

>lcl1A6XKD2_9PEZI/6-138 (A6XKD2)
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>lcl1A7LM72_FUSOX/47-179 (A7LM72)
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>lcl1Q3T4F0_RHIOR/50-182 (Q3T4F0)
FLAMLVGLDGDGYIATDIIISLDLIDINYSVKIGRVNKLITSRITLFPFNREAQFDKVMFILQNWIVG
FTIAEGSFVVDICFSLKQELLFEAFKIIFYSKFMVSQKVVDFSFYKLTQYNLWLNIRE
>lcl1Q6UVR9_PSEAK/23-155 (Q6UVR9)
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>lcl1Q6UVV4_PSEAK/49-181 (Q6UVV4)
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>lcl1Q9T2T0_MARPO/24-156 (Q9T2T0)
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>lcl1Q3T4A6_SMICU/31-163 (Q3T4A6)
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FIEAEGNFKLISRQFIQKYLIIKTYLPLHYRISNNLKHFKENKLLSYNIWYNSFKV
>lcl1Q950P9_9FUNG/4-136 (Q950P9)
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>lcl1YMRFL_YEAST/85-217 (P03881)
FYKLVGFTDGDGSIYIKFYGRMDKACLEKIRNMNMPNSFEMLVNSQIVTFPKYYSYKWKMMAMIIWILG
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>lcl1A5J038_GIBZE/134-266 (A5J038)
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>lcl1YMN3_PODAN/143-275 (P15563)
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>lcl1Q35928_SCLSC/134-266 (Q35928)
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>lcl1Q7YEU6_SACSE/415-547 (Q7YEU6)
MHSFFVGLFEGDGSIQVNRILVILNMMNLTIMNYGTMKINKVMNNSKFIIDFPKRYQLAFMKSMFENWVFG
FIEAEGCFNRNYSFSSQKMLMLFLKNYFTYILEVYMFICDFFNKYKLYQFNWNNYKCH
>lcl1Q6DN58_KLULA/138-270 (Q6DN58)
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>lcl1O20960_CRYPA/124-256 (O20960)
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>lcl1Q00IP1_OLTVI/28-160 (Q00IP1)
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>lcl1Q36472_PODAN/60-192 (Q36472)
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>lcl1Q6U7W7_CRIPE/39-171 (Q6U7W7)
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>lcl1A5J035_GIBZE/133-265 (A5J035)
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>lcl1Q8HHC4_CRYPA/181-313 (Q8HHC4)
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>lcl1Q9XKY8_AGRAE/8-140 (Q9XKY8)
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>lcl1Q6V9C2_PENMA/88-220 (Q6V9C2)
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>lcl1Q85MA9_9FUNG/42-174 (Q85MA9)
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>lcl1Q8W9R2_MESVI/5-137 (Q8W9R2)

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>lcl|Q33761_ALLMA/84-216 (Q33761)
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>lcl|Q33639_AGRAE/108-240 (Q33639)
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>lcl|Q02692_PODAN/138-270 (Q02692)
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>lcl|A7UG12_PHANO/102-234 (A7UG12)
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>lcl|Q35135_NEUCR/136-268 (Q35135)
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>lcl|O47564_AGRAE/110-242 (O47564)
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>lcl|A5J058_GIBZE/104-236 (A5J058)
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>lcl|Q3T4F6_RHIOR/77-209 (Q3T4F6)
FQQVLVGTGDSGSFVSLTLTFKINLRALYYIKQKQVGSVSVSFRIRDILPFPKYFNYAKFKSAYASWLIG
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>lcl|A5J042_GIBZE/12-144 (A5J042)
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>lcl|A5J063_GIBZE/116-248 (A5J063)
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>lcl|Q8SHQ9_TRIRE/1-133 (Q8SHQ9)
MARPQGGFSDGEATFTNFYIITLDLPLLALIQKYNQQLQILTISSAVIKFPLVDYLLFKQVYTYWLAG
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>lcl|A5J046_GIBZE/53-185 (A5J046)
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>lcl|MBI3_DEBHA/262-394 (A9RAG7)
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>lcl|Q5EM51_9FUNG/8-140 (Q5EM51)
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>lcl|Q950N2_9FUNG/92-224 (Q950N2)
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FVEGDGFSISKNSYFISQQLIYIEIKNLFQVLSLEITSILPLFYSRKQIDDFRFFIVWQG
>lcl|Q3T4D3_SMICU/10-142 (Q3T4D3)
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>lcl|O20958_CRYPA/58-190 (O20958)
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>pdb|2AB51A|pdb|2AB51A|gi|175766112/16-148 [Saccharomyces cerevisiae] Bi3 Laglidag Maturase
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>lcl|Q32X64_AGRAE/34-166 (Q32X64)
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>lcl|O47502_VENIN/98-230 (O47502)
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And Group I Intron Splicing Factor
TYAYLVGLFEGDGYFTELIELDVQLIYKIKKIGIGIVSFALRIRDFLPPKQDYDLRFRNALLAWLIG
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>lcl|PAN3_X55026.1/55-187
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>lcl|Q9B6E3_YARLI/119-251 (Q9B6E3)
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>lcl|Q950N7_9FUNG/30-162 (Q950N7)

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>lcl|Q8HIS8_MONBE/8-140 (Q8HIS8)
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>lcl|AI2_USTMA/255-387 (Q08X8)
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>lcl|Q6U7Z6_CRIPE/105-237 (Q6U7Z6)
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>lcl|Q6V9C4_PENMA/91-223 (Q6V9C4)
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>lcl|Q02690_PODAN/78-210 (Q02690)
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>lcl|O20959_CRYPA/42-174 (O20959)
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>lcl|YMC1_SCHPO/107-239 (P22191)
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>lcl|Q3T4A5_SMICU/96-228 (Q3T4A5)
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>lcl|A5J033_GIBZE/141-273 (A5J033)
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>lcl|Q950N5_9FUNG/95-227 (Q950N5)
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>lcl|Q36232_WILSA/55-187 (Q36232)
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>lcl|Q85MA7_9FUNG/40-172 (Q85MA7)
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FIEGEGTFGIKNSMAQFLTRAISTPIIHVVITYSYADYLLPFFLARKYVDFYLWAIIVIC
>lcl|Q950N0_9FUNG/21-153 (Q950N0)
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>lcl|A5J050_GIBZE/93-225 (A5J050)
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FVEGEGYFSTNSLKFQIIVLEAIQKYFMAQLVITNVIIPFFDKKKFKDYVDWKLILD
>lcl|A6XKD1_9PEZI/6-138 (A6XKD1)
FIEWFSGVDGAEFCFHIKEFVKLNVLVFKIHEGTGIGRIAITFEVGSILIDLPKVLDLFSFKKAFYKLLG
LFEFGDSFVIQTPKFEIELKLLNEIQKYLIDQLKAKITGDIFLNNDKSKDFEICTICES
>lcl|B2XX70_9MYCE/18-150 (B2XX70)
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>lcl|C5GYN7_AJEDE/76-208 (C5GYN7)
FEQWLVGFTDGDGNSITGLSFKLNRLVNYIKKEGVGSITKQYIIRDILPFPKYFDYIKFKKALASWLVG
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>lcl|Q3T4A8_SMICU/129-261 (Q3T4A8)
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>lcl|Q8SMI8_9CHLO/4-136 (Q8SMI8)
TDKVVVGFVDGDFKIIICFVVSQSVNVLALKKKGGCSVNRKVSCKIILPFPKLDKDFQILYEDLTDWLTG
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>lcl|Q8WL00_9CHLO/14-146 (Q8WL00)
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>lcl|Q8M0D4_AMOPA/78-210 (Q8M0D4)
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>lcl|Q02695_PODAN/86-218 (Q02695)
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>lcl|A7LCP3_YEAS7/92-224 (A7LCP3)
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>lcl|Q950N9_9FUNG/24-156 (Q950N9)
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>lcl|Q7YEV1_SACSE/73-205 (Q7YEV1)
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>lcl|Q85QA2_CANGA/74-206 (Q85QA2)
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>lcl|Q8HMZ3_SCHJP/74-206 (Q8HMZ3)
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>lcl|C5K415_AJEDE/48-180 (C5K415)
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>lcl|A5J062_GIBZE/80-212 (A5J062)
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>lcl|YMC2_SCHPO/86-218 (P22190)
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>lcl|Q6V9C3_PENMA/93-225 (Q6V9C3)
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>lcl|C5GYN8_AJEDE/38-170 (C5GYN8)
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>lcl|Q33796_EMENI/79-211 (Q33796)
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>lcl|Q539C3_OPHUL/70-202 (Q539C3)
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>lcl|Q8HQ86_SCHOT/87-210 (Q8HQ86)
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>lcl|Q6UVQ9_PSEAK/61-193 (Q6UVQ9)
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>lcl|Q3T4B0_SMICU/19-151 (Q3T4B0)
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>lcl|A5J061_GIBZE/83-215 (A5J061)
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>lcl|O47565_AGRAE/43-175 (O47565)
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>lcl|Q3T4A9_SMICU/33-165 (Q3T4A9)
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>lcl|Q2LCQ3_DICCI/19-151 (Q2LCQ3)
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>lcl|Q3ZIZ1_PSEAK/13-140 (Q3ZIZ1)
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>lcl|MBI4_YEAST/404-536 (P03879)
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>lcl|Q3T4F4_RHIOR/74-206 (Q3T4F4)
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>lcl|Q8M352_SACCA/364-496 (Q8M352)
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>lcl|A12_DEBHA/409-541 (A9RAH7)
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>lcl|Q3ZEG5_EPIFL/135-267 (Q3ZEG5)
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>lcl|A5J048_GIBZE/61-193 (A5J048)
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>lcl|Q3T4F5_RHIOR/86-218 (Q3T4F5)
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>lcl|Q35136_NEUCR/60-192 (Q35136)
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>lcl|Q6U7Z4_CRIPE/75-207 (Q6U7Z4)
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>lcl|Q3T4B1_SMICU/24-156 (Q3T4B1)
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>lcl|A14_USTMA/264-396 (Q0H8Y0)
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>lcl|Q6U7Z5_CRIPE/65-197 (Q6U7Z5)

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>lcl|Q2LCQ1_DICCI/37-169 (Q2LCQ1)
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>lcl|A15B_YEAST/88-220 (Q9ZZX0)
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>lcl|Q3ZEH1_EPIFL/83-215 (Q3ZEH1)
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>lcl|Q3T4A7_SMICU/75-207 (Q3T4A7)
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>lcl|A7KCU1_PLEOS/97-229 (A7KCU1)
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>lcl|Q8HIS7_MONBE/64-196 (Q8HIS7)
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>lcl|B8R1A7_VOLCA/92-224 (B8R1A7)
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>lcl|Q02673_PODAN/40-172 (Q02673)
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>lcl|Q6U7X9_CRIFE/112-244 (Q6U7X9)
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>lcl|B3V4M7_OEDCA/9-141 (B3V4M7)
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>lcl|Q3ZIZ2_PSEAK/49-181 (Q3ZIZ2)
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>lcl|Q950M1_9FUNG/122-254 (Q950M1)
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>lcl|A15_USTMA/294-426 (Q0H8Y1)
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>lcl|Q02679_PODAN/54-186 (Q02679)
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>lcl|Q6ED53_CANZE/513-645 (Q6ED53)
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>lcl|A5J077_GIBZE/52-184 (A5J077)
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>lcl|Q3T4B2_SMICU/82-214 (Q3T4B2)
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>lcl|Q8HIS6_MONBE/14-146 (Q8HIS6)
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>lcl|Q02687_PODAN/89-221 (Q02687)
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>lcl|O21044_DICDI/9-141 (O21044)
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>lcl|VS73/4-136 A 0|gi 0
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>lcl|HJE2_AF447590.1|/5-137
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>gi1257097864|gb|ACV41152.1|/186-318 ribosomal protein 3/homing endonuclease-like fusion protein [Grosmanina piceiperda]
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FTEGEGCFVSVSLIFQITQIVLMQNIKFLAVDILVTEKVIIPFFESLKLKNFTDFSKAADI
>gi134538660|gb|AAQ74268.1|/39-171 intronic ORF at intron 1 of nad4 [Moniliophthora perniciosa]
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>gi1466464|gb|AAC48982.1|/134-266 ORF1 [Sclerotinia sclerotiorum]
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>gi1156106283|gb|ABU49446.1|/102-234 unknown [Phaeosphaeria nodorum SN15]
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FVSAEGNFVDRQLRFRISQLMLQKIVEYLSISLITVNLVPPFDEIKLHDYLDWCKIHS
>gi186142508|gb|ABC86623.1|/134-266 LAGLIDADG endonuclease [Gibberella zeae]
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>gi17159925|emb|CAA38767.2|/143-275 Dod ND3 i1 grp IC protein [Podospora anserina]
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