Pathways conservation

Starch and sucrose metabolism

(link to KEGG)

Synthetic pattern of the pathway : `sckdy`

Reference Protein	EC Number	Genolevures gene families		
		Phyletic pattern	Profile	Family name
HXK1 (YFR053c)	2.7.1.1	sckdy	5 5 2 3 3	GLR.3217
HXK2 (YGL253w)	2.7.1.1	sckdy	5 5 2 3 3	GLR.3217
SUC2 (YIL162w)	3.2.1.26	s-kdy	1 0 1 1 1	GLR.1234
MAL32 (YBR299w)	3.2.1.20	s-kd-	7 0 1 2 0	GLC.151
YGR287C (YGR287c)	3.2.1.20	s-kd-	7 0 1 2 0	GLC.151
MAL12 (YGR292w)	3.2.1.20	s-kd-	7 0 1 2 0	GLC.151
YIL172C (YIL172c)	3.2.1.20	s-kd-	7 0 1 2 0	GLC.151
YJL216C (YJL216c)	3.2.1.20	s-kd-	7 0 1 2 0	GLC.151
FSP2 (YJL221c)	3.2.1.20	s-kd-	7 0 1 2 0	GLC.151
GSC2 (YGR032w)	2.4.1.34	sckdy	3 3 3 2 2	GLR.23
FKS1 (YLR342w)	2.4.1.34	sckdy	3 3 3 2 2	GLR.23
FKS3 (YMR306w)	2.4.1.34	sckdy	3 3 3 2 2	GLR.23
YHL012W (YHL012w)	2.7.7.9	sckdy	2 1 1 1 1	GLR.2246
UGP1 (YKL035w)	2.7.7.9	sckdy	2 1 1 1 1	GLR.2246
TPS1 (YBR126c)	2.4.1.15	sckdy	4 4 3 3 3	GLR.1979
TPS2 (YDR074w)		sckdy	4 4 3 3 3	GLR.1979
TSL1 (YML100w)	2.4.1.15	sckdy	4 4 3 3 3	GLR.1979
TPS3 (YMR261c)	2.4.1.15	sckdy	4 4 3 3 3	GLR.1979
GSY1 (YFR015c)	2.4.1.11	sckdy	2 2 1 1 1	GLR.110
GSY2 (YLR258w)	2.4.1.11	sckdy	2 2 1 1 1	GLR.110
PGM1 (YKL127w)	5.4.2.2	sckdy	2 2 1 1 1	GLR.2142
PGM2 (YMR105c)	5.4.2.2	sckdy	2 2 1 1 1	GLR.2142
GLK1 (YCL040w)	2.7.1.2	sckdy	5 5 2 3 3	GLR.3217
PGI1 (YBR196c)	5.3.1.9	sckdy	1 1 1 1 1	GLR.582
GLC3 (YEL011w)	2.4.1.18	sckdy	1 1 1 1 1	GLR.790
NTH2 (YBR001c)	3.2.1.28	sckdy	2 2 1 1 1	GLR.157
NTH1 (YDR001c)	3.2.1.28	sckdy	2 2 1 1 1	GLR.157
ATH1 (YPR026w)	3.2.1.28	sckd-	1 1 1 1 0	GLR.1078
BSC1 (YDL037c)	3.2.1.3	sckdy	45 35 26 36 48	GLC.1
SGA1 (YIL099w)	3.2.1.3	sckdy	1 1 1 1 1	GLR.507
MUC1 (YIR019c)	3.2.1.3	sckdy	7 4 12 8 43	GLC.11
PGU1 (YJR153w)	3.2.1.15	s----	1 0 0 0 0	none
GPH1 (YPR160w)	2.4.1.1	sckdy	1 1 1 1 1	GLR.500
EXG2 (YDR261c)	3.2.1.58	sckdy	4 4 2 5 2	GLR.3219
BGL2 (YGR282c)	3.2.1.58	sckdy	1 1 1 2 2	GLR.3339
EXG1 (YLR300w)	3.2.1.58	sckdy	4 4 2 5 2	GLR.3219
SPR1 (YOR190w)	3.2.1.58	sckdy	4 4 2 5 2	GLR.3219
VPS8 (YAL002w)	2.7.1.-	sckd-	1 1 1 1 0	GLR.1058
CDC15 (YAR019c)	2.7.1.-	sckdy	57 58 49 54 42	GLC.2
VPS15 (YBR097w)	2.7.1.-	sckdy	1 1 1 1 1	GLR.2300
DUN1 (YDL101c)	2.7.1.-	sckdy	57 58 49 54 42	GLC.2
KIN1 (YDR122w)	2.7.1.-	sckdy	57 58 49 54 42	GLC.2
SNF1 (YDR477w)	2.7.1.-	sckdy	57 58 49 54 42	GLC.2
SPS1 (YDR523c)	2.7.1.-	sckdy	7 5 4 4 3	GLC.52
YCK3 (YER123w)	2.7.1.-	sckdy	4 4 2 2 2	GLC.92
YCK1 (YHR135c)	2.7.1.-	sckdy	4 4 2 2 2	GLC.92
CTK2 (YJL006c)	2.7.1.-	s-k-y	1 0 1 0 1	GLR.2832
IME2 (YJL106w)	2.7.1.-	sckdy	22 19 19 21 17	GLC.8
PBS2 (YJL128c)	2.7.1.-	sckdy	7 5 4 4 3	GLC.52

YAK1 (YJL141c)	2.7.1.-	sckdy	22 19 19 21 17	GLC.8
ELM1 (YKL048c)	2.7.1.-	sckdy	57 58 49 54 42	GLC.2
CTK1 (YKL139w)	2.7.1.-	sckdy	22 19 19 21 17	GLC.8
CTK3 (YML112w)	2.7.1.-	sck--	1 1 1 0 0	GLR.1303
YCK2 (YNL154c)	2.7.1.-	sckdy	4 4 2 2 2	GLC.92
NPR1 (YNL183c)	2.7.1.-	sckdy	57 58 49 54 42	GLC.2
MCK1 (YNL307c)	2.7.1.-	sckdy	22 19 19 21 17	GLC.8
MKK1 (YOR231w)	2.7.1.-	sckdy	7 5 4 4 3	GLC.52
SSN3 (YPL042c)	2.7.1.-	sckdy	22 19 19 21 17	GLC.8
MKK2 (YPL140c)	2.7.1.-	sckdy	7 5 4 4 3	GLC.52
HRR25 (YPL204w)	2.7.1.-	sckdy	4 4 2 2 2	GLC.92
ENA5 (YDR038c)	3.6.1.-	sckdy	5 4 4 4 5	GLC.54
ENA1 (YDR040c)	3.6.1.-	sckdy	5 4 4 4 5	GLC.54
RAD3 (YER171w)	3.6.1.-	sckdy	2 2 2 2 2	GLR.3298
BRR2 (YER172c)	3.6.1.-	sckdy	5 5 6 5 8	GLC.40
SLH1 (YGR271w)	3.6.1.-	sckdy	5 5 6 5 8	GLC.40
HPR5 (YJL092w)	3.6.1.-	sckdy	2 2 3 2 1	GLR.3280
DDP1 (YOR163w)	3.6.1.-	sckdy	1 1 1 1 1	GLR.894

See detailed view

Detailed view

Reference Protein	EC Number	Annotation	Systematic gene deletion	Gene deletion effects (growth rate)					Genolevures gene families				
				20 gen. in YPD	60 gen. in YPD	YNB	YPD + NaCl	YP + lactate	Phyletic pattern	Profile	Family name	Gene Name	Gene Annotation
HXK1 (YFR053C)	2.7.1.1	sp|P04806 Saccharomyces cerevisiae YFR053c HXK1 hexokinase I P4.22.f4.1	viable	NA	NA	NA	NA	NA	sckdy	5 5 2 3 3	GLR.3217	YALI0E15488g	similar to sp|P17709 Saccharomy cerevisiae YCL040w GLK1 aldohe specific glucokinase, hypothetical
												CAGL0A04829g	highly similar to sp|P04807 Saccharomyces cerevisiae YGL25 HXK2 or sp|P04806 Saccharomy cerevisiae YFR053c HXK1, start similarity
												DEHA0F26092g	similar to tr|Q9C0M1 Candida albi CaNAG5 protein, hypothetical st
												CAGL0M00682g	similar to tr|Q06204 Saccharomy cerevisiae YLR446w, hypothetical
												CAGL0F00605g	highly similar to sp|P17709 Saccharomyces cerevisiae YCL04 GLK1 or Q04409 Saccharomyc cerevisiae YDR516c, start by simil
												CAGL0B00726g	weakly similar to sp|P17709 Saccharomyces cerevisiae YCL04 GLK1 aldohexose specific glucoki start by similarity
												YALI0E20207g	weakly similar to tr|Q9C0M1 Can albicans CaNAG5 protein, hypothe start

												DEHA0F15169g	highly similar to sp|P50506 Debaryomyces occidentalis Hexoki (EC 2.7.1.1)., start by similarity
												KLLA0C01155g	similar to sp|P17709 Saccharomy cerevisiae YCL040w GLK1 aldohe specific glucokinase, start by simil
												CAGL0H07579g	highly similar to sp|P04807 Saccharomyces cerevisiae YGL25 HXK2 or sp|P04806 Saccharomy cerevisiae YFR053c HXK1, start similarity
												KLLA0D11352g	gi|462368|sp|P33284|HXK_KLUI Kluyveromyces lactis HEXOKINA start by similarity
												YALI0B22308g	highly similar to tr|O74996 Yarro lipolytica Hexokinase, hypothetical
												DEHA0E07007g	highly similar to CA0263|CaGLI Candida albicans aldohexose spec glucokinase, start by similarity
HXK2 (YGL253W)	2.7.1.1	sp|P04807 Saccharomyces cerevisiae YGL253w HXK2 hexokinase II P4.22.f4.1	Exhibits growth defect on a fermentable carbon source.	0.4	0.2	0.6	Non	0.7	sckdy	5 5 2 3 3	GLR.3217	YALI0E15488g	similar to sp|P17709 Saccharomy cerevisiae YCL040w GLK1 aldohe specific glucokinase, hypothetical
												CAGL0A04829g	highly similar to sp|P04807 Saccharomyces cerevisiae YGL25 HXK2 or sp|P04806 Saccharomy cerevisiae YFR053c HXK1, start similarity
												DEHA0F26092g	similar to tr|Q9C0M1 Candida albi CaNAG5 protein, hypothetical st
												CAGL0M00682g	similar to tr|Q06204 Saccharomy cerevisiae YLR446w, hypothetical
												CAGL0F00605g	highly similar to sp|P17709 Saccharomyces cerevisiae YCL04 GLK1 or Q04409 Saccharomyc cerevisiae YDR516c, start by simil
												CAGL0B00726g	weakly similar to sp|P17709 Saccharomyces cerevisiae YCL04 GLK1 aldohexose specific glucoki start by similarity
												YALI0E20207g	weakly similar to tr|Q9C0M1 Can albicans CaNAG5 protein, hypothe start
												DEHA0F15169g	highly similar to sp|P50506 Debaryomyces occidentalis Hexoki (EC 2.7.1.1)., start by similarity
												KLLA0C01155g	similar to sp|P17709 Saccharomy cerevisiae YCL040w GLK1 aldohe specific glucokinase, start by simil
												CAGL0H07579g	highly similar to sp|P04807 Saccharomyces cerevisiae YGL25 HXK2 or sp|P04806 Saccharomy cerevisiae YFR053c HXK1, start similarity
												KLLA0D11352g	gi|462368|sp|P33284|HXK_KLUI Kluyveromyces lactis HEXOKINA start by similarity
												YALI0B22308g	highly similar to tr|O74996 Yarro lipolytica Hexokinase, hypothetical
												DEHA0E07007g	highly similar to CA0263|CaGLI Candida albicans aldohexose spec glucokinase, start by similarity
SUC2 (YIL162W)	3.2.1.26	sp|P00724 Saccharomyces cerevisiae YIL162w SUC2 invertase (sucrose hydrolyzing enzyme) singleton	viable	NA	NA	NA	NA	NA	s-kdy	1 0 1 1 1	GLR.1234	YALI0E26719g	sp|Q12724 disrupted by Saccharom cerevisiae Invertase 2 precursor identified start
												DEHA0F28468g	similar to sp|P24133 Debaryomy occidentalis invertase precursor (3.2.1.26) (Beta-fructofuranosida (Saccharase), start by similarity
												KLLA0A10417g	gi|4808541|gb|AAD29850.1|AF079 Kluyveromyces lactis invertase, sta similarity
		sp|P38158										DEHA0E00627g	similar to tr|Q8J2T6 Aspergillus or Alpha-glucosidase, hypothetical s
													highly similar to CA3405|IPF86

MAL32 (YBR299W)	3.2.1.20	Saccharomyces cerevisiae YBR299w MAL31 alpha-glucosidase P7.4.f7.1	-	NA	NA	NA	NA	NA	s-kd-	7 0 1 2 0	GLC.151	DEHA0A14300g KLLA0D00231g	highly similar to CA3405|IPF86 Candida albicans IPF8644 maltase homology), start by similarity gi|5441460|emb|CAB46746.1 Kluyveromyces lactis maltase, star similarity
YGR287C (YGR287C)	3.2.1.20	sp|P53051 Saccharomyces cerevisiae YGR287c strong similarity to maltase P7.4.f7.1	viable	0.8	0.5	0.7	Non	0.6	s-kd-	7 0 1 2 0	GLC.151	DEHA0E00627g DEHA0A14300g KLLA0D00231g	similar to tr|Q8J2T6 Aspergillus or Alpha-glucosidase, hypothetical s highly similar to CA3405|IPF864 Candida albicans IPF8644 maltase homology), start by similarity gi|5441460|emb|CAB46746.1 Kluyveromyces lactis maltase, star similarity
MAL12 (YGR292W)	3.2.1.20	sp|P53341 Saccharomyces cerevisiae YGR292w MAL12 alpha-glucosidase of the MAL1 locus P7.4.f7.1	-	Non	Non	Non	ND	Non	s-kd-	7 0 1 2 0	GLC.151	DEHA0E00627g DEHA0A14300g KLLA0D00231g	similar to tr|Q8J2T6 Aspergillus or Alpha-glucosidase, hypothetical s highly similar to CA3405|IPF864 Candida albicans IPF8644 maltase homology), start by similarity gi|5441460|emb|CAB46746.1 Kluyveromyces lactis maltase, star similarity
YIL172C (YIL172C)	3.2.1.20	sp|P40439 Saccharomyces cerevisiae YIL172c identical to FSP2P and similarity to other alpha-glucosidases P7.4.f7.1	-	NA	NA	NA	NA	NA	s-kd-	7 0 1 2 0	GLC.151	DEHA0E00627g DEHA0A14300g KLLA0D00231g	similar to tr|Q8J2T6 Aspergillus or Alpha-glucosidase, hypothetical s highly similar to CA3405|IPF864 Candida albicans IPF8644 maltase homology), start by similarity gi|5441460|emb|CAB46746.1 Kluyveromyces lactis maltase, star similarity
YJL216C (YJL216C)	3.2.1.20	sp|P40884 Saccharomyces cerevisiae YJL216c strong similarity to Mal62p P7.4.f7.1	viable	NA	NA	NA	NA	NA	s-kd-	7 0 1 2 0	GLC.151	DEHA0E00627g DEHA0A14300g KLLA0D00231g	similar to tr|Q8J2T6 Aspergillus or Alpha-glucosidase, hypothetical s highly similar to CA3405|IPF864 Candida albicans IPF8644 maltase homology), start by similarity gi|5441460|emb|CAB46746.1 Kluyveromyces lactis maltase, star similarity
FSP2 (YJL221C)	3.2.1.20	sp|P40439 Saccharomyces cerevisiae YJL221c FSP2 strong similarity to alpha-D-glucosidase P7.4.f7.1	-	NA	NA	NA	NA	NA	s-kd-	7 0 1 2 0	GLC.151	DEHA0E00627g DEHA0A14300g KLLA0D00231g	similar to tr|Q8J2T6 Aspergillus or Alpha-glucosidase, hypothetical s highly similar to CA3405|IPF864 Candida albicans IPF8644 maltase homology), start by similarity gi|5441460|emb|CAB46746.1 Kluyveromyces lactis maltase, star similarity
GSC2 (YGR032W)	2.4.1.34	sp|P40989 Saccharomyces cerevisiae YGR032w GSC2 1,3-beta-D-glucan synthase subunit P3.64.f3.1	viable	0.3	0.3	0.3	0.3	0.2	sckdy	3 3 3 2 2	GLR.23	YALI0E21021g YALI0C01411g KLLA0B05841g CAGL0G01034g DEHA0C02112g CAGL0M13827g KLLA0C08888g KLLA0C14069g CAGL0K04037g	tr|Q9UVK9 Yarrowia lipolytica gl synthase, identified start similar to tr|Q9UVK9 Yarrowia lipolytica Fks1p, hypothetical st highly similar to sp|P40989 Saccharomyces cerevisiae GR032 GSC2 1, 3-beta-D-glucan syntha subunit, start by similarity highly similar to sp|P40989 Saccharomyces cerevisiae YGR03 GSC2 or sp|P38631 Saccharomyc cerevisiae YLR342w FKS1, start similarity highly similar to tr|O13428 Candi albicans Beta-1, 3-glucan syntha catalytic subunit 1, start by simila similar to sp|Q04952 Saccharomy cerevisiae YMR306w FKS3, hypothetical start similar to sp|O13423 Candida albic Glucan synthase, start by similar similar to sp|Q04952 Saccharomy cerevisiae YMR306w FKS3, start similarity tr|Q9P8N8 Candida glabrata 1, 3-b glucan synthase, identified star similar to sp|Q04952 Saccharomy

												DEHA0A07436g	cerevisiae YMR306w FKS3 1,3-b glucan synthase, start by similari
FKS1 (YLR342W)	2.4.1.34	sp|P38631 Saccharomyces cerevisiae YLR342w FKS1 1,3-beta-D-glucan synthase, catalytic subunit P3.64.f3.1	Exhibits growth defect on a fermentable carbon source.	NA	NA	NA	NA	NA	sckdy	3 3 3 2 2	GLR.23	YALI0E21021g	tr|Q9UVK9 Yarrowia lipolytica glu synthase, identified start
												YALI0C01411g	similar to tr|Q9UVK9 Yarrowia lipolytica Fks1p, hypothetical sta
												KLLA0B05841g	highly similar to sp|P40989 Saccharomyces cerevisiae GR032 GSC2 1, 3-beta-D-glucan syntha subunit, start by similarity
												CAGL0G01034g	highly similar to sp|P40989 Saccharomyces cerevisiae YGR03 GSC2 or sp|P38631 Saccharomyc cerevisiae YLR342w FKS1, start similarity
												DEHA0C02112g	highly similar to tr|O13428 Candi albicans Beta-1, 3-glucan syntha catalytic subunit 1, start by simila
												CAGL0M13827g	similar to sp|Q04952 Saccharomy cerevisiae YMR306w FKS3, hypothetical start
												KLLA0C08888g	similar to sp|O13423 Candida albic Glucan synthase, start by similar
												KLLA0C14069g	similar to sp|Q04952 Saccharomy cerevisiae YMR306w FKS3, start similarity
												CAGL0K04037g	tr|Q9P8N8 Candida glabrata 1, 3-b glucan synthase, identified star
												DEHA0A07436g	similar to sp|Q04952 Saccharomy cerevisiae YMR306w FKS3 1,3-b glucan synthase, start by similari
FKS3 (YMR306W)	2.4.1.34	sp|Q04952 Saccharomyces cerevisiae YMR306w FKS3 similarity to 1,3-beta-glucan synthases P3.64.f3.1	viable	0.4	0.5	0.4	0.7	0.7	sckdy	3 3 3 2 2	GLR.23	YALI0E21021g	tr|Q9UVK9 Yarrowia lipolytica glu synthase, identified start
												YALI0C01411g	similar to tr|Q9UVK9 Yarrowia lipolytica Fks1p, hypothetical sta
												KLLA0B05841g	highly similar to sp|P40989 Saccharomyces cerevisiae GR032 GSC2 1, 3-beta-D-glucan syntha subunit, start by similarity
												CAGL0G01034g	highly similar to sp|P40989 Saccharomyces cerevisiae YGR03 GSC2 or sp|P38631 Saccharomyc cerevisiae YLR342w FKS1, start similarity
												DEHA0C02112g	highly similar to tr|O13428 Candi albicans Beta-1, 3-glucan syntha catalytic subunit 1, start by simila
												CAGL0M13827g	similar to sp|Q04952 Saccharomy cerevisiae YMR306w FKS3, hypothetical start
												KLLA0C08888g	similar to sp|O13423 Candida albic Glucan synthase, start by similar
												KLLA0C14069g	similar to sp|Q04952 Saccharomy cerevisiae YMR306w FKS3, start similarity
												CAGL0K04037g	tr|Q9P8N8 Candida glabrata 1, 3-b glucan synthase, identified star
												DEHA0A07436g	similar to sp|Q04952 Saccharomy cerevisiae YMR306w FKS3 1,3-b glucan synthase, start by similari
YHL012W (YHL012W)	2.7.7.9	sp|P38709 Saccharomyces cerevisiae YHL012w similarity to UDP Glucose pyrophosphorylase P2.308.f2.1	viable	0.4	Non	Non	0.6	0.3	sckdy	2 1 1 1 1	GLR.2246	KLLA0F25652g	highly similar to sp|P32861 Saccharomyces cerevisiae YKL03 UGP1 UTP--glucose-1-phospha uridylyltransferase, start by simila
												DEHA0G24310g	highly similar to CAGL-IPF7445 Candida glabrata IPF 7445.3, start similarity
												YALI0A02310g	highly similar to sp|P32861 Saccharomyces cerevisiae YKL03 UGP1 UTP--glucose-1-phospha uridylyltransferase, start by simila
												CAGL0L01925g	highly similar to sp|P32861 Saccharomyces cerevisiae YKL03

												CAGL0L01925g	UGP1 UTP--glucose-1-phospha uridylyltransferase, start by simila
UGP1 (YKL035W)	2.7.7.9	sp|P32861 Saccharomyces cerevisiae YKL035w UGP1 UTP--glucose-1-phosphate uridylyltransferase P2.308.f2.1	inviable	0.3	Ess	Ess	0.5	Ess	sckdy	2 1 1 1 1	GLR.2246	KLLA0F25652g	highly similar to sp|P32861 Saccharomyces cerevisiae YKL03 UGP1 UTP--glucose-1-phospha uridylyltransferase, start by simila
												DEHA0G24310g	highly similar to CAGL-IPF7445 Candida glabrata IPF 7445.3, start similarity
												YALI0A02310g	highly similar to sp|P32861 Saccharomyces cerevisiae YKL03 UGP1 UTP--glucose-1-phospha uridylyltransferase, start by simila
												CAGL0L01925g	highly similar to sp|P32861 Saccharomyces cerevisiae YKL03 UGP1 UTP--glucose-1-phospha uridylyltransferase, start by simila
TPS1 (YBR126C)	2.4.1.15	sp|Q00764 Saccharomyces cerevisiae YBR126c TPS1 alpha,alpha-trehalose-phosphate synthase, 56 KD subunit P4.6.f4.1	Exhibits growth defect on a fermentable carbon source.	0.7	Ess	Ess	0.4	Ess	sckdy	4 4 3 3 3	GLR.1979	KLLA0E11231g	similar to sp|P38426 Saccharomy cerevisiae YMR261c TPS3 alpha, a trehalose-phosphate synthase, 115 subunit, start by similarity
												CAGL0J09812g	highly similar to sp|Q00764 Saccharomyces cerevisiae YBR12 TPS1 alpha, alpha-trehalose-phosp synthase, hypothetical start
												CAGL0J06468g	similar to sp|P38426 Saccharomy cerevisiae YMR261c TPS3 or sp|P3 Saccharomyces cerevisiae YML10 TSL1, hypothetical start
												YALI0D14476g	similar to sp|P31688 Saccharomy cerevisiae YDR074w TPS2 alpha, a trehalose-phosphate synthase, 102 subunit, (trehalose 6-P phosphata activity), start by similarity
												DEHA0E23210g	highly similar to CA4084|CaTPS Candida albicans CaTPS1 TREHALOSE-6-PHOSPHATE SYNTHASE, start by similarity
												CAGL0H02387g	similar to sp|P38426 Saccharomy cerevisiae YMR261c TPS3alpha sp|P38427 Saccharomyces cerevis YML100w TSL1, start by similar
												CAGL0G05335g	highly similar to sp|P31688 Saccharomyces cerevisiae YDR07 TPS2 alpha, alpha-trehalose-phosp synthase, hypothetical start
												KLLA0B08822g	gi|586113|sp|Q07158|TPS1_KLU Kluyveromyces lactis Alpha, alph trehalose-phosphate synthase [UD forming] 56 kDa subunit (Trehalos phosphate synthase) (UDP-gluco glucosephosphate glucosyltransfera start by similarity
												YALI0E14685g	sp|O74932 Yarrowia lipolytica Al alpha-trehalose-phosphate syntha [UDP-forming], identified star
												DEHA0F07392g	similar to CA5505|CaTPS3.3 Cand albicans CaTPS3.3 alpha,alpha trehalose-phosphate synthase, regul subunit, 3-prime end (by homolog hypothetical start
												YALI0E31086g	similar to tr|Q9P918 Pichia angu Trehalose phosphate synthase subu hypothetical start
												KLLA0E10120g	similar to sp|P31688 Saccharomy cerevisiae YDR074w TPS2 alpha, a trehalose-phosphate synthase, 102 subunit, start by similarity
												DEHA0G13233g	similar to CA5066|CaTPS2 Cand albicans CaTPS2, hypothetical st
												KLLA0E11231g	similar to sp|P38426 Saccharomy cerevisiae YMR261c TPS3 alpha, a trehalose-phosphate synthase, 115 subunit, start by similarity
													highly similar to sp|Q00764

TPS2 (YDR074W)		sp|P31688 Saccharomyces cerevisiae YDR074w TPS2 alpha,alpha-trehalose-phosphate synthase, 102 KD subunit P4.6.f4.1	Exhibits growth defect on a fermentable carbon source.	Ess	Ess	Ess	0.3	Ess	sckdy	4 4 3 3 3	GLR.1979	CAGL0J09812g	Saccharomyces cerevisiae YBR12 TPS1 alpha, alpha-trehalose-phosp synthase, hypothetical start
												CAGL0J06468g	similar to sp|P38426 Saccharomy cerevisiae YMR261c TPS3 or sp|P3 Saccharomyces cerevisiae YML10 TSL1, hypothetical start
												YALI0D14476g	similar to sp|P31688 Saccharomy cerevisiae YDR074w TPS2 alpha, a trehalose-phosphate synthase, 102 subunit, (trehalose 6-P phosphata activity), start by similarity
												DEHA0E23210g	highly similar to CA4084|CaTPS Candida albicans CaTPS1 TREHALOSE-6-PHOSPHATE SYNTHASE, start by similarity
												CAGL0H02387g	similar to sp|P38426 Saccharomy cerevisiae YMR261c TPS3alpha sp|P38427 Saccharomyces cerevis YML100w TSL1, start by similar
												CAGL0G05335g	highly similar to sp|P31688 Saccharomyces cerevisiae YDR07 TPS2 alpha, alpha-trehalose-phosp synthase, hypothetical start
												KLLA0B08822g	gi|586113|sp|Q07158|TPS1_KLU Kluyveromyces lactis Alpha, alph trehalose-phosphate synthase [UD forming] 56 kDa subunit (Trehalos phosphate synthase) (UDP-gluco glucosephosphate glucosyltransfera start by similarity
												YALI0E14685g	sp|O74932 Yarrowia lipolytica Al alpha-trehalose-phosphate syntha [UDP-forming], identified star
												DEHA0F07392g	similar to CA5505|CaTPS3.3 Cand albicans CaTPS3.3 alpha,alpha trehalose-phosphate synthase, regul subunit, 3-prime end (by homolog hypothetical start
												YALI0E31086g	similar to tr|Q9P918 Pichia angu Trehalose phosphate synthase subu hypothetical start
												KLLA0E10120g	similar to sp|P31688 Saccharomy cerevisiae YDR074w TPS2 alpha, a trehalose-phosphate synthase, 102 subunit, start by similarity
												DEHA0G13233g	similar to CA5066|CaTPS2 Cand albicans CaTPS2, hypothetical st
TSL1 (YML100W)	2.4.1.15	sp|P38427 Saccharomyces cerevisiae YML100w TSL1 alpha,alpha-	viable	0.7	0.4	ND	Non	ND	sckdy	4 4 3 3 3	GLR.1979	KLLA0E11231g	similar to sp|P38426 Saccharomy cerevisiae YMR261c TPS3 alpha, a trehalose-phosphate synthase, 115 subunit, start by similarity
												CAGL0J09812g	highly similar to sp|Q00764 Saccharomyces cerevisiae YBR12 TPS1 alpha, alpha-trehalose-phosp synthase, hypothetical start
												CAGL0J06468g	similar to sp|P38426 Saccharomy cerevisiae YMR261c TPS3 or sp|P3 Saccharomyces cerevisiae YML10 TSL1, hypothetical start
												YALI0D14476g	similar to sp|P31688 Saccharomy cerevisiae YDR074w TPS2 alpha, a trehalose-phosphate synthase, 102 subunit, (trehalose 6-P phosphata activity), start by similarity
												DEHA0E23210g	highly similar to CA4084|CaTPS Candida albicans CaTPS1 TREHALOSE-6-PHOSPHATE SYNTHASE, start by similarity
												CAGL0H02387g	similar to sp|P38426 Saccharomy cerevisiae YMR261c TPS3alpha sp|P38427 Saccharomyces cerevis YML100w TSL1, start by similar
												CAGL0G05335g	highly similar to sp|P31688 Saccharomyces cerevisiae YDR07

(YML100W)		trehalose-phosphate synthase, 123 KD subunit P4.6.f4.1								3		CAGL0G05335g	TPS2 alpha, alpha-trehalose-phosp synthase, hypothetical start
												KLLA0B08822g	gi|586113|sp|Q07158|TPS1_KLU Kluyveromyces lactis Alpha, alp trehalose-phosphate synthase [UI forming] 56 kDa subunit (Trehalos phosphate synthase) (UDP-gluco glucosephosphate glucosyltransfer start by similarity
												YALI0E14685g	sp|O74932 Yarrowia lipolytica Al alpha-trehalose-phosphate syntha [UDP-forming], identified star
												DEHA0F07392g	similar to CA5505|CaTPS3.3 Cand albicans CaTPS3.3 alpha,alpha trehalose-phosphate synthase, regul subunit, 3-prime end (by homolog hypothetical start
												YALI0E31086g	similar to tr|Q9P918 Pichia angu Trehalose phosphate synthase sub hypothetical start
												KLLA0E10120g	similar to sp|P31688 Saccharomy cerevisiae YDR074w TPS2 alpha, a trehalose-phosphate synthase, 102 subunit, start by similarity
												DEHA0G13233g	similar to CA5066|CaTPS2 Cand albicans CaTPS2, hypothetical st
TPS3 (YMR261C)	2.4.1.15	sp|P38426 Saccharomyces cerevisiae YMR261c TPS3 alpha,alpha-trehalose-phosphate synthase, 115 KD subunit P4.6.f4.1	viable	0.3	0.4	Ess	Ess	0.2	sckdy	4 4 3 3 3	GLR.1979	KLLA0E11231g	similar to sp|P38426 Saccharomy cerevisiae YMR261c TPS3 alpha, a trehalose-phosphate synthase, 115 subunit, start by similarity
												CAGL0J09812g	highly similar to sp|Q00764 Saccharomyces cerevisiae YBR1 TPS1 alpha, alpha-trehalose-phosp synthase, hypothetical start
												CAGL0J06468g	similar to sp|P38426 Saccharomy cerevisiae YMR261c TPS3 or sp|P Saccharomyces cerevisiae YML1 TSL1, hypothetical start
												YALI0D14476g	similar to sp|P31688 Saccharomy cerevisiae YDR074w TPS2 alpha, a trehalose-phosphate synthase, 102 subunit, (trehalose 6-P phosphata activity), start by similarity
												DEHA0E23210g	highly similar to CA4084|CaTPS Candida albicans CaTPS1 TREHALOSE-6-PHOSPHAT SYNTHASE, start by similarity
												CAGL0H02387g	similar to sp|P38426 Saccharomy cerevisiae YMR261c TPS3alpha sp|P38427 Saccharomyces cerevis YML100w TSL1, start by simila
												CAGL0G05335g	highly similar to sp|P31688 Saccharomyces cerevisiae YDR07 TPS2 alpha, alpha-trehalose-phosp synthase, hypothetical start
												KLLA0B08822g	gi|586113|sp|Q07158|TPS1_KLU Kluyveromyces lactis Alpha, alp trehalose-phosphate synthase [UI forming] 56 kDa subunit (Trehalos phosphate synthase) (UDP-gluco glucosephosphate glucosyltransfer start by similarity
												YALI0E14685g	sp|O74932 Yarrowia lipolytica Al alpha-trehalose-phosphate syntha [UDP-forming], identified star
												DEHA0F07392g	similar to CA5505|CaTPS3.3 Cand albicans CaTPS3.3 alpha,alpha trehalose-phosphate synthase, regul subunit, 3-prime end (by homolog hypothetical start
												YALI0E31086g	similar to tr|Q9P918 Pichia angu Trehalose phosphate synthase sub hypothetical start
												KLLA0E10120g	similar to sp|P31688 Saccharomy cerevisiae YDR074w TPS2 alpha, a

												KLLA0E10120g	trehalose-phosphate synthase, 102 subunit, start by similarity
												DEHA0G13233g	similar to CA5066|CaTPS2 Cand albicans CaTPS2, hypothetical st
GSY1 (YFR015C)	2.4.1.11	sp|P23337 Saccharomyces cerevisiae YFR015c GSY1 UDP glucose--starch glucosyltransferase, isoform 1 P2.249.f2.1	viable	0.7	0.7	0.9	0.9	0.7	sckdy	2 2 1 1 1	GLR.110	YALI0F18502g	similar to sp|P23337 Saccharomy cerevisiae YFR015c GSY1 UD glucose--starch glucosyltransfera isoform 1 or sp|P27472 Saccharom cerevisiae YLR258w GSY2 UD glucose--starch glucosyltransfera isoform 2, start by similarity
												CAGL0F04719g	highly similar to sp|P27472 Saccharomyces cerevisiae YLR25 GSY2 UDP-glucose--starch glucosyltransferase, start by simila
												DEHA0B05764g	highly similar to sp|P23337 Saccharomyces cerevisiae YFR01 GSY1 UDP glucose--starch glucosyltransferase, isoform 1, star similarity
												KLLA0F23133g	highly similar to sp|P23337 Saccharomyces cerevisiae YFR01 GSY1 UDP glucose--starch glucosyltransferase, isoform 1, star similarity
												CAGL0K10626g	highly similar to sp|P23337 Saccharomyces cerevisiae YFR01 GSY1, start by similarity
GSY2 (YLR258W)	2.4.1.11	sp|P27472 Saccharomyces cerevisiae YLR258w GSY2 UDP-glucose--starch glucosyltransferase, isoform 2 P2.249.f2.1	viable	NA	NA	NA	NA	NA	sckdy	2 2 1 1 1	GLR.110	YALI0F18502g	similar to sp|P23337 Saccharomy cerevisiae YFR015c GSY1 UD glucose--starch glucosyltransfera isoform 1 or sp|P27472 Saccharom cerevisiae YLR258w GSY2 UD glucose--starch glucosyltransfera isoform 2, start by similarity
												CAGL0F04719g	highly similar to sp|P27472 Saccharomyces cerevisiae YLR25 GSY2 UDP-glucose--starch glucosyltransferase, start by simila
												DEHA0B05764g	highly similar to sp|P23337 Saccharomyces cerevisiae YFR01 GSY1 UDP glucose--starch glucosyltransferase, isoform 1, star similarity
												KLLA0F23133g	highly similar to sp|P23337 Saccharomyces cerevisiae YFR01 GSY1 UDP glucose--starch glucosyltransferase, isoform 1, star similarity
												CAGL0K10626g	highly similar to sp|P23337 Saccharomyces cerevisiae YFR01 GSY1, start by similarity
PGM1 (YKL127W)	5.4.2.2	sp|P33401 Saccharomyces cerevisiae YKL127w PGM1 phosphoglucomutase, minor isoform P2.202.f2.1	viable	0.9	Non	Non	Non	Non	sckdy	2 2 1 1 1	GLR.2142	YALI0E02090g	similar to sp|P37012 Saccharomy cerevisiae YMR105c PGM2 phosphoglucomutase, major isofor sp|P33401 Saccharomyces cerevis YKL127w PGM1 phosphoglucomu minor isoform, start by similarit
												DEHA0C05940g	highly similar to sp|P37012 Saccharomyces cerevisiae YMR1 PGM2 phosphoglucomutase or sp|P33401 Saccharomyces cerevis YKL127w PGM1 phosphoglucomu start by similarity
												KLLA0B12694g	highly similar to sp|P37012 Saccharomyces cerevisiae YMR1 PGM2 phosphoglucomutase, ma isoform, start by similarity
												CAGL0K03421g	highly similar to sp|P37012 Saccharomyces cerevisiae YMR1 Phosphoglucomutase 2, start by similarity
												CAGL0K07480g	highly similar to sp|P37012 Saccharomyces cerevisiae YMR1 PGM2 phosphoglucomutase, hypothetical start

PGM2 (YMR105C)	5.4.2.2	sp|P37012 Saccharomyces cerevisiae YMR105c PGM2 phosphoglucomutase, major isoform P2.202.f2.1	Exhibits sensitivity at 15 generations when grown in galactose.	0.6	0.1	Ess	0.7	ND	sckdy	2 2 1 1 1	GLR.2142	YALI0E02090g	similar to sp|P37012 Saccharomy cerevisiae YMR105c PGM2 phosphoglucomutase, major isofor sp|P33401 Saccharomyces cerevis YKL127w PGM1 phosphoglucomu minor isoform, start by similarit
												DEHA0C05940g	highly similar to sp|P37012 Saccharomyces cerevisiae YMR1 PGM2 phosphoglucomutase or sp|P33401 Saccharomyces cerevis YKL127w PGM1 phosphoglucomu start by similarity
												KLLA0B12694g	highly similar to sp|P37012 Saccharomyces cerevisiae YMR1 PGM2 phosphoglucomutase, ma isoform, start by similarity
												CAGL0K03421g	highly similar to sp|P37012 Saccharomyces cerevisiae YMR1 Phosphoglucomutase 2, start by similarity
												CAGL0K07480g	highly similar to sp|P37012 Saccharomyces cerevisiae YMR1 PGM2 phosphoglucomutase, hypothetical start
GLK1 (YCL040W)	2.7.1.2	sp|P17709 Saccharomyces cerevisiae YCL040w GLK1 aldohexose specific glucokinase P4.22.f4.1	viable	NA	NA	NA	NA	NA	sckdy	5 5 2 3 3	GLR.3217	YALI0E15488g	similar to sp|P17709 Saccharomy cerevisiae YCL040w GLK1 aldohe specific glucokinase, hypothetical
												CAGL0A04829g	highly similar to sp|P04807 Saccharomyces cerevisiae YGL2 HXK2 or sp|P04806 Saccharomy cerevisiae YFR053c HXK1, start similarity
												DEHA0F26092g	similar to tr|Q9C0M1 Candida albi CaNAG5 protein, hypothetical st
												CAGL0M00682g	similar to tr|Q06204 Saccharomy cerevisiae YLR446w, hypothetical
												CAGL0F00605g	highly similar to sp|P17709 Saccharomyces cerevisiae YCL04 GLK1 or Q04409 Saccharomyc cerevisiae YDR516c, start by simil
												CAGL0B00726g	weakly similar to sp|P17709 Saccharomyces cerevisiae YCL04 GLK1 aldohexose specific glucoki start by similarity
												YALI0E20207g	weakly similar to tr|Q9C0M1 Can albicans CaNAG5 protein, hypothe start
												DEHA0F15169g	highly similar to sp|P50506 Debaryomyces occidentalis Hexok (EC 2.7.1.1)., start by similarity
												KLLA0C01155g	similar to sp|P17709 Saccharomy cerevisiae YCL040w GLK1 aldohe specific glucokinase, start by simil
												CAGL0H07579g	highly similar to sp|P04807 Saccharomyces cerevisiae YGL2 HXK2 or sp|P04806 Saccharomy cerevisiae YFR053c HXK1, start similarity
												KLLA0D11352g	gi|462368|sp|P33284|HXK_KLU Kluyveromyces lactis HEXOKINA start by similarity
												YALI0B22308g	highly similar to tr|O74996 Yarro lipolytica Hexokinase, hypothetical
												DEHA0E07007g	highly similar to CA0263|CaGL Candida albicans aldohexose spec glucokinase, start by similarity
PGI1	5.3.1.9	sp|P12709 Saccharomyces cerevisiae YBR196c	inviable	NA	NA	NA	NA	NA	sckdy	1 1 1 1	GLR.582	KLLA0E23595g	gi|120740|sp|P12341|G6PI_KLU Kluyveromyces lactis Glucose- phosphate isomerase (GPI) (Phosphoglucose isomerase) (P (Phosphohexose isomerase) (PHI), by similarity
												CAGL0H05445g	highly similar to sp|P12709 Saccharomyces cerevisiae YBR1 PGI1, hypothetical start

(YBR196C)	5.3.1.9	PGI1 glucose-6-phosphate isomerase singleton	inviable	NA	NA	NA	NA	NA	sckdy	1	GLR.582		PGI1, hypothetical start
												DEHA0F14289g	highly similar to sp|P12709 Saccharomyces cerevisiae YBR1 PGI1 glucose-6-phosphate isomer hypothetical start
												YALI0F07711g	highly similar to sp|P12709 Saccharomyces cerevisiae YBR1 PGI1 glucose-6-phosphate isomer start by similarity
GLC3 (YEL011W)	2.4.1.18	sp|P32775 Saccharomyces cerevisiae YEL011w GLC3 1,4-glucan branching enzyme (glycogen branching enzyme) singleton	viable	0.7	Non	0.6	0.8	0.6	sckdy	1 1 1 1 1	GLR.790	CAGL0M03377g	highly similar to sp|P32775 Saccharomyces cerevisiae YEL01 GLC3, hypothetical start
												DEHA0B01650g	similar to sp|P32775 Saccharomy cerevisiae YEL011w GLC3 1,4-gl branching enzyme (glycogen branc enzyme), hypothetical start
												KLLA0A11176g	highly similar to sp|P32775 Saccharomyces cerevisiae YEL01 GLC3 1, 4-glucan branching enz (glycogen branching enzyme) singl start by similarity
												YALI0C06798g	highly similar to tr|Q9P5P3 Neuros crassa Probable branching enzyme hypothetical start
NTH2 (YBR001C)	3.2.1.28	sp|P35172 Saccharomyces cerevisiae YBR001c NTH2 alpha,alpha-trehalase P2.445.f2.1	viable	0.5	0.2	0.6	0.5	0.6	sckdy	2 2 1 1 1	GLR.157	DEHA0B02673g	similar to sp|P52494 Candida albi Neutral trehalase (EC 3.2.1.28), sta similarity
												CAGL0M10439g	highly similar to sp|P32356 Saccharomyces cerevisiae YDR0 NTH1 neutral trehalase or sp|P35 Saccharomyces cerevisiae YBR0 NTH2, hypothetical start
												YALI0D15598g	similar to sp|P32356 Saccharomy cerevisiae YDR001c NTH1 neut trehalase, hypothetical start
												KLLA0E17325g	gi|1351293|sp|P49381|TREA_KLU Kluyveromyces lactis NEUTRA TREHALASE (ALPHA, ALPHA TREHALASE) (ALPHA, ALPH TREHALOSE GLUCOHYDROLA start by similarity
												CAGL0C04323g	similar to sp|P32356 Saccharomy cerevisiae YDR001c NTH1 neut trehalase, hypothetical start
NTH1 (YDR001C)	3.2.1.28	sp|P32356 Saccharomyces cerevisiae YDR001c NTH1 neutral trehalase (alpha,alpha-trehalase) P2.445.f2.1	viable	Ess	Ess	Ess	0.1	Ess	sckdy	2 2 1 1 1	GLR.157	DEHA0B02673g	similar to sp|P52494 Candida albi Neutral trehalase (EC 3.2.1.28), sta similarity
												CAGL0M10439g	highly similar to sp|P32356 Saccharomyces cerevisiae YDR0 NTH1 neutral trehalase or sp|P35 Saccharomyces cerevisiae YBR0 NTH2, hypothetical start
												YALI0D15598g	similar to sp|P32356 Saccharomy cerevisiae YDR001c NTH1 neut trehalase, hypothetical start
												KLLA0E17325g	gi|1351293|sp|P49381|TREA_KLU Kluyveromyces lactis NEUTRA TREHALASE (ALPHA, ALPHA TREHALASE) (ALPHA, ALPH TREHALOSE GLUCOHYDROLA start by similarity
												CAGL0C04323g	similar to sp|P32356 Saccharomy cerevisiae YDR001c NTH1 neut trehalase, hypothetical start
ATH1 (YPR026W)	3.2.1.28	sp|P48016 Saccharomyces cerevisiae YPR026w ATH1 acid trehalase, vacuolar singleton	viable	0.7	0.9	0.7	0.5	0.5	sckd-	1 1 1 1 0	GLR.1078	KLLA0E06622g	similar to sp|P48016 Saccharomy cerevisiae YPR026w ATH1 aci trehalase, vacuolar singleton, hypothetical start
												CAGL0K05137g	similar to sp|P48016 Saccharomy cerevisiae YPR026w Vacuolar a trehalase precursor, hypothetical s
												DEHA0D15774g	similar to CA2574|CaATH1 Canc albicans CaATH1 acid trehalase vacuolar, hypothetical start
													similar to CA3841|IPF16640 Canc

DEHA0G07777g	albicans IPF16640 unknown funct hypothetical start
KLLA0E24959g	no similarity, hypothetical start
KLLA0C05016g	some similarities with sgd|S00059 Saccharomyces cerevisiae YOR38 hypothetical protein, hypothetical
DEHA0C12155g	some similarities with tr|Q1221 Saccharomyces cerevisiae YOR009 start, frameshift
DEHA0F20570g	weakly similar to CA4243|IPF164 Candida albicans IPF16491, hypoth start
YALI0D08140g	similar to sp|P36110 Saccharomy cerevisiae YKR013w PRY2 prote precursor (Pathogen related in Sc 2) by similarity
DEHA0F27148g	similar to CA1909|IPF20091 Canc albicans IPF20091, hypothetical s
CAGL0C05665g	some similarities with sp|P3617 Saccharomyces cerevisiae YKR10 FLO10, no start, frameshift
KLLA0A04367g	some similarities with sgd|S00059 Saccharomyces cerevisiae YOR38 hypothetical protein, hypothetical
YALI0B18568g	no similarity, hypothetical start
DEHA0D16907g	similar to CA0605|CaUTR2 Cand albicans CaUTR2, hypothetical st
CAGL0J11913g	some similarities with sp|P0864 Saccharomyces cerevisiae YIR01 STA1, no start, frameshift
CAGL0L03289g	similar to sp|P46955 Saccharomy cerevisiae YJL116c NCA3 or sp|P3 Saccharomyces cerevisiae YKR04 UTH1, hypothetical start
YALI0D13255g	No Similarity, Hypothetical Star
KLLA0D02420g	some similarities with sp|P3611 Saccharomyces cerevisiae YKR01 PRY2, hypothetical start
CAGL0J08910g	similar to tr|Q05790 Saccharomy cerevisiae YLR213c CRR1, hypoth start
KLLA0F04433g	similar to sp|P53616 Saccharomy cerevisiae YNL066w SUN4, start similarity
CAGL0G04125g	weakly similar to sp|P20840 Saccharomyces cerevisiae YJR00 SAG1 alpha-agglutinin, hypotheti start
YALI0A00506g	weakly similar to sp|P43633 Saccharomyces cerevisiae YGL02 ALK1 DNA damage-responsive pro hypothetical start
YALI0C21186g	no similarity, hypothetical start
CAGL0G03421g	some similarities with sp|P0864 Saccharomyces cerevisiae YIR01 STA1, hypothetical start
CAGL0D02530g	weakly similar to sp|P42835 Saccharomyces cerevisiae YNL32 EGT2 cell-cycle regulation prote hypothetical start
YALI0B14795g	some similarities with sp|P4055 Saccharomyces cerevisiae Cell w protein TIR3 precursor, hypothetica
YALI0E34463g	some similarities with wi|NCU066 Neurospora crassa NCU06697. hypothetical protein (67439 - 697 hypothetical start
DEHA0F22803g	weakly similar to CA4237|IPF63 Candida albicans IPF6375, hypothe start
YALI0E08008g	weakly similar to tr|Q08294 Saccharomyces cerevisiae YOL15 hypothetical start

DEHA0C15092g	highly similar to sp|P36135 Saccharomyces cerevisiae YKR04 UTH1, start by similarity
KLLA0E24937g	no similarity, hypothetical start
CAGL0H09592g	highly similar to sp|P10863 Saccharomyces cerevisiae YER01 TIR1 or sp|P33890 Saccharomyc cerevisiae YOR010c TIR2, start similarity
YALI0E19635g	no similarity, hypothetical start
YALI0A07601g	weakly similar to sp|P08640 Saccharomyces cerevisiae YIR01 STA1 extracellular alpha-1, 4-glu glucosidase, hypothetical start
YALI0F02343g	weakly similar to tr|O42970 Schizosaccharomyces pombe SPBC1E8.05 Serine rich protein, sta similarity
KLLA0F04906g	some similarities with sgd|S00042 Saccharomyces cerevisiae YLR21 CRR1, hypothetical start
YALI0C14630g	weakly similar to sp|Q04893 Saccharomyces cerevisiae YMR31 hypothetical start
YALI0C08349g	Weakly similar to sp|P08640 Saccharomyces cerevisiae YIR01 STA1 extracellular alpha-1,4-gluc glucosidase, 5 end
YALI0A18381g	no similarity, hypothetical start
YALI0C09680g	similar to sp|P53301 Saccharomy cerevisiae YGR189c CRH1 family putative glycosidases might exer common role in cell wall organizat start by similarity
DEHA0G22066g	some similarities with sp|P5330 Saccharomyces cerevisiae YGR18 CRH1 family of putative glycosida might exert a common role in cell organization, hypothetical start
YALI0E18700g	no similarity, hypothetical start
YALI0D26257g	weakly similar to sp|P08640 Saccharomyces cerevisiae YIR01 STA1 extracellular alpha-1,4-gluc glucosidase, hypothetical start
CAGL0A00231g	similar to sp|P43633 Saccharomy cerevisiae YGL021w ALK1 DN damage-responsive protein, hypothe start
CAGL0G05896g	similar to sp|P38844 Saccharomy cerevisiae YHR143w, start by simil
CAGL0K09130g	some similarities with tr|Q0867 Saccharomyces cerevisiae YOR24 SRL1, hypothetical start
KLLA0C04928g	no similarity, hypothetical start
DEHA0C05566g	similar to sp|P53832 Saccharomy cerevisiae YNL283c WSC2 glucoamylase III, hypothetical st
DEHA0B02222g	weakly similar to sp|P08640 Saccharomyces cerevisiae YIR01 STA1 extracellular alpha-1,4-gluc glucosidase, hypothetical start
YALI0E15015g	no similarity, hypothetical start
CAGL0C00209g	some similarities with sp|P4717 Saccharomyces cerevisiae YJR15 hypothetical start
DEHA0E10109g	similar to sp|Q04893 Saccharomy cerevisiae YMR317w similarity mucins, glucan 1, 4-alpha-glucosic and exo-alpha-sialidase, hypothet start
YALI0D21230g	some similarities with tr|Q0065 Emericella nidulans FlbD, hypothe start

BSC1 (YDL037C)	3.2.1.3	Saccharomyces cerevisiae YDL037c strong similarity to glucan 1,4-alpha-glucosidase P2.341.f2.1	viable	NA	NA	NA	NA	NA	sckdy	45 35 26 36 48	GLC.1	YALI0F27203g	no similarity, hypothetical start
												YALI0D06149g	similar to sp|P47032 Saccharomy cerevisiae YJL079c PRY1 prote precursor (Pathogen related in Sc 1) by similarity
												DEHA0F18271g	some similarities with wi|NCU069 Neurospora crassa NCU06981.1 hypothetical start
												YALI0C16148g	no similarity, hypothetical start
												KLLA0E14982g	similar to sp|P36135 Saccharomy cerevisiae YKR042w UTH1 involv the aging process, start by similar
												YALI0F10175g	no similarity, hypothetical start
												YALI0E04532g	no similarity, hypothetical start
												DEHA0F04158g	similar to CA0076|IPF8866 Cand albicans IPF8866, hypothetical st
												DEHA0G22902g	some similarities with sp|P5330 Saccharomyces cerevisiae YGR18 CRH1, hypothetical start
												DEHA0E03377g	similar to CA4245|IPF4303 Cand albicans IPF4303 unknown functi hypothetical start
												YALI0A00682g	no similarity, hypothetical start
												CAGL0L05434g	similar to sp|P36135 Saccharomy cerevisiae YKR042w UTH1 or sp|P46955 Saccharomyces cerevis YJL116c NCA3, hypothetical sta
												DEHA0B02266g	
												CAGL0C02211g	similar to sp|P32623 Saccharomy cerevisiae YEL040w UTR2 cell w protein, hypothetical start
												YALI0F26081g	no similarity, hypothetical start
												DEHA0F14531g	weakly similar to ca|CA5614|IPF Candida albicans IPF522, hypothe start
												CAGL0A04081g	weakly similar to tr|Q05777 Saccharomyces cerevisiae YLR19 hypothetical start
												DEHA0B10868g	some similarities with sp|P4703 Saccharomyces cerevisiae YJL07 PRY3 closely related to the plant P class of pathogen proteins, hypothe start
												KLLA0E10967g	no similarity, hypothetical start
												CAGL0G09449g	similar to sp|P53301 Saccharomy cerevisiae YGR189c CRH1, hypoth start
												DEHA0G02618g	weakly similar to tr|Q9Y8F2 Canc albicans Agglutinin-like protein 6, by similarity
												YALI0E18722g	no similarity, hypothetical start
												KLLA0E04939g	some similarities with sgd|S0006 Saccharomyces cerevisiae YLR39 Secretory Stress Response protein hypothetical start
												DEHA0F00638g	
												KLLA0B11055g	no similarity, hypothetical start
												DEHA0F22242g	highly similar to CA0883|CaSUN Candida albicans CaSUN41 Putative wall beta-glucosidase (by homolog start by similarity
												KLLA0C17985g	some similarities with sp|P3233 Saccharomyces cerevisiae YGR01 MSB2 multicopy suppressor of a C bud emergence defect, hypothetical
												YALI0B15510g	similar to sp|P32623 Saccharomy cerevisiae YEL040w UTR2 cell w protein P3.82.f3.1, start by similar
												CAGL0F01463g	similar to sp|P10863 Saccharomy cerevisiae YER011w TIR1, start similarity
												DEHA0D05093g	no similarity, hypothetical start

CAGL0C03872g	similar to sp|P40552 Saccharomy cerevisiae YIL011w TIR3, start similarity
DEHA0G15543g	similar to CA3335|IPF8682 Cand albicans IPF8682, hypothetical st
CAGL0J02530g	some similarities with tr|Q1221 Saccharomyces cerevisiae YOR00 hypothetical start
CAGL0J09922g	similar to sp|P53616 Saccharomy cerevisiae YNL066w SUN4 or sp|P40472 Saccharomyces cerevis YIL123w SIM1, start by similari
DEHA0B04213g	similar to sp|P32334 Saccharomy cerevisiae YGR014w MSB2 multic suppressor of a CDC24 bud emerg defect, hypothetical start
YALI0D19316g	no similarity, hypothetical start
YALI0F27687g	no similarity, hypothetical start
YALI0F20548g	no similarity, hypothetical start
DEHA0C17644g	weakly similar to sp|P08640 Saccharomyces cerevisiae YIR01 STA1 extracellular alpha-1, 4-glu glucosidase, hypothetical start
CAGL0F05137g	similar to sp|P47032 Saccharomy cerevisiae YJL079c PRY1, start similarity
DEHA0B10659g	weakly similar to sp|P54867 Saccharomyces cerevisiae YOR00 SLG1 required for cell wall integrit for stress response, hypothetical s
CAGL0A03608g	some similarities with tr|Q0829 Saccharomyces cerevisiae YOL15 hypothetical start
KLLA0E19657g	no similarity, hypothetical start
KLLA0E02046g	some similarities with sp|P4283 Saccharomyces cerevisiae YNL32 EGT2 cell-cycle regulation prote singleton, hypothetical start
YALI0D02024g	weakly similar to KLLA-IPF530 Kluyveromyces lactis, hypothetical
CAGL0J11902g	some similarities with sp|P0864 Saccharomyces cerevisiae YIR01 STA1, no start, frameshift
CAGL0G10175g	some similarities with sp|P4717 Saccharomyces cerevisiae YJR15 hypothetical start
KLLA0C01496g	some similarities with sp|P4703 Saccharomyces cerevisiae YJL07 PRY1, hypothetical start
KLLA0C04730g	some similarities with sp|P2902 Saccharomyces cerevisiae YLR28 CTS1 endochitinase singleton, hypothetical start
YALI0C20779g	no similarity, hypothetical start
CAGL0G00858g	similar to sp|P36027 Saccharomy cerevisiae YLR332w MID2 mati process protein, hypothetical sta
DEHA0B01232g	similar to sp|P36110 Saccharomy cerevisiae YKR013w PRY2 similar the plant PR-1 class of pathogen re proteins, start by similarity
CAGL0F03003g	some similarities with sp|P3233 Saccharomyces cerevisiae YGR01 MSB2 or sp|P41809 Saccharomy cerevisiae YDR420w HKR1, hypothetical start
CAGL0H06413g	similar to sp|O13547 Saccharomy cerevisiae YLR390wa CW14, star similarity
KLLA0C12177g	some similarities with sp|Q1221 Saccharomyces cerevisiae YOL10 WSC3 cell wall integrity and stre response component 3, hypothetical

												DEHA0A05302g	similar to CA5213|CaSSR1 Cand albicans CaSSR1 Secretory Stre Response protein 1, start by simila
												CAGL0H09614g	highly similar to sp|P10863 Saccharomyces cerevisiae YER01 TIR1 or sp|P33890 Saccharomyc cerevisiae YOR010c TIR2, start similarity
												KLLA0E00704g	gi|5531272|emb|CAB50897.1 Kluyveromyces lactis WSC4 homol start by similarity
												DEHA0G19877g	some similarities with sp|P5330 Saccharomyces cerevisiae YGR1 CRH1 family of putative glycosid might exert a common role in cell organization, hypothetical start
												YALI0E33539g	similar to sp|P53616 Saccharomy cerevisiae YNL066w SUN4, start similarity
												DEHA0C11814g	no similarity, hypothetical start
												KLLA0A03179g	some similarities with sp|P3602 Saccharomyces cerevisiae YLR33 MID2 mating process protein, hypothetical start
												CAGL0J11176g	some similarities with sp|P5388 Saccharomyces cerevisiae YNL17 hypothetical start
												YALI0E23969g	no similarity, hypothetical start
												KLLA0E24893g	no similarity, hypothetical start
												YALI0E35090g	weakly similar to sp|P32323 Saccharomyces cerevisiae YNR04 AGA1 a-agglutinin anchor subu singleton, hypothetical start
												DEHA0B05478g	similar to CA0728|IPF7345 Cand albicans IPF7345 unknown functi hypothetical start
												YALI0E33913g	weakly similar to sp|P08640 Saccharomyces cerevisiae YIR01 STA1 extracellular alpha-1,4-glu glucosidase P2.341.f2.1, hypothet start
												KLLA0D08239g	some similarities with sp|P5388 Saccharomyces cerevisiae YNL1 singleton, hypothetical start
												CAGL0J00253g	similar to sp|P53214 Saccharomy cerevisiae YGR023w MTL1, hypothetical start
												KLLA0F02497g	weakly similar to sp|P39732 Saccharomyces cerevisiae YAL0 FUN21 hypothetical protein single hypothetical start
												YALI0E20757g	some similarities with sp|O1354 Saccharomyces cerevisiae YLR390 SSR1 Secretory Stress Response pr 1, hypothetical start
												CAGL0G05808g	weakly similar to sp|P53882 Saccharomyces cerevisiae YNL17 start by similarity
												YALI0F04213g	emb|Z69781 Yarrowia lipolytica T gene, thermosensitive suppressor 7SRNA defect, involved in the sig recognition particle-dependent translocation pathway of secreto proteins, identified start
												YALI0D13266g	No Similarity, Hypothetical Sta
												CAGL0G08668g	similar to sp|P53616 Saccharomy cerevisiae YNL066w SUN4 or sp|P40472 Saccharomyces cerevis YIL123w SIM1, hypothetical sta
												KLLA0D14377g	weakly similar to sp|P54867 Saccharomyces cerevisiae YOR0 SLG1 required for cell wall integrit for stress response singleton, start similarity

												DEHA0B01804g	no similarity, hypothetical start
												CAGL0C03575g	some similarities with sp|P4717 Saccharomyces cerevisiae YJR15 hypothetical start
												YALI0E05819g	weakly similar to sp|P08640 Saccharomyces cerevisiae YIR01 STA1 extracellular alpha-1, 4-glu glucosidase, hypothetical start
												CAGL0F01485g	similar to sp|P10863 Saccharomy cerevisiae YER011w TIR1 or tr|Q1 Saccharomyces cerevisiae YOR00 hypothetical start
												CAGL0M11792g	weakly similar to sp|P39732 Saccharomyces cerevisiae YAL0 FUN21, hypothetical start
												DEHA0D05423g	similar to Candida albicans CaWS Cell wall integrity
												YALI0F05720g	weakly similar to sp|P53214 Saccharomyces cerevisiae YGR02 MTL1 potential cell wall stress se
												YALI0D09185g	some similarities with sp|P3232 Saccharomyces cerevisiae YNR04 AGA1 a-agglutinin anchor subur hypothetical start
												YALI0D07854g	no similarity, hypothetical start
												KLLA0F22671g	some similarities with sp|P5330 Saccharomyces cerevisiae YGR1 CRH1 family of putative glycosida might exert a common role in cell organization, hypothetical start
												YALI0F05786g	some similarities with sp|P1086 Saccharomyces cerevisiae YER01 TIR1 cold-shock, hypothetical st
												DEHA0E21890g	no similarity, hypothetical start
												YALI0A16214g	weakly similar to sp|P53832 Saccharomyces cerevisiae Cell w integrity and stress response compo 2 precursor, hypothetical start
												KLLA0C11583g	weakly similar to sp|P43633 Saccharomyces cerevisiae YGL02 ALK1 DNA damage-responsive pro start by similarity
												DEHA0D10780g	similar to CA2150|IPF19940 Canc albicans IPF19940 unknown funct start by similarity
												YALI0C08140g	no similarity, hypothetical start
												DEHA0F26862g	similar to sp|P47032 Saccharomy cerevisiae YJL079c PRY1, hypothe start
												YALI0E24673g	weakly similar to sp|P53301 Saccharomyces cerevisiae YGR1 CRH1, hypothetical start
SGA1 (YIL099W)	3.2.1.3	sp|P08019 Saccharomyces cerevisiae YIL099w SGA1 sporulation specific glucan 1,4-alpha-glucosidase singleton	viable	0.9	0.7	0.6	Non	0.8	sckdy	1 1 1 1 1	GLR.507	YALI0E05203g	some similarities with sp|P0801 Saccharomyces cerevisiae YIL09 SGA1 sporulation specific glucan alpha-glucosidase, hypothetical s
												DEHA0A12705g	similar to sp|P08019 Saccharomy cerevisiae YIL099w SGA1 sporula specific glucan 1,4-alpha -glucosic hypothetical start
												KLLA0F04059g	weakly similar to sp|P08019 Saccharomyces cerevisiae YIL09 SGA1 sporulation specific glucan alpha-glucosidase singleton, hypoth start
												CAGL0G02717g	similar to sp|P08019 Saccharomy cerevisiae YIL099w SGA1 sporula specific glucan 1, 4-alpha-glucosic hypothetical start
												YALI0E33715g	weakly similar to sp|P08640 Saccharomyces cerevisiae YIR01 STA1 extracellular alpha-1,4-glu glucosidase P2.341.f2.1, hypothet start

												DEHA0F13915g	similar to ca|CA2024|IPF9616 Can albicans IPF9616 unknown functi start by similarity
												KLLA0B14927g	no similarity, hypothetical star
												KLLA0E21131g	no similarity, hypothetical star
												YALI0B06919g	no similarity, hypothetical star
												YALI0B12606g	no similarity, hypothetical star
												YALI0B17028g	weakly similar to tr|Q8XQP2 Ralst solanacearum Putative hemagglutinin/hemolysin-related pr hypothetical start
												YALI0D18436g	no similarity, hypothetical star
												KLLA0C11517g	no similarity, hypothetical star
												KLLA0A04345g	no similarity, hypothetical star
												YALI0E16731g	no similarity, hypothetical star
												YALI0C05390g	no similarity, hypothetical star
												CAGL0E06600g	some similarities with sp|P3889 Saccharomyces cerevisiae YHR21 FLO5, hypothetical start
												DEHA0G20141g	weakly similar to CA2769|IPF15 Candida albicans IPF15870, hypoth start
												YALI0C09031g	no similarity, no start
												KLLA0C01276g	no similarity, hypothetical star
												YALI0E33737g	weakly similar to CA2714|CaIFI Candida albicans CaIFF2, hypothe start
												YALI0E29425g	weakly similar to sp|P08640 Saccharomyces cerevisiae YIR01 STA1 extracellular alpha-1,4-gluc glucosidase, hypothetical start
												YALI0D02299g	similar to sp|P08640 Saccharomy cerevisiae YIR019c STA1 extracel alpha-1, 4-glucan glucosidase, hypothetical start
												KLLA0A11748g	no similarity, hypothetical star
												KLLA0D07942g	no similarity, hypothetical star
												YALI0D00627g	weakly similar to sp|P32334 Saccharomyces cerevisiae YGR01 MSB2 multicopy suppressor of a Cl bud emergence defect, hypothetical
												KLLA0F24486g	no similarity, hypothetical star
												YALI0C24211g	no similarity, hypothetical star
												DEHA0B02244g	
												CAGL0M14069g	some similarities with sp|P3889 Saccharomyces cerevisiae YHR21 FLO5, hypothetical start
												YALI0A01870g	similar to sp|P29029 Saccharomy cerevisiae Endochitinase precursor 3.2.1.14 Soluble cell wall protein 2) by similarity
												YALI0E16841g	no similarity, hypothetical star
												YALI0C13970g	weakly similar to sp|P08640 Saccharomyces cerevisiae YIR01 STA1 extracellular alpha-1, 4-glu glucosidase P2.341.f2.1, hypothet start
												YALI0A09559g	no similarity, hypothetical star
												YALI0F15653g	some similarities with sp|P0864 Saccharomyces cerevisiae YIR01 STA1 extracellular alpha-1, 4-glu glucosidase, hypothetical start
												CAGL0M09779g	similar to sp|P29029 Saccharomy cerevisiae YLR286c endochitina hypothetical start
												KLLA0C04994g	weakly similar to sgd|S000294 Saccharomyces cerevisiae YDR5 start by similarity
												YALI0D13530g	no similarity, hypothetical star
													some similarities with sp|P2084

	MUC1 (YIR019C)	3.2.1.3	sp|P08640 Saccharomyces cerevisiae YIR019c STA1 extracellular alpha-1,4-glucan glucosidase P2.341.f2.1	viable	NA	NA	NA	NA	NA	sckdy	7 4 12 8 43	GLC.11	KLLA0E09658g	Saccharomyces cerevisiae YJR00 SAG1 alpha-agglutinin singleto hypothetical start
													YALI0D22396g	weakly similar to sp|P29029 Saccharomyces cerevisiae YLR28 CTS1endochitinase singleton, hypothetical start
													YALI0F10802g	weakly similar to sp|P08640 Saccharomyces cerevisiae YIR01 STA1 extracellular alpha-1, 4-glu glucosidase, no start
													YALI0D13992g	no similarity, hypothetical start
													YALI0E22572g	weakly similar to sp|P08640 Saccharomyces cerevisiae YIR01 STA1 extracellular alpha-1, 4-glu glucosidase
													YALI0C16247g	no similarity, hypothetical start
													YALI0C08476g	weakly similar to sp|P08640 Saccharomyces cerevisiae YIR01 STA1 extracellular alpha-1, 4-glu glucosidase, hypothetical start
													DEHA0A14784g	similar to CA1678|IPF5185 Cand albicans IPF5185 putative cell w protein (by homology), start by simi
													YALI0C03916g	weakly similar to KLLA-IPF618 Kluyveromyces lactis IPF 6186. hypothetical start
													KLLA0E10945g	
													DEHA0G19096g	some similarities with CA1898|IPF1 Candida albicans IPF11998, hypoth start
													YALI0E32395g	weakly similar to sp|P08640 Saccharomyces cerevisiae YIR01 STA1 extracellular alpha-1, 4-glu glucosidase P2.341.f2.1, hypothet start
													YALI0E14993g	no similarity, hypothetical start
													YALI0D18249g	some similarities with tr|Q8WZS Neurospora crassa Dynactin (150 dynein-associated polypeptide) ro hypothetical start
													YALI0E31273g	weakly similar to tr|Q8SY55 Droso melanogaster GH09355p, hypothet start
													YALI0E02442g	no similarity, hypothetical start
													YALI0A15796g	no similarity, hypothetical start
													YALI0B15422g	no similarity, hypothetical start
													YALI0C03894g	weakly similar to DEHA-IPF878 Debaryomyces hansenii IPF 8785 hypothetical start
													YALI0A13079g	no similarity, hypothetical start
													KLLA0A01826g	some similarities with sp|P4180 Saccharomyces cerevisiae YDR42 HKR1 Hansenula MrakII k9 killer t resistance protein, hypothetical st
													DEHA0G01573g	weakly similar to sp|P08640 Saccharomyces cerevisiae YIR01 STA1 extracellular alpha-1, 4-glu glucosidase, start by similarity
													YALI0D22825g	no similarity, hypothetical start
													YALI0F07216g	similar to sp|P08640 Saccharomy cerevisiae YIR019c STA1 extracel alpha-1, 4-glucan glucosidase, hypothetical strart, start by simila
													YALI0D25014g	weakly similar to tr|Q97P71 Streptococcus pneumoniae Cell w surface anchor family protein, hypothetical start
													YALI0C18293g	weakly similar to tr|Q9N4S7 Caenorhabditis elegans Y51B11A protein, hypothetical start
														weakly similar to sp|P32334

												CAGL0F08833g	Saccharomyces cerevisiae YGR01 MSB2 multicopy suppressor of a C bud emergence defect, hypothetical
												YALI0E22550g	weakly similar to sp|P08640 Saccharomyces cerevisiae YIR01 STA1 extracellular alpha-1,4-glu glucosidase, hypothetical start
												YALI0D02915g	no similarity, hypothetical start
												DEHA0G06655g	similar to sp|P29029 Saccharomy cerevisiae Endochitinase precursor 3.2.1.14) (Soluble cell wall protein start by similarity
												YALI0B16676g	no similarity, hypothetical start
												DEHA0G01595g	weakly similar to sp|P40442 Saccharomyces cerevisiae YIL16 realated to glucan 1, 4-alpha-glucos hypothetical start
												YALI0E20229g	no similarity, hypothetical start
PGU1 (YJR153W)	3.2.1.15	-	viable	0.4	Ess	0.1	0.4	Ess	s----	1 0 0 0 0	none	-	-
GPH1 (YPR160W)	2.4.1.1	sp|P06738 Saccharomyces cerevisiae YPR160w GPH1 glycogen phosphorylase singleton	viable	NA	NA	NA	NA	NA	sckdy	1 1 1 1 1	GLR.500	KLLA0F10065g	highly similar to sp|P06738 Saccharomyces cerevisiae YPR16 GPH1 glycogen phosphorylase sing start by similarity
												CAGL0F04895g	highly similar to sp|P06738 Saccharomyces cerevisiae YPR16 GPH1 glycogen phosphorylase, sta similarity
												DEHA0F23782g	highly similar to CA5206|CaGPH Candida albicans CaGPH1 Glycog phosphorylase (by homology), hypothetical start
												YALI0F04169g	similar to sp|P06738 Saccharomy cerevisiae YPR160w GPH1 glyco phosphorylase, hypothetical sta
EXG2 (YDR261C)	3.2.1.58	sp|P52911 Saccharomyces cerevisiae YDR261c EXG2 exo-beta-1,3-glucanase minor isoform P3.33.f3.1	viable	NA	NA	NA	NA	NA	sckdy	4 4 2 5 2	GLR.3219	KLLA0F18788g	similar to sp|P38081 Saccharomy cerevisiae YBR056w singleton, sta similarity
												CAGL0M08756g	similar to sp|P52911 Saccharomy cerevisiae YDR261c exo-beta-1 glucanase, hypothetical start
												CAGL0I00484g	similar to sp|P23776 Saccharomy cerevisiae YLR300w EXG1, start similarity
												DEHA0D09196g	similar to sp|P29717 Candida albic CaEXG1 Glucan 1, 3-beta-glucosi precursor, hypothetical start
												DEHA0F01485g	similar to CA4180|CaEXG2 Cand albicans CaEXG2, hypothetical st
												KLLA0C05324g	gi|1150442|emb|CAA86949.1 Kluyveromyces lactis exo-1, 3-be glucanase/1, 3-beta-D-Glucan glucanohydrolase, start by similar
												DEHA0F01716g	similar to tr|O93939 Hansenula ano Exo-1,3-beta-glucanase (EC 3.2.1. hypothetical start
												YALI0F05390g	sp|Q12725 Yarrowia lipolytica Gluc 3-beta-glucosidase precursor (E 3.2.1.58) (Exo-1, 3-beta- glucana identified start
												CAGL0H10120g	similar to sp|P38081 Saccharomy cerevisiae YBR056w, start by simil
												DEHA0G07095g	no similarity, hypothetical start
												YALI0E34155g	some similarities with KLLA-IPF6 Kluyveromyces lactis IPF 644.1 hypothetical start
												CAGL0G09515g	similar to sp|P23776 Saccharomy cerevisiae YLR300w EXG1 exo-be 3-glucanase (I/II), hypothetical st
												DEHA0F26378g	similar to ca|CA5339|IPF885 Canc albicans IPF885 glucan 1,3-beta glucosidase (by homology), hypothe start

BGL2 (YGR282C)	3.2.1.58	sp|P15703 Saccharomyces cerevisiae YGR282c BGL2 endo-beta-1,3-glucanase of the cell wall P4.19.f3.1	viable	NA	NA	NA	NA	NA	sckdy	1 1 1 2 2	GLR.3339	YALI0F13299g	weakly similar to tr|Q96W35 Ophiostoma novo-ulmi Glucan 1, 3 glucosidase-like protein (Fragmen hypothetical start
												YALI0B03564g	similar to sp|P43070 Candida albic Glucan 1,3-beta -glucosidase precu (EC 3.2.1.58) (Exo-1, 3-beta-glucanase), start by similarity
												DEHA0G19943g	similar to sp|P15703 Saccharomy cerevisiae YGR282c BGL2 endo-be 3-glucanase of the cell wall, hypoth start
												CAGL0G00220g	highly similar to sp|P15703 Saccharomyces cerevisiae YGR28 BGL2, start by similarity
												KLLA0F03036g	highly similar to sp|P15703 Saccharomyces cerevisiae YGR28 BGL2 endo-beta-1, 3-glucanase of cell wall, start by similarity
												DEHA0E22715g	some similarities with CA2245|IPF Candida albicans IPF7409 unkno function, hypothetical start
EXG1 (YLR300W)	3.2.1.58	sp|P23776 Saccharomyces cerevisiae YLR300w EXG1 exo-beta-1,3-glucanase (I/II), major isoform P3.33.f3.1	viable	0.8	Non	Non	Non	Non	sckdy	4 4 2 5 2	GLR.3219	KLLA0F18788g	similar to sp|P38081 Saccharomy cerevisiae YBR056w singleton, sta similarity
												CAGL0M08756g	similar to sp|P52911 Saccharomy cerevisiae YDR261c exo-beta-1 glucanase, hypothetical start
												CAGL0I00484g	similar to sp|P23776 Saccharomy cerevisiae YLR300w EXG1, start similarity
												DEHA0D09196g	similar to sp|P29717 Candida albic CaEXG1 Glucan 1, 3-beta-glucosi precursor, hypothetical start
												DEHA0F01485g	similar to CA4180|CaEXG2 Canc albicans CaEXG2, hypothetical st
												KLLA0C05324g	gi|1150442|emb|CAA86949.1 Kluyveromyces lactis exo-1, 3-be glucanase/1, 3-beta-D-Glucan glucanohydrolase, start by similar
												DEHA0F01716g	similar to tr|O93939 Hansenula ano Exo-1,3-beta-glucanase (EC 3.2.1. hypothetical start
												YALI0F05390g	sp|Q12725 Yarrowia lipolytica Gluc 3-beta-glucosidase precursor (E 3.2.1.58) (Exo-1, 3-beta- glucana identified start
												CAGL0H10120g	similar to sp|P38081 Saccharomy cerevisiae YBR056w, start by simil
												DEHA0G07095g	no similarity, hypothetical start
												YALI0E34155g	some similarities with KLLA-IPF6 Kluyveromyces lactis IPF 644.1 hypothetical start
												CAGL0G09515g	similar to sp|P23776 Saccharomy cerevisiae YLR300w EXG1 exo-be 3-glucanase (I/II), hypothetical st
												DEHA0F26378g	similar to ca|CA5339|IPF885 Canc albicans IPF885 glucan 1,3-beta glucosidase (by homology), hypothe start
												KLLA0F18788g	similar to sp|P38081 Saccharomy cerevisiae YBR056w singleton, sta similarity
												CAGL0M08756g	similar to sp|P52911 Saccharomy cerevisiae YDR261c exo-beta-1 glucanase, hypothetical start
												CAGL0I00484g	similar to sp|P23776 Saccharomy cerevisiae YLR300w EXG1, start similarity
												DEHA0D09196g	similar to sp|P29717 Candida albic CaEXG1 Glucan 1, 3-beta-glucosi precursor, hypothetical start
												DEHA0F01485g	similar to CA4180|CaEXG2 Canc albicans CaEXG2, hypothetical st

SPR1 (YOR190W)	3.2.1.58	sp|P32603 Saccharomyces cerevisiae YOR190w SPR1 exo-1,3-beta-glucanase precursor P3.33.f3.1	viable	0.6	0.8	ND	0.3	0.4	sckdy	4 4 2 5 2	GLR.3219	KLLA0C05324g	gi|1150442|emb|CAA86949.1 Kluyveromyces lactis exo-1, 3-be glucanase/1, 3-beta-D-Glucan glucanohydrolase, start by similar
												DEHA0F01716g	similar to tr|O93939 Hansenula ano Exo-1,3-beta-glucanase (EC 3.2.1. hypothetical start
												YALI0F05390g	sp|Q12725 Yarrowia lipolytica Gluc 3-beta-glucosidase precursor (E 3.2.1.58) (Exo-1, 3-beta- glucana identified start
												CAGL0H10120g	similar to sp|P38081 Saccharomy cerevisiae YBR056w, start by simil
												DEHA0G07095g	no similarity, hypothetical start
												YALI0E34155g	some similarities with KLLA-IPF6 Kluyveromyces lactis IPF 644.1 hypothetical start
												CAGL0G09515g	similar to sp|P23776 Saccharomy cerevisiae YLR300w EXG1 exo-be 3-glucanase (I/II), hypothetical st
												DEHA0F26378g	similar to ca|CA5339|IPF885 Canc albicans IPF885 glucan 1,3-beta glucosidase (by homology), hypoth start
VPS8 (YAL002W)	2.7.1.-	sp|P39702 Saccharomyces cerevisiae YAL002w VPS8 vacuolar sorting protein, 134 kD singleton	Exhibits sensitivity at 15 generations when grown in 10 uM nystatin.	NA	NA	NA	NA	NA	sckd-	1 1 1 1 0	GLR.1058	DEHA0A09020g	similar to sp|P39702 Saccharomy cerevisiae YAL002w VPS8 vacuo sorting protein, 134 kD, start by similarity
												KLLA0C18491g	weakly similar to sp|P39702 Saccharomyces cerevisiae YAL00 VPS8 vacuolar sorting protein, 134 singleton, start by similarity
												CAGL0A00781g	similar to sp|P39702 Saccharomy cerevisiae YAL002w VPS8, hypoth start
												KLLA0F11319g	similar to sgd|S0006071 Saccharom cerevisiae YPL150w, start by simil
												CAGL0L07810g	similar to sp|P25333 Saccharomy cerevisiae YCR008w SAT4 serine/threonine-specific protein ki start by similarity
												CAGL0K11550g	similar to sp|P28708 Saccharomy cerevisiae YKL116c, hypothetical
												YALI0F11385g	weakly similar to SP|P38691 Saccharomyces cerevisiae YHR0 KSP1 ser/thr protein kinase and DE IPF5974.1, start by similarity
												KLLA0A09713g	similar to sp|Q03533 Saccharomy cerevisiae YMR291w, start by simi
												KLLA0E17127g	similar to sp|P38691 Saccharomy cerevisiae YHR082c KSP1 ser/t protein kinase, start by similarit
												YALI0C04158g	similar to sp|P18961 Saccharomy cerevisiae Serine/threonine-prote kinase YPK2/YKR2, hypothetical
												DEHA0F24676g	similar to sp|P24719 Saccharomy cerevisiae YOR351c MEK1 ser/t protein kinase
												DEHA0G14817g	similar to CA2643|CaHSL1 Cand albicans CaHSL1, hypothetical st
												DEHA0C18150g	similar to sp|P40494 Saccharomy cerevisiae YIL095w PRK1 serine/threonine protein kinase, sta similarity
												CAGL0K10604g	similar to sp|P27466 Saccharomy cerevisiae YFR014c CMK1 Ca2+/calmodulin-dependent ser/ protein kinase type I, hypothetical
												DEHA0C08591g	similar to sp|P22204 Saccharomy cerevisiae YGR092w DBF2, hypothetical start, sequence gap
												YALI0F13629g	some similarities with sp|P2356 Saccharomyces cerevisiae YLR36

												YALI0F15629g	STE11 ser/thr protein kinase of t MEKK family, hypothetical sta
												KLLA0C06138g	similar to sp|P32562 Saccharomy cerevisiae YMR001c CDC5 involv regulation of DNA replication, sta similarity
												YALI0F16159g	some similarities with wi|NCU009 Neurospora crassa NCU00914. hypothetical protein, hypothetical
												CAGL0K08514g	similar to sp|P34244 Saccharomy cerevisiae YKL101w serine/threon protein kinase, hypothetical sta
												DEHA0F25278g	similar to ca|CA1881|CaRCK2 Can albicans CaRCK2 Ca/calmoduli dependent ser/thr protein kinase (homology), hypothetical start
												KLLA0F26983g	some similarities with sp|P3280 Saccharomyces cerevisiae YKL0 ELM1 ser/thr-specific protein kin hypothetical start
												DEHA0C11484g	similar to sp|P22211 Saccharomy cerevisiae YNL183c NPR1 or tr|Q1 Saccharomyces cerevisiae YDL02 hypothetical start
												YALI0C00891g	similar to sp|O14019 Schizosaccharomyces pombe Prob serine/threonine-protein kinase C29A4.16 (EC 2.7.1.-), hypothetica
												KLLA0F23507g	similar to sp|P24719 Saccharomy cerevisiae YOR351c MEK1 ser/t protein kinase, start by similarit
												CAGL0F03245g	similar to sp|P32361 Saccharomy cerevisiae YHR079c IRE1, hypothe start
												CAGL0K11990g	some similarities with sp|P3808 Saccharomyces cerevisiae YBR0 AKL1 Ark-family Kinase-Like pro hypothetical start
												DEHA0G10417g	similar to CA1971|CaPKH2 Cand albicans CaPKH2 Ser/Thr protei kinase(by homology), hypothetical
												YALI0B17556g	weakly similar to tr|Q9Y898 Emeri nidulans Calcium/calmodulin depe protein kinase C, hypothetical st
												CAGL0G03047g	highly similar to sp|P22204 Saccharomyces cerevisiae YGR09 DBF2 ser/thrprotein kinase or sp|P3 Saccharomyces cerevisiae YPR11 DBF20, hypothetical start
												YALI0F27093g	weakly similar to DEHA-IPF372 Debaryomyces hansenii, hypothet start
												DEHA0C14091g	similar to sp|P37292 Saccharomy cerevisiae YBR263w SHM1, hypothetical start
												DEHA0C18601g	similar to CA4433|CaBCK1 Canc albicans, hypothetical start
												KLLA0C04213g	similar to sp|P22209 Saccharomy cerevisiae YAR018c KIN3 ser/thr p kinase, hypothetical start
												YALI0A04697g	similar to sp|O42626 Neurospora c Serine/threonine-protein kinase n (Nonrepressible conidiation protei hypothetical start
												YALI0D26015g	similar to sp|P32562 Saccharomy cerevisiae Cell cycle protein kina CDC5/MSD2 (EC 2.7.1.-), hypothe start
												DEHA0G14839g	highly similar to sCA3870|CaYP Candida albicans CaYPK1, start similarity
												KLLA0C14278g	similar to sp|P28708 Saccharomy cerevisiae YKL116c, hypothetical
													similar to tr|CAD79666 Neurospo

												YALI0E13750g	crassa B1D14.230 Related to serine/threonine-protein kinase a DEHA-IPF6149.1 Debaryomyc hansenii, no start
												CAGL0B04147g	highly similar to sp|P22204 Saccharomyces cerevisiae YGR09 DBF2 ser/thrprotein kinase related DBF20P or sp|P32328 Saccharomy cerevisiae YPR111w DBF20 cell c protein kinase related to DBF2F hypothetical start
												DEHA0F13497g	similar to ca|CA1299|CaPTK2 Can albicans CaPTK2 serine /threoni protein kinase involved in polyam uptake (by homology), hypothetical
												DEHA0D13684g	similar to CA4865|IPF4085 Cand albicans IPF4085, start by similar
												CAGL0L06006g	similar to sp|P53104 Saccharomy cerevisiae YGL180w APG1 essenti autophagocytosis, hypothetical st
												CAGL0E05720g	similar to sp|P38991 Saccharomy cerevisiae YPL209c IPL1 ser/thr pr kinase, start by similarity
												KLLA0F18612g	some similarities with sp|P3808 Saccharomyces cerevisiae YBR05 AKL1 Ark-family Kinase-Like pro hypothetical start
												YALI0E24563g	similar to tr|Q12152 Saccharomy cerevisiae YPL150w, hypothetical
												DEHA0F24013g	similar to ca|CA5226|CaRIM15 Ca albicans CaRIM15 Protein kinas involved in the RIM pathway (b homology), hypothetical start
												CAGL0I04422g	some similarities with sp|P2220 Saccharomyces cerevisiae YAR0 KIN3 ser/thr protein kinase, hypoth start
												CAGL0K01661g	some similarities with tr|Q1210 Saccharomyces cerevisiae YDL02 hypothetical start
												DEHA0E15741g	highly similar to CA3361|CaSNI Candida albicans CaSNF1 serine/threonine protein kinase hypothetical start
												CAGL0M02233g	highly similar to sp|P22216 Saccharomyces cerevisiae YPL15 SPK1 ser/thr/tyr protein kinase hypothetical start
												CAGL0F04741g	similar to sp|P22517 Saccharomy cerevisiae YOL016c CMK2 Ca2+/calmodulin-dependent ser/ protein kinase, type II, hypothetical
												YALI0E06523g	weakly similar to sp|P34244 Saccharomyces cerevisiae YKL10 HSL1 ser/thr protein kinase, coup septin ring assembly to cell cycl progression, hypothetical start
												KLLA0E11979g	some similarities with sp|P2533 Saccharomyces cerevisiae YCR00 SAT4 serine/threonine-specific pro kinase, hypothetical start
												CAGL0J11308g	similar to sp|P22211 Saccharomy cerevisiae YNL183c NPR1 ser/t protein kinase, hypothetical star
												DEHA0G11638g	similar to sp|P25333 Saccharomy cerevisiae YCR008w SAT4 serine/threonine-specific protein ki hypothetical start
												CAGL0H10208g	similar to sp|P38080 Saccharomy cerevisiae YBR059c AKL1 Ark-fa Kinase-Like protein, hypothetical
												CAGL0B02739g	similar to sp|P23561 Saccharomy cerevisiae YLR362w STE11 ser/ protein kinase of the MEKK fam hypothetical start

												YALI0D07150g	weakly similar to tr|Q9C2E8 Neuro crassa Conserved hypothetical pro start by similarity
												DEHA0F10197g	highly similar to ca|CA2265|CaCM Candida albicans CaCMK2 Ca /calmodulin-dependent ser/thr pro kinase, type II (by homology), hypothetical start
												DEHA0B12628g	similar to sp|P06245 Saccharomy cerevisiae YPL203w TPK2 cAM dependent protein kinase 2, cataly chain, start by similarity
												DEHA0E13574g	similar to CA2193|IPF14273 Cand albicans IPF14273 Probable ser/ protein kinase
												KLLA0D07348g	weakly similar to sgd|S000606 Saccharomyces cerevisiae YPL14 start by similarity
												DEHA0B12650g	some similarities with sp|P3897 Saccharomyces cerevisiae YJL16 HAL5 ser/thr protein kinase, hypoth start
												DEHA0F04114g	similar to CA0576|CaNPR1 Cand albicans CaNPR1, hypothetical st
												DEHA0C13211g	similar to sp|P22216 Saccharomy cerevisiae YPL153c SPK1, hypothe start
												KLLA0B07205g	some similarities with sp|P0598 Saccharomyces cerevisiae YKL16 TPK3 cAMP-dependent protein kin catalytic chain, hypothetical sta
												CAGL0K06479g	some similarities with tr|Q0330 Saccharomyces cerevisiae YDR46 start by similarity
												KLLA0C12485g	weakly similar to sp|Q12236 Saccharomyces cerevisiae YOL10 PKH2, start by similarity
												KLLA0E06413g	gi|22858696|gb|AAN05732.1 Kluyveromyces lactis protein kinas start by similarity
												YALI0D26213g	weakly similar to tr|Q96WJ8 Blum graminis Protein kinase C-like pro hypothetical start
												DEHA0G14707g	similar to CA6135|CaCMK1 Cand albicans CaCMK1, hypothetical s
												DEHA0E16115g	similar to CA5074|IPF3607 Cand albicans IPF3607 putative serine/threonine protein kinase hypothetical start
												CAGL0M13167g	similar to sp|P32801 Saccharomy cerevisiae YKL048c ELM1 ser/t specific protein kinase, hypothetical
												KLLA0F01408g	weakly similar to sgd|S000218 Saccharomyces cerevisiae YDL02 hypothetical start
												DEHA0F25212g	highly similar to tr|Q9HEW0 Cand albicans cAMP-dependent protein k catalytic subunit, hypothetical sta
												CAGL0M08404g	some similarities with sp|P0598 Saccharomyces cerevisiae YKL16 TPK3 or sp|P06244 Saccharomy cerevisiae YJL164c SRA3 or sp|P0 Saccharomyces cerevisiae YPL20 TPK2, hypothetical start
												KLLA0A03806g	gi|2181934|emb|CAA61235.1 Kluyveromyces lactis putative kin start by similarity
												YALI0D19470g	similar to tr|Q871H9 Neurospora cr B16M17.090 Related to Ste20-li kinase Don3, hypothetical start
												YALI0A10230g	similar to sp|P22211 Saccharomy cerevisiae YNL183c NPR1 ser/t protein kinase, start by similarit
													some similarities with

DEHA0F10461g	ca|CA1288|CaKSP1 Candida albic CaKSP1 SERINE/THREONINE PROTEIN KINASE by homolog hypothetical start
YALI0F01716g	tr|Q9P860 Yarrowia lipolytica Wee protein, mitosis inhibitor protein ki hypothetical start
YALI0E27632g	tr|O93955 Yarrowia lipolytica SS protein, multicopy suppressor of S secretory defects, putative calmodu dependent ser/thr protein kinase identified start
CAGL0I09504g	similar to sp|P38147 Saccharomy cerevisiae YBR274w CHK1 regu inhibitory Cdk phosphorylation of F start by similarity
CAGL0F09075g	similar to sp|P11792 Saccharomy cerevisiae YHR205w SCH9 serine/threonine protein kinase, sta similarity
DEHA0C17996g	similar to CA2348|IPF12811 Cand albicans, putative serine/threonin kinase, hypothetical start
CAGL0H00979g	similar to tr|Q12003 Saccharomy cerevisiae YPL236c, hypothetical
KLLA0C03828g	similar to sp|P54199 Saccharomy cerevisiae YDL028c MPS1 serine/threonine/tyrosine protein ki hypothetical start
KLLA0F14190g	gi|3021329|emb|CAA06336.1 Kluyveromyces lactis MAP kinase k kinase, start by similarity
CAGL0M10153g	some similarities with sp|Q0349 Saccharomyces cerevisiae YHL0 ser/thr protein kinase of the pheron pathway, hypothetical start
KLLA0F24618g	similar to sp|P38070 Saccharomy cerevisiae YBR028c, start by simil
CAGL0K07458g	similar to sp|P12688 Saccharomy cerevisiae YKL126w or sp|P189 Saccharomyces cerevisiae YMR1 ser/thr-specific protein kinases, sta similarity
KLLA0D03190g	highly similar to sp|P06245 Saccharomyces cerevisiae YPL20 TPK2 cAMP-dependent protein kin catalytic chain, start by similarit
DEHA0D19833g	similar to CA5851|CaKIN2 Cand albicans CaKIN2, hypothetical st
KLLA0D14905g	gi|28565036|gb|AAO32601.1 Kluyveromyces lactis DBF2, start similarity
KLLA0C18568g	gi|6967028|emb|CAB72435.1 Kluyveromyces lactis MUP1 prot hypothetical start
CAGL0M13541g	similar to sp|Q03533 Saccharomy cerevisiae YMR291w, hypothetical
KLLA0E03487g	similar to sgd|S0002874 Saccharom cerevisiae YDR466w, start by simil
DEHA0C08635g	similar to sp|P22204 Saccharomy cerevisiae YGR092w DBF2, hypothetical start, sequence gap
CAGL0G02607g	similar to sp|P40494 Saccharomy cerevisiae YIL095w PRK1, start similarity
CAGL0K11275g	similar to tr|Q03785 Saccharomy cerevisiae YDR247w, hypothetical
DEHA0E05753g	similar to CA0719|IPF9779.5 Can albicans IPF9779.5 serine/threon protein kinase 5-prime end, hypoth start
YALI0B05588g	some similarities with sp|Q1223 Saccharomyces cerevisiae YOL10 PKH2 related to ser/thr protein kin

CDC15 (YAR019C)	2.7.1.-	sp|P27636 Saccharomyces cerevisiae YAR019c CDC15 protein kinase of the MAP kinase kinase kinase family P108.1.f6.1	inviable	0.3	Ess	Ess	0.8	Ess	sckdy	57 58 49 54 42	GLC.2		P108.1.f16.1, hypothetical star
												DEHA0A08822g	similar to CA0577|IPF16051 Canc albicans IPF16051 unknown funct start by similarity
												KLLA0C17160g	similar to sp|P53104 Saccharomy cerevisiae YGL180w APG1 essenti autophagocytosis, start by similar
												KLLA0A02717g	some similarities with sp|P5323 Saccharomyces cerevisiae YGR05 hypothetical start
												YALI0C21758g	similar to KLLA-IPF4914.1 Kluyveromyces lactis IPF 4914. hypothetical start
												CAGL0C03509g	similar to sp|P53739 Saccharomy cerevisiae YNR047w or sp|P25 Saccharomyces cerevisiae YCR09 KIN82, hypothetical start
												KLLA0B03586g	similar to sp|P11792 Saccharomy cerevisiae YHR205w SCH9 serine/threonine protein kinase invo in stress response and nutrient-sen signaling pathway, start by simila
												YALI0C15444g	similar to tr|Q12706 Schizosaccharomyces pombe Prob serine/threonine protein kinase PS (EC 2.7.1.-), hypothetical start
												YALI0E34067g	weakly similar to DEHA-IPF394 Debaryomyces hansenii IPF 394 hypothetical start
												CAGL0C05005g	similar to sp|P27636 Saccharomy cerevisiae YAR019c CDC15, hypothetical start
												DEHA0B04895g	similar to CA2018|CaSTE11 Canc albicans CaSTE11 ser/thr protein k of the MEKK family, hypothetical
												KLLA0B12716g	similar to sp|P12688 Saccharomy cerevisiae YKL126w YPK1 ser/t specific protein kinase, start by simi
												CAGL0F03707g	similar to sp|Q08732 Saccharomy cerevisiae YOR267c, start by simil
												YALI0E22858g	Weakly similar to CAAL-CA55 CaAKL1 serine/threonine protein k (by homology), Hypothetical sta
												KLLA0F09031g	similar to sp|P43565 Saccharomy cerevisiae YFL033c RIM15 prote kinase involved in expression of me genes, hypothetical start
												DEHA0E12782g	similar to sp|P38070 Saccharomy cerevisiae YBR028c, putative ribos protein kinase
												CAGL0B01925g	similar to sp|P13185 Saccharomy cerevisiae YDR122w KIN1 or sp|P1 Saccharomyces cerevisiae YLR09 KIN2, hypothetical start
												KLLA0C07535g	some similarities with sgd|S00057 Saccharomyces cerevisiae YOR26 hypothetical start
												CAGL0D02244g	similar to sp|P24719 Saccharomy cerevisiae YOR351c MEK1 ser/t protein kinase, hypothetical star
												DEHA0C13387g	similar to tr|Q08732 Saccharomy cerevisiae YOR267C, hypothetical
												YALI0E17743g	no similarity, hypothetical start
												CAGL0C02893g	similar to tr|Q08732 Saccharomy cerevisiae YOR267c, hypothetical
												KLLA0F19536g	similar to sp|P13186 Saccharomy cerevisiae YLR096w KIN2 ser/t protein kinase, start by similarit
												CAGL0M11396g	similar to sp|P13186 Saccharomy cerevisiae YLR096w KIN2 ser/t protein kinase, hypothetical star
												YALI0B13178g	similar to sp|P32490 Saccharomy cerevisiae YOR231w MKK1 ser/

	protein kinase, start by similarit
DEHA0F27489g	similar to CA1288|CaKSP1 Cand albicans CaKSP1 serine/threonin protein kinase (by homology), star similarity
KLLA0B02332g	similar to sp|P38991 Saccharomy cerevisiae YPL209c IPL1 ser/thr pr kinase, start by similarity
CAGL0L07326g	similar to sp|P39009 Saccharomy cerevisiae YDL101c DUN1 prote kinase, start by similarity
KLLA0F11143g	similar to sp|P22216 Saccharomy cerevisiae YPL153c SPK1 ser/thr/ protein kinase, start by similarit
DEHA0E14641g	similar to CA4097|CaGIN4 Cand albicans CaGIN4 ser/thr protein ki (by homology), hypothetical sta
CAGL0J03872g	similar to sp|Q01919 Saccharomy cerevisiae YOR233w KIN4 ser/t protein kinase or tr|Q03002 Saccharomyces cerevisiae YPL14 start by similarity
YALI0D14542g	similar to sp|P11792 Saccharomy cerevisiae YHR205w SCH9 serine/threonine protein kinase invo in stress response and nutrient-sen signaling pathway, start by simila
KLLA0B06501g	some similarities with sp|P4711 Saccharomyces cerevisiae YJR05 PTK2 involved in polyamine upta hypothetical start
DEHA0C05742g	some similarities with sp|P4189 Schizosaccharomyces pombe Ce division control protein 7 and CA2669|IPF17494.3eoc Candid albicans and CA2404|CaCDC15 Ca albicans, hypothetical start
DEHA0F20878g	similar to CA0044|IPF17347 Canc albicans IPF17347, hypothetical s
KLLA0E08371g	similar to sp|P40494 Saccharomy cerevisiae YIL095w PRK1 serine/threonine protein kinase invo in regulation of actin cytoskeleto organization, start by similarity
KLLA0F13552g	gi|33386566|emb|CAD87727.1 Kluyveromyces lactis protein kina start by similarity
CAGL0J11638g	highly similar to sp|P32562 Saccharomyces cerevisiae YMR0 CDC5 involved in regulation of D replication, hypothetical start
CAGL0K02167g	similar to sp|P38990 Saccharomy cerevisiae YER129w Serine/threon protein kinase, start by similarit
DEHA0F09493g	similar to ca|CA2909|IPF11424 Ca albicans IPF11424 unknown funct hypothetical start
CAGL0G05720g	similar to sp|P22211 Saccharomy cerevisiae YNL183c NPR1 ser/t protein kinase, start by similarit
DEHA0C09823g	similar to CA1205|CaSSK2 Cand albicans, hypothetical start
YALI0D22770g	Similar to CAAL-CA5851 CaKI ser/thr protein kinase (by homology start
CAGL0M08910g	highly similar to sp|Q00372 Saccharomyces cerevisiae YDR47 carbon catabolite derepressing ser protein kinase, hypothetical star
KLLA0C04191g	weakly similar to sp|P27636 Saccharomyces cerevisiae YAR0 CDC15 protein kinase of the MA kinase kinase kinase family, hypoth start

DEHA0B16071g	similar to sp|P22209 Saccharomy cerevisiae YAR018c KIN3 ser/thr p kinase, start by similarity
CAGL0K03399g	highly similar to sp|P12688 Saccharomyces cerevisiae YKL12 Serine/threonine-protein kinase, sta similarity
CAGL0J04972g	some similarities with tr|Q1210 Saccharomyces cerevisiae YDL02 hypothetical start
DEHA0F10923g	highly similar to ca|CA2986|CaCD Candida albicans CaCDC5 Cell-cy protein kinase (by homology), star similarity
YALI0B04840g	similar to tr|Q12003 Saccharomy cerevisiae YPL236c, start by simila
KLLA0C01650g	similar to sp|Q12263 Saccharomy cerevisiae YDR507c GIN4 ser/thr p kinase, start by similarity
YALI0F08165g	some similarities with sp|P4189 Schizosaccharomyces pombe 7 CD OR SPBC21.06C gene Cell divis control protein, start by similarit
KLLA0E01584g	highly similar to sp|P39009 Saccharomyces cerevisiae YDL10 DUN1 protein kinase, start by simil
DEHA0C02882g	similar to CA4039|CaSKS1 Cand albicans, start by similarity
KLLA0F01276g	similar to sp|P38147 Saccharomy cerevisiae YBR274w CHK1 regul inhibitory Cdk phosphorylation of P start by similarity
CAGL0G09020g	highly similar to sp|P06245 Saccharomyces cerevisiae YPL20 TPK2 cAMP-dependent protein kin catalytic chain, hypothetical sta
DEHA0G16302g	similar to tr|Q12706 Schizosaccharomyces pombe Prob serine/threonine protein kinase PS start by similarity
CAGL0I06248g	similar to sp|P38970 Saccharomy cerevisiae YJL165c HAL5 ser/thr pr kinase, start by similarity
YALI0B08558g	weakly similar to tr|Q00863 Nect haematococca Ran1-like protein ki hypothetical start
DEHA0G05544g	similar to CA1375|IPF7158 Cand albicans IPF7158 putative serine/threonine kinase, hypothetica
KLLA0B13607g	weakly similar to sp|Q03497 Saccharomyces cerevisiae YHL00 STE20 ser/thr protein kinase of t pheromone pathway, hypothetical
YALI0F27159g	some similarities with sp|P4704 Saccharomyces cerevisiae YJL057c probable serine/threonine-protein ki hypothetical start
CAGL0I05390g	similar to sp|Q12505 Saccharomy cerevisiae YPL026c SKS1 suppres kinase of SNF3 or tr|Q03785 Saccharomyces cerevisiae YDR24 start by similarity
YALI0E31361g	similar to tr|Q9HF33 Arthrobotr dactyloides Calmodulin-binding pro kinase, hypothetical start
YALI0B14201g	similar to sp|P32328 Saccharomy cerevisiae YPR111w DBF20 cell c protein kinase P108.1.f3.6 or sp|P2 Saccharomyces cerevisiae YGR09 DBF2 ser/thr protein kinase P108.1.f16.1, hypothetical star
DEHA0C16181g	similar to CA1447|CaNRK1 Cand albicans, hypothetical start
CAGL0K04301g	similar to sp|P53233 Saccharomy

												CAGL0K04301g	cerevisiae YGR052w, hypothetical
												KLLA0A06820g	some similarities with sp|P3897 Saccharomyces cerevisiae YJL16 HAL5 ser/thr protein kinase, hypoth start
												KLLA0C00979g	similar to sp|P08458 Saccharomy cerevisiae YDR523c SPS1 ser/thr pr kinase, hypothetical start
												YALI0D02101g	similar to sp|O94168 Candida tropi Carbon catabolite derepressing pro kinase (EC 2.7.1.-), hypothetical s
												YALI0C08305g	highly similar to sp|P06245 Saccharomyces cerevisiae YPL20 TPK2 cAMP-dependent protein kin catalytic chain, hypothetical sta
												KLLA0D12100g	some similarities with sgd|S00026 Saccharomyces cerevisiae YDR24 hypothetical start
												CAGL0M10791g	highly similar to sp|P53599 Saccharomyces cerevisiae YNR03 SSK2 MAP kinase, no start, frame
												YALI0A05247g	similar to tr|Q876Z5 Neurospora cr OS-4 Putative SSK22 like MAPK kinase, hypothetical start
												DEHA0F24684g	similar to sp|P24719 Saccharomy cerevisiae YOR351c MEK1 ser/t protein kinase
												KLLA0B13112g	similar to sp|P23561 Saccharomy cerevisiae YLR362w STE11 ser/ protein kinase of the MEKK family by similarity
												CAGL0F03311g	similar to sp|P38691 Saccharomy cerevisiae YHR082c KSP1 ser/t protein kinase, start by similarit
												KLLA0C03938g	some similarities with sgd|S00021 Saccharomyces cerevisiae YDL02 hypothetical start
												CAGL0M08360g	some similarities with sp|P3897 Saccharomyces cerevisiae YJL16 ser/thr protein kinase, hypothetical
												YALI0E34375g	similar to wi|NCU00108.1 Neurosp crassa NCU00108.1 hypothetical pr (93222 - 91750), hypothetical sta
												KLLA0B07579g	weakly similar to sp|P32944 Saccharomyces cerevisiae YJL18 SWE1 ser/tyr dual-specifity prot kinase, start by similarity
												YALI0D25388g	similar to tr|Q8TFN2 Pichia angu Serine-threonine kinase Pdd7p hypothetical start
												DEHA0C04840g	some similarities with sp|P3899 Saccharomyces cerevisiae YPL20 IPL1 ser/thr protein kinase, hypothe start
												YALI0B00880g	similar to sp|P22211 Saccharomy cerevisiae YNL183c NPR1 ser/t protein kinase, hypothetical star
												YALI0D08822g	some similarities with sp|P3899 Saccharomyces cerevisiae YER12 PAK1 DNA polymerase alpha suppressing protein kinase, hypothe start
												DEHA0G22440g	similar to CA4770|IPF9382.3 Cand albicans IPF9382.3, hypothetical s
												KLLA0C08525g	similar to sp|P53599 Saccharomy cerevisiae YNR031c SSK2 MAP k kinase kinase of the high osmolar signal transduction pathway, start similarity
												YALI0F09746g	similar to sp|P24583 Saccharomy cerevisiae YBL105c PKC1 ser/t protein kinase, start by similarit
												DEHA0D07601g	similar to Candida albicans CA42 start by similarity

												CAGL0I07513g	similar to sp|Q12236 Saccharomy cerevisiae YOL100w PKH2, start similarity
												DEHA0D11242g	highly similar to CA5299|IPF219 Candida albicans IPF2190, start similarity
												DEHA0F26994g	similar to CA0206|IPF14089 Canc albicans IPF14089 putative serine/threonine protein kinase hypothetical start
												CAGL0M09361g	highly similar to sp|P24583 Saccharomyces cerevisiae YBL10 PKC1 ser/thr protein kinase, start similarity
												YALI0E06501g	similar to sp|P12688 Saccharomy cerevisiae YKL126w YPK1 ser/t specific protein kinase, hypothetical
												CAGL0K05709g	similar to sp|Q12263 Saccharomy cerevisiae YDR507c GIN4, start similarity
												DEHA0C09130g	similar to sp|P38147 Saccharomy cerevisiae YBR274w CHK1, hypothetical start
												CAGL0M02299g	similar to tr|Q12152 Saccharomy cerevisiae YPL150w, start by simil
												CAGL0B04301g	similar to sp|P38070 Saccharomy cerevisiae YBR028c, start by simil
												CAGL0J03432g	similar to sp|P53974 Saccharomy cerevisiae YNL020c ARK1 or sp|P4 Saccharomyces cerevisiae YIL09 PRK1, start by similarity
												DEHA0D13706g	similar to CA4864|IPF4087 Cand albicans IPF4087, hypothetical st
												KLLA0D09328g	some similarities with sp|P3899 Saccharomyces cerevisiae YER12 PAK1 DNA polymerase alpha suppressing protein kinase, hypothe start
												DEHA0B13519g	some similarities with sp|P5373 Saccharomyces cerevisiae YNR04 related to ser/thr protein kinases hypothetical start
												CAGL0M02519g	highly similar to tr|Q03002 Saccharomyces cerevisiae YPL141 sp|Q01919 Saccharomyces cerevis YOR233w KIN4, hypothetical st
												CAGL0G04609g	similar to sp|Q12236 Saccharomy cerevisiae YOL100w PKH2, hypothetical start
												KLLA0F23155g	similar to sp|P22517 Saccharomy cerevisiae YOL016c CMK2 Ca2+/calmodulin-dependent ser/ protein kinase, type II, start by simi
VPS15 (YBR097W)	2.7.1.-	sp|P22219 Saccharomyces cerevisiae YBR097w VPS15 ser/thr protein kinase singleton	viable	0.7	Ess	Ess	0.3	0.1	sckdy	1 1 1 1 1	GLR.2300	DEHA0F16742g	weakly similar to sp|P22219 Saccharomyces cerevisiae YBR09 VPS15 ser/thr protein kinase single hypothetical start
												CAGL0H08437g	similar to sp|P22219 Saccharomy cerevisiae YBR097w VPS15, star similarity
												YALI0E33781g	similar to tr|Q9UVG6 Pichia paste VPS15 protein, hypothetical sta
												KLLA0B11924g	similar to sp|P22219 Saccharomy cerevisiae YBR097w VPS15 ser/ protein kinase singleton, start b similarity
												KLLA0F11319g	similar to sgd|S0006071 Saccharom cerevisiae YPL150w, start by simil
												CAGL0L07810g	similar to sp|P25333 Saccharomy cerevisiae YCR008w SAT4 serine/threonine-specific protein ki start by similarity
												CAGL0K11550g	similar to sp|P28708 Saccharomy cerevisiae YKL116c, hypothetical

												YALI0F11385g	weakly similar to SP|P38691 Saccharomyces cerevisiae YHR0 KSP1 ser/thr protein kinase and DE IPF5974.1, start by similarity
												KLLA0A09713g	similar to sp|Q03533 Saccharomy cerevisiae YMR291w, start by simi
												KLLA0E17127g	similar to sp|P38691 Saccharomy cerevisiae YHR082c KSP1 ser/t protein kinase, start by similarit
												YALI0C04158g	similar to sp|P18961 Saccharomy cerevisiae Serine/threonine-prote kinase YPK2/YKR2, hypothetical
												DEHA0F24676g	similar to sp|P24719 Saccharomy cerevisiae YOR351c MEK1 ser/t protein kinase
												DEHA0G14817g	similar to CA2643|CaHSL1 Cand albicans CaHSL1, hypothetical s
												DEHA0C18150g	similar to sp|P40494 Saccharomy cerevisiae YIL095w PRK1 serine/threonine protein kinase, sta similarity
												CAGL0K10604g	similar to sp|P27466 Saccharomy cerevisiae YFR014c CMK1 Ca2+/calmodulin-dependent ser/ protein kinase type I, hypothetical
												DEHA0C08591g	similar to sp|P22204 Saccharomy cerevisiae YGR092w DBF2, hypothetical start, sequence ga
												YALI0F13629g	some similarities with sp|P2356 Saccharomyces cerevisiae YLR36 STE11 ser/thr protein kinase of t MEKK family, hypothetical sta
												KLLA0C06138g	similar to sp|P32562 Saccharomy cerevisiae YMR001c CDC5 involv regulation of DNA replication, sta similarity
												YALI0F16159g	some similarities with wi|NCU009 Neurospora crassa NCU00914. hypothetical protein, hypothetical
												CAGL0K08514g	similar to sp|P34244 Saccharomy cerevisiae YKL101w serine/threon protein kinase, hypothetical sta
												DEHA0F25278g	similar to ca|CA1881|CaRCK2 Ca albicans CaRCK2 Ca/calmoduli dependent ser/thr protein kinase (homology), hypothetical start
												KLLA0F26983g	some similarities with sp|P3280 Saccharomyces cerevisiae YKL0 ELM1 ser/thr-specific protein kin hypothetical start
												DEHA0C11484g	similar to sp|P22211 Saccharomy cerevisiae YNL183c NPR1 or tr|Q1 Saccharomyces cerevisiae YDL0 hypothetical start
												YALI0C00891g	similar to sp|O14019 Schizosaccharomyces pombe Prob serine/threonine-protein kinas C29A4.16 (EC 2.7.1.-), hypothetica
												KLLA0F23507g	similar to sp|P24719 Saccharomy cerevisiae YOR351c MEK1 ser/ protein kinase, start by similarit
												CAGL0F03245g	similar to sp|P32361 Saccharomy cerevisiae YHR079c IRE1, hypoth start
												CAGL0K11990g	some similarities with sp|P3808 Saccharomyces cerevisiae YBR0 AKL1 Ark-family Kinase-Like pr hypothetical start
												DEHA0G10417g	similar to CA1971|CaPKH2 Cand albicans CaPKH2 Ser/Thr prote kinase(by homology), hypothetical
												YALI0B17556g	weakly similar to tr|Q9Y898 Emeri nidulans Calcium/calmodulin depe protein kinase C, hypothetical st

CAGL0G03047g	highly similar to sp|P22204 Saccharomyces cerevisiae YGR09 DBF2 ser/thrprotein kinase or sp|P3 Saccharomyces cerevisiae YPR11 DBF20, hypothetical start
YALI0F27093g	weakly similar to DEHA-IPF372 Debaryomyces hansenii, hypothet start
DEHA0C14091g	similar to sp|P37292 Saccharomy cerevisiae YBR263w SHM1, hypothetical start
DEHA0C18601g	similar to CA4433|CaBCK1 Canc albicans, hypothetical start
KLLA0C04213g	similar to sp|P22209 Saccharomy cerevisiae YAR018c KIN3 ser/thr p kinase, hypothetical start
YALI0A04697g	similar to sp|O42626 Neurospora cr Serine/threonine-protein kinase nr (Nonrepressible conidiation protei hypothetical start
YALI0D26015g	similar to sp|P32562 Saccharomy cerevisiae Cell cycle protein kina CDC5/MSD2 (EC 2.7.1.-), hypothe start
DEHA0G14839g	highly similar to sCA3870|CaYP Candida albicans CaYPK1, start similarity
KLLA0C14278g	similar to sp|P28708 Saccharomy cerevisiae YKL116c, hypothetical
YALI0E13750g	similar to tr|CAD79666 Neurospo crassa B1D14.230 Related to serine/threonine-protein kinase a DEHA-IPF6149.1 Debaryomyc hansenii, no start
CAGL0B04147g	highly similar to sp|P22204 Saccharomyces cerevisiae YGR09 DBF2 ser/thrprotein kinase relatec DBF20P or sp|P32328 Saccharomy cerevisiae YPR111w DBF20 cell c protein kinase related to DBF2F hypothetical start
DEHA0F13497g	similar to ca|CA1299|CaPTK2 Can albicans CaPTK2 serine /threoni protein kinase involved in polyam uptake (by homology), hypothetical
DEHA0D13684g	similar to CA4865|IPF4085 Cand albicans IPF4085, start by similar
CAGL0L06006g	similar to sp|P53104 Saccharomy cerevisiae YGL180w APG1 essenti autophagocytosis, hypothetical st
CAGL0E05720g	similar to sp|P38991 Saccharomy cerevisiae YPL209c IPL1 ser/thr pr kinase, start by similarity
KLLA0F18612g	some similarities with sp|P3808 Saccharomyces cerevisiae YBR0 AKL1 Ark-family Kinase-Like pro hypothetical start
YALI0E24563g	similar to tr|Q12152 Saccharomy cerevisiae YPL150w, hypothetical
DEHA0F24013g	similar to ca|CA5226|CaRIM15 Ca albicans CaRIM15 Protein kinas involved in the RIM pathway (b homology), hypothetical start
CAGL0I04422g	some similarities with sp|P2220 Saccharomyces cerevisiae YAR0 KIN3 ser/thr protein kinase, hypoth start
CAGL0K01661g	some similarities with tr|Q1210 Saccharomyces cerevisiae YDL02 hypothetical start
DEHA0E15741g	highly similar to CA3361|CaSNI Candida albicans CaSNF1 serine/threonine protein kinase hypothetical start

CAGL0M02233g	highly similar to sp|P22216 Saccharomyces cerevisiae YPL15 SPK1 ser/thr/tyr protein kinase hypothetical start
CAGL0F04741g	similar to sp|P22517 Saccharomy cerevisiae YOL016c CMK2 Ca2+/calmodulin-dependent ser/ protein kinase, type II, hypothetical
YALI0E06523g	weakly similar to sp|P34244 Saccharomyces cerevisiae YKL10 HSL1 ser/thr protein kinase, coup septin ring assembly to cell cyc progression, hypothetical start
KLLA0E11979g	some similarities with sp|P2533 Saccharomyces cerevisiae YCR00 SAT4 serine/threonine-specific pro kinase, hypothetical start
CAGL0J11308g	similar to sp|P22211 Saccharomy cerevisiae YNL183c NPR1 ser/t protein kinase, hypothetical sta
DEHA0G11638g	similar to sp|P25333 Saccharomy cerevisiae YCR008w SAT4 serine/threonine-specific protein ki hypothetical start
CAGL0H10208g	similar to sp|P38080 Saccharomy cerevisiae YBR059c AKL1 Ark-fa Kinase-Like protein, hypothetical
CAGL0B02739g	similar to sp|P23561 Saccharomy cerevisiae YLR362w STE11 ser/ protein kinase of the MEKK fam hypothetical start
YALI0D07150g	weakly similar to tr|Q9C2E8 Neuro crassa Conserved hypothetical pro start by similarity
DEHA0F10197g	highly similar to ca|CA2265|CaCM Candida albicans CaCMK2 Ca /calmodulin-dependent ser/thr pro kinase, type II (by homology), hypothetical start
DEHA0B12628g	similar to sp|P06245 Saccharomy cerevisiae YPL203w TPK2 cAM dependent protein kinase 2, cataly chain, start by similarity
DEHA0E13574g	similar to CA2193|IPF14273 Canc albicans IPF14273 Probable ser/ protein kinase
KLLA0D07348g	weakly similar to sgd|S000606 Saccharomyces cerevisiae YPL14 start by similarity
DEHA0B12650g	some similarities with sp|P3897 Saccharomyces cerevisiae YJL16 HAL5 ser/thr protein kinase, hypoth start
DEHA0F04114g	similar to CA0576|CaNPR1 Cand albicans CaNPR1, hypothetical st
DEHA0C13211g	similar to sp|P22216 Saccharomy cerevisiae YPL153c SPK1, hypothe start
KLLA0B07205g	some similarities with sp|P0598 Saccharomyces cerevisiae YKL16 TPK3 cAMP-dependent protein kin catalytic chain, hypothetical sta
CAGL0K06479g	some similarities with tr|Q0330 Saccharomyces cerevisiae YDR46 start by similarity
KLLA0C12485g	weakly similar to sp|Q12236 Saccharomyces cerevisiae YOL10 PKH2, start by similarity
KLLA0E06413g	gi|22858696|gb|AAN05732.1 Kluyveromyces lactis protein kinas start by similarity
YALI0D26213g	weakly similar to tr|Q96WJ8 Blum graminis Protein kinase C-like pro hypothetical start

DEHA0G14707g	similar to CA6135|CaCMK1 Cand albicans CaCMK1, hypothetical s
DEHA0E16115g	similar to CA5074|IPF3607 Cand albicans IPF3607 putative serine/threonine protein kinase hypothetical start
CAGL0M13167g	similar to sp|P32801 Saccharomy cerevisiae YKL048c ELM1 ser/t specific protein kinase, hypothetical
KLLA0F01408g	weakly similar to sgd|S000218 Saccharomyces cerevisiae YDL02 hypothetical start
DEHA0F25212g	highly similar to tr|Q9HEW0 Cand albicans cAMP-dependent protein k catalytic subunit, hypothetical st
CAGL0M08404g	some similarities with sp|P0598 Saccharomyces cerevisiae YKL1 TPK3 or sp|P06244 Saccharomy cerevisiae YJL164c SRA3 or sp|P0 Saccharomyces cerevisiae YPL20 TPK2, hypothetical start
KLLA0A03806g	gi|2181934|emb|CAA61235.1 Kluyveromyces lactis putative kin start by similarity
YALI0D19470g	similar to tr|Q871H9 Neurospora c B16M17.090 Related to Ste20-li kinase Don3, hypothetical start
YALI0A10230g	similar to sp|P22211 Saccharomy cerevisiae YNL183c NPR1 ser/t protein kinase, start by similarit
DEHA0F10461g	some similarities with ca|CA1288|CaKSP1 Candida albic CaKSP1 SERINE/THREONINE PROTEIN KINASE by homolog hypothetical start
YALI0F01716g	tr|Q9P860 Yarrowia lipolytica Wee protein, mitosis inhibitor protein ki hypothetical start
YALI0E27632g	tr|O93955 Yarrowia lipolytica SS protein, multicopy suppressor of S secretory defects, putative calmodu dependent ser/thr protein kinase identified start
CAGL0I09504g	similar to sp|P38147 Saccharomy cerevisiae YBR274w CHK1 regu inhibitory Cdk phosphorylation of F start by similarity
CAGL0F09075g	similar to sp|P11792 Saccharomy cerevisiae YHR205w SCH9 serine/threonine protein kinase, sta similarity
DEHA0C17996g	similar to CA2348|IPF12811 Cand albicans, putative serine/threonin kinase, hypothetical start
CAGL0H00979g	similar to tr|Q12003 Saccharomy cerevisiae YPL236c, hypothetical
KLLA0C03828g	similar to sp|P54199 Saccharomy cerevisiae YDL028c MPS1 serine/threonine/tyrosine protein ki hypothetical start
KLLA0F14190g	gi|3021329|emb|CAA06336.1 Kluyveromyces lactis MAP kinase k kinase, start by similarity
CAGL0M10153g	some similarities with sp|Q0349 Saccharomyces cerevisiae YHL0 ser/thr protein kinase of the pheron pathway, hypothetical start
KLLA0F24618g	similar to sp|P38070 Saccharomy cerevisiae YBR028c, start by simil
CAGL0K07458g	similar to sp|P12688 Saccharomy cerevisiae YKL126w or sp|P189 Saccharomyces cerevisiae YMR1 ser/thr-specific protein kinases, sta similarity

DUN1 (YDL101C)	2.7.1.-	sp|P39009 Saccharomyces cerevisiae YDL101c DUN1 protein kinase P108.1.f5.1	Exhibits sensitivity at 5 generations when grown in 10 uM nystatin.	NA	NA	NA	NA	NA	sckdy	57 58 49 54 42	GLC.2		KLLA0D03190g	highly similar to sp|P06245 Saccharomyces cerevisiae YPL20 TPK2 cAMP-dependent protein kin catalytic chain, start by similarit
													DEHA0D19833g	similar to CA5851|CaKIN2 Cand albicans CaKIN2, hypothetical st
													KLLA0D14905g	gi|28565036|gb|AAO32601.1 Kluyveromyces lactis DBF2, start similarity
													KLLA0C18568g	gi|6967028|emb|CAB72435.1 Kluyveromyces lactis MUP1 prot hypothetical start
													CAGL0M13541g	similar to sp|Q03533 Saccharomy cerevisiae YMR291w, hypothetical
													KLLA0E03487g	similar to sgd|S0002874 Saccharom cerevisiae YDR466w, start by simil
													DEHA0C08635g	similar to sp|P22204 Saccharomy cerevisiae YGR092w DBF2, hypothetical start, sequence gap
													CAGL0G02607g	similar to sp|P40494 Saccharomy cerevisiae YIL095w PRK1, start similarity
													CAGL0K11275g	similar to tr|Q03785 Saccharomy cerevisiae YDR247w, hypothetical
													DEHA0E05753g	similar to CA0719|IPF9779.5 Cand albicans IPF9779.5 serine/threoni protein kinase 5-prime end, hypoth start
													YALI0B05588g	some similarities with sp|Q1223 Saccharomyces cerevisiae YOL10 PKH2 related to ser/thr protein kin P108.1.f16.1, hypothetical star
													DEHA0A08822g	similar to CA0577|IPF16051 Cand albicans IPF16051 unknown funct start by similarity
													KLLA0C17160g	similar to sp|P53104 Saccharomy cerevisiae YGL180w APG1 essenti autophagocytosis, start by similar
													KLLA0A02717g	some similarities with sp|P5323 Saccharomyces cerevisiae YGR05 hypothetical start
													YALI0C21758g	similar to KLLA-IPF4914.1 Kluyveromyces lactis IPF 4914. hypothetical start
													CAGL0C03509g	similar to sp|P53739 Saccharomy cerevisiae YNR047w or sp|P253 Saccharomyces cerevisiae YCR09 KIN82, hypothetical start
													KLLA0B03586g	similar to sp|P11792 Saccharomy cerevisiae YHR205w SCH9 serine/threonine protein kinase invo in stress response and nutrient-sen signaling pathway, start by simila
													YALI0C15444g	similar to tr|Q12706 Schizosaccharomyces pombe Prob serine/threonine protein kinase PS (EC 2.7.1.-), hypothetical start
													YALI0E34067g	weakly similar to DEHA-IPF394 Debaryomyces hansenii IPF 394 hypothetical start
													CAGL0C05005g	similar to sp|P27636 Saccharomy cerevisiae YAR019c CDC15, hypothetical start
													DEHA0B04895g	similar to CA2018|CaSTE11 Cand albicans CaSTE11 ser/thr protein k of the MEKK family, hypothetical
													KLLA0B12716g	similar to sp|P12688 Saccharomy cerevisiae YKL126w YPK1 ser/t specific protein kinase, start by simi
													CAGL0F03707g	similar to sp|Q08732 Saccharomy cerevisiae YOR267c, start by simil
													YALI0E22858g	Weakly similar to CAAL-CA55 CaAKL1 serine/threonine protein k (by homology), Hypothetical sta

KLLA0F09031g	similar to sp|P43565 Saccharomy cerevisiae YFL033c RIM15 prote kinase involved in expression of me genes, hypothetical start
DEHA0E12782g	similar to sp|P38070 Saccharomy cerevisiae YBR028c, putative ribos protein kinase
CAGL0B01925g	similar to sp|P13185 Saccharomy cerevisiae YDR122w KIN1 or sp|P1 Saccharomyces cerevisiae YLR09 KIN2, hypothetical start
KLLA0C07535g	some similarities with sgd|S00057 Saccharomyces cerevisiae YOR26 hypothetical start
CAGL0D02244g	similar to sp|P24719 Saccharomy cerevisiae YOR351c MEK1 ser/t protein kinase, hypothetical star
DEHA0C13387g	similar to tr|Q08732 Saccharomy cerevisiae YOR267C, hypothetical
YALI0E17743g	no similarity, hypothetical start
CAGL0C02893g	similar to tr|Q08732 Saccharomy cerevisiae YOR267c, hypothetical
KLLA0F19536g	similar to sp|P13186 Saccharomy cerevisiae YLR096w KIN2 ser/t protein kinase, start by similarit
CAGL0M11396g	similar to sp|P13186 Saccharomy cerevisiae YLR096w KIN2 ser/t protein kinase, hypothetical star
YALI0B13178g	similar to sp|P32490 Saccharomy cerevisiae YOR231w MKK1 ser/ protein kinase, start by similarit
DEHA0F27489g	similar to CA1288|CaKSP1 Cand albicans CaKSP1 serine/threonin protein kinase (by homology), star similarity
KLLA0B02332g	similar to sp|P38991 Saccharomy cerevisiae YPL209c IPL1 ser/thr pr kinase, start by similarity
CAGL0L07326g	similar to sp|P39009 Saccharomy cerevisiae YDL101c DUN1 prote kinase, start by similarity
KLLA0F11143g	similar to sp|P22216 Saccharomy cerevisiae YPL153c SPK1 ser/thr/ protein kinase, start by similarit
DEHA0E14641g	similar to CA4097|CaGIN4 Cand albicans CaGIN4 ser/thr protein ki (by homology), hypothetical sta
CAGL0J03872g	similar to sp|Q01919 Saccharomy cerevisiae YOR233w KIN4 ser/t protein kinase or tr|Q03002 Saccharomyces cerevisiae YPL14 start by similarity
YALI0D14542g	similar to sp|P11792 Saccharomy cerevisiae YHR205w SCH9 serine/threonine protein kinase invo in stress response and nutrient-sen signaling pathway, start by simila
KLLA0B06501g	some similarities with sp|P4711 Saccharomyces cerevisiae YJR05 PTK2 involved in polyamine upta hypothetical start
DEHA0C05742g	some similarities with sp|P4189 Schizosaccharomyces pombe Ce division control protein 7 and CA2669|IPF17494.3eoc Candid albicans and CA2404|CaCDC15 Ca albicans, hypothetical start
DEHA0F20878g	similar to CA0044|IPF17347 Canc albicans IPF17347, hypothetical s
KLLA0E08371g	similar to sp|P40494 Saccharomy cerevisiae YIL095w PRK1 serine/threonine protein kinase invo in regulation of actin cytoskeleto organization, start by similarity

												KLLA0F13552g	gi|33386566|emb|CAD87727.1 Kluyveromyces lactis protein kina start by similarity
												CAGL0J11638g	highly similar to sp|P32562 Saccharomyces cerevisiae YMR0 CDC5 involved in regulation of D replication, hypothetical start
												CAGL0K02167g	similar to sp|P38990 Saccharomy cerevisiae YER129w Serine/threon protein kinase, start by similarit
												DEHA0F09493g	similar to ca|CA2909|IPF11424 Can albicans IPF11424 unknown funct hypothetical start
												CAGL0G05720g	similar to sp|P22211 Saccharomy cerevisiae YNL183c NPR1 ser/t protein kinase, start by similarit
												DEHA0C09823g	similar to CA1205|CaSSK2 Cand albicans, hypothetical start
												YALI0D22770g	Similar to CAAL-CA5851 CaKI ser/thr protein kinase (by homology start
												CAGL0M08910g	highly similar to sp|Q00372 Saccharomyces cerevisiae YDR47 carbon catabolite derepressing ser protein kinase, hypothetical star
												KLLA0C04191g	weakly similar to sp|P27636 Saccharomyces cerevisiae YAR0 CDC15 protein kinase of the MA kinase kinase kinase family, hypoth start
												DEHA0B16071g	similar to sp|P22209 Saccharomy cerevisiae YAR018c KIN3 ser/thr p kinase, start by similarity
												CAGL0K03399g	highly similar to sp|P12688 Saccharomyces cerevisiae YKL12 Serine/threonine-protein kinase, sta similarity
												CAGL0J04972g	some similarities with tr|Q1210 Saccharomyces cerevisiae YDL02 hypothetical start
												DEHA0F10923g	highly similar to ca|CA2986|CaCI Candida albicans CaCDC5 Cell-cy protein kinase (by homology), star similarity
												YALI0B04840g	similar to tr|Q12003 Saccharomy cerevisiae YPL236c, start by simila
												KLLA0C01650g	similar to sp|Q12263 Saccharomy cerevisiae YDR507c GIN4 ser/thr p kinase, start by similarity
												YALI0F08165g	some similarities with sp|P4189 Schizosaccharomyces pombe 7 CI OR SPBC21.06C gene Cell divis control protein, start by similarit
												KLLA0E01584g	highly similar to sp|P39009 Saccharomyces cerevisiae YDL10 DUN1 protein kinase, start by simil
												DEHA0C02882g	similar to CA4039|CaSKS1 Cand albicans, start by similarity
												KLLA0F01276g	similar to sp|P38147 Saccharomy cerevisiae YBR274w CHK1 regul inhibitory Cdk phosphorylation of F start by similarity
												CAGL0G09020g	highly similar to sp|P06245 Saccharomyces cerevisiae YPL20 TPK2 cAMP-dependent protein kin catalytic chain, hypothetical sta
												DEHA0G16302g	similar to tr|Q12706 Schizosaccharomyces pombe Prob serine/threonine protein kinase PS start by similarity
												CAGL0I06248g	similar to sp|P38970 Saccharomy cerevisiae YJL165c HAL5 ser/thr p kinase, start by similarity
													weakly similar to tr|Q00863 Nect

												YALI0B08558g	haematococca Ran1-like protein ki hypothetical start
												DEHA0G05544g	similar to CA1375|IPF7158 Cand albicans IPF7158 putative serine/threonine kinase, hypothetica
												KLLA0B13607g	weakly similar to sp|Q03497 Saccharomyces cerevisiae YHL0 STE20 ser/thr protein kinase of t pheromone pathway, hypothetical
												YALI0F27159g	some similarities with sp|P4704 Saccharomyces cerevisiae YJL057c probable serine/threonine-protein ki hypothetical start
												CAGL0I05390g	similar to sp|Q12505 Saccharomy cerevisiae YPL026c SKS1 suppre kinase of SNF3 or tr|Q03785 Saccharomyces cerevisiae YDR24 start by similarity
												YALI0E31361g	similar to tr|Q9HF33 Arthrobotr dactyloides Calmodulin-binding pr kinase, hypothetical start
												YALI0B14201g	similar to sp|P32328 Saccharomy cerevisiae YPR111w DBF20 cell c protein kinase P108.1.f3.6 or sp|P2 Saccharomyces cerevisiae YGR09 DBF2 ser/thr protein kinase P108.1.f16.1, hypothetical star
												DEHA0C16181g	similar to CA1447|CaNRK1 Canc albicans, hypothetical start
												CAGL0K04301g	similar to sp|P53233 Saccharomy cerevisiae YGR052w, hypothetical
												KLLA0A06820g	some similarities with sp|P3897 Saccharomyces cerevisiae YJL16 HAL5 ser/thr protein kinase, hypoth start
												KLLA0C00979g	similar to sp|P08458 Saccharomy cerevisiae YDR523c SPS1 ser/thr pr kinase, hypothetical start
												YALI0D02101g	similar to sp|O94168 Candida tropi Carbon catabolite derepressing pro kinase (EC 2.7.1.-), hypothetical s
												YALI0C08305g	highly similar to sp|P06245 Saccharomyces cerevisiae YPL20 TPK2 cAMP-dependent protein kin catalytic chain, hypothetical sta
												KLLA0D12100g	some similarities with sgd|S0002 Saccharomyces cerevisiae YDR24 hypothetical start
												CAGL0M10791g	highly similar to sp|P53599 Saccharomyces cerevisiae YNR0 SSK2 MAP kinase, no start, frame
												YALI0A05247g	similar to tr|Q876Z5 Neurospora cr OS-4 Putative SSK22 like MAPK kinase, hypothetical start
												DEHA0F24684g	similar to sp|P24719 Saccharomy cerevisiae YOR351c MEK1 ser/t protein kinase
												KLLA0B13112g	similar to sp|P23561 Saccharomy cerevisiae YLR362w STE11 ser/ protein kinase of the MEKK family by similarity
												CAGL0F03311g	similar to sp|P38691 Saccharomy cerevisiae YHR082c KSP1 ser/t protein kinase, start by similarit
												KLLA0C03938g	some similarities with sgd|S00021 Saccharomyces cerevisiae YDL02 hypothetical start
												CAGL0M08360g	some similarities with sp|P3897 Saccharomyces cerevisiae YJL16 ser/thr protein kinase, hypothetical
												YALI0E34375g	similar to wi|NCU00108.1 Neurosp crassa NCU00108.1 hypothetical pr (93222 - 91750), hypothetical sta
													weakly similar to sp|P32944

KLLA0B07579g	Saccharomyces cerevisiae YJL18 SWE1 ser/tyr dual-specifity prot kinase, start by similarity
YALI0D25388g	similar to tr|Q8TFN2 Pichia angu Serine-threonine kinase Pdd7p hypothetical start
DEHA0C04840g	some similarities with sp|P3899 Saccharomyces cerevisiae YPL20 IPL1 ser/thr protein kinase, hypothe start
YALI0B00880g	similar to sp|P22211 Saccharomy cerevisiae YNL183c NPR1 ser/t protein kinase, hypothetical star
YALI0D08822g	some similarities with sp|P3899 Saccharomyces cerevisiae YER12 PAK1 DNA polymerase alpha suppressing protein kinase, hypothe start
DEHA0G22440g	similar to CA4770|IPF9382.3 Can albicans IPF9382.3, hypothetical s
KLLA0C08525g	similar to sp|P53599 Saccharomy cerevisiae YNR031c SSK2 MAP k kinase kinase of the high osmolar signal transduction pathway, start similarity
YALI0F09746g	similar to sp|P24583 Saccharomy cerevisiae YBL105c PKC1 ser/t protein kinase, start by similarit
DEHA0D07601g	similar to Candida albicans CA42 start by similarity
CAGL0I07513g	similar to sp|Q12236 Saccharomy cerevisiae YOL100w PKH2, start similarity
DEHA0D11242g	highly similar to CA5299|IPF21 Candida albicans IPF2190, start similarity
DEHA0F26994g	similar to CA0206|IPF14089 Can albicans IPF14089 putative serine/threonine protein kinase hypothetical start
CAGL0M09361g	highly similar to sp|P24583 Saccharomyces cerevisiae YBL10 PKC1 ser/thr protein kinase, start similarity
YALI0E06501g	similar to sp|P12688 Saccharomy cerevisiae YKL126w YPK1 ser/t specific protein kinase, hypothetical
CAGL0K05709g	similar to sp|Q12263 Saccharomy cerevisiae YDR507c GIN4, start similarity
DEHA0C09130g	similar to sp|P38147 Saccharomy cerevisiae YBR274w CHK1, hypothetical start
CAGL0M02299g	similar to tr|Q12152 Saccharomy cerevisiae YPL150w, start by simil
CAGL0B04301g	similar to sp|P38070 Saccharomy cerevisiae YBR028c, start by simil
CAGL0J03432g	similar to sp|P53974 Saccharomy cerevisiae YNL020c ARK1 or sp|P Saccharomyces cerevisiae YIL09 PRK1, start by similarity
DEHA0D13706g	similar to CA4864|IPF4087 Cand albicans IPF4087, hypothetical st
KLLA0D09328g	some similarities with sp|P3899 Saccharomyces cerevisiae YER12 PAK1 DNA polymerase alpha suppressing protein kinase, hypothe start
DEHA0B13519g	some similarities with sp|P5373 Saccharomyces cerevisiae YNR04 related to ser/thr protein kinases hypothetical start
CAGL0M02519g	highly similar to tr|Q03002 Saccharomyces cerevisiae YPL141

												CAGL0M02519g	sp|Q01919 Saccharomyces cerevis YOR233w KIN4, hypothetical st
												CAGL0G04609g	similar to sp|Q12236 Saccharomy cerevisiae YOL100w PKH2, hypothetical start
												KLLA0F23155g	similar to sp|P22517 Saccharomy cerevisiae YOL016c CMK2 Ca2+/calmodulin-dependent ser/ protein kinase, type II, start by simi
												KLLA0F11319g	similar to sgd|S0006071 Saccharom cerevisiae YPL150w, start by simil
												CAGL0L07810g	similar to sp|P25333 Saccharomy cerevisiae YCR008w SAT4 serine/threonine-specific protein ki start by similarity
												CAGL0K11550g	similar to sp|P28708 Saccharomy cerevisiae YKL116c, hypothetical
												YALI0F11385g	weakly similar to SP|P38691 Saccharomyces cerevisiae YHR0 KSP1 ser/thr protein kinase and DE IPF5974.1, start by similarity
												KLLA0A09713g	similar to sp|Q03533 Saccharomy cerevisiae YMR291w, start by simi
												KLLA0E17127g	similar to sp|P38691 Saccharomy cerevisiae YHR082c KSP1 ser/t protein kinase, start by similarit
												YALI0C04158g	similar to sp|P18961 Saccharomy cerevisiae Serine/threonine-prote kinase YPK2/YKR2, hypothetical
												DEHA0F24676g	similar to sp|P24719 Saccharomy cerevisiae YOR351c MEK1 ser/t protein kinase
												DEHA0G14817g	similar to CA2643|CaHSL1 Cand albicans CaHSL1, hypothetical st
												DEHA0C18150g	similar to sp|P40494 Saccharomy cerevisiae YIL095w PRK1 serine/threonine protein kinase, sta similarity
												CAGL0K10604g	similar to sp|P27466 Saccharomy cerevisiae YFR014c CMK1 Ca2+/calmodulin-dependent ser/ protein kinase type I, hypothetical
												DEHA0C08591g	similar to sp|P22204 Saccharomy cerevisiae YGR092w DBF2, hypothetical start, sequence gap
												YALI0F13629g	some similarities with sp|P2356 Saccharomyces cerevisiae YLR36 STE11 ser/thr protein kinase of t MEKK family, hypothetical sta
												KLLA0C06138g	similar to sp|P32562 Saccharomy cerevisiae YMR001c CDC5 involv regulation of DNA replication, sta similarity
												YALI0F16159g	some similarities with wi|NCU009 Neurospora crassa NCU00914. hypothetical protein, hypothetical
												CAGL0K08514g	similar to sp|P34244 Saccharomy cerevisiae YKL101w serine/threon protein kinase, hypothetical sta
												DEHA0F25278g	similar to ca|CA1881|CaRCK2 Ca albicans CaRCK2 Ca/calmoduli dependent ser/thr protein kinase (homology), hypothetical start
												KLLA0F26983g	some similarities with sp|P3280 Saccharomyces cerevisiae YKL0 ELM1 ser/thr-specific protein kin hypothetical start
												DEHA0C11484g	similar to sp|P22211 Saccharomy cerevisiae YNL183c NPR1 or tr|Q1 Saccharomyces cerevisiae YDL0 hypothetical start
												YALI0C00891g	similar to sp|O14019 Schizosaccharomyces pombe Prob serine/threonine-protein kinase

	C29A4.16 (EC 2.7.1.-), hypothetica
KLLA0F23507g	similar to sp|P24719 Saccharomy cerevisiae YOR351c MEK1 ser/t protein kinase, start by similarit
CAGL0F03245g	similar to sp|P32361 Saccharomy cerevisiae YHR079c IRE1, hypothe start
CAGL0K11990g	some similarities with sp|P3808 Saccharomyces cerevisiae YBR05 AKL1 Ark-family Kinase-Like pro hypothetical start
DEHA0G10417g	similar to CA1971|CaPKH2 Cand albicans CaPKH2 Ser/Thr protei kinase(by homology), hypothetical
YALI0B17556g	weakly similar to tr|Q9Y898 Emeri nidulans Calcium/calmodulin deper protein kinase C, hypothetical sta
CAGL0G03047g	highly similar to sp|P22204 Saccharomyces cerevisiae YGR09 DBF2 ser/thrprotein kinase or sp|P3 Saccharomyces cerevisiae YPR11 DBF20, hypothetical start
YALI0F27093g	weakly similar to DEHA-IPF372 Debaryomyces hansenii, hypothet start
DEHA0C14091g	similar to sp|P37292 Saccharomy cerevisiae YBR263w SHM1, hypothetical start
DEHA0C18601g	similar to CA4433|CaBCK1 Canc albicans, hypothetical start
KLLA0C04213g	similar to sp|P22209 Saccharomy cerevisiae YAR018c KIN3 ser/thr p kinase, hypothetical start
YALI0A04697g	similar to sp|O42626 Neurospora cr Serine/threonine-protein kinase nr (Nonrepressible conidiation protei hypothetical start
YALI0D26015g	similar to sp|P32562 Saccharomy cerevisiae Cell cycle protein kina CDC5/MSD2 (EC 2.7.1.-), hypothe start
DEHA0G14839g	highly similar to sCA3870|CaYP Candida albicans CaYPK1, start similarity
KLLA0C14278g	similar to sp|P28708 Saccharomy cerevisiae YKL116c, hypothetical
YALI0E13750g	similar to tr|CAD79666 Neurospo crassa B1D14.230 Related to serine/threonine-protein kinase a DEHA-IPF6149.1 Debaryomyc hansenii, no start
CAGL0B04147g	highly similar to sp|P22204 Saccharomyces cerevisiae YGR09 DBF2 ser/thrprotein kinase relate DBF20P or sp|P32328 Saccharom cerevisiae YPR111w DBF20 cell c protein kinase related to DBF2F hypothetical start
DEHA0F13497g	similar to ca|CA1299|CaPTK2 Can albicans CaPTK2 serine /threoni protein kinase involved in polyam uptake (by homology), hypothetical
DEHA0D13684g	similar to CA4865|IPF4085 Cand albicans IPF4085, start by similar
CAGL0L06006g	similar to sp|P53104 Saccharomy cerevisiae YGL180w APG1 essenti autophagocytosis, hypothetical st
CAGL0E05720g	similar to sp|P38991 Saccharomy cerevisiae YPL209c IPL1 ser/thr pr kinase, start by similarity
KLLA0F18612g	some similarities with sp|P3808 Saccharomyces cerevisiae YBR05 AKL1 Ark-family Kinase-Like pro hypothetical start

YALI0E24563g	similar to tr|Q12152 Saccharomy cerevisiae YPL150w, hypothetical
DEHA0F24013g	similar to ca|CA5226|CaRIM15 Ca albicans CaRIM15 Protein kinas involved in the RIM pathway (b homology), hypothetical start
CAGL0I04422g	some similarities with sp|P2220 Saccharomyces cerevisiae YAR0 KIN3 ser/thr protein kinase, hypoth start
CAGL0K01661g	some similarities with tr|Q1210 Saccharomyces cerevisiae YDL02 hypothetical start
DEHA0E15741g	highly similar to CA3361|CaSN Candida albicans CaSNF1 serine/threonine protein kinase hypothetical start
CAGL0M02233g	highly similar to sp|P22216 Saccharomyces cerevisiae YPL15 SPK1 ser/thr/tyr protein kinase hypothetical start
CAGL0F04741g	similar to sp|P22517 Saccharomy cerevisiae YOL016c CMK2 Ca2+/calmodulin-dependent ser/ protein kinase, type II, hypothetical
YALI0E06523g	weakly similar to sp|P34244 Saccharomyces cerevisiae YKL10 HSL1 ser/thr protein kinase, coup septin ring assembly to cell cyc progression, hypothetical start
KLLA0E11979g	some similarities with sp|P2533 Saccharomyces cerevisiae YCR00 SAT4 serine/threonine-specific pro kinase, hypothetical start
CAGL0J11308g	similar to sp|P22211 Saccharomy cerevisiae YNL183c NPR1 ser/t protein kinase, hypothetical star
DEHA0G11638g	similar to sp|P25333 Saccharomy cerevisiae YCR008w SAT4 serine/threonine-specific protein ki hypothetical start
CAGL0H10208g	similar to sp|P38080 Saccharomy cerevisiae YBR059c AKL1 Ark-fa Kinase-Like protein, hypothetical
CAGL0B02739g	similar to sp|P23561 Saccharomy cerevisiae YLR362w STE11 ser/ protein kinase of the MEKK fam hypothetical start
YALI0D07150g	weakly similar to tr|Q9C2E8 Neuro crassa Conserved hypothetical pro start by similarity
DEHA0F10197g	highly similar to ca|CA2265|CaCM Candida albicans CaCMK2 Ca /calmodulin-dependent ser/thr pro kinase, type II (by homology), hypothetical start
DEHA0B12628g	similar to sp|P06245 Saccharomy cerevisiae YPL203w TPK2 cAM dependent protein kinase 2, cataly chain, start by similarity
DEHA0E13574g	similar to CA2193|IPF14273 Cand albicans IPF14273 Probable ser/ protein kinase
KLLA0D07348g	weakly similar to sgd|S000606 Saccharomyces cerevisiae YPL14 start by similarity
DEHA0B12650g	some similarities with sp|P3897 Saccharomyces cerevisiae YJL16 HAL5 ser/thr protein kinase, hypoth start
DEHA0F04114g	similar to CA0576|CaNPR1 Cand albicans CaNPR1, hypothetical st
DEHA0C13211g	similar to sp|P22216 Saccharomy cerevisiae YPL153c SPK1, hypothe start

KLLA0B07205g	some similarities with sp|P0598 Saccharomyces cerevisiae YKL1 TPK3 cAMP-dependent protein kin catalytic chain, hypothetical sta
CAGL0K06479g	some similarities with tr|Q0330 Saccharomyces cerevisiae YDR46 start by similarity
KLLA0C12485g	weakly similar to sp|Q12236 Saccharomyces cerevisiae YOL10 PKH2, start by similarity
KLLA0E06413g	gi|22858696|gb|AAN05732.1 Kluyveromyces lactis protein kinas start by similarity
YALI0D26213g	weakly similar to tr|Q96WJ8 Blum graminis Protein kinase C-like pro hypothetical start
DEHA0G14707g	similar to CA6135|CaCMK1 Cand albicans CaCMK1, hypothetical s
DEHA0E16115g	similar to CA5074|IPF3607 Cand albicans IPF3607 putative serine/threonine protein kinase hypothetical start
CAGL0M13167g	similar to sp|P32801 Saccharomy cerevisiae YKL048c ELM1 ser/t specific protein kinase, hypothetical
KLLA0F01408g	weakly similar to sgd|S000218 Saccharomyces cerevisiae YDL02 hypothetical start
DEHA0F25212g	highly similar to tr|Q9HEW0 Cand albicans cAMP-dependent protein k catalytic subunit, hypothetical st
CAGL0M08404g	some similarities with sp|P0598 Saccharomyces cerevisiae YKL1 TPK3 or sp|P06244 Saccharomy cerevisiae YJL164c SRA3 or sp|P0 Saccharomyces cerevisiae YPL20 TPK2, hypothetical start
KLLA0A03806g	gi|2181934|emb|CAA61235.1 Kluyveromyces lactis putative kin start by similarity
YALI0D19470g	similar to tr|Q871H9 Neurospora c B16M17.090 Related to Ste20-li kinase Don3, hypothetical start
YALI0A10230g	similar to sp|P22211 Saccharomy cerevisiae YNL183c NPR1 ser/t protein kinase, start by similarit
DEHA0F10461g	some similarities with ca|CA1288|CaKSP1 Candida albic CaKSP1 SERINE/THREONINE PROTEIN KINASE by homolog hypothetical start
YALI0F01716g	tr|Q9P860 Yarrowia lipolytica Wee protein, mitosis inhibitor protein ki hypothetical start
YALI0E27632g	tr|O93955 Yarrowia lipolytica SS protein, multicopy suppressor of S secretory defects, putative calmodu dependent ser/thr protein kinase identified start
CAGL0I09504g	similar to sp|P38147 Saccharomy cerevisiae YBR274w CHK1 regu inhibitory Cdk phosphorylation of F start by similarity
CAGL0F09075g	similar to sp|P11792 Saccharomy cerevisiae YHR205w SCH9 serine/threonine protein kinase, sta similarity
DEHA0C17996g	similar to CA2348|IPF12811 Canc albicans, putative serine/threonin kinase, hypothetical start
CAGL0H00979g	similar to tr|Q12003 Saccharomy cerevisiae YPL236c, hypothetical
KLLA0C03828g	similar to sp|P54199 Saccharomy cerevisiae YDL028c MPS1

KIN1 (YDR122W)	2.7.1.-	sp|P13185 Saccharomyces cerevisiae YDR122w KIN1 ser/thr protein kinase P108.1.f9.1	Exhibits sensitivity at 5 generations when grown in synthetic complete medium.	NA	NA	NA	NA	NA	sckdy	57 58 49 54 42	GLC.2	KLLA0C05828g	serine/threonine/tyrosine protein ki hypothetical start
												KLLA0F14190g	gi|3021329|emb|CAA06336.1 Kluyveromyces lactis MAP kinase k kinase, start by similarity
												CAGL0M10153g	some similarities with sp|Q0349 Saccharomyces cerevisiae YHL0 ser/thr protein kinase of the pheron pathway, hypothetical start
												KLLA0F24618g	similar to sp|P38070 Saccharomy cerevisiae YBR028c, start by simil
												CAGL0K07458g	similar to sp|P12688 Saccharomy cerevisiae YKL126w or sp|P189 Saccharomyces cerevisiae YMR1 ser/thr-specific protein kinases, sta similarity
												KLLA0D03190g	highly similar to sp|P06245 Saccharomyces cerevisiae YPL20 TPK2 cAMP-dependent protein kin catalytic chain, start by similarit
												DEHA0D19833g	similar to CA5851|CaKIN2 Cand albicans CaKIN2, hypothetical st
												KLLA0D14905g	gi|28565036|gb|AAO32601.1 Kluyveromyces lactis DBF2, start similarity
												KLLA0C18568g	gi|6967028|emb|CAB72435.1 Kluyveromyces lactis MUP1 prot hypothetical start
												CAGL0M13541g	similar to sp|Q03533 Saccharomy cerevisiae YMR291w, hypothetical
												KLLA0E03487g	similar to sgd|S0002874 Saccharom cerevisiae YDR466w, start by simil
												DEHA0C08635g	similar to sp|P22204 Saccharomy cerevisiae YGR092w DBF2, hypothetical start, sequence gap
												CAGL0G02607g	similar to sp|P40494 Saccharomy cerevisiae YIL095w PRK1, start similarity
												CAGL0K11275g	similar to tr|Q03785 Saccharomy cerevisiae YDR247w, hypothetical
												DEHA0E05753g	similar to CA0719|IPF9779.5 Can albicans IPF9779.5 serine/threon protein kinase 5-prime end, hypoth start
												YALI0B05588g	some similarities with sp|Q1223 Saccharomyces cerevisiae YOL10 PKH2 related to ser/thr protein kin P108.1.f16.1, hypothetical star
												DEHA0A08822g	similar to CA0577|IPF16051 Can albicans IPF16051 unknown funct start by similarity
												KLLA0C17160g	similar to sp|P53104 Saccharomy cerevisiae YGL180w APG1 essenti autophagocytosis, start by similar
												KLLA0A02717g	some similarities with sp|P5323 Saccharomyces cerevisiae YGR05 hypothetical start
												YALI0C21758g	similar to KLLA-IPF4914.1 Kluyveromyces lactis IPF 4914. hypothetical start
												CAGL0C03509g	similar to sp|P53739 Saccharomy cerevisiae YNR047w or sp|P253 Saccharomyces cerevisiae YCR0 KIN82, hypothetical start
												KLLA0B03586g	similar to sp|P11792 Saccharomy cerevisiae YHR205w SCH9 serine/threonine protein kinase inv in stress response and nutrient-sen signaling pathway, start by simila
												YALI0C15444g	similar to tr|Q12706 Schizosaccharomyces pombe Prob serine/threonine protein kinase PS (EC 2.7.1.-), hypothetical start
													weakly similar to DEHA-IPF394

YALI0E34067g	Debaryomyces hansenii IPF 394 hypothetical start
CAGL0C05005g	similar to sp|P27636 Saccharomy cerevisiae YAR019c CDC15, hypothetical start
DEHA0B04895g	similar to CA2018|CaSTE11 Canc albicans CaSTE11 ser/thr protein k of the MEKK family, hypothetical
KLLA0B12716g	similar to sp|P12688 Saccharomy cerevisiae YKL126w YPK1 ser/t specific protein kinase, start by simi
CAGL0F03707g	similar to sp|Q08732 Saccharomy cerevisiae YOR267c, start by simil
YALI0E22858g	Weakly similar to CAAL-CA55 CaAKL1 serine/threonine protein k (by homology), Hypothetical sta
KLLA0F09031g	similar to sp|P43565 Saccharomy cerevisiae YFL033c RIM15 prote kinase involved in expression of me genes, hypothetical start
DEHA0E12782g	similar to sp|P38070 Saccharomy cerevisiae YBR028c, putative ribos protein kinase
CAGL0B01925g	similar to sp|P13185 Saccharomy cerevisiae YDR122w KIN1 or sp|P1 Saccharomyces cerevisiae YLR09 KIN2, hypothetical start
KLLA0C07535g	some similarities with sgd|S00057 Saccharomyces cerevisiae YOR26 hypothetical start
CAGL0D02244g	similar to sp|P24719 Saccharomy cerevisiae YOR351c MEK1 ser/t protein kinase, hypothetical star
DEHA0C13387g	similar to tr|Q08732 Saccharomy cerevisiae YOR267C, hypothetical
YALI0E17743g	no similarity, hypothetical start
CAGL0C02893g	similar to tr|Q08732 Saccharomy cerevisiae YOR267c, hypothetical
KLLA0F19536g	similar to sp|P13186 Saccharomy cerevisiae YLR096w KIN2 ser/t protein kinase, start by similarit
CAGL0M11396g	similar to sp|P13186 Saccharomy cerevisiae YLR096w KIN2 ser/t protein kinase, hypothetical star
YALI0B13178g	similar to sp|P32490 Saccharomy cerevisiae YOR231w MKK1 ser/ protein kinase, start by similarit
DEHA0F27489g	similar to CA1288|CaKSP1 Cand albicans CaKSP1 serine/threonin protein kinase (by homology), star similarity
KLLA0B02332g	similar to sp|P38991 Saccharomy cerevisiae YPL209c IPL1 ser/thr pr kinase, start by similarity
CAGL0L07326g	similar to sp|P39009 Saccharomy cerevisiae YDL101c DUN1 prote kinase, start by similarity
KLLA0F11143g	similar to sp|P22216 Saccharomy cerevisiae YPL153c SPK1 ser/thr protein kinase, start by similarit
DEHA0E14641g	similar to CA4097|CaGIN4 Cand albicans CaGIN4 ser/thr protein ki (by homology), hypothetical sta
CAGL0J03872g	similar to sp|Q01919 Saccharomy cerevisiae YOR233w KIN4 ser/t protein kinase or tr|Q03002 Saccharomyces cerevisiae YPL14 start by similarity
YALI0D14542g	similar to sp|P11792 Saccharomy cerevisiae YHR205w SCH9 serine/threonine protein kinase invo in stress response and nutrient-sen signaling pathway, start by simila

KLLA0B06501g	some similarities with sp|P4711 Saccharomyces cerevisiae YJR05 PTK2 involved in polyamine upta hypothetical start
DEHA0C05742g	some similarities with sp|P4189 Schizosaccharomyces pombe Ce division control protein 7 and CA2669|IPF17494.3eoc Candid albicans and CA2404|CaCDC15 Ca albicans, hypothetical start
DEHA0F20878g	similar to CA0044|IPF17347 Canc albicans IPF17347, hypothetical s
KLLA0E08371g	similar to sp|P40494 Saccharomy cerevisiae YIL095w PRK1 serine/threonine protein kinase invo in regulation of actin cytoskeleto organization, start by similarity
KLLA0F13552g	gi|33386566|emb|CAD87727.1 Kluyveromyces lactis protein kina start by similarity
CAGL0J11638g	highly similar to sp|P32562 Saccharomyces cerevisiae YMR0 CDC5 involved in regulation of D replication, hypothetical start
CAGL0K02167g	similar to sp|P38990 Saccharomy cerevisiae YER129w Serine/threon protein kinase, start by similarit
DEHA0F09493g	similar to ca|CA2909|IPF11424 Can albicans IPF11424 unknown funct hypothetical start
CAGL0G05720g	similar to sp|P22211 Saccharomy cerevisiae YNL183c NPR1 ser/t protein kinase, start by similarit
DEHA0C09823g	similar to CA1205|CaSSK2 Cand albicans, hypothetical start
YALI0D22770g	Similar to CAAL-CA5851 CaKI ser/thr protein kinase (by homology start
CAGL0M08910g	highly similar to sp|Q00372 Saccharomyces cerevisiae YDR47 carbon catabolite derepressing ser protein kinase, hypothetical star
KLLA0C04191g	weakly similar to sp|P27636 Saccharomyces cerevisiae YAR0 CDC15 protein kinase of the MA kinase kinase kinase family, hypoth start
DEHA0B16071g	similar to sp|P22209 Saccharomy cerevisiae YAR018c KIN3 ser/thr p kinase, start by similarity
CAGL0K03399g	highly similar to sp|P12688 Saccharomyces cerevisiae YKL12 Serine/threonine-protein kinase, sta similarity
CAGL0J04972g	some similarities with tr|Q1210 Saccharomyces cerevisiae YDL02 hypothetical start
DEHA0F10923g	highly similar to ca|CA2986|CaCI Candida albicans CaCDC5 Cell-cy protein kinase (by homology), star similarity
YALI0B04840g	similar to tr|Q12003 Saccharomy cerevisiae YPL236c, start by simila
KLLA0C01650g	similar to sp|Q12263 Saccharomy cerevisiae YDR507c GIN4 ser/thr p kinase, start by similarity
YALI0F08165g	some similarities with sp|P4189 Schizosaccharomyces pombe 7 CI OR SPBC21.06C gene Cell divis control protein, start by similarit
KLLA0E01584g	highly similar to sp|P39009 Saccharomyces cerevisiae YDL10 DUN1 protein kinase, start by simil
DEHA0C02882g	similar to CA4039|CaSKS1 Cand

DEHA0C02882g	albicans, start by similarity
KLLA0F01276g	similar to sp|P38147 Saccharomy cerevisiae YBR274w CHK1 regul inhibitory Cdk phosphorylation of P start by similarity
CAGL0G09020g	highly similar to sp|P06245 Saccharomyces cerevisiae YPL20 TPK2 cAMP-dependent protein kin catalytic chain, hypothetical sta
DEHA0G16302g	similar to tr|Q12706 Schizosaccharomyces pombe Prob serine/threonine protein kinase PS start by similarity
CAGL0I06248g	similar to sp|P38970 Saccharomy cerevisiae YJL165c HAL5 ser/thr pr kinase, start by similarity
YALI0B08558g	weakly similar to tr|Q00863 Nect haematococca Ran1-like protein ki hypothetical start
DEHA0G05544g	similar to CA1375|IPF7158 Cand albicans IPF7158 putative serine/threonine kinase, hypothetica
KLLA0B13607g	weakly similar to sp|Q03497 Saccharomyces cerevisiae YHL00 STE20 ser/thr protein kinase of t pheromone pathway, hypothetical
YALI0F27159g	some similarities with sp|P4704 Saccharomyces cerevisiae YJL057c probable serine/threonine-protein ki hypothetical start
CAGL0I05390g	similar to sp|Q12505 Saccharomy cerevisiae YPL026c SKS1 suppre kinase of SNF3 or tr|Q03785 Saccharomyces cerevisiae YDR24 start by similarity
YALI0E31361g	similar to tr|Q9HF33 Arthrobotr dactyloides Calmodulin-binding pr kinase, hypothetical start
YALI0B14201g	similar to sp|P32328 Saccharomy cerevisiae YPR111w DBF20 cell c protein kinase P108.1.f3.6 or sp|P2 Saccharomyces cerevisiae YGR09 DBF2 ser/thr protein kinase P108.1.f16.1, hypothetical star
DEHA0C16181g	similar to CA1447|CaNRK1 Cand albicans, hypothetical start
CAGL0K04301g	similar to sp|P53233 Saccharomy cerevisiae YGR052w, hypothetical
KLLA0A06820g	some similarities with sp|P3897 Saccharomyces cerevisiae YJL16 HAL5 ser/thr protein kinase, hypoth start
KLLA0C00979g	similar to sp|P08458 Saccharomy cerevisiae YDR523c SPS1 ser/thr pr kinase, hypothetical start
YALI0D02101g	similar to sp|O94168 Candida tropi Carbon catabolite derepressing pro kinase (EC 2.7.1.-), hypothetical s
YALI0C08305g	highly similar to sp|P06245 Saccharomyces cerevisiae YPL20 TPK2 cAMP-dependent protein kin catalytic chain, hypothetical sta
KLLA0D12100g	some similarities with sgd|S00026 Saccharomyces cerevisiae YDR24 hypothetical start
CAGL0M10791g	highly similar to sp|P53599 Saccharomyces cerevisiae YNR03 SSK2 MAP kinase, no start, frame
YALI0A05247g	similar to tr|Q876Z5 Neurospora cr OS-4 Putative SSK22 like MAPK kinase, hypothetical start
DEHA0F24684g	similar to sp|P24719 Saccharomy cerevisiae YOR351c MEK1 ser/t protein kinase

												KLLA0B13112g	similar to sp|P23561 Saccharomy cerevisiae YLR362w STE11 ser/ protein kinase of the MEKK family by similarity
												CAGL0F03311g	similar to sp|P38691 Saccharomy cerevisiae YHR082c KSP1 ser/t protein kinase, start by similarit
												KLLA0C03938g	some similarities with sgd|S00021 Saccharomyces cerevisiae YDL02 hypothetical start
												CAGL0M08360g	some similarities with sp|P3897 Saccharomyces cerevisiae YJL16 ser/thr protein kinase, hypothetical
												YALI0E34375g	similar to wi|NCU00108.1 Neurosp crassa NCU00108.1 hypothetical pr (93222 - 91750), hypothetical st
												KLLA0B07579g	weakly similar to sp|P32944 Saccharomyces cerevisiae YJL18 SWE1 ser/tyr dual-specifity prot kinase, start by similarity
												YALI0D25388g	similar to tr|Q8TFN2 Pichia angu Serine-threonine kinase Pdd7p hypothetical start
												DEHA0C04840g	some similarities with sp|P3899 Saccharomyces cerevisiae YPL20 IPL1 ser/thr protein kinase, hypothe start
												YALI0B00880g	similar to sp|P22211 Saccharomy cerevisiae YNL183c NPR1 ser/t protein kinase, hypothetical star
												YALI0D08822g	some similarities with sp|P3899 Saccharomyces cerevisiae YER12 PAK1 DNA polymerase alpha suppressing protein kinase, hypothe start
												DEHA0G22440g	similar to CA4770|IPF9382.3 Can albicans IPF9382.3, hypothetical s
												KLLA0C08525g	similar to sp|P53599 Saccharomy cerevisiae YNR031c SSK2 MAP k kinase kinase of the high osmolar signal transduction pathway, start similarity
												YALI0F09746g	similar to sp|P24583 Saccharomy cerevisiae YBL105c PKC1 ser/t protein kinase, start by similarit
												DEHA0D07601g	similar to Candida albicans CA42 start by similarity
												CAGL0I07513g	similar to sp|Q12236 Saccharomy cerevisiae YOL100w PKH2, start similarity
												DEHA0D11242g	highly similar to CA5299|IPF21 Candida albicans IPF2190, start similarity
												DEHA0F26994g	similar to CA0206|IPF14089 Cand albicans IPF14089 putative serine/threonine protein kinase hypothetical start
												CAGL0M09361g	highly similar to sp|P24583 Saccharomyces cerevisiae YBL10 PKC1 ser/thr protein kinase, start similarity
												YALI0E06501g	similar to sp|P12688 Saccharomy cerevisiae YKL126w YPK1 ser/t specific protein kinase, hypothetical
												CAGL0K05709g	similar to sp|Q12263 Saccharomy cerevisiae YDR507c GIN4, start similarity
												DEHA0C09130g	similar to sp|P38147 Saccharomy cerevisiae YBR274w CHK1, hypothetical start
												CAGL0M02299g	similar to tr|Q12152 Saccharomy cerevisiae YPL150w, start by simil
												CAGL0B04301g	similar to sp|P38070 Saccharomy cerevisiae YBR028c, start by simil

												CAGL0J03432g	similar to sp|P53974 Saccharomy cerevisiae YNL020c ARK1 or sp|P4 Saccharomyces cerevisiae YIL09 PRK1, start by similarity
												DEHA0D13706g	similar to CA4864|IPF4087 Cand albicans IPF4087, hypothetical st
												KLLA0D09328g	some similarities with sp|P3899 Saccharomyces cerevisiae YER12 PAK1 DNA polymerase alpha suppressing protein kinase, hypothe start
												DEHA0B13519g	some similarities with sp|P5373 Saccharomyces cerevisiae YNR04 related to ser/thr protein kinases hypothetical start
												CAGL0M02519g	highly similar to tr|Q03002 Saccharomyces cerevisiae YPL141 sp|Q01919 Saccharomyces cerevis YOR233w KIN4, hypothetical st
												CAGL0G04609g	similar to sp|Q12236 Saccharomy cerevisiae YOL100w PKH2, hypothetical start
												KLLA0F23155g	similar to sp|P22517 Saccharomy cerevisiae YOL016c CMK2 Ca2+/calmodulin-dependent ser/ protein kinase, type II, start by simi
												KLLA0F11319g	similar to sgd|S0006071 Saccharom cerevisiae YPL150w, start by simil
												CAGL0L07810g	similar to sp|P25333 Saccharomy cerevisiae YCR008w SAT4 serine/threonine-specific protein ki start by similarity
												CAGL0K11550g	similar to sp|P28708 Saccharomy cerevisiae YKL116c, hypothetical
												YALI0F11385g	weakly similar to SP|P38691 Saccharomyces cerevisiae YHR08 KSP1 ser/thr protein kinase and DE IPF5974.1, start by similarity
												KLLA0A09713g	similar to sp|Q03533 Saccharomy cerevisiae YMR291w, start by simi
												KLLA0E17127g	similar to sp|P38691 Saccharomy cerevisiae YHR082c KSP1 ser/t protein kinase, start by similarit
												YALI0C04158g	similar to sp|P18961 Saccharomy cerevisiae Serine/threonine-prote kinase YPK2/YKR2, hypothetical
												DEHA0F24676g	similar to sp|P24719 Saccharomy cerevisiae YOR351c MEK1 ser/t protein kinase
												DEHA0G14817g	similar to CA2643|CaHSL1 Cand albicans CaHSL1, hypothetical st
												DEHA0C18150g	similar to sp|P40494 Saccharomy cerevisiae YIL095w PRK1 serine/threonine protein kinase, sta similarity
												CAGL0K10604g	similar to sp|P27466 Saccharomy cerevisiae YFR014c CMK1 Ca2+/calmodulin-dependent ser/ protein kinase type I, hypothetical
												DEHA0C08591g	similar to sp|P22204 Saccharomy cerevisiae YGR092w DBF2, hypothetical start, sequence gap
												YALI0F13629g	some similarities with sp|P2356 Saccharomyces cerevisiae YLR36 STE11 ser/thr protein kinase of t MEKK family, hypothetical sta
												KLLA0C06138g	similar to sp|P32562 Saccharomy cerevisiae YMR001c CDC5 involv regulation of DNA replication, star similarity
												YALI0F16159g	some similarities with wi|NCU009 Neurospora crassa NCU00914. hypothetical protein, hypothetical
													similar to sp|P34244 Saccharomy

												CAGL0K08514g	cerevisiae YKL101w serine/threon protein kinase, hypothetical star
												DEHA0F25278g	similar to ca|CA1881|CaRCK2 Car albicans CaRCK2 Ca/calmoduli dependent ser/thr protein kinase (homology), hypothetical start
												KLLA0F26983g	some similarities with sp|P3280 Saccharomyces cerevisiae YKL0 ELM1 ser/thr-specific protein kin hypothetical start
												DEHA0C11484g	similar to sp|P22211 Saccharomy cerevisiae YNL183c NPR1 or tr|Q1 Saccharomyces cerevisiae YDL02 hypothetical start
												YALI0C00891g	similar to sp|O14019 Schizosaccharomyces pombe Prob serine/threonine-protein kinase C29A4.16 (EC 2.7.1.-), hypothetica
												KLLA0F23507g	similar to sp|P24719 Saccharomy cerevisiae YOR351c MEK1 ser/t protein kinase, start by similarit
												CAGL0F03245g	similar to sp|P32361 Saccharomy cerevisiae YHR079c IRE1, hypothe start
												CAGL0K11990g	some similarities with sp|P3808 Saccharomyces cerevisiae YBR0 AKL1 Ark-family Kinase-Like pro hypothetical start
												DEHA0G10417g	similar to CA1971|CaPKH2 Cand albicans CaPKH2 Ser/Thr protei kinase(by homology), hypothetical
												YALI0B17556g	weakly similar to tr|Q9Y898 Emeri nidulans Calcium/calmodulin depen protein kinase C, hypothetical st
												CAGL0G03047g	highly similar to sp|P22204 Saccharomyces cerevisiae YGR0 DBF2 ser/thrprotein kinase or sp|P3 Saccharomyces cerevisiae YPR11 DBF20, hypothetical start
												YALI0F27093g	weakly similar to DEHA-IPF372 Debaryomyces hansenii, hypothet start
												DEHA0C14091g	similar to sp|P37292 Saccharomy cerevisiae YBR263w SHM1, hypothetical start
												DEHA0C18601g	similar to CA4433|CaBCK1 Canc albicans, hypothetical start
												KLLA0C04213g	similar to sp|P22209 Saccharomy cerevisiae YAR018c KIN3 ser/thr p kinase, hypothetical start
												YALI0A04697g	similar to sp|O42626 Neurospora c Serine/threonine-protein kinase n (Nonrepressible conidiation protei hypothetical start
												YALI0D26015g	similar to sp|P32562 Saccharomy cerevisiae Cell cycle protein kina CDC5/MSD2 (EC 2.7.1.-), hypothe start
												DEHA0G14839g	highly similar to sCA3870|CaYP Candida albicans CaYPK1, start similarity
												KLLA0C14278g	similar to sp|P28708 Saccharomy cerevisiae YKL116c, hypothetical
												YALI0E13750g	similar to tr|CAD79666 Neurosp crassa B1D14.230 Related to serine/threonine-protein kinase a DEHA-IPF6149.1 Debaryomyc hansenii, no start
												CAGL0B04147g	highly similar to sp|P22204 Saccharomyces cerevisiae YGR0 DBF2 ser/thrprotein kinase relate DBF20P or sp|P32328 Saccharom cerevisiae YPR111w DBF20 cell c protein kinase related to DBF2 hypothetical start

DEHA0F13497g	similar to ca|CA1299|CaPTK2 Can albicans CaPTK2 serine /threoni protein kinase involved in polyam uptake (by homology), hypothetical
DEHA0D13684g	similar to CA4865|IPF4085 Cand albicans IPF4085, start by similar
CAGL0L06006g	similar to sp|P53104 Saccharomy cerevisiae YGL180w APG1 essenti autophagocytosis, hypothetical st
CAGL0E05720g	similar to sp|P38991 Saccharomy cerevisiae YPL209c IPL1 ser/thr pr kinase, start by similarity
KLLA0F18612g	some similarities with sp|P3808 Saccharomyces cerevisiae YBR05 AKL1 Ark-family Kinase-Like pro hypothetical start
YALI0E24563g	similar to tr|Q12152 Saccharomy cerevisiae YPL150w, hypothetical
DEHA0F24013g	similar to ca|CA5226|CaRIM15 Ca albicans CaRIM15 Protein kinas involved in the RIM pathway (b homology), hypothetical start
CAGL0I04422g	some similarities with sp|P2220 Saccharomyces cerevisiae YAR0 KIN3 ser/thr protein kinase, hypoth start
CAGL0K01661g	some similarities with tr|Q1210 Saccharomyces cerevisiae YDL02 hypothetical start
DEHA0E15741g	highly similar to CA3361|CaSNI Candida albicans CaSNF1 serine/threonine protein kinase hypothetical start
CAGL0M02233g	highly similar to sp|P22216 Saccharomyces cerevisiae YPL15 SPK1 ser/thr/tyr protein kinase hypothetical start
CAGL0F04741g	similar to sp|P22517 Saccharomy cerevisiae YOL016c CMK2 Ca2+/calmodulin-dependent ser/ protein kinase, type II, hypothetical
YALI0E06523g	weakly similar to sp|P34244 Saccharomyces cerevisiae YKL10 HSL1 ser/thr protein kinase, coup septin ring assembly to cell cycl progression, hypothetical start
KLLA0E11979g	some similarities with sp|P2533 Saccharomyces cerevisiae YCR00 SAT4 serine/threonine-specific pro kinase, hypothetical start
CAGL0J11308g	similar to sp|P22211 Saccharomy cerevisiae YNL183c NPR1 ser/t protein kinase, hypothetical star
DEHA0G11638g	similar to sp|P25333 Saccharomy cerevisiae YCR008w SAT4 serine/threonine-specific protein ki hypothetical start
CAGL0H10208g	similar to sp|P38080 Saccharomy cerevisiae YBR059c AKL1 Ark-fa Kinase-Like protein, hypothetical
CAGL0B02739g	similar to sp|P23561 Saccharomy cerevisiae YLR362w STE11 ser/ protein kinase of the MEKK fam hypothetical start
YALI0D07150g	weakly similar to tr|Q9C2E8 Neuro crassa Conserved hypothetical pro start by similarity
DEHA0F10197g	highly similar to ca|CA2265|CaCM Candida albicans CaCMK2 Ca2 /calmodulin-dependent ser/thr pro kinase, type II (by homology), hypothetical start
DEHA0B12628g	similar to sp|P06245 Saccharomy cerevisiae YPL203w TPK2 cAM

DEHA0B12628g	dependent protein kinase 2, cataly chain, start by similarity
DEHA0E13574g	similar to CA2193|IPF14273 Canc albicans IPF14273 Probable ser/t protein kinase
KLLA0D07348g	weakly similar to sgd|S000606 Saccharomyces cerevisiae YPL14 start by similarity
DEHA0B12650g	some similarities with sp|P3897 Saccharomyces cerevisiae YJL16 HAL5 ser/thr protein kinase, hypoth start
DEHA0F04114g	similar to CA0576|CaNPR1 Cand albicans CaNPR1, hypothetical st
DEHA0C13211g	similar to sp|P22216 Saccharomy cerevisiae YPL153c SPK1, hypothe start
KLLA0B07205g	some similarities with sp|P0598 Saccharomyces cerevisiae YKL16 TPK3 cAMP-dependent protein kin catalytic chain, hypothetical sta
CAGL0K06479g	some similarities with tr|Q0330 Saccharomyces cerevisiae YDR46 start by similarity
KLLA0C12485g	weakly similar to sp|Q12236 Saccharomyces cerevisiae YOL10 PKH2, start by similarity
KLLA0E06413g	gi|22858696|gb|AAN05732.1 Kluyveromyces lactis protein kinas start by similarity
YALI0D26213g	weakly similar to tr|Q96WJ8 Blum graminis Protein kinase C-like pro hypothetical start
DEHA0G14707g	similar to CA6135|CaCMK1 Canc albicans CaCMK1, hypothetical s
DEHA0E16115g	similar to CA5074|IPF3607 Cand albicans IPF3607 putative serine/threonine protein kinase hypothetical start
CAGL0M13167g	similar to sp|P32801 Saccharomy cerevisiae YKL048c ELM1 ser/tl specific protein kinase, hypothetical
KLLA0F01408g	weakly similar to sgd|S000218 Saccharomyces cerevisiae YDL02 hypothetical start
DEHA0F25212g	highly similar to tr|Q9HEW0 Canc albicans cAMP-dependent protein k catalytic subunit, hypothetical st
CAGL0M08404g	some similarities with sp|P0598 Saccharomyces cerevisiae YKL16 TPK3 or sp|P06244 Saccharomy cerevisiae YJL164c SRA3 or sp|P0 Saccharomyces cerevisiae YPL20 TPK2, hypothetical start
KLLA0A03806g	gi|2181934|emb|CAA61235.1 Kluyveromyces lactis putative kin start by similarity
YALI0D19470g	similar to tr|Q871H9 Neurospora c B16M17.090 Related to Ste20-li kinase Don3, hypothetical start
YALI0A10230g	similar to sp|P22211 Saccharomy cerevisiae YNL183c NPR1 ser/t protein kinase, start by similarit
DEHA0F10461g	some similarities with ca|CA1288|CaKSP1 Candida albic CaKSP1 SERINE/THREONINE PROTEIN KINASE by homolog hypothetical start
YALI0F01716g	tr|Q9P860 Yarrowia lipolytica Wee protein, mitosis inhibitor protein ki hypothetical start
YALI0E27632g	tr|O93955 Yarrowia lipolytica SS protein, multicopy suppressor of S secretory defects, putative calmodu

SNF1 (YDR477W)	2.7.1.-	sp|P06782 Saccharomyces cerevisiae YDR477w SNF1 carbon catabolite derepressing ser/thr protein kinase	exhibits growth defect on a non-fermentable (respiratory) carbon	NA	NA	NA	NA	NA	sckdy	57 58 49 54 42	GLC.2		dependent ser/thr protein kinase identified start
												CAGL0I09504g	similar to sp|P38147 Saccharomy cerevisiae YBR274w CHK1 regul inhibitory Cdk phosphorylation of P start by similarity
												CAGL0F09075g	similar to sp|P11792 Saccharomy cerevisiae YHR205w SCH9 serine/threonine protein kinase, sta similarity
												DEHA0C17996g	similar to CA2348|IPF12811 Canc albicans, putative serine/threonin kinase, hypothetical start
												CAGL0H00979g	similar to tr|Q12003 Saccharomy cerevisiae YPL236c, hypothetical
												KLLA0C03828g	similar to sp|P54199 Saccharomy cerevisiae YDL028c MPS1 serine/threonine/tyrosine protein ki hypothetical start
												KLLA0F14190g	gi|3021329|emb|CAA06336.1 Kluyveromyces lactis MAP kinase k kinase, start by similarity
												CAGL0M10153g	some similarities with sp|Q0349 Saccharomyces cerevisiae YHL00 ser/thr protein kinase of the pheron pathway, hypothetical start
												KLLA0F24618g	similar to sp|P38070 Saccharomy cerevisiae YBR028c, start by simil
												CAGL0K07458g	similar to sp|P12688 Saccharomy cerevisiae YKL126w or sp|P189 Saccharomyces cerevisiae YMR1 ser/thr-specific protein kinases, sta similarity
												KLLA0D03190g	highly similar to sp|P06245 Saccharomyces cerevisiae YPL20 TPK2 cAMP-dependent protein kin catalytic chain, start by similarit
												DEHA0D19833g	similar to CA5851|CaKIN2 Cand albicans CaKIN2, hypothetical st
												KLLA0D14905g	gi|28565036|gb|AAO32601.1 Kluyveromyces lactis DBF2, start similarity
												KLLA0C18568g	gi|6967028|emb|CAB72435.1 Kluyveromyces lactis MUP1 prot hypothetical start
												CAGL0M13541g	similar to sp|Q03533 Saccharomy cerevisiae YMR291w, hypothetical
												KLLA0E03487g	similar to sgd|S0002874 Saccharom cerevisiae YDR466w, start by simil
												DEHA0C08635g	similar to sp|P22204 Saccharomy cerevisiae YGR092w DBF2, hypothetical start, sequence gap
												CAGL0G02607g	similar to sp|P40494 Saccharomy cerevisiae YIL095w PRK1, start similarity
												CAGL0K11275g	similar to tr|Q03785 Saccharomy cerevisiae YDR247w, hypothetical
												DEHA0E05753g	similar to CA0719|IPF9779.5 Can albicans IPF9779.5 serine/threon protein kinase 5-prime end, hypoth start
												YALI0B05588g	some similarities with sp|Q1223 Saccharomyces cerevisiae YOL10 PKH2 related to ser/thr protein kin P108.1.f16.1, hypothetical star
												DEHA0A08822g	similar to CA0577|IPF16051 Canc albicans IPF16051 unknown funct start by similarity
												KLLA0C17160g	similar to sp|P53104 Saccharomy cerevisiae YGL180w APG1 essenti autophagocytosis, start by similar
												KLLA0A02717g	some similarities with sp|P5323 Saccharomyces cerevisiae YGR05 hypothetical start

		P108.1.f9.1	source										hypothetical start
												YALI0C21758g	similar to KLLA-IPF4914.1 Kluyveromyces lactis IPF 4914. hypothetical start
												CAGL0C03509g	similar to sp|P53739 Saccharomy cerevisiae YNR047w or sp|P253 Saccharomyces cerevisiae YCR09 KIN82, hypothetical start
												KLLA0B03586g	similar to sp|P11792 Saccharomy cerevisiae YHR205w SCH9 serine/threonine protein kinase inv in stress response and nutrient-sen signaling pathway, start by simila
												YALI0C15444g	similar to tr|Q12706 Schizosaccharomyces pombe Prob serine/threonine protein kinase PS (EC 2.7.1.-), hypothetical start
												YALI0E34067g	weakly similar to DEHA-IPF394 Debaryomyces hansenii IPF 394 hypothetical start
												CAGL0C05005g	similar to sp|P27636 Saccharomy cerevisiae YAR019c CDC15, hypothetical start
												DEHA0B04895g	similar to CA2018|CaSTE11 Canc albicans CaSTE11 ser/thr protein k of the MEKK family, hypothetical
												KLLA0B12716g	similar to sp|P12688 Saccharomy cerevisiae YKL126w YPK1 ser/t specific protein kinase, start by simi
												CAGL0F03707g	similar to sp|Q08732 Saccharomy cerevisiae YOR267c, start by simil
												YALI0E22858g	Weakly similar to CAAL-CA55 CaAKL1 serine/threonine protein k (by homology), Hypothetical sta
												KLLA0F09031g	similar to sp|P43565 Saccharomy cerevisiae YFL033c RIM15 prot kinase involved in expression of me genes, hypothetical start
												DEHA0E12782g	similar to sp|P38070 Saccharomy cerevisiae YBR028c, putative ribos protein kinase
												CAGL0B01925g	similar to sp|P13185 Saccharomy cerevisiae YDR122w KIN1 or sp|P1 Saccharomyces cerevisiae YLR09 KIN2, hypothetical start
												KLLA0C07535g	some similarities with sgd|S00057 Saccharomyces cerevisiae YOR26 hypothetical start
												CAGL0D02244g	similar to sp|P24719 Saccharomy cerevisiae YOR351c MEK1 ser/t protein kinase, hypothetical star
												DEHA0C13387g	similar to tr|Q08732 Saccharomy cerevisiae YOR267C, hypothetical
												YALI0E17743g	no similarity, hypothetical start
												CAGL0C02893g	similar to tr|Q08732 Saccharomy cerevisiae YOR267c, hypothetical
												KLLA0F19536g	similar to sp|P13186 Saccharomy cerevisiae YLR096w KIN2 ser/t protein kinase, start by similarit
												CAGL0M11396g	similar to sp|P13186 Saccharomy cerevisiae YLR096w KIN2 ser/t protein kinase, hypothetical star
												YALI0B13178g	similar to sp|P32490 Saccharomy cerevisiae YOR231w MKK1 ser/ protein kinase, start by similarit
												DEHA0F27489g	similar to CA1288|CaKSP1 Cand albicans CaKSP1 serine/threonin protein kinase (by homology), star similarity
												KLLA0B02332g	similar to sp|P38991 Saccharomy cerevisiae YPL209c IPL1 ser/thr pr kinase, start by similarity
												CAGL0L07326g	similar to sp|P39009 Saccharomy cerevisiae YDL101c DUN1 prot

													kinase, start by similarity
												KLLA0F11143g	similar to sp|P22216 Saccharomy cerevisiae YPL153c SPK1 ser/thr protein kinase, start by similarit
												DEHA0E14641g	similar to CA4097|CaGIN4 Cand albicans CaGIN4 ser/thr protein ki (by homology), hypothetical sta
												CAGL0J03872g	similar to sp|Q01919 Saccharomy cerevisiae YOR233w KIN4 ser/t protein kinase or tr|Q03002 Saccharomyces cerevisiae YPL14 start by similarity
												YALI0D14542g	similar to sp|P11792 Saccharomy cerevisiae YHR205w SCH9 serine/threonine protein kinase invo in stress response and nutrient-sen signaling pathway, start by simila
												KLLA0B06501g	some similarities with sp|P4711 Saccharomyces cerevisiae YJR05 PTK2 involved in polyamine upta hypothetical start
												DEHA0C05742g	some similarities with sp|P4189 Schizosaccharomyces pombe Ce division control protein 7 and CA2669|IPF17494.3eoc Candid albicans and CA2404|CaCDC15 Ca albicans, hypothetical start
												DEHA0F20878g	similar to CA0044|IPF17347 Canc albicans IPF17347, hypothetical s
												KLLA0E08371g	similar to sp|P40494 Saccharomy cerevisiae YIL095w PRK1 serine/threonine protein kinase invo in regulation of actin cytoskeleto organization, start by similarity
												KLLA0F13552g	gi|33386566|emb|CAD87727.1 Kluyveromyces lactis protein kina start by similarity
												CAGL0J11638g	highly similar to sp|P32562 Saccharomyces cerevisiae YMR0 CDC5 involved in regulation of D replication, hypothetical start
												CAGL0K02167g	similar to sp|P38990 Saccharomy cerevisiae YER129w Serine/threon protein kinase, start by similarit
												DEHA0F09493g	similar to ca|CA2909|IPF11424 Car albicans IPF11424 unknown funct hypothetical start
												CAGL0G05720g	similar to sp|P22211 Saccharomy cerevisiae YNL183c NPR1 ser/t protein kinase, start by similarit
												DEHA0C09823g	similar to CA1205|CaSSK2 Cand albicans, hypothetical start
												YALI0D22770g	Similar to CAAL-CA5851 CaKI ser/thr protein kinase (by homology start
												CAGL0M08910g	highly similar to sp|Q00372 Saccharomyces cerevisiae YDR47 carbon catabolite derepressing ser protein kinase, hypothetical star
												KLLA0C04191g	weakly similar to sp|P27636 Saccharomyces cerevisiae YAR0 CDC15 protein kinase of the MA kinase kinase kinase family, hypoth start
												DEHA0B16071g	similar to sp|P22209 Saccharomy cerevisiae YAR018c KIN3 ser/thr p kinase, start by similarity
												CAGL0K03399g	highly similar to sp|P12688 Saccharomyces cerevisiae YKL12 Serine/threonine-protein kinase, sta similarity
												CAGL0J04972g	some similarities with tr|Q1210 Saccharomyces cerevisiae YDL02 hypothetical start

												DEHA0F10923g	highly similar to ca|CA2986|CaCD Candida albicans CaCDC5 Cell-cy protein kinase (by homology), star similarity
												YALI0B04840g	similar to tr|Q12003 Saccharomy cerevisiae YPL236c, start by simila
												KLLA0C01650g	similar to sp|Q12263 Saccharomy cerevisiae YDR507c GIN4 ser/thr p kinase, start by similarity
												YALI0F08165g	some similarities with sp|P4189 Schizosaccharomyces pombe 7 CD OR SPBC21.06C gene Cell divis control protein, start by similarit
												KLLA0E01584g	highly similar to sp|P39009 Saccharomyces cerevisiae YDL10 DUN1 protein kinase, start by simil
												DEHA0C02882g	similar to CA4039|CaSKS1 Cand albicans, start by similarity
												KLLA0F01276g	similar to sp|P38147 Saccharomy cerevisiae YBR274w CHK1 regul inhibitory Cdk phosphorylation of P start by similarity
												CAGL0G09020g	highly similar to sp|P06245 Saccharomyces cerevisiae YPL20 TPK2 cAMP-dependent protein kin catalytic chain, hypothetical sta
												DEHA0G16302g	similar to tr|Q12706 Schizosaccharomyces pombe Prob serine/threonine protein kinase PS start by similarity
												CAGL0I06248g	similar to sp|P38970 Saccharomy cerevisiae YJL165c HAL5 ser/thr p kinase, start by similarity
												YALI0B08558g	weakly similar to tr|Q00863 Nect haematococca Ran1-like protein ki hypothetical start
												DEHA0G05544g	similar to CA1375|IPF7158 Cand albicans IPF7158 putative serine/threonine kinase, hypothetica
												KLLA0B13607g	weakly similar to sp|Q03497 Saccharomyces cerevisiae YHL00 STE20 ser/thr protein kinase of t pheromone pathway, hypothetical
												YALI0F27159g	some similarities with sp|P4704 Saccharomyces cerevisiae YJL057c probable serine/threonine-protein ki hypothetical start
												CAGL0I05390g	similar to sp|Q12505 Saccharomy cerevisiae YPL026c SKS1 suppre kinase of SNF3 or tr|Q03785 Saccharomyces cerevisiae YDR24 start by similarity
												YALI0E31361g	similar to tr|Q9HF33 Arthrobotr dactyloides Calmodulin-binding pr kinase, hypothetical start
												YALI0B14201g	similar to sp|P32328 Saccharomy cerevisiae YPR111w DBF20 cell c protein kinase P108.1.f3.6 or sp|P2 Saccharomyces cerevisiae YGR09 DBF2 ser/thr protein kinase P108.1.f16.1, hypothetical star
												DEHA0C16181g	similar to CA1447|CaNRK1 Cand albicans, hypothetical start
												CAGL0K04301g	similar to sp|P53233 Saccharomy cerevisiae YGR052w, hypothetical
												KLLA0A06820g	some similarities with sp|P3897 Saccharomyces cerevisiae YJL16 HAL5 ser/thr protein kinase, hypoth start
												KLLA0C00979g	similar to sp|P08458 Saccharomy cerevisiae YDR523c SPS1 ser/thr p kinase, hypothetical start
												YALI0D02101g	similar to sp|O94168 Candida tropi Carbon catabolite derepressing pro

	kinase (EC 2.7.1.-), hypothetical s
YALI0C08305g	highly similar to sp|P06245 Saccharomyces cerevisiae YPL20 TPK2 cAMP-dependent protein kin catalytic chain, hypothetical sta
KLLA0D12100g	some similarities with sgd|S00026 Saccharomyces cerevisiae YDR24 hypothetical start
CAGL0M10791g	highly similar to sp|P53599 Saccharomyces cerevisiae YNR03 SSK2 MAP kinase, no start, frame
YALI0A05247g	similar to tr|Q876Z5 Neurospora cr OS-4 Putative SSK22 like MAPK kinase, hypothetical start
DEHA0F24684g	similar to sp|P24719 Saccharomy cerevisiae YOR351c MEK1 ser/t protein kinase
KLLA0B13112g	similar to sp|P23561 Saccharomy cerevisiae YLR362w STE11 ser/ protein kinase of the MEKK family by similarity
CAGL0F03311g	similar to sp|P38691 Saccharomy cerevisiae YHR082c KSP1 ser/t protein kinase, start by similarit
KLLA0C03938g	some similarities with sgd|S00021 Saccharomyces cerevisiae YDL02 hypothetical start
CAGL0M08360g	some similarities with sp|P3897 Saccharomyces cerevisiae YJL16 ser/thr protein kinase, hypothetical
YALI0E34375g	similar to wi|NCU00108.1 Neurosp crassa NCU00108.1 hypothetical pr (93222 - 91750), hypothetical sta
KLLA0B07579g	weakly similar to sp|P32944 Saccharomyces cerevisiae YJL18 SWE1 ser/tyr dual-specifity prot kinase, start by similarity
YALI0D25388g	similar to tr|Q8TFN2 Pichia angu Serine-threonine kinase Pdd7p hypothetical start
DEHA0C04840g	some similarities with sp|P3899 Saccharomyces cerevisiae YPL20 IPL1 ser/thr protein kinase, hypothe start
YALI0B00880g	similar to sp|P22211 Saccharomy cerevisiae YNL183c NPR1 ser/t protein kinase, hypothetical sta
YALI0D08822g	some similarities with sp|P3899 Saccharomyces cerevisiae YER12 PAK1 DNA polymerase alpha suppressing protein kinase, hypothe start
DEHA0G22440g	similar to CA4770|IPF9382.3 Cand albicans IPF9382.3, hypothetical s
KLLA0C08525g	similar to sp|P53599 Saccharomy cerevisiae YNR031c SSK2 MAP k kinase kinase of the high osmolar signal transduction pathway, start similarity
YALI0F09746g	similar to sp|P24583 Saccharomy cerevisiae YBL105c PKC1 ser/t protein kinase, start by similarit
DEHA0D07601g	similar to Candida albicans CA42 start by similarity
CAGL0I07513g	similar to sp|Q12236 Saccharomy cerevisiae YOL100w PKH2, start similarity
DEHA0D11242g	highly similar to CA5299|IPF21 Candida albicans IPF2190, start similarity
DEHA0F26994g	similar to CA0206|IPF14089 Cand albicans IPF14089 putative serine/threonine protein kinase hypothetical start

												CAGL0M09361g	highly similar to sp|P24583 Saccharomyces cerevisiae YBL10 PKC1 ser/thr protein kinase, start similarity
												YALI0E06501g	similar to sp|P12688 Saccharomy cerevisiae YKL126w YPK1 ser/t specific protein kinase, hypothetical
												CAGL0K05709g	similar to sp|Q12263 Saccharomy cerevisiae YDR507c GIN4, start similarity
												DEHA0C09130g	similar to sp|P38147 Saccharomy cerevisiae YBR274w CHK1, hypothetical start
												CAGL0M02299g	similar to tr|Q12152 Saccharomy cerevisiae YPL150w, start by simil
												CAGL0B04301g	similar to sp|P38070 Saccharomy cerevisiae YBR028c, start by simil
												CAGL0J03432g	similar to sp|P53974 Saccharomy cerevisiae YNL020c ARK1 or sp|P4 Saccharomyces cerevisiae YIL09 PRK1, start by similarity
												DEHA0D13706g	similar to CA4864|IPF4087 Cand albicans IPF4087, hypothetical st
												KLLA0D09328g	some similarities with sp|P3899 Saccharomyces cerevisiae YER12 PAK1 DNA polymerase alpha suppressing protein kinase, hypothe start
												DEHA0B13519g	some similarities with sp|P5373 Saccharomyces cerevisiae YNR04 related to ser/thr protein kinases hypothetical start
												CAGL0M02519g	highly similar to tr|Q03002 Saccharomyces cerevisiae YPL141 sp|Q01919 Saccharomyces cerevis YOR233w KIN4, hypothetical st
												CAGL0G04609g	similar to sp|Q12236 Saccharomy cerevisiae YOL100w PKH2, hypothetical start
												KLLA0F23155g	similar to sp|P22517 Saccharomy cerevisiae YOL016c CMK2 Ca2+/calmodulin-dependent ser/ protein kinase, type II, start by simi
SPS1 (YDR523C)	2.7.1.-	sp|P08458 Saccharomyces cerevisiae YDR523c SPS1 ser/thr protein kinase P108.1.f6.1	viable	NA	NA	NA	NA	NA	sckdy	7 5 4 4 3	GLC.52	YALI0F21065g	tr|Q9Y7W8 Yarrowia lipolytica ser/thr/tyr MAP kinase kinase, no
												YALI0B15906g	similar to sp|P08018 Saccharomy cerevisiae YJL128c PBS2 tyrosi protein kinase of the MAP kinase k family P108.1.f2.4, start by simila
												DEHA0B12672g	similar to sp|O14427 Candida albi Serine/threonine-protein kinase CL start by similarity
												CAGL0M03729g	similar to sp|P48562 Saccharomy cerevisiae YNL298w CLA4, start similarity
												KLLA0A07403g	similar to sp|P48562 Saccharomy cerevisiae YNL298w CLA4 ser/t protein kinase, start by similarit
												CAGL0L05632g	similar to sp|P08018 Saccharomy cerevisiae YJL128c PBS2, hypothe start
												KLLA0E15378g	some similarities with sp|P0801 Saccharomyces cerevisiae YJL12 PBS2 tyrosine protein kinase of the kinase kinase family, hypothetical
												CAGL0I03498g	similar to sp|P06784 Saccharomy cerevisiae YDL159w STE7 ser/thr protein kinase of MAP kinase kin family, hypothetical start
												CAGL0H01639g	similar to sp|P08458 Saccharomy cerevisiae YDR523c SPS1 ser/thr pr kinase, hypothetical start
												YALI0D07502g	weakly similar to sp|P08458 Saccharomyces cerevisiae YDR52

												YALI0D07502g	SPS1 ser/thr protein kinase, start similarity
												DEHA0C17204g	similar to CA4577|CaMKK2 Canc albicans, start by similarity
												KLLA0C16577g	some similarities with sp|P0678 Saccharomyces cerevisiae YDL15 STE7 ser/thr/tyr protein kinase of M kinase kinase family, hypothetical
												KLLA0D07304g	some similarities with sp|P3249 Saccharomyces cerevisiae YPL14 MKK2 protein kinase of the map ki kinase (MEK) family, hypothetical
												CAGL0J03828g	similar to sp|P32490 Saccharomy cerevisiae YOR231w MKK1 ser/ protein kinase or sp|P32491 Saccharomyces cerevisiae YPL14 MKK2, start by similarity
												DEHA0C09416g	similar to sp|P08018 Saccharomy cerevisiae YJL128c PBS2, hypothe start
												DEHA0F15719g	similar to ca|CA1623|CaSTE7 Can albicans CaSTE7 MAP Kinase Kin hypothetical start
YCK3 (YER123W)	2.7.1.-	sp|P39962 Saccharomyces cerevisiae YER123w YCK3 casein kinase, isoform 3 P108.1.f4.1	Exhibits sensitivity at 5 generations when grown in synthetic complete medium.	0.1	Ess	0.1	0.2	Ess	sckdy	4 4 2 2 2	GLC.92	KLLA0D11044g	gi|730472|sp|P40230|RAG8_KLU Kluyveromyces lactis CASEIN KIN I HOMOLOG RAG8, start by simil
												YALI0E26609g	similar to tr|CAD79679 Neurospo crassa, start by similarity
												DEHA0A09933g	similar to sp|P23292 Saccharomy cerevisiae YNL154c YCK2 casein k I isoform, hypothetical start
												CAGL0G06138g	similar to sp|P23291 Saccharomy cerevisiae YHR135c YCK1, start similarity
												DEHA0D04466g	similar to YALI-IPF3384.1 Yarro lipolytica, start by similarity
												YALI0F08305g	similar to sp|P29295 Saccharomy cerevisiae YPL204w HRR25 case kinase I, start by similarity
												CAGL0H03553g	highly similar to sp|P29295 Saccharomyces cerevisiae YPL20 HRR25, start by similarity
												CAGL0J05940g	similar to sp|P23291 Saccharomy cerevisiae YHR135c YCK1 or sp|P2 Saccharomyces cerevisiae YNL15 YCK2, hypothetical start
												CAGL0K02299g	similar to sp|P39962 Saccharomy cerevisiae YER123w Casein kinas hypothetical start
												KLLA0E13563g	some similarities with sp|P3996 Saccharomyces cerevisiae YER12 YCK3 casein kinase, isoform 3 hypothetical start
YCK1 (YHR135C)	2.7.1.-	sp|P23291 Saccharomyces cerevisiae YHR135c YCK1 casein kinase I isoform P108.1.f4.1	viable	Ess	Ess	Ess	Ess	Ess	sckdy	4 4 2 2 2	GLC.92	KLLA0D11044g	gi|730472|sp|P40230|RAG8_KLU Kluyveromyces lactis CASEIN KIN I HOMOLOG RAG8, start by simil
												YALI0E26609g	similar to tr|CAD79679 Neurospo crassa, start by similarity
												DEHA0A09933g	similar to sp|P23292 Saccharomy cerevisiae YNL154c YCK2 casein k I isoform, hypothetical start
												CAGL0G06138g	similar to sp|P23291 Saccharomy cerevisiae YHR135c YCK1, start similarity
												DEHA0D04466g	similar to YALI-IPF3384.1 Yarro lipolytica, start by similarity
												YALI0F08305g	similar to sp|P29295 Saccharomy cerevisiae YPL204w HRR25 case kinase I, start by similarity
												CAGL0H03553g	highly similar to sp|P29295 Saccharomyces cerevisiae YPL20 HRR25, start by similarity
													similar to sp|P23291 Saccharomy

												CAGL0J05940g	cerevisiae YHR135c YCK1 or sp|P2 Saccharomyces cerevisiae YNL15 YCK2, hypothetical start
												CAGL0K02299g	similar to sp|P39962 Saccharomy cerevisiae YER123w Casein kinas hypothetical start
												KLLA0E13563g	some similarities with sp|P3996 Saccharomyces cerevisiae YER12 YCK3 casein kinase, isoform 3 hypothetical start
CTK2 (YJL006C)	2.7.1.-	sp|P46962 Saccharomyces cerevisiae YJL006c CTK2 carboxy-terminal domain (CTD) kinase, beta subunit singleton	viable	0.8	0.4	0.5	0.1	Ess	s-k-y	1 0 1 0 1	GLR.2832	YALI0E13640g	weakly similar to tr|O59748 Schizosaccharomyces pombe Cyc homolog and sp|P46962 Saccharom cerevisiae YJL006c CTK2 carbox terminal domain (CTD) kinase be subunit, start by similarity
												KLLA0D09482g	similar to sp|P46962 Saccharomy cerevisiae YJL006c CTK2 carbox terminal domain (CTD) kinase, b subunit singleton, start by similar
												DEHA0C07139g	some similarities with sp|P2329 Saccharomyces cerevisiae YPR16 SGV1 ser/thr protein kinase, hypoth start
												KLLA0E14828g	gi|27526973|emb|CAD36964.1 Kluyveromyces lactis serine/threon protein kinase KIN28, start by simi
												DEHA0C06314g	some similarities with sp|P0624 Saccharomyces cerevisiae YDL01 CDC7, hypothetical start
												DEHA0B08701g	similar to CA4995|CaYAK1 Canc albicans CaYAK1 putative Ser/t protein kinase, hypothetical star
												CAGL0J00539g	highly similar to sp|Q00772 Saccharomyces cerevisiae YHR03 SLT2, hypothetical start
												KLLA0E12177g	gi|4096112|gb|AAC99804.1 Kluyveromyces lactis CTD kinase la subunit, hypothetical start
												DEHA0B00770g	similar to sp|P32581 Saccharomy cerevisiae YJL106w IME2 ser/thr p kinase, hypothetical start
												YALI0D25190g	highly similar to sp|P17157 Saccharomyces cerevisiae YPL03 PHO85, hypothetical start
												DEHA0E21219g	similar to CA1378|CaERK2 Cand albicans CaERK2 mitogen-activa protein kinase, start by similarit
												DEHA0F08987g	similar to CAGL-IPF1383.1 Cand glabrata, hypothetical start
												CAGL0I05896g	some similarities with sp|P1468 Saccharomyces cerevisiae YJL14 YAK1 ser/thr protein kinase, hypothetical start
												KLLA0F20053g	highly similar to sp|P32485 Saccharomyces cerevisiae YLR11 HOG1 ser/thr protein kinase of M kinase (MAPK) family, start by similarity
												DEHA0E22110g	sp|Q9UV50 Debaryomyces hanse Mitogen-activated protein kinase H identified start
												DEHA0A14080g	highly similar to CA6039|CaCKA Candida albicans CaCKA1 casein k II, catalytic alpha chain, start by similarity
												YALI0E33803g	similar to tr|Q9Y7V6 Emericell nidulans MAP protein kinase MPI hypothetical start
												YALI0E25135g	highly similar to sp|P32485 Saccharomyces cerevisiae YLR11 HOG1 ser/thr protein kinase of M kinase (MAPK) family, hypothetica
													highly similar to tr|Q9UW09 Glom

YALI0E23496g	lagenarium Mitogen activated pro kinase, hypothetical start
CAGL0L06820g	highly similar to sp|P38615 Saccharomyces cerevisiae YMR13 MDS1 Serine/threonine-protein ki
CAGL0G02035g	highly similar to sp|P19454 Saccharomyces cerevisiae YOR06 CKA2 casein kinase II alpha chain, by similarity
DEHA0G02750g	similar to CA4014|CaCTK1 Cand albicans CaCTK1 probable cell div protein kinase, start by similarit
YALI0B02816g	similar to sp|Q00772 Saccharomy cerevisiae Mitogen-activated prot kinase SLT2/MPK1 (EC 2.7.1.-) (M kinase MPK1), start by similarit
KLLA0D11814g	similar to sp|P39073 Saccharomy cerevisiae YPL042c SSN3 cyclin dependent CTD kinase, start by simi
KLLA0B11902g	gi|7385125|gb|AAF61706.1|AF2267 Kluyveromyces lactis MAP kinase, by similarity
CAGL0D02002g	similar to sp|Q03957 Saccharomy cerevisiae YKL139w CTK1 carbo terminal domain kinase, hypotheti start
KLLA0F02838g	some similarities with sp|P3258 Saccharomyces cerevisiae YJL10 IME2 ser/thr protein kinase, hypoth start
KLLA0D10527g	similar to sp|P23293 Saccharomy cerevisiae YPR161c SGV1 ser/t protein kinase, hypothetical star
CAGL0D01694g	similar to sp|P41808 Saccharomy cerevisiae YPR054w SMK1 sporula specific MAP kinase, hypothetical
YALI0D04334g	similar to sp|P06242 Saccharomy cerevisiae YDL108w KIN28 cycl dependent ser/thr protein kinase, sta similarity
CAGL0I08349g	similar to sp|P23293 Saccharomy cerevisiae YPR161c SGV1 ser/t protein kinase, hypothetical star
CAGL0K01815g	similar to sp|P06243 Saccharomy cerevisiae YDL017w Cell divisio control protein 7, hypothetical st
DEHA0F09713g	similar to ca|CA1467|IPF5082 Can albicans IPF5082 similar to Saccharomyces cerevisiae Cak1p c activating protein kinase (by homol hypothetical start
KLLA0D11990g	gi|2499590|sp|Q92241|PH85_KLU Kluyveromyces lactis NEGATIV REGULATOR OF THE PHO SYS hypothetical start
YALI0D04114g	weakly similar to tr|Q8X0V5 Neuro crassa Related to putative dual speci protein kinase pom1, hypothetical
CAGL0K04169g	similar to sp|P14681 Saccharomy cerevisiae YGR040w KSS1, start similarity
KLLA0E07414g	highly similar to sp|P21965 Saccharomyces cerevisiae YNL30 MCK1 ser/thr/tyr protein kinase, sta similarity
YALI0B18700g	similar to tr|Q8TG13 Neurospora c Casein kinase II alpha subunit CKA by similarity
YALI0D16863g	tr|Q92390 Yarrowia lipolytica case kinase II catalytic subunit, identified
KLLA0C04345g	similar to sp|P06243 Saccharomy cerevisiae YDL017w CDC7 prote kinase, start by similarity
	highly similar to sp|P06242

IME2 (YJL106W)	2.7.1.-	sp|P32581 Saccharomyces cerevisiae YJL106w IME2 ser/thr protein kinase P108.1.f12.1	viable	0.8	0.5	0.5	0.3	0.2	sckdy	22 19 19 21 17	GLC.8	CAGL0H10318g	Saccharomyces cerevisiae YDL10 KIN28 cyclin-dependent ser/thr pro kinase
												YALI0B22528g	weakly similar to tr|O14098 Schizosaccharomyces pombe Puta serine/threonine protein kinase, sta similarity
												DEHA0G22528g	highly similar to CA3004|CaKIN Candida albicans CaKIN28, start similarity
												KLLA0B11946g	similar to sp|P41808 Saccharomy cerevisiae YPR054w SMK1 sporula specific MAP kinase, start by simil
												DEHA0F26268g	similar to sp|P41808 Saccharomy cerevisiae YPR054w Sporulatio specific mitogen-activated protein k SMK1 (MAP kinase SMK1), hypothetical start, frameshift
												KLLA0B09790g	highly similar to sp|P00546 Saccharomyces cerevisiae YBR16 CDC28 cyclin-dependent protein ki start by similarity
												DEHA0F26257g	similar to sp|P41808 Saccharomy cerevisiae YPR054w Sporulatio specific mitogen-activated protein k SMK1 (MAP kinase SMK1), hypothetical start, frameshift
												YALI0F03113g	some similarities with sp|P3258 Saccharomyces cerevisiae YJL10 IME2 ser/thr protein kinase, hypoth start
												KLLA0F16467g	highly similar to sp|P19454 Saccharomyces cerevisiae YOR06 CKA2 casein kinase II alpha chain, by similarity
												CAGL0L12474g	highly similar to sp|P17157 Saccharomyces cerevisiae YPL03 cyclin-dependent protein kinase, sta similarity
												CAGL0M11748g	highly similar to sp|P32485 Saccharomyces cerevisiae YLR11 HOG1, start by similarity
												CAGL0E01683g	highly similar to sp|P21965 Saccharomyces cerevisiae YNL30 MCK1 or sp|Q12222 Saccharomy cerevisiae YOL128c, start by simila
												KLLA0A02497g	highly similar to sp|P14681 Saccharomyces cerevisiae YGR04 KSS1 ser/thr protein kinase of the kinase family, start by similarity
												CAGL0J04290g	similar to sp|P16892 Saccharomy cerevisiae YBL016w FUS3 or sp|P1 Saccharomyces cerevisiae YGR04 KSS1, start by similarity
												KLLA0A05819g	similar to sp|P14680 Saccharomy cerevisiae YJL141c YAK1 ser/thr p kinase, start by similarity
												YALI0D20966g	highly similar to tr|Q9HE92 Neuros crassa Probable glycogen synthase k 3 alpha, start by similarity
												KLLA0F08877g	gi|27526975|emb|CAD36965.1 Kluyveromyces lactis cyclin-depen kinase activating kinase 1, start b similarity
												DEHA0E05819g	highly similar to CA2027|CaMC Candida albicans CaMCK1 ser/thr protein kinase, hypothetical star
												DEHA0C07469g	highly similar to sp|P19454 Saccharomyces cerevisiae YOR06 CKA2, hypothetical start
												YALI0E11077g	similar to sp|Q07538 Schizosaccharomyces pombe SPCC777.14 PRP4 Serine/threoni protein kinase, hypothetical star
													similar to sp|Q00772 Saccharomy

												DEHA0E19217g	cerevisiae YHR030c SLT2 ser/thr p kinase of MAP kinase family P108.1.f12.1 Length = 484, start similarity
												KLLA0F17006g	gi|3127831|emb|CAA61157.1 Kluyveromyces lactis protein kina start by similarity
												KLLA0E10527g	similar to sp|P16892 Saccharomy cerevisiae YBL016w FUS3 mitog activated protein kinase (MAP kina start by similarity
												YALI0D19492g	similar to wi|NCU07880.1 Neurosp crassa NCU07880.1 hypothetical pr (15912 - 17477), hypothetical sta
												YALI0B10758g	highly similar to sp|P43063 Cand albicans cell division control protei hypothetical start
												DEHA0F09735g	similar to ca|CA1468|CaSRB10 Ca albicans CaSRB10 cyclin-depend kinase by homology, 3 end, hypothe start
												DEHA0F09647g	similar to wi|NCU04185.1 Neurosp crassa NCU04185.1 hypothetical pr ((AL451015) probable glycoge synthase kinase 3 alpha [Neurosp crassa]) (47604 - 49112), hypothe start
												DEHA0G11660g	highly similar to sp|P43063 Cand albicans Cell division control prote (EC 2.7.1.-), hypothetical start
												DEHA0D14256g	highly similar to CA4448|CaPHO Candida albicans CaPHO85 Nega regulator of PHO system, start b similarity
												YALI0C10967g	similar to sp|P39073 Saccharomy cerevisiae YPL042c SSN3 cycli dependent CTD kinase, hypothetica
												CAGL0K12496g	similar to sp|P43568 Saccharomy cerevisiae YFL029c CAK1 cdk activating protein kinase, hypothet start
												CAGL0L12650g	similar to sp|P39073 Saccharomy cerevisiae YPL042c cyclin-depend CTD kinase, hypothetical start
												CAGL0G04455g	similar to sp|P32581 Saccharomy cerevisiae YJL106w IME2 ser/thr p kinase, hypothetical start
												KLLA0E04136g	similar to sp|P15790 Saccharomy cerevisiae YIL035c CKA1 casein k II, catalytic alpha chain, start by similarity
												CAGL0H07535g	highly similar to sp|P00546 Saccharomyces cerevisiae YBR16 CDC28, start by similarity
												CAGL0I05192g	highly similar to sp|P15790 Saccharomyces cerevisiae YIL03 CKA1 casein kinase II, start by simi
												DEHA0E04290g	highly similar to CA0722|CaER Candida albicans CaERK1 mitog activated protein kinase (FUS3 homolog), hypothetical start
												YALI0C24321g	weakly similar to sp|P43568 Saccharomyces cerevisiae YFL02 CAK1 cdk-activating protein kina hypothetical start
												YALI0F21065g	tr|Q9Y7W8 Yarrowia lipolytica ser/thr/tyr MAP kinase kinase, no
												YALI0B15906g	similar to sp|P08018 Saccharomy cerevisiae YJL128c PBS2 tyrosi protein kinase of the MAP kinase k family P108.1.f2.4, start by simila
												DEHA0B12672g	similar to sp|O14427 Candida albic Serine/threonine-protein kinase C start by similarity

PBS2 (YJL128C)	2.7.1.-	sp|P08018 Saccharomyces cerevisiae YJL128c PBS2 tyrosine protein kinase of the MAP kinase kinase family P108.1.f2.4	Exhibits sensitivity at 15 generations when grown in medium of pH 8.	Ess	Ess	Ess	0.3	Ess	sckdy	7 5 4 4 3	GLC.52	CAGL0M03729g	similar to sp|P48562 Saccharomy cerevisiae YNL298w CLA4, start similarity
												KLLA0A07403g	similar to sp|P48562 Saccharomy cerevisiae YNL298w CLA4 ser/t protein kinase, start by similarit
												CAGL0L05632g	similar to sp|P08018 Saccharomy cerevisiae YJL128c PBS2, hypothe start
												KLLA0E15378g	some similarities with sp|P0801 Saccharomyces cerevisiae YJL12 PBS2 tyrosine protein kinase of the kinase kinase family, hypothetical
												CAGL0I03498g	similar to sp|P06784 Saccharomy cerevisiae YDL159w STE7 ser/thr protein kinase of MAP kinase kin family, hypothetical start
												CAGL0H01639g	similar to sp|P08458 Saccharomy cerevisiae YDR523c SPS1 ser/thr pr kinase, hypothetical start
												YALI0D07502g	weakly similar to sp|P08458 Saccharomyces cerevisiae YDR5 SPS1 ser/thr protein kinase, start similarity
												DEHA0C17204g	similar to CA4577|CaMKK2 Cand albicans, start by similarity
												KLLA0C16577g	some similarities with sp|P0678 Saccharomyces cerevisiae YDL15 STE7 ser/thr/tyr protein kinase of M kinase kinase family, hypothetical
												KLLA0D07304g	some similarities with sp|P3249 Saccharomyces cerevisiae YPL14 MKK2 protein kinase of the map k kinase (MEK) family, hypothetical
												CAGL0J03828g	similar to sp|P32490 Saccharomy cerevisiae YOR231w MKK1 ser/ protein kinase or sp|P32491 Saccharomyces cerevisiae YPL14 MKK2, start by similarity
												DEHA0C09416g	similar to sp|P08018 Saccharomy cerevisiae YJL128c PBS2, hypothe start
												DEHA0F15719g	similar to ca|CA1623|CaSTE7 Can albicans CaSTE7 MAP Kinase Ki hypothetical start
												DEHA0C07139g	some similarities with sp|P2329 Saccharomyces cerevisiae YPR16 SGV1 ser/thr protein kinase, hypoth start
												KLLA0E14828g	gi|27526973|emb|CAD36964.1 Kluyveromyces lactis serine/threon protein kinase KIN28, start by simi
												DEHA0C06314g	some similarities with sp|P0624 Saccharomyces cerevisiae YDL01 CDC7, hypothetical start
												DEHA0B08701g	similar to CA4995|CaYAK1 Cand albicans CaYAK1 putative Ser/t protein kinase, hypothetical star
												CAGL0J00539g	highly similar to sp|Q00772 Saccharomyces cerevisiae YHR0 SLT2, hypothetical start
												KLLA0E12177g	gi|4096112|gb|AAC99804.1 Kluyveromyces lactis CTD kinase la subunit, hypothetical start
												DEHA0B00770g	similar to sp|P32581 Saccharomy cerevisiae YJL106w IME2 ser/thr p kinase, hypothetical start
												YALI0D25190g	highly similar to sp|P17157 Saccharomyces cerevisiae YPL03 PHO85, hypothetical start
												DEHA0E21219g	similar to CA1378|CaERK2 Cand albicans CaERK2 mitogen-activa protein kinase, start by similarit
												DEHA0F08987g	similar to CAGL-IPF1383.1 Cand

DEHA0F08987g	glabrata, hypothetical start
CAGL0I05896g	some similarities with sp|P1468 Saccharomyces cerevisiae YJL14 YAK1 ser/thr protein kinase, hypothetical start
KLLA0F20053g	highly similar to sp|P32485 Saccharomyces cerevisiae YLR11 HOG1 ser/thr protein kinase of M kinase (MAPK) family, start by similarity
DEHA0E22110g	sp|Q9UV50 Debaryomyces hanse Mitogen-activated protein kinase H identified start
DEHA0A14080g	highly similar to CA6039|CaCK Candida albicans CaCKA1 casein k II, catalytic alpha chain, start by similarity
YALI0E33803g	similar to tr|Q9Y7V6 Emericell nidulans MAP protein kinase MP hypothetical start
YALI0E25135g	highly similar to sp|P32485 Saccharomyces cerevisiae YLR11 HOG1 ser/thr protein kinase of M kinase (MAPK) family, hypothetica
YALI0E23496g	highly similar to tr|Q9UW09 Glom lagenarium Mitogen activated pro kinase, hypothetical start
CAGL0L06820g	highly similar to sp|P38615 Saccharomyces cerevisiae YMR1 MDS1 Serine/threonine-protein ki
CAGL0G02035g	highly similar to sp|P19454 Saccharomyces cerevisiae YOR06 CKA2 casein kinase II alpha chain, by similarity
DEHA0G02750g	similar to CA4014|CaCTK1 Cand albicans CaCTK1 probable cell div protein kinase, start by similarit
YALI0B02816g	similar to sp|Q00772 Saccharomy cerevisiae Mitogen-activated prot kinase SLT2/MPK1 (EC 2.7.1.-) (M kinase MPK1), start by similarit
KLLA0D11814g	similar to sp|P39073 Saccharomy cerevisiae YPL042c SSN3 cycli dependent CTD kinase, start by simi
KLLA0B11902g	gi|7385125|gb|AAF61706.1|AF2267 Kluyveromyces lactis MAP kinase, by similarity
CAGL0D02002g	similar to sp|Q03957 Saccharomy cerevisiae YKL139w CTK1 carbo terminal domain kinase, hypotheti start
KLLA0F02838g	some similarities with sp|P3258 Saccharomyces cerevisiae YJL10 IME2 ser/thr protein kinase, hypoth start
KLLA0D10527g	similar to sp|P23293 Saccharomy cerevisiae YPR161c SGV1 ser/t protein kinase, hypothetical star
CAGL0D01694g	similar to sp|P41808 Saccharomy cerevisiae YPR054w SMK1 sporula specific MAP kinase, hypothetical
YALI0D04334g	similar to sp|P06242 Saccharomy cerevisiae YDL108w KIN28 cycl dependent ser/thr protein kinase, sta similarity
CAGL0I08349g	similar to sp|P23293 Saccharomy cerevisiae YPR161c SGV1 ser/t protein kinase, hypothetical star
CAGL0K01815g	similar to sp|P06243 Saccharomy cerevisiae YDL017w Cell divisi control protein 7, hypothetical st
DEHA0F09713g	similar to ca|CA1467|IPF5082 Can albicans IPF5082 similar to Saccharomyces cerevisiae Cak1p c

YAK1 (YJL141C)	2.7.1.-	sp|P14680 Saccharomyces cerevisiae YJL141c YAK1 ser/thr protein kinase P108.1.f3.5	viable	0.4	0.1	Ess	0.1	0.6	sckdy	22 19 19 21 17	GLC.8		activating protein kinase (by homol hypothetical start
												KLLA0D11990g	gi|2499590|sp|Q92241|PH85_KLU Kluyveromyces lactis NEGATIV REGULATOR OF THE PHO SYS hypothetical start
												YALI0D04114g	weakly similar to tr|Q8X0V5 Neuro crassa Related to putative dual spec protein kinase pom1, hypothetical
												CAGL0K04169g	similar to sp|P14681 Saccharomy cerevisiae YGR040w KSS1, start similarity
												KLLA0E07414g	highly similar to sp|P21965 Saccharomyces cerevisiae YNL30 MCK1 ser/thr/tyr protein kinase, sta similarity
												YALI0B18700g	similar to tr|Q8TG13 Neurospora c Casein kinase II alpha subunit CKA by similarity
												YALI0D16863g	tr|Q92390 Yarrowia lipolytica case kinase II catalytic subunit, identified
												KLLA0C04345g	similar to sp|P06243 Saccharomy cerevisiae YDL017w CDC7 prote kinase, start by similarity
												CAGL0H10318g	highly similar to sp|P06242 Saccharomyces cerevisiae YDL10 KIN28 cyclin-dependent ser/thr pro kinase
												YALI0B22528g	weakly similar to tr|O14098 Schizosaccharomyces pombe Puta serine/threonine protein kinase, sta similarity
												DEHA0G22528g	highly similar to CA3004|CaKIN Candida albicans CaKIN28, start similarity
												KLLA0B11946g	similar to sp|P41808 Saccharomy cerevisiae YPR054w SMK1 sporula specific MAP kinase, start by simil
												DEHA0F26268g	similar to sp|P41808 Saccharomy cerevisiae YPR054w Sporulatio specific mitogen-activated protein k SMK1 (MAP kinase SMK1), hypothetical start, frameshift
												KLLA0B09790g	highly similar to sp|P00546 Saccharomyces cerevisiae YBR16 CDC28 cyclin-dependent protein ki start by similarity
												DEHA0F26257g	similar to sp|P41808 Saccharomy cerevisiae YPR054w Sporulatio specific mitogen-activated protein k SMK1 (MAP kinase SMK1), hypothetical start, frameshift
												YALI0F03113g	some similarities with sp|P3258 Saccharomyces cerevisiae YJL10 IME2 ser/thr protein kinase, hypoth start
												KLLA0F16467g	highly similar to sp|P19454 Saccharomyces cerevisiae YOR06 CKA2 casein kinase II alpha chain, by similarity
												CAGL0L12474g	highly similar to sp|P17157 Saccharomyces cerevisiae YPL03 cyclin-dependent protein kinase, sta similarity
												CAGL0M11748g	highly similar to sp|P32485 Saccharomyces cerevisiae YLR11 HOG1, start by similarity
												CAGL0E01683g	highly similar to sp|P21965 Saccharomyces cerevisiae YNL30 MCK1 or sp|Q12222 Saccharomy cerevisiae YOL128c, start by simil
												KLLA0A02497g	highly similar to sp|P14681 Saccharomyces cerevisiae YGR04 KSS1 ser/thr protein kinase of the I kinase family, start by similarit

CAGL0J04290g	similar to sp|P16892 Saccharomy cerevisiae YBL016w FUS3 or sp|P1 Saccharomyces cerevisiae YGR04 KSS1, start by similarity
KLLA0A05819g	similar to sp|P14680 Saccharomy cerevisiae YJL141c YAK1 ser/thr p kinase, start by similarity
YALI0D20966g	highly similar to tr|Q9HE92 Neuros crassa Probable glycogen synthase k 3 alpha, start by similarity
KLLA0F08877g	gi|27526975|emb|CAD36965.1 Kluyveromyces lactis cyclin-depen kinase activating kinase 1, start b similarity
DEHA0E05819g	highly similar to CA2027|CaMC Candida albicans CaMCK1 ser/thr protein kinase, hypothetical star
DEHA0C07469g	highly similar to sp|P19454 Saccharomyces cerevisiae YOR06 CKA2, hypothetical start
YALI0E11077g	similar to sp|Q07538 Schizosaccharomyces pombe SPCC777.14 PRP4 Serine/threoni protein kinase, hypothetical star
DEHA0E19217g	similar to sp|Q00772 Saccharomy cerevisiae YHR030c SLT2 ser/thr p kinase of MAP kinase family P108.1.f12.1 Length = 484, start similarity
KLLA0F17006g	gi|3127831|emb|CAA61157.1 Kluyveromyces lactis protein kina start by similarity
KLLA0E10527g	similar to sp|P16892 Saccharomy cerevisiae YBL016w FUS3 mitog activated protein kinase (MAP kina start by similarity
YALI0D19492g	similar to wi|NCU07880.1 Neuros crassa NCU07880.1 hypothetical pr (15912 - 17477), hypothetical st
YALI0B10758g	highly similar to sp|P43063 Cand albicans cell division control protei hypothetical start
DEHA0F09735g	similar to ca|CA1468|CaSRB10 Ca albicans CaSRB10 cyclin-depend kinase by homology, 3 end, hypothe start
DEHA0F09647g	similar to wi|NCU04185.1 Neuros crassa NCU04185.1 hypothetical pr ((AL451015) probable glycoge synthase kinase 3 alpha [Neurosp crassa]) (47604 - 49112), hypothe start
DEHA0G11660g	highly similar to sp|P43063 Cand albicans Cell division control prote (EC 2.7.1.-), hypothetical start
DEHA0D14256g	highly similar to CA4448|CaPHO Candida albicans CaPHO85 Nega regulator of PHO system, start b similarity
YALI0C10967g	similar to sp|P39073 Saccharomy cerevisiae YPL042c SSN3 cycli dependent CTD kinase, hypothetica
CAGL0K12496g	similar to sp|P43568 Saccharomy cerevisiae YFL029c CAK1 cdk activating protein kinase, hypothet start
CAGL0L12650g	similar to sp|P39073 Saccharomy cerevisiae YPL042c cyclin-depend CTD kinase, hypothetical start
CAGL0G04455g	similar to sp|P32581 Saccharomy cerevisiae YJL106w IME2 ser/thr p kinase, hypothetical start
KLLA0E04136g	similar to sp|P15790 Saccharomy cerevisiae YIL035c CKA1 casein k

												KLLA0E04136g	II, catalytic alpha chain, start by similarity
												CAGL0H07535g	highly similar to sp|P00546 Saccharomyces cerevisiae YBR16 CDC28, start by similarity
												CAGL0I05192g	highly similar to sp|P15790 Saccharomyces cerevisiae YIL03 CKA1 casein kinase II, start by simi
												DEHA0E04290g	highly similar to CA0722|CaERI Candida albicans CaERK1 mitog activated protein kinase (FUS3 homolog), hypothetical start
												YALI0C24321g	weakly similar to sp|P43568 Saccharomyces cerevisiae YFL02 CAK1 cdk-activating protein kina hypothetical start
												KLLA0F11319g	similar to sgd|S0006071 Saccharon cerevisiae YPL150w, start by simil
												CAGL0L07810g	similar to sp|P25333 Saccharomy cerevisiae YCR008w SAT4 serine/threonine-specific protein ki start by similarity
												CAGL0K11550g	similar to sp|P28708 Saccharomy cerevisiae YKL116c, hypothetical
												YALI0F11385g	weakly similar to SP|P38691 Saccharomyces cerevisiae YHR0 KSP1 ser/thr protein kinase and DE IPF5974.1, start by similarity
												KLLA0A09713g	similar to sp|Q03533 Saccharomy cerevisiae YMR291w, start by simi
												KLLA0E17127g	similar to sp|P38691 Saccharomy cerevisiae YHR082c KSP1 ser/t protein kinase, start by similarit
												YALI0C04158g	similar to sp|P18961 Saccharomy cerevisiae Serine/threonine-prote kinase YPK2/YKR2, hypothetical
												DEHA0F24676g	similar to sp|P24719 Saccharomy cerevisiae YOR351c MEK1 ser/t protein kinase
												DEHA0G14817g	similar to CA2643|CaHSL1 Cand albicans CaHSL1, hypothetical st
												DEHA0C18150g	similar to sp|P40494 Saccharomy cerevisiae YIL095w PRK1 serine/threonine protein kinase, sta similarity
												CAGL0K10604g	similar to sp|P27466 Saccharomy cerevisiae YFR014c CMK1 Ca2+/calmodulin-dependent ser/ protein kinase type I, hypothetical
												DEHA0C08591g	similar to sp|P22204 Saccharomy cerevisiae YGR092w DBF2, hypothetical start, sequence gap
												YALI0F13629g	some similarities with sp|P2356 Saccharomyces cerevisiae YLR36 STE11 ser/thr protein kinase of t MEKK family, hypothetical sta
												KLLA0C06138g	similar to sp|P32562 Saccharomy cerevisiae YMR001c CDC5 involv regulation of DNA replication, star similarity
												YALI0F16159g	some similarities with wi|NCU009 Neurospora crassa NCU00914. hypothetical protein, hypothetical
												CAGL0K08514g	similar to sp|P34244 Saccharomy cerevisiae YKL101w serine/threon protein kinase, hypothetical star
												DEHA0F25278g	similar to ca|CA1881|CaRCK2 Can albicans CaRCK2 Ca/calmoduli dependent ser/thr protein kinase (homology), hypothetical start
												KLLA0F26983g	some similarities with sp|P3280 Saccharomyces cerevisiae YKL0 ELM1 ser/thr-specific protein kina hypothetical start

DEHA0C11484g	similar to sp|P22211 Saccharomy cerevisiae YNL183c NPR1 or tr|Q1 Saccharomyces cerevisiae YDL02 hypothetical start
YALI0C00891g	similar to sp|O14019 Schizosaccharomyces pombe Prob serine/threonine-protein kinase C29A4.16 (EC 2.7.1.-), hypothetica
KLLA0F23507g	similar to sp|P24719 Saccharomy cerevisiae YOR351c MEK1 ser/t protein kinase, start by similarit
CAGL0F03245g	similar to sp|P32361 Saccharomy cerevisiae YHR079c IRE1, hypothe start
CAGL0K11990g	some similarities with sp|P3808 Saccharomyces cerevisiae YBR0 AKL1 Ark-family Kinase-Like pro hypothetical start
DEHA0G10417g	similar to CA1971|CaPKH2 Cand albicans CaPKH2 Ser/Thr protei kinase(by homology), hypothetical
YALI0B17556g	weakly similar to tr|Q9Y898 Emeri nidulans Calcium/calmodulin deper protein kinase C, hypothetical sta
CAGL0G03047g	highly similar to sp|P22204 Saccharomyces cerevisiae YGR09 DBF2 ser/thrprotein kinase or sp|P3 Saccharomyces cerevisiae YPR11 DBF20, hypothetical start
YALI0F27093g	weakly similar to DEHA-IPF372 Debaryomyces hansenii, hypothet start
DEHA0C14091g	similar to sp|P37292 Saccharomy cerevisiae YBR263w SHM1, hypothetical start
DEHA0C18601g	similar to CA4433|CaBCK1 Cand albicans, hypothetical start
KLLA0C04213g	similar to sp|P22209 Saccharomy cerevisiae YAR018c KIN3 ser/thr p kinase, hypothetical start
YALI0A04697g	similar to sp|O42626 Neurospora c Serine/threonine-protein kinase n (Nonrepressible conidiation protei hypothetical start
YALI0D26015g	similar to sp|P32562 Saccharomy cerevisiae Cell cycle protein kina CDC5/MSD2 (EC 2.7.1.-), hypothe start
DEHA0G14839g	highly similar to sCA3870|CaYP Candida albicans CaYPK1, start similarity
KLLA0C14278g	similar to sp|P28708 Saccharomy cerevisiae YKL116c, hypothetical
YALI0E13750g	similar to tr|CAD79666 Neurospo crassa B1D14.230 Related to serine/threonine-protein kinase a DEHA-IPF6149.1 Debaryomyc hansenii, no start
CAGL0B04147g	highly similar to sp|P22204 Saccharomyces cerevisiae YGR09 DBF2 ser/thrprotein kinase relate DBF20P or sp|P32328 Saccharom cerevisiae YPR111w DBF20 cell c protein kinase related to DBF2 hypothetical start
DEHA0F13497g	similar to ca|CA1299|CaPTK2 Car albicans CaPTK2 serine /threoni protein kinase involved in polyam uptake (by homology), hypothetical
DEHA0D13684g	similar to CA4865|IPF4085 Cand albicans IPF4085, start by similar
CAGL0L06006g	similar to sp|P53104 Saccharomy cerevisiae YGL180w APG1 essenti autophagocytosis, hypothetical st

CAGL0E05720g	similar to sp|P38991 Saccharomy cerevisiae YPL209c IPL1 ser/thr pr kinase, start by similarity
KLLA0F18612g	some similarities with sp|P3808 Saccharomyces cerevisiae YBR05 AKL1 Ark-family Kinase-Like pro hypothetical start
YALI0E24563g	similar to tr|Q12152 Saccharomy cerevisiae YPL150w, hypothetical
DEHA0F24013g	similar to ca|CA5226|CaRIM15 Car albicans CaRIM15 Protein kinas involved in the RIM pathway (b homology), hypothetical start
CAGL0I04422g	some similarities with sp|P2220 Saccharomyces cerevisiae YAR0 KIN3 ser/thr protein kinase, hypoth start
CAGL0K01661g	some similarities with tr|Q1210 Saccharomyces cerevisiae YDL02 hypothetical start
DEHA0E15741g	highly similar to CA3361|CaSNI Candida albicans CaSNF1 serine/threonine protein kinase hypothetical start
CAGL0M02233g	highly similar to sp|P22216 Saccharomyces cerevisiae YPL15 SPK1 ser/thr/tyr protein kinase hypothetical start
CAGL0F04741g	similar to sp|P22517 Saccharomy cerevisiae YOL016c CMK2 Ca2+/calmodulin-dependent ser/ protein kinase, type II, hypothetical
YALI0E06523g	weakly similar to sp|P34244 Saccharomyces cerevisiae YKL10 HSL1 ser/thr protein kinase, coup septin ring assembly to cell cycl progression, hypothetical start
KLLA0E11979g	some similarities with sp|P2533 Saccharomyces cerevisiae YCR00 SAT4 serine/threonine-specific pro kinase, hypothetical start
CAGL0J11308g	similar to sp|P22211 Saccharomy cerevisiae YNL183c NPR1 ser/t protein kinase, hypothetical star
DEHA0G11638g	similar to sp|P25333 Saccharomy cerevisiae YCR008w SAT4 serine/threonine-specific protein ki hypothetical start
CAGL0H10208g	similar to sp|P38080 Saccharomy cerevisiae YBR059c AKL1 Ark-fa Kinase-Like protein, hypothetical
CAGL0B02739g	similar to sp|P23561 Saccharomy cerevisiae YLR362w STE11 ser/ protein kinase of the MEKK fam hypothetical start
YALI0D07150g	weakly similar to tr|Q9C2E8 Neuro crassa Conserved hypothetical pro start by similarity
DEHA0F10197g	highly similar to ca|CA2265|CaCM Candida albicans CaCMK2 Ca2 /calmodulin-dependent ser/thr pro kinase, type II (by homology), hypothetical start
DEHA0B12628g	similar to sp|P06245 Saccharomy cerevisiae YPL203w TPK2 cAM dependent protein kinase 2, cataly chain, start by similarity
DEHA0E13574g	similar to CA2193|IPF14273 Canc albicans IPF14273 Probable ser/t protein kinase
KLLA0D07348g	weakly similar to sgd|S000606 Saccharomyces cerevisiae YPL14 start by similarity
	some similarities with sp|P3897 Saccharomyces cerevisiae YIL16

DEHA0B12650g	Saccharomyces cerevisiae YJL1 HAL5 ser/thr protein kinase, hypoth start
DEHA0F04114g	similar to CA0576|CaNPR1 Cand albicans CaNPR1, hypothetical st
DEHA0C13211g	similar to sp|P22216 Saccharomy cerevisiae YPL153c SPK1, hypothe start
KLLA0B07205g	some similarities with sp|P0598 Saccharomyces cerevisiae YKL16 TPK3 cAMP-dependent protein kin catalytic chain, hypothetical sta
CAGL0K06479g	some similarities with tr|Q0330 Saccharomyces cerevisiae YDR46 start by similarity
KLLA0C12485g	weakly similar to sp|Q12236 Saccharomyces cerevisiae YOL10 PKH2, start by similarity
KLLA0E06413g	gi|22858696|gb|AAN05732.1 Kluyveromyces lactis protein kinas start by similarity
YALI0D26213g	weakly similar to tr|Q96WJ8 Blum graminis Protein kinase C-like pro hypothetical start
DEHA0G14707g	similar to CA6135|CaCMK1 Cand albicans CaCMK1, hypothetical s
DEHA0E16115g	similar to CA5074|IPF3607 Cand albicans IPF3607 putative serine/threonine protein kinase hypothetical start
CAGL0M13167g	similar to sp|P32801 Saccharomy cerevisiae YKL048c ELM1 ser/t specific protein kinase, hypothetical
KLLA0F01408g	weakly similar to sgd|S000218 Saccharomyces cerevisiae YDL02 hypothetical start
DEHA0F25212g	highly similar to tr|Q9HEW0 Cand albicans cAMP-dependent protein k catalytic subunit, hypothetical st
CAGL0M08404g	some similarities with sp|P0598 Saccharomyces cerevisiae YKL16 TPK3 or sp|P06244 Saccharomy cerevisiae YJL164c SRA3 or sp|P0 Saccharomyces cerevisiae YPL20 TPK2, hypothetical start
KLLA0A03806g	gi|2181934|emb|CAA61235.1 Kluyveromyces lactis putative kin start by similarity
YALI0D19470g	similar to tr|Q871H9 Neurospora c B16M17.090 Related to Ste20-li kinase Don3, hypothetical start
YALI0A10230g	similar to sp|P22211 Saccharomy cerevisiae YNL183c NPR1 ser/t protein kinase, start by similarit
DEHA0F10461g	some similarities with ca|CA1288|CaKSP1 Candida albic CaKSP1 SERINE/THREONINE PROTEIN KINASE by homolog hypothetical start
YALI0F01716g	tr|Q9P860 Yarrowia lipolytica Wee protein, mitosis inhibitor protein ki hypothetical start
YALI0E27632g	tr|O93955 Yarrowia lipolytica SS protein, multicopy suppressor of S secretory defects, putative calmodu dependent ser/thr protein kinase identified start
CAGL0I09504g	similar to sp|P38147 Saccharomy cerevisiae YBR274w CHK1 regul inhibitory Cdk phosphorylation of F start by similarity
CAGL0F09075g	similar to sp|P11792 Saccharomy cerevisiae YHR205w SCH9 serine/threonine protein kinase, sta similarity

ELM1 (YKL048C)	2.7.1.-	sp|P32801 Saccharomyces cerevisiae YKL048c ELM1 ser/thr-specific protein kinase P108.1.f3.2	Exhibits growth defect on a fermentable carbon source.	0.4	0.1	Ess	0.3	0.2	sckdy	57 58 49 54 42	GLC.2	DEHA0C17996g	similar to CA2348|IPF12811 Can albicans, putative serine/threonin kinase, hypothetical start
												CAGL0H00979g	similar to tr|Q12003 Saccharomy cerevisiae YPL236c, hypothetical
												KLLA0C03828g	similar to sp|P54199 Saccharomy cerevisiae YDL028c MPS1 serine/threonine/tyrosine protein ki hypothetical start
												KLLA0F14190g	gi|3021329|emb|CAA06336.1 Kluyveromyces lactis MAP kinase k kinase, start by similarity
												CAGL0M10153g	some similarities with sp|Q0349 Saccharomyces cerevisiae YHL00 ser/thr protein kinase of the pheron pathway, hypothetical start
												KLLA0F24618g	similar to sp|P38070 Saccharomy cerevisiae YBR028c, start by simil
												CAGL0K07458g	similar to sp|P12688 Saccharomy cerevisiae YKL126w or sp|P189 Saccharomyces cerevisiae YMR1 ser/thr-specific protein kinases, sta similarity
												KLLA0D03190g	highly similar to sp|P06245 Saccharomyces cerevisiae YPL20 TPK2 cAMP-dependent protein kin catalytic chain, start by similarit
												DEHA0D19833g	similar to CA5851|CaKIN2 Cand albicans CaKIN2, hypothetical st
												KLLA0D14905g	gi|28565036|gb|AAO32601.1 Kluyveromyces lactis DBF2, start similarity
												KLLA0C18568g	gi|6967028|emb|CAB72435.1 Kluyveromyces lactis MUP1 prot hypothetical start
												CAGL0M13541g	similar to sp|Q03533 Saccharomy cerevisiae YMR291w, hypothetical
												KLLA0E03487g	similar to sgd|S0002874 Saccharom cerevisiae YDR466w, start by simil
												DEHA0C08635g	similar to sp|P22204 Saccharomy cerevisiae YGR092w DBF2, hypothetical start, sequence gap
												CAGL0G02607g	similar to sp|P40494 Saccharomy cerevisiae YIL095w PRK1, start similarity
												CAGL0K11275g	similar to tr|Q03785 Saccharomy cerevisiae YDR247w, hypothetical
												DEHA0E05753g	similar to CA0719|IPF9779.5 Can albicans IPF9779.5 serine/threon protein kinase 5-prime end, hypoth start
												YALI0B05588g	some similarities with sp|Q1223 Saccharomyces cerevisiae YOL10 PKH2 related to ser/thr protein kin P108.1.f16.1, hypothetical star
												DEHA0A08822g	similar to CA0577|IPF16051 Can albicans IPF16051 unknown funct start by similarity
												KLLA0C17160g	similar to sp|P53104 Saccharomy cerevisiae YGL180w APG1 essenti autophagocytosis, start by similar
												KLLA0A02717g	some similarities with sp|P5323 Saccharomyces cerevisiae YGR05 hypothetical start
												YALI0C21758g	similar to KLLA-IPF4914.1 Kluyveromyces lactis IPF 4914. hypothetical start
												CAGL0C03509g	similar to sp|P53739 Saccharomy cerevisiae YNR047w or sp|P253 Saccharomyces cerevisiae YCR09 KIN82, hypothetical start
													similar to sp|P11792 Saccharomy cerevisiae YHR205w SCH9

												KLLA0B03586g	serine/threonine protein kinase invo in stress response and nutrient-sen signaling pathway, start by simila
												YALI0C15444g	similar to tr|Q12706 Schizosaccharomyces pombe Prob serine/threonine protein kinase PS (EC 2.7.1.-), hypothetical start
												YALI0E34067g	weakly similar to DEHA-IPF394 Debaryomyces hansenii IPF 394 hypothetical start
												CAGL0C05005g	similar to sp|P27636 Saccharomy cerevisiae YAR019c CDC15, hypothetical start
												DEHA0B04895g	similar to CA2018|CaSTE11 Canc albicans CaSTE11 ser/thr protein k of the MEKK family, hypothetical
												KLLA0B12716g	similar to sp|P12688 Saccharomy cerevisiae YKL126w YPK1 ser/t specific protein kinase, start by simi
												CAGL0F03707g	similar to sp|Q08732 Saccharomy cerevisiae YOR267c, start by simil
												YALI0E22858g	Weakly similar to CAAL-CA55 CaAKL1 serine/threonine protein k (by homology), Hypothetical sta
												KLLA0F09031g	similar to sp|P43565 Saccharomy cerevisiae YFL033c RIM15 prot kinase involved in expression of m genes, hypothetical start
												DEHA0E12782g	similar to sp|P38070 Saccharomy cerevisiae YBR028c, putative ribos protein kinase
												CAGL0B01925g	similar to sp|P13185 Saccharomy cerevisiae YDR122w KIN1 or sp|P1 Saccharomyces cerevisiae YLR09 KIN2, hypothetical start
												KLLA0C07535g	some similarities with sgd|S00057 Saccharomyces cerevisiae YOR26 hypothetical start
												CAGL0D02244g	similar to sp|P24719 Saccharomy cerevisiae YOR351c MEK1 ser/t protein kinase, hypothetical star
												DEHA0C13387g	similar to tr|Q08732 Saccharomy cerevisiae YOR267C, hypothetical
												YALI0E17743g	no similarity, hypothetical start
												CAGL0C02893g	similar to tr|Q08732 Saccharomy cerevisiae YOR267c, hypothetical
												KLLA0F19536g	similar to sp|P13186 Saccharomy cerevisiae YLR096w KIN2 ser/t protein kinase, start by similarit
												CAGL0M11396g	similar to sp|P13186 Saccharomy cerevisiae YLR096w KIN2 ser/t protein kinase, hypothetical star
												YALI0B13178g	similar to sp|P32490 Saccharomy cerevisiae YOR231w MKK1 ser/ protein kinase, start by similarit
												DEHA0F27489g	similar to CA1288|CaKSP1 Cand albicans CaKSP1 serine/threonin protein kinase (by homology), star similarity
												KLLA0B02332g	similar to sp|P38991 Saccharomy cerevisiae YPL209c IPL1 ser/thr pr kinase, start by similarity
												CAGL0L07326g	similar to sp|P39009 Saccharomy cerevisiae YDL101c DUN1 prote kinase, start by similarity
												KLLA0F11143g	similar to sp|P22216 Saccharomy cerevisiae YPL153c SPK1 ser/thr protein kinase, start by similarit
												DEHA0E14641g	similar to CA4097|CaGIN4 Cand albicans CaGIN4 ser/thr protein ki (by homology), hypothetical sta
													similar to sp|Q01919 Saccharomy cerevisiae YOR233w KIN4 ser/t

CAGL0J03872g	protein kinase or tr|Q03002 Saccharomyces cerevisiae YPL14 start by similarity
YALI0D14542g	similar to sp|P11792 Saccharomy cerevisiae YHR205w SCH9 serine/threonine protein kinase invo in stress response and nutrient-sen signaling pathway, start by simila
KLLA0B06501g	some similarities with sp|P4711 Saccharomyces cerevisiae YJR05 PTK2 involved in polyamine upta hypothetical start
DEHA0C05742g	some similarities with sp|P4189 Schizosaccharomyces pombe Ce division control protein 7 and CA2669|IPF17494.3eoc Candid albicans and CA2404|CaCDC15 Ca albicans, hypothetical start
DEHA0F20878g	similar to CA0044|IPF17347 Canc albicans IPF17347, hypothetical s
KLLA0E08371g	similar to sp|P40494 Saccharomy cerevisiae YIL095w PRK1 serine/threonine protein kinase invo in regulation of actin cytoskeleto organization, start by similarity
KLLA0F13552g	gi|33386566|emb|CAD87727.1 Kluyveromyces lactis protein kina start by similarity
CAGL0J11638g	highly similar to sp|P32562 Saccharomyces cerevisiae YMR0 CDC5 involved in regulation of D replication, hypothetical start
CAGL0K02167g	similar to sp|P38990 Saccharomy cerevisiae YER129w Serine/threon protein kinase, start by similarit
DEHA0F09493g	similar to ca|CA2909|IPF11424 Can albicans IPF11424 unknown funct hypothetical start
CAGL0G05720g	similar to sp|P22211 Saccharomy cerevisiae YNL183c NPR1 ser/t protein kinase, start by similarit
DEHA0C09823g	similar to CA1205|CaSSK2 Cand albicans, hypothetical start
YALI0D22770g	Similar to CAAL-CA5851 CaKI ser/thr protein kinase (by homology start
CAGL0M08910g	highly similar to sp|Q00372 Saccharomyces cerevisiae YDR47 carbon catabolite derepressing ser protein kinase, hypothetical star
KLLA0C04191g	weakly similar to sp|P27636 Saccharomyces cerevisiae YAR0 CDC15 protein kinase of the MA kinase kinase kinase family, hypoth start
DEHA0B16071g	similar to sp|P22209 Saccharomy cerevisiae YAR018c KIN3 ser/thr p kinase, start by similarity
CAGL0K03399g	highly similar to sp|P12688 Saccharomyces cerevisiae YKL12 Serine/threonine-protein kinase, sta similarity
CAGL0J04972g	some similarities with tr|Q1210 Saccharomyces cerevisiae YDL02 hypothetical start
DEHA0F10923g	highly similar to ca|CA2986|CaC Candida albicans CaCDC5 Cell-cy protein kinase (by homology), star similarity
YALI0B04840g	similar to tr|Q12003 Saccharomy cerevisiae YPL236c, start by simila
KLLA0C01650g	similar to sp|Q12263 Saccharomy cerevisiae YDR507c GIN4 ser/thr p kinase, start by similarity

												YALI0F08165g	some similarities with sp|P4189 Schizosaccharomyces pombe 7 CI OR SPBC21.06C gene Cell divis control protein, start by similarit
												KLLA0E01584g	highly similar to sp|P39009 Saccharomyces cerevisiae YDL1 DUN1 protein kinase, start by simil
												DEHA0C02882g	similar to CA4039|CaSKS1 Cand albicans, start by similarity
												KLLA0F01276g	similar to sp|P38147 Saccharomy cerevisiae YBR274w CHK1 regu inhibitory Cdk phosphorylation of F start by similarity
												CAGL0G09020g	highly similar to sp|P06245 Saccharomyces cerevisiae YPL20 TPK2 cAMP-dependent protein kin catalytic chain, hypothetical sta
												DEHA0G16302g	similar to tr|Q12706 Schizosaccharomyces pombe Prob serine/threonine protein kinase PS start by similarity
												CAGL0I06248g	similar to sp|P38970 Saccharomy cerevisiae YJL165c HAL5 ser/thr pr kinase, start by similarity
												YALI0B08558g	weakly similar to tr|Q00863 Nect haematococca Ran1-like protein ki hypothetical start
												DEHA0G05544g	similar to CA1375|IPF7158 Cand albicans IPF7158 putative serine/threonine kinase, hypothetica
												KLLA0B13607g	weakly similar to sp|Q03497 Saccharomyces cerevisiae YHL0 STE20 ser/thr protein kinase of t pheromone pathway, hypothetical
												YALI0F27159g	some similarities with sp|P4704 Saccharomyces cerevisiae YJL057c probable serine/threonine-protein ki hypothetical start
												CAGL0I05390g	similar to sp|Q12505 Saccharomy cerevisiae YPL026c SKS1 suppres kinase of SNF3 or tr|Q03785 Saccharomyces cerevisiae YDR24 start by similarity
												YALI0E31361g	similar to tr|Q9HF33 Arthrobotr dactyloides Calmodulin-binding pr kinase, hypothetical start
												YALI0B14201g	similar to sp|P32328 Saccharomy cerevisiae YPR111w DBF20 cell c protein kinase P108.1.f3.6 or sp|P2 Saccharomyces cerevisiae YGR09 DBF2 ser/thr protein kinase P108.1.f16.1, hypothetical star
												DEHA0C16181g	similar to CA1447|CaNRK1 Canc albicans, hypothetical start
												CAGL0K04301g	similar to sp|P53233 Saccharomy cerevisiae YGR052w, hypothetical
												KLLA0A06820g	some similarities with sp|P3897 Saccharomyces cerevisiae YJL16 HAL5 ser/thr protein kinase, hypoth start
												KLLA0C00979g	similar to sp|P08458 Saccharomy cerevisiae YDR523c SPS1 ser/thr pr kinase, hypothetical start
												YALI0D02101g	similar to sp|O94168 Candida tropi Carbon catabolite derepressing pro kinase (EC 2.7.1.-), hypothetical s
												YALI0C08305g	highly similar to sp|P06245 Saccharomyces cerevisiae YPL20 TPK2 cAMP-dependent protein kin catalytic chain, hypothetical sta
												KLLA0D12100g	some similarities with sgd|S0002 Saccharomyces cerevisiae YDR24 hypothetical start
													highly similar to sp|P53599

CAGL0M10791g	Saccharomyces cerevisiae YNR0 SSK2 MAP kinase, no start, frame
YALI0A05247g	similar to tr|Q876Z5 Neurospora cr OS-4 Putative SSK22 like MAPK kinase, hypothetical start
DEHA0F24684g	similar to sp|P24719 Saccharomy cerevisiae YOR351c MEK1 ser/t protein kinase
KLLA0B13112g	similar to sp|P23561 Saccharomy cerevisiae YLR362w STE11 ser/ protein kinase of the MEKK family by similarity
CAGL0F03311g	similar to sp|P38691 Saccharomy cerevisiae YHR082c KSP1 ser/t protein kinase, start by similarit
KLLA0C03938g	some similarities with sgd|S00021 Saccharomyces cerevisiae YDL02 hypothetical start
CAGL0M08360g	some similarities with sp|P3897 Saccharomyces cerevisiae YJL16 ser/thr protein kinase, hypothetical
YALI0E34375g	similar to wi|NCU00108.1 Neurosp crassa NCU00108.1 hypothetical pr (93222 - 91750), hypothetical st
KLLA0B07579g	weakly similar to sp|P32944 Saccharomyces cerevisiae YJL18 SWE1 ser/tyr dual-specifity prot kinase, start by similarity
YALI0D25388g	similar to tr|Q8TFN2 Pichia angu Serine-threonine kinase Pdd7p hypothetical start
DEHA0C04840g	some similarities with sp|P3899 Saccharomyces cerevisiae YPL20 IPL1 ser/thr protein kinase, hypothe start
YALI0B00880g	similar to sp|P22211 Saccharomy cerevisiae YNL183c NPR1 ser/t protein kinase, hypothetical star
YALI0D08822g	some similarities with sp|P3899 Saccharomyces cerevisiae YER12 PAK1 DNA polymerase alpha suppressing protein kinase, hypothe start
DEHA0G22440g	similar to CA4770|IPF9382.3 Can albicans IPF9382.3, hypothetical s
KLLA0C08525g	similar to sp|P53599 Saccharomy cerevisiae YNR031c SSK2 MAP k kinase kinase of the high osmolar signal transduction pathway, start similarity
YALI0F09746g	similar to sp|P24583 Saccharomy cerevisiae YBL105c PKC1 ser/t protein kinase, start by similarit
DEHA0D07601g	similar to Candida albicans CA42 start by similarity
CAGL0I07513g	similar to sp|Q12236 Saccharomy cerevisiae YOL100w PKH2, start similarity
DEHA0D11242g	highly similar to CA5299|IPF21 Candida albicans IPF2190, start similarity
DEHA0F26994g	similar to CA0206|IPF14089 Cand albicans IPF14089 putative serine/threonine protein kinase hypothetical start
CAGL0M09361g	highly similar to sp|P24583 Saccharomyces cerevisiae YBL10 PKC1 ser/thr protein kinase, start similarity
YALI0E06501g	similar to sp|P12688 Saccharomy cerevisiae YKL126w YPK1 ser/t specific protein kinase, hypothetical
CAGL0K05709g	similar to sp|Q12263 Saccharomy cerevisiae YDR507c GIN4, start

													similarity
												DEHA0C09130g	similar to sp|P38147 Saccharomy cerevisiae YBR274w CHK1, hypothetical start
												CAGL0M02299g	similar to tr|Q12152 Saccharomy cerevisiae YPL150w, start by simil
												CAGL0B04301g	similar to sp|P38070 Saccharomy cerevisiae YBR028c, start by simil
												CAGL0J03432g	similar to sp|P53974 Saccharomy cerevisiae YNL020c ARK1 or sp|P Saccharomyces cerevisiae YIL09 PRK1, start by similarity
												DEHA0D13706g	similar to CA4864|IPF4087 Cand albicans IPF4087, hypothetical st
												KLLA0D09328g	some similarities with sp|P3899 Saccharomyces cerevisiae YER12 PAK1 DNA polymerase alpha suppressing protein kinase, hypothe start
												DEHA0B13519g	some similarities with sp|P5373 Saccharomyces cerevisiae YNR04 related to ser/thr protein kinases hypothetical start
												CAGL0M02519g	highly similar to tr|Q03002 Saccharomyces cerevisiae YPL141 sp|Q01919 Saccharomyces cerevis YOR233w KIN4, hypothetical st
												CAGL0G04609g	similar to sp|Q12236 Saccharomy cerevisiae YOL100w PKH2, hypothetical start
												KLLA0F23155g	similar to sp|P22517 Saccharomy cerevisiae YOL016c CMK2 Ca2+/calmodulin-dependent ser/ protein kinase, type II, start by simi
												DEHA0C07139g	some similarities with sp|P2329 Saccharomyces cerevisiae YPR16 SGV1 ser/thr protein kinase, hypoth start
												KLLA0E14828g	gi|27526973|emb|CAD36964.1 Kluyveromyces lactis serine/threon protein kinase KIN28, start by simi
												DEHA0C06314g	some similarities with sp|P0624 Saccharomyces cerevisiae YDL01 CDC7, hypothetical start
												DEHA0B08701g	similar to CA4995|CaYAK1 Canc albicans CaYAK1 putative Ser/t protein kinase, hypothetical star
												CAGL0J00539g	highly similar to sp|Q00772 Saccharomyces cerevisiae YHR0 SLT2, hypothetical start
												KLLA0E12177g	gi|4096112|gb|AAC99804.1 Kluyveromyces lactis CTD kinase la subunit, hypothetical start
												DEHA0B00770g	similar to sp|P32581 Saccharomy cerevisiae YJL106w IME2 ser/thr p kinase, hypothetical start
												YALI0D25190g	highly similar to sp|P17157 Saccharomyces cerevisiae YPL03 PHO85, hypothetical start
												DEHA0E21219g	similar to CA1378|CaERK2 Canc albicans CaERK2 mitogen-activa protein kinase, start by similarit
												DEHA0F08987g	similar to CAGL-IPF1383.1 Canc glabrata, hypothetical start
												CAGL0I05896g	some similarities with sp|P1468 Saccharomyces cerevisiae YJL14 YAK1 ser/thr protein kinase, hypothetical start
												KLLA0F20053g	highly similar to sp|P32485 Saccharomyces cerevisiae YLR11 HOG1 ser/thr protein kinase of M kinase (MAPK) family, start by similarity
													sp|Q9UV50 Debaryomyces hanse

DEHA0E22110g	Mitogen-activated protein kinase H identified start
DEHA0A14080g	highly similar to CA6039|CaCKA Candida albicans CaCKA1 casein k II, catalytic alpha chain, start by similarity
YALI0E33803g	similar to tr|Q9Y7V6 Emericell nidulans MAP protein kinase MPI hypothetical start
YALI0E25135g	highly similar to sp|P32485 Saccharomyces cerevisiae YLR11 HOG1 ser/thr protein kinase of M kinase (MAPK) family, hypothetica
YALI0E23496g	highly similar to tr|Q9UW09 Glom lagenarium Mitogen activated pro kinase, hypothetical start
CAGL0L06820g	highly similar to sp|P38615 Saccharomyces cerevisiae YMR13 MDS1 Serine/threonine-protein ki
CAGL0G02035g	highly similar to sp|P19454 Saccharomyces cerevisiae YOR06 CKA2 casein kinase II alpha chain, by similarity
DEHA0G02750g	similar to CA4014|CaCTK1 Cand albicans CaCTK1 probable cell div protein kinase, start by similarit
YALI0B02816g	similar to sp|Q00772 Saccharomy cerevisiae Mitogen-activated prot kinase SLT2/MPK1 (EC 2.7.1.-) (M kinase MPK1), start by similarit
KLLA0D11814g	similar to sp|P39073 Saccharomy cerevisiae YPL042c SSN3 cyclin dependent CTD kinase, start by simi
KLLA0B11902g	gi|7385125|gb|AAF61706.1|AF2267 Kluyveromyces lactis MAP kinase, by similarity
CAGL0D02002g	similar to sp|Q03957 Saccharomy cerevisiae YKL139w CTK1 carbo terminal domain kinase, hypotheti start
KLLA0F02838g	some similarities with sp|P3258 Saccharomyces cerevisiae YJL10 IME2 ser/thr protein kinase, hypoth start
KLLA0D10527g	similar to sp|P23293 Saccharomy cerevisiae YPR161c SGV1 ser/t protein kinase, hypothetical star
CAGL0D01694g	similar to sp|P41808 Saccharomy cerevisiae YPR054w SMK1 sporula specific MAP kinase, hypothetical
YALI0D04334g	similar to sp|P06242 Saccharomy cerevisiae YDL108w KIN28 cycl dependent ser/thr protein kinase, sta similarity
CAGL0I08349g	similar to sp|P23293 Saccharomy cerevisiae YPR161c SGV1 ser/t protein kinase, hypothetical star
CAGL0K01815g	similar to sp|P06243 Saccharomy cerevisiae YDL017w Cell divisio control protein 7, hypothetical st
DEHA0F09713g	similar to ca|CA1467|IPF5082 Can albicans IPF5082 similar to Saccharomyces cerevisiae Cak1p c activating protein kinase (by homol hypothetical start
KLLA0D11990g	gi|2499590|sp|Q92241|PH85_KLU Kluyveromyces lactis NEGATIV REGULATOR OF THE PHO SYS hypothetical start
YALI0D04114g	weakly similar to tr|Q8X0V5 Neuro crassa Related to putative dual speci protein kinase pom1, hypothetical
CAGL0K04169g	similar to sp|P14681 Saccharomy cerevisiae YGR040w KSS1, start

CTK1 (YKL139W)	2.7.1.-	sp|Q03957 Saccharomyces cerevisiae YKL139w CTK1 carboxy-terminal domain (CTD) kinase, alpha subunit P108.1.f3.4	viable	Ess	Ess	Ess	0.3	Ess	sckdy	22 19 19 21 17	GLC.8		similarity
												KLLA0E07414g	highly similar to sp|P21965 Saccharomyces cerevisiae YNL30 MCK1 ser/thr/tyr protein kinase, sta similarity
												YALI0B18700g	similar to tr|Q8TG13 Neurospora c Casein kinase II alpha subunit CKA by similarity
												YALI0D16863g	tr|Q92390 Yarrowia lipolytica cas kinase II catalytic subunit, identified
												KLLA0C04345g	similar to sp|P06243 Saccharomy cerevisiae YDL017w CDC7 prot kinase, start by similarity
												CAGL0H10318g	highly similar to sp|P06242 Saccharomyces cerevisiae YDL10 KIN28 cyclin-dependent ser/thr pro kinase
												YALI0B22528g	weakly similar to tr|O14098 Schizosaccharomyces pombe Puta serine/threonine protein kinase, sta similarity
												DEHA0G22528g	highly similar to CA3004|CaKIN Candida albicans CaKIN28, start similarity
												KLLA0B11946g	similar to sp|P41808 Saccharomy cerevisiae YPR054w SMK1 sporula specific MAP kinase, start by simil
												DEHA0F26268g	similar to sp|P41808 Saccharomy cerevisiae YPR054w Sporulation specific mitogen-activated protein k SMK1 (MAP kinase SMK1), hypothetical start, frameshift
												KLLA0B09790g	highly similar to sp|P00546 Saccharomyces cerevisiae YBR16 CDC28 cyclin-dependent protein ki start by similarity
												DEHA0F26257g	similar to sp|P41808 Saccharomy cerevisiae YPR054w Sporulation specific mitogen-activated protein k SMK1 (MAP kinase SMK1), hypothetical start, frameshift
												YALI0F03113g	some similarities with sp|P3258 Saccharomyces cerevisiae YJL10 IME2 ser/thr protein kinase, hypoth start
												KLLA0F16467g	highly similar to sp|P19454 Saccharomyces cerevisiae YOR06 CKA2 casein kinase II alpha chain, by similarity
												CAGL0L12474g	highly similar to sp|P17157 Saccharomyces cerevisiae YPL03 cyclin-dependent protein kinase, sta similarity
												CAGL0M11748g	highly similar to sp|P32485 Saccharomyces cerevisiae YLR11 HOG1, start by similarity
												CAGL0E01683g	highly similar to sp|P21965 Saccharomyces cerevisiae YNL30 MCK1 or sp|Q12222 Saccharomy cerevisiae YOL128c, start by simil
												KLLA0A02497g	highly similar to sp|P14681 Saccharomyces cerevisiae YGR04 KSS1 ser/thr protein kinase of the I kinase family, start by similarity
												CAGL0J04290g	similar to sp|P16892 Saccharomy cerevisiae YBL016w FUS3 or sp|P1 Saccharomyces cerevisiae YGR04 KSS1, start by similarity
												KLLA0A05819g	similar to sp|P14680 Saccharomy cerevisiae YJL141c YAK1 ser/thr p kinase, start by similarity
												YALI0D20966g	highly similar to tr|Q9HE92 Neuros crassa Probable glycogen synthase k 3 alpha, start by similarity

												KLLA0F08877g	gi|27526975|emb|CAD36965.1 Kluyveromyces lactis cyclin-depen kinase activating kinase 1, start b similarity
												DEHA0E05819g	highly similar to CA2027|CaMCK Candida albicans CaMCK1 ser/thr protein kinase, hypothetical star
												DEHA0C07469g	highly similar to sp|P19454 Saccharomyces cerevisiae YOR06 CKA2, hypothetical start
												YALI0E11077g	similar to sp|Q07538 Schizosaccharomyces pombe SPCC777.14 PRP4 Serine/threoni protein kinase, hypothetical star
												DEHA0E19217g	similar to sp|Q00772 Saccharomy cerevisiae YHR030c SLT2 ser/thr p kinase of MAP kinase family P108.1.f12.1 Length = 484, start similarity
												KLLA0F17006g	gi|3127831|emb|CAA61157.1 Kluyveromyces lactis protein kina start by similarity
												KLLA0E10527g	similar to sp|P16892 Saccharomy cerevisiae YBL016w FUS3 mitog activated protein kinase (MAP kina start by similarity
												YALI0D19492g	similar to wi|NCU07880.1 Neurosp crassa NCU07880.1 hypothetical pr (15912 - 17477), hypothetical sta
												YALI0B10758g	highly similar to sp|P43063 Cand albicans cell division control protei hypothetical start
												DEHA0F09735g	similar to ca|CA1468|CaSRB10 Ca albicans CaSRB10 cyclin-depend kinase by homology, 3 end, hypoth start
												DEHA0F09647g	similar to wi|NCU04185.1 Neurosp crassa NCU04185.1 hypothetical pr ((AL451015) probable glycoge synthase kinase 3 alpha [Neurosp crassa]) (47604 - 49112), hypothe start
												DEHA0G11660g	highly similar to sp|P43063 Cand albicans Cell division control prote (EC 2.7.1.-), hypothetical start
												DEHA0D14256g	highly similar to CA4448|CaPHO Candida albicans CaPHO85 Nega regulator of PHO system, start b similarity
												YALI0C10967g	similar to sp|P39073 Saccharomy cerevisiae YPL042c SSN3 cyclin dependent CTD kinase, hypothetica
												CAGL0K12496g	similar to sp|P43568 Saccharomy cerevisiae YFL029c CAK1 cdk activating protein kinase, hypothet start
												CAGL0L12650g	similar to sp|P39073 Saccharomy cerevisiae YPL042c cyclin-depend CTD kinase, hypothetical start
												CAGL0G04455g	similar to sp|P32581 Saccharomy cerevisiae YJL106w IME2 ser/thr p kinase, hypothetical start
												KLLA0E04136g	similar to sp|P15790 Saccharomy cerevisiae YIL035c CKA1 casein k II, catalytic alpha chain, start by similarity
												CAGL0H07535g	highly similar to sp|P00546 Saccharomyces cerevisiae YBR16 CDC28, start by similarity
												CAGL0I05192g	highly similar to sp|P15790 Saccharomyces cerevisiae YIL03 CKA1 casein kinase II, start by simi
												DEHA0E04290g	highly similar to CA0722|CaERK Candida albicans CaERK1 mitog activated protein kinase (FUS3

												homolog), hypothetical start
											YALI0C24321g	weakly similar to sp|P43568 Saccharomyces cerevisiae YFL02 CAK1 cdk-activating protein kina hypothetical start
CTK3 (YML112W)	2.7.1.-	sp|P46963 Saccharomyces cerevisiae YML112w CTK3 carboxy-terminal domain (CTD) kinase, gamma subunit singleton	viable	0.9	0.6	ND	Non	ND	sck--	1 1 1 0 0	GLR.1303	CAGL0J06754g	similar to sp|P46963 Saccharomy cerevisiae YML112w CTK3 carbo terminal domain kinase, start by similarity
											KLLA0D01815g	weakly similar to sp|P46963 Saccharomyces cerevisiae YML11 CTK3 carboxy-terminal domain (C kinase, gamma subunit singleton, st similarity
YCK2 (YNL154C)	2.7.1.-	sp|P23292 Saccharomyces cerevisiae YNL154c YCK2 casein kinase I isoform P108.1.f4.1	viable	Ess	Ess	Ess	0.1	Ess	sckdy	4 4 2 2 2	GLC.92	KLLA0D11044g	gi|730472|sp|P40230|RAG8_KLU Kluyveromyces lactis CASEIN KIN I HOMOLOG RAG8, start by simil
											YALI0E26609g	similar to tr|CAD79679 Neurosp crassa, start by similarity
											DEHA0A09933g	similar to sp|P23292 Saccharomy cerevisiae YNL154c YCK2 casein k I isoform, hypothetical start
											CAGL0G06138g	similar to sp|P23291 Saccharomy cerevisiae YHR135c YCK1, start similarity
											DEHA0D04466g	similar to YALI-IPF3384.1 Yarro lipolytica, start by similarity
											YALI0F08305g	similar to sp|P29295 Saccharomy cerevisiae YPL204w HRR25 case kinase I, start by similarity
											CAGL0H03553g	highly similar to sp|P29295 Saccharomyces cerevisiae YPL20 HRR25, start by similarity
											CAGL0J05940g	similar to sp|P23291 Saccharomy cerevisiae YHR135c YCK1 or sp|P2 Saccharomyces cerevisiae YNL15 YCK2, hypothetical start
											CAGL0K02299g	similar to sp|P39962 Saccharomy cerevisiae YER123w Casein kinas hypothetical start
											KLLA0E13563g	some similarities with sp|P3996 Saccharomyces cerevisiae YER12 YCK3 casein kinase, isoform 3 hypothetical start
											KLLA0F11319g	similar to sgd|S0006071 Saccharom cerevisiae YPL150w, start by simil
											CAGL0L07810g	similar to sp|P25333 Saccharomy cerevisiae YCR008w SAT4 serine/threonine-specific protein ki start by similarity
											CAGL0K11550g	similar to sp|P28708 Saccharomy cerevisiae YKL116c, hypothetical
											YALI0F11385g	weakly similar to SP|P38691 Saccharomyces cerevisiae YHR0 KSP1 ser/thr protein kinase and DE IPF5974.1, start by similarity
											KLLA0A09713g	similar to sp|Q03533 Saccharomy cerevisiae YMR291w, start by simi
											KLLA0E17127g	similar to sp|P38691 Saccharomy cerevisiae YHR082c KSP1 ser/t protein kinase, start by similarit
											YALI0C04158g	similar to sp|P18961 Saccharomy cerevisiae Serine/threonine-prote kinase YPK2/YKR2, hypothetical
											DEHA0F24676g	similar to sp|P24719 Saccharomy cerevisiae YOR351c MEK1 ser/t protein kinase
											DEHA0G14817g	similar to CA2643|CaHSL1 Cand albicans CaHSL1, hypothetical st
											DEHA0C18150g	similar to sp|P40494 Saccharomy cerevisiae YIL095w PRK1 serine/threonine protein kinase, sta similarity

CAGL0K10604g	similar to sp|P27466 Saccharomy cerevisiae YFR014c CMK1 Ca2+/calmodulin-dependent ser/ protein kinase type I, hypothetical
DEHA0C08591g	similar to sp|P22204 Saccharomy cerevisiae YGR092w DBF2, hypothetical start, sequence gap
YALI0F13629g	some similarities with sp|P2356 Saccharomyces cerevisiae YLR36 STE11 ser/thr protein kinase of t MEKK family, hypothetical sta
KLLA0C06138g	similar to sp|P32562 Saccharomy cerevisiae YMR001c CDC5 involv regulation of DNA replication, star similarity
YALI0F16159g	some similarities with wi|NCU009 Neurospora crassa NCU00914. hypothetical protein, hypothetical
CAGL0K08514g	similar to sp|P34244 Saccharomy cerevisiae YKL101w serine/threon protein kinase, hypothetical star
DEHA0F25278g	similar to ca|CA1881|CaRCK2 Car albicans CaRCK2 Ca/calmodulin dependent ser/thr protein kinase (homology), hypothetical start
KLLA0F26983g	some similarities with sp|P3280 Saccharomyces cerevisiae YKL0 ELM1 ser/thr-specific protein kin hypothetical start
DEHA0C11484g	similar to sp|P22211 Saccharomy cerevisiae YNL183c NPR1 or tr|Q1 Saccharomyces cerevisiae YDL02 hypothetical start
YALI0C00891g	similar to sp|O14019 Schizosaccharomyces pombe Prob serine/threonine-protein kinase C29A4.16 (EC 2.7.1.-), hypothetica
KLLA0F23507g	similar to sp|P24719 Saccharomy cerevisiae YOR351c MEK1 ser/t protein kinase, start by similarit
CAGL0F03245g	similar to sp|P32361 Saccharomy cerevisiae YHR079c IRE1, hypothe start
CAGL0K11990g	some similarities with sp|P3808 Saccharomyces cerevisiae YBR0 AKL1 Ark-family Kinase-Like pro hypothetical start
DEHA0G10417g	similar to CA1971|CaPKH2 Cand albicans CaPKH2 Ser/Thr protei kinase(by homology), hypothetical
YALI0B17556g	weakly similar to tr|Q9Y898 Emeri nidulans Calcium/calmodulin deper protein kinase C, hypothetical sta
CAGL0G03047g	highly similar to sp|P22204 Saccharomyces cerevisiae YGR09 DBF2 ser/thrprotein kinase or sp|P3 Saccharomyces cerevisiae YPR11 DBF20, hypothetical start
YALI0F27093g	weakly similar to DEHA-IPF372 Debaryomyces hansenii, hypothet start
DEHA0C14091g	similar to sp|P37292 Saccharomy cerevisiae YBR263w SHM1, hypothetical start
DEHA0C18601g	similar to CA4433|CaBCK1 Canc albicans, hypothetical start
KLLA0C04213g	similar to sp|P22209 Saccharomy cerevisiae YAR018c KIN3 ser/thr p kinase, hypothetical start
YALI0A04697g	similar to sp|O42626 Neurospora c Serine/threonine-protein kinase n (Nonrepressible conidiation protei hypothetical start
	similar to sp|P32562 Saccharomy

												YALI0D26015g	cerevisiae Cell cycle protein kina CDC5/MSD2 (EC 2.7.1.-), hypothe start
												DEHA0G14839g	highly similar to sCA3870|CaYP Candida albicans CaYPK1, start similarity
												KLLA0C14278g	similar to sp|P28708 Saccharomy cerevisiae YKL116c, hypothetical
												YALI0E13750g	similar to tr|CAD79666 Neurosp crassa B1D14.230 Related to serine/threonine-protein kinase a DEHA-IPF6149.1 Debaryomyc hansenii, no start
												CAGL0B04147g	highly similar to sp|P22204 Saccharomyces cerevisiae YGR09 DBF2 ser/thrprotein kinase relate DBF20P or sp|P32328 Saccharomy cerevisiae YPR111w DBF20 cell c protein kinase related to DBF2I hypothetical start
												DEHA0F13497g	similar to ca|CA1299|CaPTK2 Can albicans CaPTK2 serine /threoni protein kinase involved in polyam uptake (by homology), hypothetical
												DEHA0D13684g	similar to CA4865|IPF4085 Cand albicans IPF4085, start by similar
												CAGL0L06006g	similar to sp|P53104 Saccharomy cerevisiae YGL180w APG1 essenti autophagocytosis, hypothetical st
												CAGL0E05720g	similar to sp|P38991 Saccharomy cerevisiae YPL209c IPL1 ser/thr pr kinase, start by similarity
												KLLA0F18612g	some similarities with sp|P3808 Saccharomyces cerevisiae YBR05 AKL1 Ark-family Kinase-Like pro hypothetical start
												YALI0E24563g	similar to tr|Q12152 Saccharomy cerevisiae YPL150w, hypothetical
												DEHA0F24013g	similar to ca|CA5226|CaRIM15 Ca albicans CaRIM15 Protein kinas involved in the RIM pathway (b homology), hypothetical start
												CAGL0I04422g	some similarities with sp|P2220 Saccharomyces cerevisiae YAR0 KIN3 ser/thr protein kinase, hypoth start
												CAGL0K01661g	some similarities with tr|Q1210 Saccharomyces cerevisiae YDL02 hypothetical start
												DEHA0E15741g	highly similar to CA3361|CaSNI Candida albicans CaSNF1 serine/threonine protein kinase hypothetical start
												CAGL0M02233g	highly similar to sp|P22216 Saccharomyces cerevisiae YPL15 SPK1 ser/thr/tyr protein kinase hypothetical start
												CAGL0F04741g	similar to sp|P22517 Saccharomy cerevisiae YOL016c CMK2 Ca2+/calmodulin-dependent ser/ protein kinase, type II, hypothetical
												YALI0E06523g	weakly similar to sp|P34244 Saccharomyces cerevisiae YKL10 HSL1 ser/thr protein kinase, coup septin ring assembly to cell cycl progression, hypothetical start
												KLLA0E11979g	some similarities with sp|P2533 Saccharomyces cerevisiae YCR00 SAT4 serine/threonine-specific pro kinase, hypothetical start
												CAGL0J11308g	similar to sp|P22211 Saccharomy cerevisiae YNL183c NPR1 ser/t protein kinase, hypothetical star
													similar to sp|P25333 Saccharomy

DEHA0G11638g	cerevisiae YCR008w SAT4 serine/threonine-specific protein ki hypothetical start
CAGL0H10208g	similar to sp|P38080 Saccharomy cerevisiae YBR059c AKL1 Ark-fa Kinase-Like protein, hypothetical
CAGL0B02739g	similar to sp|P23561 Saccharomy cerevisiae YLR362w STE11 ser/ protein kinase of the MEKK fam hypothetical start
YALI0D07150g	weakly similar to tr|Q9C2E8 Neuro crassa Conserved hypothetical pro start by similarity
DEHA0F10197g	highly similar to ca|CA2265|CaCM Candida albicans CaCMK2 Ca2 /calmodulin-dependent ser/thr pro kinase, type II (by homology), hypothetical start
DEHA0B12628g	similar to sp|P06245 Saccharomy cerevisiae YPL203w TPK2 cAM dependent protein kinase 2, cataly chain, start by similarity
DEHA0E13574g	similar to CA2193|IPF14273 Canc albicans IPF14273 Probable ser/t protein kinase
KLLA0D07348g	weakly similar to sgd|S000606 Saccharomyces cerevisiae YPL14 start by similarity
DEHA0B12650g	some similarities with sp|P3897 Saccharomyces cerevisiae YJL16 HAL5 ser/thr protein kinase, hypoth start
DEHA0F04114g	similar to CA0576|CaNPR1 Cand albicans CaNPR1, hypothetical st
DEHA0C13211g	similar to sp|P22216 Saccharomy cerevisiae YPL153c SPK1, hypothe start
KLLA0B07205g	some similarities with sp|P0598 Saccharomyces cerevisiae YKL16 TPK3 cAMP-dependent protein kin catalytic chain, hypothetical sta
CAGL0K06479g	some similarities with tr|Q0330 Saccharomyces cerevisiae YDR46 start by similarity
KLLA0C12485g	weakly similar to sp|Q12236 Saccharomyces cerevisiae YOL10 PKH2, start by similarity
KLLA0E06413g	gi|22858696|gb|AAN05732.1 Kluyveromyces lactis protein kinas start by similarity
YALI0D26213g	weakly similar to tr|Q96WJ8 Blum graminis Protein kinase C-like pro hypothetical start
DEHA0G14707g	similar to CA6135|CaCMK1 Canc albicans CaCMK1, hypothetical s
DEHA0E16115g	similar to CA5074|IPF3607 Cand albicans IPF3607 putative serine/threonine protein kinase hypothetical start
CAGL0M13167g	similar to sp|P32801 Saccharomy cerevisiae YKL048c ELM1 ser/tl specific protein kinase, hypothetical
KLLA0F01408g	weakly similar to sgd|S000218 Saccharomyces cerevisiae YDL02 hypothetical start
DEHA0F25212g	highly similar to tr|Q9HEW0 Canc albicans cAMP-dependent protein k catalytic subunit, hypothetical st
CAGL0M08404g	some similarities with sp|P0598 Saccharomyces cerevisiae YKL16 TPK3 or sp|P06244 Saccharomyc cerevisiae YJL164c SRA3 or sp|P0 Saccharomyces cerevisiae YPL20 TPK2, hypothetical start

KLLA0A03806g	gi|2181934|emb|CAA61235.1 Kluyveromyces lactis putative kin start by similarity
YALI0D19470g	similar to tr|Q871H9 Neurospora cr B16M17.090 Related to Ste20-li kinase Don3, hypothetical start
YALI0A10230g	similar to sp|P22211 Saccharomy cerevisiae YNL183c NPR1 ser/t protein kinase, start by similarit
DEHA0F10461g	some similarities with ca|CA1288|CaKSP1 Candida albic CaKSP1 SERINE/THREONINE PROTEIN KINASE by homolog hypothetical start
YALI0F01716g	tr|Q9P860 Yarrowia lipolytica Wee protein, mitosis inhibitor protein ki hypothetical start
YALI0E27632g	tr|O93955 Yarrowia lipolytica SS protein, multicopy suppressor of S secretory defects, putative calmodu dependent ser/thr protein kinase identified start
CAGL0I09504g	similar to sp|P38147 Saccharomy cerevisiae YBR274w CHK1 regul inhibitory Cdk phosphorylation of P start by similarity
CAGL0F09075g	similar to sp|P11792 Saccharomy cerevisiae YHR205w SCH9 serine/threonine protein kinase, sta similarity
DEHA0C17996g	similar to CA2348|IPF12811 Cand albicans, putative serine/threonin kinase, hypothetical start
CAGL0H00979g	similar to tr|Q12003 Saccharomyc cerevisiae YPL236c, hypothetical
KLLA0C03828g	similar to sp|P54199 Saccharomy cerevisiae YDL028c MPS1 serine/threonine/tyrosine protein ki hypothetical start
KLLA0F14190g	gi|3021329|emb|CAA06336.1 Kluyveromyces lactis MAP kinase k kinase, start by similarity
CAGL0M10153g	some similarities with sp|Q0349 Saccharomyces cerevisiae YHL0 ser/thr protein kinase of the pheron pathway, hypothetical start
KLLA0F24618g	similar to sp|P38070 Saccharomy cerevisiae YBR028c, start by simil
CAGL0K07458g	similar to sp|P12688 Saccharomy cerevisiae YKL126w or sp|P189 Saccharomyces cerevisiae YMR1 ser/thr-specific protein kinases, sta similarity
KLLA0D03190g	highly similar to sp|P06245 Saccharomyces cerevisiae YPL20 TPK2 cAMP-dependent protein kin catalytic chain, start by similarit
DEHA0D19833g	similar to CA5851|CaKIN2 Cand albicans CaKIN2, hypothetical st
KLLA0D14905g	gi|28565036|gb|AAO32601.1 Kluyveromyces lactis DBF2, start similarity
KLLA0C18568g	gi|6967028|emb|CAB72435.1 Kluyveromyces lactis MUP1 prot hypothetical start
CAGL0M13541g	similar to sp|Q03533 Saccharomy cerevisiae YMR291w, hypothetical
KLLA0E03487g	similar to sgd|S0002874 Saccharon cerevisiae YDR466w, start by simil
DEHA0C08635g	similar to sp|P22204 Saccharomy cerevisiae YGR092w DBF2, hypothetical start, sequence ga
CAGL0G02607g	similar to sp|P40494 Saccharomy cerevisiae YIL095w PRK1, start

NPR1 (YNL183C)	2.7.1.-	sp|P22211 Saccharomyces cerevisiae YNL183c NPR1 ser/thr protein kinase P108.1.f7.1	Exhibits sensitivity at 20 generations when grown in 1 M NaCl.	0.3	Ess	Ess	0.4	Ess	sckdy	57 58 49 54 42	GLC.2		similarity
												CAGL0K11275g	similar to tr|Q03785 Saccharomy cerevisiae YDR247w, hypothetical
												DEHA0E05753g	similar to CA0719|IPF9779.5 Cand albicans IPF9779.5 serine/threoni protein kinase 5-prime end, hypothe start
												YALI0B05588g	some similarities with sp|Q1223 Saccharomyces cerevisiae YOL10 PKH2 related to ser/thr protein kin P108.1.f16.1, hypothetical start
												DEHA0A08822g	similar to CA0577|IPF16051 Cand albicans IPF16051 unknown funct start by similarity
												KLLA0C17160g	similar to sp|P53104 Saccharomy cerevisiae YGL180w APG1 essenti autophagocytosis, start by similar
												KLLA0A02717g	some similarities with sp|P5323 Saccharomyces cerevisiae YGR05 hypothetical start
												YALI0C21758g	similar to KLLA-IPF4914.1 Kluyveromyces lactis IPF 4914. hypothetical start
												CAGL0C03509g	similar to sp|P53739 Saccharomy cerevisiae YNR047w or sp|P253 Saccharomyces cerevisiae YCR09 KIN82, hypothetical start
												KLLA0B03586g	similar to sp|P11792 Saccharomy cerevisiae YHR205w SCH9 serine/threonine protein kinase invo in stress response and nutrient-sen signaling pathway, start by simila
												YALI0C15444g	similar to tr|Q12706 Schizosaccharomyces pombe Prob serine/threonine protein kinase PS (EC 2.7.1.-), hypothetical start
												YALI0E34067g	weakly similar to DEHA-IPF394 Debaryomyces hansenii IPF 394 hypothetical start
												CAGL0C05005g	similar to sp|P27636 Saccharomy cerevisiae YAR019c CDC15, hypothetical start
												DEHA0B04895g	similar to CA2018|CaSTE11 Cand albicans CaSTE11 ser/thr protein k of the MEKK family, hypothetical
												KLLA0B12716g	similar to sp|P12688 Saccharomy cerevisiae YKL126w YPK1 ser/t specific protein kinase, start by simi
												CAGL0F03707g	similar to sp|Q08732 Saccharomy cerevisiae YOR267c, start by simil
												YALI0E22858g	Weakly similar to CAAL-CA55 CaAKL1 serine/threonine protein k (by homology), Hypothetical sta
												KLLA0F09031g	similar to sp|P43565 Saccharomy cerevisiae YFL033c RIM15 prote kinase involved in expression of me genes, hypothetical start
												DEHA0E12782g	similar to sp|P38070 Saccharomy cerevisiae YBR028c, putative ribos protein kinase
												CAGL0B01925g	similar to sp|P13185 Saccharomy cerevisiae YDR122w KIN1 or sp|P1 Saccharomyces cerevisiae YLR09 KIN2, hypothetical start
												KLLA0C07535g	some similarities with sgd|S00057 Saccharomyces cerevisiae YOR26 hypothetical start
												CAGL0D02244g	similar to sp|P24719 Saccharomy cerevisiae YOR351c MEK1 ser/t protein kinase, hypothetical star
												DEHA0C13387g	similar to tr|Q08732 Saccharomy cerevisiae YOR267C, hypothetical
												YALI0E17743g	no similarity, hypothetical start

												CAGL0C02893g	similar to tr|Q08732 Saccharomy cerevisiae YOR267c, hypothetical
												KLLA0F19536g	similar to sp|P13186 Saccharomy cerevisiae YLR096w KIN2 ser/t protein kinase, start by similarit
												CAGL0M11396g	similar to sp|P13186 Saccharomy cerevisiae YLR096w KIN2 ser/t protein kinase, hypothetical star
												YALI0B13178g	similar to sp|P32490 Saccharomy cerevisiae YOR231w MKK1 ser/ protein kinase, start by similarit
												DEHA0F27489g	similar to CA1288|CaKSP1 Cand albicans CaKSP1 serine/threonin protein kinase (by homology), star similarity
												KLLA0B02332g	similar to sp|P38991 Saccharomy cerevisiae YPL209c IPL1 ser/thr pr kinase, start by similarity
												CAGL0L07326g	similar to sp|P39009 Saccharomy cerevisiae YDL101c DUN1 prote kinase, start by similarity
												KLLA0F11143g	similar to sp|P22216 Saccharomy cerevisiae YPL153c SPK1 ser/thr protein kinase, start by similarit
												DEHA0E14641g	similar to CA4097|CaGIN4 Cand albicans CaGIN4 ser/thr protein ki (by homology), hypothetical sta
												CAGL0J03872g	similar to sp|Q01919 Saccharomy cerevisiae YOR233w KIN4 ser/t protein kinase or tr|Q03002 Saccharomyces cerevisiae YPL14 start by similarity
												YALI0D14542g	similar to sp|P11792 Saccharomy cerevisiae YHR205w SCH9 serine/threonine protein kinase invo in stress response and nutrient-sen signaling pathway, start by simila
												KLLA0B06501g	some similarities with sp|P4711 Saccharomyces cerevisiae YJR05 PTK2 involved in polyamine upta hypothetical start
												DEHA0C05742g	some similarities with sp|P4189 Schizosaccharomyces pombe Ce division control protein 7 and CA2669|IPF17494.3eoc Candid albicans and CA2404|CaCDC15 Ca albicans, hypothetical start
												DEHA0F20878g	similar to CA0044|IPF17347 Canc albicans IPF17347, hypothetical s
												KLLA0E08371g	similar to sp|P40494 Saccharomy cerevisiae YIL095w PRK1 serine/threonine protein kinase invo in regulation of actin cytoskeleto organization, start by similarity
												KLLA0F13552g	gi|33386566|emb|CAD87727.1 Kluyveromyces lactis protein kina start by similarity
												CAGL0J11638g	highly similar to sp|P32562 Saccharomyces cerevisiae YMR0 CDC5 involved in regulation of D replication, hypothetical start
												CAGL0K02167g	similar to sp|P38990 Saccharomy cerevisiae YER129w Serine/threon protein kinase, start by similarit
												DEHA0F09493g	similar to ca|CA2909|IPF11424 Ca albicans IPF11424 unknown funct hypothetical start
												CAGL0G05720g	similar to sp|P22211 Saccharomy cerevisiae YNL183c NPR1 ser/t protein kinase, start by similarit
												DEHA0C09823g	similar to CA1205|CaSSK2 Cand albicans, hypothetical start
												YALI0D22770g	Similar to CAAL-CA5851 CaKI ser/thr protein kinase (by homology

	start
CAGL0M08910g	highly similar to sp|Q00372 Saccharomyces cerevisiae YDR47 carbon catabolite derepressing ser protein kinase, hypothetical star
KLLA0C04191g	weakly similar to sp|P27636 Saccharomyces cerevisiae YAR0 CDC15 protein kinase of the MA kinase kinase kinase family, hypoth start
DEHA0B16071g	similar to sp|P22209 Saccharomy cerevisiae YAR018c KIN3 ser/thr p kinase, start by similarity
CAGL0K03399g	highly similar to sp|P12688 Saccharomyces cerevisiae YKL12 Serine/threonine-protein kinase, sta similarity
CAGL0J04972g	some similarities with tr|Q1210 Saccharomyces cerevisiae YDL02 hypothetical start
DEHA0F10923g	highly similar to ca|CA2986|CaCI Candida albicans CaCDC5 Cell-cy protein kinase (by homology), star similarity
YALI0B04840g	similar to tr|Q12003 Saccharomy cerevisiae YPL236c, start by simila
KLLA0C01650g	similar to sp|Q12263 Saccharomy cerevisiae YDR507c GIN4 ser/thr p kinase, start by similarity
YALI0F08165g	some similarities with sp|P4189 Schizosaccharomyces pombe 7 CI OR SPBC21.06C gene Cell divis control protein, start by similarit
KLLA0E01584g	highly similar to sp|P39009 Saccharomyces cerevisiae YDL10 DUN1 protein kinase, start by simil
DEHA0C02882g	similar to CA4039|CaSKS1 Cand albicans, start by similarity
KLLA0F01276g	similar to sp|P38147 Saccharomy cerevisiae YBR274w CHK1 regul inhibitory Cdk phosphorylation of F start by similarity
CAGL0G09020g	highly similar to sp|P06245 Saccharomyces cerevisiae YPL20 TPK2 cAMP-dependent protein kin catalytic chain, hypothetical sta
DEHA0G16302g	similar to tr|Q12706 Schizosaccharomyces pombe Prob serine/threonine protein kinase PS start by similarity
CAGL0I06248g	similar to sp|P38970 Saccharomy cerevisiae YJL165c HAL5 ser/thr pr kinase, start by similarity
YALI0B08558g	weakly similar to tr|Q00863 Nect haematococca Ran1-like protein ki hypothetical start
DEHA0G05544g	similar to CA1375|IPF7158 Cand albicans IPF7158 putative serine/threonine kinase, hypothetica
KLLA0B13607g	weakly similar to sp|Q03497 Saccharomyces cerevisiae YHL00 STE20 ser/thr protein kinase of t pheromone pathway, hypothetical
YALI0F27159g	some similarities with sp|P4704 Saccharomyces cerevisiae YJL057c probable serine/threonine-protein ki hypothetical start
CAGL0I05390g	similar to sp|Q12505 Saccharomy cerevisiae YPL026c SKS1 suppres kinase of SNF3 or tr|Q03785 Saccharomyces cerevisiae YDR24 start by similarity
YALI0E31361g	similar to tr|Q9HF33 Arthrobotr dactyloides Calmodulin-binding pro

	kinase, hypothetical start
YALI0B14201g	similar to sp|P32328 Saccharomy cerevisiae YPR111w DBF20 cell c protein kinase P108.1.f3.6 or sp|P2 Saccharomyces cerevisiae YGR09 DBF2 ser/thr protein kinase P108.1.f16.1, hypothetical star
DEHA0C16181g	similar to CA1447|CaNRK1 Canc albicans, hypothetical start
CAGL0K04301g	similar to sp|P53233 Saccharomy cerevisiae YGR052w, hypothetical
KLLA0A06820g	some similarities with sp|P3897 Saccharomyces cerevisiae YJL16 HAL5 ser/thr protein kinase, hypoth start
KLLA0C00979g	similar to sp|P08458 Saccharomy cerevisiae YDR523c SPS1 ser/thr pr kinase, hypothetical start
YALI0D02101g	similar to sp|O94168 Candida tropi Carbon catabolite derepressing pro kinase (EC 2.7.1.-), hypothetical s
YALI0C08305g	highly similar to sp|P06245 Saccharomyces cerevisiae YPL20 TPK2 cAMP-dependent protein kin catalytic chain, hypothetical sta
KLLA0D12100g	some similarities with sgd|S00026 Saccharomyces cerevisiae YDR24 hypothetical start
CAGL0M10791g	highly similar to sp|P53599 Saccharomyces cerevisiae YNR03 SSK2 MAP kinase, no start, frame
YALI0A05247g	similar to tr|Q876Z5 Neurospora cr OS-4 Putative SSK22 like MAPK kinase, hypothetical start
DEHA0F24684g	similar to sp|P24719 Saccharomy cerevisiae YOR351c MEK1 ser/t protein kinase
KLLA0B13112g	similar to sp|P23561 Saccharomy cerevisiae YLR362w STE11 ser/ protein kinase of the MEKK family by similarity
CAGL0F03311g	similar to sp|P38691 Saccharomy cerevisiae YHR082c KSP1 ser/t protein kinase, start by similarit
KLLA0C03938g	some similarities with sgd|S00021 Saccharomyces cerevisiae YDL02 hypothetical start
CAGL0M08360g	some similarities with sp|P3897 Saccharomyces cerevisiae YJL16 ser/thr protein kinase, hypothetical
YALI0E34375g	similar to wi|NCU00108.1 Neurosp crassa NCU00108.1 hypothetical pr (93222 - 91750), hypothetical sta
KLLA0B07579g	weakly similar to sp|P32944 Saccharomyces cerevisiae YJL18 SWE1 ser/tyr dual-specifity prote kinase, start by similarity
YALI0D25388g	similar to tr|Q8TFN2 Pichia angu Serine-threonine kinase Pdd7p hypothetical start
DEHA0C04840g	some similarities with sp|P3899 Saccharomyces cerevisiae YPL20 IPL1 ser/thr protein kinase, hypothe start
YALI0B00880g	similar to sp|P22211 Saccharomy cerevisiae YNL183c NPR1 ser/t protein kinase, hypothetical star
YALI0D08822g	some similarities with sp|P3899 Saccharomyces cerevisiae YER12 PAK1 DNA polymerase alpha suppressing protein kinase, hypothe start
DEHA0G22440g	similar to CA4770|IPF9382.3 Can albicans IPF9382.3, hypothetical s

												KLLA0C08525g	similar to sp|P53599 Saccharomy cerevisiae YNR031c SSK2 MAP k kinase kinase of the high osmolar signal transduction pathway, start similarity
												YALI0F09746g	similar to sp|P24583 Saccharomy cerevisiae YBL105c PKC1 ser/t protein kinase, start by similarit
												DEHA0D07601g	similar to Candida albicans CA42 start by similarity
												CAGL0I07513g	similar to sp|Q12236 Saccharomy cerevisiae YOL100w PKH2, start similarity
												DEHA0D11242g	highly similar to CA5299|IPF21 Candida albicans IPF2190, start similarity
												DEHA0F26994g	similar to CA0206|IPF14089 Canc albicans IPF14089 putative serine/threonine protein kinase hypothetical start
												CAGL0M09361g	highly similar to sp|P24583 Saccharomyces cerevisiae YBL10 PKC1 ser/thr protein kinase, start similarity
												YALI0E06501g	similar to sp|P12688 Saccharomy cerevisiae YKL126w YPK1 ser/t specific protein kinase, hypothetical
												CAGL0K05709g	similar to sp|Q12263 Saccharomy cerevisiae YDR507c GIN4, start similarity
												DEHA0C09130g	similar to sp|P38147 Saccharomy cerevisiae YBR274w CHK1, hypothetical start
												CAGL0M02299g	similar to tr|Q12152 Saccharomy cerevisiae YPL150w, start by simil
												CAGL0B04301g	similar to sp|P38070 Saccharomy cerevisiae YBR028c, start by simil
												CAGL0J03432g	similar to sp|P53974 Saccharomy cerevisiae YNL020c ARK1 or sp|P4 Saccharomyces cerevisiae YIL09 PRK1, start by similarity
												DEHA0D13706g	similar to CA4864|IPF4087 Cand albicans IPF4087, hypothetical st
												KLLA0D09328g	some similarities with sp|P3899 Saccharomyces cerevisiae YER12 PAK1 DNA polymerase alpha suppressing protein kinase, hypothe start
												DEHA0B13519g	some similarities with sp|P5373 Saccharomyces cerevisiae YNR04 related to ser/thr protein kinases hypothetical start
												CAGL0M02519g	highly similar to tr|Q03002 Saccharomyces cerevisiae YPL141 sp|Q01919 Saccharomyces cerevis YOR233w KIN4, hypothetical st
												CAGL0G04609g	similar to sp|Q12236 Saccharomy cerevisiae YOL100w PKH2, hypothetical start
												KLLA0F23155g	similar to sp|P22517 Saccharomy cerevisiae YOL016c CMK2 Ca2+/calmodulin-dependent ser/ protein kinase, type II, start by simi
												DEHA0C07139g	some similarities with sp|P2329 Saccharomyces cerevisiae YPR16 SGV1 ser/thr protein kinase, hypoth start
												KLLA0E14828g	gi|27526973|emb|CAD36964.1 Kluyveromyces lactis serine/threon protein kinase KIN28, start by simi
												DEHA0C06314g	some similarities with sp|P0624 Saccharomyces cerevisiae YDL01 CDC7, hypothetical start
													similar to CA4995|CaYAK1 Canc

DEHA0B08701g	albicans CaYAK1 putative Ser/t protein kinase, hypothetical star
CAGL0J00539g	highly similar to sp|Q00772 Saccharomyces cerevisiae YHR03 SLT2, hypothetical start
KLLA0E12177g	gi|4096112|gb|AAC99804.1 Kluyveromyces lactis CTD kinase la subunit, hypothetical start
DEHA0B00770g	similar to sp|P32581 Saccharomy cerevisiae YJL106w IME2 ser/thr p kinase, hypothetical start
YALI0D25190g	highly similar to sp|P17157 Saccharomyces cerevisiae YPL03 PHO85, hypothetical start
DEHA0E21219g	similar to CA1378|CaERK2 Cand albicans CaERK2 mitogen-activa protein kinase, start by similarit
DEHA0F08987g	similar to CAGL-IPF1383.1 Cand glabrata, hypothetical start
CAGL0I05896g	some similarities with sp|P1468 Saccharomyces cerevisiae YJL14 YAK1 ser/thr protein kinase, hypothetical start
KLLA0F20053g	highly similar to sp|P32485 Saccharomyces cerevisiae YLR11 HOG1 ser/thr protein kinase of M kinase (MAPK) family, start by similarity
DEHA0E22110g	sp|Q9UV50 Debaryomyces hanse Mitogen-activated protein kinase H identified start
DEHA0A14080g	highly similar to CA6039|CaCKA Candida albicans CaCKA1 casein k II, catalytic alpha chain, start by similarity
YALI0E33803g	similar to tr|Q9Y7V6 Emericell nidulans MAP protein kinase MPK hypothetical start
YALI0E25135g	highly similar to sp|P32485 Saccharomyces cerevisiae YLR11 HOG1 ser/thr protein kinase of M kinase (MAPK) family, hypothetical
YALI0E23496g	highly similar to tr|Q9UW09 Glome lagenarium Mitogen activated pro kinase, hypothetical start
CAGL0L06820g	highly similar to sp|P38615 Saccharomyces cerevisiae YMR13 MDS1 Serine/threonine-protein ki
CAGL0G02035g	highly similar to sp|P19454 Saccharomyces cerevisiae YOR06 CKA2 casein kinase II alpha chain, by similarity
DEHA0G02750g	similar to CA4014|CaCTK1 Cand albicans CaCTK1 probable cell div protein kinase, start by similarit
YALI0B02816g	similar to sp|Q00772 Saccharomy cerevisiae Mitogen-activated prot kinase SLT2/MPK1 (EC 2.7.1.-) (M kinase MPK1), start by similarit
KLLA0D11814g	similar to sp|P39073 Saccharomy cerevisiae YPL042c SSN3 cyclin dependent CTD kinase, start by simi
KLLA0B11902g	gi|7385125|gb|AAF61706.1|AF2267 Kluyveromyces lactis MAP kinase, by similarity
CAGL0D02002g	similar to sp|Q03957 Saccharomy cerevisiae YKL139w CTK1 carbo terminal domain kinase, hypotheti start
KLLA0F02838g	some similarities with sp|P3258 Saccharomyces cerevisiae YJL10 IME2 ser/thr protein kinase, hypoth start
	similar to sp|P23293 Saccharomy

MCK1 (YNL307C)	2.7.1.-	sp|P21965 Saccharomyces cerevisiae YNL307c MCK1 ser/thr/tyr protein kinase P108.1.f12.1	Exhibits sensitivity at 20 generations when grown in 1 M NaCl.	0.1	Ess	Ess	Ess	Ess	sckdy	22 19 19 21 17	GLC.8	KLLA0D10527g	cerevisiae YPR161c SGV1 ser/t protein kinase, hypothetical star
												CAGL0D01694g	similar to sp|P41808 Saccharomy cerevisiae YPR054w SMK1 sporula specific MAP kinase, hypothetical
												YALI0D04334g	similar to sp|P06242 Saccharomy cerevisiae YDL108w KIN28 cycl dependent ser/thr protein kinase, sta similarity
												CAGL0I08349g	similar to sp|P23293 Saccharomy cerevisiae YPR161c SGV1 ser/t protein kinase, hypothetical star
												CAGL0K01815g	similar to sp|P06243 Saccharomy cerevisiae YDL017w Cell divisio control protein 7, hypothetical st
												DEHA0F09713g	similar to ca|CA1467|IPF5082 Can albicans IPF5082 similar to Saccharomyces cerevisiae Cak1p c activating protein kinase (by homol hypothetical start
												KLLA0D11990g	gi|2499590|sp|Q92241|PH85_KLU Kluyveromyces lactis NEGATIV REGULATOR OF THE PHO SYS hypothetical start
												YALI0D04114g	weakly similar to tr|Q8X0V5 Neuro crassa Related to putative dual speci protein kinase pom1, hypothetical
												CAGL0K04169g	similar to sp|P14681 Saccharomy cerevisiae YGR040w KSS1, start similarity
												KLLA0E07414g	highly similar to sp|P21965 Saccharomyces cerevisiae YNL30 MCK1 ser/thr/tyr protein kinase, sta similarity
												YALI0B18700g	similar to tr|Q8TG13 Neurospora c Casein kinase II alpha subunit CKA by similarity
												YALI0D16863g	tr|Q92390 Yarrowia lipolytica case kinase II catalytic subunit, identified
												KLLA0C04345g	similar to sp|P06243 Saccharomy cerevisiae YDL017w CDC7 prot kinase, start by similarity
												CAGL0H10318g	highly similar to sp|P06242 Saccharomyces cerevisiae YDL10 KIN28 cyclin-dependent ser/thr pro kinase
												YALI0B22528g	weakly similar to tr|O14098 Schizosaccharomyces pombe Puta serine/threonine protein kinase, sta similarity
												DEHA0G22528g	highly similar to CA3004|CaKIN Candida albicans CaKIN28, start similarity
												KLLA0B11946g	similar to sp|P41808 Saccharomy cerevisiae YPR054w SMK1 sporula specific MAP kinase, start by simil
												DEHA0F26268g	similar to sp|P41808 Saccharomy cerevisiae YPR054w Sporulation specific mitogen-activated protein k SMK1 (MAP kinase SMK1), hypothetical start, frameshift
												KLLA0B09790g	highly similar to sp|P00546 Saccharomyces cerevisiae YBR16 CDC28 cyclin-dependent protein ki start by similarity
												DEHA0F26257g	similar to sp|P41808 Saccharomy cerevisiae YPR054w Sporulation specific mitogen-activated protein k SMK1 (MAP kinase SMK1), hypothetical start, frameshift
												YALI0F03113g	some similarities with sp|P3258 Saccharomyces cerevisiae YJL10 IME2 ser/thr protein kinase, hypoth start

												KLLA0F16467g	highly similar to sp|P19454 Saccharomyces cerevisiae YOR06 CKA2 casein kinase II alpha chain, by similarity
												CAGL0L12474g	highly similar to sp|P17157 Saccharomyces cerevisiae YPL03 cyclin-dependent protein kinase, sta similarity
												CAGL0M11748g	highly similar to sp|P32485 Saccharomyces cerevisiae YLR11 HOG1, start by similarity
												CAGL0E01683g	highly similar to sp|P21965 Saccharomyces cerevisiae YNL30 MCK1 or sp|Q12222 Saccharomy cerevisiae YOL128c, start by simil
												KLLA0A02497g	highly similar to sp|P14681 Saccharomyces cerevisiae YGR04 KSS1 ser/thr protein kinase of the kinase family, start by similarit
												CAGL0J04290g	similar to sp|P16892 Saccharomy cerevisiae YBL016w FUS3 or sp|P1 Saccharomyces cerevisiae YGR04 KSS1, start by similarity
												KLLA0A05819g	similar to sp|P14680 Saccharomy cerevisiae YJL141c YAK1 ser/thr p kinase, start by similarity
												YALI0D20966g	highly similar to tr|Q9HE92 Neuros crassa Probable glycogen synthase k 3 alpha, start by similarity
												KLLA0F08877g	gi|27526975|emb|CAD36965.1 Kluyveromyces lactis cyclin-depen kinase activating kinase 1, start b similarity
												DEHA0E05819g	highly similar to CA2027|CaMC Candida albicans CaMCK1 ser/thr protein kinase, hypothetical star
												DEHA0C07469g	highly similar to sp|P19454 Saccharomyces cerevisiae YOR06 CKA2, hypothetical start
												YALI0E11077g	similar to sp|Q07538 Schizosaccharomyces pombe SPCC777.14 PRP4 Serine/threoni protein kinase, hypothetical star
												DEHA0E19217g	similar to sp|Q00772 Saccharomy cerevisiae YHR030c SLT2 ser/thr p kinase of MAP kinase family P108.1.f12.1 Length = 484, start similarity
												KLLA0F17006g	gi|3127831|emb|CAA61157.1 Kluyveromyces lactis protein kina start by similarity
												KLLA0E10527g	similar to sp|P16892 Saccharomy cerevisiae YBL016w FUS3 mitog activated protein kinase (MAP kin start by similarity
												YALI0D19492g	similar to wi|NCU07880.1 Neurosp crassa NCU07880.1 hypothetical pr (15912 - 17477), hypothetical st
												YALI0B10758g	highly similar to sp|P43063 Cand albicans cell division control protei hypothetical start
												DEHA0F09735g	similar to ca|CA1468|CaSRB10 Ca albicans CaSRB10 cyclin-depend kinase by homology, 3 end, hypoth start
												DEHA0F09647g	similar to wi|NCU04185.1 Neurosp crassa NCU04185.1 hypothetical pr ((AL451015) probable glycoge synthase kinase 3 alpha [Neurosp crassa]) (47604 - 49112), hypothe start
												DEHA0G11660g	highly similar to sp|P43063 Cand albicans Cell division control prote (EC 2.7.1.-), hypothetical start
													highly similar to CA4448|CaPHO

													DEHA0D14256g	Candida albicans CaPHO85 Nega regulator of PHO system, start b similarity
													YALI0C10967g	similar to sp|P39073 Saccharomy cerevisiae YPL042c SSN3 cyclin dependent CTD kinase, hypothetica
													CAGL0K12496g	similar to sp|P43568 Saccharomy cerevisiae YFL029c CAK1 cdk activating protein kinase, hypothet start
													CAGL0L12650g	similar to sp|P39073 Saccharomy cerevisiae YPL042c cyclin-depend CTD kinase, hypothetical start
													CAGL0G04455g	similar to sp|P32581 Saccharomy cerevisiae YJL106w IME2 ser/thr p kinase, hypothetical start
													KLLA0E04136g	similar to sp|P15790 Saccharomy cerevisiae YIL035c CKA1 casein k II, catalytic alpha chain, start by similarity
													CAGL0H07535g	highly similar to sp|P00546 Saccharomyces cerevisiae YBR16 CDC28, start by similarity
													CAGL0I05192g	highly similar to sp|P15790 Saccharomyces cerevisiae YIL03 CKA1 casein kinase II, start by simi
													DEHA0E04290g	highly similar to CA0722|CaERK Candida albicans CaERK1 mitog activated protein kinase (FUS3 homolog), hypothetical start
													YALI0C24321g	weakly similar to sp|P43568 Saccharomyces cerevisiae YFL02 CAK1 cdk-activating protein kina hypothetical start
MKK1 (YOR231W)	2.7.1.-	sp|P32490 Saccharomyces cerevisiae YOR231w MKK1 ser/thr protein kinase P108.1.f6.1	viable	NA	NA	NA	NA	NA	sckdy	7 5 4 4 3	GLC.52		YALI0F21065g	tr|Q9Y7W8 Yarrowia lipolytica ser/thr/tyr MAP kinase kinase, no
													YALI0B15906g	similar to sp|P08018 Saccharomy cerevisiae YJL128c PBS2 tyrosin protein kinase of the MAP kinase k family P108.1.f2.4, start by simila
													DEHA0B12672g	similar to sp|O14427 Candida albic Serine/threonine-protein kinase CL start by similarity
													CAGL0M03729g	similar to sp|P48562 Saccharomy cerevisiae YNL298w CLA4, start similarity
													KLLA0A07403g	similar to sp|P48562 Saccharomy cerevisiae YNL298w CLA4 ser/t protein kinase, start by similarit
													CAGL0L05632g	similar to sp|P08018 Saccharomy cerevisiae YJL128c PBS2, hypothe start
													KLLA0E15378g	some similarities with sp|P0801 Saccharomyces cerevisiae YJL12 PBS2 tyrosine protein kinase of the kinase kinase family, hypothetical
													CAGL0I03498g	similar to sp|P06784 Saccharomy cerevisiae YDL159w STE7 ser/thr protein kinase of MAP kinase kin family, hypothetical start
													CAGL0H01639g	similar to sp|P08458 Saccharomy cerevisiae YDR523c SPS1 ser/thr p kinase, hypothetical start
													YALI0D07502g	weakly similar to sp|P08458 Saccharomyces cerevisiae YDR52 SPS1 ser/thr protein kinase, start similarity
													DEHA0C17204g	similar to CA4577|CaMKK2 Canc albicans, start by similarity
													KLLA0C16577g	some similarities with sp|P0678 Saccharomyces cerevisiae YDL15 STE7 ser/thr/tyr protein kinase of M kinase kinase family, hypothetical
														some similarities with sp|P3249

												KLLA0D07304g	Saccharomyces cerevisiae YPL14 MKK2 protein kinase of the map k kinase (MEK) family, hypothetical
												CAGL0J03828g	similar to sp|P32490 Saccharomy cerevisiae YOR231w MKK1 ser/ protein kinase or sp|P32491 Saccharomyces cerevisiae YPL14 MKK2, start by similarity
												DEHA0C09416g	similar to sp|P08018 Saccharomy cerevisiae YJL128c PBS2, hypothe start
												DEHA0F15719g	similar to ca|CA1623|CaSTE7 Can albicans CaSTE7 MAP Kinase Kir hypothetical start
												DEHA0C07139g	some similarities with sp|P2329 Saccharomyces cerevisiae YPR16 SGV1 ser/thr protein kinase, hypoth start
												KLLA0E14828g	gi|27526973|emb|CAD36964.1 Kluyveromyces lactis serine/threon protein kinase KIN28, start by simi
												DEHA0C06314g	some similarities with sp|P0624 Saccharomyces cerevisiae YDL01 CDC7, hypothetical start
												DEHA0B08701g	similar to CA4995|CaYAK1 Cand albicans CaYAK1 putative Ser/t protein kinase, hypothetical star
												CAGL0J00539g	highly similar to sp|Q00772 Saccharomyces cerevisiae YHR03 SLT2, hypothetical start
												KLLA0E12177g	gi|4096112|gb|AAC99804.1 Kluyveromyces lactis CTD kinase la subunit, hypothetical start
												DEHA0B00770g	similar to sp|P32581 Saccharomy cerevisiae YJL106w IME2 ser/thr p kinase, hypothetical start
												YALI0D25190g	highly similar to sp|P17157 Saccharomyces cerevisiae YPL03 PHO85, hypothetical start
												DEHA0E21219g	similar to CA1378|CaERK2 Cand albicans CaERK2 mitogen-activa protein kinase, start by similarit
												DEHA0F08987g	similar to CAGL-IPF1383.1 Cand glabrata, hypothetical start
												CAGL0I05896g	some similarities with sp|P1468 Saccharomyces cerevisiae YJL14 YAK1 ser/thr protein kinase, hypothetical start
												KLLA0F20053g	highly similar to sp|P32485 Saccharomyces cerevisiae YLR11 HOG1 ser/thr protein kinase of M kinase (MAPK) family, start by similarity
												DEHA0E22110g	sp|Q9UV50 Debaryomyces hanse Mitogen-activated protein kinase H identified start
												DEHA0A14080g	highly similar to CA6039|CaCK Candida albicans CaCKA1 casein k II, catalytic alpha chain, start by similarity
												YALI0E33803g	similar to tr|Q9Y7V6 Emericell nidulans MAP protein kinase MPK hypothetical start
												YALI0E25135g	highly similar to sp|P32485 Saccharomyces cerevisiae YLR11 HOG1 ser/thr protein kinase of M kinase (MAPK) family, hypothetica
												YALI0E23496g	highly similar to tr|Q9UW09 Glom lagenarium Mitogen activated pro kinase, hypothetical start
												CAGL0L06820g	highly similar to sp|P38615 Saccharomyces cerevisiae YMR13 MDS1 Serine/threonine-protein ki
													highly similar to sp|P19454

SSN3	2.7.1.-	sp|P39073 Saccharomyces cerevisiae YPL042c	exhibits growth defect on a non-	NA	NA	NA	NA	NA	sckdy	22 19 19 21	GLC.8	CAGL0G02035g	Saccharomyces cerevisiae YOR06 CKA2 casein kinase II alpha chain, by similarity
												DEHA0G02750g	similar to CA4014|CaCTK1 Cand albicans CaCTK1 probable cell div protein kinase, start by similarit
												YALI0B02816g	similar to sp|Q00772 Saccharomy cerevisiae Mitogen-activated prot kinase SLT2/MPK1 (EC 2.7.1.-) (M kinase MPK1), start by similarit
												KLLA0D11814g	similar to sp|P39073 Saccharomy cerevisiae YPL042c SSN3 cyclin dependent CTD kinase, start by simi
												KLLA0B11902g	gi|7385125|gb|AAF61706.1|AF2267 Kluyveromyces lactis MAP kinase, by similarity
												CAGL0D02002g	similar to sp|Q03957 Saccharomy cerevisiae YKL139w CTK1 carbo terminal domain kinase, hypotheti start
												KLLA0F02838g	some similarities with sp|P3258 Saccharomyces cerevisiae YJL10 IME2 ser/thr protein kinase, hypoth start
												KLLA0D10527g	similar to sp|P23293 Saccharomy cerevisiae YPR161c SGV1 ser/t protein kinase, hypothetical star
												CAGL0D01694g	similar to sp|P41808 Saccharomy cerevisiae YPR054w SMK1 sporula specific MAP kinase, hypothetical
												YALI0D04334g	similar to sp|P06242 Saccharomy cerevisiae YDL108w KIN28 cycl dependent ser/thr protein kinase, sta similarity
												CAGL0I08349g	similar to sp|P23293 Saccharomy cerevisiae YPR161c SGV1 ser/t protein kinase, hypothetical star
												CAGL0K01815g	similar to sp|P06243 Saccharomy cerevisiae YDL017w Cell divisio control protein 7, hypothetical st
												DEHA0F09713g	similar to ca|CA1467|IPF5082 Can albicans IPF5082 similar to Saccharomyces cerevisiae Cak1p c activating protein kinase (by homol hypothetical start
												KLLA0D11990g	gi|2499590|sp|Q92241|PH85_KLU Kluyveromyces lactis NEGATIV REGULATOR OF THE PHO SYST hypothetical start
												YALI0D04114g	weakly similar to tr|Q8X0V5 Neuro crassa Related to putative dual speci protein kinase pom1, hypothetical
												CAGL0K04169g	similar to sp|P14681 Saccharomy cerevisiae YGR040w KSS1, start similarity
												KLLA0E07414g	highly similar to sp|P21965 Saccharomyces cerevisiae YNL30 MCK1 ser/thr/tyr protein kinase, sta similarity
												YALI0B18700g	similar to tr|Q8TG13 Neurospora c Casein kinase II alpha subunit CKA by similarity
												YALI0D16863g	tr|Q92390 Yarrowia lipolytica case kinase II catalytic subunit, identified
												KLLA0C04345g	similar to sp|P06243 Saccharomy cerevisiae YDL017w CDC7 prot kinase, start by similarity
												CAGL0H10318g	highly similar to sp|P06242 Saccharomyces cerevisiae YDL10 KIN28 cyclin-dependent ser/thr pro kinase
												YALI0B22528g	weakly similar to tr|O14098 Schizosaccharomyces pombe Puta serine/threonine protein kinase, sta

(YPL042C)		SSN3 cyclin-dependent CTD kinase P108.1.f2.5	fermentable (respiratory) carbon source							17			similarity
												DEHA0G22528g	highly similar to CA3004|CaKIN Candida albicans CaKIN28, start similarity
												KLLA0B11946g	similar to sp|P41808 Saccharomy cerevisiae YPR054w SMK1 sporula specific MAP kinase, start by simil
												DEHA0F26268g	similar to sp|P41808 Saccharomy cerevisiae YPR054w Sporulation specific mitogen-activated protein k SMK1 (MAP kinase SMK1), hypothetical start, frameshift
												KLLA0B09790g	highly similar to sp|P00546 Saccharomyces cerevisiae YBR16 CDC28 cyclin-dependent protein ki start by similarity
												DEHA0F26257g	similar to sp|P41808 Saccharomy cerevisiae YPR054w Sporulation specific mitogen-activated protein k SMK1 (MAP kinase SMK1), hypothetical start, frameshift
												YALI0F03113g	some similarities with sp|P3258 Saccharomyces cerevisiae YJL10 IME2 ser/thr protein kinase, hypoth start
												KLLA0F16467g	highly similar to sp|P19454 Saccharomyces cerevisiae YOR06 CKA2 casein kinase II alpha chain, by similarity
												CAGL0L12474g	highly similar to sp|P17157 Saccharomyces cerevisiae YPL03 cyclin-dependent protein kinase, sta similarity
												CAGL0M11748g	highly similar to sp|P32485 Saccharomyces cerevisiae YLR11 HOG1, start by similarity
												CAGL0E01683g	highly similar to sp|P21965 Saccharomyces cerevisiae YNL30 MCK1 or sp|Q12222 Saccharomy cerevisiae YOL128c, start by simil
												KLLA0A02497g	highly similar to sp|P14681 Saccharomyces cerevisiae YGR04 KSS1 ser/thr protein kinase of the kinase family, start by similarity
												CAGL0J04290g	similar to sp|P16892 Saccharomy cerevisiae YBL016w FUS3 or sp|P1 Saccharomyces cerevisiae YGR04 KSS1, start by similarity
												KLLA0A05819g	similar to sp|P14680 Saccharomy cerevisiae YJL141c YAK1 ser/thr p kinase, start by similarity
												YALI0D20966g	highly similar to tr|Q9HE92 Neuros crassa Probable glycogen synthase k 3 alpha, start by similarity
												KLLA0F08877g	gi|27526975|emb|CAD36965.1 Kluyveromyces lactis cyclin-depen kinase activating kinase 1, start b similarity
												DEHA0E05819g	highly similar to CA2027|CaMC Candida albicans CaMCK1 ser/thr protein kinase, hypothetical star
												DEHA0C07469g	highly similar to sp|P19454 Saccharomyces cerevisiae YOR06 CKA2, hypothetical start
												YALI0E11077g	similar to sp|Q07538 Schizosaccharomyces pombe SPCC777.14 PRP4 Serine/threoni protein kinase, hypothetical star
												DEHA0E19217g	similar to sp|Q00772 Saccharomy cerevisiae YHR030c SLT2 ser/thr p kinase of MAP kinase family P108.1.f12.1 Length = 484, start similarity
												KLLA0F17006g	gi|3127831|emb|CAA61157.1 Kluyveromyces lactis protein kina

													start by similarity
												KLLA0E10527g	similar to sp|P16892 Saccharomy cerevisiae YBL016w FUS3 mitog activated protein kinase (MAP kin start by similarity
												YALI0D19492g	similar to wi|NCU07880.1 Neurosp crassa NCU07880.1 hypothetical pr (15912 - 17477), hypothetical sta
												YALI0B10758g	highly similar to sp|P43063 Cand albicans cell division control protei hypothetical start
												DEHA0F09735g	similar to ca|CA1468|CaSRB10 Ca albicans CaSRB10 cyclin-depend kinase by homology, 3 end, hypothe start
												DEHA0F09647g	similar to wi|NCU04185.1 Neurosp crassa NCU04185.1 hypothetical pr ((AL451015) probable glycoge synthase kinase 3 alpha [Neurosp crassa]) (47604 - 49112), hypothe start
												DEHA0G11660g	highly similar to sp|P43063 Cand albicans Cell division control prote (EC 2.7.1.-), hypothetical start
												DEHA0D14256g	highly similar to CA4448|CaPHO Candida albicans CaPHO85 Nega regulator of PHO system, start b similarity
												YALI0C10967g	similar to sp|P39073 Saccharomy cerevisiae YPL042c SSN3 cycli dependent CTD kinase, hypothetica
												CAGL0K12496g	similar to sp|P43568 Saccharomy cerevisiae YFL029c CAK1 cdk activating protein kinase, hypothet start
												CAGL0L12650g	similar to sp|P39073 Saccharomy cerevisiae YPL042c cyclin-depend CTD kinase, hypothetical start
												CAGL0G04455g	similar to sp|P32581 Saccharomy cerevisiae YJL106w IME2 ser/thr p kinase, hypothetical start
												KLLA0E04136g	similar to sp|P15790 Saccharomy cerevisiae YIL035c CKA1 casein k II, catalytic alpha chain, start by similarity
												CAGL0H07535g	highly similar to sp|P00546 Saccharomyces cerevisiae YBR16 CDC28, start by similarity
												CAGL0I05192g	highly similar to sp|P15790 Saccharomyces cerevisiae YIL03 CKA1 casein kinase II, start by simi
												DEHA0E04290g	highly similar to CA0722|CaERK Candida albicans CaERK1 mitog activated protein kinase (FUS3 homolog), hypothetical start
												YALI0C24321g	weakly similar to sp|P43568 Saccharomyces cerevisiae YFL02 CAK1 cdk-activating protein kina hypothetical start
												YALI0F21065g	tr|Q9Y7W8 Yarrowia lipolytica ser/thr/tyr MAP kinase kinase, no
												YALI0B15906g	similar to sp|P08018 Saccharomy cerevisiae YJL128c PBS2 tyrosi protein kinase of the MAP kinase k family P108.1.f2.4, start by simila
												DEHA0B12672g	similar to sp|O14427 Candida albi Serine/threonine-protein kinase CI start by similarity
												CAGL0M03729g	similar to sp|P48562 Saccharomy cerevisiae YNL298w CLA4, start similarity
												KLLA0A07403g	similar to sp|P48562 Saccharomy cerevisiae YNL298w CLA4 ser/t protein kinase, start by similarit

MKK2 (YPL140C)	2.7.1.-	sp|P32491 Saccharomyces cerevisiae YPL140c MKK2 protein kinase of the map kinase kinase (MEK) family P108.1.f6.1	viable	0.2	Ess	Ess	Ess	Ess	sckdy	7 5 4 4 3	GLC.52	CAGL0L05632g	similar to sp|P08018 Saccharomy cerevisiae YJL128c PBS2, hypothe start
												KLLA0E15378g	some similarities with sp|P0801 Saccharomyces cerevisiae YJL12 PBS2 tyrosine protein kinase of the kinase kinase family, hypothetical
												CAGL0I03498g	similar to sp|P06784 Saccharomy cerevisiae YDL159w STE7 ser/thr protein kinase of MAP kinase kin family, hypothetical start
												CAGL0H01639g	similar to sp|P08458 Saccharomy cerevisiae YDR523c SPS1 ser/thr p kinase, hypothetical start
												YALI0D07502g	weakly similar to sp|P08458 Saccharomyces cerevisiae YDR52 SPS1 ser/thr protein kinase, start similarity
												DEHA0C17204g	similar to CA4577|CaMKK2 Canc albicans, start by similarity
												KLLA0C16577g	some similarities with sp|P0678 Saccharomyces cerevisiae YDL15 STE7 ser/thr/tyr protein kinase of M kinase kinase family, hypothetical
												KLLA0D07304g	some similarities with sp|P3249 Saccharomyces cerevisiae YPL14 MKK2 protein kinase of the map k kinase (MEK) family, hypothetical
												CAGL0J03828g	similar to sp|P32490 Saccharomy cerevisiae YOR231w MKK1 ser/ protein kinase or sp|P32491 Saccharomyces cerevisiae YPL14 MKK2, start by similarity
												DEHA0C09416g	similar to sp|P08018 Saccharomy cerevisiae YJL128c PBS2, hypothe start
												DEHA0F15719g	similar to ca|CA1623|CaSTE7 Can albicans CaSTE7 MAP Kinase Kin hypothetical start
HRR25 (YPL204W)	2.7.1.-	sp|P29295 Saccharomyces cerevisiae YPL204w HRR25 casein kinase I, ser/thr/tyr protein kinase P108.1.f4.1	inviable	Ess	Ess	Ess	0.1	Ess	sckdy	4 4 2 2 2	GLC.92	KLLA0D11044g	gi|730472|sp|P40230|RAG8_KLU Kluyveromyces lactis CASEIN KIN I HOMOLOG RAG8, start by simil
												YALI0E26609g	similar to tr|CAD79679 Neurospo crassa, start by similarity
												DEHA0A09933g	similar to sp|P23292 Saccharomy cerevisiae YNL154c YCK2 casein k I isoform, hypothetical start
												CAGL0G06138g	similar to sp|P23291 Saccharomy cerevisiae YHR135c YCK1, start similarity
												DEHA0D04466g	similar to YALI-IPF3384.1 Yarro lipolytica, start by similarity
												YALI0F08305g	similar to sp|P29295 Saccharomy cerevisiae YPL204w HRR25 cas kinase I, start by similarity
												CAGL0H03553g	highly similar to sp|P29295 Saccharomyces cerevisiae YPL20 HRR25, start by similarity
												CAGL0J05940g	similar to sp|P23291 Saccharomy cerevisiae YHR135c YCK1 or sp|P2 Saccharomyces cerevisiae YNL15 YCK2, hypothetical start
												CAGL0K02299g	similar to sp|P39962 Saccharomy cerevisiae YER123w Casein kinas hypothetical start
												KLLA0E13563g	some similarities with sp|P3996 Saccharomyces cerevisiae YER12 YCK3 casein kinase, isoform 3 hypothetical start
												YALI0B22066g	highly similar to wi|NCU01680. Neurospora crassa NCU01680.1 pla membrane ATPase (proton pump hypothetical start
													similar to sp|Q12691 Saccharomy

ENA5 (YDR038C)	3.6.1.-	sp|Q12691 Saccharomyces cerevisiae YDR038c ENA5 P-type ATPase involved in Na+ efflux P16.2.f7.1	-	NA	NA	NA	NA	NA	sckdy	5 4 4 4 5	GLC.54	YALI0A01023g	cerevisiae YDR038c ENA5 P-ty ATPase involved in Na+ efflux, sta similarity
												DEHA0A09295g	similar to sp|P38929 Saccharomy cerevisiae YGL006w PMC1 Ca2 transporting P-type ATPase, hypoth start
												CAGL0A00517g	similar to sp|P38929 Saccharomy cerevisiae YGL006w PMC1, hypothetical start
												YALI0E19338g	similar to tr|Q96X39 Debaryomy hansenii Plasma membrane Na+ AT hypothetical start
												YALI0E09471g	sp|O43108 Yarrowia lipolytica Calc transporting ATPase 1, identified s
												DEHA0G09878g	tr|Q96X39 Debaryomyces hanse Plasma membrane Na+ ATPase identified start
												KLLA0F20658g	similar to sp|Q12691 Saccharomy cerevisiae YDR038c ENA5 P-ty ATPase involved in Na+ efflux, sta similarity
												DEHA0F14619g	highly similar to tr|Q9P872 Cand albicans Calcium/mangenease P-t ATPase PMR1, start by similari
												CAGL0J01870g	highly similar to sp|P13586 Saccharomyces cerevisiae YGL1 PMR1, hypothetical start
												CAGL0I04312g	highly similar to sp|P13586 Saccharomyces cerevisiae YGL1 PMR1 Ca2+-transporting P-typ ATPase, start by similarity
												DEHA0C02937g	tr|Q9C1R0 Debaryomyces hanse ATPase ENA1p, identified star
												YALI0D04873g	similar to sp|P38929 Saccharomy cerevisiae YGL006w PMC1 Ca2 transporting P-type ATPase, start similarity
												KLLA0E14630g	similar to sp|Q01896 Saccharomy cerevisiae YDR039c ENA2 P-ty ATPase involved in Na+ efflux hypothetical start
												KLLA0A03157g	gi|3288523|emb|CAA04476.1 Kluyveromyces lactis Ca++ ATPa start by similarity
												KLLA0A08910g	similar to sp|P38929 Saccharomy cerevisiae YGL006w PMC1 Ca2 transporting P-type ATPase, start similarity
												CAGL0K12034g	highly similar to sp|P13587 Saccharomyces cerevisiae YDR0 ENA1 or sp|Q01896 Saccharomy cerevisiae YDR039c ENA2 or sp|Q Saccharomyces cerevisiae YDR0 ENA5, hypothetical start
												YALI0B22066g	highly similar to wi|NCU01680 Neurospora crassa NCU01680.1 pl membrane ATPase (proton pum hypothetical start
												YALI0A01023g	similar to sp|Q12691 Saccharomy cerevisiae YDR038c ENA5 P-ty ATPase involved in Na+ efflux, sta similarity
												DEHA0A09295g	similar to sp|P38929 Saccharomy cerevisiae YGL006w PMC1 Ca2 transporting P-type ATPase, hypoth start
												CAGL0A00517g	similar to sp|P38929 Saccharomy cerevisiae YGL006w PMC1, hypothetical start
												YALI0E19338g	similar to tr|Q96X39 Debaryomy hansenii Plasma membrane Na+ AT hypothetical start
												YALI0E09471g	sp|O43108 Yarrowia lipolytica Calc

ENA1 (YDR040C)	3.6.1.-	sp|P13587 Saccharomyces cerevisiae YDR040c ENA1 P-type ATPase involved in Na+ and Li+ efflux P16.2.f7.1	-	NA	NA	NA	NA	NA	sckdy	5 4 4 4 5	GLC.54	YALI0E09471g	transporting ATPase 1, identified s
												DEHA0G09878g	tr|Q96X39 Debaryomyces hanser Plasma membrane Na+ ATPase identified start
												KLLA0F20658g	similar to sp|Q12691 Saccharomy cerevisiae YDR038c ENA5 P-ty ATPase involved in Na+ efflux, sta similarity
												DEHA0F14619g	highly similar to tr|Q9P872 Cand albicans Calcium/mangenease P-t ATPase PMR1, start by similari
												CAGL0J01870g	highly similar to sp|P13586 Saccharomyces cerevisiae YGL1 PMR1, hypothetical start
												CAGL0I04312g	highly similar to sp|P13586 Saccharomyces cerevisiae YGL1 PMR1 Ca2+-transporting P-typ ATPase, start by similarity
												DEHA0C02937g	tr|Q9C1R0 Debaryomyces hanser ATPase ENA1p, identified star
												YALI0D04873g	similar to sp|P38929 Saccharomy cerevisiae YGL006w PMC1 Ca2 transporting P-type ATPase, start similarity
												KLLA0E14630g	similar to sp|Q01896 Saccharomy cerevisiae YDR039c ENA2 P-ty ATPase involved in Na+ efflux hypothetical start
												KLLA0A03157g	gi|3288523|emb|CAA04476.1 Kluyveromyces lactis Ca++ ATPa start by similarity
												KLLA0A08910g	similar to sp|P38929 Saccharomy cerevisiae YGL006w PMC1 Ca2 transporting P-type ATPase, start similarity
												CAGL0K12034g	highly similar to sp|P13587 Saccharomyces cerevisiae YDR0 ENA1 or sp|Q01896 Saccharomy cerevisiae YDR039c ENA2 or sp|Q Saccharomyces cerevisiae YDR0 ENA5, hypothetical start
RAD3 (YER171W)	3.6.1.-	sp|P06839 Saccharomyces cerevisiae YER171w RAD3 DNA helicase/ATPase P2.76.f2.1	inviable	0.7	Ess	Ess	0.3	Ess	sckdy	2 2 2 2 2	GLR.3298	YALI0F20746g	highly similar to sp|P06839 Saccharomyces cerevisiae YER17 RAD3 DNA helicase/ATPase, star similarity
												DEHA0A02519g	similar to CA3942|CaCHL1 Cand albicans CaCHL1 protein of the D box family, start by similarity
												CAGL0L11924g	highly similar to sp|P06839 Saccharomyces cerevisiae YER17 DNA helicase/ATPase, start by simi
												YALI0C23639g	similar to sp|P22516 Saccharomy cerevisiae YPL008w CHL1 protei the DEAH box family, start by simi
												DEHA0G12815g	highly similar to CA5581|CaRA Candida albicans CaRAD3, start similarity
												KLLA0C17776g	highly similar to sp|P06839 Saccharomyces cerevisiae YER17 RAD3 DNA helicase/ATPase, star similarity
												CAGL0L08844g	similar to sp|P22516 Saccharomy cerevisiae YPL008w CHL1 protei the DEAH box family, start by simi
												KLLA0F27181g	similar to sp|P22516 Saccharomy cerevisiae YPL008w CHL1 protei the DEAH box family, start by simi
												YALI0A13519g	similar to sp|P35207 Saccharomy cerevisiae YLR398c SKI2 antivi protein and putative helicase, hypothetical start
												CAGL0C02563g	similar to sp|P35207 Saccharomy cerevisiae YLR398c SKI2, hypothe start

BRR2 (YER172C)	3.6.1.-	sp|P32639 Saccharomyces cerevisiae YER172c BRR2 RNA helicase-related protein P5.1.f3.1	inviable	NA	NA	NA	NA	NA	sckdy	5 5 6 5 8	GLC.40	DEHA0C14025g	highly similar to sp|P47047 Saccharomyces cerevisiae YJL05 MTR4, start by similarity
												YALI0E07689g	similar to sp|P35207 Saccharomy cerevisiae YLR398c SKI2 antivi protein and putative helicase, frame
												YALI0F20724g	similar to sp|P32639 Saccharomy cerevisiae YER172c BRR2 RN helicase-related protein, start b similarity
												CAGL0H07601g	weakly similar to sp|P51979 Saccharomyces cerevisiae YGL2 HFM1, hypothetical start
												YALI0D12210g	similar to sp|P47047 Saccharomy cerevisiae ATP-dependent RNA hel DOB1, start by similarity
												KLLA0C17798g	similar to sp|P32639 Saccharomy cerevisiae YER172c BRR2 RN helicase-related protein, start b similarity
												KLLA0B03190g	similar to sp|P35207 Saccharomy cerevisiae YLR398c SKI2 antivi protein and putative helicase, hypothetical start
												DEHA0G13761g	similar to CA4411|CaBRR2 Cand albicans CaBRR2, hypothetical s
												YALI0A11869g	similar to sp|P35207 Saccharomy cerevisiae Antiviral protein SKI hypothetical start
												YALI0E07645g	similar to sp|P35207 Saccharomy cerevisiae YLR398c SKI2 antivi protein and putative helicase, frame
												YALI0E07700g	similar to sp|P35207 Saccharomy cerevisiae YLR398c SKI2 antivi protein and putative helicase, frame
												KLLA0B03179g	similar to sp|P35207 Saccharomy cerevisiae YLR398c SKI2 antivi protein and putative helicase, start similarity
												DEHA0A11715g	similar to sp|P35207 Saccharomy cerevisiae YLR398c SKI2 antivi protein and putative helicase, hypothetical start
												CAGL0G00506g	highly similar to sp|P53327 Saccharomyces cerevisiae YGR27 start by similarity
												CAGL0L11946g	similar to sp|P32639 Saccharomy cerevisiae YER172c RNA helica related protein, start by similarit
												KLLA0A09889g	highly similar to sp|P53327 Saccharomyces cerevisiae YGR27 start by similarity
												DEHA0G21681g	highly similar to CA3403|IPF86 Candida albicans IPF8650, start similarity
												KLLA0D11462g	similar to sp|P51979 Saccharomy cerevisiae YGL251c HFM1 DNA/ helicase, start by similarity
												KLLA0F01364g	highly similar to sp|P47047 Saccharomyces cerevisiae YJL05 MTR4 involved in nucleocytoplas transport of mRNA, start by simila
												CAGL0J04928g	highly similar to sp|P47047 Saccharomyces cerevisiae YJL05 MTR4, start by similarity
												YALI0B13904g	similar to sp|P53327 Saccharomy cerevisiae YGR271w strong similar S.pombe RNA helicase or sp|P32 Saccharomyces cerevisiae YER17 BRR2 RNA helicase-related prot hypothetical start
												DEHA0F08877g	similar to ca|CA4212|CaHFM1 Ca albicans CaHFM1 DNA/RNA heli by homology, start by similarit

SLH1 (YGR271W)	3.6.1.-	sp|P53327 Saccharomyces cerevisiae YGR271w strong similarity to S.pombe RNA helicase P5.1.f3.1	-	0.9	Non	Non	Non	0.6	sckdy	5 5 6 5 8	GLC.40	YALI0A13519g	similar to sp|P35207 Saccharomy cerevisiae YLR398c SKI2 antivi protein and putative helicase, hypothetical start
												CAGL0C02563g	similar to sp|P35207 Saccharomy cerevisiae YLR398c SKI2, hypothe start
												DEHA0C14025g	highly similar to sp|P47047 Saccharomyces cerevisiae YJL05 MTR4, start by similarity
												YALI0E07689g	similar to sp|P35207 Saccharomy cerevisiae YLR398c SKI2 antivi protein and putative helicase, frame
												YALI0F20724g	similar to sp|P32639 Saccharomy cerevisiae YER172c BRR2 RN helicase-related protein, start b similarity
												CAGL0H07601g	weakly similar to sp|P51979 Saccharomyces cerevisiae YGL2 HFM1, hypothetical start
												YALI0D12210g	similar to sp|P47047 Saccharomy cerevisiae ATP-dependent RNA hel DOB1, start by similarity
												KLLA0C17798g	similar to sp|P32639 Saccharomy cerevisiae YER172c BRR2 RN helicase-related protein, start b similarity
												KLLA0B03190g	similar to sp|P35207 Saccharomy cerevisiae YLR398c SKI2 antivi protein and putative helicase, hypothetical start
												DEHA0G13761g	similar to CA4411|CaBRR2 Cand albicans CaBRR2, hypothetical s
												YALI0A11869g	similar to sp|P35207 Saccharomy cerevisiae Antiviral protein SKI hypothetical start
												YALI0E07645g	similar to sp|P35207 Saccharomy cerevisiae YLR398c SKI2 antivi protein and putative helicase, frame
												YALI0E07700g	similar to sp|P35207 Saccharomy cerevisiae YLR398c SKI2 antivi protein and putative helicase, frame
												KLLA0B03179g	similar to sp|P35207 Saccharomy cerevisiae YLR398c SKI2 antivi protein and putative helicase, star similarity
												DEHA0A11715g	similar to sp|P35207 Saccharomy cerevisiae YLR398c SKI2 antivi protein and putative helicase, hypothetical start
												CAGL0G00506g	highly similar to sp|P53327 Saccharomyces cerevisiae YGR27 start by similarity
												CAGL0L11946g	similar to sp|P32639 Saccharomy cerevisiae YER172c RNA helica related protein, start by similarit
												KLLA0A09889g	highly similar to sp|P53327 Saccharomyces cerevisiae YGR27 start by similarity
												DEHA0G21681g	highly similar to CA3403|IPF86 Candida albicans IPF8650, start similarity
												KLLA0D11462g	similar to sp|P51979 Saccharomy cerevisiae YGL251c HFM1 DNA/ helicase, start by similarity
												KLLA0F01364g	highly similar to sp|P47047 Saccharomyces cerevisiae YJL05 MTR4 involved in nucleocytoplas transport of mRNA, start by simila
												CAGL0J04928g	highly similar to sp|P47047 Saccharomyces cerevisiae YJL05 MTR4, start by similarity
													similar to sp|P53327 Saccharomy cerevisiae YGR271w strong similar

												YALI0B13904g	S.pombe RNA helicase or sp|P32 Saccharomyces cerevisiae YER17 BRR2 RNA helicase-related prot hypothetical start
												DEHA0F08877g	similar to ca|CA4212|CaHFM1 Can albicans CaHFM1 DNA/RNA heli by homology, start by similarity
HPR5 (YJL092W)	3.6.1.-	sp|P12954 Saccharomyces cerevisiae YJL092w HPR5 ATP-dependent DNA helicase P2.136.f2.1	viable	Ess	Ess	Ess	Ess	Ess	sckdy	2 2 3 2 1	GLR.3280	KLLA0C03674g	similar to sgd|S0005455 Saccharom cerevisiae YOL095c HMI1 mitochondrial DNA helicase, start similarity
												DEHA0B14509g	weakly similar to sp|P12954 Saccharomyces cerevisiae YJL09 HPR5 ATP-dependent DNA helic start by similarity
												CAGL0L03454g	similar to sp|P12954 Saccharomy cerevisiae YJL092w HPR5 ATP dependent DNA helicase, hypothe start
												KLLA0F14234g	weakly similar to sp|P12954 Saccharomyces cerevisiae YJL09 HPR5 ATP-dependent DNA helic hypothetical start
												KLLA0F14256g	weakly similar to sp|P12954 Saccharomyces cerevisiae YJL09 HPR5 ATP-dependent DNA helic start by similarity
												CAGL0I07623g	similar to tr|Q12039 Saccharomy cerevisiae YOL095c HMI1, hypoth start
												DEHA0A13948g	weakly similar to tr|Q12039 Saccharomyces cerevisiae YOL0 HMI1 mitochondrial DNA helica hypothetical start
												YALI0E27269g	weakly similar to sp|P12954 Saccharomyces cerevisiae YJL09 HPR5 ATP-dependent DNA helic hypothetical start
DDP1 (YOR163W)	3.6.1.-	sp|Q99321 Saccharomyces cerevisiae YOR163w DDP1 diadenosine hexaphosphate (Ap6A) hydrolase singleton	viable	NA	NA	NA	NA	NA	sckdy	1 1 1 1 1	GLR.894	DEHA0F15389g	similar to sp|Q99321 Saccharomy cerevisiae YOR163w DDP1 diaden hexaphosphate (Ap6A) hydrolas hypothetical start
												YALI0A04675g	similar to sp|Q99321 Saccharomy cerevisiae Diadenosine and diphosphoinositol polyphosphat phosphohydrolase 1 (EC 3.6.1.- (Diadenosine 5, 5 -P1, P6-hexaphos hydrolase) (AP6A hydrolase), star similarity
												KLLA0F20273g	similar to sp|Q99321 Saccharomy cerevisiae YOR163w DDP1 diaden hexaphosphate (Ap6A) hydrolas singleton, start by similarity
												CAGL0L04422g	similar to sp|Q99321 Saccharomy cerevisiae YOR163w DDP1, hypothetical start

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'Ess' indicates that the gene is essential for growth under the condition tested.
'Non' indicates that the gene is not essential.
A number indicates that the gene when mutated exhibits an intermediate phenotype; the number is the relative growth score.
'ND' indicates that no data are available.
'NA' indicates that no gene deletion experiments are available.

N.B. : conservation percentage color code 0% 1% to 20% 21% to 40% 41% to 60% 61% to 80% 81% to 90% 91% to 99% 100%

URL: http://cbi.labri.fr/Genolevures/path/pathway-00500.html
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