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Heterothallism revealed in the root rot fungi Berkeleyomyces basicola and B. rouxiae

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#### 14 Abstract

15 Berkeleyomyces basicola and B. rouxiae, two cryptic sister species previously treated collectively as Thielaviopsis basicola, reside in the Ceratocystidaceae (Microascales, 16 17 Ascomycota). Both species are important plant pathogens that infect the roots of many important agricultural crops and ornamental plants. Although T. basicola has been known for 18 more than 150 years, a sexual state has never been found and it has been assumed to be 19 an asexual pathogen. The aim of this study was to determine the mating strategy of the two 20 21 Berkeleyomyces species. Investigation of the genome sequences of two B. basicola isolates 22 allowed for the complete characterization of the MAT locus. This revealed that it has a typical heterothallic mating system with the MAT1-1 and MAT1-2 idiomorphs occurring in 23 different isolates. PCR amplification using mating type primers developed in this study, 24 showed that the MAT1-1-1 and MAT1-2-1 genes were also present in different isolates of B. 25 rouxiae. Pairing of isolates representing the two mating types of both B. basicola and B. 26 rouxiae using a variety of techniques failed to produce sexual structures. Although we have 27 28 found no direct evidence that they reproduce sexually, these fungi are clearly heterothallic 29 with both mating types occurring in some countries suggesting that a cryptic sexual cycle 30 could exist for them.

31 **Keywords:** Black root rot, Sexual reproduction, mating, plant pathogen, *MAT* locus

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#### 33 **1. Introduction**

34 Berkeleyomyces basicola and its sister species B. rouxiae are filamentous Ascomycete fungi that reside in the Ceratocystidaceae (Nel et al. 2018; De Beer et al. 2014). The two species 35 36 are plant pathogens, causing a disease commonly known as black root rot on many important crops such as tobacco (Stover 1950), cotton (Pereg 2013) and carrots (AbdAllah 37 et al. 2011). Despite being important pathogens of agricultural crops, both species are only 38 known from their two asexual states: the first being the chlamydospore state that gives rise 39 40 to distinct dark-coloured, club shaped spores only known to Berkeleyomyces; and the second being the endoconidial state characterized by phialides that give rise to endoconidia 41 (Nel et al. 2018). 42

Until recently, these two pathogens were treated as a single species Thielaviopsis basicola, 43 44 originally introduced by Ferraris (1912) based on morphological-characteristics. In a reclassification of the Ceratocystidaceae, De Beer et al. (2014) suggested that the generic 45 level placement of the species required revision. This was because the isolate included in 46 47 their study grouped outside Thielaviopsis and all other known genera in the Family. Based 48 on phylogenetic and clear biological and morphological differences from other genera in the 49 Ceratocystidaceae, Nel et al. (2018) described the new genus Berkeleyomyces. They also showed that isolates previously described as T. basicola represent two cryptic species. The 50 epithet "basicola" was retained for the type species of the new genus and the second 51 52 species was described as *B. rouxiae*.

Although [the former] T. basicola has been known for more than 150 years (Berkeley & 53 54 Broome 1850) nothing is known regarding its mating strategy. Soon after the original description of the fungus, Zopf (1876) described a sexual state as Thielavia (Th.) basicola. 55 However, during the early 1900's experiments involving single spore cultures were used to 56 show that the sexual structures of *Thielavia* and the asexual structures of *Berkeleyomyces* 57 belonged to two unrelated fungi (McCormick 1925, Lucas 1948, Lucas 1949, Stover 1950). 58 There has subsequently been only a single report attempting to induce sexual structures in 59 60 [the former] T. basicola. Johnson & Valleau (1935) performed co-culture experiments using 61 multiple single spore isolates of the fungus but no sexual structures were observed over a 62 period of more than one year. The absence of a sexual state has led to a view that the 63 species represents an exclusively asexual pathogen (Tabachnik & DeVay 1980, Paulin & 64 Harrington 2000, Paulin-Mahady et al. 2002).

65 Mating and sexual reproduction in filamentous Ascomycetes, including the 66 *Ceratocystidaceae,* is controlled by a single region in the genome known as the mating type 67 or *MAT* locus (Yoder *et al.* 1986, Wilken *et al.* 2017). This region can be present as two non-

68 homologous idiomorphs known as MAT1-1 and MAT1-2 (Yoder et al. 1986, Turgeon & 69 Yoder 2000, Wilken et al. 2017). The MAT1-1 idiomorph contains at least the MAT1-1-1 70 open reading frame (ORF) encoding a protein with an  $\alpha$ -box domain. Similarly, the MAT1-2 idiomorph contains at least the MAT1-2-1 ORF encoding a protein with an HMG-box domain 71 (Butler 2007, Wilken et al. 2017). When both the MAT1-1-1 and MAT1-2-1 genes are found 72 73 in the genome of a single isolate, the species is considered homothallic and sexual reproduction can take place independent of a second isolate (Butler 2007, Wilson et al. 74 2015a, Wilken et al. 2017). However, when the MAT1-1-1 and MAT1-2-1 genes occur in 75 different isolates of a species, the species is considered heterothallic and at least two 76 isolates, each containing one of the MAT idiomorphs, are required for sexual reproduction to 77 take place. There are, however, exceptions to these norms. The first exception is known as 78 mating type switching, whereby a single isolate contains both MAT1-1-1 and MAT1-2-1 79 80 genes in its MAT locus but this locus undergoes structural changes before sexual 81 reproduction can occur (Wilken et al. 2014). The other exception is known as unisexuality, in 82 which any isolate of a single mating type can undergo sexual reproduction without the need of an opposite mating type (Wilson et al., 2015a, 2015b). Although the overall genetic 83 organization at the MAT locus can vary among species, certain genes, such as those 84 85 encoding the cytoskeleton assembly control protein (SLA), the AP endonuclease (APN), the 86 anaphase promoting complex (APC), and subunit VIa of cytochrome C oxidase (COX), are 87 frequently found flanking the MAT locus in species of the Ceratocystidaceae (Butler 2007, 88 Wilken et al. 2017).

The *Ceratocystidaceae* includes examples of a wide variety of sexual reproductive strategies. These include species that are heterothallic (Wilson *et al.* 2015b, Wilken *et al.* 2018, Mayers *et al.* 2017) and primary homothallic (Mbenoun *et al.* 2014). Some species have secondary homothallic reproductive strategies including mating type switching (Harrington & McNew 1997, Witthuhn *et al.* 2000, Wilken *et al.* 2014) and unisexuality (Wilson *et al.* 2015b).

95 Against the background of this diverse array of reproductive strategies in the 96 *Ceratocystidaceae*, we asked what the mating type strategy could be for the 97 *Berkeleyomyces* species, and would the mating type locus suggest the absence of a sexual 98 cycle as has previously been speculated. The aim of this study was thus to characterize the 99 mating locus in these fungi and to consider their possible mating strategy. We also 100 attempted to induce sexual reproduction of these species by carrying out various mating 101 crosses.

#### 102 **2. Materials and Methods**

#### 103 **2.1.** Isolates

104 Cultures used in this study were obtained from various collections including the Culture 105 Collection (CMW) of the Forestry and Agricultural Biotechnology Institute (FABI), University 106 of Pretoria, South Africa, the Westerdijk Fungal Biodiversity Institute (CBS), Utrecht, The 107 Netherlands, and the International Collection of Microorganisms from Plants (ICMP), New 108 Zealand. Cultures (**Table 1**) were maintained on 2 % Malt Extract Agar (MEA – 2 % malt 109 extract, 2 % Difco<sup>®</sup> agar Biolab, Midrand, South Africa).

#### 110 **2.2.** Characterization of the *MAT1-2* idiomorph

The genome of *B. basicola* isolate CMW49352 (Wingfield et al. 2018) was investigated to 111 identify the contig containing the MAT locus. The tBLASTx algorithm in CLCbio Genomics 112 Workbench 9.5 (CLCbio, QIAGEN, Aarthus, Denmark) was used to screen the assembled 113 114 genome for MAT idiomorph sequences using reference sequences for MAT genes from Ceratocystis fimbriata (GenBank accession number: APWK02000000; Wilken et al. 2013). 115 116 The scaffold containing the greatest similarity to the reference sequences was extracted and annotated using Augustus 3.3.2 (Stanke et al. 2004) using the pre-optimized species model 117 118 of Fusarium graminearum. A BLASTp analysis was made using the NCBI database to identify each of the predicted protein sequences. 119

## 120 **2.3.** Genome sequencing and characterization of the *MAT1-1* idiomorph

### 121 **2.3.1.** Identification of putative *MAT1-1* idiomorphic isolates

CLCbio Genomics Workbench 9.5 (CLCbio, QIAGEN, Aarthus, Denmark) was used to 122 design primers for the MAT1-2-1 and MAT1-2-7 genes identified in section 2.2, along with 123 124 two additional MAT locus associated genes (SLA and a gene of unknown function [UNK]) (Table 2). Thirteen isolates of *B. basicola* and 26 isolates of *B. rouxiae* were screened by 125 126 PCR, using these primers. Isolates that do not give positive PCR amplification for these 127 MAT1-2 genes were presumed to have MAT1-1 idiomorph. DNA extraction and PCR amplification were conducted using the methods described by De Beer et al. (2014) and the 128 annealing temperatures for the different primer pairs are indicated in Table 2. 129

130 **2.3.2. G** 

#### 2.3.2. Genome sequencing

Based on the amplification results for the different isolates, *B. basicola* isolate CMW25440 (putatively identified as containing the *MAT1-1* idiomorph) was selected for additional genome sequencing. A single spore culture of isolate CMW25440 (= CBS142829 collected in Indonesia from *Styrax benzoin*) was grown in YM broth (2 % malt extract, 0.5 % yeast extract, Biolab, Midrand, South Africa) for 3-5 days. Mycelium was collected in 1.5 mL Eppendorf tubes by centrifugation and lyophilized. The tubes containing the lyophilized

mycelium was submerged in liquid nitrogen and the mycelium ground to a fine powder using 137 138 a sealed sterile pipette tip. Total genomic DNA was extracted from the powdered mycelium using the method described by Duong et al. (2013). A paired-end library (350 bp average 139 insert size) was prepared and sequenced using the Illumina HiSeq2500 Platform at 140 Macrogen Inc. (Seoul, Korea). The 101 bp pair-end reads obtained were assembled into 141 contigs using SPAdes 3.9 (Bankevich et al. 2012) using default settings and k-mer sizes of 142 21, 33, 55 and 77. Completeness of the assembly was assessed using the Benchmarking 143 Universal Single-Copy Orthologs (BUSCO 1.1b1) tool using the Ascomycota dataset (Simão 144 et al., 2015). 145

#### 146 **2.3.3. Characterization of the** *MAT1-1* **idiomorph**

The newly assembled genome of *B. basicola* isolate CMW25440 was investigated to identify the *MAT1-1* idiomorph using the same method described in section 2.2. In this case, the genes identified flanking the *MAT* locus in the genome of isolate CMW49352, as well as the *MAT1-1-1* gene from *C. fimbriata*, was used to screen the genome of isolate CMW25440 for the *MAT1-1* idiomorph. The scaffold containing the greatest similarity to the reference sequences was extracted and annotated again as described in section 2.2. and the putative genes were identified by BLASTp.

## 1542.4.Development of multiplexPCR-based mating type markers for155Berkeleyomyces

A primer set targeting the MAT1-1-1 gene was designed based on the MAT1-1 sequences 156 identified from the genome of *B. basicola* isolate CMW25440 (Table 2). The primer 157 parameters were selected to be compatible with multiplex PCR amplification together with 158 the MAT1-2-1 primer set designed in section 2.3.1. The MAT1-1-1 primer pair was selected 159 160 to produce a longer amplicon size but with the same annealing temperature as the MAT1-2-1 primer pair. These primers were combined in a multiplex PCR reaction following the 161 protocol described by Duong et al. (2013) with an annealing temperature of 56 °C for all 162 isolates of *B. basicola* and *B. rouxiae*. From the PCR result, three putative MAT1-1-1 and 163 three MAT1-2-1 amplicons from B. rouxiae isolates were selected for Sanger sequencing to 164 confirm the identity of the amplified products. Sequencing reactions were carried out 165 following the protocol described in De Beer et al. (2014) 166

## 167 2.5. Comparison and phylogenetic analyses of the HMG and α-box amino 168 acid sequences

169 The *MAT* locus and its flanking regions were extracted and annotated from the available 170 genomes of various species in the *Ceratocystidaceae* (**Table 3**) in the same manner as

171 described in section 2.2. The amino acid sequences of the HMG and  $\alpha$ -box were identified 172 using the conserved domain function of BLASTp. Datasets were compiled and aligned to the 173 HMG and  $\alpha$ -box amino acid sequences of *B. basicola* and *B. rouxiae* using the online 174 version of MAFFT v.7.0 (Katoh & Standley 2013). Neighbour-joining analyses were 175 performed on the amino acid alignments using MEGA v.6.0 (Tamura *et al.* 2013) using the 176 poisson method with 1000 bootstrap replicates.

177 **2.6. Mating crosses** 

#### 178 **2.6.1. On carrots**

The mating types of *B. basicola* and *B. rouxiae* isolates were determined using the newly developed multiplex PCR primers. Isolates, of opposite mating type, were selected and paired on carrot slices in an attempt to induce mating. Thirteen isolates of *B. basicola* (three *MAT1-1* and 10 *MAT1-2*) and 26 isolates of *B. rouxiae* (18 *MAT1-1* and 8 *MAT 1-2*) were paired in all possible combinations on carrot pieces. The experiment was conducted in triplicate for each pair of isolates.

Whole carrots were surface disinfected using 70 % ethanol and these were cut into 5 cm 185 186 thick pieces. These pieces were halved lengthwise and rinsed in a solution of streptomycin (0.3 g Streptomycin, 500 mL distilled water). The pieces were air dried after which isolates 187 representing either the MAT1-1 or MAT1-2 were inoculated on the surface of one half 188 approximately 2 cm apart. The uninoculated half carrot slice was then placed against the 189 inoculated half and the pieces were wrapped with parafilm to form a tight "sandwich". The 190 carrot "sandwiches" were placed in a sealed sterile plastic container and incubated for two 191 weeks at  $\pm$  20 °C, after which the halves were separated and inspected for the presence of 192 sexual structures. Once inspected, the carrot halves were returned to the plastic containers 193 and incubated for a further two weeks after which they were again inspected for sexual 194 195 structures.

Because sexual structures were not observed during the initial incubation period, the inoculated carrot slices were transferred to a 4 °C incubator for 12 weeks after which the experiment was terminated.

#### 199 **2.6.2.** In culture

Isolates, of opposite mating type, were selected and paired in culture in an attempt to induce
mating. Thirteen isolates of *B. basicola* (three *MAT1-1* and 10 *MAT1-2*) and 15 isolates of *B. rouxiae* (nine *MAT1-1* and six *MAT1-2*) were paired in all possible combinations on 0.2 %
MEA, 10 % Carrot agar (900mL MEA and 100 mL organic carrot juice, Rugani, South
Africa), and 2 % MEA supplemented with Thiamine (200 mg/L, Sigma Aldrich). The

experiment was conducted in triplicate for each pair of crossed isolates. A total of 90 combinations of *B. basicola* and 162 combinations of *B. rouxiae* were tested on each medium.

Inoculum for the pairing experiment was taken from a two-week-old culture. Squares (3mm x 3mm) of agar bearing mycelium of the test isolates were inoculated 25 mm apart from one another in the centre of Petri dishes. The paired isolates were incubated for one month at 20 °C ( $\pm$  2 °C) and inspected regularly for the presence of sexual structures. After one month, the plates were transferred to a 10 °C incubator to induce a stress response that might give rise to sexual structures. The paired isolates were inspected monthly for the appearance of sexual structures for six months.

#### 215 **3. Results**

#### 216 **3.1.** Characterization of the *MAT1-2* idiomorph of *B. basicola*

tBLASTx searches using the reference *Ceratocystis fimbriata MAT1* gene sequences identified highly similar sequences to *MAT1-2-1* in scaffold 18 of the genome of isolate CMW49352 (Wingfield *et al.* 2018). Annotation of the 2 Mb scaffold using Augustus 3.3.2 identified 1001 putative ORFs. BLASTp of the predicted protein sequences identified the structure of the *MAT1-2* idiomorph. A *MAT1-2-1* and a *MAT1-2-7* encoding ORF was identified, flanked at one side by *COX*, *APN*, *APC*, and *SLA* encoding genes, and at the other side by a gene of unknown function (*UNK*) and an importin gene (*IMP*) (**Fig. 1A**).

# 3.2. Genome sequencing and characterization of the MAT1-1 idiomorph of B. basicola

Illumina sequencing of the genome of the putative MAT1-1 isolate (CMW25440), produced 226 227 approximately 39.6 million paired reads. De novo assembly of the genome using SPAdes 3.9 produced 841 scaffolds longer than 500 bases. The assembly produced a genome of 228 229 approximately 25.1 Mb in size with an N50 of 90Kb and a GC content of 52%. This draft assembly was similar in size to that available for *B. basicola* (Wingfield et al. 2018). BUSCO 230 analysis predicted an assembly completeness of 97%. The assembly contained 1276 231 complete single-copy BUSCOs, 1 complete and duplicated BUSCO, 10 fragmented 232 BUSCOs and 28 missing BUSCOs from a total of 1315 BUSCO groups searched. 233

tBLASTx searches using the identified *MAT* flanking genes from isolate CMW49352 and *MAT1-1-1* from *C. fimbriata* identified highly similar sequences in scaffold 63 of the genome
of isolate CMW25440. Annotation of the 100Kb scaffold identified 41 putative ORFs.
BLASTp of the predicted protein sequences allowed for the identification of the *MAT1-1*idiomorph. The organization of the genes flanking the *MAT1-1* from CMW49352 and *MAT1-2*

from CMW25440 were almost identical (Fig. 1B) and only the presence of the different *MAT*genes allowed for delineation between the two isolates.

In both the MAT1-1 and MAT1-2 isolates, the region from the COX encoding gene to the 241 IMP encoding gene spanned about 31Kb and closely resembled that of the MAT flanking 242 regions in other Ceratocystidaceae species (Supplementary figure 1). The predicted 243 MAT1-2-1 gene was 909 bases long, composed of three exons with a combined sequence 244 length of 798 bases and two introns (53 bases and 55 bases). The predicted protein 245 sequence included 265 amino acids and harboured the characteristic HMG-box domain. The 246 predicted MAT1-2-7 gene was 857 bases long, composed of three exons with a sum 247 sequence length of 603 bases and two introns (53 bases and 201 bases). The predicted 248 MAT1-2-7 protein sequence included 200 amino acids and contained no known conserved 249 structural domains. The predicted MAT1-1-1 gene was 1233 bases long, composed of two 250 exons with a total sequence length of 1176 bases with a single intron of 56 bases. The 251 predicted protein sequence included 391 amino acids and harboured the characteristic a-252 253 box. The predicted MAT1-1-2 gene region was 1518 bases long, composed of five exons of 254 1284 bases in total and four introns (59 bases, 57 bases, 141 bases and 59 bases). The 255 predicted protein sequence included 427 amino acids and contained the HPG/PFF pfam 256 domain (accession pfam17043). The scaffold sequences, together with their MAT gene 257 annotations, were deposited in NCBI GenBank (Table 1).

258 **3.3.** Multiplex and other PCRs

The *MAT1-1-1* and *MAT1-2-1* primer pairs were successfully used in multiplex amplification of the *MAT* genes from both *Berkeleyomyces* species. Multiplex amplification of 13 *B. basicola* isolates identified three isolates containing the *MAT1-1-1* gene region and ten isolates containing the *MAT1-2-1* gene region (**Fig. 2A**). Multiplex amplification of 26 *B. rouxiae* isolates identified 18 isolates containing the *MAT1-1-1* gene region and eight isolates containing the *MAT1-2-1* gene region (**Fig. 2B**).

Additional support for the identity of *MAT1-1* and *MAT1-2* idiomorph isolates was provided by PCR amplification of the *MAT1-2-7* gene region. This region was successfully amplified in all the isolates where the *MAT1-2-1* region was amplified, and no amplification was observed in isolates where the *MAT1-1-1* region was amplified (**Supplementary figure 2A**). The *SLA* gene and the conserved *UNK* region were successfully amplified for all *B. basicola* and *B. rouxiae* isolates included in this study (**Supplementary figure 2B & 2C**).

From the multiplex PCR results, we selected three MAT1-1-1 and three MAT1-2-1 containing isolates for MAT amplicon sequencing. Sequencing of the MAT1-1-1 region produced a product of around 810 base-pairs spanning the entire  $\alpha$ -box region (**Fig. 2A**). Sequencing of

the *MAT1-2-1* region produced a product of around 500 base-pairs containing the intron region and encoding 53 of the 81 amino acids of the HMG-box domain (**Fig. 2B**).

## 276 3.4. Comparison and phylogenetic analyses of the HMG and α-box amino 277 acid sequences

Neighbour joining analyses of the HMG-box and α-box amino acid sequences for various
isolates of the *Ceratocystidaceae* produced phylogenetic trees with similar topology (Fig. 4
A & B). In both trees, *B. basicola* and *B. rouxiae* grouped together with high bootstrap
support. The included *Ceratocystis* species formed a strongly supported sub-group to the *Berkeleyomyces* species, except for *C. adiposa* that grouped together with *Huntiella* species
in both trees.

#### 284 **3.5.** Mating experiments

None of the pairings between the identified *MAT1-1* and *MAT1-2* idiomorph isolates of *B. basicola* and *B. rouxiae* resulted in the production of sexual structures under any of the conditions tested. All isolates produced abundant mycelium, asexual endoconidia and chlamydospores. In many cases a zone of vegetative incompatibility developed between the isolates preventing the mycelium of the different isolates colonizing a plate from making contact.

#### 291 **4. Discussion**

Whole genome sequencing and investigation of the genomes of two *B. basicola* isolates 292 allowed for the identification and characterization of the MAT locus for Berkeleyomyces. 293 294 From the genome of *B. basicola* isolate CMW49352 (Wingfield et al. 2018) we were able to 295 identify and characterize the MAT1-2 idiomorph. From genome sequencing results of B. 296 basicola isolate CW25440, we were further able to identify and characterize the MAT1-1 297 idiomorph. The presence of the MAT1-1 and MAT1-2 idiomorphs in different isolates of B. basicola is similar to that of other species of Ceratocystidaceae and other ascomycete fungi 298 299 that have a heterothallic mating system. This heterothallic mating systems was found in both B. basicola and B. rouxiae. Although no sexual state is currently known for these closely 300 301 related species, the presence of an apparently functional mating-type locus in these species suggest that cryptic sexual reproduction could occur in nature (Kuck & Poggeler 2009, Dyer 302 303 & Kuck 2017). However, more in-depth sampling of natural populations followed by various 304 population genetic analyses are needed to determine if mating is taking place in nature.

Characterization of the genes located at the *MAT* locus of two isolates of *B. basicola* allowed us to elucidate the structure of both the *MAT1-1* and *MAT1-2* idiomorphs for the fungus. Each idiomorph was flanked on one side by the *COX APN*, *APC*, and *SLA* genes and on the

other side by a gene of unknown function (here referred to as UNK) and an IMP gene. This 308 309 arrangement is very similar to that of Ceratocystis fimbriata (Wilken et al. 2014) and appears 310 to be conserved among the various genera of the Ceratocystidaceae and Gondwanamycetaceae (Aylward et al. 2016, Wilken et al. 2018, Wilson et al. 2015b). Our 311 results also showed that *B. rouxiae*, the cryptic sister species of *B. basicola*, is also 312 heterothallic. Although the MAT locus of B. rouxiae was not fully characterised, using PCR 313 and sequencing it was possible to confirm that the MAT1-2 idiomorph in B. rouxiae contains 314 homologs to the MAT1-2-1 and MAT1-2-7 genes and that the MAT1-1 idiomorph contains a 315 homolog of the MAT1-1-1 gene. We also confirmed the presence of homologs to the SLA 316 and UNK genes in B. rouxiae. 317

The MAT1-1 idiomorph of B. basicola included the additional MAT gene, MAT1-1-2 originally 318 described from Neurospora crassa (Turgeon & Yoder 2000). Like many other heterothallic 319 species in the Ceratocystidaceae the gene was located adjacent to the MAT1-1-1 gene. We 320 were able to identify the conserved HPG/PFF domain in this gene. Like the MAT1-1-2 gene, 321 322 its conserved domain was also first identified in Neurospora crassa (Turgeon & Yoder 2000). 323 The MAT1-2 idiomorph included the MAT1-2-7 originally described in Huntiella omanensis 324 (Wilson et al. 2015b). This gene was located adjacent to MAT1-2-1, but is in the opposite 325 orientation. Prior to the present investigation, a full length MAT1-2-7 gene had been characterized only in Huntiella omanensis and a truncated version of this gene had been 326 characterized in Huntiella moniliformis (Wilson et al. 2015b). The present study revealed 327 homologs of this gene in both *Berkelevomyces* species, as well as putative homologs to this 328 gene in other species of Ceratocystidaceae where they had not previously been identified. 329

330 Alignment of the  $\alpha$ -box amino acid sequences in *B. basicola, B. rouxiae* and various other genera in the Ceratocystidaceae showed relatively low conservation of this region. On the 331 other hand, alignment of the HMG-box amino acid sequences showed that the region is 332 more conserved than that of the  $\alpha$ -box region, but overall conservation between the genera 333 was low. A similar situation was seen when aligning the HPG/PFF domain amino acid 334 sequences (results not shown). The low level of conservation of these conserved domains 335 336 among genera was not unexpected and has for example been found in the Ophiostomatales (Duong et al. 2013) and Pleosporales (Yun et al. 2013). 337

Phylogenetic analyses of the α-box amino acid sequences and HMG-box amino acid sequences grouped *B. basicola* and *B. rouxiae* distinct from the other *Ceratocystidaceae* genera. This region had little resolution and the two species could not be separated in these analyses. The trees generated from these sequences were also not congruent, which is consistent with the findings of other studies (Goodwin *et al.* 2003, Yokoyama *et al.* 2006,

Bihon *et al.*, 2014). Mating type genes are under selective and evolutionary pressure (Duong *et al.* 2013, Bihon *et al.* 2014), which makes them unsuitable for phylogenetic analyses
(Schmitt *et al.* 2009, Stielow *et al.* 2015).

It was not possible to induce sexual structures in cultures of either B. basicola or B. rouxiae, 346 even though isolates of known opposite mating type were paired in many different 347 combinations and grown under a relatively wide range of conditions. While these 348 experiments provide some evidence that sexual reproduction does not occur in B. basicola 349 or *B. rouxiae*, many different biological, ecological and environmental factors could influence 350 the ability of these fungi to reproduce sexually. Various other fungi known to include isolates 351 of two different mating types typical of heterothallism have yet to reveal sexual states 352 (Gordon 2017). In some cases such as Aspergillus fumigatus, many years passed before 353 sexual structures were found even though the fungus was known to be heterothallic (Paoletti 354 et al. 2005, O'Gorman et al. 2009). For the present, it is not possible to know whether sexual 355 reproduction can occur in the two cryptic species of Berkeleyomyces. 356

PCR amplification of the MAT genes using the mating type markers developed in this study 357 358 identified three MAT1-1 and ten MAT1-2 isolates of B. basicola, and 18 MAT1-1 and eight 359 MAT1-2 isolates of B. rouxiae in our collection of isolates. Our collection of isolates of the two species showed that both B. basicola and B. rouxiae occur in South Africa and the 360 Netherlands. Available isolates of *B*. basicola from these countries included only a single 361 mating type. In contrast, the collection of isolates of *B. rouxiae* from South Africa and New 362 Zealand included both MAT1-1 and MAT1-2 isolates. This implies that sexual reproduction 363 could occur in *B. rouxiae* in these countries. A population genetics study of a sufficiently 364 large collection of isolates would shed light on this question. 365

#### 366 **Conflict of interest**

367 The authors report no conflict of interest.

#### 368 Acknowledgements

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#### 545 Figures Captions

- **Figure 1:** The structure of the *MAT1-2* and *MAT1-1* idiomorphs of *B. basicola* elucidated from its genomes. (**A**) The structure of the *MAT1-2* idiomorph and its flanking genes was identified from the genome of CMW49352; (**B**) The structure of the *MAT1-1* idiomorph and its flanking genes was identified from the genome of isolate CMW25440.
- Figure 2: Results obtained from a multiplex PCR assay to determine the MAT-1 genotype of 550 551 isolates of B. basicola and B. rouxiae. (A) Electrophoresis gel for 13 isolates of B. basicola; (B) Electrophoresis gel for 13 isolates of *B. rouxiae*. The molecular weight maker used was a 552 GeneRuler 100 bp DNA Ladder (Fermentas). Fragments were separated on a 2 % agarose 553 gel stained with GelRed and visualized under UV light. The band sizes of 1 kb, 500 and 100 554 bp are indicated for the molecular weight marker lane. Amplification of the MAT1-1-1 gene 555 region produced an amplicon size of 845 bp and amplification of the MAT1-2-1 gene region 556 produced an amplicon size of 530 bp. 557
- Figure 3: Alignment of the amino acid sequences of the (A) α-domain and the (B) HMG-box
  domain from *B. basicola, B. rouxiae* and other *closely related* species..
- 560 **Figure 4:** Neighbour joining trees derived from phylogenetic analyses of the (**A**) α-domain
- and (B) HMG-box amino acid sequences for various Ceratocystidaceae species including B.
- 562 *basicola* and *B. rouxiae*. Bootstrap values above 75 % are indicated at nodes.

## Tables

**Table 1:** Isolates included in this study with the GenBank accession numbers of the respective *MAT* gene sequences obtained for the different isolates

|                | Collection             | Other collection   |             |           | GenBank accession |
|----------------|------------------------|--------------------|-------------|-----------|-------------------|
| Current name   | number                 | numbers            | Country     | ldiomorph | numbers           |
|                |                        |                    |             |           | MAT scaffolds     |
| Berkleyomyces  |                        |                    |             |           |                   |
| basicola       | CMW4098 <sup>a</sup>   |                    | Ecuador     | MAT1-2    |                   |
|                | CMW5896 <sup>a</sup>   |                    | Uganda      | MAT1-2    |                   |
|                | CMW6714 <sup>a</sup>   |                    | Australia   | MAT1-2    |                   |
|                | CMW7065 <sup>a</sup>   | CBS341.33/MUCL9545 | Netherlands | MAT1-2    |                   |
|                | CMW7067 <sup>a</sup>   | CBS487.48/MUCL9542 | Belgium     | MAT1-2    |                   |
|                | CMW7069 <sup>a</sup>   |                    | Netherlands | MAT1-2    | 7                 |
|                | CMW49352 <sup>a</sup>  | CBS142796          | Netherlands | MAT1-2    | MH522765          |
|                | CBS414.52 <sup>a</sup> | MUCL8363           | Netherlands | MAT1-2    |                   |
|                | CBS430.74 <sup>a</sup> | CMW7071            | Netherlands | MAT1-2    |                   |
|                | CMW25439 <sup>a</sup>  |                    | Indonesia   | MAT1-1    |                   |
|                | CMW25440 <sup>a</sup>  | CBS142829          | Indonesia   | MAT1-1    | MH522766          |
|                | CMW26479 <sup>a</sup>  |                    | Indonesia   | MAT1-1    |                   |
|                |                        |                    | South       |           |                   |
|                | CMW51564 <sup>a</sup>  |                    | Africa      | MAT1-2    |                   |
|                |                        |                    |             |           | MAT1-1-1 or MAT1- |
|                |                        |                    |             |           | 2-1               |
| Berkeleyomyces |                        |                    | South       |           |                   |
| rouxiae        | CBS118120 <sup>a</sup> |                    | Africa      | MAT1-2    |                   |
|                | CMW5472 <sup>a</sup>   | CBS117825          | Ethiopia    | MAT1-2    | MH522760          |
|                | CMW7064 <sup>a</sup>   | CBS194.26/MUCL9544 | Unknown     | MAT1-1    | MH522756          |
|                | CMW7066 <sup>a</sup>   | CBS342.33/MUCL9456 | Netherlands | MAT1-1    |                   |
|                | CBS413.52 <sup>a</sup> |                    | Netherlands | MAT1-1    |                   |
|                | CBS150.67 <sup>a</sup> | IHEM3832           | Switzerland | MAT1-1    |                   |
|                | C                      |                    | South       |           |                   |
|                | CMW7622                | CBS117826          | Africa      | MAT1-1    |                   |
|                |                        |                    | South       |           |                   |
|                | CMW7623                | CBS118119          | Africa      | MAT1-1    | MH522757          |
|                |                        |                    | South       |           |                   |
|                | CBS117827              |                    | Africa      | MAT1-1    |                   |
|                |                        |                    | South       |           |                   |
|                | CMW7625 <sup>a</sup>   | CBS117828          | Africa      | MAT1-1    |                   |
|                | CMW14219 <sup>a</sup>  |                    | Chile       | MAT1-2    |                   |
|                | CMW14220               |                    | Chile       | MAT1-2    |                   |
|                | CMW14221               | CBS142830          | Chile       | MAT1-2    | MH522761          |
|                | CMW14222               |                    | Chile       | MAT1-2    |                   |
|                | CMW14223               |                    | Chile       | MAT1-2    |                   |

|              | Collection             | Other collection |         |           | GenBank accession |
|--------------|------------------------|------------------|---------|-----------|-------------------|
| Current name | number                 | numbers          | Country | ldiomorph | numbers           |
|              |                        |                  | South   |           |                   |
|              | CMW44562               |                  | Africa  | MAT1-1    |                   |
|              |                        |                  | South   |           |                   |
|              | CMW44563               |                  | Africa  | MAT1-1    |                   |
|              |                        |                  | South   |           |                   |
|              | CMW44564               |                  | Africa  | MAT1-1    |                   |
|              |                        |                  | South   |           |                   |
|              | CMW44565               |                  | Africa  | MAT1-1    |                   |
|              |                        |                  | South   |           |                   |
|              | CMW44566 <sup>a</sup>  |                  | Africa  | MAT1-1    | MH522758          |
|              |                        |                  | South   |           |                   |
|              | CMW44567               |                  | Africa  | MAT1-1    |                   |
|              |                        |                  | South   |           |                   |
|              | CMW44568               |                  | Africa  | MAT1-1    |                   |
|              |                        |                  | South   |           |                   |
|              | CMW44569               |                  | Africa  | MAT1-1    |                   |
|              |                        |                  | New     |           |                   |
|              | ICMP2460 <sup>a</sup>  |                  | Zealand | MAT1-1    |                   |
|              |                        |                  | New     |           |                   |
|              | ICMP13276 <sup>a</sup> |                  | Zealand | MAT1-2    | MH522762          |
|              | CBS178.86 <sup>a</sup> | MUCL40417        | Canada  | MAT1-1    |                   |

<sup>a</sup>Isolates used in single mating crosses

Sh 

| Namo        | Sequence $(5^{\prime} \rightarrow 3^{\prime})$ | Annealing        | Fragment    |
|-------------|--|------------------|-------------|
| Name        | Sequence $(3 \rightarrow 3)$                   | Temperature (°C) | length (bp) |
| Tbas_SLA_F  | CAACACCAAGGGTCTACTCCG                          | 50               | 887         |
| Tbas_SLA_R  | TCCACCTGCTGCTCCATCTC                           | 39               | 007         |
| Tbas_M127_F | TGAAGGAAGTAAGTCCGCACAG                         | 50               |             |
| Tbas_M127_R | GGGAAACTCAACCCAGAAGC                           | 59               | 445         |
| Tbas_Unk_F  | GACTGCCTACATCGCCTACC                           | 57               | 1000        |
| Tbas_Unk_F  | TTGCCGTCACTACCAACCTG                           | 57               | 1000        |
| Tbas_M121_F | AAGACTTTACTCCGTGACTTTAGG                       |                  | 520         |
| Tbas_M121_R | CCAATTCTTGATAGTGGGTGC                          | 30               | 550         |
| TBAS_M111_F | GCTGAAATGGGTGGTGTT                             | 56               | 945         |
| TBAS_M111_R | CTTGGTTTTGGTTGGGTTG                            | oc               | 040         |

Table 2: Newly designed primer sets for amplification of Berkeleyomyces mating genes

REAL

| Species                     | Genome accession number | Reference                        |
|-----------------------------|-------------------------|----------------------------------|
| Ceratocystis adiposa        | LXGU0100000             | Wingfield et al. 2016a           |
| C. fimbriata                | APWK0000000             | Wilken <i>et al.</i> 2013        |
| C. manginecans              | JJRZ0000000             | Van der Nest <i>et al.</i> 2014b |
| Chalaropsis thielavioides   | BCGU00000000            | Unpublished                      |
| Endoconidiophora laricicola | LXGT0000000             | Wingfield <i>et al.</i> 2016a    |
| E. polonica                 | LXKZ01000000            | Wingfield <i>et al.</i> 2016a    |
| Huntiella buthanensis       | MJMS0000000             | Wingfield <i>et al.</i> 2016b    |
| H. moniliformis             | JMSH0000000             | Van der Nest <i>et al.</i> 2014b |
| H. omanensis                | JSUI0000000             | Van der Nest <i>et al.</i> 2014a |
| H. savannae                 | LCZG0000000             | Van der Nest et al. 2015         |
| Thielaviopsis musarum       | LKBB00000000            | Wingfield <i>et al.</i> 2015a    |

LAEV0000000

LNGK0000000

LNGL0000000

Wingfield et al. 2015b

Aylward et al 2016

Aylward et al 2016

T. punctulata

K. proteae

Knoxdaviesia capensis

 Table 3: Accession numbers of Ceratocystidaceae and Gondwanamycetaceae genomes

 used in this study





| F MAFE          A YYQ          F A YYQ          F A YZQ          F I AFE          A YZQ          A YZQ <th>в</th> <th></th> <th>F. graminearum</th> <th>E. polonica</th> <th>K. proteae</th> <th>C. adiposa</th> <th>H. savannae</th> <th>H. omanensis</th> <th>H. buthanensis</th> <th>T. musarum</th> <th>Ch. thielavioide.</th> <th>C. manginecans</th> <th>C. fimbriata</th> <th>B. rouxiae</th> <th>B. basicola</th> <th>4</th>  | в |                               | F. graminearum   | E. polonica  | K. proteae  | C. adiposa   | H. savannae   | H. omanensis  | H. buthanensis  | T. musarum  | Ch. thielavioide.  | C. manginecans  | C. fimbriata  | B. rouxiae  | B. basicola   | 4 |
|---|---|-------------------------------|--|--|---|--|---|---|---|---|--|---|---|---|---|---|
| MAP       XAYYQKIFAQFPQKN-FAQFPQKN-1SPFITKLWRKDPFQSRWLMASVYSFYRDSIGNKGAKLITFLDIAAPLMCTPKPEEYLKSLCWNTANDKGEIQFLQDS         MAP       XAYYQKIFAQVQKIFAQQKPQKN-1SPFITKLWRKDPFQSRWLMASVYSFYRDSIGNKGAKLITFLDIAAPLMCTPKPEZYLKSLCWNTANDKGEIQFLQDS         MAP       XAYYQKIFAQVQKIFAQVQKIFAQQKS       SUMTANDKGEIQFLQDS         MAP       XAYYQKIFAQVQKIFAQQKIFAQ       SUMTANDKGEIQFLQDS         MAP       XAYYQKIFAQVQKIFAQVQKIFAQ       SUMTANDKGEIQFQ         MAP       XAYYQKIFAQVQKIFAQVQKIFAQ       SUMTANDKGEIQFQ         MAP       XAYYQKIFAQVQKIFAQ       SUMTANDKGEIQF       SUMATANDKGEIQFQ         MAP       XAYYQKIFAQVQKIFAQ       SUTANDKAS       SUMATANDKAS       SUTANDKAS         MAP       XAYYQKIFAQVQKIFAQ       SUTANVIKAIS       SUTANXA       SUTANXA       SUTANXA         MAP       XAYYQKIFAQVQKIFAQ       SUTANXA       SUTANXA       SUTANXA       SUTANXA       SUTANXA         1 47       SUTAYQKIFAQVQKIFAQ       SUTANXA       SUTANXA       SUTANXA       SUTANXA       SUTANXA       SUTANXA       SUTANXA          1 47       SUTANQA       SUTANXA  |   | ÷                             | ы  | ы  | Ħ   | ч  | F   | ы   | Ħ   | ħ   | F  | М   | ч   | ч   | μų.   |   |
| IF RAYYQKIFAQFPQKN-ISPTIKLWRKDPFQSRWLMASVSFVRDSIGNKGAKLTFLDIAAPLMCTPKPEZKLKSLCWNTANDKGEIQFLQDS         FR AVYQKIFAQFPQKN-ISPTIKLWRKDPFQSRWLMASVSFVRDIA         FR AVYQKIFAQFPQKN-ISPTIKLWRKDPFQSRWLMASVSFVRDIA         FR AVYQKIFAQFPQKN-ISPTIKLWRKDPFQSRWLMASVSFVRDIA         FR AVYQKIFAQFPQKN-ISPTIKLWRKDPFQSRWLMASVSFVRDIA         FR AVYQKIFAQFPQKN-ISPQKN-ISPTIKLWRKDPFQSRWLMASVSFVRDIA         FR AVYQKIFAQFPQKN-ISPTIKLKIF         FR AVYQKIFAQFPQKN-ISPTIKL         FR AVYQKIFAQFPQKN-ISPTIKL         FR AVYQKIFAQFPQKN-ISPTIKL         FR AVYQKIFAQFPQKN-ISPTIKL         FR AVYQKIFAQFPQKN-ISPTIKL         FR AVYQKIFAQFPQKN-ISPTIKL         FR AVYQKIFAQFPQKN-ISPQKN-ISPTIKL         FR AVYQKIFAQFPQKN-ISPTIKL         FR AVYQKIFFAQFPQKN-ISPTIKL         FR AVYQKIFFAQFPQKN-ISPTIKL         FR AVYQKIFFAQFPQKN-ISPTIKL         FR AVYQKIFFAQFPQKN-ISPTIKL         FR AVYQKIFFAQFP   |   | р.<br>р.                      | ΜA   | I A  | I A   | I A  | IA  | I A   | I A   | I A   | ΜA   | - 0   | -   | ΜA  | ΜA  |   |
| RAYYQKIFAQFPQKN-ISPFITKLWRKDFQSRWMLMASYYSFYRDSIGNKGAKLLTFLDIAAPLMCTPKPEEYLKSLCWMTANDKGEIQFLQDS         RAYYQKIFAQPPQKN-ISPFIKLWRKDFFQSRWMLMASYYSFYRDSIGNKGAKLLTFLDIAAPLMCTPKPEYLKSLCWMTANDKGEIQFLQFLQDS         RAYYQKIFAQPPQKN-ISPFICKURAISKUPFQSRWMLMASYYSFYRDSIGNKGAKLLTFLDVAAPLMCTPKPEYLKSLCWMTANDKGEIQFLQFLQDS         RAYYQKIFAQPPQKN-ISPFICKUPKTANDKASYYSFYRDSIGNKGAKLLTFLDVAAPLMCTPKPEYLKSLCWMTANDKGEIQFLQFLQFLQDS         RAYYQKIFAQPPQKN-ISPFICKUPKTANDKASSPFQSRWMLMASYYSFYRDSIGNKGAKLLTFLDVAAPLMCTPKPEYLKSLCWMTANDKGEIQFLQFLQFLQFLQDS         RAYYQKIFAQPPQKS-ISSFITALWRKSDFFQSRWMLMASYYSFYRDSIGNKGAKLLTFLDVAAPLMCTPKPEYLKSLCWMTANDKGEIQFLQFLQFLQFLQF         RAYYQKIFAQPPQKS-ISSFITANPLKAISKLWRSDFFQSRWMLMASYYSFYRDSIGNKGAKLLTFLDVAAPLMATLUNDSPQRYLRXLKSLCWWTANDKGEIKFLQF         RAYYQKIFAQVPQKS-ISSFITANPLKAISKLWRSDFFQSRWMLMGRYYSFYRFYKTYSFYRDJAIGNVGAALAPLMATLNUPSPQRYLRXLCWIYLKLCWNTGDDNGEIKFPQDS         RAYYQKIFAQVPQKS-ISSFITANDKKASSDFQSRWMLMGRYYSFYRFYKTYSFYKDJAIGKNTAKLSDFLEVAVPIMCTPPP2         RAYYQKIFAQVPQKS-ISSALTTKANSSDFQSRWMLMKSDFT         RAYYQKIFAQVPQKS-ISSALTTKANSSDFQSRWMLMKSDFT         RAYYQKIFAQVPQKS-ISSALTTKANSSDFQSRWMLMKSDFT         RAYYQKIFAQVPQKS-ISSALTTKANSDFQSRWMLMKSDFQSRWMLMGRYYSFTKDT         RAYYQKIFAQVPQKS-ISSALTTKANSDFQSRWMLMKSDFT         RAYYQKIFAQVPQKS-ISSALTTKANSDFQSRWMLMKSDFT         RAYYQKIFAQVPQKS-ISSALTTKANSDFQSRWMLMKSDFT         RAYYQKIFAQVPQKS-ISSALTTKANSDFQSRWMLMKSDFT         RAYYQKIFAQVPQKS-ISSALTTKANSDFT         RAYYQKIFAQVPQKS-ISSALTTKANSCONCTONUNCALITAKTYSFY  |   | ÷                             | F  | F  | Y   | F  | F   | F   | F   | F   | F  | -   | -   | F   | F   |   |
| IVYQKIFAQFPQKN-ISPFITKLWRKDPFQSRWLMASVSFVRDSIGNKGAKLLTFLDIAAPLMCTPKPEYLKSLCWMTANDKGEIQFLQDS         IVYQKIFAQFPQKN-ISPFITKLWRKDPFQSRWLMASVSFVRDSIGNKGAKLLTFLDIAAPLMCTPKPEZKLKSLCWMTANDKGEIQFLQDS         IVYQKIFAQFPQKN-ISPFIKLWRKDPFQSRWLMASVSFVRDSIGNKGAKLLTFLDIAAPLMCTPKPEKLKSLCWMTANDKGEIQFLQDS         IVYQKIFAQFPQKN-ISPFIKLWRSDPFQSRWLMASVSFVRDSIGNKGAKLLTFLDIAAPLMCTPKPEKLKSLCWMTANDKGEIQFLQDS         IVYQKIFAQFPQKS-ISSTITKLWRSDPFKSWMLMASVSFVRDSIGNKGAKLLTFLDVAAPLMCTPKPEKLKSLCWMTANDKGEIQFLQFLQES         IVYQKIFTQVPQKS-ISSTITKLWRSDPFKSWMLMGRVSFVRSFILARDVGFLARDVGTAARLKLSDFLUNLPSPEKLCWVTANDKGEIGTTRRNKIRFVQDS         IVYQKIFTQVPQKS-ISSLITKLWRSDPFKSWMLMGRVSFVRSFILARDVGTAARLKLSDFLUAAPLMCTPKPEZGUNGTSKAKLKIKTGDDNGEIKF         IVYQKIFTQVPQKS-ISSLITKLWRSDPFQSRWMLMGRVSFFILARDVGFLARDVSFVLAARLSDFLUAAPLMCTPKPEZGUNGTSKAKLKIKTGDDNGEIKF         IVYQKIFTQVPQKS-ISSLITKLWRSDPFQSRWMLMGRVSFFILARDVSFVRFILARDVGTAALSDFLUAAPLMCTPKPEZGUNGTSKKKUKIKTANDKGEIGTLAFFQDS         IVYQKIFTQVPQKS-ISSLITKLWRSDPFQSRWMLMGRVSFFILARDVSFVRFILARDVGKAKLSDFLUAAPLMCTPKEZGUNTTGDDNGEIKF         IVYQKIFTQVPQKS-ISSLITKLWRSDPFQSRWMLMGRVSFFILARDVSFVRFILARDVGKAKLSDFLUAAVPIMGTDNGCUNTGDDNGEIKF         IVYQKIFTQVPQKS-ISSLITKLWRSDPFQSRWMLMGRVSFFILARDVSFILARDVGKAKLSDFLUAAVPIMGTDNGCUNTGDDNGEIKF         IVYQKLFTQVSKGLFFUCKSLS         IVYQKLFFQVSKS-ISSLOV      ISSLITKLWRSDPFQSRWMLMGRVSFFILARDVSFILARDVSFILARDVSKLSDFLUAAVPIMGTDNGCUNTGDDNGELAFFQDS         IVYQKLFTQVPQKS-ISSLTTKKVST       ISSLTTKLWRSDPFQSRWMLMGRVSFFILARDVSFILARDVSFILARDVSKLSDFLUAAVPIMGTDNST         IVYQKIFTQVPQKS-ISSLTTKLWNSDFGSRW   |   | Ra                            | RI   | V BI   | RS  | RA   | R A   | V B   | Ą R   | ų B   | RA   | RΝ  | RV  | RA  | ų B   |   |
| YQK1 F AQF P QKN - 1 S PF1 TKL WRK D P F Q S WML MAS VYS F VRD 1 G NKG AKLL TFL DI AAPLMC TP KPEE YLKS L CWMT ANDK GEI Q F L Q 5 9<br>YQK1 F AQF P QKN - 1 S PF1 TKL WRK D P F Q S R WML MAS VYS F VRD 1 G NKG AKLL TFL DV AAPLMC TP KPEE YLKS L CWMT ANDK GEI Q F L Q 5 9<br>YE KCLRF MPRHTNVLKAI S KL WR G D F KS HWAI I AQAFTL ARD VYG TKAARL RD V ALAATLLNL P S P Q R YLKS L CWMT ANDK GEI Q F L Q 5 9<br>YQK1 F THL P QKS - 1 S ALI TRL WKS D P F Q S R WML MAS VYS F VRD 1 G NKG AKLL TFL DV AAPLMC TP KPEE YLKS L CWMT ANDK GEI KFL Q 5 9<br>YQK1 F TQ V P QKS - 1 S ALI TRL WKS D P F Q S R WML MAS VYS F VRD 1 I G NKG AKLL TFL DV AAPLMC TP KPEE YLKS L CWMT G N K G E L RF N R F V Q 5 9<br>YQK1 F TQ V P QKS - 1 S ALI TRL WKS D P F Q S R WML MG R VYS F I R D TV G KNAARLS S F LE AAPI MG V P V P E AYLAKL CWI YTG NEV G ELAF F Q 5 9<br>YQK1 F TQ V P QKS - 1 S ALI TRL WKS D P F Q S R WML MG R VYS F I R D TV G KNTAKLS D F LE VA V P I MG V P V P E AYLAKL CWI YTG NEV G ELAF F Q 5 9<br>YQK1 F TQ V P QKS - 1 S ALI TRL WKS D P F Q S R WML MG R VYS F I R D TV G KNTAKLS D F LE VA V P I MG V P V P E AYLAKL CWI YTG NEV G ELAF F Q 5 9<br>YQK1 F TQ V P QKS - 1 S ALI TRL WKS D P F Q S R WML MG R VYS F I R D TV G KNTAKLS D F LE VA V P I MG V P V P E AYLAKL CWI YTG NEV G ELAF F Q 5 9<br>YQ R I F TQ V P Q K - 1 S LI T KL WKS D P F Q S R WML MG R VYS F I R D TV G KNTAKLS D F LE VA V P I MG V P V P E AYLAKL CWI YTG NEV G ELAF F Q 5 9<br>YQ R I F AQF P Q K - 1 S LI T KL WKS D P F Q S R WML MG R VYS F V S F I R D TV G KNTAKLS D F LE VA V P I MG V P V P E AYLAKL CWI YTG NEV G ELAF F Q 5 9<br>YQ R I F Q V P Q K - 1 S LI T KL WKS D P F Q S R WML I G R V S F V S F I R D TV G KNTAKLS D F LE VA V P I MG V P V E AYLAKL CWI YTG NEV G ELAF F Q 5 9<br>YQ R I F Q V P Q K - 1 S LI T KL WK D P F Q S R WML I S R VYS F V S F I R D V G K A A L A Y I M K I V P F A YLAKL CWI YTG NEV G ELAF F Q 5 9<br>YQ R I F Q V P Q K - 1 S LI T KL WK D P F Q S R WL I S R VYS F V S F I R D V G K A A L A Y I A YLA A A P I MG V P V E AYLAKL CWI YTG N A D A C N Y A A C Y Y F Y A C Y Y A A C Y Y A A C Y Y F Y A A C Y Y  |   | ¥                             | Υ  | M  | ¥   | X  | M   | M   | ×   | M   | M  | Y   | Y   | M   | X   |   |
| XIF       AQFPQKN-IS       YFITKLWRKDPFQSRWMLMASVYSFVRDSIGNKGAKLTFLDIAAPLMCTPKPEVLKSLCWMYTANDKGEIQFLQDS         XKIF       AQFPQKN-IS       YFITKLWRKDPFQSRWMLMASVYSFVRDSIGNKGAKLTFLDIAAPLMCTPKPEVLKSLCWMYTANDKGEIQFLQDS         XKCLRF       MPRHTNVLKAISKLWRKDPFQSRWMLMASVYSFVRDSIGNKGAKLTFLDVAAPLMCTPKPEVLKSLCWMYTANDKGEIQFLQDS         XKIFTQVPQKS-IS       YKIK       YKIFTQVWRKDPFQSRWMLMASVYSFVRDSIGNKGAKLTFLDVAAPLMCTPKPEVLKSPQRYLRDIGWVTANDKGEIQFLQFLQ5         XKIFTQVPQKS-IS       YKIK       YKIKTTANDKGEIQFLQ5       YKIFTQVVSFVRD         XKIFTQVPQKS-IS       YKIK       YKIWKSDPFQSRWMLMASVYSFVRD       YKDTAKAAPIMKLNL       YKIFTQVVSFVRD         XKIFTQVPQKS-IS       YKIKNS       YKIWSDPFQSRWMLMASVYSFVRD       YKDTAKAAPIMKLNL       YKIFTQVVSFVRD       YKIFTQVVSFVRD         XKIFTQVPQKS-IS       YKIKN       YKIWSDPFQSRWMLMASVYSFVRD       YKDTAKAAPIMKL       YKIFTQVVSFVRD       YKIFTQVVSFVRD       YKIFTQVVSFVRD         XKIFTQVVS       YKSITTRTVK       YKIKNON       YKIFTQVVSFVRD       YKIFTQVSF   |   | Υq                            | Τ  | Q M  | YK  | Q A  | N N   | Q M   | Q M   | Q M   | Q A  | ΎΕ  | ΥE  | Q A   | N N   |   |
| I F AQF P Q KN - I S P F I TKL WR KD P F Q S RWL MAS VYS F V R D S I G NK G AKLLTFL D I AAP L MCT P KP E EXL KS L C WMYTANDK G E Q F L Q D S         I F AQF P Q KN - I S P F I TKL WR KD P F Q S RWL MAS VYS F V R D S I G NK G AKLLTFL D I AAP L MCT P KP E EXL KS L C WMYTANDK G E Q F L Q D S         CLRF MP RHTNVLKAI S KL WR GD P F KS HWAI I AQAFTL AR D V G TKAARL LTFL D I AAP L MCT P KP D Z Q KYLR D L G W G TETRRNR I R F V Q D S         I F TQV P Q KS - I S F I TRL WR S D P F Q S RWL MAS VYS F V R D I G K V G TKAARL AAT LLNL P S P Q R YLR D L G WVG TETRRNR I R F V Q D S         I F TQV P Q KS - I S ALI TRL WR S D P F Q S RWL MAS VYS F V R D I G K V G TKAARL AAT LLNL P S P Q R YLR D L G WVG TETRRNR I R F V Q D S         I F TQV P Q KS - I S ALI TRL WK S D P Q S RWL MG R VYS F I R D TI G KNTAKL S FLE VALAAT LNL P S P Q R YLR D L G WVG TETRRNR I R F Q D S         I F TQV P Q KS - I S ALI TRL WK S D P Q S RWL MG R VYS F I R D TI G KNTAKL S D FLE V ALAAT LNL P S P A XLAKL C WI YTG NEV G E L AF F Q D S         I F TQV P Q KS - I S ALI TRL WK S D P Q S RWL MG R VYS F I R D TI G KNTAKL S D FLE V ALAA I LNL P S P A XLAKL C WI YTG NEV G E L AF F Q D S         I F TQV P Q KS - I S ALI TRL WK D P F Q S RWL I G R VS F I R D TI G KNTAKL S D FLE V AV P I MG V P V P E AYLAKL C WI YTG NEV G E L AF F Q D S         I F TQV P Q KS - I S ALI TRL WK D P F Q S RWL I G R VS F I R D TI G KNTAKL S D FLE V AV P I MG V P V E AYLAKL C WI YTG NEV G E L AF F Q D S         I F Q Q V P Q KS - I S ALI TRL WK D P F Q S RWL I G R VS F I R D I G S E ALL S D FLE V AV P I MG P V P E AYLAKL C WI YTG NEV G E L AF F Q D S         I F Q Q V S Q S F L TQ L W K A D P F Q S RWL I G R V S F TR D I G R AC U N F L S V Q V A A D G C Y F A A A G Y P I  |   |                               | ×  | ĸ  | Ģ   | R  | R   | R   | R   | ĸ   | R  | ×   | ×   | ĸ   | ĸ   |   |
| A Q F P Q KN - I S P F I TKL WR KD P F Q S R WL MAS VYS F V RD S I G NKG A KL T F L DI A A P L MC T P K P E V L K S L C WLYT A ND K G E I Q F L Q D S         A Q F P Q KN - I S P F I TKL WR KD P F Q S R WL MAS VYS F V RD S I G NKG A KL L T F L DY A A P L MC T P K P D E V L K S L C WLYT A ND K G E I Q F L Q D S         R M P R HTNVL KA I S L T KL WR G D P F K S HWAI I A Q A F T L A D V R D K G A KL L T F L DY A A P L MC T P K P D E V L K S L C WLYT A ND K G E I Q F L Q D S         T H L P Q K S - I S S I T T L WK S D P F Q S R WL MAS VYS F V R D X J T I A R D V G T K A A R L R D F V L A A P L MC T P K P D E V L K L C WLYT A ND K G E I K P Q D         T Q V P Q K S - I S S I T T L L WK S D P F Q S R WL MAS VYS F V R P K D T I G KNTAKL S D F L Z A A P I MC T P K P E B A L A C W V R T A ND K G E I K F L Q D S         T Q V P Q K S - I S A L I T R L WK S D P F Q S R WL MA K Y S F V S F I R D T I G KNTAKL S D F L Z A A P I M G V P V B E A YL A KL C WL WN R T D N G E L A F F Q D S         T Q V P Q K S - I S A L I T R L WK S D P F Q S R WL M G R V S F I R D T I G KNTAKL S D F L Z A V P I M G V P V B E A YL A KL C WL WN R T D N G E L A F F Q D S         T Q V P Q K S - I S A L I T R L WK S D P F Q S R WL M G R V S F I R D T I G KNTAKL S D F L Z A V P I M G V P V B E A YL A KL C WL WN R T A ND K E Z L A F Q D S         T Q V P Q K S - I S S L I T K L W N D P F Q S R WL M G R V S F I R D N G R V S F I R D T V G KNT A KL S D F L Z A V P I M G V P V B E A YL A KL C WL W N S O N C E L A F E Q D S         T Q V P Q K S - I S S L I T K L W N D P F Q S R WL I G R V S F I R D N G N S S D F L S V C P I M G V P V B E A YL A KL C W Y S G D F G N A C D N C L A F Q D S         T Q V P Q K S - I S S L I T K L W D P F Q S R WL I A K V S F T R D N G  |   | -                             | F  | F  | F   | IF   | IF  | F   | F   | IF  | IF   | Ê   | 6   | IF  | IF  |   |
| Q F P Q K N - I S P F I T K L W K K D P F Q S R W M L M S V Y S F V R D S I G N K G A K L L T F L D I A A P L M C T P K P E Y L K S L C W M T A N D K G E I Q F L Q D 98         Q F P Q K N - I S P F I T K L W K K D P F Q S R W M L M S V Y S F V R D S I G N K G A K L L T F L D V A A P L M C T P K P E Y L K S L C W M T A N D K G E I Q F L Q D 98         F M P R H N V L K A I S K L W R K D P F Q S R W M L M S V Y S F V R D S I G N K G A K L L T F L D V A A P L M C T P K P D S Y L K S L C W M T A N D K G E I Q F L Q D 98         F M P R H N V L K A I S K L W R G D P F K S H W A I I A Q A F T L A R D V G T K A A R L R D F V A A P L M C T P K P D S Y L K S L C W M T A N D K G E I K Q L F H Q A F T A R D Y A F L M K S P Y A D A T L N L P S P Q R Y L R D L G W G T E T R R N R I R F V Q D 98         R P P Q K S - I S A L I T R L W K S D P F Q S R W L M A R V Y S F I R D T I G K N T A K L S F L E A A P L M R T P K P E E Y L K L C W N T G D N G E I K R A R L R D F V A A P L M R T P Y P E A Y L A K L C W I T G N E V G E L A F F Q D 98         Q V P Q K S - I S A L I T R L W K S D P F Q S R W L I A Q K Y S F I R D T I G K N T A K L S D F L E V A V P I M G V P V P E A Y L A K L C W I T G N E V G E L A F F Q D 98         Q V P Q K S - I S A L I T R L W K S D P F Q S R W L I A Q K Y S F I R D T I G K N T A K L S D F L E V A V P I M G V P V P E A Y L A K L C W I T G N E V G E L A F F Q D 98         Q V P Q K S - I S A L I T R L W S D P F Q S R W L I A G R V S F I R D T I G K N T A K L S D F L E V A V P I M G V P V P E A Y L A K L C W I T G N E V G E L A F F Q D 98         Q V P Q K S - I S S L I T K L W N D P F Q S R W L I A K V Y S F T R D Y G K N S E A K L S D F L E V A V P I M G V P V E A Y L A K L C W Y S G N A L A F F Q D 98         Q V P Q K S - I S S L I T K L  |   |                               | ٣  | •  | ×   | A  | н   | н   | н   | н   | A  | 20  | 20  | A   | A   |   |
| P Q K N - I S P F I T K L W R K D P F Q S R W M L M S V Y S F V R D S I G N K G A K L L T F L D I A A P L M C T P K P E Y L K S L C W M T A N D K G E I Q L A P L A P L M C T P K P E Y L K S L C W M T A N D K G E I Q L Q D S S         P Q K N - I S P F I T K L W R K D P F Q S R W M L M S V Y S F V R D S I G N K G A K L L T F L D V A P L M C T P K P D E Y L K S L C W M T A N D K G E I Q L Q D S S         P Q K N - I S P F I T K L W R K D P F Q S R W L M S V Y S F V R D S I G N K G A K L L T F L D V A P L M C T P K P D E Y L K S L C W M T A N D K G E I Q L Q D S S         P Q K N - I S P F I T R L W R D P F Q S R W L M S V Y S F V R D S I G N K G A K L L T F L D V A P L M C T P K P D E Y L K S L C W W T A N D K G E I Q L Q D S S         P Q K S - I S S F I T R L W S D P F Q S R W L M R V Y S F V R D I G R V G T K A R L R D F V A L A T L L N L P S P Q R Y L R D L G W G T E T R R N R I R P V Q D S S         P Q K S - I S A L I T R L W S D P F Q S R W L M R V Y S F V R D I G K N T A K L S D F L E V A V P I M C T P Y P E A Y L A K L C W I T G N E V G E L A F P Q D S         P Q K S - I S A L I T R L W S D P F Q S R W L M R V Y S F I R D T I G K N T A K L S D F L E V A V P I M C T P Y P E A Y L A K L C W I T G N E V G E L A F P Q D S         P Q K S - I S A L I T R L W S D P F Q S R W L I G R V S F I R D T I G K N T A K L S D F L E V A V P I M G V P Y P E A Y L A K L C W I T G N E V G E L A F P Q D S         P Q K S - I S A L I T R L W S D P F Q S R W L I G R V S F I R D T I G K N T A K L S D F L E V A V P I M G V P Y P E A Y L A K L C W I T G N E V G E L A F P Q D S         P Q K S - I S A L I T R L W S D P F Q S R W L I G R V S F I R D T G K N T A K L S D F L E V A V P I M G V P Y E A Y L A K L C W Y S G N A W L G R V S F Q A R A F I N C Y S F I R D Y G Y R   |   |                               | DI   | 1 Q  | GΥ  | Qγ   | QV  | QΛ  | Qν  | ΗL  | R F  | FN  | FN  | QF  | QF  |   |
| 2 X N - I S       2 F I T X L W X K D 2 F Q S R W M M M S V Y S F V R D S I G N K G A K L L T F L D I A A P L M C T P K D E Y L K S L C W M Y T A N D K G E I Q F L Q D 98         2 X N - I S       2 F I T K L W X K D 2 F Q S R W M M M S V Y S F V R D S I G N K G A K L L T F L D V A A P L M C T P K D E Y L K S L C W M Y T A N D K G E I Q F L Q D 98         2 X N - I S       2 F I T K L W X G D 2 F K S H W A I I A Q A F T L A R D V V G T K A A R L R D F V A L A T L L N L P S P Q R Y L R D L G W V G T E T R R N R I R P V Q D 99         2 K N - I S       5 F I T R L W R G D 2 F K S H W A I I A Q A F T L A R D V V G T K A A R L R D F V A L A T L L N L P S P Q R Y L R D L G W V G T E T R R N R I R P V Q D 99         2 K N - I S       5 F I T R L W R D 2 F Q S R W L M A R V Y S F V R D A I G I K V A K L S F L E A A P I M R T P V P E E Y L E K L C W Y T G D N G E I K F L Q D 98         2 K N - I S       5 F I T R L W R D 2 F Q S R W L M A R V Y S F I R D T I G K N T A K L S F L E A A P I M R T P V P E E Y L E K L C W Y T G D N G E L A F P Q D 98         2 K N - I S A L I T R L W K S D P F Q S R W L M G R V Y S F I R D T V G K N T A K L S D F L E V A V P I M G V P V P E A Y L A K L C W I Y T G N E V G E L A F P Q D 98         2 K N - I S A L I T R L W K S D P F Q S R W L M G R V S F I R D T V G K N T A K L S D F L E V A V P I M G V P V P E A Y L A K L C W I Y G N E V G E L A F P Q D 98         2 K N - I S A L I T R L W K D P F Q S R W L M G R V Y S F I R D T V G K N T A K L S D F L E V A V P I M G V P V P E A Y L A K L C W I Y G N E A G D E L A F P Q D 98         2 K N - I S A L I T K L W K D P F Q S R W L I A K V Y S F T R D H V G K A K L S D F L E V A V P I M G V P V P E A Y L A K L C W V Y S G N E A G L  |   | p                             | 0  | P O  | ×   | P  | P   | P<br>Q  | P   | P   | P  | P   | P   | P   | P   |   |
| N-1 S PFI TKL WRKD PFQ S RWMLMAS VYS FYRDSI GNKGAKLLTFLDIAAPLMCTPKPEVALSIC WMYTANDKGEI QFL QD 98<br>N-1 S PFI TKL WRKD PFQ S RWMLMAS VYS FYRDSI GNKGAKLLTFLDVAAPLMCTPKPEVALSIC WMYTANDKGEI QFL QD 98<br>TNVLKAI S KL WRGD PFKS HWAIIAQAFTLARDVYGTKAARIRDVAGTADVAPLMCTPKP QRYLRDLGWVGTETRRNRI RFVQD 99<br>S - 1 S FI TRLWRD PFQ S RWMLMAS VYS FYRDAIG KARLRDFVALAATLLNLPS QRYLRDLGWVGTETRRNRI RFVQD 99<br>S - 1 S FI TRLWRSD PFQS RWMLMARVYS FYRDAIG KARLRDFVALAATLLNLPS 2 QRYLRDLGWVGTETRRNRI RFVQD 99<br>S - 1 S ALI TRLWKSD PFQS RWMLMARVYS FYRDAIG KARLRDFVALAATLLNLPS 2 QRYLRDLGWVTGDNGEI 84 C<br>S - 1 S ALI TRLWKSD PFQS RWMLMARVYS FYRDAI GKNTAKISDFLEVAVPIMAPV PE 2 VLEKLCWVTGDNGEI 84 F<br>S - 1 S ALI TRLWKSD PFQS RWMLMGRVS FIRDTV GNTAKISDFLEVAVPIMAPV 2 E AYLAKLCWI YTGNEVGELAFFQD 98<br>S - 1 S ALI TRLWKSD PFQS RWMLMGRVS FIRDTV GNTAKISDFLEVAVPIMAP 1 MGVPV 2 E AYLAKLCWI YTGNEVGELAFFQD 98<br>S - 1 S ALI TRLWKSD PFQS RWMLMGRVS FIRDTV GNTAKISDFLEVAVPIMAF 2 8 VLAKCWI VTGNEVGELAFFQD 98<br>S - 1 S ALI TRLWKSD PFQS RWMLMGRVS FIRDTV GNTAKISDFLEVAVPIMAC 2 MAVPIMAC V 2 8 AYLAKCWI YTGNEVGELAFFQD 98<br>S - 1 S ALI TRLWKD 9 FQS RWMLMSVF FXDH 1 GKVF RDH 1 GKS AKCN 1 N FLEVAVPIMAF 2 8 VLAKCWI VFHADDTG VVTF - Q 99<br>S - 1 S ALI TRLWKDD 9 FQS RWMLISRVS FIRDTV 6 1 1 0 VVQVAAP AND 1 0 VVQVAAD A 1 0 VVVYAADDTG 0 VVTF - Q 99<br>S - 1 S ALI TRLWKDD 9 FQS RWMLISTV 7 8 TRDH 0 GKAKCN 1 N FLEVAVPIMAF 2 8 0 LTKKCWI VTGNEVGELAFFQD 1 4 F<br>S - 1 S S LI TKLWKDD 9 FQS RWMLISTV 7 8 TRDH 0 VS FIRDVQVAAP A 0 S FLEVAVPI A ALC WVYAADDTG 0 VVTF - Q 99<br>S - 1 S S LI TKLWKDD 9 FQS RWMLISTV 7 8 TRDH 0 S V 2 F 0 N V 1 V 2 1 MGV 9 1 2 0 VLTK 1 CWVYAADDTG 0 VVTF - Q 99<br>S - 1 S S LI TKLWKDD 9 FQS RWMLISTV 7 8 TRDH 0 VS F 0 N V 1 V 2 1 MGV 9 1 2 0 VLTK 1 CWVYAADDTG 0 VVTF - Q 99<br>S - 1 S S LI TKLWKD 0 F 0 S RWMLISTV 7 8 TRD 1 V 2 1 A 0 N V 1 V 2 1 MGV 9 1 2 0 VLTK 1 A 0 VVYAADDTG 0 VVTF - Q 99<br>S - 1 S S LI TKLWKD 0 F 0 S RWMLISTV 7 8 TRD 1 Q 0 1 0 CV 7 7 0 0 V 7 0 0 V 7 0 0 V 7 0 0 V 7 0 0 0 0  |   | *                             | ĸ  | ĸ  | ĸ   | ĸ  | ĸ   | ĸ   | ĸ   | ĸ   | ĸ  | Ĥ   | Ĥ   | ĸ   | Хĸ  |   |
| I S PFI TKL WR KD PF Q S R WML MAS VYS F V RD S I G NK G AK LLTFL DI AAPLMCTP KP E E VLKS L C WMYTANDK G E I QFL Q D 98         I S PFI TKL WR KD PF Q S R WML MAS VYS F V RD S I G NK G AK LLTFL DV AAPLMCTP KP E E VLKS L C WMYTANDK G E I QFL Q D 98         I V L KAI S KL WR G D PF KS HWAII A Q AFTL AR D V G TKAAR L R DF V AL AATLLNL PS P Q R VLRS L C WMYTANDK G E I QFL Q D 99         I S FI TRL WR S D PF Q S R WML MAR VYS F V RD AI G I KVA AR L R DF V AL AATLLNL PS P Q R VLR DL G WV G TE TRRN R I RFV Q D 99         I S FI TRL WR S D PF Q S R WML MAR VYS F V RD AI G I KVA AR L R DF V AL AATLLNL PS P Q R VLR DL G WV G TE TRRN R I RFV Q D 98         I S ALI TRL WR S D PF Q S R WML MAR VYS F I RD TI G KN TAK L S DF L E V AV P I MR T P V P E E VLE KL C WI YT G DN G E I KFL Q D 98         I S ALI TRL WR S D PF Q S R WML MAR VYS F I RD TI G KN TAKL S DF L E V AV P I MG V P V P E AVLAKL C WI YT G NEV G E L AFF Q D 98         I S ALI TRL WK S D PF Q S R WML MG R VYS F I RD TI G KN TAKL S DF L E V AV P I MG V P V P E AVLAKL C WI YT G NEV G E L AFF Q D 98         I S ALI TRL WK S D PF Q S R WML MG R VYS F I RD TI G KN TAKL S DF L E V AV P I MG V P V P E AVLAKL C WI YT G NEV G E L AFF Q D 98         I S ALI TRL WK S D PF Q S R WML MG R VYS F I RD TI G KN TAKL S DF L E V AV P I MG V P V P E AVLAKL C WI YT G NEV G E L AFF Q D 98         I S G L T KL W ND PF Q S R WML MG R VYS F I RD H I G S V Q F AL A TL L VL P S P G L F Q L K C W Y S G NEA G D I VL F Q 0 98         I S C L T KL WK S D PF Q S R WML NG R VYS F T RD H G S V C F L C V V Q V A A P AMG V P I E A VL A KL C WI Y S G NEA G D I VL F Q 0 98         I S C L T KL W ND PF Q S R W ML I A VYS F T RD H V C T F Q L Y C A A P A M C V I F S  |   |                               | U.   | 59   | -   | 52   | \$  | 52  | -   | -   | -  | H   | T   | Ν.  | N -   |   |
| S P F I       T K L W K K D P F Q S K W L M S V Y S F V K D S I       G N K G A K L L T F L D I A A P L M C T P K P K D E Z L K S L C W Y T A N D K G E I Q F L Q D 98         S P F I       T K L W K K D P F Q S K W L M S V Y S F V K D S I       G N K G A K L L T F L D V A A P L M C T P K P D E Y L K S L C W Y T A N D K G E I Q F L Q D 98         L K A I       S K L W K G D P F K S H W A I I A Q A F T L A R D V V G T K A A R L R D F V A L A A T L L N L P S P Q R Y L K S L C W Y T A N D K G E I R N R I R F V Q D 98       S A L I T R L W R D P F Q S R W L I A Q A F T L A R D V V G T K A A R L R D F V A L A A T L L N L P S P Q R Y L K S L C W Y T G D D N G E I K F L Q D 98         S F I       T Q L W K S D P F Q S R W L I A Q A F T L A R D V V G T K A A R L R D F V A L A A T L L N L P S P Q R Y L K S L C W Y T G D D N G E I K F L Q D 98         S A L I T R L W R S D P F Q S R W L I A Q A F T L A R D V V G T K A A R L R D F V A L A A T L L N L P S P Q R Y L K L C W V M S T D D C D V T F       Q D 98         S A L I T R L W R S D P F Q S R W L M A R V S F V R D I I       G K N T A K L S D F L Z A A P I M R T V L P E A A P I M S L C W V M S T D C D V D C D V T F       Q D 98         S A L I T R L W R S D P F Q S R W L M G R V S F I R D T V       G K N T A K L S D F L Z A A P I M S L C W V M S T D C D V M S T D C D V T F       Q D 98         S A L I T R L W S D P F Q S R W L M G R V S F I R D T V G K N T A K L S D F L E V A V P I M G V P V P E A Y L A K L C W I Y T G N E V G E L A F F Q D 98       S A L I T R L K K S D P F Q S R W L M G R V S F V R D I I G K N T A K L S D F L E V A V P I M G A P V P E A Y L A K L C W I Y T G N E V G G L A F F Q D 98         S L I T R L   |   |                               | Þ  | н  | н   | н  | н   | н   | н   | н   | н  | 4   | V   | н   | н   |   |
| FINT NEL WRX D P F QS R WML MAS VYS F VRDS I G NKGAKLLTFLDI AAPL MCTP KPEE YLXS L CWMYT ANDX G EI QFL QD 98         FIT TKL WRX D P F QS R WML MAS VYS F VRDS I G NKGAKLLTFLDVAAPL MCTP KPEE YLXS L CWMYT ANDX G EI QFL QD 98         AI S KL WR G D F KS HWAI I AQAFTLARD VY G TKAARLRDY ARL RDFVAL ALL NLP S Q RYL RDL GWYG TETRRNRI RFVQ D 99         FI TRL WRN D F QS R WML MAS VYS F VRDS I G NKGAKLLTFLDVAAPL MCTP KPE Q RYL RDL GWYG TETRRNRI RFVQ D 99         FI TRL WRN D F QS R WML MAS VYS F VRDAI G KVAARLRDY G TKAARLRDY ALL LLLP S Q RYL RDL GWYG TETRRNRI RFVQ D 99         FI TRL WRS D F QS R WML MAR VYS F VRDAI G KVAARLRDY G TKAARLRDY ALL LLLP S Q RYL RDL GWYG TETRRNRI RFVQ D 99         FI TRL WRS D F QS R WML MAR VYS F VRDAI G KVAARL RDY ALARLARDY ALL LLLP S Q RYL RDL GWYG TETRRNRI RFVQ D 98         FI TRL WRS D F QS R WML MAR VYS F VRDAI G KVAALS ARL RDY ALL AL ATLLNLP S Q RYL RDL GWYTG DDNGE I KFLQ D 98         FI TRL WRS D F QS R WML MAR VYS F VRDAI G KVAALS ARL RDY ALL AL ATLLNLP S Q RYL RDL GWYTG DDNGE I KFLQ D 98         L1 TRL WRS D F Q S R WML MAR VYS F I RD TY GKNTAKLS DFLEVAV FI MGT P VE E AYL KLC WW TG NEV G EL AFF Q D 98         L1 TRL WRS D F Q S R WML MG R YS F I RD TY GKNTAKLS DFLEVAV PI MGT P VE E AYL AKL CWI YTG NEV G EL AFF Q D 98         L1 TRL WRS D F Q S R WML MG R YS F I RD TY GKNTAKLS DFLEVAV PI MGT P VE E AYL AKL CWI YTG NEV G EL AFF Q D 98         L1 TRL WRS D F Q S R WML MG R YS F TRD HY G KNTAKLS DFLEVAV PI MGT P VE E AYL AKL CWI YTG NEV G EL AFF Q 0 98         L1 TRL WRS D F Q S R WML MAS YS F TRD HY G KN ALL S DY Q VALS DFLEVAV PI MGT P VE E AYL AKL CWI Y AADDTG VYTF Q 0 14 F Q 0 98         L1 TYL WA   |   | 60                            | s<br>G   | 22   | S   | S  | 2   | SA  | N N   | 52  | s  | L K   | LK  | S P   | 52  |   |
| I T KL WR K D P F Q S R WML MAS V Y S F V R D S I G N K G A KL L T F L D I A A P L M C T P K P E Y L K S L C WMY T AN D K G E I Q F L Q D 98<br>I T KL WR G D P F K S H WAI I A Q A F T L A R D V V G T K A A R L R D F V A L A A T L L N L P S P Q R Y L R D L G W G T E T R R N R I R F V Q D 99<br>I S KL WR G D P F K S H WAI I A Q A F T L A R D V V G T K A A R L R D F V A L A A T L L N L P S P Q R Y L R D L G W G T E T R R N R I R F V Q D 99<br>I S KL WR G D P F K S H WAI I A Q A F T L A R D V V G T K A A R L R D F V A L A A T L L N L P S P Q R Y L R D L G W G T E T R R N R I R F V Q D 99<br>I T R L WR D P F Q S R WML MAR V Y S F V R D A I G I K V A KL S F L E A A A P I M R T P V P E E Y L E K L C W M Y T A N D K G E I K F L Q D 98<br>I T R L WR S D P F Q S R WML M R V Y S F V R D I I G K N T K L S F L E A A A P I M R T P V P E A Y L K L C W M Y T G D D N G E I K F L Q D 98<br>I T R L WK S D P F Q S R WML M G R V Y S F I R D T I G K N T A KL S D F L E V A V P I M G V P V P E A Y L A K L C WI Y T G N E V G E L A F F Q D 98<br>I T R L WK S D P F Q S R WML M G R V Y S F I R D T I G K N T A KL S D F L E V A V P I M G V P V P E A Y L A K L C WI Y T G N E V G E L A F F Q D 98<br>I T R L WK S D P F Q S R WML M G R V Y S F I R D T V G K N T A KL S D F L E V A V P I M G V P V P E A Y L A K L C WI Y T G N E V G E L A F F Q D 98<br>I T R L WK A D P Y H C K WAL N G R V Y S F I R D T V G K N T A KL S D F L E V A V P I M G V P V P E A Y L A K L C WI Y T G N E V G E L A F F Q D 98<br>I T N L WK A D P F Q S R WML I G R V Y S F I R D N I G R D Q V R L C D Y V Q V A A P A M G V P V P E A Y L A K L C WI Y T G N E V G E L A F F Q D 98<br>I T N L WK A D P F Q S R WAL I S R V Y S F I R D N I G R D Q V R L C D Y V Q A A P A M G V P I P E A Y L A K L C WI Y A A D D T G V V F F I R D I I G K V Y S F I R D V G K A X C N L V P I M G V P I P E A Y L A K L C WI Y A A D D T G V T F - Q D 98<br>I T N L W A D P N R N K A L I A K V Y S F T R D N I G R D Q V R L C D Y V Q A A P A M G V P I P S E Y L A R L C W Y A A D D T G V T F - Q E 9 9<br>I T N L W A T D N R N K A L I A K  |   |                               | ч  | ы  | н   | H  | H   | H   | H   | ы   | ы  | ₽   | Þ   | ы   | ы   |   |
| INKL       WR       G       WK       G       WK       I       G       WK       G       WK       I       I       A       P       I       I       A       P       I       I       A       WK       G       I       I       A       I       I       I       A       I       I       I       A       I       I       A       I       I       A       I       I       A       I       I       I       A       I       I       I       A       I       I       I       A       I  |   | -                             | Н  | H  | H   | H  | H   | Ц   | H   | H   | H  | I S   | IS  | H   | Ц   |   |
| L WR K D P F QS R WML MAS V YS F V RD S I G N K G A K L L T F L D I A A P L M C P K P E YL K S L C WM Y T A ND K G E I Q F L Q D 98<br>L WR G D P F K S H WA I I A Q A F T L A R D V V G T K A A R L R D F V A L A P L M C P K P S P Q R YL K S L C WM Y T A ND K G E I Q F L Q D 99<br>L WR G D P F K S H WA I I A Q A F T L A R D V V G T K A A R L R D F V A L A P L M L P S P Q R YL R D L G WV G T E T R R N R I R P V Q D 99<br>L WR G D P F K S H WA I I A Q A F T L A R D V V G T K A A R L R D F V A L A P L M L P S P Q R YL R D L G WV G T E T R R N R I R P V Q D 99<br>L WR S D P F Q S R WML MA R V YS F V R D A I G I K V A K A R L R D F V A L A P I M R T P V P E E YL E K L C WM Y T G DD N G E I K F L Q D 99<br>L WR S D P F Q S R WML M G R V YS F I R D T I G K N T A L S S F L E A A A P I M R T P V P E A YL E K L C WM Y T G DD N G E I K F L Q D 98<br>L WK S D P F Q S R WML M G R V YS F I R D T V G K N T A K L S D F L E V A V P I M G V P V E A YL A K L C WI Y T G N E V G E L A F F Q D 98<br>L WK S D P F Q S R WML M G R V YS F I R D T V G K N T A K L S D F L E V A V P I M G V P V E A YL A K L C WI Y T G N E V G E L A F F Q D 98<br>L WK S D P F Q S R WML M G R V YS F I R D T V G K N T A K L S D F L E V A V P I M G V P V E A YL A K L C WI Y T G N E V G E L A F F Q D 98<br>L WK S D P F Q S R WML I S R V YS F V R D H I G K S E A K L S D F L E V A V P I M G P P S P A YL A K L C WI Y T G N E V G E L A F F Q D 98<br>L WK X D P F Q S R WML I S R V YS F I R D H I G K S A A L S D F L E V A V P I M G P P S P A YL A K L C WI Y S G N E A G D I A F F Q D 98<br>L WK N D P F Q S R WML I S R V YS F I R D H I G K D S A Q L S T F L T V C P I M G P P S P A L A K L C W V YA A D D T G V V F F Q D 98<br>L WK N D P F Q S R WML I S R V YS F T R D H Y G K A C N L N F L C T Y Q A A P A M K Y V F I P S L YL K L C W V YA A D D T G V T F - Q S 97<br>L WA T D P N R N K WALL I A K V YS F T R D H Y G K A C N L N F L C Y V Q A A P A M K Y V E P S D YL T K L C W V S H D S F G N YL Y F - Q S 97<br>L W Y D P F Q S R WML I S R V S F T R D H Y G K A C N L Y F A Z C Y Y Y A A D Y T - Q Y A A P  |   |                               | ø  | ×  | U   | 20   | 20  | ×   | ×   | ø   | 20   | ×   | ×   | ×   | ×   |   |
| R K D P F Q S R WML MAS       W X S F V R D S I G N K G A K L L T F L DI A A P L M C T P K P E E YL K S L C WMY T A ND K G E I Q F L Q D Q S         R K D P F Q S R WML MAS       W X S F V R D S I G N K G A K L L T F L D V A A P L M C T P K P D E YL K S L C WMY T A ND K G E I Q F L Q D Q S         R G D P F K S H WAI I A Q A F T L A R D V V G T K A A R L R D F V A L A A T L L N L P S P Q R YL R D L G WV G T E T R R N R I R P V Q D Q D Q S       99         R M D P F Q S R WML MAR       W Y S F V R D A I G I K V A R L R D F V A L A A T L L N L P S P Q R YL R D L G WV G T E T R R N R I R P V Q D Q D Q D Q D Q D Q D Q D Q D Q D Q   |   | 1                             | L  |  | M   | L  |   |   | L   | L   | F  | L   | L   | L   | L   |   |
| KD P F Q S R WML MAS WYS F V R D S I G N K G A K L T F L D I A A P L M C T P K P E E Y L K S L C WMY T A N D K G E I Q F L Q D 98         KD P F Q S R WML MAS VYS F V R D S I G N K G A K L T F L D V A A P L M C T P K P D E Y L K S L C WMY T A N D K G E I Q F L Q D 98         G D P F K S H WAI I A Q A F T L A R D V V G T K A A R L R D F V A L A A T L L N L P S P Q R Y L R D L G WV G T E T R R N R I R P V Q D S 99         G D P F K S H WAI I A Q A F T L A R D V V G T K A A R L R D F V A L A A T L L N L P S P Q R Y L R D L G WV G T E T R R N R I R P V Q D S 99         G D P F Q S R WML MA K V Y S F V R D T I A R D V V G T K A A R L R D F V A L A A T L L N L P S P Q R Y L R D L G WV G T E T R R N R I R P V Q D 99         S D P F Q S R WML M A R V Y S F I R D T I G K N T K L S E L Q I A A P I M R T P V P E E Y L K L C WV M S T D D C D V F [ Q D 98         S D P F Q S R WML M G R V S F I R D T V G K N T A K L S D F L E V A V P I M G V P V P A A Y L A K L C WI Y G N R V G R U G E L A F Q D 98         S D P F Q S R WML I G R V S F I R D T V G K N T A K L S D F L E V A V P I M G V P V P A A Y L A K L C WI Y G N R V G R U G E L A F Q D 98         S D P F Q S R WML I G R V Y S F I R D T V G K N T A K L S D F L E V A V P I M G V P V P A A Y L A K L C WI Y S G N R A G D I A F Q D 98         S D P F Q S R WML I S R V Y S F I R D H I G K S A Q L S T L L V V C F I L I A G P V P E A Y L A K L C WI Y S G N A A D D T G V V F A Q P 98         S D P F Q S R WML I S R V Y S F I R D H I G R S A Q Q V R L C D Y V Q A A P A M M K I V E P S P L A R L C W Y S G N A A D D T G V V F A Q P 1 0 98         S D P F Q S R WML I S R V Y S F T R D H V G W N A C D Y V Q I A A D A A M A W K I V E P S P L A R L C W Y A A D D T G V V A A D   |   | 4                             | A  | K  | K.  | K  | K   | K   | K   | K   | R  | R   | R   | R   | R   |   |
| P       Q       R       M       M       M       X       Y       S       Y       K       G       X       K       L       T       L   |   | U                             | I  | U  | A D   |  | U   |   |   | Ð   | Ð  | G   | G   | ΚĐ  | κĐ  |   |
| P Q S R WML MAS VYS F VRDS I G NKG AKLLTFLDI AAPLMCTPKPLMCTPKPEVLKS L CWMYTANDKGEI QFLQ 5         P Q S R WML MAS VYS F VRDS I G NKG AKLLTFLDI AAPLMCTPKPLMCTPKPLS L CWMYTANDKGEI QFLQ 5         P Q S R WML MAS VYS F VRDS I G NKG AKLLTFLDI AAPLMCTPKPLMCTPKPLS P QRYLKS L CWMYTANDKGEI QFLQ 5         P K S H WAII AQAFTLARDVVG TKAARL ARLRDFVALAATLULPS P QRYLKS L CWMYTANDKGEI QFLQ 5         P Q S R WML MAR VYS F VRDTI ARDVVG TKAARL ARLRDFVALAATLULPS P QRYLRDL GWVG TETRRNR I RF VQ 5         P Q S R WML MG RVYS F VRDTI G KNTKAR KLS DFLEVALAATLULPS P QRVCTPK P V 2 E VLEKL CWWYTGDDNGEI KFLQ 5         P Q S R WML MG RVYS F VRDTI G KNTAKLS DFLEVALS DFLEVAV P I MG V P V 2 E VLEKL CWVTS GNEVGELAFFQ 5         P Q R WML MG RVYS F VRDTI G KNTAKLS DFLEVALS DFLEVAV P I MG V P V 2 E AVL AKL CWI YTGNEVGELAFFQ 5         P Q S R WML MG RVYS F I RDTV KNTAKLS DFLEVALS DFLEVAV P I MG V P V 2 E AVL AKL CWI YTGNEVGELAFFQ 5         P Q S R WML I G RVYS F VRDHI GKSEAKLS DFLEVALS DFLEVAV Q         P Q S R WML I G RVYS F VRDHI GKSEAKLS DFLEVALS DFLEVAV Q         P Q S R WML I S RVS F VRDHI G KND AKLS AQLS TFLIVVCPI AAP N G V V 2 E AVL AKLCWI YTGNEVGELAFFQ 5         P Q S R WML I S RVS F F RD HI G KS AKLS AQLS TFLIVVCPI AAP N G V V 2 ALGLFHHMGEE G DI AFF Q 0 58         P Q S R WML I S RVS F F RD HI G R AKLS AQLS TFLIVVCPI AAP N 0 V 1 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0   |   | P                             | Pl   | ΡI   | Ч   | ΡI   | ΡI  | PI  | ΡI  | P   | ΡI   | PI  | PI  | ΡI  | ΡI  |   |
| S R WML MAS VYS F VRD S I G NKG AKLLTFLDI AAPLMCTPKPLMCTPKPE VLKS LCWMYTANDKGEI QFLQF         S R WML MAS VYS F VRD S I G NKG AKLLTFLDI AAPLMCTPKPLMCTPKPLS         S R WML MAS VYS F VRD S I G NKG AKLLTFLDI AAPLMCTPKPLMCTPKPLS         S R WML MAS VYS F VRD S I G NKG AKLLTFLDI AAPLMCTPKPLMCTPKPLS         S R WML MAS VYS F VRD TLARDYG G TKAARLARLS         S R WML MAR VYS F VRD TLARDYG G TKAARLARLS         S R WML MAR VYS F VRD TLARDYG G TKAARLS         S R WML MAR VYS F VRD TLARDYG G TKAARLS         S R WML MAR VYS F VRD TLARDYG G TKAARLS         S R WML MAR VYS F VRD TLARDYG G TKAARLS         S R WML MAR VYS F VRD TLARDYG G TKAARLS         S R WML MAR VYS F VRD TLARDYG G TKAARLS         S R WML MAR VYS F VRD TLARDYG G TY KAARLS         S R WML MAR VYS F VRD TLARDYG G TY         S R WML MAR VYS F VRD TLARDYG G TY         S R WML MAR VYS F VRD TLARDYG G TY         S R WML MAR VYS F VRD TLARDYG G TY         S R WML MAR VYS F VRD TLARDYG G TY         S R WML MAR VYS F VRD TLARDYG G TY         S R WML MAR VYS F VRD TLARDYG G TY         S R WML MAR VYS F VRD TLARDYG G TY         S R WML MAR VYS F VRD TLARDYG G TY         S R WML MAR VYS F VRD TLARDYG G TY         S R WML MAR VYS F VRD TLARDYG G TY         S R WML TARDYG G TY         S R WML TARDYS F TRD TTY         S R WAL VAR YS F TRD TTY         S  |   |                               | R  | õ  | H   | Q  | õ   | õ   | õ   | Q   | Q  | ×   | ×   | Q   | õ   |   |
| RVML MAS VYS FVRD SI GNKGAKLLTFLDIAAPLMCTPKPEE YLKSLCWMYTANDKGEI QFLQDS         RVML MAS VYS FVRD SI GNKGAKLLTFLDIAAPLMCTPKPEE YLKSLCWMYTANDKGEI QFLQDS         RWML MAS VYS FVRD SI GNKGAKLLTFLDIAAPLMCTPKPEE         RWMI MAS VYS FVRD SI GNKGAKLLTFLDIAAPLMCTPKPEE         RWMI MAS VYS FVRD SI GNKGAKLLTFLDIAQ         RWMI MAS VYS FVRD SI GNKGAKLLTFLDIAP         RWMI MAS VYS FVRD SI GNKGAKLLTFLDIAP         RWMI MAS VYS FVRD SI GNKGAKLLTFLDIAP         RWMI MAS VYS FVRD SI GNKGAKLLTPL         RWMI MAR VYS FVRD SI GNKGAKLLTPL         RWMI MGRVYS FVRD SI GNKGAKLLTSDFVALAATLLNLPS         RWMI MGRVYS FVRD SI GNKTAKLSSFLQIAAPI         RWMI MGRVYS FVRD SI RDTVGKNTAKLSSFLQIAAPI         RWMI MGRVYS FVRD SI RDTVGKNTAKLSSDFLCVVQVAAP         RWML MGRVYS FVRD SI RDTVGKNTAKLSSDFLCVVQVAAP         RWML MGRVYS FVRD SI RDTVGKNTAKLSSDFLCVVQVAAP         RWML SVS FVRD SI RDTVGKNTAKLSSDFLCVVVQVAAP         RWML SVS FVRD SI RDTVGKNTAKLSSDFLCVVVQVAAP         RWML SVS FVRD SI RDTVGKNTAKLSSDFLCVVVQVAAP          SUSSAGNTKLSSDFLCVVVQVAAP  |   |                               | NK   | 52   | CF  | AF   | 22  | 52  | 52  | 52  | S H  | SI  | S   | S H   | 52  |   |
| MI MAS VYS F VRD S I GNKG AKLLTFLDI AAPLMCTPKPEE YLKSLCWMYT ANDKGEI QFLQ D 98<br>AII AQAFTLARD V G TKA ARLRDFVAL A TLNLPSPARE QRYLRDLG WVG TETRRNRI R F V Q D 99<br>AII AQAFTLARD V G TKA ARLRDFVAL A TLNLPSPARE QRYLRDLG WVG TETRRNRI R F V Q D 99<br>ML MAR V S F V RD AI GIKVAR LRDFVAL AATLNLPSPARE QRYLRDLG WVG TETRRNRI R F V Q D 99<br>ML MAR V S F V RD AI GIKVAR LS S F L Q AAPI MRTPVE 2 Q RYLRLC WMYTGDDVG EI KFLQ D 99<br>ML MG R V S F V RD AI GIKVAR LS S F L Q AAPI MRTPVE 2 E YL KLC WMYTGDDVG EI KFLQ D 99<br>ML MG R V S F I RD TI GKS N KLS S F L Q AAPI MRTPVE 2 E YL KLC WMYTGDDVG E AFF Q D 98<br>ML MG R V S F I RD TV GKNTAKLS D F L E VAV PI MG V P V P E A YL KLC W MS TDDC D V F Q 1 4 F Q 0 98<br>ML MG R V S F I RD TV GKNTAKLS D F L E VAV PI MG V P V P E A YL KLC W NS TDDC D V G E AFF Q D 98<br>ML M KV S F I RD TV GKNTAKLS D F L E VAV PI MG V P V P E A YL AKLC WI YT GNE V G E AFF Q D 98<br>ML M KV S F V S F I RD TV GKNTAKLS D F L E VAV Q A P M MG V P V P E A YL AKLC WI YT GNE V G E AFF Q D 98<br>ML M KV S F V S F I RD TV GKNTAKLS D F L C V V Q A P M MG V P V P E A YL AKLC WI Y GNE V G E A F Q D 98<br>ML S V Y S F V RD NI GRD Q V R L C D Y V Q V A P M MG V P V P E A YL AKLC WI Y A ADD TG V TF - Q 5 98<br>ML S V Y S F V RD NI GRD Q V R L C D Y Q V A P M MG V P V P E A YL AKLC WV A ADD TG V TF - Q 5 98<br>ML I A K V Y S F T RD V G KAKCNLN F L C V V Q A P M MKI V E P S I F Q L F G WQ V S HD S F G NMVLV Q D 98<br>ML I A K V S F T RD V G KAKCNLN F L V F F F M M F P * VI I C W Y A ADD TG V TF - Q 5 98<br>ML I A K V S F T RD V G KAKCNLN F I F F F Y Q A P M MKI V E P S I F G L F G WQ S HD S F G NMVLV V Q D 98<br>ML A V S F T RD F F G W V F F F F F F F F F F F F F F F F F F  | _ | W                             |  | ŝ  |   |  | ŝ   | é   | é   | Ĩ   | é  | W   | W   | Ĩ   | ŝ   |   |
| MAS       VYS       F       RDS       I       GNKG       AK       LTFLD       I       AP       LMCTPKP       E       E       VLKS       L       WMYTANDKGEI       QFLQ   |   | B 1                           | ΑL   | MI   | A L   | MI   | ML  | MI  | MI  | MI  | ML   | ΑI  | ΑI  | ML  | MI  |   |
| AS       V Y S       F       V RD S       I       G N K G       A K L L T F L D I       A A P L M C T P K P E E YL K S L C WMY T A N D K G E I       Q F L Q D S       Q F L Q D S         A S       V Y S       F       R D S I       G N K G A K L L T F L D V A P L M C T P K P D E YL K S L C WMY T A N D K G E I       Q F L Q D S       Q F L Q D S         A Q A F TL A R D V V G T K A A R L R D F V A L A T L L N L P S       P Q R YL R D L G WV G T E T R R N R I R F V Q D S       Q A F TL A R D V G T K A A R L R D F V A L A T L L N L P S       P Q R YL R D L G WV G T E T R R N R I R F V Q D S       Q A F TL A R D V G T K A A R L R D F V A L A A T L L N L P S       P Q R YL R D L G WV G T E T R R N R I R F V Q D S       Q A F TL A R D V G T K A A R L R D F V A L A A T L L N L P S       P Q R YL R D L G WV G T E T R R N R I R F V Q D S       Q A S S V S F V R D A I G I K V A K L S S F L E A A A P I M R T P V M C T P K P I E Y L K L C WW M S T D D C D V G E L A F F Q D S       Q A S S V Y S F I R D T I G K N T A K L S D F L E V A V P I M Q V P V P E A YL A K L C WI Y T G N E V G E L A F F Q D S       Q B S         G R V Y S F I R D T V G K N T A K L S D F L E V A V P I M G P V P I A G V P V A A K L C WI Y T G N E V G E L A F F Q D S       Q A F T A O V R G E L A F F Q D S       Q B S         G R V Y S F I R D N I G K D S A Q L S T F L T V V C P I A G P I M G V P V P E A YL A R L C WV Y S G N E A G D T G V T F - Q S S F       Q D S       Q D S       Q L F H H M G E E G N W L V C P I A G P N M C T P O L A R L C WV Y S A D T G V T F - Q S S F       Q D S       Q D S         S N Y S  |   |                               | H  | Ĥ  | ~   | ÷.   | ×   | ×   | ×   | ÷.  | ×  | н   | н   | ×   | ×   |   |
| VYSFVRDSIGNKGAKLLTFLDIAAPLMCTPKPEEVLKSLCWMYTANDKGEIQFLQFLQDS         VYSFVRDSIGNKGAKLLTFLDVAAPLMCTPKPEEVLKSLCWMYTANDKGEIQFLQFLQDS         AFTLARDVVGTKAARDVVGTKAARLRDFVALAAPLNCTPKPRO         AFTLARDVVGTKAARDVVGTKAARLRDFVALAAPLNLPSPQRYLRDLGWVGTETRRNRIGEVQDS         VYSFVRDJIGKKAARLRDFVALAAPLNDFVALAAPLNLPSPQRYLRDLGWVGTETRRNRIERVRIERVQDS         VYSFVRDJIGKKAARLSSFLQIFAAAPINKTPVPEEVLEKLCWMYTGDDNGEIKFUQDS         VYSFVRDJIGKKAARLSSFLQIAAPINKTPVDS         VYSFVRDJIGKKAARLSSFLQIAAPINKTPVDS         VYSFVRDJIGKKAARLSSFLQIAAPINKTPVDS         VYSFVRDJIGKKAARLSSFLQIAAPINKTPVDS         VYSFVRDJIGKKAARLSSFLQIAAPINKTPVDS         VYSFVRDJIGKKTAKLSSFLQIAAPN         VYSFVRDJIGKKTAKSTARLSS         VYSFVRDJIGKKTAKSTARLSS         VYSFVRDJIGKKTAKSTARLSS         VYSFVRDJIGKKTAKSTARLSS         VYSFVRDJIGKKTAKSTARLSS         VYSFVRDJIGKT         VYSFVRDJIGKT         VYSFVRDJIGKT         VYSFVRDJIGKT         VYSFVRDJIGKT         KUSSTARLSS          VYSFVRDJIK         KUSSTARLSS         KUSSTARLSS         KUSSTARLSS          KUSSTARLSS         KUSSTARLSS         KUSSTARLSS          KUSSTARLSS         KUSSTARLSS         KUSSTARLSS  |   |                               | A K  | SR   | A K   | GR   | GR  | GR  | GR  | GR  | A R  | AQ  | AQ  | AS  | AS  |   |
| YSF       YKDSI       GNKGAKLLTFLDI       AAPLMCTPKPEE       YKPEE       YLKSLCWMYTANDKGEI       QFLQFIQ       QFLQFIQ         YSF       YKDSI       GNKGAKLLTFLDI       AAPLMCTPKPEE       YKPEE       YLKSLCWMYTANDKGEI       QFLQFIQ       QFLQFIQ         FTLARDY       GNKGAKLLTFLDV       AAPLAP       MCTPKP       QRYLRSLCWMYTANDKGEI       QFLQFIQ       QFLQD       99         FTLARDY       QTKAARDKARLK       FVALAAPL       FVLNLPS       QRYLRDL       RDI       GWVGTETRRNRI       RFVQD       99         FTLARDY       QTKAARDK       RLRDFVALAAPL       FVLNLPS       QRYLRDL       RDLGWYGTETRRNRI       RFVQDNGTETRRNRI       RFVQDS       99         YSFVLARDY       QTKAARDK       RLSSFLQIAAPI       AAPINARTLNLPS       QRYLRDL       QWVGTETRRNRI       RFVQDNGTETRRNRI       RFVQDS       99         YSFVLARDY       QTVARDY       ALAAPINAAPIN       MRTPVPE       PEEYLEKUCWNYTANDSTONGTETRRNRI       RFVQDS       99         YSFVLS       RDTIGKNTAAKLS       RFLQIAAPINAAPIN       MRTPVPE       PEEYLEKUCWNYTANSTONGTEN       90       98         YSF       RDDTIGKNTAAKLS       RFLQIAAPINAAPIN       MRTPVPE       PEANLAKLKUNKUNSTONGTEN       91       90       98         YSF       RDDTIGKNTAAKLS   |   | 4                             | <  | 4  | <   | <  | <   | 4   | <   | H   | <  | A   | A   | V   | <   |   |
| F       V R D S I G N K G A K L L T F L D I A A P L M C T P K P E E YL K S L C WMY T A N D K G E I Q F L Q D 98         F       V R D S I G N K G A K L L T F L D V A A P L M C T P K P D E YL K S L C WMY T A N D K G E I Q F L Q D 99         L A R D V V G T K A A R L R D F V A L A T L L N L P S P Q R YL R D L G WV G T E T R R N R I R F V Q D 99         F V R D A I G I K A A R L R D F V A L A A T L L N L P S P Q R YL R D L G WV G T E T R R N R I R F V Q D 99         F V R D A I G I K V A K L S S F L E A A A P I M R T P V P E E YL L K L C WMY T G D D N G E I K F L Q D 98         F V R D A I G I K V A K L S D F L E V A L A P I M R T P V P E E YL L K L C WW M S T D D C D V T F         F V R D A I G K N T A K L S D F L E V A V P I M R T P V P E E YL L K L C WW M S T D D N G E L A F F Q D 98         F V R D A I G K N T A K L S D F L E V A V P I M R T P V P E E YL L K L C WW M S T D D N G E L A F F Q D 98         F V R D N I G K N T A K L S D F L E V A V P I M R T P V P E E YL L K L C WW M S T D D N G E L A F F Q D 98         F V R D H I G K S N T K L S D F L E V A V P I M G V P V P E A YL A K L C WI Y T G N E V G E L A F F Q D 98         F V R D N I G R D Q V R L C D Y Q V A A P A M G V P I A G V P V P E A YL A K L C WV Y S G N E A G D I A F F Q D 98         F V R D N I G R D Q V R L C D Y Q V A A P A M G V P I P E D YL T K L C WV Y A A D T G V T F - Q S 97         F V R D N I G R D Q V R L C D Y Q V A A P A M G V P I P A ' N A C W Y A A D D T G V V T F - Q S 98         F V R D N I G R D Q V R L C D Y V Q V A A P A M G V P I P A ' N A C W Y A A D D T G V T F - Q S 98         F V R D W G K A K C N L Y I A K L ' Y A   |   | y s                           | ΥS   | YS   | YS  | ΥS   | YS  | YS  | YS  | YS  | ΥS   | F   | FI  | ΥS  | YS  |   |
| W R D S I G N K G A K L L T F L D I A A P L M C T P K P E E YL K S L C WMY T A N D K G E I Q F L Q D 98         W R D S I G N K G A K L T F L D V A A P L M C T P K P E E YL K S L C WMY T A N D K G E I Q F L Q D 99         A R D V V G T K A A R L R D F V A L A T L L N L P S P Q R YL R D L G WV G T E T R R N R I R F V Q D 99         A R D V V G T K A A R L R D F V A L A T L L N L P S P Q R YL R D L G WV G T E T R R N R I R F V Q D 99         A R D V V G T K A A R L R D F V A L A T L L N L P S P Q R YL R D L G WV G T E T R R N R I R F V Q D 99         V R D A I G I K V A K L S S F L E A A A P I M R T P V P E E YL L K L C WMY T G D D N G E I K F L Q D 98         V R D T I G K S N T K L S E F L Q I A A P V M C T P K P E E YL L K L C W M S T D D C D V T F Q D 98         V R D T I G K N T A K L S D F L E V A V P I M G V P V P E A YL A K L C WI Y T G N E V G E L A F F Q D 98         V R D T V G K N T A K L S D F L E V A V P I M G V P V P E A YL A K L C WI Y T G N E V G E L A F F Q D 98         V R D H I G K S E A K L S D F L E V A V P I M G V P V P E A YL A K L C WI Y T G N E V G E L A F F Q D 98         V R D H I G K S A C N L S D F L E V A V P I M G P F S P G L Y F Q K L G L F H H M G E E G D I V L G D 98         V R D N I G R D Q V R L C D Y Q V A A P A M G V P I P E N L K C W Y A A D T G N E V G E L A F F Q D 98         V R D N I G K A K C N L W F L S V Q V A A P A M G V P I P E N Y L X K L C WV Y A A D T G V V T F - Q S 98         V R D N I G K A K C N L W L Y L Y Q V A A P A M G V P I P E N Y L X K L C WV Y A A D T G V T F - Q S 98         V R D N I G K A K C N L W L Y L Y Q V A A P M M C P N P P E N Y L Y K A D T G N Y Y A A   |   | ÷                             | Ħ  | ы  | ы   | Ħ  | ы   | ы   | ы   | ы   | Ħ  | H   | F   | Ħ   | μų.   |   |
| D S I G NKG AKLLTFLDI AAPLMCTPKPEN PL K 2 E VL KSLCWMYTANDKGEI QFLQDS         D S I G NKG AKLLTFLDI AAPLMCTPKPK         D S I G NKG AKLLTFLDI AAPLMCTPKPK         D V V G TKAARLRDF VALATLLNLPS         D V V G TKAARLSS FLEAAAPI NKTAADKPK         D AI G I KV AKLSS FLEAAAPI NKTP V P         D TI GKSNTKLSS FLEAAAPI NKTP V P         D TI GKSNTKLSS FLEAAAPI NKTP V P         D TI GKSNTKLSS FLEVAAAPI NKTP V P         D TI GKSNTKLSS FLEVAAAPI NKTP V P         D TV G KNTAKLSS FLEVAAAPI NKTP V P         D TV G KNTAKSTK         D TV G KNTKAARLSS FLEVAAAPI NKTP V P         D TV G KNTAKSTK         D TV G KNTAKSSTK         D T V G KNTAKSSST <td< th=""><th></th><th></th><th>н.</th><th>&lt;</th><th></th><th>&lt;</th><th></th><th></th><th></th><th></th><th><math>\sim</math></th><th></th><th></th><th>&lt;</th><th>&lt;</th><th></th></td<>  |   |                               | н.   | <  |   | <  |   |   |   |   | $\sim$   |   |   | <   | <   |   |
| I G NKG AKLLTFLDI AAPLMCTPKPERVLKSLCWMYTANDKGEI QFLQD:98         I G NKG AKLLTFLDV AAPL MCTPKPERVLKSLCWMYTANDKGEI QFLQD:98         I G NKG AKLLTFLDV AAPL MCTPKP         I G NKG AKLLTP I         I G NKG A R I R D F V AL AATLLNLP S         I G K N T AKLS S F L E A AA P N MCTP V P E E VLLKLCWWNSTGD NGE V F Q D 98         I G K N T AKLS D F L E V AV P N MG V P V P E A YL AKL CWI VTGNNS TDD CDV TF Q D 98         I G K N T AKLS D F L E V AV P N MG P N P P E A YL AKL CWI VS G N E Q G L AF F Q D 98         I G K N T AKLS D F L T V V C N A P A MG V P V P E A YL AKL CWI VS G N E Q G D 1 AF F Q D 98         I G R D Q V R L C N V P I A Q A P A MG V P I P P A YL AR L CWI V A AD T G V V T F - Q 0 98         I G K A K C N L N P F L S V A C P MMKI V E P A V F I P A VL K CWI V A AD T G V T F - Q 0 98         I G K A K L K L F I  |   | 7                             | R  | 20   | R   | ₩.   | R   | 72  | R   | R   | R  |   | 72  | R   | ×   |   |
| G N K G A K L L T F L D I A A P L M C T P K P E E YL K S L C WM Y T A N D K G E I Q F L Q D 98<br>G N K G A K L T F L D V A A P L M C T P K P S P Q R YL R D L G WY G T E T R R N R I R F V Q D 99<br>G T K A A R L R D F V A L A A T L L N L P S P Q R YL R D L G WY G T E T R R N R I R F V Q D 99<br>G T K A A R L R D F V A L A A T L L N L P S P Q R YL R D L G WY G T E T R R N R I R F V Q D 99<br>G T K A A R L R D F V A L A A T L L N L P S P Q R YL R D L G WY G T E T R R N R I R F V Q D 99<br>G T K A A R L R D F V A L A A T L L N L P S P Q R YL R D L G WW Y G T E T R R N R I R F V Q D 99<br>G T K A A R L R D F V A L A A T L L N L P S P Q R YL R D L G WW Y G T E T R R N R I R F V Q D 99<br>G T K A A R L S D F L E A A A P I M R T P V P E E YL L K L C WM W S T D D O G E I A F F Q D 98<br>G K N T A K L S D F L E V A V P I M G V P V P E A YL A K L C WI Y T G N E V G E L A F F Q D 98<br>G K N T A K L S D F L E V A V P I M G V P V P E A YL A K L C WI Y T G N E V G E L A F F Q D 98<br>G K N T A K L S D F L E V A V P I M G V P V P E A YL A K L C WI Y G N E V G E L A F F Q D 98<br>G K N T A K L S D F L E V A V P I M G V P V P E A YL A K L C WV Y S G N E A G D I A F F Q D 98<br>G K N T A K L S D F L E V A V P I M G F P S P G L YF Q K L G L F H H M G E E G D I V L G Q D 98<br>G K N T A K L S D F L T V V C P I M G Y P I P A ' P A ' T K L C WV Y A A D D T G V V T F - Q S 97<br>G K A K C N L N P F L S V A C P M M K I V E ' P A ' Y I ' I C ' W Y A A D D T G V V T F - Q S 97<br>G K A K C N L N P F L S V A C P M M K I V E ' P A ' Y I ' I C ' W Y I A A D D T G V V T F - Q d ' 98<br>G K A K C N L M Y A ' I ' A A ' M A ' M M Y A ' M A ' M A ' Y I ' Y G N Y S ' G N Y A A D T ' Y ' Y ' Y ' Y ' Y ' Y ' Y ' Y ' Y '   |   | RD                            | RDH  | R D 1  | RDI   | R D I  | R D   | R D   | R D   | R D   | R D /  | RD  | RD  | RDS   | R D S   |   |
| 4 K G A K L L T F L D I A A P L M C T P K P E E YL KS L C WM Y T A N D K G E I Q F L Q D 98         4 K G A K L L T F L D V A A P L M C T P K P E P N E YL KS L C WM Y T A N D K G E I Q F L Q D 99         6 A K L T F L D V A A P L M C T P K P E P Q R YL R D L G W V G T E T R R N R I R F V Q D 99         7 K A A R L R D F V A L A A T L L N L P S P Q R YL R D L G W V G T E T R R N R I R F V Q D 99         7 K A A R L R D F V A L A A T L L N L P S P Q R YL R D L G W V G T E T R R N R I R F V Q D 99         7 K A A R L R D F V A L A A P I M R T P V P E E YL L R L C WM Y T G D D N G E I KF L Q D 98         7 K A K L S S F L E A A A P I M C T P K P E E YL L KL C WW M S T D D C D V T F         0 D 98         7 K A K L S D F L E A A A P I M G V P V P E A YL A KL C WI Y T G N E V G E L A F F Q D 98         7 N A K L S D F L E V A V P I M G V P V P E A YL A KL C WI Y T G N E V G E L A F F Q D 98         7 N A K L S D F L E V A V P I M G V P V P E A YL A KL C WI Y T G N E V G E L A F F Q D 98         7 N A K L S D F L E V A V P I M G V P V P E A YL A KL C WI Y T G N E V G E L A F F Q D 98         7 N A K L S D F L E V A V P I M G V P I P E N V A A L C WV Y A A D T G V T F - Q D 98         7 N A K L S D F L E V A V P I M G V P I P P E A YL A KL C WV Y A A D T G V T F - Q D 98         7 N A K L S D F L E V A V P I M G V P I P 2 B Q L Y F A KL C WV Y A A D T G V T F - Q D 98         7 N A K L S D F L E V A P A M G V P I 2 P 0 2 F 0 0 1 Y 0 V Y A A D T G V T F - Q 0 98         7 A K L S D F L S V Q P A A P A M G V P I 2 P 0 2 F 0 0 1 K 0 V Y 0 N V 0 V Y 0 0 V 0 V T 7 - Q 0 98 <th></th> <th>R D</th> <th>R D H V</th> <th>R D N I</th> <th>RDEV</th> <th>RDHI</th> <th>RDTV</th> <th>RDTV</th> <th>RDTI</th> <th>RDTI</th> <th>R D A I</th> <th>RDVV</th> <th>RDVV</th> <th>RDSI</th> <th>R D S I</th> <th></th>   |   | R D                           | R D H V  | R D N I  | RDEV  | RDHI   | RDTV  | RDTV  | RDTI  | RDTI  | R D A I  | RDVV  | RDVV  | RDSI  | R D S I   |   |
| G A K L L T F L D I A A P L M C T P K P E E YL KS L C WMYT A N D K G E I Q F L Q D 98<br>G A K L L T F L D V A A P L M C T P K P D E YL KS L C WMYT A N D K G E I Q F L Q D 99<br>A A R L R D F V A L A A T L L N L P S P Q R YL R D L G W V G T E T R R N R I R F V Q D 99<br>A A R L R D F V A L A A T L L N L P S P Q R YL R D L G W V G T E T R R N R I R F V Q D 99<br>V A K L S S F L E A A A P I M R T P V P E E YL L KL C WM Y T G D D N G E I KF L Q D 98<br>N T K L S S F L E V A V P I M R T P V P E E YL L KL C WM W T G D D N G E L A F F Q D 98<br>T A K L S D F L E V A V P I M G V P V P E A YL A KL C WI Y T G N E V G E L A F F Q D 98<br>T A K L S D F L E V A V P I M G V P V P E A YL A KL C WI Y T G N E V G E L A F F Q D 98<br>S A Q L S T F L T V Q V A A P A M G V P I S P C L YF Q L A KL C WI Y G N E V G E L A F F Q D 98<br>S A Q L S T F L T V Q V A A P A M G V P I P E N Y I A KL C WV Y S G N E A G D I V G F P Q D 98<br>S A Q L S T F L T V Q V A A P A M G V P I P E N Y I A KL C WV Y S G N E A G D I V G Q D 98<br>S A Q L S T F L T V Q V A A P A M G V P I P E N Y I A KL C WV Y A A D T G V T F - Q S 97<br>A K C N L N P F I S V A C P M M K I V E P S I C Y I G KL G L F H H M G E E G N M V L V Q D 98<br>S A Q V R L C D Y V Q V A A P A M G V P I P P S Y I S C Y S H D S F G N M V L V Q S 98<br>A Q V R L C D Y V Q V A A P A M G V P I P S O Y I S C F G W Q V S H D S F G N M V L V Q S 98<br>S A Q V R L C D Y V Q V A A P A M G V P I P S Y I S C Y F S S S G N M V L V Q S 98<br>S A Q V R L C D Y V Q Y A A P A M G Y P I Y S S S S G N M V L V Q S 98<br>S A Q V R L C S Y Y Q Y A A P A M G Y P I S S S S A Y S S S S A Y S S S S A Y S S S S  | 1 | R D G                         | R D H V G K  | R D N I G R  | RDEVGK  | RDHIGK   | R D T V G K   | RDTVK   | RDTIGK  | R D T I G K   | R D A I G I  | RDVVGT  | RDVVGT  | R D S I G N   | R D S I G N   |   |
| KLLTFLDIAAPLMCTPKPEEYLKSLCWMYTANDKGEIQFLQDS         KLLTFLDIAAPLMCTPKPEEYLKSLCWMYTANDKGEIQFLQDS         KLLTFLDVAAPLMCTPKPEEYLKSLCWMYTANDKGEIQFLQDS         RLRDFVALAATLLNLPSQPREE         RLRDFVALAAPLMCTPKPEE         RLRDFVALAAPLMCTPKPEE         RLRDFVALAAPLMCTPKPEE         RLRDFVALAAPLMLPS         RLRDFVALAAPLMLPS         RLRDFVALAAPLMLPS         RLRDFVALAAPLMLPS         RLRDFVALAAPLMLPS         RLRDFVALAAPLMLPS         RLRDFVALAAPLAAPLMLPS         RLRDFVALAAPLAAPLMLPS         RLRDFVALAAPLAAPLANLPS         RLSSFLQIAAP         RLSSFLQIAAP         RLSSFLQIAAP         RLSSFLQIAAP         RLSSFLQIAAP         RLSSFLQIAP         RL   | 1 | R D G                         | RDHVGKA  | R D N I G R D  | R D E V G K D   | R D H I G K S  | R D T V G K N   | r d t v k n   | R D T I G K N   | R D T I G K S   | R D A I G I K  | RDVVGTK   | R D V V G T K.  | R D S I G N K   | RDSIGNK   |   |
| LL TF L DI AAPLMCTP KPEEYLKS LCWMYT ANDKGEI QF L Q 59<br>LTF L DV AAPLMCTP KPEEYLKS LCWMYT ANDKGEI QF L Q 59<br>LTF L DV AAPLMCTP KPEYLEN L & CWMYT ANDKGEI QF L Q 59<br>RDF VALAATLLNLP S 0 Q 7 L RDL G W G TETRR NR I RF V Q 59<br>S F L E AAAPI MR TP V P E EYLEKLCWMYTGDDNGEI KF L Q 59<br>S F L E AAAPI MR TP V P E EYLEKLCWMYTGDDNGEI KF L Q 59<br>S F L E V AV P I MG V P V P E AYLAKLCWIYTGDDNGEI KF L Q 59<br>S DF L E V AV P I MG V P V P E AYLAKLCWIYTGDNGE G L AFF Q 59<br>S DF L E V AV P I MG V P V P E AYLAKLCWIYTGDNGE G L AFF Q 59<br>S DF L E V AV P I MG V P V P E AYLAKLCWIYTGUN VS GNEVGEL AFF Q 59<br>S DF L E V AV P I MG V P V P E AYLAKLCWIYTGUN VS GNEVGEL AFF Q 59<br>S DF L E V AV P I MG V P V P E AYLAKLCWIYTGUN VS GNEVGEL AFF Q 59<br>S DF L E V AV P I MG V P V P E AYLAKLCWIYTGUN VS GNEVGEL AFF Q 59<br>S DF L V C P I MG V P V P E AYLAKLCWIYTGUN VS GNE G 1 AFF Q 59<br>S TF L T V C P I MG V P I P E AYLAKLCWIYTGUN VS GNE G 1 AFF Q 59<br>S TF L T V C P I MG V P I P E 2 V A F ALAKLCWIYTGUN VS GNE G 1 V C 7 F 0<br>S A C V V Q V A A P A MG V P I P E 2 V A C V F A A D D T G V T F 0<br>S A C V V Q V A A P A MG V P I P E 2 S YF GLF G W V S HD S F G NMVLV V Q 59<br>S A C V V Q V A A P A MG V P I P C 2 S YF 0<br>S C Y V Q V A A P A MG V P I P C 2 S YF 0<br>S C Y V Q V A A P A MG V P I P C 2 S YF 0<br>S C Y V Q V A A P A MG V P I P C 2 S YF 0<br>S C Y V Q V A A P A MG V P I P C 2 S YF 0<br>S C Y V Q V A A P A MG V P I P C 2 S YF 0<br>S C Y V Q V A A P A MG V Y I P C 2 S YF 0<br>S C Y V Q V A A P A MG V Y I P C 2 S YF 0<br>S C Y V Q V A A P A M Y V Z Y C 2 S YF 0<br>S C Y V Q V A A P A M Y V Z Y 0<br>S S YF C C Y V C 2 S Y 0<br>S S S S S S S S S S S S S S S S S S S  |   | RD G ₂                        | RDHVGKAKC  | R D N I G R D Q V  | R D E V G K D S A   | R D H I G K S E A  | R D T V G K N T A   | r d t v k n t a   | R D T I G K N T A   | R D T I G K S N T   | R D A I G I K V A  | RDVVGTKAA   | R D V V G T K A A   | R D S I G N K G A   | R D S I G N K G A   |   |
| T F L DI       A A P L MC T P K P E E Y L K S L C WMY T A N D K G E I       Q F L Q D S       Q F L Q D S         T F L DV       A A P L MC T P K P E E Y L K S L C WMY T A N D K G E I       Q F L Q D S       Q F L Q D S         D F V AL A T L L N L P S       P Q R Y L R D L G W G T E T R R N R I R F V Q D S       Q S S       Q S T R R N R T P N P P P P E E Y L E K L C WMY T G D D N G E I K F L Q D S       S         S F L E A A A P I M R T P V P E E Y L E K L C WMY T G D D N G E I K F L Q D S       S       Q S S T L E N A P N MC T P P P P E E Y L L K L C WMY T G D D N G E L A F F Q D S       S         S F L E V A V P I M G V P V P E E Y L L K L C WM W S T D D C D V T F       Q D S       S       S       Q S S S T L C N A P N G V P V P E A Y L A K L C WI W S G N E V G E L A F F Q D S       S       S         D F L E V A V P I M G V P V P E A Y L A K L C WI V S G N E V G E L A F F Q D S       S       S S C V T F S S S S S S S S S S S S S S S S S S  |   | RD G ₂k]                      | RDHVGKAKCNI  | R D N I G R D Q V R I  | R D E V G K D S A Q I   | RDHIGKSEAK   | R D T V G K N T A K I   | R D T V K N T A K   | R D T I G K N T A K I   | R D T I G K S N T K I   | R D A I G I K V A K I  | RDVVGTKAARI   | RDVVGTKAARI   | R D S I G N K G A K I   | R D S I G N K G A K I   |   |
| 1 DI AAPL MCTPKPEEYLKSLCWMYTANDKGEI QFLQD9         1 DV AAPL MCTPKPEEYLKSLCWMYTANDKGEI QFLQD9         1 DV AAPL MCTPKPEEYLKSLCWMYTANDKGEI QFLQD9         1 DV ALAATLLNLPS         1 DV ALAATLLNLPS         1 D ZAAPI MRTPVPEEYLEKLCWMYTGDDNGEIKFUQD99         1 L AATLLNLPS         1 L AAPI MRTPVPEEYLEKLCWMYTGDDNGEIKFUQD99         1 L ZAAPI MRTPVPEEZYLEKLCWMYTGDDNGEIKFUQD99         1 L ZAAPI MRTPVPEEZYLEKLCWINTGDDNGEIKFUQD98         1 L ZV AVPI MGVPVPEEAYLAKLCWI YT GNEVGELAFFQD99         1 L ZV AVPI MGVPVPEEAYLAKLCWI YT GNEVGELAFFQD99         1 L ZV AVPI MGVPVPEEAYLAKLCWI YT GNEVGELAFFQD99         2 L ZV AVPI MGVPVPEEAYLAKLCWI YT GNEVGELAFFQD99         2 L ZV AVPI MGVPPPPEEAYLAKLCWI YT GNEVGELAFFQD99         2 L ZV AVPI MGVPPPPEEAYLAKLCWI YT GNEVGELGD1 AFFQD99         2 L ZV AVPI MGVPPPPEEAYLAKLCWVYSGNEVGELAFFQD99         2 L ZV AVPI MGVPPPPEEAYLAKLCWVYSGNEGUEGD1 VLGD99         2 L ZV AVPI MGVPPPPEEAYLAKLCWVYSGNVYADDTGVTF         2 AVPI MGVPPPEEAYLAKLCWVYSGNVYADDTGVTF         3 Z A MMXI VEPPE         4 Z A MMXI VEPE         4 Z A MMXI VEPE         5 Z YFGLFGLFGWYSHD2         4 Y A P MMXI VEPE         6 S Z YFGLFGLFGWYSHD2         7 1 S Z A P MMXI VEPE         7 2 2 3 M  |   | RDG akL                       | R D H V G K A K C N L N  | R D N I G R D Q V R L C  | RDEVGKDSAQLS  | R D H I G K S E A K L S  | R D T V G K N T A K L S   | RDTV KNTAKLS  | R D T I G K N T A K L S   | R D T I G K S N T K L S   | R D A I G I K V A K L S  | R D V V G T K A A R L R   | R D V V G T K A A R L R   | R D S I G N K G A K L L   | R D S I G N K G A K L L   |   |
| DI AAPL MCTP KPEEYLKS LCWMYTANDKGEI QFLQ D98<br>DVAAPL MCTP KPEEYLKSLCWMYTANDKGEI QFLQ D99<br>ALAATLLNLP SPQRYLRDLG WVGTETRRNRI RFVQ D99<br>ALAATLLNLP SPQRYLRDLG WVGTGDDNGEI KFLQ D99<br>EAAAPI MRTP VPEEYLEKLCWMYTGDDNGEI KFLQ D98<br>EVAVPI MGVP VPEEYLLKLCWMYTGDDNGEI KFLQ D98<br>EVAVPI MGVP VPEEYLAKLCWI YTGNEVGELAFF QD98<br>EVAVPI MGVP VPEEYLAKLCWI YTGNEVGELAFF QD98<br>SVACPI MGVP I PEYLAKLCWVYSGNEAGDI AFF QD98<br>SVACPMMKI VEPS 2 GLYFQKLGLFHHMGEEGGI VTF-QS97<br>SVACPMMKI VEPS 2 SZYFGLFGWVYSHDSFGNMVLVQ098<br>SVACPMMKI VEPS 2 SZYFGLFGWVYTV<br>SVACPMMKI VEPS 2 SZYFGLFGWVYT<br>SVACPMMKI VEPS 2 SZYFGLFGWVYT<br>SVACPMMKI VEPS 2 SZYFGLFGWVYT<br>SVACQVANAVI VEPS 2 SZYFGLFGWVYT<br>SVACPMMKI VEPS 2 SZYFGLFGWVT<br>SVACPMMKI VEPT 2 SZYFGLFGWVYT<br>SVACPMMKI VEPT 2 SZYFGLFGWVT<br>SVACPMMKI VEPT 2 SZYFGLFGWVT<br>SVACPMMKI VEZ 2 SZYFGLFGWVT<br>SVACPMKI VEZ 2 SZYFGGLFGWVT<br>SVACPMKI VEZ 2 SZYFGGLFGW   |   | RDG akL f                     | R D H V G K A K C N L N P F  | R D N I G R D Q V R L C D Y  | R D E V G K D S A Q L S T F   | R D H I G K S E A K L S E F  | R D T V G K N T A K L S D F   | RDTV KNTAKLSDF  | R D T I G K N T A K L S D F   | R D T I G K S N T K L S E F   | R D A I G I K V A K L S S F  | RDVVGTKAARLRDF  | R D V V G T K A A R L R D F   | R D S I G N K G A K L L T F   | R D S I G N K G A K L L T F   |   |
| A A P L MC T P K P E E Y L K S L C WMY T A N D K G E I Q F L Q D 98         A A P L MC T P K P D E Y L K S L C WMY T A N D K G E I Q F L Q D 99         A A T L L N L P S P Q R Y L R D L G WY G T E T R R N R I R F V Q D 99         A A T L L N L P S P Q R Y L R D L G WY G T E T R R N R I R F V Q D 99         A A T L L N L P S P Q R Y L R D L G WY G T E T R R N R I R F V Q D 99         A A T L N L P S P Q R Y L R D L G WY G T E T R R N R I R F V Q D 99         A A P I MR T P V P E E Y L L K L C WMY T G D D N G E I K F L Q D 98         A A P V MC T P K P E E Y L L K L C WI W MNS T D D C D V T F         A V P I MG V P V P E A Y L A K L C WI Y T G N E V G E L A F F Q D 98         A V P I MG V P V P E A Y L A K L C WI Y T G N E V G E L A F F Q D 98         A V P I MG V P V P E A Y L A K L C WI Y T G N E V G E L A F F Q D 98         A A P A MG V P V P E A Y L A K L C WI Y T G N E V G E L A F F Q D 98         A A P A MG V P I P E A Y L A K L C WI Y A A D D T G V T F - Q S 97         A A P A MG V P I P E D Y L T K L C WV Y A A D D T G V T F - Q S 97         A A P A MG V P I P E S Q L F G L F G WQ V S H D S F G NMV L V Q D 98         A A P M MX I V E P S E Y I I C W Y I C W Y H A N D X F G N MV L V Q D 98         A P M M Y P P P * Y I I C Y I C W Y S H D S F G N MV L V Q D 98   |   | RD G ₂kL f1                   | R D H V G K A K C N L N P F L  | R D N I G R D Q V R L C D Y V  | R D E V G K D S A Q L S T F L   | RDHIGKSEAKLSEFL  | R D T V G K N T A K L S D F L   | RDTV KNTAKLSDFL   | R D T I G K N T A K L S D F L   | R D T I G K S N T K L S E F L   | R D A I G I K V A K L S S F L  | R D V V G T K A A R L R D F V   | R D V V G T K A A R L R D F V   | R D S I G N K G A K L L T F L   | R D S I G N K G A K L L T F L   |   |
| $ \begin{array}{c} A \ p \ L \ MC \ T \ p \ K \ p \ E \ E \ Y \ L \ K \ S \ L \ C \ WM \ Y \ T \ A \ N \ D \ K \ G \ E \ I \ Q \ F \ L \ Q \ D \ .98 \\ A \ T \ L \ ML \ P \ S \ P \ Q \ R \ Y \ L \ R \ D \ L \ Q \ D \ .98 \\ A \ T \ L \ ML \ P \ S \ P \ Q \ R \ Y \ L \ R \ D \ L \ Q \ D \ .98 \\ A \ T \ L \ ML \ P \ S \ P \ Q \ R \ Y \ L \ R \ D \ L \ Q \ D \ .98 \\ A \ T \ L \ ML \ P \ S \ P \ Q \ R \ Y \ L \ R \ D \ L \ Q \ D \ .98 \\ A \ T \ L \ ML \ P \ S \ P \ Q \ R \ Y \ L \ R \ L \ R \ M \ R \ T \ G \ D \ S \ R \ R \ R \ R \ R \ R \ R \ R \ R$   |   | RDG akL f1                    | R D H V G K A K C N L N P F L S V  | R D N I G R D Q V R L C D Y V Q V  | R D E V G K D S A Q L S T F L T V   | RDHIGKSEAKLSEFLEI  | R D T V G K N T A K L S D F L E V   | R D T V K N T A K L S D F L E V   | R D T I G K N T A K L S D F L E V   | R D T I G K S N T K L S E F L Q I   | R D A I G I K V A K L S S F L E A  | R D V V G T K A A R L R D F V A L   | R D V V G T K A A R L R D F V A L   | R D S I G N K G A K L L T F L D V   | R D S I G N K G A K L L T F L D I   |   |
| $ \begin{array}{c ccccccccccccccccccccccccccccccccccc$  |   | RDG akLf1 a                   | R D H V G K A K C N L N P F L S V A  | R D N I G R D Q V R L C D Y V Q V A .  | R D E V G K D S A Q L S T F L T V V   | RDHIGKSEAKLSEFLEIA   | R D T V G K N T A K L S D F L E V A   | RDTV KNTAKLSDFLEVA  | R D T I G K N T A K L S D F L E V A   | RDTIGKSNTKLSEFLQIA.   | R D A I G I K V A K L S S F L E A A .  | R D V V G T K A A R L R D F V A L A .   | R D V V G T K A A R L R D F V A L A .   | R D S I G N K G A K L L T F L D V A .   | R D S I G N K G A K L L T F L D I A.  |   |
|   |   | RDG akL flaap                 | R D H V G K A K C N L N P F L S V A C P  | R D N I G R D Q V R L C D Y V Q V A A P  | R D E V G K D S A Q L S T F L T V V C P   | R D H I G K S E A K L S E F L E I A G P  | R D T V G K N T A K L S D F L E V A V P   | R D T V K N T A K L S D F L E V A V P   | R D T I G K N T A K L S D F L E V A V P   | R D T I G K S N T K L S E F L Q I A A P   | R D A I G I K V A K L S S F L E A A A P  | R D V V G T K A A R L R D F V A L A A T   | R D V V G T K A A R L R D F V A L A A T   | R D S I G N K G A K L L T F L D V A A P   | R D S I G N K G A K L L T F L D I A A P   |   |
| $ \begin{array}{c ccccccccccccccccccccccccccccccccccc$  |   | RDG akLfl aapr                | R D H V G K A K C N L N P F L S V A C P M1   | R D N I G R D Q V R L C D Y V Q V A A P A I  | R D E V G K D S A Q L S T F L T V V C P I 1   | RDHIGKSEAKLSEFLEIAGPI1   | R D T V G K N T A K L S D F L E V A V P I 1   | RDTV KNTAKLSDFLEVAVPI1  | R D T I G K N T A K L S D F L E V A V P I 1   | R D T I G K S N T K L S E F L Q I A A P V I   | R D A I G I K V A K L S S F L E A A A P I 1  | R D V V G T K A A R L R D F V A L A A T L I   | R D V V G T K A A R L R D F V A L A A T L I   | R D S I G N K G A K L L T F L D V A A P L 1   | R D S I G N K G A K L L T F L D I A A P L 1   |   |
|   |   | RDG akL flaap m               | R D H V G K A K C N L N P F L S V A C P MMK  | R D N I G R D Q V R L C D Y V Q V A A P A MG   | RDEVGKDS AQLS TFL TVVCPI MG   | RDHIGKSEAKLSEFLEIAGPIMG  | R D T V G K N T A K L S D F L E V A V P I MG  | RDTV KNTAKLSDFLEVAVPI MG  | R D T I G K N T A K L S D F L E V A V P I MG  | R D T I G K S N T K L S E F L Q I A A P V M C   | R D A I G I K V A K L S S F L E A A A P I MR   | R D V V G T K A A R L R D F V A L A A T L L N   | R D V V G T K A A R L R D F V A L A A T L L N   | R D S I G N K G A K L L T F L D V A A P L M C   | R D S I G N K G A K L L T F L D I A A P L M C   |   |
|   |   | RDG akL flaapm p              | R D H V G K A K C N L N P F L S V A C P M M K I V  | R D N I G R D Q V R L C D Y V Q V A A P A MG V F   | RDEVGKDSAQLSTFLTVVCPI MGFP  | RDHIGKSEAKLSEFLEIAGPIMGAP  | R D T V G K N T A K L S D F L E V A V P I MG V F  | RDTV KNTAKLSDFLEVAVPIMGVF   | R D T I G K N T A K L S D F L E V A V P I MG V P  | R D T I G K S N T K L S E F L Q I A A P V M C T F   | R D A I G I K V A K L S S F L E A A A P I MR T P   | R D V V G T K A A R L R D F V A L A A T L L N L F   | R D V V G T K A A R L R D F V A L A A T L L N L F   | R D S I G N K G A K L L T F L D V A A P L MC T P  | R D S I G N K G A K L L T F L D I A A P L M C T F   |   |
| $ \begin{array}{c ccccccccccccccccccccccccccccccccccc$  |   | RDG akL flaapm p              | R D H V G K A K C N L N P F L S V A C P MMKI V E   | R D N I G R D Q V R L C D Y V Q V A A P A MG V P I   | RDEVGKDS AQLSTFLTVVCPI MGFPS  | RDHIGKSEAKLSEFLEIAGPIMGAPV   | R D T V G K N T A K L S D F L E V A V P I MG V P V  | RDTV KNTAKLSDFLEVAVPI MGVPV   | R D T I G K N T A K L S D F L E V A V P I MG V P V  | R D T I G K S N T K L S E F L Q I A A P V M C T P K   | R D A I G I K V A K L S S F L E A A A P I MR T P V   | R D V V G T K A A R L R D F V A L A A T L L N L P S   | R D V V G T K A A R L R D F V A L A A T L L N L P S   | R D S I G N K G A K L L T F L D V A A P L M C T P K   | R D S I G N K G A K L L T F L D I A A P L M C T P K   |   |
| $ \begin{array}{cccccccccccccccccccccccccccccccccccc$   |   | RDG akLflaapmpPe              | R D H V G K A K C N L N P F L S V A C P MMK I V E P S  | R D N I G R D Q V R L C D Y V Q V A A P A M G V P I P E  | R D E V G K D S A Q L S T F L T V V C P I M G F P S P G   | RDHIGKSEAKLSEFLEIAGPIMGAPVPE   | R D T V G K N T A K L S D F L E V A V P I MG V P V P E  | RDTV KNTAKLSDFLEVAVPIMGVPVPE  | R D T I G K N T A K L S D F L E V A V P I MG V P V P E  | R D T I G K S N T K L S E F L Q I A A P V M C T P K P E   | R D A I G I K V A K L S S F L E A A A P I MR T P V P E   | R D V V G T K A A R L R D F V A L A A T L L N L P S P Q   | R D V V G T K A A R L R D F V A L A A T L L N L P S P Q   | R D S I G N K G A K L L T F L D V A A P L M C T P K P D   | R D S I G N K G A K L L T F L D I A A P L M C T P K P E   |   |
|   |   | RDG akLf1 aapm pPe            | R D H V G K A K C N L N P F L S V A C P MMKI V E P S E   | R D N I G R D Q V R L C D Y V Q V A A P A MG V P I P E D   | R D E V G K D S A Q L S T F L T V C P I MG F P S P G L  | RDHIGKSEAKLSEFLEIAGPIMGAPVPEE  | R D T V G K N T A K L S D F L E V A V P I MG V P V P E A  | R D T V K N T A K L S D F L E V A V P I MG V P V P E A                                | R D T I G K N T A K L S D F L E V A V P I MG V P V P E A  | R D T I G K S N T K L S E F L Q I A A P V M C T P K P E E   | R D A I G I K V A K L S S F L E A A A P I MR T P V P E E   | R D V V G T K A A R L R D F V A L A A T L L N L P S P Q R   | R D V V G T K A A R L R D F V A L A A T L L N L P S P Q R   | R D S I G N K G A K L L T F L D V A A P L MC T P K P D E  | R D S I G N K G A K L L T F L D I A A P L M C T P K P E E   |   |
| $ \begin{array}{c ccccccccccccccccccccccccccccccccccc$  |   | RDG akL flaapm pPeY1          | R D H V G K A K C N L N P F L S V A C P MMKI V E P S E Y F   | R D N I G R D Q V R L C D Y V Q V A A P A M G V P I P E D Y L  | R D E V G K D S A Q L S T F L T V V C P I MG F P S P G L Y F  | R D H I G K S E A K L S E F L E I A G P I M G A P V P E E Y L  | R D T V G K N T A K L S D F L E V A V P I MG V P V P E A Y L  | R D T V K N T A K L S D F L E V A V P I MG V P V P E A Y L                            | R D T I G K N T A K L S D F L E V A V P I MG V P V P E A Y L  | R D T I G K S N T K L S E F L Q I A A P V M C T P K P E E Y L                                       | R D A I G I K V A K L S S F L E A A A P I MR T P V P E E Y L                                       | R D V V G T K A A R L R D F V A L A A T L L N L P S P Q R Y L   | R D V V G T K A A R L R D F V A L A A T L L N L P S P Q R Y L   | R D S I G N K G A K L L T F L D V A A P L M C T P K P D E Y L   | R D S I G N K G A K L L T F L D I A A P L M C T P K P E E Y L                                       |   |
| $ \begin{array}{c c c c c c c c c c c c c c c c c c c $   |   | RDG akLflaapm pPeY1           | R D H V G K A K C N L N P F L S V A C P MMKI V E P S E Y F G I                                     | R D N I G R D Q V R L C D Y V Q V A A P A MG V P I P E D Y L T I                                     | R D E V G K D S A Q L S T F L T V V C P I MG F P S P G L Y F Q I                                    | R D H I G K S E A K L S E F L E I A G P I M G A P V P E E Y L A I                                    | R D T V G K N T A K L S D F L E V A V P I MG V P V P E A Y L A I                                    | R D T V K N T A K L S D F L E V A V P I MG V P V P E A Y L A I                        | R D T I G K N T A K L S D F L E V A V P I MG V P V P E A V L A I                                    | R D T I G K S N T K L S E F L Q I A A P V M C T P K P E E Y L L I                                   | R D A I G I K V A K L S S F L E A A A P I MR T P V P E E Y L E I                                   | R D V V G T K A A R L R D F V A L A A T L L N L P S P Q R Y L R I                                     | R D V V G T K A A R L R D F V A L A A T L L N L P S P Q R V L R I                                     | R D S I G N K G A K L L T F L D V A A P L M C T P K P D E V L K S                                     | R D S I G N K G A K L L T F L D I A A P L M C T P K P E E Y L K S                                   |   |
| $ \begin{array}{c ccccccccccccccccccccccccccccccccccc$  |   | RDG akLflaapmpPeY11           | R D H V G K A K C N L N P F L S V A C P MMKI V E P S E YF G L F                                    | R D N I G R D Q V R L C D Y V Q V A A P A MG V P I P E D Y L T K L                                   | R D E V G K D S A Q L S T F L T V V C P I MG F P S P G L Y F Q K L                                  | R D H I G K S E A K L S E F L E I A G P I MG A P V P E E Y L A R L                                   | R D T V G K N T A K L S D F L E V A V P I MG V P V P E A Y L A K L                                  | RDTV KNTAKLSDFLEVAVPIMGVPVPEAYLAKL  | R D T I G K N T A K L S D F L E V A V P I MG V P V P E A Y L A K L                                  | R D T I G K S N T K L S E F L Q I A A P V M C T P K P E E Y L L K L                                 | R D A I G I K V A K L S S F L E A A A P I MR T P V P E E Y L E K L                                 | R D V V G T K A A R L R D F V A L A A T L L N L P S P Q R Y L R D L                                   | R D V V G T K A A R L R D F V A L A A T L L N L P S P Q R Y L R D L                                   | R D S I G N K G A K L L T F L D V A A P L M C T P K P D E Y L K S L                                   | R D S I G N K G A K L L T F L D I A A P L M C T P K P E E Y L K S L                                 |   |
| $ \begin{array}{cccccccccccccccccccccccccccccccccccc$   |   | RDG akLflaapmpPeYilev         | R D H V G K A K C N L N P F L S V A C P MMKI V E P S E Y F G L F G V                               | R D N I G R D Q V R L C D Y V Q V A A P A M G V P I P E D Y L T K L C V                              | R D E V G K D S A Q L S T F L T V V C P I MG F P S P G L Y F Q K L G I                              | R D H I G K S E A K L S E F L E I A G P I M G A P V P E E Y L A R L C V                              | R D T V G K N T A K L S D F L E V A V P I MG V P V P E A VL A K L C V                               | RDTV KNTAKLSDFLEVAVPIMGVPVPEATLAKLCV  | R D T I G K N T A K L S D F L E V A V P I MG V P V P E A Y L A K L C V                              | R D T I G K S N T K L S E F L Q I A A P V M C T P K P E E Y L L K L C V                             | R D A I G I K V A K L S S F L E A A A P I MR T P V P E E Y L E K L C V                             | R D V V G T K A A R L R D F V A L A A T L L N L P S P Q R Y L R D L G V                               | R D V V G T K A A R L R D F V A L A A T L L N L P S P Q R V L R D L G V                               | R D S I G N K G A K L L T F L D V A A P L M C T P K P D E Y L K S L C V                               | R D S I G N K G A K L L T F L D I A A P L M C T P K P E E Y L K S L C V                             |   |
| $ \begin{bmatrix} A & N & D & K & G & E & I & Q & F & L & Q & D & 98 \\ F & A & N & D & K & G & R & I & R & F & V & Q & D & 99 \\ F & E & T & R & R & N & R & I & R & F & V & Q & D & 99 \\ F & G & D & D & G & E & L & A & F & F & Q & D & 98 \\ F & G & N & E & V & G & E & L & A & F & F & Q & D & 98 \\ F & G & N & E & V & G & E & L & A & F & F & Q & D & 98 \\ F & G & N & E & V & G & E & L & A & F & F & Q & D & 98 \\ F & G & N & E & V & G & E & L & A & F & F & Q & D & 98 \\ F & G & N & E & V & G & E & L & A & F & F & Q & D & 98 \\ F & G & N & E & V & G & E & L & A & F & F & Q & D & 98 \\ F & M & G & E & G & D & I & V & T & F & Q & D & 98 \\ F & M & G & E & G & D & I & V & T & F & Q & D & 98 \\ F & M & D & T & G & V & V & T & F & Q & D & 98 \\ H & D & S & F & G & N & M & V & L & V & Q & D & 98 \\ H & D & S & F & G & M & M & L & V & Q & D & 98 \\ H & D & S & F & G & M & M & L & V & Q & D & 98 \\ H & D & S & F & G & M & M & L & V & Q & D & 98 \\ \end{bmatrix} $   |   | RDG akLflaapmpPeY1lcw         | R D H V G K A K C N L N P F L S V A C P MMKI V E P S E Y F G L F G WQ                              | R D N I G R D Q V R L C D Y V Q V A A P A M G V P I P E D Y L T K L C W V                            | R D E V G K D S A Q L S T F L T V V C P I MG F P S P G L Y F Q K L G L F                            | R D H I G K S E A K L S E F L E I A G P I MG A P V P E E Y L A R L C W V                             | R D T V G K N T A K L S D F L E V A V P I MG V P V P E A Y L A K L C WI                             | R D T V K N T A K L S D F L E V A V P I MG V P V P E A Y L A K L C WI                 | R D T I G K N T A K L S D F L E V A V P I MG V P V P E A Y L A K L C WI                             | R D T I G K S N T K L S E F L Q I A A P V MC T P K P E E Y L L K L C W V                            | R D A I G I K V A K L S S F L E A A A P I MR T P V P E E Y L E K L C W M                           | R D V V G T K A A R L R D F V A L A A T L L N L P S P Q R Y L R D L G W V                             | R D V V G T K A A R L R D F V A L A A T L L N L P S P Q R Y L R D L G W V                             | R D S I G N K G A K L L T F L D V A A P L M C T P K P D E Y L K S L C W M                             | R D S I G N K G A K L L T F L D I A A P L M C T P K P E E Y L K S L C W M                           |   |
| $ \begin{array}{c ccccccccccccccccccccccccccccccccccc$  |   | RDG akL flaapmpPeY11cwyt      | R D H V G K A K C N L N P F L S V A C P MMK I V E P S E YF G L F G WQ V S                          | R D N I G R D Q V R L C D Y V Q V A A P A MG V P I P E D Y L T K L C W Y A                           | R D E V G K D S A Q L S T F L T V V C P I MG F P S P G L Y F Q K L G L F H H                        | R DHIGKSEAKLSEFLEIAGPIMGAPVPEEVLARLCWVYS   | R D T V G K N T A K L S D F L E V A V P I MG V P V P E A Y L A K L C WI Y 1                         | R D T V K N T A K L S D F L E V A V P I MG V P V P E A Y L A K L C WI Y 1             | R D T I G K N T A K L S D F L E V A V P I MG V P V P E A Y L A K L C WI Y 1                         | R D T I G K S N T K L S E F L Q I A A P V M C T P K P E E Y L L K L C W V M N                       | R D A I G I K V A K L S S F L E A A A P I MR T P V P E E Y L E K L C WMY 1                         | R D V V G T K A A R L R D F V A L A A T L L N L P S P Q R Y L R D L G W V G 1                         | R D V V G T K A A R L R D F V A L A A T L L N L P S P Q R Y L R D L G W V G 1                         | R D S I G N K G A K L L T F L D V A A P L MC T P K P D E Y L K S L C WMY 1                            | R D S I G N K G A K L L T F L D I A A P L M C T P K P E E Y L K S L C W M Y 1                       |   |
| $ \begin{array}{c ccccccccccccccccccccccccccccccccccc$  |   | RDG akL flaapm pPeY1 low yt   | R D H V G K A K C N L N P F L S V A C P MMKI V E P S E YF G L F G WQ V S H                         | R D N I G R D Q V R L C D Y V Q V A A P A M G V P I P E D Y L T K L C W V Y A A                      | R D E V G K D S A Q L S T F L T V V C P I MG F P S P G L Y F Q K L G L F H H M                      | RDHIGKSEAKLSEFLEIAGPIMGAPVPEEYLARLCWVYSG   | R D T V G K N T A K L S D F L E V A V P I MG V P V P E A Y L A K L C WI Y T G                       | R D T V K N T A K L S D F L E V A V P I MG V P V P E A Y L A K L C WI Y T G           | R D T I G K N T A K L S D F L E V A V P I MG V P V P E A Y L A K L C WI Y T G                       | R D T I G K S N T K L S E F L Q I A A P V M C T P K P E E Y L L K L C W V M N S                     | R D A I G I K V A K L S S F L E A A A P I MR T P V P E E Y L E K L C WMY T G                       | R D V V G T K A A R L R D F V A L A A T L L N L P S P Q R Y L R D L G W V G T E                       | R D V V G T K A A R L R D F V A L A A T L L N L P S P Q R Y L R D L G W V G T E                       | R D S I G N K G A K L L T F L D V A A P L M C T P K P D E Y L K S L C W M Y T A                       | R D S I G N K G A K L L T F L D I A A P L M C T P K P E E Y L K S L C WMY T A                       |   |
| $ \begin{array}{c ccccccccccccccccccccccccccccccccccc$  |   | RDG akL flaapm pPeY1 lowyt    | R D H V G K A K C N L N P F L S V A C P MMKI V E P S E Y F G L F G WQ V S H D S                    | R D N I G R D Q V R L C D Y V Q V A A P A MG V P I P E D Y L T K L C W Y A A D E                     | R D E V G K D S A Q L S T F L T V V C P I MG F P S P G L Y F Q K L G L F H H MG E                   | R D H I G K S E A K L S E F L E I A G P I MG A P V P E E Y L A R L C W V Y S G N E                   | R D T V G K N T A K L S D F L E V A V P I MG V P V P E A Y L A K L C WI Y T G N E                   | R D T V K N T A K L S D F L E V A V P I MG V P V P E A Y L A K L C WI Y T G N E       | R D T I G K N T A K L S D F L E V A V P I MG V P V P E A Y L A K L C WI Y T G N E                   | R D T I G K S N T K L S E F L Q I A A P V M C T P K P E E Y L L K L C W V M N S T L                 | R D A I G I K V A K L S S F L E A A A P I MR T P V P E E Y L E K L C WMY T G D E                   | R D V V G T K A A R L R D F V A L A A T L L N L P S P Q R Y L R D L G W V G T E T R                   | R D V V G T K A A R L R D F V A L A A T L L N L P S P Q R Y L R D L G W V G T E T R                   | R D S I G N K G A K L L T F L D V A A P L M C T P K P D E Y L K S L C W M Y T A N E                   | R D S I G N K G A K L L T F L D I A A P L M C T P K P E E Y L K S L C W M Y T A N L                 |   |
| $\begin{array}{c ccccccccccccccccccccccccccccccccccc$   |   | RDG akL flaapm pPeY11cwyt     | R D H V G K A K C N L N P F L S V A C P MMK I V E P S E Y F G L F G WQ V S H D S F V               | R D N I G R D Q V R L C D Y V Q V A A P A MG V P I P E D YL T K L C W V Y A A D D T                  | R D E V G K D S A Q L S T F L T V V C P I MG F P S P G L Y F Q K L G L F H H MG E E                 | R D H I G K S E A K L S E F L E I A G P I MG A P V P E E Y L A R L C W V Y S G N E A                 | R D T V G K N T A K L S D F L E V A V P I MG V P V P E A Y L A K L C WI Y T G N E V                 | R D T V K N T A K L S D F L E V A V P I MG V P V P E A Y L A K L C WI Y T G N E V     | R D T I G K N T A K L S D F L E V A V P I MG V P V P E A Y L A K L C WI Y T G N E V                 | R D TI G K S N T K L S E F L Q I A A P V M C T P K P E E Y L L K L C W V M N S T D D                | R D A I G I K V A K L S S F L E A A A P I MR T P V P E E Y L E K L C W M Y T G D D N               | R D V V G T K A A R L R D F V A L A A T L L N L P S P Q R Y L R D L G W V G T E T R R .               | R D V V G T K A A R L R D F V A L A A T L L N L P S P Q R V L R D L G W V G T E T R R .               | R D S I G N K G A K L L T F L D V A A P L M C T P K P D E Y L K S L C W M Y T A N D K                 | R D S I G N K G A K L L T F L D I A A P L M C T P K P E E Y L K S L C WMY T A N D K                 |   |
| $ \begin{array}{c ccccccccccccccccccccccccccccccccccc$  |   | RDG akLflaapmpPeYilcwytg      | R D H V G K A K C N L N P F L S V A C P MMK I V E P S E Y F G L F G W Q V S H D S F G N            | R D N I G R D Q V R L C D Y V Q V A A P A MG V P I P E D Y L T K L C W V Y A A D D T G V             | R D E V G K D S A Q L S T F L T V V C P I MG F P S P G L Y F Q K L G L F H H M G E E G D            | R D H I G K S E A K L S E F L E I A G P I M G A P V P E E Y L A R L C W V Y S G N E A G D            | R D T V G K N T A K L S D F L E V A V P I MG V P V P E A Y L A K L C WI Y T G N E V G E             | R D T V K N T A K L S D F L E V A V P I MG V P V P E A Y L A K L C WI Y T G N E V G E | R D T I G K N T A K L S D F L E V A V P I MG V P V P E A Y L A K L C WI Y T G N E V G E             | R D T I G K S N T K L S E F L Q I A A P V M C T P K P E E Y L L K L C W V M N S T D D C D           | R D A I G I K V A K L S S F L E A A A P I MR T P V P E E Y L E K L C WMY T G D D N G E             | R D V V G T K A A R L R D F V A L A A T L L N L P S P Q R Y L R D L G W V G T E T R R N R             | R D V V G T K A A R L R D F V A L A A T L L N L P S P Q R Y L R D L G W V G T E T R R N R             | R D S I G N K G A K L L T F L D V A A P L M C T P K P D E Y L K S L C W M Y T A N D K G E             | R D S I G N K G A K L L T F L D I A A P L M C T P K P E E Y L K S L C W M Y T A N D K G E           |   |
| L Q D 98<br>L Q D 98<br>V Q D 99<br>V Q D 99<br>L Q D 99<br>F Q D 98<br>F Q 09<br>F Q |   | RDG akLflaapmpPeYilcwytgi     | R D H V G K A K C N L N P F L S V A C P M M K I V E P S E Y F G L F G WQ V S H D S F G N M         | R D N I G R D Q V R L C D Y V Q V A A P A MG V P I P E D Y L T K L C W V Y A A D D T G V V .         | R D E V G K D S A Q L S T F L T V V C P I MG F P S P G L Y F Q K L G L F H H M G E E G D I )        | R D H I G K S E A K L S E F L E I A G P I MG A P V P E E Y L A R L C W V Y S G N E A G D I .         | R D T V G K N T A K L S D F L E V A V P I MG V P V P E A Y L A K L C WI Y T G N E V G E L .         | RDTV KNTAKLSDFLEVAVPIMGVPVPEAYLAKLCWIYTGNEVGEL.                                       | RDTI GKNTAKLS DFLEVAVPI MGVPV <mark>P</mark> EAYLAKLCWI YTGNEVGEL.                                  | R D T I G K S N T K L S E F L Q I A A P V M C T P K P E E Y L L K L C W V M N S T D C D V .         | R D AI GI K V A K L S S F L E A A A P I MR T P V P E E Y L E K L C WMY T G D D N G E I 1           | R D V V G T K A A R L R D F V A L A A T L L N L P S P Q R Y L R D L G W V G T E T R R N R I I         | R D V V G T K A A R L R D F V A L A A T L L N L P S P Q R Y L R D L G W V G T E T R R N R I I         | R D S I G N K G A K L L T F L D V A A P L M C T P K P D E Y L K S L C W M Y T A N D K G E I (         | R D S I G N K G A K L L T F L D I A A P L M C T P K P E E Y L K S L C W M Y T A N D K G E I (       |   |
| 0     0 <th></th> <th>RDG akLflaapmpPeYilcwytgif</th> <th>R D H V G K A K C N L N P F L S V A C P MMKI V E P S E Y F G L F G WQ V S H D S F G N M V L</th> <th>R D N I G R D Q V R L C D Y V Q V A A P A MG V P I P E D Y L T K L C W V Y A A D D T G V V T F</th> <th>R D E V G K D S A Q L S T F L T V V C P I MG F P S P G L Y F Q K L G L F H H MG E E G D I V L</th> <th>R D H I G K S E A K L S E F L E I A G P I MG A P V P E E YL A R L C WV Y S G N E A G D I A F</th> <th>R D T V G K N T A K L S D F L E V A V P I MG V P V P E A YL A K L C WI Y T G N E V G E L A F</th> <th>RDTV KNTAKLSDFLEVAVPIMGVPVPEAYLAKLCWIYTGNEVGELAF</th> <th>R D T I G K N T A K L S D F L E V A V P I MG V P V P E A Y L A K L C WI Y T G N E V G E L A F</th> <th>R D T I G K S N T K L S E F L Q I A A P V M C T P K P E E Y L L K L C W V M N S T D D C D V T F</th> <th>R D A I G I K V A K L S S F L E A A A P I MR T P V P E E Y L E K L C WMY T G D D N G E I K F</th> <th>R D V V G T K A A R L R D F V A L A A T L L N L P S P Q R Y L R D L G W V G T E T R R N R I R F</th> <th>R D V V G T K A A R L R D F V A L A A T L L N L P S P Q R Y L R D L G W V G T E T R R N R I R F</th> <th>R D S I G N K G A K L L T F L D V A A P L M C T P K P D E YL K S L C W M Y T A N D K G E I Q F</th> <th>R D S I G N K G A K L L T F L D I A A P L M C T P K P E E Y L K S L C W M Y T A N D K G E I Q F</th> <th></th>  |   | RDG akLflaapmpPeYilcwytgif    | R D H V G K A K C N L N P F L S V A C P MMKI V E P S E Y F G L F G WQ V S H D S F G N M V L        | R D N I G R D Q V R L C D Y V Q V A A P A MG V P I P E D Y L T K L C W V Y A A D D T G V V T F       | R D E V G K D S A Q L S T F L T V V C P I MG F P S P G L Y F Q K L G L F H H MG E E G D I V L       | R D H I G K S E A K L S E F L E I A G P I MG A P V P E E YL A R L C WV Y S G N E A G D I A F         | R D T V G K N T A K L S D F L E V A V P I MG V P V P E A YL A K L C WI Y T G N E V G E L A F        | RDTV KNTAKLSDFLEVAVPIMGVPVPEAYLAKLCWIYTGNEVGELAF                                      | R D T I G K N T A K L S D F L E V A V P I MG V P V P E A Y L A K L C WI Y T G N E V G E L A F       | R D T I G K S N T K L S E F L Q I A A P V M C T P K P E E Y L L K L C W V M N S T D D C D V T F     | R D A I G I K V A K L S S F L E A A A P I MR T P V P E E Y L E K L C WMY T G D D N G E I K F       | R D V V G T K A A R L R D F V A L A A T L L N L P S P Q R Y L R D L G W V G T E T R R N R I R F       | R D V V G T K A A R L R D F V A L A A T L L N L P S P Q R Y L R D L G W V G T E T R R N R I R F       | R D S I G N K G A K L L T F L D V A A P L M C T P K P D E YL K S L C W M Y T A N D K G E I Q F        | R D S I G N K G A K L L T F L D I A A P L M C T P K P E E Y L K S L C W M Y T A N D K G E I Q F     |   |
| 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8   |   | RDG akLflaapmpPeYilcwytgif(   | R D H V G K A K C N L N P F L S V A C P MMKI V E P S E Y F G L F G WQ V S H D S F G N M V L V      | R D N I G R D Q V R L C D Y V Q V A A P A MG V P I P E D Y L T K L C W V Y A A D D T G V V T F - (   | R D E V G K D S A Q L S T F L T V V C P I MG F P S P G L Y F Q K L G L F H H M G E E G D I V L G    | R D H I G K S E A K L S E F L E I A G P I MG A P V P E E Y L A R L C W V Y S G N E A G D I A F F (   | R D T V G K N T A K L S D F L E V A V P I MG V P V P E A YL A K L C WI Y T G N E V G E L A F F      | RDTV KNTAKLSDFLEVAVPIMGVPVPEAVLAKLCWIYTGNEVGELAFF                                     | R D T I G K N T A K L S D F L E V A V P I MG V P V P E A Y L A K L C WI Y T G N E V G E L A F F     | RDTIGKSNTKLSEFLQIAAPVMCTPKPEEYLLKLCWVMNSTDDCDVTF  | R D A I G I K V A K L S S F L E A A A P I MR T P V P E E Y L E K L C WMY T G D D N G E I K F L (   | R D V V G T K A A R L R D F V A L A A T L L N L P S P Q R Y L R D L G W V G T E T R R N R I R F V V   | R D V V G T K A A R L R D F V A L A A T L L N L P S P Q R V L R D L G W V G T E T R R N R I R F V V   | R D S I G N K G A K L L T F L D V A A P L M C T P K P D E YL K S L C W M Y T A N D K G E I Q F L (    | R D S I G N K G A K L L T F L D I A A P L M C T P K P E E Y L K S L C WMY T A N D K G E I Q F L C   |   |
|   |   | RDG akLflaapmpPeYllowyt gifQd | R D H V G K A K C N L N P F L S V A C P MMKI V E P S E Y F G L F G W Q V S H D S F G N M V L V Q D | R D N I G R D Q V R L C D Y V Q V A A P A MG V P I P E D Y L T K L C W V Y A A D D T G V V T F - Q S | R D E V G K D S A Q L S T F L T V V C P I MG F P S P G L Y F Q K L G L F H H MG E E G D I V L G Q D | R D H I G K S E A K L S E F L E I A G P I MG A P V P E E Y L A R L C W V Y S G N E A G D I A F F Q D | R D T V G K N T A K L S D F L E V A V P I MG V P V P E A Y L A K L C WI Y T G N E V G E L A F F Q D | RDTV KNTAKLSDFLEVAVPI MGVPVPEAYLAKLCWIYTGNEVGELAFFQD                                  | R D T I G K N T A K L S D F L E V A V P I MG V P V P E A Y L A K L C WI Y T G N E V G E L A F F Q D | R D T I G K S N T K L S E F L Q I A A P V M C T P K P E E Y L L K L C W V M N S T D D C D V T F Q D | R D A I G I K V A K L S S F L E A A A P I MR T P V P E E Y L E K L C WMY T G D D N G E I K F L Q D | R D V V G T K A A R L R D F V A L A A T L L N L P S P Q R Y L R D L G W V G T E T R R N R I R F V Q D | R D V V G T K A A R L R D F V A L A A T L L N L P S P Q R V L R D L G W V G T E T R R N R I R F V Q D | R D S I G N K G A K L L T F L D V A A P L M C T P K P D E Y L K S L C W M Y T A N D K G E I Q F L Q D | R D S I G N K G A K L L T F L D I A A P L M C T P K P E E Y L K S L C WMY T A N D K G E I Q F L Q D |   |

|                                      | F. graminearum                                 | E. laricicola                                    | E. polonica                                    | K. capensis                                  | C. adiposa   | H. omanensis  | H. moniliformis   | T. punctulata  | C. manginecans   | C. fimbriata   | B. rouxiae   | B. basicola  |  |
|--------------------------------------|--|--|--|--|--|---|---|--|--|--|--|--|--|
| ъ                                    | P  | V S  | V S  | P  | L P  | L<br>P  | L<br>P  | н<br>Р   | ΥP   | νP   | н<br>Р   | P  |  |
| RF                                   | RI   | RΕ   | RΕ   | RΕ   | RΕ   | RΕ  | RΕ  | RΕ   | RΕ   | RΕ   | RΕ   | RΕ   |  |
| Þ                                    | P  | P  | P  | P  | P  | P   | P   | P  | P  | P  | P  | P  |  |
| NA                                   | ΝA   | ΝA   | ΝA   | ΝA   | ΝA   | ΝA  | ΝA  | ΝA   | ΝA   | ΝA   | ΝA   | ΝA   |  |
| ΥI                                   | ΥI   | ΥI   | ΥI   | ΥI   | ΥI   | ΥI  | ΥI  | ΥI   | ΥI   | ΥI   | ΥI   | ΥI   |  |
| -                                    | E V  | M  | MN   | L  | L  | L   | L   | L  | L  | L  | M  | M  |  |
| R                                    | C R I  | R  | R  | R  | R  | R   | CR 1  | R  | R  | R  | R  | C R  |  |
| d d                                  | κE   | D  | D  | ð  | K D  | Ε   | ж<br>Н  | E  | D  | Ď  | D  | K D  |  |
| r H                                  | R  | R  | R  | R  | R  | R   | R   | R  | K  | K  | R  | R  |  |
|                                      | QI   | QД   | QD   | QΑ   | ΗS   | ΗS  | ΗS  | ΗE   | RG   | RG   | RΕ   | RΕ   |  |
| v k                                  | VK   | VK   | VK   | LK   | VK   | VK  | VK  | VK   | VK   | VK   | I R  | I R  |  |
|                                      | GI   | AI   | AI   | N  | RE   | U   | D   | K  | AF   | A  | A  | AF   |  |
| μ.                                   | C R  | TH I   | TH I   | Ê  | N  | 1   | 1   | R  | ĩ  | ŝ  | F  | F  |  |
| P                                    | P<br>G   | PN   | P  | 52   | P G  | P G   | P<br>G  | Ģ  | PH   | ΡH   | Ð  | Ð  |  |
|                                      | H  | н<br>И   | н<br>И   | I<br>S                                       | ГС   | ГС  | I C   | Ð  | MD   | MD   | Ð  | IJ   |  |
| NN                                   | NN   | NN   | NN   | NN   | ΝN   | NN  | ΝN  | ΝN   | ΝN   | NN   | NN   | ΝN   |  |
| e                                    | Ħ  | μ  | Η  | Η  | н  | Ħ   | Η   | Η  | U  | D  | Η  | Ħ  |  |
| S                                    | 6/2  | 62   | 62   | 6/2  | 6/2  | 62  | 6/2   | 6/2  | 62   | 62   | 62   | 62   |  |
| 1                                    | QV   | RV   | RV   | RI   | RΙ   | RI  | RI  | CI   | W  | W  | RI   | RI   |  |
| LG                                   | LG   | LG   | LG   | LG   | LG   | LG  | LG  | LG   | LG   | LG   | LG   | LG   |  |
|                                      | RO   | ΚI   | K  | RS   | KΒ   | RB  | RI  | K  | E  | E  | K  | K  |  |
|                                      |  | ~  | 20   |  |  | ~   | 20  | 22   | 20   | 22   |  | 0  |  |
| MI                                   | M  | C M H  | R WH   | WB   | Č M H  | Č M F   | R W F   | K W H  | R M F  | RWB  | Q<br>M<br>H  | QWH  |  |
| Mr e I                               | WN MB  | WR E   | RWRE   | WK E   | UWR E  | <b>WKE</b>  | RWKEB   | KWREB  | R WR F I   | RWRFI  | QWREI  | QWRE   |  |
| Wr e E                               | WN ME H  | WREDS  | RWREES   | WKEEE  | UMREEDI  | WKEES :   | RWKEBSI   | KWREEPI  | R WR F E T   | RWRFET   | QWREES.  | QWREES.  |  |
| WreE                                 | WN MEHPD                                       | WREBSTG  | RWREESTS                                       | WKEBECS                                      | WREBDEI  | <b>WKEBSET</b>  | RWKEBSET  | KWREEPEN   | R WR F E T S K   | R WR F E T S K   | QWREBSAS   | QWREESAS   |  |
| WreE vR                              | WN MEHPDIR                                     | <b>WREBSTGVR</b>                                 | RWREBSTSIR                                     | WKEBECSVR                                    | WREBDEIVR  | R WKEBSETVR   | RWKEBSETVR  | KWREBPENVR   | R WRFBTSKIR  | R WR F E T S K I R   | QWREBSASVR   | QWREESASVR   |  |
| WreE vR                              | WNMEHPDIRTY                                    | R WREESTGVREF                                    | R WREBSTSIREF                                  | WKEBECSVRLH                                  | WREEDEIVRIF  | R WKEBSETVRAF   | RWKEESETVRAF  | K WREEPENVRMH  | R WR F E T S K I R N H   | RWRFBTSKIRDH   | Q WREESASVRTH  | QWREESASVRTH   |  |
| WreE vR Yk                           | WNMEHPDIRTYYK                                  | WREESTGVREFYK                                    | R WREESTSIREFYK                                | WKEEECSVRLHYK                                | WREBDEIVRIFYK  | R WKEESETVRAFYK   | RWKEESETVRAFYK  | K WREEPENVRMHYK  | R WR F E T S K I R N H Y Q   | RWRFETSKIRDHYQ   | Q WREESASVRTHYQ  | Q WREESASVRTHYQ  |  |
| WreE vR Yk                           | WNMEHPDIRTYYKKI                                | WREESTGVREFYKT(                                  | RWREESTSIREFYKK                                | WKEBECSVRLHYKEI                              | WREEDEIVRIFYKE (   | WKEESETVRAFYKE (  | RWKEESETVRAFYKE(  | K WREEPENVRMHYKKI  | R WR F E T S K I R N H Y Q K T   | RWRFETSKIRDHYQK  | Q WREESASVRTHYQEI  | Q WR E E S A S V R T H Y Q E I   |  |
| WreE vR Yk a                         | WNMEHPDIRTYYKKMA                               | R WREESTGVREFYKTQA                               | R WREESTSIREFYKKQA:                            | WKEEECSVRLHYKEKA:                            | WREEDEIVRIFYKEQA:  | WKEESETVRAFYKEQS:   | R WKEESETVRAFYKEQS:   | K WREEPENVRMHYKKLA:  | R WRFETSKIRNHYQKTA   | RWRFETSKIRDHYQKTA  | Q WREESAS VRTHYQEL n :   | QWREESASVRTHYQELA:   |  |
| WreE vR Yk a                         | WN MEHPDIRTYYKK MADD                           | WREESTGVREFYKTQAET                               | R WREESTSIREFYKKQAET                           | WKEEECSVRLHYKEKADL                           | WREEDEIVRIFYKEQADA   | WKEESETVRAFYKEQSEN  | R WKEESETVRAFYKEQSEA  | K WREEPENVRMHYKKLAED   | R WR F E T S K I R N H Y Q K T A T D   | RWRFETSKIRDHYQKTATD  | Q WREESAS VRTHYQELnnn  | Q WREBSAS VRTHYQELAIS  |  |
| WreE vR Yk a yK                      | WN MEHPDIRTYYKK MADDIK                         | RESTGVREFYKTQAETYK                               | R WREESTSIREFYKKQAETYK                         | WKEEECSVRLHYKEKADLFK                         | I WREEDEI VRIFYKEQADAYK  | R WKEESETVRAFYKEQSENYK  | R WKEESETVRAFYKEQSEAYK  | K WREEPENVRMHYKKLAEDYK   | R WR F E T S K I R N H Y Q K T A T D Y K   | R WR F E T S K I R D H Y Q K T A T D Y K   | Q WR E E S A S V R T H Y Q E L n n n n                             | QWREESASVRTHYQELAISYK  |  |
| WreEvRYk ayk                         | WN MEHPDIRTYYKK MADDIKEE                       | X WREESTGVREFYKTQAETYKKS                         | R WREESTSIREFYKKQAETYKKS                       | WKEEECSVRLHYKEKADLFKKE                       | NREEDEI VRIFYKEQADAYKRN  | r wkees tvrafykeqs en ykqn  | R WKEESETVRAFYKEQSEAYKQN  | K WREEPENVRMHYKKLAEDYKTQ   | R WR F E T S K I R N H Y Q K T A T D Y K E N   | R WR F E T S K I R D H Y Q K T A T D Y K E N                                     | Q WR E E S A S V R T H Y Q E L n n n n n n                         | Q WR E E S A S V R T H Y Q E L A I S Y K K I                                     |  |
| cWreE vR Yk a yK fr                  | WN MEHPDIRTYYKK MADDIKEEHH                     | R WR E E S T G V R E F Y K T Q A E T Y K K S F M | R WREESTSIREFYKKQAETYKKSF1                     | WKEEECS VRLHYKEKADLFKKEFI                    | N W R E E D E I V R I F Y K E Q A D A Y K R N F M                            | X WKEESETVRAFYKEQSENYKQNFM  | R WKEESETVRAFYKEQSEAYKQNF1  | K WREEPENVRMHYKKLAEDYKTQF1   | R WR F E T S K I R N H Y Q K T A T D Y K E M F M                                       | R WRFETSKIRDHYQKTATDYKEMF1   | Q WREESAS V R THYQEL nnnnnn n                                      | Q WR E E S A S V R T H Y Q E L A I S Y K K I F M                                 |  |
| :WreE vR Yk a yK fm                  | WN MEHPDIRTYYKK MADDIKEEHKR                    | WREESTGVREFYKTQAETYKKSFME:                       | R WREESTSIREFYKKQAETYKKSFME:                   | WKEBECSVRLHYKEKADLFKKEFLE                    | WREEDEIVRIFYKEQADAYKRNFMK.   | X WKEESETVRAFYKEQSENYKQNFMN   | R WKEESETVRAFYKEQSEAYKQNFMN   | K WR E E P E N V R MH Y K K L A E D Y K T Q F M K .                                | R WR F E T S K I R N H Y Q K T A T D Y K E M F M L                                     | R WR FETSKIRDHYQKTATDYKEMFML   | Q WR E E S A S V R THYQEL nnnnnnnn                                 | QWREESASVRTHYQELAISYKKIFME.  |  |
| :WreEvRYk ayK fm                     | WN MEHPDIRTYYKK MADDIKEEHKRLY                  | X WREESTGVREFYKTQAETYKKSFMEMY                    | R WREESTSIREFYKKQAETYKKSFMEMY                  | WKEEECS VRLHYKEKADLFKKEFLEDH                 | NREEDEI VRIFYKEQADAYKRNFMKAY   | X WKEESETVRAFYKEQSENYKQNFMNTH   | R WKEESETVRAFYKEQSEAYKQNFMNTH   | K WR E E P E N V R MH Y K K L A E D Y K T Q F MK A F                               | R WR F E T S K I R N H Y Q K T A T D Y K E M F M L T Y                                 | R WR F E T S K I R D H Y Q K T A T D Y K E M F M L T Y                           | Q WR E E S A S V R T H Y Q E L n n n n n n n n n n n n             | Q WREESAS VRTHYQELAISYKKIFMEAF   |  |
| r WreE v RYk a y Kfm Pd              | WN MEHPDIRTYYKKMADDIKEEHKRLYPD                 | WREESTGVREFYKTQAETYKKSFMEMYPD                    | R WREESTSIREFYKKQAETYKKSFMEMYPD                | WKEEECS VRLHYKEKADLFKKEFLEDHPN               | WREEDEI VRIFYKEQADAYKRNFMKAYPD   | UWKEESETVRAFYKEQSENYKQNFMNTHPD  | R WKEESETVRAFYKEQSEAYKQNFMNTHPD   | K WR E E P E N V R MH Y K K L A E D Y K T Q F MK A F P D                           | R WR F E T S K I R N H Y Q K T A T D Y K E M F M L T Y P D                             | R WR F E T S K I R D H Y Q K T A T D Y K E M F M L T Y P D                       | Q WR E E S A S V R T H Y Q E L n n n n n n n n n n n n n n n       | Q WREESAS VRTHYQELAIS YKKIF MEAFPD   |  |
| rWreE vR Yk a yK fm PdYg             | WN MEHPDIRTYYKK MADDIKEEHKRLYPDYQ              | WREESTGVREFYKTQAETYKKSFMEMYPDYR                  | R WREESTSIREFYKKQAETYKKSFMEMYPDYR              | WKEBECS VRLHYKEKADLFKKEFLEDHPNYQ             | N WREEDEI VRIFYKEQADAYKRNFMKAYPDY  | X WKEESETVRAFYKEQSENYKQNFMNTHPDYQ   | R WKEESETVRAFYKEQSEAYKQNFMNTHPDYQ   | K WR E E P E N V R MH Y K K L A E D Y K T Q F MK A F P D Y Q                       | R WR F E T S K I R N H Y Q K T A T D Y K E M F M L T Y P D Y Q                         | R WR F E T S K I R D H Y Q K T A T D Y K E M F M L T Y P D Y Q                   | Q WR E E S A S V R T H Y Q E L n n n n n n n n n n n n n n n n n   | Q WREESAS VRTHYQELAIS YKKIF MEAFPDYQ   |  |
| cWreE vR Yk a yK fm PdYqYr           | WN MEHPDIRTYYK KMADDI KEEHKRLYPDYQYR           | X WREESTGVREFYKTQAETYKKSFMEMYPDYRYK              | R WREESTSIREFYKKQAETYKKSFMEMYPDYRYK            | WKEEECS VRLHYKEKADLFKKEFLEDHPNYQYA           | N WREEDEI VRIFYKEQADAYKRNFMKAYPDYQY  | X WKEESETVRAFYKEQSENYKQNFMNTHPDYQY  | R WKEESETVRAFYKEQSEAYKQNFMNTHPDYQY  | K WREEPENVRMHYKKLAEDYKTQFMKAFPDYQYK  | R WR F E T S K I R N H Y Q K T A T D Y K E M F M L T Y P D Y Q Y K                     | R WR F E T S K I R D H Y Q K T A T D Y K E M F M L T Y P D Y Q Y K               | Q WREES AS VRTHYQEL nnnnnnnnnnnnnnnn                               | Q WREESAS VRTHYQELAISYKKIFMEAFPDYQYK   |  |
| WreE vR Yk a yK fm PdYqYrP.          | WN MEHPDIRTYYKK MADDIKEEHKRLYPDYQYRPI          | X WREESTGVREFYKTQAETYKKSFMEMYPDYRYKPI            | R WREESTSIREFYKKQAETYKKSFMEMYPDYRYKPI          | WKEBECS VRLHYKEKADLFKKEFLEDHPNYQYRPI         | N W R E E D E I V R I F Y K E Q A D A Y K R N F M K A Y P D Y Q Y R P I      | X WKEESETVRAFYKEQSENYKQNFMNTHPDYQYRPI   | R WKEESETVRAFYKEQSEAYKQNFMNTHPDYQYRP1   | K WR E E P E N V R MH Y K K L A E D Y K T Q F MK A F P D Y Q Y R P I               | R WR F E T S K I R N H Y Q K T A T D Y K E M F M L T Y P D Y Q Y R P I                 | R WRFETSKIRDHYQKTATDYKEMFMLTYPDYQYRPI  | Q WREES AS VRTHYQEL nnnnnnnnnnnnnnnn                               | Q WREESAS VRTHYQELAIS YKKIFMEAFPDYQYRP   |  |
| r WreE v RYk a y Kfm PdYqYrPRk       | WN MEHPDIRTYYKK MADDIKEEHK RLYPDYQYRPRK        | N WREESTGVREFYKTQAETYKKSFMEMYPDYRYKPRK           | R WREESTSIREFYKKQAETYKKSFMEMYPDYRYKPRK         | WKEEECSVRLHYKEKADLFKKEFLEDHPNYQYRPRR         | N WR E E D E I V R I F Y K E Q A D A Y K R N F M K A Y P D Y Q Y R P R K     | X WKEESETVRAFYKEQSENYKQNFMNTHPDYQYRPRK  | R WKEESETVRAFYKEQSEAYKQNFMNTHPDYQYRPRN  | K WR E E P E N V R MH Y K K L A E D Y K T Q F MK A F P D Y Q Y R P R K             | R WR F E T S K I R N H Y Q K T A T D Y K E M F M L T Y P D Y Q Y R P R K               | R WRFETSKI RDHYQKTATDYKEMFMLTYPDYQYRPRK  | Q WR E E S A S V R T H Y Q E L n n n n n n n n n n n n n n n n n n | Q WREESAS VRTHYQELAISYKKIF MEAFPDYQYRPRK   |  |
| r WreE vR Yk a yK fm PdYqYrPRka      | WN MEHPDIRTYYKK MADDIKEEHKRLYPDYQYRPRKSR       | N WREESTGVREFYKTQAETYKKSFMEMYPDYRYKPRKPG         | R WREESTSIREFYKKQAETYKKSFMEMYPDYRYKPRKPG       | WKEEECS VRLHYKEKADLFKKEFLEDHPNYQYRPRRS R     | N WR E E D E I V R I F Y K E Q A D A Y K R N F M K A Y P D Y Q Y R P R K A G | X WK E E S E T V R A F Y K E Q S E N Y K Q N F MN T H P D Y Q Y R P R K A G     | R WKEESETVRAFYKEQSEAYKQNFMNTHPDYQYRPRNAG  | K WR E E P E N V R MH Y K K L A E D Y K T Q F MK A F P D Y Q Y R P R K A A         | R WR F E T S K I R N H Y Q K T A T D Y K E M F M L T Y P D Y Q Y R P R K A N           | R WRFETSKIRDHYQKTATDYKEMFMLTYPDYQYRPRKAN   | Q WR E E S A S V R T H Y Q E L n n n n n n n n n n n n n n n n n n | Q WREESAS VRTHYQELAIS YKKIFMEAFPDYQYRPRKAN                                       |  |
| :WreE vR Yk a yK fm PdYqYrPRkae      | WN MEHPDI R TYYKK MADDI KEEHKRLYPDYQYRPRKS RER | N WREESTGVREFYKTQAETYKKSFMEMYPDYRYKPRKPGER       | R WREESTSIREFYKKQAETYKKSFMEMYPDYRYKPRKPGEK     | WKEEECS VRLHYKEKADLF KKEFLEDHPNYQYRPRRSRER   | N WREEDEI VRIFYKEQADAYKRNFMKAYPDYQYRPRKAGEK                                  | N WK E E S E T V R A F Y K E Q S E N Y K Q N F MN T H P D Y Q Y R P R K A G E K | R WK E E S E T V R A F YK E Q S E A YK Q N F MN T H P D Y Q YR P R N A G A K        | K WR E E P E N V R MHYK K L A E D Y K T Q F MK A F P D Y Q Y R P R K A A E K       | R WR F E T S K I R N H Y Q K T A T D Y K E MF ML T Y P D Y Q Y R P R K A N Q R         | R WR F E T S K I R D H Y Q K T A T D Y K E M F M L T Y P D Y Q Y R P R K A N Q R | Q WR E E S A S VR THYQEL nnnnnnnnnnnnnnnnnnnnnnnn                  | Q WR E E S A S V R T H Y Q E L A I S Y K K I F M E A F P D Y Q Y R P R K A N E K |  |
| r WreE vR Yk a yK fm. PdYqYrPRkae kı | WN MEHPDI RTYYKK MADDI KEEHKRLYPDYQYRPRKSRERR  | N WREESTGVREFYKTQAETYKKSFMEMYPDYRYKPRKPGERKK     | R WREESTSIREFYKKQAETYKKSFMEMYPDYRYKPRKPGEKKK   | WKEBECS VRLHYKEKADLFKKEFLEDHPNYQYRPRRSRERRA  | N WREEDEI VRIFYKEQADAYKRNFMKAYPDYQYRPRKAGEKKK                                | N WKEESETVRAFYKEQSENYKQNFMNTHPDYQYRPRKAGEKKH                                    | R WK E E S E T V R A F Y K E Q S E A Y K Q N F MN T H P D Y Q Y R P R N A G A K K H | K WR E E P E N V R MH Y K K L A E D Y K T Q F MK A F P D Y Q Y R P R K A A E K K H | R WR F E T S K I R N H Y Q K T A T D Y K E MF ML T Y P D Y Q Y R P R K A N Q R K K     | R WR FETS KI RDHYQKTATDYKE MF ML TYPDYQYRPRKANQR K K                             | Q WR E E S A S V R T H Y Q E L n n n n n n n n n n n n n n n n n n | QWREESASVRTHYQELAISYKKIF MEAFPDYQYRPRKANEKKK                                     |  |
| r WreE vR Yk a yK fm PdYqYrPRkaekrR  | WN MEHPDIRTYYKK MADDIKEEHKRLYPDYQYRPRKSRERRR   | N WREESTGVREFYKTQAETYKKSFMEMYPDYRYKPRKPGERKRR:   | R WREESTSIREFYKKQAETYKKSFMEMYPDYRYKPRKPGEKKRR: | WKEEECS VRLHYKEKADLFKKEFLEDHPNYQYRPRRSRERRR. | N WREEDEI VRIFYKEQADAYKRNFMKAYPDYQYRPRKAGEKKRR:                              | N WKEESETVRAFYKEQSENYKQNFMNTHPDYQYRPRKAGEKKKR:                                  | R WKEESETVRAFYKEQSEAYKQNFMNTHPDYQYRPRNAGAKKKR:                                      | K WREEPENVRMHYKKLAEDYKTQFMKAFPDYQYRPRKAAEKKHR:                                     | R WR F E T S K I R N H Y Q K T A T D Y K E MF ML T Y P D Y Q Y R P R K A N Q R K R R : | R WR FETSKIRDHYQKTATDYKEMFMLTYPDYQYRPRKANQRKRR:                                  | Q WR E E S A S V R TH Y Q E L n n n n n n n n n n n n n n n n n n  | QWREESAS VRTHYQELAIS YKKIFMEAFPDYQYRPRKANEKKRR:                                  |  |

A *MAT1-1-1* α-domain Neighbour-Joining 1000 bootstraps





- The mating type loci of *Berkeleyomyces basicola* and *B. rouxiae* were characterized.
- Both species were found to have the genes required for heterothallic mating.
- The sexual states of neither species have been observed in nature and could not be induced in laboratory crosses.
- Primers were designed that can distinguish the two mating types in multiplex PCR.