

a

```
... 3' end of PIKa -->
M I T Q G I Y S *
8801 AATGATAACGCAAGGAATTTATAGTTAGAGTTTGCTATTTAATATCAAATTATAAATACGAGAAAGCAGCATGCAAAAAAATTGATGCATTTTTTAACAC 8900

                                MTLa2 gene -->
                                M P Y T F N F P K S Q S S F K Y S I K
8901 GTTCTCTCTTTTTGATTAGTTTTTAAAGACAAATACCCAATAATATGCCATATACCTTTAATTTTCCAAGCTGCAGTCAAGTTTCAAATATTCTATTTAAA 9000
S L T N S R S F P M I S I Y V T P Q S T P K F I N N Q S I D K M T V
9001 AGTCTTACTAATTCTCGGTCATTCCCAATGATATCCATCTATGTTACACCACAATCAACACCTAAGTTTATCAATAATCAGTCCATTGATAAAAATGACAG 9100
L S S F R S R N S F I I A R S I L S K L L R K N K A D F K K V S K
9101 TATTGAGTCTTTTCAGATCAAGAAACAGTTTCATTATTGCTAGAAGCATACTTTCCAAGCTATTAAGAAAAAATAAAGCTGATTTCAAGAAAGTGCCAA 9200
S V S L                               intron                               L W G S V D N S F K N
9201 GAGTGATCTTTAgtatgtataataaaattgattgaaatcctttgacagagtactaacataatatacagCTTTGGGGTTCGGTTGACAATCTTTCAAAAA 9300
Y F E Y L S I L E S Q W H D K K S S N L N P I S S T R T T S E L N
9301 CTATTTCGAATACTATCTATTTTAGAGTCGCAATGGCAGCATAAAAAAAGCTCAAACCTCAATCCAATATCTTCTACTAGCAGTACTAGTGAGTCAAC 9400
Y I E L C S S I Y N Q S R K H P R S V Q G N K A K F R L Y K N V S K
9401 TATATCGAACTTTGTTCAGTATTTACAATCAATCAAGAAAAACATCCAAGATCTGTACAGGTAACAAGCAAAATTCAGATTATACAAAAACGTTTCAA 9500
K S N R K P R R L K N G F K V S R S T I N C S Y G I Y T E D V F Q
9501 AAAAGCTGAATAGGAAACCAGGAGATTAAAAAATGGTTTTAAGTAAGTCAAGCACTATAAACTGCAGTTATGGCATCTATACTAGGAGACGTTTTTCA 9600
*
9601 ATAGTTTTTTTTCTGCGTATTGTGATAAATAAATCTTTTTTCCCTCTAAAAATATTGATTAGAGGCACAAAAAATAAAATCACCTTCAACCTCCTCGTTTTT 9700

5' end of MTLa1 -->
M N S E I E S S L T L L K S V E K L V Q A T S V Y K N E D N
9701 CCAAAGCAATGAACTCAGAAATAGAAAGTAGCTTAAACACTTTTAAAAAGTGTAGAGAAACTAGTTCAAGCAACATCAGTATATAAGAATGAAGACAACGA 9800
```

b

T-COFFEE, Version_1.41(Fri Jun 28 14:24:48 MDT 2002)

Notredame, Higgins, Heringa, JMB(302)pp205-217,2000

CPU TIME:7 sec.

SCORE=27

*

BAD AVG GOOD

*

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C.albicans_HMG      -----MPYTFN-----FPKSQSSFK-----
S.kluyveri_HMG     MSSTEIYFVECVLPKRQHVKTPSNYNDRLLHLLSDFPFSNAKQKKVDIKCHFVET
K.lac_MATa2_HMG    -----MANSTLRRTTFFKLT-----TTEDEDTIP-----
Y.lip_MATa2_HMG    MENTILHIHSFQLPQTEQPYPEAMLFDR-----DT
Cons                [red] [red] [red] [red] [red] [red] [red] [red] [red]
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```
C.albicans_HMG      -----YSIKSLTNSRSFPMISIVTPOSTPKFINNQS-----
S.kluyveri_HMG     RSKLIVLGNTSDGNQOKCPPLNLFKEKNKFQNTNSKTPFDGDAERKEKSDYEV
K.lac_MATa2_HMG    -----KLLQPNNNSVAFPNL-----KRTGKAFTNDT-----
Y.lip_MATa2_HMG    SDSRTVLTQKPNGLEISLNFL-----QYDGHK-----GLFIRQD-----
Cons                [red] [red] [red] [red] [red] [red] [red] [red] [red]
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```
C.albicans_HMG      -----IDKMTVLSSFRSRNSFIIARSILSK-----
S.kluyveri_HMG     KKMPSSKDTDVYLESKSHNYITRPRNKFIIMRTVFHNQIINSLMRLAEPNRQSK
K.lac_MATa2_HMG    -----I-KENTKKYTRPRNQFVLMRTLFRNRVNNHILQYYNKSLEK
Y.lip_MATa2_HMG    -----SRTNEPEYIEP-----KVLKPRNSYILFRNATSR-----
Cons                [red] [red] [red] [red] [red] [red] [red] [red] [red]
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```
C.albicans_HMG      -----LLRKNKA-----DFKKVSKSVSLLWGSVDNS--F
S.kluyveri_HMG     TAFKWKHRGLNNNLDKNEILVNLSLENIAEHLSEFEDISVVASNIWRNNRNG--F
K.lac_MATa2_HMG    KM-----FTLTSKITSELWNESSPD--L
Y.lip_MATa2_HMG    -----CSQSIDPN-----SAFVSRVSSYIWGSGIPNPIV
Cons                [red] [red] [red] [red] [red] [red] [red] [red] [red]
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```
C.albicans_HMG      KNYFEYLSILESQWHDKKSSNL--N-----PISSTRTTSELNY--
S.kluyveri_HMG     QNYFKLLSEFEKWHMTMKHPHF--SHCPRGHKRLAFAEAYSQNTASEHGERAR
K.lac_MATa2_HMG    KSYFLLATLEENWHKYTH-----YCSWDRNSAQTLSMEPIELSQ
Y.lip_MATa2_HMG    RRWFKYMGFFEALYHEVDYPEYIPNKLPKSPKKPKVQKGATSKKKKGAKGKNKV
Cons                [red] [red] [red] [red] [red] [red] [red] [red] [red]
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```
C.albicans_HMG      -----IELCSSIYN
S.kluyveri_HMG     --RPQTGTDAGILESFSGRAVLGKLTAVLGRGKS-----LVVSSYEYD
K.lac_MATa2_HMG    V--RPRI-----ISSLTVGAGSSVSTY--TLRELLLVKIKS
Y.lip_MATa2_HMG    TALQVLVGPVGV-----GGRMTVSPMTAFFSNNSHVTCYDPNFVL-----D
Cons                [red] [red] [red] [red] [red] [red] [red] [red] [red]
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C.albicans_HMG   QSRKHPRSVQGNKA-----KFRLYKNVS---
S.kluyveri_HMG   SLRREYGVAGAKKEAADPIAQSKN TYKALKKAKLCGRFSVKKTAGSKI IADAS
K.lac_MATa2_HMG  RKRKTTTLTQDS-----SPTTKFKY-----KFKKQPKTKMNS
Y.lip_MATa2_HMG  TPTREFLMMPLDDITLPSQGPRSDS QE QHVPRQPPDGQDYFDILDIDDFVSPYD
Cons             :

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C.albicans_HMG   -----KKSNRKPRRLKNGFKVSRSTINCSYGIYTEDVFQ--
S.kluyveri_HMG   CQERLVRAGKVKKRGTTQPKTFSLRRSTFS--KDFVVEDVFVRR
K.lac_MATa2_HMG  NLSKLRF--KSKQPPTPEENS NVFKKRYTS--ENRIEDLFM-
Y.lip_MATa2_HMG  DL'TTRSFTNRQLFKHATLG-----
Cons             : : .

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