==> Acanthomorphata.txt <==
>MSA Consensus of 880 seqs, protein
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==> Aconoidasida.txt <==
>MSA Consensus of 1031 seqs, protein
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==> Actinobacteria.txt <==
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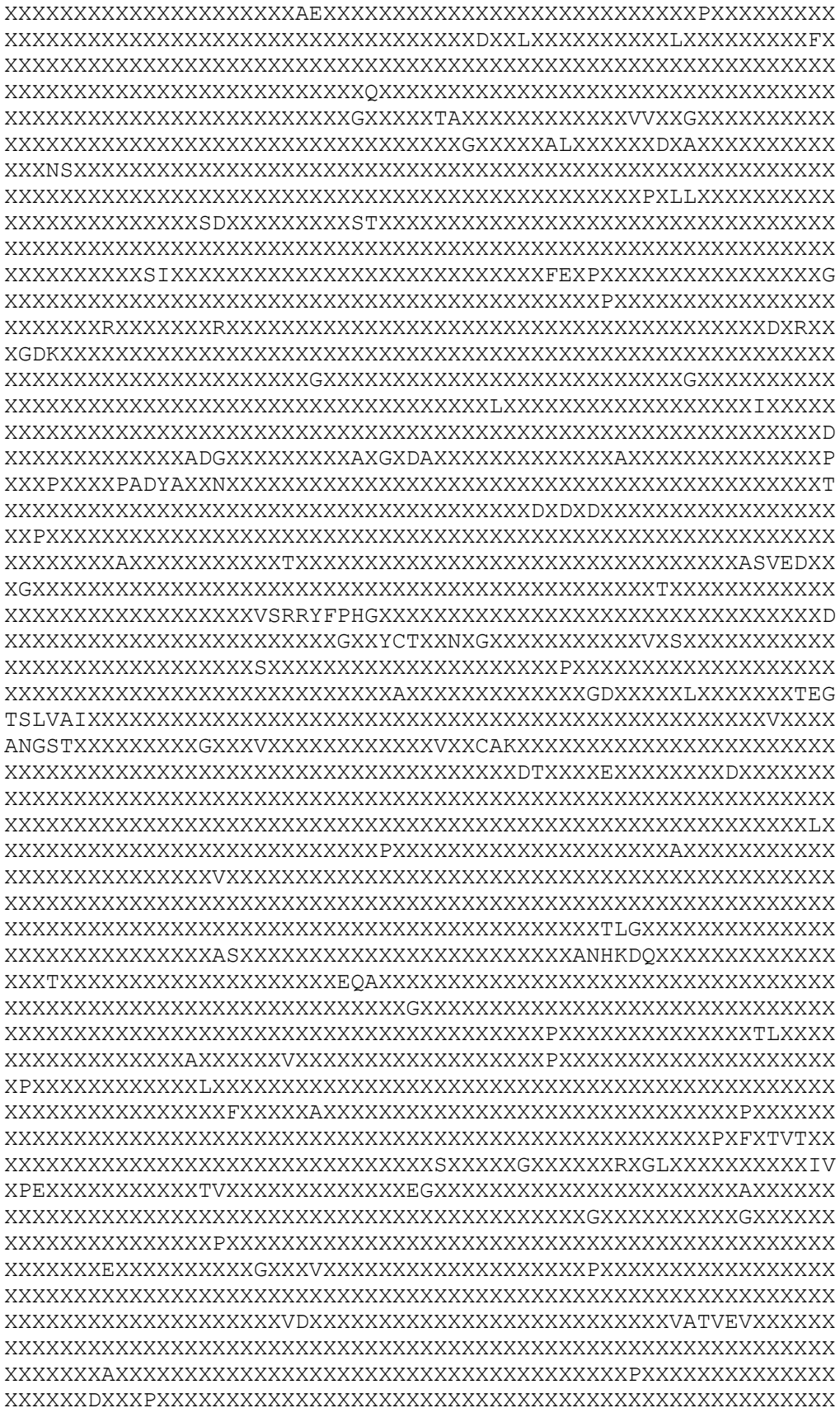

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==> Actinomycetaceae.txt <==
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==> Actinomycetales.txt <==
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VCEHCDKAFARRPSLRIHRLLHCSRMIYTQPPKIDIRNLECHLRIHNGEKPYPCTECDQS
FSQKPELRRHMFYHTGGGFLCSYCGKSLRDPHSLKSHERLHTGERPHHCPVCEKGYTLAT
KLRRHIKSSHLMEKPYSCHCGASYTVRQSLLRHQAQHRTEGGAQEEVKAAESDGECGEEA
NDSKKEDVQELGSSHSKPVRGRPKKKSLREEGEKKAGRVKQKKGRGKGEEKEARQVERKG
EETSGAGRVGDGEDSGDIQHTVVYVHTDDLSVESSLPAGMGQELVEVVISEGEEQCIVVH
GQQTVGELLILQEEGSGLCSVAQTVEIDTV

==> Alphaproteobacteria.txt <==
>MSA Consensus of 559 seqs, protein

```
MXXXXXXXXXAXXXXXXXXXTATGLSVVXAXPXXAXPXXXXXXXXXXXXXXXXXSLGXXAX
XXNEFXXXXQXGXXXXXXXXXXXXXXXXXXXXXGXXXXXXXXXPGXXXXXXXXXXXXXXX
DXXXXXXXXXXXXXXXXXXXXXREGXSQXXVVVPKXXXXAXXXSXXXXXXXXXXXNAXXX
XXXXXAXXXXAQQVAEEXKRVSEXXXXXWXXXXXXXXALTTSHEXXXXXXXXTTASLA
KDTADTAKGLAEEAKNASDAAKXXXXXGXXXEQXXXXXXXGXXXXXXXXSXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXEXGXXAXXXXXXXXXXXXXXXXXGXXXXXXXXGXXXX
XXLXXXXXXXXXXXXXXXXXXXXXXXXXXXVXXXXXXXXXXXXXXAXXXXXXXXXXXG
XXXXXXXXXXXXXKXXXXXXXXXDXXXXLXXXXXXXXXXXXXXXXGXXXXXXXXXXXXXX
LXRXXXXXXXXXXXXXXXXXXXXXXXXXXAXXXXXXXXXXXXXXXXXTXEXXLXXXXXXKS
XXDXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPGXXXXXXXXSXXXXXXXXXXXX
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XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXDRXXXXXXXXXXXXXXXXXXXGGXX
XXXXERXIRXIXDXXPXGXXXXGXXKAVLSKIXXXXXXXXXXXXXXXXXXXXXXXEEAX
XVXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXAXXEXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXRXXXFXXXXXXXXN
XXXXXXXXGXXXXXXXXXXXXXXXRXXXXXXDXGXXXXFXXXXXXXXXXLXXXXXXXXGX
XXXXXXXXXXXXXLPXXXXXXXXXXXXXXXDTNXXXXXXXXXXTAXXXXXXAXXXXXXXXX
XXXXXXXXXXXXXXXXXRXXXXXIXXXXXXXXXXXXXXAXXXXXXXXXXXXXXXXXXXXVNX
LXXXXXXQXXXXXXXAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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TXXVXXSXXXXXXXXSXQXXXGXXXXXXXGXXXGXXYXXXGXXXXAXXXXXXXXXXGXGR
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XXXLXXXXXXXYXXXXXXXXXXXGXVXXXXEXXLXXXXXXXXXXXXXXSXXXXNXXXXXX
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QXXXXXXXXXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXXAXXXAXXXYXXGXXXXXXXX
AXXKAGXXXVENXXXXXXXXXSXXXXXXXYANXXLXXXXXXGPXXXXXXXXXXXRXIXXX
XXXGSXXXXAXXXXXXXNXXXXXXXXEXNYNIRSXGXDXXXGXXEEAXXXXXXXXXXMLYI
XXXXXXXXXMXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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GVFXXXXXXXXXXXXXXXXXXDXRGLXXXDXXXXXLLSPXXXXXXANGXXXXXXXXXXX
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GSXXXXXXXGXXXXXXXXXXXXXYDXXYVDGRLAIXXXXXXACSXXXGXXXXCXXXXRYP
XXXXXLNDQAPIEVVXP


==> Alteromonadales.txt <==
>MSA Consensus of 166 seqs, protein
MMXXXXXXXXXXXXXXXXXXXXXXLXXXXXXXXXXXXVXXXKXXXXXXXXXXXXXXXVNXX
XXXXXXXXVXXXXXXXXXVXXXXXXXXXXXXXXXXXXXXXAXXXXFXXXXXLXGXPXXXXX
XXXXANNXIADLWTXXXFXXXXXFXXLEDPXTXLNLXXGXXXXXXAXXTXXXXXXFFGDX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXWXXXXXXXXXXXXXXXXLSXXXXXXXXXXX
XLGASFXXAVTVAQLQRXXXXXXXXXXXXXXXGSXXXXXXXXXXXXXXXXXXXTVXXGV
GXXDSIXLRLMQXTGPXXXXXXNXXXVYXXXXXAYXXXXXIXSDXXXXGXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXNXXXXXXXXX
XXXXXXFYXXXXXXXXEXIGHMLVTDNXXXXXXXXVPXXXXXGLXXXXXXXXWXTDAXXX
XXXXXSXXXXXXXRXXXXXXXXXXXXGXXXXGIXNXXXXXHEDQSGIXXXXPXXXXXXXX
LXXXXXXXXAXEXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXLXNXXXXX
```

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XRXXXXXFXERXXLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXYXXXXXXXXXXXXXXXX
XXXXXXXXXXAXXXEXXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
WXXXXXXXXGXXXXXXXXAITQXXGXXXLTXXXXXXXXXXXXXXXXXXXVDXVXXXXXXG
DXXFXXXXXSXXAXXXXWXRSATGQXSDAXXXXXXXXXXXXXXXXXXXXLNXXXXXXXXL
ASPKGEXXXXXISVAAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
LXXXXXXXAXXXXXYXGXXXXXXXXWXXXXXXXXXXXXXXXXXXGXXXXXXXXXXXXXXX
XXXXXXAXXXXXXXXXXXXXXXXXXXXXXXRXXXXXXXXXXXXXXXXXXXXXXXLXXXXXX
XXXXXXXXXXXXXXXXXGXXXXXXEXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXD
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XXXXXXDXDXXXXXXXXDXXXXXXXXSETXXDXXXXXXXXXXXXXXXXXKIAXXNXSXXXX
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XDGIGXNXXXXXDGXXXXXXXDXYXNNXXXXXXXXXXXGQLXXXXXXXXXXXXXXXGXXXX
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PXXXXXIXXXXXXXXXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXDNWXVXXXXXXXXXX
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XDXDGXXXXXXXDXXXXGDGXXXXXXXXPXDXXEXXDXDXDXXGXXXDXDXDXXIGXXXX
XDWADVHXXVXGXXXXXXXXXXXXXXGXDXCPXXXXXXXXXCXGXVDXDGGXQTYVTHNG
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XLXSXXXLXVXXXXXXXYXXSLIAXXXXVEXXDXDGDXXXXXXXXXAXXXXXXXXXXXNN
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AVXRDLDXXXXXXXXXXXXXXXXXDXXXXTXXXXXXNEVGCEVEPEIDSEYXXXXXLXVG
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XYXVXXXXSXXXXXYXXXXLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGXXRLXXXXDNL
XQXQXIXXXXXXXXGXXXXXXXXXXXXXXXXXXXXGXFXXXLXLXENGXLXLXXXXGXXX
VXXXXXXXXXXXXXXXXXVXXXXXXADGQLDSXXXXXGXXXXXXXXXXXXXFXXXXXXXQX
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ISQLQANGVNVIQ

==> Alveolata.txt <==
>MSA Consensus of 1393 seqs, protein
MAAPEKSETSSADMSLVWGXDXXXSXXXXXXXXXXSAXWXXXGVXXXXXXXGGRGASGSP
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RLXXXXAXXXXXXXPXXXTXXXXXGXXXXXXXGGXXXEGXXXYGSYGAELXXSXXXXWXX
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AALEVXXXXXXXXXXXXXXGXXXXXXPAXXXXXXXXXXXXXXXXXXXXXXGXXXXXXXXX

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SIXQXXDAWDLRLQAVXXXXXXXXXXXXXXXXXXXXXXLXXXXHXXXXXXXXXXXXXEXX
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XXLXXNKYXXXXXXXLXXVKSIXYXXXXXXSXXXXFXXXXXXXXXXXXXXXXXXXXXXXX
WXXXXXFDXXXGXXSXXXRXRKEPLELXXFELXNXLXXXXXXXXXXXXXXIXXXXXXXXX
XXXXXXXXXXXCXXGXXXXTCFXLYXDXXXXXXAXXDXXXXXNXXXIXDXIEEILKQSGS
XXXXXXPXXXXXVKNPKTWWDQXHXILWXDXXXXXXXXXXXTQXXXXKXIXQXXXXYXLX
XXXXGXXEELESELXHXXXXKYXXXXLXPXXXIXXXXXXXAXLXXPXCXXXXXXGXEDES
DPXVVXVDXGXGXIXXFXXXLXEVXKSNXSERAXXSGXRXXXXXLNXXXXDXXXXXXXX
XNIINPXLXEXGTLXXXQKXXXXXXXQXFXXXXXXXXXVXXCXXXXNFLENXEXEIAIXX
XXXXXXXXXXPXXXXXFSKXXXXXXXXXYIXXXXXYXXEXDAVHNTSXXXLXYXXXXXGX
XXXXXXXXXRSSESFCXXXXXXXXXXXXXIYXXXXXXXXXGLETXXYXTXXDXXXXXIXY
YKYXXNEXXYNITQYXSYXIXSXXXXSXXXXXXXXXXXXXDXXFINXXIXXXXXXIYXXG
ETFKAEXQXXXXXAITSFXXEASDLDFXLXXXXXXXXYXXXXXWXXXXLRIEAIXXXXXX
XXXXXXXXXXXKYFSIXYXXDXXKXNXSNVLXXXEXXXNXDXXXXXXXXXXXXXXXXXXX
XXIXXXTGVXXIXLXXDGNXNXNXXXXXXXXVXXXGXXXXXXXXXXFXXXCXXGHYXXXX
NXXXXXXXESXKCXXCXXGXYNXLXXIKXXXXXXXXXYXXDSKCXXVQANNSEGRRCXXN
XTTXXXXXXXXEXXCLCXXGYEYXXXPXNXXXXAXCXPCXXGEYKDXXSNENERKKIXL

CXXGXXCXXNXSXXXXXXKXXXXSXCXCNXGYYLXXDXXXXXXCXKCXXXHYCPXXXXXX
XXXCDIRSWPXHNXTXXXXRXXGXXXTXFXTIXSCLCXXGYEPINMXKXXXXXWDKFYSG
QKGVSRXXHYYNXFXXXGVSMPLIRSSRFGAKEYXXLNXXXXXXXXXXXXICMECXXGXYK
XXXSSXXCXKCPXXSXXXXXGSXXIXXCNSCXXGYYKXENSCCGLPQDFRTXXXXEGCGS
LIYDXVCSXCLXNHFCVGXXXXXDKCFLRFQXXXXXYXGDAXYVDVDXICPNXSVTXXPX
EXNDXXSFKXCLCXXGYXXXXQXXYNXXXQAPRDYYKDFVGNRDXXXXPNXSXXLXXXAX
XXDSCVCERENXXXVXKXXEXNXXXXXXLGXXXXYVXXXXXXNXHCKXAPLNFYKXXDTX
SNDXXXPCPXNSITLXXGAXSIXXCICXKGFFYXXXXXXKCXXCPXGYYCXEKXXXMXXK
XXXPIKCPXNXXXTXXXGSYXXXXCXCXXGYTXXXXIVXHDXXXSLVLKKEEISEKRXXX
NXXIXXXXSXRRXXXXXXSEQXRSISRXPSFVXFGKVLXRRNLKKSXFITGSNRHXXXNX
XATXXXXXXLQXXXXXXXCXXCPXSXYKSXIXNEXCHXCXXNSXTLXXXEVLLEENNSDX
XFCLCXSTSSGTHCQXGYYXXISXXXCKPCXFXXLYCXGEXIXXXXXXXYXXXIXXIXXX
IXXXXXXSXDPXXXFXNXXIXXYXXXWGXGAHRGXXXXXXXXXXXXXSXXXXGNXXXXXX
XXXXDXXXXXXXIXXRXGXXXXKXRXXXXXRXXXPISSYFXKPLPXMXXXXXXXIXDXST
SLFLXRXXLXXXXNKIIAXXNXKLTXXXXXNXNXDXXXXXLXXXFYXXXXNXXYXKXQXL
XXCXXNTXIPLXXXXXMXGVDSXXNXDDCKCXKGYYLEXXXXXKXXKXCXPCXEGTFKNX
XGDXXXCXXCPPKSTSXXGSXYPXHCNDFCKXGFFYSKXXXCLXCLEGAXCXGGLYXNAM
XXIXGTDNDXXXXNEIXXXXXVXXXNSPASTGMTNIXLXXENVXXIXXXDHVKPESXXGY
YLDXXXXXEGHRLIDYXIDVSEWXFIKCPIXXADEKCLXXNXCHXXMXNYLCXECXKGYT
NXFXXGSXCXXCPNNXXNXXXXXXIYIXFCFIIIXISYLNXSPHGGGSSISSGFYRRSIH
SIXIKIAVNYXSSMLXXNILXDXXLXLPXXXXXXYXXXTXXXXXXXQXXXIISIDCLLRX
YFXLXNXXXXXXXXXXXXXXXPXXPLXXXXXXXXXLXXXRKHXXXSXXXXYXDSFFPFYS
XTXLXXSXSDXSXXXFFXXXPXXLMXTLTXXLFVILKIXXXXXKXXIXXXXXXKXXCNXX
XXGXQENGKKEXCKXXXEXXXXXLXXNKLXLLXXAKXXXIXXXXXXQXXXSXXXXXXXX
AXXFLXXSLXXXXXNVEXYKXLXXXXXXXXXXXXXXXXLKERXIMILRYIKXXMDYPPKE
IGXXXXXXLXXXXXTWXDXXXXFFEDMIPXYXTFLFXIHXKTSXXXRMXQLFDCSYIXYT
KKGXXGSXXXXXYILXXXSSVQCXXXXXXXYLKFSPDFILGXSGTXXXSSGXXXXXXXXX
XVXWXLGIPXLXFFVLXXXYXNRHNLFXENXRIKYGFLHNGYLPNRWCXSDDXXXXXXXI
XXXIXXXNKHNXXYWEXXRVFXRKXXXXFXTTVXXFPSXXXXXXKLXXQXXXXITFVAIF
SLCXHFIFQPFDKRNFFXLXXXXXXXFXXLXXIEXXXXXXXXISXXXKXKIXXSTXNXXI
XXXEXXXIXXXIXDXXKXLXXLDEAIRRGXXLXXXXXNKLENXSLXIWXXTIXXXSXLKX
XIEXXLXXFXNXKXXXFXXILLHXXFXXKLLICLFYIFRYECIXNXRXXXXXXXVENXXX
XLPXXXXXXXXLXXXXXXXXKXQEPXXXYDKXXENRQXXXXLPDXXXXXXXXVRLFAXXXX
XIXXXVXXFXXKXXXXXXXXXXXXXXRRASDGGXXXXXXXXXXXXNXXIXGXXXXXXTXX
GXXXGXXXXYXXXXXXXXXXXXXXXXXXXXXXXXXEXXKRRPTCGAXXXXQHGSLNXQXK
KGXXNXXXXXXXXXXXXQKLXXXSXFXXXXNXIMNETKRISNTDXYTNIXXXSXXXXITE
XXEXRMFAIEIYKELLDIFXKXVTXTYIXXXXFEFIFKIXXNIGXXIDXXDXXDKIFXSX
XQKRKVKEITDNIEXXXXNIXEQWSLEXXXXXXXXXXXXXKXXXXFIXNXXXNXXXDXNEL
LGLXNXXXDXXXXXSXXFXXXXXXXXXXRXEXEXXXXXXKXAXGESSXEXSGKXXLXXEX
QKXKDEXXXXXXSXEEXQXQEEXXKLFSFXFSDDLLXXXXVKGDKILXXXXQXXIXLSXX
XFYXILXELKXKYXXXLXXYFYXFXXXXXXXXXXXXLYKLXXXXXXXXKKVLXXXXXXXV
LSXGTSLAELGMTEEAFQSKXAELXMLNKKLXKXXXXXXXNEXRXXXXXXNPDXXXXXXP
XXNXKKXXXEQXQXXDXXXXXXXIKXKTAXXIXXXXXXLXIHXLYKEXXXIXXNXDXXXX
XSXXXXXXKXLXKXLXKXXNQXKXXYXNXKEDDSNQSXSNXRSQXENEXXXXXXXXIXXX
XXSRNDSEXFXXXXXXXIDXXSDAPXPEGTFRLIGQXXXXSXEXGXXDXDGXXXXSSGXX
XXMDXXLIXDSIDTDENADHRHXXNXXXXXXXXXXLSMXXDQKXIXEXXXXXESXXRNES
KEYESQTEQTHEEGIXXXNXYSISEVDGIKLXXXXXXXXTXXLVDIXPXXXXXXYTNKLS
DNGEXXXXXXXNXXXXXXXSXXXXXXDXTXXXXXXXXXXXNXXXXSXXXXXXXXXYTAGX
VXXCVLXFXSIXXXXXXXXXXDXXXXXXCXEXXXXXXXXXXXXXKXEIIEIXFXXNXXXXF

==> Arachnida.txt <==
>MSA Consensus of 118 seqs, protein
MDXXXFVPSVNQSIETSVEEIRVQVAEPLKDCFXXXXXXSEMSTCQLXXXXXXXXXXXXX

XXXREXXXXXXCXXGXXXXXXXXXXXXXCXXXXXXXXXHXXXGXXXXXXXXXXXRXXXXX
XXXXNLXXLLXXKXXXXXXXXKDARXXXXXXXXXXAXXXXXXXXXXXXXXNXXLCXXICXX
XCXXXXCXXXXCXXXXNXXXXCXCXXXXXXXXXXXXCXXCXCGXXXXCXXXXXXXXXXXK
XXXXXXGXXXXXXXXXXXCXXNPCXNXGTCXXXXXXXXXXXCXCXXXXXGXXXXEXXXXX
XCEXXXXXXCXXNPCKNXXXCSSXGXXXXCXCXXXFXXXXXXXXXXXXXXXXCXXXXXXX
XXXXXXXXXXXXCXXXXXMYXXXXXXXXXXXXXXCXXNPCXNXNGXCXXXXXXXXXXXXC
XCXXXXXGXXCXXXXXPCXXNXXCXCXXXXCVXLEXXNTXXCICPLXXXXYXXXCKIPDH
CISXXCXXXXGICSSEGEKYSCTCLQNFRGINCEEEIQDRCNPNPCKNNGXCXXXXGXXX
XXXCXCXXXXXGXXCXXXIQDXCXXXPCXNXGXCXXXXDVNHFNQNGPLDIFIXSXXXXX
XXCXCXXXXXGGXXCEXEKVXXXXXCXXXPCXXNXGXCXXXXXXXXXCXCXXXXXXXXXX
XEXXXCXQDRCXXXXCXNXGXCXKDGSTXXXXXWESLKNWEKXXXXCXCXXXXXGXXCEX
XXCXXXCXXXXXXXXXXXXGCXXXXXXCXXNPCXNXGXCXXXXXGXXXTCSFXXXXXXXC
XCXXXXXGXXCEXXXXDXXXXXPCXXXNXGXCXXXXXXXXXXCXCXXXXXXXXXXXXXCX
EXXXCXYXCXXXPCRXXXGXCXXXGXGXXXXXXCXCXXXXRGXXXXXXCKXXXCXXXXFP
XXXCXXXXXXXXXXXPMEXCXCXXXXXXXXXXCXXXXXDRXXXNPXKNNGKCSSDGDKYS
CTCVQRFRGTXXXXXXXXPCXXNPCXNXXXXXXXGXCXXGXXXXXXCXCXXXXXGXXCEX
XXXXXXXXXXNXXXCXXXECSPHEXXSFRCECNATYTGKTDGILCNKDLMQXEGGDTXDT
XXINAQCVEAPDFNEGYACNCEIVYASGGAGFFLLVCQIKKNEENCLKMNVLGILDDKXX
XXXXXXXXXXXXTNKKKCXXXXHSXXGXXXXXRXXXSWXXXEXXXIQNXDXSSTXSDXXS
GXXXXXXXXXXXXXXXXXLXXGXXXXXXXXXXXXXXRXDXXXXXXXXXXXXACECLXXXX
KXXXXXXLLDSIADXXXCXXGXXSXXCXXXXXXXXXCXXXXXXCXXGXXXXXGXCXECPK
GIRCXXNXXCGXXXXXXXXIXXXXXXXCXXXXXXXXXXXCXCXXGYXXXXVXXXXXXXXX
XXGXCXXXXXXXXCXXXXCXXXXXCXXXXXXXXXXPXXXXXXCXCXXXXXXXXCXXXXXX
XXXXXXXXXXPXXXXXXXXXXXXXXXXNPTPXXXXXXXXXXXXXXXXKXXXXXSXXXXSXQ
YDWNLNXXXXXXXKXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGXXXXXXXXXXXXXXXXXXX
XXXPXXXXXXXXXXPXVXXXXXXXPPXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXVDXX
LXXXXXXPXXXXXXXXXXXXXXXXXXXXXXYXXXXXXXXXXXXXXYXXXXXXXXXXXVRXX
XXXXXXXXXXXXXXXXXXPXXXXXXXXXGXXYXXXXXXXXXXXXXPXQXQXYXXXXXXXXX
XXXXXXXXXXXXXXXXQXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXHX
XXXXXXVXPXXXXSXXXXXXXXXXXXXXXXXYXXXXXXXXXXXXXYHAAPXXXXXXXXXX
XXYXXXXXXXHXXXXXXXXXXXXXXXYXXXXXDXKXXVSXXXXPXXXXXXXXXXXXXVP
SXXXXXXXXXXXXXXXXXXXXXSAPXXXXXXXVVSXXXXXXXXVYYXXXXXXXPXTSXX
XXXXXXXXXXXEXXXXXXXXXAXXXXXXXXXXAXPXXXXXXXXXXXXXXXXXXXXXXXX
XXXXSVKXXXXXXXXXVXXXXXSSXXXXXXPXXXXXXXXPXXXXXXXXPXXXXXXXXY
XXXXXXXXXXXPXXXXXXXXXXXXXSXPXYXXPXXXXPXXXXXXXXXXPXXXXXXXXXX
XXXXXXXXXXYXXXXXVXXXXXYXXXPXXXXXXXXXXXXXXXXXXXXXXXPXXXXXS
XXXXXXXYXXXXXXXXXXXXXXXXXXXXXXXSXXXPXXSXSXLSTPXXXXXAXXXPXXX
XXSXXXXXYXXXXXXXXXXXXPXVXXYXXXXXPXXTXXXXXXXXPXYXXYPXXXSXXXXX
XXXXXXXXXXXXXXXXXXXPAXXXXXXXXXXPXYXXXXXXKXPKPDXXPXXXXYXXPXYX
XXXXXXXXXXXPXXXXXXPXXXXXPXXXXXXXVXTXXXYXXXXXXXXXXTXXXXXXPXXX
XXXXXXXXXXXPXXXYXXXXXXXXXXXXXXXXPXYXXXXXXXXXXXXXXXXXXXXPXXXX
XPXXYXXXXXXXXXXXXXXXXXXXXYXXXXXAXXXXXTAXXXXPAXXXXXXXXXXQXXX
PXXXPXXXXSSXXXXYPXXXXXXYXXXTPXXXXXXXXFXXXPXXXXPXXXXXPXXXXXXP
XXXXXYXXXPXXXXXXXXXXXXPXVXXXXXAXXXXXXXXXXXXXXXXXXXXPXXXXXXXX
PXYXFGXXXXXPXXXXAXXXXPXXXXPXXSXXXXSXPXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXPXXXXXXXXXXKXXXXXXXXPXXXXXXXXXXXXXXXXXXXXXXYXXXXXXXXX
XXXPXYXFGIKYKXXXXXXXPAPGAYDVEKXXXXXXXXXPXXXXXXXXXXXXXXXXXFXX
XXXXXXGXXXXXXXXPXXXXYXXXXXXXYXXXXTXXXXXYXXXXAXXXVXXXXXXXXXXX
XXXXXXIXXXXXXXXXXXXXXXAXXXXXXXXXXXXXXXXXXXAVXXXXXXXPXXXXXXXX
XPXXLXXXXXXXXXXXYXPPXXXXXXXAYXXXXXXXXXXXXXXXXXXXXXXXXXPXXKXX
XXYXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXAXXXXPXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXVHXXXXXXXXXXX
XXXXGXXXSXGYXXGXXXYGXXXGXXXXXXXAXXXXXXXXXXXXPGSYXXXXXXXXXXXXX

XXXXXAPKKNLTKVIPPKTDXXXGXXXXXAEXXXXXXXXXXSYXXXXXXXXXXXPGXADX
XXXXXXXVXKXXPXFXFXXXXXXXPYXHXYALLSXXXXXYXXXXXYDSDKKMXXXXXXXX
FXXSXXXKXXXSFXXXKXXXEIIQQXGXXVXXXXXNXXXXXXXXXYXXXKXXEEXXAQXX
XPEXXKVXXSSRQKKKILRNPPYYSDDHQGXXKGRDDDXSXXNKXXXXKXXXKITYA

==> Archaea.txt <==
>MSA Consensus of 161 seqs, protein
MGPIVTADPARAAQQSTETTTAIQEDSLTSRQQAYQAXXXXXXXXKKGPELRTTLNETLG
VYTDENRVSTAVFATDRKVAAQTQSHATPVSTNLLASDAKLARTAVTDXRRXFXXXXXXD
XEFXXXXXQXXLXXAESSLEKGDELRRKGSMGAFSHYERAWTAAQRALDRMDAATKPTVT
ITHRTDLPHNGSVTYTVKGTVSDVRMHDLENTTLTVNGERREVSFYKNTTPGGTSHFYTN
VTLTDRINNITVRTTDPGTTYAANELETTGANNRGQSKKGGKKNKNKGKDTDKKRGSDGK
QTDVAVERQTGRDTLLLDADGLPDYYERETTETNPLNPDSDSANTSANESANGLIDGAED
FDDDRVTNFLEFRNQLNPFDEDTDGDRLTDWFELTYTQLNPRVVDSDADGTTDDLEDFDD
EGFENIREQQWETDPHDPDTDADNLTXKXEXXXXGXAPTXPDSDSNHTAANESNDGLLXG
XXXFXXXXXXTXXXFXXXTDXXXEXTXXXXXXDAFEXXXEXXXPXXXDTDDDGXXXXXXX
XXXXTLXXVGKGXLXXXFMXXXXXXXXXXXXXXXXXKXXXXXXXXXLXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXSXXXXXXGXXXXXXXXXXXXXXXXXXXDXXXXXXXXXLXXXXX
XXXPXXXXXDXPXXXLXXXXXXXXXXXXPXXXXTXQDGIRDDRTXXXXXXXXXXLXXXXGX
XXXXXDXXXXXXXXXXEXXXXXXXXXXPXSXXXXXXXDXXGXDXXXXREDXDXDXLXXXX
EXXXXXXXXXPXTXXDXXXXXXEXXXXPXDPXXXDXDGXXXXXXXXDXDXDGVXXXXDXC
PXXNPLXEDYXPQYGXXIDGCPXXFVPWYDXDXDGIXDHXDXCPTXXEXYNXXSXSXNPX
XXNXXXXXXXGXGXGXXXXXXGXXXXXGXFQDXDGCPDXXPXXGXXXXXXXXDXXGXGXG
XXXXXXXXXGTGTXDGDGXXDXXDXGCPXXXXXQPETFNGXXDXDGCNPXPDXXXXXXDX
DXDGXXDXXDXCPLXXETYNXXXDXDGCPDXXXXXXXGTAFXDTDNDGIXDXXDLACXXE
PDGREVXDNXYRDTDGCPDVXXXXXFXDXDGDGIXDXXDXCXXXPEXXNXXXDXDGCPDX
XXXXXXXXXDXDXDXIXDXXDXCPXXXEXXNXFQDXDGCPDXXXXXXXXDXDXDGIXXXX
DXCPXXXETYNXFXDXDGXXDXXXXTVXXXXXXXDXDGDGIXDXXDXCPXXPETXNGXXD
XDGCPDXXXLRLGTDXXXXDXDXDGIXXXXDXCPTSXXXXETYNXXXDXDGCPDXXXXXX
XXYXXXDXDGDGIXDXXDXCXXXPEXXNGXXDXDGCPDXXXXXDADRDGVADASDACPGE
PETWNRFQDDDGCPXXXXXDXDYDXIPDXXDXCPTXXEXYNXFQDEDGCPDXXXXXXXXD
XDXDGIXDXXDXCPXXXETYNXXXDXDGCPDXYEYEXXXXXKXXXDTDGDXXGDXCXXXX
XXXXXXXSGVTXDXDGDGIXDXXDXCPXQPETXNGFQDXDGCPDXXXXXXGNATKNXSXL
DSDXDGIXDXXDXCPXXPETYNXXQDXDGCXXPDXXXXXXXXXXXXXXXXXXXXXXYXTX
FNXXXXXXXXXVXXXXXRXXXXSSXXCXXXCXXXXXXXXVGXXXXXXXXXXXLIXXXXXX
XXXRNKTRRTRTKXXXXXXXMXXXXXXXXYXFXDXDGDGIXDXXDXCXXXXEXXNRXXDX
DGCPDXPXXXXXXXXXXXDXDXDGIXDXXXDXXXXDXCPXXXERYNXXXDGXXDXDGCPD
XPXXXXXXDXDXDGIXDXXDXCPXXXEXYNXFQDXDGCPDXVXXXXXXPDXDXDGIXDXX
XXYXXXXXXXXXXXXNQPETXNGILDXDGCPDXXIXXXDXDXDGXXXXIDXXXXXXXXXX
XQDDDGCPXXXXXXXXXXXDXDXDGXXDXXDXCPXXXEXYNGFXDXDGCPDXXXXQXDXD
XDXXXDXXDXXXXXXEXXXXXXXXXXXGVPPASLLNXYFXXXXDKGETLSSINNPVCQSNP
TDPACQSXDXDGCPDXXXXXXTXPXXXDXDXDGXXDXXDXCPXXXXXXXKXXDXDGXPDX
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XXXXXGCPXXXXGXXXXXXXXXCYSXFFGXXXXXXXNNXDALELXXXLSKXXXXDDCHFX
SXXXXXXXXXXXXXXXNXXXXXDXXXXXXSXDHEXGHXXXXXXXXXXXXXXXXRSLDGLXXX
XXCXXXXGXXXXXXXXXXFHXXXXXXXXXXXXYXXRVITEQICXXXIXXXXXXXXXXXXX
XXXXXXXXXGXXXXGXSXYHIILDEPXDCXHGXGHGXXHYFXXDLXXXXXXCXXXSXXQX
XXXGXCDXXXXXXXXXXXXGXXXXYTDNXLGXXXGXXXXXXXXXXXXXCXXXXLXXXXXXX
CXXXXGXXLXFXXNHDXXXEGXXXCXXIXXXXXXAVXXXXXXCXDPXGLXXEIXXXXXXL
XXXXXXXXXDTDGXXXXXXXXXXPDCXTXXXXXKXQPXXXXXXXXXXXXXXXXXXSXKXX
XDXXXXXXXXXFXXXXXXXXXXXXXXXYXRXXXXDTPEPPSIFXXXXXXXXEXXXXXXV
XXXXXXXXXXFXXDXPXYXXXYXXXEXXXXXKXXVXXXGXXXXXLXXXXXNXPTXXSXXX
XXXXIXMIXFVPXXSGXVNMSDRSRRXFXXXXXXXXXXSXXXLXXXXXXXXXXXXXXLPX

GXXXXXXXXXXIXXGXXLXXXXVXXSXXXXXGXPXXXDFXXXTVTXMXXRXXXXXXXXXX
XXXXXXVYXXKXPLXXPXAQXXXXXXPXXXDXXIXXNDXXXXXALPGXXXXXXXXXXIDX
XXAXPYXXXLXXPILXXXXXXLXITVTTPQXXTXAXLXYSYXVQXXXXXVXVDGXXQVYT
YIIGEXXXAXSXXVXXXLXXXXGXXVXRIGGXXRXETAXKLXXXXXXXXXXXXXXXXLXV
XXAXXXDXXXXXXAXXXXXXGFFXXGXYXXPXLXXXXXXXXXXXXXXXXXXXXXLXXXXV
XLXGXXXXIXXXGSPVVASGXXKXXXXXXXFGHVQRIPXXXXXXXPXXXXGYXTYWXXEX
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XXXXXXXEXXXEXXRXVXXXXIXXXXXXXXXIXXXXXXXXXXXXXXXXXXXXXXXEGATV
SXXXXXXXXPXXAIXXXGGXXKQEELPELTGYSRPTISRIIQXLEKLKXXFXIXXXXXXX
XKXLVXREKXGKTFXVXLXKXIXXXXYXXAYXLXXXAXXXXXXXXXXXYXXXXXXYXXXX
XXXXXGWSAXXXALYPXQLEXMXXVLXXXXXXVXXXXXLXXXXXXXXXXGXXXXXXXXI
XXIKXXXXXXXXNEXIXXTXXXYXXXXXXXXXXIXPXXXXXSXXXXXXXPXXXXGXXXXXX
XXXXXXXXGXXYXXXXXFALXXXXEXXXXXXXXXXXPKXEXKXTTSGKXVSLQXVNTTXX
XNTSIEINDXXXNXFXXXTXVGXKSIXXXIPTTNTSDTSXXXXXXXXLEXXXXVLXRAXK
XKNTSXXXEXXIXPXXXASKDVXXVSVXXKNXXIXEXXXXXTXXXXXSFNXXXNXXYVVX
AIPXGNNSVXKXXXXGXGXXXXYXGXGXQXNYXXYDAXNGXXXLFXKDDPLXXITLXXXX
VNQPPVIXYTXXXXGLNVLINASESYDPEGKXLTFKWXXPGXXXXXXXXXXXXXNXXYPX
XGTYDITLXVSDGVYEVSSVIXXXXXQXXXXXPAXXXXAXGKXXXFXGQXXXTLXIXXXX
XIXXPXXXAXVNVVDKXDXXKXXXIXFKDNXSVXXIIXAMNXFXXXXXXXXGXNXXXXNP
ENWXXXXXXXXXXXXXXXXXXXXXXXXXXNNXDXXXXXXXLNXXXVXXYXTXLXXXHEXA
PYDRKXXXXWXXXXXXXXXXXXXXITXXXNXXXXXRVQAXLHAMLQEPXGXQTXXXXXXX
XXAXXGXXXXXXXXXXXXXXXXXXXXXYDFNXXIXXXXXPXNXXRYXXXXIXXXXXXXX
XXXXGTXPNXXLFXVSXVGXXGXXXDXXXNXXXXXLXAXKXXXXXXXXFXXXXXXXXYSX
XXXXNXXXLXXXXXXXXXXYXIGIAYDTXXKKIVAXXQXSID

==> Archelosauria.txt <==
>MSA Consensus of 981 seqs, protein
MLAFRVVRGASEEPFILAGGNVQSIVQKEVYIIQVSVGSHQWTVKHRYSDFHDLHEKLVS
EKKIDKNLLPPKKIIGKNSKSLVEKREKELEVYLQMXXXXXXXXXAXXLLXXXXXFHLFX
XXGXXXXIXXXXXHRGEXXXXXXXXFSLXXXXLXXIXXXXXXXXPTCANGDAKTXXXXXX
XXXCXXXXXXVTGTEGPFGTSNIQEHLLPFDLSXFXSLHXXXXXXGANRIKGLTSSKHT
LTTMXXXXXXTXMKEILVPEXXXXXXXXXXXXXSXXXXXXXXEXGXSXXXXXXXXXXSX
XPXXXDERKXSXXADEYITNNILNFVHCSEDDLISFENVQHLYNLITFEVXXNKLASLEG
VHXXXXGXXXXXXXXKYLEDVTGQXXXXXXXXXXXXXXXXXLSSNKIDQVCLDNISTTEK
ELDTVEVLKAIQKAKEVKYKLNNSDKKVPTSLLDLSKXYXXXXXXXXXXXXEEHGALSDX
XXXXXXXXXXXXXXXXNXXXXXHLSTLIAQALXXSXXXGXXXGXXXXXXXXXXXXXXXX
LXXXXXGXRXXXXPXTSDIAPPAXXCXXXXXXXXXKVLWSFCIQVHKGGVRQFASCLVLT
DSVVAVFEIPHQDXXXXXXXXXAALKLALCFPYTDLTEFGFLMPEICLTLKVXXXGNILF
LXXXXQNAXTFXXXAXXXDXXXXSXXXXXXXHEPXLRDXXXXCXXVXXLXYXXXXLXXXX
LXXQKAXXXXXXXCXXXXLVXXXXXXXXKXXXXXXXXXXXXXXXXXXPWXXXXXXLXXXL
EDFKSNLXLXCXXXXXXHGEATLLXLXMXXLXLXXXXWXXLXXXXXXXSXXPFYIMNGXX
XXSEDARXVXXXNXQXXXASVVXXXXXXXXXXXKXXXXXGHVLELXXXXXXVTXXFXXXXX
DNXXXXXXXXXXXXXLRTLLQDXXXXXXXXXXXXXESXXXXLXHARSEXXXXXXXXXXXXX
XGXXXXLPCXXXSSLYPSEFLMQKITEDNQIPSYLPXXXXXXXXXXGRGXXXXXXFXXXI
XXXXXXXXXRXKWXKXXXXXXXXXXDXXXXXXFXXXXXXXXXXXXXXVAXXXXIXXGXXXEL
KXXXXXXXXXXXXXXXXXXGRXXXXXXNLKQXXXTXXXXXXXXXXXXXLPXXXLXXXXXX
XXXXXASLXXXXXXXLXDXNXXXGXXYXCXVXXGXEDXXXXEXXAMXXQTRQTFXXGKAKX
XXLXXXGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXRXHXXXGXX
PXXXXXXXXXRXXXXXXXXXXXAPXGXGXEGXGSQXXXXXXXXXXXXXXXXXXXXXXMAX
GSXRXMXXFXXXXXXXXAXXXXXXFXLXXXSXXXXXXXXXXNVGSXXXXTXFNVSCHRYG
XVFXFVXXXXXXXYECEVTNELEDDTXXXXLESTXXRXVEKNXRYXLXXXEAXXXCXXLX
LXXXXXLATXXXXXXXXKKXCXXKXXXXXXTXXXGXXXXCXXAXXXXGFEWTKXXXXCXX
GXXXXXXVTXGXGXXDCXYXXXIPRINXDMFLAVQGLGNFLRRATDNVKHNRALTADYTS

GKCNNKTQIWHFTRLPTSFSPYHVGLAQYLTVWTIXCXXXXXXXXXXXXXXXGXXXXCXX
XXXXXXXXDXXWGXXXMXLXXCXXXXXXXXGGXXXPCXXXGXCXXGIXXXXXCXPXXXXP
SFPMQRHTILHGDTXXXXXXXXIQDXLLYVCAQGYXXXXXXXXXXXXXVYFXXXCXXXXX
GXACXXXXXXGXXXXXXXXXHXQCETGVLHTALKLKXXGXXXTXXXXXXXXNVGSGXXXX
XXXXDXSXXRYESCXXXYXGXXCDXXXPXXXXXXXXXNXXXXXXXXXXXCDCKXGYRKXG
SXXQXQXLSFSXXXTPXXXEXXXTGXXXXXXXXPXXXSGXGXKXXPXXXXXXQTXXDXXX
XXDSRAGXTXXXXSXLSQKXXXXFPXXXXXXXXXEKETDDXXXXXXXXXPXSXXXXXXXX
XXXXXXXXXXXXXXSTKAQFSEGDNHIGVKTXYDAXDXXXXXXXXXXXXXXXXGPXXXYX
XXXXXXXXXCTCXEGXXGDXXGXXXQXCXPIXPCXXXXGXXXXPXXXXXXXGXXCSXXXX
XLPENAVTXXXEIXXXXXXRXXSPHXRHSNXXPXXSXSTXXXXXXPGXVIDLVNXXLPDV
KISXXXXXXXXXXXXXFVSXTXXXXXXXXXXXXXXPWWXSLNSXXXXXXXXXXXXXXXXX
XXPXXXXXXXXXXXXXXXXILTXXXXXXXXXXCXCKXXXXYCXXXPXXXCSXXXXXETXX
XXXCXXXXXCXXXXXGXXXPXXXCXXXXXXXXXXXXCYXXXXXQXXXXXNXEVXXWXPXX
PXXXWXXXXXXXXXXXXDXQXXQXXXXXXDXXXXSXXXXXXXXLTXDXXXXEXXXXXXX
XXXXXXXGNGSXXXXXGLTQIVAATTXXDDXXXKXXXXPLXXXXXXXXXXXXXXXXXXXW
XXXXXXXXXXXXXNDXXXKTQEXXXXTXXXXXXSLKTXXXETNXXXXXXXXSVXVXXXXX
XXXXXXPXXXXXXXXSXXXXXASXXXXXDEXXXEXXXEXXXPXXXXXXXXXXXXNXXAXL
LXNXXXAXXXXXXHXXXGXXXXXXXXXXXXXXXXXXXXXXXTXXXNPXXXXXXXPXXXXXX
XXXXXXXXXXXXQXXXXXXXXXXXXXXXXXXXGXXXXXXXXXPCEXXXXXXXXXXXXXXXX
XXLXXXXXXXXXXXXXXXWXPXLTEKEVEXXGLXXXXXXXXXXXXXXXTGXXEXPXXFXX
XEXXHSSSXXXXXXEXKPTQDPLXVXXXXXXNXXXXXXXXXNDXVXXXXLXYXXXXXXSX
TAXXXXXGXXXXDXXQXXXXXXHXXXXXXXXXXXXXNVTXXXHIXXMAXXXXSXHSSTAE
XXXXGDKXXXXXXXSXXPFEPGWXXXXXXXXNLXRTXEKDHXTXXXLMEXKKLAXQXXXX
XXXSXXXXHXXXXXGXXLXXXXGIXXXXXXXVAXPXGXIXTLXGXXIPPXIXPILPHRCX
EXSXXXXXXXXXXVLXXLXXXXEXGXXNGEXDXEXXXXXXXLXCXXCXXXXXSXXXXXCP
XXSXXXEXXXXXXXXXXXXXXXXXXXXXXXXXXXLNVXXXXXXXXXXXXXXXXXXXXGX
XXXXXXXXXXXXXXXXXXXXEPLCPGGFSXXPXXQATTTDGSXVXXIXXXXXXXXDXXXXX
XXXXXFXHTPXXXXXXXXXXXXXXCXGXLAWLSQARQQHHKHPEXXXXXXXXXXXXXXXS
XXXXXFGKGXXXXXXXXXXXGXXXXXXXXXXXXFXGXXXXXCSXPXESPDKXXXXXXSXX
XCXCXXGXCXNRXXXXXSXGXCXXXSCXXXXXGKXCXXXXXXXXXXXXXXXXHKTRSWPS
AXXAXXXLXDXXXXXXCXXXGXXXXXXXXXXXXXTXXXXXXXXXXXXXTXXXXXXXXDXX
XXXXXXXCXXXNLQHLASXXXXXXXXXXXXXXCXXGWXXDGXXXXXXXXSCXXXXXGXXX
XXXXXXXXXXXXXXXXXEAXXEXLLXSTTDYKEPLXXXXXXGNDCKCKXGXXGXXXXXXSX
DVLXPEDXTXEXWXPXXXXIXXXXXXXXXXXXXXXXXXXXXXXXXXXXYSXCXXXEXXXGX
XGXTXXXXXXXXXXXXXXXXVPXXTXAXAXXXXXXXXXXXXXXXXXXXXXXXXXLXXXXXS
XXAXFXXWXKXXXXXXEQXLKNXXFRXXXXXETILPTXGTTXXXTXXPEEXSXXDSPNXT
XXXAFKNXAXXXSXXSXXXGXNXXSESEQATTXXGXXTXXIPTXLXPSXXLXXXAIXNXX
XXEXEXXXXLHXXXXTTVTXXXGXXXXKXFWXXXXXXXXXDXXXXXXXXRETKRRLGNFY
RRFGMGXPXLXXXHXLXGXXXXXXXXXXXXXXDXLPTXXXXXXXKGGTAGVTHATNTPRDE
VLHGLNGMRKGXXXTXXXSXDXXXXEXXTXXPLXPXXXXXXXXXXXXTXXXXXIVXSEXX
XXXXXXGXXXXXXXDXXXXLXTPXXXXSTXXXXXXQGPXXGXXXXTXXPXXXTTXXXXXX
QXRXXXXPXXXIXXXXXXXXXXXXVLAXXXXXXXXXXLAVCXXXNSRRRCGQKXXXXXXXXQ
YXLXXXXXXPKKLXXXXIEXXXXYTVXXXGXXAXEXYXXXXXXXXLXXXXKTXXLNGDXX
XXQXXVXLXXKXXXXXXXLLXXXLXXGXHXXSXXXMLGXSYXXXFXXXXXQXFXXXXXXX
XXXXXXXXXXXXXTALKEAXXXVLXXQKNRCXXNXTXIXXSRCXKCXXXXEKXXLFXXCR
IXXXXPEKXXXXXGXXXXEXKTKPXXXXNXTXXXDXQXXXXXXXGXKXLXXCXLXXXXMX
XYKXTXXXXXXCXXXXLXXXXXXPXXSXXXXXXKXXIXXXXXXXXXXXXXXXXXXXXXXX
QSXXXXXXXXXXXXXXSCQASLWMGRVKQLXLXXXCCXGXXGXXXXCXXCPGKXXXXXXX
XXXXXXXXXXXXXXXXENNPXXXGXXCXRXGNGXCXDGIXGXGXCXCXEGFXGTAGXXCE
XCXXGXXXXYGXXCXXXEXXXQDTQEXSXXXXXQXXXXXXXXXXXXXXXGQWLAPISPT
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VSVGGQTEEXPHFSSSNQDMTDSVMLLILLPPXXXXXXXXXXXXXXXXXXXXXXXSXX
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XCVGPSGAAGAXCXXGYXGDGXXCXEIXXCLEXNGGCXXNAECXXTGPXXFQTKHLFSPQ
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FXTXXXXXNXXXXDMKXGVXXXXXXXXXXXXXDXXXXXXXXXXXXXXXXXLFXXPXXXXXXX
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XPGRHKCCYGXXCRXKGXXSCVXWXXXXGFVQRWLWHXXXXXXXXXXXXPXXXEXKXXXX
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XXFXXXLTXGTXXXXXXGXXLXXXXXXXXXXXXXXXPAXXXXXXXXXXXXXXXIVEWXXX
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HQHHXXXXXXXXXXXXKHXXXXXXXWXXXXXYF

==> Archosauria.txt <==
>MSA Consensus of 910 seqs, protein
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KLLVTPSSGGKTNQLILQNTATKAIIQGLIPDQNYALQIIAFSDDKESKPAQGQFRIKDI
ERRKETSKSKVKDPEKTNASKPTPEGNLFTCKTPAIADIVILVDGSWSIGRFNFRLVRLF
LENLVSAFNVGSEKTRVGLAQYSGDPRIEWHLNAYGTKDAVLDAVRNLPYKGGNTLTGLA
LTYILENSFKPEAGARPGVSKIGILITDGKSQDDVIPPAKNLRDAGIELFAIGVKNADIN
ELKEIASEPDSTHVYNVADFNFMNSIVEGLTRTVCSRVEEQEKEIKGTIAASLGAPTDLV
TSDITARGFRVSWTHSPGKVEKYRVVYYPTRGGQPEEVVVDGSSSTAVLKNLMSLTEYQI
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EGLAADEKEIKIGEASTELELDGLLPNTEYTVTVYAMFGEEASDPLTGQETTLPLSPPSN
LKFSDVGHNSAKLTWDPASKNVKGYRIMYVKTDGTETNEVEVGPVSTHTLKSLTALTEYT
VAIFSLYDEGQSEPLTGSFTTRKVPPPQHLEVDEASTDSFRVSWKPTSSDIAFYRLAWIP
LDGGESEEVVLSGDADSYVIEGLLPNTEYEVSLLAVFDDETESEVVAVLGATIVGTTAIP
TTVTTTTTTTATTPKPTIAVFRTGVRNLVIDDETTSSLRVVWDISDHNAQQFRVTYLTAK
GDRAEEAIMVPGRQNTLLLQPLLPDTEYKVTITPIYADGEGVSVSAPGKTLPLSAPRNLR
VSDEWYNRLRISWDAPPSPTMGYRIVYKSINVPGPALETFVGDDINTILILNLFSGTEYS
VKVFASYSTGFSDALTGVAKTLYLGVTNLDTYQVRMTSLCAQWQLHRHATAYRVVIESLV
DGKKQEVNLGGGVPRHCFFELMPGTEYKISVHAQLQEIEGPAVSIMETTLPFPTQPPTSP
STTLPPPTIPPAKEVCKAAKADLVFLVDGSWSIGDDNFNKIISFLYSTVGALDKIGPDGT
QVAIIQFSDDPRTEFKLNAYKTKETLLEAIQQIAYKGGNTKTGKAIKHAREVLFTGEAGM
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MEPGTFNVYPCYRLHKDALVSQPTKYLHPEGLPSDYTITFLFRILPDTPQEPFALWEILN
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DAXXXXXXXXXXXXXXXXXXXXXKGEPGEDXXXMKMXXXXXXXFXXAXXXXXXLXXXXXXX
XLXXXXXXXXXXXXQXXXXXXKXXCXXKLXHIXXXXXXTXCXXCXXXXXXXCPXGXXKXT
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LXXXXXXXXXSXFXXXXEXXGLXXXLXQXXXPXTVFVPSNXXXXXXXXXXLXXXXXAEXX
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==> Arthropoda.txt <==
>MSA Consensus of 758 seqs, protein
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TXXXXXXXXXXXXXXXXXXXXXXXXXGXXXXXXXAXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXPXXXXXXXXXXXXXXXXXXXGXXXXXXGXXXXXXXXXXXXXXXXXXXXXXGX
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XXXLXPXXXXXXXIXXXXXXXXXXXGXXXXXXXXXXXXXXXGXXXLXXXXXXXXXXXXXX
WXXXXXXXXXXXXXXXXXXXXXXXXXXPXXXXXXXXXPKQXXXXXXXXXXXXXXXXXPAX
XPXXVXXXCXXXXXXXXXXXXXXXXCXXXXXXXXSXXXXXXXXEGTXXXXXXXHXXXSXX

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XXLTXXHXXXXXXXXXXXXXXXLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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XXXXXXLXXXXLXXXXXXXXXXXDXTSYETXXXXTTXXXXXXFXXXXXXIXXXXXDXXXX
XIXXGXXKLXXMXXXXPXXXLXXRAPLDHXXXXYXXXXXXCXXXXXXSXXXXXXXXXXXI
DENDNAPQFXXXXLXXXYXXXXDXDXFVGXXXXXDRDIGRNAELSFTLSSQTQDFTIDTR
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XPXXXXXXXXXXXPXXXXXGXFXXXXXXPXXXXXXXXXXXXYXXXXXXQXXFDIXXXTXX
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AMSEDVXXXXXITKVXXXXXXXXXXXXXRYAIXXXXXXXXXXXXXXXGXXXXXQXXXXXX
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KNXXXXXXXXXXXLNVTXXXXXXXXXXXVXXXXXXXXXXXNXXXXXXXXXXRXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXHSXXXXXXRXXXXXXXXXXXXXXXXXXXXXX
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XHXLXXXXXXHXXXXHSLXXXXXXXXXPPSLXXXXXXXXXXXXXXXXXXRDRTKSAXXX
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PTRGAAEXXXXXXXSXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXTXXXXXXXXP
XXXAXXTXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXLX
FVVWAHHMFTXXXXXXXXXXXSXXXXIXXXXXXXXXXTDXXXXXXXXXXXXXXXYARTS
XVXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXYPXXXXXXXXXXXXXXXX
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RXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXYXXXXXXXXXXXXCXXXXXXXXXXXX
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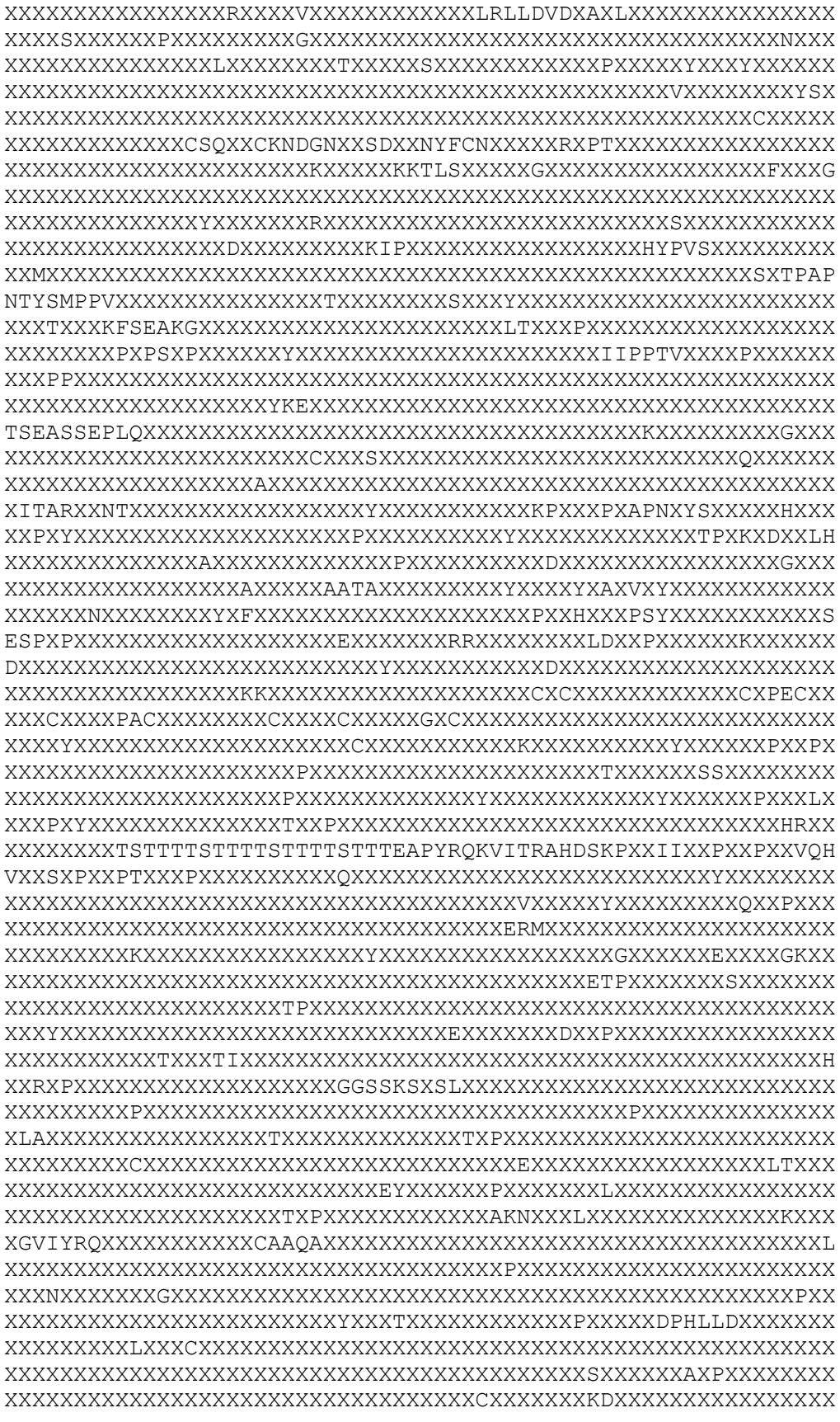
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXREXRXXXXXXXXXXXXXXXX



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XXXXXXXXXXXXXXXXPXXXXXXXXYYXXXXXXXXXXXXXXXXXXXKXXXXXXXYXXXX
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XHXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXVXXXP
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XVEXTEEXXEXXXXEXXPXXXXXXXXEXXPXTEXXXXXXXXXXXXFPDESEEPXXXXXXXP
VXXXXXXXEEPXXPXXXXXXXSTPXXXXXEYPDQXVTGEXNPHFPXHGGSYLNPDEDYDE
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==> Artiodactyla.txt <==
>MSA Consensus of 471 seqs, protein
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XXCXXXXXXXLXXXXXXXXXXXXXASIXRXXXXKGAGXQKXXXXMLQXXILXFLGLXXQNL
GDLPDXXXXXXXCSXXXXXXXXXXXXXNXXXXXXXXXXXXXXTXXQXXRCDXKXXXXXXXX
CXXASHHQSCXXXXXXXCPXGXXXXXXXXXLXXXXXXXXXXDCRYXXXXXXXXLSXXGXX
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XLXXXAAXXXXXXKXXXXXXKVVHXLEXGXXXXSXXVQXXXXXPGXVCSXXXXPAXXXX
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KWTXXXXXXXXXCXXGXXXRGXXPCXXXXXXXXGXGXCXXXXXXXVAXXXXXRXXXXXXX
RXXLXXGXXXXXXXXXXXXXXFHXXXXXXXXXXXXXXXXTYXXXXXXXXXXXXCXVXXX
XFEDXXXXVXXXXXGXXFXXXXXXGXAYXLXFXEXXXXRXXXXXXCXXXXXXXXXXXXXX
XXLEAXRAHACXXXXXXXXXXXXXXXXXSCXXXXCXXSDGRDCLCDAVATYAAACARRG
VHIGXXXDGXXXXXXXXGXXXRXRXXXXXXCXXXXXXGSAGAGGGXSCXALXCXXNXXXS
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XGVXLXXXXVXAXNGXIXXLXGXLXPPXIXPILPXXCXEXXXXXXXGXCVXCXXXXXSXC
PXNSXXXXXXXXXCVYXXXPTGXXXLKXGCAXYCNXTXXXPXCCKGFXGPDCXQCPGGFS
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AXCXXXXXXARCXCXXGXEGDGXXCXXXXPCSXXEEXRGGCSXNAECXXXXXGXHXCXCX
XGWXAAHGXGXXXXXXXXCXLXXXXXXXXXXAXCXYVGPGQXXXXCKXGFPPXXXVSXXXG
DGXXCXPXXXXXXXXXVCXXXXXXXXXXXXXXGXCHXLATCXXXXXGXXXCXXXXXXXADF
AIXPXXXXXPXAXXXXCXXXXXPXXGYXGDGXXXXXXCXXXXXXSXXXXGXXXXXWXXXX
XXXXXXXXXXXXFXCYXXXGXXXXXXXXXXXPXXXELDSAXXXXXXXXXXXPEXTXVXXX
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RLXXXXLCLVQLXXXXXXGXXXXXXXXVQGSLQLXXXXXLSSXXQIDLNITCRYXGXFPX
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PAPTNXXXXXXXPTSXXXXXXXXXLXXXXXXXRIVQRXXXXXXXXXNLAPDXXXVXXSXL
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==> Atherinomorphae.txt <==
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MEVLIRSGSAGHCWSTALLVIQEPGGSLETASRQDLLFLQVFSAGRVHLEKNLRPNMETF
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EGVKLGTQTEDESSVGQTDESSVGQTDESWRPESSESAGRRLSAMTEVQPEAPGGRQVLN
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GFXXXXXSXXSXCXYXXXXXXGXXLXXXGCXXXCXXXXXXPXCCPGXWGPXCXXCPXXSX
RXCXXXGXCXDGXXGNGTCXCXXGFXGXACXXCXNPXXXGXXCXSGTVTFFHPDPGRYRQ
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CXGXXEXXLTXXXXCXCLPGYXKXXXXCXXXXXCXQXXCXXXAXCXXXXXXXXXCXCXXG

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EVXPCVTNPCLHGGXXXXQGTGYSCYCPXGXXGEXXXXDXXDCXXXPXXSXNXGXXVXXI
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SXXSXXEQEXXNGXGXXXXWXGLXXXXXXXDFQWTDGNXLVYENWRESQPDNFFAGGEDC
VVTIAHEXGKWNDVPCNYNLPYICKKGTVLCGTPPAVENAHLXGRRRSHYXIHSVVRYQC
SEGFXQRHIPTXRCRADGSWERPRIXCTKSRXSHRYRRHHHNQHXXXRRNRRHGGEGHKX
REDXXSYYRTK

==> Autobranchia.txt <==
>MSA Consensus of 208 seqs, protein
MXXXXXXCLLYTIVYCIPYVCGIVYCIPYVCGIVYCTPYVCGIVYCTPYVCGIVYCTPYV
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CWIVYCTPYVCEIVYCIPYVCGIVYCIPYVCGIVYCTPYVCGIVYCTPYVCGIVYCTPYV
CGIVYCTPYVCGIVYCTPYVCGIVYCTPYVCGIVYCTPYVCGIVYCTPYVCGIVYCTPYV
CGIVYCTPYVCGIVYCTPYVCGIVYCTPYVCGIVYCTPYVCGIVYCTPYVCGIVYCTPYV
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CGIVYCTPYVCGIVYCTPYVCGIVYCTPYVCGIVYCTPYVCGIVYCTPYVCGIVYCTPYV
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CGIVYCTPYVCGIVYCTPYVCGIVYCTPYVCGIVYCTPYVCGIVYCTPYVCGIVYCTPYV
CGIVYCTPYVCGIVYCTPYVCGIVYCTPYVCGIVYCIPYVCGIVYCIPYVCGIVYCTPYV
CGIVYCTPYVCGIVYCTPYVCXXXXXXXKYRXAAYDDNYVCGXXXYRXXXXRVYCTPXX
XXXXYXXXYXXXXXYXLPYAXDXXYXXXYXXXXXYXLPYAXDXXYXXXYXCRXXYXXXPX
XXLVYAXXXXXRXXYXXXXXRIVLXXXXXXRXXYXXXXVCGIXXXXXXXXXXXXXXXXX
XXRXXXXXXXXXTPYVXXHVXXXXXXXRXXXXXXPEYRLAADDNYXXXYXTXXXXXXXXA
DXXXRXXXXXXXXXXXXXGXXXXXXXXXXRXXXXXXXXXXXXXXXXYXXXXXXXXXXXXX
XRXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXLXXXLX
GSASXXXXXXXXXXXXXXXXXXXXVXXXXXXXXXXXXXXXXXXXXTPKPXXXXXXXPXX
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XXXLXAXXXXXXXXXALPEYRLAADDNYRSIYRALPEYRLAXXXXXXXXXXXXXXXXXXX
XKPXXXXXXXXXXXXXXXXPXPXXXXXXXXXXXXXXXXXXXXSXXXXXXXXXXXXXXXX
XXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXXXXXXXXKPWXXRXXXXXXXXXXXXIXXXL
XLXXXXXVXSDAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXXX
XXXXKXXXXXXXXXXXXYXXXXXXXXXXGXYXXYXCXXXXXXXXXXXXNKXXXCXXXXXX
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XAPXPXXXXXXXXGXXXXXXXXXXXXXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX

XXXXXRXXXXXAXXXXXXXXXXXXXCXXXXFXDXXXXXXXXXXXXXXXXXXXEGXXXXXXXXX
VXXXXXXXXXCXXXGXCXXXXSXXYXXXXXXXXXGXXCXXXVCKPNPRKNSGRCVNKGSS
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XCKPNPXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGXXXX
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EVKPSEVKLXXXXXXXXXXPXXXXXXXXXPXXXXXXXXXXXXXXPXXXXXXXXPXXXXX
XXXLQQPXXXXLXPXXXSXXXXXCXXXXPXXXXXXXXXXXXXXXXXXXXXXXXXXXLXX
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EVKPSXXXXXXXXXXXXPXXXXXXXXXXXXXXXPXXXXPXXXXXXXPXXXXXXXXXXXXX
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XXXXQXXXXXXXXXXPXXXXPXXIXXXXXXXXXXXXXXXXXVSFXXXXXXXXXXKMXXXXX
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XXXXTLITXXXXXPXXXRXXXXXXPXXXXXXXXXXXXYSXPXXDPPPXXXXXXXXXPXXXL
XPXXXXXXXXXPXYXXXXXXXNXXXXPTYXPXXXXXXXXXPXYXXXXXXXXXXXXPXXXXXX
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HXXXXXXXXXXXPXXXXXXXXXPSXXXXXXXXXXXXXXXXSXXPSXXXXXSXXPSXXXXXS
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XXXXXXPTIXXXPXXXXXXXXXXPXYXXXLXXXXXYLXXXXXXPXXXXXXXXXXPSYLPXIX
XXPXXXXXXXXXPXYXXXXXTXXXXXPXYXXYISHCPXXXXXXXXXXPXYXXYISHCPXLX
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ISHCPSLXTXXXXVPXXXXXXIHCXXXXXXXTXXPXXXXXXXXXXPXYXXXLXHCPSYLXX
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XNTADVPTP

==> Aves.txt <==
>MSA Consensus of 877 seqs, protein
MLCWNEVQSCFLLAFLAVAAYSVSDAQGQVSPPTRLRYNVVNPDSVQISWKAPKGQFSGY
KLLVTPSSGGKTNQLILQNTATKAIIQGLIPDQNYALQIIAFSDDKESKPAQGQFRIKDI
ERRKETSKSKVKDPEKTNASKPTPEGNLFTCKTPAIADIVILVDGSWSIGRFNXXLXXLF
XXXXXSAFNVGSEKTRVXLXXXXGXPRIEWHLNAYGTKDAVLDAVRNLPYKGGXXXXLX
XTYILENSFXPEAGXRXRHSXXXKXXILXXXGXSXXXXXXXXKNLRDAGIELFAIGVXXA
XXXEXXXIASEPDXXXVXNVADFNFMNSIVEGLTRTXCSRVEEQEKEIKGTIXXXLGXXX
XXVTSDITARGXXXXWXXXXXXXXRXXXXXXXXXXXXXXXXXXXXXGXXXXXXXXGXXXX
XXXRXXXXXTEYQXAVXXXXXXXXXXGXEGCGSQXXEXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXMKMXXXXXXXFFXAXXXXXXXXXXXXXXXLXXXXXXXXTXX
CXXSXXXXXXXKXCXXKXXXXXXTXCXXCXXXXXXXCPXGXXKXTXXXXGXGXXDCRYXX
XXXXMFGEEXXXXXXXXXXTLSXPGCXHXCXKEXEXXXCCXGXWGXXCXXCPGGXXXPCN
XXGXKXXXXVXXGPXXXXSSVXRRXCITXXXXRTXLTGHSWXXXXXXXEXCXXGIXXXGT
CXCXXXXXGXACXXCXXXNXFGNSRPXCXSXXXXXTXXXXXXXKXTSSDIAXXRXXXXXX
SVCXCVHGXCNSVGXXGXGXCTCXXGYXGXXCDQXXXXCXXXXCXANSXCXXXXXDGXXX
XCXCXXXYXXXGXXCXATTPKPTIAVFRTGXRNLXXXPECXXXLRXCXPXAXCXXLGPXX
XYXTXXXXXXXXCTCXEGXXGDAVGXXCXPIXPCXXXXGQDALPQMRMAEXCPXXVXSTI
CXYXXPGXVXXXXXXXXXXXXXXXXLRVSDEWYNRLXXXXXXXPXXXMGYRIVYKSXXXP
XXXXXXXVGXDXXXXLLXXXXXXXXXXXXXXXXCXCKXXXXXXXPXXXCSXXXXXETXRQX
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VGTKGSNXRGRXXXKLXXAXXXXXXXXXXXLXXPXGPFTVXVPXTXKGLKEVCKGTNIKX
XXXVXXXXXXXXXXXXXXXSXXXSTVGAXXXXXXXXXXVFVPSLPIXDXMEFNXXAXXXX
XDLLNNXXXAXXXXXXHXXXGXXXXXXXXXXXXXXTLXGXXXXXSXXXXXXXXRXXXXXG
RXXXXXLQXNXXAXNGIXHIXXXXXXXXXXXXXXXXXXTIXXXLXXXXXXSXFXXXXEXX
GLXXXLXQXXXPSERXTVFVPSNXXXXXXXXXXLXYLXXAXXXXXPLVXEGGDKLAXXKL
XEMFGLVEKEFSAIDGVSMEPGXXHIXXXXXXXVXXLXXXXHIYLHPEGLPSDYTITFLF
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FYGSFHKLHVVISKTXGXXLXXESEAGXKXXXXXDIVAXNGXIXLGTLXGXXIPPXXXXX
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RGEKGEKGAPGPRGRDGEPGXLXXPGPPGPPGPXXPXXXXGCXXXXXXXGLNVXKXGCAR
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XCSXPXKXGXXCDXXXXCXCXXGXCDNRGPXXSXGXRGFPGTPCXXXVSCXXGYTGKXCD
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XNGXCHXLATCXXXXXXXXXXCXCPXGYXGDGXXCYGXGXXXELXXXSXXAAFNQWVNTX
LRMNYAXFXXWVXEAXXXGXXXXXXXXXACLICSFLFFGQQKXXXSXXXXTXXXTVLVPS
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XNXXPXXXXXXXTXXGXXPEFTPVREEMEAVXXGXPGXXXXXXXXXXXXVLXIQKNRCXX
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TACEXCXXGXYGXXCXXGXXXPXXXQXLXXXXXXXXLPXXXGQXXXXXXXXXXXXXRSXX
XXXXXXXXXXXCACXXGPPXXXGXXXXXGXXCXXGXXGDGSCECXXGXXXXXXXXXXXXX
PDXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPRSXXXXXXXRXXXXXXXLXXXXXXG
HVIDLVXXXXXXXXXXXXDKKXXXXXXXXXXXXXXXXXWXGXTCXXXIKEXDXCNXXCH
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XXXXGDGFXCRGXXXQELXPXRXXXXSXFXXXXXAXXIXXXXGXGPXXDXXXXXFXXXXX
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DXFXXVXXXGSXESCXXXGLCGFEPPCPAGSVQRGETXXCYYYXXXXILLLFSSPFSKAI
FCFKCGKPTNFSAQICCLXXXXXXXPXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
PXXXXXXXNSXXXPXXXXXXXXXXXXXXXXXSXXXXXXTALLXXXXXXXXXXXXXXXXX
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GSXXCXXXSSPTDXXXXXXXXXXFLXXIXXXXXLXXXPXCXPXXXXXAXXXXXXXXCXX
XYXGDGXTCXXXIXXXXXDXCXXXXXXXXXRXKWXKXXXXNGXRXGXEXXXXXAXXXXXX
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QALTTDQPNHVEVRKXGNGSPAPEEGLTQIVAAPPTTTTSPDGXHXXDDTQPPLPXXXXQ
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GXQLTLT

==> Babesia.txt <==
>MSA Consensus of 234 seqs, protein
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ICLCGLXASAXPXXXNXXXNKKLAAFXKXXXXXLSYXXGXXXXXXXXFNGSNVIXXTXEX
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XXXXXXPQYVTTHKKDLLSKVEQVMKQVRDYXSXXXXCXNNCXXXXXCXGXXXXXXXXXX
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LTFVPXXXXEXEYKQESDWYKPGTSGNDQSDFEXMSREEIKKMEEDKGCTGDLIADSRIA
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VSAGKDYVIAVEDTTHFGEEFWKTELHSFVKLLAYGLSATKGTNTLSLVRYSNTVEKVLD
RTAAVTDLLQSVQLEYXGYQXXXKXXXXXXXGAALKFMRENVYPNHDRFVRRGDTTTLS
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RYGGEGHGNDKNGCKGXXAQHKGSPWCCXGKGHKTLLTXXXXXXXXXGXTCXXXLXXXXX
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DYSEDEDYEEPDYLDDRGNIITDDFHEGDYDMDARRGPYGIDYGRYNGEXXYEDQQENEY
GGGNXMFDGKMPLFWEYKAYILAGFAGLLLITVVYYGSHIVRSNKQEEELNDETEYLQSG
DGDDVEAGGREQVADANEAMWA

==> Babesiidae.txt <==
>MSA Consensus of 234 seqs, protein
MLGVGIISTFAVLSAICSGQASAYRHAAYGSHSPSQDVEDRVVPSTEHTHQLGSHEAVIK
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ICLCGLXASAXPXXXNXXXNKKLAAFXKXXXXXLSYXXGXXXXXXXXFNGSNVIXXTXEX
WXXXXXXXXXTVTXVSKRIDKMFESMSNAEESKPGEALKFLRESVYXNANKYLLNDKTTE
LNLNSXXGKDTXXXXXXXGXXSXMQXXXDXXCXXXNGGXTLFVIEXCAXCEXXXXXXCXC
XXXXXXPQYVTTHKKDLLSKVEQVMKQVRDYXSXXXXCXNNCXXXXXCXGXXXXXXXXXX
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XSAXXXXIDGDEXXXXXXXXXXXXXGXXXPCMXXXXGLNPIRTINPMAVDWDRXXRXXGX
XXFLXLHXXAXDXYXERXAXXXXXXXXXXXXXXXXXAXXXXGENEDGDGDEXRTRGDDLE
LTFVPXXXXEXEYKQESDWYKPGTSGNDQSDFEXMSREEIKKMEEDKGCTGDLIADSRIA
NILRKRKYDVYTGKWSLKYAKENKRDLELRYYIPTLNGDERGLENMLKYAKRVNHWLGVC
VSAGKDYVIAVEDTTHFGEEFWKTELHSFVKLLAYGLSATKGTNTLSLVRYSNTVEKVLD
RTAAVTDLLQSVQLEYXGYQXXXKXXXXXXXXGAALKFMRENVYPNHDRFVRRGDTTTLS
VENAAGKDTVVIMVNSGSVSDSALAXXXXXXXXXNXXXXXXXXXGXXSSGFWKQVVGCRA
GXXXXXYXXXLXQELLEKVGTMVXNLCEPDGRXXXXLXXWSXXXXCXXXXGXXXXTSTLC
RYGGEGHGNDKNGCKGXXAQHKGSPWCCXGKGHKTLLTXXXXXXXXXGXTCXXXLXXXXX
KXXXCXXXXCXXXXXXXXXXHXXXXXXGXXXXXXXXXXXSDXRNGCXCGXXGXGSAXCSP
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EVHADPYPGXDPTXXEXDHHSQSTVGSVSEHSAHEEVGGRSXXDEXXXXMGXTTTXXDDV
SDRQLSTGSTHDRQVSGSHALVPDVISSVLPTXEEXEXEDQTXDQTDDQTDDQTDDEESX
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DYSEDEDYEEPDYLDDRGNIITDDFHEGDYDMDARRGPYGIDYGRYNGEXXYEDQQENEY
GGGNXMFDGKMPLFWEYKAYILAGFAGLLLITVVYYGSHIVRSNKQEEELNDETEYLQSG
DGDDVEAGGREQVADANEAMWA

==> Bacillaceae.txt <==
>MSA Consensus of 786 seqs, protein
MXXXXXXXXXXXXXXXXXXXXXXXXXXXSXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXH
IKXXXXXXXXXXFXXXDSXXEXGXXXXXXXAXXXXVQLPSTXXXXXXLXXXXXXXXXXVX

XXXXXXTDEAGXXXFXXLXXXDXSGXXXGXXXXXXXXXXXXAXXXXXXXXXXXXIVLQEGXX
XXXXXXXKXXXXXXXXXXXXXXXXXXXXXXXXXXSTXXXXXXXXXXXXXXVXXVXXXXXXSV
XYRXXXXXXXXXXXXXXXXXXXXPXXXXXSXQDYXXXXXXXXXXXXXXXXXGXGXXVXXID
XGXXXXHXXXXXXXXXXXXXXDSGEXXEXXXXXXRKXGXSKIXXVXXXXXXXXXXXXTXX
XXXXXXXXTXXXXYTXXAXXGXXXXXXXXXXFXXXXXEXDXIXXXEXXXXTXGIXXXXXX
XXXXXXXXXXXXPXPXXXXXXXXXXXLNXXGXXXXXXDGEXXXNXXXXFXVLLXXDXVYIDT
DXDXDFTDETAYXXXXXXTXDXXXXDXXXGXXXXXXXXXXXXXXXXXXXXXXXXXXXXNX
XXXXXXHGXXVXGXXXXXXXXXXXXEEEEEKEEVKDEEKEEKATXXXXXGXTXAVAXEGVA
PXXXXXXXXXXFXXXXXXXXXXXXXXXXXXXXXXXXXGXXXXXXXXDVXNPSXSXXXXXX
XXXXGXXXXXXXXXXAEKLQTRXXXXXXXXXXXXXXXXXXXXXXXXXGNXXXXXXXXXSXD
XSXXXGEXXXXXXXNXXXXIXAXXXXXGXXXXXXVXXXXXXXXXXXXXGXXXXMXDXSTN
RETXXISVGAXIXXXMWAXXXXXXXXXXXDVNXXGVIXIXXXXXEXXXXXXAXXXXXXXXX
EVGXTYEXXXXXXXXXXXXEGXXXXGXXXFSXXGPXXXXXXXXXXXELXXXXGXXXXXXY
TXXXKPXXVXXXXAXXXXXXVXGXVXXXXXXXLXFXDKTXNAAXAGAXGXXXYXXXXXXX
FXXDQGGXXXPFMKXSXXDGXAXXXXXXXXXXXXXXXXXLXXXEXPEXGRMTELQVSLEK
AXXXXWXXXXNXXGTTPSLEXXXXXXXPXXXXXXXXXXXXXXXXXXXXXXXXSKSXGTS
MXXXXXXXXXXXFXXXXXXFXXXXXAXXXXXXXXRXXXXYEXXXXXXXXXAXXXGXXXXX
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XXXXXGXXXXXXXXXXHXXXXXXXXXXXXXXKXXXXPVXXXXXXXXXXXXXXXXXXXXXX
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VTLXEGTKGXATXAXAYENGSLTLNPXXXXXXXXXXXXXXXXXXGPXXXXXXXXXXXXXD
XQGXXXXXXXXXXMXVXXXXXXXXAXXGXXXXYXXXXXNXXXXXXXXXEYXXXXMTIEXX
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XEAXXXXXXXXXXTSXXXXXXXXXQMXXXXXXXXXXXXXXXXXXXRXXGXXNRQNERXXTA
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PLXAXYFSXXXXAPILLVTXXXXXXEGGLQXSGSXXXKLXXXXXXEXXRLXQXXXXXXHY
XSXSXPXXXXXXGGXXXAXSXXVXXXLXXLDGXXAXXXXXXXXXXXXXXXNXXRIXXXXXX
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FQDXXXXXXXXXXXXXXXGGXXXXXXXXXXYNSXXXXXXXXXXXXXXQFXXXXXXXXXXX
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XXXXXXXXXXXXXXXXXXXXXXRXXXXXXXXXXXXXXXXXXXXLXXXXXXXIXXHXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXPXXXXXFXTXXXXXXXXXXXXXXXXXXXXXXXXXXX
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QGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXSLNNLLVLSLALNEXXX
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SAXXXXXXXXXXXFXXXLXPXXXXPAKEXXXXXXXXXXXXXXXXXXXXXPXXXXXXXXG
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXDXXXXXXXXXXXXXXXXXXXXYXXXLXXX
XTXXXXXVANMVLDNKDSEYXXXXYSLGGFIAQIIGSEFADXXXXAFWSASXXXXLXXS
XAXVXXXSXYXXXXXXXTXXXXPXXXXGXXXXXXXXIRXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXSLXXXKKYXMKTTDEIKGLLGRHGIGFFMKDPITTKLSKNY

==> Bacillales.txt <==
>MSA Consensus of 1066 seqs, protein
MXXXXMXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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XFTXXXXXXXXAXDXXEXXEXXXXXTRKSIXGXXXXXXXKXXXXXXXNXXXXXTXXXXXE
XXYXXXXXXXXXXXXXXXXXXGDVXXXXXXXXXXKVYXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXDGEXXXNXXXXX
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TQXXXXXXXXXXGVAPXAXXXXXXXFXXXXXXXXXXXXXXXXXXXXXXXXGXXXXXXXX
DVXNXSXGXXXXXXXEGXXXXXXXXXXXXXXXXXXXXXXXXGNXXHXGXGWXXXXXXXXX

XXXXXPXXXXXXXDNXXVXAXXXXXXXXTLXXXXXXXXXXXXXXXXXXXPYGKXXXGXXX
XXXXXXXFXXXGXXXXXXXXXXAXXXXSAXXSKPXKXXXXXXXXXXXXXXXXXDXEXXXXX
XXXXXXXXXXXXXXVXGXXXXXXXXXXXFXXXXXXXXGGXTXXXXXXXXXGXXXXXXXXX
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XXPXXXXXXXXXXXXXXGEXXXXXXXXLNEXEXXXXXXTIEKAEDKXXXXXXXXXXXXXX
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XXXXXTAXXXXXXXXXXXYVNXXFGXXXXXXXXXXXGXXXXXXXXXXXXXRXXXXXXGXX
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TXXIXYTXXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXXXDHSTXXXXXVXXXXXXXXXX
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GILPXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXYXXPXXXXXX
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XYXXXATSXXXYQMXXXXXXXXXXXXXXXXXXXXXXXXXXKEFIXXXXXXXXXXXXXXX
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AXXXXXGXXXXXXXXGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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XXXTXXXXXXXXXXXXXXXXXLXXXXXXXXXXXXXXXXXXXXSXXXXXXXXXXXXXXXX
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XXXXXXXXXXXXXXXXXXXXXDXXXXXXXXXXXXXXXXXXXXXSXXXXXXXXXXXXX
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MTRXXXEXXXXXXXXXXXTXXXXXXXXXXXLXXXXXXXXXXSLXNXXXXXXXXXXXXXX
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XXXXXXXXXXXXXXXXXXXXXXXYAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXDXXDXI
XXXXXQXXXXXXXXXXXXXXXXXXXXXXXXNXXXXXXXXXXXXXXXXXXSGPXXXXXX
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XVXXDXXXDIXXXXXXXXXDXXXXXXEXXXXXSXXXXXXXXXXXXXXXXXXXXXXXXXX
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PXXXXXNXXXXXXXXXXXVXXAXXXDXXGXXXXXXXDALXXXPLAXXXXXXXAPXLLTXXX

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GXXXXXSXXVXXXXLVLDGXXXXXXXXXXXXXXXXXXXXXRGESVWSIXGXGMPXRXXT
XXXIAXXLKSXNXXXXNXXFPNQVLKVSGSSSRASNSXXXXXXEVXXXXRXXXXXXXXXT
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SXXLXXXDXXXXXXGXXXXXXXXXXXXXXXXXXXXXLXXXXXXXXXXXXXXXXXXXXXX
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STVSANXNHXXXXXLXXXXXXXEYWXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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GGXXXXXXXXXGXYEXXLXXGXXXXXXXXXXXXXXXXXXSXXXXXXXXXXXXXXXXXXX
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XXXXRXXLXWXXXXXDLDXHLTGXXXXXXXXXXXXXXXXXXXXXXXXXXAXXXXXDXXXXX
NXPETXTXXLFXTDXXXGXYXYXVXXXXXXXXXXXXXXXXXXXXXXXXXXXXXTXXDEVX
XXXXXXLXXXXXXPXNXXGXXWXXXXLXXXXIXPXNXXXXXXXXXXSRSXXXXXXXXXXX
XXXSLXXXKKYE

==> Bacilli.txt <==
>MSA Consensus of 4441 seqs, protein
MGFLCFNRNCKYYESIKRRMXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXLXXXXXVXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXHDGXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXWYXXXXXXXXXXXXTHXXXXLQSXXXXDXXXEXXXXXXNXLXXXX
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XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXSXX
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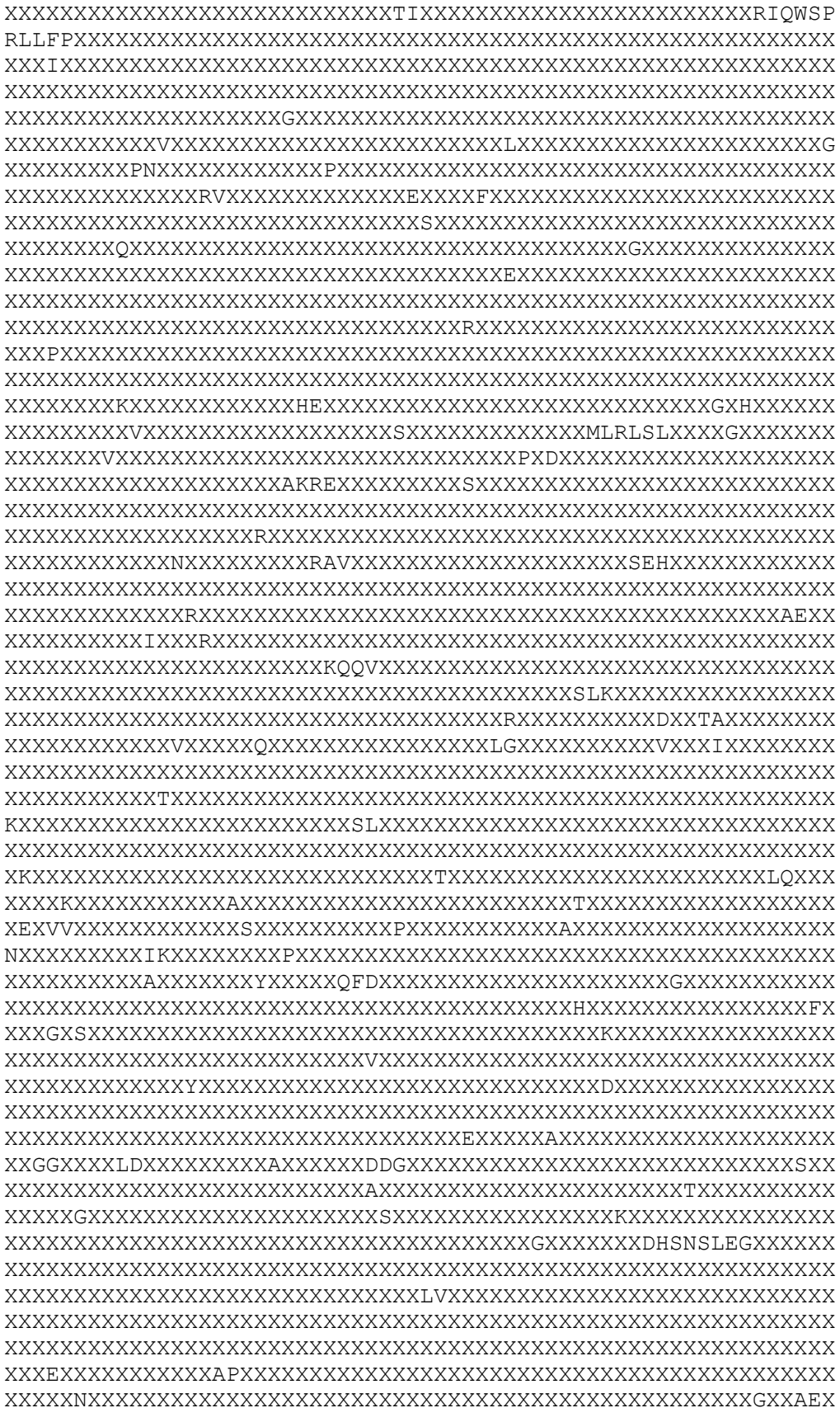
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXEXXXXXXXXHXXXXXXXXIXXXXX
XITALXXXXXXXXXXXXXXXXXXXXXTQXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX



XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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RNAKEVXYNXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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XVXXXXXXXXXXXXXXXXXXXXXXXXXXXAXXXXYXQYXXXXXXXXXXXXXXXXXXXXX
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FXDALXGSXLAAFVYYXVYYGXASVXPMSXXXXLXXXIQXXXEXXXXNXXXXXXXXLXXT
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XAASXXKXXXXXXXXXXXXXXXXXXXXXXXXXXXXYGXXXXYXXXXXXXXSDMXXASDA
LSDAKXXXXXXXXXXXKASXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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ASXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXLXXXXXXXXXXXXXXXXXXXXX
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==> Bacillus.txt <==
>MSA Consensus of 454 seqs, protein
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XGXXLSXXYYKXAPFXSXKMVFSKXLGGXXGDXXXXXXXXRDXVYXDLVQLKXLFADVAX
XGSXSXYXITXXDQXAINXLYXXALXXXXXXXELPXXXXXXXXXSXPXXXXXXXXXXXXX
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VAXXXXXXXXXXXXXXXVXXXXXXXXXXXXXXXXXXXAAXXEXXGXXXXXXGXDXXNXSL
GXXXXXXXXXXXXXXAXXXXXXXXXXXXXXXXXXPXPXSXXXXXXXXXXXXXXXXXXXXD
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IVYVXXGXPXXYXXGXXAXXXXLXXXXTXXXGNVSDATLVTVXDXXGXXXXXXXXXXXXX
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XEXGXXSXXXXXXXXDERXXXLXXXXXXXXXXXXXXXXXXXXXXXXXXXHXSPXXXXXXG
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==> Bacteria.txt <==
>MSA Consensus of 15579 seqs, protein
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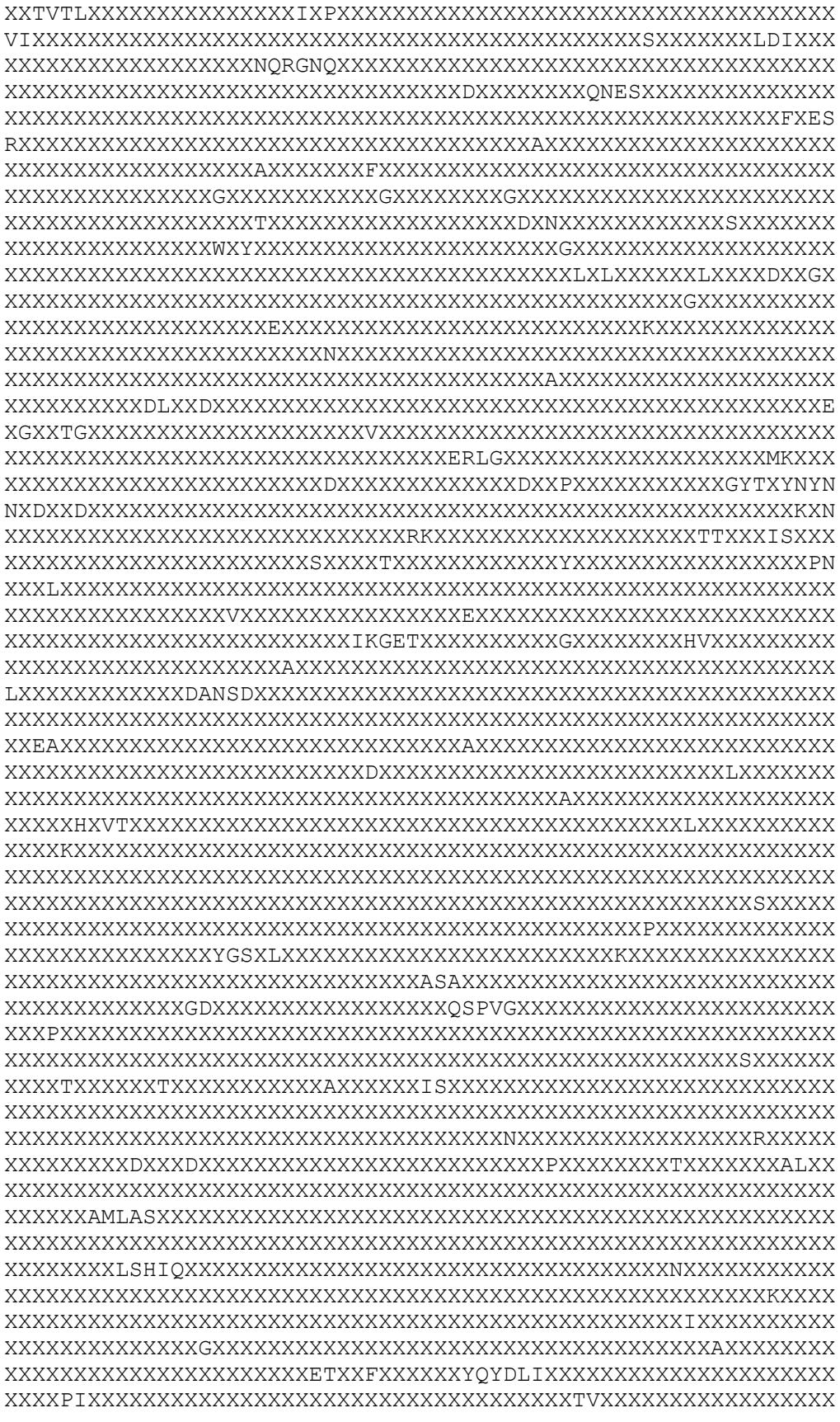

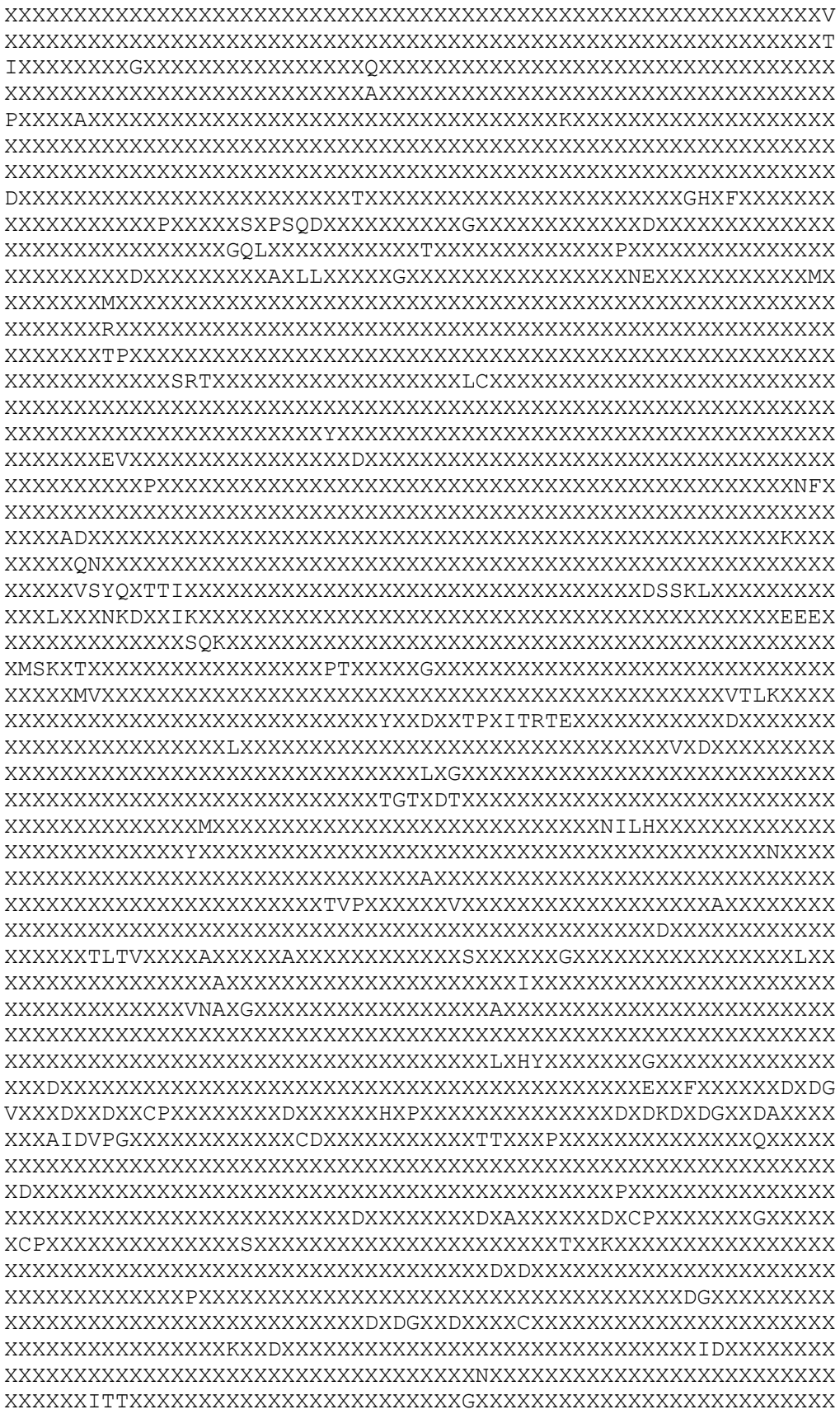

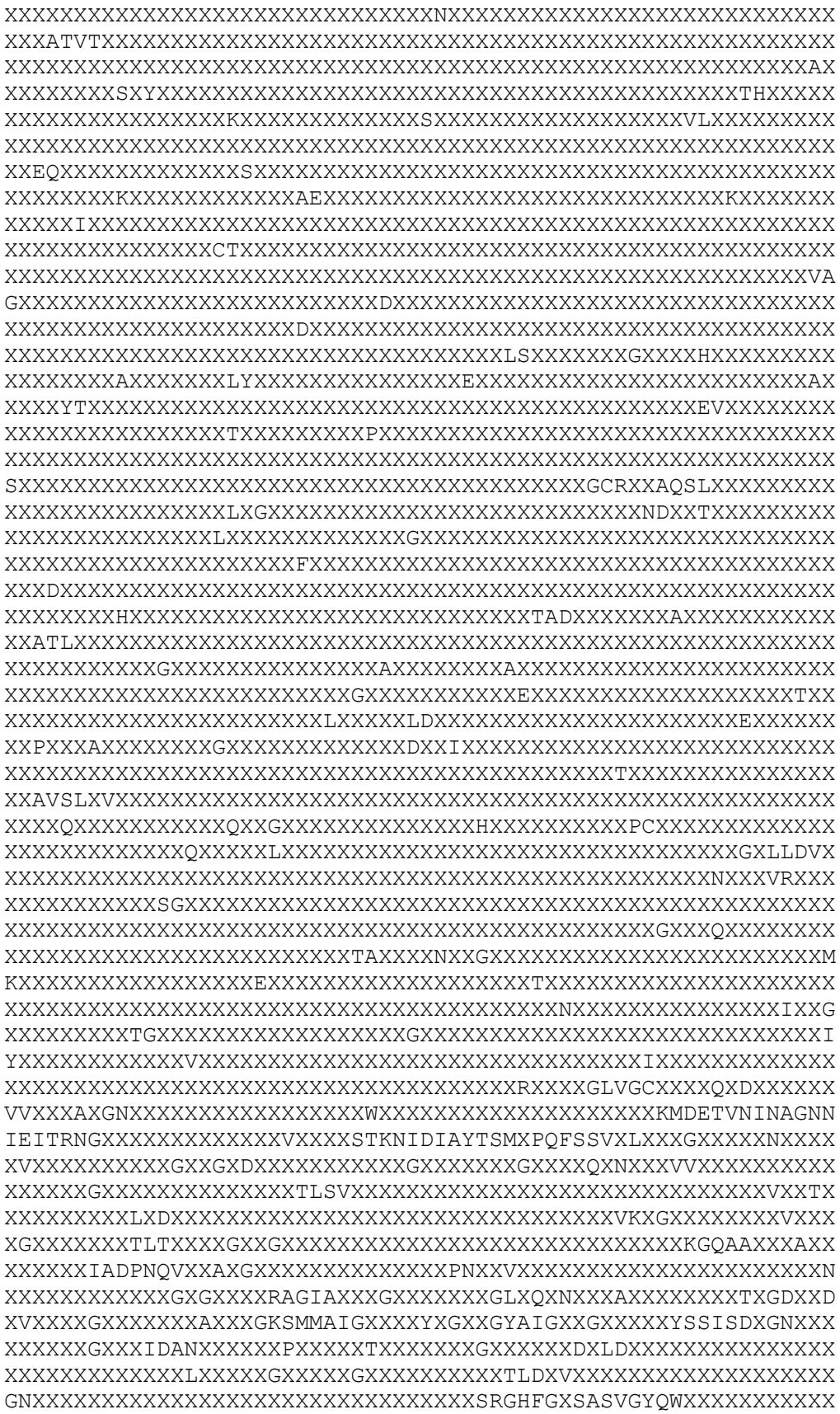

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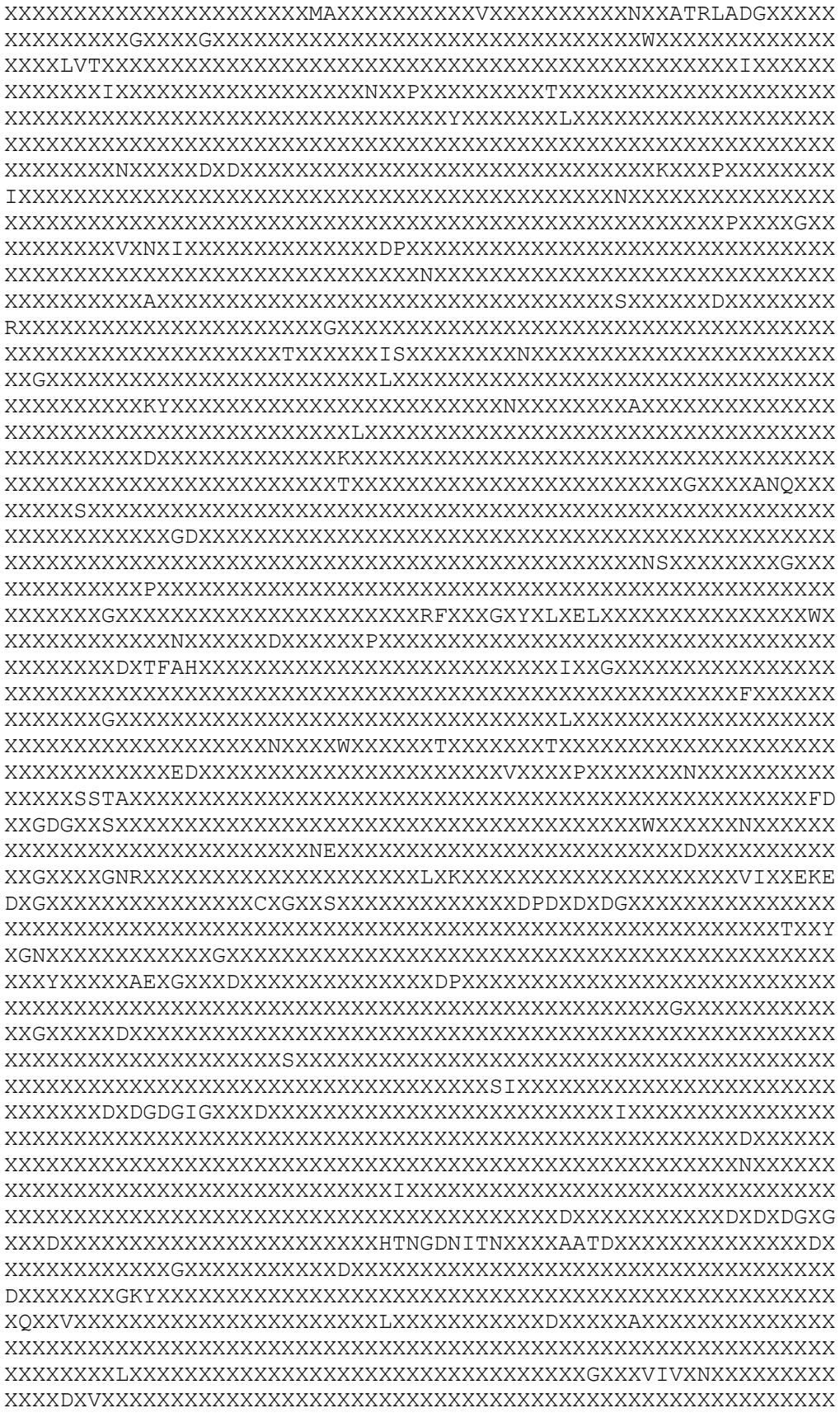

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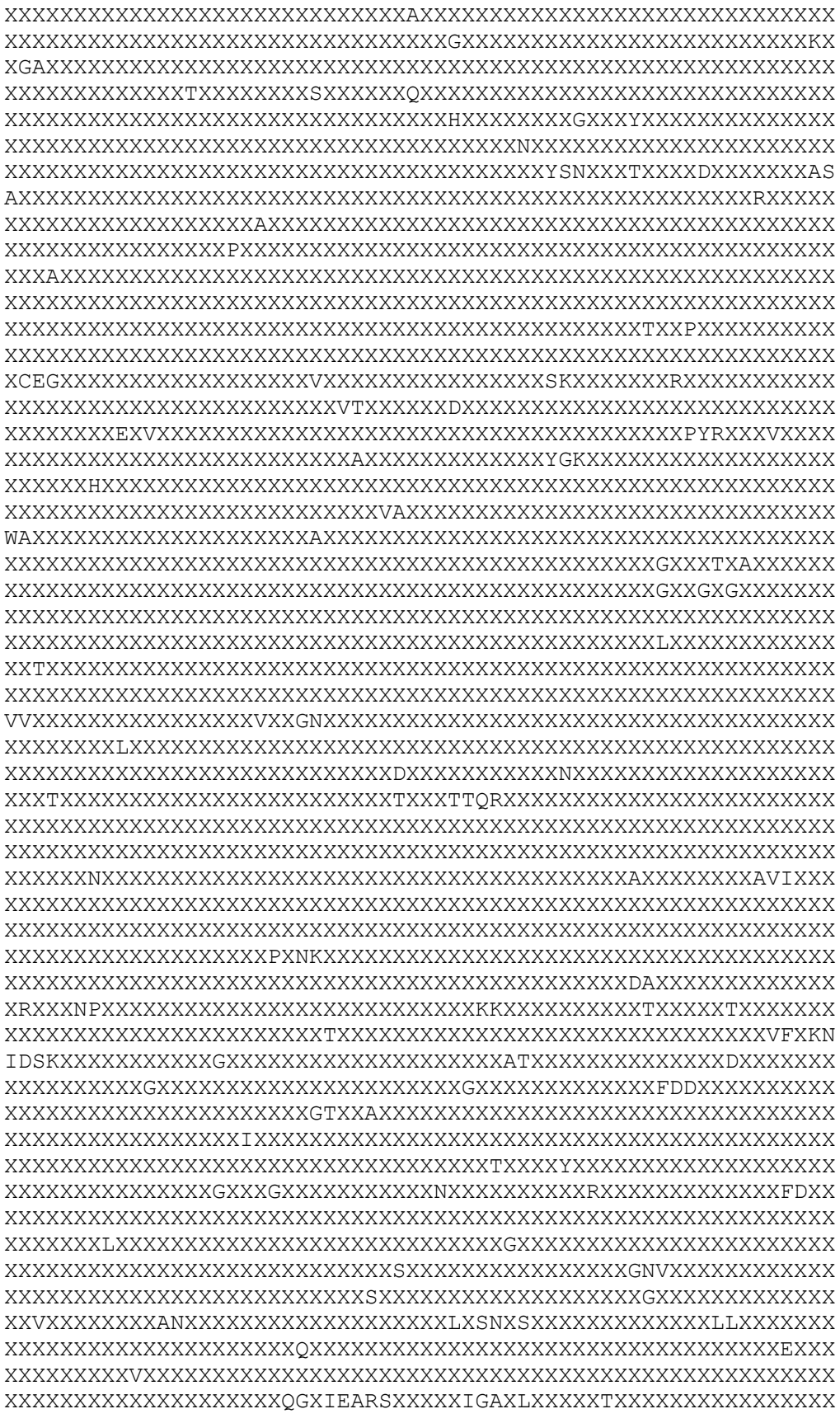

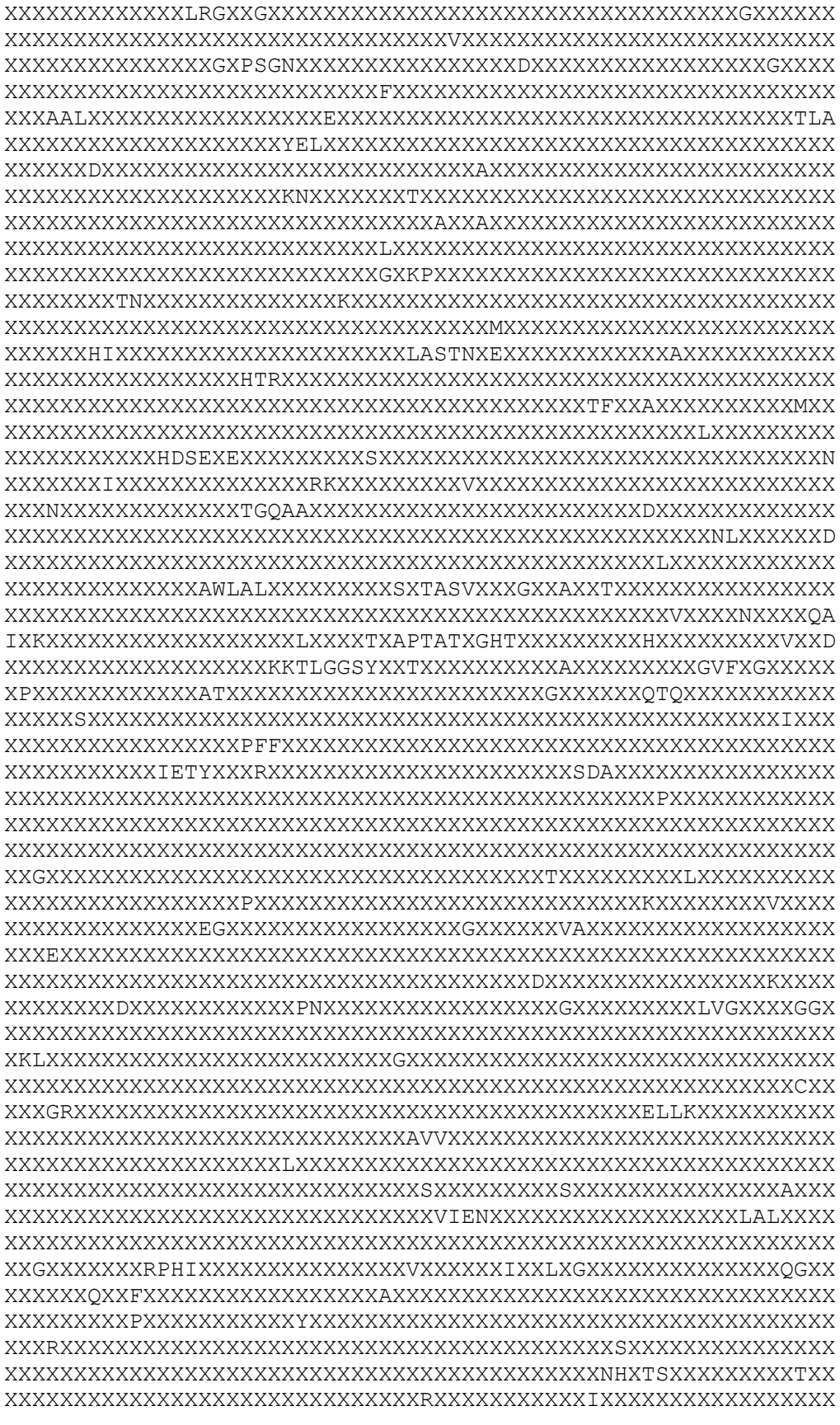

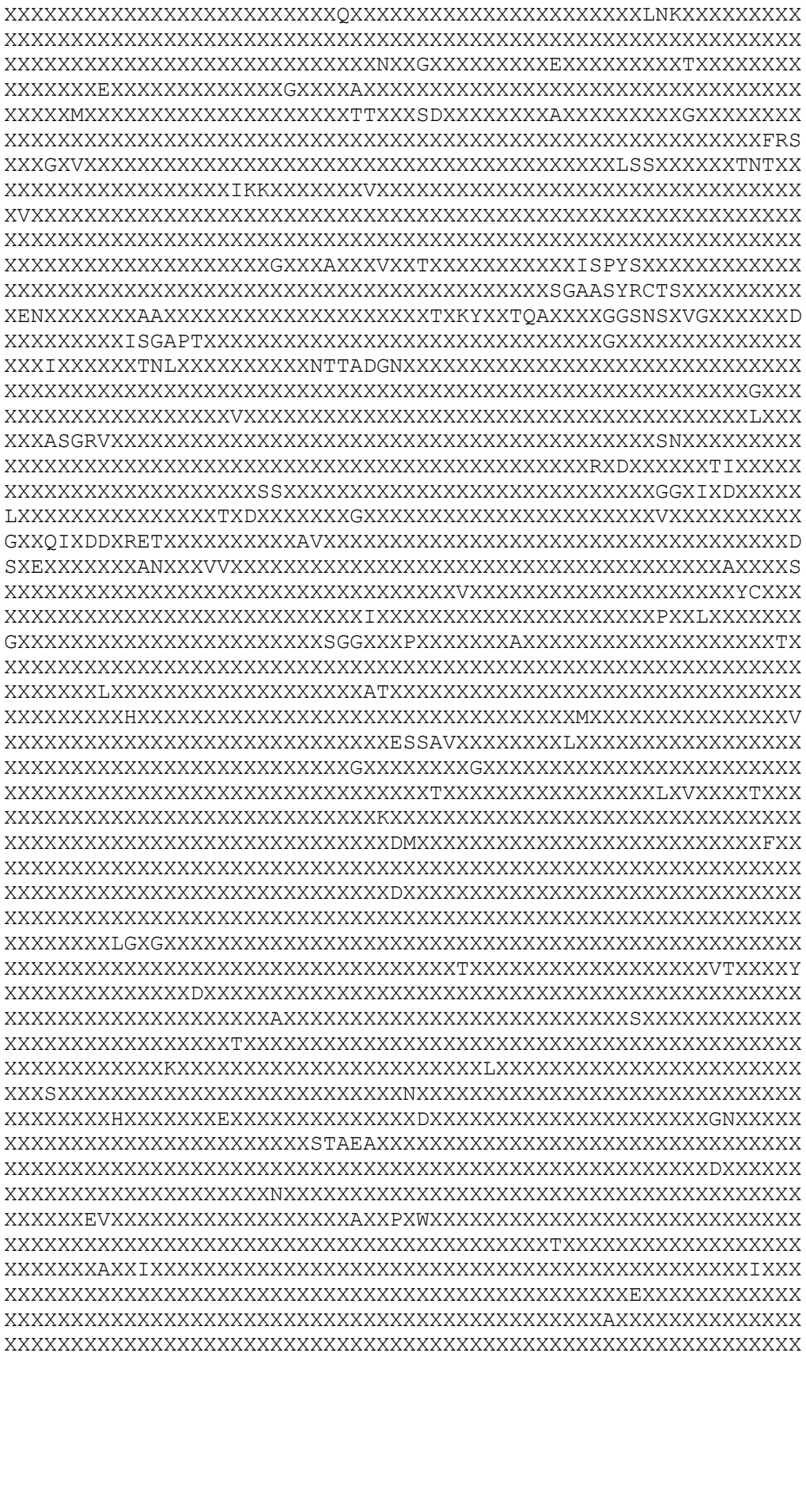

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==> Bacteroidetes.txt <==
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XDGNGQVXTPDXIVDELPETDGXXXLSFAXLXXXNXXLXXXXXXXXXGVXXXTXXXXXXX
XXXXXXEKEXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPXXXNXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXIXXXXXXXXXXXXXXXXXCXYXXSXXEGLXXXXIXXXGXXXXXXXSXXXXXXFX
XDXXXXXXXXXXXXXXEXLXLXXXFQQLP

==> Betaproteobacteria.txt <==
>MSA Consensus of 159 seqs, protein
MXXIXADGGPAFGQVVELSPDGIRRVLIEGDRIFTGEQILTGAAGSVSLALERCVRVEMX
GXTEWEPEAPDIAQPSDDAVDGAPSIAELQQTIIAGADPTQSLEATAAGEQISGDTSDAG
DSHSVTTPVVLQETAGVVDPAVGMPTGTFDGARSNNSEFLGAPDRNTQPAQVPTNTAATP
AAAVDTASSDTSTAPVDPPASGDTSNAGTTTPGTATPGDTTTPGTTTPGDTTTPGTTTPG
GTTNPGTPTPGGTTNPGTTTPVDTTTPGTTTPGGTTNPGTTTPGGTTNPGTTTPGGTTNP
GTTTPGGTTTPGTTTPGGSTTPGTTTPGGTTSPGTTTPGGTTSPGTTTPGDTTTPGTTTP
GGTTTPGTTTPGGTTNPGTTTPGDNTTPGTTTPGGTTTPGTTTPGGTTNPGTTTPGDTTT
PGTTTPGGTTTPGTTTPGGTTSPGTTTPGDTTTPGTTTPGGTTTPGTTTPGGTTSPGTTT
PGDTTTPGTTTPGGTTTPGTTTPGGTTSPGTTTPGDTTTPGTTTPGGTTTPGTTTPGGTT
SPGTTTPGDTTTPGTTTPGGTTTPGTTTPGGTTSPGTTTPGGTTTPGTTTPGGGTTTPAN
KAPLLDLNSTDGATTTGNAFSVNQGASGVAIAPSVSLSDDGTTLKNVTLDVTSHQTGDKL
DTSAISGAVKVDDVSSTATHVVLISSDAANPATVAEFQAAIAAITFSTTSAGTPRTISVT
ADDGSATTTANSVVTVAPINSLTLSADVAAVAENGTVTYTATLGQPASAALTVTLSNGQS
IIIPKDATSGSXXXTXXXDXYXXXPLSXTXXXTXXXTXGGXFXXLXXXXXAXXTXXTDXX

DTTTXXXVSTXXXXVXEGGXXXXXXXLXNKAXXDVTVTXXXXXGSVTGSKNVTIASGSSN
AMYTVDVPDNTGIGSNADLVVTLSNPAGGKFESLILGTATVTTAIGDNDRASELTADTNL
TTPEDNAAIGNVLSNDKAGTIGLSVSTFSVDGMTGTFNAGTTAVPITTGSGSTASTIGTL
TLSSTGAYVFTPIANWNGTVPTITYTTAEGASQTLNISIQAVNDAPVLDLNSADGSATTG
NAISVSQGGAAVAIAPAVSLSDIDSNSAKSVTIAIQGTHIAGDTLVIGSGVPAAVKAELS
SDGSSVVLTSTDATTPATLAQFEAAIAAVNFSTTSVGVPRTINVSVDDGSNSGTSTSTAS
TVVNVTAVNHLTLSADVATVAEKGAVTYTVTLDRATDTALVVQLSNGQTINIAKDAISGT
SLPFAVGNDAWTGAPELSVTISSYSGGSAAANLSITPTPAVTTVTDAIDTTSISIISTDT
APVIEGSTAHFQLNLSNKAEADVTVTVSYSYGSVTGTKDVTIASGSTSATYTVDVPENTT
VGVNPSLIVTLSNPAGGKFESLILGTASVTTAIGDNDRASELTADSNLTTLEDNAAIGNV
LTNDKAGTNGLSVSTFSVDGMTGTFNAGSAAVPVNVGASNIGTLSITSTGAYVFTPTAMX
HGGVPTITYTTAEGASQTLNISIQAVNDAPVLDLNSADGITTTGNAISVSQGGAAVAIAP
AVSLSDIDSNSAKSVTIAIQGTHIAGDTLVIGSGVPAAVKAELSSDGSSVVLTSTNATTP
ATLAQFEAAIAAVNFSTTSAGAPRTINVSVDDGSNSGTATSTASTVVNVTAVNHLTLSAD
VATVAEKGAVTYTVTLDRATDTALVVRLSNGQTINIAKDAISGTSLPFAVSNDVWTGAPG
LSVTISSYSGGSAAANLSITPTAAVTTVTDAIDATSISIISTDTAPVIEGSTAHFQLNLS
NKAEADVTVTVSYSYGNVTGTKDVTILSGSSTAQYTVDVPENTTVGVNPSLIVTLSNPAG
GKFESLTLGTATVTTAIGDNDRASELTADSNLTTLEDNAAIGNVLTNDKAGTIGLSVSTF
SIDGMTGTFNAGTTAVPVTTGSGSTTTNIGTLTLSSTGAYVFTPTANWNGSVPTITYTTA
EGASQTLNISIQAVNDAPVLDLNSADGSATTGNAISVSQGGAAVAIAPAVSLSDIDNSSA
KSVTIAIQGTHITGDTLVIGSGVPAAVKAVLSSDGSSVVLTSTNATTPATLAQFEAAIAA
VNFSTTSAGAPRTISVTADDGSGSDTAISTANSVVTVTAVNHLTLSADVATVAEKGSVIY
TVKLDRAADSDLTVLLSNXXXXXMXXXXLXXXSXXFXVGNDSWXXAXXLSVSISSYSGGS
AAANLAITPTAAVTTVTDAIDATSISXXXTDXAXXXXGXXXXFQLNLSNKAEADVTVTVS
YSYGNVTGTKDVTISSGSSTAQYTVDVPENTTVGANPSLVVTLSNPAGGKFESLTLGTAT
VTTAIGDNDRASELTADSNLTTLEDNAAIGNVLSNDKAGTNGLSVSTFSIDGMXXXXXAG
TTAXPXXXXSGSTASTIGTLTLSSTXXXXXXLXXXXXXXXXXXXXXTAEGASQTLXXXXX
XCXXXXXXXXXXXXXAXAXDSVGXXXXXXXXRDPXGXXXXXXXALEXXXXDSTSAKSVTI
AIQGXXXXXGXLXXXXXXPAAVKAELSSDGXXVVLRXXNAXTPAXXAQXEAXXXAVNXXX
XXAXXXXXXNVSVDDGSNSGTSTSTASTVVNVTAVNHLTLSADVATVAXXXXXXYXYVPV
XXXXAXDXXLXXXXXXGXXXXXXXXMNKIYRXIWNXXXASGRGXXAWXVXXXXXXXXXXX
LGXYXXXXXXXADDXXXXTPAXXTVATAVLATXXSLXXXXXXXADSNAXXXXXXDDXXL
EXVXRXXXXXXXXXYRDXEGXXXXXXXXXXXXXXXXXXXXXXXXXXXRTLNXXXXXXXX
XXXXXXXXXXFXXXXXXXXXXXXXXGXXXSXXXXXXXAXGXXFLXXXLXXXXXTXXXGXX
XXXXXXXXXXXXXXLXFEFXGITPEELQRAXXXXXXXXXXXXXLXXXXXXXXXAYXXXT
XFAXXXXXXXFXNTDXXVXRLXGXLVXXXXTLXXXGSGXSQSFXVTXPAPTLADAXARXX
FXXFXXXXXXXXXXXXXXXXXXXXXFXAXXXXXXXXXXXXXXXSYXXXXXXXXXXC
XXXXIQAVNXXXXFDLNSAXXXXXXXXAXXXXXXXXXXXXXXXXXNXPIYXXXXXXXXV
ALXXXXXXNXXXHHPXXXXXXXXXXXXXXXXXXXXXXXXXXXXQXXXXXXXXISGQDDK
YELSLDITSKLGTLLXADGGXVXXXAXXXXXXXXXXXXXXXXXXXXNXXXAAXXLXXXXX
XXTTSAXXAXXIXLDGXMXXGTVXXXXXXXXSAXGXXXGXXXXXXXGXXVNXXXQELVH
IDAXVAXLEQLVXXEXXXXXXXXXLMLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXTX
VXLXXXXXXXXXXGXXXVXXXXPXXXXXRCINXXXXWXXXXXLXXXXXXYSGGSAXXXXX
XXXXXXXXXAXAXXXXXXXXXVXXXXXXXXXGXXXXXXXXXXXKXXXXXXXTVXXXYGSV
TGTKDXXXXXXXTSATYTVDVPENTVVGSXXXXXVTLSGPXXXXXXXXGXXXXXVXXXXX
XXXXAXXXXXXXXXXXXXXNLXGXXXXXXXXXGXXXXXXXXXTXXXXXXXXXXXSXXPXX
XXXXFXXXXEXXLXDLTSVXXGYXXXRXYXAXXIEXXEXXXFXXXGXXXNITSDXKGLNW
XXXXXXXXXXXXXXXXXXXXXXXXXXGXXXXXXXXXXFFADEMIKARDLTIKPVSDXXN
LXXXXXXXXXXXXXXXXPXETAGTNGXXXXXXXXXGXLXGXNXGXXXNXXXXXXXVXXXX
XXXXNXXMELXXXXGDXXXXXXXXXXXXXGXNXXGXXXXXXXXGXXXXXXXXXXXGGLXGX
XXXXXXXXXXXXXXXXLPVXXXXXXXXXXXVXXXXXXXXXXGGXVXXXXXXQEXXNXGXXXX
XXXXXXVXXXXXSDTDSSXDXTVHLNGIGSTLTDXXXXLXXXXAXXXXXXXXXXXXXXXR
XXSXKDVLXXGXXXKGVKXGXTTXXSXXVDXXXXXXXXXXGXAXXTSXTPVEFVVRTYDA
LVADTNSVREDXXXXGDXLXXAYXXXXXXXXXXAXXXXXGXVXXXSXXTXXXXVNVXXXXT

SGATXXXXXXXYEXKDNGKXRMARYSRALGTQLLRXXXXXRXXXXXXXLDWKGTIXXXR
XXXXXXXXXXXXXXXXXXXXAKTXVXXXXXXXXXXXXXTGKGKXEXXXSTDEGEGLVTX
XXXXXXXXXXXXXXXXXXXXDAXXXXXWXXXXXXXXXXXXXXAXAXXDXYXQXXKFXXXX
XGXWXXXXXXXXXGXXXXXXXDXXXXXXVXVRXXXXXXXXXXXXXXXXXXXXXXVXXXX
XXCXXXXXXRPXQGXXXXDXXXXLXXXXXTXXXXXXXXXXXXXXXXXXXXDXXXXXXXXX
XXXXXXXXXXXLXKXXXXXXKXXQNSGWXLDXXXXXXXXXXXXXVAGXXXXXXXGNVSPS
KGKXDETVNINAGNNIEITRNGKNIDXXXXXIXXXXAXGXXXXXXPXSXXSMXPQFSSVS
LGXKAGXXAPTXXXXXXXXXXXXXDEGALNVGSKDXXXXXXXXVXXXVXXXXXGXXNKPV
RITNVAPGVKXXDXXXXAQLHXXXAXXKGXXXXLXXXXXXXSLXXPXXYXXXXXXIXXXA
XXXDNVDGNARAGIXXXXXXXAQAIATAGLXXAXLPGXXXXXXXGXGXVAXXXXDXXPXX
XXXXGXXXYXIGYSXXXXXXXXXXXXXXXXXXXXXXXXXDXXXXXXSISDXGNWXIKXA
TDKAXNXXXXXXXXXXXXXXXXXXXXXINGIADLPPGLQPQVDTLLASAXXSXKGSLWSH
XGTASXXXXGNSXXXXGXXXXXXXXXXXXXXXXXXGXXXXDAXXXXXXXXXXXXXGXXXG
XXXXXXXXXXXXXXXXXXTXGKNANPVVVDYQSNTAPDXRLDAIEXANRHRLGGXGAVNI
GGVSRTIVDSNGQVHLFTXXXXXXXXXXXXXXXRXXGXXRXXXXXXXAXXXXXXGXXXXX
VXNGXXFPDALSXXXXAXKXGXXILXXXXXXXXXXTXXXXXXLNVYDSNGQALTNISADN
LGAAIKXXXEXXVXGGXXXVXXXXXXXLPGDVFAYTSXXXXXEGXXXXXGSXRYXTNXXX
AXXFXXXXXHQYIAGHSADFDVSRETDGRDTLLGGDGDDILFGQGGKDSLDGGAGNDLLY
GGTGDDTLIGGQGNDTLIGGAGNDXXXXAXGXXXXDXXXXXXLAAXXXXXXXLVXXXXXX
XXXXXXXXXXXXXXXXFGGXXXVXXXXXXLLXXXXXXXXXXGSNADLTIXLEGVQFSSST
TIXXXXXGGDPTIKIDNPTG

==> Bifurcata.txt <==
>MSA Consensus of 770 seqs, protein
MLEXXXXXFFXMXXXXXXXXXXXXXXXXXXXXXXXXXXXXXCDXKXXXXXXTXCXXCX
XXSXXXXCPXGXXXXXXXXXXXXCRYXXXXXXDXXLSXXGCXXXCXXEXXXXXCCXGYWG
XXCXECPGGXXXXCXXXGXCXXGXXXNGTCXCXXXXXGXACXXCXXXXXFGPXCXSVCXC
XHGICNXGXXGDGXCTCXXGYXGPXCDQXXPXCXXXXCXXNSXCXVXXXDXXQXXCXCLP
XYXXXGXXCXXXXPCXXXXCXXXAXCXXLGPXXXXCTCXXGYXGDGXXCXPIXPCXXXXG
XCPXXSTXCXXXXPGKXXCXCKXXXXXXXXXXXRRXXXCXSXXXXCXXXNXXXXXAXCXXX
XXGXXXCXCQXGXXGDGXXCYXXXXXXIXXXNMXPXXXXXLXXAXAIFGKGCXXXLXXYG
PFTVXLXTXTIFPPFHISPRIPVTTMXSXHWLLAWXGLXXXXXVFXLRDTKEMGEYAKSG
IPVFSIELNTLXXXPXIXKXXHPRATEAXTKYFLXQXXAAXXILXAXTXNAWXTGQWXIX
XXXXXXXXXXXXXAXXXKLGXXAPXHXWYPXXXVXQGXTXXTALXXSTWREITAQKXAPL
XXLXGQXXXXXXXXXXXLXXGLXSXXXXXXGELYLIEPLKFPXXXXXXXXRXSYXGGXX
GLNQTQTRKIXAXSSIAHMGWLXXAXKKASXXXXXLXTLTXXXYXXXTXXXFXXLXXXXX
KTXXDVXLXXLXXXWXXXPXXXXXXXXXLXSLGGLPPLTGFXPKXLIXXXLXXXXLXXXX
XXXXXXXLXSXFXXHLSLXRXDTXYXXXAALTXPPXTXXXXXQXXXWRXXXXXXXXXTAI
NFQGNIIGRAYTXXXXVXXXXXXIXAXNGXIXXXXXXXXXXXXXLPXXPXXXXXXXXXXX
XGXCXXCXXLXXELSFEFSXCPXXSXXXXXXXFPXDXXXCXYXXXXLGLNXXXXGCXXXC
NXTXXXPXCCKGFFGXXCXXCPGGFXNPCXGXGXCXDGXXGNGXCXCXXXFXGXXCXXCX
XPNKXGXXCDXXCXCXXGXCDNXXXSXGXCXXGXCKXGYXGXXCDXXXXXCXXXDXAXXX
CXXXAXCXXXXTGXXXCXCXXGYEGDGXXCXXXDXCXXXXXXXCXXNAXCXXTGPGTXXC
XCXXGWTGXGXXCXXIXNCXXXXXGGCHXNAXCXYIGPGQXXCXCKXGXXGXGYXCXPXX
XCXXXNXXCHXLAVCQLXNXXKEDETCLRKYXGDGXXCYGXXMXELXXXXXXXXFXEWXX
XXXXXTXXXXXXNXTXLVPXXXCSKNSLASRQSFWAELNVARLDHQNVVRXIAASTCSPA
GQDSLTGTIIMEYVGNSTLHHVIYGTXWXTXKRKXXXIXXAXIXXGDIXAXNXXIXXID
KVLFLXPXXXXIKRCMXDMHQXLSFGPXYGXLSELQXGEQFLEXIEKERKTTTFXIGGHS
IEXNTRPPNLYKLDXDXXXYHXXLGXKLLXXDLXNGXXXXTMLGXSXXXXFXXXXXQXYX
NXXXXXXXXVXTXXGXXXGXXXVXXIXKNRCXXNXTXXXXXXCXXCXLXXXXCPXGSXXA
XXPXXGXXXXCXXXXXXXXXXXXGCXXXCXKXXXXXXCCXGXYGXXCEXCPGXXGXXCXG
NGXCXDGIXGXGXCXCXXGXXGXACEXCXXGXYGXXCXXECXCXXGXCNXGXXGDGXCKX
CXXGXXGVXCLKAXXXXXXDXCNXTCXXXANCXXXXTXXXXXCXCXAGXXGNGTXCTXIX

XCXXXNGGCSXXAXCXXXXPGXRXCXCKXGYXGDGXXCXEIXXCLEXNGGCXXNAECXXX
GPXXXACNCLXXYXGDGXXXCXXXXXCXXNNGGCXXXAXCXXTXXXXRXCXCXXXYXGDG
FTCXGXXXXEXLXXXXXXXXFXXXXXXXXXXXXXXGXGPXTVFXPXXXXXXXXXXXXWX
XKGXXXXXLRYHIVXCXXLLXXDLXSXXXXTXLXGXXXKXXPXEXHXXNNDXXKXAASXX
XVXXGVIXXIDXXLXPQXPFHXXXXLXXGXXXXXXXXXXXVXDKXXXXXXQXEXEXHXVX
XXXXCXXXGGISVSSXXXXXXKRSHPVHGPVDXXXXXLDDEMQXLLXKKEXXATSWPDLL
XKXIXXXXXMFKXDVXXPRXDXDTIHPTXFCHXCXXDXXXXGXXXXXXXXXXIXQRXXHH
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RAQXXMYXRSQKQXNSKXXMKKITXCKKIHLSTKMLTXDYPXDFVKSISCQICEHILADP
VETXGXCDXGXXGXGXCXCNXXFXGTXCEXCXPGXYGXXCKXCXCTXXGXCXEGXXGXGX
CFCXXGWXGXXCETXLAXXPXCSPXCXXNAVCXXXXXXXXXXXXXPXXXXXXXLXXXXLX
XXXGXXAXHDNICXCXXXXXGXGXXCXXXXXXXXXXXXXXXXXXXXQXGSXXXXXXVXX
XCXXXYXXDGXXCXPXXXPXDFTDEHDPXXXXXXXXKVXXXXXXCXEXAXXXXXGXXXXF
TXXGXXXGXXXXXXXXXHXXXXSLXXXXXXLXXAXGXYXLXSCXXXXXXXGLXFLHXXXX
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XXXXDXYCXXXXXXXXXXFXXXXXXXGXXXNSSDXWXXXXXXXXXCXXVXXXXVXLXDXS
TEMNSTXXXXXXXXXXXXXXXXXXXXGXXXXXDGSXXXXXXXGCGFGVXXTAXXXXXXX
XPXXXXXSXSAXXRXTXXPXXXXXFGXXXXXXXXXALXXXXXXXXXXFXXXXXXXXXXX
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XXHRXXFDDDDXGXXXXXXXXXXXXXXXXXXNXXXXLEWXXXXXXXXXXSPXXAVXXXXX
VKNXXSXXXXXXXXXXXXXXXXEVXYSTNXXXXXXXPXXXXXVPXGXXXXXSXXXXPXLLV
YRGXXXXXXYXXXXDVLXXGXXSNFXXXTEQFXXTEESPTAXSSSDDXFXQEXXXXXXXX
XXGXXXXLXXXXXXXTAXXXSDXLHXXXXPSXXXEXXLEXXSXHHXXXXXNXSXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXTNRTILQVXXXVXXXLXXPXEXXXENXSSQXX
SXXVDEQPLQPSETTGHQEEKETSNESSTVSITQTNKEKQXLDXXTXDQGQSPAXPRXXX
XSKWSKIKIVTKQPSGVDVYXXNXXXXEXXXXXXPXXXXXXXXXPXXXXXXXDXXXXXXX
XVSXXXTXXEXXXXXXAXXXXXXXXXXXXDVXLHXXHSXXXXEEXXSGVTFIDTKLFEVT
TPSPXXEXGXXXXXXXGLPXTNTSXXXXLPGIXXXXXXXXXXXXXXXXGXXXXXTXXXXXX
SXXXGKXXXTTQXPHFYXXHPGXXXXXXXTXNXTXDXXXXXIXLXXEXKXEXETXXTXXX
XXXXXXXXXSXXDXXXHXXXXXDXXXGPXFEDXIXLXXXXXXXXEPETLHFVNQEETMSL
LDIAGKDTVLKQSSQHSEEASELRGHEAVTLSPXXXXXXXPGXXXXXXXXXXPEKTXXXX
XEXXXXXNXSXXXXXPGIXXXXXXXHXXEXSHXXXXSSXDXKXXHEXXXXXPXXHDXXXE
XGREDXYXTNXTXXXXXXXXXXIPPTGTXXXXEXXXXXXIXLXNTKKGAXXTADKDXXXS
TXXXLXGKXXXXXPXXXXPXWXXEEXXPXNXXRXXXXXXXXXXXXEHXXXXXDXXXHXX
XKEDXTXEPVXQWXXEDXYTTXXXXDVLXPGIVPRRGIXQKNXTDHTXXVPPIYILLIID
LTIVTPVXXSXDGXKXEESTQXPXXHGLXRLVWAQEMNXXLLXETXXXXXXXXXXXXXXX
XPXXSXXXEPLVNXTXDXXXPXXXXEXXSXXXXXXXXSXXRXXXSTAXXXXXXXXXXXXX
XXKXXFCXXXXXXCLKXXXXXXPXXXCRYPCFPXXXXXXXXXXXXXLXXLAXXLGVCXXX
NSRXXCXXKXKLXINNGKGGIXEKXXGGLNGEXXXXXXXXHLXXXXXXXXXXTXXSXXXX
XXWXGLXDRXXEXDFXWXDXXXLXYENWXXGXXDEFXAIDETQNXXXXXXXGXXQXVXLK
SXXPXXGXGXXXXCXXPXXXMYGSXXXXXXGXXFGXGXGXXXXYXXGXGXGXGXXXPXXXX
GXXXXXXXXXXXXLGXXXPXIXXGXNGXWXXPXXXCXXQXPXSEVXIQPPPXXVXXPGPX
LXAXXEPXRVGGYTXCXXXXXXXXSSXXXXXSXXXXXXXXXXXXXSFXXXXXRXGSXGGC
XRGXLILGXXXXGXXCXXPXN

==> Bivalvia.txt <==
>MSA Consensus of 208 seqs, protein
MXXXXXXCLLYTIVYCIPYVCGIVYCIPYVCGIVYCTPYVCGIVYCTPYVCGIVYCTPYV
CGIVYCTPYVCGIVYCTPYVCGIVYCTPYVCGIVYCTPYVCGIVYCTPYVCGIVYCTPYV
CGIVYCTPYVCGIVYCTPYVCGIVYCTPYVCGIVYCTPYVCGIVYCTPYVCGIVYCTPYV

CGIVYCTPYVCGIVYCTPYVCGIVYCTPYVCGIVYCTPYVCGIVYCTPYVCGIVYCTPYV
CGIVYCTPYVCGIVYCTPYVCGIVYCTPYVCGIVYCTPYVCGIVYCTPYVCGIVYCTPYV
CGIVYCTPYVCGIVYCTPYVCGIVYCTPYVCGIVYCTPYVCGIVYCTPYVCEIVYCKPYA
CWIVYCTPYVCEIVYCIPYVCGIVYCIPYVCGIVYCTPYVCGIVYCTPYVCGIVYCTPYV
CGIVYCTPYVCGIVYCTPYVCGIVYCTPYVCGIVYCTPYVCGIVYCTPYVCGIVYCTPYV
CGIVYCTPYVCGIVYCTPYVCGIVYCTPYVCGIVYCTPYVCGIVYCTPYVCGIVYCTPYV
CGIVYCTPYVCGIVYCTPYVCGIVYCTPYVCGIVYCTPYVCGIVYCTPYVCGIVYCTPYV
CGIVYCTPYVCGIVYCTPYVCGIVYCTPYVCGIVYCTPYVCGIVYCTPYVCGIVYCTPYV
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CGIVYCTPYVCGIVYCTPYVCGIVYCTPYVCGIVYCIPYVCGIVYCIPYVCGIVYCTPYV
CGIVYCTPYVCGIVYCTPYVCXXXXXXXKYRXAAYDDNYVCGXXXYRXXXXXRVYCTPXX
XXXXYXXXYXXXXXYXLPYAXDXXYXXXYXXXXXYXLPYAXDXXYXXXYXCRXXYXXXPX
XXLVYAXXXXXRXXYXXXXXXRIVLXXXXXXRXXYXXXXVCGIXXXXXXXXXXXXXXXXX
XXRXXXXXXXXXTPYVXXHVXXXXXXXRXXXXXXPEYRLAADDNYXXXYXTXXXXXXXXA
DXXXRXXXXXXXXXXXXXGXXXXXXXXXXRXXXXXXXXXXXXXXXXYXXXXXXXXXXXXX
XRXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXLXXXLX
GSASXXXXXXXXXXXXXXXXXXXXXVXXXXXXXXXXXXXXXXXXXXTPKPXXXXXXXPXX
XXXXXAXPXXWTAWKAPPPXXXXXXXXXXXXXXXXXXPXXXXAWKATXKXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXAXXXYXXXXXXXX
XXXLXAXXXXXXXXXALPEYRLAADDNYRSIYRALPEYRLAXXXXXXXXXXXXXXXXXXX
XKPXXXXXXXXXXXXXXXXPXPXXXXXXXXXXXXXXXXXXXSXXXXXXXXXXXXXXXX
XXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXXXXXXKPWXXRXXXXXXXXXXXXIXXXL
XLXXXXXVXSDAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXXX
XXXXKXXXXXXXXXXXXYXXXXXXXXXXGXYXXYXCXXXXXXXXXXXXNKXXXCXXXXXX
XXXXXXXXXXXXXXXXXXPXXGGYXXXXGXNXGWXXXCXXXGXXXXXXXXXYXXXGYXXX
XAPXPXXXXXXXXGXXXXXXXXXXXXXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXRXXXXXAXXXXXXXXXXXXXCXXXXFXDXXXXXXXXXXXXXXXXXXEGXXXXXXXX
VXXXXXXXXXCXXXGXCXXXXSXXYXXXXXXXXXGXXCXXXVCKPNPRKNSGRCVNKGSS
YNCICKGGYSGPTCGVNXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPTCGEXX
XCKPNPXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXPVYKPVXXSYXXXXXXXXXXXXXXXXXPXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXSECXHXXXXXXXXXXXXXXXVYKXXXXX
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XXXXXXXKKLSSXXXXYXPXXXXPCKNXXKXXXXXXXXXTXYPPVYXXXXXXPPTXXXXX
XYPXTXXXXXXXXXXXKPKTTYPPTYXXXXXXXXXXXXXXXYPSXXXXXXXXPXXXXXXX
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XXYPXXXXXXXXYXXXXXXXXXXXXXXXXXXXXXXTTHPXXXXXXXXXPXXXXXXXXXP
XXXXXXXXXXXXXYXXXXXXXXXYXXXXXXQGPPSNQGTNTHKSSTKXXXXXXXXXXXTX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPXXXXXXXXXXPXXXXXXXXXXXXX
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XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXYXXXXXXXSYPXXYXXXXXXPXXXY
XXXXXXXXXYXXXXXXXTXYXXTYKXXXXYXPTYKXKXXYXXXXXXXXXXXXXXXXXXX
XXXXXXXXXYXXXXXXXXPXXXXXXXXXXXXXXPTHTRFXXXXPXXXXXXPXXPXXXX
XXXXXXXXXXXXPTXXXXXXXXXXXXXYXXXXXXXXXIXXXXXXXXXPPXXXXXXXXXX

XXXXXXXXXXXXXXXXXXXXXXXXXXXXLDXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXLXXXXXXXXXXXXXXXXXXXXXXXXXYXXXXXYXXXPXXXXXXXXXST
XXXXXXXXXXDXXXXXXXPXXXPXXXXXXXXXXPXXXXSHTXXXXXXXPXXXPGQRPPTH
XXXXXXXXXXXXXXXYXXXXXXXXXXXXXXXXXXXXXXXXXXXXPXXXXXXXXXPXXXXX
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PXXXXXXXXXXXXXXXXXXXXXQXXKLSMFXXXXXXXXXXXPXXXXXXXXRGXXXXXXX
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EVKPSEVKLXXXXXXXXXXPXXXXXXXXXPXXXXXXXXXXXXXXPXXXXXXXXPXXXXX
XXXLQQPXXXXLXPXXXSXXXXXCXXXXPXXXXXXXXXXXXXXXXXXXXXXXXXXXLXX
XXXTPYRASNCPCDXXXXXNPXLXXXXXXXXXXXXXXXLXXXXPXXXXXXXXXPXXVKPS
EVKPSXXXXXXXXXXXXPXXXXXXXXXXXXXXPXXXXPXXXXXXXPXXXXXXXXXXXXX
XXXXXXXXLXXXGXPXXXLXXXXXXXXXXXXXXXXXXXPXXXXXXXXXXXXXXXTTXXXX
XXPXXXXXXXXXLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXPXXXXXXXANPXXXXXLXXXXXXXXXXXXXXHXPXXLXXI
XXXXXXXXXXXXXXXXLXXXXXXXXXXXXXXXXXYXXXXXXXXXXXXXXXXXXXXXXXX
XXXXQXXXXXXXXXXPXXXXPXXIXXXXXXXXXXXXXXXXXVSFXXXXXXXXXXXKMXXXXX
XXXXXIXXCPSYLDYISHCPSYXXXXXXXXXXXXXXXXXXNXYXXXXXXXXXSXXXXXXXXP
XXXXTLITXXXXXPXXXRXXXXXXPXXXXXXXXXXXYSXPXXDPPPXXXXXXXXXPXXXL
XPXXXXXXXXXPXYXXXXXXNXXXXPTYXPXXXXXXXXXPXYXXXXXXXXXXXPXXXXXX
XXXXXXXXXXXXXPXXXXXXXXXXXYXXXIXHXXXXXXXXXXXPXYXXXXXXXPSXXDXX
XXXPXXXXXXXXXPXXLXXIXHXXXYLXXIXHXXXYLXXIXHXXXYLXXIXHXXXYLXXI
XXXXXXXXXXXXXXXYXXXXXXNTXXXXXYXXYISHCPXXXXXXXXXXYLXXXXXXPXX
XXXXXXXPXXXXXXXXXXXDVPXXXXXXXXXXXXXPXYXXXXXXXXXXXXXXXXXPTXXL
PXXXXXXXXXPXXXXTXXXXXXXXXXYXXXXXXXXXXXXXXXXPXYXXXIXHXXXXXXX
XXXXPXYXXXIXHXXXXXXXXXXXPXXXLPPXXXXXXXXPEVSLXXXXXXXXXXXXXXXX
HXXXXXXXXXXPXXXXXXXXXPSXXXXXXXXXXXXXXXSXXPSXXXXXSXXPSXXXXXS
XXPXXXXXXXXXXXXXXXXSXXPXYXXXXXXXXXXXXXXXXXXXTXXXXXPXVEYXPXXX
XXXXXXPTIXXXPXXXXXXXXXPXYXXXLXXXXXYLXXXXXXPXXXXXXXXXPSYLPXIX
XXPXXXXXXXXXPXYXXXXXTXXXXXPXYXXYISHCPXXXXXXXXXPXYXXYISHCPXLX
XXXXXXPXYXXXLXXXXXXVPXXLDYISHXPXXXXXXXXXPXYXXXXXXXXXXVPXYXXX
ISHCPSLXTXXXXVPXXXXXXIHCXXXXXXXTXXPXXXXXXXXXPXYXXXLXHCPSYLXX
XXXXPXYXXXISHCPSLXXXXXXVPXYXXXLXTXXXXVXTXXXXXXNXXXXXXXKPTLI
XNTADVPTP

==> Bovidae.txt <==
>MSA Consensus of 133 seqs, protein
MAGPRGHLLLCFLALCLAGPSFFGEQKGPGPXLQSVILFFLGLVVQNLGDLPDQGIEPVL
XXLXXXXXXXKRCDXKXXXXXXXXCXXCXXXXXXXCPXGXXXXXXXTXXXXDCRYXXXXX
XXXLSMSGCSLECWKDMVQKACCPGYWGSQCYECPGGAETPCSGHGTCLDGLDGNGTCVC
QENFSGSACQECRDPNRFGPDCQSVCRCVHGVCRHGXXGDGSCLCFAGYTGAXCDQELLA
CQALNCPRNSQCSEESKDEIXPSCSCLPGYTQQGHECXASDPCRPSPCSPLAQCSVGPGG
QAQCRCPENYHGDGTVCLPQDPCTTNNGGCPSNSTLCLYRKPGQASCLCKPGLVSIXHDX
SAGCFAHCESAFSCDRSATCQVTPDGKTSCVCKEGEVGDGRACYGHLLHEVQKASQEPRT
SMLLRLRVTFXXLDXGXXXXLSXXGPFTXXXSNXXXXXXXXXXXFDVLXPXXXXRKXXXX
XXFXXXXXSSXAQXXXXXHIIPXXAGQXXXXXXXAXRXXXXXXXXEXXXTXXTQXXXXXX
TLXGXXXXXSXFXXXXFSXXXXXXXXXKXXXXXXXXTXXIHKXNXXAANGLXHXXTXXXX
QPPPELPEDPKRTIGQILASNEVFSRFETILENCGLPSFLXEDGGXGPXTVFXPSXEAXX
XXXDGXLXYLFXXXXASIXRXXXXKSAGXXXKLXELXRYHXXXXGQLXVEXLLSXXXXXX
MANQILXXNIXXXGXILXXSPXXXXXXXGPXGVXLXXXXVXAXNGXIXXLXGVLXPPXIX
PILPXXCNEXXXXVXAGSCVXCXXXXXSXCPXXSXXXXXXXXCXYXXDPTGXXXXKXGC
AXYCNXTXXXXSXGSAXXCXCXXXSRXTXCXXXSXPPXCCKGFXGPDCXQCPGGFSNPCX
XXGWSPWXEWTXGXGXCXDGXQGXGXCLCFPDYKGIXCXXCSNPNKXGXXCXXXCXCXXG
XCDNRXXSXGXCXXGSPWSSCSVTCGXGXXTRIRLCNSPXPGXXGRFCXXXTXXCGXXEQ

XQXCHXHXXCXXPXXPXGXXXCXCXXGXEGRXRCTSRNXCNXPXPXXGGKDCVGXXXEDG
XXCXXXDPCSXXXXGGCSXXAECXXXXRGXHXCXXCXXGWXTSAGDGRXCXXXDECXLXX
XGGCXXHXXAXCXYVGPGQXXCXCKXGFXHCVTDGXXXXGVGXXXAXTQGGXGXVCXPIX
PCXXXXXXCHXLATCXXXGGXXXXXPCXXXYIGDQMRGCKMERNCRDPELNPXXXXAXCI
YLGHXXXGXXXCXCXXXYXGDGXXCYGDXXXELXXXXXXSVFYQWIKGAGIXHLLXXXSX
XTALVPSESAIRRLSTEDQAFWLXXXXXPXLXRAHFLQGXXXXEXLXXLHGQNVSTLNLP
XVXWEIHNVSGRXXXXXASVDXXDXXATNGVXHXXXXVLXPPRXDVXGGQXLLXQLDXXP
XXXXFRXXXXXXXLXXQIEAAXAYTXFXPXNXXXEXXAREKNSSSLDSDVVRXHVILGEA
LSXEALGKGGHRNSLLGPAHWLVFYNHSGQPEVNHVPLEGPVLXXXXXXXXGLXXVLXXX
XSRCLHXXXXXXRXKCXXCXXXXXCXXGXXXDXXXXXRXXCXYXSGYMGRRSFXRGCSYT
CAKKIQVXXCCXGXFGXXCXPCPGXXXXVCXGXGXCXXXXXGXGXCXCXXGFXGTACEXC
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XGXXGDGXCXCXVGWXGXXCDXXIXXXXCXXXCXPXANCVQDSAAAPVCVCAAGYSGDGV
SCSAXXTPPPCXXXXGGCSXHAXCXXXXPGXRXCTCXXGYTGDGXXCXXXXCPEXNXXXX
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XXLXXXXXXXXAXKVNLXTXLXGXXLXXSXXXXXXXXXXLXXXXXXXXXXXXXXXXPXXX
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XKXTIXDLPXXXPXXTXXXXXASXXXXXXXXXGXXXSXXCXXXXXXGXLXXXXXXXXRIV
QRXLXFXXGXXYGIDXLLXXPXLGXXXDXFXAQQXTXXXXPTXXXXLXXXXDTXXCXXXX
PXXXHXCXXXPXCXXXPXXXXXPXXXXXXXXXXDXXGXXXXXXXXXXXKFWTSPXLXXXXL
RSVQPGSEWTRPXVAVXWGXXXXXXXGCXXXCXXXXXXPXXXXXXXXXXXCXACPGXXXX
PXXXXXXCXDXRXSQGGSXSXXCXXXXXXXXFXGTACELCXXGXXXVYTISVLXXXXXDX
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XXXXHXXXXXTGPXXXXXXCXXXYVGDGLXXXXEPXXPXDRCXXXXXXXXXXAXAXXXXX
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XSMVHPSPDQXXXSXXXXXXXXLNXXXXXXXXXXXXXXGAXXPAHSGXXLXIGXXXPENTS
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VINNGNGTMEERKPSCAGGKCPSLGRGPIIATIVTVLCTPPXXXXXXXHTPTCXPXPXXX
XVXEEIQIGXXXXXXXLLLFLAGVGLNGEASKSQEMVXXGVWGYRSCQHKSSVYKLHLV
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GXXXXXDDSCFDPYTVSHYAIGDETRNLQNVDMKIGVXCLGXGXGHXXXXSXKXXXDXGX
NYXIXXXWXXQGENGQMMSCTCLGNGKGEFKCDPHEATCYDDGKTYHVGEQWQKEYLGAI

CSCTCFGGQRGWRCXXXXRXGXEPGNEXXXXHXXXXXSQRYHQRTNTNVNCPIECFMPLD
VQADREDSRE

==> Bovinae.txt <==
>MSA Consensus of 129 seqs, protein
MAGPRGHLLLCFLALCLAGPSFFGEQKGPGPXLQSVILFFLGLVVQNLGDLPDQGIEPVL
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XXXLSMSGCSLECWKDMVQKACCPGYWGSQCYECPGGAETPCSGHGTCLDGLDGNGTCVC
QENFSGSACQECRDPNRFGPDCQSVCRCVHGVCRHGXXGDGSCLCFAGYTGAXCDQELLA
CQALNCPRNSQCSEESKDEIXPSCSCLPGYTQQGHECXASDPCRPSPCSPLAQCSVGPGG
QAQCRCPENYHGDGTVCLPQDPCTTNNGGCPSNSTLCLYRKPGQASCLCKPGLVSIXHDX
SAGCFAHCESAFSCDRSATCQVTPDGKTSCVCKEGEVGDGRACYGHLLHEVQKASQEPRT
SMLLRLRVTFXXLDXGXXXXLSXXGPFTXXXSNXXXXXXXXXXXXFDVLXPXXXXRKXXXX
XXFXXXDPXSXAQXXXXXHIIPXXADXXXXXXXXAXRXXXGQXXXEXXXTXXTQXXXXXX
TLXGXXXXXSXFXXXXXSXXXXXXXXXKXXXXXXXXTXXIHKXNXXAANGLXHXXTXXXX
QPPPELPEDPKRTIGQILASNEVFSRFETILENCGLPSFLXEDGGXGPXTVFXPSXEAXX
XXXDGXLXYLFXXXXASIXRXXXXKSAGXXXKLXELXRYHXXXXGQLXVEXLLSXXXXXX
MANQILXXNIXXXGXILXXSPXXXXXXXGPXGVXLXXXXVXAXNGXIXXLXGVLXPPXIX
PILPXXCNEXXXXVXAGSCVXCXXXXXSXCPXXSXXXXXXXXXCXYXXXPXGXXXXWXVX
SXGSAXXCXCXKXGCAXYCNXTXXXPXCCKGFXGPDCXQCPGGFSNPCXXXGWSPWXEWT
XGXGXCXDGXQGXGXCLCFPDYKGIXCXXCSNPNKXGXXCXXXCXCXXGXCDNRXXSXGX
CXXGSPWSSCSVTCGXGXXTRIRLCNSPXPGXXGRFCXXXTXXCGXXEQXQXCHXHXXCX
XPXXPXGXXXCXCXXGXEGRXRCTSRNXCNXPXPXXGGKDCVGXXXEDGXXCXXXDPCSX
XXXGGCSXXAECXXXXRGXHXCXXCXXGWXTSAGDGRXCXXXDECXLXXXGGCXXHXXAX
CXYVGPGQXXCXCKXGFXHCVTDGXXXXGVGXXXAXTQGGXGXVCXPIXPCXXXXXXCHX
LATCXXXGGXXXXXPCXXXYIGDQMRGCKMERNCRDPELNPXXXXAXCIYLGHXXXGXXX
CXCXXXYXGDGXXCYGDXXXELXXXXXXXVFYQWIKGAGIXHLLXXXSXXTXLVPSESAI
RRLSTEDQAFWLXXXXXPXLXRAHFLQGXXXXEXLXRLHGQNVSTLNLPXVXWEIHNVSG
XXXXXXASVDXXDXXATNGVXHXXSQVLLPPRXDVXGGQGLLQQLDSVPAFHLFRELLQR
HXLVXXIEAAXAYTXFXPXNXXXEXXXXXKNSSSLDSDVVRXHVILGEALSXEALGKGXH
RXXXLGPAXWLXFYNHSGQPEVNHVPLEGPVLQAPGRSLFGLSGVLXVGSSRCLXXXXXX
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XXXFGXXCXPCPGXXXXVCXGXGXCXDDGITXXXGXGXCXCXXGFXGTACEXCXXGRYGX
XCXXVCXCXHGXCXXGXXGDGSCVCNVGWQGLRCDQKIXGXXCXXXCDXXANCVQDSAAA
PVCVCAAGXXGXGXXCXAXXNXPPCXXXHGGCSXXAXCXXXXPGXRXCXCXDGYTGDGXX
CXXXXEXNXCLXXHGGCHXXXHAECXGDXPTGPXQVSCXCXXXXXGDGXRXCXXXXXCXX
NNGGCSXXAXRXXQXXXXXPXXXXQMDTFWWRAAWGLCLVQLSTCXCXXXLAQIDLNITC
RYAGVFHVEKNGRASXYSISKTXXXXEAADLCKAFNSTLPXXAXSESGYQXXXXXQMEAA
RXIGXXXXXCRYGXIXXHVXXPRIHPNSICAANNTGVVNLKECLQSASYILTSDPXXXXX
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XSXPXXXPEASLQTXXTTRMTDVXXXSXXXCXXXXXXXWTXXPXXSXXXLXXXXXXXVQX
XXWTRPXXXXHPXXXXXXXXXGXXXXCXXXXXXPXXXXXXXXXGXXYXFXXXXXXXXXXX
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TPGXXGPXCQXXXXXXXCXXHGXCDXGXXXXGXCXXXXPLXNLQPGSEYAXXXXGXXXXE
ETXHXXXXQXXXXPXXAXXDLLFXCXXPPCXXXAXXXXGLHXXXXEXXXXXXXXGXXGXX
VVXTVXXXXXXXXGXXXXXEXXXSXAGTXVXXXXTPGVXYVYTISVLRDGQERDAXIXXX
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XLXXXXXXXXXXXGXXXXXXGXXXXXXXXXPXXXXXXDGRXXCGXXXXXGGAGSAGAGGG
XXGGXXPXXXXXSVXSSPVPXXXXXXSXVGXVXXGXXXXXDTXEXXXXXCXXXXXPXXXX
XXXXCXXPXXPTKTGSPGVTEXXXXGXSXXXXXXXXXPXXYXXXXEXAXXXXXXXXXXXYG
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PXXKPQIPEXLXXLASLXXXXXXXXVCXXVNSRRRCGQKKRHKLVINNGNGTXEERKPSG
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XLXXQXXXVXXXXXXVGXXXXQGXXXXXDDSCFDPYTVSHYAIGEXMEKVXXXGXXLXXX
CLGXGXGHXXXXSXKXXXDXGXNYXIXXXWXXQGENGQMMSCTCLGNGKGEFKCDPHEAT
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QRYHQRTNTNVNCPIECFMPLDVQADREDSRE

==> Brevundimonas.txt <==
>MSA Consensus of 183 seqs, protein
MTAAYGEAWQAVLNNHDPDWDAGCLPTXXXCXXMMXXMXXXXXXXXXXXXXXXAXXXXXX
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YTGXVSXDGGRQITXGASLMAXXALAKAGAXXVERYDTSVSEXELRYANNXLIGDXXXAX
XXXTXXXXXXXXXXXXXXXXXXYXVGGXXXXXXXXXXXXXXGYXXXXXXXAEEXXXXXX
XXGXXXXXXXVMXXXXXLXXXQXXXXXXXAXXXXXXXGXXXXXXXXXXXXXGXXXXXXXX
XXXXXXXXXXXQXXXGXXXXAXXXXXXXXXXXXXGGXXXXXAXXNXVALXGXGTGXQXXX
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XXXXXXXXNXXXXXNXGXXXXXXXDXXXXXXXRDXXXRXXXXXXGXXXXXAXXVXNEXXX
GNNDIYXXXDNTQXNXGGVXAXAXXXGXGSGXGYDAYVGXXAXGNXVTGXACSXCXGGXX
XXXNXQTNXGXVXATXXXTXXXXGRXXXXGANAVGNXAXFYVXRPGXXXXXH

==> Burkholderiales.txt <==
>MSA Consensus of 119 seqs, protein
MXXIXADGGPAFGQVVELSPDGIRRVLIEGDRIFTGEQILTGAAGSVSLALERCVRVEMX
GXTEWEPEAPDIAQPSDDAVDGAPSIAELQQTIIAGADPTQSLEATAAGEQISGDTSDAG
DSHSVTTPVVLQETAGVVDPAVGMPTGTFDGARSNNSEFLGAPDRNTQPAQVPTNTAATP
AAAVDTASSDTSTAPVDPPASGDTSNAGTTTPGTATPGDTTTPGTTTPGDTTTPGTTTPG
GTTNPGTPTPGGTTNPGTTTPVDTTTPGTTTPGGTTNPGTTTPGGTTNPGTTTPGGTTNP
GTTTPGGTTTPGTTTPGGSTTPGTTTPGGTTSPGTTTPGGTTSPGTTTPGDTTTPGTTTP
GGTTTPGTTTPGGTTNPGTTTPGDNTTPGTTTPGGTTTPGTTTPGGTTNPGTTTPGDTTT
PGTTTPGGTTTPGTTTPGGTTSPGTTTPGDTTTPGTTTPGGTTTPGTTTPGGTTSPGTTT
PGDTTTPGTTTPGGTTTPGTTTPGGTTSPGTTTPGDTTTPGTTTPGGTTTPGTTTPGGTT
SPGTTTPGDTTTPGTTTPGGTTTPGTTTPGGTTSPGTTTPGGTTTPGTTTPGGGTTTPAN
KAPLLDLNSTDGATTTGNAFSVNQGASGVAIAPSVSLSDDGTTLKNVTLDVTSHQTGDKL

DTSAISGAVKVDDVSSTATHVVLISSDAANPATVAEFQAAIAAITFSTTSAGTPRTISVT
ADDGSATTTANSVVTVAPINSLTLSADVAAVAENGTVTYTATLGQPASAALTVTLSNGQS
IIIPKDATSGSXXXTXXXDXYXXXPLSXTXXXTXXXTXGGXFXXLXXXXXAXXTXXTDXX
DTTTXXXVSTXXXXVXEGGXXXXXXXLXNKAXXDVTVTXXXXXGSVTGSKNVTIASGSSN
AMYTVDVPDNTGIGSNADLVVTLSNPAGGKFESLILGTATVTTAIGDNDRASELTADTNL
TTPEDNAAIGNVLSNDKAGTIGLSVSTFSVDGMTGTFNAGTTAVPITTGSGSTASTIGTL
TLSSTGAYVFTPIANWNGTVPTITYTTAEGASQTLNISIQAVNDAPVLDLNSADGSATTG
NAISVSQGGAAVAIAPAVSLSDIDSNSAKSVTIAIQGTHIAGDTLVIGSGVPAAVKAELS
SDGSSVVLTSTDATTPATLAQFEAAIAAVNFSTTSVGVPRTINVSVDDGSNSGTSTSTAS
TVVNVTAVNHLTLSADVATVAEKGAVTYTVTLDRATDTALVVQLSNGQTINIAKDAISGT
SLPFAVGNDAWTGAPELSVTISSYSGGSAAANLSITPTPAVTTVTDAIDTTSISIISTDT
APVIEGSTAHFQLNLSNKAEADVTVTVSYSYGSVTGTKDVTIASGSTSATYTVDVPENTT
VGVNPSLIVTLSNPAGGKFESLILGTASVTTAIGDNDRASELTADSNLTTLEDNAAIGNV
LTNDKAGTNGLSVSTFSVDGMTGTFNAGSAAVPVNVGASNIGTLSITSTGAYVFTPTAMX
HGGVPTITYTTAEGASQTLNISIQAVNDAPVLDLNSADGITTTGNAISVSQGGAAVAIAP
AVSLSDIDSNSAKSVTIAIQGTHIAGDTLVIGSGVPAAVKAELSSDGSSVVLTSTNATTP
ATLAQFEAAIAAVNFSTTSAGAPRTINVSVDDGSNSGTATSTASTVVNVTAVNHLTLSAD
VATVAEKGAVTYTVTLDRATDTALVVRLSNGQTINIAKDAISGTSLPFAVSNDVWTGAPG
LSVTISSYSGGSAAANLSITPTAAVTTVTDAIDATSISIISTDTAPVIEGSTAHFQLNLS
NKAEADVTVTVSYSYGNVTGTKDVTILSGSSTAQYTVDVPENTTVGVNPSLIVTLSNPAG
GKFESLTLGTATVTTAIGDNDRASELTADSNLTTLEDNAAIGNVLTNDKAGTIGLSVSTF
SIDGMTGTFNAGTTAVPVTTGSGSTTTNIGTLTLSSTGAYVFTPTANWNGSVPTITYTTA
EGASQTLNISIQAVNDAPVLDLNSADGSATTGNAISVSQGGAAVAIAPAVSLSDIDNSSA
KSVTIAIQGTHITGDTLVIGSGVPAAVKAVLSSDGSSVVLTSTNATTPATLAQFEAAIAA
VNFSTTSAGAPRTISVTADDGSGSDTAISTANSVVTVTAVNHLTLSADVATVAEKGSVIY
TVKLDRAADSDLTVLLSNNQTVTLVKGAISASSLPFTVGNDVWTGAPELSVSISSYSGGS
AAANLAITPTAAVTTVTDAIDATSISIISTDTAPIIEGSTAHFQLNLSNKAEADVTVTVS
YSYGNVTGTKDVTISSGSSTAQYTVDVPENTTVGANPSLVVTLSNPAGGKFESLTLGTAT
VTTAIGDNDRASELTADSNLTTLEDNAAIGNVLSNDKAGTNGLSVSTFSIDGMTGTFNAG
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XXGXXXXXXXXXXXXXXXXXIXXXXXXXXXXXXXXGFXXXLXXXXXXXXXXGXXGXSXXT
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SXXXXLXXXXXXLXXXXXXXXXXXXXXXXXXXXXXXXXXXXLXLXXXXXXPGXXXXXXXXX
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XVXAXXVGNAYGLPAGXHVMELERLAGDPSDXXXXXGGLVGXNXXGXXXXXXXXGXVXGX
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NGIADXXPXXXXXXXXXXXRAVXXEELQXPXXXXXXXXWXXXXATSKLXXXAXXXAXXXY
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WXAXXXXXXXXXXXXXXGXXXXXXXXXXXXGXXXGXXXXXXXXXXXXXXXDAFKTAANFFT
SSTATSNTGXXNXXXXXXXGXPXFXTXXXXXXXVXXXXXPXXXSXNXXXXXDVXXXXXXXX
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FAILSALSNXDAXXXXXLRXEXNXYXXXGXXXXXXXXYXXXXGXQXXXXXTXXXRXXXXX
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XXRXXXXXXXXGXXXXXXXXXXXXXXWXXXXXXXXXXXXXSXXXXVSAEXXXXYXAGXXX
DFXXXXXXXGXXXLLXXXXXXXXXXXXXXXXXXDXXXXXXXXVGGTGDDRXXXXXXXXXXX
GGAGAXXXXXXXXXXVXXXXXXCXXXXXXXXXXXXXXXXXXXLLADRLSTQXXXTSXXXX
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XXXXVXXXXXXXXXXXXXRLXAXXXXXXXXXVXXXXVXXXXXXXXXXXXXXXXXXXXXXGR
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XXFXXXXXXXXXXXXGGXXXVXXXXXXXLXXXXX

==> Caniformia.txt <==
>MSA Consensus of 159 seqs, protein
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PCXGXGXCXXGXXGNGTCXCQXXFGGXACXXCXDXNXFGPNCXXVCSCVHGVCXXGXXGD
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XPGXXXCXCKXXXXXXXXXXXXXXXXXXCEXXXXCXRXAXCXXXXXGXXXCXCXXGXVGDG
XXCYGXXXXXXXXXXXEPXGXXXXRLXXXXXXLDXXXXXXLXXXGPFTVLXPXXXXXXXF
XXKEXXMXXXXAXXXXKXHIIAGQXXXEXXGTXXTXXXXTLXGXXXXXXXXXXXXXXXXK
XXEXXXXXXXIXXXXXXAXNGXXHXXXXXXXXXPXXXXXXKXTIXXXLASXXXXSXFXX
XLEXXXXXXXLDXDGXXGPXTXFXPSNEAXDXXXDGXLXYLXXPXGXXKLXELVXYHIXX
XXQLXXXXLIXXXXXXTXANQXXXXNXXXXGXILXXPEXXXXXXXXVXAXNGXIXXLXGV
LXPPXIXPILPXXCXEXXXXXXXGXCVXCXXXXXSXCPXNSXXXXXFXXXCVYTXXPTGX
XXLKXGCAXYCNXTVXXPXCCKGFXGPDCXQCPGGFSNPCXGXGXCXDGXXGNGXCXCXX
XXXGXXCXXCSXPNKXGXRCXXXCXCXXGXCDNRXXSXGXCXXGTCXXGXXGRFCXXXXX
XCGPXEQXQXCHXHAXCXXXXGXXXCVCXXGXEGDGXXCXXXXPCXXXXRGGCSXNAECV
XXXXGTHXCXCXXGWXGDGRXCXXIDXCXLXXXGGCHAXAXCXYVGPGQXXCXCKXGFXG
DGXXCXXXXXCXXXXGXCHXLATCXXXGXGXXXCXCXXGYXGDGXXCYGXXXXELXXXXX
XXXFXQWIXXAXLXPMLXXXSXXTXLVPSXXAIXXXXXXXXXFWLXXXXXPXLXXXHXLX
GXXXXXXLXXLXXXDXLATXXPXXXXXXXXXGXVXXXXASVXXXDXXATNGVXHVXXXV
LXPXRXXXXXXXXLLXXLDXXPXXXXFRXXXXXXXLXXXIEAAXAYTXFXPXNXXXEXXI
REXXXXXLXXDXXRXHVILXEXLXXXXLXXGXHRXXXLGXXYLLGFPPPPPRQPAAPMRH

WLVFGMDSTXXHXXQXXVNXXXXXXXXXXXXXXXXXGLXXVLXXXXXRCXXXXXXXXRXK
CXXCXXXXXCXXGXXXXXXXXXXCXYXXXFMGKXSXXXGCXXXCXKXIXXXXCCXGFFGX
XCXPCPGXXGXVCXGXGXCXDXXXGXGXCXCXEGFXGTACEXCXXGXYGPXCXXVCXCXH
GXCXXGXXGDGSCXCXVGWXGXRCDXXITXXXCXXXCXXXANCXXXXXXXXXCXCAAGXX
GNGXXCXXKRGRXXXXCXXXXGGCSXXAXCXXXXPGXRXCXCXXGYTGDGXXCXEXNXCL
XXXGGCHXXAXCXXTGPXQXXCXCXXXYXGDGIXXCXLXXXCXXXNGGCSXXAXCXXTGX
XXRTCTCXXAXXXGDGFTCRXXXXXELXRXXXXSXXXXXLLXXXXXXLXGXGPFTVFXPX
XXXXXXXXQXXXXXXXXXXXXVXRYHVXXCXQLXXXXLXXXXXXTXLXGXXXXIXXXEXX
XYXNXXAXXXSSDXXXXNGXXHXIDXXLXPXXXLXXXXDAXXXXXXNXTXXAXXXGYXXF
SXLXXXXGLLXXXXDXXHXPXTXXWPXDXALQALPPXXQXXLXXXDXXDKLXXXLXXHVI
RXXXVGLPPPSPWSPLPATQPAPPAPTVAPSAQXLAXDLPXXXXXXTXXGXXXXXXCXXG
AGXXXGELXXXMTSEXXXXRIVQRXLXFKXXGXAYGIDXLLXXPXLGXRCDXFXTXXXXX
KXCXXCXXXPXCSXSESPDKXPXXSXXXGXXEXCXXYXXXFWTSPPLXSLALRSIWARSS
LWGQXXGXXXGCXXXCXXXXXXPXCCXGXXGXXCXACPGGAXXPCSXXGVCXDXXSGXGX
CXCXXXFVSRAGGXGXACELCXXGXFGPXCQAPAXCXCSXHGXCXXGXXGSGXCFCXXGW
TGXXCXXXXXXXPXXXXPCXXXAXCXXXXXXEXXSPLXXEGDMXGXXXXVXDXCXXXXGG
XXXXXXXSXXGXXVXXXCXXXYATFXXXXXSCHIRLVPIQDTQAVAIKEITVQTNLLPRD
VXXXXXXXXXXXXXXGCXEXXXXXXXGPXXXXXXXYRXXXXXXGDGXXXXXXXXXXXXW
GLXLLXLSLXXVEEXXXXXXCXCXVXXXXXXDXGLXXXXXXXGVFHXXXXXGXYXXXXXE
AXXXCXXXXXXLXXXXQXXXAVXXXGFXXCXXGXXXXGXVXXPXXXPXXXCXXXXXAGSA
GTGXXGGTASXGVXXXXXRXXXXXXXKSPGFPNEYEDDXYCXXXXXPPXEDCTSVTHLPX
XXXXXITXXIVNXXGXXXXXCXXXXXXXAKVGQLRXXXXXXXXXXXXXXXYXXXELPEXI
VXWSXXGXYRTNPEXXXDXXXSXPXXXXPXLXXXNXXXXGXXXXXXXXXXSXXXXYNXFX
XXXXXVYPTXXXXXTXXXXXXEEXXXQXHXXNXXXXXXNXXXXXTXXXXXXGXXLXXXXX
XPDNXXXXPKNTSXXHSXXXXXVXXXXXXXWXPAEXXXXXGXXXQDHTXXATTXXXSXSG
TXPKTATKRREAQDWLSWWFQPSESKNHLHXTTIMXGTDSXXXXAXXXPXXXXXXEXDKX
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XSGTXXXXXXXXXXXXXTXXXXXXXXXXXXXEDEXXXXXXEGTXXXXXXXPXXXXXXXAT
XKEQWXENGWPGEYXXXPXEXXHSTAGTXAPAQDXHPDQRXTTQSQEDSSWTYFFDPISH
PMGRXHXXEXXXDXXXXXXXXDXXXLALRPXNVSETXQPSADPNTHLVEDLDRTGPXSVT
XQQSXTXSFSTSHGGLEEDKDXXXXXXPTSSSKSXRTDGRGGRRGGHLPEDSATSVEGST
SHSPATGEYRTLIPVTPAXTGSPGVTEVNIAGDXNSNXIHFFSEDQDSSVHPSGTSHTTH
GSESAGHSSGSELLPXVEXCQEGGANTTSEGPMRKPQIPEWLIILASLLALALILAVCIA
VNSRRRCGQKKKLVINNGNGAVGDRKPSGINGEASKSQEMVHLVNKEPSETPDQYMTADE
TRNLQNVDMKIGV

==> Carnivora.txt <==
>MSA Consensus of 317 seqs, protein
MAXXXGXLXLXLLXXXXXXSXXXXXXXXXXXRCDXKXXXXXRXXCXXCXXXXXXXCPXGX
XXXXXXXXGXXDCRYXXXXXXXXXSXXGCXXXCXKDXVXXXCCPGXWGXXCXECPGGAXX
PCNGRGXCXXGXXGNGTCXCQXXFXGXACXXCXDXXXFGPXCXXVCSCVHGVCXXGXXGD
GSCXCXXGYTGPXCDXXXPXCXXLXCPXNSXCSXSSQDEXXXXCXCLPXXXXXGXXCXXX
NPCXXXXCXPXAXCXXXXXXXXXCXCXXXYHGDGXVCLPXDPCXXNYGXCPXXSTXCXYX
XXGXXXCXCKXXXXXXXXXXXXXXXXXCXXXXXCXRXAXCXXXXXGXXXCXCXXGXVGDG
XXCYGXXXXXXXXXXXEPXGXXXXRLXXXXXXLDXXXXXXLXXXGPFTVLXPXXXXXXGF
XVKXXXMXXXXAXXXXKXHIIAGQXXXEXXXTQXTXXXXTLXGXXXXXXXXXXXXXXXXK
XXEXXXXXXXIXXXNXXAXNGXXHXXXXXXXXXPXXXXXXKXTIXXXLASXXXXSXFXX
XLEXXXXXXXLDXDGAXGPXTXFXPSNEAXXXXXDGXLXYLXXPXGXXKLXELVXYHIXX
XXQLXXXXLISXXXXXTMANQXXXXNXXXXGXILXGPXGVXXXXXXVXAXNGXIXXLXGV
LXPPXIXPILPXXCXEXXXXXXXGXCVXCXXXXXSXCPXNSXXXXXFXXXCVYTXXPTGX
XXLKXGCAXYCNXTXXXPXCCKGFXGPDCXQCPGGFSNPCXGXGXCXDGXXGNGXCXCXX
XXXGXXCXXCSXPNKXGXXCXXXCXCXXGXCXNRXXSXGXCXXGTCXXGXXGXFCXXXXX
XCGPXEXXQXCHXHAXCXXXXGXXXCVCXXGXEGDGXXCXXXXPCXXXXRGGCSXNAECV

XXXXGXHXCXCXXGWXGDGRXCXXIDXCXLXXXGGCHAXAXCXYVGPGQXXCXCKXGFXG
XGXXCXXIXXCXXXXGXCHXLATCQXXXXGXXXCXCXXGYXGDGXXCYGXXXXELXXXXX
XXXFXQWIXXAXXXXMLXXXSXXTXLVPSXXAIXXXXXXXXAFWLXXXXXPXLXXXHXLX
GXXXXXXLXXLXXXDXXATXXPXXXXXXXXXXGXVXXXXASVXXXDXXATNGVXHVXXXV
LXPXRXXXXXXXXLLXXLDXXPXXXXFRXXXXXXXLXXXIEAAXAYTXFXPXNXXXEXXI
REXXXXXLXXDXXRXHVILXEXLXXXXLXXGXHRXXXLGXXYXXGFPPPPPRQPAAPMRH
WLVFGMDSTXXHXXQXXVNXXXXXXXXXXXXXXXXXGLXXVLXXXXXRCXXXXXXXXRXK
CXXCXXXXXCXXGXXXXXXXXXXCXYXXXFMGKXSXXXGCXXXCXKXIXXXXCCXGFFGX
XCXPCPGXXGXVCXGXGXCXDXLXGXGXCXCXEGFXGTACEXCXXGXYGPXCXXVCXCXH
GXCXXGXXGDGSCXCXXGWXGXRCDXXIXXXXCXXXCXXXANCXXXXXXXXXCXCAAGXX
GXGXXCXXKRGRXXXXCXXXXGGCSXXAXCXXXXPGXRXCXCXXGYTGDGXXCXEXNXCL
XXXGGCHXXAXCXXTGPXQXXCXCXXXYXGDGIXXCXLXXXCXXXNGGCSXXAXCXXTGX
GXRTCTCXXAXXXGDGFTCRXXXXXELXRXXXXSXXXXXLLEXXXXXLXGXGPFTVFXPX
XXXXXXXXQXXXXXXXXXXXXVXRYHVXXCXQLXXXXLXXXXXXTXLXGXXXXIXXXEXX
XYXNXXAXXXSSDXXXXNGXXHXIDXXLXPXXXLXXXXDAXXXXXXNXTXXAXXXGYXXF
SXLXXXXGLLXXXXDXXHXPXTXXWPXDXALQALPPXXQXXLXXXDXXDKLXXXLXXHVI
RXXXVGLPPPSPWSPLPATQPAPPAPTVAPSAQXLAXDLPXLETAQXXXXXXXXXXXLRT
XXGXXXXXXCXXXXXXXGELXXXXXXXRIVQRXLXFXXGXAYGIDXLLXXPXLGXRCDXF
XTXXXXXKXCXXCXXXPXCPXXSXXXGXXXXCXXYYXXFWTSPPLXSLALRSIWARSSLW
GQXXGXXXGCXXXCXXXXXXPXCCXGXXGXXXQHAECXACPGGAXXPCXXXGVCXDXXSG
XGXCXCHSPRVSRXXFXGTACELCXXGXFGPXCQXCXCXXHGXCDXGXXGSGXCFCXXGW
TGXXCXXQXXLXPXCXPPCXXXAXCXXXNXCECXLXYEGDGXXXXVXDXCXXXXGGXXXX
XXXSXXGXXWRPVXXXCXXXYEXXGXXXSPRSRXXXXXXXXXXVRXKWXKXXXXXXXXXEP
KCNICLGKTSGPLNDVXXXDPCAXGXXXXXXXXXXGRXXXXXXGXXXXXCXCXXXXXXXX
XXXXXEXXXXXXXCLXXXXXCHXDALEXXXDLXXXXXXXGVFHXXXXXGXYXXXXXEAXX
XCXXXXXXLXXXXQXXXAXQXXGFXXRQNCXXGXXLXXXXGXVXXPXXXPXXXCXXXXXX
XXXGTXFTDIENPRGXXQXXXXXGVXXLXXRXXXXXXXDXYQPECXXXXXXXXEDCXSXT
XXXXXXXXXIXXXXGXLLXVLXXXXXXXXFXXVCRGPALGRRXXIVNRDGTRYXQXXEYR
TNPEDIXPSXPTDDDQAXASPQPHLLAPLPXQDVVHLALYNLXXGQXXLFXAXXXXLXXX
XXXWELXXXXDEXXXNXXXRGXXXXXXLXDXXXXXXXXXXXXXXFXXXXXXXXPTXXPXX
XXXKXXXDXXXDPTESMASSRTXXEEDRXXXXXXXXXXXXXXXTXXXXXXXXXXXXXXXA
QDTXXXPXXXXXXXXXXXXXVXXXXXXXWXXXXXXXXXXXDHXAXXXXAXXXXXAXVXXE
XPPVXXGXXXXXAXXXXLGXXAXAXXXXXRXXXXXXXXLSWWXQXXXXXXXXXXXXXMXG
TDSNIISAGWEPTEENEDERDKHPSYSGSGIDXXXDFXXSTIXTTPRLFNHPKQNQDXTX
XXXGXSXXXVLLQTTDXXPNXXXXXTXXXXTSXXXXXXXXXXXRXLXXXXAVTXXXXXXP
XXXXXXXDXXXXXXDQXXXXXXXXXXXXXXXXEXXSPLIHHEXHDEEEXQHXXSTTQXIXS
XXMEETATXKEQWVENGWXGEYXQSXKEDSHSTAGTXXPAXDXHPDQRMTTQSQEDSSWT
YFFDPISHPMCGRXHQTERWMDXDSSHSTTXQPSADPNTHXVEXLDRTGPLSVTTQQSXT
XXXXGXQSFSTSHGXXEEDKDHPXTSTPTXSETESPSXSKXXRTDGXGGRRXGHXPEDSA
TSVEXXTSXSPATXEXRTLIPVTPAXTGXPXVTEVNIAGDXXSPSNVXXFFSTPXEDQXX
QDSXVHPSGXSHTTHGSESAGHXSGSQEGPTVGANTTSXGPXRKPQIPEWLIILASLTVL
ALNFNCDRSALILAVCIAVNSRRRCGQKKKLVINNGNGAVXXRKXDTTSCSGXNGEACNG
RGICECGACKCTDPXXXGPTCEMCQTCLGXCSKSQEMVHLVXXXNKEXSXTXDQYMTADE
TEKVXXXRNLQNVDMKIGVLXXXXXXXXXXXWXXXXXXXYXXXGXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXGXXXXXXXXXLXXXXXXGXPRRRYEVDTVLRYRCXXXLXXXXXXXXX
XXXXXXXXNXXXXXXXXXXXXXXXARXXXXXXXXXXXGXLXXXWXXXLXXXXXXXXXXXX
ARPXPALPSPHHRLTTWEGAAALQAAVPQGVCGXHLGGSSLD

==> Catarrhini.txt <==
>MSA Consensus of 732 seqs, protein
MELXNYXXXXXLXXXXXRXXXXXXXRGXXXGPXXXXXXLXXXXLXXXXGTNXXXXXXXXX
XXXDXXXXXXXXXXXXXXXXXXXXXXXXXGXXXXDLVQVIEXXXXXXXXXLXXXXXXXXX
XXXXXXXXXXGPXXXXXXXXXXXXKXXXNVTNRSXXXXXXXXXXXXXXXXXXXXXXXXX

DCPEMSIXXXXXXLXXXXPXXXXXXXXXARSKDYRLTHEVXXFXXXXXPXVXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXSSEXXXXXXXXXXRKXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXPCXXXXXXXXLKWVEXXXXXXXXXXXXXXXXXXLXXGXXXXXXXXXXXXXRXX
XXXXLYXXCXXXXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXXXXXXFXXXXXXXXXXXX
XXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXNSALSLT
DTDHERKSDGENXXXXXXXXCXXXXXXXXXXXXXXXXXNXSSPXXXXTFRXXXXXXXXXX
XXXCXXXXXXXXXXXXXXXXXXXXXXXISTPARIXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXSWVLNSXXXXXXXXXXXXXAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXGEXXXPGMXXXXXXXXXXXXXXXXXXXXXIPCSVDSLLPFTLSFVRNGVTLGVD
QYLKXXXXXXXXDXXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXRCWPSDSADDGWSPW
SEWTSXXXXXXXXXXXXXXXXXXXXXXEPPPRPLPXXXXXXXXXXXCXXXXXXXXXXXXX
XXXXYLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXHRSSCSVTCGXXXXXXXXXXXXXXXX
XXXXXCXXXXXXXKACKKDXCXXXXXXXXXXXXXXXALPLLXXXXXXXXXXXXXXXXXLAX
XXXXXXXXXXGXYXXXXXXXXXGAGSXXXGXXXXXXVXENXXXXXXXXXXXXXXXXXCXXG
VXCXXTXXXXXXXXXXXGPCXXXXXXNGXXXXXXXXXXXXPDXCXXXIGGKVXXXXXXXV
XXXXGXXXXXVVEKXXXXXXXXXXCMXXCXXXXXXXXXXXIXXXXXMAGPXGLXXXXLLAF
CLAXFSQXXCXXXXXXXXXXXXDXXXLMDGKQLVKQDSKGSDDXQHSPRXFXRGQVLFKX
CDXXTXXXXXXXXXXCXXXXXXTXXXGXLXELPDQITQDCRYEVQLGGSXXSXXGCXRRX
CRKXXXQXXCCPGRGGYWGSRCXECPGGAETPCNGHGTSVSSISQXXXXXFXXXXXXXXX
AXXXXXXDGMXXNGTCXCXXXFXGXXXXXCXDXNXFXXXPXXXLGPXCXSVCXCXXXXCX
XXPNSGQEDXXXXXXXXXCXXXXXXDXXXXXXGXXGDGXCXCXXGYTGPXCDXXLPXCQE
LRCQXXXXXXXXCSXXXXXTTAEFXXXXXXXXXXXXXXXXXXXXXXCXXXXXPXNXXCS
XXTXXXXXXXCXCLPGYTXXGXXXXXXXXXXXXPXXXCXXXXXXCXXXAXXHXXXXLXXL
XXXXLXXXCXXXXNXXPSVXXDXXXDXXGXXSAKFSCXXCXXXXXXSXXXXXXXXPKGQA
QCHCXENYHGDGXVCLPKDPCTDNLGGCPSNSFGNGTXCVYQKPGQAXCXCXXHYQNXXX
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XXXXXXXDDDNDGIPXXXXPXXXNCXXTPXXXGXXXXXXXXGXXCXXXXXGDGRACYGHL
LHEXXXXXXXXXXXXXXXXXXXXXXXXFXQLRVAXXXDPXXXXRXXXXXPXXXXXXXGXX
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XTXAGPFTVLVPSXSSFSSRTMNAXXXXXXXXXXXXXXXXXLAQQXCRXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXFLPEXXXXXXXXXXXXQEXXXXXXXXXXXXXXXXXXXXXXVVV
ENSASRANLSXXXXXXXXXXXXXNFIXXXXXXXPXXXXXXXXXXXXXXXXXXXLXXXXXX
XPIPKXLKGFNXLXXXXGRTPGXXXLXXXXXLXXXXXXXXXXXXXXXVXXXXXXDXXXXQ
XXXXXXXXXXEXTVTFNXXXXXXXXXXXXXXXXXXXXXXXYXDXXXXXXXXXKXXXXAAN
GVFHVVTXXXXXXGLXWQXXXXXPGXDPKRXIXQILXXTXAFSXXXXXXXXXXXXXXXXX
RLDSPTFHLTLHYPTEHXXTILENCGLPSILDGPGXXXXXXXXXXGXXXXXXXXXXXXKP
FTVFAPSNEAXDSXXXXXXXXXXXXXRLXXXXXXXXXKLQXLVTXXXXXYXXXXXXLXX
XXXXGHAXXXXGXGXXXXXXVXXXEXXXXXXXGXXQADXSXXXNSGXXXXXXXXXXXXPX
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XXXXXTEXGXXXFTLIPDSTXXXEQGCCKGFFGPDXXXXVXXXXXXXXXXXXKSTLXXPX
XXVXTXXXXXXXDPXXXXXXXLXGLXXXXXXXXXXXCTQCPGGFSNPCYGXXWXXPXXXX
XXXXGXXXXXXNNXVLQISEKGNCXXXXXGNXXCXXXXXYKXXXXXXAXHXTLESXRAIS
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GTCXPGXXGXXCXXSMGAPSSLAVXXCGPXXXXXXGNXXXXTGLAQXCHLHAXXXYXXXX
CVSXXGXXXXXXTXWVYLLEPXXXXXHXXXCXCXXXXXXXXXQXXXXXXXXXXGXXXDGX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPXGQVYWLTISSNGVLKRVSAQGY
NLALMTYPGNTGLLATKSNENGWTTVYEYDXXXXXXXXXXXXXXXXXFXCTPSNPXXHPD
RGGCSENAECXXXXXGTHHCTCHKGWSGXGRVCVXXXXRDCXXXAIXXCXLXXSDRGGCH
XDAXXXXXXXXGXCXPXPAKPMHPENKLTLCSYVGPGQXXCXCKXGFXGXGXXCXPIXXC
RAGNGGCHGLAXCXXVGXGXXXCXXXXXXXXXXXXXXXXXXXXXDGGQRXCTCPPGFGG

DGFSCYGDIFXXELEXXXNAXXXXXXXXXKSXXIXLXXXXXSNFERRLRAXNXXVTAXXX
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XXXXRAFWLQPRXXXXXXXXXFLQXXXXXXXXXXXXXXEXXXAXLXXXXXXDXXXXXXPX
XXXXLGELKRXXXXXXXXXXTTRWEIRNXXXLXXXXXXXXXXSGRVDGNXXVQXNASVDV
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XXXXLXXXXXXXXXXXXXXXXXXXXXXXXXXXFXXXXNCXHXXXXXXXXXHXLVXQIEXX
XXXYXXXXEXXXXGXXXXXXXGXXXXXHLXXGXXGXXXXXXXXXVPTNRSLEAQHRSPEN
ISVVXGNSXXXXXXXXXXXXXXXXXXXXXXXXXXDTVRHHVXSVLGEALSMETLXKGXX
RXXXXXXXXXXXXXXXXXXXXXXCXLXXXXGEXWXXXXXXXXXXXXXXXXXPXXXXEXX
XXXXXVXXXXXXXXXXXXXXXXXXXXXXXXPLEGPMLEAPGXSXXXXSXXXXXXXXXXR
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RGCSYTCXXXIQXXDCCXGFFGXXCXPCPGXXXXXXXGHGXXXXXXXXXXXXXXXFLGSG
ECHCHEGXXXXXXXXXXXXXXXMXXXXXXLGXXGXXXTXXCDCXXXNITLXXXXXXGDGS
CXCXVGWXGXXCDQKITXXXXXXXXXXXXXXXXXXXXXXXXPXXXXXKYEEPLQXXXXX
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GPQQGAGQLLAPSSPXHTGQVEVSCSCREGYXGDGXXXXXXXXXXXXXXXXXLGRRVAXX
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ASFFSLRLLEYKELKGDGPFXXXXXXXXLMXXXXXXXXXXRIRAHXXQLXXXXTAXVXXC
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KYTTXXXXXXXXXXXXXXXXXXXXXXTXXXGXXXXXXXXXXXRXXXXXXXSXXXGXXXXX
XXXXVXXGXXXXXXXXXXXXXXXXXXXXXXXXRXXXPXXXXXXXXXXQXXLXXXXXXDX
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XXXXXXXXXXXXXXXXXRFAXXXXXXXXXXXXXXXXXXXXXXXVXXXXXXXXXXXXPSXXXXX
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XPGXXXXXXXXXXXXXXXXXXXXXXXXXXXHMEKKXXXXXXXXXXXXXXXXXXXXXXXXX
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LLEPPGLGARCDXFXTXPLXXXXXXXXXRLNTCSXXXXXXXPXXXXXSXXXXXXFDXXX
EQGXXXXXWRXYPXXXXXXXLXSLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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YXLXFXEAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPXXXXXXXXXXXXXXXXXQLGX
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XXXXXXECKSXXXXXXXXXXXPXXXXXXTMFPXXXSXXXXXXXFXXDXXXXXXGXXXNPS
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XXXTSXTXXXXXXXGPITITIVNXDGTRYVXKGEYRTNPEDIYXXXPTXDDVSSGSSSER
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AXXXXXXXXXXXXXXXXXPXXXXLGXXXXXXXPXXXXXRTNATRXLXXXXXXXAXGXXGI
XXXXXXXXXXXXXAXXXXNSAXXXXXXXXXXXXXXXXXXXXXXXXPFXWXXXXXXXXFXX
XXXXXXXXHTSXXTXXXXXXSSXSXXIXXDIXXXXGXXXXVHALAXXXLXPPXXXAXLXP
XAPPVAAGVGXXXXXXXXXXXXXXXXXXDTGEXXXXXXXLRAXXXPXXXXXXXXXXXXXL
XXEXXXXXXXXXXXXXXXXXXXXXXXXERDRXXXXXXXXXXDXXXXXISSTISXTPRXX
XFDHTKQXXXXXXXXXXXXXXXXVLLQTTXRXTXDVDRNGXTAXEGXWNPEAHPPLIHHX
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XXXXXXXVAXLXXXXXXXXXXXXXXPPMRSLSXXXXXXXXPXXXXXXTXXTAPXXXXXXX
XPXXXXXCXXXXXGXXXXXXXXFXRAXXXXXXXXXXXXXPXXXXXXXXXXXXXCXXXXXAK
XXLVXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXLXRXXXXXXXXXXXXXXXXX
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DSSXTXXXDXXXXXXXXXXXXXXXGRXRMXMDSSHXTTLQXXXXXXXXXNTGLVEDLDRT
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SGNGAVXDRKPSGLNGEASKSQPQXXXXKEMVHLVNKXXXXXXXXXXXXXEXSETPDQFM
TADETRNLQNVDMKIGVXXXXXXXXXXXXXXXPXXPXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXLDXXXXXXXXXXXXXXXXXXXXTEXXXXXXXXXXXXXX
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SXPESXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGPXXXXXXXXXXX
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XXEGAANLXXXXXXXXXLXXXXXXXXXXXXXXXXXLXVXXXXXXXXXXXXXXXXXXXXX
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XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPXXXXXXXIDNDRVVCAXXPCPXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXNNSNNTA
SKAMSDDTVXXXXXXXXEVITKNMENAKAXXXXXXXXXXXXXXXXKGDKHSPKXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXTXXXCXXXXXXXXXY
XXXXXXSXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXXXXXXLXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXTIXXDXXXXXXXXXXXXXXXXPSIXXXXXXXXXXX
ASAPASPREXXXXKXXXXXXXXXXXXXXXSXXXQCSXXXXXXXTXXXXXXXXXXXXXXX
XXXXXXXXXXXSXXXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXWXXXXXXXXDTXXXXX
XXPVXXXTDERLNWIYXXPXRXDXXXYQPFQXXXXXXXYDESFFEDQVHHRXXXXRXIR
AKITNVPRSLGSAMRKIVSXLXPXXWXXXXXXXXXASEYTMXXXXXLXXXXXXXXXXXL
QMSHIXXXXXXXXXXXXAXXXRXFXLXXXSPAXXSXXXXXXXXXXXXXXXXXXXXXXXX
RXXQXXXXXSAAPASXAXXXXWXXXXXXXXQXXXKXLTEFXEPXXXXXXXXXXXXLXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXKQVGEKAMNAXXXPXXXXXXXXXGXXXXRXXXX
XXXXXXYXXXSXFXXXSVGPXXXXRXXCXXGXXCXXSCXXXXXXXXXXCXXXXXXXXXAX
XXXXCXXXXXCAXGXXXCXXXXXXXXXXGXADRQXXCXXXXRXRRXXXFXXXAXLXXXXX
XXXCXDINECXXXSHTXXXHXXXXXXXXXXXXXXXXXXXXGXXCXXXXEXXXKXXXRXX
XXXXXXXXXXXXXXPXXXXLXXLLXXXXVDSXWSVAQALLVLXXXXXXXXXXPXXXXXXX
XXXXXXXXXXXXXGXXXXGXXXXXGXXXXXEKMKEGLEDEKRXEKALKNDIEXXXXXXXX
XXPXXXGXTPLXVXXXSXXXXXXGXXXVXXXXXXXXLEXXXXXXXXXXCXXXXGXXXXXX
DXXXXXXXXXXXXXXXSXVXXXXXXXXIGXXAXHXXXXPXLXGXXXXXGXXXXLXPXXQ
PXXXXGXXCXXXXYRLXGDXXGXQYSSYNLXXXXXXXXXXXXXXXXXXXXXXKWKTXXX
XXYXGTXXXKXXXXXXERXXGXXGXXXXXGXXXXXXXCVDIDECEXTDACXXXXXXXFGX
XXXXCPXXXLXXXXXXXXXXXXXXXXXKGNXXVGTQGPRGPPGPXGPXXXSRPGSPGPPG
XXXXRGXXXXXXXPXPXXXXXXPVSXXXXXSXCXXXXXEXXXXPXXXEXXXVSLPFGIAT

XQDXXXXXXXXXXGVMHPRTTFLMVDEEQTVPFALRDENLKGVVYTTRPLREAETYRMRV
RASSYSANGTIEYQTTFIVYIAVSAYPY

==> Caulobacter.txt <==
>MSA Consensus of 142 seqs, protein
MTAAXPXSVKGIDPKAREXXKXLAXXSXXXXXXWXXXMXXEGXXXXXXPXLXXXDVPNRX
XXEXVRAXXXXPDRVKXXIXXXPXXEVGXXAXXXXRXXQXXXXXXGXXMCXXXXXXXXMX
XKXXXXXXXXXXXAXXXLXXCXXGRXMVXXXFXXXXXXXXXXXARAGNYAXPIGXAPVGT
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XIXAGQVXGSDFYXXGGXTELNYNIXSXGXDXXXGDXDTXNPXXXRXXXGXXSLAATLTQ
KMEAARLEXAAGLKXXXXXRXFVXMXXXXGNXAXDLRLXNXRTLEVXDVXSYQKQXXGRE
XVGVADXFXRXXXXAXXRXXGXFXFXNXNXFDXSXGXXHXXXXXXSVQAGALEPLGGEIA
RITEKLAERIGSAERRNALAIDDVGEQVARXQLAVRXLXERXXXEXXANLYGXPGRTLRM
RRPAXXRLAGTXXAXXXCXXXXXGXXXXXXXDPXXXXXXTXXXXXXXXXXXXXXXXXXX
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FAHADXXXXXGXXPESPRYEVEPEVSDFAPAEPSRPMSTSNQXNXGXVXXHXVVXXXXXX
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GVGNSXXXXXAXGXXXXXDXVXXXGXXXXVXSSXXXSSXGXXXXXSXXXXXXXXXPDXXX
XXTAXGNXXXXXXXXXXXXXXXXXXXQXNXXXVXAXXXXXXXXXXXXXXGXXTAXGNNAX
FXVXXXXXN

==> Caulobacteraceae.txt <==
>MSA Consensus of 409 seqs, protein
MTAASPWSVKGIDPKAREVAKDLARRSGMTLGEWLNRMXXEGDGQTADPRLAGDDVPNRX
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RLXXXXXXXXALXXPXVSXXFXXAXXXAXXXXARXTEXXXAXESEARGXRGXXXAFXAXX
LRXDVAMXXXGPMGXYXALISAPGVTMXXXDXXXXXXXGXXXACHXYXXXDXGXXXXXET
LAXXXRNAXXLXXWXXGXPXXXXXXXAERKXAXXGXRLXXXXXXXXXAXREXGXCXFXAX
XXXXXAXXXXXXXATGVQEGXXXXXXXLTXXXXXXRLEXAAXXXXXLXGRFXXXXXXXXGX
XXXXXXXXQXXAVXIEXXGEXXXXVAXAWLXXXXAAEXRXASAIEQVGGEVARIAASVEH
KLNRADSVQXXXLEXXXXXXXXXXXXLXXXXGXXXXXXXLXXXDXXXQXXXXXXXLXXXX
XXXXXXXXXRXXXXXXXXXXMXXXXXXXXXXXXXXXXXXXAXXXXLXXCXXXXXXXXXGX
YAXPIGXAQRPVTXNPTPYSXNYFSQAASFSTSEDEADXXXXXXXXXXXXXXXXXXXXXX
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XXXXXXXXXXGYXXXXXXAXGXXXXXXSGXXXXXXKKEXXXXXXXXXXGXXXGXXGFXXX
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YAR

==> Caulobacterales.txt <==
>MSA Consensus of 409 seqs, protein
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GRXXXXXXXAXGNXAXFYVXXPGXXXXXXALRMAIAAYQRDQGLPPTGSVDAETLNRLSV
YAR

==> Cellvibrionales.txt <==
>MSA Consensus of 124 seqs, protein
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XXXXYXXXXXXGXXXSSSTSXXXXXXXXXXEXWXXXXXXXXXXXXPVXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXEQXXXXXXXXXXXXXXXXCXXXXXXXXXXXXXXXXXX
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XGXXXXXXXXXXXXXXVLEXXXXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXDPXXXXXXXX
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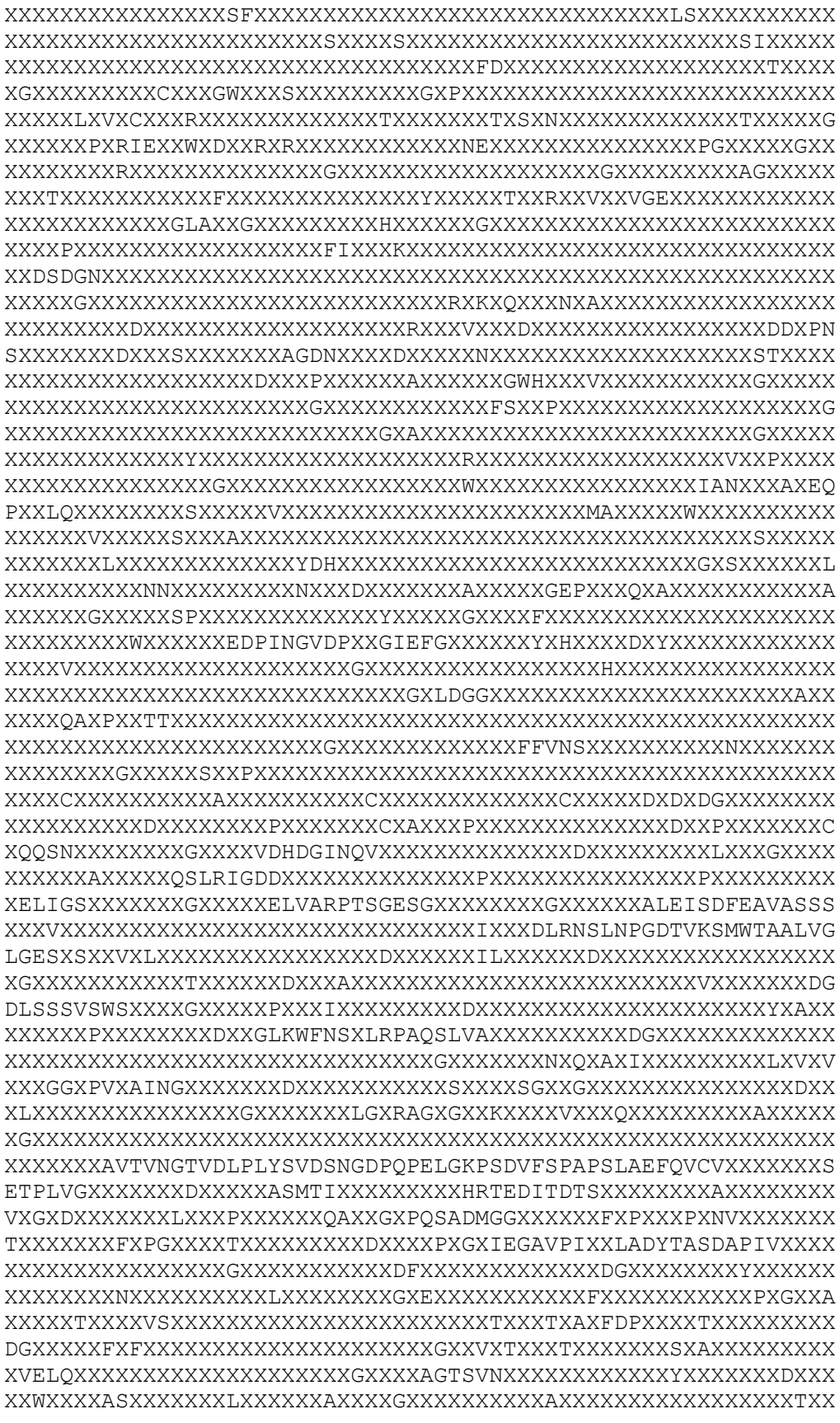

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==> Cercopithecidae.txt <==
>MSA Consensus of 212 seqs, protein
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HGTCLDGMDRNGTCVCQENFRGSACQECQDPNRFGPDCQSVCSCVHGXCNRGPRGDGSCL
CFAGYTGPHCDQELPICQELRCPQNTQCSAEAPSCKCLPGYTQQGSECRAPNPCWPSPCS
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RPGLVSINSNASAGCFAFCSPFSCDRSATCQVTADGKTSCVCRESEVGDGRACYGHLLHE
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FGGDGFSCYGDIFDSTQKQLEEITDRELEANAHFSIFYQWFKSAGITLPADGRVTALVPS
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ISGRVWVQNASVDVADLLATNGVLHILSQVLLPSRGDVPGGQGLLQQLDLVPAFSLFREL
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==> Cercopithecinae.txt <==
>MSA Consensus of 176 seqs, protein
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APGFSGRFCNESMGDCGPTGLAQHCHLHARCVSQEGVARCRCLDGFEGDGFSCTPSNPCS
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VAIDECELDVRGGCHADALCSYVGPGQSRCTCKLGFAGDGYQCSPIDPCRAGNGGCHPPG
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LGGQEVATLNPTTRWEIRNISGRVWVQNASVDVADLLATNGVLHILSQVLLPSRGDVPGG
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GLGGVMEETCSGHGQCQDRFLGSGECHCHEGFHGTACEMCELGRYGPNCTGVCDCAHGLC
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IXGXXXXVXXXEXXVXARILDXXXXXTXXPVTLGIEXFXXEVXXGSPXVESFXXXXXSXE
XXXLXGXXEESVXXXXXXXXXXXDXCXXNPCLXGGTCXXXXTXYXCXCXXGXXGXXCEXDX
DXCXXXPCXNGXTCXDXXNXFXCLCLPSYXGXLCEXDTEXCDXGWHKFQGXCYXYFAHRR
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==> Cetacea.txt <==
>MSA Consensus of 222 seqs, protein
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IKRLKSAREERGRPAVAGAVVLGHWGPDEAAPAKKDLAEQPVKPALMTTYLDPAVQQDTC
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HGVCXXGXXGDGXCXCXXGXTGPXCDXXXPXCXALXCPXNSXCSXXXEDETKXXCXCXPX
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CPXXSTXCXYXXPGQAXCXCXXXXXXXXXXXXXXXXXCEXXXXCXRXAXCXXXXXGXTX
CXCXXGXVGDGXXCYGXXXXXXXXXXXXXXXXEWXXRLXXXXXXLDXXXXXXLSXXGPFTV
LXPXXXXXKGFNVKEXXXNXXXAQXXXXXHIIAGQXXXEXXGTXXTXXXXTLXGXXXXVX
FXXXXQXXXXKXKXYXXXXXXXIXXXNXXAXNGXXHXXXXXXXXXXPXXXXXXXXTIGXX
XXXXXXXXXFXXXLEXXXXXXXLDXDGIXGPXTVFXPSXEAXXXXXDGXLXYLXXSXGXX
KLXELVRYHVXXXXQLXVXXLISXXXXXXMANQXXXXNXXXXGXILXXPEXVXXXXXXVX
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GQXXCXCKXGFXGDGXXCXPXXXCXXXXGXCHXLATCXXXXXTQPVSLLLLVSGVVFAKR
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AWLWQHGDSSSLGIIELXXXXXXXIFXQWIXXAXXQPXLXAXSXXTXLVPSXXAIXXXXX
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QRIQXXXCCXGXFGXXCXPCPGXXXXVCXGXGXCXDXXXGXGXCXCXEGFXGTACEXCXX
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GKQQPENISNPMYENTXQSQEDRSWTYFXDPVSHPMGRGHQTERRMDVDTXSXSTTLQPS
ALDPNTGLVEDLDRTGPLSVTTQQSXTQSFSTSRGGLEEDKDHPXTATPTSSNRNDGTGG
RRGXNLPEDSTTSVEGYTPYSPDTNEYRTLIPVTPAKTGSPEVTEVTIVGDSTSNVDLSL
SXDXDSSHDPSGXSYTTHGSESAGXGXXHSSGXPXXXSQXRGAAITVTTGHNTTSGPXXS
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ETSGIPDLSGQPSGLPGFSGTTSGIPDLVSSAVSGSGESSGITFVDTSLVEVTPTTFKEE
EGLGSVELSGLPSGKADLSGTSGIVDVSGLSSGVIDSSGFXPXPPXXLXGXPXXXXXVXX
EXXXAETGSSXPSGAYDGRGLPSGFSTVSLVDRTLVESVTQAPTAXEXGEGEPPSGILEX
SGXPXGXPXXSVDTSVVMSLMSLDLGDXSGLLDXSGLQSGXXEPSXEPSSTPYFSGDFSG
TTDVSGESSAPTSTSGEASGLPEVTLIISEFVEGVTEPTVSQELGQRPPVTYTPQRFESS

GEASXSGDAPXXPGSGVEAXXVPEXXSETSAYPEAEVGASAVPEASGGTSRSPDLSGTTS
ALHEADLEGASGLGVTGSTSAFQEGPREGSAAPEVSGESTTTYDVGTEASGSPSATPMAS
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IRCQXXGXWEXPXIXCTXXXXXXXXXXXRSTNTTTSITTTNRTRSXXPXRSTQQRTGRRX
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==> Chelicerata.txt <==
>MSA Consensus of 125 seqs, protein
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DCKKKDFCGTSNETSCMYDITQMQAVCNCSDSSKQFDYVEQICKTRCEDDSNCENGHKCI
RDGASKYCQCIPGKDINICSHVMDCDEPDSCGIDNNVTCEYDATQMKGRCQCSNASKQFD
YREKICKEPCQDSDCENGGKCTGHGDFKFCECLPGTTGDACSDVTDCNETDFCGTGNDTT
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==> Chiroptera.txt <==
>MSA Consensus of 175 seqs, protein
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RCLPXDPCXXXXGXCPXXSTXCXYXGPGXASCXCKPGLVSINXNXXXGCXXXCKSXXSCD
RSATCQVTXXGKTSCVCXEXQVGDGXACYGHLLXEXXXXXXXXXGKXXXXLXXXXXXLDX
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==> Chordata.txt <==
>MSA Consensus of 6080 seqs, protein
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VKQKKGRGKGEEKEARQVERKGEETSGAGRVGDGEDSGDIQHTVVYVHTDDLSVESSLPA
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==> Cichlidae.txt <==
>MSA Consensus of 117 seqs, protein
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XSXCXCXSGXXXXXGSPEXGCXLXXXCXXDXCXXXAXCXTXXXGXXXCXCXXXXIGXGXX
CXGNXMERXXXLXTEXXGXWXGXXXXAIXXFXXXXPXXLXXXGPFTXFIPXXKXXXGTPV
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RKXXXXIQXXXXASNGIIHIIXXXXXXXXSSPXXEXXXXXXXXXIXXXXXKXXXFXSLXX
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XTSCXCXXXXXGXGXXCXXXXXCRXNNGXCXRNARCXXXGXGXXXCTCXXXXIGDGXXCX
GXXXXEXXXXXXXXFXXXXMXMXGXXXLXGXGPXTVFXPXXEXXXXXXXXEMRQXWXXXX
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XYXXXXXXXXXXXXXGWXXXXXXXXXXXXPXXEXXXXXXPXXXXXXXXXVXXXXXXXXXX
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LSGDXSGDLSXNXXXXXXXXXXGDXXXDLSGDXSGXXSGDXSGDXXXXXXXXXXXXGXXXX
XPXXIXXXGSGXTEXXGSSXXXXXXXXXXPXXXXXXSXAEGXXXYXXXXXXXXXXXXXXX
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XHXXRRXGGEGXXXXXXXXXYYXXXXXPGAKTNPTTTRPHTKPPGYSYPLYYPYNFYYPY
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==> Cichliformes.txt <==
>MSA Consensus of 117 seqs, protein
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CXGNXMERXXXLXTEXXGXWXGXXXXAIXXFXXXXPXXLXXXGPFTXFIPXXKXXXGTPV
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RKXXXXIQXXXXASNGIIHIIXXXXXXXXSSPXXEXXXXXXXXXIXXXXXKXXXFXSLXX
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==> Cichlomorphae.txt <==
>MSA Consensus of 117 seqs, protein
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CXGNXMERXXXLXTEXXGXWXGXXXXAIXXFXXXXPXXLXXXGPFTXFIPXXKXXXGTPV
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==> Clostridia.txt <==
>MSA Consensus of 3472 seqs, protein
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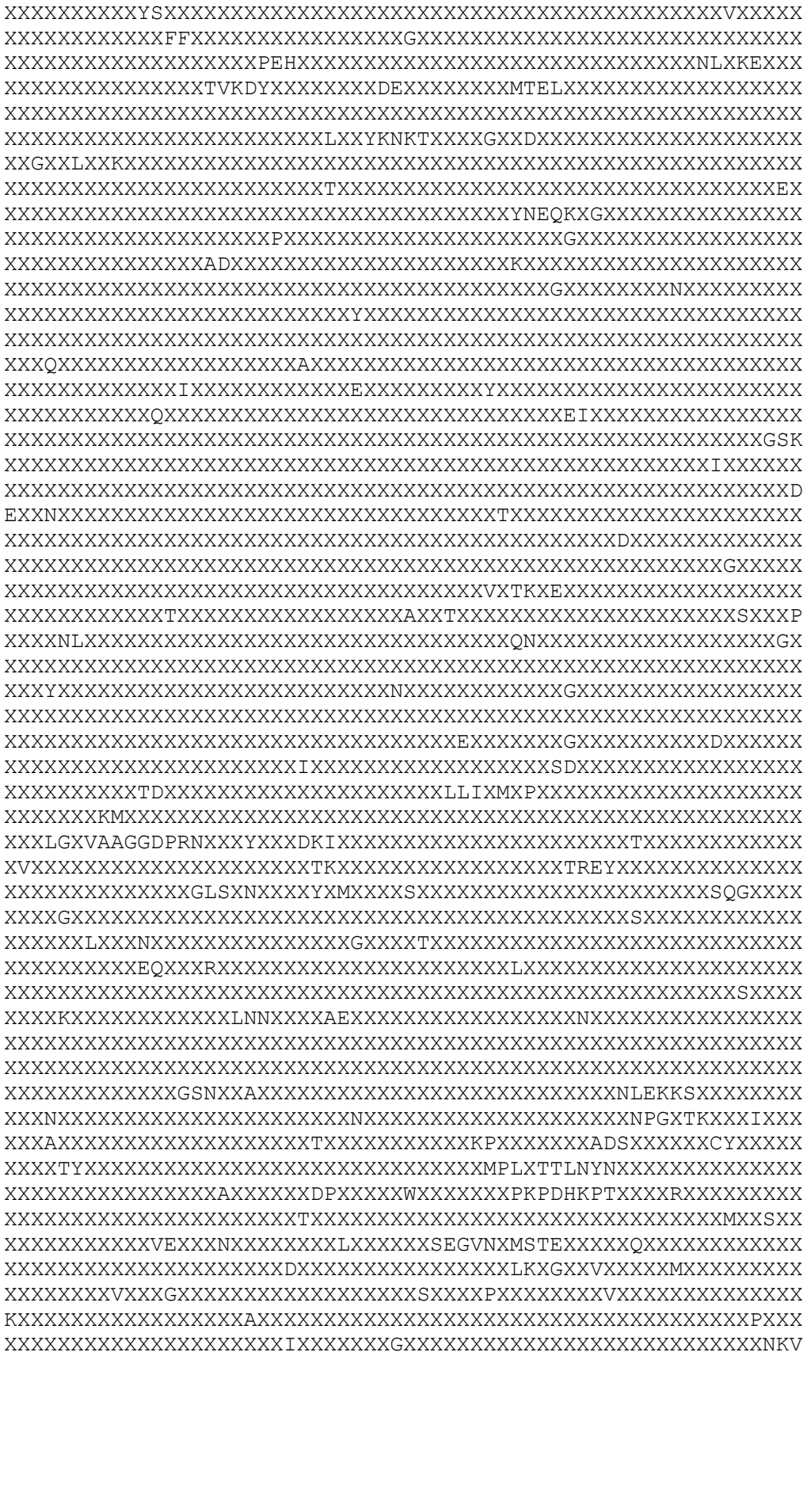

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==> Clostridiaceae.txt <==
>MSA Consensus of 1259 seqs, protein
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XLGEALAAXXXXGXXXXXXXXXXXXXXXXXXXXXXXTXXXXXXXLNVNAXXXALEVTNG
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SGXXXXXXXXIXXXXXXXXXXXXXXXXXXXXXXXVAXXXXXXXXVTVQTENLXXXXXXXX
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GTPTXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXAXXXXXXXXXXXM
EYXXXXXXXXXXXXXXXXXXXXXXXXSHXXXDXFXATXXXXXXXXXXXXXXXXXXXPT
AXTYTPAQDYXXXXXFXXXXXXXXXTATXXXXXXXXXXXXXTSVNAMNSAELTEAINNPA
VAXIILTSNTTYQIGGAEINXPXXXXXXXTIEVLSGVGQXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXSXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXLLX
XXXXXXXXXXXXXXXXXXXXXXXKAXLXXXXXXXDNIDYXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXGVYGXYXXXXXXXXDHSXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXEXXXXXXXXXXXXXXXXXXLPAXHNXXXXXXXXXXXXXXGXXXXXXMXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXVXAXXXXXXXXXXXXWXXXXXGXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXEAIVSXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXTXKAVXXXXXXXXXXXXXXXXXXXXXXXXXXKXXXXXXXXXXXXXX
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SXXXXXKYNXXXXGXXXXXXXTPXXXXXXNXXXXXXXXXXXXXXXXXXXGGQAXXXRYDEA
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXYVXXXXXIXXXXXXXXXXXXXXXXXXX
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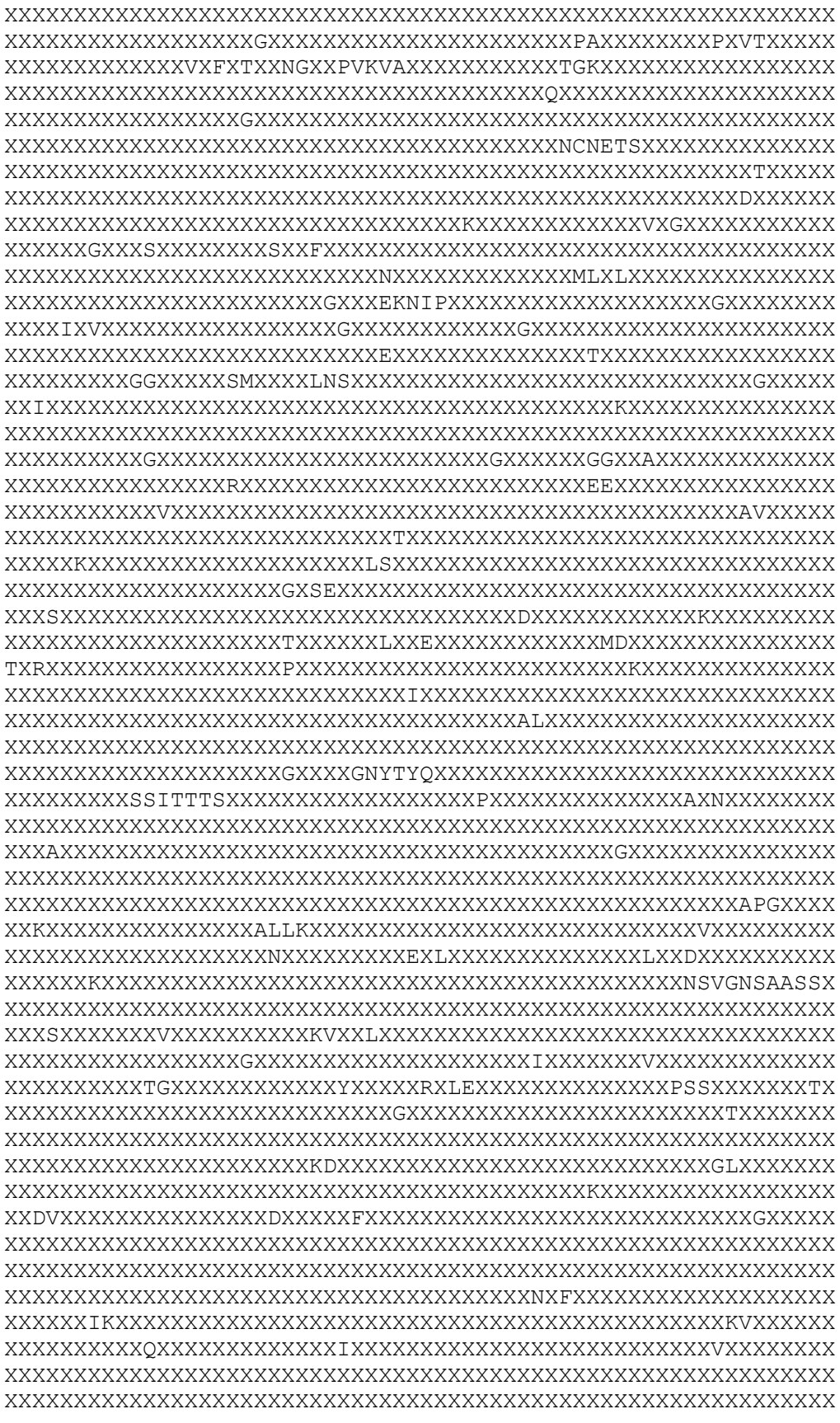

XXXXXXXXXXXXXXXXXXXXSXXXXXXXXXXXXXXXXXXXQNXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXWXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXXXXDXXXNXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXLXXXXXDXXXXXXXXXXXXXNDVXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXNXXXXXTXXNXFXXFXDDEGSGFXXYXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXTYNDXIVXXXMXXXGXDGXXXXXXXXXXXXXXXXXXXXX
ILXXXXXXXXXXXTXXXGDXXXXXXXXXXXXRVXSXXXXXXAMENNADXNXXXEKKRXXX
XXXXXXXXXXXXXXXXXXXXVSVXFXXXXXXXXXXXXXXXXXXXYXXXXXXXXXXXXXXXQ
XAXXXXXXXXXXXXYXXXXXXXXXXXXXXXXXXXXLLXXXXXXDXPXXXXXXXXXXXXXX
XXXXXNXXXXXXXXXXXXXXXXXXXXXXXXXXLLXXXXXSXXXXXXXXXXXXXXXXXXX
XXXXXGXXXXXXXXXXXXXXXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXAXXXXXXXXXXXXXXXGXXXINYNXXXXXXXXKXXXXXXXXXYGXXXXXXXFXXXMXX
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XIXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXQXXXXXXXXXXXXXXLXXMX
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XXXXNELKRRGTGDIIISGGVDSXTATVLANERNCXXXXXXXXXXXXXSXXXXXXLVXXX
XIXRVMNLKNTXXXXXXLLXXXXXXXXXXXXXXXXXXGXXXXXTIXGGXAXXXSXGXXKS
RXGXXXXXXXXXKXXXXXXXXXXXXXXXXXXQSHXXXXTXXXXXXXEXRHXXSYTDSKGX
XGQKYGDXXXXXRYXTXXXXXXXXXXXXXXXXXXAAXXMXXXXXTXXXXXXXXXXXXXXX
XXXXISIQXXXXXXXXXXXXXVVXXXDXXXXXXXXXXXXXXGNXXXXXDXGXXXXXXXX
GXDLRAVXXDAXSPQKNIINFLSPSTYNTIMPXXXXAXXXXXXXXXNPTSIXXXXXXXXR
XXXXXXXTVDXKXXXXXXXXXXXXXKXDATPSVEKSNYLKTNGQTIPATIGGIPLIXLAXX
XXXXXXXXTTENVPEAWSXALATQKRVPILITNXXXXXYGXMXXXXXXYXXXXXXXXKXL
XXXXXXXXXXXXXXXXNSXXXNXXXXXXXSSNNXXXXXXXXXXXXXXXXXXTNNXXXXXX
GGXXGXTTXXXXKEVNNTLPSVTKIAGSDNNKXXXXXXIXXXXXNSXXXXXXNNXXXXXX
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NGXXXRXRXXTNXXXXXXXXFXXXXXXXXXXNHNNQTXXXXXXGXXTXXXVXXTXXXXSX
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XXXXXXXXXXXXKXXXXYLTXXXXGXXXXXXXXXXXNXDXATVAGLXXVNNXXXXXXXXX
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XXXXXXXXXXXXTEATLXKSXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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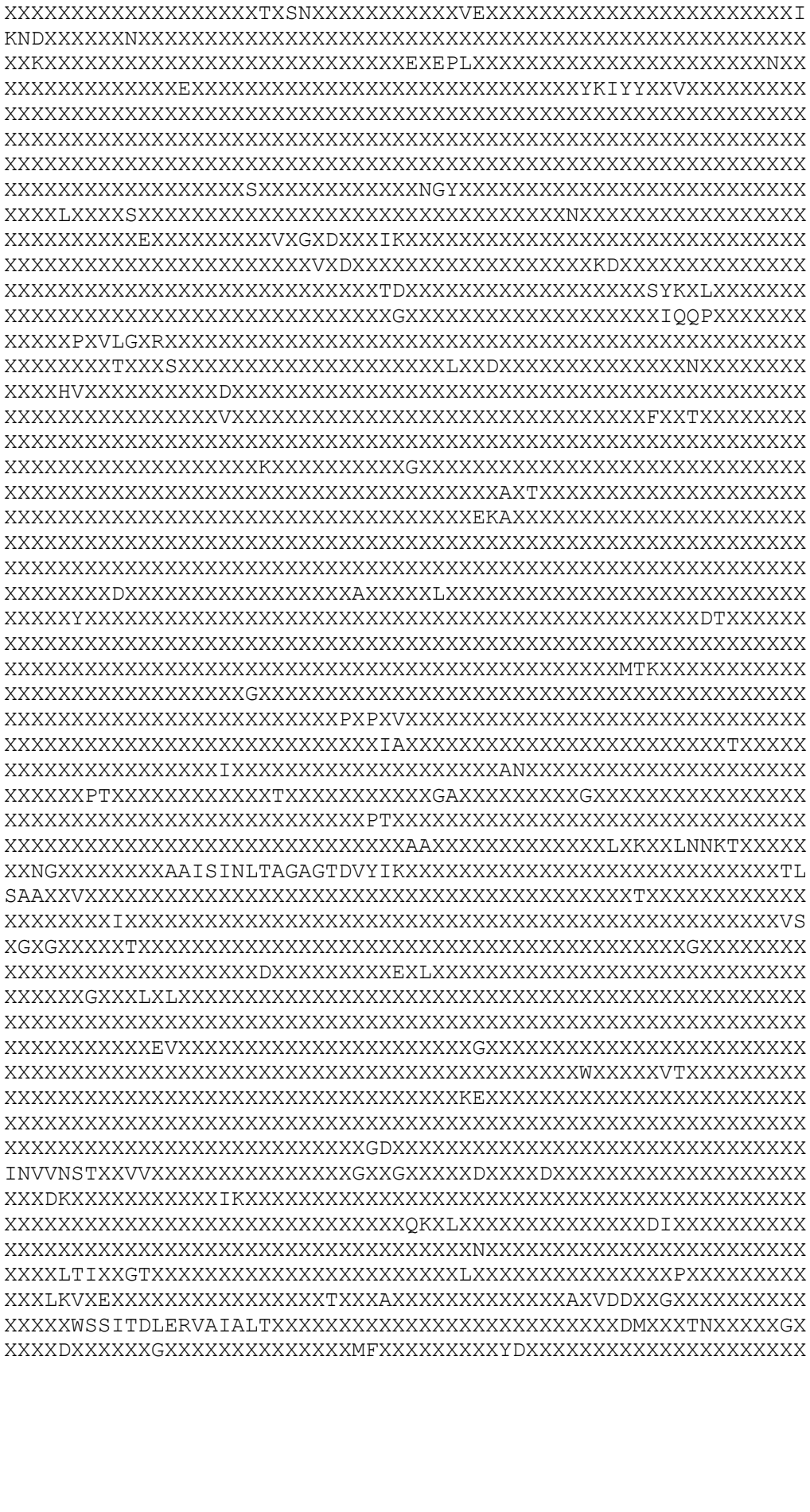

XXXXXXXXXXXXXXXXXXXXXXXXXXGYXXXXXXXXXXXXXXXXXXXXXXXXGXXXXXY
XXTXXXXXXGXXXXXXEXXSXVXXXXXXXXXXXXXXXXXXXXXXXXAXXXXXXXLXXXXXXX
XXXXXXXXXXXXXDXXXXNXXXXXXGXXXXXXXXXXXXXXXXXXXXYXXNXXXRXXSSTP
IISGDVAETDFSIILKWEEN

==> Clostridioides.txt <==
>MSA Consensus of 1099 seqs, protein
MNXXXKXLLXILNMILILSNVYIPXNALEXDVXVXVXQXPDIDIVLVAGKTXTSLXXFEX
DIKNSLKXKGVXINKVNVQAIQSSQXTAESNFTWQKYDHGKGSVSGXDVIFNGYTEEGYS
DFWFCNNTKIGEKTFTFTLNESQVKXXXXMXXGXXXGMKDYGDGTFEGYTLLIDSGTMSI
KKIPRVSXTXFXXXXXXQXXXENXXXXXTEEKSNLNKHKERXSVXKXXXXXXXIXXXLXX
NSXKXYXXNXLKLDYTLXXXXXXEGFXXXXDHNSHNCNXXXXXRLXXLXMXXXXXXXXE
VLRXPXXXDNSVKFIVNVEDKERTDFNSXTALGEIXXRXXXXXXXXXXGXSXXKXXIDX
LIXSNNNXGXXXXXXXXXSXIXXXXXXXXEXXXXIXKPXXXXXXXTNLKDXFXXSIXXXE
LKTXXXXXXXPDGXXXXXXXXXXXXXXXXKXXXXIXXGXXNGNPRXXXXXXXXXXLYMXXX
XLKXXXXXXXXXXXXXLXXXXXXXSXXXXXXXXXXXNXXXXXXSXXXXXXXXXXXXXXEA
SYDEDGXXXXXXXXXXXXXKYKNDFPVELSXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXEIKNXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXTVXSXXXEYXXXXXQYXXXXXXXXNXXXXXNXXXXXXXXXXXXXXXXXX
XXNGXXXXXGXXXXXXXXXXXXXXYKSXXXXXXXXXXXXXXXXXXXXXAXXXRLXXXXXX
NVXXXXXXXXXXXXXXXXXXGXIXXGXXXXXXXXXXXPXXXXXXXXXXXXXXXXXXXXX
LKXXXXGXXXXXXXXXXXWXXXXXXXXKXXXXGWXXLXXXXXXXYXXXXXXXXXXXGXXX
XXXXXXXXXXXXXXXXXXXXXVQELXXXXXXXXXXXXTXLXXXXXXXXXXDXXXXAXLXX
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NXXXSXXXXXXXXXXXXXXXXXXXXXDXXXXXNXXXXXXXKXXXXXXXXXXXXXXXXXX
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IKETXXXXXXXXXXXXXXXXXXGNXXLXXXXXXXXXXXXGXXXXXXXXXXXXXVXXXXX
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TLXYKXYXXPLXTTLNYNQSTXXXSXXXXHRXXXEAAIAXXYEGTIKDLXNXXYNXDXX
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XXXXIXXXXXXXXVXXXXXXXXXXXXXXXGXXRYETAXXIAXXXAYKTAYKTAYKTXNXX
XXDXXXDHSAXXXXGXXXRXXXXNXEDXXXXDXXXXXPXASRTARSASLSESVAXXXNAP
ILLXXKXXXXXXXXXEXKRLXXKXXXTXXXKXXKXXXXIGXXXXXSXXXXXXXKSTXXXX
XXXXXXSXXXRXXGXXRXXTDTTSXXXAKXXXXELGRKGXKXXVNDGXKXXXXNXKXXGX
XDAXXXXXQVTRDGDGVXAXXXXXPIILXDXXXXTXXXXXXXXXXXFXXXXXXXXYXXGG
XXXXSNXXEVNNTLPSVTKIAGSDNNKEXXXXXXXXTKDXXXXXRXXGXDRXXTNXXVIX
XFYXXLXNGXLXXXXXXXXXXXXXGXXXXXXXLXDALXXXXLAXXXXXPTWMRMYPQLRH
XXLXXXXGXXXXXHKXXLXXKXXXXXTXXGXXXNGNXXXXXXXXXXXXXXXXXXXXXXX
XXXKXXXXGGKXXAIXXXXXXXXXXXXXXXXXXXXXXAXXXGXXNXTGXXXXXXXXXXXX
XTXKAXXXXXXXXXXXXVXXXXXTIXMPNGXXXNXXXXXXXXXXXXXXXXXXXXXXTX
XNXGXIXXXXXXDXXGXXXXXXXXXXXXVXXXXXXXXXXXXXXXXXXXXXLXXXXXXXXXX
XXXGXIXXXXNXXXXXXIXXXGXXXXXXXGXXXXXXXXXXXXXXXXXSVXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXLXXXXIAGQXXXXXXXXXXXXXXXXXTXXTXXXXXXXXXXX
XXXNESVIXXXXXYKXXXXXXXXXPSXXXXXXXXXXXXXXXXXXXXXXVXXXXXXXXXX
XXXXXXXXIXXXXXXXXXXXXXXVXXXXXXXXXXXXXXXXXXXXXFXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXVXXXNXXXXYXXXXXXXXXXXXXXXXXXXXXXGXGDXXXXXX
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DXXXXXXXXXYXXXXXXXXXXXXPXXXXXXXXXNXXXXXVXXKXKATGYDDIKIQIETVK
EAGXXXXXXXXXXXXXXXXFGXXXXXXXXVXXKYIELVELXXSXXXXXXXGXXXKXXXX

XXXXPAXXXXXXXXXTXXXXGXXXYXXXXVXATXEFLNXNXGGXXXXXXXXXXXXIXXXX
XXXXXXXXXXXTXXXXGXXXXXXXXXXXNXAVXXKXXXVXXXXXTXXXXXXXXXXXLXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXATXXXXXXXFXXXXXVAAXXXXXLXXDAXX
XXXXXYXXXXXXXXXXXGDXTXXXXDXXXVXXLXXGTXXXGXXXXXXXVTGLPXGXXXXX
XXXXXXNTITITXXGXAXXXXXXXXXXXXXXXXXTVKAGAVSETTATDSXANXXFXXXXXX
XXXXXXXXXXXXXXXXXXXXTXYSXXXKXXYXXVXXXXXXXDXSXXXXXIXXXXXDAEGY
KDNKLEIDLSKENSDINIKRDRENNILVTLDKEIKQKFKGXXXXXXXXXXXXXXXGXXXX
XXXXXXXXXXXXXXXXKFXXXXNNTXXXXAXXXXXXXXGXXXXSXGXXDLGGFSLXXNXXX
XYXXXATTPVXXXXGXXXGXXXXXXYKXDXXXXXXVDXXXXXXXNXXXXXKXXXXXXXXV
XKVFNNDYQNKIEEVLVNNNVVXNXXXXXXFYXXXVXGXNXXXVGGXXXTXKSSGYENFS
TKVKIHGDKISVPNIEASKSVMGEYTFKSDAKYINDITDVKLNGKSMGSSEWSKQGDKVV
LSASINSSDVITFESNNYENYVYTVPKKSVDSVGVSIISSGYYKFKHNESGWSKDVEVYL
NGSLLSKDSDYITSDGEIVITKKLNLGDKLSVKSGKYVDYNYTVELLDNKVEIKYNSYNE
NYSFNSSDSYWRDNITSVSINGSEINMTTDFQPTAGYKNNYSGGIDIYNSLTTNDEVVIE
SNGYKDYKIIIE

==> Clostridium.txt <==
>MSA Consensus of 1202 seqs, protein
MXXKXXXXXXXXXXXXXXXXAXXXXXXXXXXXXXXXXXXXXXXXXAXXXXXXXXXXXXXXX
XXXXXXXXXTXTXXTXENXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXTXXXXXYX
XXXXXXXXXXXXXXXXPXXXXXXXXXXXXXXSXGXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXYVXXXXXXXXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXIXVXXXXXXX
XXXXXXXXYXXGXDXXXXXXXXXXXXXXXXXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXX
XXPXXGXXXXXXXXXXXXXXXXXXXXXXXXXXXXQINXXXXXXXXXXXXXXXXXXXXXXXP
XXXXXXXXXXXXXXXXTXXXXXXXXXXXXXXXXXXWXXXXXXXXXXXXXXXDXXCMAXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXSDGXNXXXXXXXXXXXXYXXXDXSXXTVTSXXXXXEXXXXGXXXXXXXXXXXXXSXXXX
XXXXXXDSXXXXNGXXXXXKAXXXXXXXXXXXXXXXXXWXXXXXXXXXXXXXXXWXXXXXXX
XXXXXXXXXXXXXXXXXLXVXXYXTXXPXXXNXXXXXXXXXXXXXXGXXXXXXXXXXXXYX
XXXXXXXXXXXXRYTXXXXXXTXXXXXXXXXXXXXXXXVXXXXXXXXXXXXXXXXXXXXXX
IPMSXXXXXXXXXNXXXGGXXXKXXXXXXXXXXXXXXXXXXXXAXXXXXXPPXXXXXXXXI
XVXXXXXXXXPXXXXXXSXXXXNXXXXGXAGSXXXXXAXXXXXXXXXTXKKEYXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXDXXXXAXXXXXXTXXXFXXXXXXXXXXXXTXXXXSAAXXX
EXXXXXXXXXXXXXXXXXXXXXXXXXXXNHVXXXXXYXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXRXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXKXXXXXXXXXXXXX
XXGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXVXXXXXXXXXXXXXXXXXDXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXITXXXXXXXXXXXXXXXKXXXXXXXXXXXXXX
XXXXXXXXXXYXXXXXHXXXXXDXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXTXXXXXXXXXX
XXXXXSXXXXXXXXNXXXXXXXXXXXPXXXXXXXXTIXXXXXXXXXXXXGDXXXVXXXXXX
GXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXKXLXXXXXXXNRXXXXXXX
XXXXXXXXXXXXXXXXXXXXTXXXXXXXXXXXXXXXXXXXXNXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXKXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXN
PTVEFXTXXNGXXXXXXXXXXXXXYXRXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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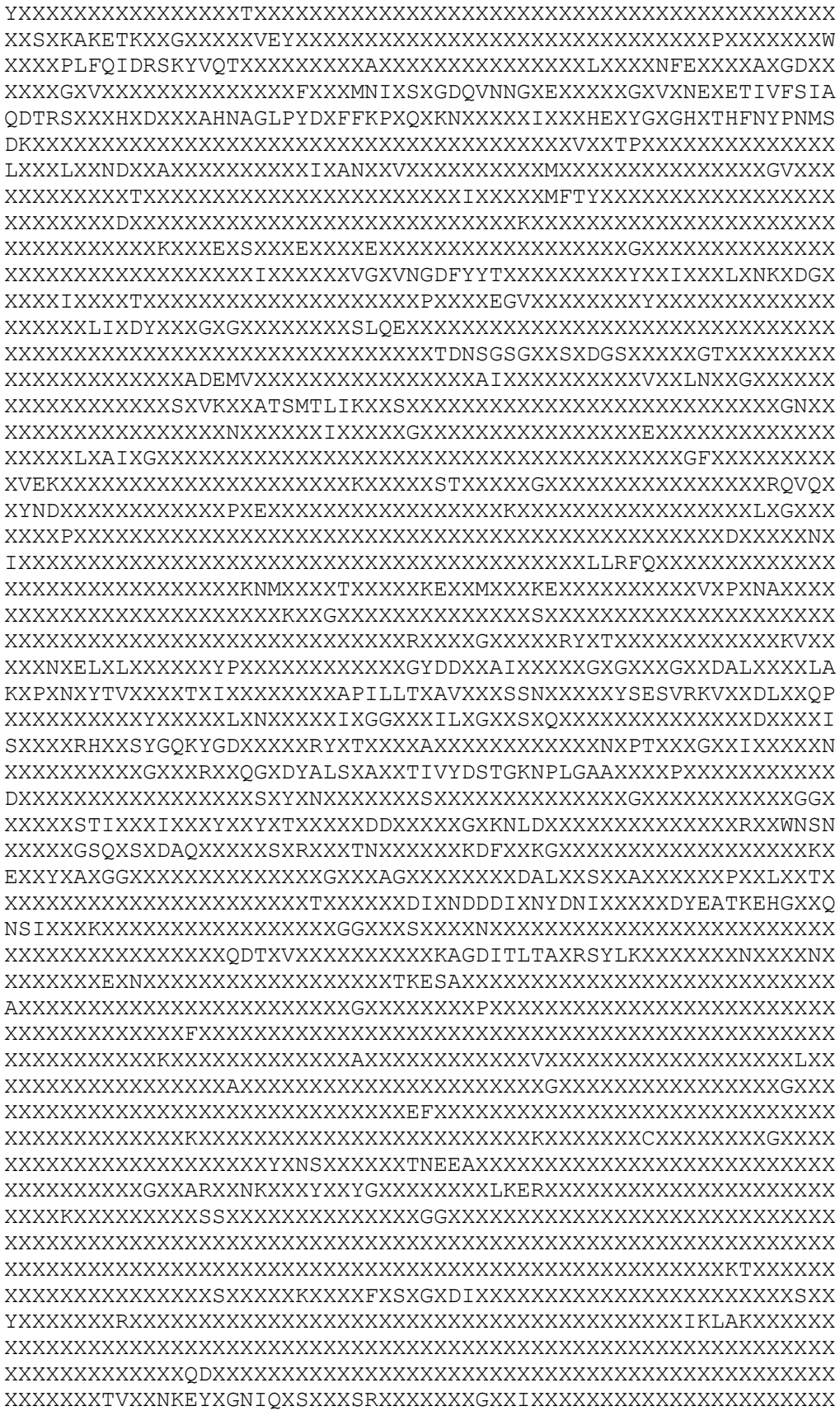
XXXXXXXXXXXXXXXXXXXXXXXXXEXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXLXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXGXNXXXXXXXXXXXXXXXXXXXXTTSSSFXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXTXXTAXXXXXVXXXXXXXXXXXXXXXXXXXXXXXXTFXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXGXXXSXXXAXXXXXXXXXXXXXTXXXXGXXXXXXXXXXXXXXXXXX
XXXXVXXTXXXXXXXXXXXXXXXXXXXXXXXTXQXXXXXXXXXXXXXXXXXXXXXXXXXX
EXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXTKTAALTXXXXXXXXXXXXXXXXX
XXXXGXXSXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXVTXNTNXX



XXXXXXXXXXXXXXXXXXXXXXXXXYKGQXXXXXXXXXXXXXXXLXXXXXXXXXXXXXX
XDXXXXXXNPTXSNIPXXXXXXXXDXXXXXPXIXXXXXYXXPXTVXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXLQTVQANNXXGXXXXXXXXXXXXXXXXXXXKXXXXXXXX
XXXXXXXXXXXXXXTVXXXXXXXXXNVXXXXXXXXXXINIGSXXXXXRTNKDENXXXXAVX
KXGNTDXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXDXXXXXXXXXXXXNXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXANEAGXXXFXXXXXXXXXXXXXXXXXYXXXXXXXXGXXYXX
XXXXXXXXXXXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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XXXXNEKXXXXXXXXXXXXXXXXXSXXXXXXXXXPXXEEXXKXKXXXXXXXXXXXXXXXXX
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XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXVXXXXXXXXXXX
XXXXXXXXXXKXXXXXXXXXSXGXXTXXXXXXXXXXXXXXXXXXXXXXXXFKNXXXXXXRX
XXXXXXXXXXXXXXXXXXXXXXXXXTXXXIATXXDXXXXXXXXXXXXXXXXXXXXKXXXXX
XXXXXXXXXYXXXXXXXXXXDXXXXXXTXXXXXXXXXXXXMXVXXXXXXIXXXXXXXXXX
XXKNLKXXXXXXXXXXXXXXXXXXXXXXAGAXXXXXXXXXDXXXXXXXVXXXXXXXXXXXX
XXXXXXVXXXXGSTXXXXXXXSXXXXXXXXXXXXXXXXXXXXXXXXXXXXXIXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXDXXKXXXXXXXXXXXXXXXXXXXXXXXXXXX
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XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXSAIKXXXXXXXGX
XXXXXXXXXXXXXXXSXXXXXXXXXXXXXXXXXNDXXXXXAAXLGNNXXXXXXXXDMDKX
XXXGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXIAX
XXXXXXXXXXNXXXXXXSTXXXXXXXXXXXXLDPKISGITMKKSVSQSIXXXXXDGXXXX
XXXXXXXXXXXXXXXXXXXGXXXXWXXXKLDNEWYNLDATWDDPXXXXNXXXXXXXXXNS
XXXXXXXXXXXPXXXXXXXXXXXGSGSVXLXXGIKVVSGDDXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXVKXXXXKYXYXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXSVDPSDSKXXXXXXXXXXGXXXXXNXXXXXXXXXX
XXXXXXXXXXXXXXXXXKXXXXXXXXXXXXXXXXXXXFXXXGXXXXXXPXXXXXXXXTX
XYIXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXWXXXXXTGNNGGXXDXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXVGAXXXXXXNDSS
LSTVXXXXXXXXGXXXXXXSXPXXXXXXXXIXLSCXNGIXXXXXXXXXXXXXXXXXIXXX
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XXXXXXXVXXXXXXXXXXXXXXXXXXXXXXXXXXXLXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXTXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXGXXXXXXXXXXXXXXXXXYXXXXXXXXXXXNIKVXXGXXVXXXXXXXXX
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XTNIXXXXXXXXXXXXXXXXXXXXXXXXXXXSAAXTXXXXXXXXXXXXXXXXXXXXXXXXX
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XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
AGTXXXXXXXXXXXXXXXXXXGGTTXXXXXXXXXXXXXXXXXXXXPXXXIPVTGISLXXX
XXXXXXXXXXXXXXXVLNLYYVDGENHLQKVNSNXXXXXPXXXXXXXXXXXXXXXXXXXX
DXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXTNLINXXGDXXLNI
XXTXXGXIKXXXXXXXXXTTMXXSXXIXXTXXXXXXXAXSSVEMXYXNXXXGXXXXXTKX
XXGXYXGYXXXSXXXXXXXKLNLSTLQPNNNNNSSITXIXXXXXXXXXXXXXXXXXDXXX
XXXXXXXXXLXXXXXXLXVGDVEXXTAAXXXXXXXXXXXXSDXXXXXAXDXXPNLMPQS
EGXXXXXXXGXXXXXXXXXYXXXXXRNDSSTPIISGDVAETXXSXXXXXXEN

==> Coccidia.txt <==
>MSA Consensus of 334 seqs, protein
MNXXXLLXYXXXIXXAFXXXXXGVXXXGGXPXXXSSXXVXXXXPXHQAAVEXXXXYSXXX
LAXXXGGFLGXXXXXXXLXQXXLGGSXXXXPXXXXXXXACXNESSVSSXXXXREXXXXCX
XWXXGXXXXXXEXXXXXXXFXXXXXWXXXXXXXXXXXSXXXSSSLXSXXXGXGXXXXRXXX
XPSLSVLGSIXXXPRXGGETXGXXXXXXXXCXXHDIPCPLSCTVSEWGNWSRCSLTCGIG
HQMRERSVIKAPKDQNLFQCPETRQIRECIQDTCSSNCTLGEFKFKSAVSGSPCLMEKGC
VERREILHPPFKPELGNFTCKVEEXSRXXITNSRVSRPSDCLGLSEAATGDDDGSSAXEE
AGDQQYDMLVSKLVHLSHLGCXXXXXFXALEALLXXXXXXXSGCPXXXEXXXXXXXXXXF
XXXXXXXXXXXXXXFXXCXXXXXXXXXXXXEXXXXXLXXXXXXXXXXXXXXXXXXXEXEX
XXXXXSXXXXXXXXXXHLXXXXXXXRXXVXSTXXXXGXXXXXXXXXXXXXXXLSXFXXXXX
XSXXXXXXXXXLXALXXGSANXXXXTNNNXXXXXVXGEMXXXXXXSXXXXXXSXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXELMTXXXXXXXXEXXXXXXLXXIXXXXXX
XXXXXXXXXXXXXXEXXXXXXXXXLXXXXKXVXXLEXXFSXXXXXXKSXXXXXGXFNXXX
KVXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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XXXXXGXXXXPXXXXXXXXXXXXXXXXXXXXXXXXXWXXXXXXXXXXXXXXXXXLTXLXPX
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XXXXXXXATXXXXXXWXXEXXXXXXXXXXXXPXAPXXXXXXXXXXXXXXXXXXXSXXXXR
XRSXLXXXXXXXXYCPXXIEYSNCVVXNKCPENCPQXXVXXXXXXCXXXXTFXXXXXXNX
XXNXDSNXXXXXXXXXXXXXXXPVVSXXXPXXXXXXXXKXXXXXXXXXXXXXXXXXXXXX
XXXVAXXXXXXXXXXXXXXXAXXXGXXXXXXXXXXXXXXXXRXCXXXXXXXCXXXXXXXXX
XXXXXXXXXVXXXXEXXXXKXXXXXXXXXXXXXXXXXWXXXXXXXXXXXXXXXXXCXXXCXX
XXXXXRXXXXXXXXXXXXXXXXXXXLXEXXXXXXXXXXXXXXXXXXXXIXXXXXXXXXXP
XXXXXXXXXXXXXXXXXXXXXXXXPXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXLQXX
XXXXCXXXPQXXXXXXXXXXCXXXXXXXXSIETCXXCXXXXWXXWXXXXXXRKEDCXXXX
XXXXRXXXTRXXXXXXXXSXXXGXXXXXXXXWAASGGPQKETXXXXXGXXCXXXXXXXLC
NGTEXTXXXXXSXXXXXXXXCXDVXCGXXXXCXGXVXXXXXXXSSXXXXXXXXXXXXREX
XXGXWSXXXXXXXXXXXCSXXQXXXXXXXXXCGXXXXXXXXXXXXXXXXXXXEXXXEESE
TEXXSXXXXXXXXXXXXXXXCXXXXXXSXXXVMSXXXXWXXXXXXCXXGVVRRYRDFDF
XXXGXXARXXXGXXXXQXXXXXXCXXXXXXXEYSXXXXXXXCXXXCXXXXXCXXGXXXXX
XXXXLXXXXXXXXXXXXXXXXXXLXAHXPXXDCSGTQTRDRXXXGTAAQAXXXXXXXXXX
XXXXXXXXXVIDEXXXXXCXXXXXXXXDTRRSIGCXXPXXCXXXXXXXXXXXXXXXXPXX
XXXXXXXDATLAIAXXXXXXXXXXXXXXXLCIIXXSXXXXGGXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPXXXXXLXXXXXXXXEXEXXKAXXXXQX
XXXXXXXQXXXDXXCQXXXXXXCXXXKXTXXXXXXXXARXXXXXXXSXXXXXWRCXXXXX
LXFXXXXXXCXDXCXNXXXCXGXXXXXXXXXXXXXXXXXXXXXXVXXXXEXXXPAGPXX
LXXXXATXXXCXXXGXXXXQXAXNXXXXXXXADXGXXGXXXXXXXFSXXXARLXXXXXXX
XXXXXTXXXXCXXXXXXXXXXXKLLNLPXXXXXXCXXXCXXXXXXXXXXXXXXXXXXXXX
XXXXXHXXXXXXXXXXXXXCXXXXXXXXXXSGXXXDRXGXXXLXXXXXXXXXXXXXXSXX
XXXXXXXXXXXXXEVXGXXXLXVRXXXGEXCXPTXXXQXXXXXPXYCSXXXXXXEXLXYX
XXXXXXXPXXXXXXXXXXXXXXCXXXXRXXXXXXFLGESXISEXXLYPFHDFVKGAXLAX
XXXXXXXXXXXRXDXGXXXXXXXXXWRXGXXXXGXXXXXXXXCXXXXIXNXXXFXXXXXX
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KXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXVXV
XSGTGYIXXXXXXXXVXGXXXLQXXLDXXXXXXXXXXCXXXXXXCXXAVANPQXXXSXXX
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XLXXELXXXXXXXXXXXXXXXXXVXXXFSGKTLIYVAEGDEAASAYPLLLTKVDEEETLH
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PNDSDLSXXXXXXXYXXXXASKNNNSGKNSCKDNPIXXXXFNRSCEELKTSFGCSINLEK
IXPXXXXVXXXXTXXTKXXAXXXXXCVHSDNKGSRAPXIGXXXXXVTNKNADIKTERPYT
IIFNEKRSLEQXXXXXKXXXXCXXXXYXDXXXMCXXCXXGXXXXXXLXXXXXXXSXXXXR
XCXEXHXXXFXXXXCKXXXWXXXXXXCXXXXXXXXCXXXXDXXXGVQSEQNDNEIXGXXX
XXXXXXCQXXCAADPSXXIKENRGSDERNGSYKGSDLDREFFXXXXEXXXXCXXXXXGXX
AFKERGVLGXPXVXSXXCPXXXXXXXCXEXNWGKMXXXXLXDEGGKLTQELXGXXXPDDI
PXXXLXXXXXXXNCXXYXXGCXXXSXXXXXXXXXEXXEPMEXXXXXXCXXRCXCDXXXXX
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KEAXCVVKRKGFYKHSXGAHXXXXCXXNXXXXXXXXXSXXXXXXCXXXYYQTRKTGVTGV
TVGPREFCVGSEPTVSSLSQYAGAKIMCPDNTATVPPNAQNDHPYKCMCQEGXXXSKVDS
VXPTVICQPXRVGDXXGXIXDREEADAPVGSSTQSDDGXNAEATMANPGYXFSXASGXXX
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CDAXEDXCXXGXKXXXXXXCPXHXXXXXXXXXXWXXXTSXCXXGXXIXSGXSAXXXXXXE
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SHGVCSETMTEYXXSECXXXXTNTFSXGEXCTXCPSMXXNIXXXXGYYLXXLLFNIVMXY
MNVAAGFNRRSIHKSIVIKIASNXLTXXSVLSXXDFSXIXXPSWXXXXXXXXXXXXXXXX
XTDRNMKSKFXXXXVDCXLRXXXDLSXSXSFFXGMDEEATMXFYALXPIXLPIXATXIFG
AKMXXIVXRXXXXYXNSTQRKLELLKQTMQYGLYXLAQQLKEKYEEDRVFMIFRYXALPG
ESIXRRAAKFMEDMXPIYVTSVLFFXYSSTTRTSGYSDPENSCCGLPQDFRXMLSLLXCT
XIXFGRXHXAKYFLXAXMXVXCTXXXSGPYFKFFAVGITGLXVWSIGIPLSCFLVLYVNR
KXLNSREXRLKYGFLHNGFVXKYWYWEXVVFARKXXVXKENGIQDTGADXVSSVXLIXDS
NSDSXXKXGSRXXXXXXIAXXFLIXHLXXQPFDKRSYLTLDKLENHSMXXWTIXXIXXXX
MIGXDFXGXVNXALLXFXXVLSCXFXLEVXVSLXXAYFDNVXXXXTXXXXPXXGYVFRFF
AXLSEKRRAREPIVVSFDTETGNIESEGVTGSSPNSSTYNEVIQLVAAKRXXWXLFRXXX
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XLXVXXXXXXXXXXXXXXXXXXXXXTXXXXXRSXXXXLXXLXXXIXKLXXRLQELKXNPX
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==> Coelurosauria.txt <==
>MSA Consensus of 877 seqs, protein
MLCWNEVQSCFLLAFLAVAAYSVSDAQGQVSPPTRLRYNVVNPDSVQISWKAPKGQFSGY
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GXQLTLT

==> Conoidasida.txt <==
>MSA Consensus of 334 seqs, protein
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VERREILHPPFKPELGNFTCKVEEXSRXXITNSRVSRPSDCLGLSEAATGDDDGSSAXEE
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XXXXXXXXXXXXXXFXXCXXXXXXXXXXXXEXXXXXLXXXXXXXXXXXXXXXXXXEXEX
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XSXXXXXXXXXLXALXXGSANXXXXTNNNXXXXXVXGEMXXXXXXSXXXXXXSXXXXXXX
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KVXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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==> Coriobacteriia.txt <==
>MSA Consensus of 115 seqs, protein
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TGATTXXELXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXYYXXXXXXDRL
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GXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXLAEA
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XXXXXXXXXXXXXXXXXXXXXXPQXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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ISGTXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXTATSGGTGAXXXXXXXXXXXGX
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==> Craniata.txt <==
>MSA Consensus of 6061 seqs, protein
MLAFRVVRGASEEPFILAGGNVQSIVQKEVYIIQVSVGSHQWTVKHRYSDFHDLHEKLVS
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DDSVKLIPKIEFLELSHNDVSLIENVQHLYNLIHLDLSYNKLASLEGVHTKLGNIKTLNL
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LNNSDKKVPTSLLDLSKEYGRGHHICLDHSDEEHGAXSDXXXXXXXXXXXXXXXXXXXX
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APPALDSTRAESIDIVKXXXDXXXXVXXXXXXXFASCXXXXXXXXXXXXIXXXXXXXXXQ
HIPAALKLAXXXXXXXXXXXXFHXXXXGXXXXXXXXXXXXXVVSDSQXXXXXXXXXXXSC
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XYSNXTXXXXXXRXXXGXXXXXXXDXXXXXXXXXXXGXXXXXXXXXXXXXXLHXXXXXXX
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SXXXXXXXXXXXXXXXXXXXXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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XCSPLXXXXXXXXXXXXXXCXXGWXXXXXXXXXXXXXXXXXXXXCXXXXXGXXCXXCXXX
PNKIXXXXXGXXXXXRXYGXXXQCXXXXXXXXXXXERXXXXXXXXXYCXAXXPCXXKXXX
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XTTXPXXXXXXXWXXXXXXEDIXAXNGEXXXXXXXIHXXXXPLXXXXXXPXXXXXXXXXX
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XIXXEDTEXXXXXXTXXPEEXXXXDSPXXXXFXXFXXXXXXXDXFSXXXXXXXXXXXXXG
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XLLILGXXXXCXXXXVTXXHXPXXPPPIXXXXXXXXYXXXXXXXXXXXXXXXXXXXXXXX
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==> Crustacea.txt <==
>MSA Consensus of 224 seqs, protein
MLEISXLXLXXPPXXXXXXXXXRXSXXXXXPPXXRISSLLLXXPPFARISSLXLEYPPF
CSNIXXFXXXSSLXLXXXPXXSXIXRISSLLLEYPPFARISSLXXXXXXXXXXXXXPPP
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XXXXXXXXXXXXXXXXTQLRPSXXXXXXXXXXXXSLRHHSLRLXXXXXLXCXXTHXXVXXXX
XXXXXXXXXXXXXXXVXXXXXXPXDIXXXXXXXXXLXXXXXXXXXXXXXXHXXXXXXXXXX
XXXLRHHSLRHHSXXXLTXXHSXXXXXFXXXXXXSSFXXXXXXXXXXXRXXSXXXXXXXXX
XXXXXXXXFVXXXXXXXXLXXXXXXXXXXXXXXXXPXILPFARIXXXXXXXPXXXXXXXX
XXXXXXXLXXXXXXXXXXXSTSFTSXXLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXIXX
XDIXLXPXXXSXXXXXXPXXDITHFDXXXXXXXXXXXXXPSXXXXXIXXXXXXXFXXPXX
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SLRHSSLSTXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXEYPLLNILPLLEYPEFPFARI
NILXXXXXXLXXXXXXXXXXXXXSXXXXXLTSTSXXSTSLLHSXXXXXXXXXXXLXXEXX
XXXXXXLLXXXXXXXXXXXXXXXRHHTSTSSLRHXXLXXXXXXXXXXXYSXXFXXXXFXXX
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XLRPXXLXXXXXXXXFXXXXXXXXXXHSLRHHXPXLXXXSXXXXSXXXXXXXPSXXXXS
SXXXXXXXXXXXXXXXXXXPXXNIXPPFARISSLLLESSLLLEYPSFCSNILPFARISXL
FXXXXXFCSNILPFARISSLCSXXXXRLXXXXXCSNILXXXXXXPXXXXXXLXXXXXXFD
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PPXXXXXPXXXXXXXXXXXXXXXXXXXXXXXXXPSXXXXSXXXXXXXXXXXXTTXXXX
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XYXNXANXXXXXXXXXXXXXXXXXXPXXXXXXXXXHXXXXXXXXXXXXXXXXXXXGXXXX
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PXPXXXPXXXXXXXXXXXXENXXXYXXXXXXXXXXXXXXXXXXYXXXXXXXXXXXXXXXXX
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XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXTXXXXXXXXXXXXXXXXXXXXXXX
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XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPXXXXXXXXXXXXXXXXXXXXXXXXXXXX

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KQDSLXXPTXXXXXSXXXXXPXXQISSVXXXXXXXXXXLVXXXXXXXXXXXXXXXXXXXX
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PXXSXXSNQTPXXXXLXXXXXXXXNHQSHQPQKSSTSXXXXKXXXXKXXXXSHNLGXPXX
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==> Cutibacterium.txt <==
>MSA Consensus of 171 seqs, protein
MAVEATTTCKRVVGPVVAAALMVGAVGVXAXPAQAAXXSGPADYAXQAXXAADYIDGHXA
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AGEXTTYGGXDYAKPVTSLPXSXXXERPFHQALDMIALERLGKPIPQXLFKSITDYXXXX
PXRAGAFGYTKRNHDXXXNXPSXXXTDGLMLAALSHVVSNPHLIXTAYXQXGITAVKAAL
VKRLDADRQXDGWGWXXAXGAXVRATTRVAPGLYRAGDANHKDQAVKGQAWLAXQQXXDG
VGXXXXXSFXXXVXSPAWXXXATXQAVPVLRGLQSASTWSGKTPKNTPTCXDXIGANPAR
AVTVDGWVPPRRLVKMTVLGDSYSAGNGTLVDDGYPADGSYRSPKNYGSVLTRRLNREFG
DDTTFQTDVRAWSGAQITTGDHTIVSQADGMDPHTXVVLMTAGGNDLDFTXVVENCFXEX
XWSAAXCGGSVDAXRKKIDATMTKTTTLLSHIQXRLADPAHTRVILIGYPYLIPADXDXP

XXDVPSTRVRAAEDEFRTRQAATIKAWNTSHALKVTYTPTTSLFNTHEPEPLVHNSTSPG
GXQNPXRWINXVXETAGXXXXXXGXXXXPILXXXSEPSQDXXNWYHPNVXGHEQIAGLVH
DALLSRXARSASLSAXXGXXESVAQVASXPGVRMRAAVIGQSQVRRGNPLSLDASSSYTA
FGHIRRWQWDLDGDRHYEIDXXTPEITRTLTRIGTYQAHLRITDTTGTTDTLTFPIQVTR
DGDGVPDTQDNCPTIANQDQTDTDHDGIGDACDPHTTTKTPR

==> Cypriniformes.txt <==
>MSA Consensus of 129 seqs, protein
MDKTGCGTHXXXXXXXXXXXXCXLXXXQTXSXMXXXXXXXGXXXXLGCAHLPLSYRQKEL
CARKPHLLPSVKEGARLGISECQSQFRHERWNCSTRRDPNVFGYELTSGTKETAFIYAVM
AAGLVHAVTRSCSAGNMTECSCDTSLLGTGSPTEGWHWGGCSDDIAFGTLFSRRFIDNSV
KNISTRGEEALFIMKQHNSEAGRQAVAKTMLTDCRCHGVSGSCAVKTCWRTMAAFERVGA
YLKERYETSVQVVDRTKRKVRRKEKEKRQTPIAKEDLIFFNKSPNYCLEDRRLGVTGTRG
RKCNRTSAGPDGCNLLCCGRGYNTHVVRHVERCECTGKREGGIAVKAKGQLVLPQSGEGP
QRARIGESVIIMXFXLXXVCXXXXLXXGXXXLXXXXXXAVXNRCDXXXTXXXKXXCXSCX
XSXXAXCPXGXRKXXXXXSXXXCXYXVXXGXRXXXXXGCXXXCXXXXXXXXCCPGXWGXX
CXXCPXXXXXXCXXXGXCXXGXXGNGTCXCXXGXXGXACXXCXXGXXXGXXCXXXCSCXN
GXCXSGXXXXXXCTCXSGYTGXXCXXELXXCXXLXCXXXSXCXXXXXXGXXAVCXCXPGY
XKXXXDGVQCXXIXXCXRXVCHANAXCAHTGPNXHVCTCXEGXXGDGXXCXPIXPCXTNX
GXCXXXSTXCXXXGPGXXXCXCLXGXEXXXXXXGCXXKXXCXPXSCHXXAXCXXXXXGTX
XCXCXXXXIGXGXXCXGNXXXXLXEXXXXPGGXXXGXLXXXXXXXXXXXXXXLXXXGPFT
XFVPXXXXXXXIXXGSXSXXXLNEGSEYFKIDNMTGDLSTNERRIDREKXCKXHLILGQN
EXLYXFXVKXLXAXXMXTYGGERXRXXXXXXXXXXIHPSIHPSIHPSIHPSIHPSIHPS
IHPSXNXPSXXPSIXPXXXXSXXXSXXXGILXLLPTATDRDFGRNGIERXXLXXMXAESX
XRRIGTSGSGSVDXXQXXIXXXXXXXXXXXXXLQVSDXXASNGXIHLXIDKXXXXXXXXS
SELTLRVRDNNXXXXXXXXXXEIMIXXXXXXFXXFXSLLXXXXXXXXXXXXGPXTXXXPT
NXAXXXXXXXGXLXYXXSEEXKXKLXXLXXXHESTGXXSXXXXXXXXXXSXXXXXTMARDR
GQPPKTDKATVIINIKDEAXXILXXNXXXXGXXXXXXXGVXXXXXDXXAXNGXXHXXXGX
LXPXSIXPIXPHRCDXXXXXXXXXXCVXCXXXXXXXCQLKPXGXXXLXXXXXGCXXXXXX
XRWXXSLXXXGCAXXCNXTXXXXQCCXGFXGXDCXPCXGGFXXPCXXXGTCXXGIXGNGX
CXCEPXFXGXXCXXCXDXXKXGXNCDXXCXCXHGXCDNXPXXXGXCXXGSCXXGXXGEXC
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NAXCXXKSTVEVSFPENXGPGXXXCXCLXGWXXDGXXCXXINNCLXXSRGGCHXXAXCXX
XGPGQXDCXCKXGXXGXGXXCXXXNXCXXXXGGCHXLAXCXGMPVXXXPXXXXCXCXXXY
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VNXXXVXXXXXXXDLXXXXXXXPNIRTVVRXXXXXKXXXXXXSXXXXXXXXXXXIXXXDX
XAXNGXIHXIDXVLXXXXXXXPXXXXGLXXXLXXXXXXSLFXXXXLXXXLXXXXXXXXXX
TXFXPXDXAXXXYLXXTXXXXXXXXXXXYHXXXXEXLXXXXLXXXLXKXTXLGXXXQXXF
FXXQTXXXLXXNXXXVNXXXXETXXGXXXXXXXVLXXXXNXCXXXXXXXXKXXGRCXDCX
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NHMMIENVKIPLTSFXXXXLFXXXXXXXXXAXXXGFKXFXXLXXXXXXXXXXXXDXXXXX
SXXXXXXXXXXXXTXXXXXXLXXXXKXXLYXXXXRDXLXXXXCXFXYXSXIXXXXXXXXX
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FXXXDXXXXXXXLXXXNXXXXXXXXXXXXLXXXXXGXXXXCXXXXXXXXPPXXXXRXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXLXXXXXXXXXCRXCGXXXLXXXXXXXXXGK
IQRVSTXXQXCXXXXXXXXXXXXCXXXXXXVXXWKXXXXXXXXXXEPXCXXXXXSHIXAS
LHXXXXEMYRIPTSXXXXXXXMSXLXXXXXILICXXCDXXXXGXGXXXXXXXXXXXXXXX
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QXGXXSXTPXSXXXGXXXXXGXXXXXLXXXXXYXXRXXXXXXXXXXXXEXXXXXXXXXXXD
XCQPNXCPXXXXXXXRXXXXXXXXXXXXXXXXXXXXRTNRVXXXXXXXXXXXXXXXXXAX
XXCXXXXXXXXXXXPAEXXXXXXXXWXXXPXXXXXXXXXXXXXXXXXXPXXXXXXXXXXX
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NVGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXEXSXXXXXXXXXPXXXXXXXXX
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SXXXXXXXXXXXXXXFXTESTILKXXXXXXXXXXXXXXXXXXXXXGNPXXXXXXXXXXX
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PTXPXXXXXXXXXXXXXXXXXXXXEXXXXXXXXXEXXXXXXXXXXTXXXXXAXXXXXX
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XPXXAKXXXXXXXXXXXXXXXXXXPXXXXXXXGXXXXXXXXXXXTIXXXXXXXXXXXXXX
LXXXPQXPXXXXXXXXXXXFGRDSLGDDNLIDRKETIXXXXXXXXXXXXXXXXXWXXXXX
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SXXXXXXXXXXXXXXXXXPXXXXXXXXXXXXXXXTXXXTXXIKXXXXXXXXXXXXXXXP
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DKYGRXXXXXXXXXXXXXXSXXXXXXXXXXXXXXXXXXXXGXXXXXXXXXXXXXXXXXXX
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GXLXXNMGXXXXXXXXXXXXXXRXXXXVLGXXLXXXXXXXXXXXXXXXXXXXXXXPXXX
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GXXXXXXXXXXXXXXXXSXSXXXLXXXXXXXQXXXXXXXLXXXSXAXTXXXXXXXXEXXX
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SERVXSPGXPXXXXXXXXXTSPXXXXXXXXXXSXXXXXXXSXXXSXXGXXXXXSXXSXSX
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==> Cyprinodontiformes.txt <==
>MSA Consensus of 147 seqs, protein
PTFSPTFSPTFSPTFSPTFSPSFSPTFSPNFSPTFSPTFSPTFSPTFSPTFSPTFSPTFS
PTFSPSFSPTFSPNFSPTFSPTFSPTFSPXFXXXXXXXXXPTFXXXXXXXXXPTFXXXXX
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QLXVXXXLXXXPXXXTMANQXXXIXXXXXGXXLXXXKGXXXXXXXXXAXNGXXXXXXGXL
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SFRXHILXGXXSXXXLXXXXXXXLSXLXPAXXXXXXXXXXXXXXXGXAXIIXXXXXAXNGX
IHXIXXVLXPXXXXLPPEXXXLXAXLXXXXXFSLFRXXXXXXNLTXXXXXAEEFTXXXPT
DXAXTXXLXXXXXXXLXXXXXXYHVXXXEXLLXXXLXXGXXKXTLLGXXXQXXXXXXXTX
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XGXCXCXXGWXGXXCXXXIXSKADXXCXXVXCXXXANCXXXPXGSAAXCXCXAGXEGNGT
FCXXXDXCXXXNGGCSXXAXCXXXXXGXRXCXCXXGYTGDGXVCXEIXXCLXXNGGCHXX
AECIXXGPNXTXCXCXXGXXGXGXXCXXVNXCXTXNGGCXXXXXCXXXGXGXRXCTCXXX
XXGDGFXCXGTXXXELXXXXXXXFXXXXXXXXDXIXLXGXGPFTVFXPXXXXXXXXNSLX
XDLKEXXXXKXXXXXXXXXRXHXVXCXXLXXXDLXXTXXXXSLSGXXLXXXXVXXGXXXI
NXXSXXXXSDXXXXNGXIHXIDXXLXPXXLXXXXXXLXXXXXXXNXXXXAXXXGYCTSSF
CLXXFYKLXXDXGXXXXXXXXIXQGAKPXTXFXPSDXXXXXLPXXXXXXLSXXLQXXXXQ
LXXXXKXHIVRXIXXKXXXXGQXXXXXSXRTXXGSXXXFSCXXXXKIVNTAEKETIEEEE
EVKLSSESVAVLVDVGXXXXNXXXXRXXXRHLXFXXGXXXGIDXLLXPPXLGXXCDXXXX
XTXAXXXALKEGHEDLXXXCGXCXXXXXXCSXXHVDTGKXXQCFRXRXXXXXXXXNCDXX
XXXXDXXXXXGCXXIHFHIXXXXXXXCXXXXWXXXXXXXXYGRXCXVCXGGVXXXXXXXX
XWXXXXXXXXXPCSSRAPXMXQSQSADQTQDXXGXCXDGXXGXGTCXCXXGXXSGXWGXX
CEXXXSXXXXXXXIXGXXXXXXXXXXXXXXXXXXAXFSYXPXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXLSDPKGGXXXXXXXXLPCXXXXXXXXXXXXXXGPYDAVXXXXXXXXXXX
WTXXXXXXXGHGAXXXXXXXXAXXXXXXXXXXXXXXRXDXXXXXXXXLXXXXXXXXXXXX
XXXXXXXXXXXXXCXXXXXXXXXXXXVXLXXXGXXFXXXXXXXRYXXXFXXAXXXCXXXX
XXGCXXXAXCXXALXXXXXXXGIVLFQNISYPHVRDICAVWFCHNNPLLLAAXXXGXXXC
XAGWXXDXXTVXYXXXXXXXXCXGXXEXXAKMLQCFKCXXGXXXXXXXXXXXXXXXXRX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGXFHXXXXXXXXXXXXXAX
XXCXLDEXXXXXAXXXQLXXAXXXXXXXXCXXGWXXXXXXXPXXXXXXCGXXXXXGX
XXXXXXTRKEVPXHTNQTXXXXXXXXXXXXXCXXXXXXXXXXXXXXXXXXXXKACXGXLX
XXXXXXXXXXXXLXXXXXXXXXXXXSSXXXXXXXXTXTDSSESSXXXXXXXXXXXXXXS
XXXXXXXXXXXXXXXXXXXXXXXFXXXYXXXXXXXXXXXXXXXXXXXXXXXXKKHTXXXX
XXXXXXXXPXXXXXXXXXXXXRXXXXXXXXXXXXXXXWXXXXEXXXXXXEXXXXHAAXXX
XXXXXXXXXXXXXXXXXSIXXXXXXXXXXXXXEXGXXXXXXXEXDXXXXXXTXXXXXXXXX
SXXSXXLFSWXXXWFXXXXXXXSSXXXXXXXXXPXXXXXXXXXDQPGVRTYGLRPAEERY
DVYCYTTXXXXXXXXXXXXEGXXXXXAXTIKXXXPXXXXENHSPPVXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXSIPNPLYSXXXXXXXXXXXXXXX
XXXXXXXHXXXXXXXXXXXXXPXARFDAYCDHDDQHDDHDDIRHDHKDQXXXXXXXXXXX
LDQXXDIXXXXXXDXXDQTSXXDXLXXDXXXXXXXXXXXXXXXGXGXXDFDSGXXXXXXG
XXXXXGXXXXXGXXRGKXEEEGSGEXXGAEAKGEIQVQSGXXDQXTXXXHHDXPXXXHDD
QSGSGDQXXXXDQSGSGXQSGSGDQSGXXDXVSSGYQSGSXXQXXXXXRPXXXXXPXXXX
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XXAXEXSXLSXPQEXXXTXXDXXXXPXXXXXXSXXXSXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXDXXLSGFSGFLXXXXXXXXXXXXXXSXSXXXPXXXXXDXXXDXXXX
YXXDXXXXXXXXXXXXXXSXXXXXSXXXXDXXXXXXXXXXXPXXSXXXXXXXXXTQXXXG
SPSGEXXXXXGGLFYSSGPEXXXXXXGXXXXXCSFDXXXXXXSXXXXSKSEXSTTKGEEE
GSXXFFTQXXXXXXPXDXXXXXXXQXXXXXXXXXQTXGXXPXXQANVKDXSXDXXXXXXX
APKSDQXXXXXXXXGXXXSXXXXDXLXXXXXPLXLXXXXXXPQXXXXXXXWXXXXXXTEL
THNSXXXXXXGPAXXXXXXXAPXAXXXPGXXXEXXVXGGEGGNISXTTVSPTAEVEPCVT
XPCLHGGXXLPXXXGYSCYXXXGXXGXXXXXDXXDCXXXPXXXXXQGTCVXXIXXFXCLC
LPSESAVATAVYGGXXCXXXXXXCEHGWRKFHGXCYXXXSHRHXWXXAEXXCRXXXXHLX
XVXXXXEQXFXNGLGHDNAWIGLNDRTVEEDFQWTDGNXLVYENWRESQPDNFFAGGEDC
VVTIAHEXGKWNDVPCNYNLPYICKKGTVLCGTPPAVENAHLXGRRRSHYXIHSVVRYQC
SXGFYQRHIPTXRCRADGSWERPRIXCTKXXXXXRXRRHHHNQHXXXRRNRRHGGEGHKP
REDAQSYY

==> Cystobacterineae.txt <==
>MSA Consensus of 147 seqs, protein
MRSSPRLLLAALGAVLLLGSACXSDXXEVXNXXVCGDGKKEGAEQCDDGNTXGGDGCEAN
CTXTPTTPGXKCGDGVKXXXEACDDGNTXXGDGCEADCTXTPXXXXQCWATPPAPLANGA
TCXVTKXGTAGXLFTGIVLKDGXTLXGGQVLVDAQGVITCXXCDCSKAAGAAEATXVTCP
TGVXSXXXXNPHDHITYPXXPXAAXXXSXERYEHRHXWRXGXNXHTXLXNXXNXKAXXXR
XXXXXXXXXXXXXXXXXXXVGAXXNXXXAXXXXXXXXXXXXRXXXXGAXXXXXXXXXXA
XXXXXXXXGXXXXXXXXRXXXXXXXXXXXLXXXXXXXXXXXCSYSXXXXXXXXXXXXXAX
XPXXXXXXXXXXXXXXRCXSXQXSXVXXXXGXXXXXXXLFXXXXXXPXXXXXXXTXXXXX
XXXXXXQXXXXXXDXXXXXXXXXXXXXXWXXRXXXCSDNSECTGNVXXXXXXXXXLXGXXX
XXGXXXXXXXXXXYQATAXXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXXXGXXXXXXXP
XXXXXRXXGXXXXXXXXXXXXRXXXXXXXXXXXXXXXXXXPXGXXXXXXXXXXGXXXXXX
XXXXXXXADXXXXXXGXXXXXXXXAVIXXXXGXXXXXXXXPLXXRXPXXXXXXXEXAPXX
RDGDXXXXXXXXXXXXXXXXXGXXXXXXXXXXXXDXXXXXDXXXXXXXXXXXXXXXGXX
XXXXXXXXXXAXXXXXXXGXXXXAQXPXXXXXDNPXCXGXXCGXXXEXGXXXXCXXGXS
XXXXXXVXXXXXXXXXXXXXDXDGDGXXDLPPGATEAPSCHPGRMEGXXDXCPXXXXXXX
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XXVXXXXXXPEXXXXXXXXXXQXXDXDGCVSTTQXXDGXXGDXXXXDXDXDGXXXXXPDX
CPXXXXXPLVPNQXXXDXDXDTXXXXXDPANXLIVXGXXCDXXXXXXXXXXXXXXWXXXG
XXXXCSVXXXXDXDXDGXXDXXDXCPXXXXXXQXXXPXDXDXXXCRVDADXDNXSLXXXX
XCPXXXRXXXNPDQXDXDXDGXGDXCDXDXDXDXDXXXXXGPDGKXXDNCPXXXXXXXXQ
XXXXXXXXXVXGDXDGXGXACDXXYCXVXXXLGAGPRXXXXXXLXXXXXXXXXXGGFKGX
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XXGXXXXXXXXXXARAXXVXXXLXXXXVXRTXXXXXXXXXXXXXXXXXXGXXXXXPXXXX
XXXXXXXXANTXLENRXXEXXXXVXXXXXXXXXDXXXYSXXXXXRPXXSXAVVEXPXGXX
XXAVTXSRXWXYXYVDGSVPXFXPDXXGXYXLQXXXRLAFADRVFPXXRXSXSXLXXXVG
XXXXXGXXCXSXPAGXSXXALGAXXLXXXXXXXXGXXXXXXXXXXXGXXXXXXXXXXKXX
PRSAADXVXPLPEXIXXXXXXXXXDGSFVGLXXXDGXVLDGVDAVSTRVAELMATGEWRW
FSSLEDPPXXALTXFXSXXLXRRRXXXXAXXXPXXXXXXXAYPVDVTVXIXSSDAAALXA
XXGQVVIPAGQTSAXVXXXALXXXXXAXXXXQXXVXLTAPTLGTSSQXXXLRVLGXXEXX
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FDLTVDEASTGXGTVXXXXLXATVNVITDVPRLXSLTPSTATVNAGAXQVFTVTLXXXPX
XPVQVLLALAXPAAATPFGALSATXVTVXAGXTTATVTFXAXXXGXGXGXXXXSXXGXXX
XXDXXXXXXXXAXLTVLXPPXKXXSVTPXXXXXXXXXXXXXXXXWXXXXLGEXFTXXLXX
XXXRXXXXQEXXGGAXVXVAFXDLSDGKQEVGXXPXXXGXXXXXTVXXXEXQTXATVXFT
AXXXTGXGQLTAXYXXXGVTKQAKXVTVAXXQGHVVISEXXGXGXXXXXDXXIELYNPTX
XXVXXXGWKXXYRXAXXTSXXXXFXXXXXXXXAXIKAHGYYLVXXXXYXXXTPXVXXDXX
WGXXXXXSXSRXXXGXVRLGXAXXXXXXXXXXXXVDTXGXGXGXXXXXGXAAPXXXXXGG
SXERKARAXSTXATMXXGGXDELAGNGQDXDXNAADFXXRTXRXPQNXXSPXEXP

==> Deltaproteobacteria.txt <==
>MSA Consensus of 329 seqs, protein
MKRFRSVVSICMLVVISHVVFVAEAFALGNLKQPPILEFSSEKSEISQGESVRLTWSSTY
AESCTIEPDIKQNSACSGSETISPDQTTTYVFSASNGDGDASQTLTIIVNAPVDSDNDGV
KDDDDACPDTPSGESVDSNGCSASQKDSDNDGVNDNADTCPDTPSGESVDASGCSSSQKD
SDSDGVMDNVDMCPGTAPGVSVDSRGCSSSQKDTDKDGVKDNVDSCPGTPAGEAVDGKGC
SDSQKDTDDDGVTDNLDMCAGTPAGESVDANGCSDSQKDTDGDGVMDNLDTCAGTPAGES
VDANGCSDSQKDTDGDGVTDNLDMCASTPAGEPVDANGCSDSQKDTDGDGVTDNLDICAD
SPAGEAVDANGCSDSQKDTDSDGVTDNLDTCAATPAGEAVDANGCSDPQKDTDGDGVTDN
LDTCAGTPAGESVDTNGCSDSQKDTDSDGVTDNLDTCAATPAGEPVDANGCSDSQKDTDG
DGVTDNLDTCANTPAGEAVDGNGCSDSQKDTDGDGVTDNLDTCAGTPAGEAVDGNGCSDS
QKDTDGDGVTDNLDTCAGTPTGEAVDANGCSDSQKDTDGDGVTDNLDTCAGTPEGELVDA
NGCSDSQKDTDGDGVTDNLDTCAGTPEGELVDANGCSDSQKDTDGDGVTDNLDTCAGTPA
GEAVDANGCSDSQKDTDGDGVTDNLDTCAGTPAGEAVDANGCSDSQKDTDGDGVTDNLDT
CAGTPAGEAVDANGCSDSQKDTDGDGVRDNLDTCAGTPTGEAVDVNGCSDSQKDTDGDGV
TDNLDTCAGTPAGESVDANGCSGSQKDTDGDGVTDNLDTCAGTPAGESVDVNGCSDSQKD
TDGDGVTDNLDICAGTPAGESVDGNGCSDSQRDTDGDGVTDNLDTCAGTPAGESVDGNGC
SDSQKDTDGDGVTDNLDICAGTPAGESVDDSGCSDSQKDTDGDGVTDNLDACVTTPVGEP
VDSNGCSDSQKDTDGDGVTDNLDTCAGTPAGESVDVNGCSDSQKDTDGDGVTDNLDICAG
TPAGESVDGNGCSDSQRDTDGDGVTDNLDTCAGTPAGESVDGNGCSDSQKDTDGDGVTDN
LDICAGTPAGESVDDSGCSDSQKDTDGDGVTDNLDACVTTPVGEPVDSNGCSDSQKDTDG
DGVTDNLDMCASTPAGEPVDIDGCACSERELVWAYISLGTNHTAGITSEGLIYCWGYNNS
GELGDGTTESKPSPTLVDGDRWASVSSGGGYTLALKDDGTLYAWGRNTYGQLGDGANENK
HSPVQVGGDNDWQFVSAGSNHTVGLKRDGALYAWGKNDNGQLGDGTHVNRIYPVQIGTEN
DWAFVNASYDKTIGIKKDGSLYAWGWNQFGWLGDGTTEDKNVPTQIGSDTDWISVSSSYG
HTLAIKRNGALYGWGSNGYWALGMKYADFSVPVQIGTSFDWQSVQCGKNHSIGIKADGSL
FVWGDNRYGQLGDGTTERTFTPTPITSNSNWSCISGGGWHSAALDNKGQIYIWGNNNHGQ
VGDGTIGHSLRPQSVGTTHDWVSVATSGSTTLSIREDGSLYAWGDNSFGRLGNGTQTPTD
TPVRVGSDDDWASVAASNDHTVALRTDGRLYSWGSNYWGQLGYGAYSRVPVTVPTQVDES
SDWYAVTAGNCFTVAIKKDGTLYAWGKNDRGQLGDGTTERRDQPVQIGDENDWGAVYSGR
YHTLALKNDGSLYAWGDNLYGKIGDGGTEDRLTPVRIGLDNDWRIISASYTHSAAIKTDG
SLYVWGANRDGTLGIGSTELARVPTRVPGGSDWAAVAAGRSYTLAIKENGTLYAWGENIL
GKLGDGTTLSRTVPVQVGYSHQWKMVAATDEHSAAIQESGALYTFGSNYFGQLGNGNAWR
ENLVGFEPNSCFDLTGDNDSDGVIDSIDFCDDTPSSEHPDSSGCSNSQKDTDSDGVTDDM
DICPNTPGGEPVDSMGCSDSQKDSDGDGVTDNLDTCINTPAGEKVDTNGCSDPQKDTDGD
GVTDNLDICPNTPDDETIDVNGCSDSQRDTDGDGVTDDLDACANTPYGEVPDTKGCSDSQ
KDTDGDGVTDNIDICPNTSVGTVVDTSGCSCDQVEIVWMMVSSGGGHAAGITLDGELFGW
GDNHWGQVGDGTTESKLSPVQIGDGHWISVSCSGSFTVALKEGGSLYAWGRNAEGQLGDG
SVENRLTPVQIGLENNWKSVSVGSAHAIGLKKDGTLHAWGSNEWGQLGNGNQKNEVVPIQ
VGTDNDWVFIDASYDRSFAIKSDGTLYAWGKDTFGSLGHGEGVNRDVPTQIGSDSDWNFI
DGGYCHTLAINSDGXXXXXXXXXDGXXGXXXXXXXXXXXXXXXXXXXXXXXXXGXAXX
XXXXXXAAXELFTWGGXXXXXXXXXXXXXXFPXXXAXXXXXXXXXXAXXXXXXXLXXXGX
XFAXXXXXXXXXXGXXXXXXXXXXXXXXXXPXXXWDRVVSGEXXXXXXXXXGXXXXXXXX
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GGXSFWXXXXGGXXXXLXXXPXAXXXXGXXXXXXXXXWXXXGXXXRXXGXXVXXXDXXGX
XRLIGRDNDXVTAPXGAHHVLAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXDXXXD
WVKIXXXXXXXXXIXXXXXXYXWXXXXXXXXXXXXXXXRLXXXXXXXXXXXXXXXEXXXX
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XXXXXXXWXXXXXXXXXXXXXXXXXXXXXXXXXDXDXXXXXXGXXXCXXXXXXXXXXX
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XXXXXXXXXGXXXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXXXXXXXXGXXXXXXXXXX
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XXXXXXXXXXSASDSRXXXXXXXXXXXXXXXXXXXXXXSXXXPXXXXXXXXXXGXXXXXX
XXPLXXXXXHXXXXXXXXXXGXXXXXGXXXXXXXXXXXSSXXGXXXXXXXXXLDXXXXX
XXXXLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGXXXGXXXXXXXXXXXXX
AXXXXXXXXXXXXXXXXXXXDWXXXXXXXXXXITRXNXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXLXXXXXICXGXXXXAGXXXXXXXXXXXXXX
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VXXXXXXXXXXXXXXXXXXXXXXXXGXXXXXXXXAXXXXXXXXXXXXXXXXXXXXXXXX
RYXYXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGXQIKKEKVXXXXXXXXXXXXXXXX
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XXXXXXXXXXXXXXXXXXXXXXXXXXXDXXXXXXXXXXXXXXXXCXXWXXNXXXXQXXXXX
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XXXXYXTXFVXXXXXXXGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPX
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XVNVXXXXXXXXXXGXXXXGXXXXXXXXXXXXXXXXXXXXXLXXXXXXXXXXXXXXXXXX
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YXFXTPEFXXXPXTXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXVX
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XXXXXXXXXXXXXXXXXXXXXXXXXQXXXXXXXXXXXXXXXXXXXXXAXXECLGDXCGXP
XXXXXXXXXGXXXXXXXXXXXXXXCXXXXXXXXXXXXXXXXXXXGXXXXXXXXXXXXXX
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XXGXXNXXPQXXDXDXNGPXDTXXXXXDPANGXXDXCDXXXXXXXXXXXXXXXXXXXXXX
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PDGXXXDXCXXXLXNXXXXXXXXXCXXXXDXDXDXXXDXXDXXXXXXXXXXXXXVTXXXX
XCXXXXXXPXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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ETXXXXXXXXXXXPXXXXXXXXNXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPXXXXXXXXXXXXXXXGXGQXXXXXXXGXX
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XXXXXXXCXXXPXXXXXXXXXXXXXXXXXXLXXXXXXXXXXXXXXXXXXXXXXTXXXVXX
XXXXXXXXXGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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XXXXXXXXXXXXXXXXXXXXXXXXXXXAXXGXXANAGXXXXXXXXXXXXXXXXXXXXXXX
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AXTEXXXXPXXXXXXXXGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXNDXXXXXXXX
XXXXXXXXXPXXXXXXXXXTXXXPXGXXXXXXXXGXXXXXXXXXXXXXXXXXXXXXDXXX
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GQSXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXXXXXXXXXX
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DGVXXXXEXXXXGXDXDXXNSXXXXXXXXXXDXXXXAXXXXXXXFXXXXRXXXXXXPXXX
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LXAXXXXNNXXYSFXSXXXXXXGRGSXXDXYXXXRINRDRXXXXXXXGXXXXXXXXXXXS
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SLFCWGKNSSGQLGDGTTHADYRPKQVGTEIDWQYISXXXXHXLXXXXXXLYAXXDXXX
XXXXPXXXXXXXXXXLVXXTXDXLQXXSPXXXPQDXXXXXPTDTSXXCTLXRXXXXXXXX
WXXKXXXXXGEKXLXXXLXXXKXXYXXXXXXNVXXADXDPXXXGXLGXGXXYAXDYXXGL
IENEGNWEDVSAGLNHTLAIKDXAXFXXXXXNXXXLGDGTRNDRAXXSXXXXXXNXVXVX
XGEXXXXXXXXXGXXXXXXXGXXXXLGXXXLTDTMVPTRIGDENDWVYIXAGXXXXXXXX
XDXXXXXLXGXGXXXCXXXXXXSXXXXXPXXXXXXPIDADMDCVYDHLDLCLETPPEARV
DSYGCSDSQVDLDYDGVPYNLDICLNTLDGEIXDDSGCSATQRDSDDDGVADYFDICGAT
PEGEMVDASGCSNSQKDSDDDVIVDNLDTL

==> Desulfitobacterium.txt <==
>MSA Consensus of 160 seqs, protein
MTKEGNKRRGKGARGLVSLILSLLLLLQGFVGSTPVYADPGSKVFTFDIANGLESFSDPT
HAQWTEGGYTLDFSVTGSSTQMXGSXXFDDXESWXVXNXXXXGPIXLTXXXPXXXXXLXX
XDLXNXXXDITGXXXXYXXSTNKGGSXSGXIXXXNGXXTXXXLNFSGAXFTGISSFTLTY
TGXXXDAXXYSIDNLXXXXXTXLTTDPLSNDAXLXSVLGQXITAGGEAGTXXXPKTAAIT
VXNXXXXVXAXXXXXXXXGXIXXFXXXXXXXAXXAVPLGTXXXXLXXXXTXDXXXXVXXX
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XXXXXXXAXPEMXEXXXXXXXXXXXXXXYXXXXXGTYXFXXXXXHSSWYYVTKSVGGQES
LSSFVNPTFRIPVATKGVESVDXTNVSSNATIRLYKXVEGTDPDILXSEXPTPVGNGTYR
FENITPDSAGFYVTQYANTIESANCPFFGVDLRTPSISGGNGQXTVSXXXPXXXXTXXXX
XGXXQTANNVTTATHQFSNVVPGNGYYVQQTINGVISXPSNSATTYSSGPQFVGGXPXIX
VRQYPNXXXXXXQLYXXXXXXXXXXXWXXXXXXXXXXXXXGTXXXXPXXXXXXXXXEXXQ
RPPDXXGXXPXXGXXXXXXXPXXXXQTXXGXXXXXXXXXXXXXXAQXXVGXXXXXXXXXX
GTXXAXXTXXXGXXXXXXXXXXXXXSAELTEXIXXPXXXXXXXXXXXTYQIGGXXIXXXX
XXXXXXXXXXXYXXXXXXGXXXXXXXIXXLXXXXXXXGXXXXXXXXXXXXGXXXXXSSGD
GGPAGXATXXXXXXXXXXXXXXXXXLTLRNXYIXXXXXXXXGXXXXXXXXXXXXXXXXG
VXXXXXXXXXXXXXXXVXXXXXXXXXXXXXXXXXXXXXXXXXGXXXYXXXXXXXXXXYXXX
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KLQNCYAIGNVIGKSSXXXXXGXXYXDRLRXXXXXXXXXYXXXGXXXXXXXXXXGGXXXX
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XXXXXXIXXXTXDXXXXXGXXXXXXXXXXXGXXXXXXXKXXXXXXXXXXXXXXXXXXSG
XNXXXXXXXXXXXXXXIEXXXXXXTXXXXXXXXXGXXWXXXXXXXXXXXXXXXXXXXXA
NKXXXLRVKMTHXNXXTXXXXXTXYXNAVTFXXXXGXXXXXXPXXXXXXXXXXYXXXXXX
XXTVXXXXXXGXGXLTXXXXGXXXGXXXXXXXXXXXXXXGSXNIGGXXXXXXXXNXGXXX
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XXXXXXXXXYAWXGXXXXXXXXXXXXXXXXXXXXXXGXXXXXXXXXXXXXXXXXXXAYSSEG
XXXXXXXXXXXXXYXXGXXXXXXVXXLXXGDXXXIXXXXXXXXXXXXXXXXXXXXXXXGX
XXVXXXXXXXSXXXXXXXXXXXXXGYXXSXXXXXXXXXXXXXXXXKXXXXXGXWXXXXXX
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KFXGNQWXXXXLXXXXXXXXXDGAXXXDXXXXXXXXXXXXXXXXXXXXYXXXDXXXXXYX
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TIAAXXXNXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXRPIXXXXXXXXXXXX
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LPLXXXYGTPTXGXYXXXXXXSXXXXXXXXXXXXXXXXXXXXXXXXXXXYXXXXXXXXTA
GXTXXXXXXXXXXXXYXXXXXXXXXXXXXXXXXLXAKXXXXXXXXXXXXNXXXXXXXXXV
TIXXXXXXXXXXXXXXXXXXIXXXXXXXXXXNXXXXXXXXXXXXXXXXXXMDMXNSXKX
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SXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXIVGGXXXXXXXXXXXXXXTXXXWXXXXX
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SNAVTXQXXXXXXXXXXXXXXXNGXXXXXXXXXXXXXLLXXXXLXXXXXXXXXGXXXXXX
XXPXXEXXXGXXXXXVXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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XPXXPPAENXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXYXXXXXXXXXXXELLPXXXX
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RXQIILANSPENSSDDPPXXXXXXSADSEXXXXXXXLXXXXXXXXPDALXXXXLAXSSXX
XAPILLTXXXXXXXXXXXXXIXXXXLXXXXXXXXXXXXGGXGXXXXXXXXXLXXIXXGXXX
XXXXRXXGXXRYXTAXXIAXAXXXXXXXXXXXXAXGXXXIQTISXXXXXXXXXXXXXXGX
XTEXXXXDALSXXXXAAXXXXPILXXXXALXXXXXXXXXXLXXXXAXXXXXXXXGXXXXX
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XXXTXXXSXXVXXXDXANGTGXXXXDALXGXXXAAXXXXPXXLXXXXXXXXXXXPRXXXX
XXXXXQTLTVPVASLXXXXXXXXXXXXGGXXXXXXXXXXXXXXXXXXTGXXXXXXXXXX
NXXPXXXXXXXXXXXXXXXAXXXXXXXXXXXXXXXXXXXXXLTXXXXXXXXXXXXXNL
TXXXXXXXXXXXDXXXXXWXXAXXXXXXSXXXXGXXXXXXXXXXXXXXXXXXXXXXXX
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XXXEVNXXXXXXXXXXXXXXXXXYXXYXXXSXXGXXXXXXXXXXXXXXXXXXXXXXXX
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PXXXXXXXXXGXXXXXGGXXXGXXXXXXXXXXXXGXXXXXXXXXVXXXXXXXXXXXXXX
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VXTXXXXXXXXXXGXXXXXXXXXXXXXXXEXXLXXXXXXXXXXXXXXXAXXXXXXXXXXX
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IXXTFXXXXXXXXXXXXXXXXXDGXXXXXXGXGXXXXXXXIXXXXXXXXXXXXLXXIDL
TKVTLSVXXGAFADXNXXXXXXXXXXXXXXXXVGLXXVXVXXXXXXXXXXXGXDXXXXXX
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XAXXKINXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXDQYGKXXXXXXXXXXXXX
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XXXXNLVNLLXAXXXXXXXXAXXXXXXXGXXXXXXXXGXXXXXFXXXXXESNXXYXISX
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==> Desulfosporosinus.txt <==
>MSA Consensus of 260 seqs, protein
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YXSENSEAMFDSMVSXXXXXEXGXXXXXXXXXDGXAXXTXDQXXXXXNXPGVDLTKEVXX
XXXXVXXAXIXXLXXXXXXXXXXXEXXXLXNXXXXTDXXXXXXXXLXNRTXXNXXGXXXXN
MSXXXXXXAVXXXXXXXAXXXXXXXXIXXXXSDDFGGAVXXXXTXTXXGGXXXXXXXXSX
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VYMPGNGTTTLNSDVQSITVTQAATPVISTFTVTQPSTIGGTGSIXXXXXXXYXXXSGS
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LLSLLMIVNMFXXXXXXXXXXXXXWXXXXXXXXXXAXXXXXXXXXXGXXXTXXXXXXXXY
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KWTPXXKXXXXXXXXXXXXXXDGNGYTXXGXXXXXXXXXXXALXRXXXXXXXXSIXXXXX
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CXXXXXXXLXXXXXGXXXXXGGVYXXXXXXXDRXXXXXXXXXXWXXXXXXXXXXXXXQX
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TXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPXXSXXXTXGXKXXXX
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DXXXXXXXXXXXXXXXXXXXXXXXXXXGDFNHDGRTDLAXTXXXXXXYXXXXXXXXXX
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GXGXXXXXXXXXXXXXXXXXXXXXXXXXXXPIXXXXXXXXXGXXXXXXXXXXXXXXG

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XTKXFVVTVKGQ

==> Dinosauria.txt <==
>MSA Consensus of 877 seqs, protein
MLCWNEVQSCFLLAFLAVAAYSVSDAQGQVSPPTRLRYNVVNPDSVQISWKAPKGQFSGY
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CXCXXXXXGXACXXCXXXNXFGNSRPXCXSXXXXXTXXXXXXXKXTSSDIAXXRXXXXXX
SVCXCVHGXCNSVGXXGXGXCTCXXGYXGXXCDQXXXXCXXXXCXANSXCXXXXXDGXXX
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XCNXTXXXPXCCKGFFGPDCXPCPGGFXSXPCXGXGXCXDGXXGNGXCXCXEXFXGXXCX
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XNXXPXXXXXXXTXXGXXPEFTPVREEMEAVXXGXPGXXXXXXXXXXXXVLXIQKNRCXX
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PDXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPRSXXXXXXXRXXXXXXXXLXXXXXXG
HVIDLVXXXXXXXXXXXXDKKXXXXXXXXXXXXXXXXXXWXGXTCXXXIKEXDXCNXXCH
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DXFXXVXXXGSXESCXXXGLCGFEPPCPAGSVQRGETXXCYYYXXXXILLLFSSPFSKAI
FCFKCGKPTNFSAQICCLXXXXXXXPXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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XGXXXDSXXXGXXYXXXDXTXXXXXXXXXXVTEXEQXLKNXKFXXXXXXXXXXXXXGXXL
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XSNXXXXXKXXXEMXYXTXXXGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXTTQAXWNP
FXXXXWXXXXXXXXQXXTXNXXXXXXXXXXXXXXXXXXEXXXXXXXXTSXXNGIIHXXXXX
LXAXXXXPXXXLXXXXGXXXXXXXXXTGXXXXXCXXXWAXXXXXAXHSFCQKCXGXXYXX
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EDXXTEGXTXXTDXXAPXXXVLLXFXXXXXXXXXXEXXXXXEXTKEPLAPGTQRGSESE
QALTTDQPNHVEVRKXGNGSPAPEEGLTQIVAAPPTTTTSPDGXHXXDDTQPPLPXXXXQ
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TEXXXPXXXXXXXXHXXXXXXXXVLXXXXXXXXXXXXXXXXXXXKVXXVXXXXXXXXXXXX
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GXQLTLT

==> Ecdysozoa.txt <==
>MSA Consensus of 785 seqs, protein
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XNXXXXXXXXXXFNXXXXXXXXXXPXXXXXXXXXXXXXXXXXXXXXXXSXXCXSLNETALP
GTPVVTVMASDNXXXXXXXIXXXLXEXXXXXSXXXPXXXXSSFCSXXLXXXXXXXXXXXX
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ILPFCSXXXXXAXXXXXXXXXXXXLXXYXXXXXXXXFXXXXXXXXXXXXXLXXXXXXXXX
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XMXXXXXXXXXXXXXXNIXXXSSXXXXXAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XPXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXYXXXXXXXXXXXXXXXXXXNFXXXXXX
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XNRKDXDXXXXXXXXXXXXXXXXXXXXXXXRXXXXXXXXXXXXXXXXXXXPKRXXXXX
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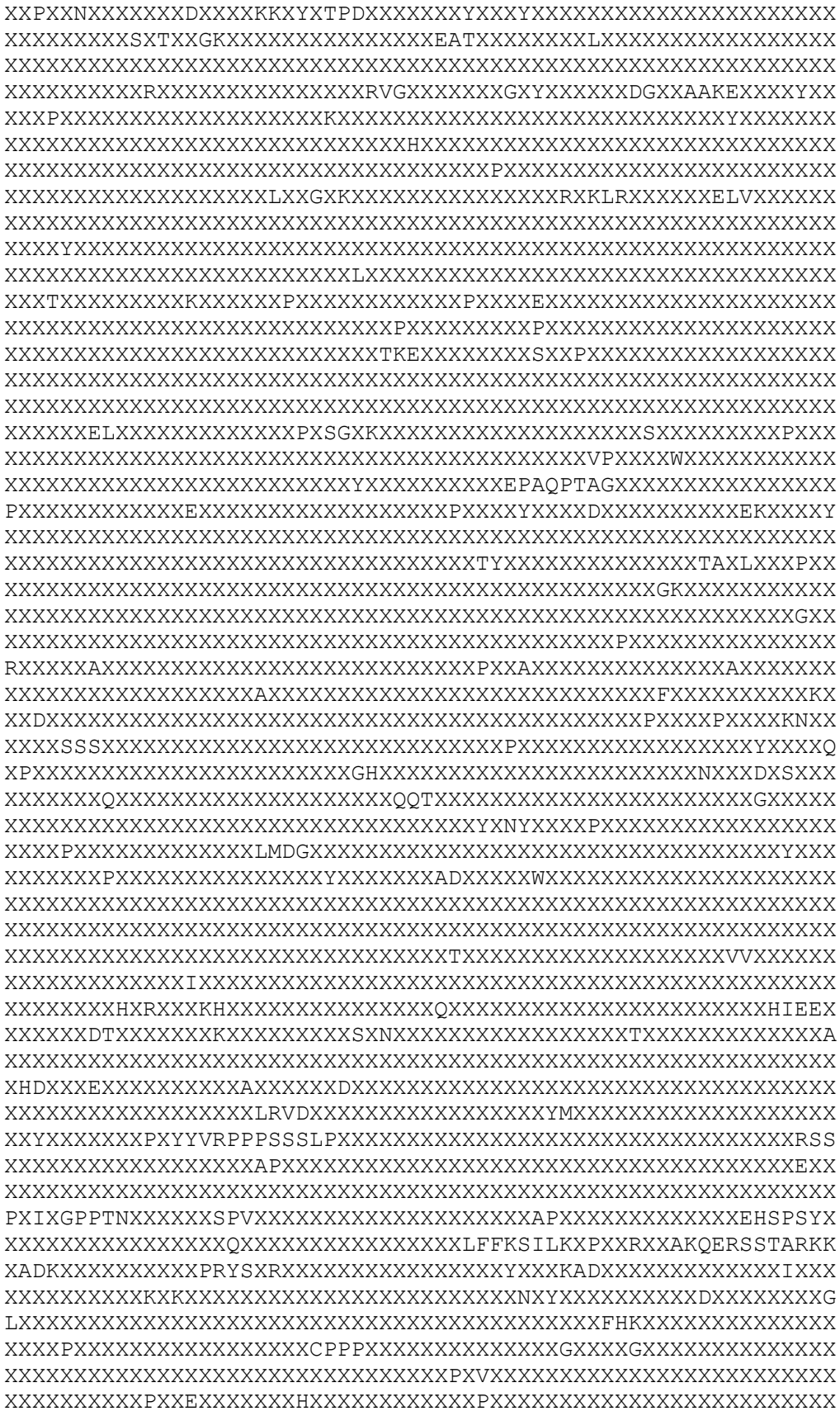
STPXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPXXXXXXXXXXX



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HHSLRHHSLRHHSLRHXXXXPXXXXXXXXXXXCXCXXXXXGXXCXXXXXXXXXXXXGNFX
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EXXTKXXXLPXEPXXVEXTEEXXEXXXEEXXPXXXXXXXXEXXPXTEXXXXXXXXXXXFP
DESEEPXXXXXXXPVXXXXXXXEEPXXPXXXXXPTSTPXXXXXEYPDQXVTGEXNPHFPX
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==> Eimeriorina.txt <==
>MSA Consensus of 334 seqs, protein
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VERREILHPPFKPELGNFTCKVEEXSRXXITNSRVSRPSDCLGLSEAATGDDDGSSAXEE
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XXXXXXXXXXXXXXFXXCXXXXXXXXXXXXEXXXXXLXXXXXXXXXXXXXXXXXXXEXEX
XXXXXSXXXXXXXXXXHLXXXXXXXRXXVXSTXXXXGXXXXXXXXXXXXXXLSXFXXXXX
XSXXXXXXXXXLXALXXGSANXXXXTNNNXXXXXVXGEMXXXXXXSXXXXXXSXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXELMTXXXXXXXXEXXXXXXLXXIXXXXXX
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KVXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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XXXXXGXXXXPXXXXXXXXXXXXXXXXXXXXXXXWXXXXXXXXXXXXXXXXXXLTXLXPX
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KXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXV
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==> Embryophyta.txt <==
>MSA Consensus of 117 seqs, protein
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YXXPXXXPPXXXXXXXYXXXXXPXXXXXXXXXXXVGSHXXXXXXXXSXXXPXXXXXPPYXY
XSXXXPXXXPXXXXXXXXXXXXXXXXXXXXXXFGXPLPXXXXXXRWFRRXXXXXXXXXXH
XXXXXXXXXXXXXXXTVACYDXXXXXXXXXXXXXXAXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXLHVAXXXXXXEGXXXXXXXXXXXXXXXXWXXXXXXXXXXXXXXXXXYDPX
XXXXXXXXXXXXXXXXXXLXXXXXXXXXATLATGELVLALHXXSYXXXXXXXXXXXXXVXX
XXXXXPGXXXXXXXXXXXXXXXXXXXXXXRSXXSXXXXXHXXXXXXXXXVXXXYATPXX
XXXXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXSXXXXXVPAX
XXXXXXXXXXXXVTAKYXXXLXXXXXXXXXXRIIQVXXXXXXXXXXXXXXXXXXXXXQWX
XXXXXXXXXXXCXXXXXXXXXXXALKASEVIGXXXXXXAXXXXXXXCXXXXXXXXXXXXX
XXXXXXXXLXXLXRNXXXMSLFXXXXXXXXXXXXXXXXWXXXXXXAXSTGXXXKXXXXXX
XXXXXFXXXXXXXXXXXXXXXXXXXXXXXXXXKSTGRVXXXXXXXCXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXGKEXXXXXXPXNDPVEXXXXXXXXXXXXXXXXXXXXXXXXX
XXXMXXXMKXXXXXXXXXXXXXXXXXXXXAYSPXXSCTHQXXXXXXXXXXXXXXXXXXXX
XXKXPSXXXKEXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXVXXDXXYKX
XXXXXGXXXXXXSVSEDTYKKVSSVXXXXXXXXXXXXXXXYXXKPXXXXXXXXXXXXXPX
XNXYKXXXXXXXXXXXXXXXXXSXSXSRSYSSDRGRSYXXXXGRRGRSSXXXXXXXXXXX
XXXXXXXXXXXXXXKXXYXKXXXVPXXXXKNDYYKKPSVSEDTPXXXXXXXXXXXXXXKX
DYYKKPXXXXXXXKNDYYKKPPXXXXXXXXDYXXKPXXXXXXXXXXXXXXXXXXXXXXX
XXXXLXXXXXXXXXXGXXXXXXXEXPXXXXXXXXXXXXXXXXXXXXPXXXSKVEFEPRF
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPXPXXPXXXRKXXXXXXXXXIXPXX
XEXXIXXXXXXXXXXXXXXXXXFXXXXXXXXXFPTHLXXXXXXXXXTTDTYXLPKXXXX
XXXXXXEXXXXXXPXXXEDXXYXXXXXXPXXXXXXXGXXXXXXXXXXGGXXXXXXXXXX
XXXXXXXXXXXXXAFSQLVSXXXXXYXXXXXXXXXXXXXXISKIYXXXXXXXXXXDXXX
XXXXXXXXXXXKXXXXXXXXXXXXXXXXXRXGXLXXXXXXXXXXXXPXXXSXXXXXXXXXX
XXXPXXXXXXXXXFXPXXXXXXXXXXXXXXXIXXXXXXXXXVHKTKXXXXXPXXXXXXXX
XYKXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXIAPEISTKLNRNFKLAPHXXXXXX
XXXXXXXXXXXXXXXXGXRXXERERSXXXXXXXXXXXXXXXXXXXXXYXXXXXXXXXSY
SXXXXXXXXXKSXXXXXXXXXXXXXXXXXVPKXXTEPKPXXXXXXXXXXXYXXXSLPXXX
YYXXXXXPXXXXXXPXXYYKSPPPXXXXXPXXXXXXXXXXXXXXAYPXXPXXXXXXPXXX
YXXPXXPXXXPPPXXYYKKPSXXXXXYXXXXXXXXXXPPPXXXPXPPXXXXXXXXPPPXX
XPPXXXXXXXXXQSXXXXXXXXXXXXPXXXYXXPSXXXPXPXXXXXXXYKXPXXXEXXXXX
PXPXYXXXXXXXXXXXYKVPSXPXXEYXXPSXXXXXXYXXXXKSHTYPRXXXDYYKKXXX
YXPXXXXEXXXKKVXXXVPXXXXXKXPXXXXXSXXYXXPSXXPXXXYXXXXXXXXPXYXX
XSPPXXXXXPXPXXYXXXPXPPXPXPPPPXYXXSXXXPXXXPXPXYXXXXPSVPXXXXKX
XXXPXXXXXXXXPXYXXXXRLXXXXXXKXXXXLXXXXXXLXXXXXXSLPKXXXXAXXXXX
XXXXPPKNDCHKKPYVPXYXXKSXPPPSPXXXXPXVYKXPXXXXQVYEAPSXPKNDYYKK
PYXXXXXYXXXPXXPKNNYYKTPSVPKQVYXXPXPXXXXXYXXPXXYXXPSXXPXXXXXX
KXXSSPPPSNDYKAPXVPXPXYXXXSXPPPSPXPXXPYXXKSXPXPSPXXXXPXYXKSXX
XYXXXXKXXXPSLPKNDYYKKPXXPXXXYXXXXXLXXXPXXXPXPXYXXXXPXXXXXXXX
PXYXXXXXXXXXXXXKVPSVPKNNYYKTPSVPKQVYEAPXXXXXXYXXXPXXXXXXXXXX
XXXPXXXYXYXXXXXPXXVYEAPSPPXPXYXXXPXXPXXXPXPXXXXXXXXPPXXXXXPX
YXKKPCVXXXXPXPXXXXPXXXXYXXXPXXKXVYTTLPKNDYHKKXXPPXYXYSXXXXPV
KSPXXPXYYXXPPPPXXXXXXXXXYXXXSTXXXXXXXXXXYXXXXXXXXXXXXGXXXQN
NTKMSPPISNFSPQELIEECXXXXXXXXXXXXXXXSYQNNQSDTTEXXXGXXXXXXCXX
XXXXGXXXLXYARKGGVXXXXXXXXXXXXXGXFXXXXXXXXXXCREFKKRIKKTVTFPP
PLTXXYXXXXXXXKHPXXXXXXXLVLRAXXXXXCXXXLXSSXXXTCXXXXXXXXGXXGAX
XXXXXEQDVEXXXXXXXXYXXEAKVIEHENGDXLXXXXXAPXFXYXXXXXYXXCXKPKXX

XXXXXYKXXXPPXPXXXYKXPXXXPXXXVYKXPXXXXPXXXYXXPSYYKXPXXXXPXXXY
KXPXXXXXXXXXKXXXXXXPXXXYKXPXPXYXXXXXXPKXXYXXPXXXPXXYVYKXXXXX
PXXYXXXXXXXXXXXXXXXSXPPPXXXXXYKPPXXXXPXYVYKPPXXXXPKXVYKXPXXX
XPKXVYKXPXXXXPKXVYKXPXXXXPKXVYXXPXXPPXYYKXPXXXXPYSXXXPXXYYXX
PPPPXXXPPPXYYYKSPPPDDKPXXXPXPPYYYKXPPXXXPXXXYPPXYXKSPPPPSPXP
XPXYYYKSPPXXXPYXXXPPYYYKSPPPPSPXPXXPYYYKSPPPPSPSPXPPYYYKSPXP
PSPSPPPPYYYKSPPPPSPSPPPPYYYKSPPPPSPSPPPPYYYKSPPPPSPSPPPPYYYK
SPPPPSPSPPPPYYYKSPPPPSPSPPPPYYYKSPPPPSPSPPPPYYYKSPPPPSPSPPPP
YYYKSPPPPSPSPPPPYYYKSPPPPSPSPPPPYYYKSPPPPSPSPPPPYYYKSPPPPSPS
PPPPYYYKSPPPPSPSPPPPYYYKSPPPPSPSPPPPYYYKSPPPPSPSPPPPYYYHSPPP
PVKSPPPPYYYSSPPPPXXSPPPPXYIYXSPPPPXHYPCQSSFSWATVIRDCPKKGRFLS
QSPTKFLWGIGNKGLYHAMKSLNHETADLRASMVAILHALVLAFSSRIGFIRETGQGISI
KKQKPF

==> Enterobacterales.txt <==
>MSA Consensus of 629 seqs, protein
MMXXXXXXXXXXXXXXXXHWRLXXXXXXLXLXXXXXXXXXXXXXLXXXQAXXIRXXTXI
TSSXXMXXXFRXXXXTXXXXXRXXXXXXXXXXXXXXXFMKKWFPALLFSLCXXXXXXXXX
XXXXXXXLXXXXXXXXXXXXAXXXXXSXXXXXXXSSXWMTTVMLDMVVGRVVVPPDLPXX
NSVXXXXXXTXXXEGENXAGIILXXTDXXXXXXXGXXXYRXXXXXXXXXXXXXXXXXXG
ATDLXXXXXEAXXXXGNKIXXYXTXXXYEXXXXXXXXKNXPGXXXXXXXXIGMRFSXXGX
XXXXVXPDXXXXXXXSXXXXXWXDXXXSXXPXXXXXTNXXXXXXXXXXXXXXXXXXTSXN
XXXXXSXXSXXXXDRXXFXCXXXXIXXXSXXXXXXQXDXSXXXXXXXNGXXXXXXXXXXX
XXXXXXXNXXXXXXXXGXXDISXXXXXNXSXXXXWNNIVFYSLGXVNSXSEKANVXXXXX
XXXXXXXYXXGXXXXTXXXXXITSWRPGIATVTXXXTWNQCNGXXXXXXXWXXXTXXXXX
XXXYXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXTXXXXXXXIAWVVXSMXXXXXXGXX
XXXXXXTXXXXPLFIEVHXEAXXSCSXXXXXXXXXXXXXXXDXGXIXXXXXXGXXXXXXXX
DGXXNKXXXXXXXQXXXXXNXXXXXXXSXXXXANNVTXXYAGXYIXNSSXNSANNNHXNX
AXTDIXXXGXXTXXXXXXFXXXXXXXXXXXXXKGYKWXTXXXXXXXXXXXXXXXXNIXXX
XXALXXXXXXXERXXXXXNLXXXXGXXXXXXXXGTLATSTTAXXGALLNEXXXXXXXTKA
GSXXXXGXXXXXXFXDXIFKVALPADLPLGDYSVXIPYTSGXQRHFXXXLGAXXXIPXXX
XKXXXXXNEMLFLFKNIGGCRPSXFTDDGXXXXXXXXLXRXNXQXXXXXXXXSLXXXXXX
XXXXWLXXXXXXSXEAXXXQXXXTSRYXXXPLNHAXXXXXXPXXXXXXXGGXXXXXAXXX
XXGHLXXXXAQSLEIKHGDLSINSANNHYAAXXXXXXXXXGDXPANIRFMLLRNTTPTXX
HXXXFSXXXXXXYDXXXXXXXXXXXXVGLGXGWDSIVSVNGXXXXXXXXXXXXXXXXXXX
XYXXXXXGIXLXXXXXXXXXLXXXXXXXXXXXXXXXXXXXXXXVXXXXXYXXXXLXXXX
GXTTGXXXMRWXDNXXXXXXXXKXXALVSQXGYGINXEXXXADTYVTVGGXLVHAGTQNL
TIGSRLYGXXSXXXPGVLSGSATLLMILXLXXXXXXEXXTXXYSXTYSTXXXXXXXXXXX
XXXXXXXXXXSPLRRGXXTXXXXXXXXXXXXXXXXYXXXXXLVFXGXYXXINDAALDLA
NSHLVLGGXGDAXFDLTRIDNREEAILDGDPNRITGFGTLTKTNXSXEKQLRILLQTVNS
THQRXXXIWTXXXXXTGXNMADGDANAXLXANIAGXXLVLDNATLGLTPXXXAXXXXXXN
RLSAXXXADIAADXXXVAXXXXXXXXXXXXXXETGXXTLXEGGALXSXXLGDSVLXLSGNX
XSXXGXXXXXXLXXXXXNXXXXXXXXXXXXXXXXXXXXXGXXXXXXXXXSXXYTAXXXXXX
XXXXXTTXXXGXXXXXXXXXXXXGNGAXTXXXXXXXXXQTVSXXXXXXXXXXXXDXXXXX
AXKQTXXAXXXXXXXXXXVXVXDAAXXXXXXXXXXXXXLTVXGXYXGXNNGSGEGAWLALDT
VLGDDDSATDRLVINGDATGTTSVRVNNAGGLGDKTLNGINLITXDGLAQDDTFLLAGPX
IXXXGDNXXXXXXXXXGXXXXXXXXXXXTLQADGEAATAGRNWYLSSXXXLTXXVXXQXG
VPXYXQXVXXXXXXGXXXXXXXXXXXXXXQXPQXXXALNTLPTLQQRVGNXYGAXGALX
XXXFDXNQXXXXXXXXXXXXXXXXXXTFRXXVTDPARSTSGSQREIDVWKLQTGIDVPL
YQSQXXSXLTGGVNFXYGKAKADIHSFFGDGRINSXGYGXRXXXXDXXGXXXXGXSLTW
YGNNGVYVXGXXXTMWFDGXATSDLSSRTAGHAVATAXVXXQXXXXSXXXFADDSTAXXX
PLXXXXXXDXXXXSGNNGRGYTSAXEAXXXNXXXXXXLDEXGXVXXXXXXGXXNXXXXGX
XGXXXXXATATXYALGNGXSLXXXXXXXXXTXQMQVXXSRVGXXXXDFXDTFRDPFXXXV

SLXXGDXXXXXXXXXXXXXLXXXXXXRRGRXGVSXDSPXXXVXXXXKETTWXLKGEXQA
XXXXXXXXSHIYSHLDLHNEFTXXXXXXXXXXXXVXXTXXXXXXXXXXXXXXXADGXXTX
XXTXXXAGHSVVTATLNGSKQTVSTTVXXXXXXXXLXXXXLXXXXXXXXANGVQVSGVEF
ATRDERQSVGLGAGGTYEWQNGRGKQLCXSLGSXXASXXAXXXLYAXYGNVYXXXXXXXX
XXXXXXNLLGATRNXYVTSTDYLAASSGSAEHQAXXXFXXXSTATLTSDNYAVGGTIGAR
VSWXXTGFACXXXXXXXNPXXGRTGVVSGXXXSGXXXSXTAXXXXXXXXXXXXXXGADGIA
XXXLXXXAXXHSVVTAXXNGXSXXVSTTVVADDSTXXLXXANLTVTSDNAVANGTATXGX
XARXXDXXXXXXXXXXXXFTATNGATVTTVXGXXXXDXXXXAXXTNTAAGHSVVTATVNG
SSQTVSTTVVADDSTAXLTAANLTVTSDNAVANGTATNGVQARVTDAHSNPVAGQXXSFT
ATNGATVTTVIGTTGADGIATATLTNTAAGHSVVTATVNGSSQTVSTTVVADXSTAXLTA
ANLTVTSDNAVANGTATNGVQARVTDAHSNPVAGQSVSFTATNGATVTTVIGTTGADGIA
TATLTNTAAGHSVVTATVNGSSQTVSTTVVADDSTATLTAANLTVTSDNAVANGTATNGV
QARVTDAHSNPVAGQSVSFTATNGATVTTVIGTTGADGIATATLTNTAAGHSVVTATVNG
SSQTVSTTVVADXSTATLTAANLTVTSDNAVANGTATNGVQARVTDAHSNPVAGQSVSFT
ATNGATVTTVIGTTGADGIATATLTNTAAGHSVVTATVNGSSQTVSTTVVADDSTAXLTA
ANLTVTSDNAVANGTATNGVQARVTDAHSNPVAGQSVSFTATNGATVTTVIGTTGADGIA
TATLTNTAAGHSVVTATVNGSSQTVSTTVVADXSTAXLTAANLTVTSDNAVANGTATNGV
QARVTDAHSNPVAGQSVSFTATNGATVTTVIGTTGADGIATATLTNTAAGHSVVTATVNG
SSQTVSTTVVADDSTATLTAANLTVTSDNAVANGTATNGVQARVTDAHSNPVAGQSVSFT
ATNGATVTTVIGTTGADGIATATLTNTAAGHSVVTATVNGSSQTVSTTVVADDSTAXLTA
ANLTVTSDNAVANGTATNGVQARVTDAHSNPVAGQSVSFTATNGATVTTVIGTTGADGIA
TATLTNTAAGXSVVTATVNGSSQTVSTTVVAVPAFTGVSVNGTTFATNNGFPSTGFTGAE
FSLTVTGAASDYTWSSSASSWAPVDSSGKVSFTSQGNASPVTITATPTGGGTPLTYIFTV
GSWFINNGSTVMNWANASTWCTNQSLSQPTRGELTMGGDTRAVGSLWSEWGVMGNYSGSG
FDSGYHWTSEADGIGYYYGVXLYNGDVGSNYDSGDLYVVCRQGL

==> Enterobacteriaceae.txt <==
>MSA Consensus of 546 seqs, protein
MNRIYSLRYSAVARGFIAVSEMXXXXXXXXXXXXXXXXXXXXXLLSXXXXXXXXAXEX
NXXXGXXXXXXFAXXXGXXXXXXXXXXXYXXXGXXXXXXXXXAMPDFSAVDSEIGVATLX
XGQYXXDVXVNGXXXXXSXGXXXNRAXLXIXXXXPXLSXXXXXXXXXXXXXXXXXXXXX
XXAXMSEYMKNEILEFLNRHNGGKTAEIAEALXXXXXPXXGAXXLXXXXXXAVTDYQARY
YLLLLEKXGXVXXXXXXXXXXXXXGLXLDYXXXXXXXXXXXXXGDQRSPXXXXXXXLTLRR
GMATYWXLKGEXQAGQXCSSXXTTXXXIPLDMXXXXXXXXXXXXXXFXXXXXXXXTWXXX
SSXXXXXXTQGTTTYAMHGQQGNDLNAGKNLIFQGQNGQXXLXXAIXXXXXXLTLGXNXX
XXTXXFXXWXXXGXXLXSXXXXXXXXXXGXXXXXXXKIXLGTLXXXXTGXXXGXXXXXXX
RVVVXQQGXXXXXXXXXXXXXXXXXXXFXXXXXXXXXXXXXXXXXXWXXXXXXLXVXXXG
XXXXXHRIKXTPTXXXXXNNXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
FXXXXXXXXLGXXXXGXXXQXXXXXXXXXXXXXXXQXNCNXXXXXXXXXXXXDVXNXXXL
FXGXXXGXLXXXXRLPEGXXXXXLXSXXXDIXXXYXQXSXNXKXXXIXXXXXXXXXXXXX
XYXXLXXXGXXXXXXXXXXXXXXXXXXXXXXXXXXXNXXXXXXGXXXXXNSARVRXXXS
XXXXXXXXXXXXXGGMARXXXXXXXXXXXGXXXXXXXXXXXXXXXXYYQXGRXDRXXXXX
XXXGXXXXXXXXXXXIXXXXXGXXVXXXXXXXXXXXXXXXXXXXXXXXLAXXXGXRXGT
TQSXXXXXXXXXXXXXXDINELKXXXXXPXXXXXTXFXXXXXXXXXXXXXXWXXXXXXXX
XXXXXLXXXXXXXXXXXIXEXXXXXXEXXXPXXXXXAEXXXXXXXXXXXXXXXLALLVNEM
PGXXWDVXXXXGXIXNXXXRYXXXQXNHKSXXNXXXXXPXXXXXXXQXXXXXXXXXQXXX
XXXXXXXXXXXXXXXXXXXXXXXXLXYEKEGLTNXXXXXXXXGXXXXXXXXNMSLRKLL
TLFIVSXXXXXXXXXLMALGTTSSXXXXXXXXXXXXXXDMVVXXXXXPPDLPVGSVILTR
XWXXXXPGGASXYSLGXVNSYXXXXGXXNKIXXVVITQRPQFITSWRPGDXXGXXSASXX
IATVTWNQCNGPXFADGSWAYYREYIAWVVFPKKVMTXNGYPLFIEVHNKGXXXXXXXXX
CPXXXXXXXXXXXXXXXXXKXYXXXERAFDNGXXADNVXXXXLXXXXXXXXXXXXRFXXX
XXXXXXXXXXXXXXXXXGEXXXLXXXXXXXXFXXXXXXXXXXKGDYSVXIPYXGXVXXXX
XXXXTXXGXXXXELLNSLAAVKSGXKAKRAQRPAXXXXGKXXXXXSYXXXXXXXPXXEXK

XXXXXXXLQIALXVAXXXXYXXXXXXXXXXXXXXXXXGXXXXXXXXSXXXXIXXXXXXXN
XXGXKXFNIXXXANXXXXXXXXXXXXXXXXXXXFLDEXXXXXXXXXXXXXXXAXXXXXXXXX
XXXXXXXXXXXXXXXXLXXXXXXXXXXXXXXXXRNTTPXXXXXXFXXXXXCXVXAXXXXX
XXXXXXXXGXXIXXXXXXXXXXXXXXXXTYSHGKKFSVGLXXGWDSIVXXXGXLVDVXDP
LQFNXXYTXGXLXXQXXPXXXXRXETRYITXXXXXRXYXXGTQNLTIGSRLYGXXXXXXX
GXIESSKIQPGVLSGXXXXXXMIXPLTXXXXXXXXXXXXXXXXXXXXXXXXXXXXXNXX
XXLXGXXXXXXXXXXXXXXXXXXXXXXXXXXXGXXXXXXXXXXXXXEQXXXXXXPXXXL
XXXXXEXXXXXXXXXXEXXXXLFGLSVXRLXXXXXFXXXXEFGXXXXXXXXXGXXXXXXL
XXXXXDXXXXXXXXXXXXXXXXXXXXXXXXXXXXXRXXXXXXXXEGVEXXXXXXXXXXXX
XXXXQGXGEXXADXXPXPXXXXXXXXXXXXXXXXRHNGXIXXXMPXX

==> Episquamata.txt <==
>MSA Consensus of 117 seqs, protein
MLEXXXXXFFMXXXXLXXXXXXXXXXXXXXXXXXXXXXXXXXCDXXXXXXXXTXCXXCXX
XSXXXXCPXGXTKXXXXXGXXXCRYXXXXXXXXXLSXXGCXXXCXXXXXXXXCCXGXWGXX
CXECPGGXXXXCXXXGXCXXGXXXNGTCXCXXXXXGXACXXCXXXXXFGPXCXSVCXCXH
GICNXGXXGDGXCTCXXGYXGPXCDQXXXXCXXXXCXXNSXCXVSSVXXXQXXCXCLPXY
XXXGXXCXXXXPCXXXXCXXXAXCXXLGPNXXXCTCXXGYXGXGXVCXPIXPCXXXXGXC
PXXSTXCXYXXPGKXXCXCKXXFXXXXXXXRREXXCXSXXXXCXXXNXXXXXAXCXXXXX
GXXXCXCQXGXXGDGXXCYXXXXXXIXXXNXXXXXXXXXXXALAIFGKGCSLLLENYGPF
TVLVPTGSIFPPFHISPRIPVTPLHVPHMLFAXLLXXXXXVFXLRDTKEMGEYAKSGIP
VFSIMVAALYIPPIVLTXXXXSXIXXXGXXXXXXXXYXXXXXXLIKKNXGGXWQXXLIXA
IXXFEXXXXXXLXXXGPXTVLVPXXKXXXXXNXKXXXXXXXXREITAXXXXKXHIXXGXX
XXXXXXXXXXXXTLXGXXXXXXXDGELYLIEPLKFPXXXXXXXXRXXDXXXXXXXIXXXX
XXAXNGIXHIXXXYEPXXXASQLXXXXXXXXXXXKXXXLXXLXXXXXXSRFXXILENXXX
XXXLDXXPGPXTVFXPXNXAXXXLXDGXLXYLXXSEGXXKLXELVXXHIXXXXDXXXVXX
AALIXXXXIXTMAXQXXXXXXXXXGXILXTAINFQGNIIGRAYTXXXXVXXXXXXIXAXN
GXIXTLXGXXIPPSIXPILPXXCXEXXXXXXGXCXXCXXLXXXXCPXXSXXXAXXLSEE
LSFEFSDCSLNQYQXFPXDXXXCXYXXXPLGLXXXXXGCXXXCNXTXXXPXCCKGFFGXX
CXXCPGGFXNPCXGXGXCXDGXXGNGXCXCXXXFXGXXCXXCXXPNKXGXXCDXXCXCXX
GXCDNXXXXXGXCXXGSCKXGYXGXXCDXXXXXCXXXDXXXXXCXXXAXCXXXXTGXXXC
XCXXGYEGDGXXCXXXDXCXXXXXXXCXXNAXCXXTGPGTXXCXCXXGWTGXGXDCXXIX
NCXXXXXGGCHXNAXCXYIGPGQXXCXCKXGXXGXGYXCXPIXXCXXXNXXCHXLAVCQX
XXXGXXXCXCSXGYXGDGXXCYGNXMXELXXXXXXXXFXEWXXXXXXXTXXXXXXNXTXL
VPXXXAIQNXXXXEXXFWXXXXXXXXLXXXHXLXGXXTXXXLXXXXXXXGXXTXXXXXXX
XXXXXXGXXXIXXAXIXXGDIXAXNXXIXXIXKVLLLXXLXXXXXXXPXLXXXLXXXPXX
SXFXXXXXXYXLXXXIEXXXXYXXFXPXNXXIEXYXXXXXXXXLDXXXXXYHXXLGXKLL
XXDLXXGXXXXTMLGXSXXXXFXXXXXQXYXNXXXXXXXXVXTXXGXXXGXXXVXXIXKN
RCXXNXTXXXXXXCXXCXLXXXXCPXGXXXAXXPXKXXXXXXXXXXXXXXXXGCXXXCXK
XXXXXXCCXGXYGXXCEXCPGXXGXXCXGNGXCXDGIXGXGXCXCXXGXXGXACEXCXXG
XYGXXCXXECXCXXGXCNXGXXGDGXCKXCXXGXXGVXCRXAXXEXXXDXCNXTCXXXAN
CXXXXXXXXXXCXCXAGXXGNGTXCXXIXXCXXXNGGCSXXAXCXXXXPGXRXCXCXXGY
XGDGXXCXEIXXCLEXNGGCXXNAECXXTGPXXXACNCXXXXXGDGXNXCXXXXPCXXNN
GGCXXXAXCXXTXXXXRXCXCXXXYXGDGFTCXGXXXXELXIXXXXXXXFXXXXXXXXXX
XXIXGXGPFTVFXPXXXXXXXXXXXXXWXXKGXXXXXLRYHIVXCXXLLXXDLXSXXXXT
XLXGXXXKXXXXXNXVXLNXXAKIXXSDIXXXNGVIHXIDKXLXPXXXQXXXXXXXXXXX
XXXXXXAXXXGYXXXXXLXXXXGLXXLXNXXLHQPXTIPCYFIDXXWPXDXXXXXLPXXP
XQXXLXXXXXXXKVLXXYLKXHXIXXXKXXAXXXLXXXXXLXTDATLEIKTLRSNDTGIY
RCEVIHGIEDSQDMVEVKVKGRDGTLXGSXXSXXCXXDXTXXGXXXXXXXXXXIXQRXXH
HPREGCYGXXDXFXXGIAYGXDXXLXXPXLGXRCDXFXXXEXPXXXXCXXCXXXXXCPXG
SXXXGXXQXCXYXXXXXXXXXXXXXXXRXSXWXXXXXAXXXXXXXXXXXXXPXXXXXXX
GCXXXCXXXXXXPQCCXXXXGXXCQXCPGGXXXPCXNXGXCDXGXXGXGXCXCNXXFXGX
XCEXCXPGXYGXXCKXCXCXXXGXCXEGXXGXGXCXXXXXWXXXXXXXXXXXXXTXXXXX

XXXXXPGXXXXXXLXXXCXXXXXXXXXXXXXXXXXXXXXCXXXXXGXGXXXXXXXXXXXX
XXXXXXXXXXXXQXGSIXXXXXVXXXCXXXXXXXAXXXXPXXXGDGXXCXXXXXXXXXXW
XXVXXXXGXXXEXAXXXXXGXXXNFRXCEXXXXXXGXXXXXXXXXMXXXXLCXAXGFYXX
XXXXXLXXXNXXXXXXXXXXXXXXXXCXXXXGTAAXXEDXXXXXXLXLXGGVFHXXXXXX
RYXXXXXXAXXXCXXXXXTXXTXXQXXXAXXXGFXXCXXGXXXXXXETXXXXPXCXXXGX
RXFGRGXXXXPXXXCXXXXXGIXXXXSNIXXXXXXYCFNXSXXXDXXCXXXXXXXXXXXX
XXXXXXNXXXXXXXQXXXXXXXXXXXXXXXXXXXXKXXXXXYRXXCXXXXXXXXXXXXXX
XXXXLYSXXPXXXXXXXXXXXXXDGSXYXXGXXXTXRXPXXEPXXXXXGXGXAXXRXTXD
XXXXXXXXXSXFPXXXHXXXXXXXXXXXCVKDEMKQTEGHXXXXXXXXXXXXXXXXXXDA
XXXXXTXXXXXXXXXXXDQXXXXXNLDSXXKXXXPXXEYKTPGLEGDKYGRKTQLSPSIT
XXXXNXXXXXXXXXXXXXTPMXXXXXXXXHXXXEVFPTXXXXXEXXXXXXXXXXXXXFX
XWXXXXIMSXEHKEXXXXXXXXXXXXKDXXXEXHRDVFDXDDXGXXDDGYPXXXEXXAXDD
XXXXEGSGXXXSXXXNXETVLEWXXXSGXXXXXXSXXXAXXXXXDXKXXXSXHXXXXHXV
HSXKDQSEVXYSTNXXXXXVXXXXXPXXXXEXXXXXXXXXXXXXXXXXXXXXXGSDXXFX
QEDSXQXXSGSPSGEXXLDGAXXXLXXXXXXXXXXXXSDXISIKXXXXXXXXXXXLXGXX
XXXHXXXXXSXXXGXIHXIXXPLXXXXXLXMTSXMQXXTTXPXXXXFTDXEXXLEXEXXX
XXXXXHXVXXXXXSXXXXEXSSXXXXXXXXXXXXXXRSXXSSXTXXXXLXXXXXXXXXXX
XXEXXXXXXXXQXXXXXXXXXXXXEXXXQXPXSXGXXXXWXXSGXXSEEXXXXXXXIXXS
XXXSXXXXXDSKEXXPXIXXPXXXXXXXXXXXXXYXVSSXSTDXEXXXXXXXXXLHXXXX
XXXXXXXXXXXTSXXXXLPGILHXXXXXXXXXXXXXGIXXXXXVXSXXXGKXXXTTQXPH
FYXXSXXXXXXHPGXXXXXXXTXNXTXDXXXXXIHXXXXEXTXXXLXXEXKXEXETXSSQ
HSEEASEXXXTAVXXXXXXXXEXSTXDXXXXEXXXXXHXEXXXXXXEXXXXXNXSXXXXX
PGIXXXXXXXHXXEXSHXXXXSSXDXKHEXATQSMENHXRDPXXHDIHXEXGREDXYXTN
XTXDXXXXEXIPPXGXXXXXXXXHTXXIXXDXEDSXQXPLPPXHQPXWXXEEXXPTNTSR
XXXXXXXXXXXENEHXXSXXDXXXXXXKEDXXSTXEPVRQWXXGXEDXYTTXXXXXXXXN
PLXXDVLXPGIVPRRGIXQKNXTDHTXVVXPXPILLIIXXTIXTPVXXSXDGXKXEESTQ
XPXXHGLXRPXXSQEXXXXLLXETXAETETXXXXXPXLXXXXXXXXXXEPLVNXTXDYXXP
GVFXEXXSXSXXRXXXSTXAXXXXXXXXXXXXXXXXXXXCXXXXXXGEXXXXXPRXAXIP
DWLIVVASLLALALILGVCIAVNSRRRCGQKXKLXINNGKGGIXEKXKGGLNGEASXSXE
MVHLVHXEKPEXQXFXXSXXXXXXWXGLXDRGXXDEFXAIDETQLXYENWXXNQQXVALK
SGXXCVXXXXXXXGXWXDXPCXYXLPXXCKXXXXXCXXPPXVXXAXXXGXXKXXYXXXXX
XRYXCXXGXXQXXXPXIXCXXNGXWXXPXXXCXXXXXTEPGGTTVITAGSITTTNPARSG
GNTRSSVQSWTGQRMAATTFNLXPQWKHKL

==> Escherichia.txt <==
>MSA Consensus of 428 seqs, protein
MXTSDNXXXXXXXXXXXXXITXXXXXXXALLQHXMXXXXXXXXXXXXXXXXXXXXXXXL
XXXXXXXXXXXXXXXXDXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XSHXLYDXXXXXXXXXXXXXXXXXXKXXXXXRPAXXXXXXXXINVLXXXSFXXXXNXXCXX
XXXXXXNXXXXXXXTXXXLXFTXXXVXVIVTEVXXTXVXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXNXXXXXXXXXXXXXXXXXXXXXXXXXXXGXXXLGITDXXXXXXXWXXXQEL
TSXXXGXXXXXXXXXXXXXXXXXXXRHDXXKLLXXXXXXXXXXRXXXXXXXXXXXXXXX
XXXLXXWXXXXXXXXXXFLIFLXXVXXXXXXXAXXXXXLPXPXXXXXXXXXWXXXXRLTX
XXXPXXXLXMXXXXXXXPXXXPVXSEXXFXXXXXXXXXSSTGAGALTQGLXXXXXXXXXG
XXXXDXXXXCXXXGYGXXELXXXXFXXXXGXXXXXXXXFXXXXXXXXXLXXXXXXXXXXX
RXYAPXITGIAXTXARXVXSXIXXXXWXXXXXXGXXXXXXXXXXXXXXXXXXGXXLXXXX
XXXXXXXXXXXDGXXXXEKQXNHKXXXXXXXXXXXXXXXXXVXXXXXXXXXXXXXXMKK
WFPALLFSLCVSGEXSFSXXSXXXSAWNNIVLXXXXXXXXXGXFYSLGDXGXLSXXXXXS
VNSYQGGNVVITQRPQFITSWXXXXXXXXXXXXXXXYRVLNKEGEVXXXXXXXXXXTSXX
XXXXXGXXXXXXRPGIATVTWNQCNGPXFADGSWAYYREYIAWVVFPKKVMTXNGYPLFI
EVHNKGXWSEENXGDNVDIGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXDSYFFLKGY
KWDERAFDXXNFXDXNVXXXLCQKPGETXRLTEKFXDIIFXLXRXKXXFAXXXXXXXXXX
XXXXXXXXXXXXNXXXXXXXXXXXKXXXXXYXKVALPADLKXXXXXXXXXPLGDYSVXIP

YTSGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXQRHFXXXXIXXKNGMXXXXXXXXXV
XXXXXXXXXXXXXXSYXGXXXXXXXXFKIPXXXXXXXXSYXXXXXXYNVAXXXXXXXX
XXXXXXXXXVSPXXXKTLPRENEMLFLFXXXXXXXXXXXXXXXXGXXXXXXGXXVXXXX
XXXXXXXXXXXXXSXXXXXXXXKNXGGCRPSAQSLEIKHGDLSINSAXLXXXYXXXXXXX
XXXRXNGGKTXXXXXXXXXXXSVSCDVPANXXDXXXXIXFMYALGIANGXXIEATFNQA
XXXLLRNTXPXXXXXXXKKFSVGLXXXXXXXXXXKXXXVXTGETTMRWYKAGTQNXLTIG
SRLYGESSKIQPGVLSGSATLLMILPXXXXXXXXNXXGXXXCXXXXXXXXXXXXVXNXRX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXNXXXDXXXLXXXWXXXXXXXXXXXXXXXXXX
XXXXXXXXXXVXXXXXXXXDAXSXXAXXRLSIXXXXXXXXXXXXRLSXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXXXKXXYRXAXIKXXXXXXXX
XLXXXXXGXXXXXXLNKVSGGYXXXXPTPXXXXXIXXGGSEXXXEEGXXEXVXXXXXXXX
XXXXXXXXXNFXXXXYXTFXXXRSPLRRGMATYWXLKGEXQAGQXXXXTPAVIKXXXXXX
CSSXTTXLIXQXXXXXXXXLGXXXXXXXVXLXXVMXTXXXTDXXXXXXXXXXXXWGGXXX
XXXXLXXGXYFAVXGFRVDYEXXXDXXXXGXGKQNFRSHSLYAGAEVGYRYHLTDTTFVE
PQAELVWXXLQXXXFXXXXSGMDVSMRRNSVNPXXGRXGXXXXXXXXGXXXXXAXXXXT
YXFDLTDSADVHLKDAAGEHQINGRKDSRMLYGVGLNARFGDNTRLGLEVERSAFGKYNT
DDAINANIRYSF

==> Euarchontoglires.txt <==
>MSA Consensus of 1574 seqs, protein
MXXXXWXXPXXXXXXXXLXXXLXXLXXXLXXXXXXXLXXXXXXXXRXXXXXXXXXXXXXX
XXXXXXXXXXXXXXVXCXXXXXXXXXTXXXXXXXXXXXXXXXXXXXXXXXXXLVPFXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXSXXXXXXAXXXXXXGXXXXVFXXXXXK
DYRLTHEVLQLIQQKQSXXXXXLXXXCXXXXXXXAEQXXXXXXXXLXXXXGXXXXXXXSW
ALSSQVTFTHXXXXPXXXCXCXXXXXPPVLAXXXXELLXXXXXXXXXXKVHLLSTDHLEX
AVNTWXIPFDPSLXXXXXXXXXXXXPXIEIRNPXGKLIKKGFGLXELLNIHNSAKVVXCXE
PEAGMWTVKTSSSGRXXXXXXXXGXXDXXXXCSXXGXXXXKKTXSRPVQGIPTYVLLNTS
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XXAXXXXXXXXXGPXXXXLXXXXXXXPSST

==> Eucoccidiorida.txt <==
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==> Eukaryota.txt <==
>MSA Consensus of 8936 seqs, protein
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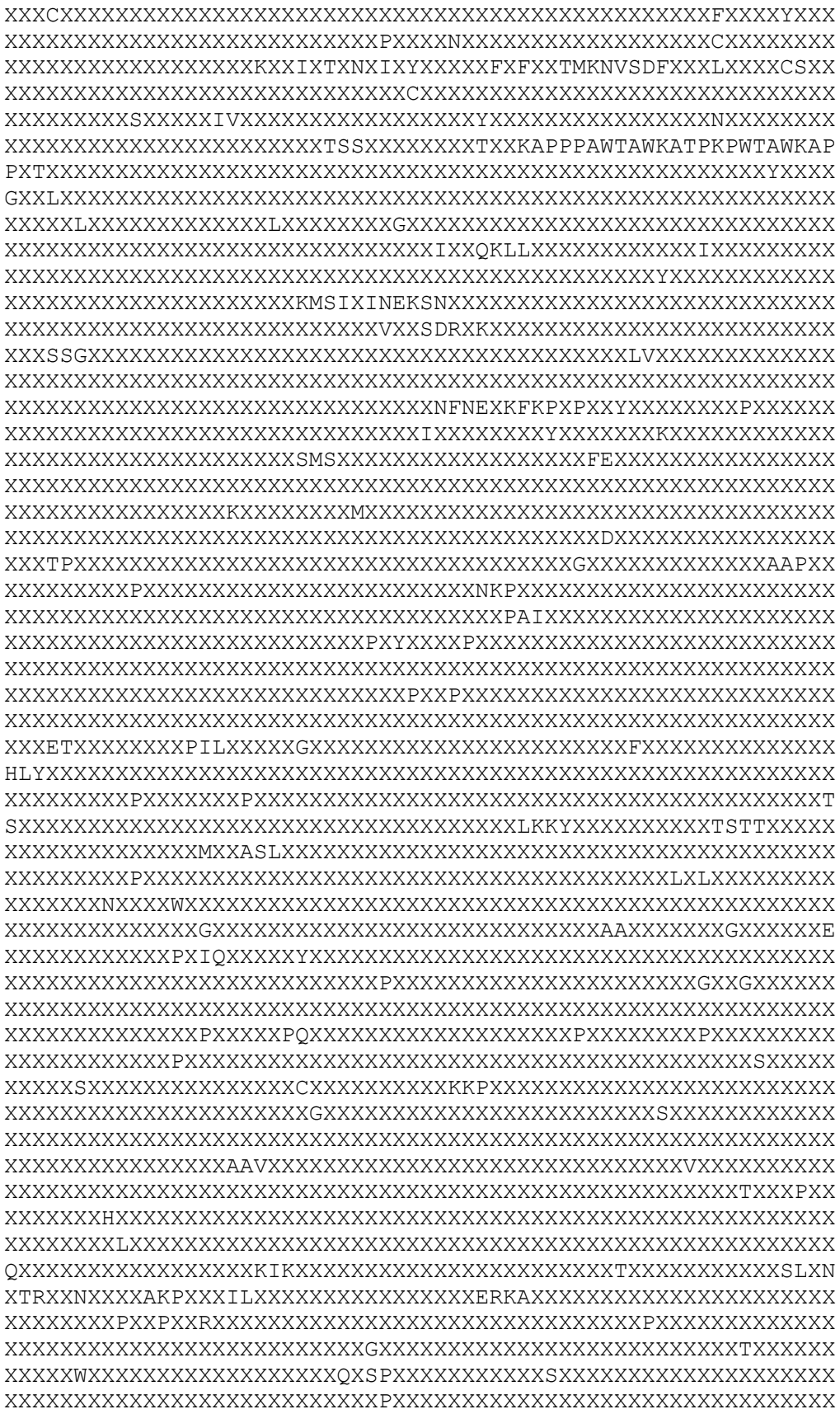

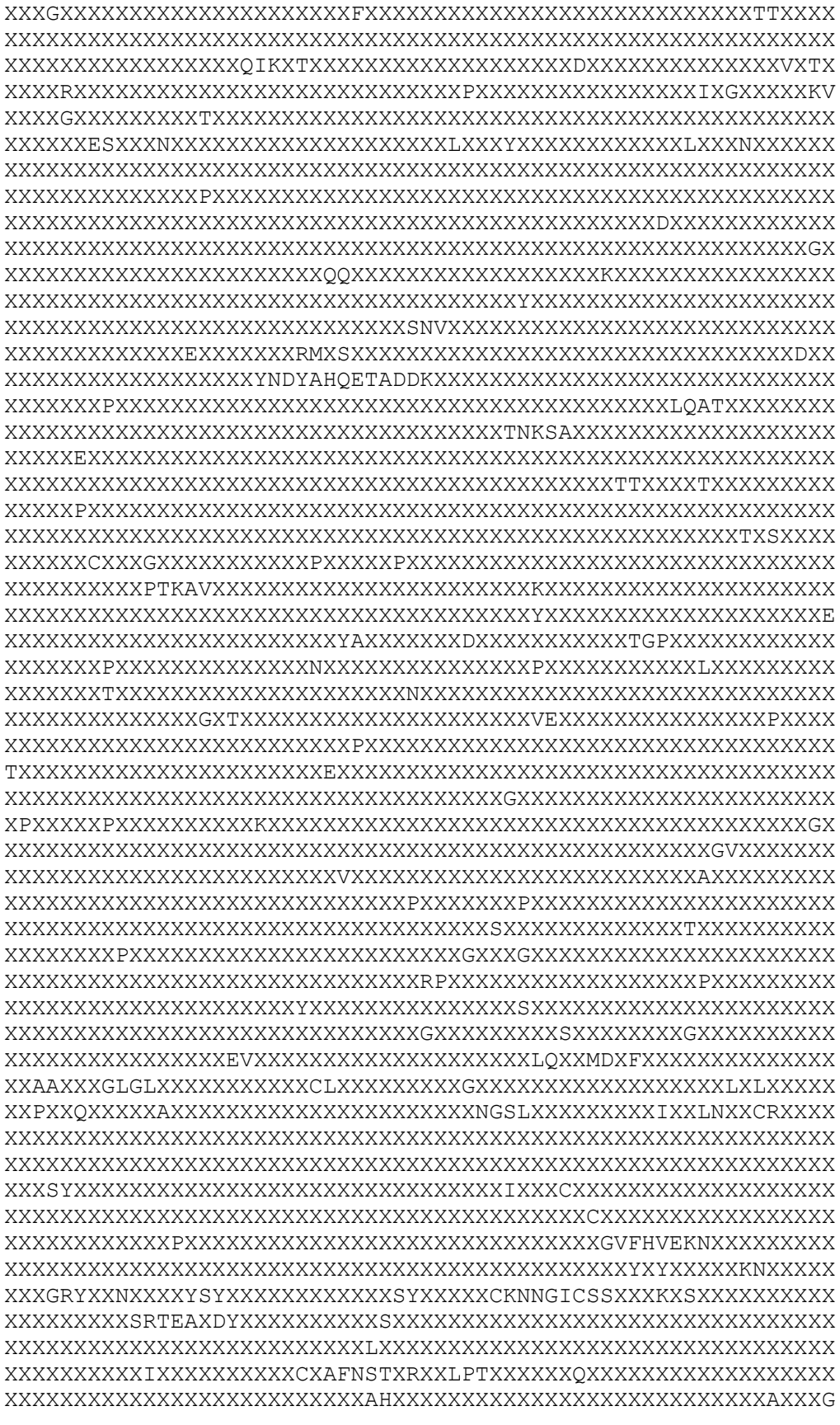

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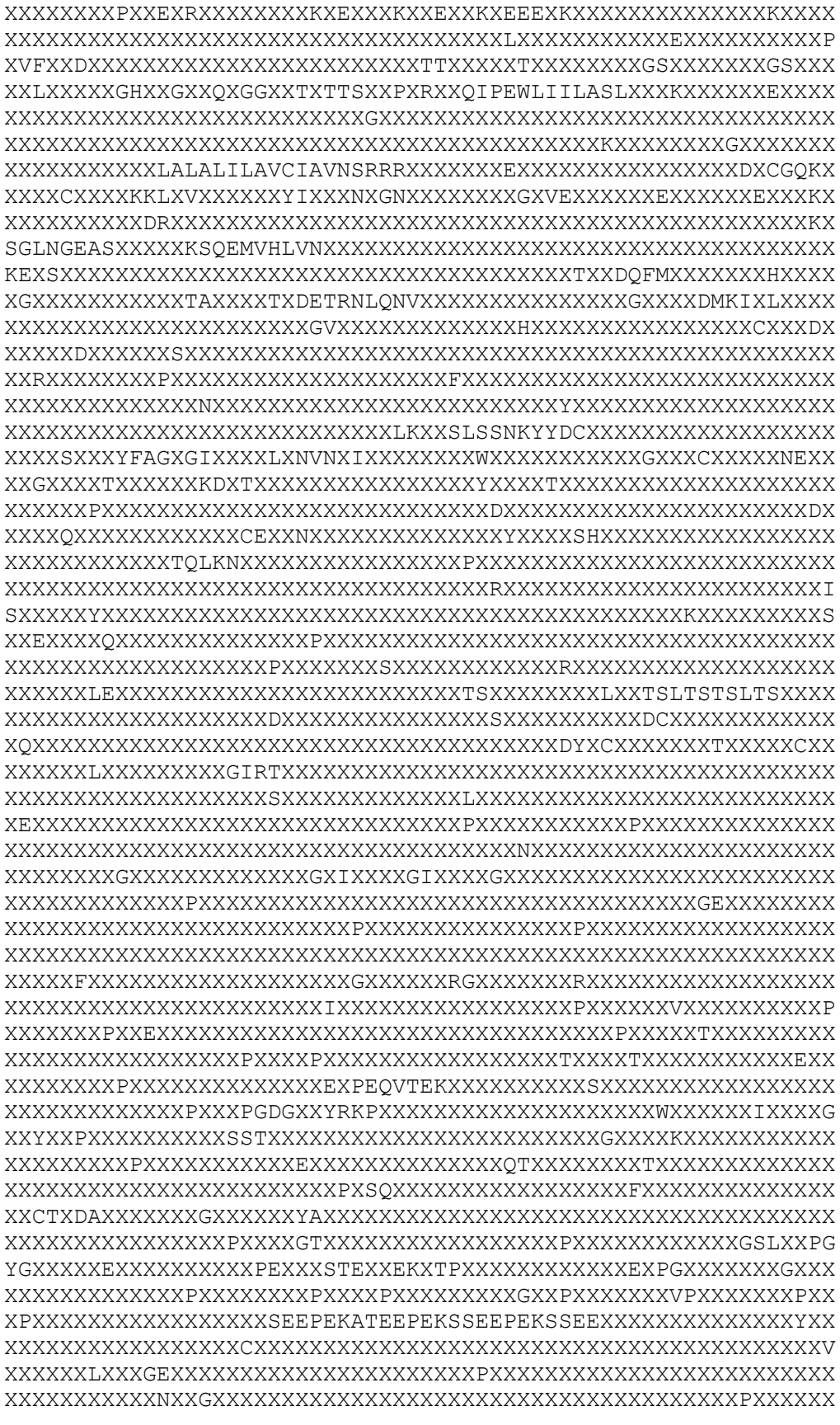

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==> Eupercaria.txt <==
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SXXXXXXXXXXTIXXXXXXXXXXXXXXPXAXXGXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXSXXXXXXXXXXXXXXXXXXXSXXXXXXXXXLXXXXXXXXXXXXXXXXXXXXXXQ
XRXXXXEEXXXVGXXXXXXLXXXLXPXXXXXFXXXXXXXXXXXXXXXXXKNSSLXXXVLK
NPSHSLPXIXXXXXGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXKCIXXXXXX
XXKAENGTXXXXXXXXXXXXXXXXXXXCXXXXXXXXXXXXXGYXXQGXXXXXXXGXXXXX
XXXXXKXXXXXXXSXXXXXXXXXXXXXXXXXXIXNXXXXXXXXXXXXXGXLRFXXXXCXCX
XGQXXXXXXXXXXXXXXXXXXXPXXXXGXYXYXXXVAFXAXXTXXXXXPXAGXALAAXSX
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XXXXXXXLXXXXXXXXXXQARQERXXXXXEXRXXVXFXXXSXXXXXDXMXXXXXXXXYX
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==> Euzebyales.txt <==
>MSA Consensus of 297 seqs, protein
MXXXXXXXXXXXXXXXXXXXLXXXXXXXXXXTVPXXXXXXXXXXXXXXXXXXXXXXXXX
XXXAXXXXXXXXXEDXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXXXXXXAXX
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XXXXXXXXXXXXQXXXXXXXXXXXXVXXXXXXXXXXXXRXXRXXXXXXXXXXXXRXXPXX
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AAAXGXAXMHVSSXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPX
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XXXXXXXXXXXXXXXXXGEXPXRAXXXXXXXXXXXXXXXXXXXXXXXXXXXXLXXXYTNX
VXDXXXPVXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGXXXXXXXXXXXXXXXXX
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XXXXXXXXXXPXXXXXXXXXXXXLGTASSTXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXAXXXXXXXXXXXXL
XXEEIXXXXXXXXXXXXXXXXXVXXXXXXXXXXXGXXXVXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXAXXXXXXXXXXXXXXXXXXXXXXDXXXXXXXXXXXXXXXXXX
XXXXXLXXXXXXXXXXXXPXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
PTXXXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXXXXXXSXXXXXXXXXXXXXXPXXGX
XXXXXGXXXXXXXXXXXXXXXXXXVXXXXXXXXXXXXXXXXXXXXXVXXXXXXAXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXAXXXXX
XXXXXXXXXXXXXXXXAAAXXXXXXXTPXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXAGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXGXXXXXXXXXXXXXAQIYVDALEAAXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXAXXXXXXXXXXXXXXXAGRIXXXXXXX
XXXXXXXXXXGXXXXXXXXAAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXSXXCXXXXXXXXXXXXXXXXAXXXFXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXLXXXXXXXXXXXXXPXXXXXXXXXXXXXXXXXXXLXXXXXX
XXXXFXXXXQARRDGQVDAHRDLLXXXXXXXXXXXXXXXXXXXXXXXXTXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXRVVXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXGXXXXXRYXXXXXXXXXXXXXXXXXASXGLXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXVQXXXXXXPXXXXXXXXXTLXXXXAXPV
LXXXXXXXXXXXXLXXXXXXXXXXXXXHTYXXXXXXXPXXXXXXXXXXXXXXXXPXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXAXXXXXXXCXXXXXXXXSSXXXXXXXXXXXXXXXX
DXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXAX
XXXXXXXAXXXXXXXXXXXXXXXXXXXXXXXXXXXDXXXXXXXXXXXXXXXXXXXXXFX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXDXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXTPXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXRXXXXXXXXXXXX
XADLXXXXXXXXXXXXXXFQRXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXGXXXXXXXXXXXXXXXXXXXXXXXXXXDXYXXXXXXXXXXXGXXXDNEXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXTXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGXXTXXXXLXDXXXXXXXXXXXXXXXXXX
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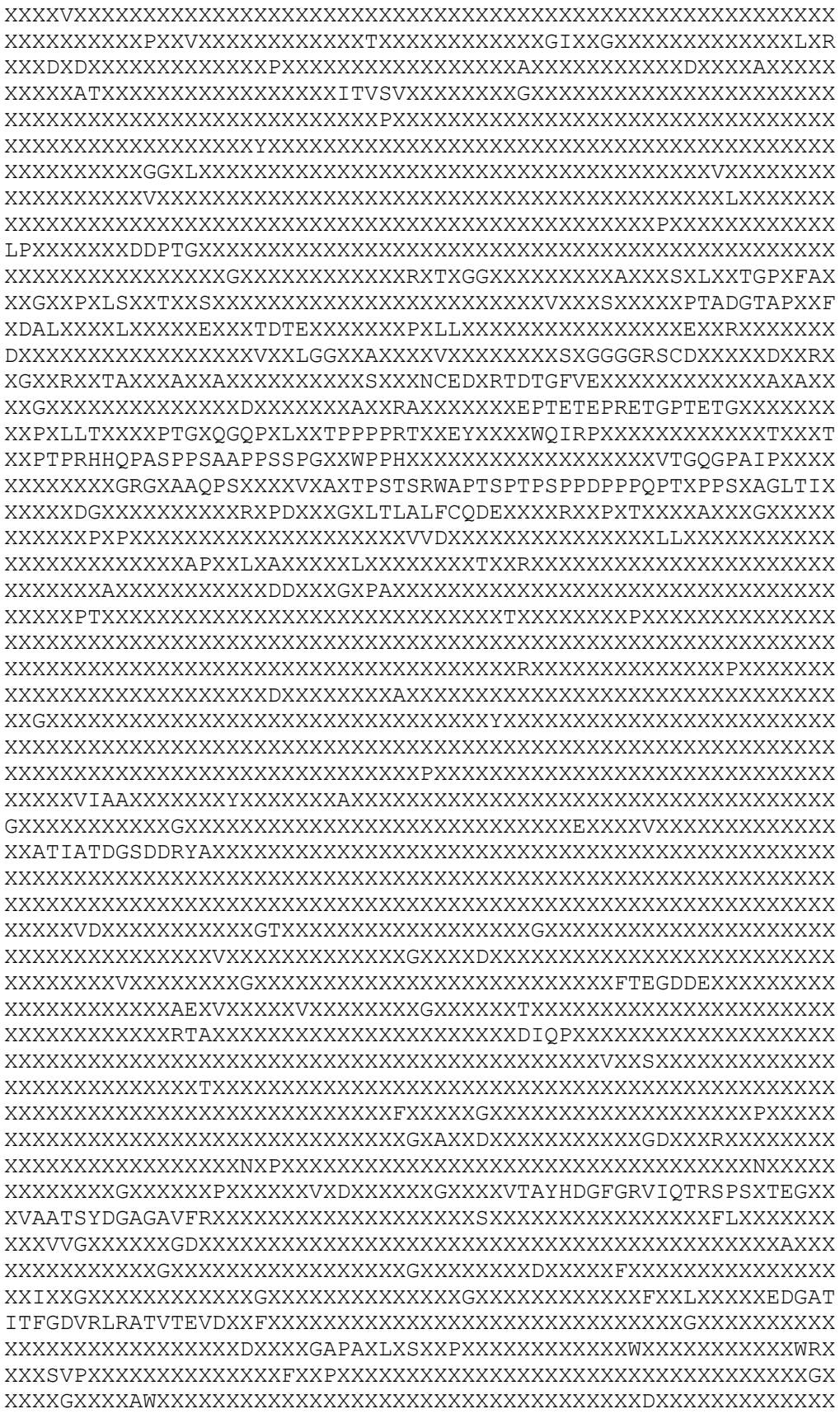
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXNXXGXXX



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XADXXXXPXGXXXXXXXXXXXXXXXXGXDDXXXXXXXXXXXXXXXIXXDGXXXXXXXXXX
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PXXVXXXXXXXGXXXXXXAXXFXXGTLGLXAGGGXXGXXXXXXSXVSRGXEXXXXGXTIT
EGLLXPXNXLXXXXXGXXXXXXPXTPPAGXWXXXXPXXXXQXXXAAGDASGGTDXXXXXX
FXXGXXXXXDXTPXXXXXPXXXXXTPQSXXXXXXXXXXXXXXXXXXXGXXXXXXXXXXX
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XXXIXXIGGANTKLNYVQXXXXXXXXXXTXXXXXXXXXXXXXXXXAVXAXVXXXGXXXXVX
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DXXXXXXGXXXXTXGXTXTXXXXDXXXXXXXXXXXGXXXXYXWXXXXXLXXWXXXXXXXX
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GAPXXVXXXGXXHDTXXXVXXXXXXXXXXGXXXVPPTFVTXXXVXXXGTXXXXXXXXGXX
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XXGXXTXXXGXXVVXXXXXXXXXXXXXXDPXGXXXXYXYDXXGXXXXXXDXXGXRXXXXYX
XXXDXXXXTXXXXPXXXXXXXXXXYDXXGXXXXXXXKSPNGVIEYTSEXXGGALQXRXXIV
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DXTGXXXXXGGXXXGXGXXXXXXXXXXXXVXXXXXXGXXXXXXGXXXXXGXSVSIDPXXXX
XGXXXXXXXRXXXGXXXXXXXXDKGDDXFXXXXXXXXPXXPXXXXXXXXFXXPXXXXXXD
XXXXLXXXXXXXXGXXXXXXPXXXGAXXXXXXXXXXXXXXYYDSXXXXXVXXXXXARNXXG
VAXXXXXXPLPGDTFLVGFEDASNGDYQDYVFVLENVVAAGDGGGGXXXGXXXXXXXXXX
XXXXXXXXXXGXLXXXXXXXGXXTXADQGTGLTXXWIDDETXDXXSLVGNXXXRDSNDDQ
RLDTLMHMXXXPXGQGGVLAXXXXXXXXXXXXXEVTVSVGDPNLGGADETHTINVEGITA
VDAFGXXTXXXGXXXXHTTSTVQVEVTDGAXTXDXXGXXXTXINYIEITPLDGGIGETIG
QVNXXPXGXXTXXXXVXXXGXLXXXTDPXGXXXXXXXVDTEGGADKTDDXXXRXXXTXXX
DGXXXXXXXDXXXXXXSXTDAXXXXRXXXXXXXNGXYXXXASXXXXXXXXXXXXXXXGX
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XXXXXXXXXXEXXXXXXXFTGPXXXXXXAXXXXXXXXDXVVDXXXXXXXXXXXXXPXXXX
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XAGRXXTXXXXNGXTTXXXXDXXXRXXXXXXXXXXXXXXXXXXXRDXXXXXXXXXXXDGX
ETITXSXXXXDXXXXXXXEXHRXXXXXXXXXXXXXXDXXXNRXXXXXXXGTGXXXXXXXD
XVLLVSHDGADXXXXXXXXXXXXXXXXXGXXXXXXXXGXXXXGXXXXXXLXXXRXXXXA
XXXXXXXXXXGXXXXEQDTSXXXXXLXDPXXPXXXXXXXXXXXXXXXATYXXXXXGXXX
XXVXGPXXXXXXXXLTHDXXXXXXXLXXXXXGXVXXXXXXXXFXXXPDEFTLRIDPESGD
WTXXXXXXXXXXXXXXGXXXXXXXXXXXXXXRXXXPXXGXXXXVXXXXGTXXXXXXXXXY
XXXXXXPXTXXXXTAPAVPAGLAGTAVDGEVELTWDGVADADLTGYQVERATSPTGPWTS

LTGIAVSGTTFVDAPPASGTYSYRVLAEDVSGXXXXXXXXXTXXVXGXXXXAXRINAGXX
XVTSGGXAXXXXXXXXXXSXXXXGXXXXXXXXXAXXXXXXXXXXXXXXGXXXXXXXNGT
YDVTLHMAEIYFGAXXXXXXGXXXXXXXXXXXXXXXVXXLXXXXXIXXXXXXXXXXXGXX
XXGAVXXXXALXXXXXXXXXXXXXXXXXQXXXXXXXXXXXXXXXXXXXXYLXXXXXXPGD
PPATASG

==> Felidae.txt <==
>MSA Consensus of 134 seqs, protein
MAGXXXXXXLXLLXXXXXXXXXXXXXXXXXXRCDXXXXXXXRXXCXXCXXXXXXXCPXGX
XXXXXXXXGXXDCRYXXXXXXXXXSXXGCXXXCXKDXVXXXCCPGXWGXXCXECPGGAXX
PCNGRGXCXXGXXGNGXCXCQXXFXGXXCXXCXDXXXFGPXCXXVCSCVHGXCXXGXXGD
GSCXCXXGYTGXXCDXXXPXCXXLXCPXNSXCSXXXQDETKXXCXCLPXXXXXGXXCXXX
NPCXXXXCXPXAXCXXXXXXXXXCXCXXXYHGDGXVCLPXDPCXXNXGXCXXXSTVCXYX
XXGXXXCXCKXXXXXXXXXXXXXXXXXCXXXXXCXRXAXCXXXXXGXTXCXCXXGXVGDG
XXCYGXXXXXXXXXXXEPXGXXXXRLXXXXXXLDXXXXXXLXXXGPFTVLXPXXXXXXXF
SVKEXXMXXXXAXXXXKXHXIAGQXXXEXXXTQXTXXXXTLXGXXXXXXXXXXXXXXXXK
XXXHXXXXXXIXXXNXXAXNGXXHXXXXXXXXXXPXXXXXXXXTIXXXLASXXXXSXFXX
XLEXXXXXXXLDEDGXXGPXTVFVPSNEAXXXXXDGXLXYLXXPXGXXKLXELVXYHIXX
XXQLXXXXLISXXXXXXMANQXXXXNXXXXGXILXGPXGVXXXXXXVXAXNGXIXXLXGV
LXPPXIXPILPXXCXEXXXXXXXGXCVXCXXXXXSXCPXNSXXXXXFXXXCVYTXXPTGX
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XXXXGXHXCXCXXGWXGDGRXCXXIXXCXLXXXGGCHXXAXCXYVGPGQXXCXCKXGFXG
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XXXXXXXXGLGDEVXXVLXXXXXRCXXXXXXXXXXKCXXCXXXXXCXXGXXXXXXXXXC
XYXXXXMGKRSXXLQXGCXXXCXKXXXXXXCCXGFFGXXCXPCPGXXXXVCXGXGXCXDX
LXGXGXCXCXEGFXGTACEXCXXGXYGPXCXXXCXCXHGXCXXGXXGDGSCXCXXGWXGX
XCDXXIXXXXCXXXCXXXANCXXXXXXXXXCXCAARDNTNEGXXGXGXXCXXXXXCXXXX
GGICSXXAXCXXXXPGXRXCXCXXGYTGDGXXCXLEXNXCLXXXGGCHXXAECXXTGPXQ
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XTCRXXXXXEGQVDPLSHCLXXXXXXSXYFFXLXXXXXXXLXGXGPFTVFXPXXXXXXXX
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XXXSSDXXXXNGXXHXIDXXLXPXXXLXXXXDXXXXXXXNXTXXAXXXGYXXFXXLXXXX
GLLXXXXDXXHXPXTXXWPXDXALQALPPXXQXXLXXXDGGXXDKLXXXLXXHVIRXXXX
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XXNXCECXLXYEGDGXXCTVXDXCXXXXXXXXXXXXXSXXGXXVXXXCXXXYEXXPFTEX
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EAXXXCXAXXXXLXXXXXXXAAXQXXGFXXRQNCRXGXXXXGXVXXPXXXPWSSXXXCXX
XXGXXXXXXGGGAAXXGVXXLXXRXXXXXXXDTYCXXXXXXXXXXXXXXXXXLQGRTGL
ETGDEGXSVCXXXXXXXXXXXXXTILCXXXXXXXXXXTQTGXXYXXXXAEDIXXYPSXRX
XXDDVXXXXXXXXSTSXXXXXFXXXXXXXXXXXXRXPGXXXXXXPXXXXXXXNXXXXXSXN
XXXXXXXXXXXGLSLXXSXVXXXXXSWAPXXXXXVXXXXXXXWXXXXXXXXXXXXHTAAA

TTALMSSSGTTSRFLCKTATKRREAXXXXXXXXXPXXXXXXXXXTTIMAGTDSNIISAGW
EPTEENEDERXXHPXXXGXGXXXXEDFISSTISTTPRLFNHPKQNQDRTQWSPGESXXGV
XXLXXXAXXXDVDRSSTIANGXXXXRXXXXXFGXXXXXXXDXXEXQHSTSPTPAHDSHPD
QRMTTQSQEDXXXXXFFDPIXEXXSXXXXXXXXXTERWXXXDSXXXHXXXLXPXXDPXXX
XXXXXXXTXXLXXTTQXXXXQSFSTSHGDWEEDKDHPVTSTPTXSSKDXRTXXXDGKGGR
RSGXXPEXXXXXKSPVATLPYELTSSAPETVATSVEXXTSXSPATKEXRTLIPVTPAKTG
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GGANTTSGPTRKPQIPEWLIILASLLALALILAVCIAVNSRRRCGQKKKLVINNGNGAVE
ERRSWEEAETQCRMYGAHLASXXTPEEQNFINSRKASGLNGEASKSQEMVHLVNKESSVT
CDQYMTADETRQAQHYHQQINLQNVPCNYHLSVDMKIGVVSCGPPPELPLAQVFGRPRRR
YEVDTVLRYRCREGLTQRNQPLIRCQENGRWEPPQISCVPRRPARALHLAKAPGHQGRLL
GRWKELLTPPSSPSPGPXGARPCPALPSPHHRLTTWEGAAALQAAVPQGVCGKHLGGSSL
D

==> Feliformia.txt <==
>MSA Consensus of 158 seqs, protein
MAGXXXXXXLXLLXXXXXXXXXXXXXXXXXXRCDXXXXXXXRXXCXXCXXXXXXXCPXGX
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PCNGRGXCXXGXXGNGXCXCQXXFXGXXCXXCXDXXXFGPXCXXVCSCVHGXCXXGXXGD
GSCXCXXGYTGXXCDXXXPXCXXLXCPXNSXCSXXXQDETKXXCXCLPXXXXXGXXCXXX
NPCXXXXCXPXAXCXXXXXXXXXCXCXXXYHGDGXVCLPXDPCXXNXGXCXXXSTVCXYX
XXGXXXCXCKXXXXXXXXXXXXXXXXXCKXXXXCXRXAXCXXXXXGXTXCXCXXGXVGDG
XXCYGXXXXXXXXXXXEPXGXXXXRLXXXXXXLDXXXXXXLXXXGPFTVLXPXXXXXXXF
SVKEXXMXXXXAXXXXKXHXIAGQXXXEXXXTQXTXXXXTLXGXXXXXXXXXXXXXXXXK
XXEXXXXXXXIXXXNXXAXNGXXHXXXXXXXXXPXXXXXXXXTIXXXLASXXXXSXFXX
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XXQLXXXXLISXXXXXXMANQXXXXNXXXXGXILXGPXGVXXXXXXVXAXNGXIXXLXGV
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LXEAYNXLXXXXLXXGXHRXXXLGXXXXXSYXFXXXXXQXXVNXXPXXXXXXXXXXXXXX
GLXXEVQFVLXXXXXRCXXXXXXXXXXKCXXCXXXXXCXXGXXXXXXXXXXCXYXXXXMG
KRSXXLQXGCXXXCXKXGIXXXXXCCXGFFGXXCXPCPGXXXXVCXGXGXCXDXLXGXGX
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XXXXCXXXCXXXANCXXXXXXXXXCXCAAGXXGXGXXCXXXXXCXXXXGGICSXXAXCXX
XXPGXRXCXCXXGYTGDGXXCXLEXNXCLXXXGGCHXXAECXXTGPXQXXCXCTXXXYXG
DGIXXCXXXXXCXXXNGGCSXXAXCXXTGXGXRTCXCXXECAXXXGDGXTCRXXXXXELQ
VDPLSHCKXXXXXXSXYFFXLXXXXXXXLXGXGPFTVFXPXXXXXXXXXXXXXXXXXXX
XXVXRYHVXXCXQLXXXXLXXXXXXTXLXGXXXXIXXXEXXXYXNXXAXXXSSDXXXXNG
XXHXIDXXLXPXXXLXXXXDXXXXXXXNXTXXAXXXGYXXFXXLXXXXGLLXXXXDXXHX
PXTXXWPXDXALQALPPXXQXXLXXXDGGXXDKLXXXLXXHVIRXXXXLAXDLPXXXXXX
TXXGLAXXXXXXXCXXXRXXGELXXXXXXXRIXQRXLXFXXGXAYGIDXLLXXPXLGXXC
DXFXXXXXXXKXCXXCXXXPPCPXXSXXXGXXXXRXCXXYXSKFWXSPPLHSLAFYNGFY
YSLRSIWALGRSSLWGXXXGXXXGCXXXCVXXXXXPXCCXGXXGXXCXACPGGAXXPCXX
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XLXXXGXXXCXXXLSLXXXXDLXXXXXXAGVFHXXXXXGXYXXXXXEAXXXCXAXXXTLX
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DELLYVXXXXAPGPXXXRDGTRYXXXXXXXXXXXXXXXLSDXXYXXXXXXXEYRTNPXXX
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VHSNSHAAVQEXXXXXXXWXXXXQPKTQDXXXXXXTXLXXXSGXXXXXXXXXXXXXXWXX
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RXXXXXXXXXXXXXXHXXXXXXXXXXXEXXTQHSXSXXXEXXXXXXETATRKEQWVENG
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GHTSGSQEGGANTTSGPXRKPQIPEWLIILASLLALALILAVCIAVNSRRRCGQKKKLVI
NNGNGAVEERRSWEEAEKASGLNGEASKSXXTQEEQNFINSGLGTGLEGMVQHLVNKESS
VTXDQYMTADETRNAQHYHQQIELQNVPCNYHLSVDMKIGVVSCGPPPELPLAQVFGRPR
RRYEVDTVLRYRCREGLTQRNQPLIRCQENGRWEPPQISCVPRRPARALHLAKAPGHQGR
LLGRWKELLTPPSSPSPGPXGARPCPALPSPHHRLTTWEGAAALQAAVPQGVCGKHLGGS
SLD

==> Finegoldia.txt <==
>MSA Consensus of 335 seqs, protein
MRXSIRKEIRRFLCFLMTFIMILTSMPVHLLAANVDHNNLXNSKSXIINNKTPVMVAKPE
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LPDLXGYXXPQDDFTIDYXTXKNAAXGXXXTGNXXNGXRYXANXXFXYKAKSNXIXIKHV
FQDLEDFTKYTNPDGSVGEXGXXITTQXGNTGSTMEVSPLXXXDPXXKGFVPEAXXIXMQ
VPENAENFILEYRYNRAHYDVVFDTXGGTALPTRTLYYGQXMPKIADXXIPTKVGGEFQG
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FWAEKADHADGASLXDKYDYIGTRVYKDXDTGSRPXLDNEXVXXIVFPDLDQARLXKIWA
GARFNRGKDLYLNKFYVYNQALTHXQNKDPXNVNLVKSVDSTGKTVYNIYYDRQVYDLYF
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PGYQSFGWGPNYTXPNWPLHLDTPPYRLNADEFLDMXNYXXWGGYTKHIDKGDGTXIDLD
XXDFXTLSFGIKQXKPSIPHHMDFWMDGFKXGETIIRYDLVRTKADTXXXDYXHXYPXVX
GFTPYGYXPXXAWPXIXEXXEEXGRVXEXXINXLNDERXEITPNNSGXYYNNXGXKLPIG
QLDFIXXFFSDXDEFGDPLXDXDGXPXVXXFEENGYLRFKYTRNKYPLRFNYDPSKIKDD
SEFNXTNXLDTFYEFPLKALSPDLXXDKTPREXEEYKKENXKNLLDNPEKLXELGLTDLV
FNDPXDXNKLKVKRPDNLSDQMVFKGWALDPAGSKLIWENPXEXMPXHPVNLYAKWGEPD
YKWKVTFDPNGGXLRNIKEENLTTSRKKIQEGDIGQEEINTYAKKEANXGXKQIFTVIQR
QKLVEPKXKPTRKGYDFMGWEVIRYKKDAXTGDYTXEXDTSYRDTYKVPELYSFGNDVVA
PVYLKAIWVPNXRVDVKVEHYMLDKDYSKLVKKLEDTLEXKRANYLVATTGDKQDDEYIL
APHEELEKKLTGDLKTTYEXYNXRVKXXNTXFQXFRVEPAQILNTXTSNKXXDNXXXXXX
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IDYDLSYVLGXXGKTQYKXXVPXGYVXXTXXXXKGGXFTXDXSDGXXXTXLXYDVIKGLX
XXXLPXXXXXXXGXXXXXXXXXKXXXXXXITXGNYKRVYAYXXGKXSMDXXXWXXXXXLN
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==> Firmicutes.txt <==
>MSA Consensus of 8306 seqs, protein
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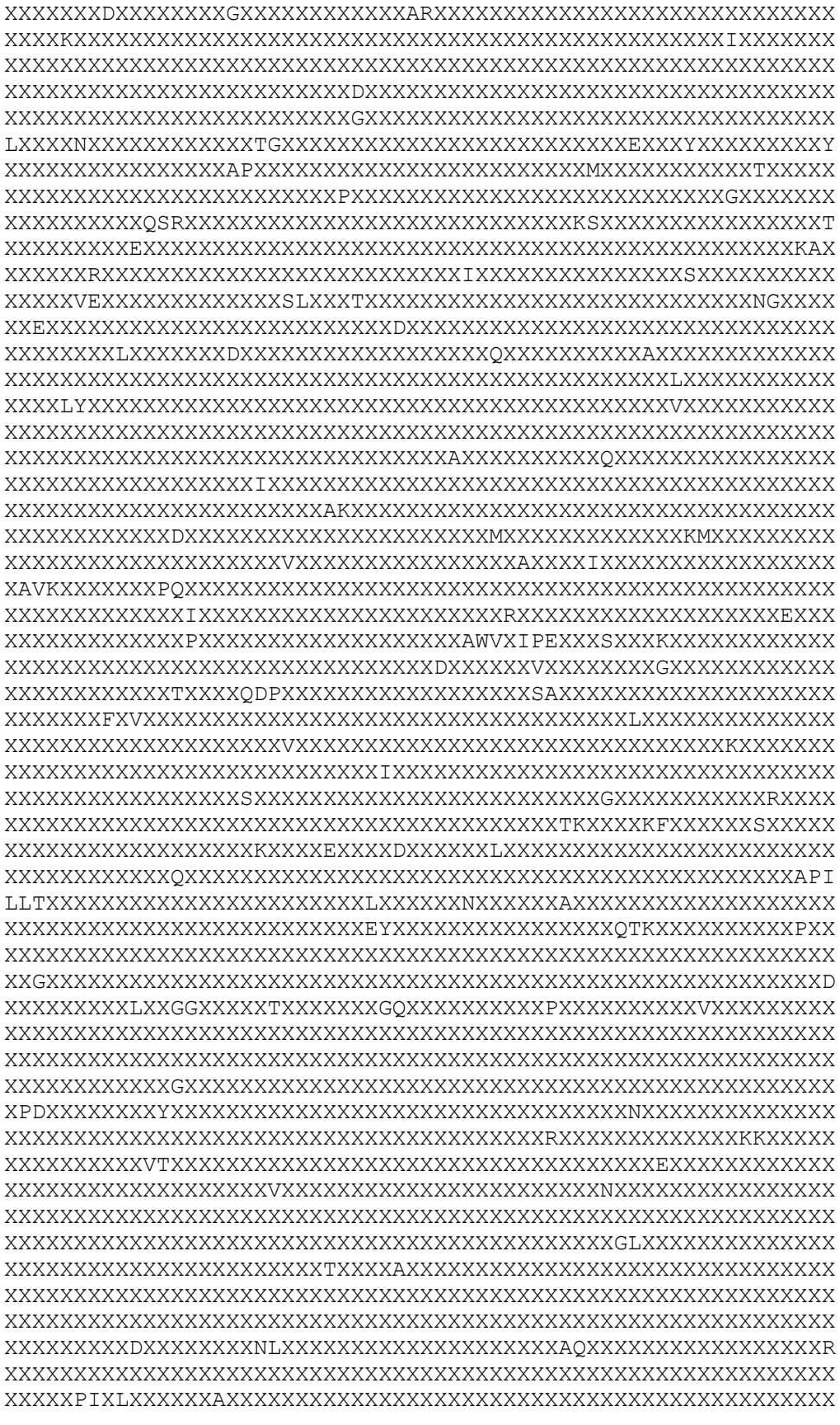

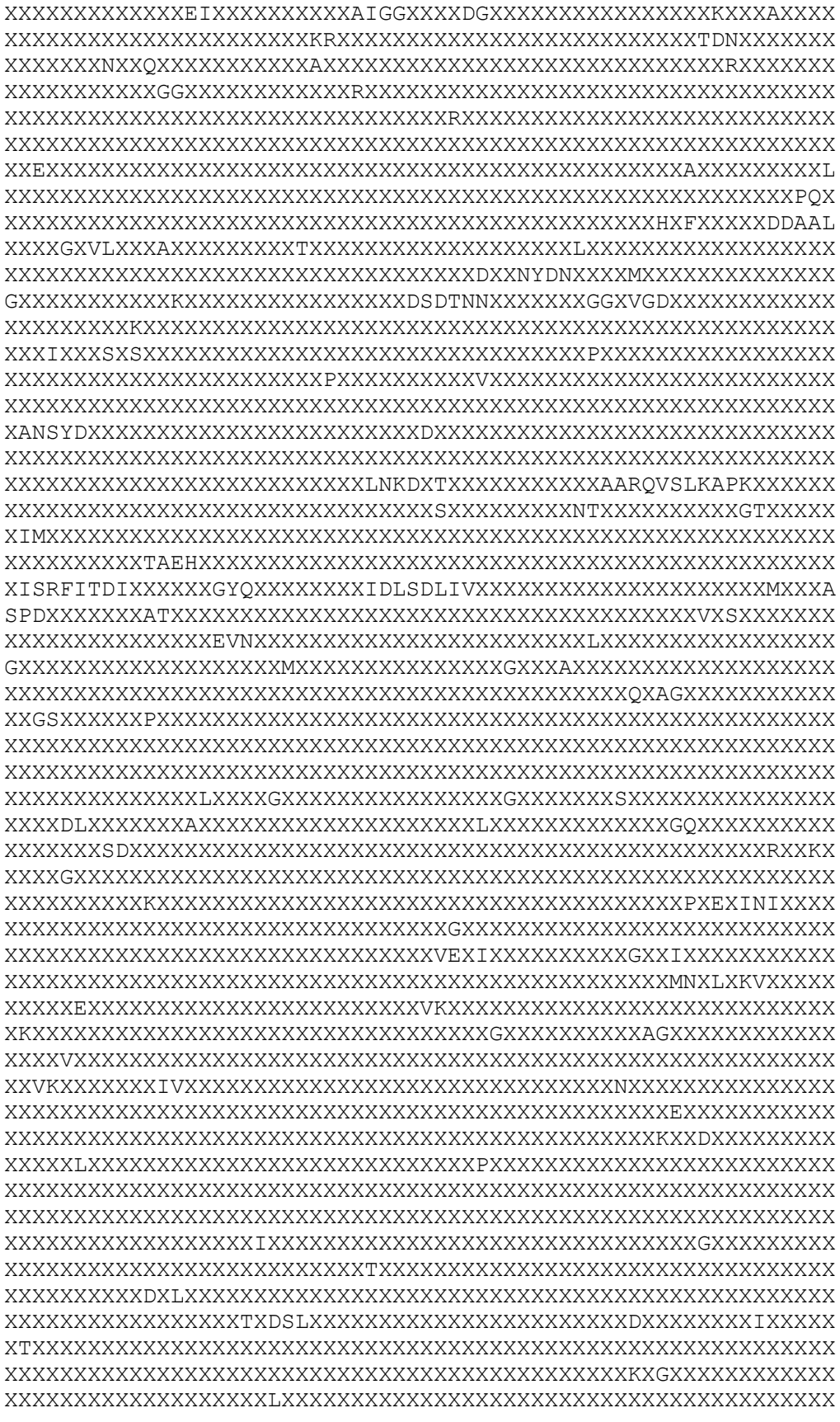

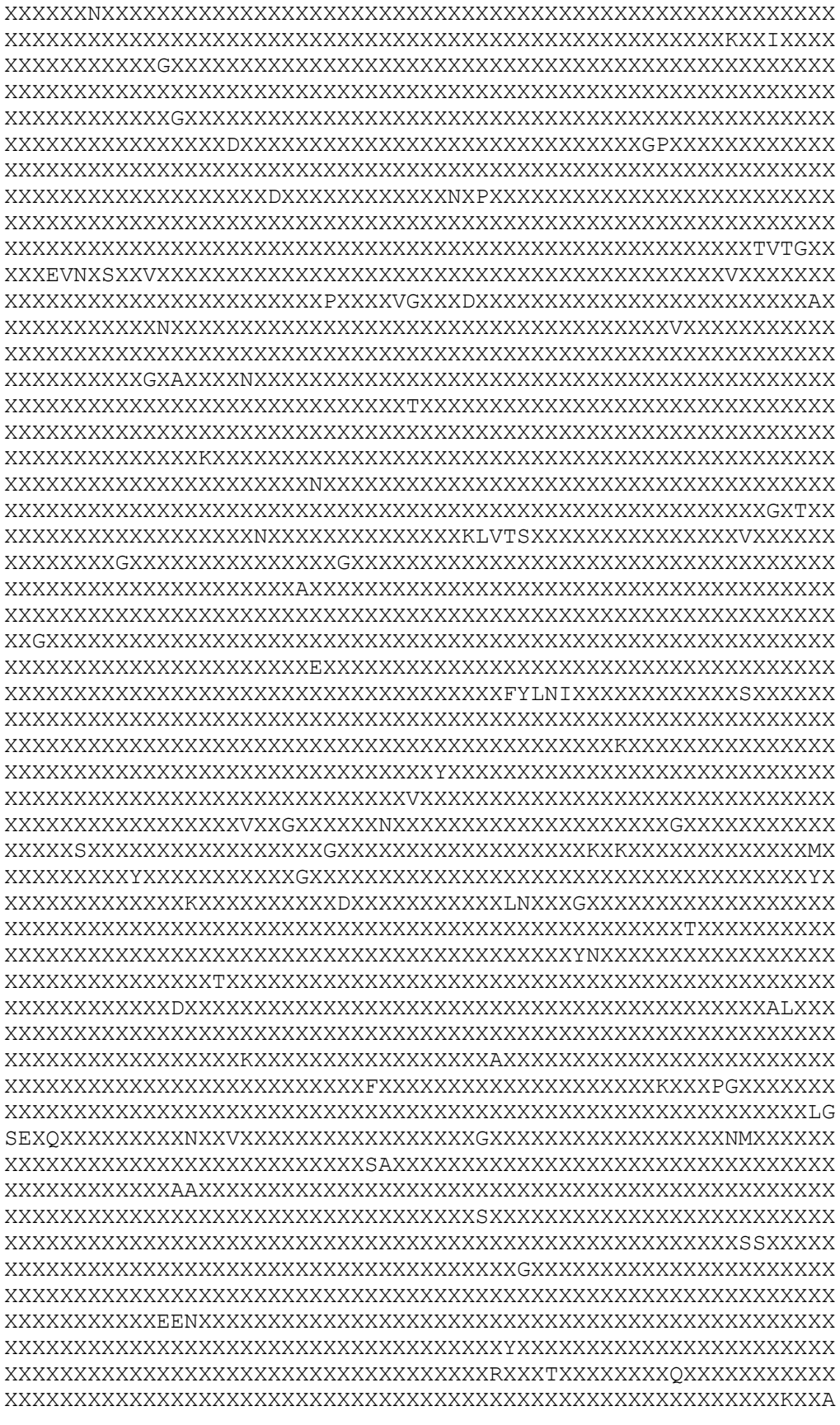

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==> Flavobacteriaceae.txt <==
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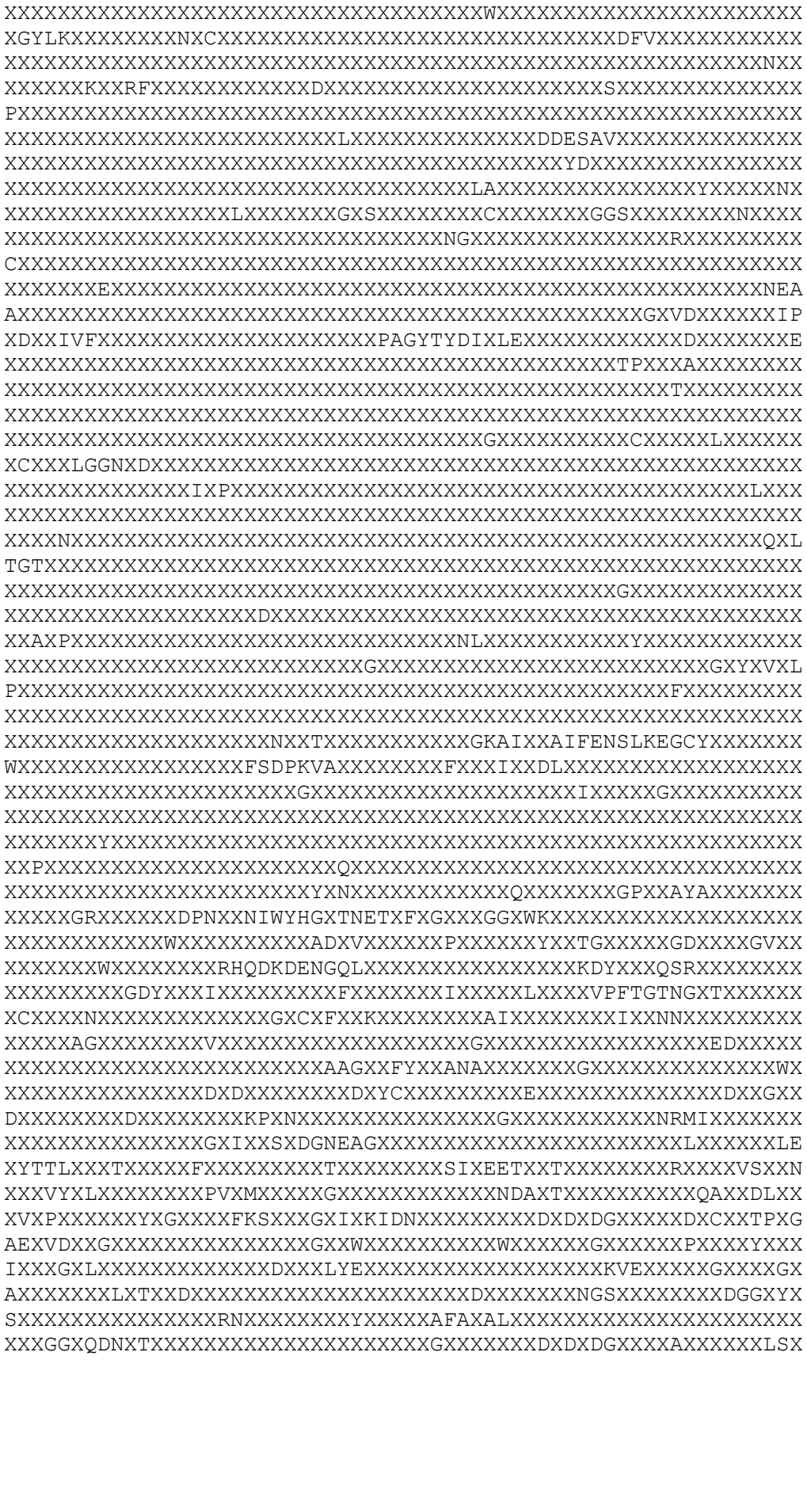

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TGAXXDXCXXXXNXXXQXXXXGCXXXXXXXXXXDXXXXXGIXXXXDGXXXXXAXXXSGDR
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LDXXDXCXXXXXXXXDXDXDGIGNNXDXDDDNDGXXDXXXXXXXXDAVNLXXXXYXXXXD
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==> Flavobacteriales.txt <==
>MSA Consensus of 537 seqs, protein
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XXXQXXXXXXXXXXXXXXXPXXFXXXXXXXXXXXXXXXXSXXXXXXXXXXXXLXXXTXG
XXLPXFTXGDXXXXXXXXTLXXXXPXNLXXXXXXXXXXXXXXXXXXXXXXXXPXXXXX
GXXXXXXXXXXXXXIXSXXXXXXYXXXXXXXGXXXXXXXXXXXXXXXXXXXNFDXXXXX
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VTVSQDPNRXXXXLXKXXRXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXK
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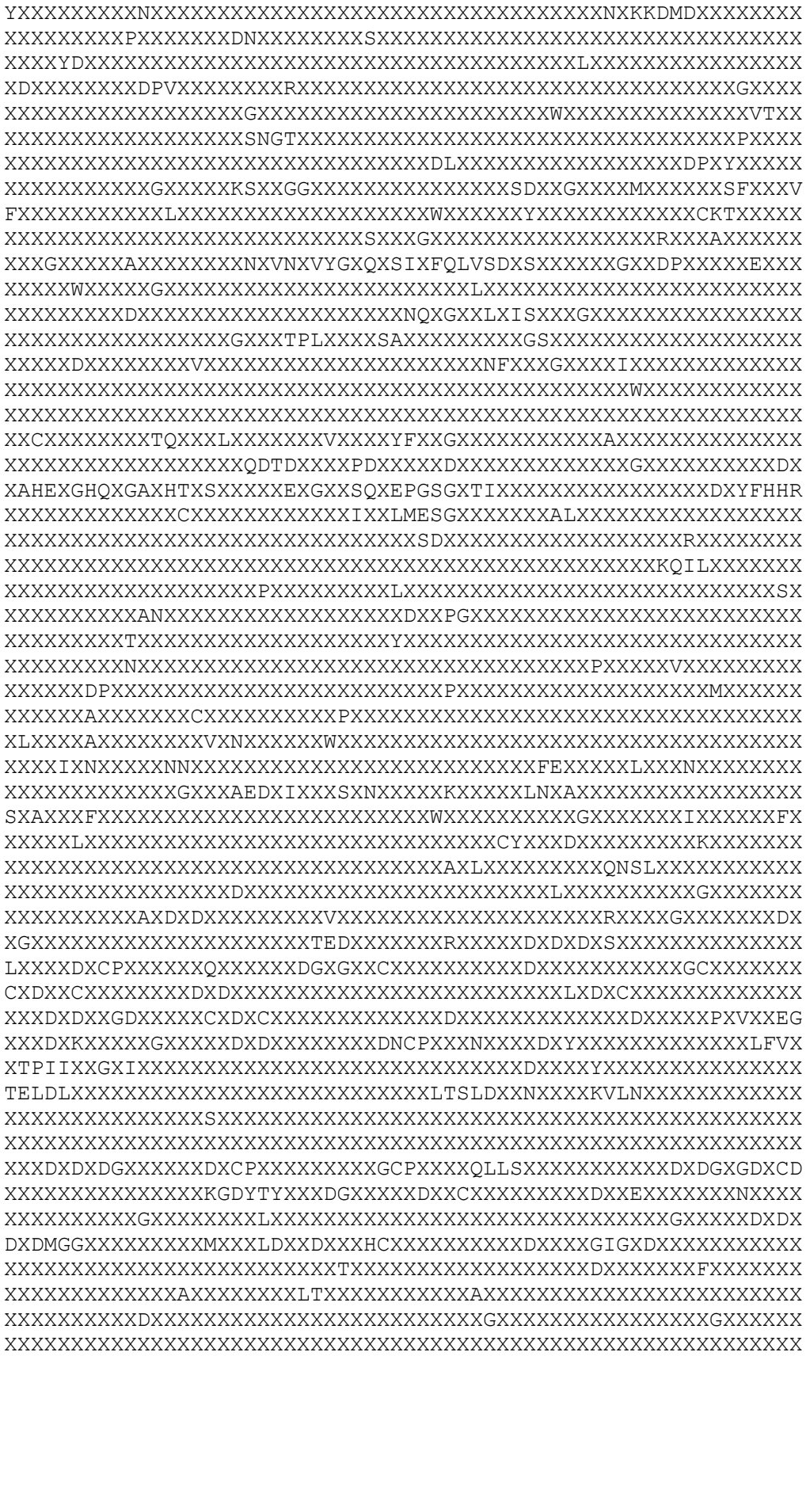

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==> Flavobacteriia.txt <==
>MSA Consensus of 537 seqs, protein
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XXXQXXXXXXXXXXXXXXXPXXFXXXXXXXXXXXXXXXXSXXXXXXXXXXXXLXXXTXG
XXLPXFTXGDXXXXXXXXTLXXXXPXNLXXXXXXXXXXXXXXXXXXXXXXXXPXXXXX
GXXXXXXXXXXXXXIXSXXXXXXYXXXXXXXGXXXXXXXXXXXXXXXXXXXNFDXXXXXX
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XXXFXXXXXXXXXXXXXXXXXXXXXDXDNDGIPXXXAXXXPXXXXXXXXXXXXXXXXXX
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XXQXXXXXXXXXXXXXXXXXYXXXXXXNXXXXXXFXXXVGXXXXXXXXXVXDPNXQXXX
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VTVSQDPNRXXXXLXKXXRXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXK
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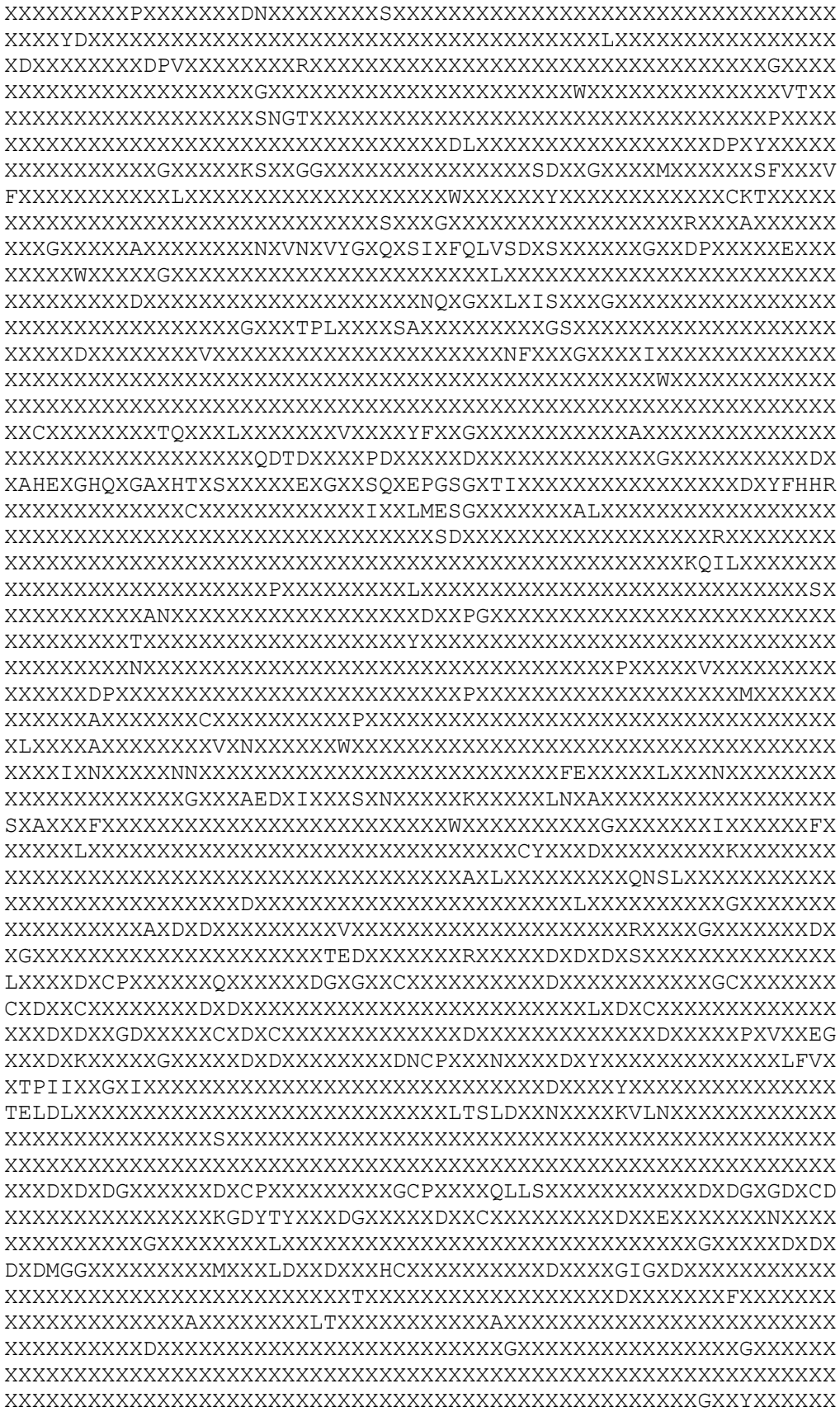

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==> Galliformes.txt <==
>MSA Consensus of 146 seqs, protein
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XXPISVTGXLHMPDHSSGGGEKDXXVKXYXXEXSXXPXXXSTXIXATAXDFXXEDDVQXC
XHPASTTXXXXXXXXXXXXTQXXWXPXXXXXXXXXXXXXXXEXXXXXXADXXSSGNGSXD
EDXSEXXXXXXXXXXXXIXXXXXXXXXXXXXXXHHXXXXXXXXXXXXXXXXXXSXLXXXX
XXXXXAXCTDXPXXLLXYXXXXPXXXXXXXSXGNGSXDXDXSXEXMXSTXVXXXEXSXAX
NEXAXXXXXXXHXDNXEXTXXXXXXXXGXXFXXXXXXXNPXXXXLXXXXXXXXXXAREVD
SXEXGXXEXLXXVXTQDYWXPSYTXEXERYPSSXXXAXXXXEXXXXXXXXXXAXXXGXXX
XFXXPLLHSXXXGWXXXGXNPXXTTGXXXXXXXXXXGENXXEKETSYTAMVSNHGAXXXX
XXVGXVXXXXRXXXPXVXXXWXXXXYXXRMTQRKTHCXXPXIMDRVIPSXESNXEKXXXN
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XXXXXXXXXXNXGQXXXGXXVXXXXXXXXXXXXXSXXXXXXXXXXSXXXXXXXXXXRXLX
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PVLLGLDPXSXXEAXXESLLXSTINLXIIXTXTDSNDXLXPXXXXXEXWTPRVIXXXXLX
LTXXXXXXXXXXXQXDTAXATXDXXXXAXHXXXXQXXXXXXXXXXXXXXXXETCVYPTPX
TLPSDNEAAQSTEGXTHXTDXXXXXXGXXAXPGXPTVLLGLDPXSTXXXXXXXPXXXXXX
EAGXESLLXXXXXXXTXTXXTXXNKMVSXXXFHXEEXTXXXXXXXXXXXXXXXXXGKTEXX
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SDQGPXXGLGXDXEPTXXPGXSTTTTXXXXXEGXIXXXAXXSDVXSQPXXXXXXXXXXIX
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KEQXXMQDXTGACDEFLTVDXXXTQNHQPXXXXXSVXEXXLXXDXKEPXXXYXXXSALXP
SXPXYXXXXXDXXXXMKSGVQXVXXDXGXXPXXXPXDXXXXXSSMAECIMQSLRSRWRSP
PHEGAQ

==> Galloanserae.txt <==
>MSA Consensus of 166 seqs, protein
MLCWNEVQSCFLLAFLAVAAYSVSDAQGQVSPPTRLRYNVVNPDSVQISWKAPKGQFSGY
KLLVTPSSGGKTNQLILQNTATKAIIQGLIPDQNYALQIIAFSDDKESKPAQGQFRIKDI
ERRKETSKSKVKDPEKTNASKPTPEGNLFTCKTPAIADIVILVDGSWSIGRFNFRLVRLF
LENLVSAFNVGSEKTRVGLAQYSGDPRIEWHLNAYGTKDAVLDAVRNLPYKGGNTLTGLA
LTYILENSFKPEAGARPGVSKIGILITDGKSQDDVIPPAKNLRDAGIELFAIGVKNADIN
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TSDITARGFRVSWTHSPGKVEKYRVVYYPTRGGQPEEVVVDGSSSTAVLKNLMSLTEYQI
AVFAIYSNAASEGLRGTETTLALPMASDLKLYDVSHSSMRAKWNGVAGATGYMILYAPLT
EGLAADEKEIKIGEASTELELDGLLPNTEYTVTVYAMFGEEASDPLTGQETTLPLSPPSN
LKFSDVGHNSAKLTWDPASKNVKGYRIMYVKTDGTETNEVEVGPVSTHTLKSLTALTEYT
VAIFSLYDEGQSEPLTGSFTTRKVPPPQHLEVDEASTDSFRVSWKPTSSDIAFYRLAWIP
LDGGESEEVVLSGDADSYVIEGLLPNTEYEVSLLAVFDDETESEVVAVLGATIVGTTAIP
TTVTTTTTTTATTPKPTIAVFRTGVRNLVIDDETTSSLRVVWDISDHNAQQFRVTYLTAK
GDRAEEAIMVPGRQNTLLLQPLLPDTEYKVTITPIYADGEGVSVSAPGKTLPLSAPRNLR
VSDEWYNRLRISWDAPPSPTMGYRIVYKSINVPGPALETFVGDDINTILILNLFSGTEYS
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==> Gammaproteobacteria.txt <==
>MSA Consensus of 2117 seqs, protein
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XXXXXXXXXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXVQNNTE
XVXDXSVQITGLSANTLYNLTVASNDAAGNRATQTREIQFQTASTSDTEPPLIIGRALVE
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ESSDLSGNQVHSNMSSVTTQSQSVSNGFEIISQPVIERLTGXXXXLXXAXXRYSDSVAIV

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VDPTIGFPTAGXXXXXXXXXXXXGXXXXXXXXXXGNXXXXXXXXLXXSTLXLSATPXITE
AGGVLVYTATXTQAVPXTDLTXTLSNGXVIXIXAGQXTGTVNVPLAPNDXVYXDPXQIXV
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LDAGXVTNVXXTATXXXAEGGKTSTVXYTAXXXXXDXDXDXAPVTGSPVVVTLXNGQXIT
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VIQ

==> Gekkonidae.txt <==
>MSA Consensus of 488 seqs, protein
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==> Gekkoninae.txt <==
>MSA Consensus of 475 seqs, protein
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GXCTCXXXYXGPXCDQXXPXCXXXXCXXXSXCXVXXTDKXXXXCXCLPXYXXXGXXCXAX
XPCXXXXCXXXAXCXXLGPXXXXCXCXXGYXGDGXXCXPIXPCXXXXXXCPXXXTXCXXX
GPGKSXCXCKXXMXPXXWXXXXTPXLXXXXXXXXXXXXHWLXXWXXLXXXXLXXXXXXXXX
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FXXXXXXXXTIYIXXXXXXXXXXXXXXXXXXXXDLXXXXXXXXXXXXXGGISVSSAIVTQ
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NGSEHDPLHTDVVSHDGTKXKGSTLAPVKYDSEDKYSTSSAEGVLLPGIVPRRGTNHKNN
TYHTGLVPNQPEDRGSQQGDSTPETQPRAAHIPDWLIVVASLLALALILGVCIAVNSRRR
CGQKQKLVINNGKGVVDNKNMGGLNGEASKSHEMVHLVHKEQPEDQTGSHDEFLQIDETN
NLQEVDLKSGV

==> Gekkota.txt <==
>MSA Consensus of 652 seqs, protein
MXXXXXVLFXXXXXIXXXYXXXGQXXXLXXXXCXXKXXXTXXTXCXXCXXXXXXQCPXGX
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PCNXXGXCXXGITXNGXCXCXXXXXGXACXXCXXXXXFGPXCXSVCXCXHGXCNXGXXGD
GXCTCXXXYXGPXCDQXXPXCXXXXCXXXSXCXVXXTDKXXXXCXCLPXYXXXGXXCXAX
XPCXXXXCXXXAXCXXLGPXXXXCXCXXGYXGDGXXCXPIXPCXXXXXXCPXXXTXCXXX
GPGKSXCXCKXXXXXXXXXXGCXXXXXXXXXXXCXXXXXCXXXXXXXXXCXCXXGXXGXG
XXCYXXXIXXIXXXNXLPXGXXXGXLXXAXXXFXXXXXXXLXXXGPFTVLXPXXXXXXXX
XMADXXXXXXXAXXYVLPELQSGFSFHLSLTRNDTIYIIGGHSIETNTRPPNLYKXKIDL
PIGSPAVNCCVLSGGISVSSAIVTQVKTXXXXXXXXXXGNXXKXIXXXLXXXXXXSXFXX
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XXXXXXLXXXXXIXTMXXQXXXXNITXXGXILXXDXGXAXXXXXIXAXNGXIXXLXGXXX
PPSIIPXLPXRCXEXXXXXVAGSCVDCDALNTSVCPPQSTPMEXXIXXXXCXYXXXPLGL
NXXXXGCXXYCNXTXXXPXCCKGFFGPDCXXCPGXXXXPCXGXGXCXDGXXGNGXCXCXX
GFXGXXCXXCSXXXKYGXXCDXXCXCXXGXCDNRXXSXGXCXXXXCKXGYXGXXCDXXXX
XCXXXXXXLSCXXXAXXXXNXXXXCXCXXGYEGDGXXCSXXDXCXXXXXXXCSXXAXCXX
TGPGTXXCXCXXGWXGXGXXCXXIXNCXXXXXGXCHXXAXCXXXGPGQXXCXCKXXXXGX
GXXCXXXXPCLXXNXXCHXXAXCXXXXXXXXCXCXXGYXGDGXXCYXXXXXXLXXXXXX
XXFXXWXXXXXXXALLXXXXNXTKSLPEEXHLANNXXXEXXXWXXXXXXPXXXXXHXLXG
XXXXXXXQXXXXXXXXXXNXXVRWQXXXXXXXXXIXXXXXVXGDIXAXNXXIXXXDXVLX
PXXRXXXXXXPXLXXXLXXXXXXXXFXXXXXQYXLXXEIEXXXXYTIFXPXXXXXXXYXK
XXXXTXLDXDXXXXHXXXXXKLXXNDLXNGXXXXTMLGXSXXXXFXXXXXQXXXNXXXXX
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XGXGXCXCXXGFXGXACXXCXXGXYGXXCXXECXCXXGXCXXGXXGDGSCXCXXGWXGXX
CDXXXXXDXCNXTCXXXANCXXXXTXXXXXCXCXAGXXGNGTXCTXIDXCXXXNGGCSXX
AXCXXXXXGXRXCXCKXGYXGDGXXCXEIXXCXXNXGGCXXXAECXXMXPXXXACNCLXX
YSGXGXKTXXLIXXCXXNXXXCSKNXLXTXTIITMXSXHWLLAWXGLELNTLXXXPXXXX
XXXXXAXXXXXXXXXXQXXAAXXILXAXTXNAWXTGQWXIXXXXXXXXXXXXXXAXXXKL
GXAPXHXWYPXVXQGXTXXTALXXSTWQKXAPLXLLXXXXXXLXXXXXLXXGLXSXDLXX
XGGXXGLNQTQTRKIMAFSSIAHMGXAWLXXAXXXXXXLXTLTXXXYXXXTXXXFIDXXX

XLXXTXXKTXXDLXXXWXXXPXXXXXXXXXLXSLGGLPPLTGFXPKXLIXXXLXXXXLXX
XXXXLXXXSLPSLXFYXRXXYXTXLTXPPXTTXXXVXXKWRXXXXXXXXXXXXXXXXXXX
XXXLPXXXXXXPXXXLXXXXXXXISXXCSXXXXEIGEXYIXXXXXXIXXXYXEFXXGXAY
GIDXXLXXPXXGXRCDXFXXXXXSXXXCGXXXXXPXCASXPAIXXGXXXXGXXXXHSGXC
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GXXPCCPKPCCPKXXCPXXXXXPCXSPCGXPXXGXGXXXXCXXXXXFXGTXCXXCXPXRY
GPDCXXCXCTEXGXCXEGXXGXGXCXXXXXXXXXFCXXXLXXXXXCSPXCXXNXVCXXXN
XCXCXXXYXXXXXXXTXXXXXXXXXXXXXXXXXLGXXXGXXVXXXCINQIPPSEVXIQPPP
XXXXXPNVVRXXAASTCSPAGQDSLGTIIMEYVGNSTLHHVXXXXIYGTXXXTAKRKXDD
GXGXGXESLXDXXXXXXXXXXSLXXXXXXXXXXIVAGLXFLHSQLXVXXXXKPAXXXXXEX
XXXGXXXXXXXXXXXCXXXXXXXXXXXXXXEXEAPEWTPDIKHXKXGXXXXXXHXVNLQXL
CRICGGSFKNDPVXXXXDXQXKXXXXXSXXXDXXCXXXXXXRSHPVHGPVDDEMQALLRK
KERRATSWPDLLNKVFKIDVRGDXXXXGXXXXXXLPPXXXXXXSSMGXXXXXXXXDTIHPT
NFCHXCWXXIQRKFSXXPCEVYXXXXXXXXXWXPHSXSCXXFLKSPLXXXXNXNNCLTSSH
GIKRKXXKKAVEDGTKXXLXXXXXXXXXXXXXXXXGPXXXXXXVKEEVXXXXXXXNNXTG
ATLIXXGKXDEXXLXXXXXXXXQDMXXKEXXXXXXXXGSXXXXXXXXQXLXXXXADQXGQ
SPXXSSDVKKERKTTXXXRVNXXXXXXKIKIVTKQTGTECITAIEIVADXXXAXSTPIXX
XXXXXXXXXXXXXXXXRKIMYXRSQKQXNSKXXXAXXXXXXXXQDGIHLSTKMLTVDYPVD
FVKSISCQICEHILADPVETTCXHLFCAALTTVVFVNGSXEXKDXXSXXXXRLCILKCLK
VIGSXXXXCXXXXXXTGAGDRFXXDXXXXXXXXXXXXXXXXXXXXVXXXTXXXXEXVXLG
XXXXXXXXXXXXXXXXXXXXXKYSHHLSSHKXXXXXXXXXXXXPXXXXXXXEXFNXXXSXX
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EGLAFFPPPENSNEGFHTAVIHNNDAHHEDSTQEPLPPVHQPDWHTEEEYSTNISRDDIL
MGVIANNGSEHDPLHTDVVSHDEXKXKGSTLAPVKYDSEDKYSTSSAEGVLLPGIVPRRG
TNHKNNTYHTGLVPNQPEDRGSQQGDSTPETQPRAAHIPDWLIVVASLLALALILGVCIA
VNSRRRCGQKQKLVINNGKGVVDNKNMGGLNGEASKSHEMVHLVHKEQPEDQTGSHDEFL
QIDETNNLQEVDLKSGV

==> Glires.txt <==
>MSA Consensus of 711 seqs, protein
MPLGAPALLALALGLGLWLGALAGDPGRGCGPCPLPCFCGPAPDAACRVNCSGRWLQTLG
PSLRIPADATALDLSHNLLQTLDIGLLVNLSALVELDLSNNRISTLEEGVFANLFNLSEI
NLSGNPFECXXGXXWXXXWAKEHQVHVVQSEATTCRGPIPLAGQPLLSIPLLXXXCXXXX
XXXLPDXXXXXXXXTPXXXXXXXXXXXXXXXAXXSSTXXXXXXXXXEQXSTRDTPXXXXX
XXQXXXXXXMETSKXXXXXXXXXXXSXXSAXXXXTXXQHTFXXXXXXXXXXPXGXXXSXQ
PADFHITSSLPISSTRWXXGDGXPXXXSXAEEIPEGAPXXTHXXXXTXSSXXXTXXVXXG
XXXAXXTQGLXXXXXQVXXTPXXXNXXXVXFVXXPXXXXLTXRXXXGSXQTSSKSQXXXV
TSTXSXXXXDXXPAQXXXXXXXSSDKRTKPSTSGVSSTSLTTTEVXXXXXXTXXXPGNXX
CXRXXXXXXXXXTKVSTTSTPQXXXXXXTXXXXXXXMXXXPXXQHXXXXXXSRQPQTTXX
XXVXXXXXSXXXXXXXXXRGEAFXXXSXXXXXPGEXXXXXAXXCXRXXPXXXXNXXLXXX
PXXXXXSVXXXXXXAITTXVXXXXXXXXXMXXXXXXXPXHXXXXQEXXXXXXXXVEVXXX
XGXSXSREAFLTAAEFSTQKXXXXXXXXXXXXXPSXXXXXXIQXEXSSQRTXXPGXXRTX
XXPXXXSSAPXTTHXLXXXXXNXXXXXDXXXXXXVXXXGSXXXXXQTSLTPSSQNXSTVS
TPITSTXXLSTLXQSQHTGSKGXSXXPXXTXXXEXXXSXPXXXXXXXXXTXXSXXXXXXP
GXXIGLQHDAGPGTXXXXPXXXXSXPXXXXXXXTXXXXXXXXXXVHLEEAWAGPVCSLQL
LLVTXXXTXLXXXGXXPXXXXPGHYEVRATVGXSXSXQNXSCSXXVXXPIXXXXXXXXXX
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XXXXSXVSTXXXXXXXLXXLXXXXXXXXXVXXXGXXXXXLXNIHNSAXXXXXXXXPXXXXX
XXXXXXXXXXXXXXXTETSSQRTIXXGXXXXXXXPXXXXXXXXXXXXXXXXKXXLXFXXTX
XNVIXXXAXXXXXXXXXXRHXXXIXTXXXXXXXXXXXXSGXSSXXXXTVXXPXXXXXXIXX
XXXXSQHTGSKGTSXXPQTTTXPVXXXSXXXXXXXXXXXXXXXXXXRXXXPXXXXXXLKVT
GYDKDGYLFQRVSSVSFSSXVPDXXXXXVXXXXXTTHXXXTXXXXXXTXXXXRXTXXXXT

QXXTXXXXXVLPXXXIGMXXXXXXXXXXITXTQILXXXXXXXXXXXXXXWDFXXXXXXXX
XXXXXXXXXXXXTGXXXXXXVXXXXXXXXXXXXXXXXXXXXXTXXPGXXXXXXXXXSX
SXXXXXXXXXXSSXXXXNXTWXXDGRDIRLADSARIRTLANLSLELRSVKXGXXTEYRC
VXXXXGXXXAASVFLTVQEXTXXXVXPXXQNXXXXSXXSIMCSATGXXXXXIXXTXXXXX
XXGSHRYRMTSXGTXXIKNAXXXXXXXXXVXXSXPXGXXXXXXXXXXXXLEXRXIXPXXX
XXXXXXXXXXXXPXTTXMXXTTSSTXXXXGXXXXXXXXXXXGXXXXXVTVHGHPSVTHXX
TXXXXXPLXXXXXXXXXXXXXXXXXXXXXXXTGXXXTXXXXXXXXXPXXXXXXPSATS
RXXXQXETSSXXXXXXGXXXXXXXXSLXXXXPXXXXXXXRLDNMPXXXXXXSXSXXTXXX
TXXXTXGSXXXXXXXXPXSXLXXXXXXXXIXXXXXXXXXXXXQXXVXVTGXXXXXXXXXX
XXXPXXXXXXXSXXXXXXXXXXXXXXXTXXXGXXXXXXXXXMXSXXPXXTHXXSXXXXXX
XXSXXXXHXXXXXXQXXXXYTCXXXXVXXXXXXXXXXXVHVLPXXXXXXXXSTXXXXXX
XGXXXXSGIPXXXXXWXXXXXXXXXXXXXXXXXXXXXXXSXXXXXXXXXXXXXAPXXXXN
AAGXXXRKXXXXXYXLXXXXXXXXXXXDXGXXXXXXYTLQXQXSXXXXXXAILPCEAKSL
PPXSXXXXXXXEXXLIXXFXXXXXXLPSGSMXXTXTRXXXXXXXXXLXXXXXXGSXXXXX
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HXLXXXXSTXXTSXIEQAVISDAXXXXXXAXXXXGXXXAXXXXXXQEXPXXXXXXXXXXX
XVXSXXXXXXXXXXXXXXXQXXXXXXTXXNPQXTXXXEXXXXXXXXXSXXQXXTXXXXXR
XXXPGXXXPSFGSVAPFLXXLXXXXXLGNVYYREDXXPFXXXXXXSXXXXXXXEXXXXXP
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XXXXXGXYXPXXXXXXXXXXEXXXXXVLXXXXXXXXXXXXXXXXXQXXXXXXXXXXXXXX
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LXXXXXXPXXXXXXXXRGLASPEQGPRSSTQGSVXXAXXXACXXXXXXXXXXXXXXXXXX
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XXXXPXXXXXLXTXXSXXXXXXXXXXXXXXXXYXXGXXXXXXXXXXXXXXXXXXXXXXXX
XVDRGQYICXTNXXXXXXDCRYXXXXXXXPAVEGGEETSYFIVLANNLLELDCQVSGSPX
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GGAXXXXXXXXXXXXXXXXXXXTIKSSDLPEPCXGXGXCXXXXXXXXXXXXXXXXXXXXD
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PFTXLXPXXXXXXXXXXSSXXXXXXXXXXXXXXXXRYFVXXXXHXXXXXXXXXXXXXXXX
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YHIYXXXXXQXXVXXLXXCXXXXXXXXXXKKEYNLQVXXXXSIXXXGXXXXXLXXXXGXXX
XXXXXXXRXXXXAXXXXXXXXXXXXKXXXXXIXDIXXXGXILXXXXXXXXXXDFKRNPSPR
XXXXXXXXXXXXXXXXXXXXXXXXXQXALQLNXAANGXIXXLXGXLXPPXXXXXLXXNKX
XXXPXXCXEXXXXXXXXXXXXXXGXCXXXVXCXXXXXSXCPXXSXXXXXXXXXXGXXXXL
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XXXXGXXXXXXXXXGSXXXXXXXXXXXXXXXXXXGXXXXXXXSPXXXXXXXXXXPGXXXPC
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXG
XXXCXCXXGWXGXGXXEXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
CVXIXXCXLXXXHXXXXXXXXXHLVXXXXXXXGGCTTXXXXPXXXXXXXXXXXXXXXXXX
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NYLVXXIXCXXXXXXCXXXXXXXAXXXXXXXXXXXXXXXXXXXXXGXXXCXCXXXXXGDG
XXCYXXXXXSXXXXXXXXXXXXXXELXXLXEXXXXXXXXXXVCEASLQXXRVCTCXPSXX
GXGFNCYGDIXXELEANAHFSXXXXXXXXXXXXXPXXXXXXXXXXXXXXXXXXXXGGVRE
KXTXXXXGXXXPXXXXXXXXXXXPXXXXXSXXXXTXXVPSESAXXDPXXXEXXXXXXXXX
XXXXXXXXLXXXXXPXLXKXHXLXGTXXXXDLQXLXXXXXXATXXXXXWXIRNIQTMLXG
RVWVQNASXDVADLLATDGXXXXXNQVLLPPRGDVQVGQGXLXQXXXXPXXXLRAHFLQG
XFSEEXLAXLXGQXVXTLSXXXXXXXXXXXGXXXXXXASXXXXDXXATNGXXXXXXXXLX
XXKASIXXXXXXXXXXRXXXXXXXXXXXXLXXLXXXPXXXXFXHPGPHSXXXXXEVVXXX
XXDXXXXXXXXXXXXXXSIQXXXXXXXQLSXXXXXXEXLXXXXLXXXIEAAXAYTXFXPX
NXXXXXXXXXXXXXXLXXXXXXXXXXXXXLAAVXXXXXXXXXXXXXXXXXXXXXXXXXXX
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CEXCXXGXYGXXCXXGEAWEGKHGGALESRADWTSWQGQGLGMALTLSCLIPLTXCXCXH
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LAXXXXLNXXXXXXXXXXXXXXXXXXXXXXXXXCXXXXXXXXXXXGXXGXXXXXXXXXXX
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YALPXXXXXXXXXLIXXXDXDVSSGSXXEXSTXXGYXIXHTXLPTXXPTXXXDXXXXXXX
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XRXXDVXXXEXXXPXXXXXXXXXXXXXXXXXXXGXGISXXXXKXXXXXXXGQRXXXXYLL
XVLXXXSXLXNATANFSTFXXMVLXYXXXXXRGXXFLXHLXDEDLSXXXXLXXXXXDPAX
XXXXXXXXXXXXPDXXXXXXEXRNLQXVDMKIGVXXXASPEQIQRLASEMAGSSSVSSTL
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XXXXGXXXXXXXXXXXXAXAXYXXXRXXXXXXGFXXFXXEXXXDXXXXXXQEGPXXPTLX
XXXNPXXXXXXXXXPXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXPXXX
XXXXXDFPXXXXXXXXXXXLXXXXXXXXXXXXXTVEXXXXXXXXXXXXXXXXXXAGMAEXQLSL
TLQXXXXXQXXXVXXXXXXGXEGVLAXXXXXEPXXXXXXXXXXXXXXXXXXLSMLPNSSL
YIAXXXXXXXXXXXXXXXXXLEVKAAQLXXXXXXXXXXXXXXXXXXXXXXXXQXXXXCQVTC
XXXXXXXXRXCXXPXPXXXXRPCQGADSEARHCHNKLCPVDGHWSEWSFWEDCSRSCXXX
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XXXXXXDKXXXXXXXXSXXXXXCHXXXXXXXFXXXXXXXXXXXXXXXXXXVXXXXXXXXX
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XPXPXXXXAXXXXLXXXXXXXXXXXXXXXXXGXXXXXXXXXXXTDXXGXLVXXXXXXXXXX
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XATQXXXCXXXXXXXGXXRARGSVIGNIXXXXXXIXXXXXXXXXXPXXXXXXXXXXXXX
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XXXXXXYXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXIHHXXXXXXXXXXXXXXXXXXXXXHTQXXXXXXXXXXXXXXXXXXXXXSDYNQLE
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XXXXXNLHXXXXXXXXXXXXXXXXXXXXXXXVXIXXSXXXXXXXXCXXXXXXXXXXXXX
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XXXXXXXXGXXVQQRNISCPXXXXPXXXXXLXXXXXPLXXXPXXXXXXXDXXXXXGXTDL
GLAASLLFLLLXXXXXXXXXXXXXXVXVXXXXXCXCXXXXXXXXXXXGIXXXXXXXXXFX
AXXRXAKXSXXXQPQXXIXVXXXPXXXXXEXXGTCXDXXXXXXGXXXLXPXXCXVDLKGL
FHFEEXTXXLYXCXGXXXXXXXXXXXXXXXXXXPXXCXXGXXXXXXXXXXXXXXXXXXVS
XGPPPELPLXQXXXSPRPRYEVDTVXXXXXXXCXXQXXXXXXXXHXXXXXXXXXXXXXXX
XXXXXXGXXPXXXXGXXXXXXXXXXXLLGDGKXXXXXXXXXXXXXXXXXXXXXXXXPXP
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XXXXXXXXXXXYSIXXPXXXXXCXXXXXXRXXLNGKXXXXXXXCXXXXXXXXNRXXXXX
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XXXXXXXXXLXXXXXXXXXXXXXWXXGXXXXXXXXXXXXXXAXXXXXXXEXLKGXXXXX

XXLREAETYRMKVGALSYSAXGXXXYXXXXXXXIAVSAYPY

==> Haemosporida.txt <==
>MSA Consensus of 794 seqs, protein
MXXKXXSIFXXIXWLXXXXXXXKXXXXRIFDVNXXEXXXKKXXXXXEXYKCFSKRXXXX
XIXXXQXIXXXXXXXXXLNXXRXXXXXXXIXQATXXXGXXHXXXNGQGDNRTDEIQTXXX
XXPXXXFKFXXXLNXLXYXDXXXXLXSXLXIXLXXYCXPXIPKGXRCXXXXXXXXXCXXX
XKXXXXXXXXXCXDNCGXXXXCXXXXXXXXXXXIPXXXVXXXXXXXCXXSXXQRKLXNLC
GXNKXFRXXXXXXYCIPXLXNXSALDKIXNXXXDADVCLAALXEXXSXXQXYPKYQAQYX
XXXXPSQMXXXXXXCXSXXXXVIXCXGXXXXXKKEKLDLEKNLKXXXXKXYXXXXXXRAK
DHFXXXXXXXFIXXXEDXXXXXXFXXXXXXXXXXGESDKYXXXXXCXEXXXXNGXXYXGC
QXXSISXXXCLPWXXXNIXXIXXXXXXTHNXCRNXEXXXXXYXXXXXXXXXXXXXXXXXX
XXIXNNXXXXXXXXXGXXXEXXCXXXGKTDFXXFDXXXXHVNVSDFXIXLXXXXCXXGXX
XXXXXXXXIXXXXXXYXKXYHXXDXEIAXTXXFXXXXXXXXSXXXXXXXXXXCXXXXXXX
XYXXEXSXXCXXXXYXXXXGKXXXXXXXXXXXYXEXXLXXNEXXXXXXNXXXXXXXEXXEX
KNIPXXXSXXXXYXGFNDNIELFXXXXXXXXXXXXXXXEXXXXMXFXKXXNXXXXXXXXX
IXPXLXXSXXXSXXYXYXXXXXXXXXXXXXXXXXXXKXXXXXXXFXXXGXGGRLGXXXXXPL
HXYXXXEXXXXKXMXXXXXXXXXXXXXLXXXSXXICIXXXXXXXXYXXXIGXXXXXDXXNS
XXKYXLXNXXXXXNDNXCFXXXXXXXXXDXXXXSXXNXXFXXXXXXCXXXXTHXXXXXXX
XXXXEXXIXRXXXXSXXXXXXXXXXFXXXXXNXXXXXXXXXXXXXXXXEKGXXXXXFXLX
XTXXXXXXXXXYLCXXXXXXXXXXXXXXXXXLXXXETIXXXXYDIIISEKASMDEMEKKE
LSLNNYXYXSSFXXXXYXXXXXPXXXXXXXXFGYFNYXTGXCEXXXXXXXXYXXXXXXXX
XXXXXFXXXXXXXXXXXXXXXXLWXXXXDNXVSLWXXXXLXXXXXEXXXXXXXXIEXXXX
XLTPXFLXKYXXXXPXXSXXXLXXXXXXXXXXXKXXXXXXXXXSXXXXXTXXXXXTXPXX
XXXNXXXXXXXXXXXAXXYXFSXXXLXXXKYXTXXFXXLXXXXSXXXXXXXXXXXIXXFT
XXXXXFFXXLXKNNXXSXXNXNXXXXXXXXXXXXXXXXXXXPIKXXCXXXXXXXTCXXXXX
XHXSXXXXXXXXFXXXXXXXXXXTIIXKXXXNIXYPXRXXXXXXXXXXXXXXXXXXXXXX
XXXKNXXXXXXXXXXXXXXXXXXKXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXHDXXXXXXKLXXYXXXXXXXXXX
XNXXXXXXXXXXXXXXXXXVXXXXXXXXXXKDAIQNIKNKISDDIKIXXXXXXXXXXXXXX
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TKXXXXQSXXXXXXHEXLXQTLNIGXXXCPNXXXXXWXXXXXXXXXXPXXXXXXXXXXXX
XXXXKXXXXXXXNXXXLXXXXXXXXXXXXXXXXXXFXXXXXDXXXVELXYXXXXXXIXXX
XXXXXXXXXDXXXTDPXXSXXXMHXXFXXXXXXXXLXXXXXXXCXXXXXXXXXXXXXXXX
XNXXXCKXXXXXXXXXXXKXXDXXXXXXXXXXXLAVGSYGLGGRLGSNXXYXXCXXXXXXX
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ITLPMXNPXXXXXXXXCSXCXXGEYXDXYXXGXCXENXYXNXCXXNLXXYXXXXXXXXXS
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XRXXXXTRXXIIXXSKXNXCXNXXXXXXXXXXFXDXXXXXXXXLFXIHAKTSXRMXXLXX
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FXXXXXXXXXXFXXXXXXXXXXXVXXFPSXXXXXXXXXXITFVXIXXXXXXXIXXXXXXX
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NNXXXXXKSXRYIPXSXLXXXXXVNEKXDNERKQXXPXXXDNXXXXXVPNXNKTVHPGRKD
SAXVPXDRXXRPHGXXXXNXXXXXXXXDXPXXPERXXXXXXXXXXKXXXXSXNXYKIADX
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EXXQFXIVILPEXNXWN

==> Haplorrhini.txt <==
>MSA Consensus of 795 seqs, protein
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SXXXTXXXXXXXXXXDDLVXXXTXXXXXXGXXXXXPXXXXXXXXXXXXXXXXXXGXXXXXX
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XKSTQEXXXXXXXXXXXXXXXXLXYXXXXGKXHXVXXXXXXLXXXXXXXXXXGXXXXXXX
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XCXXXXXXXXXXXXXXXXXXXXXXXXXXPXXSXXXLXXXXXXXGXXXXXXXXXXXXXXXX
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IVYIAVSAYPY

==> Herbiconiux.txt <==
>MSA Consensus of 159 seqs, protein
MXMXXPRXXXXXXXRXPLXXVAGXXXAAXXXGALXXXAXAAXXXAXAAPXAPAAXXXXXX
PVXXAXXAXXAXPVXXXXXXYDSRNELGAIFDXDVXXGAXXXXXSXXXXDXXLVXXGTDX
XXXGXXXGXXAXXLXGGAVXXXTXXXVXXPXXLXXXXXXXTVSAXXKXXSXXDXXQWXFX
XGXXXXXXXXXXXXXGXGXXXXVAXXXXIXGXGXYTITVTVDGQXXXXTEAXXXXXXXXX
XWXXVXXXXDXXXXXVXTXYIXXXXVAXTXXXXXXSGGAKSVTLGASXXXTTXXXXXEXX
GXXGXXLXXVTTVXPXFXGXVDXXXVXDXALTXXXXXXXXGSAXXXVQLGFVTPETXXXR
TXXXXXXXXDXAXAXXXXVTAYNAWWADNVPXXXTXXDXXXXXXXXXWXXXXXXXLDXXA
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XYXXXXXXGYXXXXXXXXXXXXXXXSHXXYXXXXXXVXVXDXTXXMXXXXXXXXQANEXX
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==> Hexapoda.txt <==
>MSA Consensus of 409 seqs, protein
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DIICLQQSCPPPIXGCHEEPIXGFCCPRYECXVSMATSLNXTTTTTTRTTTTLPPHFXXH
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==> Holometabola.txt <==
>MSA Consensus of 238 seqs, protein
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DXXXLXXXXXXXXXXXXXXXXXRXXXXXXXGXXXXXXPXGPPSLGQAXXXXFXXXXXXXX
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KDSATAXYXXXXXXPXXXXXXNXLXXTPSTXXXXXXXXXXXXXYXAEXXXQXXXXPXXXX

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XXPPPXXXXXXXXXXXXXXXCXXXXXXXXCXXXPXTCPXXXXXCXXXXXXLXXXXXXXQ
XXPXXXLXPXXXXTXXXXXXXXXXXXXXXXCXXXXXXXXXXXXXCXPXXXXXXXXXXC
XXXPXXXXXXCPXXXXGXXXXXAPSCAQQCPIDSECVGGKCVCKPGSSGYNCQTSTGDGA
SALALTPINCNATNGKCLNGGTCSMNGTHCYCAVGYSGDRCEKAENCSPLNCQEPMVCVQ

NQCLCPENKVCNQCATQPCQNGGECVDLPNGDYECKCTRGWTGRTCGNXXPTXPXXPKIC
GNGICKNEKGSYKCYCTPGFTGVXXXXXXPXCXXXPCXXXPXCXXXXPXXXXXXXXCXPG
XXXXXCXXXXXXPXXXXXXPXXXPXXXXXXXPXXXXXXXXXXPXXPXXXXXXXXXKXXCX
PXXXXXXCXXXXXXXXXXXXTPXYXXPTTTRAPITXXXXXXXXXXXXPXXXXXXXTTXXX
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XXXXXXXXXXXXCXPXXXXXXCXXXXXXXXXXXXXXXCXXXXXXXXXXXXCXXXXXXXXX
XXXXXXXXXXXXXXXXXXMQLXXXXXXXXXXXXXXPXXXXXXAXSXXXXAXXCXXXXXPX
VXXSXXLXTSXXXPXXXPXXXYXXXXXXRCXXPXGXXXYXXXXXWKXXXXXPXXXXXXXX
XXGXLXXXXAVQRCDRXXXXXWXYXPXXXDXGYXXXXXXXXXXXXVXXXXXXXXXXWXXXX
XXXXXXXLXXXXNXXXXXFPVGSYETANNSQPSFXXXXXXGXXXXLXXYLXXLXXXXEXF
VGCXXXXXVXXEXXXXXXXXXXXXXXXXXGXXXXXCXXXEQCKPNPCHSNGECTDLXXXX
AXXXXXXXXGHTCQHNMTAATXXXXXXXXXXXIXVVAXXXXXXXRXXXXXXXXXXXLXXX
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XXXXVGGXXLXXGYXXXXXXVXXXXLVQVKLXGXEYFRKTLSTTGLLDAQVLYLGGPAPT
RESLLGATTEPGIIPVPGAGIPIEDTTVPKEADDSRDYFKGIIQDVKVSNGSLNLIVEMY
SLNVTDVQVNAKPLGAVTIDRASVLPGEVSDDLCRKNPCLHNAECRNTWNDYTCKCPNGY
KGKXXXXXXFXXXXTCXXXXXXXXXXXXYECVTNTTFTGXXXXPLAFFYFQEQXXXXXXX
XXSPXXXXXXXXPXXXXXXXXXXXXXXXSSVDXGXXXXEHYDLENASSIXXXXXDXXXXX
XGXXXXXXXXXXXXXXXXXXXXXXFXKXXXXGXXXXXXXXXXXXXXXXXXXXXESMXXX
XXXXXXXXXQXXXXXXXXXSXXVYLGGMXXSXQXRXXTLXXXXGXXXKGCVGEARVGDLL
LPYFSMAELYSRTNVSVQQKAQFRLNATRPEXXXXXXXXXXXXXXGFCQSPSDEYACTCQ
PGFEGXXXXXXXXXXLNXXXXXXXXXXSSSAXXXXXXXXXCXPXXXXXXXEQXXXXXXXX
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CXCVPGFEGPLCDXXXXEXXXXXXXXXXXXXXXXXXXCXXXXXXXGXXXXXDINECESXXX
XXGXXXXXXXGXXXXACXXCXXXXXXXXXXXLTCXXXXXXXXXXXXXXXXXXXXXXXGXX
XRXXNXPXXXQXXXXXXXXXXYXXXXXXXXXXXXCSNGGRCVXXXXXXXDXYCECPEGFA
GXXXXXXIXXKXXGXXXXXXXXXXXXXXXXXXXXXXXLXGXFXXXAXXXXXTRGTXXPSX
QXQQQTXXXXXLXMXXXXXPXXXEXXX

==> Hominidae.txt <==
>MSA Consensus of 507 seqs, protein
MAAAARXRXXXXXXXWXXXXXXLLXXLXXXXXXXXXXXXXXXXXXXVXXPXXXXPXXXXX
XXXXXXXXXXXXXXXXXXHTXXGXXXXXXXXXXXXXAIPXXAXRXXXXXXCXXXXPXXXXX
XXXXXXXXXXEVXXXXXXXXXXGXXXXXVXXXXXXXXXXXXXXXXXXXXXXXXXTXILLFX
XGXXVXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGXQYXXXXXXXLXXX
XXXXXXITHLPGALLXXXXXXXXXXXXXXXXXXXXXXXDXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXLEVPEFXXXXXXXXXXXXXXXXXXXXXLEXTVSLXXXXXXXXXXX
XXXXXEPXXXXPRXXXXXXXXXXXXXXXXXXXXXXXXXRXXXXXXXXXXXXXXXXXXXXXX
XSXXXXXXXXXXXXXXXXXXXYXXXXXXXXXXGXXXXXXXCXGXXXXXXXXXXXXXXXXXV
FTDXXSXXYRXTHEVLQLXXXXXXXXXXXXLXXXCXXXEXXXXXXXXXIASTRXXXXFSFV
RGQVXXXXXXXVKXXXXXXXXXXXXCXXXXKQTCPSGWLREXXXXXXXXDCXXXXXLXXXX
XSLXTXXXXXXXXXHTSEXXGXXXCXXGXXSXXXXCXXXXXXVXEKIXXXXXXGXWSXXX
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FXXXXCXXCXXXNRFXPXXXXXXXXXXXXFPXSCXXXXXXXXXXSISGSSIXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXCXCXXGXXXXXXVFDXLXXXXXXXXXXCXXLXCPXXXQXS
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VXXXXXXXCXCXEXYXGDGCTRSKIVYKXLDKENPSGCSECKCXXXXVXLXXXXXXXXXG
XCXXXXXXXXXXYXXPXXIXXXXXXXXXXXINSXASIXXXXXXXXXXXXXXXXXXXXXX
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XXXKATXXGXXXXXXXXXXXXXXXGXRXXXXXXXXXXXXXWXXXXXXXIVLVPSVSSFSS

RTXXXVELSLXXXXXRXXXXXXXQHILXRDTXTXXXRXXXXXXXXXXXXXXXXXXXXPXXX
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LXXGKKXXXIXXXXXIAANGVFXXXXXLXXXXXXPXQXGXXVVVXXXXXEAAQLXXXDXA
MXKXXXXXXGXXXXXSCNYSVLCRSAVIDHMSRITIGQILASTEAXXXXXXXXXRXXLXX
XXXXXXXXLDGDGVPXXXXXXXXXXXXVDSXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXDDQLXXXXXXXXXXXXXXXXXXSKLXELVRYHIYXHXXXXAHPTXXX
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GXLXPPXIXPILPKHCSEEQHKIXAGXCVXXXXXXXXXXXXXXXXTXXXXXXXXXXXXXX
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CXXXXXXXXXXXXXGXXXXXXXGXGXCSDXXXXXQXXCXXGXGXCXCXXXXXGXXCXX
CSXXXKHGXXXXXXXXXXXXXCXXXXXXXGXXXXXXXXXXXXLXXXXXXTNPLXXXXGXX
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XXXXXDXXAWGLCLVXXXXXXAMXXXXXXXXXXXXXPLSLAQXPXXXXNAECVXXDLGXX
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HVEKNGRYSISRXTEAXDLCXAFNSTLPGITLVXTMAQMEKALSIGFEXCXXGFIEXXXX
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XXXXXXXXXXXXXXTDALCSXXAPXEXXCTXVTDLXXXXXGXXXXXXXXPIVNXXXXXSX
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XGXXXXXXXXRXXXXXXXXXXPXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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VXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXXQRXXXXSXXXXXXXLXXXXXXXXXXXXX
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EGXWXXXXXXXXXNXXPXXXXXXXXXXXXXXXXXXXXXRXMXXXXXXXXXXXHEHXEXXX
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GPIXLXXXXXXXXXLXXXXXXLXMXXXXXSXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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IXXXXXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXVWXSPPLXXXXXXXXXXQ
XSXXRCXXSXWVHXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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XXAGXIEXXXXXXXXXHXLKLRXXXXXXXLXSPSXPXXXXXXXXXXXXXXXXXXXDX
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DAXCTDLHFXXXXXGXXXLXXXXXXXXXXXXXFXXXXXXXXXXXXXXXXXXPGXXXXXN
RXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXYEXXGXXXXXXXXXXXXXXXXXXXX
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XSXXPXXXXXXXXXXXXXXXAPXXXPXXXXXXXXXXFXGXXXXXQLXXXXXXXXSXXXX
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XXXXXXWXXXXAXXXXXXXXXXXXXXXXXXXXXXXXXQXXXXXXXXXXXNXXXXYXXXX
VXXXXXXXXXXXXXNXXXXXXXGXXXXXXXXXXATTXXXTXXXXXXXXXXXXXLXVXXXX
QXXXXCXAXXXTXXXXXXXWXXXXXXXFXXXQRATXXXXXXCLXXXXXXXXYXXXXXXXX
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MXXXXXXCXXXXXXXXLXXXXLXXXXXXXXXXXXXGXDXXXXXXXXXXXXXARXXXXXXXXX
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ELTXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGXXXSGXXIXLXXXXXXXXXVXXXGX
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LGXXSTXXXXXXXXXXXVVXXXXXXXXTXXXGXXXXXXWXXXXXXXXXXXXXDXXXXXXLX
LNQXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXYXXG
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DGIXNXXDNCXXXXNXXQXDXDXDGVGDXCDXCPXXXXNPXQXDXDXDXVGDXCDXNXDX
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VGXXXXXXXECXXXPXXXXXXXSXTXGXFXXXYVAMXPXXXXXXGXXXSXXGLERLPNYX
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ASHDTCVDIDECENTDACQHECKNTFGSYQCICPPGYQLTHNGKTCQDIDECLEQNVHCG
SQEMVFFSDLKYECRDXPCPPNYQRDPVSGFCLKNCPPNDLECALSPYALEYKLVSLPFG
IATNQDLIRLVAYTQDGVMHPRTTFLMVDEEQTVPFALRDENLKGVVYTTRPLREAETYR
MRVRASSYSANGTIEYQTTFIVYIAVSAYPY

==> Homo.txt <==
>MSA Consensus of 363 seqs, protein
MEQTDCKPYQPLPKVKHEMDLAYTSSSDESEDGRKPRQSYNSRETLHEYNQELRMNYNSQ
SRKRKEVEKSTQEMEFCETSHTLCSGYQTDMHSVSRHGYQLEMGSDXXXXTXXXAXXXXX
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FKFSPVCCDMEAQAGSTQDVQSSPHNQFTFRPLPXXPXPXXPXXCXCXRXXXKXXXDXXP
GXXRXXXXXXXXXXXXXXXXXXXXXXXLXXXXXXXXNIXXXXXXXXXXXXXXXXXXXX
XXXXXXXXYPXXXXXXXXVXXSMXDDLXXVXXXXXXXMXXXXARPXXXXFXXXXXPXXXX
XXXXLXSPXPRPXXXXXXXXXXXXXXFXXXXXXXXXXGXGXXXXXXXGXXXXXXXXXXXX
XXXXXXXXXLXXCXAXXXXXGXXXXHXXXXXXLXXXXXXXXXXXXXXWXXXXXEXXXXXX
XCXXXXXXXXXXXXEXXXXXXXXXGGXXXXXXXCTSGHTXXXXXXXXXXKSXLLQTSVSV
HPDAIEXXXXXIMELKKINPDVNPQLGISLQACLLQIVGYRNLIADVEXXRXXXXXXXXX
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LQYFAERDXXXXXXXXXXXXXXXXXLXLSXNXXXXXXXXXXXXXXXXXXFXXXXXXXXXX
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XGXXXXXXXXXXGXPXXXXXXXXXXXXXXXCXXXXXXXXXXXXXXXXXLSVXXXXAXXX
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XXXRVXSXXXXXXXXXXXXXXXXXGXXXXXXXXXXXXFXXXXXXXXXXWXXXXXXXXXX
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XCXXXXXXXXXGXXTSFXXXXXXXXETYTICSGXXXXXLXXXXXXXXXLXXDFXXXXXSX
XXXXISLVCLVLXXXXXXXXXXXXXXXXXXGXXXXXXXXXKXXFLXXXXXTNQVXXXXX
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XPXXXXXGXLXVSCXEXLXXXLXXXXXXXXXXXXXXXXXXXXXXXXXXHXXXXXXXXXXX
VXVAIDECXXXXXGXHGKVFLTVPSXXXXXXXXYXXXGXXXXXDSLXXXDXEXXAFXAXK
VAXVGGXXXNXXLXXXXXLPGFVGCLELATLNXXXXSLXXXXLXXXXXXXXXXXXXXXXX
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NQXXTEAADLCXXXXXXLXXXXXXXAQXEXALXXGFETCXYGFXXGXXVXXXXXXXXXXX
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PDKXEDSXXXXXSXXDRIPAXXXXXQHMSXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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XPXXXXXXXXXXTXXXLXXXXXXXXXXXXXXLXXXNXEFXXXXXXXXXXXXXXXXXXXXX
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YSXXXXXXXXXXXXXXXXXXXXXXXSEDNQDGVTHSDXXGXXDETXXXXXXXXXYPHETT
XXXXXXXXXXXXXEXXXXXAEVXXXXXXXXXXXXXXXSAXXXXXXXXXXXXXXXXXXXXX
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NKILXTCDTAHTXXXAKSSTTVRTFIPVXXXXXXXFXXXXXXXXXGXXXKXXXXXXXXXX
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XXXEPXLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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XFTIQVXXXXXXXXYXXXXXXXXXXXXXXXWXXXXXXXXXXXXXYPVTTTVGLFXXXXXXX
SXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXNXXYWESHCDMINGTDAAS
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XLXXXXXXXXXXXXXWXXXXXXXXXXXXXXXXXXXXXXXXXXLXXXXXXXXXXXXXXL
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XIRXAXXVXXXDQRXXXXXXXXXXXXXSXXXXXXXXXXXXXXXXXXXXGXXXCXXXESPY
AXXXEXXXXXXPXXXXXXXXXXXXXXXXXXXXXXXXXXXXWXXXXXXXLEVPQRTNXXXX
XXXQAVXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXYTKGXX
SSXPXXXXXXXXXGXXXXXNGXXXXXXXXXXXXXXSSXXXGXXQXXXDAXXFTSXXXXXXX
XXXXLXXXXXXGXXXXXXXXXXXXXXXXXXXXXXXXXXGXXDXXXXXXXXXXXXXXXXPXXX
XXXXXXXXXXTXXXXXXXXXXXXXXXXXXXXXTXXXXXXXXXXXXXXXXXXXXXXXXXI
NQMXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXQXXXXXXXXXXXXGXX
WXXXXXXXXTCXXXXXXXXXXXXXXXXXXXXXXXXXXXXEXGVMTLXXXXXVMXPPXXXXX
XXXXXXXXXXXXXXXXXXVRSPTGSPXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
CXXXXNCSQVGXXXXXXXXXXXXXXXXXXXXXXSSSSAPXXXXXXGXXEGXXNTTSSPDP
TPSQNPLXXXXXXXXXXXXXXXXXXCXXXXXXXXXXSXXXXXXDRPXXXXPXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXPXXXXXXXXXXXXXXXPXXXXXXXXXXXXXXXXXX
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XXXXXACEATNXXXTXXXXXXXXXXXXAAQQXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGKXXXXXXXXXXKKXXXKKSXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXWXXXXXXXXXXXXXVDSKNVAYRHSXXXXXXXXXXF

XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXAPXXXXXXXXSXXXXXXXGXSTXXXXX
XXXXXXLXXXXXXXXXXQXXFXXXXXXXXXXLXNXXXGXXXXXXXXXXXXXXXSKXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGXXXXXXXWXXXXXXXLXXGXXXXXXXXXP
XXXXXXXXXXTXXXXLXXXVCXXXXSRXLXXXXXXXXXXXXXXXXXXLVINXXXXXXXXX
XPXXXNXXXSKSKXXXXXXXXXVXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
AXXXVXXXXXXXXXXXXXXXXXXXXXXXAXXXXXXXXXXXXXXXXXXXXXXXXASXXXXX
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XXXXAXXXXXXPXSHLLFXXXXXXXXXXXXXXXXTXXXXXXXXXXXXXXXXXXCXXXXXX
XXXXXLYLSXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGXXXXXXX
XXXXCXXXXXXXXXXXGXKXXXXXRKXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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XXXXXXXXXXXXXXXXNXXXNYXXXXXXXXXXXXXXXXXXRPPAXXXXXXXXXXXXXXPXX
XPXXXXXVXXXXXGXXXXGXYXSXXXGHVVLXXXXXXXXXXXXXXXXRPXXXXEXXXXXX
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XXXXXXXXXXXXLXXXXXXXXXXXXXGGTXXXXXXXXXXXXCXXXXXXXTIKXXXXXXXX
XXXXXXXXXXXXXXXTEQKGXXXXXXXCXXXXXXPXXXXXXXXXXXXDXXXXCXXNNXX
XXXXXXXXXXXXXXXXXPXXXXXXXSTAPPXXXPAXXXXXXXXXXXXXXXXXXXXXXXXX
RLIRXXHYTDADGDGIXNXTQSLIQXXXXXXXXXXXDXXXXXXXXXXXXXXXNXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPXXXXXXXXXWXXXXXGXXX
XXXGXXXXXXXXXLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGNXSXQXDXDXD
XXXXXXXXXXXXXXXXXXXXLXXXXXXXXXXXXXXVXXXXXXXDXCXXXXXXXXXXXXXX
XXXXPXXXNSXQXXXXXXGXGDECDXXXXXXXXXXXXXXXXXXXXXXXXPTXXXXXXXXX
XXXAXXXXXTXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXAXXXXXXXXXGXXXXXXX
CRXXXXXXXXXXXXXXXXXXXXSXXTXXXXXXXXXXXXXXXXXXGXXXXPXXXXXXXXXX
LXXXXXXXXXXXXGVGDXCEXDFDXDXXXXXXXXVXXXXXXXXXXXXXXXXXXXXXXXXP
XXXFXXXXXXXXXVXPEGXXXXXXXXXXXXXXXXXEIVQXXXXXXXLXXGXXXXNGVDXE
XXXXXXXXXXXXVXXXXXXXXXXXXXXXXSXXXXXXXXXXXXVXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXAQRXXXXXXXXXXXXXXPXXXXXXDXXXFXXXXXXQTEQXXXX
XXXXXXXXXAXXXXXXXXXXXXXXXVXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGRX
XXXXXXXXXXXXXXXXXPXXXXXXXXXXXXXXXXXDXXXXXXLXXXXXXGXXXXXXXXXX
XXXXXXXXXSXXXAXXXXXXXXXXXXXXXXXGXXXXXXXXSGYGYGYXXGLXXXXXXXXXX
XXXXXXXLXXXXFXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXTXXXXXXGXXXXXXXXXXXXXXXXXXXXXLXXXAPXXXXPXXXXAXXAPEXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXNGXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXLXPXXXXXXXXXXAXXEXXXSXAXXXXXXXXXXXXXXXXGQTSEESXX
RXXXLXXTXXXXXXXXXXXXXXXXXXXXXXXXPXXXXXXXXXXXXXXXXXXXMAXXX
XXXXXXLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXTNXXXXXLXXXXXXXXXGXXXXXXXXXXXXXXSXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXQXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXWXXXXXXXXXXXXXXRLCXXXXXXXXXXXXXXXXXXXXXX
XXLXXXXXXXXXWXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXLXXXXXXLXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXQFXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXGXXXXXXXXXLXXXTXYXAXXXXXXXPXXXXXXXXXXXXXXXXXXXXXX
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XPSAKAPSPXTPXXXXLXXWXXWGTPSXXXXXXXXXXXXXXXXXXXXXXXXLRQVRLQE
ALYPDPPXXXXTXXXXXGXXXXTXYXXXXQAXXXXXXXXPXXXXXTTDELTGGXXXXXPX
XXXXEXXXXXXXXXXXXXXXXXXXXDXGXYVQELXIXLXGXXXXXLXVXXXXXXXXXXX
XXXXXXXXXXXXXXXXXGXXXXPGXXXXAGAPGXXXXXXXXXPXXXXXXXXXXXXXXXX
XXXXXFXXXXXXXXXXXXXXXXXXGXXXXXXXXXXXXXXXXRYXXXXXXXXXXXRXXH
XTESQSEASTEXXXXXLXXGXXXXXXXXXXXXXXXXXXXXXXXXXAXXXXXXXXGQXXLX
XXXXXWXXXXXXXXXXNXXXXXXAXFXXXXXXXXFXXGXXLXXXXXXXXLXXXXXXXXXX

XXVXXXXXXXXXXVREXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXAXXXXXXTIDXVXX
XXXXXXXXXYXQAXXRXXXXXXXXXXSXXXXXXXXXXXXXXXXXXXXXSXXXXXXXXXXX
XXXXXXXXXXFXXXXXXXXAGNPXXXXCXXXXXGXXXXXXXXGXXXXADGRXCHXXXXNA
LGRHTCHXXXXXXXXIXXYXXVXXXXXGXXXXXXGXXXXELFLXXXXXXXGXXKVXEFRX
XXXXXEMXXXPXXXXXXXXXXXXXXGCXXXXXXXGXXXXDXXECXXNXCRXXXXCXXXXX
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RPXXXXXXXXXXPXPXGXXXXSXPXXXXCICPXXXXXXXXXXXXXXXXRLXXXXXXXXXX
XXXXFXXXXXXXDRXXQXXXXXYXXYXXXXXSXXXXRXSRXXXXXXRGPSXXXXXXXPXX
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XGPXRXXXXXXGSYQCIDTPCPPNYQRDPVSGFCLKNCPPNDLECALSPYALEYKLVSLP
FGIATNQDLIRLVAYTQDXXXHPXXTFLMVDEEQTVPFALRDENLKGVVYTTRPLREAET
YRMRVRASSYSAEGLINMXXXXXXXXXVXXYPXLSHL

==> Hystricomorpha.txt <==
>MSA Consensus of 130 seqs, protein
MRRGSMGMAEXXXXLXXXLLXXXLXXSXXXXXXXXQXXRCDXKXXXXXXTXCXXCXXXXX
XXCPXGXXXXXXXXXXXXXCRXXXXXXXXXXSXXGCXXXCXKXXXQXXCCPGXWGXXCXE
CPGGAXXPCXGXGXCXXGMXGNGXCXCQEXFHLRRFALPELYNSQCRVLCCGVYRHISYK
DTVXGXACYIPXXCXXXXXFGXMXCXSXCXCVHGXCXXGXXGDGXCXCXXXYTGPXCDXX
XPXCXXLXCPXNSXCSPXXEDRTXXXCRCLPXYXXXGXXCXXXXPCXXXPCXXXAXCXXX
XXXQXXCXCXXXYXGDGXVCLPXDPCXXXXGXCPXXSTXCXYXXPGXXXCXCXXXXXXXX
XXXXXXXXXXCXSXXXCXXXAXCXXXXXGXXXCXCXXGXVGDGXXCYGXXXXXXQXXXXA
PXGXXXXRLXXXIXXLXXXXXXXLXTXGPFTXLXPXXXXXXXSXXVTXXXXXXXXAXXXX
XXHIIAGQXXXEXGXXXXXXTXXTLXGXXXXXXXXXXDXXXXXXXXXXXXXXXXXXNXX
ASNGXXHXXXXXXXXXXPXLPGDLKVLPGXXXXXKXTXXXXLXSNXXXXXFXXXLEXXXL
XXXLXXRGXXGXXTXFXPSNEAXXXXXXXXLXYLXXPXGXXXLXELXRYHIXXXXQXXVA
XLXSXXXXXTMANQXXXXNXXXXGXILXXPEGXXXXXXXXXXXNGXIXXLXGXLXPPXXL
XXLSXNKPGDVPXXCXXXXXXXXXGSCVXCXXXXXSXCPXXSXXXQXXFXXXCXYXXXSX
GXNXXKXGCAXYCNXTXXXXXCCXGFXGPDCTXCPGGFXNPCXGXGXCXDGIXGNGXCXC
XXXXXGXXCXXCSXPNKXGXXCXXXCXCXXGXCDNRXXSXGXCXXXTCXXGXXGXFCNXX
XXXCGXXXLAXXCHXHAXCXXXXHTIRLRRARDNVSTVYRPIAERLKELRLPSVNQTEKF
VIRTGPHHSKSLSLXXXXCVCXDGXEGDGXXCXXXXPCXXPDRGGCSXNAECXXXXXPGX
HXCXCHXGWXGXGRXCXXIXXCXLXXXGGCHXXAXCXYVGPGQXXCXCXXGFXGXGXXCX
PIXXCXXXXGXCHXLATCXAVXXGXXXCXCXXXXXGDGXXCYGDVAXELXANAYFSTFYQ
WFKATCKAVGAGQRVCTCPPHFGGDGFNCYGDIXRELEXXXXXXXFXQWXXXAXXQPXLS
XXSXXTXLVPSXXAIXXXXXXXKXFWLXXXXLPXLXXXHXXXGXXXXXDLXXLXXXXXXX
XXXXXXWEIRNISGRVWVQNASVDVADLLATDGVLHIINQVLLPPRGDVQVGQGVLQQLD
QVPAFRLFRELVQGALSEEDLARLGGQEVATLSPTTFXXLXKADXNVTXGGASIXDXDXX
ATNGXXHIIXXVLXPXRGXXXXXXXXLXXLXQXPXXXXFRXXXXHXXLXXXIEAAXXYTX
FXPXNXXXEXXXXXKKVXXLVVPAGWVIGNPQLAAVLTDRPGCAMQXXDTXRXHVXLXEX
LXXXXLXXGXHRXSMLGPXXXLXFXXXXXQXXVNXXPXXXXXXXXXXXXXXGLXXVLXXX
XXRCXXXXXXXXRXKCXXCXXXXXCXXGXXXXXXXXXXCXYXXXFXGKXSXXXGCXXTCV
XXXXXXXCCXGXFGXXCXXCPGXXGXXCXGXGXCXDXXXGXGXCXCXXGFHGTACEXCXX
GXYGXXCXXXCXCXHGXCXXGXXGDGSCXCXVGWXGXRCDXXITXXXCXXXCXXXANCXX
SXXGXXXCXCAAGXXGNGXXCXXXXPCXXXXGGCSXXAXCXXXXPGXRXCXCXXGYTGDG
XXCXEXNXCLXXXGGCXXXAECXXTGPXQATGQLLAPRSPTDRDLGQXXCXCXXXYSGDG
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XSQYFFXLXXXXXRELXGXGPFTXFVPXXXXXXXXXQXXXXXXXXXXXXVXRYHVVXCXQ
LXXXXLXXXXXXTXLXGXXXXXSXXQFHLDWIXXXXYXNXXAXVXSXXXXXXNGVXHXID
XXLXPXXXLXXXXDAXXXXXXNVTLTTXAXXXGYXXFSXLXXVLPLRICSPSPGNEQXXG
LLXXXXXXXHXPXTXXWPTDXALQALPXXXXXXLXXXDXSSACNTEERSPXXXDKLXXXL
XXHVIRXXXGELFLNGXXCXIVQRELFFDLGVAYGIDCLLTDPSLGGRCDSFSTFNVPXL
AXDLPXXXXXXTXXGXXXSXXCGXGXDXGELXXXXXXXRIVQRXLXFXXGXAYGIDXLLX

XPXLGXRCDXFXXXXLXLVRETTGQVXXXCXXCXXXPXCPXXXXXXGXXXXCXXXXXKXW
TNXXXRXFMXGXXWXRPSXWGQPXXGXXXXGCXXXCXXXXXXPXCCXGXXXXXCQGHRXX
XXXXLXXPGXXXXXXXSXXRYVXEHVCLSACGTILPXEGAGVVPRHVWALSQXXXPPXXX
XNNYERMTRPXQXXXXXRXXXXXPACPGGPXXPVGPXXGPLCSXXGXCXXXXSXXGQCRC
XXGFXGTACELCXPGXEVXXXXXXXXXXXXXXXXXXXXXXXFGPXCQXCXCXXHGXCDXGX
XGSGXCXCXXGWTGXXCXXXXXXXAGALWAAXXPVCTPPCXXXAXCXXXNXCECXLXYEG
DGXXCTVXXXCXXXXGGXXVVQCXXXAXCSQXGTXVXCXCXXXYXGDGXSCXXXRLKWTK
VVXPCXXFXDXXVALGXQHRAFGSYRGRAELQXYXGPGXGGCXEHAXCXXTXXXXXCEC
XXXYXGDGLXCXXEAXXPXDRALMCLXXXXXCXXXAXCXXXXFWXXAAWGXCLXXXXLXX
XQXXXLNITCRXAGVFHXXXXXGXYXXXXXEAXXXCXXXXXXLXXXXQXXXAXQXXGFXX
CXXGXXXXGXVXXPXXHLFDXPXXXCXXXXGXGXXGPXXXXXXXGVXXXXXRXNXXXXXD
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XXXGHXETAXXXLCNSXXXXXXXXLXYXXXEAAAEXHXDVSSGXXXXRXXXGGYSIFXXX
LXXXXXXXXXXXTXXXXXXPXXXXXXXNXTLSXXXXXXHXXXXXXXXXXXXXXXXXLXX
XXXXXXXXXGXXXLXXXXXXXXTXXWFSWLFQPSXXXSHLXTTTKMAGNKLWLSYMFFDS
TDSNTXXXXWXPXXXXXEXXDXHLSFSXXXXXXXXDXXXSTISTTPRVSDHTKQXXXWXQ
WXXXHXXXXXLXXXXXXXXXXXXGXXXXXXAXXXXXGXXXSDVDRNXXXXGXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXDXEXXXHXXXXXWAAPSSTTXETAATQKEQWFEXXW
HGEYPQTPREDSDSTXGTTVTTVSAHXSHPSQRMTTQSQEDXXXXXXXXXXXXXXXPXXX
XXXXXXXXDVDTSHSXXVXPXXXPXXDLXXXXXRXRPXPSXPSXVLXXXXLXXXXXNVSS
VTTXXQSDSQLTKYQSXVPWSFSTSHGELEEDKXHPTTSTLTSGNRXPAXGGRRGXNLPE
DSTTSLEGYTPXYPXTKENXTLIPVTPANTGXXGETEVTVPVXEXNSDVDHXLPXDXXXX
XDXDPXXXSHTTSDSKSDGHXSGTXXGAXTXSXPXRRPQIPEWLIILALLGYSLLALALI
LAVCIAVNSRRRCGQKKKLVINNGNGRXVEDRKPSGXNGEASKSQEMVHLVXEXXXLXGX
SLAQQGQXXEXXXXGXXXRXXXGXXXXSDGVPVLYENKEPSETPDQFMTADETRNXXXPE
STXXXGXWXXXXXXXXLXVASESSEARSQNVDMKIGVXGIQQXPXXLXXXXVFXSXXPXY
XXDXXXXXRXLEXXXXXXLPLIRCXEXGXXEXPXIACVPRRPARXXXXXXGXXXXXXXWX
RXXXXXXPXXXXXXGPXXXXXLLP

==> Insecta.txt <==
>MSA Consensus of 398 seqs, protein
MERLLLLFFLLLAGRESLCQTGDTKLELLAPRGRSYATTYEQYAAFPRRRSSSSSPSGEM
QSRAVDTSADFEVLEGQPRGTTVGFIPTKPKFSYRFNEPPREFTLDPVTGEVKTNVVLDR
EGMRDHYDLVVLSSQPTYPIEVRIKVLDVNDNSPEFPEPSIAISFSESATSGTRLLLDAA
TDADVGENGVTDQYEIVAGNVDNKFRLVTTANPSGDTSYLHLETTGNLDRESRGSYQLNI
SARDGGSPPRFGYLQVNVTILDVNDNPPIFDHSDYNVSLNETALPGTPVVTVMXTWPXXX
DNSKITYYLXXXXXQXTVXXETXXXSTTXXXNCPQQTNVKSSASXXSXXXXXXXXDSXSP
XXXQXXXXHXXXXXXXMXXXXXXXIVXXXXXXXIXXXXKVATVDENAVNGTXXXXXXXXX
XXXXXXXXXELXWTXXXXXXXXXXLXFIADXXXXXXXXXXXXXXXXXYNLTVVAMDQGTP
ARTTTAHLIIDVNDVNDHEPVFXXXXYXXVXXXXXXXLXXXXXMXXIXXPMXTTXXXGXX
WXWXILSXXXXXXXXXXXXXXYMINXXXXXXXXXXDVDXRXXXXSXXXXXTXIXKXXXTXX
XXXXSWXXXXXGXXXXXXPXXLXXXXXXXXXXXXXXXXXLXXGXXXXXEQNVTXXXNXSXX
XXXXXXXXXXHDQGTXGXXXXXXXXXXXTYYVXAFALDALTGQLTTRRPLDREKMSQYEI
SVIARDQGAPTPQSATATVWLNVADVNDNDPQFYPRHFHXXLXSMXXXXXXXXKXXXEXX
RILLHVTASDKDDGDNALIEYRLESGGAXXFQLDARSGAXXXXXXXXXXXXWXXXXXXXX
XNXXXLKXQXXXXXXXXXXXXXPQHXLXLXXXXXXXXXXXAGMPRXYXXXDHEQXXXXXP
XXXXXXCXXXXXXDXXXXXXXYPDXXXXXXXXXXXXXXXXXXXXXGXXXXARPLDXXXXX
XXRXXXXXXXSXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGCRXX
ECXXNXXCXXXXXXXXXXCXXXISCXXXCXXGXXCYLSXXXXXYXXXXXCXXXXYSLTNN
PNXXXXXXXXXXXXXXXXXXXXXPXXXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXCXXXPXXXCXPMHLPPSXXXSPCGXNXXCXXXXXXXXCXCXXXXXX
XXXXXCRXXXXXXXXCXXXXXCXYXXXLXXTVEPTPGLXXXXXXXXCXXXXXCXXXXXCS
XXIIEGNTEXXXXXXXXGXLXXXXXXXXXCXCXXXXXXLTCXGXXCXXXCPXXXXXXXXX

XXXXXXXXXXXXXXXXXXXXXXTYXXXXXXXXLGLLXXXXXXXXXXXXXXGXXXXXXXX
XXXXXXXXXTXXXXXXXPXXXXXXFPXXXXXXXXXXGRNAXXXXXXSSGXXSXXXXXX
XXXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXDXXXXXXAXXXXTXXXXETT
QXXTETSXXXXXPXXXEPXEEXXVXXEXXXTXXXXXXXXXXXXTEXXXXXXXXXXXXXX
XXXXXXCXXXXXXXXXXXXXXXXXXXXSXXXAXXXXXXXXVXXXXXXEKXTXAXEXPS
XXXXXXXXXXXEXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXKQQXXXXXXXXXXXXXXXXXXXXXXXXGXEPXEXXXEXXETV
XXXXXXXXTXKPXXXXPXXXXXXXXXXXXXXXPEXXXXXXXLXXXXXXXXXXXXXGXXXX
XXXXXXXXXXXXAGCXXXXXXXXXXXXXXXXXXXXDXXDIXKXXXXXXXXXXXXXXXXXX
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XXXPXXXXXXXXXXXXXXXXXXXXXXXXNXAXXXXXXXXXXPXXXXXXGXXXXEAPXX
KXXXXXXPXXXXXXIXXXXGXXXXXXXXXXXXXXXXXXXXXXXXXXXXTTSTTTXSAXXX
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XXXXXXXXXXXXXXXXXXXXXXXTXXPXXGXXXXINXXXXXXXXXXPPXVXPXPXXXXXX
XXXXXXXXXXXXXTXXXXXXXSXNGXXXXXXXXXXXXXXXXXXXXXXXXXXXPXXXXXX
XXXXXXXXLXXXXXXXXXXXXXXXXXXXXXXXXXXXNEXXXLXXSAGXGXXXXXXXXXX
AXEXXKRAAXXXXITGRGKFXXXXXXXXXXXXXXXXCXXXXXXXXXXXXXXXXXXXXXX
GXXXXXXXXXXXXXXXXXXXPXXXXXXXXXAXXXXEXXXXXXXYXYXXXPXXXXXXXXX
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XXXXXXXXXXXXXXXXXXXXPXXXXXXXXEXXXXXEXXXXXXXXXXXXXXXXXXXX
XXYXPDXXXXXXXXXPXXXXXXKXXLXXXRXXXXXXXXXXXXXXXXXXXXXXXXXX
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XXTPXXNXLXXXXXXXXXXXPXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXSX
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XGDSDLXXXXXXXXXXXXXXXXXXXXXXXXYXXXXXXXXXYXXXXXXEAXPXXXXXXXXX
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XNDXDPXXXXXXXXRXXXXXPXXXXXXXXXXXXXTXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXGXXEVKXXXXXXXXXXXXXXXLXXXXXXXXXXXXKRYSLYXX
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AKXXXXXXXXXXXXXPXXYXXXSXXXXXNXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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AXXXCGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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XXXXXXXXXXXXXXXXXXXXXXXXSSXXXXXEXXXXXXXXXXPXPXXXXXXXXXXYNPXKX
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KXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXKXXXTPXXXXYXXXXXXXXXX
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PXXXXXXXXXXXXXVXXXXXXXXXXGXLXPXXXXXXYXXXXXXXXXXXXXXXXXXPXXXX
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RYEDXXXXXXXXXXSXXXXXXGRPGNHGXNGXPXXXXXXTXXXTXXXXXXXXXXXKXXXX
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IAVSLFNXXXPXNVKLXPXXPXXXXXXXXXXXPSQPXEEXXXXXXXXXXXXXXXEAQPXV
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XXXXXXXXXXCXXXXXXXXXXXXXXXXXXXXFXXXXXXXXICLPHHKXXXIXXLDHINQX
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CTPXXXXXXCXRFSYGFQPXXYXXXXXLXXTTXXXXXVFXTXXXXXLLLYNYGMQSGGRS
DFLAIELXXXXXXXXXGXXXXAXXXXXXGXXXADGGWHKVTATXXGXXXXXXXGXXXDXG
DVCTECXXXXXXCXXXXXXPXGXXNXXXXPXXXXSELFVLEPRPXPXXCXPEPXXXXXXX
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GXXXFVEFXXXXXXXXXXXXXXXXXXXXNXXXXXXXXXMRERRAVSXXXTXXXXXXXXXX
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VSLXXXXXXXXXIVDXXXXXXXXXXXGXRXXXXXXXXXLXXLXXXXEXXXXCXXXXXVN
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TGTHESAXXXXXXXXYXXXXXXXXXXXXXXXXHRXXXPXXXHCAAXXXGXXXXPXPXXAS

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SSSEAPRVSSSALHMSLGGDVDAHSSTSTDESGNDSFTCSEIEYDNNSLSGDGKYSTSKS
LLDGRSPVSRALSGGEXXRNXXXXXXKTPPIPPHAYDGFESSFRGSLSTLVASDDDIANH
LSGIYRKANGAASPSATTLGWEXXXXXGPSYENLMGVFKDIAELPDTNGPSQQQQQQTQV
VSTLRMPSSNGPAAPEEYV

==> Kineosporiaceae.txt <==
>MSA Consensus of 132 seqs, protein
MLMXXXXXXXXXXXXXXXXVXXXXXRTXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXAS
XXQTPATSLVGDAXPXXAXXXXXXXXXXLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXGXXXXXXXXXXXXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXGXGXXXXXXXXXXPX
XXXXXXAXXXXXXXXXXXXDXXXXXXXXAXXXXXXXXXXXXXXGXXXXXXGXXXGXXXXXXX
XXXXGXAXXSXXGXSXLXXXXXXXXXXPXXXAVXXFAFEXXGXXYXADXXXXXXXXXXXXX
XXLXXXAGXGXXXXXXXGXXXPXAXXXXXXGXXXXXXXXXXXXXGGXPXXXXXXXXXXXXX
XXVQXXPAXXXXXXXXXXXLXXPXXXAXXXDXXGXXXXXXXXXXXXXXXXXXXXXGXXXXXA
GXGXXXGXXXXXXCXGHGTXVAGXXXQVDGXXXXXGGTGQXXAXXXXXXXPXXXXXXVXX
AAXXXXXXXDXXXXSXXVXXXXXSXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPXXXXX
XXXGXXXXXXXXXXXXLXAGXXXDPVTGTLSGTPTIAQSAXXXXVXXXXXXXXGXAXXXX
XXSXXXXXXXXXXXXXXXXXXAXWXXXXXXXXXXXGXXXXLXXXXXXXPXXXXXXXGXXX
XXXXXXXXXXXXGXXXXXXXAXXXXXXXXXXXXXXXXXXXXXXXPXXXSXXPXXVTXVTAA
SPGGTXAXXVGXXXXXXXXXXAXXGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XEGTADXXXXXXXXXXXXXXXXXXXXAXXXXGXXXXXXXXXXXXXXXXXXGXXXXXXXXXR
XDXTXXXXYYAXGXXXXXXXXXXXXXXXXXXXXXXXXXXHGEXXXTXXXXPXXXXDPXXLX
XVXXXXXXXXXXAAXXXXXXXXXXXXXAXXXXXXXXXXXXXXXXXXXXXXAXXXXXXXXXX
XXXXXPATXAVTIXVXPXXXPXXXLXXXXPXXXXXXGXXXXXXXXXXXXXXXXXXXXSXSX
SPSXSXXXXXXXPXXXXAXXXXXXXXXXXXXXXXXXXXXRXXXXXXSXXXXXXXXXXXXXX
XXXXXXXXXXXXVXXXXDXXXXXXXXARQPARXSXDXEAVAASRXXXXXXXXXXXXXPXX
XTXXTVXPXXXXXSXGXXXXLPXXXXXXXXPXXLXLXXXXXAXXAXXVXXGXGSXXXXXX
XXGXXXXXXXXXXXXXXXXXVXPAXPXXXXXXXGXXXXXXAGTXXVXVTAXXXXXXXAAXX
XLXXXXXXXXXXXXXXXXXXXRXXGXDRXXTVLAPVSGSFFNAXXXXXXXXXXXXXXXXX
XXXXXXXXXXXDXXXXXXDXLXAXXLAXXXXXVXXXPXLLXXXXXXXXXXXXXXXXXXLX
XXXAXXASXTXXXXXAAAXXXXXXXXXXXXXVXXXGGXXXXXXXXXXXXDGELXXXXXXX
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XDALXXXXXAXVVDXXXXXXXXXXLLXTXXXXXPXXTXXXLXXGGTTGXXXXXVNXXXLX
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DQQVAEQSNTTAQXXXXXDAXXXXXXXXXXXXXGGXXXXXXXXXXXXXXXXXXXXGXX
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XXXXNXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGARVVNARTVXXXXXXXXXXXGXXX
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VXXXXXTXXGXXTXXXXXTXXXRFASXXXXXXGXXGXXXXXGXXXXXXETXXTXXXXXXA
GPXXXXEXXGXGXXXXXXXXXXAXXXXXXXNGXXXXXXTXXXXXGXXIXSVDXXXXXXXXX
XXXXXXLXXXXXXXXXTTXXXXXXXXXXXXXXXXXXXXXXXXXXVXXXXFXXXXXXGDXXX
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GATXXXXXXXXXXDXXXXXGXXXXXXXXXXXXXXGXPXXXXXXXXXXXXGDXXXXXXGG
VXXFXLXXXXXXXXXXXXXXXTMSSXXXXXDXXXXXXXXXXXXXXXXXXXXXXXXXXXX
RXXXXGXXXXXXXXXXXXXXXXXXXXXXXXXTXXXXXXXXXXXXXXXXXXXDXXXAXG
XXXXXXXXXXXXXXXXXGXXXXXXXXXXXXXXXXXXXDXXXPXXXXXXXXXXXXXXXXXX

XXXXXXXXXXXXXXXXXXXPMEDYAGXXXFXXXXXXTLETRLAXVXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXGXXXXXLXXXXXXXXXXXXXXXXXXXGXXXXVXTXXVXXXXXXXXXX
XXATXXXXXXXXXPXTXXXXXXXXDXXXXXXXXXXXXXXXXXXXSAXXXXXXATANAAGT
AXXXTXXTXXXXSGNSVAXXXXXXXXXVXXVXXXXXTXAAXXXDTXGXVEAAIDAATSXXX
XXXXSANAATAVAVAGPTXXTXXTNQSNADTVIAP

==> Kineosporiales.txt <==
>MSA Consensus of 132 seqs, protein
MLMXXXXXXXXXXXXXXXXVXXXXXRTXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXAS
XXQTPATSLVGDAXPXXAXXXXXXXXXLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXGXXXXXXXXXXXXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXGXGXXXXXXXXXXPX
XXXXXXAXXXXXXXXXXXXDXXXXXXXXAXXXXXXXXXXXXXXGXXXXXXGXXXGXXXXXXX
XXXXGXAXXSXXGXSXLXXXXXXXXXXPXXXAVXXFAFEXXGXXYXADXXXXXXXXXXXXX
XXLXXXAGXGXXXXXXXGXXXPXAXXXXXXGXXXXXXXXXXXXXGGXPXXXXXXXXXXXXX
XXVQXXPAXXXXXXXXXXXLXXPXXXAXXXDXXGXXXXXXXXXXXXXXXXXXXXXXGXXXXXA
GXGXXXGXXXXXXCXGHGTXVAGXXXQVDGXXXXXGGTGQXXAXXXXXXXPXXXXXXVXX
AAXXXXXXXDXXXXSXXVXXXXXSXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPXXXXX
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XXSXXXXXXXXXXXXXXXXXXAXWXXXXXXXXXXXGXXXXLXXXXXXXPXXXXXXXGXXX
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SPGGTXAXXVGXXXXXXXXXXAXXGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XEGTADXXXXXXXXXXXXXXXXXXXAXXXXGXXXXXXXXXXXXXXXXXXGXXXXXXXXXR
XDXTXXXXYYAXGXXXXXXXXXXXXXXXXXXXXXXXXXXHGEXXXTXXXXPXXXXDPXXLX
XVXXXXXXXXXXAAXXXXXXXXXXXXXXAXXXXXXXXXXXXXXXXXXXXXXAXXXXXXXXXX
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SPSXSXXXXXXXPXXXXAXXXXXXXXXXXXXXXXXXXXRXXXXXXSXXXXXXXXXXXXXXX
XXXXXXXXXXXXVXXXXDXXXXXXXXARQPARXSXDXEAVAASRXXXXXXXXXXXXXPXX
XTXXTVXPXXXXXSXGXXXXLPXXXXXXXXPXXLXLXXXXXAXXAXXVXXGXGSXXXXXX
XXGXXXXXXXXXXXXXXXXVXPAXPXXXXXXXGXXXXXXAGTXXVXVTAXXXXXXXAAXX
XLXXXXXXXXXXXXXXXXXXXXRXXGXDRXXTVLAPVSGSFFNAXXXXXXXXXXXXXXXXX
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XXXAXXASXTXXXXXAAAXXXXXXXXXXXXXXVXXXGGXXXXXXXXXXXXDGELXXXXXXX
XXXXXRXXGXDRYXTAXXXAXXXXXXXXXXXXGXXXXXXXXXXXXXXXAXGXXXXXGXXX
XDALXXXXXAXVVDXXXXXXXXXXLLXTXXXXXPXXTXXXLXXGGTTGXXXXXVNXXXLX
XXDXXXXXXXXXGGXXXXXXXXXXXXXXXXXXXXYQQXXXXXXXXXXGXDRXXTAXXXAX
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DQQVAEQSNTTAQXXXXXDAXXXXXXXXXXXXXXGGXXXXXXXXXXXXXXXXXXXXXGXX
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XXXXNXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGARVVNARTVXXXXXXXXXXXGXXX
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VXXXXXTXXGXXTXXXXXTXXXRFASXXXXXXGXXGXXXXXGXXXXXXETXXTXXXXXXA
GPXXXXEXXGXGXXXXXXXXXAXXXXXXXNGXXXXXXTXXXXXGXXIXSVDXXXXXXXXX
XXXXXXLXXXXXXXXXXTTXXXXXXXXXXXXXXXXXXXXXXXXXXVXXXXFXXXXXXGDXXX
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GATXXXXXXXXXXDXXXXXGXXXXXXXXXXXXXXGXPXXXXXXXXXXXXGDXXXXXXXGG
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RXXXXGXXXXXXXXXXXXXXXXXXXXXXXXTXXXXXXXXXXXXXXXXXXXDXXXAXG
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XXXXXXXXXXXXXXGXXXXXLXXXXXXXXXXXXXXXXXXGXXXXVXTXXVXXXXXXXXXX
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AXXXTXXTXXXXSGNSVAXXXXXXXXXVXXVXXXXXTXAAXXXDTXGXVEAAIDAATSXXX
XXXXSANAATAVAVAGPTXXTXXTNQSNADTVIAP

==> Lacticaseibacillus.txt <==
>MSA Consensus of 3193 seqs, protein
MXXXXXXXFXGXXXXXXXXXXXXXTSDWTQAQHEEQXXXXXXFXXXXXXXXXXXXXXXXX
XSXXXXTVXXXXXXXXXXXXXXXXXXMXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPXXXX
XXXXXXXXXXAXXXXXXXXXXXXXXXGXXXXXXXAXKIEXXXXXXXXXPXXXHXXXXXXPAXX
XXEPQXXXXXXXXXXXXXXXXXXDXXXXXXXXXXXXXXXXXXPXXXXXXXXXXPXXXXXXX
XXXXKAXXXXXXXXXVXXXXXXXXXXXXXXXXXXXXXXXXXXFXXXXXXXXXXXXXXAXXX
XXXXXAXXXXXKXXXWXXXXHLHXXXXXXXXXXXXXXXXXLSQAXXXXXXPXXXXXXXXX
XXXXXXXXXIXXXXXXXXXXXTXXXXNXXXXXXXXXXXGXXXXXXANLXXXKKDSVXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXQXXXXXXXXXXXXXXXXXXXXXXXXXXXXAXXR
KMXXXXXXXXXXXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXAXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXYXXXXXXL
XXXXXAXVXAXXXXXXXXXXIXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXKX
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XXXXXXXXXXXXXXXXXXXMSSXXXXXXXXXXXXXXXXXXXXXXXXAXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXQNXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXTXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXKXXXXTXXXXXXXXXXXXXXXXXXXXEXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
IINXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXVXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXTXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXMXXX
XXXXXXXXXXXXXXTXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXNAXXXXXXXXXXXXXXXXXXXXXXXXXXXEXXXXXXXXXTXT
XXXXAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXTXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXIXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXFXXXXXXXXXXXXXXXX
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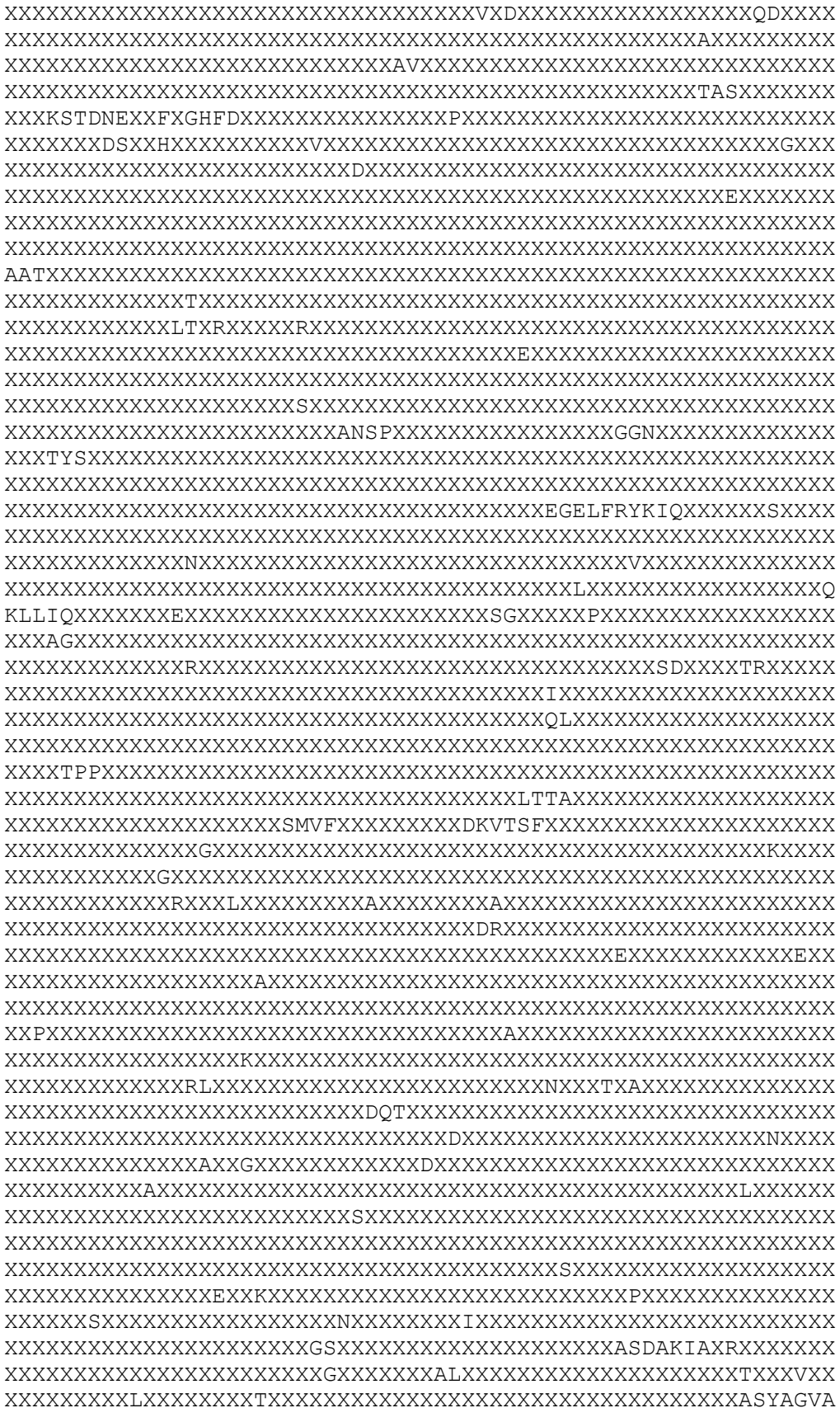

SXXXXXAXXXXXXXXXXXXXXXXXXXXXXXXAXLXXXGAXXXXXXXXXXXXXXXXXXXX
XXXXNAAAXXXXXXXXXXXXXXXXXXXXXXXXXXXTAXXXXXXXXXXXMQSNVASAQAVAX
NXXNXXSXXXXXXXXXXXXXQAXXXSDAATSXAXXXXXDXXXXXSXDXXXXXXXXXXLXX
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XFGXXXTXXXXXXXXXXXXESSNHATXXXXXXDXXXXAXXXPXXXXIXXXAXKXXXXXXX
AXXXXXXXXXXXSDXKSXXDXXDXXXAXXKNXXXKXXDXEXTXXXAASEAASADADXXXK
DXXXXXXXAAESAKKXSDASXXTXGIASNYPSDSGIASDAAKASNAASDXXXQXGLXXXX
XKXAXXAXAKGXXXXXTSAXKQXXXXEKTXAXXXXXXKXAXXALXXXXXXXSXHXXXXXX
IXASDAAKAASDAAESAKKASDASSEXTGXXXXXXXXXGXXSXXXXXXNAASDAKSQAGL
ASDAAKAASDAAAKSDASGAASAGKQASDAASKAASDAKVASDALSDAKAKASDHASSDA
KASASDAAKAASDAAESAKKASDASSDTTGIASNYPSDSGIASDAAKASDAASDAKSQAG
LASDAEKAASDAAAKSDASGAASAGKQASDAASKAASDAKVASDALSDAKAKASDHASSD
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GLASDAAKAASDAAAKSDASGAASAGKQASDAAAKAASDAKVASDALSDAKAKASDIASG
KAASDAKVSASDAAKAASDAAESAKKASDASSETTGIASNYPSDAGIASDAAKASNAASD
AKSQAGLASDAAKAASDAAAKSDASGAASAGKQASDAAAKAASDAKVAKAKASDHASSNA
NISASDAAKAASDAAESAKKASDASSETTGIASNYPSDAGIASDAAKASNAASDAKSQAG
LASDAAKAASDAAAKSDASGAASAGKQASDAAAKAASDAKVALSDAKAKASDIASGKAAS
DAKVSASDAAKAASDAAESAKKASDASVKLLDCIELPE

==> Lactobacillaceae.txt <==
>MSA Consensus of 3228 seqs, protein
MMXXXLKLGQAQYYKRYYTPQVDEXXXXVAALXXXXXFXGXXXXXXHXXXXXXXXXEXXT
XXXXVXAAQALHFXXXXXXXXXTXXXXXXXXYXXXVXVXXRGEXXXXXXXXCEXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXDAXXXXXXXIAPEPQYQXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXQAAA
SXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXAXXXXXX
XKAXXXXXXXXXXXXXXXXXXXXXPXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXANXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXDXXXXXX
XXXXXXXMXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXGXXXXXXXXXXXXXXXXRPTVXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXAXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXMXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXEXXXPXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXKMXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXDXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXAXX
AAKXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXMXXXXXMXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXRXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXIXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXDHXXXXXXXXXXXDXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
VSXXXXXXXXXXXXXXTXXXXXXXXXXXXXEXXXXXXXXAXXXXXXXXXXXXXXXRXXXX
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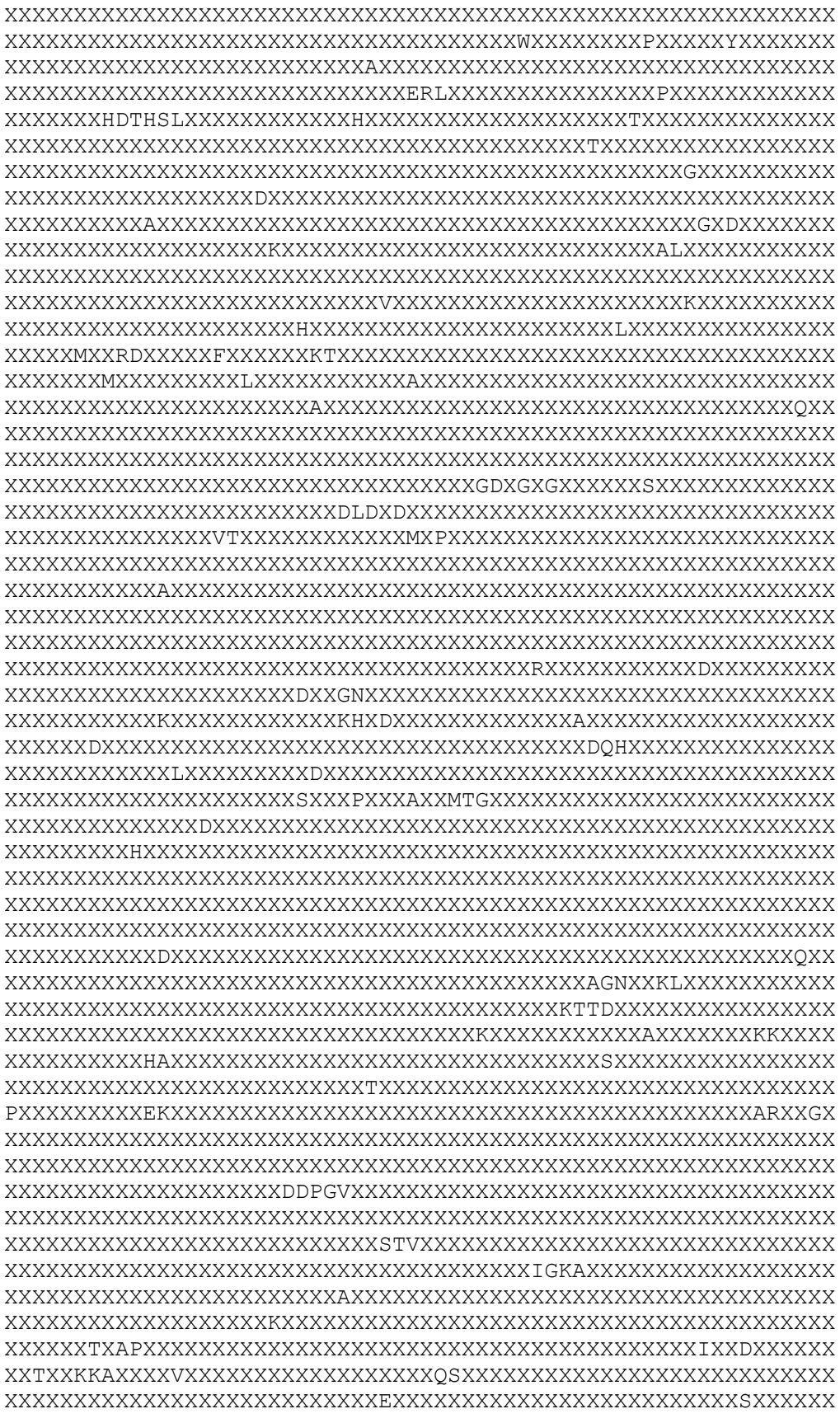

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XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXEXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXASGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXADXKXXAXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGQXXXXXTXXXXXXXXXXX
XXXXXXXXXXXIXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXAXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXLDXXXXXX
XXXXXXXXXXAGNXXXXXXXXXXXXXASPTADXAXEATXESVNVEXXXXHPXXLVYXXX
XXXXKSQXXXXXXXXXVXXXXXSXXXXXXXXXXXXTXXXTXXXXXXSXXXXXXXXXX
XXXXAXDXXKXXSXXXXXXXXXDXXXXXXXXXXSXXXXXXXXXXXXXXXATXXXSDAAV
XXXXSSXXXXXASEXPXXPXXXXXXXAASAANAASAAAXTXXXXDXXXXXXXQXXSDX
XXXTXXXXXXPXXXXKXXXXXVXXAQGVASAASXXXXXXXXXXXXXXXXSXXXIVXXXX
AXXXXXXXXXXXXXXXXXEXXXXXXXXXXLKAXXXXXKXXXXXXXXXXXXXXXGXXXX
GQGAKLAAASDAAQAATAASDAAAAAKQASXAAXXXXXXXXLXXXXXXXXXXXXXXXXX
XXXXXXXAXIXXXXSXXXXXXAXXXXXXXXXXXXXXXXXXXXXGSSAASGAQSYAXXXGK
YASAAASDAKIASDAAGVTSGFAAKHPEDLVYADLDSTAQSQSAIAGSAAATAASAASAA
SAAASTANAAAKSGDVPTAQAAASAAASYAGVASDEADKAKAAAKIASDAAASAAARDQA
GSSASDSAAISGSALTTHGYASAAASDAANAAATAAAADSAAQSAAAKFNSDFASAQAKG
QQLPAAYVKAMQSNVASAQAVASNAANVASSDAEVAKKALAAAQAAINSDAATSSASAAT
IDANHAAADAAKAASDAKLAAGYASNAASDHSKYPSDPVLTGLDSQAQGAKSAAASDAAS
ASAAAGIADSAAKQASAAAGSGDNSGAASYSAIASSAAKDASDAASDAHRQAGIASDAAA
SAAARAKELDGFGSSATSHASGASDAASAAQSSASDAASTAKDNPSDSAIASDAAKASDA
ASTAKSAASEASDAASDAKSAADKGDTSAASDATKKASDAESTAKSAASEAASADADAKA
KDAAHHASDAAESAKKASDASSETTGIASNYPSDSGIASDAAKASNAASDAKSQAGLASD
AAKAASDAAAKGDVSGATSADKQASDAAASAASDAKVASDALSDAKAKASDHASSNANIS
ASDAAKAASDAAESAKKASDASSETTGIASNYPSDAGIASDAAKASNAASDAKSQAGLAS
DAAKAASDAAAKSDASGAASAGKQASDAASKAASDAKVASDALSDAKAKASDHASSDAKA
SASDAAKAASDAAESAKKASDASSDTTGIASNYPSDSGIASDAAKASDAASDAKSQAGLA
SDAEKAASDAAAKSDASGAASAGKQASDAASKAASDAKVASDALSDAKAKASDHASSDAK
ASASDAAKAASDAAESAKKASDASSDTTGIASNYPSDAGIASDAAKASDAASDAKSQAGL
ASDAAKAASDAAAKSDASGAASAGKQASDAAAKAASDAKVASDALSDAKAKASDIASGKA
ASDAKVSASDAAKAASDAAESAKKASDASSETTGIASNYPSDAGIASDAAKASNAASDAK
SQAGLASDAAKAASDAAAKSDASGAASAGKQASDAAAKAASDAKVAKAKASDHASSNANI
SASDAAKAASDAAESAKKASDASSETTGIASNYPSDAGIASDAAKASNAASDAKSQAGLA
SDAAKAASDAAAKSDASGAASAGKQASDAAAKAASDAKVALSDAKAKASDIASGKAASDA
KVSASDAAKAASDAAESAKKASDASVKLLDCIELPE

==> Lactobacillales.txt <==
>MSA Consensus of 3375 seqs, protein
MNIXXXXXXXXXXXXMXXXXXXXXXXXXXXXXXAXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGXXXXX
XVXXXXDXXXXXXXXXXXCXXXXXLXTLQXXXXXXXXXXXXADXXXXXXXXXXXXXXTNX
XXEPQXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXTXXXXXXXXXXXXX
XXXXXXXXIXXXXDXXXXXXXXXXXXSLXXXXXXXXXXXXXXXXQXXXXXXXXXXXXXXXA
QXXXXAXXXAXXXXXXXXXXXXXXXVGXXXXXQXXXXXXXXXXXXXXXXXXXXXXXXXXX
VXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXAIXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXSMXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXQEXXKXXXXXXXXXXXXXXXXXXXXXXXXXXX
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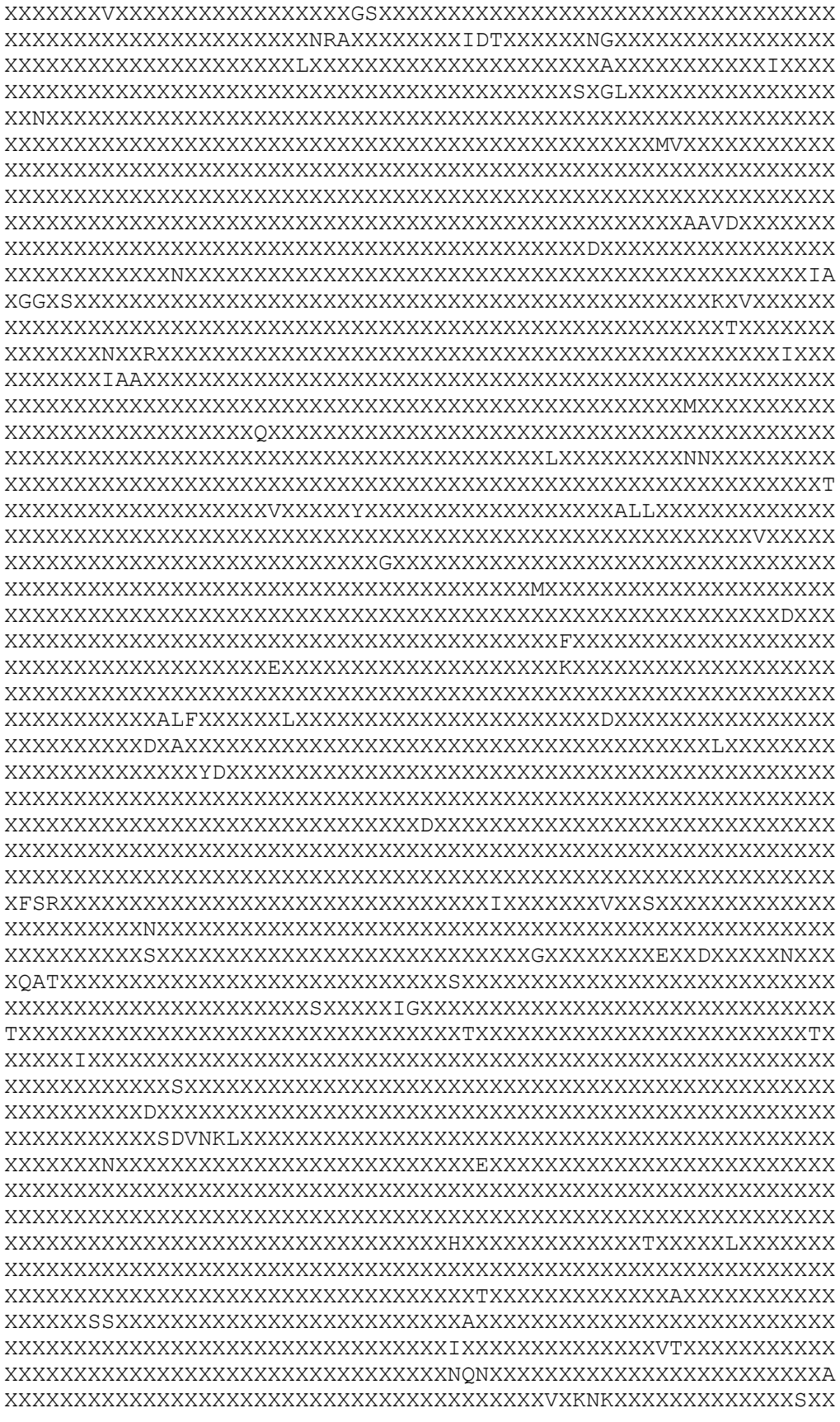

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XXXXXXXXXXXXXXXXXXXXXXXXVXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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XXXXXXXEXXXXXXXXXXXXXXXXXXXQXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XLXXXXXXXXXXXXXXXVXXXXXXXXXXXXXXXXXXXXXXXXXXXLNXXXXXXXXXXX
XXXXXXXXXXXXXXXSVTXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXAKRAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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TLXXXXXLPLGXXXXXXXXXXXLXYXXXXXXVTXXXXXXXXXXXXXXXXXXXXXXXXX
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KSXXXXXXXXXXXXXSNIFNSXXXXXXXXXXXXXXXXXXXSXXXXXXXXXXXXXXXXXX
QKXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXKXXXXXXVXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXLXXXXXXXXXXXXXXXXXXXXXX
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XXXXXXXXXXFXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXAXXX
XXXXXXXXXXHXXXXXXXXXXXXXXXXXAAADAAKAASDXXXXXXXXXXXXXXXXXP
XXXXIXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXAXXX
XXXXXXXXXXXXXXXXXXGXXXXXXXXXXXXXXXXVXXXXXXXXXXXXXXXXXXXXX
AASAXXXXXXXXXXXXXXXKXXXXXXXXXXXXXXXXXTDXXGXXXXXXXXXXXXXXXX
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TDXXXXXXXXXXXXXEGKVXGXXXXXXXXXXXXXXXXXXAXXTAAXXXXXXXXXXXXX
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XXXXXXGXXXXXXXXXXXTXSPVTDPAIXXXXXXNSDXXXXXXXXATIDANHAAADAAKA
AXXXKXXXXXXXXXXXXXXXXXXXPXLXXXXXXXXGXXXXXXSXAXXXSAAXXXXDXXA
KQASAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXSKTTVTXXXXXXXXXXXXXXXXAXXX
XXXXXFGXXXTXXXXXXXXXXXXXSSNHATNXXXXXXXXXXXXXXPXXXXXXXXXXXXD
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XXDXXHHASDAAESAKKASDXXXXXXPXXXXXXXXXXXXXXDXXXXSXXXXKXXXXXXXXX
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XXXXXXXXXXXXXXXXXXXXEXXGXXXXXXXXXXGXXXLXXXXXXXXXXXXXXXKXXXXAA
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==> Laurasiatheria.txt <==
>MSA Consensus of 1072 seqs, protein
AADTQEEILAGSCGAHSPRRLPXXXXXXXAXXXXPXMAGPRXXLLLCLLAXCXXXXXSXX
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SAVQATGAQTAWTNIWXXXXXXSXXGCKXXXCXKDXVQXXLKYSNETIKRLKSAREERGR
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GVRCXXGXXGDGSCXCXXGYTGPXCDXXXPXCXALXCPXNSXCSXXSXDETXXXCXCLPX
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PXXXXXXRLXXXXXXLDXXXXXXLXXXGPFTVLXPXXXXXXXFXMNVRPGSSXMLVPPLS
SVKEXXMNXXXAQXXXXXHIIAGQXXXEXXXXQQXTXXWFXTLXGXXXXXXXXXXXXXXX
XKXKXXXXXXXXIXXXNXXAXNGXXHXXXXXXXXXXPXXXXXXXASQCPNACSFLQXTIX
XXLAXXXXXSXFXXXLEXXXXXXXLDXDGXXGPXTVFXPSNEAXXXXXDGXLXYLXXXXG
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ERNAWLWQHGDSSSLGIXXVXXXXXXXXFXQWIXXAXXQXXLXAXSXXTXLVPSXXAIXX
XXXXXXAFWLXXXXXPXLXXXHXLXGXXXXXXLXXLXXXXXXXXSLPXXXXXXXXXXGXX
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XXXXXXXXLLXXLDXXPXXXXFRXXLXASIMFSAWPSAQVTWERESLTQXXXXXXXXXXL
XXXIEAAXAYTXFXPXNXXXEXXXXXXXXVRSLGPGPPGAGQPAIPRPLSFSSXTLXXDX
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XXQXXVNXXPXXXXXXXXXXXXXXGLXXVLXXXXXRCXXRXXXXXLRXKCXXCXXXXXCX
XGXXXXVRLDWRIPFPCHLLSLPPALLAQXXXXKXCXYXXYFMGXXSXXXGCXXXCXKXI
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GSCXCXVGWXGXRCDXXITXXXCXXXCXXXANCXXXXXAXXXXCXCAAGXXGXGXXCXXV
DGXXINXCXXXXGGCSXXAXCXXXXPGXRXCLXCXXGYTGDGXXCXEXNLSXXCLXXHGG
CHXHAECXQXXXXPQXXTGPXQGAGPLLGSSSPTDQDLGQXXCXCXXXYXGDGXXXXXXX
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EARGPFPRAGRGVLGXXXXXXXXCLTXNGGCSNLFXXAXCVQYVXXXTGXXXRTCTCXXX
XXXXXXFTCRXXXXLELLEHXXSXRDXHXTXXXXXXXXXXXXCXXXXXXXXXXXXXXQEL
PXNPXXSQXFFXLXXXSXXXXXXXHXGXXXXXGXXLXXXCEXXXLXGXGPFTXFXPXXXX
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PNATXSGQRMRGTWVWPQIPLTTTLQGESIVXXXXISVSXDXXXXXXGXXYXNXXAXXXS
SDXXXXNGXXHXIDXXLXPXXXLXXXXDXXXXXXXNXTXXAXXXGYXXFSXLXXDLLLCX
XXLXXXLXDXXHXPXTXXWPXDSAXALXXXALPPXXQXXLXXXDXXDKLXXILRGXXXXK
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TWKPXCCXGXXXPGXXCXALSECPGGXXXPCXXXALPALLENGKTNGGXCXDXXXXLXXX
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XXXXXXXXXXXXXXXXXXVCRNXARXXAAXCXXGXXGSGXCXCXXGXXGPXCEVQLEXXA
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XNXCECXLXXXXYEGXGXXXDGXXCTVXDXCXXXXXXXGGCXXXAXXCSXXVRWEAPLPS
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XVVIPXXPXXXPXXXXXXXXXXXPXXXXXXCIYXXXXXGXXGXXXXAXXXGVVXGXLGXA
SXGVRXYGYILXXXTSXXSXYDGXXXYXAXXXXXXXXXXCFNXSAPXXXEXXSCXXXTXL
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XXXXXXXXHXTGXXXXXXXFXLXCNSXXXWLADGXXXXYYXXXXXXDXSSGSXSERSTSG
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XXXXXXXXXXXNXGXXXXXTXXXXXXEXXXXXXXXXXXXXXXXKXXXXXPFXXXXXQKE
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GXXXXVDGXXXXXWDIXAXNGIIHXHVXXXPLXXXXXXXXXXXAPXQXXXXXXXXLXXXV
XXXVAAXPVGEEXXXXXXFXXXXXXXXXXXXAYXXXGXXXXXGTDSNIISAGWXPTEENE
DEXDXHPSYSGSGIGXXXDDDEDXXXXTISTXPXXFEXXHXXXTTLTPXQNXDWXXXXPG
XSNPXXXXAGLGXXXXXXXXXXXXXXXXAXYXXXRXXXXXXXXXSXXGEXWTXEXHSXLX
HHXXHDEEETQHXTSTTXALAXXXSTXEETATQKEQWXENGWXGEYPQPLIHHEXPKEDS
HSTAGTXVTXXXXXXXXXXXXTTQSXXXSXWXXXXXPXSHPMXRXAAGRXHQTXXXXPN
PXXXXSXXTXTXQPSADPXXXXXXXXDXTGPLSXTTXQQSXTQSFSXSXXXLEEDKDHPX
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GXXXXQXXWXXPXXXXAFXLXXXRCGQKKXXXLVINNGNGXXEXXXXGVXXXXXRKXXX
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XXGXXXGXXXXXXXXXXXXPFXDSXXXXXXXXXXPSXXXXHLETSAXXXXXXXXLXXGXE
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KXXXMXXXXXXDNXXXXXXXXXXXXEXXGXXXXXXXXXXPXXXXTXXXGXXXXXXXXXGXX
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XPDLSGXXXXXXXXSGXXSGXPXXXVSXXXGXXXXXVXXXXGXXETXXLXGLXXXXXYXV
SXXXXXXXXXXXXXXXXGTXXXTIXXXXXXXXVEVTPTXFXXXXXXXXXXXXSXXXXXXP
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LMDDSALXXYSMKDDLXNXKXLGTDLMNEMXXXXVDVSGXXSGXXXXXGXXXGXXXXPXX
FSGLPSXXAEXSGXXXXXXXXXXXXXXXXXXXXXXXXXGXPXXSXXXXXXXXXXXXXPXXXX
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LXYXXGXXPXXXXXXXXXXXAXXXXXXXXXXXXTXXXDKGXXXXXXXXCXXXXXXXXXXXX
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XXXXSXXXXXXXXXXXXXLXXXXXXXXXSXXXXXXPXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXGXXSXSXDLXGXXXXXXXXGXXHLXXXXXTXXXXXXXXXXXX
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DXXXXXHIXXXXXXASTXQXXXXXXXXXXXXXXSXXXXXXXCXXXXGXXXXXXXXXXXXX
XXEXAXXXXXXXXXXXIXXLXXXXXXXXXXXXXXXXCXXQXXXIPXXXXXXXGXAXXXXXXX
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CVCRKRDNTXXXXXGXXXXXXXXXXXRXNGXXXXXGEKWDRNGENGGXXXXXXXXXXXXX
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VYNXDQXDXDXXXXGXXCXXXPXXXXXXXXXGXXXXXYXXXXXXRYXCXEGXXQXXXPXI
RCXXXGXWXXPXIXCXXXXXXXXXXXXXXXXXXXGDXCDXCEEDDDNDGIPDLQXXXXXN
CRXXXXXXXXDSDGDXXGXXXXXXXXXXXXXXXXXPDXXDXCXXXXXIXXXXXXXXQXXP
LDPKGTXQXDPNWVVRHQGKELVQTXNXDPGLAVGYDEFNXVDFSGTFXXNTXRDDDYAG
FVFGYXXSSXXYXXXWXXXXXXXWXXXPXXAXXXXXXXXXKVVXSXTGPXXHXRNALWHTG
NTSGQVRTLWHDPRXIGWKDXTAYRWHLXHRPKTGXIRVXXYEGKXXMADSGPIYDXTYA
GGRLGLFVFSQEMVXFSDLKYECRDXIPEDFQEFQTQNFDRLDK

==> Leifsonia.txt <==
>MSA Consensus of 128 seqs, protein
MTRSGFARLRALALIPLVVASMLLPVAATSASAAPVPTAITDVASGLPDPMDRGSYTPAV
IQETKLGLVSLQEPSSSGSAPTSGTAQAPENLQIRGQLYYPADRSEPSPVLVLVHGNHGS
CDSGQSSSTATCAEYKRNEAGYAYLAENLATWGYTTFSVSQDQMMXXXXXXXXXXXXRR
XLXAATXXXLSAANEPGGLPVDADTTXXXXLVGXXXXXXXGXXXXXXXXXGVXXXIXXXX
XXTXXPXXXXXXXIXXAXVXXEXXXXXXXXXXVFPXXXXXXSGXXXNXXKLMXTXXFXXX
XXXXXXXXRXXWXXXXGDAALXAXXXFXXXISMRXPRTPRXXXNXXXXXAXXXXIXLLPX
XXXXXAXXXXXGXXAXXXXXXXXXXXXXXXXXXXXXTXXXXXXXXXXXXXXXXXXXXXXX
XXXXWXXXXSXXXXXXXXXAXXXXXXXXXXXXXNXXLXXXXXXAGXDXXXXXVNXXXXQKA
AXRVTNNXXVXXXXXGXXXXXGXXXXXXXXXXXXXXXGXXXXSDGTYSIGGLXXXXXXXR
YXXXXXXXXXXXTXXXXXXXNXXXXXXXXXXXXXLXXXXXXXXXXXXXXXXXXXXXXPXX
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XXXAXAXXXXPXXXXLTGXXXXXXXXXXXXXXXXXXGXXXXXXXGXXXXXXXXXXXXXXX
RXXXXDXXXXXXXXGXXXXXXXXXXXXXDPANVGDXXXXXXXXXXXXXXXXXXXXGXXXXX
XXXXXXXXXXXXGXXXXXXXXXXXXXXXXXXXRXXXXXXXXDSXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXAAVXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXTXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGXXXXXTAGLEXXXXXXX
XXXXXXXXXXXXXXXWXXXXXXFGXXXXXXXXXXXGXXXXXXXXXXXXXPXXXXXXXXXX
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XXXXXXXXXGXXXXXXXXXXXXXXGXDXYXXXXXXXXXXLGXXXXXXXXXXXXGXXXXXX
XXXXXXXXGXXXXXIXXXXXXXXXXXIXXXXXXXXWXXXXXXXXXXXXXHEXGHNXGLXX
XXXXXXXXXXXXXXXEDXXXXXXXXXXXXXXXXXXXXXYXXXYXXXXXXXXXXXXXXXX
XXXXXXXXAXXXXXXXXXXXXXXXXPXVXXXXAXXXXTXXXTXXXXGAAXXXXXXXXXX
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DXXXXXXXXPXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXY

XXXXXXXXXXXXXXXSXXXXXXXXXXTXXXXXXXXXXXXXXXXXXXEESSDSTSIGYERS
XXXSXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXADTDXXXXXXNXDXDXDXDGXXXX
XXXXXXXXXXXXXXXVDSDSXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXMXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXAXXXXXXXXXXXXX
XXXXXXXXXXXXXPXXXXXXXXXXTAXXXEXXXXXXXXXXXXXPXXXXXXXXXXXXXXX
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XXXPXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXTXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXAYENDXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGXEXXXXX
XXXXXAXXIXXXXXXXXXXXXXXXXXXXXVXLXXLXKXXXLXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXTXXXXXXXXXXGGSXXCXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXPASXXGXXXXXXXXXXXXXXXXXGXXXXXXXXXXXXGXXXXX
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TGSLGYPTNYPANXESXXXXXXXFXXXGXXXXXXXXXXXXXXXXTNXXXXXXXXXXXXLX
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XXXPXPEPSAXXXXXPXXEPTXXXTXXXXGXVXAXXXRPXXXXXXPXXGXXXXXXXXXXX
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PAAAXXXGPLLLXXXXXXPXXXXXEXXRLXPXXIVVXGGXXXXXXXVXXXLXXXXXXXXS
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XXPVXLVXGXXXXXDXXTXXXLXXXXGXXXXXXXGGXXXXXXXXXXXLXXXXXXDYPWXX
XVXRXXGXDRXXTXXXXXXXXFXXXXXXXXXXXGXXXXXXXXXXAXGXXFPDALXXXXXA
GXXXXXXPLXXXXXXCXPXXXXXXXXXXLXXXXXXXXGGXXXLXSSXXVXXXXXXCXXXX
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XAXYGXXXXXXXXXXXXXXXXXXXXGXXXXXXHTXRXXXXWYXYXXPXXXYXXXXXXX
XXXGXXXGXAHIVTGGXLXXXXXXXXXXXXXXWXXAADRTWTSFXXAKXGXAPSSXLXXX
XHLXFEXYXXGXQXDXXPXXXLXGXXXXMFGLYDYWRXTGNXEXARYFTGGXTTVLXRMM
PLVRVKGGVSYYCVQXTYCHSPLWQNQTYHVIHSWQLDTLARLTGDAXFTXWADRLRXDW
XXXDASXRRVXPXXGXGDLGEAGETGEPTDPADPGATGEVGEXXDXGXXVPXPXLXPPPX
XGPRAGTGGDXXWIEP

==> Lepidosauria.txt <==
>MSA Consensus of 770 seqs, protein
MLEXXXXXFFXMXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXCDXKXXXXXXTXCXXCX
XXSXXXXCPXGXXXXXXXXXXXCRYXXXXXXDXXLSXXGCXXXCXXEXXXXXCCXGYWG
XXCXECPGGXXXXCXXXGXCXXGXXXNGTCXCXXXXXGXACXXCXXXXXFGPXCXSVCXC
XHGICNXGXXGDGXCTCXXGYXGPXCDQXXPXCXXXXCXXNSXCXVXXXDXXQXXCXCLP
XYXXXGXXCXXXXPCXXXXCXXXAXCXXLGPXXXXCTCXXGYXGDGXXCXPIXPCXXXXG
XCPXXSTXCXXXXPGKXXCXCKXXXXXXXXXXRRXXXCXSXXXXCXXXNXXXXXAXCXXX
XXGXXXCXCQXGXXGDGXXCYXXXXXXIXXXNMXPXXXXXLXXAXAIFGKGCXXXLXXYG
PFTVXLXTXTIFPPFHISPRIPVTTMXSXHWLLAWXGLXXXXXVFXLRDTKEMGEYAKSG
IPVFSIELNTLXXXPXIXKXXHPRATEAXTKYFLXQXXAAXXILXAXTXNAWXTGQWXIX
XXXXXXXXXXXXXAXXXKLGXXAPXHXWYPXXXVXQGXTXXTALXXSTWREITAQKXAPL
XXLXGQXXXXXXXXXXXLXXGLXSXXXXXGELYLIEPLKFPXXXXXXXRXSYXGGXX
GLNQTQTRKIXAXSSIAHMGWLXXAXKKASXXXXXLXTLTXXXYXXXTXXXFXXLXXXXX
KTXXDVXLXXLXXXWXXXPXXXXXXXXXLXSLGGLPPLTGFXPKXLIXXXLXXXXLXXXX
XXXXXXXLXSXFXXHLSLXRXDTXYXXXAALTXPPXTXXXXXQXXXWRXXXXXXXXXTAI
NFQGNIIGRAYTXXXXVXXXXXXIXAXNGXIXXXXXXXXXXXXXLPXXPXXXXXXXXXX

XGXCXXCXXLXXELSFEFSXCPXXSXXXXXXXFPXDXXXCXYXXXXLGLNXXXXGCXXXC
NXTXXXPXCCKGFFGXXCXXCPGGFXNPCXGXGXCXDGXXGNGXCXCXXXFXGXXCXXCX
XPNKXGXXCDXXCXCXXGXCDNXXXSXGXCXXGXCKXGYXGXXCDXXXXXCXXXDXAXXX
CXXXAXCXXXXTGXXXCXCXXGYEGDGXXCXXXDXCXXXXXXXCXXNAXCXXTGPGTXXC
XCXXGWTGXGXXCXXIXNCXXXXXGGCHXNAXCXYIGPGQXXCXCKXGXXGXGYXCXPXX
XCXXXNXXCHXLAVCQLXNXXKEDETCLRKYXGDGXXCYGXXMXELXXXXXXXXFXEWXX
XXXXXTXXXXXXNXTXLVPXXXCSKNSLASRQSFWAELNVARLDHQNVVRXIAASTCSPA
GQDSLTGTIIMEYVGNSTLHHVIYGTXWXTXKRKXXXXIXXAXIXXGDIXAXNXXIXXID
KVLFLXPXXXXIKRCMXDMHQXLSFGPXYGXLSELQXGEQFLEXIEKERKTTTFXIGGHS
IEXNTRPPNLYKLDXDXXXYHXXLGXKLLXXDLXNGXXXXTMLGXSXXXXFXXXXXQXYX
NXXXXXXXXVXTXXGXXXGXXXVXXIXKNRCXXNXTXXXXXXCXXCXLXXXXCPXGSXXA
XXPXXGXXXXCXXXXXXXXXXXXGCXXXCXKXXXXXXCCXGXYGXXCEXCPGXXGXXCXG
NGXCXDGIXGXGXCXCXXGXXGXACEXCXXGXYGXXCXXECXCXXGXCNXGXXGDGXCKX
CXXGXXGVXCLKAXXXXXXDXCNXTCXXXANCXXXXTXXXXXCXCXAGXXGNGTXCTXIX
XCXXXNGGCSXXAXCXXXXPGXRXCXCKXGYXGDGXXCXEIXXCLEXNGGCXXNAECXXX
GPXXXACNCLXXYXGDGXXXCXXXXXCXXNNGGCXXXAXCXXTXXXXRXCXCXXXYXGDG
FTCXGXXXXEXLXXXXXXXXFXXXXXXXXXXXXXXGXGPXTVFXPXXXXXXXXXXXXWX
XKGXXXXXLRYHIVXCXXLLXXDLXSXXXXTXLXGXXXKXXPXEXHXXNNDXXKXAASXX
XVXXGVIXXIDXXLXPQXPFHXXXXLXXGXXXXXXXXXXXVXDKXXXXXXQXEXEXHXVX
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RAQXXMYXRSQKQXNSKXXMKKITXCKKIHLSTKMLTXDYPXDFVKSISCQICEHILADP
VETXGXCDXGXXGXGXCXCNXXFXGTXCEXCXPGXYGXXCKXCXCTXXGXCXEGXXGXGX
CFCXXGWXGXXCETXLAXXPXCSPXCXXNAVCXXXXXXXXXXXXXPXXXXXXXLXXXXLX
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XCXXXYXXDGXXCXPXXXPXDFTDEHDPXXXXXXXXKVXXXXXXCXEXAXXXXXGXXXXF
TXXGXXXGXXXXXXXXXHXXXXSLXXXXXXLXXAXGXYXLXSCXXXXXXXGLXFLHXXXX
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TEMNSTXXXXXXXXXXXXXXXXXXXXGXXXXXDGSXXXXXXXGCGFGVXXTAXXXXXXX
XPXXXXXSXSAXXRXTXXPXXXXXFGXXXXXXXXXALXXXXXXXXXXFXXXXXXXXXXX
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VKNXXSXXXXXXXXXXXXXXXXEVXYSTNXXXXXXXPXXXXXVPXGXXXXXSXXXXPXLLV
YRGXXXXXXYXXXXDVLXXGXXSNFXXXTEQFXXTEESPTAXSSSDDXFXQEXXXXXXXX
XXGXXXXLXXXXXXXTAXXXSDXLHXXXXPSXXXEXXLEXXSXHHXXXXXNXSXXXXXXX
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SXXVDEQPLQPSETTGHQEEKETSNESSTVSITQTNKEKQXLDXXTXDQGQSPAXPRXXX
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XVSXXXTXXEXXXXXXAXXXXXXXXXXXXXDVXLHXXHSXXXXEEXXSGVTFIDTKLFEVT
TPSPXXEXGXXXXXXXGLPXTNTSXXXXLPGIXXXXXXXXXXXXXXXGXXXXXTXXXXXX
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XXXXXXXXXSXXDXXXHXXXXXDXXXGPXFEDXIXLXXXXXXXXEPETLHFVNQEETMSL
LDIAGKDTVLKQSSQHSEEASELRGHEAVTLSPXXXXXXXPGXXXXXXXXXXPEKTXXXX
XEXXXXXNXSXXXXXPGIXXXXXXXHXXEXSHXXXXSSXDXKXXHEXXXXXPXXHDXXXE
XGREDXYXTNXTXXXXXXXXXXIPPTGTXXXXEXXXXXXIXLXNTKKGAXXTADKDXXXS
TXXXLXGKXXXXXPXXXXPXWXXEEXXPXNXXRXXXXXXXXXXXXXEHXXXXXDXXXHXX
XKEDXTXEPVXQWXXEDXYTTXXXXDVLXPGIVPRRGIXQKNXTDHTXXVPPIYILLIID
LTIVTPVXXSXDGXKXEESTQXPXXHGLXRLVWAQEMNXXLLXETXXXXXXXXXXXXXXX
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XXKXXFCXXXXXXCLKXXXXXXPXXXCRYPCFPXXXXXXXXXXXXXXLXXLAXXLGVCXXX
NSRXXCXXKXKLXINNGKGGIXEKXXGGLNGEXXXXXXXXHLXXXXXXXXXXTXXSXXXX
XXWXGLXDRXXEXDFXWXDXXXLXYENWXXGXXDEFXAIDETQNXXXXXXXGXXQXVXLK
SXXPXXGXGXXXXCXXPXXXMYGSXXXXXXGXXFGXGXGXXXXYXXGXGXGXXXPXXXX
GXXXXXXXXXXXXLGXXXPXIXXGXNGXWXXPXXXCXXQXPXSEVXIQPPPXXVXXPGPX
LXAXXEPXRVGGYTXCXXXXXXXXSSXXXXXSXXXXXXXXXXXXXSFXXXXXRXGSXGGC
XRGXLILGXXXXGXXCXXPXN

==> Lophotrochozoa.txt <==
>MSA Consensus of 353 seqs, protein
MISXXXXXLXXXXXMXXXXXXXXFALFVLXALXXXXXXXXXYGXGXIXXPIXPRNXXXXM
XXXXYXXXXWYLNGILPRXSXXXXXSXXXXXXXXXXXXXXXXXXXGXXXXXXXXXXXXXF
AVXSXXXXXQXGXXXLXXXXPXXPLPXXXXXXXXXXXXQLYWXXXKGLFPPXXXXXVKPX
XXPVYKPVKTSXSXPXXXKPPTYXXXLXXXXQPEWKPXXXYHPTXXXXWMKXPXXNSYPP
TYGSKTEWKPKPNYLPXXXXLAKKLSSXXPXXTTXWKXXPXXXXLXXXXXXXXPEXXXKX
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XXXXXPXXXXXXXSXPXYXPXXXXYPLPVIXXXPXXYXXXXFPFSEXXYXXXXXXPXPYV
PIXXXXXYXXXXXXXYXXXXXXXXXXXXXXXXXXTYPPTYXXXXXXXXXXXXXXXXXXXY
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ISTXXXXXXXXXXXPXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXYXXS
XXXSXXXXXXXXSXXXYXXXXXXXXXXXXXXXXXXXPXXXQQEDEGEAXXXXXSXXXXXXX
XXXXXQXXXXXXXXXPXXXXDSXXXXXXPPTXXXXXXXXXXXXXXXXXPXXXXXXXXXXX
XXXXXXXXXXXXXPXXXXXXXSXXXXXXXYXNXPXXXXYSXXXXXXYXXXXXXSYXXXXX
SXXXXXXKXSYXXXYXXXXXXXXGXXXXASYGYSNQADHTYSNQXXXXYXXXXAXXYXXX
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XPXXYXXXXXPXXSXXXXXXPXXXXXXXXXXXXXXTXPXXXXXXXXXXXXXXXXXXXXXX
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PXXXXXXXXXXXXXXXXXXXXDNANYQNTQLVDSSXXXXXXXXXXXXXXXXXXXXXPXXX
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LXXXXXXXXXXLXXPXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXSXXXXXXXXPXXX
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YXXXXXXXXXXXXXXXXXXSXPXXXTANXXPHXXIXXXXSIPVIXXXXXXXXFXXXXXPX
XXXXXXXXXSXXXXXXXXPSXPXXXXXXXXXXXYXXXXXXXXXXXXXXXXXXXYVCGXXX
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XXXYXCXXXXXXXYXXXIXXXXXYXXXXXXXXXYXXXXXXXXXYXXXXXYXTXYVCGXXX
XXXYXXXXXXXXXYXXXXXXXXXYXXXIXXXXXYXXXIXXXXXYXXXIXXXXXYLXXXXX
XXXYXXXXXYXXXYXXXXXXXXXYXXXIXYXXXYXXXXXYXPTYXXXXXYXXXYXXXIXX

XSXYXXXXXXXXXYXXXXXXXXXYXXXXXXXXXYVCEXVXXIPXXXXXVXXIPXVXYRXX
XXXXXYXXXXXXXXXYXXXIXXXXXYXXXIXXXXXYXXXXXXXXXYXXXXXXXXXYXXXX
XXXXXXXXXXXYXTXYVCGXVXYTPXXXGXXXXXXXXXXXXXXXXXXXXXYXTPXVCGX
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CXIXXXTXXXCYXXXXTXXXCXXXXXXXXXXXXXXXXXPXXXXXXXXXPXXXXXXXXTP
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YXXXIVXXTXXXXXXXXXXXXXXXGXIXXXXXXXSXXXHPPSXXXWIXXXXXYXXXXXXX
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YGXXXXXXXXGXGXXXXXXXXXXXXXXXXXXXXXXXXXXSSSSSSXXXXXXXXXXXXXXX
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==> Mammalia.txt <==
>MSA Consensus of 2785 seqs, protein
MRGPHWXXXWXXXXXXXXXLLXXXXXXXXSXQTPMSLSSXXRXXXXXXXASTXXXXXDX
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XQXETSSXRXXXXXGXXTSXXPXXSIGAIKIALEXSXPXXXXXXXTXXSTESXSXDXGHT
TAITTQXLTXXXXQVSLTXXXQXXSXVXXXXTXXXXXRXHXGXKXXXEIASTSSGQVFHL
XKXQVNXVXXXXXXXVQASKVHLLSTDHLEXAVNTWXIPFDPSLKEVTVSLSGPSPXIEI
RNPXGKLIKKGXGXXELLXIHNSAKVXXXXXPXXXMXXVXXSSXXRXXXXXXGXSXXXXX
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XTXPXXXXXESMXXXXXPXXXXXIXVTTSTPSASSLHQIQTETNSXKTISPGETTTSXXP
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XXSXXXXXXXXXXQXXXXLFNLSXXXXSXXXXXXXXXGXXXXXXXWXXXXXXXXXXSSQN
TXXXXEXXTXXXPXXXXSAPSTTHMLSTTSSTQSTSVVSRHXYXXXXXGXXXATTQVSPS
SQNMSTVXXPXXXXXXXXXXPXSXXXGXXXXXXXXXXXXXXXXXXSXXXXXEAPKLXXXQ
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DXKXXXXKXXXXXTVTXXXLXAXXIXXSPSXAXVIEXXXXCXXASHHQSCXXXXXXXCPX
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CXKDXVQXXXXXSNXXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXXPXXXXXXXFXXX
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PCXGXGXXXXXXCXCXDGXXXNGXCXCQEXFXGXXXXXXXXVXXXXXXXXACXXCKXXXX
XXNRIGXXXXXXXXXXXXXXXXXXDXNXFGPXXXXXCXSVCSCVHGVRCXXCAAMGGXXG
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XPXXXXXXXXXXXXXXXXXXXXXXQXXXXVXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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SSLQSXXGXXXAXGXXXXRXXXXXXXXXXXXXXXXXXXXXXXXXVPFALRDENLKGVVYTT
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==> Metazoa.txt <==
>MSA Consensus of 7317 seqs, protein
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CSSDGDKYSCICKGNFXXXTXCXEEIXDPYXCXXNPCKNXXXGXXXDXXYXXXXNGXCSS
XGXKYXCXCXXXXXGXXCXXXDXXEEXXXXXXXXXXXKNNGXCXXXXXKYXXXXXXRKCX
XNFXGXXXXXSSXXXXNXXSXEEAGXEIXDXCXPNPCKNNGXCSXLXXXGXXXXXXXXSX
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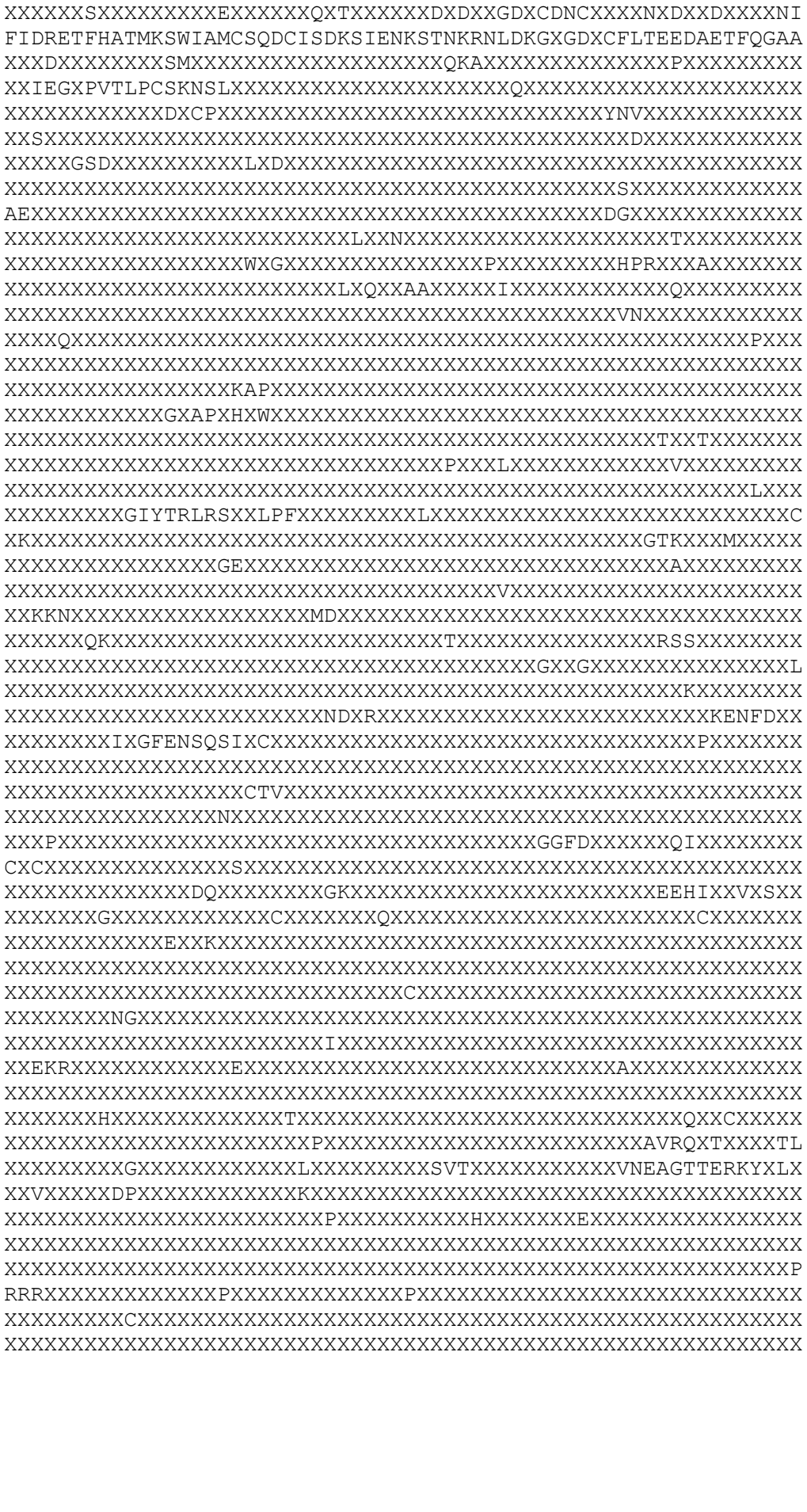

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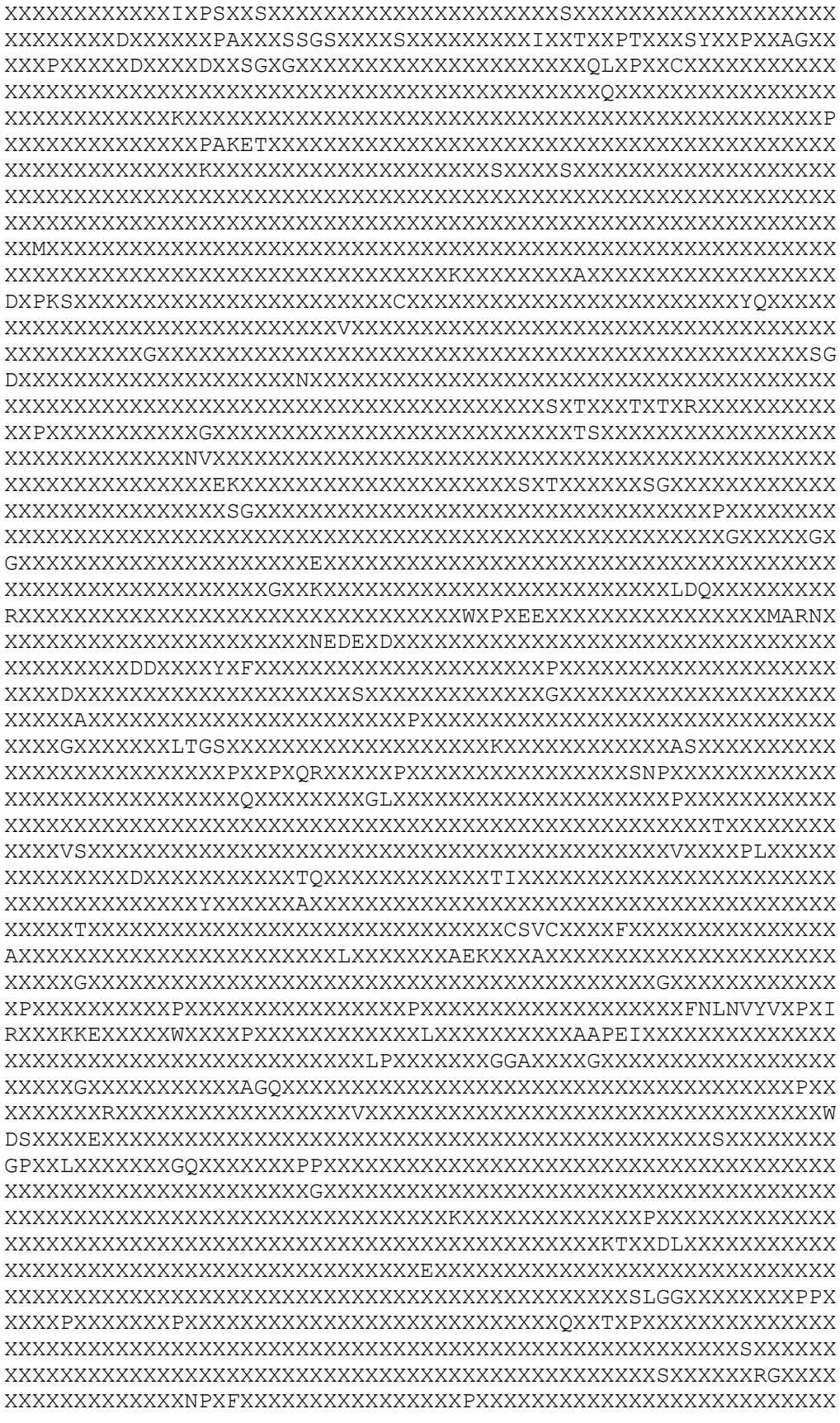

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QQVNVEQIKAGTLARSCSDPHVADEALKGEENKCVEKQSFVEQRLHLQHECVQGADTSGS
NLSSLQVRECQHKRSKRLRKARSCDCCAKRLKQQSASLSESKNEGPVELLEPQTTPVPTA
VNTSEVSGSSNLEESLSITPCAMSTPLPLAKESSVLDLERGRKGEGNLEGNSGVKEEDVE
NPARTAGEVSDSEVGRKEADKNDSAEQHVSECALDEPSDSSVAAEDQSREQAAVEEQSQS
GEMEGILEALVDGSKPETEQVNELESSQDNKEEAGNAQGEVCNTPDEEMREELPEAEMTA
PENVAAGNEEAVGNSSAASPQKPEGLDSFSSVNESPNSVQARCTWSPSASPSTSILKRGI
KRHHDDDSLSPANKIRRVSFANPIYQEGLADDIDRRSPVIRSHSSPSSRSLKILSNIQTK
MTEMVKESLPSPAECVYPALAGCKAPVDVILPQITSNICARGLGQLIRAKNIKTVGDLST

LTASEIKTLPIRAPKVSNVKRALKGYHEQQKNPQAKSRGCEEIGALEDVEKTANSAEDKS
SSVDEEKLATDLAEPAALSSSSSSSSSSPPRADLLSQMDVLAAQLASEDLGRYPGSRLFE
MQEKLSSMAECIMQSLRSRWRSPPHEGAQ

==> Microbacteriaceae.txt <==
>MSA Consensus of 1050 seqs, protein
MXAXRXXXGXXXVXXATVVVXXXAACAXXXXTIXAGXXXGXXXVXXVCAXXXXXAVAAYX
AVXAXWXLXXXXXXXDRXAXXXXRXXLXGXLAVXXAXXLXXXSXXXLGXXXXGAGAAPXH
XXXXXXXXXGXLXXAXXXVSMXXPAXXVXXVXXXXAXXXXXXXXXXXXXXXXXXXXXXXX
XHXXXXXXXXXXXXXXXXXXVAXXXXXXXXXXXXXXAXXXXXXXXXXXXXXXXXXXRQA
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXWXXXXXXPXXXPXXX
AXXXXXXXXXXXXXXXXXVXXXXXXXXXXXPXXXXXXXXXXXXXXXXXXXXXXXVPXXXT
XADXXXGXPXXGXXXXXXXXXXXXXXXXXVXIXXXNXLXXXXXXXXLXXXXXXXXXXXXX
XXYNXXXSXXAXXXXXPXGXXGXXXXVXXXXXXXWXXXXXXXXXXXXXXXXXXXAXXDGG
XAXXXLXXXXXXXXXXXXXXXXXXXXXLSSXXPDQQYAXVXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXQDXXDXXXXXXXXXXXXXXXXXXXAVXXGXXXXXXXXXXXXXXXXX
XXXXXGXXXXXXXXXXRSXXXXXXXXXXXXXXSVXXXXXXXXGXXXXXXXXXXXXXXGMV
KLXXXMXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPXXXXXXXXXXXXXXXADNXX
XXXXNSVXXXXXXXXXXXXXXPXXXXXXXXXXXXXXXXXXXXXXXXXXXAXXXXXXXXXXX
XXXXXPXXXXPAGXXPPXPTXXXXXXXXXXXXXXXXXXXXXXXXXXXFXXXXXXXXXXX
XXXXXXXXXXXXXXXVLTXXXGXXXXDLXXXRDPXYXXGXWVSAGEAAKSYKXXXXXXXX
XXXXXXYXXXXXXXXWXXXXXHXXXXPXXXXXGXXXXXXXXGXXXXXXXXXXXXXPXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXGXXXXXXXXXXXXXPXXXXXXXXXXXXXXXXX
EXLXXXXXXXXXXXXXXXXXXXXXXXXAXXXXNALAXXSXXDXXGDXXXAXXMRXXXTX
XXXPXXXXXTQXXXVDXAXXGXLXLXFXGXXXXVXLPATAXQXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXWXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
GXXXIXXXMXTLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGXX
XXXXXXXXXXXTSAXXXXXXXXXXXXGXXXXXXXXXXXXXXXXXXPXXDXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXAXXXGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXLXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXLXXXXXXXXXXXXXXXXXXXXFXLXXRXXXXX
XXXXXXXXXXXXXXXXXXXXXXXDXXXXXXXXXXXXXXXXXXXXXXAXXXXXXXXXXXXX
XXXXXXGXXXXXGFAGTAHXXXXXXXXXXEAQSXXXXXXXXXXXXXXXXXXXXXXMNYA
XXXXXXXXXXXXXXXXWXXXXXXXXXXXXXXXXXLHXWTEGXTXXXXXXXYXXXDXXXXX
XXXXXXXXXXXXXXGXXXXXXXXXXXXXXXXXXVXXXGXXXXXFXXXXXXXAXXXXXXXX
XXXXXPXXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXXXXXXXGXXSTXXXXXXXXXXXX
XXXXXXXXXXXXXXGXXXXXXXXXXXXXXAXXXXXXXXXXXXXXXXXXXXXXAXXAXXXXXXXX
XXXXKXXXXXXXAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGXXXXXXXXLXX
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LXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXAXGXEIGXXXXXXXDLXXXXXXXSXXXX
XDAALXXXXXXCXXXXXLXXXXXXXGXXXXXXFAYPXXXXXXXXXXXXVXAGXXXXXXXGX
XSXRXLGDXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXAXX
XXXXXXXXXXXXXXXXXXXXXXXXAXXXXXXXXXEXXTXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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XXXDXXXXXXXXXXXXXXXFXXXXXQXXXXXXXXXXXXXXPXXXXXXXXXXXXXXXCXXX
XXXXXXXXXXXXXXXXXXXXXCXXXXXXXXXXXXXXXXXXXXXCXXXXXXAYXGXXXX
XAAXIXXXVXXACGIXXXXXXVXXQKEXXXXXXXXXXXXXXXXPGXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXNPXXXXXXXXXXXXGXXXXXXXXXXXXXXXXXPXXXXXXXXXX
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XXXXXXXXXXXXXXPXXXXXXXXXXXXXXXXXXXXXXXXXDXAXLXXXXXXXXXXXXXX
XXXXDXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXQEXGXXXXXXXX
SVRXXXXPLGXXXXXXXXXXXXXXXXXXXXXXXXXXLGXXLTDADXLXXPXXXXXXGX
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XXXXXXXXXXXXXXXXXXXXTXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXVXX
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XXXXXXXXXXXXXXXSIXXVXXXXXXXXXXXXXXXXXXXXXSXXXXXXXXXXXXXXXXG
XXXXXXXXXXXXXXXXNNXXXXXXXXXGLXXXXXXXXXTDXXXXXXXXXPXXXXIXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXFXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXSAVVXXXXXXXXXXXXXXXXXXX
XXTXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPAXXXAXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXPXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXRXXXXXXX
XXXXXDXXXXXXXXXXXXXXXXXXXXXLXXXXXXPXXXXXXXXXXXXXXXLXXXXNXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGXXVXXXXXGXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXWXXXXXXXXDGDXXXIXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXAXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
GXXGXXXXXXXXPSXXXKXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXRXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPXXXXXXXXXXXXXXXXXXLXXXX
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XXXXXXXXXGGXXXIPXGAXXXXXXXXXXXXXXXXXXXXXXXXXXXAXGDQXXXXXXXX
XXXXXXXXXXXXXXXXXXXXPXXXYRXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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XXXXXXXXXXXXXXXXXXXXXXXXXXXXGXXXXXXXXQXXXXXXXXXXXXXXXXXXXX
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XAAMXXXXXXXXXXXXXXXXXXXXXXXXXXXRXXGXDRXXTXXXXSXFARSXGXXTPX
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XPDALSAXXXXXXXXTXXXXPGXXXXXXAAXXAGQRXSXXHXXPXLLXXILXXXXXXXXX
XXPXXXXXELXXGRLXYRGPAARAVGAXXIVXXGGXXXVSXXVXXXXXAAAEXXSFXTXX
AXRXXLXGATVXVDELPASTDVEQTTEQPSEPAATTEPTPSATAEPTPADTAEPVPSESA
EPTASAEVDPAXXXXPAGPDASASPQPSPTATAGSAPTSASELARSQETLAATAADXXXX
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VGXXXXXXXXXXXXXXXXTGXDXXXXAXVXYSXXSXXXAXXAXXXXXPXXGXXFPDALXA
XXXAXXXXSTXXXXXXXPVXLVXXGXXXXIPDATEIAAVPAAXXXXXXXXXXWAXXXXXX
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XXRPHLXXXXXXXXXXXXXXXXXXXXXXRXXGXDGRXXTXRXXXXXXXAANQKGKIQQL
IETPAVASLXXXALDRGXXXTXXXXXXXXXXXXXXXXXTPXXXXXXXXGXXXXXXXXXX
XXXXAXGXXFPRPSSRRDXDALXGXXXAXSVDGXXXXSATYKPAAAXXXXXPXXXXXXXX
TTXXXCYGSVSKTSAAXPXXXXLLAXGXXXXXXVXXXXXXGAQXXXXXXXXXSXRKXASX
XXXXXXXLGGXXXXXXXXXXXXXXRRQNPXXXXCXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXGXXXXXXXXXAXXXXXXXXXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXAGVXXXXXXXXXXGHASXXFXXLXXXXXXXXXXXXXXSXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPPXXPPXXPXXGXXXGXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGDGXXDXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXAXXXXXXXXXXXXXXTXXXXXXXXXXXXXXXXXXXXXXIVLNXXXX
DXXLLXXXLXXGXXXXXXXXXXXXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGXXX
XXXXTLTXXXXXXXGDXXXXXXXXXXXXXXXWXXXXXXXXXXXXXXGXXXXXXXXXXXX

XXXXXXDSXDWXXXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXRXXXXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGPSXXXX
XXXXXDYWXXTXXTYDXXXXXXXXXGXAXXXXXXXXXXXXXXXXXXXXLFPDGXXXXXGXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGXXXXXXPXXXXXXXXTGXFXXXX
GXRXXXXXXXXXXXXXXVXXXXXXXXXXXXGXXXXXXWXXXXXXXXXXXXXPVXXXXXXXX
XXXXXXXXXXXXXXXXXXEXXLRPXXXHXXXXXXXXXXXXXXLXXXXXXXXXXXXXXXXXX
XXXXXXXXXXDGXXXXXIXGXGXDXXEGRXGXDXXDGDXXXXXXLXXXXXXXXVQATLXX
XXXXXXXXXXXXXXXXXGRNTXXXGXVSKAXXXXLXXXXDXAXXLXXXXXXGXXXXRVXW
XXXXXXXXXXXXXXXXXPXXXXXXLPNVXXXXXXXXDGXXXXXXXXXXXXXXXXXXXXXX
XXXXXAXADXXXXXXXXXXXXXXXXXXXXTNQXXXPXXXXXXXXXXXIXXXRGTGXIXX
XXXXAPAAPPGALXXXXXXDXXXXXXXXXXXXXXXXXXAXXXXXXDSXYXXXXXXXXXX
XXXXXXNGXXGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXYXXXXXXXXXXEXXXSX
GXDXXXXXEXXQXXXXGSXXHDXXXXFXXXXXXXXXXXXXXXXXXXXXXPTQXVXXXXXX
XXXXXXXXLXXXXXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXXXXXRXXAPVTXXXXXX
XGXXXDXXXXXXXXXXXXXXKXXXXXXXXWXXGXXXXXXXXXEWEXLXXXXXXXGXXTX
XXXXXXPXYLXXDXXXXXXXLXXAXXXVXXXVXRAEXXPXXXXGFXXXXXXXTDAXXGXX
LXVXVXYXXXADGXXXYXYXXXGXXXXXDXXXXXXXXWXXXXXXXXXXXXXXXXXXXVGX
XXXXXXXXXXXXXXXPXXXXPXXXXVGXXXXXXXXXXXXDGXXXAXXXXXXYXWXXXXXXXX
XXXXXXXWXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXAYXXXAX
DXGXXIRVXXXGLTDVASMAVSYTDXXGXXXXXXXXXXPVXXXXPAPXPVXPXXXGXES
LXPEAEPPVTP

==> Microbacterium.txt <==
>MSA Consensus of 119 seqs, protein
MXAXRXXXGXXXVXXATVVVXXXAACAXXXXTIXAGXXXGXXXVXXVCAXXXXXAVAAYX
AVXAXWXLXXXXXXXDRXAXXXXRXXLXGXLAVXXAXXLXXXSXXXLGXXXXGAGAAPXH
XXHXXXXXXGXLXXAXXXXSXLAPAXXVXXVXXXXAXXXXXXXRSXXXGXXXRXRRXXXP
XXATXGXLLAXTXPXXXAPAAXAXVPXXPACXAXXAVRXYDXAAVXXXIPXSRWXNDSRV
PEXDPVVDGVDHLXDGDPXGMLFVLQXDKXAVQNWHVPXVGTAADGYAGDPAXGRRXRPR
PLVLRANVGECVXITLXNELDPXAXAXFLPQXDPXVXXRAXGVSYNXAXSGXAXVGYXPD
GXXGVGESXTYXWVAPKSEGVYLFRDXGMXXXAXXDGGXAEHGLYGALAVQPXGAXWFDP
XTGRELSSXXPDQQYAXVADQSGDLYIXAVIXDAXQXRFREXVXXSQDILPXQDRADLXX
EELAXLPEPFERFGXNXGSDPEPKRXXFNXEGXERWCEDCSXEETXLSSWVYGDPGMVKL
ASGXGPWLPXAPDFGGXDPXSAPGGLVADNXEDCXLXLTXAAXEXRPASCYVTNVXRAYQ
GDPIKXRFXHAGNYETHVFHLHAHTWXAEPDDXGPAGXXPPXPTXXXQPRATTIDSKTYS
PWTAFTADLNYGAGARVGTXGDXIFHCHLYTHFSHGFWXLXRXHDVLEDGXXALPDGTRV
XXXVPLXXXXXXLGXXAXVPPXKXXXXXXVPGYPRFIPGEXGARXPQXPXSXWQREFDXN
GDPVLDXXGXPVXXXXXRXXXTXXLDPXLLXATQXXXVDXAXXGXLXLXFXGXXXXVXLP
ATAXQXXXALESLDXXXXVXXXXXXXXXXPWXXXXXXXXXXXAXXXVXXXXXAXXXPXAX
AXTDXXPXXXXXXXXXXXIXXXXXXXXXXXAXXXXPXXXXXXXXXXXXXXXXVXXXXHX
XXGVXXVXGXXXXXXCPAXXXXGXYXXXXXXXXXXXXXXXXXXXLXXXXWRXXXXXXLXL
XXXXXXXXQXXXXXXXXXXXYXXXXGXXXDXXXXXXXXNXIXDXXXXXPAXXXXXXAGXX
IXXVNFDVLASDGASNGWNYQQAAFXXXQAXXXXXLLXGXXXCAVGXXCLPAMPXGXXXV
XXXXXAXXXXLXXXXXXXERWYADXXXXXXFXHDXXXAXXXXXXGXYXXXXXXPXXXXXX
XXXXXXWXXXXXXAXHAXAAGKXXCVXACXGEAXGXAMDMXGPXXXPTXEXXXXXXXXXX
XXXXXXDXXXAXXVXXXXXXATXXDILDPXNALEPPXAXLXXXXXXXGXXXXPXXXAPLX
DRQFAGXXPXXPAXPXXXXTXXQLAAAGWXXXXXXXPXGXXXXXXXXXXLXXXXXXXXXX
AXXGDTVXXXXXXXXPXXXXXXIXXXXXXXXXXXXXXXXXXXXXNLXXPXXXXXXXXXXX
XXXVXXXXXXEXXXXXXXXXGXXXXXXXXLXXXXXXXXXRVXDFXXXXXXXXXWXXXXX
IMRVFDXXXXXXGLXXXXXNXXXXPXXNXXXXXXXXXXXXXXPXPXCPXXAPXXXXDXX
XXSXXXXXXXXXXXXXXXXXXPQXXXXXXXXXXXXXGXXXXXXLXXXXXXGDXXXXXXXXX
XXXXXSXXXXXXXXXXXXXXXXXRXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXLL
PRFXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGXIX

XXXXFXXXXXXXVXXVXXXXXQIXXXXXXXXXXCXXGSDXXGPXXGXXXXXXCLXX
XXXXXXEXPAXYXXXXXXXXXXXXXXXXXXXAXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXGXXXHXGXXVXXXXXGEGXDYRXXXXFQXXXXXXXXXGXXXXXXXXXXP
XXXXXXXXXXXXXXNAPXXXXXGXXXXXXPSTXXXXXXXXXXIATNPXXXXXIXXXPXXY
LTDSIXXXXXXXXXRSVRSVTXXXXXXGXXXANFXXXXXXXXXXXXXXXXXXPDXXXXXX
XXGXHGDXXXXXXXXXXXXXXXXXXXXXXXEXXXTXXXATXXXXXXXXXXXIDXXXXXXX
SXXPGARXXXXXXXXXYXXXXXVXXGXXXXXXXXXXXXXXXXXXGXXXXXXXXXXXEXX
VXXXXXXXRTLXXXXXXXXXXXXXXXXGAPSXXXXXXGXXXXXPGSSPXXXXXXXXXXXX
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XXXXXXXXXXXXXXXXXXXXXXXXXXYGXXXXXXXXXXAXXXXWXXXXXXXXXXXXXPX
XXXXXXXXXXXXXXXXXXXXXTAASLNXRTAPTEKXTXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXVDSPEHGHETAXXXXXXXXXXXEXXXXGXXXVATSXXXXXPXXXXXX
CXXXXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXWXXXXXXXXXXXXXXXXXXXXXXXX
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XXXXXXXXXXXXXXXXXXXXXXXPXXXXXXXXXXXXXXXXXXXXXXXPXPXXTPTXXXXX
XXXXXXXXXXXXXXXXXXXXXXXRXXGXXRXXTXXXXSXXXXXXXXGXXXXXXAXGEXXF
PDALXXALXPXXXXTEDVLPGGXXXXXAAXXXXXPXLLVTXXXXXXGXXPXXXXXEXXRL
XPXXXXXXGGXXXVXXXVXXXXXXXXXXXXXEXXXXRXXGXXRYXTXXXXXXXXXXXXXX
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XGGXGXVSXXXXXXXXXXXXXXXXXXVXRXXGXXRYXTAXXXXXXXFXXXSXXXXXXXXA
XGXXFPDALXGAAXAGXXXXPXXXXXXAXXXXXXXXXXXXXXXXXXXXXXXGGXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXYXXXXXXXXXXXXXXYQWXANGXXXX
GATXXXXXXXXXXXGKXXXVXXXXXXXGXXXXXXXXXXXXXXXXXXAAXXXXXXXXXXXX
XGXTXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXWXXXXXXXXXXXX
XXXXXPXXXXXXXXXPXXXXGXXYXXXXGNXXXXXXXXELXXXXXXXXXXXXXXXXXXX
XXXXHGXXXXDXXXGXXXXXXXWXXXXXXXXXXXXXXXXAXXGGXGDDIXTXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXGXDFXXXXXGXXXTXWXXXXDDXXXXXXXXXXXXX
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XXGXXXXXXXXXXXXXXXXXXXXGXXXXXYXXXXXXXCXXXXXQXXXXXXXXXXXXXXX
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XXXXXXXXXXXXXXXXXSSGDXGXXXXXXXXXXXXXXXXXQEAXXXXXXXXXXXXXXXXL
XXXXGXXXXLXXXXXXHXEXXGEXXXXXXFXVXPXXRXXXXXDXXGXXXXXXXXKAXXYX
XXXGPXXXXXXXXGGXXYXXXXXXPXXXXXLXVXLXXXXXXXXXXXXXXTXXXXXXGXXX
XXXXXXXXXLVGGPEXLXXXVXXGXXNPGXXXXXRTAVKIDXXRXIXXDXXAXXAXDTAX
YXXXXXXYXXXXNGTVWAWGNNLXGXXGSGYXXVXHTXVXXPXXSDGTELTAQGSVVALR
GDGTVWSWGDGETLVXDXXXGXERXQFXDGCXXXXXDGXXWVXCXXXXXXXXMXXTXPXE
XXPVTAXLWXXXXXGXAXXXXFXXXXXTNYAKNXXXTWWXGXGXXXXXXXEWEXLXNPXG
XXSXXXVPXQXXLSVXXXLRVXVXGNAYAYSASGSALAWXXXAXGXXRXXXSXVSXXPVX
XXXXXXXXLXXXXXXPXXXGXXIXXGXPXDPDGXIXXXGXLXYXWXXXXXDTPXXXGXXX
XWXXXXXXXXXXXXXXYAPTXXDXGRXIRVTILXYXDGXSMAVSSSDAYAVXXXXTXXAX
XSXXXXXXPVKIGG

==> Microchiroptera.txt <==
>MSA Consensus of 138 seqs, protein
MXXXXXLXLLXLXXXCLAGSRXXGGQKAVGPVLYLRNFXSPXGXXXXXXRCDXKXXXVXX
XXCXXCPXXXXXXCPXGXXXXXXXXIGXXDCRYXXXXXXXXXXSXXGCXXXCXKDXXQXXC
CPGXWGXXCXECPGGAXXPCXGXGXCXXGXXXNGXCXCQEXFXGXACXXCXDXNXFGPXC
XXVCSCVHGVRCXXGXXGXGXCXCXXXYTGPHCDXXXPECXALXCPXNSXCSXXSEDETX
XXCXCLPXYXXXGXXCXCQLLDXXXPCXXXXCXPXAXCXXXXXXQXXCXCXEXYXGDGXV
RCLPXDPCXXXXGXCPXXSTXCXYXGPGXXXCXCKXXXXXXXXXXXXXXXXXCKSXXXCX
RXAXCXXXXXGXTXCXCXXXXVGDGXXCYGXXXXXXXXXXXXXXGKXXXXLXXXXXXLDX
XXXXXLXXXGPFTVLXPXXXXXXXXXVKELLMXXXXXQXXXXXHIIAGQXXXEXXXXXXQ

TRRXXXTLXGXXXXXXXXXXXXXXXXKXXDXXXXXXXXXXXNXXAXNGXXHXXXXXXXXX
XPXXXXDXQASQCPNACSFLXKTIXXILXXXXXXSXFXXXLEXXGXXXXLDXDGVXGPXT
VFXPSNEAXXXXXDGXLXYLXXPXGXXKLXELVRYHIXXXXQLXVXXLISXXRXXTMANQ
XXXXNXXXXGXILXXPEXVXXXXXDVXAXNGXIXXLXGXLXPPXIXPILPXXCXXXXXXX
XVGXCVXCXXXXXXSXCPXNSXXXXLXXXXCVYTXXXTGLXXLKXGCAXYCNXTXXXPXC
CKGFXGPXCXQCPGGFSNPCXGXGXCSDGXXGNGXCXCXXXXXGXXCXXCSXPNKXGXXC
XXXCXCXHGXCDNRXXSXGXCXXGTCXXGXXGRFCXXXTXXCGXXEQXQXCHXHAXCXXX
XGXAXCXCXXGXEGDGXXCXXXXPCXXXXXGGCSXNAECVXXXXGTHXCXCXKGWXGDGR
XCXXIDXCXLXXXGGCHXXAXCXYVGPGQSXCXCKXGFXGXGXXCXPIXXCXXXXGXCHX
LATCQXXXGGXXXCXCXXGYXGDGFXCYGXXXXELXXXXXXXXFXQWXXXAXXHPXLXAX
SXXTYTXLVPSXXAITYXXXXXXXAXAFWLXXXXXPXLXXXHXLXGXXXXXXLXXMLXXX
XXXXXSXXXXXXXXXXXXGXXXXXXASXXXXDXXATNGVXHIXAMITXXVLLPPRKDXPX
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XHAMIRXXXXXXLXXDXXRXHVVLXEXLXXXXLXXGXHRXSXLGXXXXLXFXXMIXXXQX
XVNXXPXXXXXXXXXXXXXGLXXVLXXXXXRCXXSHXXXLRXKCXXCXXXXXCXXGXXX
XVRLDWRIPFPCHLLSLPPALLAQDXXXKXCXYXXXXMGKRSXXXGCXXTCXKXIXMPSP
LPAFCFSLMSVLACAGLSLHPSPQXXXCCXGFFGXXCXPCPGXXXXVCXGXGXCXDXXXG
XGXCXCXEGFXGTACEXCXXGXYGXXCXXVCACXHGXCXXGXXGDGSCXCXVGWXGXRCD
XXIXXXXCXXXCXXXANCXXXXXAXXXXCXCAAGXXGNGTXCXGNXXXXCXXXNGGCSXX
AXCXXXXPGXRXCXCXXGYXGDGXXCXEXNXCLXXHGGCHXHAECXXTGPXQXXCXCXXX
YXGDGIXXCXLXXPCXXXNGGCSXXAXCXXTGXXXRTCTCXPXXSXGDGFTCRGXXXXEL
XXXXXXSQYFFXLXXXXXXXLXGXGPFTVFXPXXXXXXXXRXEXXXXXAXXXXVXXXXX
XXXXXLXXXDLXXXXXVTXLXXXXXXXXXXXSXXXXXXYINXXAXXXXSSDXXXXNGXXX
XIXXVXXXXXXXXXXXXXXAXXXXXXXXXXAXXXGYXXFSXLXXXAGLLXXXXXXSHXXX
XXXWXXXXXXXXXXXXXXVAXGXQXRAXGXYXGRXXLXXXPXXXXXAXLXXXXXXXXXXX
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GLLYICEPHVSHTLCLXGELXXXXXXXRIXQXXEXRXLXFXXGXAYGIDQLLXXXGLGXR
CKDXFXXRPXXXXXXXCXXXXRGVGXTXXXXXXXCXXXPXCPXXXXEXGSPQXCLXYXSK
XWTSPALRXXTLRNLWGXXXXXXXXCXXXXXXXXXKPSCCXGHYGSXCXACPGGPXXPCX
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CXDXXXGGIKTAPCXEHAXCXXTGPXXXXCXCXXXYVGDGXXCXXEPXXPXXXXXXXLA
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LXXXXXXXXXYDXYCXXXXXXXXXXXXXITNLXNAXXXXILQXXIXXXNXXXLXXXAXXX
HVTGHRDXTXYTXXXXYXXXXXXINNTXXDEAEXEXDXXXGXXXXRXXXEXYXXXXXXXP
TGXXDNXTLXXPTXXXTFFSDXPXVDXXSXXXXXXXXXXXXPXDTXXTXXXSNXXXIXVY
CXXXXXXKRRAAEAXXXXXXXNXXXXXXXXXXXXXHSGSXXXXXXXXXSXTXXXXXTIXX
PXXXPPXPXXXXXXXXXXXXXGXGXXXXXXXXXXXXXXXXXXXXXQWSXXXXXXXXXLQ
TTXRXXXXXXXXXXXXDRSXXXXXXXXXXXXXXXPLXXXXXXXXXXXXXETKVXXSXTDG
XSGPXXXXXXXXXXXPXXXXXXXXXXXXXPXXXXILAXKGSGEXLQTPXEDGSXSXSXSX
XSAHDXHPNQXXTTXSXEDSSWVTSAAGSGLPVGSGLASGXEDTXFXDPISHPMGXPXGG
EGHQTXXXRXXMDSSHSTTLEXXXXGXEXXXXQPSADSNTXLVEDXDRTXPLPXTTXQDX
SHLETSTSGVDLSGLPSGGXXXPXSXTXXTQXFSTSHGGXEEDXDPXXGDXXXXXXXXQX
MPXXXESHMSTPTSSXRHDGGGGXXXGNLPEDXATSVEGYTPHSPDTKEYTTXLIPVTPA
NTELPSGGTXTPXXETAAPEXQDXSPGVGETHLATSTXXXTEVTXLXXGDSNVNVDGXLP
XDXXXLXXXXXDXSXXXXGDXXLGGRXHTTXGSXXTPEASGLPXGFSGHXSGSDLGSGPQ
EGGXXTTSGPXRKPQIPEWLIILASLLALALILAVCIAVNSRRRCGQKKKLVINNGNXGA
VEXDRKPSGXXXXXELNGEASKSQEMVGETSGXHLVNKEXXETPDQCMTADGLFELSGQP
SGFPEETRNLQNLSGQSSGQPGVSGEASVDMKSGXPIGXXDXSGETSGVPDLSGQXSXXP
GXSXXPXGXPXLVSGXASGSGDASGVTFVDSXFVEVTPTPFRXXEEGLGSVELSGLPSGE
TDLSGXSGMVDXSGQXSGAXGAXSGXXXXPPXXXGXPXXXXXXSGEASGAEVGSXLPSGA

YDGSGXPRGFPTVSLXDRXLVESVTQPPTXXEAGEGPSGXLXXXXXPXGAXDXXGXXXGX
XXLXGXXXGXXEXXGXXXXXPXFSGDFXGXTDXSGXSSAAAXXTSGEASGLPDVTLITSE
FVEGVTEPTVSQELGQRPPLTHTPQXXEXSGEAXTSGDLSGATPSFPXSGVEASSVPESS
SETXAXPEAGVGAXAAPEAXXXXXGTXXLXETTSAFXXADLEGASGLGVSGXPSXFQEGP
TEGSTPSGMSGEXXTTYDVATETSGWPSATPXASGDGXEXSGXPXXXXSGXXVXXGTSVX
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XXXXCXXSPCXNGXTCXXXXXXXXCLCLPXYXGDXCXXXXXXCXXGWXXFQGXCYXHFXX
RXSWXXAEXXCRXXXXHLXSIXTPEEQXFXNXXXXXYQWIGLNDRXIEGDFXWSDGXXLX
XXXXXPXQXXXXFXSGENCVVMVWHXXGXWXDVXCNXHLXXTCKXGXXXXXXXPXXXXXQ
LFGRXXLRYEVDTVLRYRCLEGXAQRNQPLIRCQENGRWEAPQISCVPXRPSRALXPXXA
LEGRQXRLLGRWTPPSXPVPAP

==> Micrococcales.txt <==
>MSA Consensus of 1525 seqs, protein
MXXXRXXXGXXXVPGXGRXGXXXATVVXXXXXACAXXXXXXXXXXXXXXXXXAAAPXXVXX
XXXXXXXXXXXXXXAXRXXXXXXXRXXXXXXXXXXXXXXXXXAXVXXXXXXXXLXXXXXX
XXXGXXXXXXXXXHXXXXXXGXLXXAXXXXXXXAPXXXVXXSGLALLAAXXXXXAXXXXX
XXRXXXXXXXXRXXXXXXXXXATXXXXLXXXXPXXXXPXXXAXVPXXPACXAXXAVRXYD
XAAVXXXIPXSRWXNDXXXPXXDPVVXGXXHLXDGDPXGMXFXLXXDXXAXQXWHVPXXX
XAADGXAXDPAXXRRXRPRPLVLRANXGXCVXITLXNXLDPXXXXXXLPQXDPXVXXXAX
GVSYNXXXSXXXXXGXXXDXXXXXGESXTYXWVAPXSEGXYLFRDXGMXXXAXXDGIGXA
EHGLYGALAVQPXGAXWFDPXXGXELSSXXPDXQYASVAXQXGDLYXXAVIXXXXXXXXX
RXREXVXXSQDXLPXXXXADXXPXXXAXXXEPFERFXMXXGSXPEXXXXXXXXXXXXXXX
XXXXXXXXXXLXRSXXXXGXXXXXXLASGSGPWLPXXPDXGGXDXXXXXGXXNXXXLXXX
XXXXXXXXXXXXXXXXXXXXXAXXXXXPXXXXXPXXXXXXXXXXXXXXXXMXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXALXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPXXAX
XAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXAXXXXXPXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXLXXXAXXXXXXSQXXXXXVKQXXXAXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXLXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXCXXXXXVLXXESXXXXXXXXXXXXTXXXGXXXXXXXEXXXXDXXAXXXXXXXXXXGX
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XXXXXXXXXXXXXXXXXXXXXXXXXXXXLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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XXXXAXXXXXXXXXXXAXXXXXXXXXXXXXXPTXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXSXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXIG
VXXXXXXXXXXXXXXXXXXXXXXXXRXXGXXRXXTXXXXXXXXXXXXXXXXXXXXXXXXN
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XXXXXXXXXXXXXXXXXXXXTVAPTAXXXXXXXXXXXXXXXGXXXXXXAXXXXXXXXXXXA
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PXAXXXXGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXRXRXXXXXXXXXXXXX
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XXXXXXXXXGXXXXXXXXXXDXXXXXXXXXXXXXXXXXXYXXXXXXXXXXXXXXPFXAXX
XXXXXXXXXXXXXXXXXRXXXXXXXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXCXXXXXXXXXXXXXXXXXXXXDXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXXXXXXX
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XIXXXXRXXXXXXXXXXXXXXXXXXXXXLVXDLXLXXXXXXXXXXXXXXXXXXXXXD
GXXXXXXXXXXXXXXXXXXXXXTXXXXKAXXXXXXXXXXXXXXXXXXXXXXXXXXX
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SVEHTXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXWQXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXSDXXXXXXXXXXHXXXXXXXXXXXXX
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LLGRRNAXXXGXXXXXPDALSAXXAXXAAXXXALEFRXXXXAXLXXXXXDXXVADPXXXX

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LAYTNQASAPXALVLTVXXDVNGNATNITTSSXGXXXXXYXXNTATVTFTRPDXSTQTST
VTVAGGSSTVSADDTYTFTXXDXXXXXXXXXPXXXXXXXXXXXGXVDPAEAVAPAGPDAS
ASPQPSPTATAGSAPTSASELARSQXXXXXXXXDPXXPXXXXXXXXGXXXXXXXRXXGXX
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LXXXXXEXXXXXXXXXXXXLXXLXXVSGVAXXGXXVXXXGGXXXXXXXXXXXXVXXXXAX
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SPARAGGXXXXXXXXXXGXPDGRXXTDXXPXXXXXAXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXYXXXXXXXXXXXXXXXXXLXXXXXXXAXSAGXXXXXXXXX
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RSTSXXXXXXXXXXXCXXXPXXXXXXXXXXXXXPXXXXXXLXXXXXXGXTXXXXXVXXXX
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FXXLXAXXXXXXXXXAAXXXXXXXXGDXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGX
XXXXXXXXVTXXXXXXXXXXKSAXXGXXXXXXXXXXXLXXFXXXXXXXXRXXGXEHXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXRXXXXXTXXLXXXXXXXXXXXXXXXXX
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XXXRXDXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPXXXXXXXXXXXXX
XXDXXXXGXXXXXXXXXXXXXXXXXXXXXXXXRXXGALXXXXGXXXXXWXTYXCXIXXXXD
SSMQTLXXXXXXXXXXXXXXXXXXXXXTXXXXRXRXXXXESVTAPYDVFALSGLXXXXXX
XXXXXXXRXXXXXXXXXXXXXGXXXXXXQSPXXXXXXGAXGXXXXVXXXXXXXXXPXXXX
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XXRXXYXXXXXXXAXXXXXXXXXXXXXXXXXXXXXXXXGXXXXXXXXXXXXXXXXXXRX
XTRGSISVNAXFMXXXXXXXXGXXXXXXXDGDAXLXVXXXXXXXXGXEPXXXXXXXXXX
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XXXXXXXXXXXXAXXXXXXXXXYXXPFGNXLXSXDMTGXXXXXXXXXXGXXXXXXXXXGX
XXVXXXXXXXXXXEXEXGXXXGXXXXXXXEXXGXXQXXXXGXXXXXXXXXXXXXXXXGX
XXXXXXXXXXXEXXXXTAXXXXVXDXXXXXXXXXXXXXXXXXXXXXXXXGXXXTXXXXGX
XXXXGPEXXXXXVXXXXXXPXLXAPXDXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XTQXXXXXXXXXXXXXXGXXXYDHXXXXXXSXPXRXXXXXLGDRVXVXXXXQXRXRXXAG
EPXXXXXXDXXXGXXXXXXSXXXXXXXXXDXXXXXVXNXNDXPXXXXXXXXXXXAXXXXV
GXXXXXXXXXXDXDGXXXXXXXXXXXYXWXXXXXXXPLTQAGSGDTVXXXXXXXXWXXXX
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XXXXXVXXXXXXXXXXXPXXXXXSAANQKGKIQQLIEXPAXASLIKSFYDDDGMXXLXXX
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==> Mobiluncus.txt <==
>MSA Consensus of 456 seqs, protein
MKISRTLAAVSATILTTTLLSAIPAVATPALAFPTLPNRSHPAVSTAXXRXXXXXKXXXX
XXXAXXXVXGXXLAXXLXXXAGXXXXXXAXDLXXPTXXXAIXXXXXAYPGAXXXXXGXXT
QHGNPAWXXDGKRXXXXSDXXXXXXXVXDXSXXDXXGGXRVTGKVVTYRSGERXXANXXX

GXXXXXXGXXVYARXXXNLARXGAXSPXXXATTXDASTDSKTGXPXXYAIXMXXFVDXNG
EXXXFRXXPXXXDVLNDEISELGVQXXXXXXVWXXXXXXXXXXQLTXSEXXXXVXXXYXX
XKDXXXXXXXXXXXQXXXXXXXXXXKSTXVXXXXXXXXXXXXXXXXLXXXXXVXXXXYIP
LLAXXXXXXXXXXXXXXXXXXXXXXGXVXWXXXXXXXGLXXXXXSVQRSXXXXXXXXXXX
XXVDXXDXXPXXXAXXXXXPXXXXXVXXXXXXXXXIRRIMTGYKDKNXXXEXXXTXXXXX
XXXXXXXXXWXXXXXXXXXXXXXXXXETXXXXXXXXGKYXXQXRXXXXXXNMVXXXXXXX
XXXXXXGKAKNXKAAKLRXXXXXXXXXXXGXXXLERXXXXXXXWSXXXXXXXXXXXXXXX
XXXVAVXDAXXXRXXXXXXXXXXXXNXXXXXXXPXXXXXXXXXXXLDDXSFTSDXXXXXX
XLXXXXXXXXPXXXXXXXXXXXXXFXAXXXXXXXXXPXXXXXXXXXXXGXXNXDXXXXPI
DSINFKAXGXXXXXSXTXNXXXXXXXXXXXWXXXXXQXXXXXXXXXXXGXXXXWQXVGDE
XDIAQXXKDXXXXXXXWXSXXXXXXXXXXXXXXXXXXAXXKXXXXXXXXXXXXXXXXXX
XXXXXXXGXAPXAXXXXXKXXXXXXXXXXXXXDGXXXXXXXXXDXXXXXXXXXXXXXXXX
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XXXXXXXXXXXXXXXXXNXXXXXXXXXXXXXXXXXAXXXXWGDIXYXXLVXXXXXXWQG
RXXXXXXXXXXGGXXXVAXXXXXXXXXSLRDGXXGXXLXXXXXXXXXXXXGXXXXXSXP
XXXXYXXXXXXXXXXXXXSXXXXXXXXXXXXXXXXXIXXXXXXXXXXXXEXRXXXXXX
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XXXXXXXXXXXXXXXXGGPELSXXXXXNXXXXXXXXXXXXXTYXXXXXXXXXTXXXXXC
STQXXXXXXXXXXXXXXXXXGGRVXLGRXXXXXXXXXXXXXXXMXXXXKXXXXXXXKAA
XXALXAXXXXLXXXXXPAXXXXXXXXXXXXXXXXXXXXAXXXXXXXXXXAXXXXXXXXXX
XRXXGXXRXSIASGDFTNXXTXXXXAXXXXXXXXXXXXXXWXXXXXXXXVYXAGGXXXXA
NYTFSAXGXXXDATMXXXGXLXDXXXXXGPXXLXXXXXXXXXXXXXXXXKDDXCXXTPX
DXXXXXXXXXXXXXXLXXXXXXGGXXXXXXXXXXXXXXXXXXXXXXXXXXXRXXGXXRGG
NRXXTXXXIAXXXXAQAKAGXYKXXXXXXXXXXXXXFXXXXVYXXXXXGXXGXXXXDAXXX
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KGVNPKIRETQTLSEXQLDVLXAXXXXXXXXXXXXXXXXXYXXARXXXXXXXXXXXXXXXX
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XXAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPXXLXXXXXXXXXXXXXXXX
XXXXXXENHXXXAXXXXXXXXXXXKDXVXGXXXXXXXXXXXXXXXGXXXXXXXXXLTXXX
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EKXXXXXXXXXXXXXXXXPXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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XTGXXXXXXXXXXXXXXXXXXXDXXXXKXXXXXXXXXAEGNRVVFRANHXXXLAXXDXXVX
XXXXXXXXXXXXXXXGXXXXXXXXXXXXXQXXKXXXXXXXXXXXXXXXXXTXXXAXXGXXXX
XXXXXXXNAXXXXXXXXXXXXXXXXXAQXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXAXXXXXXXXXESIAXXXXXXXXXXXXXXXXXXXXTXXXXXXXXXX
XRLXGNALXDRYXTXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXSDXXXXXXXX
XDXXVAGXXXXXXXXXXGPXXLLXXXXXXXXXXXXXXXXXXXXXYXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXFQAGSKHRXXXXXXXXXXXXXXXKLSKGXXXXXXXXXXXXGGXX
XXXDXXXXXXXXXXXXXXXWLPQSCRXXXXXXXXXXXATXXXXXXXXXXXXXGXXXXX
XXXXXXXXXXXXXXXXXXXEKXXXXXXXXXXXXXXXXXXXXXXXXXXXXATXXXXXXKNXXX
XXXXXXXXXXXXXXXXXXXTXXXTXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGXXXX
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XXXXXRATKINAEVDXXPXGXXXXXKTXXXXQVXXXXXGXGXXXXXXKXXXXXXXXXXXX
XXXXXXXXXXVLTVTGTPXXXXXXRXXXKXKTAXXXXXXPXXXXXXXXXVXVXVTDXNGN
VSESXTQKTGEVXSDXAXXXTXTVEDNXXXXXPXPXXXXGPFSVNAXDXXNXXXXXLXXL

TNGSSXDXXGCSXXPSXXSXXRDLTGTEGQGIQGWTPLPKXXXXXGXKXXXXXXXXEGLPX
GXXFXXXXGXLXXNKIAXXXXXXXPIXXXXXXXNXXXXXXXXXXXVRASXXTXXXSPXXX
XXLXGXXLTSPVTVATVSGGXXXXXXXXXLXNGXXXXLDXXGXXXLTXXXXXXAGXXXX
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SGTLXXVSNDSKLEXXXXPXXXXXXXXXXXXXXXXXXXXTXXEIRXXXXDICLXXXXXXX
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IHGGTPDSQXXXXXGXXIGGEGKPTXXXXXPXXXLXGTXXXXXXXADXGXXGXFXXXXXX
VXXQXXXXXXSXEXPXXXXPXXXXXTXXDXXXPXXXPXXXXTXXXXEVXXXADGXXXGVX
XXSGXXXXTAKNKCTKQDSAVAKDIXXXXPXXEXXXCXXXXXXXXXNVXXDXXXXGIAID
KDTGTWTVSENXVPXXXXXXXXXXXXCXXXXXXXNXXXXXXXXXXXXNDXXXXXFXXXXX
XMXXXXGRXXXXXXXXXXAXVTXGXXXXXTTXXXXXXXXXVXXXXXDXXXXXXLXXVXXA
GLPEXXXVXXXXGTXXXPVXVSNGTKEVKXXXGAXXXXXXXXXXXVGXXXXXXXXXXXXX
XXTIXXXTQNSVSAERQPTNLTAXXXIXXRXFASPLQLNTKTVGTPVGMIRGAANYNSPI
GTVDYLXGTITPTTXXXXXXXXSXXXWXXXXXXXXXXXXXXXXXAXXXXXXXXXVSGHSD
GLTITAANSXXAAMPTGSQAGCDGLKAQTLTLSSAGTDAIPRGTTSLAVELXXXXGXXIV
RSAXXXXPXXXXXEXXXPXXXXXXSXXXXXXXGXQGAPYPXYYAQXXXGXXXFXXXLXEX
XXXXXTXXXXXXXXXXXXXXXXXXXXXXXXYXXXXXXXCXXXXXXNXXXXXPKCFPIPG
LGGTIPADNAWNNXXXXXXXXXXXXXXXXSXXIPVDAAXGVXTAQVLVIXGSDXXXXXXX
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TXXXXXXXXXXXXXXXXTXXXXXXXADVGDXXXXXXXXXXXXXXXXKXAXXXXDPXXIXX
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XXXXXXXXXXXXXXXXXEXXXXAEVGTTIQASEGAFGTSLVAIGDVNGDDXXDFAVGAPEA
NGSTGAVAIIXXXXQTTGTVSXDVCXASQIPVVRNGHPAGTLIRQAXXXXXXXXXXXXVXX
YXXXXXXXXXXXXXXXXXXXXVKLENKPAXNXXXXXXXXXXXXXXXNTXXXXXXXXXXXX
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EGDTLXLDKSAYRLEWKYTXXXXXXXXXXXXXXWXXXXXXXXXTTPPXXXXXXXXXXXXX
APXXQXVDEADXXXXXXXXXXGFXXXXXXXXXXXTXXGXXXLVXGXTVPYHETLKXXXKX
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PXXXXXXXKXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPXXXXXXXXXXX
PXXTXFYXXGXXXXFXXXVXXXXXDXXIXGLTVTGXXXTGSADPRSCSVTVTXXXXVXXX
XXXXXXXXXXXMXXXXXXLXXXXXXXXXXXXXXXXXXXXXKXXXXGXXXXXXXXXXXXX
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XSXXXXXXXXQTYXXXXXXXGXXXXXXXXXXXXXXXXXXXXXXXXXXWXXXXXXXXXXXX
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XAXXXAXXXXGXXXLXXXXXXXXXXXXXXXXLGXTVXXXXXXXXXXXXGGXAXXAXXXXX
AHADXXWXXXXSXXXXXXXGXDRYXTAXXLAXWSXXXXXPXXXXXXVXXGXNXXXDXLXA
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GWXMSQLGXXXXDXLXKXLXXXXXXXNHARNDDELSKMWATXXXXKKPDXAKPELDKSSA
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XYGRXVXXXXXXXXXXXXXXXXIXXXXVXXXKIEGXXVGXXGXEQMIDASGXXXXXRXXX
XXXGADYFTHPL

==> Mollusca.txt <==
>MSA Consensus of 250 seqs, protein
MKRGXXXXXXITXVLXXXXXXYGXXYGEPSGXXXIXXXRXXXXXXXFXXHSHVHGHHLLH
RHVXXHSVXHGHVHMHRVSHRIXXXXXXXXXXXXHXXRXXXXXXXXXXXXXXXXXHXXXXXX
XXLXLNDLTIXXXXXXXXXXHXXXXXXNXXHXXSXXXXXXHXXXXXXXXVHXXXXXXXXX
HXXXVLHKHXHXXXVXHXXXHXXXXXHXXXHXXXVXHXXXHXXXXXXXXXHXXXXXXXXX
HXXXVXHXXTHYNXXHXXXXXHXXXHXXXVXHXXIHXXXXXHXXXHXXXVXHXXXHXXXX
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RXXXXMNXMXXXXXXXXLLXXXVLXGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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WKAPPPXXTXXKXXXXXPXXXXXXXGXXXXXXXXXXXXXXGCXXXXXXXXXXXXXXXXXX
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XGXXXXXGXXXXXXXXXXXXXXXXXXGXXXXXPXXXXXXXXSXXXXXXNXXXXXXXXXY
XXXXXXXXXXXTNXXXXXXXXXXXXXXXXXXXXGXXXXXXPXXXXGTXXDTCASXTXX
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XXXXXXXXTAXXXXTXSXPPTXXXTTXXXXXXXXXXXXXXXXXXXXXYXSKTNYXPXX
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DXXXXXXXXXXPXXXXXXXXXPXXXXXXITXXTXXPXXXXXXXXXXXXXXXXXXXXXXP
TLXXXXXXXPXXXXLLKPXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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DCNXCXCXXXXXXXXXXXXXXXXXXXYXXXXXXRYEXXXXXXPXXXXXXXXXXXYXXXXX
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XXXPXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXTXXX
PXXXXXXXXXXXPXXXYXXXXXXXXXXYXXXXXXXXXXXXXXXXXXXXYXXXXXXXXPXXXS

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YXXXXXYXPTYXXXXXYXXXYXPXXXXXPXYXXXXXYXXSYXXXXXYXXXYXXXXXYXXX
YXXXXXYXXXYXXXIXYXXXYXXXXXYXXXYXXXXSYPPXYXXKIXXXPXXXXXISYPSX
YXXXXSYXPXYXXXXXYCXXYXXXIXXCXXYXXXXXXCXXYXXXIXXCXXYXXXIXYXTP
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YXXXIXXCXXYXXXIXXCXXYXXXIXXCXXYXXXIXXCXXYXXXIXXCXXYXXXIXXCXX
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YXXXIXXCXXYXXXIXXCXXYVCEIVYCIPYXXXIXXXXXYXCEIVYCIXXVCXXXXCKP
YVCEIVYCIPYVCEIVYCKPYVCEIVYCIPYVCEIVYCKPYVCEIDYCIPYVCEIVYCKP
YVCEIVYCTPYVFEIVYCKPYGVGLSTV

==> Multicrustacea.txt <==
>MSA Consensus of 171 seqs, protein
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CSNIXXFXXXSSLXLXXXPXXSXIXRISSLLLEYPPFARISSLXXXXXXXXXXXXXPPP
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XDIXXXPXXXXRXXXXXPXXXXTXXDXXXXXXXXXXXXEXXPXXXXXXXXXXXXXXXXXX
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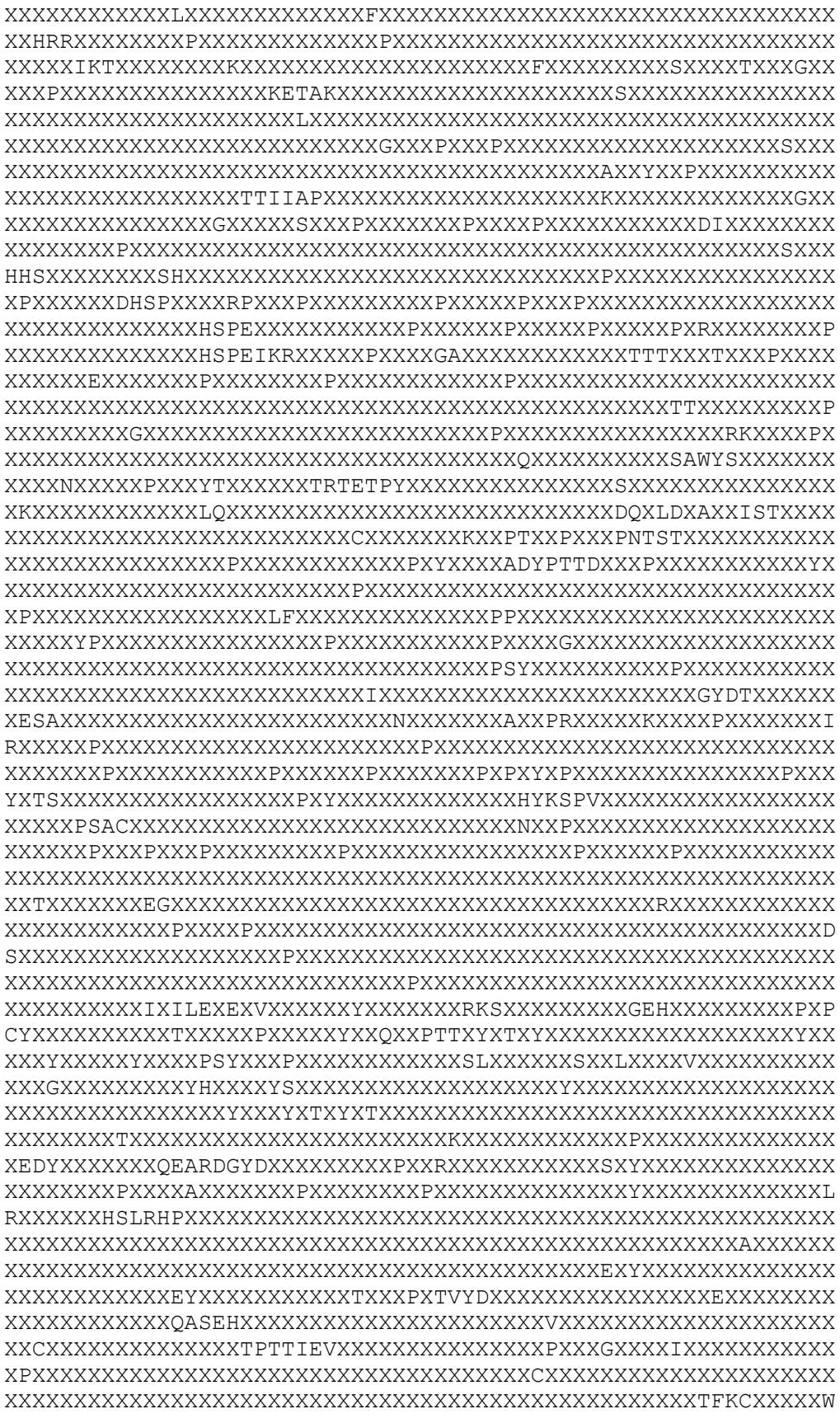

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GXXXXXXXXGXXXTIALTTTEAPTXXXXXXXLXXXXXXXXPXXXXXXXXXXXXXXXXLXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPXXXXXXXXXXXXXXXXXXXXXXXX
LNNLNYXXXVXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXEPFPDXXXXXXX
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TTTXXXXXXXXXXXXXXXPXXXXXXXPXXXXXXXXXXXXXXXXXXXXXAPXXXXXPXXXX
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EYLLKDNSW

==> Muridae.txt <==
>MSA Consensus of 360 seqs, protein
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GPQGDRGFPGTPGRPGIPGEKGAVGQPGIGFPGLPGPKGVDGLPGEIGRPGSPGRPGFNG
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==> Murinae.txt <==
>MSA Consensus of 353 seqs, protein
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XXXXXXXXLXXXXXXXXXXXXXXXXXXXXEXXXXXLVFNIXXXXXXPXGXHXGXXXXXHX
XDPXXXXXXXXXXXXXXXXXXXXXXLQKNRDTPGKLSRKSEXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXDXXXXXXXPXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXTXXXXXXXXXXXXXGXXXXXXXXXXXXXXXXXXXPXXXXXXXXXXXX
XXXXXXXXXXXXXXXXPXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXSXXXXXXXXXSPSNSXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX

GXYXXXQEDIMDASNXIDXDVSSQEDASXXXXXXXXXXXXXIXXXNXXAEHTXLPTXXPT
GXXXXXKVSRVGSXMVNAKDDEXXXXXXLAXXXTXXXXXXXXXXXXXXXXXNNWIXXXXXX
XXXXXXXXXXXXXAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPXXXXXXXXLTPXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXTTKXXXXESNTNPTGWEPNEXNXXETDKY
PSXXXXXXXXXEXXXXXXXXXXXXXEPFXXXXXXXXXXXQDWTQWKPXHXXXXXXXQXXXX
XXXXXXXXXXXXXXXWXXXXXXXXXXXXXXXXEEMXXXXXXXXDELGVVDRAQAGDXIFXX
XXXXXXXXTTXXXXXXXXEXAXGALAXXXXXWXXXXXXXXXXXXXXXDXXXXXAVKXXXE
XXXXXXXXXXXXHXSXRXXTQSXXXXXWXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXGXXXXXXXXXXLXSXXXXXXXXXDXXXXXXXXXXXXXXXXXXXXXXXXXXGXILXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXSXXXXXXXXXXXPXXXLXXXX
XXXXXXXXXXXXXXXXXXXXXGXXXXXXCXXXGXXXXXXGXXXXXXXXPLXXXAXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPXL
AXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXYXXXXXXXXXLKXGXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXPXXXXXXXXXXXXXXXXXXXXXLXXXXXXX
GXXXXXYXXXXXXXXXXXXXXXXXXXXXTXXXXXXFXXXPAKNXXXXXXXXXXXXXXX
XXXXFXXXXXXXXXXXGXXXXGXXXXXXXXXXXXXXXXXXXXXXXXXXXXPXXXXXXX
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NQDSGVTTTSGPXXXXXXQSSLTQEELMXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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XXXXRXXXXXXXSXXXXXXXXXXXLNGEAXSKSQEMVHLVNKEPXEGXXXYXXTPDQXM
XAXXXXXXXXXXXXXXXXXXXXXXXXXXXEXEXXXXXXXXXXXXXXXXXXXXXXKI
GXXXXXXXXCXEAXXXXXXXXXXXXXXXXXXXXCXXXXXGXGXXXXXXXXXXXXXXXX
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XXXXXXXSSPGPXXXSMVLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXYXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
LXXXFXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXCVXIXXXXXXX
XXXCHXXAXCXYVGPGQXXCXCKXGFXGXGXXCXPXXXXXXXXXXCHXXXXXXXXXXGXX
XCXCXXXXXXXGXGXXXXXXXXXXLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXPXXXAXXXXXXXXXXLDXXXXXFXXXXXXXXXXXXPXLXXXXXXXXXXXX
XXXXXXXXYXXXXXXXDLXXSGAXXXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXXXX
XVEQXXXXXMXXXXXXXXXXXXXXXGPXXXXLXXLXXXXXXXXXXXXXHXLXXAXXXXXX
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XXXXRXXXXXXXXXGXXXXXXXXXXXXXXXGXXXXXDDXXXXXXXXXXXXXXXXXXXXX
PXXLXXXXXVLXPXXXXXXXXXXXXXXXXXXGXXXXXPXLLXXLXXXXXXXILXXPXXXX
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XXXXXXXXXXXSNLXXXXXXXXXYXXXXXXXXXXXXXXXXXXXXXXXGEXXXXXXXXXH
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXPXPXXXXXXXXXXXEXPXXXXXXXXXXXXXX
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XXXXXXXXXXXXXXXXXXXXXXXXXXXIXXXXXXXXXQXXXXXXXXXXXXXXXCXXCXX
XXXXXXXXXAXXVXRSMXXXXXXSPXIXXXXXXXXXXXXXXXXXXXXXXXXPTTDLXXX
RXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXXXXXXXSXXXXXXYXXYXXXX
XSXXXXXXXXXXXXXXXXXCXXXXXXPXXXXXXXXXXXXXXXCXXCPGXNSVXXXXXXV
CXXXGXXXXXXXXXXXXXXXXXXXXXXXPXXXCXXXXXXXXXXXXXXXXXXXXXXXXX
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XNNGGCSXXXXCXXXXXXXXXXCXXXXXXXLETXXXXXGXGXXXXXXXXXXLXXNXXXSQ
XFFXLXXXXXXEXXGXGPFTXXXXGXXXXXXXXXPXXDXXXXXXXXXXXXXXXXXXXXX
XRYHVVXCXXLXXXXXXXXXXXTXLXGXXXXXSXXXXXXXXXXXXXXXXXXXXXXXXXX

XXXXXXXXXXXXGXXXXXXXLPLPLSSXXXXXXXXXXXXXXGXXXXXXXXXXXXXXXXXX
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XXNXTXXAXXXGYXXGGXXXXXPXXXXALDRLCAHRXVXXXXXXXXXXXXXXXXXXXXXX
XKXQAXXGXXXFSXLXXXXGLLXXXXXXXXXXXXXXXXXDXXLXALPXXXXXXLXXXDXX
DKLXXXLXXXXXRXXXXAQCIEEXXXXXXXXXXXXXXXXXXXXXGXXXXXXXXXXXXXXX
XCXXXXXXXXXXXXXXCXXXXXXGXLXXXXXXXRIXQRXLXFXXXGXXVXXXXXXLXXXX
XXGXXXDXFXXXXXXMXXXXXCXXXPXCPXXSXXXGXXXXXXCXXXXXXXXXXXXXSXXX
RXPXXREXXXXXXXXRSXXXXXXXXGXXXXCWXXXXXXXXXXPXCCXGXXXXXCXACPGG
PXXPCXXXGXCXXXXDXXXXXGXXXCXXGXXXXQXXLWXVAWXETDXXXXGXACXXXXXX
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GNCXXXXXXXXXXPVCDXXXXXXXXXXXXXXXXXRGGXXXXXCXXXXXXXXXXXXXDGX
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XPXQXXXXXXGXGXXCXXXXXCXXXXXGXXXXXAXCXXXGXXXXXXXCXXXLXXXNVTLX
XYXXXXXXXXXEXXXXXXXXXXXXXXXXXXPXXXCXXXXXXXXXDAXXXXLHFXDXXXX
VFXXXXXXGXYXXTFXXAXXACXXXXXXXAXXXXXXXXXXXXXXXCXXGWXXXGXXXXPX
XXXXXXCXXXXXXXXXVGXXXXGXXQXXXXXXXXXXXXXXXXPXXXXXXXXXXXXNXXXD
DDLLXXXXXXXXXXXXXXXXXXXRXNXXXXXXXXCXXXNLPGRVXXEKLPQPVFFLXXXX
XXXXXGXXXXXXXXXXXXXXXXXXXXGXXXXXWXXXXLXXXSTQCHXXXPXXXXXXXXF
XXXXLXXXXXXXXGXXFXXXLXDXXXXXTLXXXXNXGXXXXXXXXGXSCXXXXXXXXXX
XXYXXXXXGTXLXXXXGXXLXIXXXXXXXXXXXXLXXXXXXXXXXXXWDIXAXNGXXXXX
XXXXXXXXXXXXXXXISEKYXXXXXXXXXFXXYCXXXXXXXXXXXXXXXXWXXXXXXXX
XXWXXXXXXEXXXXXGXXXXXXXXRXSYQCIDXXXXXXXXXPLXXXXXXXAWXPXXXPX
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XXXXXXPSXXXXGCXXGXXPXLPXXXSRXXXXXDXTXGXXXXXXXXPNNKVHPSST

==> Muroidea.txt <==
>MSA Consensus of 460 seqs, protein
MXXXXXXXXLXXXXXXXXXXXXXGXXXRXXXXXPPTXXTLXXLXXXXXXAXXXXXXXXCS
GRWLQTLGPSLRIPADATALDLSHNLLQTLDIGLLVNLSALVELDLSXXRXXXXXEGVFA
NLFNLSEINLSGNPFECNCGLAWLPRWAKEHQVHVVQSEATTCRGPIPLAGQPLLSIPLL
DNACXXEYVACLPDNSSGAXXXXXFXFXXXGXXXXXXCSAFCFSAGEGLAALSEQXQXXX
GAGQASNSSAACSSWCSSISLSLNSACGXXXXLXXTFMAAGGAXLXXPXXPLXXXXXXXF
HXXXXXPXXITTDXXXXQYELRELYVXXGXXXPEXXXXXXXXXXXXXLPGSXXXXXXXAX
XXXXXLXETEVQVEATXXVXXLXCPSFVHSNESLELGIRHRGGSALEVTYSILALXXXXX
QVVXXLTGXCXXXXHIGYKVYEEIXXXXXGXXXXLDKKQVXEXXXWXXXXXQXXTWAGAA
LAMVDSPXXXXXXXXXXXXXXXXWXXXXSXXXXEGXDPXXXXXSLESCXXXLXGEPXPXX
XIRXXXXXXXXXGXXXXXLLCXAXXXYXXXXRXXXXXXXXXXXXXSXXHGXXIXXXSTID
FRAGFSXXXXXQXXXXXXGPXXXXXXXVXPGLSPSREAFLTAAEXXTXXXXXPAXVXRLX
XXXXSGGXXXXXXGXSXXXNRXXXXXXCXXEXXFXXLHXXXPXXXXCXXFXXXXXXHVCI
NGSVXXXXXXRXXYXXXXXXFFXXPXEAFFLKVTGXXXXXYXXXXVXSVSFSSIVXXXPK
PXXXXXXLXXQXXXXPXXXGXXATXXXKXXXXXXXXXXCXFTLSFMRDGIALXQXXYXXE
XAXXXWXXXLPXXLEEAWAGPVCSLQLLLVTERLTPLXXXGXXXGXXXXGXXXXXXXXXX
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XXXXXXXXDXXXQXLXLCXXXCPXXXXXXXXXXXXEEANGXLFXXLXLXXXKXGDXGEXXX
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XVXXXXXXXGXXXXXXPINXXXPXXXXXXXXXXXXXXCXAXXXXXXXXXXXXXXXGXXXXX
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XGXXAXXXCXXXXFQXXXXXXXXXXWXXLAACRCNXXXXXXXXRXFSXXXXXMXXPXXLX
XLXXXXXXXXXLXXXXXXNXXXXXXXXXXXXXKRCXXXPFXXEERXXXDXXXXXXXXXXCX
XXXAXXXXXCPXGXXXXXXXWXXNXFPXXXXXDXRYXVXXXXXXXXXXXXXXXTSQXXXXX

XYXCXXXXXXXXXXXXXTXXXFSXXXXXXXXXXXTTKPYPXXXXXXXXXXXTXXGXXVT
LXXXXXXXXXXXXXXRXXXXPMPSTXXXXTXGAXXXXXXXNXQXXDEGLYECEAENIRGK
DKHXXXXXVXXXXXXXXXXXXVNTPNIVXPXXVVXXXXXXEVXXXXXXNCPPDIGSDLYX
PCXXXXXXXPXXXWLXXXXXXXXXVXXXXXXTXXXXXXXXXXXXXSXDXGXTTXXXXXGX
XXXXXXXXXXXXXXXXXXXXXXXXXTXXXXXXXXXKXXXXXGXXVXIXXXXXXXXXXXXS
XXXXXXXLXNXXXXQEVQVQXXXXXXXXXLXIXXXXXXXXXXXXXXXXXXXXXAXXXXXX
XXXXXXXXXXXXIXXXGXTPFQXVXXXEXXXLXCXXXXXPXXXXXXXWXXXXXXXXXXYR
LVLMDKGAIVQDTNVDRRDTSYAFHELTPGHLYNLTIVTMASGLQNSRWKLVRXXXXXVS
XLXXXXXXXXXXXXSXXXXXXGXXXXXXXXXSHQGTIKESKXXXPPXXXXQFKXXXXXRX
XXXXXXXXXXXXXVXXXXXXXSVLXXVXXXXLXXXXXXXXXXXXIXXXXXXXIXXXXXXX
XXXXXSXVXXVXXGXXXXXXXXXXXXXXXXYXXXXXXXXXXQXXXXXXVXXXXSXLGASS
PSEXXXXXXXXXXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXLXXXXXXXXXXEPYLRTAHGXXXCXXXXXXXXXXXXVTSXXXXXXXXXXXX
XGXXXXXXXAXDXXXXXXXXXXXXXXXXXXXWXXXXXXXXXXXXPXXXXXXXXXXXXX
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SGRXXXXXXXXXDAKTDPPIIXXXXXXXXXXXXXPXXXXXXXXXXXXCXAXXXXXXVXXX
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XGSXSXXXXXXXXXHVXXXXXXXXXXXXXGRYSISXXXAXXXCXXXXXXXXXXXXXCXAFN
STLPTXXPXXYXXXEXXXTTFXMXQMXXALXSKPEGXXXXXXXXXXLXXXXXXXXXXXXX
ATXXXXXXXXXXXXXXXXXGXXXCRYXXXXXGXXXXXXXXXXXXXXXXXXXXXEXPXXXX
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KLKDXXXXXXXLXXXXXXXXXXXXXXXXGXXXXXDRXXNXTXXXXENXTXXXXXPXXXX
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RNXXXLXXXXXXXXXXXXIXXXXXXXGXXXXXXTXXXXXXXXXXXXXXDXXXXXXXTX
XXXWXXXXWXXXXXRETCQXXXXRPXXXXQXXXXXXXXXXXXXXXRXIXXXPXXXXXXXX
FXXXCXYXXXXXXLXXXXXXXXXCEXXEXPXPLXXXXXXXXXXXXXXXXXXXXXXXXXX
XCAXYCXXXXXXXXXXXXXXXXGXXGXXXXXXXXXEXXXXXXXXXXXXXXSXXXXXPXX
GXGXEVLSARVCXDXXXXXXXXXXXXTKYVMQXXXXXXXXXXDXXPXXXGXXXXEXCX
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XRCXXXXXXXXXXXXXXXXXXXXXXXXYCHNSSDTWXNSCXVWKAVGYXLXXXXDMXXXX
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GCXXXCXXXIXXXXXXXXXXXXXXXXXXXXXXXXXXEXXXXXXXXXIXXXXXXXXXXXXX
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TXXXXXXXXXXXXXXGXXEIXXXXXDXXXXXPVLXXXXXXXXXXXXRXXXXXXXXXXXXX
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ILCXXXXXXXXXXXXXXXXXXXXWXXXXXXXXGCXXXCXXXXXXPXCCXXXXXXDCQAC
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PXHCTNGSVVYHXXXDXXXCXXXXXXXXXXXXGXXXXXXCXCXXXXXXXXXXXXXXXXXE
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XXRLSHXXXXXYXSXXXXCEXXDLSVKLGPYALEYAFXGILFGXLGALLLLXILXXXXXX
XXXXXXXXXXXXXXXXXPXXXXXLXXXXXKGVVYTTRPIYDXTYAGGRLGLFVXXXDSEL
EYQTTEMVXFSDXKYECRDS

==> Mus.txt <==
>MSA Consensus of 248 seqs, protein
MIAQEVVHTVFLVALFRSSLAGDGTPQSESRAEEIPEGASTLAFVFDVTGSMYDDLVQVI
EGASKILETSLKRPKRPLYNFALVPFHDPEIGPVTITTDPKKFQYELRELYVQGGGDCPE
MSIGAIKIALEISLPGSFIYVFTDARSKDYRLTHEVLQLIQQKQSQVVFVLTGDCDDRNH
IGYKVYEEIASTSSGQVFHLDKKQVNEVLKWVEEAVQASKVHLLSTDHLEHAVNTWKIPF
DPSLKEVTVSLSGPSPVIEIRNPFGKLIKKGFGLNELLNIHNSAKVMIFLATLPLFWIMI
SASRGGHWGRITGLSTIDFRAGFSRKPTLDFKKTMSRPVQGIPTYVLLNTSGAWMPSTID
RLELLSAFEGTCVSIPCRFDFPDELRPAVVHGVWYFNSPYPKNYPPFLKVTGYDKDGVVF
KSRTQVVHESFVPDAPKVQGRSRLLGDYLQLGLRNCTVESFLPFTLLLSTLSPELGGKYY
FRGDLSVNWDFTKVTLSDEGGYNQYTFSSAGTGSEHSVLDIVNTPNIXXXPXXVAVTPXX
EVEXXXXXXXXCPELXXXXXWXXXXGLGEPTVLGRLREDEGTWVQVSLLHFVPTREANGH
RLGCQAAFPNTTLQXXGXXXXDXXXGPXFEEXPXXXXXXXXVXAIXXXXVSLXCXAXXXP
XPXXXWXXXXXXXXXXXXXRYXXXXXXXXXXXXXXXXXXGVYXCLAXNXYGXXXXTXXTL

SXXYXXXFXPXXXXXVXXXEGXXXXXLCXXXXXXXXXXLXXRWXXXXXXXXITMDXRXFLV
XXXXXXXLXXXXVXXXDXGXYXCXAXXXYGXXXXXXXLSXXFXPXIXXXXXTTKXXXXXI
XXXXXXDXXXXXXXXVXXXCXXXXNPXPXXXXXXXXXXXXXTXEXEREFVYSXXXXXLXX
XXXTIRGQXXXXXXXXCXXXNXXGXXXXXXXXXXXXXXXXWXXXIXXXXAVVXXXXXXXXX
CYIXXGKPIPXXRXXKNXXXXSSXXXXSXXDNXXXLXXXXXXXXXAXDXYXXXXXXXXGX
IYAXAEXXXXXXXXXXXXTXXXXXXXXXXXXXXGXRXIXXCXXXXXPXXXXSXSXXXXGX
XXXXXSXXXXXXXDGSLXIXNIXXXDXGXYTCFAEXXXXXAXXXXXLXXXXXTXIMSTVS
TPXXXXXXXXXXXXXXQXSXKXXXXXXIXXXXXXXXXXXXXXXPXXDLXXXWXXXXXXXX
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LXVXXXXXXXXGXXXXXXXXXXXXHXXKXNTTSXXQXXPXXSXLXNXXXXXXXXXXXXHX
EGPXGXXXXXXSVXXDXXXXXXAXXXXXGXXXXXXAPRSXXXXXXXXXXXXSXXXXXXGX
XXPGTXXDDXXXAPPXXXXCNXADXXXXXXQLGPXXXXQXXXXXXXXXGXXXXAKXXXLX
PXXXXXXXXVATNTLGTGXXXXPXXXXXXXXXXXXXXXXXGSPGLPGLRSXXXXXXXXXG
GGXXXXXXXXXXPXSREYXXXXXFXTXXANXAAEAVLXXXXXXXXXXXXXXXXXXXXXXS
TAPLNTQXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
TTNTKXXXXPPXXXXXXXXGXEXSLXXXXXSXXXXXXXXXXXGTXPNXXXXXXXXXPXXX
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XXXXXXXXPGXQMXRXPGFXGMXXXXXXXXXXXXXPXXXXXXLLSSXXXXXXXXXXXSX
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PXXXXXXXXXXXXXXXXPXGXXXXXXXXXXXXXXEXXXGXXXLXXXXXXXXPGXXXXNMX
VNXNXNMXXXXQXXPQXXXXXXXXXXGXXXXXXXXDFQKMKXXXSXXMEXXXXXXXXXSXXX
LXXXXXXXXXXXXXXXXXXXXXXGXXXXXXXXXXXGPXSXXXXXXXXGPQXXXXXXXXXX
XLXXXXXXXXXXGXXGGQGPXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPMGTVGTXXXSX
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GXVXXXXXXXXXXXNSSXAXXXXXXXXXXXXXXXXXXXXXXXXXXXXSXXXXXXXXXXXX
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==> Myomorpha.txt <==
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==> Mytilinae.txt <==
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YSGPTCGENVCKPNPCQNRGRCYPXNSXDGXXCXCVGGYXGPXCXXXXCXPNPCQNKGRC
YPDXSXDGFXCXCXXGXXXXXCXXXXXXCXXXXXXNGXXXXXXGXXYXXXXAXGXRGRHC
TXKAYKXXPCVVSKPCKNRGKCIWNGKXYRCKXAYXYGXXHXPVKSYKPVKTSXXPCKNX
GXXXXKXXXYXXXCXKXXXXYXPTNSYPPTYGSKTNYLPIYKPLAKKLSSYKPIKTTYNA
YKAKTNYPPVYKPKMTYPPTYKPKPSYPPTYKXKPSYPPSYKPKTTYPPTYKPKIXYPPT
YKXKXSYPSXYKPKKTYPPTYKPKXTYPPTYKPKPSYPPTYKPKPXYPPXYKXKXSYPXX
YKXKXXYPXXYKXKXXYPPTYKXKXSYPPTYKXKPXYPPXYKXKXTYPSTYKXKPXYPPT
YKAKPTYKXKXXYPPTYKAKPSYPXXYKAKPSYPPTYKAKXXYXXKPTYKAKPXYKXKPS
YPPTYKAKPSYPPTYKAKPSYPPTYKAKXSYPPTYKAKPTYKAKPXYPPTYKAKPSYPPX
YKXKPTYKAKXTYPXTYKXKXSYPPTYKAKPSYPPXYKAKPTYKXKXXYPPTYKXKXSYX
PTYKXKPSYPPTYKAKPTYKAKPTYPSTYKXKXXYPPXYKXKPSYPPTYKAKPTYKXKXT
YPXTYKXKPXYPXXYKXKPSYPPXYKXKXSYPXXYKXKKTYPPTYKPKXTYPPTYKPKPS
YPPXYKXKXXYPPTYKXKXXYPPTYKXKXSYPXTYKXKXXYXXTYKXKPSYPXXYKXKPS
YPPXYKXKXSYPTAYKXKXXYPXTYKXKXXYPPTYKXKPSYPPXYXXKXXYPXTYKXKXX
YPXXYKXKXSYPPTYKPKXSYPPTYKAKPSYPPTYKXKXSYPPTYKXKPTYKAKPXXPXX
YKXKXSYPPTYKAKXSYPPTYKAKPSYPPTYKAKPXYXAKPTYPSTYKAXXTYKAKPXYP
PTYKAKPSYPPTYKPKPSYPPTYKSKSSYPSSYKPKKTYPPTYKPKLTYPPXYKPKPSYP
PXYKPKIXYPXTYKXKXXYPPTYKXKXSYPPXYXKKISYPSXYKAKTSYPPAYKPTNRY

==> Myxococcaceae.txt <==
>MSA Consensus of 109 seqs, protein
MRSSPRLLLAALGAVLLLGSACXSDXXEVXNXXVCGDGKKEGAEQCDDGNTXGGDGCEAN
CTXTPTTPGXKCGDGVKXXXEACDDGNTXXGDGCEADCTXTPXXXXQCWATPPAPLANGA
TCXVTKXGTAGXLFTGIVLKDGXTLXGGQVLVDAQGVITCXXCDCSKAAGAAEATXVTCP
TGVISPGLINPHDHITYPXXPLAAASTSXERYEHRHDWRTGXNXHTXLXNXXNXKXXXXX
XXXXXQXXXXXXXXAXXGXXXXXLXXXXXXXXAGXXXXXEXLXXXPXADSDTFPLGDSXX
GXXLTDGCSYSSFPSSXTITXRXSAYLXXXXXXXXXTAXXXFRXXXXXXYXXXXXLXXGX
XXXXHGVGLTXXXXXXXXXXXXXXXWXPRSNIYVFADADFNSYDKSLYGDTAXVXXXXXX
GXXXXLXTXWXXXXXXXXXXXXXGGXTAREXXCXXXLNXTRYXXXXXXXXXXXXXXXEXX
WXXXXXNAXDXXXXXXXRXEYXRXGRIAPGYQATAXXXXXXXXIXXXXXXXXXTPXXXXR
XXXXXXXXXXXXXLXXXLXVGXPXGXAXXXXXXXXXXGXXXXXXXXVXXXXGXXXXGXXX
GXXAPPAANLTYCYXXXPXXXXXXXXXRXXXXXXXXXXXXXXXXXXXXXXXXXSXXGXX
LXXXXXXXXXXXMTXXRXAXXLXLGAXLXXXXXLXPXXXXAQXPNXNPDNPECLGDXCGX
PXXTXXXXXEXGGXGCGCGXXXXXXXXXXDXXXXXXAXXXPXRXPGESSXXCXXGXNAA
AXXXXXXXXXLXXXXDADGDGEARXXXDXXXGXDXCPXXXNXXXXXXXGXXXXXXDGDX
XXXXCDXCXXXXXXXXXXDGDGXGDXXXXDXDXDGXXXXXDNCPXXXNXPLVPNQXQXD
XDXDGXGDXCDXDDDXDGXXDXXDXCPXXXXPXXXXXPFXXDXXXCRVDADXDNXSDXXD
NCPGXXNPDQGWDGXDXDXDGXXXXXXXDXDXDXVXXXXDNCXXVXGXPXLRNXXQXDXD
XDGXGDACDXXXCXXXXXXXXEXNXXCXXXXXPFXVXXGGXXXLXERIXXXXXGXXXXXX
XXPXLXXXXXVXXXXXXXXXXXXNRNGXAAAXEYXWXVXKRPXGSXXVVENPXGAVTXSR
XWXYXYVDGSVPXFXPDKXGXYXLXXXXXLAFADRVFPXXXXXXXXLXXXVGXXXXXXLX
XXXGXRGXPXXXGXXXXXXXXXXSXPGXPXXVXXAITXXXXXGXXXXALXAXXXGXLXRR
IAEYXPXEXXXVPXTGXXTXXXRXXNXRXXXXXXXXXXXXXXXPXXXXXNCVMVAXPXXV
RXDGDSQGDACDVDDDNDTVSDTAAXXGLMVDDQXXXYXXQVLGXEYXXDDDLRGVLTFX
FXXHKLXPRSAADMVIPLPPLPALTXFXSGGFXRVGXXXXAXPQPXTVTMANHGAYPVDV
TVXIXSSXXAALSAXXGQVVIPAGQTSAXVXLXAXAXAEPGXAXVTLTATLGTSSQXXXL
RVLGXXEXXXXTXLTPXTXXVAPGGTXRFTVTFDRPVPXGTTLXXXVXPXGFGTXTAXXV
TRXDALTATFDLTVDEASTGXGTVXXXXLXATVNVITDVPRLXSLTPSTATVNAGAXQVF
TVTLXXXPXXPVQVLLALAXPAAATPFGALSATSVTVXAGXTTATVTFTAAAXGEGTGXV
SASLNGITRXAXLTVLPPPAKLASVTPXXVXVTXGXTQTFTVTLDRKAPXGGAAVDVAFX
PAELGSLXASTVTVXEGQTTATVVFTAXXXTGXGQLTAXYXAQGVTKQAKXVTVAXXQGH
VVISEXXGXGXXXXXDXXIELYNPTXXXVXXXGWKLXYRXAXXTSXXXXXXXXXXXXXAX
IKAHGYYLVXXXXYXXXTPXVXXDXXWGXXXXXSXSRXXXGXVRLGXAXXXXXXXXXXXX

VDTXGXGXGXXXXXGXAAPXXXXXGGSXERKARAXSTXATMXXGGXDELAGNGQDXDXNA
ADFXXRTXRXPQNXXSPXEXP

==> Myxococcales.txt <==
>MSA Consensus of 252 seqs, protein
MXXWSMXGXXGXXXXXXXXXXXXXXXXXXAXXXAXGXXXXXXXXXAAXCXXXXTGGRFP
AXAXXVLXXXXXVTVTXXXXXAXXXXXXSTTSAXXXPXXXXXXXXXGXXGXXXXXXXXA
XLPXXGXXWXPXXXXXGXFXXRVREXGXTYYXGXGXXXXXAXXYXRXGGXSFWXXXXXGS
SXXEEWLLXXXXXXXXXXXXXXXXXXXXWXXXGAXXRXRGXXXXXXDXXGXXRXXVTAPX
AFXXXGXXXXXXXLXXXXTALVVVPADDXDTDGDGIXDYVDXXXXXXXAXXXXXXXXXXX
XXXXIXXXDXSTQSCSGRALXDXXWXXXXXGXXXSXGXXXXXXXXHTXXXLXXXXGXVXV
XGGXXXXXXXXXXXSXEXYDPXXXXWXXXXXXXXXXXXXXXXXXLXXGXRVLVXGGXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGXVLXXXGXXXXXXXXXX
XXXXXXXXXXXXXXXLVLXXXXXXXXXXXXXXXXDGXXGXXXXGGXGXXXXCTLXXXXPG
XXCGXGXXXGXYXXXXXXXXXXXXXXXXXXXXXXGXXXXCXXXXXXXXXGXXFXXXXXXXX
XSXELVRXXPXNPQLFXVYXWXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXRXXXXXXID
NLRXXXXXXXXXXXXXXXPXIXXGXXXXXXXXXXXXXXMXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXVNVXXXGXXXXGXEEQEAXXXPFAXXXXXXAXXX
XXXGXXXXXXXGXXXXXXXDCXXXXXXAXXXXXXXCPXXXXXXXXXMXXXRXXHXAXLXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXWXXXXXXHTXXXXXXXXXXXXXXXXXLRXXXXX
XRXXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXXXXXXXXGXXCXXXXDCXXXXGLGXXX
XXXXXXXXXXGXXCXXXXXXXXXXXXSXAXXXXXXXXXXXXXXXXXXGXXXXXXGXXXXXXX
XXXXCXXXXXXXXXXXXXXXXXXXXXXXGSYNXXXXXXXXXXDXNVGSXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGAXXXXXXEXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXTNAIXHXTXXXXXAXXXXXXXXXXXXXXXXXXXX
XXXXXVXXXXXXXPXXXXLXXSSDXXXXXXXXGXXAXVTXXXXXXXXXSXTXCXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGXXX
XXXXXPXXXXAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
NAAXXXXXXXXXXXXXXXGXXATXLXXXPXVXXXXXXXPXXXXXYVGAPEXXXXXXXXXX
XXXXXXXXXXXXXXXGNXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGXXXXXX
XXXXXXXXGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXEXXXXXXXXXXXXTXXDXX
XXXXXXXXXXXDLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXFXXXXXXXXXXXCXXGX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXE
XXXXDQXXXXXRXXXXXXXXXSTXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXRVXXDXXXXXXXXXXXXXXPXXLXXSXXXXXXGXXXRXXXXPXXX
XCXXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXPGXXXXXXXXXXDXXXXXXXXXXXXXXXXXXXPXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXLXLGAFXXXXPXXXXXXXPXXXXXXXXCXGXXCGXPXX
XXGXXCXXXXXXXXXXXXSXXXXXXXXCGXXXXXXXDXXXXXXXXXXXXXXXXXXXXXXX
DXDGDGXXDXXDXCPXXXNXXRPXDFPLXGXQXEDTXDAGLPAXDGXXXXLCDXCXXXXX
XXXXDXDGDGXGDXCDXDXDXDGXXXXXXXPXXGXXCXXXXXXXXXDXCPXXXXXPLVPN
QXPXXXXXXXXXXXXXVRNCPXQXDXDXDTXXXXXDPAXGXGDGTLXXXXTTXXXCDXXX
XXXXXXXXXXXGCPXXDXDXDGXXXDXXDXCPXXXXXXQXXXXXXXXXGXXCXXXXXXXX
XXXXXXXXXXXXXXXXXXXDXDXDXXXXXXXXXDXCPXXXXXXXVTTPFXXCXXXSGXXX
TVDVXXXXXXXXXXXXXXXXXXQXDXDXDGXXGDXCDXXYXPXXXXXXXXXCPQPXXXXC
XXXXCXXTPXXGXNXDQXXXXXXCXXXDXDXDXCPNPVDEGAGCPDKXXXXGPDGKXXDX
CXXXXXXXQXXXXXXXXXDXDXDXXGXXCXXXXXXXXXXXXXXXCXDXXXXXXXXXGGXX
XXXXGESXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXDXXGXPGXDXDXDGX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXGXXXXGXXXXXXXGAEPXXXXXXXXXXXXXX
XXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXXXGXXXXXGXXXXXXXXXXXXDAXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXHXXPXGAVXXXXXXXXSRXWXYXXXXXXXXXXXXX
XXRXXXXXXXXXXXXVXXXXXXAXXXXXXRXXXXPXXXXXXXXXXRXXXXXXXXXXXXXX
VGXXXXXGXXCXXXAXXXAPXXXXXXXXXXXXXXXXXXXXXXXXXXXAISGVAXXGXNXLX

XXXXXXXGXXXXGXXXXXXXXXXXXXXTXXXSLTFXXRXXXXXXXXXXXXXXXPXXXXGXXX
XXXXXXXXXXXXQXXXXXXXXXXPXXAXXXXXXXXGDACDXXXXXXDXDXDXXXDXXXXX
XXXXXGXXXXALGAXXLXXLXRRRXXXXLGDDAGGXSXYXXXGXXXGXXXQDGLXXXXDX
XXXXXXXXXXXXXXXIPXXAXPVGRNGPADLSSVRRIXXXXXXXXXXXXXXXXXXXISYL
PTXXXSPXXVPGLXXXXXXXXXXXGXXAXAXEXXXQXXXXKXGPXDXXGXXXXXXDDXDX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXDEXXXXXXPXXXXGXXXXDXXXXXXXXG
LXXXXEAXXLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXDXXXXTDXXXXIDAXDPDSD
XDGXXDXXEAGDXXLXTXXXDTDGDXXPXYRXXDXDXDGXXDXXDNCXXXXXXPXXPGEX
QXXXDXXXXGXXCXGXXXXXXXXDGVXDDANKNGVKDPXXDNCXXXXXXXXTVXXXXXXX
XGEPQXDXDXXXXXXXXXXXXXXXRSNHXDGXXXXDXDXCXXXXXXXXXXXXXGXXXAXX
XXXXXXXXCXXCVGPGXXXXXLTATXXXXXXXXXXXLXXXXXXXXXXLTPXTYLXXVAP
GGTXRFTVTFDRPXXXGXXLXXXXXPXGFXXXTAXXVXXXDXXXDDAXDNXXXXXNXXQG
LETXDXXXXGXGXXXXXXLXAXXNXXTDVPRLXTQDPEDXLTPSTATVNAGAXQXXTLGD
ACDXDXXXDXDXDGXXDXXXXXCPXXXNXXQXDXDXDXXGDXCXXXXXXXXXXXXVQXPV
QVLLALXXXXXDXXXXXXGXXXXXXXXXGXXXXXAXXXXXXXXXGEGXGXXXXXGXGXXD
XXXGXXXXXXXXXXPXXXXXXXXXXGXXCXXXXXXXXRGXGXXXXXXXXXXXXXXXXXXX
XRXXXXXGAAVDVAFXPAELGSLXASTVTVXEGQTTATVVFTXXXXXGXGXLTAXYXXQG
VTKXAXXXXVXXXXGHVVISEXXGXGXXXXXDXXIELYNPTXXXVXXXGWKLXYRLPEPA
EXXXXXXXXXXXXXXXXXXXXXXXXXXAHGYXLVXXXXYXXXXXXVXXDXXWGXXXXXSXS
RXXXGXVRLGXAXXXXXXXXXXXXVDTVGYGXGXXXXXALDALAAVGAEGXAAPXXXXXG
GSXERKARAXSTXATMXXGGXDELAGNGQDXDXNAADFXXRTXRXPQNXXSPXEXP

==> Neognathae.txt <==
>MSA Consensus of 793 seqs, protein
MLCWNEVQSCFLLAFLAVAAYSVSDAQGQVSPPTRLRYNVVNPDSVQISWKAPKGQFSGY
KLLVTPSSGGKTNQLILQNTATKAIIQGLIPDQNYALQIIAFSDDKESKPAQGQFRIKDI
ERRKETSKSKVKDPEKTNASKPTPEGNLFTCKTPAIADIVILVDGSWSIGRFNFRLVRLF
LENLVSAFNVGSEKTRVGLAQYSGDPRIEWHLNAYGTKDAVLDAVRNLPYKGGNTLTGLA
LTYILENSFKPEAGARPGVSKIGILITDGKSQDDVIPPAKNLRDAGIELFAIGVKNADIN
ELKEIASEPDSTHVYNVADFNFMNSIVEGLTRTVCSRVEEQEKEIKGTIAASLGAPTDLV
TSDITARGFRVSWTHSPGKVEKYRVVYYPTRGGQPEEVVVDGSSSTAVLKNLMSLTEYQI
AVFAIYSNAASEGLRGTETTLALPMASDLKLYDVSHSSMRAKWNGVAGATGYMILYAPLT
EGLAADEKEIKIGEASTELELDGLLPNTEYTVTVYAMFGEEASDPLTGQETTLPLSPPSN
LKFSDVGHNSAKLTWDPASKNVKGYRIMYVKTDGTETNEVEVGPVSTHTLKSLTALTEYT
VAIFSLYDEGQSEPLTGSFTTRKVPPPQHLEVDEASTDSFRVSWKPTSSDIAFYRLAWIP
LDGGESEEVVLSGDADSYVIEGLLPNTEYEVSLLAVFDDETESEVVAVLGATIVGTTAIP
TTVTTTTTTTATTPKPTIAVFRTGVRNLVIDDETTSSLRVVWDISDHNAQQFRVTYLTAK
GDRAEEAIMVPGRQNTLLLQPLLPDTEYKVTITPIYADGEGVSVSAPGKTLPLSAPRNLR
VSDEWYNRLRISWDAPPSPTMGYRIVYKSINVPGPALETFVGDDINTILILNLFSGTEYS
VKVFASYSTGFSDALTGVAKTLYLGVTNLDTYQVRMTSLCAQWQLHRHATAYRVVIESLV
DGKKQEVNLGGGVPRHCFFELMPGTEYKISVHAQLQEIEGPAVSIMETTLPFPTQPPTSP
STTLPPPTIPPAKEVCKAAKADLVFLVDGSWSIGDDNFNKIISFLYSTVGALDKIGPDGT
QVAIIQFSDDPRTEFKLNAYKTKETLLEAIQQIAYKGGNTKTGKAIKHAREVLFTGEAGM
RKGIPKVLVVITDGRSQDDVNKVSREMQLDGFSFFAIGVADADYSELVNIGSKPSERHVF
FVDDFDAFTKIEDELITFVCETASATCPLVFKDGDKLAGFKMMEMFGLVEKEFSAIDGVS
MEPGTFNVYPCYRLHKDALVSQPTKYLHPEGLPSDYTITFLFRILPDTPQEPXALXXXLN
EQYEPLVGVIXXXXXXXLXFFXXXXKGXXQXXXXXXXXXRKXXXXXXHKXXXXXKPXXXT
XXXXKSTKASAEXXXXXXXEXXXXXXXNXXXGXXXXXXGWXXXXXXPRXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXPXXXXXXXXXXPXXXXXPRXXXXPXXXXGEXXXXGXXSQ
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXMKMXXXXXXXFFLA
XXAGGXXEKAGGAQMGXXXXPMGXXXXXXXPGPXGXPGXXXXXXXPGEPGEPGAAGPMGP
RGPXXXXXXPTXXCXXGKPGKSGERGPPGPQGARGFPXXXXXXXXKXCXXKXXXXGXKGE
AGAPGAKGXTXCXXCXXXXXXXCPXGXXKXTXXXXGXGXXDCRYXXXXXGXXXXXXXXXX

XTLSIXGXPGXPGXKGEXGPTGARGPEGAQGPRGESGTPGSPGPAGXXGXPGCXHXCXKX
GSXEXEXXXCCXGXWGXXCXXCPGGXXXPCNXXGXXGXXXXXGXXGXXGPXXXXXXXXXX
GXXXXXGEXXXRXXXXXXXWQWNMHLSXXCXXGIXXXGTCXCXXXXXGXACXXGXXCXPG
XXNXFGXXXPXCTTGXXXRXXEXGXXXXAXXLXXXFSWXXQSVCXCVHGXCNXGXPGEXG
RPGXSGXXGXGXCTCXXGYXGXXCDNGEPGXXGEQXXXXCXXXXCXANSXCXXXXXDGRX
XXCXCXXXYXXXGXXCXGKRXXXPCXXXXCXPXAXCXXLGPXXXYATXXXXXXXXCTCXE
GXXGDXXPXGPXGXXCXPIXPCXXXXGXXXXPXXXXXXXCPXXVXSTICXYXXPGXXXXX
XXXLXXXXXXXXXXXXXXXGEQXPXXXXXXXXXTISPAVXXXXXLLXXXKTXXMPCSXXX
XCXCKXXXXXXXPXXXCSXXXXXETXRQXXCXXXAXCXXXXXGXXXCXCXXGXXGXGXXC
YXXXXXEXXQXLNXEVGTKGSNXRGXXXXKLXXAXXXXXXXXXXXLXXXGPFTVXVPXXX
XXXXXXXXNVTASLQLXDLLNNXXXAXXXXXXHXXXGXXXXXXXXXXXXXXTLXGXXXXX
SXXXXXXAPGKDGARGLTGPIGPPGPAGPNGEKGESGPPGPSGAAGARGAPGERGEPGAP
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GPPGEKGEPGEDGPAGPDGXXAXNGIXXXXHIXXXXXXXXXXXXXXXXXXXTIXXXLXX
XXXXSXFXXXXEXXGLXXXLQXXXXGXXGPPGLTGPAGEPGREGXPXTVFVPSNXXXXXX
XXSTXXLXYLXXAEXXSXXEGXXKLXELVXXHIXXXXXXXXXXVXXXXGXXXXLXXXXHI
XXMAXQXXXXNXXXXGXXLXXEXXXXDKSGXXXXXXDIVAXNGXIXTLXGXXIPPXIXPI
LPHRCXEXXXXXXXGXCXXCXXXXXXXCPXXSXXXXXXLXPXXPRXXXXXXXXXKXXCXX
XXXXXGLNVXKXGCARXCNXTXXXPXCCKGFFGPDCXPCPGGFPSXPCXGXGXCXDGXXG
NGXCXCXEXFXGXXCXXCSXPXKXGXXCDXXXXXCXCXXGXXXXXXKXXXXXXKXCDEVK
PYENRXXSXGXCXXXSCXXGYTGKXCDKXXXXCXPSGLRXYSRFHRDXQXCHXXAXCXLX
DGXXXCXCXXGVPIRCRGRVNVYMDEVWRSXXXEVDIQDYEGDGXSCXXXDXCXXXXXGG
CXXNXXXXXXXXXAXCXXTGPGXXTCXCXXGWTGDGXXCXAIXNSCXLXXXXXCHXNAXC
IYXGPGQSKCVXXXXXXXXXDCKCKDXXXXXCSGFXGNGXXXXXKRGYAGDGXXCXXINX
CLXXNGXXXXXXCHXLXXXXXXXXATCXXXXXXXXXXXCXCPXGYXGDGXXCYGXXXXEL
XXXSXXXXXXXGFYPXWXKXXXXXXXXXXAAFNQWVLACLICSFLFFNEAXXXXXXXXXX
NXTVLVPSXXAIXNXXXXEKXFWXXXXXXPXLXXXHXLXGXXXXXXXIXXEXXXLXGTXX
ALXXXXXXVXXXXXXXXXXXPXXXXMLPTXXXXXVXXXXXXTXXXXXXXXXXXXGXLTXX
XAXIVXXDIXXXTVXXNGIIHNLYVGCDLVXXKVLLPXXXXPLXXXXXPXLXXXLEXXXX
XSXFXXXXXQYXLXXXIEXXXXYTVFXPXNXXIEXYXQXPXXXXXXXXRXXXXXXXXXXS
XXXXEXXXXXXXCXXXXXXXXXXLXXXXXXLXXXXXXDXXXXXYHXVLXEKLLXXXLXXG
XQKXXXHXXXMLXDRSGXSYXXXFXXXXXQXFXNXXXXXXXPXXXXXXXTXXGIXXXXXG
XXXVLXIXXQKNRCXXNXTXIXXSXXXXXXXXXEXCXXCSXEDSKIVCXXXXCPPGXXLV
ESFIEGECCPVCSHSDDSEEGXXGXKXXAXCXLXXXNADXCXXXTQMRXRSCDXXXXXCX
XXXTXXXGCXXXKCAKXXXXXXXXXXXXXXXXXXXXXXXXXXITRIRLCNXPIPXXXXXXX
XGXGRETEKCEKXXXXXXXXXXXXXXXXXTXCCXGXXGXXCXXXXXPEXXXXXXCVXX
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XXXXXXXXXXXXXXXXFPFYLLTLLSXRSRKXXXXXXXXXXXCACXXGXXXCXXXXXGXX
GDXHXPGSCECXXGXXXXXXXXXXXXXXXXRNVPRPLRQAKSWQATKKGKLVSVGGQTEE
WPHFSSSNQDMTDSXXXXXLLXXXXXXVXXXXXXXXXXXXXXXXXXXXXXXXXWXGXTC
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XXCLEXNGGCXXNAECXXTGPXXXXXQXLXXXXXXXYFNXXXGXXLXXXXXXXXXXXXXX
XXXXXXXXXXCNCLXGYSGDGXXXXXXCXXXXLXXQNXXNXXNGGCSXFXXCXXTXXXXG
XVXIAXXXXRXXXXXXXXXXDXFXCRGXXXQELXRXXXXXXXIXXXXXXXXXXXGXXKIS
EEDKXXXXXXXXXGPFTXFVPXTDXLNSDVNGQAIGNTTTSLPSSPNKWDVWGKWTPEGG
ETLIHDSVDQVLSERFLXPXXXXXXXXXXGXXXXXLRYHMVXXXXLLXXMTAFDXXXPL
XDXGXVKEXYRCXVXXXXTXLXXXXXVVDLXIXXXXLXXXSAGXENSKXKLXXXKXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXMXXXXXXXXLXXXGXXXXXXGLXXXXXSLQY
QPPRGQYXXXXXCXNXNXXXXXNFXXAEXVCQXXXXDXXXLAXFXXXXXXXXDSKLKXPX
XXXXXXQLFQXWXXXXIXXXXXSEGLDWCXAGWXXDGTVXXXXXXYPXXXPXXPXXXXXX
FPYXXXXXGGXXXXPXXXXYXXXXXHLHRFDAFXGXXXXXXXXXXXXEAXXXXXXXXXXE
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NQNLSDXVGXNGVIHXINXILXPSXXMEXVXXXXXXKXXXXXXXXXXXXXXXXXLQXXKXV
AXXXGYXXXXXXXLXXXXXXXXCQDXGAEIAXVGXLYXXXVHLXXXXLSLXLIXDPXHXP
XXXXWXXDXXXXXXXXXXXXXLXXXXXXXXXXXXXXXXXXXKXXXXXGDXXXXAXGXXXX
PXXXSXXTXXGSXXSXSCXXNXXXGXXXXXWLXXXASXXXXXIXQRXXEFXGGIAYGIDX
LLXXPXLGXRCDXXYDXXXXXXXXXXCXXXXLXXXXXXXXXXXXXXXXXXFXXXXXXGSX
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VHNXSVQRGXXXXXXXPXXXXXXXXXXXXLXXXXXXXXEAXQXXXAXXXCXXXGAXXAXX
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PPPGTKXXXXXXXXXXXSXGXXRXGCRRXCXSMSLTVGKNMPRRRVXXXXXXXCCSXXXX
GXDCTXAPIXXPXXXXXXXYGKFSCHGMSPALXGQTAXXXXXACPGGXEXPCXNXGXCDT
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XYXGDGXTCXXXDXCXQXNGGCXXXAXCTQXGVXXXXXXXXXEXEXXEXXGXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXAQKIKMAXYXGVTSXVXXXXVMTFXXXG
YXXDGXXCXDLPTPIXXCADGXXXXXVXXXXXXXNGXCXEHAXSKGRXWXCXMXXGXXXX
XXCRIXXXXECKXXXXGXGXXXXXMANXXLQXISVXXXDRXXXXXGXCXXXMPQPKLXXX
XTXXXXXXXXXGVFHXXXSXXXXXXXXXXEAXXXCXXXXXXLATXXQXXXAVXXXXFXXC
XXGXXXXGXXXXPXXXXXXXCXXXTXXGIAVXXXXXXLRRATDNVKHNRALTADYTSGKC
NNKTVXYXXXXNXXXXXDXXCYXXXXXXXXXFQINSCXPXXXXXXXXXSXXXICRKTXXX
QQVIDXXDGXXXXXXXXXVLXXXXRXXXXXSXXXXXXXENXXSXSXXXXXVKXXXXXXXN
XXFXXXXXXXXDKXXILPXXXXXTTXXXXXXXXXXSPSYXXXXXXXNDXXXXXXSSGGGE
XXXXXXXXLLYVCAQGYVMGNXXXXXXDDEXXXXXXXXXAXIFFIISXXXXXXXXXXXQV
QACVKDETEAHIDYEDNFXXXRXIPXXXXXXXXXXXXIEQXXXXXXFXXXXXXXNCFLLX
AXXXXXXXXXXXXXXXXXXXXXWXXXXXXXXXXXXXQXTXXXGXKXEESXXXXXXXXXXX
XXXSXXXXXXXXXXXXXIXEXXXXSSGXXSXDEDSSEEMXLSQKXXXXFPXXXXSXAXNX
IIHXIXXSEXXXXPXXXPXXXXXXLXXXXXXXXXXXXXXFXXXXWXSNPXEXTQEXTXXX
XADVXXXGXXXXXXXXXXXXXXXXXXPGXXXSVXXXEXAXSXXXGXXYXXXXXRXXXEXD
XXXXXXXXXXDTKXEXDXVXXTXEXWLDXYPXTXXVXXEVVEDDXXEPXXXXXXXXXXXX
XXXXXXLXXXXXXXXXXXXXXXXXXXXXXPEEGLXXXXXXTQXXXXXXXXXDEXXXEX
XXPLTSVSXLEXLSVSRXXXXGYDDXXWXHXTTXXEXXXDXXLXTQEXXTTXLXDITSXX
XXXSXTSVXVSPSDHTXXXXXXXTTXYPXQVATTAPAPDXXXXXXXXXXXXXXXXXXGXX
XXXXNPANTTXXXEQXEFTXXGENXXXXSXXQAKEXSGXTXXXXAMXPXXGAKQNDSAQX
PXVYPGWXXXXXXXXXXXXXTYATXPXXXEDCDRVXPSREXXXSSKGAIIAVIVILLCLL
LVAAVLAXVWFFKKRQQKNSVYKLNGRCXGXXGXXXEXXXDXXEXXSSXTTXXAXPDGXX
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PPGXXVXXXXXXXXXXXSXQSXXXXXXAXXXSXLXXXXXXXXXXXVXLTTDTXXXXPXXXX
XXXTTXXXVSXXVFHXEEXTSRPLXPXXQPGSXPXXXXXXXXXXEXXXXXXXXXXXPXXX
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FXDXDXHLXXXXXLPXXXXXXXXXXXXXXGXSXXXXHLSTTLXTPDXAXHEXPTQPTLPS
XNEAAXXXXXXXXXXXXEXXXXXXXXXXXKESLPXXXXXXXSTEGXTXXTXXDAPGXPVLL
GLDPXSXXEAXXESLLXSTXXXXIXXXXTXTXSXXDXLXXPEPKVSNVKRALKDXTXEXW
XPXXXXTAXXXPDXGAHHDVEXXXXXTQXXLPSDXEXXQXTEGXXXXXXAXXXXXXXXXA
XXSTXXTDXPXXXVLXXXDXXSXXXAGXESLLXXXTKNXXXXXXXXXXXXXXXXXXEXX
XXXXXPXXXSXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXSAEAXXXXEXXTXXPLXPXX
XPGXXXEXANXTDGSHVHVXTDQSAXXXIPGVFXDXXDXXXXLXTPXXTTVDXXXXXXST
SXXPXXXXQGPXXGXXEXTXXXXXXXAPSXXXSGEXXTTTTXXXXXXSQPRSAXXXXXHX
XXXXXVPEXXXXXXXXPXXXXKXXXXXXXWLIIXXXXXXXXXXXXXXDXDXXCVAALXXL
SGALILAVCIAVNSXXRRRCGQKKKLVINNGKGAVEDRKTXXLNGDXSKSQEMVHLVHKE
QSNDXTXACDEFLTVASXXXXXXXXXXXXXXXTXXHXXXXTXXXCTXXXETQNHXXXXXXX
XXYXXXXXRXXWXXXXXXXXXXXXXXXHLXXXXXXXXXEEXXXDMKXGVXXXXXGLXXXX
XXXXXXWDELTVRTFXDXIPLMEEIHSGEEGPIEIXXXXXENWRXXXPDXFFXXXXXCVV
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==> Neoptera.txt <==
>MSA Consensus of 398 seqs, protein
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TDADVGENGVTDQYEIVAGNVDNKFRLVTTANPSGDTSYLHLETTGNLDRESRGSYQLNI
SARDGGSPPRFGYLQVNVTILDVNDNPPIFDHSDYNVSLNETALPGTPVVTVMXTWPXXX
DNSKITYYLXXXXXQXTVXXETXXXSTTXXXNCPQQTNVKSSASXXSXXXXXXXXDSXSP
XXXQXXXXHXXXXXXXMXXXXXXXIVXXXXXXXIXXXXKVATVDENAVNGTXXXXXXXXX
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==> Neopterygii.txt <==
>MSA Consensus of 1426 seqs, protein
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VAQTVEIDTV

==> Neoteleostei.txt <==
>MSA Consensus of 880 seqs, protein
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RRSSVXXXXXPXXXXRXSXXXXXXXLXXXXXXIXGXXXXXYXXEXXXXXXXXXXRYXXXX
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==> Nitriliruptoria.txt <==
>MSA Consensus of 337 seqs, protein
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GXXXXXXXXXXXXFXXXXXDXXXXXLXGXXXXXXXXXXXXXXXXXWXXXXXXXXXXXXX
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GDXXXXXXXXXXXXXXXXXXPXDXXXXXXXXEXXXXXXXXXXXXXXXXXPXXXXXXXXP
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VXXXXALXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXYXXXXXXXPGDPPAT
ASG

==> Oceanospirillales.txt <==
>MSA Consensus of 142 seqs, protein
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FCANEPVQGKFIVDGAEYLLNDFSRCHNLTVGDLNSNQTYAVSVEVTDISGNGPTQSHIS
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SNTNAMISWRTDESSSSVVSIGTEPDNLSRVESSPGFSAKHQLSVTNLLPASTYYFSVES
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TEKASTGQVRYGLTSDEMNQLESDFNFTAAHAIALNNXQAXXXYFXXXXXXNXXGXXXXX
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LTTNHSVVLSGLSADTAYETLVFSIDDNGLSSEQVPANFRTSPLPDSDLPFFVTGPTISS
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XTIGHXXXXXXFXXEXXXPVXNLAXXTXYXXXVXXXGXXLXXRVXXXVTXXXXXXXXXXP
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FSDGAEIFVAELSAVNTSYIFECDADWSPWFASNLTDCDNVVPIGFVAEDPDEDGIHDPI
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GDGSGLDGLNDQNAGIGFVKVYDHSSDVFXXXIHIAELAISSTTIDSHQVISFEVPELVA
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==> Odontoceti.txt <==
>MSA Consensus of 191 seqs, protein
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XXXXQXXRCDXKXXXXXXXXCXXCXXXXXXXCPXGXXXXXXXXIGXXDCRYXXXXXXXXL
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XGXACXXCXDXNXFGPXCXXXCSCVHGVCXXGXXGDGXCXCXXGXTGPXCDXXXPXCXAL
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XCXEXYHGDGXVCLPXDPCXXNXGXCPXXSTXCXYXXPGQAXCXCXXXXXXXXXXXXXXX
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RLXXXXXXLDXXXXXXLSXXGPFTVLXPXXXXXKGFNVKEXXXNXXXAQXXXXXHIIAGQ
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XXXXXXXXGXXXXXXAXVXXXDXXATNGVXHXXXXVLXPXRGXXXXXXXLLXXLDXXPXX
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==> Oncorhynchus.txt <==
>MSA Consensus of 125 seqs, protein
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PXXXXXXXXXXXXXXXXXPXXXXXXXXYXXXXXXXXXXPXXXXXXXXXPXYXXXXXXXX
XXPXXLXXXPXXXCXXXXXXXXXXXXXXXXQXXPACXAXPXLPSXXXXXXXXXXPXXQX
LXXXXXXXXXXXXXXXXXXXXPPXXXXXXXQXXXXXXXXXXXXXMXXTNPXXXXXXXXX
SSTPGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXRSXEPYRXXXXPXXXXX
XXXXXXXXXPXXXXXXXLYPPFXXXXXXXPXXXXXXXXXXXXXXXXXPXXXXXYXPXXX
LFLLTVVKEFDLXXXXXILEAEEGSCFXSXXXXXXXXXXXPXXXXXXXXTRXXXXXXX
LVDQASXXXXXPXXXXXXXXXXXXYXPXXXXXXPXXXSXPXXXXXTSXXXXXXXXXPXXX
XXXXXXXXXXXPTXXXPXXXPXXXXPXXXXXXXPXXPVAPVPAGPAQVQPHXXXXPXXQS
STXXXXXXXXXXXXXXQSXASXXXXXPXVXXXXXXXXXXXDSXXXXXXXXXXXXXXXXX
XXXPSXXXXXGXXXXXXXXXXSXXXPFXXXXXXXXXXXXSXXXXXXXXXXXXXGLXXPXX
XXXXXXXXXXXEXXXXXXXXXXXXXXXXXXXXSXEXXRPXXXXGXXXXXXXXXSXXXXX
XXTDDXXMXXXXXXGXQXXXQGXGYXXXXGDSSSQHEGSTSASGLSLGESPFAEGLSVVL
LPGSTMSYPXXXGSLGNXXXXCXXXVXDCXXXPXXXGGXXXXXYVTAPSAVFPSMTXXSX
VXXCXXAXXXXXXCXXXVXXCXXGWXXFXGXCYRXFXXRXTWXDAEXXCXXXSXHLXSIT
SXXEQEFXNXXXXDXXWIGLXDXXVXXXFXWTDXXXLXXENWRXXQPDXXFXXXEDCVVX

IXHEXGXWNXVPCNYXLPXXCKXGXVXCXXPPXVXNAXXXGXRRXXYXXXXXVRYQCXXG
FXQRHXPXXRCRXXGXWXXPXXXCTXXXXXXXXXXXXXXXXXRSXXXXXRXXRXXXXGEX
XRERERDDAHSPY

==> Ornithinimicrobiaceae.txt <==
>MSA Consensus of 208 seqs, protein
MNAGVFGVPGTGRFGPGAVGMAAVACAGAAGTAWLALAMDPLAAAAPGAVGARAVGLVPA
VLLGLLALRALRPWLGRRLPGAAVLRGALQVVAVTVVVVAATIVLSVVAGALRTGAHEHG
GGAGHPAMAEMGLLQHAVHEGAVVAPSALVVMSGLALLAAAXXXXXGTXRRXGXAGAAVV
RRRAVAVTAGTATXXXGLLVAXXXXXXTLAQXAAPXXAXXAXXAAXXXXXXXXXXAXXXX
FXPYXXWXNXXXXXXXDPVTGTPHLTDGDPDGMIFALEQDVAALQHWHVPLADDPAADPA
GNRRLRPRPLVLRANAGDCVEITLRNGLDPAQTPAWLPQVDPHVSLQAFGVSYNPQASEG
SSTGRNADSTVAPGESHTYYWVAPQSEGLYLFRDMGMPVGADGDGGAAEHGLYGGLAVQP
AGARWYDPVSGAELSSSVPDAQYASVATQNGDLYVDAVITVPYGGATLRYRESVLVSQDV
VPFLRPPDETPGEELFERFSINYGSEPEYKRADWNKTGEVWCEECTSEETVLSSWVYGDP
GAVKLASGSGPWLPTEXDMGGVDSSXRPGGXPRRALSAXAXTLTVDSTXPLXXXXXXXTR
AYQGDPIKLRFGQAGVYETHVFHLHAHTWPAEPDETGPAQSIPPRPTPYAQSRXXTXXXX
XYSPXTXXTXXXSTGTAAAATVSVNPAGGVIGLTVGEAGSXYGALGLAITXGGXXGXXGT
ASXXXXXXHLXXXFXXGXWXXXXVXDTYEDGSXXLPDXXRVNPWLALREVAXXXXAXXXV
PXXXNAPTLENPGYPRFIPGEFGSRAPQPPXGXXXXXXDAXGTXTAVVXDXXGXXXSXAP
XMRSVGTTPLDPALLEATQEVTVVDAAQDLVLSLXGAVLAPLSXXXXAXQXXXXLXXXEG
XQAVXVTGXXGXXXXXXGXXXXXPXXTVGGTXXTVTXXXXXDPADPAMXXXXXXXXMXX
XXXXXXXRXXAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXAXXXXPXXXXXGXXXXPXXXX
XGAXAXXXXXXXXXXXSTYXGXXAXGXLXXXXGXXXXXXRXILADEDVDAXGVELEVXLST
AAVRGRXXSXFXXXXXXXRXDXXXXXXXXXXXXXXXXXXXXYIVXLXXXXLXXXXGXAL
XARGXXAXXXXXXXXXXXXXXXXXXXYXXXXXXXXXXXVXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXDXXXXXXXXXXXXXXXXXXTIDXXVXXXXXRXXXXXXXXXPDGAPAX
PDVVVSPDXGXXXXDTXXXPDXLGLXXXXXVWXXXXGGXXXXXGXGXVVXXIDXGXXXXX
PXXXXXXGXPYTHXXPXXPXXXXGXXXXXXXXXXPXXXXXXXXXXCXXKXXGAITPWISD
XXXXDXXAXPGXHDYXXXXXXXXXXGXXXXXXDXXRXXTXSXXSPXDXXGHGXHXXGTXX
GXXXXXXVTGXXXNXQSARLMVAPXXXXGXXXXGXXXXXXXGXAPXAXXPAXXXXXXXXX
XCXXXXXXXXSGEWDVXXXXXXXXXXXXXXXRPLFNGQVXXXXXXXAXXXXXXVXNXSXXX
XXDXXXXXXXXXXXFMEDXXXAXXXAGXFXXXXXGNXGXXXXXPXXXXXXXXXXXGAPGS
XAGTVVXXXDXXGSXPRXXXXXYSVGXXXXXXXXPWXXTVAAVGISTHXXXXXXXXXXGX
XDAXXVXRIXGXXRYXTAAXIAXXXXXXVDTVYIATGXQFADALXGAAXAXQGXXXXXGL
DQPAXXPDGXPAPVLLTXVXXLPXATXXALEXXXPXNIVXLGGXXAVSXXVXXXLXXYGX
XVXRVXGXDRYETAAXXALXXXXXXXHVYVATGXXXXFPDALSGSAXXXXXGXPXLXXXX
XXXPXXXXXXXXXXXXXXXXXXXXXXXXXXXAXACXXXXDXXXXXGAXXXXXXXXRYXTS
VAXAXXFXXXXXXPAPVXXXAXGXDYPDALAXSALAGXQXVPVMLSXPXXXPXXVLXXMX
XXXPXXXXXLGGXXXXXXXVXXXXXXXXXXXXLXXXXXXXXXXXXXXXXXXXXXXXXXX
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AGGXGMILAXXXXXXXXXXXXXXXXPXXXXXXXXXXXXXXXXXXXXXXXXIXXTXXXXX
XXXXXXXXXXXXXXXPXXXXXXXXXXXFSSXGXXXXFXXXXXXXXXKPXXXAPGXXVXXXX
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DXXXXXXXXXXXXGXXXXXQREXXXXXXXXXXXGXXXXXXXXXXXXXXXXXRXXXGXXXX
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XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGXXXXXXXXXXXXXXGXXXXXXXX
XXXXXXXXVXXXXXWXXXXXXXRXXXXXXXXXXPGYXXXXXXXXXXXXXXTXXXXXXXXX
XXXXXXXXVXXXXXXXXXGXXXXXTXXXXXXXXFXXXXXLXXXXGRPXPXGRLLXGXDXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXEGGEGGFAXXXSDXXXXPXXXXDXXXXFXX
XXXVXXXXXXXXXXXXXXXXXXXXXXXVXXXXXXXXXXXXXXXXGXXXXXXXRXXXXXX
AXXXXPXXXXXXXXXXXAXXXXXXAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGX

PXXXXXSXXXXXXXXXLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXDXXXXXXXXXXXXXXXXXXXXXXXXGXXXXXXXEXXXXXXXXXXAVXX
XXXXXXXXXXXXXXXXVXXLDXPXXXXXXXXTPXXXXXXXXXXWXXXXXXXXXXXXXXGX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXLXXXXXXXDPXXXX
XXXXXXXDXXXXXXTXXXXGTXXXXXXXXEXXXXXXXLRADGXXXXXXXXXXXXXXGXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXEXXXPWXXXXXXXXXXXDXXXXXLXXXGA
SWYXXGGXDGXXXXXXVXRYDXXXXXWXXVAXLPXXXXAXXAXXVXGXIVVXXXXXXXGX
TXXXXXXXXXXXXXWXXXXXXPXXVSXAGXAVXDXXXYXVGGCTTGXCXPXSXXXXAYDP
AXDXWXXXAXYPXXXXXXXXXXXXXXXEXXXXXXXGGXXXXXXXXXXXXXXXXXXXXXX
XXNXXXXXXWXXXAXAPXXXXXXXXXXAXXXXXXXXXGXXXXXXXXXGXXXXXXXXXXX
XXXXXXXXXPXXXXXXXXXXXXXXXXXXXXXXXTGXXXXDXWXXXXGXXAXXPXXXG
XXACGFXXVGGXXXXXXXXXXXXXXAXXXXXXXXXXXXXXXXXXXXGNXXXXXXXXXXXXG
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPXXXXVXXXVXMXVXPDXEPXXXWXXXX
XXXXXXXXXXXXXPLXXXXXDXXPXRXXXADAEVSLXXXXXXXXXXXXXXTVEADDXXRR
XXXXXXXXXXXXXXXXXXXLTDTGQELDAIEVTLIVSDEQVPPVGVIEVDPTSVEXXXX
XXXXXSTDVTFSNTGEADAEVSLSEDVDWLSVDXXXXXVEADDSVDVAFTTDAAGLDXXE
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXVXRXXGXXRYXTAAX
XXXXXXXXXXWXXXDGXXXXXXXXVXXAXGXDAXXXDALXXXXXXXXXXXXAPXXXXXXX
XXXAXXXXXPVLLXXXXCXXXPXXTXXXLXXSRRLVXXXXPXXXVXXGGXXAVRSXXXVX
XXVVERXXXXXXXXXXXXVXRXXGXXRYXTAAXXXXXXAXQXIXXXGXXXXXXYXAXGXX
XXXXPPFGXXXXXXDALXXXAXAXXXXXPXLLXXXXXXXXPXXTXXXXRXXLXPXXXXXX
GGXXAVXXXVLXXXXXXXXXXXXXXXXXXXXXXXXXXRXXGXXRYXTAXXXXXXXXXXX
XXGMXXXXXXXAXGXXXXXXDALXXXXXAXGXXXXPXLLXXGXTHDASDXCXXXPXXXXX
XLXXDLXXXXXPXXXXXXXGGXXAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXGHXXXXGXGXXXXXXXXXXXXPXQXXXGGXXXXXXXLXXXXXXXXX
XXXXXTVAAGDLIGGXXXSXXXXXXXXXXTIRXTLIXVXXXXXXXXXXXXXXXXXXXAX
XXXXXXXXHXXXXXXXXXXXXXXXXCXXXXXXXXGXXXPXXGADFXXXXXXXXXXXXXXX
XXXXXXPXXXXXXLPXXXXXXXXGXXXGXXRXVXXGGGFIXXXLEXXXXXXXXXIXXGXX
XXXXLXXXXXXXXXXXXXXXXXXXXXXWXXXXXXXPXXXXXXXXXXXXXLXXXXXXNAX
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XXXXXXXXXXXXXXXGXTXFXXXGXXXXVXXXNQYXXXVTETALXXXXXXXXXXXXXXXXX
LXXXDNXXXXXXXXXDDPXMXXVVXKWXAXAXVLXXXXXGTVAEDITGDAGGDRGXXXXX
XXXXADXILXXTXXXXXGXXXXXXXXXXGGTDXXXXXXGXXXXXYXXXXXXXDHGIXADXX
XXXXXPXXVXXXRXXXXXXVXXXSNXXGDDVIRGXGXXXGXXTXXXAXXXXXXXNXXXXX
XXXGXXXXAXXEQXXXXXXXXDXXXXXXXXGXRXXLALGXSEGFXYTWXDXXXXGSKVSX
XXXDGXXXXXXXXXRVXXLNFLTGXRYXSAXXXXAXVFXGXINPGDIXIXREXVXXXXXX
XXXDTAXYXDPFXQXAGXPNYXIXXLXDGYXEXXHXGGDXFTESEGXDILXNIEXXXFGD
GGCFXLXXXXEEXTXCXXXGXVAFTXGTNLXGGPEDLAXXVXYLXXNPXLTADPXXRXXX
XXXXXGEXXEXWXPXXXXXXXVTXXXXXNXXXQTFXPGDGXAGAILRVVVTFXDDXGVLR
QXXSXVVGXXXXXDXXXXXVVNINDXPXGLTLSNXXPXVGQSXVPSPFXDXDGLEEAVEA
GMTYXWQTSXDXXFXXDVVXVATXVTPXTNQLGYTVQXADXGRXIRVVVXYTDDQGTXET
YXSXPTXXVXXAXXXGP

==> Ornithinimicrobium.txt <==
>MSA Consensus of 131 seqs, protein
MNAGVFGVPGTGRFGPGAVGMAAVACAGAAGTAWLALAMDPLAAAAPGAVGARAVGLVPA
VLLGLLALRALRPWLGRRLPGAAVLRGALQVVAVTVVVVAATIVLSVVAGALRTGAHEHG
GGAGHPAMAEMGLLQHAVHEGAVVAPSALVVMSGLALLAAAMXTVXXXXRRAGRAGAAXX
XXRXXAXXAGLXXXXXSVGXXLXXXXAXXXXXXXXPXXXXXXXXSXXXXXXXXXXXXXXX
XXXXXXXXXXXXIDPVTGTPHLTDGDPDGMIFALEQDVAALQXXIVXLXDXXXAXXXXXX
XXRXTAXVLRAXAXXKXDXTXXXAXSXXXXLXXXQXXXXXXXVXXXLGRXXAXXXXXXXX
XYXXXXXVTLNGXXXXRNADSTVXXXXXAXXXXXXXXVXXXXXXXXRXXXXXXXXXXXDG
XXXXXTXXXXXXLXXXXXXXXWXXXXGTGXGGVXAXXXXXXGXGXVXXXXDXGXXXXXXX

SXAXXXXXXYVDAVITVPYGGATLRYRESVLVSQDVVPFLRPPDETPGEELFERFSINYG
SEPEXXXXXXXXXXXXXGXCXXXXXXXXXXXXDXXXXXXXXSGPWXXTEPXXXGXXX
XXXXGXXXXXNIXXCXXKXXGDSTTPLSCYVANVTAXXXXXXXKLRFGQAGVYXXXGXXX
XPXEXXXXXDXXGHGSHXPPRPTPYAQSRAXTXAGXTYSPXXXXXXXXXXXXXXXXXXX
XXAPXAXXXXYXXXXXXXFXXXXWXXXXXXDXXXXGCXXXXXGIRVNPWXAXXXVAXXXX
XXXXVXXVXXXXXXXXXXXXXXXXGXXGSXXXXXXXXXXXXXFXXXXPATLVRGYVQLST
AAVPXXXXAXXXXXXDGXXVXNXSXXGXXXXXXXXXXXXXXXXPXXXAFXXXAXEVTVX
XXXXGXXXXXXXGXXGPVXXDATAAXXXSAXXXXXXXXXXXXXXXXXXXPWXXXXXAXTH
XXDLTXXXXXVXXXXXXXXXXXLXXXXGXXXXXPXXARTAHRLALXXXXXXXXXXPDYVF
GQELDPXXXXXXXXXXXXXXXXXXXXVTYRASVIQLPLTYVEGDQANPQGXXXXXGXIXX
XXRXXXXXXXXXXXXXXAGXXXXXXYFFRVNAGDCINFEXXXXXXXXXXXXXXXXXXXG
XXXXXXXXVXXXXXXXVXXXXSXGXSXXXXYXXQQXXXXXXXAXXXXXXXXAGXXXXXXXX
XCLPTAPVXXXXXXEAXXXXXXXXXXXGXLXGXXIXXXXXXXXXXXXXXXXXXXDHHFAGT
LQNRGLFXXXVVEXXXFXXXGPXXXXXXXXXXXLXPXXXXPGXXXXXXXXXXXGXXGXXX
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XXXXXXXXXXGXXXPVAPXPXXXXXXGXXXXXXXXXXXXXXXXXXRRXXXXXXXXXXXXX
XXXXAXAXXXXXXXXXXWXXXXXXXXXXXXXAXXXXXXXXXXXXXXXXXXXXXXXXXDXX
FXXXXLXXXGXXXXXXXXXXXXXXXXXXXXXXXXRGXXXXXXLXXXXXXXXXXXXXXXX
XXXXXTXXXGXXXQXXXXAXLXXXGXXDLXXXXXXXNXXXVXXXXXXXXXXXXAXXXXVX
XXXXXXXXXXXXXTXXXXXXXXXXXXXPXXXXXRAXXPXXXXXXXXXPXXXXXXXXIDADI
RYXXXXXXXXXXXXWGXXXXXXXXLAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXTXXXX
XXXXXXXXXYXGXXXGXXXXXXXPXXXXXXXXXXXXXXXXXXXXXGESIGXXXXXXXXXX
XVGXXXXIXXNPXXXXXXXXDXXXXXXXXXPGXXXXXXXXXCXXXXXXXXXXXWXXXXXXX
XXXXXXXXXXAAXXXADAAXXXXXXXXXXXXXXXXXXVNXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXGXXGXXXXXXXXXXXXXXXXXXXPXXRXXXXXXXXXXXXXQXXXPXX
XXXXXXXXXXXXXWXXXXXXXXXXNGNXGXXXDPXXGPXCXTXXXPXXXXXXXYXVGXYX
LXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXSXXXXXXXX
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DXXXXXXXXXXXXXXXXXXXXXXXXTAXXXXXXXXXXXXXXPXXXXXXXXXXXTDXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGXXXXXXXXXXXXXXXAXVXVXXXXTXX
XDXALXXAPXXXXXGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXRXXXXXXXGDXXXXXXXXXXXXXXXXXGXXXXXXGXXXTFDXXX
XPXXXXXXXXXXXXXXXXXXXXXXXXXXXXGXXXXAXXXSDXYGXXXXXXDTXLVSPXXD
XSXXXXXXXXFXXXXXXXLGXXXXXXXXVSXDXXXDASHXXXXXXXXXXXXXPXXXXXXX
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XXXXXXXXXXXXXXXXXXXXXXXXXXXXXPVADSEXXXDGXXXXXXXXEEFXXXXIFVXXXX
XXXXAXXXXXXXXXXXXXXXXXXXXXXXXGXXXXXXDPXXIXTXVXLGXXXXXXXTVT
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XXWXXVAXLPXXXXXXXAXXXXXXXXXXGXXXXXXXXXXXTXXYDXXXDSWXXXAXXPXX
VSAXGXAVXDGXXYXVGGCXTGXCXPXXXXVXXXDXXXDXWXXXAXXPXXXAFXXXXXXX
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GGXXXXXXXXXXNXXXXXXXXXXXXXXXXXXXXXXRXXXAXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXVKDSSGSXXXXDXXLXAXXXRXYLVXXXXXXXXXXXWX
XXXXXXXXXXXXXXXXXXXXXXXDXXXXXGXXXXXXXXXXXXXXXXXXXXVTTXXXXXXX
XXGXYXAXXXXXXXXXPXXXXXXXXXXXXSXXXXXXXXXXWXXXXXXXXXXXXXXXXXXX
XXXXXXLXXXXXXXALXXXXXXXXXXXXXXXGXADAEVSLXXXXXXXXVXPEEFTVEADD
SVDVXXXXXXXXXXAXXXXTXVGXXTDTGQELDAIEVTLIVSDEQVPPVGVIEVDPTSVX
XTAXXXGXXSTDVTFSNTGEADAEXXXXEXXXWXGXXXXXXXVEADDSVDVAFTTDXXXX
XXXXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXVXRXX
GXXRYXTAAXXXXXXXXXPXXXXXWXXXDGTXXXXXXXVXXAXGXXXXXXXGADALXXXX
XAXXXXXXXPLXXXXXXXXXXXXXXXPVLLXXXXCXXXPXXTXXXLXXLVXEXXPXXXVX
XGGXGXAVXXXVXXXXXXXXXAXXXXXVXRXXGXXRYXTAAXXXXXXXXXXXXXFDNXXXV
YXAXGXXXXXXPPFXXXXPDALXXXAXAXXXXXPXLLXXXXXXXXPXXXXXXXRXXENLX

PXXXXXXGGXXAVSXXVLXXXXXXXXXXXXSTXXXXRXXGXXRYXTXXXXXXXXXXXXXXX
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LXXXXXPXXXXXXXGGXXAXXXXXXXXXXXXXXXXXXXCVDFASQRKAQDXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXGXXXXXGXXXVDFWXXXXXXXXDXXXXXXGX
XXXXXXXXXXXXXLXXXXXXXRXXXXXXXXXXXXXXXXXDXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXANXXXGXXXXXXXGNXXXXXXXXXXXXLXXXXGGX
XXXXXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXVXXGGXXXCAL
XXDXXXXXXXXXXXXXXXXXXXXXXXXXXGXXXXXXXXXXXGXXXXXXXXXGXXHXCAXX
XXXXXXXXXXXXXTXXXXXXXXXXXXXXXXPXXXXFNXXSGTSMSAPXLXXXAALMXXGX
XXXXXXXXXXXXXXXXXXXXXXXPXIXXXXXXXXXXXXXXXXXXXXXGXXXXXXSXXQY
GXVVTXXAXXXXXXTGXVXXXXXAXXXXXNXXXXXXXGXXXXXXXXXXXVXGXXPXXXXX
XXXGXXHXCAXXXXXXXXXXXXXXXGXXXXXXXXXDXXGXXXXXRGIXXPMXXLXXXXIL
XXXXXGSQTVTRTXXXXXXXGGXXXXXXXXXXGXXXXXXXXXIXXXXXXXXXXXVTXXXX
XXXXXXXGXXXXXXXXXXXXXXXXLXXXXLXPXXVXXXXDXXXXXXSLXXGXGXXXXXXL
GVXXGFXXTXDXXXPXXXXVXXXXXXGXDLXDGXXELXXPAGHEQDYXXRXXXDNXXXXX
TXXVXXLXXXXXGGDXXXGXXGDXXXXDXDXXXRVXXXXXXTGXRYXXAXXXRXXVFXXX
XXPXXXXXXXXXXXXXGXVIAQSAXXXXDXAXXLXDPFXNXAXXXXYXIXXXXXXYWXXX
XIGGAEFEESEGXXILXNIEXXXFGDGGCFXLXXXXEEXTXCXXXGXVXFTXXTNXXXXX
EXXXXXVXXXXXXXXLTXXPXXXXXXXXXXXXXXXXAWXXXXXXXXXXTXXXXXNXXXXX
XXXGXXXXGXXXXXVXTXXDDXGVLRQXXSXVVGXXXXXDXXXXXVVNINDXPXGLTLSN
XXPXVGQSXVPSPFXDXDGLEEAVEAGMTYXWQTSXDXXFXXDVVXVATXVTPXTNQLGY
TVQXADXGRXIRVVVXYTDDQGTXETYXSXPTXXVXXAXXXGP

==> Ostariophysi.txt <==
>MSA Consensus of 206 seqs, protein
MXXXXXXXXXXXXFXXXXXXXXXXXXKXKXKXXXXXXXXXXXXXPXXXXXXKAKPEQXXXX
XXXXXXVXXXXXXPXXXPKEKAKPXXXPXXXXKPETPAKEKAKPEDPSKKKAKPETPXXX
KXXXEAXPKEXAKPXXXXKXKAKXXXXSXXXXXXXXXXXXXXXXXXXXXXXXXXXXKE
XXXXXKPXXXLXXXXXXXXXXXPXXKXXXXXXXVXKEKAKPEPXPKEXAKPEXXPKEKAK
XXPXXKEKAKPEXXPKEKXKXXPXPKEXAKPXPXXKEKAXPXXXPKXXXKPXXXPXXKXX
XXPXXXXXXXXXSAAKEKXKXEPXXKEXAKPEXXXXEKAXPEPXXKXXXXPEXAPKEKXK
PXPXPKXKXXXXXXXXXPKXXXXXXXXXXXXKXXXXXPXKEXXXXXXXXKXXAKKKAAAQAS
QPSVPXXXXXXXXXXAXPDLEXXXXEKXKPXXXPKXXXXPXXXXXXXXXXNXXPXXXXXX
XPYPXHXXXXXXKXXPXPKEXXKPXXXPKEKXKXEXVXKEXAXXEXXXKEKXXXXPXPXX
XPXXEXXPXXXXXAXPVPXXXXXEPVPXXXXXXXXXXEXXSXXXXHXXXEKXXPXXXPXX
XXXPXHXXXXXXTXXXXXXEKXXPXXXXXXXAKXXXVXKXKXXPXXXPKEXXXXXXXPXX
XXXXXPXPXXXXXXXXXPXXXXXXXXXPXXXAKPEPVSXEKXXXXXXXKXXXXPXXXXXX
XXKXXXXPXXXXKXXXXPXXXXXXEXXPXXXXKXXXXPXXXXXXXXXXKEXXKPEXXXKE
KXXLXPXXKXXXXXXXXAKXXXXXXXXXXPXXXXXEXXXXXXXXXXXXXPXXXXXXVXXX
XXPVXXXXXXXXXLXXXXPXXXXXXXXKXXXSSLXXPXNXXXXXXXXXNXXXXXXXXRX
XXXXXXXXXXXLXXXLEPXXKXXXXXSXXEXXKPXXXPXXXXXPXXXPKXKXXXEXXXXX
XXEPXXEPXXXXXXKPXXXXXLNXXXKXXXXXKXXPAXPXLXXXXXXXXXXXXXPKXKXX
PXXAPXXXXXPXXXXXPKXKXXXAPXXXXXXXPVVHFIIYLILVHRMSNRKQYRXXXXXX
XXEXXAXXXXXXPEPVXKKYGXXXXPXXXXXXXXLLVPIWGAVSLFSRPXXXPXXXXXXX
XXXXXXEXXXXXXXXXXXXXXXXXXXXXXAXXXXXXXXXXXAVLDCPLEILNRYVTKXXXXX
XXXVXXXXXXXXXXXXKXXXXPXXXXXPXXXPXXXXXXXLXXXSXXXXXXXXXCXXXXXX
XXXXXXXXXXXXXXXHIGAXXXXXXXXXLXRXXXHNXVXXXXXXXXXXXYXXXXXLLALRX
XXXXXXMXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXYXXXVQXXXXXKPXX
XPKEKXXXXPAPXEKXXXKPXXKEXXXXXXXPXXXXXXXXXXXXXXXXXPXXXXXXXXXX
XXXXVXXXXGXXXXLPCXXXXXPXLXXXXPXXXNXXXXXXXRXKWXXXXXXXXXXXXXXX
GXXXXXXXXXXXXXXXVXXXXXXXXXXXXXXXXXXXXXXXYLLXXXXSSFXXXXXXXXXXX
XXXXXDXXXXXXXXXXXDSCXXXXXXXCXXXXXKXXXXXXXXXXXXYXVXXGXXXXXXXXG
XVFXYXXXXXXXXXYXGXWGXXCXXSMMPRLYVGSRXXXXXAXXXCXXXXAXXAXXXQLX

XAXXXEGXXXCXXGXXXXXXXXXXXXXXXXXXXXXXXXXCXXXXXYXXXXPXXXXHIXXX
XXWXRXXCXXXXXXXXGXXXXGXXXXGXCXCXXXYXGXXCDXXXXXCXXXXXXXDXXCXX
XXXXIGXXXCXCXPGYXXXGXXCXXXXXXXXXXXXXXXXCXXXXXXXXXSVEEXAXVGQL
YXAWXFXXXXXCXXGWXXDGSVRXPIXXXXXXXGXXXXXSTXCXXXGPGXXXCXCLXGXX
XXXTXXXXXXXXXXXCXXXSCHXXAXCXTXXXGXXXCXCXXXXXGVXXXXXXXXXXXXXX
LXXXPXGXXXXXLXXXXXXXXRDSEXXXXXXXXXXXXXPXXXXXXCXXXXXXXXXXXXPX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXTDXXIXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXPXXXXXXXXXXXXXXXXDIKEFSXXXXXXXXXXXXXX
XXXPXXXXXXXXXXXXXXXXXXXXHXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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ASVRPSIYFSXXXXXGXXXXXXXXXXXXXXXXXPXXXXXXXXSXGXIHXXXKXXXTGX
XXXXXXXXXXXXXXXXSSXXXXXIXXXXXXXXXXXSLXXXXXXXXXXXXXXXXXXXXXTX
XXXXXXXXXXXXXXXXXXXXXXXXXXXKXKLXXLXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXKXXXXXXXDXXAXNGXXXX
XXCXXXXXXXXXXXXXXXXXXXXXXXXXXPXXXXXXXXXXXXSXSGXXXXXXXXXVXX
SXXQQXPXXQPXXXXXPXXXXXPXSXPXXXXXXXGXXXXXGXXXXXXXXXXXXXXXXXX
XXXPXXXXPXXXXXPHXCXXXXXXXXXXXXVXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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XXXXXXXXXXXCXPGXXGDGXXCXEXXXCXXPXRGGCXXXXXXXXXXGPGXXXCXCXXGWX
XDGXXCXXINNCLXXSRGGCHXXAXCXXXGPGQXXCXCKXGXXGXGXXCXXXNXCXXXXG
GCHXXAXCXXXXXGXXXCXCXXXYXGDGXXXXXXXXXEXXXNXDXXXFNXXXXXTLYKCY
KRILIKSNILQRAXLXXXXXXXXXXTXXVPSXXAXXXXXXXXXXFWXXXXXXSLPXLXXX
HXXXGXXXXXDLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXFSLXXXXXX
XXXXXXXXXXXXXXXXXXTXXXXXXXXXXXXXXXXXXXTXXXXXXXXXXXXXXLXXNVXXY
XXXXXEXLXXXXLLPXXXKXXSDXEXXLTVGQYVLCRWXDGLXXXXXIQRXXXXXQXXFV
TFXXXXXXXXXXXXXXXXXXXXXXXXXEXXXXXXXXXXXVLXXXXXXXXXXXXXXXXGXCG
XXXXXXXXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPSXXNS
XXLVTETKQEXSGXXKXXXXXXXXXXSXXXXXXMIXXXXXXXXXKXXXXXXXXXCXXXXX
FQVTIAAXXXXXXXXXXXXAXXXCXXXXXFCXXXXXXXXVRXXXXXXXXXXXXXGXXXX
XCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXLELQQEKKYMXXXXXXXXXXXXXX
XXXCXXXXXXXCXXXCXXXANCXXXXXXXXXXXXXXAGXXGXGXXCXXXXXXXXXDNGG
CSXXAXCXXTXXXXXCXCXXGXXGXXXXXXXXXXCXXXEXXXXXXXXXXXXXXPXXXAC
XCXXXFXXXGXIXCXXXNXCXXXXGXXXXXXXXXXXXXXXXXXXCXXGXXXXXXEXXXX
XXXXXXXXXXXXXXXXXXLXXXXXXXLXXXXXXTVFXPXXXYXXXXXXXXFIXXXWXXXX
XXXXXXRXHXVXXXXXXXXXXXXXCXXLXXXXXXXXXXXXXXXGXXXXXXXXEXGQXILX
XXXNXKXKXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXIFXLXXXXXPXXX
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XDAATRAEVTPNSTSGSATTSVSYDFRKNVGSRKRKLAADELGWSPSSNYXXLAXTTQCG
GIGXXXXXXXXXXXXXXXXXXXXFXXXGXXXXXXXXXXXXRQXPXXXXXXXXXXXXENX
IDSHXXXXXXXXXXXXXXAXSXXXXYIXXXXXXXXXXXXXXXXXXXXLXXXXXXXXXDF
ISERVXXPSXXXXTXXXXXXSXXXXSQPDIETXXXXXXXXXXXXSXSXXXXXXXXSXXXX
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XXXXXXXXXXXXXDXXXXXXXXXXXXXGCXXXXXXXXXXXXXXXEETSFETATXPXXXXX
XPVXGXXXXXDXXXXXXXXXXXXXXXXGXXXXXXXPXXXXXXXXXXXXXXXXXXXXXXX
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EXKXXXXXXXXXXXXXXXXCXXXXXCXXXXXXXXXXXXGXXXTDTXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXNGXXXXXAXXXXXXXXRXC
ECXXXYVGXGXXCXXKVXPPVXRCLXDNGXCHXXAXCXDLHXXXKTXGVFHXRSXXGXYK
LNYTXAXEACXXXXXTXATXXQLSXAQQXXXXXCXXXXXXXXXXXXXPMXXXXXXAXXPE

NXXXXXXXXXCGXXXXXXXXXXXXXXXXXXGEAEXXXYXXXXXXXXXTXXXXTXXXXXXX
XXXXXTXXTXXXXXXXXXDXXCXXXXXXXCXCXXGYXGXGXXXXXXXXXXXXXXXXXXXX
XXXSXFXXXXXXXXXXXXXXXXXXXXXXXXGXXXXXXLSXXXXXXXXXXXXXXXSXXXXX
XXXXXXXXXXXXSXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXTXIXXXXXX
XXXXXXXXXXHXXXXXXXXXXXXXXXXXXXPXXXXXXXXXXQXXXXXXXXXXXXXXXXX
XXXXXXXXQXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXTPLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXNPX
XXXXXXPXXXXXXXXXXXXXXXXXXXPXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XSXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGXXXXXXXXXXXXXXXXGPHXXXXSXX
XXXXXXXXXXXXXXXXPXXXXXXXXXXXXXPXXXXXGXGXXPXGXXXXPXXXXPXKKRXX
XXXXXXXXXIXXPXXXXXXXLPXXXXXXXXLPXXXLXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXGXXXGXXXXXXXXXXXRXXXXXXGXXXXXXXXXXXXXXXXXXFXXXXXXXXX
XXXEXXXPXXXGXXXXXPXXXLSXXXXXXKPSXXXLXXXFPXXXXXXXPXXXXXXXXXXF
LPXXXXPXXXXPXXSXXXLXXXXXXXXXXXXXXLXLXXXXXXRXSXXXXXXXPXXXXPXX
XXXKXSXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXXXXXCXXXGXXXXCXCPXGX
XXXXCXXXXDXCXXNPCXNGGTCIDXXXXFXXXCXPXXXXXXCEXDTEXCXXGXXKFXXX
CYXXXXXRXTWXXAEXXCRXXXXHLXSXXSXXEXXXLXXXXXXXXWIGLNDXTVEXDFXW
TDXXXXXYENWRXNQPXXXXXXGEDCXVMXXXEXGXXNXXXXXXXLXXXXXXXXXXCXXP
XXXXXXXXXXXXXXXXXXXSXXRYQCXXGFXQRHXXXXXCXXXGXYLPXWXXPXXSLSXX
XLPKLYLARLSLPKLYLPRLXCXKLSLPKLYLXXXXXXRXYXXXXXXXXXXXXXRRXXXX
SXXXXXXHXXHGXXXXRXXXXXPPESTPXXXXLXXXXXYXXXXSLXXXYLPXXYXXXXXX
XXLXXXSLYLSRLSVPKLLSLPKLYLARLHLPRLYLPRMSLPKPSLXXXXXXXXYXSXXY
XPXXYXSXXYXPXXYXSXXYXPXXLXXPXXXXPXXXXPXXXXXXPFLPKXYXPXXSXASR
QSSSARTSVQLTPXXXLXXXXXXRXXXXXXXXXXXXXXXLEQIGRFMXXXKXXLXXXXXS
XXSLPRL

==> Ovalentaria.txt <==
>MSA Consensus of 378 seqs, protein
MACRNSGGSKILLRLGIFMFATSXXXCXXXXXXKALXXPXXDSMQSQTKRTNQHHGRLLI
GHNPXXXXXXXXXTXXXIXXXXXXXXXXXXXWXXXXXXXXXXXXXXXXXXXXXXEXXV
ECTGXXXXXXXQXAXXMPASLFFVXXXXXLXXXXXXXXPPSCGYTIRSXXXXXXLXXPXX
XXXXXXXXPQXXXXXXXXXXXXXXXXXXXXXXXXPXXXXXXXXXXXXXNPPXXXXXXXXX
VXXXXXXXXXXXXXXXPTFXXXXXXXXXXXXXXXXXXXXXPXFSPAXXXXFSPXXPPXXXX
XXXXXXXPXXXXXXXXXXXXXXXXXXXXXXXXXPXXXXVXSVXXXPCXXXXXXXXXXXX
XXXXXXXXTXXXXXXXXXXXXXXPXXXXXXXXXXXQPXQXXXPXXPXXPXTXXXXXXXXX
XXIPPXXXXXQEPKSKESLTASYAEKAKQNXXXXXXXXXXXXXXXXXPXXXXXSYXPXXP
XXXXXXXXPXXXXPXPNXXPXXXXXXXXXXXPXXPXXXXXXXNXXXXXXPXXXXXXSXXP
XPKSTXXXPXXXXXXXXXXPIXXXXXXXXXPXXPXXPXXXXXXXXXXXXXXXXQXPXXXXX
FPPXVXPXYPXXXXPXXXXXXPKXXXXSXXXXXQXRXXXPXXPSGKKTTXDLLXTPPEPX
XXXXXNVPXXXKXPXXXXXXXXPXXXXXXNPXXXXXXXXXXPXXPXXXXXXXXXXXXXPX
XXXXXXXXXXXXXXXXXXXXPXXPXXXXQRSTNXXPTXXXXXXXPXXSYPVFQXPXXPQIX
XXPXXXPXXXXXHLPQXPQXPVXPXPXXXXXPXXXXXXXAXPVXPPXXXXXXXXXXXXXPX
XXXVPDVENPXXXLXXPXXPXXQXXPXXPXXXXXXXLNLICXXXVXXXXPXXPXXXXXXX
XPPXXPXXXDEXXXPXYXXXXXXXXXXXXPXXXPXXXPXXXXRXXXXXXPXXPXNVXXXXX
XXXXXPXXPXXXXXXPXXXXXXQXPQXXXXXMSXNPXXPXYXXXPQXXXXPXPXXXXXXP
XXXXXPXPPXXXXXPXXXXXLQTYRYXXXXXXXPQXXXXXXPPPPPXXPQXPXVXXXXXX
PPXPXXPXXXXPXXKXLXXXXXPXXXXXXPXXXPXXXXXXXXXXXXXXXXXXTXXPXXPX
XXXXXXXQPXXXXXPXXXXXXXXXXXXPPXXWPYPQXPXXHXXXXXPXXXXXPXXXXPPXX
XPXXXQXPXXXXXXXPPXXPXXXXNXQIXXPPXXXPXXXEXPXXXXXPXXXXXXXXXXXX
XXXXXXPXXXXXPXVXXPPXXXXXXXXXXPXXXXTXXXXPXXPXXXXXXXPXXXPXXXXXX
XPXXXXXPXXXXKXLXXXXXXXXXXXHXXXXXXPXXPXXXXXXXXPXXXXXXXQXXQIXXP

XXXXPLVXXPLDLQTXQXXXXXXXXXXPXXXXHXXXXXXPXXXSEENXXXXXXXPXXXXX
XXXXXXPXXXXXEFXXXXXXXXPXXXXXXSVHIQCYLXXXXXXAXXGXXSXXXXXXXXXX
XPXXXXXXXXXXXXPXXXXXPXXXXXPXXXXXXXXXXPXXXXXXPXXXXXPXXXXXXPTX
TXXXPXXPXXPXXXXXPXXXXXPXXXXXXXXXXXXXXXXXPXXXPXXXXXXXPXXXXXAPX
XXXSXXTXPXXXXPXXXXXXNXXXXXXXXPXXXXXXXXPXXXXXXXXPXXXXXXXXXXXX
XXXXXXXXXXPXXXXXXPXXXXXXXXXXXXXXXXXXXXXXXXXXXGXXXEXMEVXXXXXX
XXXXLLLXXXXXXXXXXXQXXXXXXMEXXXXXXXXXPXXXXXXXXXXXPXXPXXXXXXXX
XXXXXPIQXXXXXXXXXXXXXPXXXXXXXXXPXXXXXXQXXXXXXCXXXXXXXXXTXCTT
PXXXXPXSCXXXXXXXCPXGXXXXXXSXXXXCXYXXXXSXXXXXXXXQXXQNPXGCXXXC
XXXXXXXXCCPXXWGPXCXXXXCPXXXXXXCXXXGXCXXGXXGNGTCXCPPKVXXXXXXX
GFXGXACXXCXNXXXXGXXXCXXXXXXXXXXXXXXXXXXXXXLXXXGXKVXXXXXXCXCX
XGXCXXGXXGYDGXCXCXXXYXXXXXXXXXXXXXXXXXXXXXXXXCXXXXXXXXXXXXXX
XXXXXXXXXXXXLPGYXXXXXXXSRSKLKNDXXXXXXXXXXXXXXHCADTQXXCXXXAXC
XXXGXXXXXCXXXIENAQPLXCXXXYXGDGXXCXPXXPCXXXNGGCXXXSTXCVXXGPXX
SXCXCXXGXXXXXXSXEXXCXLXXXXXXXXXXXXAXXXXXXXGXXXCPXXXCXXXXXXXX
XXXXSXXXXXTSSYXAXGXXXXCYGNXMXXLXXLXXXXXXXXXXXXXXXXXXXXXXXLX
XXXYXSXXTSXXXXXXXXXAXXXFXXXXXXXLXXXGPFTXXLXPXXXPXXXXYXXFXPXX
XXXXGXXXXXLTAXXXXXXXXCXXHLXXGXXXXLXXXXXXXPXXQXXXXXYIHXXXXLXX
XXXXXXXXXXXXXXXXXXXXXXXXIXXXXXXXXXXXXXXDLXAXNGXIHIIXXXXXXXXX
DXXXXXXXXXXXXXXXXXIXXXXXXXXXFXSLXXXXXXXXXLXXPXPXTVFXPTXXAXXX
XXXGXXXYXXXXEXXXKLXEXLRXHXXXXXXXXXXSYXAXPVKLSYXXPVSPEXSXXXIX
XYLXXXXXXXXXXXXXXTMANQXXXIXXXXXGXXLXXXKGXXXXXXXXXAXNGXXXXXXX
XXXXXXXSIXPXLPHRCDXXXXKXXXXXCXXCXXXXXXXCXXGXXEXXXXXXXXXYXXXX
XGXXXXXXXXXXXXXXXXXXXXXXXXXCCXXXXXARLASXEXXXXPXXXXFXXPCXXXG
XCXXGXXGNGSCTSXYTXCXXXFHPPIQLYIHLXGXXCXXCSTYTALHPPIXXXIXLYIX
LYXXXXXXGXXXXXXXXXXHXXXDXRXXXXGXCXXXSCXXGXXGXXCDXXXXXXXXXGLX
XXCXXXXXCXXXXXXXXCXCXXGXXGDGXXCXXXXXCXXPXXXXXARLXXFECKXXXXCX
XXXPXXXXCXCXXGWTXDGXXCXXINNCXXXXRGGCXXXXXCXXXGPGQSXCXCKXGYXX
XGXXCXXXNXCXXXXGGXXXXXXCXXXXXGXXTCXCXDXXXGXXXXCXXXXXXXXLXXXX
XXXXXXXXXXXXXXXXXXXXXNXTXXVPXXXXXXXXXXXXXXXXFWXXXXXXXXXXRFD
VSFRXHXXXGXXSXXXLXXXXXXXLXTXXXXXXXXXXXXXXXXXXGXAXIXXXXXXAXXG
XXXXXXXVLXPXXXXLPPEXXXLXXXLXXXXXFXXXRXXXXXXNLTXXXXXXXXFTXXXP
TDXAXXXXLXXXXXXXXXXXXXXXYXXXXXXXLXXXXLXXGXXKXXLLXXXXXXXXXXXXX
XXXXXNDXXXXXXXXXXXXXXXXSKEXXSQEXLXXXXXXDXDDXDXXXDXXDXDXXXDDX
DXXRNRCXXXXXXXVQHDDHDDQHDDHDDHRHDHKDQDDXXGXHHDDQDXXXXXXXXDCX
DCXXXXHDDNDDXDDXXXXXXXXXXXXXXXXXXXXXMXXXCXXRXDQXXXXXXXXXXGCXX
XCLXXXXXXXCCXGFXGXXCXXCPGXXGXXCXXXGXCXDGXXGXGDXCXCXXGFHGTACE
XCXXGXYGVXCXHDDPDDHHDDXXCXCXXGXDRDDHHDDHXDCXXGLXGXGXCXCXXGWX
GXXCXXXIXSXADXXCGXVXCXXXANCXTXPXGXAAXCXCXAGXEGNGTXCXQPTXYXXX
DXXDXCXXXXXXXXXXXXXXXXXXXRDRXXXGXRXXXXXXXYXXDGXXXXEXHDDXXXCLX
XNGGXHXXXXXXXXXXDDHDDXXXHXDHDDXEVEXHDDXXXHXDHDXXXXXXDTDXXXHY
DXXHXXDXDXHDDXXXKXXXXXXXXXXXXXXXXGXXXXXXXXXXXXNGGCXXXAXXXXXXX
GXXXCXCXXXXXGDGXXCXGTXXXEXXXXXXXXFXXXXXXXXXXXXLXGXGPFTVFXPXX
XXXXXXXXXXXDLKXXXXXKXXXXXXXXXXRXHXVXCXXLXXXDXXXXXXXXXSXSGXXL
XXXXVXXGXXXINXXSXXXXSDXXXXNGXIHXIDXXLXPXXXXXXXXXAXXXXXXXXNXT
XXAXXXGYXXFYKLXXXXGXXXXXXXXXXXXPXTHGAKRCEXFXPXDXXXXXLPXXXIXX
XLXXXXXXXXXXXXXXXXXXXXXKPKYXXXSWXXXXXXXXXXXXXXXTXXGSXXXXXXXX
XXXFXXGXXEEHYPKSQLSYSPSQRPVTXVXEXXXXXLPGEXXXXXXXXGXXXINXXXXR
XXRLYREERDYGDHVSRSKSSVHHHXRXXXFXRETTPLSSSDKRHTYSREPKEYRGKYRY
DSSSPEHSPEPARPKQDLRRSYEHRERRYSRCSSYERSSRRHSPQHRRSHRDLCYSPREY
RXXXXXGXHSPEYRCRYSPERREGRRPSTPRYEHRRDXXXPPXXQERTYRGPTPTIPDF
NHPKPREFARLRIALDNLLPRDATERFKFQILVDHLKLEEALLVADSYSNSDYPFTDTMA
ALNQQYGQPHQLXXXCIAELMDGPNIQSXXXXXXTXXXXGAIXXXXLIVAXCXXGLKGAX
XXXXXXXXXXGXCXXXXLGKLXXXXXCXXXXXDTGXXXXCXXLLNLADWLEYELLIQEDI

AQXRRKXDTGAKSKDSKSTAKPLPKALFLMLGAGTXPVGKPXXXXXXXGXXXXQKXRXPX
XXQXXXXDXXXDVSSXXXXXXXMNVDGXXXXXXXXXXXXXXXXXXXXXXXXNNRCWRCGRD
HRSAECDLKMCCKTCNSRHLLALHEVSERMPAAGGPAERKPEPMXXXGSXXXPXXXXLGY
ALXXXXXXXXXPXGXXXXXXXXXVXXXXXXXXFXXXLXXXXXXXXXTAXXXXXXXXXXXX
XCXXXXXXXXXXXRSRMXLXXXXXXXXXXXXXXXXXXXXXXCXXGXXXXGXXXGXXXXX
XGXXXXXXXXXXXXXYXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXKXXXXXXXXXXXXXXXXXXXXPXTSQTRVDTSYTXXXNGXXCXXXXXXXXCX
XXXXGXXXXXXXXXXXXXVXCTCXXRTDSXXXXXXXXXXPXXXXXXWXXXXXXXITTAVX
XXXXXXXXXXXXAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPYXLXXXXXXX
XXXXXXXXXXXYXCXVXXXXXXXXXXXXXXQXXDXGLXXXXVFXXXXXNXLXXXXYXXXX
XXAXXXCXXXXXXXAXXXQLXXCXVCNKNIGSEXVRRLSLRWVDXVHLVLYNLSXXSKKK
YFAXXXGXXXCXAGWXXXXXXXXXNTPPAERGQHLLDALNXXXXXXXCGXXXXXXXGXXX
LRTRVPPNPPSKLFPERAQXDGXXXXXXXXXXXDLLLPAXXACXWTKRNRGDXXCFXXXX
VXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXFXXXXXXXXXXXASXXXXLXXXWXFXX
XXXCXIFDFTLDEXGXLXXXXXXXXXXXXXXXXXXXXXXXGXXXXXXRXXXXXXXXXXFP
XXXXXXYXXYCXRXXXXXXXXXXXXXXXSXXXXXXXXXXSXXXXXXXXLRSSTILTXXXSX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXTQXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXEXXXXXXXXPXXXXXXXXLHSSISSY
XXXXXXXXXXXXXXXLARXXXXXXXXQYLXXWXXXXXPXXLQFDSWHRXAYEXXYXXXXX
NIXXXXXXXXXXXXXXXXXXKXXXXXXXXXXXXXYGLRXXXXXXXXXXYXXGXXXEXXXX
XXXXXFXXXEXIXXXXXXXXXXXXXXXXIXXXXXXXXXXKXXXXXXXXXNXXXXXXXXXX
XTPFXXGXLYAAXXXGXDKCRXXWXXXXXXXXXXNXXXXXXXXXXXXXXXXXDXDXXXXX
XXLXXXXXQXXXXXXXXXXDAYCXRXXXXXIAXXXXXXXTXXXXXXXPXXXXXXSXXXXX
XXXXXXTXTXXXDKXXXXVXXXXSGXGXXXXGXXXXGKXSGVQXXSGDQXXSGXXSGSGX
KEXXXSGDQSGSXLAEXXXXXXXXSGSGDXXTRGEXXXRGXXXXGXXXXXGXXXGXAXX
EGSGEITGAEAKGGSGXQSEIQVSRRPXXXSKPXXRSRERSQVTSXXISGSGGKIXFGDQ
XGYTETVXXSXGXXXGXXXGXXXTXTTTTXTXXXXTTXXTXXXXXGTXXXXXXXXSXXGX
XQEAGXGSTXXXLXXXXXXXXXXXXXXXXDXXXXXXXXXSTESGSXXXXXXGXXTXXXXX
XXXXXXSXXXXXXXSGXXXXXXXSGDXXILXXSXXXXXXXXAXXXSSXSXXXXXXXXLXX
SXSGXXSGSGXLICDLNGDCSGDLSGDLSGDLSGXXSGDXSGDXSGDXSGNLSGDLSGDX
SGDLSGXLSGDLSGNLSGDXSGDLSGDXSGXXSGDXSGDLSGDLSXSXSXSXXXXXXXVT
XXGSGXXXXXXXXXXXXXXXXXXLXXSXXXXSXXSXGXXSXXSXXFXXXXXXFDXRAXXS
GSXXSXXXXSXTKXXXXGSXXFXXXXLMTXXXXXSXXXSXXXXXXXXXSXPPXXXXXXX
XXXXXXXXXXXXXXXXXDXSXDXXXXXXXVXXEXXSXXXXNXSLXXPXXXXXXTEXXXGPX
XDXXEXAWSHXVGSGXXLPXXXXEXXXXXXXXVXXXPAVVPXGXXXXPXXVXPXXVXTXX
SXXXXVXPCXXNPCLHGGKCLPQGTTGYSCYCPQGXXGENCEIXVDDCQSEPCXNGGTCX
DKIDSFLCLCLPSYGGDXCEKDXXXCEXGWXKFXGXCYRXFXXRXTWXXAEXXCRXHXAH
LXSXXSXXEQXFXNXXXXDXXWIGLNDRTVEXDFQWTDGXXLXYENWRXXQPDNXFXXGE
DCVVXIXHEDGKWNDVPCNYXLPXICKKGXVXCGXPPXVENAHXXGXRRSXYXIXSXXRY
QCXXGFXQRHXPXXRCXADGXWEXPXXXCTXXXXXXRXXRXXXXXXXXXXXXRRHGGEGH
KXREDAXSYYRTK

==> Passeriformes.txt <==
>MSA Consensus of 186 seqs, protein
MXXXXXXXGXXXXXAATXSXXXXXXXEXXXXLXXXDSRSQECCSXXXDDKXRGSQSQIVL
XXXXXXXXXXXXXXSXXXHPFXXXXIFSXXXXXXXXXMXXXPXXLXFFXXXAXXXXXXXX
QXQXXXXXXCXXKXXXXXXTXCXXCXXXXXXXCPXGXXKXTXXXGXXDCRYXXXXXXXTL
SXPGCXHXCXKEXEXXXCCXGXWGXXCXXCPGGXXXPCNGXGXCLDXQGPNTVISSVSRR
SCITMQRERTLLTGHSWQWNMHLSEIDKKPIXXNGTCXCXXXXXGXXCXXCXXXNXFGPD
CXSANPFLPVXCDCVHGXCXSGXAGXGSCTCXXGYXGXRCDQXXXXCXXXXCXANSXCVX
XXXDGXXXXCXCXXGXXXXXXXCXXXXPCXXXXCXPXAXCXXLGXXXXXCTCXEGXXGDG
XICXPIXPCXXXXGXCPXXSXICXYXXPGXVSVTAQEEIMLYLQKEPMRVWKQLPRKSNA
IPNFTISPAVDQEGVLLAPLKTGMTIXXCXCKXXXXXXXPXXXCSXXXSXXXXXXCXXXA

XCXXXXXGXXXCXCXXGXXGXGXXCYXXXXXXXXXXNAEXXGXXXXKLXXXXXXXXXXXX
XXLXXXGPFTVXVPXXXXXXXXNXKDXXXNXXXAXXXXXXHIXXGXXXXXXXXXAXXXXT
LXGXXXXXXXXXXXXXXRXXXXXGRXXXXILQXXXXAXNGIXHIXXXXXXXXXXXXXXXX
XKTIXXXLXXXXXXSXFXXXXEXXGLXXXLQXXXXPXTVFVPSNXAXXXXXXXXLXYLXX
AEVQSFYEGXXKLXELVXXHIXXXXXXXVXXLXXXXHIXTMAXQXXXXNXXXXGXXLXXE
SGXXXXXXDIVAXNGXIXTLXGXXIPPXIVPILPHXCXEXXXKIVMGXCVDCEALNNSIC
PPGSKEMEPTXXGXXMVQPLSPKECVYIHDPQGLNVLKKGCARYCNQXXXXPXCCKGFFG
PDCXPCPGGFSXPCXGXGXCXDGXXGNGXCXCXEXFXGXXCXXCXXPXKXGXXCDXXCXC
XXGXCDNRXXSXGXCXXXSCXXGYTGKXCXXXXXXCXPSGLXQXCHXHAXCXLXDGTXXC
XCXXGYEGDGXSCXXXDXCXXXXXGGCXXNAXCXXTGPGXXXCXCXXGWTGDGXXCXXIX
NCXLXSXXXCHXNAXCXYXGPGQXXCXCKICSCPDGFQGDYLNXXXXGIECLFXATCKRG
YAGDGXXXDAINXCLXXNGXCHXLATCXXXXXXXXXCVCXXGYXGDGXXCYGXXXXELXX
XSXXXXFXXWVXKSLRMNYFTLFILMQEAKINXXXXXXXNXTVLVPSXXAIXNXXXXXKX
FWXXXXXXPXLXXXHXLXGXXXXXXXXXXXXXXMLPTXXXXXXXXXXXXXGXLTXXXAXX
VXSDIXXXNGXIHVXXKVLLPSPXXPLXXXXXPXLXXXLXXXXXXSXFXXXXXXYXLXXX
XEXXXXYTXFXPXNXXIEXYXXXXXXXXLDXXXXXYHXVLXEKLLXXXLXXGXHXXXMLG
XSYXXXFXXXXXQXXXNXXPXXXXXXXTXXGIXXGXXXVLXXQKNRCXXNXTXILXXXCX
XCXXXXXCPXGSVRDCKSESVSGXXEXXGXXXXAXCXLXENHMXXXXXXGCXXXCAKXX
XXXXCCXGXXGXXCXXCPGKXGXXCXGNGXCXDGIXGXGXCXCXEGFXGTACEXCXXGRY
GXXCXXGTERPQDTQELHRPLSVQTFPFYLLTLLSPRSRKGQWLXPXXPTXCXCXXGXCX
XGXXGDGSCECXXGWXGXTCXXXSIVLPEXAXTPDXEIKXDXCNXXCSPHRRHSNRATRN
STSSLTSVHXXANCLXXSXDXXXXCXCXAGXXGNGTXCTXXXAXWXXLXXXPXXXIDXCX
XXXGGCSXXAXCXXXXPGXRXCXCXXGYXGDGXXCXEIXXCLXXNGGCXXNAECXXTGPX
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CXQNNGGCSXFXXCXXTXXXXRXCXCXXXXIGDGFXCRGXXXQELXRXXXXSXFXXXXXA
XSIXXXSGXGPFTXFVPXTDXXXHXXXXXXWXXXGXXXXXLRYHMVGCXXLLXXDLXXX
XXXTSLXGXXIXIXXXXNSXXLNXXAXXXXSDXVGXNGVIHXINXILXPSXXXXXXXXXK
LSXLFAFLPXQXXXXXVAXXXGYXXXSXLLXXXXLLXLXXXPXHXPXTLXWPTDXAXXXL
PXXXQXFLXXXXXXDXLXXYLKXHIXLLPLLLXAXXXLXXXXXXXLXRDXXXXAXXXPXX
XXXAXTXXGSXXSXSCXXNXXXXGXXXXXXGXXXXXQRXXEFXGGIPGSSPPLTAYGIXX
LLXXPXLGXRCDXFXXXEXXXSTEXXXXLTXFLFSLFQGXCXXCXXXXXCPXGXXXXXXT
XRCYYYGNXLLRNTFLFHXNSLLRXXWPXHSXWDPFRXXXXDIAVLRRLAARLSSRAEMV
GAVRQEKRMSKATEVMMQYVENLKRTYEKDHAELMEFKKLANQNSSRSXGXXRXGCRRXX
XXXXXXXXXCCXRRRVSVAVVPKFXXXXXXXXXXXXXXXXXXXXXXXXKFSCHGMXXXLSG
QTXXXXXXXXXGXXXXPCXXXGXXDXXXXGXGXXXXXXXRXKWXKXXXXXXXXEXXFXGT
XCXXXXPGXXXXXYGXXCRXCXCXXNGXCXXGXXGXGXCFCXXGWTGXXCEXXLXXXPXC
SPXCXAXAXCXXXNXCXCXXXYXGDGXTCXXXXXCXQXNGGCXXXAXCXQXGVXVXCXCX
XXXXGXXXXCXPIXXCADXXXGXCXXXXXXXXIXXXXXXXXXXXXCXXXXXXXXDXXXXX
XXXXXXXXXPXXXXMANFXXXXLXANXFGLXLLVSXXXXXXCLXXTYFVXXTGEFNXXCX
XXXXCXDLHFXDXTGXVFHXXSXXXXYXXXXXEAXXXCXXXXXXLATXXQLXXAEAFQKE
LLXSXXPXXSXDGXXXXXAXXXGFXXCXXGXXXXXXGXXXXXPXXXXXXXCXXXXXGIX
XXRXXNXXXXNXXXXXDAXCYXXXEXXXKSTCXPXXXXDXXXCXXNXXXXXXDXXXXSXX
XXDXXXXXNXXXXGXXXXXXXXXXSXXXXXXXXIPGYPGXTLFAPXXSGXXDXXXXSGXX
XXXHXXXXXXXXXSXXXTXGXXXXXXXXXXXXXRSSPSYXXXXTPVSXLXXXEXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXHXIXXXXLPXXXXXXXXXXEXXXXXXGXXPEPGVRX
EKGXPXXIXXXHXXFXXXXXXXGXXCXXGXXXXXXEXPSVSXXXTXPDLXXXXXYXXXXX
XTXXXXLAXXXXXXXXXXXXXXCXXXXXXAXXGXXYXXXXRXXXXXGXXXXXXXXXXKDE
TEAHIXYXXXXPXDXSIXXXXXXHXXXKEXXXXXXXNPFXXXXXXXXXXXXXXXPTXXXX
XXXTXXXXXXXXXXXXXXXTXXXXXXXVESXEXXXXXXFPSETFSXXXXXXXXXXXXXXX
XXXXXXXXXXXXTXXPXYDXPGAKMFYDSXDXPXXPXXXTNDTKTXXXXXXXTXXXWXXX
XPXXXXXXXDDXXEXXGXKXXXXXXXTXADVTSSGSDSDDEDSXXXXXXXTXXPXXXXXX
XXXXXXXAPEEGLTQIVAVSIKSATTXXXXXXXXETLXXXTXXXXXXXXXXXXXXXYPXX
AXXXXXXXXXEXXXXXXXXXXLXXXXSXXXSXXETSVTXXPXXXTXXXEXXXXTTAGXXY
PEQVATTAPAPDIITDTASQEXXXXXXLTQGLGEKPXPTSEPCEGEDXXXXSXGAIIAVI

VILLCLLLVXAKQNXXXXXXXXXXXXXXGSLXTDKNXXYXXXPAXXXRVXPSXXXXHEPS
ARESSTTAAVASPDGAHHKEPXQXPGXXXLPWDXESEMPXXAATXSTEGIXNPTDAPXDE
VVVSXXXGXXQPRHHCYHHYHHXHXXXXXXXKXPXXXXXXXXXSXXXGXXSXXXSXAASM
SXXVXXXPSXXPXXVGXXVTXXXXXEXXXXXXXXXFXXVXAVNLAFPXXEXGXXXVPXXX
XXXXTKDMIIKTVTASXDXLAPEDXTQTAKHSKXXPELSTLDEXWAPHLVVTXASSPXGA
HHXEPTQTPLXXXPXTAIQESDDEXGQGTEGITNPXDTPRDEXLHRTTXSVTXTXXXSSW
XXXXXXXVXEXXDDADQEKATKEPLAPGTAPGREGEPANTTDGXHVXVSWDSXPHVHGIP
GVFSDIEDRFIPXQTXLTTSSTSSVYGNQGPXKEXXXTXPXXXXAXATXXXGXYESTTSP
GEXXTTKIXSQPRSAXVPDWLIIVXALVVLEEEEEVTSALILAVCIAVNSRRRCGQKDXX
GXXKKLVINXEXXXASTATAVARNGXXPXXKGAVEDRKTSELNGDXXISKSQEMVHLVHK
EQSNDRTQACDEFLTVNETQNHPHEFDETHIDMKTGVTEPCTSDSVQDSSEYIILDPFFP
NYAEFEEDEDCENTTDVTTPPALQFINGKQQVTSAPKSTKAEEARSDQIESVAHSKNVTF
SQINETNTFIINESEASGTMHPSKAGEVIGAFEVTQPTSGAAMLEPVYSGESEVVTTDKP
IAITSSHEQSLQNSRETMTWQGTGETSPKDSKNLLFISSESSGDSSTESDLSTSVLEIVT
GSRKKDDEKNSEGSGDVRDSITVTSAMTEEVAVTETLSVQDISLGSSTALLTEFSVIDSE
ITSALPRAISTPYSAFDQSPEVTVATNSVSELITEKVFASSLVTEKSIDDEKEILATVYS
GHQNSATPAEENLDLNELGSTTSEAGTVSQEPLRKTVPDTISSEIKKVTTIPLLREKLFV
NEGSAEEPAHIFSGGPTSKVDATTEYEKHARTDQSAATTLSTVSESFTEGSGVESQMSLD
MFSTRKPGEPNMETKPTYTAPSDIKSGSIKETTSHIAPGVETGHSEMGEATSSPESVISN
NSHEDVVTHGTGSIKTVAESTESKDAKVVSSTVSLGKIFLIEHGSGEEFKDDSSTTKLMS
NGPTEEIFGGHFSITDQGSGEPDTSTSSFAKSDVAPSGRPETWEEDDKQAVSTSPLDLAF
TTDPDEQVTSSEHEVTSMGTAGDMQTEEKTVDELTVRTFSTKIPLMEEIHSGEEGPIEIT
PKAMESSEETTTDLFFKSTQTSHEHLGFLDVPTLSPYLEEKELETEPVKKILLPFNDDKV
TEPVTIERKYTSSPVTIIEQEEELVQNIFPTKDIPRTFLTPKEEKLSNNELIGDPLFSGQ
GSGDDLAVLPSVVPFIVKEIKSTSSPQTSHPANMGPQLTLT

==> Pecora.txt <==
>MSA Consensus of 165 seqs, protein
MAGPRGHLLLCFLALCLAGPSFFGEQKGPGPMLQSVILFFLGLVVQNPGDLPDQGIEPVL
XXLXXXXVXSKRCDXKXXXXXXXXCXXCXXXXXXXCPXGXXXXXXXXXXXXXDCRYXXXXX
XXXLSXXGCXXXCXKDXXQXXCCPGXWGXXCXECPGGAXXPCSGXGXCXDGXXGNGXCXC
QEXFSGXACXXCXXXNXFGPXCXXVCXCVHGVCXXGXXGDGSCXCXXGYTGXXCDXXXLX
CXALXCPXNSXCSXXSKDEXXXXCXCLPXYXXXGXXCXXXXPCXXXXCXPXAQCXXXXXX
QXXCXCXEXYHGDGXVCLPXDPCXXNXGXCPXXSTXCXYXXPGVGAQRSSLGSHGHGVTP
TLPGRAGQAXCXCKXXXXXXXXXXXXXXXXXCXSXXXCXXXAXCXXXXXGXTXCXCXXGX
VGDGXXCYGXXXXXXXXXXTEPXXXXXXRLXXXXXXLDXGXXXXLSXXGPFTXXXSNXXX
XXXXXXXXFDVFXXXXXXRXXXGXXXXXXXDPSXXXXXXXXXXXLXPXXXXXKXFXXXXAX
RNVXEXXXXXXXAQXXXXXHIIAGQXXXEXXXTQXXXXXXTLXGXXXXXXXFXXXXFSXX
XXXXXXXKXXLXXXXXTXXIXXXNXXAXNGLXHXXXXXXXNLHRGXXXXXLXXXCXXXXX
XXLDXPXPXXXXXXXXTIXIXXXLASXXXXSXFXXXLEXXXXXXXLXGDGXXGPXTVFXP
SXEAXXXXXDGXLXYLXXSXGXXKLXELXRYHXXXXXQLXVXXLXSXXXXXXMXXXXANQ
IXXXNXXXXGSPXXXXILXGPXGVXLXXXXVXAXNGXIXXLXGVLXPPXIXPIXXLXXXL
PKVXXXXXXXXXXXXXXXXXXXXXXXCXEXGXXXXXXXXXXXXXXXGXCVXCXXXXXSXCPX
NSXXXXXXXXXCVYXXXPTGXXXLKXGCAXYCNXTXXXPXCCKGFXGPDCXQCPGGFSNP
CXXXGWSPWXEWTXGXGXCXDGXXGXGXCXCXXXXXGXXCXXCSXPXKXGXXCXXXCXCX
XGXCDNRXXSXGXCXXGSPWSSCSVTCXXGXXTRIRLCNSPXXGXXGRFCXXXTXXCGXX
EQXQXCPVXGXWEXPWSPWXXCXVTCXGGXXXRXRCHXHAXCXXXXGXXGXCXCXXGXEG
DGXXCXXXDPCSXXXXGGCSXXAECXXXXRGXHXCXXCXXGWXTSAGDGRXCXXXXXCXL
XXXGGCXXHXXAXCXYVGPGQXXCXCKXGFXHCVTDGXXXXGVGXXXAXTQGGXGXXCXP
IXXCXXXXXXCHXLXXXQTXGGXXXXXPCXXXYIGDQMRGCKMERNCRDPELNPXXXXAX
CAXXXXXXXGXXXCXCXXXXXGXGXXXYGDXXXELXXXXXXXXXXWXXXAXXXHXLXXX
SXXTXXXXXXXXXXXXXXYLLNLALIXXLXXEXXXXXXXXXXXXXXXXXXHXLXGXXXXXX
LXXLXXXXXXXXXLXXXXXXXXXXXGXXXXXXASVXXXDXXATNGVXHXXXXVWLEGGVR

TGKLLVRPGGRDVLSGXXDNCXVLXPXRXXXXXXXXLLXXLDXXPXXXXFRXXXXXXXLX
XXIEAAXAYTXFXPXNXXXEXXXXXXXXVRSLGPGPPGAGQPAIPRPLSFSSTTLXXDXX
RXHVILXEXLXXXXLXXGXHRXXXLGXXXXLXFXXHXXQXXVNXXPXXXXXXXXXXXXXX
GLXXVLXXXXXRCXXXXXXXXRXKCXNCXXXXXCXQGXXXXXXXXXXCXYXXXXMGRRSX
XXGCXMRXXCXKXXXXXXCCXGXFGXXCXPCPGXXXXVCXGXGXCXDDGITXXXGXGXCX
CXXGFXGTACEXCXXGXYGXXCXXVCXCXHGXCXXGXXGDGXCXCXVGWXGXXCDXXIXX
XXCXXXCDXXANCXXXXXXXXXCXCAAGXXGXGXXCXAXXNXXXCXXXXGGCSXXAXCXX
XXPGXRXCXCXDGYTGDGXXCXXEXNXCLXXHGXCHXHAXXDCXXTGPTXQXXCXCXXXY
XGDGXXACXLXXXCXQXRPPXXXXXXXXRXXXXXXXXPXXXXXXDXXWXXXXXXXXXXXX
QXXXXXPGLDREARGPFPRAGRGVLGXAXXXXLXXPTNNGGCSXXAXCXXTGXXXRTCXC
XXVXXVGDGFTCRXXXXXSELXXXXXXSXFXXXLLEHXXXDLXGXGPFTVXXPXXXXXXX
XXQXXXXXXXXXXXXXXRYHVXXCXQLXXXVPSHLRAEALVGKVNLKECLQSASLILSSD
PXXXLXXXXXATXLXGXPLXXSXXXGXXXINXXARXXSSDXXXXNGXXHXIDXXXQXXXL
WXXQXXXPXXPXDPXXXXXLXPXXXLXWXXDAXSLXXXXXXXXXXXXXXXXXNXTXXAXXX
GYXXFSXLXXXXGLLXXXXDXXHXPXTXXWPXDXALQALPXXXQXXLXXXDXXDKLXXXL
XXHVIRXXXXLAXDLPXXXXXXTXXGXXXSXXCXXXXXXGXLXXXXXXXXRIVQRXLXFXX
GXAYGIDXLLXXPXLGXRCDXFXTXXXXLXXCSXCXXXPLRXLXYXCPXXXXXXGXXXXC
XXXXXKXXDXXXPXXXLPLFFXXXDDWTSPPLHSLALRSVWTRPXHWGHPXXXXXGCXXX
CXXXXXXPXCCXGXXXXXCXACPGGXXXPCNXXRGXXXXXXXXXXXCXXXXEAATXXXXF
XGTACELCXPGXFGPXCAQXCXCXXXXXXXXXXHGXCLXXXIMKRDXGXXGXGXXXXXXX
WTXXXXXXXXXXXXVCXXPPCXXXAXCXXXNXCECXXXXEGDGXXXXXXXXCXXXXGGXX
XXAXXXXXXCSXXPLXNXQXGTXYAVSLVAVXXNXXXPXXTGVXCXCXPLXXXXXYXXXV
XEXXIGDGXSCXAXXPXXDGXXXXXXXHMDXXXXGPXXXXXXXXXXXXXXDXXXCXXXXXX
XXXXXXXXXXXXXXXXXXXXXXAQXXLXXEXXXXAGVFHXTLXXRXXXXXXXXXXXXXXX
XGXYXXXXXEAXHXXXXXCXXXXLXXXXNRQVVLQIGVLNEAQFAKAVNSKTTTTMXXXV
XXXXVKDXXEXXXIXXXXLXXXXQXXXXXVDIXAXXXGXXWXXXXXXXXEINGTLXXXX
XXXXXXCXXAXCXXGXXXXXXVXXPXXXPXXXCXXXXXGGXAGAGGGXSGGVXXXXXXXS
SRKVXHRXYCXXXXXXXDXXVXCFXXXXPPGXDCTXVTDLXXXFXGPXTIXIVXLXXXXX
XXXXXXCXXXGTRYTKKGEYRTNPEDINXSXVXXXXXXWXXYXXXXYXXXXXXXXXXPS
IXXXXXXXXXXXXGXTNLLVXFLXXXXXXXXXXXXXXXXXXXXXXXTXSXPDXEXXXXX
XXXXXXXXXXXGXXXXAXXXLXXXIFHTAAXEQHESIPLRXXXXXXXHLPXXXXXPDXXX
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LQTTTRMTDVDRSSTSAYTDVDVDSIGESWXQEPHSVSXSHXGYHDEEETPHSTSTTQAP
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QEDSSWTYVFXDPVXXXXXXXXXTKXRMDXXXXXXNVQDTSPSTXXXPXXDXXXXXPNSX
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GTAXPTSXXRNDGRRGGTITGFQVDNLPEDATASXEGYTHSPDTNEYTTTGLQPGTDYKX
HLTXXXXXXXXXXXVIXXXXXXXXXPSXXXXXAXXXNXXLXXXXXXXXXXXXXXXXXXPV
TPTXSXXPTGSPGVTEVTIVGDXXPXXXXXLQXXXXXXXXXXXPXXXXXXXXLPXXXTL
PHPXLXXXXXXXXXTXXQKXPXLXXSXXXXSTXKADLTLPXDYGXSXDPSGRSYTTHASE
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LVINSEDMDAYCRXXXSXXXNNGNGTMEPXPXXXXXTXXXERXGGGXCXXLXXXXHLYXK
PSGLNGEASKSXXXXXXXXXXXXXXXXXXXXXXQEMVHLVNKGSSETXDQFMTADESASA
TLTGLTXGXTRNXXXXXXXLXXQXXXLXXXXXXVGXXXXXGXXXCQHXSXXXXXXVXXXX
XRHYXXXXEXISXXXXXGXIXXXXXXXXXXXXXXXXPKXXXXXXXXXXXXXXXXAXHKEC
VQNVDMKIGVXXXXXCXXXCXHFNITKVENXXXXXXXXXXXXLXHCKEKDXXXXXXXXXX
SXXXXXXXXXXXXXXXXCXXXGXXXXXXVAXXXXXXXXXXXXLLLIWKLXXXXXDXXKPP
XXXXXXYXXXXXXCEXXXXXXXXCXXXXXXXXXXXXXLLXXXXXXXRLXXXVDTVLRYRC
REGLTQRNXXXXXXXXXXXXXXXXXXXXXRSXXXXVXXXXXXXXXXXXXXGXXXXXXXXX
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==> Peptococcaceae.txt <==
>MSA Consensus of 495 seqs, protein
MRXXXXXMXVXLVXXXLXXFFXXPXXXXAQASNLSXSXAXXSXXXGXXXTXXXXXXXXXX
LXTSXXXXXXXXXXXXTXNPKTYGDEEIRKNIXXXXGXGARKIQRXPXAXXXXXXXXXXX
YXSENSEAMFDSMVSXXXXXEXGXXXXXXXXXDGXAXXTXDQXXXXXNXPGVDLTKEVXX
XXXXVXXAXIXXLXXXXXXXXXXXEXXXLXNXXXXTDXXXXXXXXLXNRTXXNXXGXXXXN
MSXXXXXXAVXXXXXXXAXXXXXXXXIXXXXSDDFGGAVXXXXTXTXXGGXXXXXXXXSX
XXXTLYGSGTLTMNXGXXXXXXVSEAGKGAGVXXXTXAXIXLTXGXPTXXXXXXGTSTPS
NVFLTDNIFXPXVLIXXXILTEAKDTIGIXXXGGXXXXXVXGYDSKKGXXXLXXXXFXXX
XSXXLXXNGSGGLKLSSXXXXXXXXXXXXFXXXXXXLXXVXNXNLXXXXVXKGRWHNGTYG
GEIKGNANSXXTXWXDXXXXSVVIADVTTAXGIXXXMXXXGXXXRGXRGXXXGXXSXXXX
XXXLLXXFXXXXPXXSEYXDXGXXXXTFXXXXXXXXXSXXXHNXXWTXGGYTXXXXXXGX
XTXMRXXGSNNNSXXXXPXXEXXXXXNXXXXXPXVLXXSXPXKXFXXXXXDLXNXXXDIT
GXXXXYXXSTNKGWLDXPXXXXXXXXVXXXSGXXXXXXXNGXXTXNSDVXXLXXXGAXFT
GISSFTXTXTGXXXXAXXYSIDNLDLXNITDLTTDPLSNDAGLXSVSDNLSAALGQXITX
GGXXXTXXXXXTXAXXXXXXXTTVAXXXIXKHXXGAIVTFYGTDSTFATEATGSVNLTAG
YTXTTXXYIXXEXXXXLEXXLXXXXTXTRXXXAQTPQXXXVXGGXEXXDXTTTVDPEDGQ
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MRLXXGTXXXEXEVLPXXXXXXXNGSSWXYVTSTITDISGGTTXSIKSVGXXXSLXSXXX
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IATISASTXEITXXXXGXXXXXXXAXXGXXXGTDXXXXXSEXPTPVGNGTYRFENITPTS
YGGSDGKITGTTTXXEXXXQGADSYKPATEPEITPDSAGFYVTQYANTIEFNTGAAVSAN
CPFFGXXLXXPSISGGAKNGQITVSXXXPXXXXXNXTXXXXXGVIXXXXNXTTATHQAEX
XXXTXXNVXXGXGXYSXXXXXXXXXPTXXXXXXXNAKXSXXTIPXXXXXXXXIXAXXXXX
XKXXTXXXXVXXXXXXXVGNXIXTSPPAXXXXXXXXXXXXXXXFVGPVXXXXXXXXXWXXX
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TNTTEXXXXXAQXTAGAIXXXXXXXTIEXMXXXXXXXXXWXXXXXXXXXXXXXXXFTAQI
EGXTVSAALXSXXXXXXXXXXXXXHXXXXXTHXXXXXXXXXXXXXXXXXXXXXXXXXPVY
XXXGXXXXXXXXXXXXXXXXXXXXXXXXTXXPXXGXXTXXXXXXXXXXXXSANXXXXXXX
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XXXXXXXXXXPXXXLAXXSXXXXXXXXXXXXXXXXXXXKGRKXTXXXXXXXXXXXXXXXX
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XXXXXXXXXXXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXXXXXXXXXGXXVXXXAXXXXX
XXXXRIXXXXTXXXXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXXXXXGXXTIXXXXXXXXX
XXGXXXXXXXGXXXXXXXXSXXXXXXXXXXXXXXXXXXXXXXXXXXXGXXXXXDXXXXXX
XXXXXXXXXXXXXXXXXXXXDXXXXXXXXXXXXXXXGXXXXXXXXXXXXXXXXKKTXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXNXXGXXXXXXXXXXXXXXXXX

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XXXXXXXXXXXXXXXXXXXXXGXXXXXXAXXLXXXXXXXXXXXXXXXXGXXXXXXGXXXXX
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XLXLXDXGSGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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XGXXXXXXXXXXXXGXXXXXXYXXXXXXPTXXXXXXXXXXXXXGXXXXXXXEAVSXXXXXX
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XXXXXXXXXXXXXXXXXXPXXXXXXXXXGXXKEGQVXXGXYTYSDAQSDXXXXSXXXXXX
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XXTXXXXXXXXXXXXXYXXDXXXXXPXXXXXXTPPISSSXXXXXXGXXXXXXXXXXXX
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XYXXXXXXXXXXXXXXPXXXXXXXXXXXXXXXXXAXXXXXXXLXXXXXXXXXXTXXXXXX
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XPXXXXXXXXXXXXXNXXTXXVXXXXXXXXXXXXXXXXXXXXXXQTXXXXXXXXXXXXXX
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XXXXXXSXXXXXXXXXXXXXXXXXXXXXXXXXXXXYXXXXXXXXXXXXXXXXXXXXXXX
XXXTXXXXXXXXXXXXXXXAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXLXXXXXXXXXXXXXXDXXXXTXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXSANNXTX
XXXXDXXAXXXGXXXXXXXXXXXXXXXXXXXXXXXXXXIGXATAXXXXXXXXXXXXXXXX
XXXXXXXXXXXXIIXXXXXXXXXXXXXVXGXXXXXXXXXXXXXXXXXXXXXXXXXXXGLX
GXXXXXXLXXXXXXXXXXXXXXXTXSXKRSXXXXGXXXXXXXXXXXXXXXXXXXXXXXXX

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DXXGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXYTXXXGXXXXXXYTXXXXXXXX
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XATXXXXXXXXLXXXXXXXXTXXGXAXXXXDXXXXXXXXXXAXXLPGNXXXXXGXXXXXX
AFXTXXXXXXXXXXXXXXXXAXAVXXXXXXVXXXXXXXVXXXXVXXXXXXXXXXAXXXX
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GIXXVTXXXXXXXXXXXGNXIANQTIXXXXXXXXXWXXXXTXXXXXXGTXXXSXGXVTRP
XGXDXXVTXTXTXXXXXXXXXXXSMQTXXTXXKXFVXXTXPAXXXXXVXGXXXXXXXXXX
XVXLXTGVD

==> Peptoniphilaceae.txt <==
>MSA Consensus of 366 seqs, protein
MRXSIRKEIRRFLCFLMTFIMILTSMPVHLLAAANVDHNNLXNXKSXIINXKTPVXVAKP
EXGKTAADLIKNPXQPXIYTLRTDXKVQRGEKYQVDYQPYIASVGAXAYTYKDINGVDGN
KVLTXXEKXKVXXXIXLPXXXGYXXPXXXFXIDYXXXKNXAXXXXXTGNXXXGXRYXXXX
XFXYXAKSNXIXIKHVFQXLEDFXKYTNPDGSVGEXXXXXTXQXGNTGSTMXVXPLXXXD
PXXKGFVPEAXXIXMQVPXNAXNFXLEYRYNRAHYDVVFDTXGGTXLPXRTLYYGQXXPK
IADXXIPTKVGGEFQGWKPSVDLTTKDGKTXKQTLTANEIIKXGTXXKGAXXNLDANLIM
PASKVTFTAXWKDKXKADYAXQFWAEKADHADKDDXASLXXKYDYIGTRVYKDXDTGSRP
XLXNXXVXXIXFPDLDQARLXKIWAXARFNRGKXLYLNKFYXYNQXLTXXQNKDXXNVNL
VKSVDSTGXTVYNXYYDRXVYXLYFTXSNXXXXXPXNXFXPXXWQYDEAXGEAVXKGGPG
XXYXXXARFNXXXXXXWPNDAXXTXGFXPXXXXXXXXXXXXGWXXNXXXXXXXXXLDTPP
YRLNADEFXDXXNXXXXGGXXXXXDKGXGXXIXXDXXXXXXXGXYXIXLXFGIKSQASXX
XXXXSXXHHXDFWMDGFXXXXXXIXYDLXXXKXDTXXXXYXXXXPXGIVXXGFTXXXXXX
XXXWXXIXXXXEEXGXXXXXXIXXLNXXRXEXTPXXXXXXXXXXGXKXPXGXXDFIXXFF
SDXDEFGDPLXDXDGXPXVXXXXXNXYXXXXYXRNXYXLXXNYDPXXXKDDXXFXXXNXX
DXXYEXPLKXLXXXXXXDKTPREXEEYKKENXKNLLDNPEKLXELGLTDLVFNDPXDXNK
XXXXXPDXXXDXXXFKGWALDPAGXKLIWENPXEXMPXHPXNLYAKWGEPDYKWKVTFDP
NGGXLXNIKEXXXTXXXXXXXXXXIGQEEIXTXAXXEXXXGXKQXFTVIQRQTIKEPQKL
VEPKIKPTRKGYDFMGWEXXRYXKXAXXGXYTXXXDTSYRDTYKVPELYSFGNDVVXPVY
LKAIWVPNXRVDVXVXHXXLDXDYXKXXKXXXXTLXXKRXXYLVAXXGDKQXDXYILAPH
EELEXKLTXDLKXXYXXYNXRVKXXNXXXQXXTXVXPXXIXXXXXXKXXDNXXXXXNIX
AFXFFYXPFXXRXXXXNYXXXXXXXXXXXXXXXXXLXXXXXXKXXXXXLLXXXXESKAXXX
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XXXXXXXXXXXXXXGGESYIXGTXXDXXXFXYKXXXVIXXXXDXXXXXVPXGYVXXYVSG
DGANDTIEKYANGVYTXXXXKGGXXXXXXSXGXXXXXLXYDVXXGXXSXXXPXXFXXXXX
PXXXXEGXXXXXXXXXXNXXXXXXXXXPXXGKXKXXXIARAKAGAEPXFXXWXXXXXXXX
XTISFLXIXXXXXASTKFVSEWHTXVXEXDXXXFTXYFXXXXXXDNKFNFPKNDTTRTVL
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YEALTXXXXKPLFLXXAEGKEAXXGXXXXXTXXYEPGVKVTVXPTXXXXXKDXKXXXVNX
XXWXXXXXXXXXXXXXXXXXFXXWXXXXXXQNEXXEANGXXXFXKXXXFXXIKEXXTXXX
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FXGYIXXXRXXXKXXXYKXPAXPKXXXXXXXYXXXKVTXXEPTNKNXYFPVIFDANXGKFE
SDPKDKKXXXXXXDGXNATVEKXXXKEVKDEFDXXXXXXXXXXXXFXXWXXXXXXXXKXA
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KDGKLDXXIXXDXXXKXXXPXFXGXXXXXIELNPXDXKYXLDXKATIKIYYEKLXXVIXX
XXXXGXXXXKPXGYVXVKFXPXDNXXXXXXXXFYVNPKXXXXXXXXXEXXXXANIGXXXX
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XMKXYXXXXXXXVXLXXXXXPXXTXYXFXXWXXXXXXXXXXXXXXXXXXEDXGVXAXFND
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XEXXXXXXXXXXKVKAKXXXDIXXXXKQXGVKXXXTQMKAERPKXGASPXLAXAXXXXXX
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PVITIMRNXXXXXYXIXXXDXXXLXXXXIXPIXXXXXXXXXXXXXXYXXXYVXXXXXXDX
XLDXXXXXXDIXXXXXXXXXXDXVXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXDNXXPXXXXXXXXXNXXXXXXXXDXXXXXXXXXGXXXXXTXXWXXXXXXXXXXXXXXX
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AQXXGXXXXKKEXGXXXXXXXXXXXXXXXVXXXXXXXXXXXXXXXXXWXXXXXXXXXXX
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XIXXXXXXXXXXXXXXXXXXXXXXXXXIXXIXXXXXXXXSLXXXXXXXXXXXXXXXXDXXX
KPXXYVKSELEYSGXXXXXXXXGXTXXXXXXXNXXXXXXXXXXXXEXXYXXXXXXXXXXX
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AIEXXXXXXXXXXXXXXXXXXXXXXLXXLXXXXXXXXXXXXXXXEGXXXXDXXXXXXXX
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XXXXXXXAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXKXXXXXAXXXFGXXXXXXXXX
DXXXXXXXXXXXXXXXDXXXXXXPXXXXXXXXXXXXXXXXXXSXSTKXXXXXXXEXXXX
XXXXKDXXXXXXXXXXXXXXXXXXXEKEXXXXXXXXXXXXXXEXXXXXXYXXXXDXXXXXX
XTPXXXXXXXXXXXXXXXXKXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPXXXXXXX
XXDXXXXXXXXXXXXXXXXRIXGXXRXXTAXXXXXXXXXXXKGSGKGXXXXXXVXXXXXX
XXXDXXXAXXXXXXRNGXXXPILXXXXXXXYIKKXXXXXXXXXXXXXXXXXXXGGXXXXS
XXXXXXXLXXXXXXXXVXRRXXGXDRYXXXXXXXXXXXXXXXXXXTKXXFXXXXXXASGX
XXXDXLXXXXXXXXXXXXKFNXXLXXXXXXXXXXXXXXXXXXXKKXXXXXXXXXXXXGGX
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XQRFSXXXDXLXXXXXXXXXXXXIXLXXXXXXLXXXXXYXXXXXKXXXXEXXXXXXXXXX
XXXXXXGGXXXXXXXXXXXXXXXXXXXXXXXXPKXXXXXXXXXXXXXXXXXXXXXXXXX
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XXXIKXXKPEEKXXXXXXXXXXXXXXXXXXXNPXXXXXXXXXXXXXXNRIXXSXXXEVXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXIRXXXXXXXXRXXXXX
XSVNIGKDEIIXXXXHKKXEXXXXXXXXXEDAKLLKXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXKXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XYXXXXXXSXXXXXXTYXXFXXXXXMXXNXXXXXXXXXXXXXXXXXXXXXXGXXXXXXXX
XXXXXXXXXXXXXXXXDPKATEXXXXXXXXXLGKKQFEYPXXLXXXXXXXXXXXXXXXXXN
LEXXXXXXXXXXDXXXXXXXXXXXXXXXLXXWKXSXGXXXXXXXXXXXXXXXXXXXTNXXXXA
KXXXXXXXXXXXXXXXXEXXXKXXXXXXXXXXXXXXXXXXXPXXXXXXXXXXXXXXXXNXKXX
XXVVRNYKNLXXXXXXXXXXXXIXXXXXXXXXXXXXXXXXXXXXXIXXXXXXXXXXXXXXX
XXXXXIXIXXXXXXXXXXXXXXXXXXDYGXWXXXXXXXXXKXXXXXXXXXXXXXXXXXXXYX
NIVESKXXXXXXXXXXKLXXXXXXXEXXXXEXXXXXXXXXXVXMDLXDLIKEXXXXXXXNY
XXXNXXXXXKVXLKITXXXXXXXXXXXXXXXXXYGXXXXXXXXXXXXXXXXXXXAKLNNFX
XXXXXGXXXXXXRRNTIRYNALXDXXIXXXXEFNXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXVXXXXXXXNXXXXXXXXXXXXXXXXXXXXXXXXIXXXXXKFKVAXXXXSXXXN
XXXXXXXXXRXVXXXXXXXXXXXXXXXXXXXXXXXXXXXXXEXXXFXXXXXXXSGXXXXXX
XXXXXXXXXXXXXXXXXXXXLXXXXXXDXXXXXIDXXXXXXXXXXXXNXXXXXXKGKNL
KLTAIVEGKNLKDEDXXXXXXXXXXXLPXXXXXXXXXXXXGXXXXLLXXXXVNVXENKLT
SVEALKDLTEXXXXXXXXNXIXXXXXXXNLXXLXXLXXXXNPIKDXXXXXXXXXXXXXXX
XXXXXXXXXXLXXXXXXXXXXXXXXSTQXQSVTVDXNXVSFXXXXXXXXXXXXXXXXXXX
XXXXKXXMEDXXXLXXXXXXXXEXXXXXTEGEDQXXXXTFXXXXXKXXXEXXXXXLXXXX
XXXXXXXXDFKNNXVEXXXXXXXXXXXXXXXXXXKXXXXXXEITXXXXXXXXXXXKLQVXK
XXEKXTXXXXXXEKXXXIXXXXXXXLPAKDAIAKIRVXGXINNIPSDKFIVKLVDEXXKX
XYXXXXVTGXXSKAXRXINIKVPENTXDKXKTYEIXVSSTGKKENFKKAEFXLTQEKXSG
TXEVEKTXKIXSSNKDIVITVNGEEKXXALXXXKKGDXVVVKAKXGKEISMFYVSGXNXX
GXPMKVNFKQXEKEGDXYQFXMPXSDCTLNIXTKDKEVXXENIQXLXLXTXXKVSKDSST
ATVQVXGXLXGIXNDKFVVKLVDNDGNETFPXVXVXGFEXXXDIXXXXXSGDVNKXXRTV
SFEIPKNTTTKEKEYTVYVSSTGSKXDFAXXTVKITQEKSDTEEQIPEGIMXLXLETXGX
XEXLXAAGGKVXLXXMGNFKNVXDDKFVVKLVDXKGXEWIVTXXXXTVSGXGXXRTLEFX
XXKNEEXTEKTYKVYATSTGSXXKFYXXSVELKQXXXENTKXTIEKINVLTPILKNXXEK
LRANXXGENXNPDNLXVSFYXLXXGKFVKDXSIXXXFEEELKXSGFYTTKRNAKFXQIVA
DSIALXKGNASDCFEEEEYMELIDVYKIXVRDMNXDXSKSYEXYFRVKYTEDXAXYXEIL
PSYXHASKDGKIIEVGFXEEIEEIFDXSXKXGISIRNSDKEDPNHEWDMVVESDKNADGN
YEXLXXXDTVELSDKKFVXTLEKPLDVXXLGXXKAXIKIXQGVFRXKGTEXLNXDVDYXI

NIGKPIVRQATIEGXKXITNXNRKVTIKVNGXNLSENAKVKAVMQTKLATEXXXXAXKGK
QPEVXGXISGXXXEQTITFELPENKTDRTVSYEXLYXPEXNGKFEKLPGNNPKSRANXXV
ISLLADGVDXNAATLAFMKIQTYGATSTXXGXXPDITYGXTPTIQESKKTFTHVYGTNLE
AKKTRVXIFDXRGVEWYXVNQPSLGAAAFKMVVPALXGIDGDGNYQTMEIIGPXXLIGDH
TFTYKVAVDGKNYDXXVXVXXXIXASGKTXXGKXDLDXQETTLKLNYVDXXGNXIKXSXX
KXSYSFFEECAAGIYPDXIEXYXPXKIXRKSDXXXXXEIKLXXGVDYTDYRNLQXXLGVN
KIGXNPEYTIVYEKTKKVEKPKTEYKLTLVGDNISTNHEGDKIKKGEEVILTFKPEEKHF
ITKLLVNGKDEVVKVKDNKYTFIMNEDTKIEATYEKRCELILKGENIKSSVKPSNQIKPG
TRIKITVDPDDDKAVSEFLVNGQNLITQLLNNTYEFYLDKCTTIEVKYTQKSTEPNDAKD
FDFDATTGTITDYKSYARKDVIIPEKINGVEVKHIAEYAFYYKGLNSVKIPNTVISIGEL
AFNSNNLGKVTIPESVEEIGANAFNTAGLNKIILTENIKKLGKGAFANNKLKEFTIPKNI
TNIPESLVENNILESLEIPNTVSEIGAKAFKSNELSSVKFADTVKKIDILAFADNNIKKV
ELSSDCDVHPLAFDSNVETNIPKKPEKEVSEEKDFVFDKNTQTITEYIGNDLVVKIPKQI
DGVDVKAIGGFEDFFGIKK

==> Peptostreptococcaceae.txt <==
>MSA Consensus of 1650 seqs, protein
MKLKKLNGAMTIKCLNLREVKMXXSKKXXXKXXXXXXXXXXMXMXXTSXXPXXXXXXXXX
XXXYAXXSIXXEXNXWXXXXXXXXNHGDSXIXXXXXPXXVAKXXXEXNRXXXXNXXXXXX
XXXXXLXSXXXXXXXXXXXXFXXXKXXXXKXXXTSXXXXXXXKXXXXXXXGXXYXXXEFE
XXDXXGXXXXXXIXFXQMDXXXSTXTXXXXQXXIXXXGXXXXXXXXXXXXXXXXXXXXXX
XXKPXXXEXXIDXXXXXXXKXXXXXXFXXXGXXXXXXXXXXDGXXXXXGXXXXLXYXXXX
XXXYKXXXNXXXXXXXXXXXXDXTXXXXXXXXXGXEGXXIXXXXGXXXSXXXXXXXXXXX
XXXKXXIPXXXXXXEXXXFXXXXXXXXXXXXKXXKXXXXXXXXXXXXXXXXXXXXXXXXK
XXXXXXXXXXYXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXEXXIXXEXXXXG
XXXPKIXXXXXPXKXGXXFXXXXXXXXXXTXDXXXFXXXXXXXXXXXXXXGXXXXXXEET
XXXXXXXXXXXKXXDXXXXXXXXESILKXXXXXXXXXXXXDGXXXXXXXXPXXXXXXXXVX
XXXXXXXXXXLXXXXXXXXXXKXXXXARXXXXWXXXXXXXXXXXXLXXGXXXXXXXXXXX
XXDXXXXXXXVKAKXXXXXXXXXXVXXXXKXXXXXXXXXXXKKLXXXXXXYXXXXXXXXX
XXXXDNXXXXXXXXXXXXXXXDXXXXXXXXXXXXXXXAXXXXXXXXIXXXGXXIXXXXXX
XXXXXXDNEXXVXXXXEXXXXXXXXXXXXXXXXXXXXXXXLXXXTXXXGXXXVXXXLXIK
XXXXXFPLSXXXKXXXXXXGXXXXXXXXXXXXXXXXXXXWXXXXXXXXXXXXXXLFXXX
XXXXKXGXXXXXXXXXXXMXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXTXXXXXXXXXXXXXXXXFXXXXTDXXXXXXXXHXTXXXXXKKAKIKIN
DXXXYSFXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXIXX
XXXXXXXITPNTXXXXXXXXXXXXXXXXXXDXXXLXXXSXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXIXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXNSXXXXXXXXXXXXVXXXXXXKXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXNXXKLXXXYDKXXXXXXXXXXXXXXPXXXXXXXVXXPXXXXXXXXFX
XXXXXXXXXXXXXXXXXXXXXTXXXXXXXXXXXXXEXDYXXXXXXXXXXXXXXXXXGXAGXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXNDXXXXXXX
XXXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXXXXVXXXXXXXXXXXXXPRIMQXXXXX
XXXXXXDEXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXSXXXXXXXXKLKNXXXXXXX
XXXXXXXXXXXXXXXXXXXPPKPTXKGYXXXXXXXXXXXXXXXXXXYXXXXDXXXXXGXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXVXXXXXXXXXXXLKXXVVXXNXXXXVXXXXXXXXXXXXXXXXXXXT
SKNXXXDXXXXXXXXXXXXXXXXXXDKXXTKXXKXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXGNSSXXXXXXXXXXXXXXXXXXXXXXXXXXXSXXXXXXXXXXXX
XXXXLXXXXXXXXXXXXFXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXVXXXXXXLXXXXXXXXXXTXXXXXXXXX
XXXXXXXNXXXXKXXXXXXXXXXXXXXXXXXXXXXXXXXXXXKXXXXXXNXXXXXXXXXX

XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXQSXXXXXXXXXXXXXXXXGKLYRXXXXXYXXXXEKAX
XXXXXXXXXXXXXXXXXXKXXXXXXXXXXVXXLXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXDXXXXEXXXXXXXXXXXXXXXXXXXKXXXXXXXXXXXXXXXXXXXX
DXXXXXXXXXXXXXXXXXXXXXXXXXXXXYXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXYXXXXXXXVXXXXXX
XXXXXXXXXXKXXXXXXXXXXXXXXXAPXXAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXIXXXXXXXXXXXXXXXXXXFVXXXXXXXXXXEKXXXXXXXXX
XXXXYXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
IXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXLITALENENIKIVXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXDXXXXXXGXXXXXXXXXSMXXXXXXXXXXXXXXXXLXXXLXXXXX
XXIGXXXXDGXXXXXXXXXXXXXXXXGKKXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXDLPXXXXXXXXXXXXXXX
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XDXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXMXXSXXXXXXXXX
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XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXSXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XIXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXTIXXXXX
XXXAVXXXXXXXXXXXXXXXXXXXXXXXXXXXXKXXXXXXXXXXXXXXXXXXXXXIX
XXXXXXXXXXXXXXXXXXXXXXGXNXXXLEDXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXGXXXXXXXXXXXXXEFXXXXXXXXXXXTXXXXXXXXXXXXXXXXX
XXIXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXENXXXXXXXXXXXXXXXXXXXXXX
XXGVXXXTXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXVINXRVXXXXXXXXXX
QXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXIXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXIXXXSLTKKXXXXXXXXXXXXLVIKM
RRXXXXXXXXXXXXXXXXGXXXXXXXXXXXXXXXXGXLSMXXXXXADKFXIVAPTXXF
XXXXXXXYXXXDNXXXXXXXXXXFXXXXXXXXXXXXXXXXXXAKXXXXXYXXXXXXXXXX
XXXXXXXXXXXXXXNADXXXXXXXXXXXXXXXLNIXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXTXXXXXXXXXXXXXXXXXXXXXXXXSIKDXXXXNXDXXXEKXXXXXVLXXXX
XXXXXXXXXXXXXXXXXXXXGSXSKVSVKFKEKPDAXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXYXXXXXXXXXXXXXXXXXXXXXXXXRYIXXDXXXXXXXXXXXSSI
YDMPLXXXGXXXXXXXXXXXTTLNYNQSTXXXXXXXTVXPXXXXXXXXXXXXXXXXA
GYVEVTFKVTGTYGKIADNEXTXXYXXXXXXXXXXXXXXXXXXXXXXXXXXXXGXXXX
XXXXXXXLXFXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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XXXXYXXXXXXXXXXXXXXXXXXXXXXTAXXIXXXXXXXXXXXXGXXNXXXXXXXXXXX
GXXXXXXXXXXHXXXXNXXXXXXXDXLXXXXXAXXXXXNXXXXXNXXXXXXXXXXXXXA
EPILLXXPXTXILSAKXXXXXTXXXAKFNTKGDVIPKTKNDDXTATVLANEXQKPQGFVX
XDXXXEXIXXXVXXEXXXRLXXXXXXXGXXXNXXXXXXXIGXXXDAELITISIGADXXXS
XXXXXXKXXXXXXXDXTGXXXXXXXXXXXXFKKWXXDXXXXXXXXXXXXKXXXFXXLXX
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XAXXXXXXXXXXXXXXXXXADAMSISGITVVPSPTYKHDGWDTDFATVIDKMXXXXXXX
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XXXXDXXXEXXXNXXXXXXXXYPLAQSKKAPILLASDNEIPKVTLDYLPXIIKAGPKDTA
PAGYVVIIFETDGRGTITXNAAYQLEDVTKKTNXXAXDXXXTTXXXXXXXXXGXXXXXX
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KXXXXXXXXXXXXPXXXXIXLXXXXKLTDATKYGFDQWRADIDTETPITRGRVHIAMFKX

XXXXXXXXXXPFXXXXXXIXXXXXXXXXXXXXXNXXXYXXGGXXXXSXKEVNNTLPSVTK
IAGSDNNKXXXXXXGXXXXSXXXXXXXXXXXXXXIXXXXXXXXXXXXXXXXXXXXXXXXX
XXLTXXXXXXXXXXXXNXRXXGXXRLAKKDANXXTNXXXXXNPGTXXXFYXXXXXXXLKE
DTTAYAQWTNDQNIIPYDPVXXXXXXXXGTYVKVTFAAEDXXXXXXXXXXYXKKDAGIKL
GDTGXXXDGXXXXXXXXXXXXXXXXXXIXXXXLXDALXXXXXXXAXXXXXXXXXXXXXXX
XXXXXXPXXLXXXTYVSAYXXXXXXXKNNKSTLSIILSIFKRSILXXXXXXXGRMEQAXX
XXXXXKXXXXXXLEDXXXXXXXXXXXXXXXXXXXXXGGXXXETAFNEXXXLXXXXXSXA
SSLSKXNXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPXXXXXXXXXXXXXXXF
EXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXFKPXXLNKAXAKGDANNVINKXXXXXXXX
XXXXXXXXLXXXXXXXXXXXXXXXXXXXXXXXXXAXXXXXXXXXXXXGXXXXXXXXXTX
XXXXXXXXNXXXXDXXXXRXVIXXXXXXXXXXXXXXXXXXXXGXXXXXXXXXXXXXXXXX
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XXXXXAVTITXXNXGKXXXXXXXXXXXXXXXXXXXXXXXXKIEVXXXXIXXXXXXXXXXXX
XXXXXXXXXXXXXXLLNXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXDXXXXXXXXXXXXX
XXXEXYXXIXXXXXXXXXXXXXXXEGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXGXXXPXISGXXXXXXXXXXXXXSGGSXXGXXXXXXXXXXXXXXXXXXXXXXXXXXXEI
KXPXXXATXXXXXXXXXXXXXDXXXXXXXXXXXXXXXXXXXXYXXXXXXXXXSSIXXXXX
XXYAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXIXXXTXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXEPXXXXXXX
XXXXXXXXXXXNXXXYLPXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXDXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXKXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXEXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXDXXXXXXXXXXXNXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXTTPXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXKKMLSXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXHSXXXXXXXXXXXXXXXXXXTIXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXIXVXVPAXXXXGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXKXXXXXXXXXXXQYKKXTGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXQXXXXXXXXXVFTVTHXKXXXXXXXXXXXXAXXXXXX
XXXXXXXXXXXXXXXXXXXFXXXXXXXXXXXXXXXXXXXXXXXXXXXNXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXTGXXXXXXXLXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXYXXXXXXXXXXTIPYXXGXGRDNFX
XSXXXIXXXXXXXXXXXXXXXKXRLXXXGTXRXXNXXXXXXXXXXXXXXXXXXXXXXXX
SSXXXXXXXXXDXXXXXXXXXXXXAXXXXXXXXXXXXXXXXXXXILXXXXXXXXXXXXX
FXXXXXXXXXXTSXFXXXVNKIKVTDXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXTAPXXXSXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXLXXXYXXXQXXXXXXXXA
PGEVFPDALXIXXXXXXXXAPILLSRTTPXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXYIXXXXXXXXXXXXXXXXXXXXETXXXXXXXXXTHXXXXXXXXXXXXSXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXDXFXXIXXXXXKXXLXXXXXXXXXXXXYXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXIXXXXXXVLDXXKXXXKXIXXNXX
TSXXXXXXXXXXXXXXXKXXXXXXXXXXXXXXLXXXXXXXXXXXXXXXXXXXXFXXXFE
XXXYXXXXXXPXFNKPMYXXXXKXXXXXXXLXINIXRDXGXXXXXXGXXXXXXXXXXXXX
LYNXXXXHXXGXWXXXVXXXLNGNXXXKXXXYXXXXGXXXIXXXXNXXDXXXXXXXXVVK
GXKXXXXXXXXYXXKXXXXXXPXXXXLEIXQKNXDIXXXIDXXXXXXXXXXLYXXNXXXXX
XXXNXXXXXINXAKXXXXXXXXXXXIGEXXLKKXXXXXXXXXXNXXXNXXXEXXXXXXXI
XXXXXXDXXXXXXX

==> Peptostreptococcus.txt <==
>MSA Consensus of 318 seqs, protein
MRXSIXKEIRRFLCFSIXMIMILTSMPVHLLAAXVXXNNLSXNKSXIINNNKTPVKVAKL
EXGNTAADLIKNPXXPXIYTLRTDYKVQRGEKYXVXYQPYIASVGXXAXXXXKXKVNKXI

XLPXIXGYXXPQXDFXIDYXTIKDAADXKNXXGXXXNGXRYXXNXXFXYXAXSNXIKIKH
VFQXLXDFTKYTNPXGXVGXEGXXITTQXGNTGSTMXXSPLXEXDXXRKGFXPEAXYIXX
QVPXNAENFXLEYRYNRAHYDVVFDTXGGTXXXXRTLYYXQXXPKIAXXXXPTKXGXEFQ
GWKPSVXLXTKDXKTXKXNEIIXVGTXXAXKNLDANLIMPASKVTFTAVWKDKXXADYAV
QFWAEKXDHADGASLLDKYDYXGTRVYKDXXTGSRPXLDXXXVXXXXFPDLDQARLXXIW
XGXKXNXGXXXYLNKFXVYNKXLTXXXNXDXKXXXXVKSVXATGKTVYNIYYDRQVYDLY
FTKSNXXXXXXTXYPEIXXYDXXXGKXVXXGGPGNXYHXKARFNXXMXXXWPXDXKXXXG
FXXGXXSXGWXPNXXTPXXXXHXDTPPYRLXAXXFXDXXXXXXXGGYXXXIDXGXGXTXX
ASXXXLXFXXXXXGXXXXXXXIPHHXDFWXDGFXXXEXXIXYDLXXXKXDTXXXDYXHRX
PXXXGFTPXXXXXXXXWPXIXEGXQEXXXXXXXXXXXLNXXRXEITPXXXXYSXXXXXXG
XXXXXGXXXXXXXFXSDXDEFGDXXXXEDGNXXXXXFXXNGYLXFXYTRNKYPLRFNYDP
SXIXXDXXFXXTNXXXTFYEFPLKXLSPXXVXXXXXEQKDKXXXXEYXKXXPXNXXDNPX
NLXKXXXTXLVXXDXXDEXKLKVKRPDNLXXXMXXXXWALDPXXXXXIXXNPGEXXXXXP
XNXYXKXGXXDXXXKVTFDPNGGNLXXIXEXXXTXXXKXIQXGDXGQEXXXXXAXKEXNX
GDKQVFTVIQRQKLVEPXIXPTXKGYDXMGWEXIRYXKDAKTGXYTXXIDXSYRXTYKVX
ELYXFGNDVVXPXYLMXXXXXXXXXXXKIVXXXXXXXXXXXXXXXIXXXXXXXXXXEXGXX
XXXXGXKQXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXNXXXXXXXXXPX
XXXXPXXXXXXXXDXXXXXXXGXXXXEXXXXXXGXXXXXXXXYNIKSPEYKFNFDQDFXX
XKXXXXIXKXKYXXXXXIXXXKYXXXXFETEGNXXFXXXXXXXXYXVXYIDERXXXXXXX
XXXGXXLXSXXXXXXXXXXXYXXVXXXXXXXXXXXXXXXXXXEXXXXXXXXXXXEXXXXXX
XXXXXXXXXXXXXWXXXXAXXXXXKPXXXXXXXXXXXXPNXXXXXXXXXXXXXNXXXXXXX
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XXXXXXXXXTXXXXXPXXXXXITXPKXDSXXXXXVXXXXXXXXXXXXXXYXXXXGXXXXM
TEXXPVXXXXNGGXXXXXXXXXYASDLNLDAKKEECGFXYXXXXKXXXXXXXXXXXXXXX
XXXXXXPXXXXXXXXXXGXXXSXXYXXXXXXXXXXXIKXXXTFXAXXXXXXXXXXXXXXX
XXLXKXXXXXXXXXXXXXPKXXDXXXXXXWXXXXXXXXXXXSXXXXXXXXDXXGXXXXXG
LFXXXXXXXXYXXXXEXXKAXNXXXXXXXXXFVXXXSXXXKXXXXXXDXXXXXXXXXXXX
XXKNXYEAXXXXGXXPXXXXXXXXKXEXXXXXXXVXXXXXSVXXXPXXXXXXXXXXXYYV
NXXAXXXIXXXXPXVXGXXIXAXXGXXIXXXXXXXXXXXXXXXXDXQNDDXXXXXXFXXX
XXXXXXXXXXXXXXXTXXDNXXXXXYXXXXEKXXXXXXXKAIVKTTDXAXDETXFXKTFW
VNPTKXVTIPIXXXXXSXXXXXXXDXXXXNXXXXFXKWXSTXXXXKTXXXXXXXXXKXVX
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NXELXKPGHKEETGYKFXKWDKEXXXXXXXXXXLXXXXXPHXXXXXXXXXXXXXXKXXXX
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DKDITNVTDETKEXPINSENXXXXXXXXXXXXXXXXXGXXXXXXXXIXXXXXXXXXXX
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XSXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXVXXXXLXXXXIESIPKDL
XXGXXGXXXXXXXXXKXXXXXXXXXXXXXXXXXXXXYXXLXXXXXXXXXXXXXAEDXXXX
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SXXXXXXXXXXXXXXXXXXXXXXXXXXXXXMIVXXXXFXXXXXXXXXXXXXXXXXXXXX
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ETFKSELEXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXYXXXXXAGXXXXKXXX
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XATNEAXVXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXIXXXXXXXX
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XETXXXXXXXXXXDXXXXPXXXKXXXXXXXXXXXXXXXGXPXXXQDXXXXXXXXKVX
XXXXLXXXXXXXXXXXXXXXFXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXXXNIXXXX
XXKXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXSHXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXTLKXXXXXXXXXXXXLXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXEXIXGXXXXXXDNXXXXSXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXVXXSXXX
XXXXXRAXXXXXXXXXXXXXXXYXXXXXXXXLXDXXKXIXKXXXXXXXXXXXXXXXXX
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XXXXXXXXXXXXXXXXXXKEDXXXXXXXXXXXXXXXXXXXXXXXXXXXFXXXXXXXKX
XGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXTXEXXXXXXXXXXXSXXXXXXXXXXXXXXXXXXXXXXXXVXXXXX
XXMVTAXDXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXKKXXXXXXXE
XXXXXDSEKXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGXXXXXXXXXXXXXXX
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XXXXXXXXXXXXXXXXXXXXXXXXXXXKXXXXXXXXXXXGXXXXXXXXXXXXXXXXYXXX
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GXXFXGXXXXXXRGNTGXXXKNKEYREEQKRXXXXXXXXXXXXXXXXLYXXXXXXXTXXXX
XXXXGGGXXXXXXXXVXXXXXXXXXXXLXXXXXXXXXXXNXXXDXLXXXXXAXXXXXPXL
LXXXXXXXXTETLNELKRRGTGDIIISGGVDSXTATVLANERNCPILLTGTDSISXXXXD
QRNSDYEKWKXXEXXRAXXXRIKXLXXXXXXXXGGXXSXXXXSXXXELKXLXSXXXXKDS
XXXXQAKFKVDPKATXXXXVXRXXGXXRXXTXXXXXXXXAEYTNXXXXXXXXXXXXXXXX
XXXXTPIFXTFXXXXXXXXXXXXVXETNPNTKTLPDALMELKXXDXXXXXXXXXXXXXXX
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XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXEX
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EKXXXLXXXXXXXWXXXXXSGXXXXXXXXXXXXXXXXQXXXPYXLDQXGIXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXKKGQGKVKKDFKEVRETSLEKGKXXXXXXXXXGKNXXXX
XXXXXXXXXGKXXXXXXXXNNXXXXXXXXILXXXXXXXXXXXXXXXXXXXAXXXXDXXXX
XXXXIXXXXXXXXXXXEXXSXXXXXXXXXXXXXXXLXXYXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXASFDVEVLNKSGQKIEHEITRSGSVFTVNVYDKKLYTGRAINITWAYPES
XXXXXXXNXXXXXXXXXXXXXXXXXXXXXXXKXXXXXXXXXXXXKXXXXXXVKNHNMXN
TXXXXXXEXLXXXIXXXXXXXXXXXXXXXKXXIXXXXXXXKIXXXXXGXXXXKXXXXLXXX
DXXXXXXXXXXXXXXXXXSKXFEXVXXXXXXXXXXXXXXXXXXXXNXXIXXXXXXXXXXX
VXXXXXXXXXKLXYXPXXXINXXXXXXXXXXXXGYXXXXSXXLXXKXGXWNXXXXXXIXV
NXLDDLKLFXXXVVKGXKXTYTXXDXVDLTKPAKDILDADXPTXLYLYNFXXXKNXXSTX
PQKXXXGXXXLXXXXX

==> Perciformes.txt <==
>MSA Consensus of 145 seqs, protein
MTTQRWILAFCXSLASVFGTVELFXTKEXQTYTCRTFGSGXVQPFKGEXYYVRSDCPFXL
TSFXVNRGEYSXXXRRXXXLLVXXXXXXXXXXLLXLQTSXQEQXXXXXXCXXXXXXXX
XTXCXSCXXXXXXXXXXXXXXXXGSTXXXXXXXXXXXXXXXXXXXXHXCXKXXXXXXXX
XXXWXXLXXXXXXXXXXXCXXXXXXXXRXXXXXXXKLXDHRCKXRDPVXXKXTXXCXXXF
XXXACXXCXXEXXXGXXXXXXXXCXHXXCXXGXSQECCFTLVSSLXGXXXCXXXXXXASQ
CNQSXXXXXXXXXTXCXXXXCXXXXXCXXEALXXXXXCXCLPGYXXXXXXXIPSCXXXXX
XXXRXCXVXAXCXXXXXXXXXCACXXXXXXNNXXXGXXCIPXXXCXXXXGGCXXXXXXXX
XXXXXIRSSXXXSCXCXXGXXXXXXNAEXXCXLXXACXXXXCXXXXXCXXXXXXXXXXVX
XXXXXQYXLPXKCXYXXXXXXXWIIIIXFSXXXXYXXXXTVQXXEXLXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXFXGTSLKTLXXXXXXXXXXCKXHLXXG
XXXXXXLXXXDXFXXLXGXXXXTDXSXXXXXXXIXXXXXXXXXXXQXDXXAXXXXXXXX
HXXXXXXXXXXXXXDKIKGLCGNSNSDTTDDFTTXXXXXXXXXXDEXXXXXXXXXXXXXX
XXXXXXXXLXXXXXXXXXXXXXXXXXXXXXXXLXXPGXXXXXXXXXXXXVXXXXXXXXXX
XXXAXXXXXLXXXXXXXXXXXXASXXXXXXXXXXXXXXXXXXXXXXXGPAPSEEAFXXX
XXXXXXXXXXXXXXXXXVRLXXXXXXAXXXRXXXXXXXXXXXXXXXXXPHRCDVXEXKIX
XXXCVXCSXXXXXXXPDXXFSYSXDXGXXXXXXXXGXXDXXXXVXLXXQXXLTXGXVXXY
XXXXXRXXXXXXXXXXCXXXXAXXXXXXXCPKEEXXXXXXXXXAAPGPVVIXGQXXXCX
XGXXXXXXQXXRGDGVSRPTMSIKRAPXXXXXXXXPXFIRDXXCXXXXXXXXGXXXXGXX
XXXXXXXGXXXXXCXXXXGTXEXCKSGCYCPXXQYEDXHGXXXDXDVESHXXCXCVHGXC
DNKARPXSXGXCXXXSCXXXXXXXXCXXXXXXXXSXXXXXGXXXXXXXXXLLXXXXXXXX
XXXXXXXCXXXXXXXXXXGXXXXXPXFXXXXXXXPXXXXXXXXXAXPERVLGSYSXXXXX
XGXLXXXXXXAAAPXXXXXXXXXGXXXDGXXPXGSVXXXXXXXXXXXXGXXXANAXCXXI
GPGQSXCXCKXNGYXGXXXXXXPXXXXXXXXXXXXXXXQXNXXANGXLWXXTKPXXXXXX
XXQQPSYLLLQXXXPXXXXXXXXXXIAXXXXXXMXXXXXXXXXXXXXXXPXXPXXXXXXQ

QXXXXXXXYXXXXXXXXKPXXXXXPXXXXXXXXXQXPVKYNPVRYNPVKYNPVKYNPVKY
NPRLRPQQLXXXXXXXXHSXXXXXXXXXXXPXXXAXXXXXXXXXXXXQXXXXXPXYPXXX
XXXXXXXXPXQXXYXXXXXXPQKPXXLSXXXXQNLXXXXXQPXXXKGHRLTPXXXXXXXX
XQXXXXXPXXXXXXQXPXXDDGYQQRPXQXPXXXXXPXXXXXXXXXXPXXPXXXXXXXXX
XVXXXXXDXXXXVGXXXXXXXPXXXXXXXXXXXXXXXXWXXXXXXGVXXXXXXXXXXHNXX
XXXXYPXXXXXPQXXXXPSXXXQXXYXXXPXQXXXPXXXXXXXYXXXPQXPXXPXXXXXX
XQQDGYRPRPQQXXXQXXXPXXGXXXXLPQQPSSPPXXXERLLPQXPXXXSKXXXXXXPS
EXSXXXXXXXXXXXXXPXYPXXXXXXXXXXXXXXXXYXXXXXXXXXXXXXXXXPTDXXXX
XXXXXXXXXXXXXXXXPXXXXXXXQQPPQXXXQPPXRXXXXPQXXXXXXYXXXXXXXQXP
XXXXXXXXXXXQPXXRPQXXXXXPXQXXXPDXXXXXXXXQPPPRXGXPXXPXXXKRVSXX
QXXXXXXGXXXSKAGMWDXXSXXXVXXXXXXLXXXYQXXXXXXXXXXXXXXXPXXXXYX
PXXQXPAYPSNPLQXXXXXXXXXXXXPXXXXQXXXXXXXXXXXXXXXXXXAGMWXXXXEXS
VASGSNXQXXXYXPXXPXYPPXXXXXXXXXXXXXXXXXXXXXPQXXXYPXXXXXXXXXXX
XXXPXXPSXPXXXXXLQXXXQPSYPXXAGXXXXXXXXXXXXXXXXXXPXQPXYPXXQPX
XXXPXXCLXXYXPQQPXXPXXXXXXXXQPQXPQQXXXXXXPXXXVXXXXXGXWDXXXXX
PXPXXXXXXXXXYPSXPXXXXXXXXXXXXXXXXCSXXXCPVKYCPXXXXXXXXXPXXXXX
XXXXXXXXPXXPXXXVXXXLXXPXXXXXXTXPRHHHHHHHHGHPSKHHPHHHPSKAHPQTQ
LPAPPXXXXXXXXXPQXPXXPXXXXXXXXXXXYXXXXXXXYPXXXQQXXXQQAEPXXXXX
XXXXGXWXXXXXXCXXXXXXXXXXVQXXPXQPXYPXXXQXXTXPXSXXXXXXXXYXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXNKHHPHHHPSXHGXCX
XGPAPPAEPQHQIHVXXXXXXXXXXXXXXXXXCXXXXXXXXXXXPXXAXXPXXXXXXXXX
XXPQQXSYPXXPLQSRYPRXXXXXXXXXCXXXXXXXXXXXSSXXXXXLQXXXXXKXXXXX
XPXXVXXAXXXXXQAXXXXXXXXXXXXXDXPEXXXXXXXXXXXXXPXYXXKPQHPAYPSNP
XXXXXXXXXXXPXXXXXXXXXXXXXXXXXXGYXGXGXXXXXXXXXXXXXGXXHXXXXXXX
XGXXXTASPXLXXXXXXXFPGXXPKXXXXXXGXGXXXXXXXXXXXGXXXXXXXXXGXXXX
XXXXXXXXXXXXXXSNPAXCXXXXXGDGXXCXGXXXXXXXXXXXNXXXXXXXXXGSXXX
XXXXPXXXXXPVEEXNXXXXXXXXXXXXXXXXXXXXXXKXLXSXXXXXXXXXXXXXXXXX
XXXXXXXXVASGSXVXXXPXQPAYXXXXXXXXXXXSXXXXXXXXXXXXVWINNXQXXXXX
XXSHXXXXQXXXXQXXXXXXXSXXXXPXXXXXXXXXXXXXXXXXLXXXXXXXXXQXXXPX
XXXXXXXXXXXXXXXXXXREXXXXXXXXGXXXXXXXXXPXXXXSXXXXXXXXXXXXXXXX
XXAYPLNPXXXXXXXXXXXXXXXPXXXXXXXXXXPXXXSXXXXXXXXXXXXXXGXXXXLP
XXXXQVXGXXXXXXXXXXXXXXXXXXXXXXXXXXGXXXXXKXXXXXXXXXXGXXXXXSX
XXXXXSXXXXXXXXXXXXXXXXXXXXXSXXXXXXXXGXXXXXXXXXRIVXRSKPQXLXFX
XGXXXXXXGMWDXXXXGXXASGSXXXXXXSXSHXXVDPRNSNVIPXXXXVXXXXXXEXXS
XTFLTXXXXXXXSGXXLLEXXXLGXXCDXXXXXXXXXXCGXCXXXXSCPFRHQDTGXTXX
XXXXXSXXXXXXXXXXXXXXXXXXXXGCXXXCXXXXWXXXXXXXXXXXGDXXXXXEXXXX
XXXXXGXLRXXXXXXPXXLXXXPXXEEPXXXHXXXXXGXXXXGXXXCXXXXXXXXXXXAX
SSLXVGQFVLXXXXXXXXXXXXCXXXXCXXXGXXXXXXXXXXXCXCXXEDNSKFWVGWXG
XXXXXXXGXXPEXCXXCXAQAXCXXXXXCQCXXXXXXXXXXXXPEPXXDXCXXXXXXCXX
XAXCXXXXXXXNCSCXSGXXGDGXSCXXXXXCXEEXNGGCSDFATCKFTXXXXXXXCXX
XXXXXXXXXXXXXXPXXXXXXXXXGXXXXXAXCXDXXXXXXXXXVXXXXSQHRTNQQQCY
CXXXXXGXYXXXMLQCFXXXXXXXXAXXXCXXXXXXXXXXXQXGGHGXXLXXXXXXXEXX
XXXXEXLXXXAXXXGXXDXEYXXXXXXXWXXXXXXXXYNLSVSSKKKYFELDEILAFVSA
NWDHLQLGKLSNTPPSERGQHLLDALXXXXXXXXCXXXXXGXXXXXXXXENAXXXXXXXD
XXCXXXXXXXCXXXXXXXLGXPXXXXXXXXXXXXRXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXPXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXQXSXXXXXXLXEXXXXXXXXAXXXXXXXXXXRXXXXXXXXXX
XXXXXQXXXXXXXXXXXXXXXXXXXXXXPPGXLXDAEXXXXXXXXXXXXPXXXPXXXX
XXXXXVRXXXXXXXXXVSAILXXXXXXXXXXXXXXXYXXXXXKXXXXXXXXFXXEXXXXX
XGGRTKPTLVSIPXPXYXGSRAXXXPXXXXXQXXXXXQXXEXXXXXXXXXXXEXXXXXDX
XXXXXEXXXXXXXXIDXXDRDDHXXXXHXDXXSXDDSXHXDXDDXDSHQXKDXXDDHVKH
YIPXQHDDLXRRDRHXNXDDHDDHYDMGEHEEDRDRVXXGSXEYDDTYDEHESYEEHDDV
TXXRGSDDRXXPDGSXEHPDPDDXDDHEEHYDPEEDDXDXXTDHXDXDXXDDXXXXXDHK
DDDHXHDXHDXDGHDHXDHEHDDHEHNXXXXXDHEXDXHEXXXXDHXDHEHDDHDSYDDH

DSHEDDNDSXQXVIFSIATDKXQNVTQKVAEGEAATDDTWLDGYPVVPEETEXGXSTTER
XRPXDTXRGTVVRTTDRPNEVEXXRPVPXTSLPXVPEXPTTEPALXQGGXEEMWPGFIPT
XAPSQPSDSPSYSDTLDYDTQQXAPTHXWQDDLTXHPFLDHGPVPPMHDGXNGVXEEHTV
HNLPGETGERGEXEGEXGEAICTGENCPXRPPSSSSRGPXVAAIIVAVCXXXXAVIVGVW
XXXXXQXKSSVRYEMNGKGXSQTRXXDRDXXQXIEMQXXXRGTLTEGXXXWEG

==> Piroplasmida.txt <==
>MSA Consensus of 237 seqs, protein
MXXIXRGLXXSIIXXVLLXXXXXXEVXXXXIXXXTSXXXXSXQDEDXXXYXQXXXXXXXE
NKXXKXREXXFKVKXWXKXXKXIFXXKXXRGKXXXXXDXXYSXMQXXXDXXCXXXNGGXT
XCAXCEXEXXXXXCXCXXXXXXDYXSXXXXCXNNCXXXXXCXGXXXXXXXXXXXXXXXXX
XLXRKNCGMSYDFYCXXXXVXSXLQXXXDELCGXGXIXRIVDXXGXXXCYXXXXXXYDXX
SXCLDXCGXXVXCXGXXXXXXXXRXINPXXVDWDRXXXXCXXXXXYXXDYETADXXXXYX
GCQNXXXXXXXCLNWXEXXXXXXXLYDKRFVFXXXXCRXXXXXXXIXCXTXXTEETCAES
SPKXKXSXCXPKXIPXIXXQPGXXFDIWITPYIPKYXLRIXFIDXSXXCGDXXXIAXENI
VQSYELEXFNXXXXKXXXXDEXDXFEYSPADXXXXEXSYVXXGXXXXXXXXXXSXICXXX
XSXYXYXXXXGXXXPXXSXXXXTITXGXLXVXXXXXXXXXXXXXXXXXXXXXXXXXXVX
XXXXXXXXXXXXRSXXXXRXTLXXXXSXXXLXXXEKXXRTXKIXXPEIXRRXXXKYXXXX
IXRXXIXLXXXXXFXXEKXGXYSXXXXNXNDXDXNXLIXXRXNXXGXXSNKXXXXXXXXX
XXXXXXXXXLXXXXWXXKXXXXXXXXXSKYXXXXXXCXXXXXYXXXXXXXSXXTXXXXXXX
WXXXXFXXXXTXXXXXXXXXXXXVCVFTXDXXXQXLGXGIFXXXXNXELXEXXPXXXLXX
XRESVYXNXXXYXXXDKXXXXXLXXXINDDXXFKXXXSXHXNXXXXXDXXXFIXXXXXXX
XKXXXXXXXFDXXXXGXXLFVIEXXXXXXXFWXXXXXXXXRXXXXRXXXXXPXYXGXIXV
XSPXAFXXYIXXXKXXXIVLXXXEXGXXMXXXXXXXXSXXXNXFNXXXXXXXCXEXXXXX
XXXXXPXXXXIITXXXXXXNXXXXLXTXXXXNXXILYDSXLXXXXXXCXXXXXXXXXXXX
PXXISXXXXSAXXXXIDGDXXXXGXXXXTXEXXXXEXXXXXXXXXXXXXQPXXXXXXWXX
XXXXKXXXXXXXXLXLXXXYXXGENXXXXNXXXXEXXXXXXKXXXXXDGXXDEXRTRGDT
FXXXDLELXXXPXSXXEXEXKXESXWYXPGTSGNDQSDFEXMSREEILRKRKEXNKRDLE
LRYYIPTLNGDERGLENMLKYAKRVNHWLGVCVSVHISKLXMSXXXXXXXAGKDYVIAVE
DTTHFGEEFWKTELHSFVKLLAYGLSATKGTNTLSLVRYSNTVEKVLDRTAAVTDLLQSV
QLEYXGYQXXXKXXXXXXXXGAALKFMRENVYPNHDRFVRRXXXNXKXLXGDTTTLSVEN
AAGKDTVVIMVNSGSVSDSALAXXXXXXXXXNXXXXXXXXXGXXSSGFWKQVSIXLXFXV
GCRAGHYAXXXXYXXXLXQELLEKVGTMVXNLCEPDGRXXXXLXXWSXXXXCXXXXGXXL
KTSTXGRNGCKGXXXXXCXXXXTAAQHKGSPWCCNLKGHKTLLTXXXXXXXXXGXTCXXX
LXXXXXKXXXCXXXXCXXXXXXXXXXHHSSHTDGLPSGANEYTAAYQNGEGDVVDTMRXC
XCXEGYYXXDXXEGXXXGXXXXXGYFCSDSGDSDXKNGCXCNTTXVIXXXXXGGXXXXXX
XXXXPRXXXXXXXXPLNPYDTDLIDPXYPGYXPTXXEXXXDEXXXXMGXTTXXDDXEEXE
XEDQTXDQTDDQTDDQTDDEESXXXADXTEESVTDXHPHPKXXXIPXPHPHPXHTDLEDG
IXXXLXEMDDEXHEEXXPXXXXXCXXCXXXEXXXXXXAEEXEEAEEXXXXVGSXEEEEDE
EXEEXEEDEDDYSEDEDYEEPDYLDDRGNIITDDFHEGDYDMDARRGPYGIDYGRYNGEX
XYEDQQENGSTHDREYGGGNXMFDGKMPLFTLSVGATSRDSCVCERENSKSVEPFEMNVW
EYKAYILAGFAGLLEGQSSKXIXXPXXXQAEQRXXDXXGXXXFXXPXXHXSXLITVVYYG
SHIVRSXNXXYXDXXKQEEELNDETEYLQSGDGDDVNXRQPMXCXDSNAXXEAGGREXSS
EXXXXXGXXXDXDXXXXXKEXTXXXHXXSYXSXDXXXRXDXNSXTXGXXXAQETXXXEXX
XXDXGYXXDXXXXXXNPPYHSXXXRXXXGXVXXXXXXXGSHEQDDSKRTGAGXXXVVXXS
XXXCPPNXXXXXXVXXAXXXXXXXXXXXGYXXVSEXXEXXXKXCXXCXPGXYKSSVMXSXX
XGXXTXXAXXXQVADANEAMWAXXGYXYLEGGXCSKCMEGAXCEGGLIXXXXTNSGGTDN
DTDSVNEIVDLTDVSNKNSPASTGMTNTSXXXXNXXVXIDDHVKPXAXEGYXLDKINXKL
RKXDDWKFIKCPIXGSCLGNDKCSXXMEHYLCSECKXGYTNNFVKGXLCQXCPXMXXNIS
XTXXYXXGLLLINIVMAXLNISXGXNRRSIHSVVIKIALNXXICTSVXNVXNFXXLKXPX
GLXKXXNXXXKVFDSXDXVYYTSIDCXXRXLFXXXHXDSXFYXXLYXAXXPXILLFXVTX
XMWXIXXXFKXXXYNDXRXKLALLQQXXXXXXXXXXXXLXEQYXNERLLMILRYIPLPNE
TSWDRFKNFXEDMIPIYVTVLFSVHGKITSRXLSLLDCXYIDLGRSFPGKYVLRPAMSIR

CSINPSEGYLRYLILGLXGLXXWGXGIPFLSFXXLXXNRXNLYAXSIRMKYGFLHNGFRQ
DYWYWETXVFXRKCLVLVIGSIVIVPSXNYSGSRIWMALVVAXXFLIXQLIYKPFDERDY
FVLGRLENHSMITWTFTLILVSFIIEANFTPSLSLILFFIILFINFLFILELLFYFIIFI
SSHIFYLFSVFFPRFFSRNIKISHPLSYKEPIVFYDKQDSHILLNRQIKPFGSLISFQNL
SSVYSNYFTTTLSHIFNLTACYLNLDVIPSLFIDFLIRYSISIGNIENKVIEKNFSTKSD
NEISDLIEGVTSEKYENKNKYLNIDKYKKEHSSDTFITEIENILEGYGIESDEINGIINS
LYDESYLKNNLYLSDFYQSIENLYNLDKTTLCLLYELFKHYKTYFEDQINKKIDLQINNL
MNQKTEFENSLKDRESIYHVTQEIGKINAEIEDLKIEREVKRGRLLKLKESGNIYKNEYD
KVIGRKSKYDNERNLFCKQLIENVGFKPINREDTISEVEHKDYQE

==> Planococcaceae.txt <==
>MSA Consensus of 147 seqs, protein
MXXEXXXKXXRKXXXXXXLXXXXXXXXVXXXXXXXXXXXXXXXXPXXXAXXXXXQXXXXX
XXXXGXXXXXXXXXXXXSGXXXXXVKXXXXXXXXXXXXXXXXLXXXPXXXXXXXXXXXQ
XXXXXVRXXXXXXGXXXXXXXXXAXXXXXGXXXXXXSXXXLXXXXXXYIXXXXXXEXXPX
XXIXXAXIXXXXXXTXXXXLXKXXXXXXKXXXXXXXXXXXXXXXXXXGTXXXXXKXXXXX
XXXXXXXGKLDIGVSGXXVYXXXXXXXXNXXXXXXXYXXXXXNKXXXLXXXXXXYXXNXX
XXPXXXXXXXXXVSPXXGXLQIQPXXXXXKXSXXXXXXXXXXXXAGXXXXXXXXXIXXXN
XXIXIXXXXDXXXXLXXXXXXXXXXXEXXXXXXXXXAXXDXXXXXGXXYXXXXXXXXXXX
XXNXXGXEXXKFXXXYXXXTXXXSRTXXDXXGVXXFXXXXXPXXXXXXXXXXXXXXGXX
XXXXXXXXGXTXXXXXXGXXPXXXXXXXXXPXXXXKXXXIXAXXXXXXXXXXFXXXXXXM
GXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXIXXXQSAXXXLXXXXXXXXXXXXX
XXXXXXXXXXXDXXNXXIXXXXXXXXVXXXXXXXXXXXXXXXXXXXXXXXXXXPXXXXX
XLXVAASXXXXXXXXWXXXDXXXXXXXXXXXXXXXXXXXXXXXXXXVXXXXXXXXXXXX
XXXXGXXXXXLXXXXXXXXXXVSXQQNSAXAAGLADVALXXXXXXXXYXXXXXLXXD
XDXXXXLDLXXXXXXXGXXXFFXXXXXXXXXXXXXXXXYXSXXXXXXXXXXXXXXXXXX
XAXXXXXXXXXXXYXXEXXXXXXEXXXXXXXXXXXXYXXXXXGXXXXXXXXXXXXXKSL
XXXXXXXXXXXXXXXXXXXXXCPXVXXGSXXXXXXXXXXXXXXXXXXLXXXXXXXLXP
SXXXSGXXVXXXXXXXXXXXXXXLXXXXXXXXFXXXXXVXXXXXRDXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXAXXXXXXXXXXXXXDQKXXXXXXXXXXXXXKPXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXATXXXXXXXXXXXXXXXXXLDAXXXXXXXXXXX
XXXGXAXLXXXXXXXXXXXXXXXXXNXXXXXXXXXXXXXXXXXRGXXXXXXXXXXXGXX
XXXXXXXXXXXXXXXXXXXXXXFXXXXXXXXXXXXXXXXXXXXXGGFXXXXXXXXXXX
XXXXXXXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXAXXXDXXXXXXQYXXXXXXXXXAXXXX
XXXXXXDXXXXXXXXXXIXXXXXXXXXXXXXXXXXXAXXGXXGXDDNAAXDXXXTXXXX
XXXXXXXXXXXXXXYXXIXXGXXXXXXXXXXLIDXXXXXXXXXXXXXXXXXKFXXXXXXXX
XXXXXTXXXXXXHXXXXXXEXAXDXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXWX
XXXXXXXXXXXXXXXXXXXXXXXXXXXSXXXXXXXIXXXLGXXXXXXXXXXAXXXXXXXXX
XXXAXXXXXXXXXXXQXXXXXXEXXXXXXXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXX
XXXXVXXTXXXXXXXXXXXXGXXXDXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXTXXPXP
XXXXXTXXXXXXXXXXXXXXDXXXXLLKXXXVFEXXXXXXXXXXXHXXXXXXXXGXXXVH
XXXXXXXXXXXXVXXXXXXXXXXXXXXXXXXNGVXTESXLXXXXXXXXXIXXXXXXXXXX
XXXXXXXXXXXXXXXVXDXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXEXXXXXXXXXXX
XXXXXXXXXXXSXVQSKXXXXXXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXXXXXXXXX
TXFXXXXQXDXXXXXXXXXXXXXXXXXXXDXXGPFXXXXSXEXXXXXXXYXXXXXXXXXX
RXXGXXRYXTAXXXSXXGWXXXXXSXKXXXXVVXAXGXXXXDALXXXPLAXXXGXAPXLL
TXDXXXLXXXXXXELEXXRLXXPKXXXXXXGGXXAXSXXVXXXLXXMXFXXXXXXXXXXA
XIXRIXGXXRXXTXXXIAXXXXXXXXXXXXXXVXXGXXXFXDXLSXXXXAXXXXXPILLTX
KXXXAXPXXXXXXXXXXXXXXXXXXXXGGXXXVSXXVXXXXXXXXGXXXPXXXRXXGXXRY
XTXXXXXXXSXXXXXXXXXXXXXVIFVXXXXTIMVXXAXGXXXXDALXGSXLAAXXXXPX
XLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGGXXXXXXXXXXXXXXXXXXXXXXXXPX
XXPXXXPXXXXXXXXXXXXXAITPKXXXGTXYXXGGTTXXXSDFDIVDAVDRFVMDGSGF

DCGIGMSXWGSXXXXXXXXXXGDVPVKAAYDGTVSYSGYXXYVXNTXXGIXXXRTGDXXX
GXXXXXXXVSYSXXNVTSVKLDKSTNTXKXGDXVXXXXXXXSTPXXXXHXXXXXXXGIYI
GXXXXXXXXGXXIHXEXXXXXLXXXXXXXXXXXXXXXSXXXXXXXGXXXXXXXXXVKPINV
XXIKLXXSXGVXXXXXSELKSSLXIXXLXXSXXXXNATXXEXTXXXXXXXXXXXXXXFXX
NXXXXXXXXXXXXXIATAXXGXXXXXXXXXXVXXXXXGXWXXXXXXXXXXXXXXXKXXXX
XDXSLXXXXXXXXXXXXXXXXXXXXXXXXVDXXNRTTXXSXTFXXXXXXYXEXXXXXVP
LGLTIXXVXXXXXXXXLXGKXSXXXXSXXXVKAEWNNEDNKFIYSSAPVTTKSTAELNAK
GQVNISQGVGLXXXIXXXXXXPXXXXNDLVXXVXXXXNGXXXXXRTKEXXXXNXXPXXIY
SXXXXXXXFDXGXFSTFKSRLLISSFGSEMGXXXXXXXXXMDXYXXXXXXXXXPAGKIKGS
VRGAVTKEKLADVKIVAYMDGEFYRSSISDANGDYEIELAPXXYXLXFSKLHYENEVINN
SEISTDEMTYNPELKLIHQDNLGDGTVEGTIKNALNGLPVPESVIEIRKGMNTTIGSIVK
TITTSSNGEYSTSLPAGNYTGVIKKEGYIDSSINIISIGLKTMPLQDGTITPIIDNEELR
IVLTWGDSPSDLDSHLFGRYNDSSVYHIYWGSKHAYENNQIIAMLDIDDTDDYGPETITL
LKQNPGKYEYWVHDYSNMSNTISKELSNSDAKVDIYRGSYLIKSFYVPSNKTGNVWKVFE
LNGNEIVPINVITNDVTYPESNSPLSIKQEEKSYLKEAM

==> Plasmodiidae.txt <==
>MSA Consensus of 794 seqs, protein
MXXKXXSIFXXIXWLXXXXXXXXKXXXXRIFDVNXXEXXXKKXXXXXEXYKCFSKRXXXX
XIXXXQXIXXXXXXXXXLNXXRXXXXXXXIXQATXXXGXXHXXXNGQGDNRTDEIQTXXX
XXPXXXFKFXXXLNXLXYXDXXXXLXSXLXIXLXXYCXPXIPKGXRCXXXXXXXXXCXXX
XKXXXXXXXXXCXDNCGXXXXCXXXXXXXXXXXIPXXXVXXXXXXXCXXSXXQRKLXNLC
GXNKXFRXXXXXXYCIPXLXNXSALDKIXNXXXDADVCLAALXEXXSXXQXYPKYQAQYX
XXXXPSQMXXXXXXCXSXXXXVIXCXGXXXXXKKEKLDLEKNLKXXXXKXYXXXXXXRAK
DHFXXXXXXXFIXXXEDXXXXXXFXXXXXXXXXXGESDKYXXXXXCXEXXXXNGXXYXGC
QXXSISXXXCLPWXXXNIXXIXXXXXXTHNXCRNXEXXXXXYXXXXXXXXXXXXXXXXXX
XXIXNNXXXXXXXXXGXXXEXXCXXXGKTDFXXFDXXXXHVNVSDFXIXLXXXXCXXGXX
XXXXXXXXIXXXXXXYXKXYHXXDXEIAXTXXFXXXXXXXXSXXXXXXXXXXCXXXXXXX
XYXXEXSXXCXXXXYXXXXGKXXXXXXXXXXYXEXXLXXNEXXXXXXNXXXXXXXEXXEX
KNIPXXXSXXXXYXGFNDNIELFXXXXXXXXXXXXXXXEXXXXMXFXKXXNXXXXXXXXX
IXPXLXXSXXXSXXYXYXXXXXXXXXXXXXXXXXXXKXXXXXXXFXXXGXGGRLGXXXXXPL
HXYXXXEXXXXKXMXXXXXXXXXXXXXLXXXSXXICIXXXXXXXXYXXXIGXXXXXDXXNS
XXKYXLXNXXXXXNDNXCFXXXXXXXXXDXXXXSXXNXXFXXXXXXCXXXXTHXXXXXXX
XXXXEXXIXRXXXXSXXXXXXXXXXXFXXXXXNXXXXXXXXXXXXXXXXEKGXXXXXFXLX
XTXXXXXXXXXYLCXXXXXXXXXXXXXXXXXLXXXETIXXXXYDIIISEKASMDEMEKKE
LSLNNYXYXSSFXXXXYXXXXXPXXXXXXXXFGYFNYXTGXCEXXXXXXXXYXXXXXXXXX
XXXXXFXXXXXXXXXXXXXXXXLWXXXXDNXVSLWXXXXLXXXXXEXXXXXXXXIEXXXX
XLTPXFLXKYXXXXPXXSXXXLXXXXXXXXXXXXKXXXXXXXXXSXXXXXTXXXXXTXPXX
XXXNXXXXXXXXXXXXAXXYXFSXXXLXXXKYXTXXFXXLXXXXSXXXXXXXXXXXIXXFT
XXXXXFFXXLXKNNXXSXXNXNXXXXXXXXXXXXXXXXXXPIKXXCXXXXXXXTCXXXXX
XHXSXXXXXXXXFXXXXXXXXXXTIIXKXXXNIXYPXRXXXXXXXXXXXXXXXXXXXXXX
XXXKNXXXXXXXXXXXXXXXXXKXXXXXXXXXXXXXXXXXXXXXXXXKXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXHDXXXXXXKLXXYXXXXXXXXXX
XNXXXXXXXXXXXXXXXXVXXXXXXXXXXKDAIQNIKNKISDDIKIXXXXXXXXXXXXXX
XXXXXXXXXXNPQXXXXXEXXXXXXXXXXXXXXNXXXXXXXXXXXXXXXXXXYXXIXXXX
TKXXXXQSXXXXXXHEXLXQTLNIGXXXCPNXXXXXWXXXXXXXXXXPXXXXXXXXXXXX
XXXXKXXXXXXXNXXXLXXXXXXXXXXXXXXXXXXFXXXXXDXXXVELXYXXXXXXIXXX
XXXXXXXXXDXXXTDPXXSXXXMHXXFXXXXXXXXLXXXXXXXCXXXXXXXXXXXXXXXX
XNXXXCKXXXXXXXXXXKXXDXXXXXXXXXXXLAVGSYGLGGRLGSNXXYXXCXXXXXXX
XXXXXXTTXXXXXXXXXXCXCXXXYXXXXXXXXXXXXXXXXXYYSXSXXXXKXXXXXXXN
ITLPMXNPXXXXXXXXCSXCXXGEYXDXYXXGXCXENXYXNXCXXNLXXYXXXXXXXXXS
XCXCNXXAXXXXPATASECVILGXXXXXDXXXXXXCXKCXXXHYCPXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXCXXGYEPINMXKXXXXXXXXXHXXXXXXXXXXXXXYXXXXXXIX

XXXXXXXXKXXXXXXXQXXRKTXXXKXWTYXXXALSFIRPDYEXXKXXRXXAPKVTILFT
DGNDXXXSSXXXXXXMXLXYXXXXVKLLDLVLGVXAAXXXXLXXIAGCXXKNXKCPPRXP
LXXXXXXXXXXXTGKCXSLXXXXXXXXXXXFXXCLEYXFXXXXPXXXXXSXXXXXYWGXW
XXXXXXNXXXXXXXXXXXYXXXXKXXCXXXXXNHFXXTXXXXNXKXXXXQYXGDAXICPX
XSXTXPXPXXXXXXFXXXXXXXXXXXXXXXXXXXXXTXXXXXXDVXPFXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXEX
XXKXEEXALXXXXKXXXXXPNNRXXXXXXXXXXXEXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXEXXXXXXXXXXXXXXXXXXXIXXXKGFFYXXXXTSRNNTFIDXXXXXXXXXXXXX
XXXXKXXXXXXXXXXKXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXEXPXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXEXRXKXXX
XXXXXXXXXXXKXSGXXXXXXKXXXXXXEXXXXXEXXXXXXXXXXTLXXXNXXDXXXCXC
XXXYXXXXAXKXXXXXXXXXXXXXXXEXXXXXXXXXXXXXXXEXXXKXXXXXXXXXXXXXFX
XXXXKKXXIXXXXXXXXXKXXXXXXKXXXXXXXXXXXXXXXXXXXXXXSQXXKAXXXXX
XXXXXXKAXXXXXXXXXXXXXXXXKXXXXXKXXXAXKKAEKKAXXLKKAEEKKKADEXX
KXXEXXXKAEEXXKKXXXXXKAEEXXKKAEXXXKAXXXXXXXXXXXXXXXXXXXXXXXX
XXXLFLXRXXXXGXXXXXXXXLKKXXXXXXXLLXXXXXXXXXXXXXXXGVSMAXXXXXXX
XXXXXXXXXXXPXXXXSXQNXXXXKXXEXXKKXXXXXXXXXXXXXXXXXXXAXEXXKXEXX
XXXXXXKNXXXXXXXCXXXXXKXXXXXXXXXPXHCFCKXGFFEXLYXXXKAEEXXXXXEX
XXXXXXXXXXEXXKCLPXNFCECECSCKNKTGFSXKXRXXXXXXXXXXXXXXXXLXXXK
XXXXSXXXXXXXXXXXXAEXXXKXEEXRXXXXXXXKXXXXXXXKAEQLKXXXXXXXXXE
XXXXXEXXRKIKXXXXXXKXEEEXKXXEXXXKXEEXXXXXXXXXXXXXXXXXXXXXXXX
EXXXKAEEXRKXEXXXKXEXXXKAEEXXXXXXXXXXXXXXXXXXXXXXXXEEEXXXXE
XXXXXXXXXXXXEXXXXXEXXRXFSSCKXXXXXXXEEXSCXXXXXXXXXXXXXXGYTNXF
XEEEXRXXCVXCPNNXXNXIXLXXIYIIFCXIIIXIXXXNXSSGFYRRSIHSIXIKXXXX
XXXXXXDXXXNIXXXXXLXLPXXXXXXXXXXTKXXXXXXXXXXXXXXXXXEXKVXXXXXX
XXXXXXXXXXXXXXSXXXXNSEXNXNXXXXXXXXXXXXXXXXXXXXXMXXLTXXLFVI
LKIYTXXXKXXXXXKXXXXXXXXXXXXXXXXXXXXXXXXXKERFIMILRYXXXXXYTXXXX
XRXXXXTRXXIIXXSKXNXCXNXXXXXXXXXXFXDXXXXXXXXLFXIHAKTSXRMXXLXX
XSXXXYXKXXXXYQILXXXSSVQCXXKTNDYLKXXXXGXXXXXXXXEWXLGIPXLXFFVL
XXXXHAPFEDVMADDEKGIKTXGDCPXXXKXEWXXLXDXXXXXSSKXCDXXXXXIXXGXC
XPSSGSXXERKXLCCSISXXCLXYFDXNSNFXXXXYSXXXKYYDCTKXEFXXPXXXDYXC
FXXXXXXXXXXFXXXXXXXXXXXVXXFPSXXXXXXXXXXITFVXIXXXXXXXIXXXXXXX
XXIINNNYKIVHFFXXXXXXNXSXXXXWXXTIXXTDPAXDKXXXXXXXXXXXXXXXNXXX
XXXXXXXXXXLLXXXXXXXXXXXQKXEXXXXXXXXXXXXIXXGLXXXFXXXXREXAPKXAX
LLTDSNNDXXEXXXLXXXXXXXYXXXXNXRXXXXLXXVXXXXXXXXXLXXXXXXXXXXGS
XXEPXXXXDXXXXQXXXXLPDXXXXXXXXXXXXXXSXXXXXXXVXXFXXXXXXXXXXXXX
XXXXRASDGGICNGNGNGNGNGNGNGNGNGNGNGNGNGNGNGNGNGNGNGNGNGNGNGNG
TGNGNGNGIGNGNGNGTGNGNGNGTGNGTGNGTGNGTGNGTGNGCXXXXXXXNXXXXXXY
XXXXSXXGTGSGNGNGNGTGNGTGNGNGNGTXXGSXXGSGNGNGTGNGNGNGTGNGTGNG
NXXGNXTXXYAXNXXGNGNGNGTGNGTGNGNGNGNGNGNXXDXGNGNGTGNGNGNGTGNG
NGXXXXXXXXXGNGNXXXXXXNGNGDXXDNGNGTGNGNGNGTGNGNGTGNGNGTDNGNG
NGTGXXEXXXNIXXGXXKXGXKRRNGNGNGNGTGNGNGNGNGNGNGTGNGNGNGNGNGTG
NGNGNGNGPXXXXXXXXXXXXXNXQXXGNGNGKGXXNGNGXXXGNGTXXXXXNXXXXXXX
XXMXXLXNXXYLVIVFLXXFXLXXXXXXXXXXXXVDEXXKYXEEVCNXXVDLYLLXDXSG
YIXXXXFEFIFSIXXXNWXXXXXPXXXXLIXXLXLXXXXIXLYXNXXSXDXFXNXXXXXX
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XXXXXXGESSXXXKKNAPXXXKKLIIMLVXEGXERERXXXXHLXXXXXNDRXNREXAXQL
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XEXKKLXXXNVKLXXXXXXXXXXXXXXXXXXXWSXXXXXXXXXTCNNNNSSGSNXKXXXXL
LYKEXXXXSKXXXKXPXYXXKIEAVXGIGQHXXGNSCXXLQGINXXFNRXXXGCXPXXXX
CXXYXXXXWXXXXXXCXDXIRXRXRXXXXGRGDAPLAASFQXDXXXXCQXFNXTEIXPFX
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VCSXXXXCEEXXCPXXXEPLXVPAPXPXXPEDXXPRXXXDXFAVXEKLXXXXSITTDENP
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XENXXXXDLXXXXXXPPLPLPPAVPGGSSEEFPADDRXCNVGMRXRXFIXNVXGXXXXXX
XDXCLEXXNXIQNNPDLXLPXCXXXXXXXPXNPEXETWXXXXEXXXXXXNPATSPRGASX
XNPXNPPXPXIPXQEPNIPEDSEKEVPSDVPKNPEDDREENFXXPXXXEXXXDNXAXPCX
NNXXXXKSXRYIPXSXLXXXXXVNEKXDNERKQXXPXXXDNXXXXXVPNXNKTVHPGRKD
SAXVPXDRXXRPHGXXXXNXXXXXXXXDXPXXPERXXXXXXXXXXKXXXXSXNXYKIADX
DGGXXXGLALXXCXGXAYXFVXXGXAXGMANIPYAGEPAPFDEXXXEXDKDEKDVAEXLD
EXXQFXIVILPEXNXWN

==> Plasmodium (Laverania).txt <==
>MSA Consensus of 334 seqs, protein
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CFFLLTXLXXIGDIIRXXXHXXGXXXXXHGASSXXDXXXXXEKNLKXFXGKXXNXXXXXX
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XGTQGRCRXXXXKXXGSKXXXNXVXXFXXXIXKDLTXXKXEVXVGILLXXXXXRXFXXWG
XXXXXXXXXXLXNXIEKXRGQDGSXKDXXXDXGGTDCKGXXXXXXXYXLDXYTCXXXIXX
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XXXXLXVLXXAEKXXXXHPEXXXXXXXXXDXXNKXXXFXXCXXNXXXXYXGIEEQKKXXW
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XXSDSXXXXXXXYXLXXXXXEVXSXXXDXXLXXAXXLXXXXXKXXNXXKXKLGDXKXXXX
XGYIHDXXKXXXXXXNFXXXHXXKXXIXXXXXXTXXXNXXDKXKKXEKGCKSNCECFKKW
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DTSGDNTFIXLFDCSIYSHCIGPCLYKDFNNXCFLNLPXNYEKEFNNDLKEKGYSSFNNF
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XSXXXXXXXNXXDXXNKDXIXXLIKKLQEKXXSLIXFKXPNXQTNKRVLYENNKKSKRNX
RTXXNXVNXFTIPSXLXTXEKEXLDEXXXXYNXXEVKNYPNNDXNNXSYIQVLDIAVVLD
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XNYKDKXCPNHVYEGRAHGSCPNYGKXIIVQNLXXEEGDYDXFNFGTNLXXXXXKXXNFL

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XSSFXIRPDYETKCPPXXXXXXXXXXXXXXXXXXXXXXXXSXXXNXXXXXXXXXXSTFXSX
NNXXSDXXXXXXKXYXDXXEXXXRXPLEKSKVXXXFGTFDXKTGKCKSLXXDXAYXVXGI
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XKHSVXNENNIXIANRKEXXEGCTSSQDINXEXQEXCYHLVXXVXKPQSEFDQQNQLYKK
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AEEKKKADELKKXEXKKKADELKKXXEXKKXXXXXKXXXXXKXXXXXXXXXXXXXXXXXX
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KEKEXVIEEELRKEDEKRRMEVEKKXIDXXXDNFXENIXDNXXXQEXNXKNTPXINKEIF
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XNXLETGHXENXKXINKDDIEGSNNXXXGNNNDIXYTKXXXXXXXIIKXXXXXXXXAELD
VEEYKKRDVXETREXIIKISKYSISEVDGIKLXXXXXXXXTXXLXNMCNNDFSSKYCDYM
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==> Plasmodium (Plasmodium).txt <==
>MSA Consensus of 391 seqs, protein
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XFARGDXXXXIDDXXKWKWRRLILCSRTIYDEKXXXSXLXTXXXXGTCPXXXXXGEKVVD
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XXXPXXXXXXXXKXXXXXXXHXXSRXRNCXSXXXXGXXXXXPNCKFYSYADWNEAVALIK
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FQENVRIKYGFLHNGYLPNRWYWEIIVFARKXFFXFITTVVLFPSXEXNTSKLXLITFVA
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==> Plasmodium.txt <==
>MSA Consensus of 793 seqs, protein
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XXXXXKLXXITFVXIFSLCXHXIXXXXXKRXXXXLXXXEXXXXXIXXXTIXXXSXLXXXX
LXXFXNXXXXXXXILXXXXXXXXXXXCXXXEXXXXXXXXXXXXXXVPXXXXXXXXXXXXX
XXXXXXXXXXYDAPLAASFXXXXXXXCXXFNXTEXEXCNXQXCXXXXNXEICEXXGXWXE
WSXCSXXXXXSXRXXXXXXLPXXXXXXXXXXXXXXXXFXXXXXXVXXFXXXXXCVAPXCE
XEXXXXWXXXXXXXXXXXRRASXXXXCGXXXXXXXXRLXXXXNXXXSXXXXXYXXXXSTH
XGXXXXXSTXXXXXXXXXXXXXXXXXYXQXXXEIXXXXXXXXXXXXXNIQXGXXXXKXGX
KXXNXXXLEXPXXXXXXXEXXXSLNXQXKXXXXXXXXXXXXXXXXXXXXXXXFXXXNXX
XXXXXXXXXEXRMFAIEIYKELLDIFXKXVTXTYIXXXXFEFIFKIXXNIGXXIDXXXXX
XXXXXXXXXEXXXXXXXXWXXXXXXXXXXXXXXYGLRPATSPRGASXXXXXXPXXRILXX
KXXXXXNXXXXXXXXNXXXXXXXXXTSXXCXDXXXXXEXXXXXXXGAXPCXDALCNEWXX
WXXXXXXXAXGXXSXXXXXKXXXXXXXXXLXXSXEEXXKLFSFFSDXXXXXXXXLXXXXX
XXXIXXLXXFXXGXXGLTCEXQNXXIEEXEACXHXVPACXPPXXXGXXGXXXXXXSXXX
XXXXXXXXXXGSXXXYXSXXXXXXSXGXGTGEKXSXAAGIKNILNEVLPSAIELXXXXXX
XXXXXXYXXXXXLYKXLXXXXEXKKLXXLNKKLXKXXXXXXXXXXXXXNXQDNXXXXXXK
XXXXLXXXEXXXXSXXXXQXKXXXXNXXXXXXXXXXXXXXFXXXDXXXXXXXSSGXXXXK
XSIXXXLLSMXXDQKEXIPXXXXXXESXRGEREFKXXXXXXXXXKXEIIEIXFXXNXXXX
F

==> Primates.txt <==
>MSA Consensus of 839 seqs, protein
MXXXXPXXLALALGLXXWXXXXXXXXXXXXXXXXXXXXXXXXXXVXXXXXXXAPAXXXP
XXXXXXSLHXXXXFXLXXAARXXXXXXXXXXGPXXXXPXXXXYCKXVXXXXXPXXXXXXX
XXXXXXXXXXXXEKXXXLXXSLRQXXKXXXXXXXLERXXXXXXXXXXXXSNXXXXTLXXXX
XXXXXSXSXXXXXGYQXEMGSDVDTETEGAASPDXXLXXXXXGXXXXXXXPXXXXXXXPX

SXXXXXXXMXXXXXXXXXXXAXSXCXXFAQXXXXXCXXXXAXSTXXXXXXSXXXXXEGXX
XXXXXXXXXFSXXXXXXXXXXXXWXXXXXXXXXXXXXXXXXXXXXXXXSXXXXDXEAXX
XXXXXPXXXXXXXXXXXXXXPXXXXXXXXXXXGXKXXXXXXYXXXXXGXXXXXXXXXXX
XXXXXXXXXGCXXXXXXGRLEXAXXXXXPXXXXXPXSXXXSAAAXXXWXXXXXXXXXXX
XXXXXXXXXXXRXXXPXXXXXPXXXXSXAXQXXPXXXNXXXTXXPXTXXXXXXXXXXXPX
XXSXFXXPAFXXXXXXXXCXXXXXXXXXXXXXXTXXXXXAXXXXXXLXXXXXXXXXAXXX
XXXXXLLXXXXXXXXXXXXXXXXXLXXXXXXVXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXCXXXXXXXXCXXXXXXXXHAEGXXXXXXXXXXXKXXXXXXXX
XCXXXXXXXXXXXXXXXXXXXXXXXXAIXXXXXXXXCXXXXXXMLQHXXIXCXXLXXDX
XVXXXXXXXXXXXXXNDNTDGIHCEXXXXXXXXXXXXXXXXXXXCXXXXXXXXXXXXXX
XXXXXXNXXXXXXGXXXXXXXXXXXXXXXXXXXXVXXXXXXXXXXTDAGCTQDQRLLDSKC
DCDPAXIAGPXXXXXXXXXXXPAVTGERCDRCXXXXXXXXXXXXXEXXXXXXXCXXXSXXX
XXXXXXXVHXXXXXXLXXXXXXXXPXXXXXXXXXXXWXXRXCXXXXXXXXXXXXXXXXXX
XXQXXMAXPXGXXXXXXVXXLXXXXSNVXXXXXXXXXXXXXXXXXXXXGAGLXXCLXXFS
FXRGQKVLXXXCDVXXTXXXXVXXGXXXXXXXXXXXEPXXXXXXXXGXPCTSCAAIKKQX
CPXXXXGWLREXXXXXXXXXXXXXXXXXCRXXVSQXXXXXXXXLISMXXXXXXXXXXXXXX
XXACCPGXXXGXXCXXXXXXXXXDSARXXXGXXXXXXXXXGXXLXGXXXXGXCXCXXXFX
GXXCXXCXDXNXFGPDCQXXXXXCSVCSCVHGHXXCXAESCXGXXGDGXCNXCXXGYTGP
XCXXXXXXXXXXXXXXXXXXCXXXXXXXXPXCQXLXCPXNXQPSXXXXCXXXXXXCXXX
XVSEDCSIRXXXXXXXXXXXXXXXXCXCNXPGXXXQGXXCXXXXPCWPSPCXXLAXCSXS
XXGQAQCXCXEXYHGDGXVCLPXDPCXXNXGGCPSNSTLGCXYQGXPGQXXCXCXXXKXX
XXXXGXXXXXXXXINXXXXXXXXAXCSPXXXXSTNGQCDIRTGQCSCXRSXXGXXXXXAX
CXGXXXXXGXXXXXXXNXXRXXXXXXXXXXXGXXXCXCXXXXVGDGXXXXXXXXCXXXXX
XXXQKXREANTETQTGRVFVPEEGKSGVLSVSSGAAAHXXXXXXXXXXXXXXLRVTXXLX
XXXXAXAXXXXXCXXXXXXXXXXXXXXXSAXXXXXWXLTTXGXXXXLVXXXXXXXXRXQT
MNXXXXXXXXXXXXXXXXXXXXXXXXXXXDXXXXXXXXXXSXXLXLAXXXXXXXXXXXQ
XXXXXXIIAGQXXXXXXXXNRVRDXXXLITQMQLSLAESEASXXDTXXXXXXXWXXXXGX
EITVXFNQRLAEXXXXXXXXXXXXXRFTXXXXXXXYXXKYXALHDXXXDXXXXXXDXXXX
XXXXXQXXXXXXXXXXXXXXNGXXXVVXXXXXXXXILXXRXYXDXXXXXXXXXXXXXXXX
XXXXXXXPXXXXXXXXXXXXPXXXXXWXXPSXXPGDPKRTIGQILASTEAFSRFXXXXEX
XXLXXXLXXXXXXXXGPXTVFPGXXXXXXXXXPXXXXVDSXXDGRLXAXXXXQXXXXXXX
XLSRKLHSSXXXXXYLXTXGLSNKLQELVXXXPEXXXXALXXXXPXXXXXXLXXXXXXXX
XXXXXXXXXXXGXXXXXXPXXXXXXXXXXXXXXPXRYHIYNHXXXGXXQLTVEKLISKGX
XXXXXXXXXXXPXXXXGXXXXXXXXXXXXLXMANXXXXXXXXXXXXXXGXILXXXXXXXX
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AGEALXXGXXVXXEXXXXNLEANVTADGALAMEKGXXXLRSEMRNXLXXXXXXXXGLHEL
XXXXXXAKVTXXXXXXXXXXSXXXXXXXXXXXXXVXXXXXXXXXLDGXXEVVPQLLDQL
RTVXXXCPXNSXXXXXXRXRELIAQTRSVADIFPKECVYIHXXAVEVHDPTSMDDLKAFT
XXXXXLKXGCAXYXXXETXXXXXXYXXXXXXPXXXXXGCCKGFFGPDXXXXPXGFSXPC
YGKGNCSDGIQXNGXXLCFPDYKGIACXXXXXPNXXGXXCXXDCXXXXXXCVHGXCDNXX
PGSXGVCXXXXGTCXXGFXGRFCXEXXXXCGPXGLAQHCHLHAXCVSQXGXARCTAEXXX
XXXGEXXXXXXXLXXXPXXXXXCLXGXEGDGFXCXPSNPCXHXXXGGCSXNAECVPGXLG
XTHXCTCXXGWSGXGRXCXAIXXCELXXRGGCHXDALCSYVGPGQSRCTCKXGFAGXGXX
CSPIDPCRAGKXXXXXXXXXLXXXXXXXXXXXXGXCHXLAXCRAXGXGXXXCSRXXPPGF
GGDGFSCYGDIFXELEAXXXXSXFYQWXKXAGITPTLSSLYVLDNNXXXXXXXXXXLPXX
XXXTXLVPSEAAXRXLXPEXXAFWLQPRXXPXLXRAHFLQGAXXEEELARLGGQEVATLX
XPXXXWXXXXXSGRVWVQNASVDVADLLATNGVLHILSQVLLPXRGDVPXXXGLLQXLXX
XPAFSLFRXLLXXXXLVXXIEAATAYTIFVPTNXSLEAQGNSSKVXXLDADTVRHHVVLG
EALSMETXXPEILQSRALRAHLPXDXXXXCDRNCGXXXGXXIGAXXXXXXXXXXXXXXXX
XXXXXXXXXATEXXXXXXXXXXXXTXXLXXXXXXGXXRXXXXXXXXXXXFYNHSGQPEVN
HVSXXXXXXXXXXXXPLAXXXDXXXXXXXXNXXXXXXXXXXXXXXXEXPMLEAXAPGRSL
XGLXXDXGVXXXXXXXXXVXXXXXXXXSXXXXXXXXXXXXSRCLHSHIKXXXXXXXXEXX
AXXXXCXXCXXXFRCTXQXXXXXXXXXXVGXKNPTKGKIEQTQXXXXXXXXXXXXXGXQX
TPXKSCVYRSGFXXXXXXXXRGCSXXXXXXXXXXXXXXXXXKXXXXXXCCPXEXGFFXGX

XCXPCPGXXXXXXXVXXXXXXXIGISPSVAGVCXGNXXHGQCQDRXLGSGECXCXEGXXG
XACXXCXXGXYGXXCXXVCDCXHGLCXEGXXGDGSCXCXXXXXXPXXXXVGWXGLRCDXX
XXXXXXXXXXKCDLMSTNLTAXXXXXXXXXXNPNANCXXDSXGAXXCXCAAGYSGNGXXX
XXXCXXXXXXPXXXXDPCAXXSDASISTCXXXXXXXXXXXXXXXXXXXXXXXXGGCFGA
XXXXXSPXAXCXXXVXXXXXXLLXXXXXXKXAPXXXXYDGQRTCTCQDGYXGDGELCXXX
XXXXQEXXXCXXXHGXXXXXXXXXXXXXXXXXPXXXXXXXXXGXXQDKPVXXXXXXGCHI
XAECXXTXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXVSCSCXXGYXGDGI
RTCXLLDXCXXNNGGCSPYAXCKSTGDXLXXXXXXXXXXXXXXXXXXXXGXRTCTCDXXX
TVGDGXTCRXRXGLELXXXXXXXXXFFXXXLXXYKELKGDGPFTXFVPXAXXXSXXSXDE
XXXXXXXXXPXXAXXXXXXXXXIXXXXFDEXXXXXXXXXXXXXXXXXXXXXXGXVXCRRL
RSEDLLEQGYATALSGHPXXXXXXXXXXXXXXXXXXSIYXNXXXAXXVSSDHEAVNGIL
HFIDXVLXPXXXLHXXPXDXPXXILRNTTXXXTAXAXXXGYKIXSXXXXXXXLLXXXRXA
SHXPFTMXWPTDXXXXALPXDRQAWLYXEDHXDKLAAXLXXHXIRXXXXLASDLPNXXXX
RTXXGXESGTXXHGHPISFSXXXXXKCGXGXXXGXXXXXSRXRXGELMVGXXXXXXQRH
LPFEXGXAYGIDXLLXXXXXXXXXSVLXXQXLXXXXXXXXXXSXXXXXXXXXXXXLXXXP
SEPIHVTESSVXXTXXXXFXTXXXXXSAEPTEVRDMEEEFTAXPPXLGARCDXFETRPLR
LNTXXXXXXASGXCSICXXXPLKXXXXXXXXXXXXXXXXXXXTVNQGXPXXLFXTXXXDA
GRYSICDIRVGVDANKQKXXYXLXXXRNLQTVSXXXEXCWXXYPKFWTNIXXXXXXXSXX
XXXXXLXSXLXLXXXXWXXXSLWXRPXLXXXXXXXXXXXXXNARRNDKGRYXXXXXGLGR
GCHRNCVXTXWXPXCCPGHNVTTXXXXYNXNXXLQXXXXTNKASGWTVXXXXDGXXXXXX
XXXLYISLGXXXXXXXXXXYGXVXCXXCPGGXXXPCEXXXXXRDXXXXXXXXXXXEXXXG
XXHSXXGXXXDXXSXXXXXXCXSXXXXXXCXXCXPGXFGPXCQXCXXRCXXHXXCDXXXX
XGLXGXGXXXCXEGWTGXXCEXQXELQPVCKGHSAFLTPPCAPXAXCRAGNSCECSLGYE
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CSEHAXCLSTGLXXXXXXVXXEXXXXXXXDXXXXXXXXXQVIIXXXXXXXXXXXXCXXXX
XXGYXXDXXXVXXXNXXXXXXXXXGXXXIRVIDXXHXXXXXXXXXXXXYVGDXXXXXXR
XXXXXXXXXXXXXXXXXXXXXXXXXDCXXXAMSXXXXLHFXFXXXXXXGVFHLXXFDYDX
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XXXXXXXXXXXXXXXXXXXXWXXXXXXXXHXXCXXXXQLRGFHSLDXXXXXXXXXXXXX
XXXCXXGWLXXGSXAHPVEXXXXXXXXXXLXXXXXXXXXXCGXXQXGRKYKXXXXGXVG
IVXXGXRXXXAKNLSERWDAXXXCXXXXXVXCXXXXXXXXXXYXXXXXDLTDTRCXXGFV
GDXXXXXXGXXLDVLAAXAXFSXXXXXXXXXXXXPSXTXXXXXXXXXXXXXXXXFXXXX
XXGMLLGYANATXXXXXXXXSRKAQXLXXNXNRAXXXXKXXXXXXXXXXXVXXXXXXRG
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DLELHASNXTXLXLXXXXXXXXXXXXXAFGPQALSTPQPPARXXXXKXXXXNXXXXXRXX
XXXXXXXLSVEQGXXXXXDCXEDXXPXPXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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GSHPTEIIXXXGPDNSXPXXXSWAPVXXXXXXXPXXXWXXXXXGLXXXXRAITWXXGHIF
QXXXXXXXXXXXXVXXQAPGTVVVSXXIVWDIXAFNGIIHALASPLLAPPQPQASVVLAP
XAPPVAATTVXXXXXXXXXXXXXXXXXLXAAGXLLGLVAGAXYLRXXXKPXGFGFXXFXX
EXDXXXDFSPXXXSXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGXXXXXXRXXTNP
TLVXVPNPXFGSXDXFXCEPXXXXLLEEDFPDTXXXVXXXXXXXXXXXXXXXXXXXXXXL
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XXXXXXXXXXXXXXXXXDXXXXXXXXXXXXXXXXXXXXXXGGEIFXXXXXXPPAXXXXXXX
XXXXXXXXPXXXXXXXXGXSXXXXLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXDPXXX
XCXXXXXXXXXXLXXAXXXXXXXXXXXXLXXXXXXXXXXXXVXXXXXITXXXXXXXXXXXXX
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XXXXXXPXXXXXXXXXXXXVXXXXXXXXXXXXXXXXXXXXXXXXXXXXGXXXXLNXXXXG
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CVAVNEAGEDSLQYDVRVLVXXXXXXXXXXXXXXXXXXXXXXXXXXXXLXLLLXXXWXXS
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PXXVXXXXNTXXXXXXXXXXXXXXXXSVIXXXXXXXXXXXXXXXXXXXXXXXVXXXXXXX
XXXXXXXXXXXXXXXXXSASVPPNXIXSXXIXXTXXXXXNLKLMFVIAXXXXXXXXXXXXX

XXXXXXXXXXXXXXXXXXXXXXPXXXXXXXXEXXXXXXXXXXXXXXXXXXXXXXXXXTP
PLVVSDGEAGPFVNGXXXXXXXXXXXXLXXXXXEXDATGXXXXXXLXXAXXXXXXXXXX
YQPXSIXXXXXXVVXXXXXXXXXXNHLXXTDPDTXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXSXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXP
XXXXXXXYXXXGXXXXXXXXXXEXXDXAXXXXXXXXXEXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXDLQXAXXXXXLXXXXXXXXXXXXXXXXXX
XXXXLXXXXXXXXXXXXXXXXXXXXXXXXXXXLDXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXEGQMKELDSSIXXXXXXXXXXXXXXXXXXXXXXP
LSDPVPALDLGQQLQIVRAQVXXXXXXXXXXXXRXXLXIDRGFSKDFSENXXPXXXXXXX
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XXDEHIEXXXXXXXXXXXXXXXXXXXXXXXGLXXXXXXXXXXXXXXXPQXXXXXXXXXXEX
XXXXXXXPXXXXGXXXXXXXXXKVSXXXXXXXXXXXXXXXESIPXXXXXTDXXXXXXXXX
XXXXXNRXXXXXXXXXXXXXXXXXXRNQERXQATPRVXXXSGGRYLXXFQNDMQETVAQ
LFKTVSSLSXXXEXXRXXXXXXNXXXXSLASQQKFVXXXEXXXXXXXXXELRNHIVNVRQ
XXXXXCXQEEXXXXXXXXXXTXXXXXXXXXXXXXXXXXXXXXXXXXXXXEREIAXLVEDV
QRLQASLTKLRENSASQISXLEQQLXXXXXXXXXXXXXXXXXXPXXXXXXXXVQTTLXXX
XXXXXMDKFWWXAAWGLLNVDKGQXXXXXXXKXCLXXLSLAQIDLNXDRGFXTXXXXXXX
XGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGQIITCRFAGXXXXVFHVEKNGRYS
ISRXXXXXHTKEXXXXXXXXXXXXXXXXXTEAADLCKAFXXXXXXXXXXXXXXXNSTLPTM
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XCAANXXXXXXXXXXXXXXXXXXXXXXXXFXXXXXXXXXXXXXXXTGVLYILTXSNTS
QYXXDTYCFNASAPAPPXEDCTSVTDXXXXXXTQDAEDNTVSXLXXXXXXXXPSLSVGTE
AXXXXXXNLAVAAAXXXXXXXXXXMILNXXXXXXKSFTLPNAFDGXXPITITIVNXDGTX
XLXXYXXXXTXXXXXXXXXXXXRYXXKGEYRTNPEXXXXXXXXXXXXXXXXXXXXXADIX
PSNPTDDDVSSGSSSERSLSTSGGYIFXTHFSTXHPIXXXXPGTPDEDXPWITDSTDRXP
ATXXXXXXXXGXLXXSNXXXXXXXXXXXXXXXXXXXXXDSXXXXXXXXXXXXXXXXXXXX
XGXXLXXXXXXXXXXXXXXXEXXXSNDESNDDSTQVLQXXXXXXXXXXXXXXXXXGCSXXX
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XXXXXXXXXXXNELXXXXXXXXXXXLGXXXXXXXXXXXXXXXXXXXXXXXXCXXXXXXXX
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XXXCXXGXXXXXXXXXXXXXXXXCGXXXXTXTXXEQWFGNRWHEGYXXXXXEDXXXXXG
TXANXWASAXTSHPXQXXTTPSXXXXXWTDFCXXPIXHXXXXXXXXXXXXXXMXXXXXXX
XDSSHXRKAXXSIIXXXXXXXXXXXXIXSDXXXXXXXXXSXXXXPTAXPNTGLVEDLDXX
XXXXXLLLFSLXLLHAXDXXXXXXXXXXXXXXXXXXXXGXWAIRTGPLSXTTLXXXXQXE
XXXXXSNSQSFSTSHEGLEEVIXTXXXXXXXXXXXXXXXQRXXXXXXGXXVYXDKDHPT
TSTLTXXIXSXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXVXG
GRRDPNHXXXXXXXXXXXXXTXPXEGSTTHLLEGYTSHYPXXXXXXXXXGXXXXXXXTSX
XXXXFXXXXXGXGGXXTXXXXXXXLFFGAXXXLGFXYVXXXXXXXXXXXXXXXXXXIXXX
GASRSETPQNXPXTXXPXVPVTXXXXXXXPSAKTGSFGVTXVTXVGDXXETSNSNVNXSX
SXDQDXFXPXSGGSHTTHGSESXXLXXXXXXXXXGHSHGSQEGXXXXXXXXXXXXXXTXX
XXXXXXGANTTSGPXRXXXXXXXXXXVXXXPDAIEKTIRXXXNTPQIPEWLIILASLXXX
KXXLALXXXXXTXXXXXXXXXXXXXXXXXXXXXXXXLXXXXXXXXGXXXPLXXXXXXXXX
XXXFEXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXRXXXXXXXXXXXNPNEE
XXXXXXXXXXXXXEMXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXLLEXXXXALILAV
CIAXXXXXLASXHSNXXXXXXGYXXXXXXXXXXXXXXXXXXGXXXXXXXXXXXXXXXGXX
XXXXXXXXXXXXXXCXXVXXVNSRRRCGQKKKLVINSGNGAVXDAHSALEXXXXXXXXXX
XWXXXXXXXXXXRKPSGLNGEASKGXRNYGYRHNXXXGXSQEMVHLVNKEXSETPDQFMT
ADXXXGRVFFLKPXXXXXXXXXXXXXSXXXXXXXXXXXXXXXXXLRPVPETRNLQNVXXX

XXXXXXXXXXXXXXXXXXXXXXXXGWLADGSARXXXXXPDMKIGVXXXXVXSXXFXXAXX
XXXGVYCXRAPGAXDPXXXXXXXXXXXGGXXXXXXXXXXXXXXCXXRXXXXXXXXXXXVX
XXXXPKXXPAAWTPLXXXXXXXXXXXXXXXKNTRGGYKCIDXXXXXXXXXXXXXXXXXXX
XXXXXXXXRXXXXXXXXXXXXXXXXXXXXSXXRXXXXXXEIQAXXXXXXXXXXSXSXXX
PXXXXXXDXGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXYQPQXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPP
XSXXXXXXXXKKTDKNPXXXXGPEEXXXPXXRXKSPSKTXXTVRCLEAEVXXXXXXXXXX
XXXXXXXXPXXXXXXXXXGXXXXPGXGXXXXXXPXGXXXXHNGXXGXXXXXXXXQNVXXG
XXXXXXXXXGXXGXXXXPXPXXXXRDGXXGXCXXXCPPNDLXXXXXXXXXXXPGGVVPXX
XXXXXGXXXAXXXXXXXXXXXXXXXXXXXXXXXXPXTXXXXXPXXXRXLXXAXLTXXXXX
XXXXVXXXXNXXVXXLXXXXXRXEXXEXXXXPXXXXXXXXXGXXXXIXXLXXXDXXXVXV
XXAHLLQYNHRVKKLNEIXXXXXXXXXXXXXXXXXXXXXXXXYXXPELXHX

==> Propionibacteriaceae.txt <==
>MSA Consensus of 190 seqs, protein
MQISEAHAADLLNPSSYELLCPGQDDVAQNCVSDIARPRGVRTVDGSYNNLTVSQDRWGS
SQEVFPRLLPAEWRQADAQPTGEGWPPNSAGVTDACETGVTCYEQTDGFVYDAEPRMISN
LIVDQTTGNPAIVNQVENGTAEVIPGTDRVITPNTAPDEGLSAPFNSFLSFFGQFFDHGL
DLVSKGGNGTLVVPLAEDDDLYCLPSGVNKLGDECDPRVNFLVLTRATRHENGTEHINLX
TXXXXXXXTXXXXXXXXXXLXXXXXXXAXXXXXXXXXXXXXXAXPXXXAXXXXXXXXPXX
XXXXXXXXXQAXXXXXXXXXXXXXAAXXXXXXXAXXXXGXXXPXXXGXXXLXXXXGXXXXX
XXXXXXXXXXXXXXXXIXXXXXXYXXXXXXXXXXXXXXXGXXXXXXXXXXXXXXXXXGXXX
XMTITLLXAAAGEXXXXXDXXXXXXXGLXAXXXXXXXXXXXXXXXHGXXLLXXERTTXEFL
XXXXXXXYGXXXXXXAXXXXXAXXXXXXXXXXXXXXXXXXGXDYAKPVTSLPXSXXXERP
FHQALDMIALERLGKPIPQXLFKSITDYXXXXPXRXXAFGYTKRNHDXXXNXPSXXXTDG
LMLAALSHVVSNPHLIGTAXXQXXIGXTAXKAALVKRLDADXQXXXXXXXPXXXXXDXWG
WXXXXGXXVXXRAXXTTRVAPGLYRAGDXXXXXXANHKXQAVXGQAWLAXQQXXXTXXXX
XGXXXDGXXXXXXXXXXXXSFXXXXXXXXXSPAXXXXXATXQAVSXQPVLRGLQSAXXAQ
GAAQDAXXXXXXXXXXXXKQISEQVAKLQXXPXXXXXXXDXIGANPARAVTVDGWVPPRR
LVKMTVLGXXXGXXXXXXXXXXDSYSAGNGTLXDXXXXXGYPADXSYRSPKNYXXXXXXG
SVLTRXXXXXLXXXRLNREXXXXXFGDDTTFQTDVRRXXGAWSGAQXXXITTGDHTIVSQ
ADGMDPHTXVVLMTAGGNDLDFTXVVEXCFXXXXWXXAXALCGGXVXAXRXKIXATMTKX
XXXXTTTLLSHIQXRLADPAHTRVILIGYPYLIXXADXXXXXXXLEAKLXXXGXXATRAA
AANDIRXXXDXXXXDXPXTRVRAAEDEFRTRQAAXXXXDPIVPVDPPALDETGXXAXXAX
XXXXXXTIKXXAXXXGXXGXXXXDXXXXXXXXXXXXXPXLLXXAWNXXHALKVTYXXPTT
SLFNTHEPEPLVXNGTSPGXXQNXXRWINXVXETASXXXXXXXXXXGXXXXXDRYXXXXX
XAXXXFXXXXXXXXXANGXXXXDXKTVAAXXXXENGXXXXDXXXXXXXXXXXXPXLLXXX
XXXXXXXXXEPSQDXNQTXXNXYHPNVXGHEXIAGLVHDALLSRXXRSASGGGXXAXXLS
XXXXXXXXXXXXXXXXESVAQVASXPGVRXAXXXXGXGXXDAQEAXXGXXMXRAAVIGQS
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GDTVGEXXXYAYGVPDTQDNCPTIANQDQTDXXXXWTDHDGIGDACDPTGHTTTXXXXKT
PRPLXKDXXXXXXXXXXCXXXXXXLXQXXXXAXXXXPVVTPXGXXXXXPXXXXAAXXXXX
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XTLXXXXXXXXWXXXXXXXXAGXXXXXXXXXXXXDDIIXXXFGXXNIKGMQGNDYXXASG
DXXXXXXXGXXGXXXXXDXYPEYXXPGXXXXXFAGMGDDIVTSSGGRFTGVIGGEHDDWX
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GAXWXXXXXXXXGVTSDWAFNRFFEPNNXXXXXXXXLXXXXGXARXXXXXXPLXEDXXLA
PSEIELSKMTQEALDLVDGLEEMLRPTIMHDGQPLALGDFTLPMXXXXXXXXXXXXXGLX
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IDIIRDIVYDDSTAVDTAVYENAFAAYTISPIGPLGSGYWTVTHTQVDEGEESDGTDVLR
GFERLQFADGCAELAEDGVTWESCLPTAEVTMDTDSPVEGQPVTALLWEVGGTEPFDTSN
VTNLRYTWWAGEGDTPDAIGEWEAIVNPLTSTSNVFVPTQAEVGQFLMVTASYTDADGLF

RTATSAVSANPVADLSSPGTLAPLAHPDPLVLPQTLLAGVPSDPDGLAEDQILQYQWSWS
ATDPSDEANPPQWVDFDVTVRLDAENSSFALNSTDAGRWIRVAVTYQDGGGETSTVYAHT
SVPLSGSPE

==> Propionibacteriales.txt <==
>MSA Consensus of 259 seqs, protein
MQISEAHAADLLNPSSYELLCPGQDDVAQNCVSDIARPRGVRTVDGSYNNLTVSQDRWGS
SQEVFPRLLPAEWRQADAQPTGEGWPPNSAGVTDACETGVTCYEQTDGFVYDAEPRMISN
LIVDQTTGNPAIVNQVENGTAEVIPGTDRVITPNTAPDEGLSAPFNSFLSFFGQFFDHGL
DLVSKGGNGTLVVPLAEDDDLYCLPSGVNKLGDECDPRVNMXXXXRATRHENGTEHINLT
XXXXXXNXTYVXXPGRRXXXXXXXXXXXLXXAXXXXXXXXVRSTXLXXXXTAAVXXPXAX
XXXXXXXXXXXXXXXXXXLQXXSTXXXXEXXXXXXAXXXXXXXXXPXGXXXXXXXVXXXX
QXXXXXXGNFXPXXXXXXXXXXXXXXXXXSYXXXXGGXXXPANYVXXXXXXXXXXAXXAX
XXXXAXXXXXXXXXXXXXXSGGGGASQFGXXGXXXXXXXXXXXXXGXXXXXXXXXXXX
XXXXXAXXXXXXXXXXSXXXXXXXLXXGXXXXXXXXXXXXXXGTXXXXXXXXXXXXXXX
XXXXXXXXXXXXXGXXXXXTXGXXXXXXXXPARATFFXXXXGXXXXXXXXXXXXXXXXX
GGGXXXXXXXXXXXXVXXXTAXXXXKXXPTXXXXXYNXXXXXXXXXXXXXXXXGGXSFAG
SATTGVNVADGXXXXDXXXXXXYXXXXXXXXXXXXXXXXXXXXXXXXXGXXXXXXXXXX
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XXXXXXXXGXTRXXGDXNAPVTIGSGLXXPXCXXDXSXXNVYIXXXXXXXXXXXLXGRXT
GXXXXXRXXXVXFXXXXXXXXXXXXXWXXXXXXXXXXXXXXGXXGXXXXXXXXXAXXXXX
XIXXLPAGXGXXXXXXXXXXGXXXXXXXXXXTXXXXXXXXXXXXDXXXXXPXXAXXPTXXP
XXXXRXXXXXXXXXXXXXXXXXXXXXXXXAXXXXXXXXXRXXGXPTTXRXXXXXXXXXXXX
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DGAXXXXGXXPXXXXXXXSXDPPGXXKGCXSXXXXXAXQAXXXXXYXXXVXXXXGXVXXX
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TRVAXGXXXAXDAXHXXXXXXXXXXXGXXWXXXXGXXXXXGXXXXXXXXXXXXXXXGXX
XXXXXXXXXPPPASGLTPDAGVAVAEHAXXXXXXXPTGVTLVPSAXXGXXXXXXXXXXAT
XXXXPXXXXXXXXXXXXXXXXXXXXXXRGLXXXXXXXXXXXXXXXXXXXXXXXXXCXXXX
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YXGXXXXXXGXXXXXXXDXSYRSPKNYGSVXXXPSMSPTGTLTRRLNREFGDDTXXXTXX
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LVXNXTSPGGXQNPXRWINXVXETVAAPLVINGQVFAXAGXXXXXXXGXXXXXXTXXXX
XTTMLDAYXXXXXXXXXXXXXXXXXXXXXXXXXNXYHPNVXGHEXIAGLVXXALLSRX
XXXXXLSAXXGXXESVAQVASXPGVRMRAAVIGQSQVRRGNPLSLDAXSSYXXXXXXXXX
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TLAXXXTRIGTXXXDXXGXXCDXXXXXXXYQAHLRITDTXXXXXXXXITGIKXTGTTDTL
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XRIXXXLXXQXXXXXLXXVXXXXXXXXXXMVTAXXXXXXGXXRXXXXXXXXXXVAXXXXX
XYXXXXAHXXXXXXXXXXLXXXXXXSXXXXXDXXXXXXXXWXXXXXXXXXXXXXWXXXXX
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XXXXY

==> Protacanthopterygii.txt <==
>MSA Consensus of 262 seqs, protein
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XINVLLXCXXXXCXXXAXCXXXGXXXXXCXCXXGYXGDGXXCVPIXPCXXXXGGCXXXSX
XCVYXXPGKSXCXCXXGXXXXXXXXCXLKXXCXXXXCXXXAXCXTXXXXXXXCXCXXXX
XGXGXXCYGNXMXRLXXLNXEPGGXXXGXLSXAIXLFXRXXXXXXSXXGPFTXFVPXNKX
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XXXXXXLXVXXXXSXXXXXTXANXXLXXNXXXXGQXLXXGXXXXXXXXXAXXGXXXXXDG
VXXPPSIXPILPXRCDXTEXKXXXGXCVXCXXXXXSXCPXGXXXLXXXXXDCXXXXXXXX
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CXXGYXGXGXXCYGXXXXXLXXXXXXXXFXXXXXXXXXXQLPXXXXXNXTXLVPSXXXXX
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XCPXXXXXXXXXEKCDLINPYSMLXPXXHSVMYXHDFSLYPSXXXXXXXXXMXCXXXCXX
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AIPXLXSXXXIXXXTEXXSXPXXXXXXXXXXHYRAEQPXPXLXSXXXIXXLXXXXXXXXX
XXXXXXXXXXXXDXXXRDDYS

==> Proteobacteria.txt <==
>MSA Consensus of 3187 seqs, protein
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==> Pseudomonadaceae.txt <==
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==> Pseudomonadales.txt <==
>MSA Consensus of 725 seqs, protein
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==> Pseudomonas.txt <==
>MSA Consensus of 713 seqs, protein
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XVXXTIXXAXGGNFENLVXXXTXPAVTXVTDTIDTXTVXLTTATXXVXEGGXXXYTAXXX
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FEXLXXXXXXAXTTXVDLQLTAAQXDTXDTXTVXLTATXXVAEGGXVXYTAXVXDKNGAP
VTXXGESLPDTPLSVFGSLSPVXVTLXNGQXITIXVGXXXGXVXXDXAPNDALXGXXXLX
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EXLVXSXTXXAVTXVTDTIDTXTVXLTATTXXVAEGGXVXYTAXVXDKNGAPVTNIGSPV
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XTXXVTPQAYLVTEGTGVXGXXXXXXXXAXXXXXXXAXXXXXXVXXGXXYXXXXXXXXLQ
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LSISNTXXXXXXXXXXXXXLSNLKLNNLRVSDXXXXXXXXXXXXLXGXNSGXXXXVXSAS

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==> Pteriomorphia.txt <==
>MSA Consensus of 208 seqs, protein
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DXXXRXXXXXXXXXXXXXGXXXXXXXXXXRXXXXXXXXXXXXXXXXYXXXXXXXXXXXXX
XRXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXLX
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ISHCPSLXTXXXXVPXXXXXXIHCXXXXXXXTXXPXXXXXXXXXPXYXXXLXHCPSYLXX
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==> Pterygota.txt <==
>MSA Consensus of 398 seqs, protein
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SARDGGSPPRFGYLQVNVTILDVNDNPPIFDHSDYNVSLNETALPGTPVVTVMXTWPXXX
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XXXQXXXXHXXXXXXXMXXXXXXXIVXXXXXXXIXXXXKVATVDENAVNGTXXXXXXXXX
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WXWXILSXXXXXXXXXXXXXYMINXXXXXXXXXXDVDXRXXXXSXXXXXTXIXKXXXTXX
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XGDSDLXXXXXXXXXXXXXXXXXXXXXXXYXXXXXXXXXYXXXXXXEAXPXXXXXXXXXX
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XNDXDPXXXXXXXXRXXXXXPXXXXXXXXXXXXXTXXXXXXXXXXXXXXXXXXXXXXXXX
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AKXXXXXXXXXXXXPXXYXXXSXXXXXNXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXPXXXXXXXXXXXXXXXXYXXXXXXXXXXXXXSXXXEKETXX
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VSTLRMPSSNGPAAPEEYV

==> Rathayibacter.txt <==
>MSA Consensus of 184 seqs, protein
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ADXGVXXXXXXQYXAXXHTGTKSFRAGXIXSDAXFFDXDAXXXXXXXXXXXXXXXXXSGT
XXXXPCLKXXXXXXXXXXXXXAXXXXYXGXXXESXTHINASVTRGXXVXAXLXXXXXXACG
INPLAXXXXPXXXAXXXXXXXXXPXXXXXXXXXXXXXXXXXXXXXAXXXTXXXXXXXXXX
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SXXXXXXXXXXXXXXXXXXXXXXXXXXXNXXXXXXGXXXXXXXXXDXXXSIDXXXXGXXX
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YFXXXXYXXRXXXXXXXXNPEIGRSTAPPSLVRAPRLSGEAIAGXXXXXXDXXXXXXXXN
VQXXXXVXXXXXXXXPXXTXXXXXTXTPTXTPTXTXTATPTXTPTXTXXPTXTPTPXXTP
XPXAXPXVXVXXXXXATPVXXXXXGXXXXXTXXXXXXXXXXRXAGXDRXXTXVXXXXXXF
DXXDXXXPVXYXAXGANXPDALSAGPAAAXQGGXLLLXDXXXXXXXVXXEXXRLXPXRXV
VVGSXLSVSXXVXXXXXXXXXXXXXXXRIXGXDRYDTSRXIVXXAFXXGXREXXYXXXXX

ATGXXFPDALSXXXXAGXXXXPVLLVXGXXXXXDXXTXXXXXXLXXXXXXXXGXXXSXSX
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LXXXXXAXXXGXPXXXXXXXCXPXXXXXXXXXXXXXXXXXLLGXXXTLSXXVXXLXXCXYD
FXXXXXXXVSXXXXPXPXATTTPTAAXXPXXXPXXXPXPXXXXPTADXXAPXXXXXXXEX
GAXLHXYXXXXDXPLSQAGKTQAXXTXXPXGXGXXXXXPVLSPXXXLRXAXQDAGRLTVG
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GPTPGYPYSRDYSSSGDTFLRDTWQLHVGTYDGTRAVSYLDGTAVAYPRFVDNQGNTYAK
NPYLFPDGLNPTAGDFTVGAVELSSGPGNYAKGAFAKIRVWDSALTAEQVRALYTAESSA
LR

==> Rodentia.txt <==
>MSA Consensus of 683 seqs, protein
MRGPHWRVPXXXXXXXXXXXLVALXXXXLAXXSTXTPXSLSSSTRTSQMSSQASTSSTSS
XXRTSKTEQTSXXXXPXXXXTXXXXXXVTXSMXXXXXQTTTTTEVXXSTPXASSRXXIQX
ETSXXRPKRXXXXXXXXXXXHXPXIXXXXXXTXXXXXTXXXXXXXXVXXGXXXXXXXXGXX
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XDXXXXNXXLXXXXNSTTHTTKVSTTSTPQKLSPVSXXXXSXXKXXXLXXXXXXXXXXTX
XXPXXXXXXEVTXSXXXXSXXXXIXXXTNXXKXIXXGXXTTSHAPNMRSSPPKXXXXLXX
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KXTXSXXXXGXXTXXXXNTSXXXXPXXXXRXXXXXXXXGSXXXXPXXXXNXXXXXXXHX
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XXXTXXPGXXXXXXXXXXXXXXXXXTXXRXXRDXXXXXSXRIRTLXXXSXXXRSVKIGDA
GEXXXXXXXXGXXXAXSVFLTVQEKPKXXXXXXXXXXXXGSEISIMCSATGYPKPKIVWT
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XXXXXXXXHXXXXTXXXXXXXXDXXXXXXAVXXQXXTXXXXXVLPXXQXXXXVSAPITST
QILXXXXXXXXXXXXXXXXXPXXXXXXXXXXXXXXXXXXXXXXXXXSXXXXSPGXXXXX
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DSGMYLCVATNIAGNVTQSXXILXXXPXXXXXGXXGXXXXXXXRVDILCNAHGXXXPVXT
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XLXTTSSXQXXXGXXXXXXXXXPPXXXXXXXXXXXXXXXXPXXXXXXNQRIXXXXXXXXXX
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XWXXXXXXXXXXXXXXXXXXGXXXXXXXPXXXXXXXXXXXXXSXTXXXXXGTXXXXXHXX
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==> Ruminantia.txt <==
>MSA Consensus of 165 seqs, protein
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QEXFSGXACXXCXXXNXFGPXCXXVCXCVHGVCXXGXXGDGSCXCXXGYTGXXCDXXXLX
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VGDGXXCYGXXXXXXXXXXTEPXXXXXXRLXXXXXXLDXGXXXXLSXXGPFTXXXSNXXX
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==> Salmonidae.txt <==
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==> Salmoniformes.txt <==
>MSA Consensus of 247 seqs, protein
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==> Salmoninae.txt <==
>MSA Consensus of 247 seqs, protein
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XPXLPXRCDXTENKXXXGXCVXCSXXXXSXCPXGXXEXXXXXXXCXXXXXXXXXXLXXGC
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PXXXXXXXXXTXXCSSXTVGQYVLXXXXXXXYXXXXXXXXXXXXXXXXVXXXXXXFXGGX
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==> Sar.txt <==
>MSA Consensus of 1259 seqs, protein
MKXTLFCSISFCNIIFFFLELSHEHFVGQSSNTHGASSVTDFNFSEEKNLKSFEGKNNNN
DNYASINRLYRKKPYMKRSLINLENDLFRLEPISYIQRYYKKNINRSDIFHNKKERGSKV
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LFTTSFYKDLDKSSITKINEDIEKFNEEIIKNEEQCLVGGKTDFDNLLXVXXNAEKANVR
KTLFDNTFNDYKNKKSSFYNCLKNKKNDYDKKINNIKNEITKLLKNIEGTGKMCKTESYV
MNNNLYLLRVNEVKSTPIDLYLNRAKELLESSSKLVXPXXXXXGXXKNMYSIGYIXXXIK
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XLXXXXXXNEXXLXXXFNXXXXIFXKXXXTXVDMKTIESKYTTVXXXXXXLXEYXXXVXK
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EXLXXXLAXXHXXDGXPGNTRVVDACPSSCNKCRECSPGCALWFIGNGVCDPECDNXSCX
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XSSXXTXXXXXXXXXXXXXXXXQINXXNDVVLXXCXXEELYXPYEDXKXXXXXEQXXNXX
NQXXXXIXLXXSXXXLXVHXXXXXXXXXXGXXXCNXXXDEXXHXLXXXXXXXXXXXXXX
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SXLXXXXXSLPXXGDXXXXXXXXPCXGXXXCFCQXXYDLTLIXDESXSIXXXXWXXXVXP
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GNDXCSKENEXXXAXNXXXXXXXXXXDDEXXXXXEXXPXXXCSANCDGXSXXXXXXXXXM
GXXYXXXXXKLLVLGVXXAXXXXLXXIAGCXXKXXXCPXAMKASEWXTISKKSTGPQDRR
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CPXXXXXXXXXXXXQXTAAAXXXXXXXXXEPLXVPXPLPTXPEDXXPRXXXDXFXVEXPX
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EIPLETPEESETXXXXXXXXXXXXXXXXXXXXXXNADXXXXXXXXXXSXXXXXXXXXXX
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SXSKGNYEAAPDDGL

==> Sarcocystidae.txt <==
>MSA Consensus of 164 seqs, protein
MVPLSXXMAMVXVAYFILGALVYGXANVXGXXMQPRQLAXXSXXXXXXXDEXXGXAXXXH
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NSGTFAAVXSXXXXXXKXXLFLLFSSSPLLLLLXXXXVXTSXXHAPXXXXXLGXPVKXXX
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GQAXLVEPSNIVLIYEGEEDESDPVVVLVDSGTGYIHLFDHDLQEVGKSNGQEALAQPLV
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GEVKXASSLSECRAXCXAXKXCXXXTYNVKSGXXLCYPKRGKPQFYKYLGDMTGSRXCDT
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XXXXXXTEPXXCXXHXXXXXXXXXXWSXXXXXCXXGXXXXSXXXXXNXXXXGXKXCXXXS
XXXXKSSXXDXXCNXXCGTSSTSFPGAQTQSQCFCEXGXXXXXXACXXCPIGAXCGXXXL
EEAEAKLXXXXXXXGRSIXXXXXDSFSGRXXPXXEXXXFXXKLKEELESPNDWQXXXCXX
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XXXXXFNIVMTYMNVAARLGFNRRSIHSIVIKIASNYLTGISVSLSVIDFSTIAFPXXXT
DLTATVXXTVXXXHXXRXXXXDCLLXDXXXLSXSESFFYTMVFYALXPXALPIVATIXXX
XIXYXXAGXXAWYXNSTQRKLELLKQTMQYGLYXLAQQLKEKYEEDRVFMIFQGRENSQE
RYIAXPGEXXFRRAXVXXXXXEXXXPXXVDQXXXFXXXXXXTRNMLSLLDCTYIDFGRAH
XAKYFLRAAMSVECTDILSGPYFKFFAVGITGLXVWSIGIPLSCFLVLYVNRKTLNSRET
RLKYGFLHNGFVKKYWYWEMVVFARKFLVIVVSSVALIPSADKNGSRVWLAVVIAVIFLI
IHLVTQPFDKRSYLTLDKLENHSMTIWTITLIVLAMMIGSDFSGSVNMALLLFXAVLSCM
FILEVGVSLMFAYFDNVRTQQTFFRVPVIGYVFRFFAXLSEKRRAREPIVVFDTENEVIQ
LVAAKRQTWTLFRALRKNINLAERNYFIKVMSESLGFAVVHMKLDVIPGSFLEFALRLGL
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DMEEKFAAKDETPTAEEKTEEQDERLHDLEGELVSDTELEQMKKTMTEAEEXEXDEXRGD
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AFRLRKQIQADEFSEALQKRNRKLKVMREALESLVLSXGTSLAELGMTEEAFQSKXAELX
XLNAEIEKLKTRLQELKDNPDSYXEXXXVEREEDWVDEDRAAEIEKIQEENXRRKLEKEE
REEXDREICMXGEDMENAGWFGXDDTAXIXDXSDAPXPEGTFRLIGQDAETWDEXGYSXS
KGNYEAAPDDGL

==> Saurischia.txt <==
>MSA Consensus of 877 seqs, protein
MLCWNEVQSCFLLAFLAVAAYSVSDAQGQVSPPTRLRYNVVNPDSVQISWKAPKGQFSGY
KLLVTPSSGGKTNQLILQNTATKAIIQGLIPDQNYALQIIAFSDDKESKPAQGQFRIKDI
ERRKETSKSKVKDPEKTNASKPTPEGNLFTCKTPAIADIVILVDGSWSIGRFNXXLXXLF
XXXXXSAFNVGSEKTRVXLXXXXGXPRIEWHLNAYGTKDAVLDAVRNLPYKGGXXXXXLX
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XXVTSDITARGXXXXWXXXXXXXXRXXXXXXXXXXXXXXXXXXXXXGXXXXXXXXGXXXX
XXXRXXXXXTEYQXAVXXXXXXXXXXGXEGCGSQXXEXXXXXXXXXXXXXXXXXXXXXXX
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CXXSXXXXXXXKXCXXKXXXXXXTXCXXCXXXXXXXCPXGXXKXTXXXXGXGXXDCRYXX
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XXGXKXXXXVXXGPXXXXSSVXRRXCITXXXXRTXLTGHSWXXXXXXXEXCXXGIXXXGT
CXCXXXXXGXACXXCXXXNXFGNSRPXCXSXXXXXTXXXXXXXKXTSSDIAXXRXXXXXX
SVCXCVHGXCNSVGXXGXGXCTCXXGYXGXXCDQXXXXCXXXXCXANSXCXXXXXDGXXX
XCXCXXXYXXXGXXCXATTPKPTIAVFRTGXRNLXXXPECXXXLRXCXPXAXCXXLGPXX
XYXTXXXXXXXXCTCXEGXXGDAVGXXCXPIXPCXXXXGQDALPQMRMAEXCPXXVXSTI
CXYXXPGXVXXXXXXXXXXXXXXXXLRVSDEWYNRLXXXXXXXPXXXMGYRIVYKSXXXP
XXXXXXXVGXDXXXXLLXXXXXXXXXXXXXXXCXCKXXXXXXXPXXXCSXXXXXETXRQX
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VGTKGSNXRGRXXXKLXXAXXXXXXXXXXXLXXPXGPFTVXVPXTXKGLKEVCKGTNIKX
XXXVXXXXXXXXXXXXXXXSXXXSTVGAXXXXXXXXXXVFVPSLPIXDXMEFNXXAXXXX
XDLLNNXXXAXXXXXXHXXXGXXXXXXXXXXXXXXTLXGXXXXXSXXXXXXXRXXXXXG
RXXXXXLQXNXXAXNGIXHIXXXXXXXXXXXXXXXXXXTIXXXLXXXXXXSXFXXXXEXX
GLXXXLXQXXXPSERXTVFVPSNXXXXXXXXXXLXYLXXAXXXXXPLVXEGGDKLAXXKL
XEMFGLVEKEFSAIDGVSMEPGXXHIXXXXXXXVXXLXXXXHIYLHPEGLPSDYTITFLF
RILPDTPQEPFALWEILNEQYEPLVGVILXXMAXQXXXXNXXXKGDFQTVTFEGPEIRKI
FYGSFHKLHVVISKTXGXXLXXESEAGXKXXXXXDIVAXNGXIXLGTLXGXXIPPXXXXX
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XCNXTXXXPXCCKGFFGPDCXPCPGGFXSXPCXGXGXCXDGXXGNGXCXCXEXFXGXXCX
XCSXPXKXGXXCDXXXXCXCXXGXCDNRGPXXSXGXRGFPGTPCXXXVSCXXGYTGKXCD
KGEAGAPGAKGESGSPGENGXXXXCXPSGLXQXCHXXAXCXLXDGXXXCXCXXGYEGDGX
SCXXXDXCXXXXXGGCXXNMPLHAPQAXCXXTGPGXXXCXCXXGWTGDGXXEGAQGPRGE
SGTPGSPGPCXAIXNXCXXGLXGAXGXXXXCHXNAXCXYXGPGQSKCVXXXXXCPDSPRR
DYLGQKSIKVNCLNDCKCKXGXXGXGXXXGXXXXXXXXXXGXCXPAGXXGXINXCLEXX
XNGXCHXLATCXXXXXXXXXXCXCPXGYXGDGXXCYGXGXXXELXXXSXXAAFNQWVNTX
LRMNYAXFXXWVXEAXXXGXXXXXXXXXACLICSFLFFGQQKXXXSXXXXTXXXTVLVPS
XXAIXNXXXXEKXFWXXXXXXPXLXXXHXLXGXXXXXXXXXXXXXXXLPTXXXXPGXPXX
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XNXXPXXXXXXXTXXGXXPEFTPVREEMEAVXXGXPGXXXXXXXXXXXXXVLXIQKNRCXX
NXTXIXGAPGKXXXXXXXXXXXXCXXAGCXXXXXXXCPPGXXXXEGARGXXGXKXEPGAP
GPAGFAGPPGADGXXXCXLXXXNXXXKGYTXXXGCXGXXCAKXXXXXXXXXXXXXXXXXX
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TACEXCXXGXYGXXCXXGXXXPXXXQXLXXXXXXXXLPXXXGQXXXXXXXXXXXXXRSXX
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PDXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPRSXXXXXXXRXXXXXXXLXXXXXXG
HVIDLVXXXXXXXXXXXXDKKXXXXXXXXXXXXXXXXXWXGXTCXXXIKEXDXCNXXCH
XXANCLXXSXDXXXXCXCXAGXXGNGTXCTAXXXLWFNXXXXXXXXIDXCXXXXGXKGCS
DRXXAXCXXXXPGXRXCVCXXGYXGDKGKDGXXCXEIXXCLEXNGGCXXNAECXXTGPXX
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WDVWGKWTPEGXXXXXXXXXXXXXXXXXXPXXXXWXXXGXXXXXLRYHMVGCXXLLXXD
KTPLKLXXXXXXTSLXGXXIXIXXXXXKDLQIQVAKVVVSDIIGMNGVIHFINKILIPSG
LVGRNISSEVSRVSLKHYCPVVRLHNASLNLFPMTPNPPSKETIPNNHISQFEEWRSRGL
LRDLLRYHMVGCQKLLSSDLEAQESLTQPVRMQKLTKLRENSXXLNXXAXXXXKLPELSE
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PXHXPXTXXWPTDAAXXXLPXXXQXXLXXXXXXDXLXXYLKXHXXRDXXXXAXXXPXXXS
XXTXXGSXXSEXSCXXNXXXGXLXXXXXXXXIXQRXXEFXGGIAYGIDXLLXXPXLGXRC
DXFXXVXXXGSXESCXXXGLCGFEPPCPAGSVQRGETXXCYYYXXXXILLLFSSPFSKAI
FCFKCGKPTNFSAQICCLXXXXXXXPXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
PXXXXXXXNSXXXPXXXXXXXXXXXXXXXXSXXXXXXTALLXXXXXXXXXXXXXXXXXX
LXLLLXAXXXXGXXXXGCXRXCXXXXXXINESTEILHLSXXCCXXXXGXDCXAXXXAPVP
PGPVPYGKFSCHGMSPALSGQTXXXXXXACPGGXEXPCXNXGXCDDXXXGXGXCXCXXPT
FTPAHNAXFXGTSCELCXPGRHKCCYGXXCRXXXLXXXXPWAXXXXFVQRWLWHMXLLGE
EVGAGQXXXXXSXXXXXXXXXXXXXXXXXXXXXXCXCXXNGXCXXGXXGXGXCFCXXGWT
GSXXCXXXSSPTDXXXXXXXXXXFLXXIXXXXXLXXXPXCXPXXXXXAXXXXXXXXCXX
XYXGDGXTCXXXIXXXXXDXCXXXXXXXXXRXKWXKXXXXNGXRXGXEXXXXXAXXXXXX
VXVXXXCXXGYXGXXXXXXPXXXCAXDXXNXXXXXXAEDEETPXEXXXEXEESENEDEXX
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PIWPPSTPIWPPVPIWPPSIWPPVPIWPPTAPIWPPPTWXXXXXXWXXXXXXXXXXLXXX
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XVKHXXXXXXXXXHXXXXXXXXXXCXXXHXAXXXXXXXXXXCLCLPXXXXXXXXXQHEXX
QXXXXXXXXXXXXXXXXXXXHXXXCXXXXXXXXXXCYXXFXXRXXXXDAEXXCXXXXXXXX
XLXXIXXXXXXXEEXXXXNXXXXXXXXXGLXXXXXXXXXXXXXCXXXFXXXXXXXXXXXX
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LERGRXGXXNLEGXXGXXXXXVXNXAXXXGXXXXXXQSAATTLXXXKXXXKNXXXSXXXX
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XXGXXXXXXXXXXXXXXHXXVVTHGTGXXXXVXEXXXSXDXXXXXXXXXXGXXXLIEXXX
XEEXXXXXXXXXXMSXXPXXXXXGXXXXXXXXXXXXPXKPXXXXSFXXXXXXPXSVXXXX
TWXXXXXXXXSTSXLXXXXXXXXDXXXXSXXXXXRRVSFANPIXXXGXAXDXXXXXXXXX
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XXXLXXLXXXKNIKXVXXLSPXLXXXEXXTXPIRAPKVSNVKXXLXXXXXXXXTXPXXXX
RXXTSXXXXXXEDVEKTANSAEDKSSSVXEEXLXXXXXXXXXXSSSSSXXXXXXPXXXXL
SXXXXXGDPLFXXQXXXXDLXXXPXXXXXXXXXXLSSMAECIXXXXXSXSSPQXXXPXXX
GXQLTLT

==> Spermatophyta.txt <==
>MSA Consensus of 116 seqs, protein
MEPKQETXXNNDDGVSEDLTLNQDEDEFDSKERVLHKYFLQEXXXXXXXXXXXXSXXRVS
XPXXVXXXRXXIDXYQEQGQLIEPYLESMISPLMNXXXXXXIXLXXXSDXXXXXXXPXXX
XXXXXIXXXXXXXXXXXXXXXXGPVXXXXXDTXXXXXVXXXXTCKASXXXXGYXCXXXX
XXXSXXXXXXXEMEAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXLXXPXPXXXXX
XNXXXXXPXXXPXIXXLVXXXXXXXXXXXXYPKXXXXXXXXXXXXLAXXXPKETDPXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXCXXXXXXPXSFVXXXXXXXSSXTEDILHHFQLL
GXXXXMAAXXXXGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXVXXXXXXPXXXXXXXXL
XXXXXXTXXXXRXXXXXXXXXXTKXXVXLXXXIXXXXXXXXXXGXXXXSNEVIDGAEDED
MEVPENVAEIILMLLSVLRDMDTIVRWSAAKGXXXXXXXXTXXXXXXXXXXXXXGXXXXX
XXXXXWEXKXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXQGXXIXXXC
XXXAXXPAPAKXXXXXXXXXXXCXXXXXXXXPXXXXXXXXXXXXXXXXXXXFGNDSPXXX
XXXXXXXXRSNLEQLAPHXXXXXCXXXEVXCXXXXXAAFMAQENVGRQGNYXXXXXXXXX
XXXXFXXXXXXXXXXXXXVFXXQXXGXXXXXXXXXXCXXXXXXXXXXXXXXXXXXIXXWX
XXXXXASXXXXXXXFLXXXXXXSXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXDXXXXXXXXXXXXXXXXXXXXXGKGXXXXXXXXX
XXXXXXXXXXXXXXLXXXXPXXXXXXXXXXXXTLNEXXXHPNXXXXXXXXXXXXXXXXXX
KXXIXPXXXXXXXXXXTSXXXXXXXXXXXXXXXXXXXXXXXXXAIGVLPYELLASQWRN
VILXXXXXXXXXXNPEERDAEARVNXXRXXXXXCEXXXXXRXXXXXXLIENDXXXXVLIX
XXGXDXXXXXXSRLFKALDSVXXXXXXXGXDPSXXXXXXXXPXXGRKESRSXXXXXXXXX
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XPXXXXSYPXXVXXXXXXYXXSXPXPPXXXXXXXXXXXGXXXXRTXXXXXXXGXXXXXX
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SXXXXXXXXXXSXXXXXXXXXXIDPKGXXXXXXXXXXXXXXXXXXPXYXXXXXXXXXXXX
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XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXRXXXXXXXXXXLXXXXXXSXXXXXXXXGX
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XXPXXXXXPXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPXXXXXSXNPXPXXX
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PPPXXYXXPPPPXPXPXXXXXYXXPPXPXPXPPPPYYYKSPPPPSPXPXPXYYYKSPPPP
XPXPPPPYXXXXXXPPXXSPPPXXXXXSPPPPXPXPXPPYXYKSPPPXSPXPXPPYXYXX
XPXXXPXPPPXYXYKSPPPPXPSPPPPYXYKSPPPPXPXPPPPYYYXSPPPPVKSPPPPY
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TXAYSPXNSXXXXXXXDSTYXKVPXTXVKSXDFKXPSXXEXXXYKXSXPPXPXLXKNXYY

KKPXXXXXXPXPXXYKKVPPPPSPXPXPXXVYXSPXPPSPXPXXXXXYKXPXXXXXDDYK
KPXXXXXXYXKXXSXPKEXEYXXXXXPKXXYXKKPXXXXXXPXYXKXSXVPXXXXYXXPX
XDTPXXXXXXXYXXXXPXXPXXXXXPXYYXXSPPPPSXXXXXXXXXYXKXPXXXXXXXXX
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XPXXXPXPXXXXXXPPPPXKSPXXPYXXXXXPXPXXXXXKXXXYXXXPXXXXXPKXDYXX
KKPXXPVKSPXXDXYKKXXXVXXXXXXXXXXYXXXSTXSXXXXXXXXYXXXKXXXXXXXV
XGXXXCXXXXXXXXPXXSHXKKXXXGAXXXIXCXXXDXXXXXXLXYARKGGVXXXSXXXX
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SPPSVPXXXXXXXXXXXXXXNXYXXXXXXXXXXAPXXXYXXXXXXXXXXXKPKSXXXXXYYK
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PPSPSPPPPYYYKSPPXPXXXXXKKPYVPXYXYKXXPPPSPXXXXXXYYKXPXPPSQVYE
APSPPPPYYYKXPXVSEYNYXXXPSXPXXXYYKSPXPPXXXYEAPSXXXXXYYKXPXXPX
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PPVSEYNYPPSPSXPPPYYYKSPPPPSQVYEAPSPPPPYYYKSPPPPSYNYKKVPSPPPP
YYYXSPPPPXXVYEAPSLPKNDYYKSPYPPPYYYXXXXEAPXLLKNXXXXPPCXXXXXXX
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QEYXXXSLXKKPSIPXXXXXXKXXSXXAXXXXXXLXQNNTKXSXXISNFSPQELIEENEN
VSNWSFMQILNNSSSYQNNQSDTTEEIDVQPSTKQCSSSIMNTRSLDMCTEILGSETGSN
YISESNMDXFXXXXXXGXXXXKXXXFKKRIKKTVTFPPPLTSISGMDRVQIKSYREGGRL
VLRAARISTCSPYFQAERANGTLRLSWVKYGNNNEMEVEQDVEVQNGEKAEAEVEAKVIE
HENGDDYWPKNGRRRLARKCKESGNRSKGIQNWGQLWVVIS

==> Spiralia.txt <==
>MSA Consensus of 353 seqs, protein
MISXXXXXLXXXXXMXXXXXXXXFALFVLXALXXXXXXXXXYGXGXIXXPIXPRNXXXXM
XXXXYXXXXWYLNGILPRXSXXXXXSXXXXXXXXXXXXXXXXXXXXGXXXXXXXXXXXXF
AVXSXXXXXQXGXXXLXXXXPXXPLPXXXXXXXXXXXXQLYWXXXKGLFPPXXXXXVKPX
XXPVYKPVKTSXSXPXXXKPPTYXXXLXXXXQPEWKPXXXYHPTXXXXWMKXPXXNSYPP
TYGSKTEWKPKPNYLPXXXXLAKKLSSXXPXXTTXWKXXPXXXXLXXXXXXXXPEXXXKX
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XXXXXPXXXXXXXSXPXYXPXXXXYPLPVIXXXPXXYXXXXFPFSEXXYXXXXXXPXPYV
PIXXXXXYXXXXXXXYXXXXXXXXXXXXXXXXXXTYPPTYXXXXXXXXXXXXXXXXXXY
XXXXXXPXXXXXKXXYXXXKFYXXXXXXYXXXXXXPQSKSXXXXXXXXPXXYXXXXXXNX
XXSXPXXYXXXXXXXXXXXXXXXXYXXXYKXXXXXXXXYXXXPXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXKXXXXXXXFEXXXXXXXXXXXXXXYXXXXXXXXXXXXXXPXXX
XXXXXXXXPXXXXXXXGXXXPXQXXXXXXXXXXXXXXXXXXXTXXXXXXXXXXYXXXXXX
XXXXXSXXXXXXXXXXXXXXXXXXXRPYXXXRPPXXXYXXXXHEXXXXXXXXXXYPXXXX
XXXXXXXXXXXXXPXXXXXXXXXXPXXXXXXXSXXXXXXXXXXXXXXXXXXXXXXXXXX
ISTXXXXXXXXXXXPXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXYXXS
XXXSXXXXXXXXSXXXYXXXXXXXXXXXXXXXXXXXPXXXQQEDEGEAXXXXXSXXXXXXX
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SXXXXXXKXSYXXXYXXXXXXXXGXXXXASYGYSNQADHTYSNQXXXXYXXXXAXXYXXX
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XPXXYXXXXXPXXSXXXXXXPXXXXXXXXXXXXXXTXPXXXXXXXXXXXXXXXXXXXXX
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XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPXXXXXXPXXXXXXXXXXXX
XXXXPXXXXXXSXXXXPXXXXXXXXXPXXXNPYTSYLAXXXXXXXXXXXXXXXXXXXXXX
XXXPXXXXXXXXXXXXXHILIHPXXXSLXXXXXPXXXXXXXHSPTXXXSXXXXXPXXXXL
PXXXXXXXXXXXXXXXXXXXXDNANYQNTQLVDSSXXXXXXXXXXXXXXXXXXXXXPXXX
XXXXPXXXXXXXXXPXXXXXXXTXXXXPFLXXXXXXXXXXXXXTXXXXPXXXXXXXXXXP
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXLXPTXXXXXXXXXXXXXX
LXXXXXXXXXXLXXPXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXSXXXXXXXXPXXX
XXXXXXXSXXXXXXXXXXXXXXXXXPPSXXVIXXXXXXXXYXXXXXXXXXXXXXXXXXXX
YXXXXXXXXXXXXXXXXXXSXPXXXTANXXPHXXIXXXXSIPVIXXXXXXXXFXXXXXPX
XXXXXXXXXSXXXXXXXXPSXPXXXXXXXXXXXYXXXXXXXXXXXXXXXXXXXYVCGXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXIXXXXXXLXYXXXXXXXXXCXXVYXTXYVCGXVX
XXXYXCXXXXXXXYXXXIXXXXXYXXXXXXXXXYXXXXXXXXXYXXXXXYXTXYVCGXXX
XXXYXXXXXXXXXYXXXXXXXXXYXXXIXXXXXYXXXIXXXXXYXXXIXXXXXYLXXXXX
XXXYXXXXXYXXXYXXXXXXXXXYXXXIXYXXXYXXXXXYXPTYXXXXXYXXXYXXXIXX
XSXYXXXXXXXXXYXXXXXXXXXYXXXXXXXXXYVCEXVXXIPXXXXXVXXIPXVXYRXX
XXXXXYXXXXXXXXXYXXXIXXXXXYXXXIXXXXXYXXXXXXXXXYXXXXXXXXXYXXXX
XXXXXXXXXXXYXTXYVCGXVXYTPXXXGXXXXXXXXXXXXXXXXXXXXYXTPXVCGX
VXXXXYXCXXXYXTPXXXXXVXXXXYXCXXXXXXXYXXXIXXXXXYXXXXXXXXXYXXXI
XXXXXYXXXXXXXXXYXXXXVYCTPYVCGIVYXTXYVCGXXXXXYXXXXXXXXXYLXXX
XXCXXYLXXIXXXXXYXXXXXXXXXYLXXXXXXXXYXXXXXXXXXYLXXIXXCXXYLXXX
XXXXXYXXXXXXXXXYXXXXXXXXXYXXXIXXXXXYXXXIXXXXXYXXXIXXXXXYXXXI
XXXXXYXXXXXXXTPXXCXXXXXTXIXXXXXXXXXXXXXXXXTXXXXGXXSYXPXXXXX
XXXIPXXXXXXXXXPXXXXXXXXXPXXXXXXXXXPXXXXXXXXTXXXXXXXXXTXXXXX
XXXXXXXXXXXXXTXXXXXXXXXTXXXXXXXXXTXXXXXXXXXTXXPXXXXXXXXXPXXX
XXXXXXPXYVXXXXXXPXYVXXVRVISXYXVXXXXXXXXXXXXTXXXXYXXXXXXXXXYX
XXXXXXXCXXXXXXXXXCXXVXXTXXXCYXVXXTXXXCXXVXXTVXPXYXXXXXXCXXXX
CXIXXXTXXXCYXXXXTXXXCXXXXXXXXXXXXXXXXXXPXXXXXXXXXPXXXXXXXXTP
XXXXXXXXTXXXXXXVXXXXXXCYXVXXTXXXCYXXXXTXXXCXXVXXXXXXXXXVXXTX
XXCYXVXXTXXXCYXVXXXXXXCYXXXXTXXXCXXXXXTXXXXYXVXXXXXXXXIXXCXX
YXXXIVXXTXXXXXXXXXXXXXXXGXIXXXXXXXSXXXHPPSXXXWIXXXXXYXXXXXXX
XXXXXXXXXXXXXXCXFXXDKKKEICRDKVDSHKCERWKSKGACANFPRRMGVLCKQSCG
MCDLEKIPCPKGXXXXXXXXXCXXVXXXXXTWRRANKHCRYHGGRLASVFDRDENDQIRE
KILSAGVNXXXXXGLTDXXXXKXWTXXXXXPXXWTAWKAXXXXXXXXXXXPSXXXXXXXX
XXXWXXXXXXXXXXXXXCXXXXXXXXYCTITHPPXXXCXXXXXXXXXCXXXXXXXXGCXC
XXXXXXTXXXXTXXPXPWXAWXXPXXXXXXYCXXXXXXXXXXXXXXXXXXCXXXXXXXX
XXXXXXXXXXYXXHVXXXXXXSSKKSKKTXXXXXXXXEXXYNGRIVHLGQRRKILVDSQR
XXPXXXXLGGDGIVVLXXXXXXXYXXXXXXXXAWTGRXXXVVTVNRNAWXXTXXXXXXXX
XXXPXXXXXXXXXXXXXXYXXXXXPXXXXXXXXXXXXTXXPXXXYCXXXXXXTXXXXTXXX
XXXXXXXXXXXXXXXXXXXXKXXXXXXTXXXXXXXXXXXXXXXXXXTXWXXXPKPDVXTXX
XATXXPXTAXXXAPXXAXXXXXATXXPXTXXXXTXXPXTAXXXTPXXWXXXXXTPXXWTV
WKATPXPXTXXXXXXXPXXXXXXXTXXPXXXXXXXXXXXXXXXTXXXXXAXXXXXXXXX
XXXXXXXXXXXXXXXXXXPXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXTXXCXXTXPXXXXXXXXXXXXXXXXXXXXPXXXYCXXXXX
XTXYDDXXXDYXPXXXYXXSPXXYXXXXXXXXXPXXXXXXXSXXXXXSYXXXCXXGXXXY
XXXXXXXXXXCXXGCXXXXCXXXXXCXPVXKTXKCXCXXXXXXXXXSCXXXXXXACXXXX
CXXXXXXXXXGXXXXXXXXXXXXXXXXXGXXXXXXXXXXXXXXXXXPXXXXXXXXXXXX

XXXXXXXXXXXXXXXXXCXXXXXXGXXXXXXXXXXXXXCXXXPCXXGXXXXXXGXXXCYD
XXXHLGVTYTAGGKCKDIDECELGXXXXXXXXXXXXXXFGDXXXXXXXXXXGXXXXXXG
VVHKAAGFGXGGYGXAXXXXXPXXXXXXXXXXXKAXXXGXGXGXYGXXXXGXXXXAXYGX
YGXXXXXXXXGXGXXXXXXXXXXXXXXXXXXXXXXXXXXSSSSSSXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXGXXXXXXXXXXXXXCXXXXXXXXXXXXXXXXDXXXXXXXGLXXXXX
XXXXSXXXXXXXGXXXXXXXXGXXXXGXXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXGXXXGXXXXFNKGDKCNNCTCLEXXXXXXSXXXXXXXXXXXGXXXXX
XSDXXXXCXCXXGYXXXXXXCHXXXXXPNPCXXKGRCYPXXXXKSSXXXXXXXXXSYXXX
XXXXXXXXXYAXNXXXXXPCXXXXXXXXXXXXXXXXXXXXIXXHXXXXXXXXDXXXXXX
XXXSGXXXXNXXVVSKPCXXXXXXXXXXXXXXSXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXGXXYXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXYXXXXXXXXXXXXXXXXXXXPPPXXXXXXXXXXSYXSSXXXXYXXXXX
XXXXXXXXXXXVXXXXXXXXVTIKPWTIPXXXXXXXXXXXXXXXXXXXXXXXPXXXXXX
XXXXXXXXXXXXYXXXXXXXXXXXXCXXXXXGXXXXXXXXXXXXXXXXCXXXXXXXXXX
XXXCXXXXXXXXCXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXTYXYXXXXXXXXXXXXN
XXXXYXXXXXXXXXXXXXXXXXXSIXXXXXXXXXXLLPRVYLXXXXXXXXXXXEKXXXXX
XXXXXXPXXXXXXXXXXXXXXYXXXPXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXCXXXXXCXXXXXXXGXXCXCGXXXXXGXGKXCXXXXXXXXXXXXX
XXXXXXCXXRTYXLPXVXXXPKNLSLSXXXXXXXXXXXXXXXXXXXDGXXXXPXXXXXXX
XXXXXPXXXXXLXXXXXXXXXXQXXXXXPXXXXXXXXXXXXXXXXXPXXXXXXSXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPTXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXNXXXXXXXXXXXXXXXXXXXXXXXSXGXXXXXXXXXXXXGXXXXXXXXXXXXX
XXXCXXXXXXXXXXXXXXXXXXXXXPXXXXXXXXXYXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXTXXXXYXXXXXXXXTXXXXXXXXXVFSDXXXXXXXXXXXXXXXXXXXXXYXX
XDLPPNIXRXXQXXXXXXXXXXXXXXXTXXXXXXXXXXXXXXXXXXXXXXXPXXDXXX
XXXXXXXXXXPXXXXXXXXXXXXXXXXXXXXXTXXXXXXXXXXXXXXXXPXXXXXXXXX
YRXXXXXXPXXXXXXXXXXXTXXXXXXXXXXXXXXXPXXXXXXXXSXXXXXXXXXXXXXX
XXXXXXXXXYXXXXXXXXXXXXXXXXXXXXXPXXXXXXXXXXXXXXXXXXXXXGXXXXXX
XXXXXXXXXXXXXXXXXPXXXXXXXXXXYXXXXXYVDPNEDPAFLPYNLAXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXPXXXXXXXXXXXPXXXXXXXXXXXXTXPDHPIXXX
XXXXXXXXXXXPPXXXXSXXXXXXXXXPXXXXXXXXXXXXXXXXPXXXXXXXHXXXXXXX
XXXXXXXXXXXXXXXXXXXXXPXXXXXXXXXXXXXXPXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXPXXXXXXXXXXXXXXXXXPXXXXXXXXXXXXQXXXXXPXXS
XXXXXXXXXXXXXXXXPXXXXXXXXXXXXXXXXPXXXXXXXXXXXXXXXXXXXXPPXXXX
XXPXXXTXXXXYXXXXXLPXXXXXXXXXXXXXXXPPXXXXXXQXXXXXXXXXXXXXXVXX
XXXXXXXXXXXXXXXXXRXXXXXXXGXXXXXXXXXXXXXPXXXXXXXXXPXXXXXXXXXPX
XXXXPXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPXXXXXXXXX
XXXXXXXFXQYXXXXXNSRIVXXXXXXXXXXXXXNXXXVXGXXXSXXYXXXXXXXXXXXX
EXDLDVAYVPNNNTCIKXXHXXEYMPKDDDDDYKDXXXXSXXYALMHQNVSGNV

==> Squamata.txt <==
>MSA Consensus of 770 seqs, protein
MLEXXXXXFFXMXXXXXXXXXXXXXXXXXXXXXXXXXXXXXCDXKXXXXXXTXCXXCX
XXSXXXXCPXGXXXXXXXXXXXXCRYXXXXXXDXXLSXXGCXXXCXXEXXXXXCCXGYWG
XXCXECPGGXXXXCXXXGXCXXGXXXNGTCXCXXXXXGXACXXCXXXXXFGPXCXSVCXC
XHGICNXGXXGDGXCTCXXGYXGPXCDQXXPXCXXXXCXXNSXCXVXXXDXXQXXCXCLP
XYXXXGXXCXXXXPCXXXXCXXXAXCXXLGPXXXXCTCXXGYXGDGXXCXPIXPCXXXXG
XCPXXSTXCXXXXPGKXXCXCKXXXXXXXXXXRRXXXCXSXXXXCXXXNXXXXAXCXXX
XXGXXXCXCQXGXXGDGXXCYXXXXXXIXXXNMXPXXXXXLXXAXAIFGKGCXXXLXXYG
PFTVXLXTXTIFPPFHISPRIPVTTMXSXHWLLAWXGLXXXXXVFXLRDTKEMGEYAKSG
IPVFSIELNTLXXXPXIXKXXHPRATEAXTKYFLXQXXAAXXILXAXTXNAWXTGQWXIX
XXXXXXXXXXXXXAXXXKLGXXAPXHXWYPXXXVXQGXTXXTALXXSTWREITAQKXAPL
XXLXGQXXXXXXXXXXXLXXGLXSXXXXXGELYLIEPLKFPXXXXXXXRXSYXGGXX

GLNQTQTRKIXAXSSIAHMGWLXXAXKKASXXXXXLXTLTXXXYXXXTXXXFXXLXXXXX
KTXXDVXLXXLXXXWXXXPXXXXXXXXXLXSLGGLPPLTGFXPKXLIXXXLXXXXLXXXX
XXXXXXXLXSXFXXHLSLXRXDTXYXXXAALTXPPXTXXXXXQXXXWRXXXXXXXXXTAI
NFQGNIIGRAYTXXXXVXXXXXXIXAXNGXIXXXXXXXXXXXXXLPXXPXXXXXXXXXXX
XGXCXXCXXLXXELSFEFSXCPXXSXXXXXXXFPXDXXXCXYXXXXLGLNXXXXGCXXXC
NXTXXXPXCCKGFFGXXCXXCPGGFXNPCXGXGXCXDGXXGNGXCXCXXXFXGXXCXXCX
XPNKXGXXCDXXCXCXXGXCDNXXXSXGXCXXGXCKXGYXGXXCDXXXXXCXXXDXAXXX
CXXXAXCXXXXTGXXXCXCXXGYEGDGXXCXXXDXCXXXXXXXCXXNAXCXXTGPGTXXC
XCXXGWTGXGXXCXXIXNCXXXXXGGCHXNAXCXYIGPGQXXCXCKXGXXGXGYXCXPXX
XCXXXNXXCHXLAVCQLXNXXKEDETCLRKYXGDGXXCYGXXMXELXXXXXXXXFXEWXX
XXXXXTXXXXXXNXTXLVPXXXCSKNSLASRQSFWAELNVARLDHQNVVRXIAASTCSPA
GQDSLTGTIIMEYVGNSTLHHVIYGTXWXTXKRKXXXXIXXAXIXXGDIXAXNXXIXXID
KVLFLXPXXXXIKRCMXDMHQXLSFGPXYGXLSELQXGEQFLEXIEKERKTTTFXIGGHS
IEXNTRPPNLYKLDXDXXXYHXXLGXKLLXXDLXNGXXXXTMLGXSXXXXFXXXXXQXYX
NXXXXXXXXVXTXXGXXXGXXXVXXIXKNRCXXNXTXXXXXXCXXCXLXXXXCPXGSXXA
XXPXXGXXXXCXXXXXXXXXXXXGCXXXCXKXXXXXXCCXGXYGXXCEXCPGXXGXXCXG
NGXCXDGIXGXGXCXCXXGXXGXACEXCXXGXYGXXCXXECXCXXGXCNXGXXGDGXCKX
CXXGXXGVXCLKAXXXXXXDXCNXTCXXXANCXXXXTXXXXXCXCXAGXXGNGTXCTXIX
XCXXXNGGCSXXAXCXXXXPGXRXCXCKXGYXGDGXXCXEIXXCLEXNGGCXXNAECXXX
GPXXXACNCLXXYXGDGXXXCXXXXXCXXNNGGCXXXAXCXXTXXXXRXCXCXXXYXGDG
FTCXGXXXXEXLXXXXXXXXFXXXXXXXXXXXXXXGXGPXTVFXPXXXXXXXXXXXXWX
XKGXXXXXLRYHIVXCXXLLXXDLXSXXXXTXLXGXXXKXXPXEXHXXNNDXXKXAASXX
XVXXGVIXXIDXXLXPQXPFHXXXXLXXGXXXXXXXXXXXVXDKXXXXXXQXEXEXHXVX
XXXXCXXXGGISVSSXXXXXXKRSHPVHGPVDXXXXXLDDEMQXLLXKKEXXATSWPDLL
XKXIXXXXXMFKXDVXXPRXDXDTIHPTXFCHXCXXDXXXXGXXXXXXXXXXIXQRXXHH
PREGCYGDKDEFXXGIAYGIDXXLXXPXXGCWSVIQRKFSXVPCEVYFPRKGTMEWXPHS
XXCXVCGTSSHGIKRKKQAXXPXGXKXXRXIXXXCXYXXXXXXXXXXXXYXXAERARKIXX
RAQXXMYXRSQKQXNSKXXMKKITXCKKIHLSTKMLTXDYPXDFVKSISCQICEHILADP
VETXGXCDXGXXGXGXCXCNXXFXGTXCEXCXPGXYGXXCKXCXCTXXGXCXEGXXGXGX
CFCXXGWXGXXCETXLAXXPXCSPXCXXNAVCXXXXXXXXXXXXXPXXXXXXXLXXXXLX
XXXGXXAXHDNICXCXXXXXGXGXXCXXXXXXXXXXXXXXXXXXXXXQXGSXXXXXXVXX
XCXXXYXXDGXXCXPXXXPXDFTDEHDPXXXXXXXXKVXXXXXXCXEXAXXXXXGXXXXF
TXXGXXXGXXXXXXXXXHXXXXSLXXXXXXLXXAXGXYXLXSCXXXXXXXGLXFLHXXXX
XXXXXXXAXXFHVXXXXXXXXXXXXXXXXXXCXXLXXXLXXXXXXXXXXXXCLVSHTSGF
NTSALIMGPTASNYGGXXXCXXGXXXXXXXXXPXXXXXXXCXXXXXXXXGIXXXXXXXXX
XXXXDXYCXXXXXXXXXXFXXXXXXXGXXXNSSDXWXXXXXXXXXCXXVXXXXVXLXDXS
TEMNSTXXXXXXXXXXXXXXXXXXXGXXXXXDGSXXXXXXXGCGFGVXXTAXXXXXXXX
XPXXXXXSXSAXXRXTXXPXXXXXFGXXXXXXXXXALXXXXXXXXXXFXXXXXXXXXXX
XXXXXXXKXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXEKXXKPXXFLKXPLVKQ
NNXXXKTQLSPSITXEXSXXGXXXXNDXKIEIVEREXPEWTPDIKHXKXXNXTSRKDXXX
XXHRXXFDDDDXGXXXXXXXXXXXXXXXXXXNXXXXLEWXXXXXXXXXXSPXXAVXXXXX
VKNXXSXXXXXXXXXXXXXXXXEVXYSTNXXXXXXXPXXXXXVPXGXXXXXSXXXXPXLLV
YRGXXXXXXYXXXXDVLXXGXXSNFXXXTEQFXXTEESPTAXSSSDDXFXQEXXXXXXXX
XXGXXXXLXXXXXXXTAXXXSDXLHXXXXPSXXXEXXLEXXSXHHXXXXXNXSXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXTNRTILQVXXXVXXXLXXPXEXXXENXSSQXX
SXXVDEQPLQPSETTGHQEEKETSNESSTVSITQTNKEKQXLDXXTXDQGQSPAXPRXXX
XSKWSKIKIVTKQPSGVDVYXXNXXXXEXXXXXXPXXXXXXXXXPXXXXXXXDXXXXXXX
XVSXXXTXXEXXXXXXAXXXXXXXXXXXXXDVXLHXXHSXXXXEEXXSGVTFIDTKLFEVT
TPSPXXEXGXXXXXXXGLPXTNTSXXXXLPGIXXXXXXXXXXXXXXXGXXXXXTXXXXXX
SXXXGKXXXTTQXPHFYXXHPGXXXXXXXTXNXTXDXXXXXIXLXXEXKXEXETXXTXXX
XXXXXXXXXSXXDXXXHXXXXXDXXXGPXFEDXIXLXXXXXXXXEPETLHFVNQEETMSL
LDIAGKDTVLKQSSQHSEEASELRGHEAVTLSPXXXXXXXPGXXXXXXXXXPEKTXXXX
XEXXXXXNXSXXXXXPGIXXXXXXXHXXEXSHXXXXSSXDXKXXHEXXXXXPXXHDXXXE
XGREDXYXTNXTXXXXXXXXXXIPPTGTXXXXEXXXXXXIXLXNTKKGAXXTADKDXXXS

TXXXLXGKXXXXXPXXXXPXWXXEEXXPXNXXRXXXXXXXXXXXXXXEHXXXXXDXXXHXX
XKEDXTXEPVXQWXXEDXYTTXXXXDVLXPGIVPRRGIXQKNXTDHTXXVPPIYILLIID
LTIVTPVXXSXDGXKXEESTQXPXXHGLXRLVWAQEMNXXLLXETXXXXXXXXXXXXXXX
XPXXSXXXEPLVNXTXDXXXPXXXXEXXSXXXXXXXXSXXRXXXSTAXXXXXXXXXXXXX
XXKXXFCXXXXXXCLKXXXXXXPXXXCRYPCFPXXXXXXXXXXXXXLXXLAXXLGVCXXX
NSRXXCXXKXKLXINNGKGGIXEKXXGGLNGEXXXXXXXXHLXXXXXXXXXXTXXSXXXX
XXWXGLXDRXXEXDFXWXDXXXLXYENWXXGXXDEFXAIDETQNXXXXXXXGXXQXVXLK
SXXPXXGXGXXXXCXXPXXXMYGSXXXXXXGXXFGXGXGXXXXYXXGXGXGXGXXPXXXX
GXXXXXXXXXXXXLGXXXPXIXXGXNGXWXXPXXXCXXQXPXSEVXIQPPPXXVXXPGPX
LXAXXEPXRVGGYTXCXXXXXXXXSSXXXXXSXXXXXXXXXXXXXSFXXXXXRXGSXGGC
XRGXLILGXXXXGXXCXXPXN

==> Streptomycetaceae.txt <==
>MSA Consensus of 114 seqs, protein
MTHQLHHPATHATEPRXXXXXXXXRXRXXLXRXAXGAXXXXAAXXXXXAXXXXXPXXXXX
PXXXXXXXXAXXXXXXDXXXXPXXXXKXXXTGKRVELXSERTETSXXXXXPXGXYGDFXX
XXTXXXXXXXXXGXXXXXGDYLTRIKASGGQADFFNFGYVSDXXXDSAGNAYIXXXDXXV
XXXXXPXXXXXLXXAGGXGXVAGXXSXGTGATXXXXXPXXLXXXGSXXXXVTLQWKGGLP
EPXLXXXXAXYXXXXPGAXXXXEATRTGFEQFXXMRXXXXXXDYXYXXPXXXKGLXXXXX
SXXXVXXXXXAXXXXXXXMXXXXRRXXAALXTXXXXXALAAXGXXAXXXPGXXXXXXXAP
XXXXXXXXXWPXXXGXXLXXXXTGSAAXXVXXXXXXXAXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXAWXXDGSRXXXXXSXXXXXXXXXRTXXXXGXXXXARSFIHWXXAAX
XXXXXXXVXXAXLXXXXXXXXXSXXXXXDXTFWXGGXXXVFXXXXXGXLXXXXXDXXXXP
XXLXXXXXXTXXRXXXXXXXXXXTGTPXXXXXXXXXXXXXXXXXXPXXXXXXXXQVREG
TEPLXXXXXXXXXPXXXCDXXPXXXXXXXXXXXAXXXXXXXXXXAXXTXXXXXXXLXXXP
XXXXXXXXAXAXXXXXXXXWXXXXXXXXXXXXXGXXXXXXXVXXXXXXXXXXSXXXAAGX
XXXXXXXXTRSLGXXGXXXAFXXXXXXXXRXXXXXXXXXXXXXXVXXYXXXXXXXXXXXX
XXXXXXXXXXFXXXXXXXXXXXXXXXXAXXPXXSPDGXXXAFXRXXXXGXXQXFXXXXDG
TXXXQXTXXXXXXXXXPXWSPXGXRIXXXXXXXXXXXXXXGXXXXXXXGAXDGXXXXIS
YDXXXXXXXXXXXXDXXXGXXTXVPXXXXXXXXXXXXWQPLRXXXXXXNXXXRVXGXXXX
XTXXAXSRWTWNXXGXXXXPGLXXAXXAVLXXXXXXXXXXYXXCTTAXXLAGXKXGPVLX
TXXXGLXXXVXXEXXXXLXVPATTTAAPVALAAADAXLKRXLXXGXXVYLXGGTXXLXXX
VXXXVXXXXLGXXXKRLXGXXRYXTSVAVAKXXXXXARTYALVGXXXXTXXPXYVFXXXS
XAXGTXDYXXALXAXXAAGXXGXXXXXXVXLXXGXXXTXSVXXYLNXXXPXXTXXIXVGX
XAXXALXXAXXAXXXXXWPSXXXYYXXXGXXXGRETXXXXXXXXAXFWWXXPXXXXXXXV
EAVRDAGTGDASELADDGXXDXXPXXXXTASPSSSSSPSASASASASASDPGXQDAQXXP
SVXXXXXXXXXXLAXXXXXXWXXGXSAXXAMXXXGXPXLWTXXXXXXLXXXXXXYLXXXS
AXAXXXXXXXFGGXXXXXXXXXXXXXGXXXXXXXXXXXYXAPXYAXGXXPXXXXXXXXXX
XXXXAXAPXXXXXSGXXXXXXXXXXXXXXXPXXXXXPXLXXLXXXXXXXXXXVXTXXPXX
XXXXXXXXXXGXXXXXXXXXXXXXXRXXXXXXXXXXXXXXXXXXXXXAXXTXXXXXXXX
XXXGXXXXXXXXXXXXXXXWXAXXXXXXXXXXXXXXXXXXEEIHVRPYSRSYIRASAAFVA
AVAIAGGVAPAAHADGDGADLVVXXXXXXGPKPXXXYXXXXXXXXXNXXXXXXXXXDXXA
XXXXRMXFXLXXXXXXXXXXXRXXXXXXXDVXXXXXXXXSXXXXXXXXXXXXXXXXXXX
WYESFPGXXXVDXXGXXXXXXYTXXXXXXPXXXXXXXXXXXLXNHQALGSSLGVXXXXXL
PQPVTYQLTCGXGERGETPGEGFGDSYRRLALTADSSADLVAVGDDTEALAGDAQXXXVG
XXXXXXXWXXXXEXXXXXXXXXXXXXXGTQATKVPEXXXXXXXXGPNAXXXXXXXXXXXX
XXDXXIEVGQSLQXXXXLXXDTXGXXXRANAEXXXXXXXVLPXXPXXAXXXXXXXXXXXA
XDXNXXXXXXXIXXXXXXXXXXXVXGAXXSXXXXPXXXXXSTXXXXDXXXAGGGSGSXXX
XXXXXXXXXXGTGASGTSAAGXSXGGSXXGTXXXXXXXXXPXXXGXAGXAAXXGXXLVLX
XXXXXAGXXXSLVDPTSSNALLRDTTN

==> Streptomycetales.txt <==

>MSA Consensus of 116 seqs, protein
MTHQLHHPATHATEPRXXXXXXXXXXRXXLXXXAXGAXSTAGLVAGXXXXAXXXXXAXAX
XXPXXXXXXYXXXXXXXSXXXXXXXXXXGXXXXXXXQVHNGDLYITGDYLTXXRXXGXXX
XXXXXXXXXXXXFXXXXXXXXXEXTXXXXRXXXXXXXXXXXMXXXXRRXXVXXXXXAALX
XXXALAAXGXXAXXXASXGTGATXXLXXPXAXAXDGSNNVYGXXXXXXXXXXXGXXXAKV
TPAXXXXWXXGLXXPXXXGTXARYXXAVPXTXGXXXXXXXXXXXXXXXXXXXEAQVDGQL
PXXXXXXXXXXXXXTGSAAXXXPXXXMXXXXXXXXXXXXXXWXPDGSXXXXXXXXXXXXX
XXXXXXXWXXXXXXXXXXXXXGXXXXXAAXXXXXXXXXXXXXXRXXXXXXXXVXGXXXGXX
XXXXXPXXXXPXXIXXXXXXTXXRXXXXXXXXXXTGTPTXXWXXLXXXXXXXXXXXXXXX
SXXXXXQVREGTEPLXXXXXXXDXXFXXGGXXXVXXXGGXXXXXXXXXXXXXXXTAXXXX
XLXXXXXDXXXXXXXLXXXXXXXLXNFHSGNXXXXXXPXXXCXDXXPXXXXXXXXXXXXX
XXXXXXGXXXAFXRXXXTXXXXXXXXXXXRXXXVXXYXXXXXXXXXYWASGXXXXXXXXYX
XTXDXXGXXXXXXXXXXXXXXXPXLXVTYNXRPXXXTXXAXXPXXSPDGXXXAFXRXDAX
XPAXXXGXXXXXXXXXFXXXXPAXXXDGTXXXQXXXXRXXXTXXXXXXXXXPXXXXXWSX
PXGXRIXXXXXXXXXXXTXXXXXXXXXXDXXXSAAPXXXXXYRSXGXXXXXXXDXLXXXX
GXXTXVPXXXXXXXXXXXXWQXXXXXXXXXXXPXXLXXXRXNXXXRVXGXXXXXTXXAXS
RWTWNXXGXXSXPGLXXAXXAVLXXXDXXXXXXYXXCTTAXXLAGXKXGPVLXTXXXGLX
XXVXXEXXXXLXVPATTTAAPVALAAADAXLKRXLXXGXXVYLXGGTXXLXXXVXXXVXX
XXLGXXXKRLXGXXRAVSLARYSSSQSTSXXXXCXXTSVAVAKXXTXSARTYALVGASXX
XXXPXYVFXAXGTXXYXXALXAXXAAGXXGXXXXXXVXLXXGXXXTXSAAAVXXYLNXXX
PXXTXXIXVGXXAXXALXXAXXAXXXXXWPSXXXYYXXXGXXXGRETXXXXXXXXAXFWW
XXXXXXXXXXVEAVRDAGTGDASELADDGXXDXXPXXXXTASPSSSSSPSASASASASASAS
DPGXQDAQXXPSVXXXXXPXXXXLAXXXXXSWXXGXSAXXAMXXXXGPXLWTXXXXXXLX
XXXXXYLXXXXAXAXXXXXXXFGGXXXXXXXXXXXXGXXXXXXXXXXXYXPYYAXGXXPX
XXXXXXXXXXXXXXXXXAPXXXXXSGXXXXXXXXXXXXXXXPXXXXXPXLXXLXXXXXXY
ASLXXTXAXXXXXXXXXXXGXXXXAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXAXXXXX
XTXXXXXXXXXXCXGSTXXXXXXKXXXXXXXXXWXAXXXXXXXXXXXXXXXXXXXVXXXXGX
XXXXXYIRXSAAFVAXXXXXXXXXXXXXXXXXDXXAXXXXRMXFXXSAXXXXXXXXXRXXX
XXXXXVXXXNKGNAAAQGVSFRVRLTXXXXXSXXXXXXXXXXXXXXXXXXXXWYESFPGX
XXVDXXGXXXXXXYTXXXXXPXXXXXXXXXXXLXNHQALGSSLGVXXXXXLPQPVTYQL
TCGXGERGXTPGEGFGDSYRRLALTADSSADLVAVGDDTEALAGDAQSXXVGXXXXXXXW
XXXXEXXXXXXXXXXXXXGTQATKVPEXXXXXXXXGPNAXXXXXXXXXXXXXXXDXXIEV
GQSLQXXXXLXXDTXGXXXRANAEXXXXXXXVLPXXPXXAXXXXXXXXXXXXAXDXNXXXX
XXXIXXXXXXXXXXXVXGAXXSXXXXPXXXXXSTXXXXDXXXAGGGSGSXXXXXXXXXXX
XXGTGASGTSAAGXSXGGSXXGTXXXXXXXXXPXXXGXAGXAAXXGXXLVLXXXXXXAGX
XXSLVDPTSSNALLRDTTN

==> Streptophyta.txt <==
>MSA Consensus of 117 seqs, protein
MVTDPSAEIKVGIDPKRTDPSAEIKVGIEPSTKFKVGMEPKQETXXNNDPSAEFKVGIYP
KGTNPSAEIKVGIDPSAEIKVGIDPKEDGVSEDLTLNQDEDEFDSKERXXVLHKYFXLKX
TQEXXXXXXXXXXXETDPSAEXXXXIDPXXXXPXXXXXXXXXXXXKFRXXXXXYQEQGQL
TDPXXXXXXGIXWXGXXXYXESMISPLMNIIDRSRTIXXXXXSDEILEIIKPICIIIYSL
VTVXXXXAXXKXFPHQVXXXEXXVXXLEKCHLTSSGXXLXQESTXXXXXXXVXLXXXXIX
XLXXXXXSTVDTSIANNENXXTXXXXXXXXXXLVLXXXXXXXDYLATAXXXXXXXGLXXX
XXLTPXPXXPXXFTSFXXXXXXXXXSXXXPXXXXXXXXXXXGAVEAMAAIFKAGSRNXXX
GVIPIVWNDTSILYKSXTXXXXPXXXXXXXXXXXXXXXXPXXXHRXPXXRYXXRTTKLNV
SXXXXIXXXXXXXXXXGXXXXSNEVIDGAEXXXXXVXXXXXXXXXXXXXXXXXXXXXXXX
XXAAXXXXRITSXXXXSPXXXXXSXXXXLXXXXXXXXSXXXXXXXXXXXXXXXXXXPXPP
YXXPXXXPPXXXXXXXYXXXXXPXXXXXXXXXXVGSHXXXXXXXXSXXXPXXXXXPPYXY
XSXXXPXXXPXXXXXXXXXXXXXXXXXXXXFGXPLPXXXXXXRWFRRXXXXXXXXXXXH
XXXXXXXXXXXXXXXXTVACYDXXXXXXXXXXXXXXXAXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXLHVAXXXXXXEGXXXXXXXXXXXXXXXXXWXXXXXXXXXXXXXXXXXYDPX

XXXXXXXXXXXXXXXXXXLXXXXXXXXXATLATGELVLALHXXSYXXXXXXXXXXXXVXX
XXXXXPGXXXXXXXXXXXXXXXXXXXXXXXRSXXSXXXXXHXXXXXXXXXVXXXYATPXX
XXXXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXSXXXXXVPAX
XXXXXXXXXXXXVTAKYXXXLXXXXXXXXXXRIIQVXXXXXXXXXXXXXXXXXXXXXQWX
XXXXXXXXXXXCXXXXXXXXXXXALKASEVIGXXXXXXAXXXXXXXCXXXXXXXXXXXXX
XXXXXXXXLXXLXRNXXXMSLFXXXXXXXXXXXXXXXXWXXXXXXAXSTGXXXKXXXXXX
XXXXXFXXXXXXXXXXXXXXXXXXXXXXXKSTGRVXXXXXXXCXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXGKEXXXXXXPXNDPVEXXXXXXXXXXXXXXXXXXXXXXXXX
XXXMXXXMKXXXXXXXXXXXXXXXXXXXXXAYSPXXSCTHQXXXXXXXXXXXXXXXXXXX
XXKXPSXXXKEXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXVXXDXXYKX
XXXXXGXXXXXXSVSEDTYKKVSSVXXXXXXXXXXXXXXXYXXKPXXXXXXXXXXXXXPX
XNXYKXXXXXXXXXXXXXXXXXSXSXSRSYSSDRGRSYXXXXGRRGRSSXXXXXXXXXXX
XXXXXXXXXXXXXKXXYXKXXXVPXXXXKNDYYKKPSVSEDTPXXXXXXXXXXXXXXXKX
DYYKKPXXXXXXXKNDYYKKPPXXXXXXXXDYXXKPXXXXXXXXXXXXXXXXXXXXXXX
XXXXLXXXXXXXXXGXXXXXXXEXPXXXXXXXXXXXXXXXXXXXXPXXXSKVEFEPRF
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPXPXXPXXXRKXXXXXXXXXIXPXX
XEXXIXXXXXXXXXXXXXXXXXFXXXXXXXXXFPTHLXXXXXXXXXTTDTYXLPKXXXX
XXXXXXEXXXXXXPXXXEDXXYXXXXXXPXXXXXXXGXXXXXXXXXXGGXXXXXXXXXX
XXXXXXXXXXXXXAFSQLVSXXXXXYXXXXXXXXXXXXXXXISKIYXXXXXXXXXXDXXX
XXXXXXXXXXXKXXXXXXXXXXXXXXXXRXGXLXXXXXXXXXXXPXXXSXXXXXXXXXXX
XXXPXXXXXXXXXFXPXXXXXXXXXXXXXXXIXXXXXXXXXVHKTKXXXXXPXXXXXXXX
XYKXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXIAPEISTKLNRNFKLAPHXXXXXX
XXXXXXXXXXXXXXXXGXRXXERERSXXXXXXXXXXXXXXXXXXXXXYXXXXXXXXXSY
SXXXXXXXXXKSXXXXXXXXXXXXXXXXXVPKXXTEPKPXXXXXXXXXXXYXXXSLPXXX
YYXXXXXPXXXXXXPXXYYKSPPPXXXXXPXXXXXXXXXXXXXXAYPXXPXXXXXXPXXX
YXXPXXPXXXPPPXXYYKKPSXXXXXYXXXXXXXXXXPPPXXXPXPPXXXXXXXXPPPXX
XPPXXXXXXXXXQSXXXXXXXXXXXXPXXXYXXPSXXXPXPXXXXXXXYKXPXXXEXXXXX
PXPXYXXXXXXXXXXXXYKVPSXPXXEYXXPSXXXXXXYXXXXKSHTYPRXXXDYYKKXXX
YXPXXXXEXXXKKVXXXVPXXXXXKXPXXXXXSXXYXXPSXXPXXXYXXXXXXXXPXYXX
XSPPXXXXXPXPXXYXXXPXPPXPXPPPPXYXXSXXXPXXXPXPXYXXXXPSVPXXXXKX
XXXPXXXXXXXXPXYXXXXRLXXXXXXKXXXXLXXXXXXLXXXXXXSLPKXXXXAXXXXX
XXXXPPKNDCHKKPYVPXYXXKSXPPPSPXXXXPXVYKXPXXXXQVYEAPSXPKNDYYKK
PYXXXXXYXXXPXXPKNNYYKTPSVPKQVYXXPXPXXXXXYXXPXXYXXPSXXPXXXXXX
KXXSSPPPSNDYKAPXVPXPXYXXXSXPPPSPXPXXPYXXKSXPXPSPXXXXPXYXKSXX
XYXXXXKXXXPSLPKNDYYKKPXXPXXXYXXXXXLXXXPXXXPXPXYXXXXPXXXXXXXX
PXYXXXXXXXXXXXXKVPSVPKNNYYKTPSVPKQVYEAPXXXXXXYXXXPXXXXXXXXXX
XXXPXXXYXYXXXXXPXXVYEAPSPPXPXYXXXPXXPXXXPXPXXXXXXXXPPXXXXXPX
YXKKPCVXXXXPXPXXXXPXXXXYXXXPXXKXVYTTLPKNDYHKKXXPPXYXYSXXXXPV
KSPXXPXYYXXPPPPXXXXXXXXXYXXXSTXXXXXXXXXXYXXXXXXXXXXXXGXXXQN
NTKMSPPISNFSPQELIEECXXXXXXXXXXXXXXXXSYQNNQSDTTEXXXGXXXXXXCXX
XXXXGXXXLXYARKGGVXXXXXXXXXXXXXGXFXXXXXXXXXXXCREFKKRIKKTVTFPP
PLTXXYXXXXXXXKHPXXXXXXXLVLRAXXXXXCXXXLXSSXXXTCXXXXXXXXGXXGAX
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==> Teleostei.txt <==
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IDTV

==> Theropoda.txt <==
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TWXXXXXXXXSTSXLXXXXXXXXDXXXXSXXXXXRRVSFANPIXXXGXAXDXXXXXXXXX
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XXXLXXLXXXKNIKXVXXLSPXLXXXEXXTXPIRAPKVSNVKXXLXXXXXXXXTXPXXXX
RXXTSXXXXXXEDVEKTANSAEDKSSSVXEEXLXXXXXXXXXXSSSSSXXXXXXPXXXXL
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GXQLTLT

==> Tissierellales.txt <==
>MSA Consensus of 370 seqs, protein
MMRXSXXKXXXRXLXXLXXXXMXLTXMPVXXXAXANVXXXXLXNXKSXXXNXKTPVXXAX
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GVDGNKVLTXXEKXKVXXXXXLPXXXGYXXPXXXXXIDYXXXXXXAXXXXXTGNXXXGXR
YXXXXXXXYXXXXXXIXWYRXXHXFQXLXXFXXYXXXYVDGSXGEXXXXXXXQXGXTGXX
XXXXXLXXXDPXXXGXXPEXXXXXXQVDLNPXNXXNFXXEXRYNRAXYDVVFXXXGGTXL
PXXTLYYGQXXPKXXXXXXXXXKXGXXFQGWKXSXDXXXXDGKTXKQTLTANEIIKXGTXX
KGAXXNXXXXXIMPASKVTFTAXWKDKXKADYXXQFWAEKXDXXDKXDXXXXXXKYDYIG
TRVYKDXDTGSRPXLXNXXVXXIXFPDLDQARLXKIWAXARFNRGKXLYLNKFYXYNQXL
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XGXXVXXGXXGXPYXYXARFNXXXXKXWPXDXXXTXGXXXXXXAXGXGXQSFGWGPNYXX
XNWPXXXDTPPYRLNAXXFLDXXNYXXXGXXTKHIDKGDGXXIXXXXXDXKXXGXXXXSX
XXXQXXXSXXHHMDXXXDGFXXGETXIXYDLXXXKXDTXFSXEXXYXXXYPXXXGFTXXX
XXXXXXWXXXXXXXXXXXXVXEXXIXXLNXERXEXTPXXSXXXXXXGXKXPXGXXXFIX
XFFSDXDEFGDPXXDXDGNPXVXXXXMXXYLXXKXXRNKYPLRFNYDPSXXKDDXEFXXT
NXLXXVXXFXLXXXXXXXXXXXXPXXXPYTXXYXKXXXXXXLXNPEKLXEXXLTDLXXND
XNXXXKLXXXLPXXXXFAXXXXFKGWKEQKELVALDPAGXXLXWXXXXTXXPXHPXNLYA
KWGEPDYKWKVTFDPNGGXLXNIXEXXXTXXGXTXXXKXQEXGVXAXXXXXXXVEXXXXG
XXXXFTXXXXQTIKEPQKLVEPKIKPTRKGYDFMGWEVIRYKKDAXTGDYTXXXDTSYRD
TYKVPEXYXFGNXVPVXXXXXRXXXVXXARXXKAVXXSXXXVKKTTWXXXXXDYXGGXXX
KXXXXXLXXXRXXXXXXXXXXXXXXKXXLXPHEXVXXXKXXXFXXXXXXFXXXVKXXXXX
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FXXXFXXXXXXXXXIDXXXXXXXXXXKDMXLXXXXYXKXXXXXXLXXXKYXXXVRARVLF
XXXXXXXKXXXLKGKWXXXKXXXGXXXXDXEXESXXIRXXXXXXYHGMXXXXXXXXKFPE
APTLAGXXXXGXVXAXGXXXXXXLXFDXXEXTXXFXXIXGXXXXEAQLLXXXXXXXDXXV
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VSEWHTXVXEXDXXXXXXXXXWXXXXKXXLXXXKNXXXXXXXXXXXXXTXHPAXXDPXXX
XXXXXNXXXXGTXPXXXXXXXXXXXXVXXEXXXXXXXXPXGXXXKLYDEAGXELTXXXXX
YXXXNEXKXADXXELXRTVXXXXXXXXXKDGXXGTAEGXXXXXXXXXXXXXXXXXXXXXX
YXXXTXXXXKXXFXXXXXXXXXXIXXKXGVYIXXXXXXXXXXNYVXVXVXPXXXXXXXGX
XXXXXXXXXXXXNXXXXXXXNXXXXXXXXXXXXXSXXXKXXVXXXXXXDLXXXXXXXXXX
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YIXXXRXXXKXXXXKXXXXXXXLXXVXXXXXXKVTXKEPTNKNXYFPVIFDANXXXXXXX
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QDRINLXXXYXLXXXXXTXXVGIGNPXXXEXXXXXIXXXXXXGXXGXWXXXXXXXXFXPX
DNXXXXXXXXDFXXXXXXXXXXXXXXGXXXKXXXXXXXXXGXWXXWNDXXGAWNVXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXPXXXXXXXXDXXDVPXXXPXXXXRXXXXXXXXXXXXX
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IEKNDDTEXHPGYVKVTFKAGXNGVIKEXXXLXXVXXXXXXPXKYVXLXXPTXXXXXXXX
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GGKIADXEXXTYYVDPTRQVSLKAPKTXAGTGXVFDXWRLXXNTTXXXINPADQXQYXXX
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IXXXXXXXXKTEXIXGXXXXXXXXXWXXXXTXXXXYXXXXXXXXXXXXXXXXIIPSXXPX
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NXXXXXXXXXXXXXXXXXXXXGWXXXXXXXXXXXXXNLXEXXXXXXXXXXXXXXXXXXXX
NPXTRPDDXYVXVXFXXEXNGXXKXXEXKAYYVKKDAXIXLGDAXLXXXGXXXXXGXNXX
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NKXXRTVSFEIPKNTTTKEKEYTVYVSSTGSKXDFAXXTVKITNPIIDQNQEKSDTEEQE
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GXNPEYTIGVYXKTKXXEXPXXEXXXXXXXXXXXXTXXXXDXXXKXEEVILTFKPEEKHFI
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FNSNNLGKVTIPESVEEIGANAFNTAGLNKIILTENIKKLGKGAFANNKLKEFTIPKNIT
NIPESLVENNILESLEIPNTVSEIGAKAFKSNELSSVKFADTVKKIDILAFADNNIKKVE
LSSDCDVHPLAFDSNVETNIPKKPEKEVSEEKDFVFDKNTQTITEYIGNDLVVKIPKQID
GVDVKAIGGFEDFFGIKK

==> Tissierellia.txt <==
>MSA Consensus of 387 seqs, protein
MRXSIRKEIRRFLCFLMTFIMILTSMPVHLLAAANVDHNNLXNXKSXIINXKTPVXVAKP
EXGKTAADLIKNPXQPXIYTLRTDXKVQRGEKYQVDYQPYIASVGAXAYTYKDINGVDGN
KVLTXXEKXKVXXXIXLPXXXGYXXPXXXFXIDYXXXKNXAXXXXXTGNXXXGXRYXXXX
XFXYXAKSNXIXIKHVFQXLEDFXKYTNPDGSVGEXXXXXTXQXGNTGSTMXVXPLXXXD
PXXKGFVPEAXXIXMQVPXNAXNFXLEYRYNRAHYDVVFDTXGGTXLPXRTLYYGQXXPK
IADXXIPTKVGGEFQGWKPSVDLTTKDGKTXKQTLTANEIIKXGTXXKGAXXNLDANLIM
PASKVTFTAXWKDKXKADYAXQFWAEKADHADKDDXASLXXKYDYIGTRVYKDXDTGSRP
XLXNXXVXXIXFPDLDQARLXKIWAXARFNRGKXLYLNKFYXYNQXLTXXQNKDXXNVNL
VKSVDSTGXTVYNXYYDRXVYXLYFTXSNXXXXXPXNXFXPXXWQYDEAXGEAVXKGGPG
XXYXXXARFNXXXXXXWPNDAXXTXGFXPXXXXXXXXXXXGWXXNXXXXXXXXXLDTPP
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XGWEVXRYKKDAXTGDYTXXXDTXYXDXYKVPEXYSFLIDTGNDVVXXXXLXAIWXPNXR
VDVXVXHXXLDXDYXKXXKXXXXXLXXKXXXYXVXXXXXXQXXXYILAPHEELEXKLTXD
LXXXYXXYXXXVXXXTLNXXXQXXXVXPXXIXXXXTXXXXAVSXXXXXXFXXXXNPXXXX
EXXATLXXXXXXXXXXXFFXXXXXXXXXXXXYXXXXXXXXXXXXXXXXXXXXXXXKXXXX
XKEXXFXXXXXXXXXXXXXXXXXADXXXXGASXRXXXXXXXTXFXXXXTKXXXXXXIXXX
AXXXXXEXVXNGXXXXXAXXXXKSQEXXXIXGWXXXXXXKXGGSNXXXXXXDXXXXXXXX
XGIXGTXXDXXXXXYKXXRVXXLXXXXXXXVXXGYVXVXXXXXXGGXXXXXXSDGXXXXX
LXYDVXXGXXSXXLPVPXXXXXGXXXDGXXXXKXXXXXXXXXXXXGXXFXKWXXXXXXXXX
TISFLXIXIXXXASTKFVSEWHTXVXEXDXXXFXAXFXXXXXXDNKFNFPKNDTTRTVLX
XXXXXXXXXXXXNXXXXXXXSELETXPXXVXVXXLXXXXXXXXXXXXXXXLPXXXXXXLY
DEAGXELTXXXXXYXXXNEXKXADXDELVRXVNXKAKVTFXDGKXXXXXXIPXXVYKNVY
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XIXEXXXXXXXKXXXXFXXWXAXXXXQNEXXEANGXXXFXKRHXFTXIKEXXTXIXPXFX
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VYXXGXXXTVXXXXXXXXXDEFXXXYXXXXXXXXXFKEWXXXXXXXXXXADDYEIQFKXW
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XAXXXXXXXXIPXXPXXXXPXXXXXXXVXVXFXKXXXXXXXXXXXKXXYVXXXXXXXLXXX
XLXXPXXXXXXGXXFXXWXXEXXXXXXDXXXXVTAXAXSKXXXDXXXXNKPGEXXPXXXX
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WXXXXXXXXFSLANFXXXXXXXXXTAXXXXKXAVYXXXXXXXKXXXXVXXXFKVXGXXGK
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DHAKFLAGXXLXXXXXPXXXXXXIGXLXXXXXXXXXXXXXXGXXXXXXXXXXKXXXXXX
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XLXXXXXXNVSFNXKAXXAXXXXXXXIXXXNXXXXXXXXXXXTYXRVXLSFMSGMEXKXF
PSVFISXXXGXXLXXXXXXXXXXXXXXXYXXXXWXKXDXLEIXXXDXXVTAKATKLXXXX
PXXXXXXXXXXXPXXXXEXXXXXXXXXXXXKXXXXXXXXXXXXXXXEXVXXXXPXXXXXXXX
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DXXXXXXXXXXXXXXXXXLXNXXXXXXXXXXXXXXXXXXXXVXXXXXXXGXXXXXXXGXXX
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XTAXXXXXXXXXXXXXXXGXKXXXVXXXXXXXXXDXXXAXXXXXXRNXXXXPILXXXXXX
XYIKKXXXXXXXXXXXXXXGXXVPAXXXXXGGXXXXSXXXXXXXLXXXXXXXXVXXRXXX
GXDRYXXXXXXXXXXXXXXXXGXXXXXXXXXXXXAHXGXXXXDALXXXXXXXXXXXXXL
LXXXXXXXXXLKXXXXLXXXXSXXXXXXXXXXXXGGXXXXXXXXXXXXXXXAGKDXXXXX
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YXXXXSYKNYPKIIKXAKLXNFXXXXXXIXDXSXXXXLXXXXXXXXXXXXXXXXXXXXXX
XXXLLRIKGRTVEVTFRXYXXXXXXXXXXXXXXXXXXXXXXXXVXXXKQNXXXNXXXXXXX
XXXXXXXXXXXLXXXXXXXXXXXXXXXXXXXXXXKXXRXXXXXXXKXXXDXXXXXIXXXXXX
XXXLXXXDXXXXXXXLXXQDQXXXKXXFXXXXXXXXNXXXXXVXXXXXXXTXETPXFYEX
XXNEYSNFYXXYXKLKXXKXIXXXXXXXLPAKDAIAKIXVXGXINNIPSDKFIVKLVDEX
GKETYPEIEVTGXASKAXRXINIKXPENTXDKXKTYEXXVSSXGKKENFKKAEXXLTQEK
XSGTQEVEKTXKIXSSNKDXVITVNGEEKXXAKKGDXVVXKAKXGKEIXMFYVSGXNXXG
DPMKVNFKQXGDXYQFXMPESDCTLNXXTKDKEVXXENIQXLXLXTXXKXYNVSKDSGXN
STATVQVXGXLXGIXNDKFVVKLVDNDGNETFPXVXVSGDVNKXXNIKRTVSFEIPKXXX
XNTTTKEKEYTVYVSSTGSKXDFAXXTVKITQEKSDTEEQIPEGIMXLXLETXGXXEXLX
AAGGKVXATLLLXVXGNXKNVXDDKFVVXLVDXKXXETXXXXXVSGXGAXRTLEFXXXDI
KNEEXTEKTYKXYATSTGSNEDYFETIKSXXXXXXIXIDKXXXDXXXWLKXXXXXXXXXX
XATEGEDQARXXKFYEXSVELKQXXXXNTKXTIEKINVLTPILKNXNNPXEKLXANXXGX
NXNPDNLXVSFYXLXXGKFVKDXSIXXXFEXSGKFXQIVADSIALXKGNEEDVYKIXVRD
NXDXSKSYEXYFRVKYTEDXXXYFXXIXPSYXHAXKDGKIVKXXXFEXXXXKVVNYSXPX
XYXIIEVGFXEEIEEIFDXSXKXGISIDKNADGNYEXLXXXDTVELSDKKFVXTXXLXXL
EKPKLDVXXLGXXKAXIKIXQGVFRXKGTEXLNXDVDYXINIGKPIXRQEDPYKPFSQPD

MDIPNSISXXATIXGXKXITNXNRKVTIKVNGXNLSENAKVKAVMQTKLATEXXXXAXKG
KQPEVXGXISGXXXEQTITFXLPENKTDRTVSYEXLYXPEXNGKFEKLPGNNPKSRANXX
VISLLADGVDXNAATLAFMKIQTYGATSTXXGXXPDGQKDITYGXTPXXQESKKTYFTHK
EKNIISNHAIAVVGYGTNLEAKKTRVXIFDXRGVEWYXVNQQGPSLGAAAFKMVVPALXG
IDGDGNYQTMEIIGPXXLIGDHQHDTFTYKVAVDGKNYDXXVXVXXXIXASGKTXXGKXD
LDXQETTLKLNYVDXXGNXIKXXXXKXSYSFFEECAADCFDEGIYPDXIEXYXPXKIXRK
SDXXXXXEIXLXXGVDYTDYRNLQXXLLNGVNXIGXNPEYTIGVYXKTKXXEXPXXEXXX
XXXXXXXXTXXXXDXXXKXEEVILTFKPEEKHFITKLLVNGKDEVVKVKDNKYTFIMNED
TXXXXXXXXXCXLXXXGXXXKXXXKPSNQIKPGTRIKITVDPDDDKAVXXXXXNXXNLIT
QLLNNTYEFYLDKCTTIEVKYTQKSTEPNDAKDFDFDATTGTITDYKSYARKDVIIPEKI
NGVEVKHIAEYAFYYKGLNSVKIPNTVISIGELAFNSNNLGKVTIPESVEEIGANAFNTA
GLNKIILTENIKKLGKGAFANNKLKEFTIPKNITNIPESLVENNILESLEIPNTVSEIGA
KAFKSNELSSVKFADTVKKIDILAFADNNIKKVELSSDCDVHPLAFDSNVETNIPKKPEK
EVSEEKDFVFDKNTQTITEYIGNDLVVKIPKQIDGVDVKAIGGFEDFFGIKK

==> Tracheophyta.txt <==
>MSA Consensus of 117 seqs, protein
MVTDPSAEIKVGIDPKRTDPSAEIKVGIEPSTKFKVGMEPKQETXXNNDPSAEFKVGIYP
KGTNPSAEIKVGIDPSAEIKVGIDPKEDGVSEDLTLNQDEDEFDSKERXXVLHKYFXLKX
TQEXXXXXXXXXXXETDPSAEXXXXIDPXXXXPXXXXXXXXXXXXXKFRXXXXXYQEQGQL
TDPXXXXXXGIXWXGXXXYXESMISPLMNIIDRSRTIXXXXXSDEILEIIKPICIIIYSL
VTVXXXXAXXKXFPHQVXXXEXXVXXLEKCHLTSSGXXLXQESTXXXXXXXVXLXXXXIX
XLXXXXXSTVDTSIANNENXXTXXXXXXXXXXLVLXXXXXXXDYLATAXXXXXXXGLXXX
XXLTPXPXXPXXFTSFXXXXXXXXXSXXXPXXXXXXXXXXXGAVEAMAAIFKAGSRNXXX
GVIPIVWNDTSILYKSXTXXXXPXXXXXXXXXXXXXXXXPXXXHRXPXXRYXXRTTKLNV
SXXXXIXXXXXXXXXXGXXXXSNEVIDGAEXXXXXVXXXXXXXXXXXXXXXXXXXXXXXX
XXAAXXXXRITSXXXXSPXXXXXSXXXXLXXXXXXXXSXXXXXXXXXXXXXXXXXXPXPP
YXXPXXXPPXXXXXXXYXXXXXPXXXXXXXXXXVGSHXXXXXXXXSXXXPXXXXXPPYXY
XSXXXPXXXPXXXXXXXXXXXXXXXXXXXXXFGXPLPXXXXXXRWFRRXXXXXXXXXXH
XXXXXXXXXXXXXXXXTVACYDXXXXXXXXXXXXXXXAXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXLHVAXXXXXXEGXXXXXXXXXXXXXXXXWXXXXXXXXXXXXXXXXXYDPX
XXXXXXXXXXXXXXXXXXXLXXXXXXXXXXATLATGELVLALHXXSYXXXXXXXXXXXXVXX
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XXXXXXXXXXXXXVTAKYXXXLXXXXXXXXXXRIIQVXXXXXXXXXXXXXXXXXXXXXQWX
XXXXXXXXXXXCXXXXXXXXXXXXALKASEVIGXXXXXXAXXXXXXXCXXXXXXXXXXXXX
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XXXXXFXXXXXXXXXXXXXXXXXXXXXXXXXKSTGRVXXXXXXXCXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXGKEXXXXXXPXNDPVEXXXXXXXXXXXXXXXXXXXXXXXXX
XXXMXXXMKXXXXXXXXXXXXXXXXXXXXAYSPXXSCTHQXXXXXXXXXXXXXXXXXXXX
XXKXPSXXXKEXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXVXXDXXYKX
XXXXXGXXXXXXSVSEDTYKKVSSVXXXXXXXXXXXXXXXYXXKPXXXXXXXXXXXXXPX
XNXYKXXXXXXXXXXXXXXXXXSXSXSRSYSSDRGRSYXXXXGRRGRSSXXXXXXXXXXX
XXXXXXXXXXXXXKXXYXKXXXVPXXXXKNDYYKKPSVSEDTPXXXXXXXXXXXXXXXKX
DYYKKPXXXXXXXKNDYYKKPPXXXXXXXXDYXXKPXXXXXXXXXXXXXXXXXXXXXXXX
XXXXLXXXXXXXXXXGXXXXXXXEXPXXXXXXXXXXXXXXXXXXXXPXXXSKVEFEPRF
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPXPXXPXXXRKXXXXXXXXXIXPXX
XEXXIXXXXXXXXXXXXXXXXXFXXXXXXXXXFPTHLXXXXXXXXXTTDTYXLPKXXXX
XXXXXXEXXXXXXPXXXEDXXYXXXXXXPXXXXXXXGXXXXXXXXXXGGXXXXXXXXXXX
XXXXXXXXXXXXXAFSQLVSXXXXXYXXXXXXXXXXXXXXISKIYXXXXXXXXXXDXXX
XXXXXXXXXXXKXXXXXXXXXXXXXXXXRXGXLXXXXXXXXXXXPXXXSXXXXXXXXXXX
XXXPXXXXXXXXXFXPXXXXXXXXXXXXXXXIXXXXXXXXXVHKTKXXXXXPXXXXXXXX
XYKXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXIAPEISTKLNRNFKLAPHXXXXXX

XXXXXXXXXXXXXXXXGXRXXERERSXXXXXXXXXXXXXXXXXXXXXXYXXXXXXXXXSY
SXXXXXXXXXKSXXXXXXXXXXXXXXXXXVPKXXTEPKPXXXXXXXXXXXYXXXSLPXXX
YYXXXXXPXXXXXXPXXYYKSPPPXXXXXPXXXXXXXXXXXXXXXAYPXXPXXXXXXPXXX
YXXPXXPXXXPPPXXYYKKPSXXXXXYXXXXXXXXXXPPPXXXPXPPXXXXXXXXPPPXX
XPPXXXXXXXXXQSXXXXXXXXXXXPXXXYXXPSXXXPXPXXXXXXXYKXPXXXEXXXXX
PXPXYXXXXXXXXXXXYKVPSXPXXEYXXPSXXXXXXYXXXXKSHTYPRXXXDYYKKXXX
YXPXXXXEXXXKKVXXXVPXXXXXKXPXXXXXSXXYXXPSXXPXXXYXXXXXXXXPXYXX
XSPPXXXXXPXPXXYXXXPXPPXPXPPPPXYXXSXXXPXXXPXPXYXXXXPSVPXXXXKX
XXXPXXXXXXXXPXYXXXXRLXXXXXXKXXXXLXXXXXXLXXXXXXSLPKXXXXAXXXXX
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PYXXXXXYXXXPXXPKNNYYKTPSVPKQVYXXPXPXXXXXYXXPXXYXXPSXXPXXXXXX
KXXSSPPPSNDYKAPXVPXPXYXXXSXPPPSPXPXXPYXXKSXPXPSPXXXXPXYXKSXX
XYXXXXKXXXPSLPKNDYYKKPXXPXXXYXXXXXLXXXPXXXPXPXYXXXXPXXXXXXXX
PXYXXXXXXXXXXXXKVPSVPKNNYYKTPSVPKQVYEAPXXXXXXYXXXPXXXXXXXXXX
XXXPXXXYXYXXXXXPXXVYEAPSPPXPXYXXXPXXPXXXPXPXXXXXXXXPPXXXXXPX
YXKKPCVXXXXPXPXXXXPXXXXYXXXPXXKXVYTTLPKNDYHKKXXPPXYXYSXXXXPV
KSPXXPXYYXXPPPPXXXXXXXXXYXXXSTXXXXXXXXXXYXXXXXXXXXXXXXGXXXQN
NTKMSPPISNFSPQELIEECXXXXXXXXXXXXXXXXSYQNNQSDTTEXXXGXXXXXXCXX
XXXXGXXXLXYARKGGVXXXXXXXXXXXXXXGXFXXXXXXXXXXXCREFKKRIKKTVTFPP
PLTXXYXXXXXXXKHPXXXXXXXLVLRAXXXXXCXXXLXSSXXXTCXXXXXXXXGXXGAX
XXXXXEQDVEXXXXXXXXYXXEAKVIEHENGDXLXXXXXAPXFXYXXXXXYXXCXKPKXX
XXXXXYKXXXPPXPXXXYKXPXXXPXXXVYKXPXXXXPXXXYXXPSYYKXPXXXXPXXXY
KXPXXXXXXXXXKXXXXXXPXXXYKXPXPXYXXXXXXPKXXYXXPXXXPXXYVYKXXXXX
PXXYXXXXXXXXXXXXXXXSXPPPXXXXXYKPPXXXXPXYVYKPPXXXXPKXVYKXPXXX
XPKXVYKXPXXXXPKXVYKXPXXXXPKXVYXXPXXPPXYYKXPXXXXPYSXXXPXXYYXX
PPPPXXXPPPXYYYKSPPPDDKPXXXPXPPYYYKXPPXXXPXXXYPPXYXKSPPPPSPXP
XPXYYYKSPPXXXPYXXXPPYYYKSPPPPSPXPXXPYYYKSPPPPSPSPXPPYYYKSPXP
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PPPPYYYKSPPPPSPSPPPPYYYKSPPPPSPSPPPPYYYKSPPPPSPSPPPPYYYHSPPP
PVKSPPPPYYYSSPPPPXXSPPPPXYIYXSPPPPXHYPCQSSFSWATVIRDCPKKGRFLS
QSPTKFLWGIGNKGLYHAMKSLNHETADLRASMVAILHALVLAFSSRIGFIRETGQGISI
KKQKPF

==> Unidentata.txt <==
>MSA Consensus of 118 seqs, protein
MLEXXXXXFFMXXXLXXXXXXXXXXXXXXXXXXXXXXXXXCDXXXXXXXXTXCXXCXX
XSXXXXCPXGXTKXXXXXGXXXCRYXXXXXXXXLSXXGCXXXCXXXXXXXXCCXGXWGXX
CXECPGGXXXXCXXXGXCXXGXXXNGTCXCXXXXXGXACXXCXXXXXFGPXCXSVCXCXH
GICNXGXXGDGXCTCXXGYXGPXCDQXXXXCXXXXCXXNSXCXVSSVXXXQXXCXCLPXY
XXXGXXCXXXXPCXXXXCXXXAXCXXLGPNXXXCTCXXGYXGXGXVCXPIXPCXXXXGXC
PXXSTXCXYXXPGKXXCXCKXXFXXXXXXXRREXXCXSXXXXCXXXNXXXXXAXCXXXXX
GXXXCXCQXGXXGDGXXCYXXXXXXIXXXNXXXXXXXXXXXALAIFGKGCSLLLENYGPF
TVLVPTGSIFPPFHISPRIPVTPLHVPHMXXXXLLXXXXXXVFVLRDTKEMGEYAKSGIP
VFSIMVAALYIPPIVLXXXXXSXIXXXGXXXXXXXXYXXXXXXLIKKNXGGXWQXXLIXA
IXXFEXXXXXXLXXXGPXTVLVPXXKXXXXXNXKXXXXXXXXREITAXXXXKXHIXXGXX
XXXXXXXXXXXXTLXGXXXXXXXDGELYLIEPLKFPXXXXXXXXRXXDXXXXXXXIXXXX
XXAXNGIXHIXXXYEPXXXASQLXXXXXXXXXXXKXXXLXXLXXXXXXSRFXXILENXXX
XXXLDXXPGPXTVFXPXNXAXXXLXDGXLXYLXXSEGXXKLXELVXXHIXXXXDXXXVXX
AALIXXXXIXTMAXQXXXXXXXXXGXILXTAINFQGNIIGRAYTXXXXVXXXXXXIXAXN
GXIXTLXGXXIPPSIXPILPXXCXEXXXXXXXGXCXXCXXLXXXXCPXXSXXXAXXLSEE
LSFEFSDCSLNQYQXFPXDXXXCXYXXXPLGLXXXXXGCXXXCNXTXXXPXCCKGFFGXX

CXXCPGGFXNPCXGXGXCXDGXXGNGXCXCXXXFXGXXCXXCXXPNKXGXXCXXXCXCVX
GXCDNXXXXXGXCXXGSCKXGYXGXXCDXXXXXCXXXDXXXXXCXXXAXCXXXXTGXXXC
XCXXGYEGDGXXCXXXDXCXXXXXXXCXXNAXCXXTGPGTXXCXCXXGWTGXGXDCXXIX
NCXXXXXGGCHXNAXCXYIGPGQXXCXCKXGXXGXGYXCXPIXXCXXXNXXCHXLAVCQX
XXXGXXXCXCSXGYXGDGXXCYGNXMXELXXXXXXXXFXEWXXXXXXXTXXXXXXNXTXL
VPXXXAIQNXXXXEXXFWXXXXXXXXLXXXHXLXGXXTXXXLXXXXXXXGXXTXXXXXXX
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SXFXXXXXXYXLXXXIEXXXXYXXFXPXNXXIEXYXXXXXXXXLDXXXXXYHXXLGXKLL
XXDLXXGXXXXTMLGXSXXXXFXXXXXQXYXNXXXXXXXXVXTXXGXXXGXXXVXXIXKN
RCXXNXTXXXXXXCXXCXLXXXXCPXGXXXAXXPXKXXXXXXXXXXXXXXXXXGCXXXCXK
XXXXXXCCXGXYGXXCEXCPGXXGXXCXGNGXCXDGIXGXGXCXCXXGXXGXACEXCXXG
XYGXXCXXECXCXXGXCNXGXXGDGXCKXCXXGXXGVXCRXAXXEXXXDXCNXTCXXXAN
CXXXXXXXXXXCXCXAGXXGNGTXCXXIXXCXXXNGGCSXXAXCXXXXPGXRXCXCXXGY
XGDGXXCXEIXXCLEXNGGCXXNAECXXTGPXXXACNCXXXXXGDGXNXCXXXXPCXXNN
GGCXXXAXCXXTXXXXRXCXCXXXYXGDGFTCXGXXXXELXIXXXXXXXFXXXXXXXXXX
XXIXGXGPFTVFXPXXXXXXXXXXXXXWXXKGXXXXXLRYHIVXCXXLLXXDLXSXXXXT
XLXGXXXKXXXXXNXVXLNXXAKIXXSDIXXXNGVIHXIDKXLXPXXXQXXXXXXXXXXX
XXXXXXAXXXGYXXXXXLXXXXGLXXLXNXXLHQPXTIPCYFIDXXWPXDXXXXXLPXXP
XQXXLXXXXXXXKLXXYLKXHXIXXXKXXAXYQESXXLXXXXXLPTDATLEIKTLRSNDT
GIYRCEVIHGIEDSQDMVEVKVKGRDXTLXGSXXSXXCXXDXTXXGXXXXXXXXXXIXQR
PMHHPREGCXXXXDXFXXGIAYGXDXXLXXPXLGXRCDXMEVFXXXSAEXXPXXXXXXXC
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PXYXGDGXXCXXXXXXXXXXXXXVXXXXGXXXEXAXXXXXGXXXNFXXCECXXXXXGXXX
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GXXXXXXXTXXXXPXCXXXGXXXATEAXGXGFXXXPXXXCXXXXXGXXXXXXXXXXGXXX
XCXNXSXXXDXXCXXXXXXXXXXXXXXXXXXXGXXXXFXLXWXXFXEXXXACXXXXGAXXX
XVXXLYSXXXXXXXXXXXXIXNXDGSXYXXGXXXXXRXXXXXXXXXXGSXMXDXLXXYDX
XXCXXGSAXXXXRXTXXXXXXXXXXXXXFPXXXDXXTXXXXXXXXXXCXXXXXXXFXXXX
XVLXVXXXXXXXXXXXXSXDQXXXXXXLDXXEXXXXEIXXKXXDPTEEXXTXXXEGDKYG
RXXXXXXXQLSPSITXEXSNXXKXXXNXXXXXQVXEXFPXWWXXEEHKXXXXXTXXKDXS
XEXXXDXFXXDDXGXXDDGXDDDXXXEGSGXXAXKXTPNNXETVLEWXXSGDXEXXXSXX
XTTXVXXXKDXKXXXXXSAHXXXLXXVHSXXXXXVGXXXXXXGXXXXVXXXXDXXXXXXE
SPSXXSXXXXYSTNXTXXDVXPXIXPLXDDEXXXTXTAXXXXXDFXXXXXXXXXXXXXXS
XXXXXNXXTXXXXXXGXXXXXNXXSXKXXXXXXXLEXXXXRXXXXXXXIXXPXXXXXXXX
XXXXXXXAXXXXSXXXXXXXTXXXXXXXXXXXXXXXXXXXXXXXXSXXXKXXXXXXXXXI
XEEXXLXXXXXXHXXXXXXXSXXXEEXHXXXXSXXXTERTNQEYWTKXXXXSXXXSXXXX
TIXXXXXXXXVXXXXXXXXXXXXXXXXXXQXXXXXXFXXXXXXXXXXXWXXEXXXXXXXX
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XXXXXXXLHXXHSXXXXEEXXXTNTSXXXLLPGILHXXXXXXXXXXXXXGXXXXSXVXSX
XXGKXXXTTQXPHFYXXHPGXXXXXXXTXNXTXDXXXXXIHXXXXEXTXXXLXXEXKXEX
ETXSSQHSEEASEXXXTAVXXXXXXXXXEXSTXDXXXXEXXXXXHXEXXXXXXEXXXXXNX
SXXXXXPGIXXXXXXXHXXEXSHXXXXSSXDXKHEXATQSMENAXRDPXXHDIHXEXGRE
DXYXTNXTXDXXXXEXIPPXGXXXXXXXXHTXXIXXDXEDSXQXPLPPXHQPXWXXEEXX
PTLNTSRKGAETXXXXXPXXXXXXXXXXXXENEHXXXXSXXDXXXXXXKEDSTXEPXXXX
VXQWGXEDXYTTXXXXDVLXPGIVPRRGIXQKNXTDHTXVVXPIYILLXXXXXXXXXVXX
SXDGXKXEESTQXPXXHGLXPXXSXXXEPLVNXTXDYXXPGVFXEXXSXSXXRXXXSTXA
XXXXXXXXXXXXXXXXXXXCXXXXXXGEXXXXXPRXAXIPDWLIVVASLLALALILGVCI
AVNSRRRCGQKXKLXINNGKGGIXEKXKGGLNGEASXSXEMVHLVHXEKPEXQXFXXSXX
XXXXWXGLXDRGXXDEFXAIDETQLXYENWXXNQQXVALKSGXXCVXXXXXXXGXWXDXP

CXYXLPXXCKXXXXXCXXPPXVXXAXXXGXXKXXYXXXXXXRYXCXXGXXQXXXPXIXCX
XNGXWXXPXXXCXXXXXTEPGGTTVITAGSITTTNPARSGGNTRSSVQSWTGQRMAATTF
NLXPQWKHKL

==> Vertebrata.txt <==
>MSA Consensus of 6061 seqs, protein
MLAFRVVRGASEEPFILAGGNVQSIVQKEVYIIQVSVGSHQWTVKHRYSDFHDLHEKLVS
EKKIDKNLLPPKKIIGKNSKSLVEKREKELEVYLQMLLIKFPIAAPKLLSHFLHFHLYEI
NGITAALAEELFHRGEQLLMAXEVFSLRPLQLYAITQXLXQXXPTCANGDAKTDLGHILD
FTCRLKYLXVXXXXGPXXXXNIQEHLLPFDLSIFKSLHQIEXXHCXAXXIKGLTSSKHTL
TTMSVRFSATSMKEILVPEASEFDQWEPEGTLSSFPVTAVIPTWKTLTTLDMSHNRISQI
DDSVKLIPKIEFLELSHNDVSLIENVQHLYNLIHLDLSYNKLASLEGVHTKLGNIKTLNL
AGNXXXXXXGLXXXXXXXXXDLSSNKIXXXXXXXISTTEKELDTVEVLKAIQKAKEVKYK
LNNSDKKVPTSLLDLSKEYGRGHHICLDHSDEEHGAXSDXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXPSSSTXXXNKXXXXXXSSVTDTEDGYFEMXXXXXXFXFXXXXDI
APPALDSTRAESIDIVKXXXDXXXXVXXXXXXXFASCXXXXXXXXXXXXIXXXXXXXXQ
HIPAALKLAXXXXXXXXXXXXFHXXXXGXXXXXXXXXXXXXVVSDSQXXXXXXXXXXSC
SXXXXXXRXXXXXYNSXXXXXXXXXXXXXXXXSQSXXRKEVXXXXXXMXXXXXXXXXXXX
XYSNXTXXXXXXRXXXGXXXXXXXDXXXXXXXXXXXGXXXXXXXXXXXXXXLHXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXLTXXXXXXXXXKQSQXXXXXTXXXXDXXXXXXXXGXKXXXXXXXXXXXXXFXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXVXXXXXXXXXXXXXXTXXLSXPSXXXXX
XXXXXXXXPXXXXLXEXXXXXXSAKVVNXXXXXXXXXXXXXCXXXXEXXXGXXXXSAEDX
SXXXXXXXXXXXXXXXXXXXXXXXXXXXXGXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXRXXXXXXXSTXXXXXXXXXXXXXXXXXXXXXGX
XXPXXXXXXXXXXXXXXXXXXXXXXXXXSTKAIXFLLXXSVXHTNEHXXXXGXXXXXTCL
TXXXXXXXXXXHXXXXXXXXXXRTXSPXXVANXXXXLXDXXAGXGXXXXXSXXXXRXVPX
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PXXXXXXAXXLXXXXXLXXXXXXXXXXXXXLAXXXXXXXXXXXGQXXXXXXXXXXXXLWXXL
PXXXXXXLXXXXXXXXXXXXXXXXXXXXXXCXDXKXXXXXXXXXCXXXXXXXXXXXXXXXX
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XXXXGXXXXXXQXXXXXXSXXXXXXXXXXXXSTXXLSTLXXXXXXXXXXXXXXXXXXTXXXX
XXXXDXXCRYXXXXXXGXXXXXXXXGXXXXXXXXXGYTXXXXNXXXXXXGXXXXXXSXXXX
GCRCXXXXXXCEKDXKXXXXXXCCPGXXXXXWGXXXXXXXXXXXXCXECPGGXXXXXXHX
PCXHXXXGXCXXCVGXXXXXXXXXXXXRXXXPXYXXXXXXXGXVVLXXWXXXXAAPAKKXLX
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XXCXXXXXXXXXXXLXXXXXXXXXXSLHYWLPTLLALYTXXXXXXXXXXXXXXXXXXXXX
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XCSPLXXXXXXXXXXXXXXCXXGWXXXXXXXXXXXXXXXXXXXCXXXXXGXXCXXCXXX
PNKIXXXXXGXXXXXRXYGXXXQCXXXXXXXXXXXERXXXXXXXXXXYCXAXXPCXXKXXX
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QDALXXXXXLXXCPXXXXSTXCXYXXPGXSXCXXXXEIMLYLXXXXXXXWXXXXXCXXXX
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XRXXXGCXAXXXXCXXXXXXXXXCXXXXAXCXXXXXRXXXXXXXSLHIXXXXXXXGXXXX
CXCXXGXXGDGXXCYXXXXXXXXGXXXXXXXXXXLNXXXXXXSXPNXHITQXGXXXXXLX
XXXXLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGXXXXXXXXXXXXXXX
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XXXXXXXXXTXXXXXXXXXXPXXXXXXXXXXXXXAXXXAGXXKXXXXXXXXXXXXXXXGXX
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SMXXXXXXXXXXXXXXXXXXXCRSYVTXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXS
ELIKXXXXXXXXXXXLRXXXXXXXXGCXXXGXXXXXXXXXXXPXXXXXXVSXVXRXLXVX
XGFSXVXGXXVXXXXXXXTAXXXXXXXXXPXXXXXXXXXXXXXXMXAXLXXXGPFTVXXP
XXXXSAXXXXXXXXXXXXXXXXXXPXXXXXXXXXXXXXXXXXXXXEXXXXPXXXXXX
LXXXITXAXXXXXXXXXXXXXXDXXXRXXXXXXXXXXXXXXXXXXXXXXXXXPGXX
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GXXXXXXXXGXPXXXXXXFXXXEPEVAAXXXXXXGXXXXXXXXXXXXXXXXXXXXXXXX
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XIAGQXXXXXXXXXXXLPXXXXPXXXXXXXXXXXXXXXXXXXXXXXXXXXGXXXXXXX
XXXXTLXGXXXXXXXXXXXIXPXXXXSXXXXXXXXXXXXXXXXIXSXXPXXXXXXXXXX
XGXXXXXXXXSXXXXXXXXVXXXXXXXXXXXXXPXXXXXXXXXXXXXXXXXXXXXXXX
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XNXXXEXXXFSXXXXXXXXXXXGXIXXXXXXXXXXXXXXXXLLIPREICWXXSXXXXXXX
XXXLXGXXXXXDRTSENICTEQLHTXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XSXXXXXLXPPXIXXXPILPXNKPGXXXXXCXXXXXXXXXXGXPXCXXLGXVXXRGPLRA
KAVRNQAMLTVDTRNRAKXCXXRXXXXXXXXXXXXXXGDXXFQLKLQVVCPXXSXXXXXX
XXXXXXXXPXXXXXCXYXXXXXXXXXXXXXXGXXXXLXXXXXGCAXXXAIAXXXXXXXXX
GXAXXXXXXYXXMXXXXXCNXXTXXXXQSGXPSXPXXXXEQXVLSAXXXPXXPPXXXXXX
XXXXXXXGDVXKXNXXXXXXXXXXXXXCCXGFXGPDXXXXXXXXXCXXXXXXXXXXXCPG
GFXVXXXXXXXXXXXXXXXXXPCXGXGXXCXDGAAXXXXXXXXGNGXCXCXXXXXGXXC
XXCSXPXKXGXXCXSXXDXXXXXCXCXHGXCDNRXXSXGXCXXXXCXXGXXGXXXXXXX
XXXXXXXXXQXXXXXXXXXXXXXXXXXXXXXXXXXXVXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXNXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXVXCXXXXXXC
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXQXCHXXXXXXXXXXXXXHAXCXXXXXXXXXTXXLKRARDNVSTVYXXXXXX
XXEXXXXXXXXREKFVIRTGPHYXLXFXXXXXXCXMXXFXXXXXXXXXXXXXXXLXXXXS
GNLDLSSVGDGXXCTRCSRRMMLXXXXXXDQTVRXXXXXXLQLHHFAXAXXXXXXXLXXX
CXXXKEXSXGVRXXXXXXXXXXXXXXXXXDXXXFATCXXNXXXXXXXGVFHVEXXIDIXX
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XXXXXCXXGXXXXXVXVXSXXIXXSXXXXXXXXCXANXTXXYXXXXQXPXXXPXXXXGXX
XCXXXXXXXXXXXXXXXXXXCXXXXXXXXXXEXXXXXXXXXXXXXXXXKXGXXGALPEL
GXGXXCXXXXXXXEXXXXXDLRVYXXXNXTXXXXXVSXXXTXXYDXYCXNASXXPXCQXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXCXXXXXXXXXXXXXXXXXXXXXX
XXXXXXTXXXXXXXXXXXXXXXXXXXNGXXCHXLAXCXXXXXXXXXCTCPPGXGGDGFS
CYXXXXXXXXXXXNXXXXXXPXXXXXXXXXCXXXXXXGXXXXXXXXXXXXXXXXXSXCXX
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XXXXXXXXXXXXXXLXXXXXXXXXXXXXXXXXXXXXELXXXXXXXXXFXXXXXXXXXHXXXXX

XXXAXXXXXXXXXXXXXXXXXXXXXXXXXXEYRXXXXXXXXXXXXXXXXXXXLTNXE
DIXPSXXXXXXXXXXXXXXXXXXXXXXXXXXXTXXXXXXXXXSGSXXXXXXXXXEXS
XXXXXXXEXXXXIXXXXXXXTXXPXXDXDXXTXTXXPAAKXXXXXXXXXXNPXGXAXXXX
XXXXYXXXXXXXXXXXXXXXXXXXXXXXXXXXXXTPXSXXXXXXXXPXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXPXXXXXXXXKXXXESXXXXXXXKXXXXXXXXXXXXXXXXX
XXXXXXXXPXXXXXXXXXXXXXXXXXXXXXSXXXXXXXXXXHXLXXXDXXXLXXXXXX
XXXXXXXXXXTXXFXXXXXSNXXXXXXXXXXXXXXXXXXXXXXXXYEKKXXXXXXXXEX
XXXXXXXXXXYEDKXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXSXXXXX
EEXXXXXXXXXXXXXXXXXQXXXXXDXXXYXSXXXXGXXXXXXXXXXAXXXXXXXXXXXX
XSXSGXXXXDESLVEVSFRSTQNHXLRKGPIEHPGPXSXXFLXPPXXXXXIXXXXXXXXX
XXXXXXDXXATNGXXHXXXXVXVLXPXXRXLXXXRXXXXXTXXXXXXXXXXXHHDXXEXX
XXXXXXXPXXXXXDXPPXXXXXXXXXXXGXXXXXXXXXXXXXXXVXXXXXPXXXWXXXXXXV
WVQNAXXXXXXXXXXXXXXXXPPXXVXLPPRGDVXXXXXLLXXLXXXPXXEXXTRPDRIIP
XXXEXXXXXXPXXXXXXXFRXPXXSXXXXXXGXXXXXLKNXXXXXXXEXXXXXXXXXXXX
XXXXXTXQXXXXXXXXXWXXXXXXXXXXXTQXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXEGFTRDMQLXSXXXXXXXXXXDXXXXXXXXEXXXXXXX
XXXXXXXXXXVXXXXXXXXXXXXXXSXXXXQCXEGXXEXXXXXXXXXXXXXXXXSXXXXX
XXXXXXXXXXXXXXXXXXXEXXXXXXXFXXXXXXXXXXXXXDXXXXXXXXXXXXXXXXPX
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XXXXXXXXXXXXXXTXXXXXXXXXXXXXXXXVFXFPXXXXXLXXXIEXAXXXYTXXXFXP
XNXNFSPKVXXXXXXXXXGXXXXXXXEXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXPXXXXXXXPXXXXXXXXXXGERSXXXXXXXXXXXXXSQKXWXXXX
FXXSXSXXXXXTTTXXXXXXXXXXXXXXXXXXXTXXXXXXXXXSXNXISAGWXXPXEEN
XXXXXXXXXXXVXXXXXXXXGXXXXXXXDXXXSXSGSGXDDXXDXXXXFXXSTXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPXXSNPXXXLQTTTXMTXXXXXXXXXXDX
XXXXXXXXXXXXXXEXXXXXXXHXXXYXXXDXXLXEXLXXXXLXXGXXXSXXXXXXLGXX
SXXXXXXXXXRQPAAPMRXXXXFXXXXXXXXXXQXXXNXXXXXXXXXXXXXXXXXXXGXL
XXVLXXXXXRCXXXXXXXXXXXXXXXXXXXXXQXCXXXXXXXXXNPXXXXXXXXXXXCXX
XXXXXXXNXXXXXXXXXXXXXEXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXGXXXXCXXXXXXXXXXXXXXXXXLXXXQKLTGXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXGXXGXXTXXXXYLGKIXCXXXXXPGXXGXXCXGX
GXCXDXXXGXGXXXCXCXEGFXGTACEXCXXGXXXXXXXXXXXLKTKNSLQXNNXXYGX
XXXXXCXXXXXXXVXXXXXXXXXXXXXXXSXXEXXXEXAXXXXXXXXNXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXHXXXXXXXXXXYPXXXXXXXXXXXXXXXXXXXD
DQHPXEDXXXTXQXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGXCXXXXXXXXX
XXXXXGXXGXXXXXXXXXXXXXXXXSAXXXXXXXXNXXXXXXDDXXXXXDXHDDHXXXX
XXXXXXGXXXXXXXHDXXXXVXXXXGXXXXXHXXXVXXXXXXXXXXPWXXXXXXXXQXXX
XXXXXXXXXXPCXXXXXXXXXXXXRPLRQAKSWQATKKGKLVSVGGQTEEXPHFSSSNQDM
TDSVMLLILLPPKLQKVENVPATMAYVMMDCKXXXXXLXXXXXXXGXXCXXLXXMKQVXX
XXXXXXXXWXXXXXXXXXXXXXXIXXXXLXXXXXXXXXXXXXGXXXXCXXXXXFXXXXXQX
XXXXXXXXXXXXFREXXXXANXXXXXXXXXXXXXXXCXCXAGXXXXNGYXXXXXXXXXDSXX
XXPXXXXXXXXXXXXXXXXXXXXXXWXXKMLXCXXXXGGCSXXXXXXXXXXXXCXXWXXX
XXXXXXXXXXXXXAXXXXAXCXXXXXXXXXXGXRXCXCXXGYXGGDGXXCXNNPGPTXXX
DXXXXXXXXXXXXGGXXXXAECXXTGPXXXXXXXXXXXXXXXXXXXXXLLXKKQXXCANF
XXXLXXXXGXYLFXCXXXXXXXXXXRDXXXXXXXXXXXXXXXHXXXXXXXXXXXXXXXXX
XXXXXXCXXXXXXXXXXXCXVGWAGAXSXXXXXQPXXXXXXXXXXXXXXXXXXXYXXXXX
XXXXXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGXXXXXXXXXXXXX
XXXXXXLXXXXXXXXXFSKXXXXXXXXXXAXXXXXXXXPXXXXXXXXXXXXXXSXXXXXXXL
XDXGXXXCXXXNXXEDXXXXXXXXLXXEPXXXXXPXXGVVXXXXMXXEWSVWLGASTPIV
XXXXXKXXTESPWGXXSKPXXXXXXXCXXXXXXXXXXXXXXXXXXXXGTGDAXXXXXXXXX
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XXXTXPLXXTXXCXXQXXXXLXLAXXXXXXXXXXXXXXXXXXXXXXXLXXXXXXXXXXXXX
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XXXXXXXXXXXXXXXXXXXXXXXXXCPXXXXXXXXXXXXXPXXXXXXXXXXXXXXXXXS
XTXXXXXXXXXXXXXXXXDXXXXXHXXXXXXEXXTXXXXXXXXXXXXXXXXXXXXXXX
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XXXXDVXXXXXXXXXXXXXXXXXXXLXXGXXXXXXXXXXXXXXXXAAXXXXXXXXXNA
WXTGXXXXXXXXXXXXXXXXXPXXXXXXXXXPPXHXXXXXVXXXXXXXXXXXXXXXXX
XWXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXLXRGXXXXX
XXRXXXXXXXXXXXHXXXXXXXXXQXXXXXXXXXXXXXXXXXXXXXXXXXXDXXXXXXX
LXXXXXXXXXLXXXXXXXXXXXXXXXXXXXXXXXEEXXXXXNXXSNXXXXXXXXXXXX
XXPXXYXXVXXXXXXXXXXXXXXXXXXGXXXXXMXXXEXXXSXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXHKXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXD
XXSAFXKRKXXXXXXXXXXXXXXHASIPXXTXXXXXXSHVXXXXXXXXXXXXXXXXPXXX
XXMXXXXXRXXXXXXXXXXXXXXKXXXKXXXXXXXXXXXXXXXXXXXXXXGXXXGXXXX
GXXXXXXXXXXXXXGEXXXXXXXXLXDXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXQXXXXXXXXXXTXXXXXXXXXXXXXXXXXXXXXXXXQPKXRXXXXPSXEWLXXLXXXX
XXXXXRXXXXXLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGXXXXXLXXXVXXRRRE
XCGQKXXXXXXXXXVINXGGXGXXXXXAXVXXXXGYTNXXXXXLXXXXXXXXXKXSGLNG
EAXXSQEMVHLVNKXXXPXXLXXXQQAXNPACXXXXNXXXXKXXXPXXPXXXXXXXXXXX
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XXXXXLXXXXXXXXXXXXXXXXXXXXXXXDXXXXXRNVDMKIGXXPXXXXXXXXXXXXX
XPXXXXXXXXXXXXXPRXXCXXXXXXXXXXXXXXXXXXPXXXXXXXXLPXXXXXXPXXXX
XEVXXXXXXXXXXXXXXXXXYXXVXXXXXXXXXXXXXXXXXXXXXXXXXXXXYXXXXXXX
GXPXXXXXXXXXXXXXXXXXXXAXXXXXXXXXXXXXXXXXXXXXGXXXXXXCXXXXXX
XXXXXXXXXXXXXXXXEXGALLLSSSDADVSGHIAIXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXGXLXXXXXXXXXXXXXXXXXXXXXXXXXXTPX
XXXXXXXXXXXXHXXXXXXXXXIVQRXLXXXXXXXXXFXXGXXXGXXXXXXXXXXXXXXX
XPXXXXXXXXXXXXXSXXXXXTXNXXXXXXXXPXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXPXXXXXXXXXXXXXXXAYGIXSPEXLLXXPXXPXXXXXXXXXXXXEVPQXXXXXX
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XXXXXDXFXXXQXXXXXXSXXXCXXXXXXXGXXXXXXXEXXXXXXXNXXXXXXXXXXPGX
XXXXXXXXXXXXXXXXXXXXKXCSXCGXXXXXLXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXEXXXXXXXPXXXXXXXXXXXPXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPXGXXXXXXXVLQSXGX
XXXXXXXXXXGXXXXXXXXXXXXXXXLXXXXXXXXXLPXXXXXXXXXXXXXXXXXXXXX
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VVYPXXXXXXXXXXXXXXXXXXXQXPXXXXXXXXXXXXXXXXXXXXXAERERXXXXXXX
XXXXXXXXXVXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XEXXXXXLLVAXXXXXXXXXFXXTXXXXXXXXXXXXXXXXXXXXXLXXXXXGPNIQXX
XQXXXXXXXXXXXXXXXRXXXXXXXXXXXXXXXXXXXXXXXXXXXGXXXXCXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXSXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXPXXXXXXXXXPXXXXXXXXXHAXXXXXXXXXXCXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXEXXXXXXXXXXXLXXXXXX
XXXXXXXXXXPXXXXGCXXXXXXXXXXXXPXXQLXXXXXXXXXXXPXXXXXXXX
PXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPXXXXXXXXCXX
XXXXXXXXXPXXXPXXXXXXXXXXXXXXXPXXXXXXXXXXXXXXXXXXXXXXXXXVX
XPPXXXXXXXXXXXXXXXXXXXXXXXXPXXXXXXXXXXXXXXXXCCXXXXXXXXX
XXXXXXVXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPXX
XXPXXXXXXXXXXXXXXXXXXXXXXXXXXKXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXKXXXXXXXXXXXXXXXXXXXXPEXXXK
TXLXXXXXGXXGXXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXKXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX

WXXXGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXYXXXXXXXXXXXXXX
MSLXXXXXXXXXXXTXSXXXXXXXXXXXXXXXXTXXXXXXXXXXXXXXXXXAVXXXXACPG
GXHCCXXXGYDWLSSFXXXXXPCXXXXGXCXDXXXGXGXCXCXXXXXXXXXXXXGFXXXX
XISXXXXGXXCELCXPGXXXTAGXXPXXXXXXXXXXXXXXXXXTKSPXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGPXXXCXPXXXXXXXXXXXXXXXXXXL
XXXPXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXQXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXPXXXXXXXXXXXXXXPXXXXPXXXXXXXXAXXTXXXXX
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XXXXXXXXXXXXXXXXXXXXXXXXXXXXYXXXXXLPPXXXXXXXXXXPXXXXXXXXXXX
XXXXDXXXXXXXXXXXXXXXXXXLXXXXXXXXXXXXXXXXXPVCXXXXXXXXXXXXX
XXXXXXXXXXXXXXPXCXXXAXCKXXXNPSSXLXCXYRXXXLDESPAHRRAQFEHLEAQ
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XXCXXXXXXPXXXXMXXXDXXXXXXXXXLXXXXXANTXXXXXXXXXXXXXXXXXWXXFXGX
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HGLVQGXXEXXXXXXXXXXGVFXXXXXXXXXNKXXXXGXXXXXXXXAXXXCXXXXLIEG
TEGTRGGHGXXLAXXXXXXXQXXXXEQXFXXXXXXXXXQLXXXAQXXXXXXXXXXXXXXX
XXXXXXXXXXXRXXLXXXWXXQSGXLXLEXXXRXXTSXXHLLCXRHXXXXXXGXHLXXM
ASWXAXXDXXXXXCXXGWXSLXGXXXXXPXXXXLXXXSNVXXGXYXXXXFXVIPXXXXXX
XCGXXXVGXVXXXYGXRXXXXDXXXXXXXDXXXXXDEDKPCGDPPSFPHTALHGHTGXEM
GDEXLXXCSEXYXXGNQEAAFTLLCDTCGEXXGQVQACVKATLVVTLDNPKRPTXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXTIICRKTXXXXXXXXXXDVXIEXXXXXXXXXDXXC
XXXXDXXCXCXXTDXXXXXXXPXFPXXXIXXXAIHXXIXXGXVXXXXXYWHIRXXXGQRX
XXXXXXNAVFKRETQVXXXXXXXXXXXXXKXXXXXXXXXLLLDXXVSGXVLQLXSPXXXXX
XXXXXXXXXXXXXXXFXXFDGDXXXXXXXXXXXXXXXXTXXXXXXXXXXXXXXXXXXNXXXX
XXXWIGLNDXTVEXGXXXCXGXGLLXVLXWXXXXXXXXXXFXXXXXXPXXGXXXXXXXGG
GSLGSXXXXXXXXXXXXXXXXXXXGXXLXYXXXXXXGXLXXRXXXXXXFXXXLSXLEXDX
XXXXXXXXXXXXNSXXXXXXRXXXTLFVPXNXATGXXXNXTXXXXEDLCTVVLCHVAHEL
SCLVAMERGCTQQEGRGESXXXCVVXIXHEXLXXXDXPCXXHXSXXXXXXXXXXXXXXXX
EXXXXXXXXXXXGXXXXXXXGPXVXXALXXXXXXXXXXXXXXXXXAXXRYXCXXGXXXXX
XEXXXXXXCXXXXXXGFRXXSCGXXXXXXXXXXCXKXXXXXEAHIDXEXXXPXXRXXXXX
XXXXXXXXXXXXXXXXXXAXXXXXGDARKQDXXXSXSKXSEXXRXXXXXXEXXXXXXXXX
XXSEXGSXXPTXXPXSXLXXXXXXXXXAXEXFXXPXXEKXXXXXXXDXTKXQFXXGDNHX
GXKXXXXXXXXRTKMXYXXXXDXPXGXXXXXXXXXXXXNDXKAXXXXVXXXDXXXXXXXX
XXXXXXXSXXDXYPVTXXXXXXXEAXXEEXXEEEGDKXDGSXXXXXXXXXXGXEXXXXXT
XXQPXXVEVXKXXXXXXXPXEXXTXXXXXXXXXXXXXXXXXXEDAHXXXETXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXTXXXXXXTXXXXXXX
ESASPXHXXXXXXXXSXXXXXXXXXXXXXXXXXXXXXXXXXXXTXXPAEXTQPPPXXXXXXX
XTTXPXXXXXXXWXXXXXXEDIXAXNGEXXXXXXXIHXXXXPLXXXXXXPXXXXXXXXXX
XXXXXXXAPXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXYXCXXXXXXHTENKVXXXXXS
XIXXEDTEXXXXXXTXXPEEXXXXDSPXXXXFXXFXXXXXXXDXFSXXXXXXXXXXXXXG
GXXRXXXGXRXXXRDNXXXVXXPTALLVLAXXXXXXFFXXXXXXXXCYXKXCLSGTTKLC
QYFYFTIFFSXXXYXKXFTVGLVIFFTSISXXXXXXXXXXPFXNKNQQKEXXEXXVPAXX
NGXXAASXXSSXXXXXXXXXCXXXXXXXXXXXXXXXXNPXXXXXXXXXXXXXXXXXXXXX
XXXTPFXXSXXDXXVXXXXXXXXXLYKDXTSXXXEXXXXXXXXXXXXXXXXXXXXPXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XSCPHCWXXXXXXXAFXXXXXXXXXXXXXXXXXAXXXXXXXXXXXXXXXXXPXXXXXXX
XXXXXXXXXXXXXXPXXXXXXXLXXXXXSXXXXXXXXXXXXXXXXXXXXGXXXAQXXXXL
XLLILGXXXXCXXXXVTXXHXPXXPPPIXXXXXXXXYXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXRXTXXXXXXXXXXXXXVPXXLXXXXXXXXXXKXXXXXVCXXGXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXYXVRQSLLRHQAQHRTEGGAQEEVKAAESDGECGEEANDSKK
EDVQELGSSHSXPXXXRPKKKSLREEGEKKAXXXKQKKGRGKGXXXXXXXXXXXGXXXXG

XGXVGDXXXXXXXXXXXVYXXXXXXXXXESXLPXXXXXXXXXXXXSXXXXXCXXXXXXXXX
XXLXIXXXXGSGXXSVXXXVXIXXXQFNNQDYXPXVYXSLLX

==> Vespertilionidae.txt <==
>MSA Consensus of 113 seqs, protein
MXXXXXXXLLXLXXVCLAGSRLIGGQKAVGPVLYXNFXSPXDGXXXXXXRCDXKXXXVXX
XXCXXCPXXXXXXCPXGXXXXXXXXIGXXDCRYXXXXXXXXXXSXXGCXXXCXKDXXQXXC
CPGXWGXXCXECPGGAXXPCXGXGXCXXGXXXNGTCXCQEXFXGXACXXCXDXNXFGPXC
XXVCSCVHGVRCXXGXXGXGXCXCXXXYTGPHCDXXXPECXALXCPXNSXCSXXSEDETX
XXCXCLPXYXXXGXXCXCQLLDXXXPCXXXXCXPXAXCXXXXXXQXXCXCXEXYXGDGXV
CLPXDPCXXXXGXCPXXSTXCXYXGPGXXXCXCKXXXXXXXXXXXXXXXXXXCKSXXXCXR
XAXCXXXXXGXTXCXCXXXXVGDGXXCYGXXXXXXXXXXXXXXXXWQXXLXXXXXXLDXX
XXXXLXXXGPFTVLXPXXXXXXXXXXXELLMDXXXXQXXXXXHIIAGQXXXEXXXXXXQT
RRXXXTLXGXXXXXXXXXXXXXXXXKXKDXXXXXXXXXXXNXXAXNGXXHXXXXXXXXX
PXXXXDXXASQCPNACSFLQKTIGQXXXXXXXXSXFXXXLEXXGXXXXLDXDGVXGPXTV
FXPSNEAXXXXXDGXLXYLXXPXGXXKLXELVRYHIXXXXQLXVXXLISXXRXXTMANQX
XXXNXXXXGXILXXPEXVXXXXXDVXAXNGXIXXLXGXLXPPXIXPILPXXCXXXXXXXX
VGXCVXCXXXXXXSXCPXNSXXXXLXXXXCVYTXXXTGLXXLKXGCAXYCNXTXXXPXCC
KGFXGPXCXQCPGGFSNPCXGXGXCXDGXXGNGXCXCXXXXXGXXCXXCSXPNKXGXXCX
XXCXCXXGXCDNRXXSXGXCXXGTCXXGXXGRFCXXXTXXCGXXEQXQXCHXHAXCXXXX
GXAXCXCXXGXEGDGXXCXXXXPCXXXXXGGCSXNAECVXXXXGTHXCXCXXGWXGDGRX
CXXIDXCXLXXXGGCHXXAXCXYVGPGQSXCXCKXGFXGXGXXCXPIXXCXXXXGXCHXL
AXCQXXXGGXXXCXCXXGYXGDGFXCYGXXXXELXXXXXXXXFXQWXXXAXXXPMLXAXS
XXTYHXLVPSXXAITYXXXXXXXAXAFWLXXXXXPXLXXXHXLXGXXXXXXLXXMLXXXX
XXXXSXXGXXXXXXXXXGXXXXXXASXXXXDXXATNGVXHIHAMIXXXVLLPPRKDXPXX
XXLITYHALQQLDSVPAFXLFRELHALQXYXLVXXIEAAXAYTXFXPXNAMITYXXXEXX
HAMIRXXXXXXLXXDXXRXHVVLXEXLXXXXLXXGXHRXSXLGXXXXLXFXXMIXXXQXX
VNXXPXXXXXXXXXXXXXXGLXXVLXXXXXRCXXSHXXXLRXKCXXCXXXXXCXXGXXXX
VRLDWRIPFPCHLLSLPPALLAQDXXXXXCXYXXXXMGKRSXXXGCXXXCXKXIQMPSPL
PAFCFSLMSVLACAGLSLHPSVIXXXCCXGFFGXXCXPCPGXXXXVCXGXGXCXDXXXGX
GXCXCXEGFXGTACEXCXXGXYGXXCXXVCACXHGXCXXGXXGDGSCXCXVGWXGXRCDX
XIXXXXCXXXCXXXANCXXXXXAXXXXCXCAAGXXGNGTXCXGNXXXXCXXXNGGCSXXA
XCXXXXPGXRXCXCXXGYXGDGXXCXEXNXCLXXHGGCHXHAECXXTGPXQXXCXCXXXY
XGDGIRXCXLXXPCXXXNGGCSXXAXCXXTGXXXRTCTCXPXHXVGDGFTCRGXXXXELX
XXXXXSXXFFXLXXLXXXXAATXSIEVSDPDNSLSVSLXGXGPFTVFXGTSLTIPCYXXX
PXHPVTXXXXGATXXLPXXXXXXXLXRXXXXXRXGAXXXKEXXXLVXRYHVVXCXXLXXX
XLXXXXXVTXLXGXXLXIXXXXSXXXGXXXINXXAXXXSSDXXXXNGXXHXIDXVLXPXX
XLXXXXXXAXXXXXFXXXXXXXXXNXTXXXXXILIXXAXXXGYXXFSXLXXXAGLLXLXX
DXXHXPXTXXWPTDXALXALPXXXQXXLXXXDXXDKLXXXLXXHVARTIRXXXXXXXDLP
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XXXXXXXXXXHRAFGXXXXRXELXXXGXXXXSXXLRNXXXQXXXXXXXCXXXCXXXXWKP
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DGXSCXXRNPCEDXHRGGCXEHADCXXXGPXXXXCVCHAGYVGDGXXCXXEXEXXXXXXG
SLVLLWCAXWGLCPNLFDMKDXLXXXSXLAXXXXXXDLXVXXXXAGVFHXXXXXGXYXXX
XXEAXXXCXAXXXTLXXXXQXXXAXXXXGFXXACXXGXXXXGXVXXPXXXPXXXCXAXXX
GVXXLXLXPNQTGXXXXXXXXXDXYCXXXXXXXXXXCXXITNLTNAFDGXXSIXIVNRDG
TRYTXXXXXXTXXXXXXXXXXXXVXPGVAAVPXDINNTTXXEXDXXXXXXSERSTXEXXI
XXTXXXTXXPXXXXXXXXXXFVSXXXXXTXXXXTXXXXXXXGXXXXXXXXXXYCGXXXXX

XIHSGSGIDDDEDFXXXTXXXTXXVXDHXXXGTXLXXRXGXXLXXXXVSXXNXXXXXXXP
GXXXXXVSLQTTTRMTVYINXITTDVDRSGXXXXXXXWXXXAXXXXIHXXXXXXXXPXXX
XXXXXPXXXXXXXGXGXXXXXXXXLALLFFXXXAXXXXXXXXXKXXXXXXFXXXXXXXXX
XXXXXXXXEXXSXXXXXXXXPXXXXXXXTXXXEXXSXPXXXFXXXGLASGXEDXITXXXX
XLEXSXPXGXXILEGSASGXEDXGGXXSXPEXXGHQXXXLXXXXXGXXXXXEXXXXXXXT
EXRXDMDSSHSTTLQPSADSNTXLXGGXXXPXSXTXGEDXDRXXPXGXXXXEGXXXGDLP
XTTQQSSHTQXFSTSHGGXEEDXDQXMMSETTPTSSTSGNRDLSGLPSGGETHPESSTSX
XHLXXXDGGGGXLPEDXATSVXGYTPHSPDTKEYTTLIPVTPANTESPGVTEVTVXGDSN
VNVDGXLPEDLXXXPSGKEDXXGSXSEDXDXSXDPRXXXXXRXHTTXXSXXTASDGLPXG
FSGHXSGSQEGSGPSSGGXXTTSGPXMEPCVGDECPSLSRKPQIPEWLIILASLLALALI
LAVCIAVNSRRRCGQKKKLVIXNLPFGNXDXSXGAVEDRKPSGLNGEASKSQEMVHETSG
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SGXKIGXXDXSGETSGVPDLSGQXSXXPGXSXXPXGXPXLVSGXASGSGDASGVTFVDSX
FVEVTPTPFRXXEEGLGSVELSGLPSGETDLSGXSGMVDXSGQXSGAXGAXSGXXXXPPX
XXGXPXXXXXXSGEASGAEVGSXLPSGAYDGSGXPRGFPTVSLXDRXLVESVTQPPTXXE
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TSAFXXADLEGASGLGVSGXPSXFQEGPTEGSTPSGMSGEXXTTYDVATETSGWPSATPX
ASGDGXEXSGXPXXXXSGXXVXXGTSVXEFEWTQQXQRPAEAXLEXESSSPVHSGEEAXT
AXXXVXPTDXXSXPXXAEGXXGXXAXXXXXXXCXXSPCXNGXTCXXXXXXXXCLCLPXYX
GDXCXXXXXXCXXGWXXFQGXCYXHFXXRXSWXXAEXXCRXXXXHLXSIXTPEEQXFXNX
XXXXYQWIGLNDRXIEGDFXWSDGXXLXXXXXXPXQXXXXFXSGENCVVMVWHXXGXWXD
VXCNXHLXXTCKXGXXXXXXXPXXXXXQLFGRXXLRYEVDTVLRYRCLEGXAQRNQPLIR
CQENGRWEAPQISCVPXRPSRALXPXXALEGRQXRLLGRWTPPSXPVPAP

==> Vibrio.txt <==
>MSA Consensus of 180 seqs, protein
MAKDMXXXXXXXXXXXXXAVLFWLSLLLXFAAIVIAXXXXXXXXXXLXXXXXXXLXXXF
XXXXCXXXXXXQXXXFTXXXXXXXGXXXXXXXXXXXXXXXXYXLXGXXXXXVXXXXXXXXX
XXXXXQXXXXXFPXXXYLXXXXXXXXXXXXPXRXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXWXXXXXXXXXXXXWXXXXXLXXXXXXXXGLXXXXXXXXXXXXXT
XXXXXXXXXXXXXXXXXXNXXXXXXXXXXXGPYXXYAXXXDXXXXXRXXXXYXXXXXXXXX
IENAXGXXXXXXXXXXALXXXXXXXXPXXXXXXXATPKXXXXVXAXXXXPXXPAXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXLDPMN
KXLXXXXXNXXXNKIVMALGLSVSXXLXXCGGXSSSSSGTQXXFXXXXXXXXXCXXXXXX
EXXAXXXVVSXXXSXXXXXXXVXLAXXXXXXXAXXPXXXXXXGGSSSXSYSVTAIDGYLQ
XAXVWLDLNKDGTGNNXXXXXNFIWDXXXXXXGXXXXXSSXTSRXVXFXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXLXXXXXXXGXDRXXXXXXXXXXXXXXXXXXXXXXXSX
XXXXXXXXXIVXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXFXAQ
VXXXXXXDXXNKXFXFXXXXXXXXXXMFYKXXXXXXXXXXXXXAIXXXLVXSAXXGXXSNX
PXXXIYTXPXXXXXXVTAXPLXXXXXXVGXXHLTXXXXTLXXXXSXXXDXXLTVKVIDGY
IQNXEXXXXXXXAKVXXXXXXXXXXXXXXXKXXXWLERKDXVNYILEDXXDGEXXXTTXXX
GXXXLDXTXIDDXNXXXYXXXVKTXAXXGXXXDXDXGXXIAXDXXMXAXXGXXXXXXLXT
XVXXXXXXGVTXAXXXXXXXXAVXXVAXXLGXXXXXVXXXDYIXXQXXXXXXXXXXAXXL
VXSGXXPXXXEELASEADEEXXXXXXXXXXXXDSTXXTEXQTVXXXXXXAXXYXXXXXXX
VKXETKDHIXXXEQAQNIXAXXXXXXXXXXPXXXXXXXXXXXXXXXXKSAXXXXEXXNLL
VENAXXDXXXXXDPETXXXXXXXXXXXXXXDSDGDXXXXXXXXXXXPXDXXXXXXXXXPX
XGXXXXEWXDSDGDXXGDNXDTDDDNDGTLDXDDIXFPXXPXEXKDTDXDXXGXNADTDD
DNDGTLDXDDAFPXDPXETXDXDKDGXGXNXDTDDDNDGALDGDDAFPXXXXENXXDXDX
DGXGXNXDXXPXDPXESKDSDKDGVGDNSDXFPXDXXESKDSDKDGVGXNSDXFPXDAXE
SKDXDXDGXXDXXDXXPTXXDLNPIEQXXVIQFMQNNSXXXMFYALWADHEYNDATGTES
VEIXXXKXXXXXXXGTVTEAYQMLPDGRKVXDEPDANDEDDXXLGPXGWQTFNDXXXXXX

XXXVRXTXYAIAIXXDXXXVXPXXXXXXTNTALXXXSXVTXXYGYVXXXXXXXXXXXXXE
XXVGXXXXKDXXGXXXXXXSXELGDYXTAXXXAVVTTVDADAXFPXXAXXXXXXXXLXDX
XDXDGVGDNXDAFPXDXXESKDXDXDGXXXXXDXXXLWXXPXXXXXXXNXXXXGXNATNL
TEIQVAPADIADXDDDXDXXXDXEDNQFXXXAXXXXXXGDDVXXAKXXXXXXXXXXXXXX
XGXXXXXQFXXVXXXXXRDSKLXYSIXXXXXXXXXDWWNEXTQXXXTEXXXXXXXGLXXX
XXXXXXXXXXXXXXVPXSVVEAWGDVWDNDXXXXXSXXXXIXHGSGKHXXXXGYXXXVX
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VPTIQQXHDVXLNTPLVVDYTRIHKWNTDAESPTFNQXATTLFYXGKDILNVDGXLVEVC
XSGXXGXXIEXGKXXXXXXXXXDGSNXXXXVYXXELXTXNXTAXQNLVVKSERSYMXLYNS
EYXXXXXXXXXXGWXXXXXXXXGXTXXDFXXAXXXDXXLXXXXXXXXXXXXXNSSGETRV
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DTFXXXAYRAAXXGXXXXXXXXXXXXLTXGGXSXXLSXXXTPXGKFTSTFIGEQLVMGXX
XXLWAFGXEKDEXGXXXXXXXXXXXFNEFXXXXXXXXXXWXXXXXENYXXXXXXXXXXX
XXXXXXXXXXXXXXXYXNGIQFNVKGXXXXXXWXGNTIXXXXXXWXXNSDXXIXXGSXXT
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DGXDXXDXGXXTXDXXXXXXXXGGDXPDDXLVDWRXGXVMYSQTYAGKKTINYDVDGQQY
QAEVXXCNQQFSYSTDXXXXXXXXXXRXHLGQTAIEVGEDGXXXHTSXYFDEDXXXXXXX
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PITXXXXXXXXXVXRERXXXXWXXEXXXXSXXLXXAPIWYPVXXMTXSXXNNCAXXXXIG
ESXXXXXXXXXXXXKXXXLVDENRTSTLNHXXXAVKFTPXXXXXLFXYXXXXXSXHLXNV
XXEPXXXXXXANXXXXXXXXXXXXXXXXXXKXXXXXXXXFXXXFIDQXXXXXIXXXXXX
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VGGXXXWXXXXXXXLTSAXLXXXXXIXXXXXXDDQDTKFYFRIYGRNINGQXFXXTAXXX
XXXXGSHINXGKINFXXXXXGXXXXXXXXXXXXXXXXXXXDYIENEIVNSTNTXXXXXXX
XXPKNIXXXDXXXXWXGMYSTSTGSDTVDSSSEHEXXDXXXWNXXLHXXGSXXLXXGXXX
XXAVSENSGISLXXXXXGHYRLEVKQXXXXXXLHLRSSVXGTLCXVPNGELNYNLPNXXX
XXXXXSXXXXXXAGSSWVTPTGYTLDISGTTAEAYPITTSKVNYVEAEAFXXXXEXEFXX
XXXXXXTXWXXXXXXXEHXXXXFEYWXXXSXXXXDGKVPYRSLYTSSGGRXXXXXXXGXI
XXVDRYKIRGATLADGYDDXXXXDXXXXKXXXLSTTEPXXXXXYXXXLGXXXXXXXXFST
WRNMYTKEEHERYGFHTWNWTSTPKEDGTVPYRLTVNXTXDLTFGDGNYGLPATSLYTGS
GGAVIRGAVEKASPTSKYMVTFFNDVAYQSILDEVGTICDFTYTEGDSTYELLEFTGLLA
ACXXXH

==> Vibrionaceae.txt <==
>MSA Consensus of 194 seqs, protein
MXXXXXXXXXXXXXXXXXXXXXYFGSXXXLXXLXXXXMAGLSQXXDXXLXXXXXXGXTXF
XXXAXXXXIYVXGGSPSSXGSXAXXXVXXXDTXTQXWSSXXXMXXXNXNKXXXALXXSXX
XXLXXCGGXXSXXSXXXXXXXPXXXXXWXXXXXXXXXXXXWXXXGXLXXXLXXXXXXXXX
XPXXXXXXXXXXXKPXXXXXXXXXPXXXPXXXXXXYVTXXXXXXXXXXXXXXXXXXXCX
XXGXTLSFVTXGLCXXYAXXXGXXXXXXXXXXXXXXXXXXXXXXXXXVXXIDGYXXXXXG
XXXQNAXVWLXXXXXXXXGFTLSGQTTDTNVNXIXXXGEXXXTTXXXGXXXLDXTXXXXX
XXXIDXXXXYXXXXXXPXXXXXXAXXGXXXXDXDXXRFXXXXXXDXXXXXDXXXNDXGXX
IAXDXXMXAXXGEQDIXXXXTXXXXXXXLPPXPXAXXXAXXXTXXXXXXXTPLXTXVXXX
XRXGVXXXXLEXXXXSXXXXGXXYXXGXDXPXXXTLSXEVXLXYXXXXXXXXXXTQDXXXX
XXXXXXXXXEXXXXXXAVXXVAXXLGXXXXXXVXXDYIXXXXXEAKXXXXXXXXXXXXXX
XXAXSXXXXXAXXLVXSGTSKEXXPETXEELASEXXXQXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXSXDGXXXXXXTXXSTFXXXXXTVNXEXXQXXXXXXXXXXXYGVXXXXXXXXXX
XXXXXXXXXGXHXXXXAVXLXXLSDXGQXAIXXXGPNLSXDCPXCWYQALLXXTKDHIET
YXXGXMXXEREXXXALGYYLXXXDXDXXAXWXXIXGYXDYPXXXXYEQLLXDXEGXXXXX
XXXXXXXXXEELNLXDKVGTFDPXXXXXXDXDXEXXXXTFXXDSDGDGVANSQDWAPXXX
XEXXDXXXXRIXXXGXXXXGXXXDXXXXXAXXXAXFNXXXXXXYXXXXXXXXXXXXXXXX
XXXXXXXDXDXDNGEDDGXXAGYAEMXDDXXXXXXXXXXXXEXXDXDGDXIGDNADTDD

DNDGXLDXXXDXFPXXXXXXXXXXTCIXXGXLXXEXXDTDXDGIGNNADTAXVXXXVTXGX
GXXXXGXVVXAXXSXGTEXXLXXXSXVTXXXGXXXFXVXXDXXSVXXLEXAXXXXXXSEX
VXXXXXXXXDDHIVAVVTTLXXXXXXXKDPETNELXLVSTHDXDXDXXXGXXVSFSDXXD
AFPXDXXEXXDTDXDXXGXNXDDPYLTDDDNDGALDGDDXFPLXPXSEXXDTDKDXXGXN
ADXFPXDPSETKDXDXDGXXDXXDXXPXXXXXXXXXXXXEQVIQFMQXDXDGXGXNXXXFX
XDXXEXXXKALXXDXXXXXXXXXXTGXXSXXXAXXDXDNDXXXDXXDXXXXIYVEKFXXX
XXXXXXKDXXXXXXGXXXXXXXMLPDGRKVADEPDANDEDDIVXXXXXWXTFNDXXAIAI
NSDAXXXYPEEVPSLTNXLXXPXDXXESXDSXXXGXXXNSDXFPXDKSXTXXXXGXXXVX
DNXXXXXXXXAXESKDSDKDXXGLNXDXFPXDAKXESXDSDXDGVGDNSDAXXEDAXEXX
DXDXXXXGXXSDXXXXVXKVTXDXXXXXXXXFPXDAXTEXXDXXXXXXXXNXXXXXXXXE
XSXWDXXXXXDXXXXFPXXAXXESXDXXGXXXXXXGXXGIVKLXXTADVDXXQYFLEISX
XXXWFKPWFWRASGNTSDDGHNATNLTEIXVXXXXLSXXXXXXXXVRVIXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPXXXXETXXXXXXXXXXXXV
APADISQXXXYXXSDKDGXGDXXXXXXXISIGMXXIXHVGVQFVTDGTTRSSFMTLDWWN
ESTQAPGTVTINGTGTWSQVVVNGXTIIRYSVPDSVVEAWGDVWDNDSQXXXEXXXXXGX
XXXXXXLLAGFXXXGXXXDDXXGYLXXEXXQPLEALNXPNTLXXXXXSLPEXQFXTVXXD
EXGXRDXQLTAHNTSKLYSIXRXXXXGDXQQXTXQFSQTEILLGQQSGLPNGLLXXRTFX
VTQVTXXXXXXGGXXSXWXXXLTLXXXFXXXXCXXXPIAELEYTDXXSGXYYGXXXKXXX
DTYYRWWGFXPTXQQXXDVXXYSAFATSLVEXLNTPLXXXXXXXIHXXXXXXXXXWXXXX
EXXXXXXXADXXXXTFQAQIADCQLPVMDPEGAVLYRVNSSGETRVQAYAANNEALRFKN
GTPSTKYWMVNQEGTLEFGDDAQNIWDYKRAIMDVDEDGILSMATFDPETGEIXXXXYXX
XDXXXXXXXDGXXXXXCEELXSXXXXXXXXXXXXXFFSFVEDLPLEPXXXXDTYADALKG
CVDDXXXXAXXXXSEXXXXXXXXQLPRNLVVKSERSYMEYXXXXXXXQXXDEXXXXXXTX
YXXXXXRIGXSXXXXXXXXXXXXXGXXXXXXXXXGXXXXXXTDENIQFTWXXXXXXXXXE
HELNXGVNIISIEGXDXXXXXXXXXXYGXDXXLSRIXXXDAENGIIALGVPXGEXXTFXQ
XXXXXXXXXXXXVAXXXXXXTYXXXXXRFSNGIXEFXXXXXXXXXXEWXXXXTIXXXXXX
WXXXXXXXEXXQALIXXXXXXXXXFXXXXXXXXXWFXEXXXXXPXXXXXYXXXXXHXXXG
XXLXQNGDXXGXXGXXPXQPANSXXXXIXXXXXXXXXLXWSXXXXXXXXXIPNXKMNXXX
XXXALXXXXXXXXXXXXWXXXXXTYSQFSIHDPSTQYXRXXXLADDGSTXXXXXHLXXXX
XGSDXDXDXLVDWRXTSTPTEDGXVXYSQTYASXXXXGXKTINYDVXGXXYXXXVCXXXX
XXXXXXXQXXYXXXXXXXXXDGXXXXXXXXXXXXXXXXFXEXXXXXXXMTEWQRQXXXYDXX
XXXXXXXXXXXXXXXXXXXXVQRXXXXXXWXXXXWNXTSTNHXXXXXXXXSXXXXXXXXX
XLXVXXYXEDXXXXXIXXXXNASDFLXXXXXXXXXXXXXXXGXXXXXXXXXXNGXXXXXX
XXXXXNXXSXDGXXXXXXDYXPXXGXKXDGTXXPXXXDKTGSPDGXYTXXGXXXXPXXXT
KNTALYTLXXXXXXIXHXNGKLGSTTSATNADIVXXVSSSTDXHYFGKFLEDENQILTVD
TFAVNGSXXXSXXXXXXLXXXTDTAVXXXXXXXXXXXXFYLXXXGXXXXXSGTTADDFGT
GYXXXXXXXXXPIXXXXXXXXXXXXXXXXXXXXXXSXLXXXXLXQXXXXXXXXXGXDER
CFEXXXXXXXLXXXRLFQYYKXXXXXXXXYXXXXXXXXXXSFXXXXXXXXXXXXXXXXXX
XXXLDINDPXXSGDEVDEYVTQTSTXXRWLHMTLIVXRXQDRRVKTEHYMRXFXXXXXNI
XAXGVGGGXDWXVRGGWGHLSLKTDIFPQLVNDDPFWRASHINIGFHELMHGFGYSAHAH
GXTYGYANXLGDYIENEIVNSTNTFMTPXPXQVPXXXXXXANEXXKNIITFDRDFDWQDX
SARXXISDVNDTVTXCXDSMTSSVGAISASYPSAWNVYLHSQELESGELELFAVSENSGI
SLLQMNEGHYRLEVKQPMSDIQLHLRSSVDRNLASAVISFDDMFVPITTSKVNYVFPEFE
PDEFRQSDYSKXXXXXVKLADGTYSLTFWEARRYCXEHFKGYSLAGDGSIEQLEELHRVF
GXCXXXNLVSALVFHESYINNVKDPFDGSQLSFSKNKLSYLSTTEPQAWKAYTAELGDTF
VKSEINXTXDIITLTDIYVSINSSGEDIVSLYSKELKILTFGDGNYGLVCAKDHFN

==> Vibrionales.txt <==
>MSA Consensus of 194 seqs, protein
MXXXXXXXXXXXXXXXXXXXXYFGSXXXLXXLXXXXMAGLSQXXDXXLXXXXXXGXTXF
XXXAXXXXIYVXGGSPSSXGSXAXXXVXXXDTXTQXWSSXXXMXXXNXNKXXXALXXSXX
XXLXXCGGXXSXXSXXXXXXXPXXXXXWXXXXXXXXXXXXWXXXGXLXXXLXXXXXXXXX
XPXXXXXXXXXXXKPXXXXXXXXXPXXXPXXXXXXYVTXXXXXXXXXXXXXXXXXXXXCX

XXGXTLSFVTXGLCXXYAXXXGXXXXXXXXXXXXXXXXXXXXXXXXXVXXIDGYXXXXXG
XXXQNAXVWLXXXXXXXXGFTLSGQTTDTNVNXIXXXGEXXXTTXXXGXXXLDXTXXXXX
XXXIDXXXXYXXXXXXPXXXXXXAXXGXXXXDXDXXRFXXXXXXDXXXXXDXXXNDXGXX
IAXDXXMXAXXGEQDIXXXXTXXXXXXXLPPXPXAXXXAXXXTXXXXXXXTPLXTXVXXX
XRXGVXXXXLEXXXXSXXXXGXXYXXGXDXPXXXTLSXEVXLXYXXXXXXXXXXTQDXXXX
XXXXXXXXXEXXXXXXAVXXVAXXLGXXXXXXVXXDYIXXXXXEAKXXXXXXXXXXXXXX
XXAXSXXXXXAXXLVXSGTSKEXXPETXEELASEXXXQXXXXXXXXXXXXXXXXXXXXX
XXXXXXXSXDGXXXXXXTXXSTFXXXXXTVNXEXXQXXXXXXXXXXXYGVXXXXXXXXX
XXXXXXXXXGXHXXXXAVXLXXLSDXGQXAIXXXGPNLSXDCPXCWYQALLXXTKDHIET
YXXGXMXXEREXXXALGYYLXXXDXDXXAXWXXIXGYXDYPXXXXYEQLLXDXEGXXXXX
XXXXXXXXXEELNLXDKVGTFDPXXXXXXDXDXEXXXXTFXXDSDGDGVANSQDWAPXXX
XEXXDXXXXRIXXXGXXXXGXXXDXXXXXAXXXAXFNXXXXXXYXXXXXXXXXXXXXXXX
XXXXXXXDXDXDNGEDDGXXAGYAEMXDDXXXXXXXXXXXXXEXXDXDGDXIGDNADTDD
DNDGXLDXXXDXFPXXXXXXXXXTCIXXGXLXXEXXDTDXDGIGNNADTAXVXXXVTXGX
GXXXXGXVVXAXXSXGTEXXLXXXSXVTXXXGXXXFXVXXDXXSVXXLEXAXXXXXXSEX
VXXXXXXXXDDHIVAVVTTLXXXXXXXKDPETNELXLVSTHDXDXDXXXGXXVSFSDXXD
AFPXDXXEXXDTDXDXXGXNXDDPYLTDDDNDGALDGDDXFPLXPXSEXXDTDKDXXGXN
ADXFPXDPSETKDXDXDGXXDXXDXXPXXXXXXXXXXXXEQVIQFMQXDXDGXGXNXXXFX
XDXXEXXXKALXXDXXXXXXXXXXTGXXSXXXAXXDXDNDXXXDXXDXXXXIYVEKFXXX
XXXXXXKDXXXXXXGXXXXXXXMLPDGRKVADEPDANDEDDIVXXXXXWXTFNDXXAIAI
NSDAXXXYPEEVPSLTNXLXXPXDXXESXDSXXXGXXXNSDXFPXDKSXTXXXXGXXXVX
DNXXXXXXXXAXESKDSDKDXXGLNXDXFPXDAKXESXDSDXDGVGDNSDAXXEDAXEXX
DXDXXXXGXXSDXXXXVXKVTXDXXXXXXXXFPXDAXTEXXDXXXXXXXXNXXXXXXXXE
XSXWDXXXXXDXXXXFPXXAXXESXDXXGXXXXXXGXXGIVKLXXTADVDXXQYFLEISX
XXXWFKPWFWRASGNTSDDGHNATNLTEIXVXXXXLSXXXXXXXXVRVIXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPXXXXETXXXXXXXXXXXXV
APADISQXXXYXXSDKDGXGDXXXXXXXISIGMXXIXHVGVQFVTDGTTRSSFMTLDWWN
ESTQAPGTVTINGTGTWSQVVVNGXTIIRYSVPDSVVEAWGDVWDNDSQXXXEXXXXXGX
XXXXXXLLAGFXXXGXXXDDXXGYLXXEXXQPLEALNXPNTLXXXXXSLPEXQFXTVXXD
EXGXRDXQLTAHNTSKLYSIXRXXXXGDXQQXTXQFSQTEILLGQQSGLPNGLLXXRTFX
VTQVTXXXXXXGGXXSXWXXXLTLXXXFXXXXCXXXPIAELEYTDXXSGXYYGXXXKXXX
DTYYRWWGFXPTXQQXXDVXXYSAFATSLVEXLNTPLXXXXXXXIHXXXXXXXXXWXXXX
EXXXXXXXADXXXXTFQAQIADCQLPVMDPEGAVLYRVNSSGETRVQAYAANNEALRFKN
GTPSTKYWMVNQEGTLEFGDDAQNIWDYKRAIMDVDEDGILSMATFDPETGEIXXXXYXX
XDXXXXXXXDGXXXXXCEELXSXXXXXXXXXXXXXFFSFVEDLPLEPXXXXDTYADALKG
CVDDXXXXAXXXXSEXXXXXXXXQLPRNLVVKSERSYMEYXXXXXXXQXXDEXXXXXXTX
YXXXXXRIGXSXXXXXXXXXXXXXGXXXXXXXXXGXXXXXTDENIQFTWXXXXXXXXXE
HELNXGVNIISIEGXDXXXXXXXXXXYGXDXXLSRIXXXDAENGIIALGVPXGEXXTFXQ
XXXXXXXXXXXXVAXXXXXXTYXXXXXRFSNGIXEFXXXXXXXXXXEWXXXXTIXXXXXX
WXXXXXXXEXXQALIXXXXXXXXXFXXXXXXXXXWFXEXXXXXPXXXXXYXXXXXHXXXG
XXLXQNGDXXGXXGXXPXQPANSXXXXIXXXXXXXXXLXWSXXXXXXXXXIPNXKMNXXX
XXXALXXXXXXXXXXXXWXXXXXTYSQFSIHDPSTQYXRXXXLADDGSTXXXXXHLXXXX
XGSDXDXDXLVDWRXTSTPTEDGXVXYSQTYASXXXXGXKTINYDVXGXXYXXXVCXXXX
XXXXXXXQXXYXXXXXXXXXDGXXXXXXXXXXXXXXXFXEXXXXXXXMTEWQRQXXXYDXX
XXXXXXXXXXXXXXXXXXXXVQRXXXXXXWXXXXWNXTSTNHXXXXXXXXSXXXXXXXXX
XLXVXXYXEDXXXXXIXXXXNASDFLXXXXXXXXXXXXXXXGXXXXXXXXXXNGXXXXXX
XXXXXNXXSXDGXXXXXXDYXPXXGXKXDGTXXPXXXDKTGSPDGXYTXXGXXXXPXXXT
KNTALYTLXXXXXXIXHXNGKLGSTTSATNADIVXXVSSSTDXHYFGKFLEDENQILTVD
TFAVNGSXXXSXXXXXXLXXXTDTAVXXXXXXXXXXXXFYLXXXGXXXXXSGTTADDFGT
GYXXXXXXXXXPIXXXXXXXXXXXXXXXXXXXXXXXSXLXXXXLXQXXXXXXXXXGXDER
CFEXXXXXXXLXXXRLFQYYKXXXXXXXXYXXXXXXXXXSFXXXXXXXXXXXXXXXXXX
XXXLDINDPXXSGDEVDEYVTQTSTXXRWLHMTLIVXRXQDRRVKTEHYMRXFXXXXXNI
XAXGVGGGXDWXVRGGWGHLSLKTDIFPQLVNDDPFWRASHINIGFHELMHGFGYSAHAH
GXTYGYANXLGDYIENEIVNSTNTFMTPXPXQVPXXXXXXANEXXKNIITFDRDFDWQDX

SARXXISDVNDTVTXCXDSMTSSVGAISASYPSAWNVYLHSQELESGELELFAVSENSGI
SLLQMNEGHYRLEVKQPMSDIQLHLRSSVDRNLASAVISFDDMFVPITTSKVNYVFPEFE
PDEFRQSDYSKXXXXXVKLADGTYSLTFWEARRYCXEHFKGYSLAGDGSIEQLEELHRVF
GXCXXXNLVSALVFHESYINNVKDPFDGSQLSFSKNKLSYLSTTEPQAWKAYTAELGDTF
VKSEINXTXDIITLTDIYVSINSSGEDIVSLYSKELKILTFGDGNYGLVCAKDHFN

==> Viridiplantae.txt <==
>MSA Consensus of 118 seqs, protein
MVTDPSAEIKVGIDPKRTDPSAEIKVGIEPSTKFKVGMEPKQETXXNNDPSAEFKVGIYP
KGTNPSAEIKVGIDPSAEIKVGIDPKEDGVSEDLTLNQDEDEFDSKERXXVLHKYFXLKX
TQEXXXXXXXXXXXETDPSAEXXXXIDPXXXXPXXXXXXXXXXXXXKFRXXXXXYQEQGQL
TDPXXXXXXGIXWXGXXXYXESMISPLMNIIDRSRTIXXXXXSDEILEIIKPICIIIYSL
VTVXXXXAXXKXFPHQVXXXEXXVXXLEKCHLTSSGXXLXQESTXXXXXXXVXLXXXXIX
XLXXXXXSTVDTSIANNENXXTXXXXXXXXXXLVLXXXXXXXDYLATAXXXXXXXGLXXX
XXLTPXPXXPXXFTSFXXXXXXXXXSXXXPXXXXXXXXXXXGAVEAMAAIFKAGSRNXXX
GVIPIVWNDTSILYKSXTXXXXPXXXXXXXXXXXXXXXXPXXXHRXPXXRYXXRTTKLNV
SXXXXIXXXXXXXXXXGXXXXSNEVIDGAEXXXXXVXXXXXXXXXXXXXXXXXXXXXXXX
XXAAXXXXRITSXXXXSPXXXXXSXXXXLXXXXXXXXSXXXXXXXXXXXXXXXXXXPXPP
YXXPXXXPPXXXXXXXYXXXXXPXXXXSHVRDAAXXVXWXXGXXXPPXXXXYYXXXXXPX
XXXXPPYXYXSXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPLAIPLPXXXXXXRWFXXXX
XXXXXXXXHXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXYXXVAVXXXXXEGXXXXXXXXXXXXXXXXWXXXXXXXXXXXXXXXXQXX
XXPXYFAXXXXXXXXXXXXXXXXLXXXXXXXXXXXGXXXXXXXXXXXXXXQXSYAXXSXPXQ
XXXXXXXXXXEKXXXXXXXXXXXXXRSXXSXXXXXHXXXXXXXXXVXXXYATPXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXVHNXXXXXXXXXXXKKXWXQXAHXXVP
AXXXXXXXXXXXXXXVTAKYXXXLXXXXXXXXXXRIIQVXXXXXXXXXXXXXXXXXXXXQ
WXXXXLXFFLXXXCXXXXSPXXXXXALKASEVXXXXXXPSAIASAVRGXXXXCXXXXXXX
XXXXXXXXXXXXXXXLXXLXRXLWXXRADYARHRAALXXXXXXXXXXCXXGWXXXXXXXXX
XXKXPXXXXKXXXXXXXFXXMXXXXXXXXXXXXXXXXXXXXXADLADXXKSXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXEKEXXXXXXXXNXXYKKXSXXXXX
QXXXXXXXXYXXXXXXXXXXXXTXPLXXNXXXXXXXXXXXXXXXXXXXXXXXXXCXXXX
XXXXXXXXXXXXXXXXXXXXXXXSXXEXCXXXXXXXXXXXEYXXXXXXXXXXXXXXXXXX
XXXXXXXXXYVXXXXXXXXGXXXXXXXXXXXPXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXPXSXSXSRSYSSDRGRSYSPSYGRRGRSSXXXXXXXXXXXXXXXXXX
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XXXXXXKNDYYKKPPXXXXXXXXDYXXKPXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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XYXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXDXXXXXX
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XXXKKPXXPXXXYXKXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGXXXXXXXXXGXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXKXXXXXXXXXXXXXXXXXXXXVPKIYQIXXXXXX
XQXXXXKKXXXXXXXXXXXXEXXPXXXXXXXXXXEYXXXSLXXXXXXXXXXXPXXXSXXXX
XXXXXXXXXXPXXXXXXXXXFXPXXXXXXXXXXXXXXXXXXXXXXXXXNDYYKKPSXXXX
NYKKXXXXXXXXXXXXXXXXXXXYXXXXXLXXXXXXXXXXXXXXXXXXXXXXXXXXXIA
PEISTKLNRNYKLAPHXXXXXXXXXXXXXXXXXXXXXXGXRXXERERSXXXXXGPXXXXX
XXXXXXXXXYXXXXXXXXXSYSXXXXXXXXXKSXXXXXXXXXXXXXXXXXXXXXXYXXXX
XPXXXYYYXXPPPPXXXPXPXXXXKSPPPXXPXPXXXXXXXXXXXXXXXAYPXXPXXXXX
XPXXXYXXPXXPXXXPPPXXXYXXPPPXXXXXPXPXXXXXXPPPXXXPXPPXXXXXXXXP
PPXXXPPXXXXXXXXXQSXXGXXPPPXPXPPPXXXXXSPXXPXPXXXPXXXYXXPXYXXX
PXYSPXPXYXXXXXXXPXXXYXXPXXXYXXPXXXPXXXYXXXXKSHTYPRXXXXXXXXXX
XYXPXPXXEXXXSDNSYSKXXXXYXKXPXXXSXSPXXEXXXYXPXXXXXXXXXXXPXYX
XXSPPXXXXXPXPXXYXXXPXPPXPXPPPPXYXXSXXXPXXXPXPXYXXXXPSVPXXXXK
XXXXPXXXXXXXXPXYXXXXRLXXXXXXKXXXXLXXXXXXLXXXXXXSLPKXXXXAXXXX

XXXXXPPKNDCHKKPYVPXYXXKSXPPPXKDNYYKAPSVPKQVYEAPSLPKNDYYKKPYV
SEYNYNKVPSVPKNNYYKTPSVPKQVYEAPSLPKNDYYKKPYVPEYNYKKVSSLPKNNDY
KAPSVPKQVYEAPXLPKNDYXXXPXVYKXPXXXXPSXXXXXXYXXXPVPKQXXXXPXPXX
XXXYXXPXXYXXPSXXPXXXXXXKXXPPPSXXPXPPYXYKSPPPPSPSPPPPYXYKSPXX
PSXXXXXPXYXKSXXXYXXXXKXXXXXXKKPYXPXXXYXXXPXXXXPXXXPXPXYXXXXP
XXPXQVYEAPXXXXPXYXXXXXXXXXXXXKKXXSXXXXXYXXXPXXXXXXXXNXXYXPXXX
YXYXXXXXPXXSPPXPXYXXXPXXPXXXPXPXXXXXXXXPPXXXXXPXYXKKPCVXXXXP
XPXXXXPXXXXYXXXPXXKXVYTTLPKNDYHKKXXPPXYXYSXXXXPVKSPXXPXYYXXXP
PPPXXXXXXXXXYXXXSTXXXXXXXXXXYXXXXXXXXXXXXXGXXXQNNTKMSPPISNFS
PQELIEECXXXXXXXXXXXXXXXXSYQNNQSDTTEXXXGXXXXXXCXXXXXXGXXXLXYA
RKGGVXXXXXXXXXXXXXGXFXXXXXXXXXXXCREFKKRIKKTVTFPPPLTXXYXXXXXX
XKHPXXXXXXXLVLRAXXXXXCXXXLXSSXXXTCXXXXXXXXGXXGAXXXXXXEQDVEXX
XXXXXXYXXEAKVIEHENGDXLXXXXXAPXFXYXXXXXYXXCXKPKXXXXXXXYKXXXPP
XPXXXYKXPXXXPXXXVYKXPXXXXPXXXYXXPSYYKXPXXXXPXXXYKXPXXXXXXXXX
KXXXXXXPXXXYKXPXPXYXXXXXXPKXXYXXPXXXPXXYVYKXXXXXPXXYXXXXXXXX
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YYKSPPPDDKPXXXPXPPYYYKXPPXXXPXXXYPPXYXKSPPPPSPXPXPXYYYKSPPXX
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SPPPPSPSPPPPYYYKSPPPPSPSPPPPYYYKSPPPPSPSPPPPYYYKSPPPPSPSPPPP
YYYKSPPPPSPSPPPPYYYKSPPPPSPSPPPPYYYKSPPPPSPSPPPPYYYKSPPPPSPS
PPPPYYYKSPPPPSPSPPPPYYYKSPPPPSPSPPPPYYYKSPPPPSPSPPPPYYYKSPPP
PSPSPPPPYYYKSPPPPSPSPPPPYYYKSPPPPSPSPPPPYYYHSPPPPVKSPPPPYYYS
SPPPPXXSPPPPXYIYXSPPPPXHYPCQSSFSWATVIRDCPKKGRFLSQSPTKFLWGIGN
KGLYHAMKSLNHETADLRASMVAILHALVLAFSSRIGFIRETGQGISIKKQKPF

==> Whippomorpha.txt <==
>MSA Consensus of 213 seqs, protein
FCPGQRARQPPPAMAGXXXLXLXXLXLXXXXXXXXXXXXQXXRCDXKXXXXXXXXCXX
CXXXXXXXCPXGXXXXXXXXIGXXDCRYXXXXXXXXLSAAXXGCRHISSLSAVQATGAQT
AWTNIWPNGLLNGYLGLKKHFCRKDYLXPXLKYSNETIKRLKSASXECSKDVVQKACCPG
XWGXXEAAPAKKDLAEQPVKPALMTTYLDPAVQQDTCXECPGGAXXPCXXXGKLXCXDGX
XXNGXCXCQEXFXGXACXXCXDXNXFGPXCXXXCSCVHGVCXXGXXGDGXCXCXXGXTGP
XCDXXXPXCXALXCPXNSXCSXXXEDETKXXCXCXPXXXXXGXXCXXXXPCXXXXCXPXA
XCXXXXXXQXXCXCXEXYHGDGXVCLPXDPCXXNXGXCPXXSTXCXYXXPGQAXCXCXXX
XXXXXXXXXXXXXXXCEXXXXCXRXAXCXXXXXGXTXCXCXXGXVGDGXXCYGXXXXXXX
XXXXXXXXEWXXRLXXXXXXLDXXXXXXLSXXGPFTVLXPXXXXXKGFNVKEXXXNXXXA
QXXXXXHIIAGQXXXEXXGTXXTXXXXTLXGXXXXVXXXXXXXXXXXKXXXQXXXXXXIX
XXNXXAXNGXXHXXXXXXXXXXPXXXXXXXXTIXXXLASXXXXXXFXXXLEXXXXXXXLD
XDGIXGPXTVFXPSXEAXXXXXDGXLXYLXXSXGXXKLXELVRYHVXXXXQLXVXXLISX
XXXXXMANQXXXXNXXXXGXILXXPEXVXXXXXXVXAXNGXIXXLXGXLXPPXIXPILPX
XCXEXXXXXXXGXCVXCXXXXXSXCPXXSXXXXXXXXCVYXXXPTGXXXLKXGCAXYCN
XTXXXPXCCXGFXGPDCXQFLRYQSAAMASTGPTATXXQXASRIRCPGMGRGPKESFQAE
LNLSQRSRPGNESIWDGFSNPCXPDGQGPCGXGXCXDGXXGXGXCXCXXXXXGXXCXXCS
XPNKXGXXCXXXCXCXXGXCDNRXXSXGXCXXGTCXXGXXGRFCXXXTXXCGPXXQAQXC
HXHAXCXXXXXXAXCXCXXGXEGDGXXCXXXXPCSXXXRGGCSXNAECXXXXXGTHXCXC
HXGWXGDGRXCXXIXXCXLXXXGXCHXXAXCXYVGPGQXXCXCKXGFXGDGXXCXPXXXC
XXXXGXCHXLATCXXXXXTQPVSLLLLVSGVVFAKRATKEMAFSAMETLQWGXXXCXCXX
GYXGDGXXCYGXXXQEGITPLPRVEKIIQAIKHERNAWLWQHGDSSSLGIIHLXXXXXXX
IFXQWIXXAXXQPXLXAXSXXTXLVPSXXAIXXXXXXXXAFWLXXXXXPXLXXXHXLXGX
XXXXXLXXLXXXXXXXXSXQXXXXXXXXXXGXXXXXXASVXXXDXXATNGVXHXXXXVLX
PXRGXXXXXXXLLXXLDXXPXXXXFRXXXXXHXLXXXIEAAXXYTXFXPXNXXXEXXXRE
KXXXXLXXDVXXXHVXLXEXLXXXXLXXGXHRXXXLGXXXXLXFXXXXXQXXVNXXPXXX

XXXXXXXXXXXGLXXVLXXXXXRCXXXXXXXLRXKCXXCXXXXXCXXGXXXXXXXXKXCX
YXXXXMGKRSXXXGCXXXCXKXXXXXXCCXGXFGXXCXPCPGXXXXVCXGXGXCXDXXXG
XGXCXCXEGFXGTACEXCXXGXYGXXCXXXCXCXHGXCXXGVXXGDGSCXASRHDCXVGW
XGXXKQTYCDXLQXITXXXCXXXCXXXANCXXXXXXXXXCXCAAGXXGXXGXXCXXXXXC
XXXXGGCSXXAXCXXXXPGXRXCXCXXGYTGDGXXCXEXNXCLXXHGGCHXHAECXXTGP
XQXXCXCXXXYXGDGXRXCXLXXXCXXXNGGCSXXAXCXXTGXXXRXCTCXXXXGXXXVX
XXGDGFTCRXXXXXELXXXXXXSXXXXXLLEHXXXXLXGXGPFTXXXPXXXXXXXXQXX
XXXXPVTTAXXXXXXVXRYHVXXCXQLXXXXLXXXXXATXLXGXXXXXSXXXXXXXINXX
AXXXSSDXXXXNGXXHXIDXXLXPXXXLIPSDATLEIQNLXSNDSGXXXXXXDAXXXXXX
NXXXXXTXXAXXXGYXXFSXLXXXLLLCXXGLLXXXXDXXHXPXTXXWPXDXALQALPPX
XQXXLXXXDXXPVTDKLXXXXXXHVIRXXXXLAXDLPXXXXXXTXXGXXXSXXCXXXSXX
GELXXXXXXXRIXXXXXXXXXVQRXLXFXXGXAYGIDXLLXGPHXPXLGXRCDXFXTXXX
XLXXCXXCXXXPXCPXXXXHLEEAQXXGXXXXCXXXGFRVXXKFKGWTSPPLHSLALRSV
WARPSHWGQXXXXXXGCXXXCXXXXXXPXCCXGXXXXXCXACPGGXXXPCNXXGXCXDXX
SXXGXCXCXXXFXGXACELCXPGXFGPXCQXCXCXXHGXCLATTGRNQQXXGXXGRNRAK
ASGXCXCXXGWTGXXCXXQXXXXAXPXXXGXXLGVRTVYLXXXXXXLXXVCAXPPXCXXX
AXCXXXXXCECXLXYXGEGDGXTCTVVDXXLXXXXCXXXXXGGCXXXXXXXLXSGHESGS
XVVXAXCSQXXSXRSAAWATKGMGXXXXXXXXXXXXXXXXXXXGXTXSXRXKXXWTKVXCX
CXXXYXGDGXXXXSCXXXXPCXDGXXGGCXKYFSLGLPGAARGDSXXXXXXXXEHAXCXX
TGPXXMDTFWWLGXXXXCXCXXXYVGDGLXCXXEPXXXXXXCLVQXXXXXXXXGXXXCHX
DXXXAXIDLXXXXXXXXGVFHXXVSXXXGXYSXXXXEAXXXCXAXXXTLXXXXQXXAAXX
XXGXXXCXXGXXXXGXVXXPXXXPXXXCXXXXTGVSAGXXXXXSXGXXXYXXXXNXSCCE
XXDXTPLPYCXXXXXXXXXXDCXXVXDLPNXXXFXGXXTXXIVXDXXXVXRXGXLLLKYG
QXVLMSXXRYTKKGEXRTXPDDIXXXXTPEEDMSSGSIPRKRKLICITEAFMESSERSTS
TGGYNIFHTHLPTVYPXXDQDSPXVXSNPETXXXXYXNXXXRXXXXLXXLXDXXXEAEED
RGXGEASEASQEQNNWIWPSFGNSQPXTXXXLFXXXXXXXXXXXXXXXXXXXXXXXXDW
XXXXXXXXXFXXXXLXXXXGXXXXIXXXXXXXXXXAPXXXXXXXXXXXXXXXXXXXGXXT
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YSGSXSASEEPLPXSQXXXXXXXXXXXXXFXSXXISTTXXXXXXPSEPXXXPXQXXXXXX
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>MSA Consensus of 116 seqs, protein
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