

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
MVEKRELRCRLGALLMLCATLPAGAQTADWKEQSYAYSADRTPLSTVLQDFADGHSVD
LHLGNVEDTEVTAKIRAENASAFDLRLALEHHFQWFVYNNNTLYVSPQDEQSSERLEISPD
AAPDIKQALSGIGLLDPRFGWGELPDDGVVLVTGPPQYLELVKRFSEQREKKEDRRKVM
TFFPLRYASVADRTIHYRDQTVVIPGVATMLNELMNGKRAAPASASGIDSTPGGPD
TNSMMQNTQTLLSRLSSRNKTSNRAGGRDNEIEDVSGRISADVRRNALLIRDDDKRHDEYSQ
LIAKIDVFPQNLVEIDAVILDIDRTALNRLEANWQATLGGVTGGSSLMSSGTLFVSDFKRFFAD
IQALEGEGTASIVANPSVLTLENQPAVIDFSQTAYITATGERVADIQPV
TAGTSLQVTPRAVGNEGHSSIQLMIDIEDGHVQTN
GDGQATGVKRGTVSTQALISENRALVLGGFHV
EESADRDRRIPLLGDIPWLGLQLFSSKRHEISQRQRLFILTPRLIGDQTD
PTRYVTADNRQQLSDRAMGRVERRHSSVNQH
DVENALRDIAEGQSPAGFQPQTSGTRLSEVCRSTPALLFESTRG
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	900	1305
Total score	900	1305
Query Cover	90%	100%
e Value	0	0
Percentage Identity	67%	100%
Accession Length	617	691

SWISS-PROT:

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


Commented [SD2]:

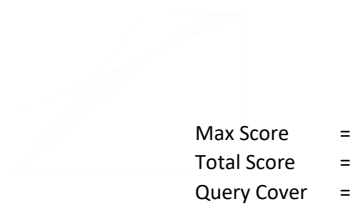
Commented [SD1]:

2. 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

- 
3. 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%

4. 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%

5. 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[string1[i:i+5]]+=1
    for i in range(len(string2)-4):
        if string2[i:i+5] not in thisdict:
            thisdict[string2[i:i+5]]=1
        else:
            thisdict[string2[i:i+5]]+=1
    return thisdict

string1="MVHWTAEKQLITGLWGKVNVAECGAEALARLLIVYPWTQRRFFASFGNLSSPTAILGNPMV
RAHGKKVLTSGDAVKNLNDNIKNTFSQLSELHCDKLHVDPENFRLLGDILIIVLAHFHFKDFTPECQAAWQ
KLVVVVAHALARKYH"
string2="MVHLTPEEKSAVTALWGKVNVDVEVGGEALGRLLVVYPWTQRRFFESFGDLSTPDVAMGNPK
VKAHGKKVLGAFSDGLAHLNDLKGTFATLSELHCDKLHVDPENFRLLGNVLCVLAHHFGKEFTPPVQAA
YQKVVAGVANALAHKYH"
```

```
print(match_pentaPP(string1, string2))
```

6. 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=' 'MVHWTAEKQLITGLWGKVNVAECGAEALARLLIVYPWTQRRFFASFGNLSS
PTAILGNPMVRAHGKKVLTSGDAVKNLNDNIKNTFSQLSELHCDKLHVDPENFRLLGDILII
VLAHFHFKDFTPECQAAWQKLVVVVAHALARKYH' '
string2=' 'MVHLTPEEKSAVTALWGKVNVDVEVGGEALGRLLVVYPWTQRRFFESFGDLST
PDVAMGNPKVKAHGKKVLGAFSDGLAHLNDLKGTFATLSELHCDKLHVDPENFRLLGNVLC
VLAHHFGKEFTPPVQAAYQKVVAGVANALAHKYH' '
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)))
```

7. 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](#), [MAFFT](#), [MUSCLE](#)

8. 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	21.4	53.2
Total score	21.4	53.2
Query Cover	42%	100%
e Value	2e-10	34
Percentage Identity	41.67%	100%
Accession Length	201	1290

There are three domain hits for the given sequence:

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

Commented [SD3]:

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      -----
sp|Q6FRT3|TIM9_CANGA      -----
sp|Q9WV98|TIM9_MOUSE      -----
sp|Q17754|TIM9_CAEEL      -----
tr|A0A072VM55|A0A072VM55_MEDTR -----
sp|Q8F3Q1|CIMA_LEPIN      MTKVE-----TRLEILDVTLRDGEQTRGVSFSTSEKLNIAKFLQKL-----NVDRV-- 47
sp|Q9SAU2|RPE_ARATH      MSTSA-----ASLC-----CSSTQVNGFGLRPERS----- 25
sp|P0A858|TPIS_ECOLI      -----
sp|Q9RUP5|TPIS_DEIRA      -----
sp|Q9Z520|TPIS_STRCO      -----
sp|Q8XKU1|TPIS_CLOPE      -----
sp|P87108|TIM10_YEAST      -----
sp|Q9W2D6|TIM10_DROME      -----
sp|Q75F72|TIM13_ASHGO      -----
sp|Q6GPY0|TI13A_XENLA      -----
sp|Q7SBR3|TIM13_NEUCR      -----
sp|P0CS01|TIM13_CRYNB      -----
sp|Q09783|TIM8_SCHPO      -----
sp|O60220|TIM8A_HUMAN      -----
sp|Q9WVA1|TIM8A_RAT        -----

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-VDYIDSEVLTPADEEF-----	
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	SSMFWMRVPLVAPEDLRDDIIENAPTSHTEEYSGEEKTWMMWHNFRTLCDYSKRIAAVALE	
207		
sp Q5R698 ANM5_PONAB	SSMFWMRVPLVAPEDLRDDIIENAPTTHTQEYSGEEKTWIWWHNFRTLCDYSKRIAAVALE	
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	PPPFLLDVGIAENYGSTS-----LTR--FMSSNASSE-----QGKNTKTK	77

sp Q8F3Q1 CIMA_LEPIN 167	PKEFFTDVSFVIEYAIKS-----GLKINVYLEDWSNGFRNSPDYVKSLVEHLS	
sp Q9SAU2 RPE_ARATH	-----VSPSILSANFAKL--GE-----	74
sp P0A858 TPIS_ECOLI	-----MRHPLVMGNWKLN--GSRHMHVELVSNLR	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 163	--A-----SMLRTKGPGTGNIVEAVRH-----	
sp A7YW45 ANM5_BOVIN 267	IGADLPSNHVIDRWLGEPKAAILPTSIFLTNKKGFPVLSKMHQRLIFRLLKLEVQFIIT	
sp Q5R698 ANM5_PONAB 267	IGADLPSNHVIDRWLGEPKAAILPTSIFLTNKKGFPVLSKMHQRLIFRLLKLEVQFIIT	
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 207	KE-----HIERIF-LPDTLGVLSPREETFQ---GVDS-----LIQKYP--DIHFEFH	
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-----NITIGPLVVDALRPVTDLPDVLHLMIVEPE	
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-----GSSAGKVDIGA	22
sp Q7SBR3 TIM13_NEUCR	-----MS-----DSTSETVKK-A	12
sp P0CS01 TIM13_CRYNB	-----MSSFFGSGAGS-----PSNDMTARKEQ	22
sp Q09783 TIM8_SCHPO	-----MAD---ATKNPIADLSESEGLE	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	---KSNSKTNINEIAITEASRLVEVFSGKRISANRPVGEDVFTQTAGVHA-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 121	IAPRMLEAMNIDYVII-GHSERREYF--NE-----TDETCNKKVKAFAHNLT	
sp P87108 TIM10_YEAST	-K-IQAAEA-----ELDLVTDMF--NK-----LVNNC-----	40
sp Q9W2D6 TIM10_DROME	AKLQLMQEM-----EIEEMSDLY--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 395	IYKCLLDRVPEEEKDTNIQVLMVLGAGRGPLVNASLRAAKQADRRIKLYAVEK-----NP	
sp Q5R698 ANM5_PONAB 395	IYKCLLDRVPEEEKDTNVQVLMVLGAGRGPLVNASLRAAKQADRRIKLYAVEK-----NP	
sp Q9XGX9 TIM9_ARATH	VERCFVDCVDSF-----	51
sp Q6FRT3 TIM9_CANGA	VERCFTDCVNDF-----	43
sp Q9WV98 TIM9_MOUSE	TETCFLDCVKDF-----	36
sp Q17754 TIM9_CAEEL	AEQCFCNSCVNEF-----	32
tr A0A072VM55 A0A072VM55_MEDTR 127	PTYN--IPEKPVTFVEGASYSLVILAGL-----GVAAAAGYSVF	
sp Q8F3Q1 CIMA_LEPIN 354	YA----NPILPERFGRKRSYALGKLAGKASISEN-----VKQLGMVLSEV--VL	
sp Q9SAU2 RPE_ARATH 192	VVLNPGTPLS-----AIEYVLDMDVLV-----L-----	
sp P0A858 TPIS_ECOLI 163	PVLCIGETEAENEAGKTEEVCAEQIDAV-----LKTQGAAAFEG--AV	
sp Q9RUP5 TPIS_DEIRA 157	PIVCVGENLDVRERGEHVPQTLAQLRGS-----LEGVGA----D--VV	

sp Q9Z520 TPIS_STRCO 169	PILCVGEELDVREAGNHVEHTLAQVEGG-----LKDLAAEQAES--VV	
sp Q8XKU1 TPIS_CLOPE 162	PILCCGETLEQRENGTTNDVIKAQITAD-----LEGLTKEQAEK--VV	
sp P87108 TIM10_YEAST	YKKCINTSYSEGELNKNNESSCLDRCVAK-----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 455	NAVVTLENWQFEEWGSQVTVVSSDMREWVAPEKADIIVSELLGSFADNELSPESLDGAQH	
sp Q5R698 ANM5_PONAB 455	NAVVTLENWQFEEWGSQVTVVSSDMREWVAPEKADIIVSELLGSFADNELSPECILDGAQH	
sp Q9XGX9 TIM9_ARATH	-----	51
sp Q6FRT3 TIM9_CANGA	-----	43
sp Q9WV98 TIM9_MOUSE	-----	36
sp Q17754 TIM9_CAEEL	-----	32
tr A0A072VM55 A0A072VM55_MEDTR 162	KELIFQPKEYKIYNKALKRIQD-----D-----GQVRGRIGSPIT-----	
sp Q8F3Q1 CIMA_LEPIN 392	QKV-LERV---IELGDQNKLV-----TPEDLPFIIADVSGRTGEKVL-----	
sp Q9SAU2 RPE_ARATH 219	--I--MSVNP--GFGGQSFIES-----QVKKIS---DLRKM-----	
sp P0A858 TPIS_ECOLI 197	IAY--EPVWA-IGTGKSATPAQ-----AQAVHKFIRDHIAKV-----	

sp Q9RUP5 TPIS_DEIRA 191	VAY--EPVWA-IGTGKTATADD-----AEELAAAIRGALREQ-----	
sp Q9Z520 TPIS_STRCO 203	IAY--EPVWA-IGTGKVCGADD-----AQEVCAAIRGKLAEL-----	
sp Q8XKU1 TPIS_CLOPE 196	IAY--EPIWA-IGTGKTATSDQ-----ANETIAAIRAMVAEM-----	
sp P87108 TIM10_YEAST	-----FETNVQVGENMQKMGS-----FNAAGKF-----	93
sp Q9W2D6 TIM10_DROME	-----LDIHEKIGKKLTAMSMQ-----DEELMKKMSS-----	92
sp Q75F72 TIM13_ASHGO 103	-----MRSWNAISQAYVARIQQ-----ASANGDI-----	
sp Q6GPY0 TI13A_XENLA	-----MDAWNTVSRAYNSRLQR-----ERAKM-----	96
sp Q7SBR3 TIM13_NEUCR	-----MAAWNVTNTTYLRRIQQ-----EMGNQ-----	86
sp P0CS01 TIM13_CRYNB	-----MAAFDQVSRSYVARISK-----ERGVAPGL-----	99
sp Q09783 TIM8_SCHPO	-----LDCNFHI----IKRYAL-----EKFGFLFCWLGFSC-----	98
sp O60220 TIM8A_HUMAN	-----IDTSQFI----LNRLEQ-----TQKSKPVFSESLS-----	97
sp Q9WVA1 TIM8A_RAT	-----IDTSQFI----LNRLEQ-----TQKSKPVFSESLS-----	97
sp P37527 PDXS_BACSU 205	-----DELM-----TEAKNLGAPYELLQIKKDGKL-	
sp A7YW45 ANM5_BOVIN 515	FLKDDGVSIPEGYTSFLAPISSSKLYNEVRACREKDRDPEAQFEMPYVVRHLNHFHQLSAP	
sp Q5R698 ANM5_PONAB 515	FLKDDGVSIPEGYTSFLAPISSSKLYNEVRACREKDRDPEAQFEMPYVVRHLNHFHQLSAP	
sp Q9XGX9 TIM9_ARATH	-----TRKSLQKQEETCVMRCAEKFLKHTMRVGMRFaelnQNAPT	91
sp Q6FRT3 TIM9_CANGA	-----TSSKLTSCKEESCILKCSEKFLKHSErVGQRfQEQNAALGQ	83
sp Q9WV98 TIM9_MOUSE	-----TTREVKPEEVTcSEHCLQKYLKMTQRISVRFQeYHIQQNE	76
sp Q17754 TIM9_CAEEL	-----GSRTVSGKEESCANNCLDKFLKMTQRVSQRfQEHQLLNAQ	72
tr A0A072VM55 A0A072VM55_MEDTR 192	-----GYGQESRNRAA---RQRIPNRVWTDEEGVEHVE-----	
sp Q8F3Q1 CIMA_LEPIN 422	-----TIKSCNIHSGI---GIRPHAQIELEYQGKIHK-----	

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	QPCFTFSPNRPMDIDNNRYCTLEFPVEVNTVLHGFAGYFET--VLYQDITLSIRPETHS	
573		
sp Q5R698 ANM5_PONAB	QPCFTFSPNRPMDIDNNRYCTLEFPVEVNTVLHGFAGYFET--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-----HGKGKVF AEMFKGADGEWSYTYLIVEIRAPS--	
231		
sp Q8F3Q1 CIMA_LEPIN	I-----S----EGDG---GYDAFMNALTKITNR	
443		
sp Q9SAU2 RPE_ARATH	NAYKVIE-A-----GANALVAGSAVFGAK---DYAEA IKG I KASKRP	
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	-----PAQLILESYPNPNK-----	
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-----
--FQQLVHQMTLCEWEKCMD-----
-----
-----
---KPGPK-----LDSRAEA-----
-----CFVNCVER-----
-----FID-----
-----TSQFILNRLEQTQ-----KSKPVFSESLSLSD-----
-----

```

```
-----
--
>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-----DSTSETVKKAIKQVLIESQSA
N-----
--ARTLMEKIGENCFTSCVP-----
-----
-----
```

```
---KPGSS-----LSNSEKT-----
-----CVTQCTEK-----
-----YMA-----
-----AWNVTNTTYLRRI-----QQEMGNQ-----
-----
```

```
--
>sp|Q6GPY0|TI13A_XENLA Mitochondrial import inner membrane translocase subunit Tim13-A OS=Xenopus laevis OX=8355
GN=tim13-a PE=3 SV=2
MEGFGSDF-----SVGG-----SSAGKVDTGAISEQVKVQIAVA
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-----IFGGGSPSQS--NL-PTSSASSSVKDQLKGQIAQELAVA
N-----
```

```
--ATELVNKVTENCFEKCLM-----
-----
-----APYTS-----KQDT-----
-----CVDQCLAK-----
-----YMR-----
-----SWNAISQAYVARI-----QQASANGDI-----
-----
-----
```

>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-----

-----AFDQVSRYSYVARI-----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-----PQLSSQQKIQA-----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-----  
--FLGTYNKLTETCFDCVK-----  
-----  
-----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-----
--SLRMYNLSVERCFVDCVD-----

--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-----LNGSRHVMHELVSNLRKELAGV
A---GCAVAIAP-----P
EMYIDMAKREAEGSH---IMLGA-----
-----QNVDLNLSG-----AFTGETSAAM-----
-----LKDIGAQYIIIG---
---HSERR-----TYHKESDE-----LIAKKFAVLKEQ-----
-GLTPVL-----CIGETEAE-----NEAGKTEEV
-----CARQIDAVLKTQGAAAFEGAVIAYEPV-----WAI
--GTGKSATPAQAQAVHK-----FIRDH--
-----IAKV-DANIAEQV--IIQYGGSVNASNAAEL-----FAQPD--
-----IDGALVGGA---SLKADAFVIVKAAEAAK-----


```

-----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-----TCNKKVKAFAH-----
-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-----MNKTPTEARSWAEELTTYAPA
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-KQGFDFLCMPVFHPRFKREFEQEPAKSRPGPQTRSDLLSGRDWNTLIVGKLSPWIRP
DSKVEKIRRNSEAAMLQELNFGA-YLGLPAFLPLNQEDNTNLARVLTNHIHTGHSSMF
WMRVPLVAPEDLRDDIIENAPTSHTTEYSGEEKTMMWWHNFRITLCDYSKRIAVALEIGAD
LPSNHVIDRWLGEPKAAILPTSIFLTNKKGFPVLSKMHQRLIFRLLKLEVQFIITGTNH
---HSEKEFC---SYLQ-----YLEYLSQNRPP---PNAYELFAKGYEDYLQS-----
-PLQPLMDNLESQTYEVFEKDPKYSQYQQAIYKCLLDRVPE-----EEKDTNIQV
LMVLGA-GRGPLVNAS--LRAAQADRIKLYAVEKNPNAVVTLENW---QF---EEW--
--GSQVTVVSSDMREWVAPEKADIIIVSELLGSFAD---NEL-SPECLDGAQHFLKDD-G
VSIPGEYTSFLAPISSSKLYNEV--RACREKDRDPEAQFEMPYVVRHLNHFHQLSAPQPCF
TFSHPNRDPMDIDNNRYCTLEFPVEVNTVLHGFAGYFETVLYQDITLSIRPETHSPGMFSW
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-KQGFDFLCMPVFHPRFKREFIQEPAKNRPGPQTRSDLLSGRDWNTLIVGKLSPWIRP
DSEVEKIRRNSEAAMLQELNFGA-YLGLPAFLPLNQEDNTNLARVLTNHIHTGHSSMF
WMRVPLVAPEDLRDDIIENAPTHHTQEYSGEEKTWIWWHNFRITLCDYSKRIAVALEIGAD
LPSNHVIDRWLGEPKAAILPTSIFLTNKKGFPVLSKMHQRLIFRLLKLEVQFIITGTNH
---HSEKEFC---SYLQ-----YLEYLSQNRPP---PNAYELFAKGYEDYLQS-----
-PLQPLMDNLESQTYEVFEKDPKYSQYQQAIYKCLLDRVPE-----EEKDTNVQV
LMVLGA-GRGPLVNAS--LRAAQADRIKLYAVEKNPNAVVTLENW---QF---EEW--
--GSQVTVVSSDMREWVAPEKADIIIVSELLGSFAD---NEL-SPECLDGAQHFLKDD-G
VSIPGEYTSFLAPISSSKLYNEV--RACREKDRDPEAQFEMPYVVRHLNHFHQLSAPQPCF
TFSHPNRDPMDIDNNRYCTLEFPVEVNTVLHGFAGYFETVLYQDITLSIRPETHSPGMFSW
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-----GVSFSTSEKLNIAKFLQLKLNVD

R----VEIASARV-----S
KGELETVQKIMEWAATEQLTERIEILGFVDGNKTVDWIKDSG-AKVL-----
-----NLLTKGSLHHLEKQLGKTPK-----EFFTDVSFVIEY---
-----AIKSGLKINVYLEDWSNGFRNSPDYVKSLEHLSKEHIERIFLPDTL
GVLSPREETFQGVDSLQKYPDIHFHFGHNDYDLSVANSQAIIRAGVKGLHASINGLGER
AGNTPLEA-----LVTIHDKSNSK-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

MFRIRILSYRALASCTRNALSSSSQP-----RSLPRSNAPILPPPFFLDVGIA
ENYGSTSLTRFM-----S
SNASSEQGKNTKTKKELKN-----
-----VEDPFDDAPT-----YNIPEKPVTf-----
-----VEGASYSLVI-----LAGLGVAAAAGY---
--SVFKE-----LIFQPKEYK-----
-----IYNKALKR-----IQDDGQ-----
-----VRGRIGSPITGYGQESRNRAARQRIPN-----RVWTD
EEGV-----EHVEVNF-----FIRGPHG
-----HGKVFAEMFKGADGEWS--YTYLIVEIRAPSPAQL-----
-----ILESYPSPYNP-----
-----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---LEAMGVVDYIDese--
-VLTPADE-----EFHLNKNEYT-----
--VPFV-----CGCRDLGEATR---RIAEGASMLRT
K---GEPGTGNIVEA---VRHMRKVNAQVRKVVMAMSEDELMTEAKNL-----
--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-----TQVNGFGLRPERSLLYQPTSFSFSRRRTHGIVKASSRVDRES
K---SDIIVS-----P
SILSANFAKLGEQVKAVELA-----G-----
-----CDWIHVDV-----
-----MDGRFVPNIT-----IGPLVVDAL-----
---RPVTDLP-LDVHL-----MIVEPEQRVP-----DFIKAGADIVSVH-----
-----CEQQSTIH-----LHRTVNQIKS
L---GA-KAGVVL-----NPGTPLSAIEYVLDMDLVLIMSVNPGF-----
--G-GQS-----FIESQ--
-----VKKISDLRKMCAEKGVPWIEVDGGVTPANAYKV-----IEAG---
-----ANALVAGSA---VFGAKDYAEAIGIKASK-----
-----RPAAV
AV

```

MUSCLECLUSTAL multiple sequence alignment by MUSCLE (3.8)

```

sp|P37527|PDXS_BACSU      -----MAQTGTERVKRGMAEMQKGGVIMDVINAEQAKIAEEAGAVAVM-----
sp|Q8F3Q1|CIMA_LEPIN      MTKVETRLEILDVTLRDGEQTRGVSFSTSEKLNIAKFLLQKLNVDREIASARVSKGELE
sp|P0A858|TPIS_ECOLI      -----MRHPLVMGNWKLNGSRHMHVHELVSNLRKELAGVAGCAVAIAPPE-----
sp|Q9RUP5|TPIS_DEIRA      -----MQTLLALNWKMNKTPTEARSWAEELTTKYA--PAEGVDLAVLA-----
sp|Q8XKU1|TPIS_CLOPE      -----MRTPIIAGNWKMHYTIDEAVKLVEELKPLVKDAKCEVVVCPTFV-----
sp|Q9Z520|TPIS_STRCO      -----MTTRTPLMAGNWKMNLNHLEAIAHVQKLAFALADKDYDAVEVAVLA-----
tr|A0A072VM55|A0A072VM55_MEDTR -----MFRIRRLSYRALASCTRNALSSSS-----
sp|Q9SAU2|RPE_ARATH      -----MSTSAASLCCSSTQVNGFGLRPER-----
sp|P87108|TIM10_YEAST      -----MSFLGFGG-----
sp|Q9W2D6|TIM10_DROME      -----
sp|Q9WV98|TIM9_MOUSE      -----
sp|Q17754|TIM9_CAEL      -----
sp|Q9XGX9|TIM9_ARATH      -----MDASMMA-----

```

sp|Q6FRT3|TIM9_CANGA
sp|A7YW45|ANM5_BOVIN
sp|Q5R698|ANM5_PONAB
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

-----MAAMAVGGAGGSRVSSGRDLNCVPEIADTLGAVAKQGFDFLCMPVFHPRFK
-----MAAMAVGGAGGSRVSSGRDLNCVPEIADTLGAVAKQGFDFLCMPVFHPRFK
-----MADATKN-----
-----MDSSSSS-----
-----MESSSSS-----
-----MEGFGSDFSV-----

-----MALSSIFGGGSPS-----
-----MSSFFGSGAGS-----

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
sp|Q5R698|ANM5_PONAB
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

-----ALERVPA-----
TVQKIMEWAATEQLTERIEILGFVDGNKTVDWIKDSGAKVLNLLTKGSLHHLEKQLGKTP
-----MYIDMAK-----
-----PALDLSA-----
-----CLDAVKK-----
-----PFTDLRS-----
-----QPRSLPR-----
-----SLLYQPT-----
-----GQPQLSS-----
-----MALPQ-----
-----MAAQIPE-----

-----GLDGLPE-----
-----MDQLNA-----
REFTQE-----PAKSRPGPQTRSDLLSGRDWNTLIVGKLSPWIRPD SKV
REFIQE-----PAKNRPGPQTRSDLLSGRDWNTLIVGKLSPWIRPDSEV
-----PIADLSE-----
-----SAAGLGA-----
-----SGSALAA-----
-----GGSSAGK-----
-----MSDSTSE-----
-----QQSNLPT-----
-----PSNDMTA-----

sp|P37527|PDXS_BACSU
sp|Q8F3Q1|CIMA_LEPIN

-----DIRAAGGVARMADPTIVEEVMNAVSIPVMAKARIGHIVEARVLEAMGVD---
KEFFTDVSFVIEYAIKSGLKINIVLEDWSNGFRNSPDYVKSLVEHLSKEHIERIFLPDTL

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
sp|Q5R698|ANM5_PONAB
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
sp|Q5R698|ANM5_PONAB

-----REAEGSHIMLGAQNVDLNLSGAFTGETSAAMLKDI-----
-----LAANLPAGIAFGGQDVSAHESGAYTGEISAAMLKDA-----
-----AVEGTNIKVG AQNMHFEEKGAFTGEIAPRMLEAM-----
-----VQTLVDGDKLKI KYGAQDISAHDGGAYTGEISGPMLAKL-----
SNAPILPPFFFLDVGIAENYGSTSLTRFMSSNASSEQGKNTKTKKELKNVEDPFDDAPT
-----SFSFSRRRTHGIVKASSRVD RFSKSDIIVSPSILSANFAKLGEQVKA
-----QQKIQA AEAE LDLV TDM-----
-----ISTADQAKLQLMQEMEIE MMSDL-----
-----SDQIKQKFKEFLGT-----
-----MTSEQNIQTFRDFLTQ-----
-----EDKAKMASMIDQLQLRDSL RM-----
-----KEQQEFQKLVEQKQMKDFMRL-----
EKIRRNSEAAMLQELNFGAYLGLPAFLLPLNQEDNTNLARVLTNHIHTGHHSSMFWMRVP
EKIRRNSEAAMLQELNFGAYLGLPAFLLPLNQEDNTNLARVLTNHIHTGHHSSMFWMRVP
-----SEQLELSKFIESEQQKVKLQQA-----
-----VDPQLQHFIEVETQKQRFQQL-----
-----VDPQLQHFIEVETQKQRFQQL-----
-----VDTGAIMEQVKVQI AVANAQEL-----
-----TVKKAIKQVLI ESQSANARTL-----
-----SSASSVKDQLKGQIAQELAVANATEL-----
-----RKEQMKQSIQQELAIANAQQL-----

-----YIDSEV
GVLSPEETFQGVDSL IQYPDIHFEFHGHNDYDLSVANSLQAIRAGVKGLHASINGLGER
-----GAQYIIIGHSERRT-----YHKESDE
-----GASCVVVGHSERRE-----YHDES DA
-----NIDYVIIGHSERREY-----FNETDET
-----KCTYVAVGHSERRQ-----YHAETDE
YNIPEKPVTFVEGASYSLVILAGLGVA AAG-----YSVFKE L
VELAGCDWIHVDM DGRFVPNITIGPLVDA-----LRPVTDL
-----FNKLVNN
-----YNRMTNA
-----YNKLTET
-----YNLVAEQ
-----YNSLVER
-----YSGLVER
LVAPEDLRDDIIENAPTSHTEEYSGE EKTMMW-----WHNFRTL
LVAPEDLRDDIIENAPTTH TQEYSGE EKTWIW-----WHNFRTL

```
sp|Q09783|TIM8_SCHPO-----IHQFTST
sp|O60220|TIM8A_HUMAN-----VHQMTTEL
sp|Q9WVA1|TIM8A_RAT-----VHQMTTEL
sp|Q6GPY0|TI13A_XENLA-----LQRMETDK
sp|Q7SBR3|TIM13_NEUCR-----MEKIGEN
sp|Q75F72|TIM13_ASHGO-----VNKVTEN
sp|P0CS01|TIM13_CRYNB-----INKINEN
```

```
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
sp|Q5R698|ANM5_PONAB
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

L-----TPAD-----EE-----
AGNTPLEALVTTIHDKSNSKTNINE-----
L-----IA-----KK-----
X-----VA-----AK-----
C-----N-----KK-----
I-----VN-----AK-----
IFQPKEYKIY-----NK-----
P-----LD-----VH-----
C-----
C-----
C-----
C-----
C-----
CDYSKRIAFALEIGADLPSNHVIDRWLGEPKAAILPTSIFLTNKKGFPVLSKMHQRLIF
CDYSKRIAFALEIGADLPSNHVIDRWLGEPKAAILPTSIFLTNKKGFPVLSKMHQRLIF
C-----
C-----
C-----
C-----
C-----
C-----
C-----
```

```
sp|P37527|PDXS_BACSU-----FHLNKNEYTVPFVCGCRD-----LGEATRRIAEGASMLRTKGEPGTGNIV
sp|Q8F3Q1|CIMA_LEPIN-----IAITEASRLVEVFSGKRISANRPVIGEDVFTQTAGVHADGDKKGNLYANPI
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
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
sp|Q5R698|ANM5_PONAB
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

-----VKAAYKHGLTPILC-----VGEE-----L
-----ALKRIQDDGQVRGR-----IGSP-----
-----LMIVEPEQRVPDFIKAGADIVSVHCEQQ-----STIH
-----YKKC-----INTS-----
-----HKKC-----IPPR-----
-----FLDC-----VKDF-----
-----FNSC-----VNEF-----
-----FVDC-----VDSF-----
-----FTDC-----VNDF-----T
RLLKLEVQFIITGTNNHSEKEFCSYLQYLEYLSQNRP-----PPNAYEL
RLLKLEVQFIITGTNNHSEKEFCSYLQYLEYLSQNRP-----PPNAYEL
-----WPKC-----IGNI-----
-----WEKC-----MDKP-----
-----WEKC-----MDKP-----
-----FRKC-----IGKP-----
-----FTSC-----VPKP-----
-----FEKC-----LMAP-----
-----FAKC-----VTKP-----

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
sp|Q5R698|ANM5_PONAB
sp|Q09783|TIM8_SCHPO
sp|O60220|TIM8A_HUMAN
sp|Q9WVA1|TIM8A_RAT

EAVRHRMRKVNAQVRKVVAMSEDELMTEAKNLGAPY-----
LPERFGRKRSYALGKLAGKASISENVKQLGMVLSEVVLQKVL-----
AENEAGKTEEVCARQIDAVLKTQGAFAFEGAVIAY-----
DVRERGEHVPTLAQLRGSLEGVGAD---VVVAY-----
EQRENGTTNDVIKAQITADLEGLTKEQAEKVVIAY-----
DVREAGNHVEHTLAQVEGGLKDLAAEQAESVVIAY-----

LHRTVNQIKSLGAKAGVVLNPGTPLSAIEYVLDMV-----

FAKGYEDYLSPLQPLMDNLSESTYEVFEKDPIKYSQYQQAIYKCLLDVPEEEKDTNIQ
FAKGYEDYLSPLQPLMDNLSESTYEVFEKDPIKYSQYQQAIYKCLLDVPEEEKDTNVQ


```
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
sp|Q5R698|ANM5_PONAB
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_STRO
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
sp|Q5R698|ANM5_PONAB
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

-GEL---NKNESSC-----LDR-----
-YSESELGKGEMVC-----IDR-----
--TTREVKPEEVC-----SEH-----
-SRTV--SGKEESC-----ANN-----
-KSL---QKQEETC-----VMR-----
-SKL---TSKEESC-----ILK-----
MREWVAPEKADIIVSELLGSFADNELSPESLDGAQHFLKDDGVSI
PGEYTSFLAPISSSK
MREWVAPEKADIIVSELLGSFADNELSPECLDGAQHFLKDDGVSI
PGEYTSFLAPISSSK
-NKL---DKSEEQC-----LQN-----
-PKL---DSRAEAC-----FVN-----
-PKL---DSRAEAC-----FVN-----
-GSL---DNSEQKC-----IAM-----
-SSL---SNSEKTC-----VTQ-----
-----YTSKQDTC-----VDQ-----
-TSL---SSSQESC-----LSQ-----

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
sp|Q5R698|ANM5_PONAB
sp|Q09783|TIM8_SCHPO
sp|O60220|TIM8A_HUMAN
sp|Q9WVA1|TIM8A_RAT
sp|Q6GPY0|TI13A_XENLA
sp|Q7SBR3|TIM13_NEUCR
sp|Q75F72|TIM13_ASHGO

-----ALMMQL-----GADGVFVGSGIFKSDNP-----
-----TGEKVLTIKSCNIHSGIGIRP-HAQIELEYQGKIHK
EISEGDDGGYDAFMNALT
-----IAKVDA-----NI-AEQVIIQYGGSVNA-----
-----LREQYG-----AR-AEGIRVLYGGSVKP-----
-----VAEMFG-----QEVADKVRIQYGGSVKP-----
-----LAELYS-----QELADKVRIQYGGSVKS-----
-----IPNRVW-----TD-EEGVEHVEVNFFIR-----
-----CAEKGV-----NP-WIEVDGGVTPANAY-----
-----CVAKYF-----ET-NVQVGENM-QKMGQ-----
-----CVAKYL-----DI-HEKIGKKLTAMSMQ-----
-----CLQKYL-----KM-TQRISVRFQYEHQ-----
-----CLDKFL-----KM-TQRVSQRFQEHQLL-----
-----CAEKFL-----KH-TMRVGMRFALNQ-----
-----CSEKFL-----KH-SERVGQRFQEQNAA-----
LYNEVRACREKDR-----DP-EAQFEMPYVVRHLN-----
LYNEVRACREKDR-----DP-EAQFEMPYVVRHLN-----
-----CVERFL-----DC-NFHIIKRYALEKFG-----
-----CVERFI-----DT-SQFIL---NRLEQ-----
-----CVERFI-----DT-SQFIL---NRLEQ-----
-----CMDRYM-----DA-WNTVSRAYNSRLQR-----
-----CTEKYM-----AA-WNVVNTTYLRRIQQ-----
-----CLAKYM-----RS-WNAISQAYVARIQQ-----

sp|P0CS01|TIM13_CRYNB

-----CMTLYM-----AA-FDQVSRSYVARISK-----

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
sp|Q5R698|ANM5_PONAB
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

-----AKFAKAIVEATHTFTDYKLI AELSKELGTAMK
KITNRLGISIPKLIDYEVRIPPGGKTDALVETRITWNKSLDLEEDQTFKTMGVHPDQTV
-----SNAELFAQPDIDGALVGGASLKADAFVIVKAAEA
-----ENIAEICGKPNVNGALVGGASLKVPDVLGMLDALR-
-----NTIAEQMAKSDIDGALVGGASLVAADFAQIVNY---
-----GNVAEIMAKPDIDGALVGGASLDSDEFVKIVRFRDQ
-----GPHGHGKVFAEMFKGADGEWSYTYLIVEIRAP
-----KVIEAGANALVAGSAVFGAKDYAEA IKG I KASKRP
-----SFNAAGKF-----
-----DEELMKKMSS-----
-----QNEALAAKAGLLGQPR-----
-----NAQANGAAIKVENGKINKIQ-----
-----APTQD-----
-----LGQGLGR-----
-----FHQLSAPQPCFTF SHPNRDP MIDNNRYCTLEFPVEVNTVLHG
-----FHQLSAPQPCFTF SHPNRDP MIDNNRYCTLEFPVEVNTVLHG
-----FLFCWLGFSC-----
-----TQKSKPVFSESLSD-----
-----TQKSKPVFSESLSD-----
-----ERAKM-----
-----EMGNQ-----
-----ASANGDI-----
-----ERGVAPGL-----

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

GIEISNLLPEQRMQERGW-----
AVHATEKMLNQLQPWQI-----
AKQA-----

SPAQLILESYP SYNPNK-----
AAVAV-----

sp|Q17754|TIM9_CAEEL
sp|Q9XGX9|TIM9_ARATH
sp|Q6FRT3|TIM9_CANGA
sp|A7YW45|ANM5_BOVIN
sp|Q5R698|ANM5_PONAB
sp|Q09783|TIM8_SCHPO
sp|O60220|TIM8A_HUMAN
sp|Q9WVA1|TIM8A_RAT
sp|Q6GPY0|TI13A_XENLA
sp|Q75BR3|TIM13_NEUCR
sp|Q75F72|TIM13_ASHGO
sp|P0CS01|TIM13_CRYNB

FAGYFETVLYQDITLSIRPETHSPGMFSWFPILFPIKQPITVREGQTICVRFWRCSNSKK
FAGYFETVLYQDITLSIRPETHSPGMFSWFPILFPIKQPITVREGQTICVRFWRCSNSKK