

PARP16

Sequences :

>NP_001303872.1 protein mono-ADP-ribosyltransferase PARP16 isoform 2 [Homo sapiens]
MQPFGWAAAREAAAGRDMLAADLRCSLFASALQSYKRDSVLRPFPPSYARGDCKDFEALLADASKLPNLKE
LLQSSGDNHKKRAWDLVSWILSSKVLTIHSAGKAEFEKIQKLTGAPHTFVPAPDFLFEIEYFDPANAKFYE
TKGERDLIYAFHGSRLNFHFSIIHNGLHCHLNKTSLFEGEGTYLTSDLSLALIYSPHGHGWQHSLLGPILS
CVAVCEVIDHPDVKQCQTKKKDSKEIDRRRARIKHSEGGDIPPKYFVVTNNQLLRVKYLLVYSQKPPKRAS
SQLSWFSSSHWFTVMISLYLLLLLIVSVINSSAFQHFWNRRAK

>XP_009248197.1 mono [ADP-ribose] polymerase PARP16 isoform X2 [Pongo abelii]
MQPFGWAAAREAAAGRDMLAADLRCSLFASALQSYKRDSVLRPFPPSYARGDCKDFEALLADASKLPNLKE
LLQSSGDNHKKRAWDLVSWILSSKVLTIHSAGKAEFEKIQKLTGAPHTFVPAPDFLFEIEYFDPANAKFYE
TKGERDLIYAFHGSRLNFHFSIIHNGLHCHLNKTSLFEGEGTYLTSDLSLALIYSPHGHGWQHSLLGPILS
CVAVCEVIDHPDVKQCQTKKKDSKEIDRRRARIKHSEGGDIPPKYFVVTNNQLLRVKYLLVYSQKPPKRAS
SQLSWFSSSHWFTIMISLYLLLLLIVSVINSSAFQHFWNRRAK

>AAH55447.1 Poly (ADP-ribose) polymerase family, member 16 [Mus musculus]
MQLSNRAAAAREASRDVLAADLRCSLFASALQSYKRDSVLRPFPPSYARHDCDKDFEALLADTGRLPNLKE
LLQSSRDTRQAWDLVSWILSSKILTIHSAKKAEFEKIQQLTGAPHTFVPPTDFLFEIEYFDPANSRFYE
TKGERDLIYAFHGSRLNFHFSIIHNGLHCHLNKTSLFEGEGTYLTSDLSLALIYSPHGHGWQHSLLGPILS
CVAVCEVIDHPDVKQCQTKKKDSKEIDRRRARIKHSEGGDIPPKYFVVTNNQLLRVKYLLVYSQKPPKRAS
SQLSWLSSHWFMIMSLYLLLLLIVSVTNSSAFHHFWNRVRAK

>XP_015147741.1 protein mono-ADP-ribosyltransferase PARP16 isoform X2 [Gallus gallus]
MGPPRLGEAVREAVRPDLGAELRCSLFAAALQSYKRDSVLRPFPPSYRGGAADASKDFEALLADTEALPG
LKELLGAAPSABERTWDLLSWILSPKTTFTIQSIKKQEYEKIQELTGMSGAAVPAPDFLFEVTVCDQMNAK
FAGTRGEQDLIYAFHGSRLNFHFSIIHNGLHCHLNKTSLFEGEGTYLTSDLSLALIYSPHGLGWQRSTLGS
ILSCVAVCEIIDHPDVKQCQVKKKDSSEIDRKRARARNSEGGDVQKYFVVTNNQLLQVKYLLVYSQKQHR
RPSGQSSWFSTRFAITMMLYLLLLLMVIGASNSAFLYYWHRMFYSEG

>XP_018108776.1 protein mono-ADP-ribosyltransferase PARP16 [Xenopus laevis]
MVEEIIITRDLISADLKCSLFAAALKSYKRDSVLRPFPPALYTSQYKDFDALITDSSALPGLPEI IQDKNN
RDQKLVNLLRWILSKDLFTVKSVPKDYEEIQALPGSPSHALPTPDFLFELEYCEKLSAKFQETRGRDRL
IYAFHGSRLNFHFSIIHNGLHCHLNKTSLFEGEGTYLTSDLGLALLYSPHGGQWTRSMGLGPVLSVAMCEM
IDHPDVKCAQKKKDSSEIDRKRARARNSEGGDVQKYFVVTNNQLLRVKYLMVYSQEQPRRRPRQPTWFS
KHRFAIMTLYLFIILIGLSSSKAFTYHWNRLLGWRP

>XP_045544515.1 protein mono-ADP-ribosyltransferase PARP16-like isoform X2 [Salmo salar]
MQPFLPDPAVRELVCCLHRDPAADLRCSLFAAQNWKYKRDSVLRPPYPRYIRDRDTKEFDLLSDVSS
LFGVRELVRLRGEGADHHLALTHWVLSSKSPAVKTLQKDEYAKLCNLTSEGISSTVPDFLFELEYCDQM
NAKFEKTRAGRDLFYAFHGSRLNFHFSIIHNGLHCHLNKTSLFEGEGTYLTSDLMAVLVSPHGNGWDRSL
LGPLLS CVAVCEVIDHPDVKQVKRKDSEITDRQSRARNSEGGVEPKYFVVTNNQLLRVKYLLVYSQR
RHLSRHSGRGSWLVRHFAIMMSLYLLLLLIVIGAFNSTTFLSFWNRLFR

>XP_032804273.1 protein mono-ADP-ribosyltransferase PARP16 isoform X2 [Petromyzon marinus]
MLAEAEARGWEPAHQAAEEGGGGGEGGGDHEDGRGVPRPGDAVREALRGDPGAADLRSLVAAALLG
YRHSLLRPFPSGYPNGGEDGKDFLTALLADMSAVPSVQQLREDVDVAPRIELLEHWALTSKHFTVCSQR
KDEFKLEALTGSPGVVPAPDFVFSVTYSETAERRFREMRGELDILYAYHGSRLNFHFSIIHNGLHCHL
NKLTALFEGEGTYLTSDLSLALLYSPHSQAWRLSALGAALSCVAVCEVIDHPDVKQVKRKDADGLDRRAR
ARHSEGGDVQKYFVVTNNQLLRVRYLLLYARKSQHHSIPWQRSWLGHRFAVGMAVYGLILLLLGALNS
PTVLHYWRRYLSGD

>XP_019627055.1 PREDICTED: mono [ADP-ribose] polymerase PARP16-like isoform X2 [Branchiostoma belcheri]
MTEDVRYNVRKLEGDVLAADLQLSLFAAALLSYRHDTVLRPFPPGFARQNDKDFPALKSVVMKGLSGVK
ELLQDSRVTSDAQTLQLVHWVLETRNFHLRSCEPAEYKEVQRLTGYSNTNIPPPSHMFEVVHSESTDARF
EETRQDRSLFYAFHGSRLDNFHSIIHNGLHAHLNKNLSLFEGEGTYLSGDLGVSI IYSHKGQGWDRSMLGET
MSCVAVCEVIDMPKVVKSYKEENGRAKNKDKHEVPEKYIYVSNELLRVKIVLVYAEKARFRVQAPSF
FQRHKFFILMTLYVIVLAVIGAANSFNLQYYLRKFFR

>XP_032233915.1 protein mono-ADP-ribosyltransferase PARP16 [Nematostella vectensis]
MDDSEVEKETQLERIVGKLRSDGFPACDLRMCLFVAALSYRHDSILRPYPYPVGLREDGSKNIQKLTNLS
IPSLSALNDSCLPVGWMLLDWVLLKKFPDVKTLDKSMFQIEKKTGHSYSNSTEPDYIFEIQYHENNAL
NARFALSEECEVL IYAYHGSRLNFHFSIIHNGLHSHLNKNSLFEGEGTYLSSDLNVSIMYSTYQAWNSG
LGEKLS CVAVCEVLNHPDVKCSLEDPRAATSSPERRRSGSGASSVRARAKGEGGDVDRYYVQNNQLL
RVKYLIVYAEKRPQRTQRTPPGTWFARLLIYIIGLVLLGSRTRAFHKLASYLQKEDTHL

>XP_002164087.1 protein mono-ADP-ribosyltransferase PARP16 [Hydra vulgaris]
MTSISEQVSIILSNDLLAAELKALFTSALNSYRHDSCLRPPFNIFGDTCDKNIAVKQMSLLSEFRPLA
EMVNIISLMSEDCQKMIHWALDSKIYSSKTCNKHVDDVQKKTGCSYQVQPDYIFEIKYNTFSSQKFD
LAKMYGVKYGFHGSMDNFHFSIYNVNLQVHMVKNVFGEGVYLSDDLVSMPYIISSGFTWQHSKLGQQIS
CVAVCEVLDPGVKCTMKTVNGANRSRANSEAGEVPKYFVVTSSDLRVVKYIFVFTDKTEKRNSAKCG
MLCFRYPVLSIMLAYMLLLAFVSIWNSKTFQLIWRNRYWYKKKF

>XP_019855808.1 PREDICTED: mono [ADP-ribose] polymerase PARP16-like [Amphimedon queenslandica]
MSKDDGDGASTGTQLKVNELREALSKDMAGCDCLLSLFWALSYYRHDTVLRYPYNPQFILSNQDKDIDG
LRSVPKTLPGINEVQQLDSDDDRVTITLYDICTCKTGRFLSFKPGDKFLSIESQTSVPAHKVQPYCFEL
QYSSEREKQRTASEYGTFLAYHGSRMENFHSIIHNGLLSHMKNVIGFEGTYLTSDLSCVMFNPSAT
SWTKSSLPCLSMMAVCEVVSHPDIRSRVQHGGEPSINQKVPERYFVVTNDEMLRVKYLIVFAQERGRPS
PTRRWFNSNHKVMVMFVLYLFLLLFLGLWNSRYVSRLYNQYTRRYITL

Alignment

| | | | |
|---------------------------------|---|------------------------------|-----|
| XP_019855808.1[A.queenslandica] | -----MSKDDGGDASTG----- | TLQLKVNELREALSKDMAGCDCL | 35 |
| XP_002164087.1[H.vulgaris] | ----- | MTSISEQVSIILSNDLLAAELK | 22 |
| XP_032233915.1[N.vectensis] | ----- | MDDSVKEETQLERVIGKLRSDGFCADLR | 28 |
| XP_019627055.1[B.belcheri] | ----- | MTEDVRTNVREKLEGDVLAADLQ | 23 |
| XP_032804273.1[P.marinus] | MLAEAEARGWEPANQAAEEEGGGGGGGEDDHEDGDRVGPGRGDAVREALGDPGAADLR | | 60 |
| XP_045544515.1[S.salar] | ----- | MQPFLFPDAVRELVCSLRHDPVADLR | 28 |
| XP_018108776.1[X.laervis] | ----- | ---MVEEIIITROLLSADLK | 16 |
| XP_015147741.1[G.gallus] | ----- | MGFPRLGGEAVREAVRDPPLGAELR | 24 |
| AAH55447.1[M.musculus] | ----- | MQLSNRAAAAREAASRDVLAADLR | 23 |
| NP_001303872.1[H.sapiens] | ----- | MQPSGWAAAREAAGRDLAADLR | 23 |
| XP_009248197.1[P.abelii] | ----- | MQPSGWAAAREAAGRDLAADLR | 23 |
| | | * ..: | |
| XP_019855808.1[A.queenslandica] | LSLFWALSYYRHDTVLRPPYPNQFILSN-GDKDIDGLRSVFKTLFGLNEVVQQLD-SLDD | | 93 |
| XP_002164087.1[H.vulgaris] | LALFTSALNSYRHDSCLRPPFNIFGDTCKNIADVQMKSLSEFRPLAEMVNIIS-LMSE | | 81 |
| XP_032233915.1[N.vectensis] | MCLFVAALLESYRHDSILRPPYPVGLRED-GSKNIQKLTNLSSSIPSLALNNDSC--LEP | | 85 |
| XP_019627055.1[B.belcheri] | LSLFAAALLSYRHDTVLRPPFPFGFARQN-DEKDFALKSVMKLSGVKELLQDSRVTSDA | | 82 |
| XP_032804273.1[P.marinus] | LSLFAAALLGYRRHSLRPPFPGYNGGDEGKDFTALLADMSAVPSVQQLREDV-DVAP | | 119 |
| XP_045544515.1[S.salar] | CSLFWAAANQYKRDSVLRPPYPPIYIRDR-DTKEFDELLSDVSSLPGVRELVRLRP-GEAD | | 86 |
| XP_018108776.1[X.laervis] | CSLFWAALKSYKRDSVLRPPFPALYTSDQ--YKDFDALITDSSALPGLPEI IQDN-NRDQ | | 73 |
| XP_015147741.1[G.gallus] | CSLFAAALKSYRRDSVLRPPFSRYGGADAASKDFEALLADTEALPGLKELLGAAP-SAE | | 83 |
| AAH55447.1[M.musculus] | CSLFSALQSYKRDSVLRPPFPASYARHD--CKDFEALLADTGRPLNKLKELLQSSR-DTDK | | 80 |
| NP_001303872.1[H.sapiens] | CSLFSALQSYKRDSVLRPPFPASYARGD--CKDFEALLADASKPLNKLKELLQSSG-DNHK | | 80 |
| XP_009248197.1[P.abelii] | CSLFSALQSYKRDSVLRPPFPSSYARGD--CKDFEALLADASKPLNKLKELLQSSG-DNHK | | 80 |
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| XP_019855808.1[A.queenslandica] | RVITLLYDIICTGFRLSFKPGDKFSLIESQTSVPAHKV-OPYCFPELQYSSE--REEKW | | 150 |
| XP_002164087.1[H.vulgaris] | DCQKMIHWALDSKIYSSKTCNKHVFDDVQKKTGCCSSYQV-OPDYIFEIKYNTF--SSQKF | | 138 |
| XP_032233915.1[N.vectensis] | GVMSLLDWLL--KKFDVKTLDKSMFQEIIEKKTGHSSYNSTEDPYIFEIQYHENNALNARF | | 144 |
| XP_019627055.1[B.belcheri] | QTLQLVHWVLETRNFHLRSCPEAEYKEVQRLTGYTSTNIPPPSHMFVSVHSES--TDARF | | 140 |
| XP_032804273.1[P.marinus] | RILELLHWALTYSKHFTVCSQRKDEFSKIEALTGSPGVPVPAPDFVFSVTYSET--AERRF | | 177 |
| XP_045544515.1[S.salar] | HHLALTHWLSSSKSFAVKTLQKDEYAKLNLTESEGISTVPDPDLFELEYCDQ--MNAKF | | 144 |
| XP_018108776.1[X.laervis] | KVLNLLRWILSSDKLFTVKSVPKDKYEEIQALPGSPSHALTPDFLFELEYCEK--LSAKF | | 131 |
| XP_015147741.1[G.gallus] | RTWDLWSILSPKTTFTIQSIKKQYEEKIQELTGMSGAAPAPDFLFEVITYCDQ--MNAKF | | 141 |
| AAH55447.1[M.musculus] | QAWDLVSWILSSKILTIHSAKKAEFEKIQQLTGAPHTVPVTPDFLFEIYFDP--ANSRF | | 138 |
| NP_001303872.1[H.sapiens] | RAWDLVSWILSSKVLTIHSAGKAEFEKIQKLTGAPHTVPVAPDFLFEIYFDP--ANAKF | | 138 |
| XP_009248197.1[P.abelii] | RAWDLVSWILSSKVLTIHSAGKAEFEKIQKLTGAPHTVPVAPDFLFEIYFDP--ANAKF | | 138 |
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| XP_019855808.1[A.queenslandica] | QRTASEGYFTFLAYHGSRMENFHSIAHNGLLSHMKNVGIFGEGTYLTDLSVCMNFPSPSAT | | 210 |
| XP_002164087.1[H.vulgaris] | DDLAKMIGVKYGFHSGSRMDNFHSIVNGLQVHMVQNAVPEGVYLSDDLSPMPYISSGF | | 198 |
| XP_032233915.1[N.vectensis] | LALSECEVLYAYHGSRLENFHSILHNLGHSLHAKNSLFGEGTYLSDSLNVSIMYSTYSQ | | 204 |
| XP_019627055.1[B.belcheri] | EETQRDSRLFYAFHGSRILDNFHSILHNLGHSLHAKNSLFGEGTYLSDSLNVSIIYSHKQ | | 200 |
| XP_032804273.1[P.marinus] | REMRGELDILYAYHGSRLENFHSILHNLGHSLHAKNSLFGEGTYLTDLSLALLYSPHSQ | | 237 |
| XP_045544515.1[S.salar] | EKTRAGRDLFYAFHGSRLENFHSILHNLGHSLHAKNSLFGEGTYLTDLSMAVLYSPHGN | | 204 |
| XP_018108776.1[X.laervis] | QETRGRDRDLFYAFHGSRLENFHSILHNLGHSLHAKNSLFGEGTYLTDLSLALLYSPHGO | | 191 |
| XP_015147741.1[G.gallus] | AETRGECDLIFYAFHGSRLENFHSILHNLGHSLHAKNSLFGEGTYLTDLSLALLYSPHGL | | 201 |
| AAH55447.1[M.musculus] | YETKGERDLIFYAFHGSRLENFHSILHNLGHSLHAKNSLFGEGTYLTDLSLALIYSPHGH | | 198 |
| NP_001303872.1[H.sapiens] | YETKGERDLIFYAFHGSRLENFHSILHNLGHSLHAKNSLFGEGTYLTDLSLALIYSPHGH | | 198 |
| XP_009248197.1[P.abelii] | YETKGERDLIFYAFHGSRLENFHSILHNLGHSLHAKNSLFGEGTYLTDLSLALIYSPHGH | | 198 |
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| XP_019855808.1[A.queenslandica] | SWTKSSLPPLCSMMMAVCEVSHPDIRSRVQHGG----- | EPSIN | 248 |
| XP_002164087.1[H.vulgaris] | TWQHSKLQQQISCVAVCEVLDPHGPKCTMTVN----- | GANRSRANNSEA | 243 |
| XP_032233915.1[N.vectensis] | AWSNSGLGEKLSCVAVCEVLNHPDVKCSLEDPRATSSPERRRSGSGASSVRARAKGSEG | | 264 |
| XP_019627055.1[B.belcheri] | GWDRSMLGETMSCVAVCEVIMDPKYVK----- | SKVEEENGRAKNKDK | 242 |
| XP_032804273.1[P.marinus] | AWRLSALGAALSCVAVCEVIDHPDVKKQVKRKD----- | ADGLDRRRRARARHSEG | 286 |
| XP_045544515.1[S.salar] | GWKRSLLGPLLSCVAVCEVIDHPDVKKQVKRKD----- | SETIDRRRARARHSEG | 253 |
| XP_018108776.1[X.laervis] | GWTRSMLGPVLSCVAVCEVIDHPDVKKQAKKKD----- | SSEIDRRRARARHSEG | 240 |
| XP_015147741.1[G.gallus] | GWQRSTLGSILSCVAVCEVIDHPDVKKQVKKKD----- | SSEIDRRRARARHSEG | 250 |
| AAH55447.1[M.musculus] | GWQHSLLGPLLSCVAVCEVIDHPDVKKQVKKKD----- | SKEIDRRRARIKHSEG | 247 |
| NP_001303872.1[H.sapiens] | GWQHSLLGPLLSCVAVCEVIDHPDVKKQVKKKD----- | SKEIDRRRARIKHSEG | 247 |
| XP_009248197.1[P.abelii] | GWQHSLLGPLLSCVAVCEVIDHPDVKKQVKKKD----- | SKEIDRRRARIKHSEG | 247 |
| | * * * * *:***.: * | . . | |
| XP_019855808.1[A.queenslandica] | QKVPERYFVVNTDEMLRVKYLIVFAQERGR--PSPTRRWFSNHKWMVFLYLFLLLFLG | | 306 |
| XP_002164087.1[H.vulgaris] | GEVPKKYFVVNTSSDLRVKYLIVFTDKTEKRNSAKCGMLCFRYPVLSIMLAYMLLAFVS | | 303 |
| XP_032233915.1[N.vectensis] | GDVPDRYVYVQNNQLLRVKYLLVYAEKRPQRNTQRTQ---PGTWFAILLIIYIIGLVLLG | | 321 |
| XP_019627055.1[B.belcheri] | HEVPKERYIVSNNELLRVKYLIVYAEKAR-PRVQAPSFFQRHKFFILMTLYVIVLAVIG | | 301 |
| XP_032804273.1[P.marinus] | GDVPQKYFVVNTNQLLRVKYLLLYARKSQHHSIPWQRSWLGRHRFAVGMVYGLILLLLG | | 346 |
| XP_045544515.1[S.salar] | GEVPQKYFVVNTNQLLRVKYLLVYSQRRHLSRHSRGSWLVRRHFAMMSLYLILLLIVIG | | 313 |
| XP_018108776.1[X.laervis] | GDVPQKYFVVNTNQLLRVKYLLVYSQEQPR-RPRQPTWFSKHRFAIMMTLYFILILIG | | 299 |
| XP_015147741.1[G.gallus] | GDVPQKYFVVNTNQLLQVKYLLVYSQKQHR-RPSGQSSWFSTHRFAIMMTLYLILLMVG | | 309 |
| AAH55447.1[M.musculus] | GEIPPKYFVVNTNQLLRVKYLLVYSQKQPK-RASSQLSWLSSHMFVIMMSLYLILLLIVS | | 306 |
| NP_001303872.1[H.sapiens] | GDIPPKYFVVNTNQLLRVKYLLVYSQKPPK-RASSQLSWFSSHMTVMISLYLILLLIVS | | 306 |
| XP_009248197.1[P.abelii] | GDIPPKYFVVNTNQLLRVKYLLVYSQKPPK-RASSQLSWFSSHMTVMISLYLILLLIVS | | 306 |
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| XP_019855808.1[A.queenslandica] | LWNSRYVSRLYNQYTRYITL | | 327 |
| XP_002164087.1[H.vulgaris] | INNSKTFQLIWRNYWYKKKF- | | 323 |
| XP_032233915.1[N.vectensis] | LSRTRAFHKLASYLQKEDTHL | | 342 |
| XP_019627055.1[B.belcheri] | AANSFNLQYYLRKFFR---- | | 317 |
| XP_032804273.1[P.marinus] | ALNSPTVLHYWRKRLSGD---- | | 364 |
| XP_045544515.1[S.salar] | AFNSTTFLSFWNRFLR---- | | 329 |
| XP_018108776.1[X.laervis] | LSSSKAFTYHWNRLGWRP---- | | 318 |
| XP_015147741.1[G.gallus] | ASNSAPFLYVYHMRMFYSEG---- | | 328 |
| AAH55447.1[M.musculus] | VTNSSAFPHFWNRVKR---- | | 322 |
| NP_001303872.1[H.sapiens] | VINSSAFQHFWRNAKR---- | | 322 |
| XP_009248197.1[P.abelii] | VINSSAFQHFWRNAKR---- | | 322 |
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Percent identity matrix:

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#
#
# Percent Identity Matrix - created by Clustal2.1
#
#
1: XP_019855808.1[A.queenslandica] 100.00 31.95 35.48 36.51 34.88 37.74 39.34 37.06 38.19 38.51 38.19
2: XP_002164087.1[H.vulgaris] 31.95 100.00 37.22 34.41 34.27 36.79 35.46 36.14 38.29 38.29 38.29
3: XP_032233915.1[N.vectensis] 35.48 37.22 100.00 41.80 44.79 42.90 46.01 42.86 42.27 42.90 43.22
4: XP_019627055.1[B.belcheri] 36.51 34.41 41.80 100.00 43.35 45.89 47.73 46.52 46.35 44.44 44.13
5: XP_032804273.1[P.marinus] 34.88 34.27 44.79 43.35 100.00 54.71 55.21 59.94 55.90 57.14 56.83
6: XP_045544515.1[S.salar] 37.74 36.79 42.90 45.89 54.71 100.00 62.22 62.96 60.25 59.63 59.63
7: XP_018108776.1[X.laevis] 39.34 35.46 46.01 47.73 55.21 62.22 100.00 66.35 62.86 62.86 62.54
8: XP_015147741.1[G.gallus] 37.06 36.14 42.86 46.52 59.94 62.96 66.35 100.00 68.63 69.25 69.57
9: AAH55447.1[M.musculus] 38.19 38.29 42.27 46.35 55.90 60.25 62.86 68.63 100.00 90.68 90.06
10: NP_001303872.1[H.sapiens] 38.51 38.29 42.90 44.44 57.14 59.63 62.86 69.25 90.68 100.00 98.76
11: XP_009248197.1[P.abelii] 38.19 38.29 43.22 44.13 56.83 59.63 62.54 69.57 90.06 98.76 100.00
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