

A

atgccgaacgctgctatcgcagctgtaccgcaacaacccccgccttcagcttcaaattcg 20
M P N A A I A A V P Q Q P P P S A S N S
gcatttgaccaggacaaagaccacagtgtgatgagtcctggctggctgtcgatagtgat 40
A F D Q D K D H S A D E S W S A V D S D
gccggctcctgctcaaaatggatcctcgcgtggcttgaacgcaggcggccactcacagtc 60
A G P A Q N G S S R G L K R R R P L T V
tcgtaagtcaaccgcccgtccccggcataatccgaccagttcttcctgccctacagtgtct 61
S
tgcagtgcttgcaatgccttgcaaccttcttgcataaccatagacctaccgcgtccctct
cggttccctcttttagacgctagattgacaagtctaggtgtgaattatgcaagcagcgcaa 69
C E L C K Q R K
ggttaaatgcggtatgttctgtggatcctgtccttgtcctggatctgactggcgctcta 72
V K C
gatcgagctcaaccaagctgtggatgggtgtacacggaatggtcaggtgtgtgagtacaag 92
D R A Q P S C G W C T R N G Q V C E Y K
gaaagaaagaagccccggccttcgtgcagggtacggaagagctagagcaacgccttaggt 111
E R K K P G L R A G Y G K E L E Q R L
acgggattccccggttacgacctatgcaccttctcattgacatttaatatgacagactggag 115
D R L E
gatatcatccaggcgcaagctcgtctcattgagacgcataatccttcaaggcgagccgcg 135
D I I Q A Q A R L I E T H I L Q G Q P R
ctctcgatgtcgaatgatctacaccagcaaggccctatcgtatagctcacccctcagag 155
L S M S N D L H Q Q G P L S Y S S P S E
ccttctgcagcacatgggcccagtcgcgaaatccgttctatttccatgagccgtcatct 175
P S A A H G P S P R N P F Y F H E P S S
gtgccctcagctccacgtccgcccggagcctgtcactactagtccaacggacatgtcggt 195
V P S A P R P P E P V T T S P T D M S V
aaaaactctatccagaaccaaatacccggtgctctccctcagtaacgcccttgccacat 215
K N S I Q N Q I T G A L P S V T P L P H
ataacgaacaccacgccgcagaacgactacaacgataacgagtcatccttaaaagtacca 235
I T N T T P Q N D Y N D N E S S L K V P
gtcaatttggtttcgaaccaagaacagtcgttctctgaccccgagctcgatcttccccct 255
V N L F S N Q E Q S F S D P E L D L P P
tatgatttactgtatgcgctggttgaccttactttgagcacctaaatacttgggtgccg 275
Y D L L Y A L V D L Y F E H L N T W C P
atcctgcatcgacgaacgacacttgacacttcttcggtcccactccttttagaggaagct 295
I L H R R T T L D T F F G P T P L E E A
gaccgcatggttctctacgctatcgtcgcgactccttctgcttttctaatgacagccga 315
D R M V L Y A I V A T T L R F S N D S R
ctcaccgaacaaaatcgcaagcggatcactcctccaagcaaaagggttctgctttac 335
L T E Q N R K R Y H D S S K Q K V L L Y
ggcctggaaaactcgtccgtaaaaggcactgcaggctctggtgattctcgccctggacctt 355
G L E N S S V K A L Q A L V I L A L D L
gttgggtcatctaacgggccccctggttgaaactccttgccttgataacaaggtcagtg 375
V G S S N G P P G W K L L A L I T R S V
gttcaattgggtctggccgtcgagtcgaagcaacccttataactcccctctatccttca 395
V Q L G L A V E S K S T L I T P L Y P S
atatatacattgcgggcccgtcactctccccgaagcggagtcgtggattgaagacgagggc 415
I Y T L R A V T L P E A E S W I E D E G
agggcgtcggcttttctggatgggtgtaccttcttgaccggtattctactctcgcaaccgct 435
R R R L F W M V Y L L D R Y S T L A T A
tttgactttgctttggatgacaaagacatcgaccgcaagcttccgtgtaaagacgagttt 455
F D F A L D D K D I D R K L P C K D E F
ttcattaagaaccagccagttgagactaggtgggttcagtcgtcgaatgaccgccagat 475
F I K N Q P V E T R W F Q S S N D R P D

catctcattcgttccgagaacggttggttcattcggactctacgtggaattcttgggtatc
 H L I R S E N V G S F G L Y V E I L G I 495
 ctttcacggatacatgtattcctcaagcggcccggttgacattgggttctatctgatgtc
 L S R I H V F L K R P V D I G V L S D V 515
 gaggagtggcaagccacgtatcgcaaattggatagcgaagttagactacctgggagttcaat
 E E W Q A T Y R K L D S E L T T W E F N 535
 cttcctacagagtacacctacgaaaacgcctctcgggcgttttagcggctcgaagcacaag
 L P T E Y T Y E N A S R A F S G S K H K 555
 gggcaccactgtgattgggttcagttacattctgtttaccagacgtgagtcgaatgtttcc
 G H H C D W V Q L H S V Y Q T 570
 taaaacggttttcgctgttcgctgaccccaactgcagggcggttaattcggcttcattcttc
 A V I R L H S S 578
 agcagcatatcccactacacggtctccgatcttcacgccgtcgtacagtgcgagccagcg
 A A Y P T T R S P I F T P S Y S A S Q R 598
 atgtctgctcgcagtcgataacattgtttcagtcacccggtttgtcgtgaacaataacat
 C L L A V D N I V S V T R F V V N N N I 618
 tttggacaagcttggaccgcccgtttgcatttacatttgggtttctgctcggttgctgct
 L D K L G P P F A F T L W V S A R L L L 638
 cgtccacggatctacaatcgcgcacacagtcagtcgccgatatcgtgtttatcgttgatc
 V H G S T I A H T V S P D I V F I V D T 658
 tctttctcaaatgggcaagtactggaaaagtagcggagaggtacagctcaatcctgcaacg
 L S Q M G K Y W K V A E R Y S S I L Q R 678
 agttctcgatgaatacggcgagtatcagcaatctggtgccggcgatggtgatcggtcac
 V L D E Y G E Y Q Q S G A G D G D R S T 698
 accttcttctgtcaaaatccttgcagacatgcgccgatgcgcgtttgacctggacttct
 P S S V K I L A D M R R C A F D L D F L 718
 gatatcgcggaaccccggttcgctcgccaaccgcaagtcaggcagcggtccgctcagctgg
 I S R Q P R S S P T A S Q A A A P S A G 738
 attgccatcgagaagccttagcacctaattgagttggagtattctagacgttttcggtttctt
 L P S R S L A P N E L E Y L D V F G F F 758
 caatgtcccgcgagtcctccgcccgttcggaccctgatattagcggctcttgacatggccga
 N V P R V P A G R T P D I S G L D M A E 778
 agctgtcaataaccccatgtcgatacctggattgactggaactggcagttcgaacccttt
 A V N N P M S I P G L T G T G S S N P L 798
 gccggtggataatgcttctaccatacaaacgagttcaatatcacgaattatttgatacc
 P V D N A S T H T N E F N I T N Y L I P 818
 ccccccgaaacggactggctgtttcgccccgggggttag
 T P E T D W L F R P G G * 830

B

<i>Myceliophthora thermophila</i> MYCTH_53224	SVSCE	CKQRKVKCDR	QPSGWC	SRNGAL	CEYK	97
<i>Colletotrichum gloeosporoides</i> Gloci1_734560	SVSCE	CKQRKVKCDR	QPSGWC	SRNGAL	CEYK	112
<i>Magnaporthe oryzae</i> MGG_08314	SVSCE	CKQRKVKCDR	QPSGWC	SRNGAL	CEYK	94
<i>Neurospora crassa</i> NCU_09033/RhaR	SVSCE	CKTRKVKCDR	QPSGWC	SRNTVV	CEYK	114
<i>Trychophyton rubrum</i> TERG_01723	MVSCE	CKQRKVKCDR	QPSGWC	ARNGHP	CEYK	106
<i>Aspergillus nidulans</i> AN5673/RhaR	TVSCE	CKQRKVKCDR	QPSGWC	TRNGVQ	CEYK	92
<i>Blastomyces dermatitidis</i> BDBG_06686	TVSCE	CKTRKVKCDR	QPSGWC	TRNGRV	CIYR	78
<i>Colletotrichum gloeosporioides</i> ELA25038	KTSCE	CKARKVKCDR	EPACSW	CARHNR	CVYL	73
<i>Saitoella complicata</i> Saico1_98448	LTACE	CKARKVKCDR	QPSCEW	CRVGV	SVYQ	65
<i>Candida lusitanae</i> CLUG_02930	SKACNS	CKKVKCDR	SPRCGY	CARNGL	TKYR	43
<i>Debaryomyces hansenii</i> DEHA2E00869g	SRSCDY	CKLKKVKCDQ	TKPNCN	CIHNES	CVYS	62
<i>Debaryomyces hansenii</i> DEHA2E01210g	SRSCDY	CKLKKVKCDQ	TKPNCN	CIHNES	CVYS	61
<i>Cryptococcus neoformans</i> CNB_05720	SITCAP	CKKVKCDSTK	PTCLNCA	SPDSCY	PP	60
<i>Saccharomyces cerevisiae</i> Gal4	EQACDI	CKLKKVKCDQ	TKPNCN	CIHNES	CVYS	41
<i>Saccharomyces cerevisiae</i> Ppr1	RTACKRC	CKLKKVKCDQ	TKPNCN	CIHNES	CVYS	64
	:	*	:	*	*	

Base-pair contacting residues in Gal4 & Ppr1

C

