Assignment 5

1. Analyze the occurrence of similar proteins in “nr” and SWISS-PROT database for the

sequence given below:>1336093|Genbank|Outer membrane integral membrane protein|HrcC MVEKRELRCRLLGALLMLCATLPAGAQTPADWKEQSYAYSADRTPLSTVLQDFADGHSVD LHLGNVEDTEVTAKIRAENASAFLDRLALEHHFQWFVYNNTLYVSPQDEQSSERLEISPD AAPDIKQALSGIGLLDPRFGWGELPDDGVVLVTGPPQYLELVKRFSEQREKKEDRRKVMT FPLRYASVADRTIHYRDQTVVIPGVATMLNELMNGKRAAPASASGIDSTPGGPDTNSMMQ NTQTLLSRLSSRNKTSNRAGGRDNEIEDVSGRISADVRNNALLIRDDDKRHDEYSQLIAK IDVPQNLVEIDAVILDIDRTALNRLEANWQATLGGVTGGSSLMSGSGTLFVSDFKRFFAD IQALEGEGTASIVANPSVLTLENQPAVIDFSQTAYITATGERVADIQPVTAGTSLQVTPR AVGNEGHSSIQLMIDIEDGHVQTNGDGQATGVKRGTVSTQALISENRALVLGGFHVEESA DRDRRIPLLGDIPWLGQLFSSKRHEISQRQRLFILTPRLIGDQTDPTRYVTADNRQQLSD AMGRVERRHSSVNQHDVVENALRDLAEGQSPAGFQPQTSGTRLSEVCRSTPALLFESTRG QWYSSSTNGVQLSVGVVRNTSSKPLRFDEANCASKRTLAVAVWPHSALAPGESAEVYLAM DPSRVLHASRESLLNR

Analysis of occurrence of similar proteins in “nr” and SWISS-PROT database:

Non redundant protein sequences(nr):

No. of sequences selected (max): 100

|  |  |  |
| --- | --- | --- |
|  | Min | Max |
| Max Score  Total score  Query Cover  e Value  Percentage Identity  Accession Length | 900  900  90%  0  67%  617 | 1305  1305  100%  0  100%  691 |

SWISS-PROT:

|  |  |  |
| --- | --- | --- |
|  | Min | Max |
| Max Score  Total score  Query Cover  e Value  Percentage Identity  Accession Length | 50.8  50.8  16%  0  22.22%  234 | 544  544  96%  3e-05  44.40%  777 |

1. List the algorithm parameters used for the search (Q1).

Algorithm Parameters used in BLAST:

* Max Target Sequences
* Short Queries
* Expect Threshold
* Word Size
* Max matches in a query range
* Matrix
* Gap Costs
* Compositional Adjustments
* Filter
* Mask

1. What is the sequence identity of the query sequence (given in Q1) with AAK81929.1?

Get the protein sequence with UniProt and use BLAST and you will get the following results:

Max Score = 530

Total Score = 530

Query Cover = 96%

E Value = 0

Per. Ident = 43.20%

Acc. Len = 713

So, the sequence Identity of query sequence is 43.20%

1. How far are hemoglobin sequences in human and chicken similar?When searched for Hemoglobin sequences in UniProt, we get Human and Chicken protein sequences which are analyzed in blast and the Percentage Identity is 69.39%. (Where the query cover is 100%)

The percentage Identity is 69.39%

1. Write a program to list all the matching pentapeptides (which occur in both the sequences)

and their frequency of occurrence in given sequences.def match\_pentaPP(s1, s2):

thisdict = {}

for i in range(len(string1)-4):

if string1[i:i+5] not in thisdict:

thisdict[string1[i:i+5]]=1

else:

thisdict[string2[i:i+5]]+=1

if string2[i:i+5] not in thisdict:

thisdict[string2[i:i+5]]=1

else:

thisdict[string2[i:i+5]]+=1

return thisdict

string1='''MVHWTAEEKQLITGLWGKVNVAECGAEALARLLIVYPWTQRFFASFGNLSSPTAILGNPMVRAHGKKVLTSFGDAVKNLDNIKNTFSQLSELHCDKLHVDPENFRLLGDILIIVLAAHFSKDFTPECQAAWQKLVRVVAHALARKYH'''

string2='''MVHLTPEEKSAVTALWGKVNVDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPKVKAHGKKVLGAFSDGLAHLDNLKGTFATLSELHCDKLHVDPENFRLLGNVLVCVLAHHFGKEFTPPVQAAYQKVVAGVANALAHKYH'''

print(match\_pentaPP(string1, string2))

1. Write a program to compute sequence identity, similarity, query coverage and gap percentage from the alignment of human and chicken hemoglobin sequences (refer Q4).string1='''MVHWTAEEKQLITGLWGKVNVAECGAEALARLLIVYPWTQRFFASFGNLSSPTAILGNPMVRAHGKKVLTSFGDAVKNLDNIKNTFSQLSELHCDKLHVDPENFRLLGDILIIVLAAHFSKDFTPECQAAWQKLVRVVAHALARKYH'''

string2='''MVHLTPEEKSAVTALWGKVNVDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPKVKAHGKKVLGAFSDGLAHLDNLKGTFATLSELHCDKLHVDPENFRLLGNVLVCVLAHHFGKEFTPPVQAAYQKVVAGVANALAHKYH'''

count=0

for i in range(len(string1)):

if string1[i]==string2[i]:

count+=1

print("query=", (100-max(len(string1), len(string2))+min(len(string1), len(string2))))

print("sequence identity", (count/min(len(string1), len(string2)))\*100)

print("Gap Percentage", max(len(string1), len(string2))-min(len(string1), len(string2)))

1. Obtain the multiple sequence alignment for TIM barrel proteins from different organisms

(Select 20 proteins, for example). Compare the results obtained with Clustal Omega, MAFFT, and MUSCLE. List 5 residue positions which are aligned differently in these three methods.

The analysis of 20 different proteins through given methods are given in the following hyperlinks.

[Clustal Omega](#_Clustal_Omega_Results:), [MAFFT](#_MAFFT_results:), [MUSCLE](#_MUSCLECLUSTAL_multiple_sequence)

1. Blast the below sequence 'EPDMRTPIAHTMAW' against PDB database. Analyze the results and discuss the significance of the results.

When blasted the sequence against PDB database, the results we get are:

|  |  |  |
| --- | --- | --- |
|  | Min | Max |
| Max Score  Total score  Query Cover  e Value  Percentage Identity  Accession Length | 21.4  21.4  42%  2e-10  41.67%  201 | 53.2  53.2  100%  34  100%  1290 |

There are three domain hits for the given sequence:

|  |  |  |
| --- | --- | --- |
| Pssm-ID, Prot Name | Bit Score | E-Value |
| 235472, PRK05447  223814, COG0743  404213, PFAM13288 | 36.21  33.72  32.41 | 3.61e-05  2.55e-04  4.55e-04 |

Resources:

# Clustal Omega Results:

CLUSTAL O(1.2.4) multiple sequence alignment

sp|P37527|PDXS\_BACSU MAQTGTERVKRGMAEMQKG-----GVIMDVINAE-----QAKIAEEAGAVAVMALER--- 47

sp|A7YW45|ANM5\_BOVIN ------------MAAMAVG-----GAGGSRVSSGRDLNCVPEIADTLGAVAKQGFDFLCM 43

sp|Q5R698|ANM5\_PONAB ------------MAAMAVG-----GAGGSRVSSGRDLNCVPEIADTLGAVAKQGFDFLCM 43

sp|Q9XGX9|TIM9\_ARATH ------------------------------------------------------------ 0

sp|Q6FRT3|TIM9\_CANGA ------------------------------------------------------------ 0

sp|Q9WV98|TIM9\_MOUSE ------------------------------------------------------------ 0

sp|Q17754|TIM9\_CAEEL ------------------------------------------------------------ 0

tr|A0A072VM55|A0A072VM55\_MEDTR ------------------------------------------------------------ 0

sp|Q8F3Q1|CIMA\_LEPIN MTKVE-----TRLEILDVTLRDGEQTRGVSFSTSEKLNIAKFLLQKL------NVDRV-- 47

sp|Q9SAU2|RPE\_ARATH MSTSA-----ASLC------CSSTQVNGFGLRPERS------------------------ 25

sp|P0A858|TPIS\_ECOLI ------------------------------------------------------------ 0

sp|Q9RUP5|TPIS\_DEIRA ------------------------------------------------------------ 0

sp|Q9Z520|TPIS\_STRCO ------------------------------------------------------------ 0

sp|Q8XKU1|TPIS\_CLOPE ------------------------------------------------------------ 0

sp|P87108|TIM10\_YEAST ------------------------------------------------------------ 0

sp|Q9W2D6|TIM10\_DROME ------------------------------------------------------------ 0

sp|Q75F72|TIM13\_ASHGO ------------------------------------------------------------ 0

sp|Q6GPY0|TI13A\_XENLA ------------------------------------------------------------ 0

sp|Q7SBR3|TIM13\_NEUCR ------------------------------------------------------------ 0

sp|P0CS01|TIM13\_CRYNB ------------------------------------------------------------ 0

sp|Q09783|TIM8\_SCHPO ------------------------------------------------------------ 0

sp|O60220|TIM8A\_HUMAN ------------------------------------------------------------ 0

sp|Q9WVA1|TIM8A\_RAT ------------------------------------------------------------ 0

sp|P37527|PDXS\_BACSU -------------VPADIRAAGGVARMADPTIVEEVMNAV-----S---IPVMAKARIG- 85

sp|A7YW45|ANM5\_BOVIN PVFHPRFKREFTQEPAKSRP--GPQTRSDLLLSGRDWNTLIVGKLSPWIRPDSKVEKIR- 100

sp|Q5R698|ANM5\_PONAB PVFHPRFKREFIQEPAKNRP--GPQTRSDLLLSGRDWNTLIVGKLSPWIRPDSEVEKIR- 100

sp|Q9XGX9|TIM9\_ARATH ------------------------------------------------------------ 0

sp|Q6FRT3|TIM9\_CANGA ------------------------------------------------------------ 0

sp|Q9WV98|TIM9\_MOUSE ------------------------------------------------------------ 0

sp|Q17754|TIM9\_CAEEL ------------------------------------------------------------ 0

tr|A0A072VM55|A0A072VM55\_MEDTR ------------------------MF--------------RIRRILSYRALASCTRN--- 19

sp|Q8F3Q1|CIMA\_LEPIN -------------EIASARVSKGELE--------------TVQKIMEWAATEQLTERIEI 80

sp|Q9SAU2|RPE\_ARATH ---------------------------------------------LLYQPTSFSFSRRRT 40

sp|P0A858|TPIS\_ECOLI ------------------------------------------------------------ 0

sp|Q9RUP5|TPIS\_DEIRA ------------------------------------------------------------ 0

sp|Q9Z520|TPIS\_STRCO ------------------------------------------------------------ 0

sp|Q8XKU1|TPIS\_CLOPE ------------------------------------------------------------ 0

sp|P87108|TIM10\_YEAST ------------------------------------------------------------ 0

sp|Q9W2D6|TIM10\_DROME ------------------------------------------------------------ 0

sp|Q75F72|TIM13\_ASHGO ------------------------------------------------------------ 0

sp|Q6GPY0|TI13A\_XENLA ------------------------------------------------------------ 0

sp|Q7SBR3|TIM13\_NEUCR ------------------------------------------------------------ 0

sp|P0CS01|TIM13\_CRYNB ------------------------------------------------------------ 0

sp|Q09783|TIM8\_SCHPO ------------------------------------------------------------ 0

sp|O60220|TIM8A\_HUMAN ------------------------------------------------------------ 0

sp|Q9WVA1|TIM8A\_RAT ------------------------------------------------------------ 0

sp|P37527|PDXS\_BACSU -------------HIVEARVLEAMG-VDYIDESEVLTPADEEF----------------- 114

sp|A7YW45|ANM5\_BOVIN -------------RNSEAAMLQELNFGAYLGLPAFLLPLNQEDNTNLARVLTNHIHTGHH 147

sp|Q5R698|ANM5\_PONAB -------------RNSEAAMLQELNFGAYLGLPAFLLPLNQEDNTNLARVLTNHIHTGHH 147

sp|Q9XGX9|TIM9\_ARATH ------------------------------------------------------------ 0

sp|Q6FRT3|TIM9\_CANGA ------------------------------------------------------------ 0

sp|Q9WV98|TIM9\_MOUSE ------------------------------------------------------------ 0

sp|Q17754|TIM9\_CAEEL ------------------------------------------------------------ 0

tr|A0A072VM55|A0A072VM55\_MEDTR --ALSSSSQPRSLP------------------RSNA---------------------PIL 38

sp|Q8F3Q1|CIMA\_LEPIN LGFVDGNKTVDWIKDSGAKVLNLLTKGSLHHLEKQL---------------------GKT 119

sp|Q9SAU2|RPE\_ARATH HGIVKASSRVDRFSKSDII----------------------------------------- 59

sp|P0A858|TPIS\_ECOLI ------------------------------------------------------------ 0

sp|Q9RUP5|TPIS\_DEIRA ------------------------------------------------------------ 0

sp|Q9Z520|TPIS\_STRCO -----------------MT----------------------------------------- 2

sp|Q8XKU1|TPIS\_CLOPE ------------------------------------------------------------ 0

sp|P87108|TIM10\_YEAST ------------------------------------------------------------ 0

sp|Q9W2D6|TIM10\_DROME ------------------------------------------------------------ 0

sp|Q75F72|TIM13\_ASHGO ------------------------------------------------------------ 0

sp|Q6GPY0|TI13A\_XENLA ------------------------------------------------------------ 0

sp|Q7SBR3|TIM13\_NEUCR ------------------------------------------------------------ 0

sp|P0CS01|TIM13\_CRYNB ------------------------------------------------------------ 0

sp|Q09783|TIM8\_SCHPO ------------------------------------------------------------ 0

sp|O60220|TIM8A\_HUMAN ------------------------------------------------------------ 0

sp|Q9WVA1|TIM8A\_RAT ------------------------------------------------------------ 0

sp|P37527|PDXS\_BACSU ------------------------------HLNKNEYTVPFVCGCRDLGEATRRIAEG-- 142

sp|A7YW45|ANM5\_BOVIN SSMFWMRVPLVAPEDLRDDIIENAPTSHTEEYSGEEKTWMWWHNFRTLCDYSKRIAVALE 207

sp|Q5R698|ANM5\_PONAB SSMFWMRVPLVAPEDLRDDIIENAPTTHTQEYSGEEKTWIWWHNFRTLCDYSKRIAVALE 207

sp|Q9XGX9|TIM9\_ARATH ------------------------------------------------------------ 0

sp|Q6FRT3|TIM9\_CANGA ------------------------------------------------------------ 0

sp|Q9WV98|TIM9\_MOUSE ------------------------------------------------------------ 0

sp|Q17754|TIM9\_CAEEL ------------------------------------------------------------ 0

tr|A0A072VM55|A0A072VM55\_MEDTR PPPFFLDVGIAENYGSTS------------LTR--FMSSNASSE-------QGKNTEKTK 77

sp|Q8F3Q1|CIMA\_LEPIN PKEFFTDVSFVIEYAIKS------------GLKINVYLEDWSNGFRNSPDYVKSLVEHLS 167

sp|Q9SAU2|RPE\_ARATH -------------------------------VSPSILSANFAKL--GE------------ 74

sp|P0A858|TPIS\_ECOLI -------------------------------MRHPLVMGNWKLN--GSRHMVHELVSNLR 27

sp|Q9RUP5|TPIS\_DEIRA --------------------------------MQTLLALNWKMN--KTPTEARSWAEELT 26

sp|Q9Z520|TPIS\_STRCO -------------------------------TRTPLMAGNWKMN--LNHLEAIAHVQKLA 29

sp|Q8XKU1|TPIS\_CLOPE -------------------------------MRTPIIAGNWKMH--YTIDEAVKLVEELK 27

sp|P87108|TIM10\_YEAST ------------------------------------------------------------ 0

sp|Q9W2D6|TIM10\_DROME ------------------------------------------------------------ 0

sp|Q75F72|TIM13\_ASHGO ------------------------------------------------------------ 0

sp|Q6GPY0|TI13A\_XENLA ------------------------------------------------------------ 0

sp|Q7SBR3|TIM13\_NEUCR ------------------------------------------------------------ 0

sp|P0CS01|TIM13\_CRYNB ------------------------------------------------------------ 0

sp|Q09783|TIM8\_SCHPO ------------------------------------------------------------ 0

sp|O60220|TIM8A\_HUMAN ------------------------------------------------------------ 0

sp|Q9WVA1|TIM8A\_RAT ------------------------------------------------------------ 0

sp|P37527|PDXS\_BACSU --A------SMLRTKGEPGTGNIVEAVRH------------------------------- 163

sp|A7YW45|ANM5\_BOVIN IGADLPSNHVIDRWLGEPIKAAILPTSIFLTNKKGFPVLSKMHQRLIFRLLKLEVQFIIT 267

sp|Q5R698|ANM5\_PONAB IGADLPSNHVIDRWLGEPIKAAILPTSIFLTNKKGFPVLSKMHQRLIFRLLKLEVQFIIT 267

sp|Q9XGX9|TIM9\_ARATH ------------------------------------------------------------ 0

sp|Q6FRT3|TIM9\_CANGA ------------------------------------------------------------ 0

sp|Q9WV98|TIM9\_MOUSE ------------------------------------------------------------ 0

sp|Q17754|TIM9\_CAEEL ------------------------------------------------------------ 0

tr|A0A072VM55|A0A072VM55\_MEDTR KE-------LKN------------------------------------------------ 82

sp|Q8F3Q1|CIMA\_LEPIN KE-------HIERIF-LPDTLGVLSPEETFQ---GVDS-------LIQKYP--DIHFEFH 207

sp|Q9SAU2|RPE\_ARATH -Q-------VKAVEL-AGCDWIHVD-VM-------------------------------- 92

sp|P0A858|TPIS\_ECOLI KE-------LAG--V-AGCAVAIAPPEM-------------------------------- 45

sp|Q9RUP5|TPIS\_DEIRA TK-------YAP--A-EGVDLAVLAPAL-------------------------------- 44

sp|Q9Z520|TPIS\_STRCO FA-------LADKDY-DAVEVAVLAPFT-------------------------------- 49

sp|Q8XKU1|TPIS\_CLOPE PL-------VKDAKC----EVVVCPTFV-------------------------------- 44

sp|P87108|TIM10\_YEAST ------------------------------------------------------------ 0

sp|Q9W2D6|TIM10\_DROME ------------------------------------------------------------ 0

sp|Q75F72|TIM13\_ASHGO ------------------------------------------------------------ 0

sp|Q6GPY0|TI13A\_XENLA ------------------------------------------------------------ 0

sp|Q7SBR3|TIM13\_NEUCR ------------------------------------------------------------ 0

sp|P0CS01|TIM13\_CRYNB ------------------------------------------------------------ 0

sp|Q09783|TIM8\_SCHPO ------------------------------------------------------------ 0

sp|O60220|TIM8A\_HUMAN ------------------------------------------------------------ 0

sp|Q9WVA1|TIM8A\_RAT ------------------------------------------------------------ 0

sp|P37527|PDXS\_BACSU -----------------------------------------------------MRKVNAQ 170

sp|A7YW45|ANM5\_BOVIN GTNHHSEKEFCSYLQYLEYLSQNRPPPNAYELFAKGYE-D----YLQSPLQPLMDNLESQ 322

sp|Q5R698|ANM5\_PONAB GTNHHSEKEFCSYLQYLEYLSQNRPPPNAYELFAKGYE-D----YLQSPLQPLMDNLESQ 322

sp|Q9XGX9|TIM9\_ARATH ---------------------------------------------MDASMMAGLDGLPEE 15

sp|Q6FRT3|TIM9\_CANGA -----------------------------------------------------MDQLNAK 7

sp|Q9WV98|TIM9\_MOUSE ------------------------------------------------------------ 0

sp|Q17754|TIM9\_CAEEL ------------------------------------------------------------ 0

tr|A0A072VM55|A0A072VM55\_MEDTR ------------------------------------------------------------ 82

sp|Q8F3Q1|CIMA\_LEPIN GHNDYD-LSVANSLQAIRAGVKGL----HASINGLGERAG------NTPLEALVTTIHD- 255

sp|Q9SAU2|RPE\_ARATH ------------DG----RFVP--------NITIGPLVVDALRPVTDLPLDVHLMIVEPE 128

sp|P0A858|TPIS\_ECOLI ------------YIDMAKREAEGS------HIMLGAQNVD----------LNLSGAFTGE 77

sp|Q9RUP5|TPIS\_DEIRA ------------DLSALAA---NL----PAGIAFGGQDVS----------AHESGAYTGE 75

sp|Q9Z520|TPIS\_STRCO ------------DLRSVQTLVDGD----KLKIKYGAQDIS----------AHDGGAYTGE 83

sp|Q8XKU1|TPIS\_CLOPE ------------CLDAVKKAVEGT------NIKVGAQNMH----------FEEKGAFTGE 76

sp|P87108|TIM10\_YEAST -----------------------M----SFLGFGGGQ--P-----------QLSSQ--Q- 17

sp|Q9W2D6|TIM10\_DROME ----------------------------------MAL--P-----------QISTA--DQ 11

sp|Q75F72|TIM13\_ASHGO -----------------------M----ALSSIFGGGSPSQ---QSNLPTSSASSSVKDQ 30

sp|Q6GPY0|TI13A\_XENLA -----------------------------MEGFGSDFSVG---------GSSAGKVDTGA 22

sp|Q7SBR3|TIM13\_NEUCR --------------------------------------MS---------DSTSETVKK-A 12

sp|P0CS01|TIM13\_CRYNB -----------------------------MSSFFGSGAGS---------PSNDMTARKEQ 22

sp|Q09783|TIM8\_SCHPO --------------------------------------MAD---ATKNPIADLSESEQLE 19

sp|O60220|TIM8A\_HUMAN --------------------------------------MDS---SSSSSAAG-LGAVDPQ 18

sp|Q9WVA1|TIM8A\_RAT --------------------------------------MES---SSSSSGSA-LAAVDPQ 18

sp|P37527|PDXS\_BACSU VRKVVAMSE--------------------------------------------------- 179

sp|A7YW45|ANM5\_BOVIN TYEVF-EKD-----PI-K---YSQY------------------QQ--------------A 340

sp|Q5R698|ANM5\_PONAB TYEVF-EKD-----PI-K---YSQY------------------QQ--------------A 340

sp|Q9XGX9|TIM9\_ARATH DKAKMASMIDQLQLRD-S---LRMY------------------NS--------------L 39

sp|Q6FRT3|TIM9\_CANGA EQQEFQKLVEQKQMKD-F---MRLY------------------SG--------------L 31

sp|Q9WV98|TIM9\_MOUSE MAAQIPESDQIKQFKE-F---LGTY------------------NK--------------L 24

sp|Q17754|TIM9\_CAEEL ----MTSEQNIQTFRD-F---LTQY------------------NL--------------V 20

tr|A0A072VM55|A0A072VM55\_MEDTR ---------------------VEDP-----------------FDDA-------------- 90

sp|Q8F3Q1|CIMA\_LEPIN ---KSNSKTNINEIAITEASRLVEVFSGKRISANRPIVGEDVFTQTAGVHA-DGDKKGNL 311

sp|Q9SAU2|RPE\_ARATH QRVPDFIKAGADIVSV-HCEQQSTIHLHRT------------VNQIK--SL--GAKAG-- 169

sp|P0A858|TPIS\_ECOLI TSAAMLKDIGAQYIII-GHSERRTYH--KE------------SDELIAKKFAVLKEQGLT 122

sp|Q9RUP5|TPIS\_DEIRA ISAAMLKDAGASCVVV-GHSERREYH--DE------------SDAXVAAKARQAQANGLL 120

sp|Q9Z520|TPIS\_STRCO ISGPMLAKLKCTYVAV-GHSERRQYH--AE------------TDEIVNAKVKAAYKHGLT 128

sp|Q8XKU1|TPIS\_CLOPE IAPRMLEAMNIDYVII-GHSERREYF--NE------------TDETCNKKVKAAFAHNLT 121

sp|P87108|TIM10\_YEAST -K-IQAAEA--------ELDLVTDMF--NK------------LVNNC------------- 40

sp|Q9W2D6|TIM10\_DROME AKLQLMQEM--------EIEMMSDLY--NR------------MTNAC------------- 36

sp|Q75F72|TIM13\_ASHGO LKGQIAQEL--------AVANATELV--NK------------VTENC------------- 55

sp|Q6GPY0|TI13A\_XENLA IMEQVKVQI--------AVANAQELL--QR------------MTDKC------------- 47

sp|Q7SBR3|TIM13\_NEUCR IIKQVLIES--------QSANARTLM--EK------------IGENC------------- 37

sp|P0CS01|TIM13\_CRYNB MKQSIQQEL--------AIANAQQLI--NK------------INENC------------- 47

sp|Q09783|TIM8\_SCHPO LSKFIESEQ--------QKVKLQQAI--HQ------------FTSTC------------- 44

sp|O60220|TIM8A\_HUMAN LQHFIEVET--------QKQRFQQLV--HQ------------MTELC------------- 43

sp|Q9WVA1|TIM8A\_RAT LQHFIEVET--------QKQRFQQLV--HQ------------MTELC------------- 43

sp|P37527|PDXS\_BACSU ------------------------------------------------------------ 179

sp|A7YW45|ANM5\_BOVIN IYKCLLDRVPEEEKDTNIQVLMVLGAGRGPLVNASLRAAKQADRRIKLYAVEK-----NP 395

sp|Q5R698|ANM5\_PONAB IYKCLLDRVPEEEKDTNVQVLMVLGAGRGPLVNASLRAAKQADRRIKLYAVEK-----NP 395

sp|Q9XGX9|TIM9\_ARATH VERCFVDCVDSF------------------------------------------------ 51

sp|Q6FRT3|TIM9\_CANGA VERCFTDCVNDF------------------------------------------------ 43

sp|Q9WV98|TIM9\_MOUSE TETCFLDCVKDF------------------------------------------------ 36

sp|Q17754|TIM9\_CAEEL AEQCFNSCVNEF------------------------------------------------ 32

tr|A0A072VM55|A0A072VM55\_MEDTR PTYN--IPEKPVTFVEGASYSLVILAGL---------------------GVAAAAGYSVF 127

sp|Q8F3Q1|CIMA\_LEPIN YA----NPILPERFGRKRSYALGKLAGKASISEN-----------VKQLGMVLSEV--VL 354

sp|Q9SAU2|RPE\_ARATH VVLNPGTPLS------AIEYVLDMVDLV-----------------L-------------- 192

sp|P0A858|TPIS\_ECOLI PVLCIGETEAENEAGKTEEVCARQIDAV-----------------LKTQGAAAFEG--AV 163

sp|Q9RUP5|TPIS\_DEIRA PIVCVGENLDVRERGEHVPQTLAQLRGS-----------------LEGVGA----D--VV 157

sp|Q9Z520|TPIS\_STRCO PILCVGEELDVREAGNHVEHTLAQVEGG-----------------LKDLAAEQAES--VV 169

sp|Q8XKU1|TPIS\_CLOPE PILCCGETLEQRENGTTNDVIKAQITAD-----------------LEGLTKEQAEK--VV 162

sp|P87108|TIM10\_YEAST YKKCINTSYSEGELNKNESSCLDRCVAK-----------------Y-------------- 69

sp|Q9W2D6|TIM10\_DROME HKKCIPPRYSESELGKGEMVCIDRCVAK-----------------Y-------------- 65

sp|Q75F72|TIM13\_ASHGO FEKCLMAPYT--S---KQDTCVDQCLAK-----------------Y-------------- 79

sp|Q6GPY0|TI13A\_XENLA FRKCIGKPGG--SLDNSEQKCIAMCMDR-----------------Y-------------- 74

sp|Q7SBR3|TIM13\_NEUCR FTSCVPKPGS--SLSNSEKTCVTQCTEK-----------------Y-------------- 64

sp|P0CS01|TIM13\_CRYNB FAKCVTKPST--SLSSSQESCLSQCMTL-----------------Y-------------- 74

sp|Q09783|TIM8\_SCHPO WPKCIGNIGN--KLDKSEEQCLQNCVER-----------------F-------------- 71

sp|O60220|TIM8A\_HUMAN WEKCMDKPGP--KLDSRAEACFVNCVER-----------------F-------------- 70

sp|Q9WVA1|TIM8A\_RAT WEKCMDKPGP--KLDSRAEACFVNCVER-----------------F-------------- 70

sp|P37527|PDXS\_BACSU ------------------------------------------------------------ 179

sp|A7YW45|ANM5\_BOVIN NAVVTLENWQFEEWGSQVTVVSSDMREWVAPEKADIIVSELLGSFADNELSPESLDGAQH 455

sp|Q5R698|ANM5\_PONAB NAVVTLENWQFEEWGSQVTVVSSDMREWVAPEKADIIVSELLGSFADNELSPECLDGAQH 455

sp|Q9XGX9|TIM9\_ARATH ------------------------------------------------------------ 51

sp|Q6FRT3|TIM9\_CANGA ------------------------------------------------------------ 43

sp|Q9WV98|TIM9\_MOUSE ------------------------------------------------------------ 36

sp|Q17754|TIM9\_CAEEL ------------------------------------------------------------ 32

tr|A0A072VM55|A0A072VM55\_MEDTR KELIFQPKEYKIYNKALKRIQD-------D--------GQVRGRIGSPIT---------- 162

sp|Q8F3Q1|CIMA\_LEPIN QKV-LERV---IELGDQNKLV--------TPEDLPFIIADVSGRTGEKVL---------- 392

sp|Q9SAU2|RPE\_ARATH --I--MSVNP--GFGGQSFIES-------QVKKIS----DLRKM---------------- 219

sp|P0A858|TPIS\_ECOLI IAY--EPVWA-IGTGKSATPAQ-------AQAVHKFIRDHIAKV---------------- 197

sp|Q9RUP5|TPIS\_DEIRA VAY--EPVWA-IGTGKTATADD-------AEELAAAIRGALREQ---------------- 191

sp|Q9Z520|TPIS\_STRCO IAY--EPVWA-IGTGKVCGADD-------AQEVCAAIRGKLAEL---------------- 203

sp|Q8XKU1|TPIS\_CLOPE IAY--EPIWA-IGTGKTATSDQ-------ANETIAAIRAMVAEM---------------- 196

sp|P87108|TIM10\_YEAST -----FETNVQVGENMQKMGQS-------FNAAGKF------------------------ 93

sp|Q9W2D6|TIM10\_DROME -----LDIHEKIGKKLTAMSMQ-------DEELMKKMSS--------------------- 92

sp|Q75F72|TIM13\_ASHGO -----MRSWNAISQAYVARIQQ-------ASANGDI------------------------ 103

sp|Q6GPY0|TI13A\_XENLA -----MDAWNTVSRAYNSRLQR-------ERAKM-------------------------- 96

sp|Q7SBR3|TIM13\_NEUCR -----MAAWNVVNTTYLRRIQQ-------EMGNQ-------------------------- 86

sp|P0CS01|TIM13\_CRYNB -----MAAFDQVSRSYVARISK-------ERGVAPGL----------------------- 99

sp|Q09783|TIM8\_SCHPO -----LDCNFHI----IKRYAL-------EKFGFLFCWLGFSC----------------- 98

sp|O60220|TIM8A\_HUMAN -----IDTSQFI----LNRLEQ-------TQKSKPVFSESLSD----------------- 97

sp|Q9WVA1|TIM8A\_RAT -----IDTSQFI----LNRLEQ-------TQKSKPVFSESLSD----------------- 97

sp|P37527|PDXS\_BACSU ----------------------DELM-----------TEAKNLGAPYELLLQIKKDGKL- 205

sp|A7YW45|ANM5\_BOVIN FLKDDGVSIPGEYTSFLAPISSSKLYNEVRACREKDRDPEAQFEMPYVVRLHNFHQLSAP 515

sp|Q5R698|ANM5\_PONAB FLKDDGVSIPGEYTSFLAPISSSKLYNEVRACREKDRDPEAQFEMPYVVRLHNFHQLSAP 515

sp|Q9XGX9|TIM9\_ARATH --------------------TRKSLQKQEETCVMRCAEKFLKHTMRVGMRFAELNQNAPT 91

sp|Q6FRT3|TIM9\_CANGA --------------------TSSKLTSKEESCILKCSEKFLKHSERVGQRFQEQNAALGQ 83

sp|Q9WV98|TIM9\_MOUSE --------------------TTREVKPEEVTCSEHCLQKYLKMTQRISVRFQEYHIQQNE 76

sp|Q17754|TIM9\_CAEEL --------------------GSRTVSGKEESCANNCLDKFLKMTQRVSQRFQEHQLLNAQ 72

tr|A0A072VM55|A0A072VM55\_MEDTR ---------------------GYGQESRNRAA---RQRIPNRVWTDEEGVEHVE------ 192

sp|Q8F3Q1|CIMA\_LEPIN ---------------------TIKSCNIHSGI---GIRPHAQIELEYQGKIHKE------ 422

sp|Q9SAU2|RPE\_ARATH -------------------------------C----AEKGVNPWIEVDGGVTPA------ 238

sp|P0A858|TPIS\_ECOLI -----------------------------------DANIAEQVIIQYGGSVNAS------ 216

sp|Q9RUP5|TPIS\_DEIRA -------------------------------Y---GAR-AEGIRVLYGGSVKPE------ 210

sp|Q9Z520|TPIS\_STRCO -------------------------------Y---SQELADKVRIQYGGSVKSG------ 223

sp|Q8XKU1|TPIS\_CLOPE -------------------------------F---GQEVADKVRIQYGGSVKPN------ 216

sp|P87108|TIM10\_YEAST ------------------------------------------------------------ 93

sp|Q9W2D6|TIM10\_DROME ------------------------------------------------------------ 92

sp|Q75F72|TIM13\_ASHGO ------------------------------------------------------------ 103

sp|Q6GPY0|TI13A\_XENLA ------------------------------------------------------------ 96

sp|Q7SBR3|TIM13\_NEUCR ------------------------------------------------------------ 86

sp|P0CS01|TIM13\_CRYNB ------------------------------------------------------------ 99

sp|Q09783|TIM8\_SCHPO ------------------------------------------------------------ 98

sp|O60220|TIM8A\_HUMAN ------------------------------------------------------------ 97

sp|Q9WVA1|TIM8A\_RAT ------------------------------------------------------------ 97

sp|P37527|PDXS\_BACSU -PVVNFAAGGVATPAD----AALMMQLGADGVFVGS-GIFKS--DNPAKFAKAIV---EA 254

sp|A7YW45|ANM5\_BOVIN QPCFTFSHPNRDPMIDNNRYCTLEFPVEVNTVLHGFAGYFET--VLYQDITLSIRPETHS 573

sp|Q5R698|ANM5\_PONAB QPCFTFSHPNRDPMIDNNRYCTLEFPVEVNTVLHGFAGYFET--VLYQDITLSIRPETHS 573

sp|Q9XGX9|TIM9\_ARATH QD---------------------------------------------------------- 93

sp|Q6FRT3|TIM9\_CANGA GLGR-------------------------------------------------------- 87

sp|Q9WV98|TIM9\_MOUSE ALAAKAGLL-GQPR---------------------------------------------- 89

sp|Q17754|TIM9\_CAEEL ANGAAIKVE-NGGKINKIQ----------------------------------------- 90

tr|A0A072VM55|A0A072VM55\_MEDTR VNFFIRG-P------------------HGHGKVFAEMFKGADGEWSYTYLIVEIRAPS-- 231

sp|Q8F3Q1|CIMA\_LEPIN I--------------------------------S----EGDG---GYDAFMNALTKITNR 443

sp|Q9SAU2|RPE\_ARATH NAYKVIE-A------------------GANALVAGSAVFGAK---DYAEAIKGIKASKRP 276

sp|P0A858|TPIS\_ECOLI NAAELFAQP------------------DIDGALVGGASLKAD---AFAVIVKAAEAAKQA 255

sp|Q9RUP5|TPIS\_DEIRA NIAEICGKP------------------NVNGALVGGASLKVP---DVLGMLDALR----- 244

sp|Q9Z520|TPIS\_STRCO NVAEIMAKP------------------DIDGALVGGASLDSD---EFVKIVRFRDQ---- 258

sp|Q8XKU1|TPIS\_CLOPE TIAEQMAKS------------------DIDGALVGGASLVAA---DFAQIVNY------- 248

sp|P87108|TIM10\_YEAST ------------------------------------------------------------ 93

sp|Q9W2D6|TIM10\_DROME ------------------------------------------------------------ 92

sp|Q75F72|TIM13\_ASHGO ------------------------------------------------------------ 103

sp|Q6GPY0|TI13A\_XENLA ------------------------------------------------------------ 96

sp|Q7SBR3|TIM13\_NEUCR ------------------------------------------------------------ 86

sp|P0CS01|TIM13\_CRYNB ------------------------------------------------------------ 99

sp|Q09783|TIM8\_SCHPO ------------------------------------------------------------ 98

sp|O60220|TIM8A\_HUMAN ------------------------------------------------------------ 97

sp|Q9WVA1|TIM8A\_RAT ------------------------------------------------------------ 97

sp|P37527|PDXS\_BACSU TTHFTDYKLIAELSKELGTAMKGIEISNLLPEQR-------------------------- 288

sp|A7YW45|ANM5\_BOVIN PGMFSWFPILFPIKQPI-TVREGQTICVRFWRCS-------------------------- 606

sp|Q5R698|ANM5\_PONAB PGMFSWFPILFPIKQPI-TVREGQTICVRFWRCS-------------------------- 606

sp|Q9XGX9|TIM9\_ARATH ------------------------------------------------------------ 93

sp|Q6FRT3|TIM9\_CANGA ------------------------------------------------------------ 87

sp|Q9WV98|TIM9\_MOUSE ------------------------------------------------------------ 89

sp|Q17754|TIM9\_CAEEL ------------------------------------------------------------ 90

tr|A0A072VM55|A0A072VM55\_MEDTR -----PAQLILESYIPSYNPNK-------------------------------------- 248

sp|Q8F3Q1|CIMA\_LEPIN LGISIPKLIDYEVRIPPGGKTDALVETRITWNKSLDLEEDQTFKTMGVHPDQTVAAVHAT 503

sp|Q9SAU2|RPE\_ARATH AAVAV------------------------------------------------------- 281

sp|P0A858|TPIS\_ECOLI ------------------------------------------------------------ 255

sp|Q9RUP5|TPIS\_DEIRA ------------------------------------------------------------ 244

sp|Q9Z520|TPIS\_STRCO ------------------------------------------------------------ 258

sp|Q8XKU1|TPIS\_CLOPE ------------------------------------------------------------ 248

sp|P87108|TIM10\_YEAST ------------------------------------------------------------ 93

sp|Q9W2D6|TIM10\_DROME ------------------------------------------------------------ 92

sp|Q75F72|TIM13\_ASHGO ------------------------------------------------------------ 103

sp|Q6GPY0|TI13A\_XENLA ------------------------------------------------------------ 96

sp|Q7SBR3|TIM13\_NEUCR ------------------------------------------------------------ 86

sp|P0CS01|TIM13\_CRYNB ------------------------------------------------------------ 99

sp|Q09783|TIM8\_SCHPO ------------------------------------------------------------ 98

sp|O60220|TIM8A\_HUMAN ------------------------------------------------------------ 97

sp|Q9WVA1|TIM8A\_RAT ------------------------------------------------------------ 97

sp|P37527|PDXS\_BACSU --MQERGW------------------------- 294

sp|A7YW45|ANM5\_BOVIN --NSKKVWYEWAVTAPVCSAIHNPTGRSYTIGL 637

sp|Q5R698|ANM5\_PONAB --NSKKVWYEWAVTAPVCSAIHNPTGRSYTIGL 637

sp|Q9XGX9|TIM9\_ARATH --------------------------------- 93

sp|Q6FRT3|TIM9\_CANGA --------------------------------- 87

sp|Q9WV98|TIM9\_MOUSE --------------------------------- 89

sp|Q17754|TIM9\_CAEEL --------------------------------- 90

tr|A0A072VM55|A0A072VM55\_MEDTR --------------------------------- 248

sp|Q8F3Q1|CIMA\_LEPIN EKMLNQILQPWQI-------------------- 516

sp|Q9SAU2|RPE\_ARATH --------------------------------- 281

sp|P0A858|TPIS\_ECOLI --------------------------------- 255

sp|Q9RUP5|TPIS\_DEIRA --------------------------------- 244

sp|Q9Z520|TPIS\_STRCO --------------------------------- 258

sp|Q8XKU1|TPIS\_CLOPE --------------------------------- 248

sp|P87108|TIM10\_YEAST --------------------------------- 93

sp|Q9W2D6|TIM10\_DROME --------------------------------- 92

sp|Q75F72|TIM13\_ASHGO --------------------------------- 103

sp|Q6GPY0|TI13A\_XENLA --------------------------------- 96

sp|Q7SBR3|TIM13\_NEUCR --------------------------------- 86

sp|P0CS01|TIM13\_CRYNB --------------------------------- 99

sp|Q09783|TIM8\_SCHPO --------------------------------- 98

sp|O60220|TIM8A\_HUMAN --------------------------------- 97

sp|Q9WVA1|TIM8A\_RAT --------------------------------- 97

# MAFFT results:

>sp|O60220|TIM8A\_HUMAN Mitochondrial import inner membrane translocase subunit Tim8 A OS=Homo sapiens OX=9606 GN=TIMM8A PE=1 SV=1

MDSSSSSSA-----------------------------AGLGAVDP-QLQHFIEVETQKQ

R-----------------------------------------------------------

--FQQLVHQMTELCWEKCMD----------------------------------------

------------------------------------------------------------

------------------------------------------------------------

---KPGPK-----------------LDSRAEA----------------------------

----------------------------------CFVNCVER------------------

------------------------------------------------------------

-----------------------------------------------------FID----

----------TSQFILNRLEQTQ-----KSKPVFSESLSD--------------------

------------------------------------------------------------

------------------------------------------------------------

--

>sp|Q9WVA1|TIM8A\_RAT Mitochondrial import inner membrane translocase subunit Tim8 A OS=Rattus norvegicus OX=10116 GN=Timm8a PE=1 SV=1

MESSSSSSG-----------------------------SALAAVDP-QLQHFIEVETQKQ

R-----------------------------------------------------------

--FQQLVHQMTELCWEKCMD----------------------------------------

------------------------------------------------------------

------------------------------------------------------------

---KPGPK-----------------LDSRAEA----------------------------

----------------------------------CFVNCVER------------------

------------------------------------------------------------

-----------------------------------------------------FID----

----------TSQFILNRLEQTQ-----KSKPVFSESLSD--------------------

------------------------------------------------------------

------------------------------------------------------------

--

>sp|Q09783|TIM8\_SCHPO Mitochondrial import inner membrane translocase subunit tim8 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=tim8 PE=3 SV=1

MADATKNPI-----------------------------ADLSESEQLELSKFIESEQQKV

K-----------------------------------------------------------

--LQQAIHQFTSTCWPKCIG----------------------------------------

------------------------------------------------------------

------------------------------------------------------------

---NIGNK-----------------LDKSEEQ----------------------------

----------------------------------CLQNCVER------------------

------------------------------------------------------------

-----------------------------------------------------FLD----

----------CNFHIIKRY-ALE-----KFGFLFCWLGFSC-------------------

------------------------------------------------------------

------------------------------------------------------------

--

>sp|Q7SBR3|TIM13\_NEUCR Mitochondrial import inner membrane translocase subunit tim13 OS=Neurospora crassa (strain ATCC 24698 / 74-OR23-1A / CBS 708.71 / DSM 1257 / FGSC 987) OX=367110 GN=tim13 PE=1 SV=1

MS------------------------------------DSTSETVKKAIIKQVLIESQSA

N-----------------------------------------------------------

--ARTLMEKIGENCFTSCVP----------------------------------------

------------------------------------------------------------

------------------------------------------------------------

---KPGSS-----------------LSNSEKT----------------------------

----------------------------------CVTQCTEK------------------

------------------------------------------------------------

-----------------------------------------------------YMA----

----------AWNVVNTTYLRRI----------QQEMGNQ--------------------

------------------------------------------------------------

------------------------------------------------------------

--

>sp|Q6GPY0|TI13A\_XENLA Mitochondrial import inner membrane translocase subunit Tim13-A OS=Xenopus laevis OX=8355 GN=timm13-a PE=3 SV=2

MEGFGSDF------------SVGG--------------SSAGKVDTGAIMEQVKVQIAVA

N-----------------------------------------------------------

--AQELLQRMTDKCFRKCIG----------------------------------------

------------------------------------------------------------

------------------------------------------------------------

---KPGGS-----------------LDNSEQK----------------------------

----------------------------------CIAMCMDR------------------

------------------------------------------------------------

-----------------------------------------------------YMD----

----------AWNTVSRAYNSRL----------QRERAKM--------------------

------------------------------------------------------------

------------------------------------------------------------

--

>sp|Q75F72|TIM13\_ASHGO Mitochondrial import inner membrane translocase subunit TIM13 OS=Ashbya gossypii (strain ATCC 10895 / CBS 109.51 / FGSC 9923 / NRRL Y-1056) OX=284811 GN=TIM13 PE=3 SV=1

MALSS---------------IFGGGSPSQQS--NL-PTSSASSSVKDQLKGQIAQELAVA

N-----------------------------------------------------------

--ATELVNKVTENCFEKCLM----------------------------------------

------------------------------------------------------------

------------------------------------------------------------

---APYTS--------------------KQDT----------------------------

----------------------------------CVDQCLAK------------------

------------------------------------------------------------

-----------------------------------------------------YMR----

----------SWNAISQAYVARI----------QQASANGDI------------------

------------------------------------------------------------

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>sp|P0CS01|TIM13\_CRYNB Mitochondrial import inner membrane translocase subunit TIM13 OS=Cryptococcus neoformans var. neoformans serotype D (strain B-3501A) OX=283643 GN=TIM13 PE=3 SV=1

MSSFF---------------GSGAGSP-----------SNDMTARKEQMKQSIQQELAIA

N-----------------------------------------------------------

--AQQLINKINENCFAKCVT----------------------------------------

------------------------------------------------------------

------------------------------------------------------------

---KPSTS-----------------LSSSQES----------------------------

----------------------------------CLSQCMTL------------------

------------------------------------------------------------

-----------------------------------------------------YMA----

----------AFDQVSRSYVARI----------SKERGVAP-------------------

------------------------------------------------------------

------------------------------------------------------------

GL

>sp|P87108|TIM10\_YEAST Mitochondrial import inner membrane translocase subunit TIM10 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TIM10 PE=1 SV=1

MSFLG---------------FGGGQ-------------PQLSSQQKIQAA-----EAELD

L-----------------------------------------------------------

--VTDMFNKLVNNCYKKCIN----------------------------------------

------------------------------------------------------------

------------------------------------------------------------

---TSYSEG---------------ELNKNESS----------------------------

----------------------------------CLDRCVAK------------------

------------------------------------------------------------

-----------------------------------------------------YFE----

----------TNVQVGENMQKMG----------QSFNAAGK-------------------

--------------------------------------F---------------------

------------------------------------------------------------

--

>sp|Q9W2D6|TIM10\_DROME Mitochondrial import inner membrane translocase subunit Tim10 OS=Drosophila melanogaster OX=7227 GN=Tim10 PE=3 SV=1

MAL-----------------------------------PQISTADQAKLQ--LMQEMEIE

M-----------------------------------------------------------

--MSDLYNRMTNACHKKCIP----------------------------------------

------------------------------------------------------------

------------------------------------------------------------

---PRYSES---------------ELGKGEMV----------------------------

----------------------------------CIDRCVAK------------------

------------------------------------------------------------

-----------------------------------------------------YLD----

----------IHEKIGKKLTAMS---------MQDEELMKK-----------MSS-----

------------------------------------------------------------

------------------------------------------------------------

--

>sp|Q9WV98|TIM9\_MOUSE Mitochondrial import inner membrane translocase subunit Tim9 OS=Mus musculus OX=10090 GN=Timm9 PE=1 SV=1

MA------------------------------------AQIPESDQIK---------QFK

E-----------------------------------------------------------

--FLGTYNKLTETCFLDCVK----------------------------------------

------------------------------------------------------------

------------------------------------------------------------

---DFTTR----------------EVKPEEVT----------------------------

----------------------------------CSEHCLQK------------------

------------------------------------------------------------

-----------------------------------------------------YLK----

----------MTQRISVRFQEYHI--------QQNEALAAK-------------------

-------------------------AGLLGQPR---------------------------

------------------------------------------------------------

--

>sp|Q17754|TIM9\_CAEEL Mitochondrial import inner membrane translocase subunit Tim9 OS=Caenorhabditis elegans OX=6239 GN=tin-9.1 PE=3 SV=1

----------------------------------------MTSEQNIQ---------TFR

D-----------------------------------------------------------

--FLTQYNLVAEQCFNSCVN----------------------------------------

------------------------------------------------------------

------------------------------------------------------------

---EFGSR----------------TVSGKEES----------------------------

----------------------------------CANNCLDK------------------

------------------------------------------------------------

-----------------------------------------------------FLK----

----------MTQRVSQRFQEHQL--------LNAQANGAA-----------IKVE----

------------------------NGGKINKIQ---------------------------

------------------------------------------------------------

--

>sp|Q9XGX9|TIM9\_ARATH Mitochondrial import inner membrane translocase subunit TIM9 OS=Arabidopsis thaliana OX=3702 GN=TIM9 PE=1 SV=2

MDASM---------------MAGL--------------DGLPEEDKAKMASMID-QLQLR

D-----------------------------------------------------------

--SLRMYNSLVERCFVDCVD----------------------------------------

------------------------------------------------------------

------------------------------------------------------------

---SFTRK----------------SLQKQEET----------------------------

----------------------------------CVMRCAEK------------------

------------------------------------------------------------

-----------------------------------------------------FLK----

----------HTMRVGMRFAELN----------QNAPTQD--------------------

------------------------------------------------------------

------------------------------------------------------------

--

>sp|Q6FRT3|TIM9\_CANGA Mitochondrial import inner membrane translocase subunit TIM9 OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) OX=284593 GN=TIM9 PE=3 SV=1

M-------------------------------------DQLNAKEQQEFQKLVE-QKQMK

D-----------------------------------------------------------

--FMRLYSGLVERCFTDCVN----------------------------------------

------------------------------------------------------------

------------------------------------------------------------

---DFTSS----------------KLTSKEES----------------------------

----------------------------------CILKCSEK------------------

------------------------------------------------------------

-----------------------------------------------------FLK----

----------HSERVGQRFQE------------QNAALGQG-----------LGR-----

------------------------------------------------------------

------------------------------------------------------------

--

>sp|P0A858|TPIS\_ECOLI Triosephosphate isomerase OS=Escherichia coli (strain K12) OX=83333 GN=tpiA PE=1 SV=1

MRHPL---------------VMGNWK------------LNGSRHMVHELVSNLRKELAGV

A---GCAVAIAP-----------------------------------------------P

EMYIDMAKREAEGSH---IMLGA-------------------------------------

-------------------------QNVDLNLSG-----------AFTGETSAAM-----

---------------------------------------------LKDIGAQYIIIG---

---HSERR----------------TYHKESDE---------LIAKKFAVLKEQ-------

-GLTPVL---------------------------CIGETEAE---------NEAGKTEEV

--------------------CARQIDAVLKTQGAAAFEGAVIAYEPV----------WAI

--GTGKSATPAQAQAVHK-----------------------------------FIRDH--

----------IAKV-DANIAEQV--IIQYGGSVNASNAAEL-----------FAQPD---

------------------------IDGALVGGA----SLKADAFAVIVKAAEAAK-----

-------------------QA---------------------------------------

--

>sp|Q9Z520|TPIS\_STRCO Triosephosphate isomerase OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=tpiA PE=1 SV=1

MTTRTP-------------LMAGNWK------------MNLNHLEAIAHVQKLAFALADK

DY-DAVEVAVLA-----------------------------------------------P

FTDLRSVQTLVDGDKL-KIKYGA-------------------------------------

-------------------------QDISAHDGG-----------AYTGEISGPM-----

---------------------------------------------LAKLKCTYVAVG---

---HSERR----------------QYHAETDE---------IVNAKVKAAYKH-------

-GLTPIL---------------------------CVGEELDV---------REAGNHVEH

--------------------TLAQVEGGLKDLAAEQAESVVIAYEPV----------WAI

--GTGKVCGADDAQEVCA-----------------------------------AIRGK--

----------LAELYSQELADKV--RIQYGGSVKSGNVAEI-----------MAKPD---

------------------------IDGALVGGA----SLDSDEFVKIVRFRDQ-------

------------------------------------------------------------

--

>sp|Q8XKU1|TPIS\_CLOPE Triosephosphate isomerase OS=Clostridium perfringens (strain 13 / Type A) OX=195102 GN=tpiA PE=1 SV=1

MRTPI---------------IAGNWK------------MHYTIDEAVKLVEELKPLVKDA

K----CEVVVCP-----------------------------------------------T

FVCLDAVKKAVEGTN---IKVGA-------------------------------------

-------------------------QNMHFEEKG-----------AFTGEIAPRM-----

---------------------------------------------LEAMNIDYVIIG---

---HSERR----------------EYFNETDE---------TCNKKVKAAFAH-------

-NLTPIL---------------------------CCGETLEQ---------RENGTTNDV

--------------------IKAQITADLEGLTKEQAEKVVIAYEPI----------WAI

--GTGKTATSDQANETIA-----------------------------------AIRAM--

----------VAEMFGQEVADKV--RIQYGGSVKPNTIAEQ-----------MAKSD---

------------------------IDGALVGGA----SLVAADFAQIVNY----------

------------------------------------------------------------

--

>sp|Q9RUP5|TPIS\_DEIRA Triosephosphate isomerase OS=Deinococcus radiodurans (strain ATCC 13939 / DSM 20539 / JCM 16871 / LMG 4051 / NBRC 15346 / NCIMB 9279 / R1 / VKM B-1422) OX=243230 GN=tpiA PE=1 SV=1

MQT-L---------------LALNWK------------MNKTPTEARSWAEELTTKYAPA

E---GVDLAVLA-----------------------------------------------P

ALDLSALAANLPAG----IAFGG-------------------------------------

-------------------------QDVSAHESG-----------AYTGEISAAM-----

---------------------------------------------LKDAGASCVVVG---

---HSERR----------------EYHDESDA---------XVAAKARQAQAN-------

-GLLPIV---------------------------CVGENLDV---------RERGEHVPQ

--------------------TLAQLRGSLEGVGAD----VVVAYEPV----------WAI

--GTGKTATADDAEELAA-----------------------------------AIRGA--

----------LREQYGAR-AEGI--RVLYGGSVKPENIAEI-----------CGKPN---

------------------------VNGALVGGA----SLKVPDVLGMLDALR--------

------------------------------------------------------------

--

>sp|A7YW45|ANM5\_BOVIN Protein arginine N-methyltransferase 5 OS=Bos taurus OX=9913 GN=PRMT5 PE=2 SV=1

MAAMA---------------VGGAGG------------SRVSSGRDLNCVPEIADTLGAV

A-KQGFDFLCMPVFHPRFKREFTQEPAKSRPGPQTRSDLLLSGRDWNTLIVGKLSPWIRP

DSKVEKIRRNSEAAMLQELNFGA-YLGLPAFLLPLNQEDNTNLARVLTNHIHTGHHSSMF

WMRVPLVAPEDLRDDIIENAPTSHTEEYSGEEKTWMWWHNFRTLCDYSKRIAVALEIGAD

LPSNHVIDRWLGEPIKAAILPTSIFLTNKKGFPVLSKMHQRLIFRLLKLEVQFIITGTNH

---HSEKEFC---SYLQ-----YLEYLSQNRPP---PNAYELFAKGYEDYLQS-------

-PLQPLMDNLESQTYEVFEKDPIKYSQYQQAIYKCLLDRVPE---------EEKDTNIQV

LMVLGA-GRGPLVNAS--LRAAKQADRRIKLYAVEKNPNAVVTLENW---QF---EEW--

--GSQVTVVSSDMREWVAPEKADIIVSELLGSFAD----NEL-SPESLDGAQHFLKDD-G

VSIPGEYTSFLAPISSSKLYNEV--RACREKDRDPEAQFEMPYVVRLHNFHQLSAPQPCF

TFSHPNRDPMIDNNRYCTLEFPVEVNTVLHGFAGYFETVLYQDITLSIRPETHSPGMFSW

FPIL---FPIKQPITVREGQTICVRFWRCSNSKKVWYEWAVTA-PVCSAIHNPTGRSYTI

GL

>sp|Q5R698|ANM5\_PONAB Protein arginine N-methyltransferase 5 OS=Pongo abelii OX=9601 GN=PRMT5 PE=2 SV=3

MAAMA---------------VGGAGG------------SRVSSGRDLNCVPEIADTLGAV

A-KQGFDFLCMPVFHPRFKREFIQEPAKNRPGPQTRSDLLLSGRDWNTLIVGKLSPWIRP

DSEVEKIRRNSEAAMLQELNFGA-YLGLPAFLLPLNQEDNTNLARVLTNHIHTGHHSSMF

WMRVPLVAPEDLRDDIIENAPTTHTQEYSGEEKTWIWWHNFRTLCDYSKRIAVALEIGAD

LPSNHVIDRWLGEPIKAAILPTSIFLTNKKGFPVLSKMHQRLIFRLLKLEVQFIITGTNH

---HSEKEFC---SYLQ-----YLEYLSQNRPP---PNAYELFAKGYEDYLQS-------

-PLQPLMDNLESQTYEVFEKDPIKYSQYQQAIYKCLLDRVPE---------EEKDTNVQV

LMVLGA-GRGPLVNAS--LRAAKQADRRIKLYAVEKNPNAVVTLENW---QF---EEW--

--GSQVTVVSSDMREWVAPEKADIIVSELLGSFAD----NEL-SPECLDGAQHFLKDD-G

VSIPGEYTSFLAPISSSKLYNEV--RACREKDRDPEAQFEMPYVVRLHNFHQLSAPQPCF

TFSHPNRDPMIDNNRYCTLEFPVEVNTVLHGFAGYFETVLYQDITLSIRPETHSPGMFSW

FPIL---FPIKQPITVREGQTICVRFWRCSNSKKVWYEWAVTA-PVCSAIHNPTGRSYTI

GL

>sp|Q8F3Q1|CIMA\_LEPIN (R)-citramalate synthase CimA OS=Leptospira interrogans serogroup Icterohaemorrhagiae serovar Lai (strain 56601) OX=189518 GN=cimA PE=1 SV=1

MTKVETRLEILDV-----TLRDGEQTR----------GVSFSTSEKLNIAKFLLQKLNVD

R----VEIASARV----------------------------------------------S

KGELETVQKIMEWAATEQLTERIEILGFVDGNKTVDWIKDSG-AKVL-------------

--------------NLLTKGSLHHLEKQLGKTPK-----------EFFTDVSFVIEY---

-------------AIKSGLKINVYLEDWSNGFRNSPDYVKSLVEHLSKEHIERIFLPDTL

GVLSPEETFQGVDSLIQKYPDIHFEFHGHNDYDLSVANSLQAIRAGVKGLHASINGLGER

AGNTPLEA----------------------LVTTIHDKSNSK-TNINEIAITEASRLVEV

-------FSGKRISANRPI-VGEDVFTQTAGVHADGDKKGNLYANPILPERFGRKRSYAL

GKLAGKASISENVKQLGMV-LSEVVLQKVLERVIELGDQNKLVTPEDL----PFIIAD--

----------VSGRTGEKVLTIKSCNIHSGIGIRPHAQIELEYQGKIHK--EISEGDGG-

------------------------YDAFMNALTKI-TNRLGISIPKLIDYEVRIPPGGKT

DALVETRITWNKSLDLEEDQTF--------KTMGVHPDQTVAAVHATEKMLNQILQPWQI

--

>tr|A0A072VM55|A0A072VM55\_MEDTR Mitochondrial import inner membrane translocase subunit Tim21 OS=Medicago truncatula OX=3880 GN=25484536 PE=3 SV=1

MFRIRRILSYRALASCTRNALSSSSQP-----------RSLPRSNAPILPPPFFLDVGIA

ENYGSTSLTRFM-----------------------------------------------S

SNASSEQGKNTEKTKKELKN----------------------------------------

------------------------VEDPFDDAPT-----------YNIPEKPVTF-----

--------------VEGASYSLVI---------------------LAGLGVAAAAGY---

---SVFKE---------------LIFQPKEYK----------------------------

----------------------------------IYNKALKR--------IQDDGQ----

--------------------VRGRIGSPITGYGQESRNRAARQRIPN--------RVWTD

EEGV-------EHVEVNF-----------------------------------FIRGPHG

------HGKVFAEMFKGADGEWS--YTYLIVEIRAPSPAQL-------------------

-----------------------ILESYIPSYNP--------------------------

----------NK------------------------------------------------

--

>sp|P37527|PDXS\_BACSU Pyridoxal 5'-phosphate synthase subunit PdxS OS=Bacillus subtilis (strain 168) OX=224308 GN=pdxS PE=1 SV=3

MAQTGTERVKRGM-----AEMQKGGVI-----------MDVINAEQAKIAEEAGAVAVMA

LERVPADI---R------------------------------------------------

--AAGGVARMADPTIVEEVM----------------------------------------

------------------------------------------------NAVSIPV-----

--------------MAKARIGHIVE--------------ARV---LEAMGVDYIDESE--

-VLTPADE--------------EFHLNKNEYT----------------------------

---VPFV---------------------------CGCRDLGEATR----RIAEGASMLRT

K---GEPGTGNIVEA---VRHMRKVNAQVRKVVAMSEDELMTEAKNL-------------

--GA----------------------------------------PYEL-----LLQ----

----------IKKDGKLPVVNFA-----AGGVATPADAALM-----------MQLG----

------------------------ADGVFVGSG----IFKSDNPAKFAKAIVEATTHFTD

YKLI---AELSKELGT-----------------------AMKGIEISNLL--PEQRMQER

GW

>sp|Q9SAU2|RPE\_ARATH Ribulose-5-phosphate-3-epimerase, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=RPE PE=2 SV=1

MSTSAASLCCSS------TQVNGFGLRPERSLLYQPTSFSFSRRRTHGIVKASSRVDRFS

K----SDIIVS------------------------------------------------P

SILSANFAKLGEQVKAVELA------G---------------------------------

-----------------------------------------------CDWIHVDV-----

--------------MDGRFVPNIT---------------------IGPLVVDAL------

---RPVTDLP-LDVHL-------MIVEPEQRVP-------DFIKAGADIVSVH-------

----------------------------------CEQQSTIH--------LHRTVNQIKS

L---GA-KAGVVL-------NPGTPLSAIEYVLDMVDLVLIMSVNPGF------------

--G-GQS----------------------------------------------FIESQ--

-------VKKISDLRKMCAEKGVNPWIEVDGGVTPANAYKV-----------IEAG----

------------------------ANALVAGSA----VFGAKDYAEAIKGIKASK-----

-------------------------------------------------------RPAAV

AV

# MUSCLECLUSTAL multiple sequence alignment by MUSCLE (3.8)

sp|P37527|PDXS\_BACSU ----------MAQTGTERVKRGMAEMQKGGVIMDVINAEQAKIAEEAGAVAVM-------

sp|Q8F3Q1|CIMA\_LEPIN MTKVETRLEILDVTLRDGEQTRGVSFSTSEKLNIAKFLLQKLNVDRVEIASARVSKGELE

sp|P0A858|TPIS\_ECOLI ---------MRHPLVMGNWKLNGSRHMVHELVSNLRKELAGVAGCAVAIAPPE-------

sp|Q9RUP5|TPIS\_DEIRA ----------MQTLLALNWKMNKTPTEARSWAEELTTKYA--PAEGVDLAVLA-------

sp|Q8XKU1|TPIS\_CLOPE ---------MRTPIIAGNWKMHYTIDEAVKLVEELKPLVKDAKCEVVVCPTFV-------

sp|Q9Z520|TPIS\_STRCO -------MTTRTPLMAGNWKMNLNHLEAIAHVQKLAFALADKDYDAVEVAVLA-------

tr|A0A072VM55|A0A072VM55\_MEDTR ----------------------------MFRIRRILSYRALASCTRNALSSSS-------

sp|Q9SAU2|RPE\_ARATH -----------------------------MSTSAASLCCSSTQVNGFGLRPER-------

sp|P87108|TIM10\_YEAST ---------------------------------------------MSFLGFGG-------

sp|Q9W2D6|TIM10\_DROME ------------------------------------------------------------

sp|Q9WV98|TIM9\_MOUSE ------------------------------------------------------------

sp|Q17754|TIM9\_CAEEL ------------------------------------------------------------

sp|Q9XGX9|TIM9\_ARATH ----------------------------------------------MDASMMA-------

sp|Q6FRT3|TIM9\_CANGA ------------------------------------------------------------

sp|A7YW45|ANM5\_BOVIN ---------MAAMAVGGAGGSRVSSGRDLNCVPEIADTLGAVAKQGFDFLCMPVFHPRFK

sp|Q5R698|ANM5\_PONAB ---------MAAMAVGGAGGSRVSSGRDLNCVPEIADTLGAVAKQGFDFLCMPVFHPRFK

sp|Q09783|TIM8\_SCHPO ----------------------------------------------MADATKN-------

sp|O60220|TIM8A\_HUMAN ----------------------------------------------MDSSSSS-------

sp|Q9WVA1|TIM8A\_RAT ----------------------------------------------MESSSSS-------

sp|Q6GPY0|TI13A\_XENLA -------------------------------------------MEGFGSDFSV-------

sp|Q7SBR3|TIM13\_NEUCR ------------------------------------------------------------

sp|Q75F72|TIM13\_ASHGO ----------------------------------------MALSSIFGGGSPS-------

sp|P0CS01|TIM13\_CRYNB ------------------------------------------MSSFFGSGAGS-------

sp|P37527|PDXS\_BACSU ---------------------ALERVPA--------------------------------

sp|Q8F3Q1|CIMA\_LEPIN TVQKIMEWAATEQLTERIEILGFVDGNKTVDWIKDSGAKVLNLLTKGSLHHLEKQLGKTP

sp|P0A858|TPIS\_ECOLI ---------------------MYIDMAK--------------------------------

sp|Q9RUP5|TPIS\_DEIRA ---------------------PALDLSA--------------------------------

sp|Q8XKU1|TPIS\_CLOPE ---------------------CLDAVKK--------------------------------

sp|Q9Z520|TPIS\_STRCO ---------------------PFTDLRS--------------------------------

tr|A0A072VM55|A0A072VM55\_MEDTR ---------------------QPRSLPR--------------------------------

sp|Q9SAU2|RPE\_ARATH ---------------------SLLYQPT--------------------------------

sp|P87108|TIM10\_YEAST ---------------------GQPQLSS--------------------------------

sp|Q9W2D6|TIM10\_DROME -----------------------MALPQ--------------------------------

sp|Q9WV98|TIM9\_MOUSE ---------------------MAAQIPE--------------------------------

sp|Q17754|TIM9\_CAEEL ------------------------------------------------------------

sp|Q9XGX9|TIM9\_ARATH ---------------------GLDGLPE--------------------------------

sp|Q6FRT3|TIM9\_CANGA ----------------------MDQLNA--------------------------------

sp|A7YW45|ANM5\_BOVIN REFTQE---------------PAKSRPGPQTRSDLLLSGRDWNTLIVGKLSPWIRPDSKV

sp|Q5R698|ANM5\_PONAB REFIQE---------------PAKNRPGPQTRSDLLLSGRDWNTLIVGKLSPWIRPDSEV

sp|Q09783|TIM8\_SCHPO ---------------------PIADLSE--------------------------------

sp|O60220|TIM8A\_HUMAN ---------------------SAAGLGA--------------------------------

sp|Q9WVA1|TIM8A\_RAT ---------------------SGSALAA--------------------------------

sp|Q6GPY0|TI13A\_XENLA ---------------------GGSSAGK--------------------------------

sp|Q7SBR3|TIM13\_NEUCR ---------------------MSDSTSE--------------------------------

sp|Q75F72|TIM13\_ASHGO ---------------------QQSNLPT--------------------------------

sp|P0CS01|TIM13\_CRYNB ---------------------PSNDMTA--------------------------------

sp|P37527|PDXS\_BACSU --------DIRAAGGVARMADPTIVEEVMNAVSIPVMAKARIGHIVEARVLEAMGVD---

sp|Q8F3Q1|CIMA\_LEPIN KEFFTDVSFVIEYAIKSGLKINVYLEDWSNGFRNSPDYVKSLVEHLSKEHIERIFLPDTL

sp|P0A858|TPIS\_ECOLI -------------------REAEGSHIMLGAQNVDLNLSGAFTGETSAAMLKDI------

sp|Q9RUP5|TPIS\_DEIRA ------------------LAANLPAGIAFGGQDVSAHESGAYTGEISAAMLKDA------

sp|Q8XKU1|TPIS\_CLOPE --------------------AVEGTNIKVGAQNMHFEEKGAFTGEIAPRMLEAM------

sp|Q9Z520|TPIS\_STRCO ---------------VQTLVDGDKLKIKYGAQDISAHDGGAYTGEISGPMLAKL------

tr|A0A072VM55|A0A072VM55\_MEDTR SNAPILPPPFFLDVGIAENYGSTSLTRFMSSNASSEQGKNTEKTKKELKNVEDPFDDAPT

sp|Q9SAU2|RPE\_ARATH -------------SFSFSRRRTHGIVKASSRVDRFSKSDIIVSPSILSANFAKLGEQVKA

sp|P87108|TIM10\_YEAST -------------------------------------QQKIQAAEAELDLVTDM------

sp|Q9W2D6|TIM10\_DROME -------------------------------ISTADQAKLQLMQEMEIEMMSDL------

sp|Q9WV98|TIM9\_MOUSE --------------------------------SDQIKQFKEFLGT---------------

sp|Q17754|TIM9\_CAEEL -----------------------------------------MTSEQNIQTFRDFLTQ---

sp|Q9XGX9|TIM9\_ARATH ---------------------------------EDKAKMASMIDQLQLRDSLRM------

sp|Q6FRT3|TIM9\_CANGA ---------------------------------KEQQEFQKLVEQKQMKDFMRL------

sp|A7YW45|ANM5\_BOVIN EKIRRNSEAAMLQELNFGAYLGLPAFLLPLNQEDNTNLARVLTNHIHTGHHSSMFWMRVP

sp|Q5R698|ANM5\_PONAB EKIRRNSEAAMLQELNFGAYLGLPAFLLPLNQEDNTNLARVLTNHIHTGHHSSMFWMRVP

sp|Q09783|TIM8\_SCHPO --------------------------------SEQLELSKFIESEQQKVKLQQA------

sp|O60220|TIM8A\_HUMAN ---------------------------------VDPQLQHFIEVETQKQRFQQL------

sp|Q9WVA1|TIM8A\_RAT ---------------------------------VDPQLQHFIEVETQKQRFQQL------

sp|Q6GPY0|TI13A\_XENLA --------------------------------VDTGAIMEQVKVQIAVANAQEL------

sp|Q7SBR3|TIM13\_NEUCR --------------------------------TVKKAIIKQVLIESQSANARTL------

sp|Q75F72|TIM13\_ASHGO ---------------------------SSASSSVKDQLKGQIAQELAVANATEL------

sp|P0CS01|TIM13\_CRYNB ---------------------------------RKEQMKQSIQQELAIANAQQL------

sp|P37527|PDXS\_BACSU -----------------------------------------------------YIDESEV

sp|Q8F3Q1|CIMA\_LEPIN GVLSPEETFQGVDSLIQKYPDIHFEFHGHNDYDLSVANSLQAIRAGVKGLHASINGLGER

sp|P0A858|TPIS\_ECOLI -----------------GAQYIIIGHSERRT----------------------YHKESDE

sp|Q9RUP5|TPIS\_DEIRA -----------------GASCVVVGHSERRE----------------------YHDESDA

sp|Q8XKU1|TPIS\_CLOPE -----------------NIDYVIIGHSERREY---------------------FNETDET

sp|Q9Z520|TPIS\_STRCO -----------------KCTYVAVGHSERRQ----------------------YHAETDE

tr|A0A072VM55|A0A072VM55\_MEDTR YNIPEKPVTFVEGASYSLVILAGLGVAAAAG----------------------YSVFKEL

sp|Q9SAU2|RPE\_ARATH VELAGCDWIHVDVMDGRFVPNITIGPLVVDA----------------------LRPVTDL

sp|P87108|TIM10\_YEAST -----------------------------------------------------FNKLVNN

sp|Q9W2D6|TIM10\_DROME -----------------------------------------------------YNRMTNA

sp|Q9WV98|TIM9\_MOUSE -----------------------------------------------------YNKLTET

sp|Q17754|TIM9\_CAEEL -----------------------------------------------------YNLVAEQ

sp|Q9XGX9|TIM9\_ARATH -----------------------------------------------------YNSLVER

sp|Q6FRT3|TIM9\_CANGA -----------------------------------------------------YSGLVER

sp|A7YW45|ANM5\_BOVIN LVAPEDLRDDIIENAPTSHTEEYSGEEKTWMW---------------------WHNFRTL

sp|Q5R698|ANM5\_PONAB LVAPEDLRDDIIENAPTTHTQEYSGEEKTWIW---------------------WHNFRTL

sp|Q09783|TIM8\_SCHPO -----------------------------------------------------IHQFTST

sp|O60220|TIM8A\_HUMAN -----------------------------------------------------VHQMTEL

sp|Q9WVA1|TIM8A\_RAT -----------------------------------------------------VHQMTEL

sp|Q6GPY0|TI13A\_XENLA -----------------------------------------------------LQRMTDK

sp|Q7SBR3|TIM13\_NEUCR -----------------------------------------------------MEKIGEN

sp|Q75F72|TIM13\_ASHGO -----------------------------------------------------VNKVTEN

sp|P0CS01|TIM13\_CRYNB -----------------------------------------------------INKINEN

sp|P37527|PDXS\_BACSU L-----TPAD-------------EE-----------------------------------

sp|Q8F3Q1|CIMA\_LEPIN AGNTPLEALVTTIHDKSNSKTNINE-----------------------------------

sp|P0A858|TPIS\_ECOLI L-------IA-------------KK-----------------------------------

sp|Q9RUP5|TPIS\_DEIRA X-------VA-------------AK-----------------------------------

sp|Q8XKU1|TPIS\_CLOPE C--------N-------------KK-----------------------------------

sp|Q9Z520|TPIS\_STRCO I-------VN-------------AK-----------------------------------

tr|A0A072VM55|A0A072VM55\_MEDTR IFQPKEYKIY-------------NK-----------------------------------

sp|Q9SAU2|RPE\_ARATH P-------LD-------------VH-----------------------------------

sp|P87108|TIM10\_YEAST C-----------------------------------------------------------

sp|Q9W2D6|TIM10\_DROME C-----------------------------------------------------------

sp|Q9WV98|TIM9\_MOUSE C-----------------------------------------------------------

sp|Q17754|TIM9\_CAEEL C-----------------------------------------------------------

sp|Q9XGX9|TIM9\_ARATH C-----------------------------------------------------------

sp|Q6FRT3|TIM9\_CANGA C-----------------------------------------------------------

sp|A7YW45|ANM5\_BOVIN CDYSKRIAVALEIGADLPSNHVIDRWLGEPIKAAILPTSIFLTNKKGFPVLSKMHQRLIF

sp|Q5R698|ANM5\_PONAB CDYSKRIAVALEIGADLPSNHVIDRWLGEPIKAAILPTSIFLTNKKGFPVLSKMHQRLIF

sp|Q09783|TIM8\_SCHPO C-----------------------------------------------------------

sp|O60220|TIM8A\_HUMAN C-----------------------------------------------------------

sp|Q9WVA1|TIM8A\_RAT C-----------------------------------------------------------

sp|Q6GPY0|TI13A\_XENLA C-----------------------------------------------------------

sp|Q7SBR3|TIM13\_NEUCR C-----------------------------------------------------------

sp|Q75F72|TIM13\_ASHGO C-----------------------------------------------------------

sp|P0CS01|TIM13\_CRYNB C-----------------------------------------------------------

sp|P37527|PDXS\_BACSU ---------FHLNKNEYTVPFVCGCRD------LGEATRRIAEGASMLRTKGEPGTGNIV

sp|Q8F3Q1|CIMA\_LEPIN ---------IAITEASRLVEVFSGKRISANRPIVGEDVFTQTAGVHADGDKKGNLYANPI

sp|P0A858|TPIS\_ECOLI ---------FAVLKEQGLTPVLC----------IGET----------------------E

sp|Q9RUP5|TPIS\_DEIRA ---------ARQAQANGLLPIVC----------VGEN----------------------L

sp|Q8XKU1|TPIS\_CLOPE ---------VKAAFAHNLTPILC----------CGET----------------------L

sp|Q9Z520|TPIS\_STRCO ---------VKAAYKHGLTPILC----------VGEE----------------------L

tr|A0A072VM55|A0A072VM55\_MEDTR ---------ALKRIQDDGQVRGR----------IGSP-----------------------

sp|Q9SAU2|RPE\_ARATH ---------LMIVEPEQRVPDFIKAGADIVSVHCEQQ-------------------STIH

sp|P87108|TIM10\_YEAST -------------------YKKC----------INTS-----------------------

sp|Q9W2D6|TIM10\_DROME -------------------HKKC----------IPPR-----------------------

sp|Q9WV98|TIM9\_MOUSE -------------------FLDC----------VKDF-----------------------

sp|Q17754|TIM9\_CAEEL -------------------FNSC----------VNEF-----------------------

sp|Q9XGX9|TIM9\_ARATH -------------------FVDC----------VDSF-----------------------

sp|Q6FRT3|TIM9\_CANGA -------------------FTDC----------VNDF----------------------T

sp|A7YW45|ANM5\_BOVIN RLLKLEVQFIITGTNHHSEKEFCSYLQYLEYLSQNRP----------------PPNAYEL

sp|Q5R698|ANM5\_PONAB RLLKLEVQFIITGTNHHSEKEFCSYLQYLEYLSQNRP----------------PPNAYEL

sp|Q09783|TIM8\_SCHPO -------------------WPKC----------IGNI-----------------------

sp|O60220|TIM8A\_HUMAN -------------------WEKC----------MDKP-----------------------

sp|Q9WVA1|TIM8A\_RAT -------------------WEKC----------MDKP-----------------------

sp|Q6GPY0|TI13A\_XENLA -------------------FRKC----------IGKP-----------------------

sp|Q7SBR3|TIM13\_NEUCR -------------------FTSC----------VPKP-----------------------

sp|Q75F72|TIM13\_ASHGO -------------------FEKC----------LMAP-----------------------

sp|P0CS01|TIM13\_CRYNB -------------------FAKC----------VTKP-----------------------

sp|P37527|PDXS\_BACSU EAVRHMRKVNAQVRKVVAMSEDELMTEAKNLGAPY-------------------------

sp|Q8F3Q1|CIMA\_LEPIN LPERFGRKRSYALGKLAGKASISENVKQLGMVLSEVVLQKVL------------------

sp|P0A858|TPIS\_ECOLI AENEAGKTEEVCARQIDAVLKTQGAAAFEGAVIAY-------------------------

sp|Q9RUP5|TPIS\_DEIRA DVRERGEHVPQTLAQLRGSLEGVGAD----VVVAY-------------------------

sp|Q8XKU1|TPIS\_CLOPE EQRENGTTNDVIKAQITADLEGLTKEQAEKVVIAY-------------------------

sp|Q9Z520|TPIS\_STRCO DVREAGNHVEHTLAQVEGGLKDLAAEQAESVVIAY-------------------------

tr|A0A072VM55|A0A072VM55\_MEDTR ------------------------------------------------------------

sp|Q9SAU2|RPE\_ARATH LHRTVNQIKSLGAKAGVVLNPGTPLSAIEYVLDMV-------------------------

sp|P87108|TIM10\_YEAST ------------------------------------------------------------

sp|Q9W2D6|TIM10\_DROME ------------------------------------------------------------

sp|Q9WV98|TIM9\_MOUSE ------------------------------------------------------------

sp|Q17754|TIM9\_CAEEL ------------------------------------------------------------

sp|Q9XGX9|TIM9\_ARATH ------------------------------------------------------------

sp|Q6FRT3|TIM9\_CANGA ------------------------------------------------------------

sp|A7YW45|ANM5\_BOVIN FAKGYEDYLQSPLQPLMDNLESQTYEVFEKDPIKYSQYQQAIYKCLLDRVPEEEKDTNIQ

sp|Q5R698|ANM5\_PONAB FAKGYEDYLQSPLQPLMDNLESQTYEVFEKDPIKYSQYQQAIYKCLLDRVPEEEKDTNVQ

sp|Q09783|TIM8\_SCHPO ------------------------------------------------------------

sp|O60220|TIM8A\_HUMAN ------------------------------------------------------------

sp|Q9WVA1|TIM8A\_RAT ------------------------------------------------------------

sp|Q6GPY0|TI13A\_XENLA ------------------------------------------------------------

sp|Q7SBR3|TIM13\_NEUCR ------------------------------------------------------------

sp|Q75F72|TIM13\_ASHGO ------------------------------------------------------------

sp|P0CS01|TIM13\_CRYNB ------------------------------------------------------------

sp|P37527|PDXS\_BACSU ----------------------------------------------------ELLLQIKK

sp|Q8F3Q1|CIMA\_LEPIN ----------------------------------------------------ERVIELGD

sp|P0A858|TPIS\_ECOLI ----------------------------------------------------EPVWAIG-

sp|Q9RUP5|TPIS\_DEIRA ----------------------------------------------------EPVWAIG-

sp|Q8XKU1|TPIS\_CLOPE ----------------------------------------------------EPIWAIG-

sp|Q9Z520|TPIS\_STRCO ----------------------------------------------------EPVWAIG-

tr|A0A072VM55|A0A072VM55\_MEDTR --------------------------------------------------------ITG-

sp|Q9SAU2|RPE\_ARATH ----------------------------------------------------DLVLIMSV

sp|P87108|TIM10\_YEAST --------------------------------------------------------YSE-

sp|Q9W2D6|TIM10\_DROME ------------------------------------------------------------

sp|Q9WV98|TIM9\_MOUSE ------------------------------------------------------------

sp|Q17754|TIM9\_CAEEL ----------------------------------------------------------G-

sp|Q9XGX9|TIM9\_ARATH ---------------------------------------------------------TR-

sp|Q6FRT3|TIM9\_CANGA ----------------------------------------------------------S-

sp|A7YW45|ANM5\_BOVIN VLMVLGAGRGPLVNASLRAAKQADRRIKLYAVEKNPNAVVTLENWQFEEWGSQVTVVSSD

sp|Q5R698|ANM5\_PONAB VLMVLGAGRGPLVNASLRAAKQADRRIKLYAVEKNPNAVVTLENWQFEEWGSQVTVVSSD

sp|Q09783|TIM8\_SCHPO ----------------------------------------------------------G-

sp|O60220|TIM8A\_HUMAN ----------------------------------------------------------G-

sp|Q9WVA1|TIM8A\_RAT ----------------------------------------------------------G-

sp|Q6GPY0|TI13A\_XENLA ----------------------------------------------------------G-

sp|Q7SBR3|TIM13\_NEUCR ----------------------------------------------------------G-

sp|Q75F72|TIM13\_ASHGO ------------------------------------------------------------

sp|P0CS01|TIM13\_CRYNB ----------------------------------------------------------S-

sp|P37527|PDXS\_BACSU DGKLPVVNFAAGGVATP---ADA-------------------------------------

sp|Q8F3Q1|CIMA\_LEPIN QNKLVTPEDLPFIIADV---SGR-------------------------------------

sp|P0A858|TPIS\_ECOLI TGKSATPAQAQAVHKFI---RDH-------------------------------------

sp|Q9RUP5|TPIS\_DEIRA TGKTATADDAEELAAAI---RGA-------------------------------------

sp|Q8XKU1|TPIS\_CLOPE TGKTATSDQANETIAAI---RAM-------------------------------------

sp|Q9Z520|TPIS\_STRCO TGKVCGADDAQEVCAAI---RGK-------------------------------------

tr|A0A072VM55|A0A072VM55\_MEDTR -YGQ---ESRNRAA------RQR-------------------------------------

sp|Q9SAU2|RPE\_ARATH NPGFGGQSFIESQVKKISDLRKM-------------------------------------

sp|P87108|TIM10\_YEAST -GEL---NKNESSC------LDR-------------------------------------

sp|Q9W2D6|TIM10\_DROME -YSESELGKGEMVC------IDR-------------------------------------

sp|Q9WV98|TIM9\_MOUSE --TTREVKPEEVTC------SEH-------------------------------------

sp|Q17754|TIM9\_CAEEL -SRTV--SGKEESC------ANN-------------------------------------

sp|Q9XGX9|TIM9\_ARATH -KSL---QKQEETC------VMR-------------------------------------

sp|Q6FRT3|TIM9\_CANGA -SKL---TSKEESC------ILK-------------------------------------

sp|A7YW45|ANM5\_BOVIN MREWVAPEKADIIVSELLGSFADNELSPESLDGAQHFLKDDGVSIPGEYTSFLAPISSSK

sp|Q5R698|ANM5\_PONAB MREWVAPEKADIIVSELLGSFADNELSPECLDGAQHFLKDDGVSIPGEYTSFLAPISSSK

sp|Q09783|TIM8\_SCHPO -NKL---DKSEEQC------LQN-------------------------------------

sp|O60220|TIM8A\_HUMAN -PKL---DSRAEAC------FVN-------------------------------------

sp|Q9WVA1|TIM8A\_RAT -PKL---DSRAEAC------FVN-------------------------------------

sp|Q6GPY0|TI13A\_XENLA -GSL---DNSEQKC------IAM-------------------------------------

sp|Q7SBR3|TIM13\_NEUCR -SSL---SNSEKTC------VTQ-------------------------------------

sp|Q75F72|TIM13\_ASHGO ------YTSKQDTC------VDQ-------------------------------------

sp|P0CS01|TIM13\_CRYNB -TSL---SSSQESC------LSQ-------------------------------------

sp|P37527|PDXS\_BACSU -------ALMMQL-------------GADGVFVGSGIFKSDNP-----------------

sp|Q8F3Q1|CIMA\_LEPIN -------TGEKVLTIKSCNIHSGIGIRP-HAQIELEYQGKIHKEISEGDGGYDAFMNALT

sp|P0A858|TPIS\_ECOLI -------IAKVDA-------------NI-AEQVIIQYGGSVNA-----------------

sp|Q9RUP5|TPIS\_DEIRA -------LREQYG-------------AR-AEGIRVLYGGSVKP-----------------

sp|Q8XKU1|TPIS\_CLOPE -------VAEMFG-------------QEVADKVRIQYGGSVKP-----------------

sp|Q9Z520|TPIS\_STRCO -------LAELYS-------------QELADKVRIQYGGSVKS-----------------

tr|A0A072VM55|A0A072VM55\_MEDTR -------IPNRVW-------------TD-EEGVEHVEVNFFIR-----------------

sp|Q9SAU2|RPE\_ARATH -------CAEKGV-------------NP-WIEVDGGVTPANAY-----------------

sp|P87108|TIM10\_YEAST -------CVAKYF-------------ET-NVQVGENM-QKMGQ-----------------

sp|Q9W2D6|TIM10\_DROME -------CVAKYL-------------DI-HEKIGKKLTAMSMQ-----------------

sp|Q9WV98|TIM9\_MOUSE -------CLQKYL-------------KM-TQRISVRFQEYHIQ-----------------

sp|Q17754|TIM9\_CAEEL -------CLDKFL-------------KM-TQRVSQRFQEHQLL-----------------

sp|Q9XGX9|TIM9\_ARATH -------CAEKFL-------------KH-TMRVGMRFAELNQN-----------------

sp|Q6FRT3|TIM9\_CANGA -------CSEKFL-------------KH-SERVGQRFQEQNAA-----------------

sp|A7YW45|ANM5\_BOVIN LYNEVRACREKDR-------------DP-EAQFEMPYVVRLHN-----------------

sp|Q5R698|ANM5\_PONAB LYNEVRACREKDR-------------DP-EAQFEMPYVVRLHN-----------------

sp|Q09783|TIM8\_SCHPO -------CVERFL-------------DC-NFHIIKRYALEKFG-----------------

sp|O60220|TIM8A\_HUMAN -------CVERFI-------------DT-SQFIL----NRLEQ-----------------

sp|Q9WVA1|TIM8A\_RAT -------CVERFI-------------DT-SQFIL----NRLEQ-----------------

sp|Q6GPY0|TI13A\_XENLA -------CMDRYM-------------DA-WNTVSRAYNSRLQR-----------------

sp|Q7SBR3|TIM13\_NEUCR -------CTEKYM-------------AA-WNVVNTTYLRRIQQ-----------------

sp|Q75F72|TIM13\_ASHGO -------CLAKYM-------------RS-WNAISQAYVARIQQ-----------------

sp|P0CS01|TIM13\_CRYNB -------CMTLYM-------------AA-FDQVSRSYVARISK-----------------

.

sp|P37527|PDXS\_BACSU ----------------------------AKFAKAIVEATTHFTDYKLIAELSKELGTAMK

sp|Q8F3Q1|CIMA\_LEPIN KITNRLGISIPKLIDYEVRIPPGGKTDALVETRITWNKSLDLEEDQTFKTMGVHPDQTVA

sp|P0A858|TPIS\_ECOLI ------------------------SNAAELFAQPDIDGALVGGASLKADAFAVIVKAAEA

sp|Q9RUP5|TPIS\_DEIRA ------------------------ENIAEICGKPNVNGALVGGASLKVPDVLGMLDALR-

sp|Q8XKU1|TPIS\_CLOPE ------------------------NTIAEQMAKSDIDGALVGGASLVAADFAQIVNY---

sp|Q9Z520|TPIS\_STRCO ------------------------GNVAEIMAKPDIDGALVGGASLDSDEFVKIVRFRDQ

tr|A0A072VM55|A0A072VM55\_MEDTR ----------------------------GPHGHGKVFAEMFKGADGEWSYTYLIVEIRAP

sp|Q9SAU2|RPE\_ARATH -------------------------KVIEAGANALVAGSAVFGAKDYAEAIKGIKASKRP

sp|P87108|TIM10\_YEAST ----------------------------SFNAAGKF------------------------

sp|Q9W2D6|TIM10\_DROME ----------------------------DEELMKKMSS----------------------

sp|Q9WV98|TIM9\_MOUSE ----------------------------QNEALAAKAGLLGQPR----------------

sp|Q17754|TIM9\_CAEEL ----------------------------NAQANGAAIKVENGGKINKIQ-----------

sp|Q9XGX9|TIM9\_ARATH --------------------------------APTQD-----------------------

sp|Q6FRT3|TIM9\_CANGA ----------------------------LGQGLGR-------------------------

sp|A7YW45|ANM5\_BOVIN ------------------FHQLSAPQPCFTFSHPNRDPMIDNNRYCTLEFPVEVNTVLHG

sp|Q5R698|ANM5\_PONAB ------------------FHQLSAPQPCFTFSHPNRDPMIDNNRYCTLEFPVEVNTVLHG

sp|Q09783|TIM8\_SCHPO ----------------------------FLFCWLGFSC----------------------

sp|O60220|TIM8A\_HUMAN ----------------------------TQKSKPVFSESLSD------------------

sp|Q9WVA1|TIM8A\_RAT ----------------------------TQKSKPVFSESLSD------------------

sp|Q6GPY0|TI13A\_XENLA ----------------------------ERAKM---------------------------

sp|Q7SBR3|TIM13\_NEUCR ----------------------------EMGNQ---------------------------

sp|Q75F72|TIM13\_ASHGO -----------------------------ASANGDI------------------------

sp|P0CS01|TIM13\_CRYNB ----------------------------ERGVAPGL------------------------

sp|P37527|PDXS\_BACSU GIEISNLLPEQRMQERGW------------------------------------------

sp|Q8F3Q1|CIMA\_LEPIN AVHATEKMLNQILQPWQI------------------------------------------

sp|P0A858|TPIS\_ECOLI AKQA--------------------------------------------------------

sp|Q9RUP5|TPIS\_DEIRA ------------------------------------------------------------

sp|Q8XKU1|TPIS\_CLOPE ------------------------------------------------------------

sp|Q9Z520|TPIS\_STRCO ------------------------------------------------------------

tr|A0A072VM55|A0A072VM55\_MEDTR SPAQLILESYIPSYNPNK------------------------------------------

sp|Q9SAU2|RPE\_ARATH AAVAV-------------------------------------------------------

sp|P87108|TIM10\_YEAST ------------------------------------------------------------

sp|Q9W2D6|TIM10\_DROME ------------------------------------------------------------

sp|Q9WV98|TIM9\_MOUSE ------------------------------------------------------------

sp|Q17754|TIM9\_CAEEL ------------------------------------------------------------

sp|Q9XGX9|TIM9\_ARATH ------------------------------------------------------------

sp|Q6FRT3|TIM9\_CANGA ------------------------------------------------------------

sp|A7YW45|ANM5\_BOVIN FAGYFETVLYQDITLSIRPETHSPGMFSWFPILFPIKQPITVREGQTICVRFWRCSNSKK

sp|Q5R698|ANM5\_PONAB FAGYFETVLYQDITLSIRPETHSPGMFSWFPILFPIKQPITVREGQTICVRFWRCSNSKK

sp|Q09783|TIM8\_SCHPO ------------------------------------------------------------

sp|O60220|TIM8A\_HUMAN ------------------------------------------------------------

sp|Q9WVA1|TIM8A\_RAT ------------------------------------------------------------

sp|Q6GPY0|TI13A\_XENLA ------------------------------------------------------------

sp|Q7SBR3|TIM13\_NEUCR ------------------------------------------------------------

sp|Q75F72|TIM13\_ASHGO ------------------------------------------------------------

sp|P0CS01|TIM13\_CRYNB ------------------------------------------------------------

sp|P37527|PDXS\_BACSU ---------------------------

sp|Q8F3Q1|CIMA\_LEPIN ---------------------------

sp|P0A858|TPIS\_ECOLI ---------------------------

sp|Q9RUP5|TPIS\_DEIRA ---------------------------

sp|Q8XKU1|TPIS\_CLOPE ---------------------------

sp|Q9Z520|TPIS\_STRCO ---------------------------

tr|A0A072VM55|A0A072VM55\_MEDTR ---------------------------

sp|Q9SAU2|RPE\_ARATH ---------------------------

sp|P87108|TIM10\_YEAST ---------------------------

sp|Q9W2D6|TIM10\_DROME ---------------------------

sp|Q9WV98|TIM9\_MOUSE ---------------------------

sp|Q17754|TIM9\_CAEEL ---------------------------

sp|Q9XGX9|TIM9\_ARATH ---------------------------

sp|Q6FRT3|TIM9\_CANGA ---------------------------

sp|A7YW45|ANM5\_BOVIN VWYEWAVTAPVCSAIHNPTGRSYTIGL

sp|Q5R698|ANM5\_PONAB VWYEWAVTAPVCSAIHNPTGRSYTIGL

sp|Q09783|TIM8\_SCHPO ---------------------------

sp|O60220|TIM8A\_HUMAN ---------------------------

sp|Q9WVA1|TIM8A\_RAT ---------------------------

sp|Q6GPY0|TI13A\_XENLA ---------------------------

sp|Q7SBR3|TIM13\_NEUCR ---------------------------

sp|Q75F72|TIM13\_ASHGO ---------------------------

sp|P0CS01|TIM13\_CRYNB ---------------------------