A

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Babela_gene_124          ------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------
Babela_gene_300          ------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------
Babela_gene_562          MVLCKPELDKLTKILFGVFISFNFYLSSMETDNKIPNKKFQNLDNIFQYEVA-QQTG---GTCGYHALYNGLTLLKALEDPSKYKL-LTSNEDRGNYFGSIDSTW--TKEIIKKRIRTLAKYYIADHLFKSFKNIEIIS---KPEENAYKLNLSNNWVKLKQFYSD--L--KNIEEYRKKFINLIVDVSSDIAN---------------------RLIIFEK--
Babela_gene_16           MSLRNLRILNLSVSALCVF--FNLNLISMQQEQK-----FKNSKKIKQYRVL-NNGD--RSFSGYHALYNSFLLFKSRENKALKSL-LTSNENRDRFFGSIEAEW--QKNVIESRIKTLAEFYLEDNLIKNLRNADISQ---DSTANDYKFHLSNDYARINIAPDN--L--NY--EKIRLFLNKIPVIVRNIID---------------------EQYQSND--
Babela_gene_252          -----MHINKYKLTLPNLFLMLSFGLNAMELSKVKPA-------NITQIDVTSQNPQ--SGTCGYHALYNGIIIAKSLKKSSDLKF-FNKENFNKRLFKDLKRIW--KEQIVKQRVKFLLKQLIVDYLFKNIILDKEIVSQKPDSGGFYELNLSHEYVKLIPVEQIENC--TYSEEERKAICDIIVEVADNIIN---------------------KDFYYYD--
Babela_gene_417          MILNKSRISKLSKIIFSMFLGITLHGPSMQVCKENPQSIVY---DIRQCEVA-QQED--GSSCGYHAFYNALVISRSIKDKSLNNL-LHDREVINSFFGSSESEW--VKHVILKRAKTLAKYYITDHLLKSLKHMEILSNEIEIDQNCYKLNLSENYIRLKNFGNSSECILSYLDKKREMFCNVISNVAQSLADNIIEEANYSYNIKTTLSYLFGNVKSYFSDRSS
Babela_gene_217          MLLHNSKLNIVYRNIFFMFICVNFSILSMRVQQET----CSFQSKICQYKVL-QQED--ESSCGYHALYNGLTIAKSLKDPSFKDF-LESNVDRNNLFGSLDSTW--IKYIILQRIQLLAKYYITDYLFKNLKNIELIS---YASDNSYKLNLRNNWIKLIPLSHGL----NDLEKARREFCNLIVNISNELAN---------------------RLMHLEE--
Babela_gene_104          MFIYNSRIKNLKTNIFFMIIVSNFYSLSMRCEKQESQS-QKSQSKISQYKVL-QQED--GSSCGYHALYNAITIAKSLKNPSFKAF-LDTDIGRSNYFGSSNSKW--ERHIIEKRVNLLAQNYIRDCLLKKLKNIEILT--KKPDSDCYELNLSSLWVKLNINDLNAL-------ATIKAFGNMITNVSKIVVE---------------------SSIVEQE--
Babela_gene_102          MFIYNSRVKNLKTNIFFMLIVSNIYSLSMRCEKQELQS------KISQYKVI-QQED--GSSCGYHALYNGITIAKSLKNPSFKAF-LDTNIGRSNFFGSSDSKW--MKHIILSRIRLLARYYIIDTLFKSLKNIEVIS---QPQEHSYKLNLSNNWIKLKPLDRG--L--NDLESPRRDLCNLIVDVSNDLAN---------------------RLIDLKE--
OrigSeq                  MFIYNSRVKNLKTNIFFMLIVSNIYSLSMRCEKQELQS------KISQYKVI-QQED--GSSCGYHALYNGITIAKSLKNPSFKAF-LDTNIGRSNFFGSSDSKW--MKHIILSRIRLLARYYIIDTLFKSLKNIEVIS---QPQEHSYKLNLSNNWIKLKPLDRG--L--NDLESPRRDLCNLIVDVSNDLAN---------------------RLIDLKE--
Jnet                     -----HHHH--H--HHHHHHHHHHHHHH-HHHHHHHHH------HH---EEE-EE----------HHHH--HEEH--------HHH-H--------------HH--HHHHHHHHHHHHHHHHHHHHHHHHH--HHEE------------------EE------------------HHHHHHHHHHHHHHHH----------------------HHHHHHH--

HHpred based alignment of the most conserved blocks and catalytically relevant amino acids

  Q ss_pred                                                        hccccccccee-eehh hCCC  CCcchHHHHhhhhhhhh
  Q Babela_gene_25                                                  KVKPANITQI-DVTS QNPQ  SGTCGYHALYNGIIIAK
  Q Consensus                                                       k~~~qkI~Qy-~V~~ Qqed  ~sscGYHALYN~i~IaK
                                                                    ...+-.+... .|.  ||++  +..||+++++++-.++.

  T Consensus                                                       ~~~~~~~~~~~~~p- qQ~n  ~~dCGv~vl~~~~~~~~
  T PLN03189                                                        DKSPFKIVRPPNVP- QQPN  GYDCGVYVLKFMECLLE
  T ss_pred                                                         -TTTCEEEEECTS-- SSSS  SSCHHHHHHHHHHHHHC

Ulp1 protease family
YPL020C                  ---------------MSFAILTDLQKYVMEESKHTIG-EDFDLIHL--DCP--QQPN--GYDCGIYVCMNTLYGSADAPLDFDYKDAIRMRRFIAHLILTDALK------------------------------------------------------------------------------------------------------------------------
                         ---------------HHHHHHHHHHHHHHHHH      -   EEEEE--   --     --   HHHHHHHHHHHHHH         HHHHHHHHHHHHHHHHHHH     ------------------------------------------------------------------------------------------------------------------------
At3g06910                ---------------ILDALARYFVDEVRDKSEVDLDVSRWRQEFVQ-DLP--MQRN--GFDCGMFMVKYIDFYSRGLDLCFTQEQMPYFRARTAKEILQLKAE------------------------------------------------------------------------------------------------------------------------
7296280                  ---------------VLDALEKYLREESIFKPKKQFDTSDFVIESVQ-NIP--RQLD--GSDCGIFSCMFAEYITCDVPITFTQSEMLYFRKKMALEIVDGEL-------------------------------------------------------------------------------------------------------------------------
SPBC19G7.09              ---------------VFDL----LRDYYIAETKGAVDVSDWENFMDD-NSP--RQRN--GHDCGVFACKTAECVSRNVPVQFSQNDMPELRIKMAASIIDAQIY------------------------------------------------------------------------------------------------------------------------
ECU05g0760               ---------------VARRVSGYLRDEW----RRIHGKDPLISIRLKRKIP--LQRN--GKDCGVFVCMFGRYRLCGDREWLSSDDIPRFRKMMLHEIMSSRILYRTFHLFA----------------------------------------------------------------------------------------------------------------
Hs7657550                ---------------ACRILLQYLKQESIDKKRKEFDTNGWQLFSKKSQIP--QQMN--GSDCGMFACKYADCITKDRPINFTQQHMPYFRKRMVWEILHRKLL------------------------------------------------------------------------------------------------------------------------
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Continued

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Babela_gene_124          --------------------------------------------------------------------------------------------------------------------------------------------------------MFIISYP------GHWISCVVYKYKNS-PTNFIFVDS-LNIDRTKCKRSIEFTNIFLD
Babela_gene_300          --------------------MLDKTIKGIPFYQENRFYTKIRRVF-YINGHVENDNIIVCEPRHSLDTERCPLANYKIDWSNIS----------KKGQALESSKPGHWVSSKEIEYLINILLDKKRSSSSFLPENTKIFCLE----GDIQDLFNLEDN---LKQTAIEFKD-NAYEGTTIFILYYP------QHWVTCVVDKKKNE-RPRFIFADS-LNIDRTKSDQAFQLIGALSN
Babela_gene_562          --DQATCRVDKQDFINIFKLFYKSQNFDKI---------------YEVIDFSSINFEIISDNKIKNLNKPN---EVYVINWQDISNQDRVKFYVNDRQEVSNEANAGEWLTSEEIEFLIET---------DKKLKHTNIFCIDTLKENEIKELFLLNAS---LKQLVIDFKS-KDYSGTAIFLLYFP------KHWITCVLTKDKDS-LPNFILMDSYYNKNRTCSKKIFNLIKQIYN
Babela_gene_16           QQDKVNFDITAEIIKSAFLSEYEETGLEVT--A--REVELIFLELF-QDEGFNLEFEVISDSQIKDARK-Q---ELYNINWTAQSGEEFVKRF--NLKTKATVEKPGHWLNAQDLDNLIKLEKDR----AIEIPEDMPVFCLD----KDIRELFNLDQ----LKNLAREFRD-INYSGSAIFLIYIKEK----RHWISCFVVKDSDE-TPKFLFTDS-LNNDRLKTDLILTLISLLSE
Babela_gene_252          ETDICRFYENSYGIFKVFKEIMLNKTIKGIPFYQNNRFYTKIRRFF-YIDCHVKKDNIINCEPLDSADTERCPLSNYKIDWSDIS----------KKGQALESSKPGHWVSSKEIEYLINILLDKKRSSSSFLPENTKIFCLE----GDIQDLFNLEDN---LKQTALEFKD-NDYEGTAIFILYYP------QHWVTCVVDKKKNE-HPRFIFADS-LNIDRTKSDQAFELIGELSD
Babela_gene_417          RFPKYFYDVKSDSIAEAFKIEFIRRGMSEE---DACKMITRISKYV--IEFTDVCFEIIADYQIKDLKTNE----TYVIDWVHRTDKDFIKLH--DINHMSSVENTGHWLSSEEIDSIMQLEKEK----KSDFSQDINVYCLE----RDIEQLFECDNN---LMEARSNFKD-KNYEGTSAFLIYSDSE----KHWFTCVVTKNNGEDFPKFIFADS-LGKNRIESRESLEFIRLLLL
Babela_gene_217          --NSAIYNIKKEDIKDVLKSQYLSKKYNKV-----NKRLSNVEKYF--IDLTDLSFEVIADGQIKNLDKDE----FYIINWSSNVGKNFARFY--KEEQNCSLLQAGHWLSSQEIESLIQLES------GDSNLDQIEILCLE----RDLKQLFDQTSGEERLINIQRKFQD-KNFSGAAIFLIYNS------VHWISCVVTKDINE-SLKFIFADS-LGCNYKSYKNANTLIKLLAG
Babela_gene_104          --DKRICRISSEYLREIFRQECIRRNIKI------DNFDELFLEIFNFTEPFDLEFEIVSDSKIVDLNNGG----IYTVNWMTSSDKRFNKVD--SENQIFTTINPGHWLSSQELESLVDL--EK----EDTELIGLEIFCLD----RDIEQLFNQNTGEELLINTQRNFQD-INYSGTAVFLIYDS------RHWITCVITKDAGE-YANFIFADS-LGNNYKSYVRARTLIRLLTN
Babela_gene_102          --EKSLYKIKIEDMIEAFKAQYLAKKYKKI-----NKLISRAIEHF--IDLPNLYFEIVGDLLIKNNDKNE----FYVVDWSNTSKRDFTKLD--ESHQNLTSLQNGHWLSSQEIESLIELEK------EDITLSDINIFCIE----RDLEQLFDEDSGQEELKNLQRNFQD-IDYSGTAIFLIYNS------MHWVTCVVTKNSNQ-SANFIFADS-LGRDFKSYSNLKTLIRLLIN
OrigSeq                  --EKSLYKIKIEDMIEAFKAQYLAKKYKKI-----NKLISRAIEHF--IDLPNLYFEIVGDLLIKNNDKNE----FYVVDWSNTSKRDFTKLD--ESHQNLTSLQNGHWLSSQEIESLIELEK------EDITLSDINIFCIE----RDLEQLFDEDSGQEELKNLQRNFQD-IDYSGTAIFLIYNS------MHWVTCVVTKNSNQ-SANFIFADS-LGRDFKSYSNLKTLIRLLIN
Jnet                     -------EEEHHHHHHHHHHHHHHHHHHHHHH-----HHHHHHHHHHH--H----HHHHHHHHHHH----------EEEEE----------------------------HHHHHHHHHH----------------EEEEEH----HHHHHHH-----HHHHHHHHH----------EEEEE----------EEEEEEE---------EEEE-------------HHHHHHHHH-

HHpred based alignment of the most conserved blocks and catalytically relevant amino acids

  Q ss_pred                                                                                                                                          --hhccccCCCccccHHHHHHHHHHHhhhccccccccccCeeEEec----hhHHHHhhhcc---HHHHHHHhhhcc--CCCceEEEEEEcc-----CceEEEEEEcCCCC-CcceEeecc-cCcchHhHHHHHHHHHHh
  Q Babela_gene_25                                                                                                                                270 --QALESSKPGHWVSSKEIEYLINILLDKKRSSSSFLPENTKIFCLE----GDIQDLFNLED---NLKQTALEFKDN--DYEGTAIFILYYP-----QHWVTCVVDKKKNE-HPRFIFADS-LNIDRTKSDQAFELIGEL
  Q Consensus                                                                                                                                     270 --q~~t~~~pGHWlSSqEiesLi~Lekdk~~~~~~~~~~~~~IfCLe----rDi~qLFn~d~----L~n~~r~F~D---nYsGtAiFLIY~~~~~~~HWiTCvVtK~~~E~pkFIFADS-Lg~dr~~~~~a~tLI~lL
                                                                                                                                                     --+.+..++||+||+.+=|+.-|++..++    ....|.. .++.+.------=.-.-...+.   |....+|=++-.  +|.=...=+|+.|    - .||.-+||..... -  .|.+-||-||-....  -+..|-+.|

  T Consensus                                                                                                                                     293 --~DL~~L~Pg~WLNDeVINfYm~LL~er---~~~~p~~~~k~h~FN----TFFytkL~~~~~~ygY~~VrRWTk~kKigv~Lfs~D~IFIPIh~~n~HWsLaVId~k~k----~I~yyDS-Lgg~~~~~-vL~~L~rYL
  T PLN03189                                                                                                                                      293 --EILRCLKPGAWLNDEVINLYLELLKER---EAREPKKFLKCHFFN----TFFYKKLVSGKSGYDYKAVRRWTTQKKLGYHLIDCDKIFVPIHQ-EIHWTLAVINKKDQ----KFQYLDS-LKGRDPK--ILDALAKYY
  T ss_pred                                                                                                                                          --HHhhccCCCCccCHHHHHHHHHHHHHh---hhcCcccccceEEEe----hHHHHHHhhcCCcCChHHHHHHhhhcccccccccCceEEeeeec-CCeeEEEEEEcCCC----eEEEEeC-CCCCCHH--HHHHHHHHH

Ulp1 protease family
YPL020C                  ------------------------------------------------------------GSLVPELNEKDDDQVQKALASRENTQLMNRDNIEITVRDFKTLAPRRWLNDTIIEFFMKYIEKST----------PNTVAFN----SFFYTNLSERG----YQGVRRWM--KRKKTQIDKLDKIFTPINLNQSHWALGIIDLKKK----TIGYVDS-LSNGPNA--MSFAILTDLQK
                         ------------------------------------------------------------        HHHHHHHHHHH      EEEEE  EEEEHHHH           BHHHHHHHHHHHHHHH ----------  EEE  ---- HHHHHHHHH ----          --            EEEEEEEE   EEEEEEEE    ----EEEEE  -       H--HHHHHHHHHHH
At3g06910                ------------------------------------------------------------------------------------------NSNIDITGKILRCLKPGKWLNDEVINLYMVLLKEREAREPKK---FLKCHFFN----TFFFTKLVNSATGYNYGAVRRWTSMKRLGYHLKDCDKIFIPIHM-NIHWTLAVINIKDQ----KFQYLDS-FKGREPK--ILDALARYFVD
7296280                  ------------------------------------------------------------------------------------------KFNLHITTEDICTFINGKWLNDEVINFYMSLLTERSEKRSGV---LPATYAIN----TFFVPRLLQAG----HAGIKRWT--RK--VDLFSKDIIPVPVHCNGVHWCMAIIHLRNK----TIRYYDS-KGKPNRP--VLDALEKYLRE
SPBC19G7.09              ------------------------------------------------------------------------------------------KFNIPITLKDLHTLRNRQWLNDEVINFYMNLISERSKIDSS----LPRVHGFN----TFFYTSLQRRG----YAGVRRWA--KKARVNIADMDAVFIPVHL-DVHWCMAVINKSKK----RFEYWDS-LAGSPGK--VFDL----LRD
ECU05g0760               ------------------------------------------------------------------------------------------------DIRRMRDGSLLNDKIINVYFELLAKHSK---------ATVYVFS----TFFYTTLSRRG----VEWVQRWT--SG--INIFENRLIYIPVHI-PGHWMLMVFDVREM----VLEHYDS-MGNVYRD--VARRVSGYLRD
Hs7657550                ------------------------------------------------------------------------------------------AFRLTITRKDIQTLNHLNWLNDEIINFYMNMLMERSK-EKG----LPSVHAFN----TFFFTKLKTAG----YQAVKRWT--KK--VDVFSVDILLVPIHL-GVHWCLAVVDFRKK----NITYYDS-MGGINNE--ACRILLQYLKQ
```

B

HHpred output for Babela_gene_300

```
   No Hit                             Prob E-value P-value  Score    SS Cols Query HMM  Template HMM

1 PLN03189 Protease specific for  91.2     2.1 4.4E-05   45.4  10.9  113  270-391   293-415 (490)
2 COG5160 ULP1 Protease, Ulp1 fa  90.2     1.1 2.4E-05   47.9   8.1   99  269-389   385-496 (578)
3 PF02902 Peptidase_C48:  Ulp1 p  89.4     5.6 0.00012   34.3  10.4  102  280-391     2-135 (216)
4 PF02902 Peptidase_C48:  Ulp1 p  75.1     2.1 4.4E-05   36.9   2.0   34   28-62    148-182 (216)


>PLN03189 Protease specific for SMALL UBIQUITIN-RELATED MODIFIER (SUMO); Provisional
  Probab=91.18  E-value=2.1  Score=45.40  Aligned_cols=113  Identities=20%  Similarity=0.317  Sum_probs=0.0

  Q ss_pred                hhccccCCCccccHHHHHHHHHHHhhhccccccccccc-CeeEEechhHHHHhhhcc---HHHHHHHhhhcc--CCCceE
  Q Babela_gene_25   270 QALESSKPGHWVSSKEIEYLINILLDKKRSSSSFLPEN-TKIFCLEGDIQDLFNLED---NLKQTALEFKDN--DYEGTA  343 (393)
  Q Consensus        270 q~~t~~~pGHWlSSqEiesLi~Lekdk~~~~~~~~~~~~~IfCLerDi~qLFn~d~----L~n~~r~F~D~--nYsGtA  343 (393)
                           +.+..++||+||+.+=|+.-|++..++    ....|.. .++.+.--=.-.-...+.   |....+|=++-.  +|.=..
  T Consensus        293 ~DL~~L~Pg~WLNDeVINfYm~LL~er-----~~~~p~~~~k~h~FNTFFytkL~~~~~~ygY~~VrRWTk~kKigv~Lfs  368 (490)
  T PLN03189         293 EILRCLKPGAWLNDEVINLYLELLKER----EAREPKKFLKCHFFNTFFYKKLVSGKSGYDYKAVRRWTTQKKLGYHLID  368 (490)
  T ss_pred                HHhhccCCCCccCHHHHHHHHHHHHHh----hhcCcccccceEEEehHHHHHHhhcCCcCChHHHHHHhhhcccccccc


  Q ss_pred                EEEEEcc----CceEEEEEEEcCCCCCcceEeeccccCcchHhHHHHHHHHHHh
  Q Babela_gene_25   344 IFILYYP----QHWVTCVVDKKKNEHPRFIFADSLNIDRTKSDQAFELIGEL  391 (393)
  Q Consensus        344 iFLIY~~~~~~~HWiTCvVtK~~~E~pkFIFADSLg~dr~~~~~a~tLI~lL  391 (393)
                           .=+|+.|    .||.-+||.....   .|.+-||||-....  -+..|-+.|
  T Consensus        369 ~D~IFIPIh~n~HWsLaVId~k~k---~I~yyDSLgg~~~~~-vL~~L~rYL  415 (490)
  T PLN03189         369 CDKIFVPIHQEIHWTLAVINKKDQ---KFQYLDSLKGRDPK--ILDALAKYY  415 (490)
  T ss_pred                CceEEeeeecCCeeEEEEEEcCCC---eEEEEeCCCCCCHH--HHHHHHHHH

>COG5160 ULP1 Protease, Ulp1 family [Posttranslational modification, protein turnover, chaperones]
  Probab=90.24  E-value=1.1  Score=47.95  Aligned_cols=99  Identities=24%  Similarity=0.496  Sum_probs=0.0

  Q ss_pred                chhccccCCCccccHHHHHHHHHHHhhhccccccccccCeeEE------echhHHHHhhhccHHHHHHHhhhccCCCce
  Q Babela_gene_25   269 GQALESSKPGHWVSSKEIEYLINILLDKKRSSSSFLPENTKIFC------LEGDIQDLFNLEDNLKQTALEFKDNDYEGT  342 (393)
  Q Consensus        269 ~q~~t~~~pGHWlSSqEiesLi~Lekdk~~~~~~~~~~~~~IfC------LerDi~qLFn~d~~L~n~~r~F~D~nYsGt  342 (393)
                           +|-+..+.+|-||+..=|+--|++.  ++++......+++-+|-      |-        ..|-...+|==+     ||
  T Consensus        385 ~~D~~~L~~~~wLNDtIIdFy~k~l--s~~sk~~s~~~~vh~FnTFFYT~Ls---------rrGy~gVrrW~k-----k~  448 (578)
  T COG5160         385 NQDFKRLRNGDWLNDTIIDFYMKLL--SKISKNTSKREQVHLFNTFFYTKLS---------RRGYSGVRRWTK-----KT  448 (578)
  T ss_pred                hHhhhhcccchhhHHHHHHHHHH--HHhccCcccccceEEeehhhHHHHH---------HHHhHHHHHHHh-----cc


  Q ss_pred                EEE---EEEcc----CceEEEEEEEcCCCCCcceEeeccccCcchHhHHHHHHHHH
  Q Babela_gene_25   343 AIF---ILYYP----QHWVTCVVDKKKNEHPRFIFADSLNIDRTKSDQAFELIG  389 (393)
  Q Consensus        343 AiF---LIY~~~~~~~HWiTCvVtK~~~E~pkFIFADSLg~dr~~~~~a~tLI~  389 (393)
                           -||   .||.|    -||..||++   +-.+++..-|||++-+   +-++++.+
  T Consensus        449 dif~~k~I~iPIni~~HW~l~II~~~~~~~~~~~i~~~DSLan~~~~~~~~v~~~~L~  496 (578)
  T COG5160         449 DIFSKKYIFIPINISYHWFLAIID---NPKKNILYFDSLANTH---DPVLEFLR  496 (578)
  T ss_pred                CccccceEEEEecccceEEEEEee---cCcceEEeccccCc---HHHHHHHH
```

```
>PF02902 Peptidase_C48:  Ulp1 protease family, C-terminal catalytic domain
  Probab=89.42  E-value=5.6  Score=34.25  Aligned_cols=102  Identities=19%  Similarity=0.289  Sum_probs=0.0

  Q ss_pred                cccHHHHHHHHHHHHhhhccccccccccCeeEEechhHHHHhh--------------------hccHHHHHHH-------
  Q Babela_gene_25   280 WVSSKEIEYLINILLDKKRSSSSFLPENTKIFCLEGDIQDLFN--------------------LEDNLKQTAL-------  332 (393)
  Q Consensus        280 WlSSqEiesLi~Lekdk~~~~~~~~~~~~~IfCLerDi~qLFn---------------------d~~L~n~~r-------  332 (393)
                           ||+++-|+..+++..++..+   .....-.+.-++--.-+...                    .+.  ...+++
  T Consensus          2 wLnd~iId~y~~~l~~~~~~~~~~~~~~~~~~~~~~f~~~l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  77 (216)
  T PF02902_consen   2 WLNDSIIDFYLEYLRHRLES---ENKNSKRVHFFSSFFYQKLTECFKQFKKDKERSKFKWNESKDF-YNGVQRWFRKKNK  77 (216)
  T ss_dssp              -EEHHHHHHHHHHHHHHHTCC---THHTSTTEEEE-THHHHHHH----HHHCCH--S-----HHHHC-HHHCGGGGTTCCT
  T ss_pred              cCCHHHHHHHHHHHHHhhcc---CccCCCCcEEEECceeeeccccccccccccccccccccccchhhhhHh-hhhhhhhhhcccc


  Q ss_pred                -hhhccCCCceEEEEEEEc-cCceEEEEEEEcCCCCCcceEeeccccCcchH---hHHHHHHHHHHh
  Q Babela_gene_25   333 -EFKDNDYEGTAIFILYY-PQHWVTCVVDKKKNEHPRFIFADSLNIDRT---KSDQAFELIGEL  391 (393)
  Q Consensus        333 -~~F~D~nYsGtAiFLIY~~~~~HWiTCvVtK~~~E~pkFIFADSLg~dr~~~~~~~~~~~~a~tLI~lL  391 (393)
                             .+.|++|   -++-|.. ..||+.+||.-..+   ++.+-|||+....   ......+++..|
  T Consensus         78 ~~l~~~~~~~~~~i~iPin~~~~HW~l~vi~~~~~~~~~~~~~~i~~~~DSl~~~~~~~~~~~~~~~~~~~~~~l  135 (216)
  T PF02902_consen  78 KNLFDKDY---IFIPININNNHWVLLVIDLPKK---RIYVYDSLGSSNNDKRYKRVIENIIPFL  135 (216)
  T ss_dssp              STGGGSSE---EEEEEEETTTEEEEEEEETTTT---EEEEE-TTSTSSH-HHHHHHHHHHHHHHH
  T ss_pred              ccccccCE---EEEEEechhhccceeEEccccc---EEEEEecccccccccccccchhhhhhhhh

>PF02902 Peptidase_C48:  Ulp1 protease family, C-terminal catalytic domain This family belongs to family C48 of
  the peptidase classification.;  InterPro: In the MEROPS database peptidases
  Probab=75.06  E-value=2.1  Score=36.88  Aligned_cols=34  Identities=24%  Similarity=0.304  Sum_probs=0.0

  Q ss_pred                hccccccccee-eehhhCCCCCcchHHHHhhhhhhhh
  Q Babela_gene_25    28 KVKPANITQI-DVTSQNPQSGTCGYHALYNGIIIAK   62 (393)
  Q Consensus         28 k~~~qkI~Qy-~V~~Qqed~sscGYHALYN~i~IaK   62 (393)
                           ...+-.+... .|. ||+++..||+++++++-.++.
  T Consensus        148 ~~~~~~~~~~~~~p-qQ~n~~dCGv~vl~~~~~~~~  182 (216)
  T PF02902_consen 148 DKSPFKIVRPPNVP-QQPNGYDCGVYVLKFMECLLE  182 (216)
  T ss_dssp              -TTTCEEEEECTS--SSSSSSCHHHHHHHHHHHHHC
  T ss_pred              ccceeeecccccc-CCCCCCCcHHHHHHHHHHHHh
```