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## Kinetics, dynamics and localization of basic amino acid transporters in *Saccharomyces cerevisiae*

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# Appendix 1

Systematic Name	Standard Name	TOPCONS > # TMS	C-terminus > Length	C-terminus > Topology	C-terminus > Sequence
YCL025C	Agp1p	12	52	in	HKDWKLFIRADKIDLDHSRQIFDEELIKQEDEEYRERLRNGPYWKRVAFWC
YBR132C	Agp2p	12	41	in	WKRKGDHFKNPHEIDFSEKTELIEHENIESSFEKFQYYSKA
YFL055W	Agp3p	12	57	in	KSNHFRTVDLRSINLDEGRRKDMEADLSDQESSLASSETMKDYKSATFFRYLSNIFT
YNL270C	Alp1p	10	46	in	QVWFKCRLLWKLQDIDSDRRQIEELVWIEPECKTRWQRVWVVLVS
YOL130W	Alr1p	2	66	in	ASYWIKRIDPPATLNEAAESGAKSVISSFLPKRKNRFNDRSKININVRAGPSNKSVASLPSRYSRYD
YFL050C	Alr2p	2	79	in	GVLLLLAVISWFLASYWIKKIDPPATLNEAAGSGAKSVISSFLPKRDKRFNDDSKNGNARVGVRRKSTVSLPSRYSRYN
YNL065W	Aqr1p	12	36	in	KWREDRLKQQRQSWLNTLAVKAKKGTQRQDNHN
YPR192W	Aqy1p	6	36	in	QLDYTTYVTAEKAASSTKEKAQKKGSTSSSAVAEV
YHL040C	Arn1p	14	44	in	RDPKLTDTVAVEYIEDGEYVDTKNDNPILDWFEKLPKFTFKRE
YHL047C	Arn2p	14	42	in	RDPRLTEDFAQKLPDREYVQTKEDDPINDWIAKRFKALGRS
YPR201W	Arr3p	10	10	in	KPYIWNRRN
YCL038C	Atg22p	12	24	in	DVKRGRREAELSQVLPESERRLD
YML116W	Atr1p	14	20	in	ESFIKRRARAAAAYDCTVA
YJR001W	Avt1p	11	1	out	S
YKL146W	Avt3p	11	7	out	TIKMWSQ
YNL101W	Avt4p	11	4	out	IFGV
YER119C	Avt6p	11	3	out	KLN
YGR224W	Azr1p	14	10	in	SNKKVTASLR
YBR068C	Bap2p	12	52	in	NRDFTLLNPLDKIDLDFHRRYDPELMRQEDEENKEKLRNMSLMRKAYHFWC
YDR046C	Bap3p	12	52	in	KRDFTLNPLDKIDLDFHRRYDPEIMRQEDEENKERLKNSSIFVRVYKFWC
YNR056C	Bio5p	12	1	in	I
YLL015W	Bpt1p	16	330	out	TKRQLSSGMVGLLMSYSLEVTGSLTWIWRVTTVTIETNIVSVERIVEY- CELPEAQSNPEKRPDENWPSKGGIEFKNYSTYRENLDVPLN- NINVKIEPCEKVGIVGRTGAGKSTLSLALFRILEPTEGKIIIDGIDISDI- GLFDLRSHLAIIIPQDAQAFEGTVKTNLDPFNRYSEDELKRAVEQAHLK- PHLEKMLHSPKPRGDDSNEDGNVNDILDVKNENGSNLVSGQRQLL- CLARALLNRSKILVLDATASVDMETDKIIQDTRREFKDRITLITIAH- RIDTVLSDSKIIVLQGSVREFDPSKLLSDKTSIFYSLCEKGGYLK
YEL063C	Can1p	12	43	in	FRCRFIWKIGDVIDSDRRDIEAIVWEDHEPKTFWDFKFWNVVA
YLR220W	Ccc1p	5	1	out	G
YGR217W	Cch1p	24	273	in	IIGNFSYVYRSGGSRGINRSEIKKIEAWSKFDTGTGELESYLPRIM- HSFDGPLSFKIWEGRLTIKSLVENYMEVNPDDPYDKIDLIGLNKELN- TIDKAKIIQRKLYRRFVQSIHYTNAYNGCIRFSDLLQIPLYTAY- SARECLGDQYVHHLYLIGKVDKYLENQRFNFDVLEMVVTRWKFCHRM- KRTIEPEWVDKPTVSSHISININVLNLEPAPGILEREPATPRMDYGVN- NFMWSPRMNQDSTMEPPEPIDNDDSANLDIR
YOR316C	Cot1p	6	144	in	SCKASKILLQATPSTLSGDQVEGDLKIPGIIAHDFHWNLTESIFI- ASLHIQLDISPEQFTDLAKIVRSKLRHYGIHSATLQPEFITREVTSTER- AGDSQGDHLQNDPLSLRPKTYGTGISGSTCLIDDAANCNTADCLEDH
YPR124W	Ctr1p	3	122	in	KIAMLKRWDIQREIQKAKSCPGFGNCQGRHPEPSPDPIAVADTTSGS- DQSTRLEKNNESKVAISENNQKQKPTQEEGCNATDSGNQANIER- DILENSKLEQESGNMQNLLPAEKFTHN

YHR175W	Ctr2p	3	16	in	CTSYSPEIDSSLACH
YJR152W	Dat5p	12	40	in	LRENKRRDKIAAERGFPETEENLEFSDLDFENPNFRYTL
YPL265W	Dip5p	12	60	in	KLIYKTKVIKSTDVLDYTFKEIYDREEEEGRMKDQKEERLKSNG-KNMEWFYKEFLGNIF
YHL016C	Dur3p	15	61	in	WEGRHGIYTTLRGLYWDLSGQTYKLREWQNSNPQDLHVVTQSJSAR-AHRQSSHFQQVEII
YOL158C	Enb1p	14	35	in	RGFTVNNKQSLSAEEREKEKLKIKQQSWLRRVIGY
YCR075C	Ers1p	5	13	out	RSRGHDLASEYPL
YCR028C	Fen2p	12	57	in	QIKENLSKKQVPYIDANDMPGEDDDDDQNENDDGDESMEVELH-NEEMAEISNPFRR
YMR319C	Fet4p	7	38	in	HNWADRQRREVTALYARRRILLSYVEKRFPEVMMLEK
YBR008C	Flr1p	12	15	in	KYGPSLRTRSSYTEE
YLL043W	Fps1p	6	141	in	VCIYQGHESPVNWSLPVYKEMIMRAWFRPPGWKKRNRARRTSDLS-DFSYNDDDEEFGERMALQKTKTKSSISDNENEAGEKKVQFKSVQRG-KRTFGGIPTILEEEDSIETASLGATTSDISGLSDTSSDSESHYGNACKVVT
YBR207W	Fth1p	7	68	in	EEKYGYIPYLPISWQKKRIMKRLSIKASLDLKHHTSELNSSTSEPD-SQRRSKDSSVPLIIDSSGSAN
YER145C	Ftr1p	7	90	in	EERRGHLPTKLNQLKHLNPGYWIKNKKQELTEEQKQQLFAK-MENINFNEDGEINVENYELPEQTTSHSSSNVATDKEVLHVKADSL
YBL042C	Fui1p	12	47	in	KGIPGDAKITDRKWLEEWVEVEEFGTEREAFFEYGGVSTGYEKIRYI
YLR081W	Gat2p	12	55	in	PETKGLSLEEIQELWEEGVLVPWKSEGWIPSSRRGNNDLEDLQHD-DKPWYKAMLE
YKR039W	Gap1p	12	52	in	KRNWKLFIAPAEKMDIDTGRREVDLDDLKQEIAEKAIMATKPRWYRI-WNFWC
YCR098C	Git1p	12	67	in	PHSLESDLMKQDVEFHNYLVNGWTKMGFDET-DEESMVRTIEVEENGTCSSKNAEII SVRQVDQS
YDR508C	Gnp1p	12	52	in	KKDWSLFIADKVDVLSHRNIFDEELLKQEEDEYKERLRNGPYWKRV-LDFWC
YGR191W	Hip1p	12	52	in	TRNWTLMVKLEMDLDTGRKQVDLTLRREEMRIERETLAKRS-FVTRFLHFWC
YGL077C	Hnm1p	12	51	in	KGKKEFHAALEESENEQAESNNFDTIEDSREFSVAASDVELENEHVP-WGKK
YNR055C	Hol1p	12	22	in	GKRIRLWTKRWYLSVNLRDGV
YHR094C	Hxt1p	12	57	in	PETKGLSLEEVNDMYAEGVLPWKSASWVPPSKRGADYNADDLMHD-DQPFYKSLFSRK
YMR011W	Hxt2p	12	36	in	ETKGLTLEEVENEMYVEGVKPKWSGWSISKEKRVSEE
YDR345C	Hxt3p	12	57	in	PETKGLTLEEVDNMYAEGVLPWKSASWVPTSORGANYDADALMHD-DQPFYKMFSGKK
YHR092C	Hxt4p	12	57	in	PETKGLTLEEVDNMYAEGVLPWKSASWVPPNKRGTNYDADALMHD-DQPFYKMFSGKK
YHR096C	Hxt5p	12	58	in	PETKGLTLEEVDNMYEENLVLPWKSTKWIPSSRRRTDYDLATRND-PRPFYKRMFTKEK
YDR343C	Hxt6p	12	57	in	PETKGLTLEEVDNMYAEGVLPWKSASWVPPSRRGANYDAEEMAHD-DKPLYKRMFSTK
YJL219W	Hxt9p	12	56	in	PETKGLTLEEVDNMYLEGVPAWKSASWVPPERRTADYDADAIDHD-DRPIYKRFSS
YDR497C	Itr1p	12	52	in	ELSGLEEEVQTIKDGFNKASKALAKKRKQQVARVHELKYEPTQEI-IEDI
YOL103W	Itr2p	12	55	in	PELSGLEEEVQTIKDGFNKASKALAKKRKQVAEGAHHHLK-LEPTQEVES
YKL217W	Jen1p	11	63	out	VGHEKFRDLSSPVMKYYINQVEEYADGLSISDIVEQKTECASVKMID-SNVSKTYEEHIEIV

YNL268W	Lyp1p	12	43	in	YKCRFIWKLEDDIDSDRREIEAIIWEDDEPKNLWEKFWAAVA
YGR289C	Mal11p	12	63	in	ETTGRTFSEINELFNQGVPAKFASTVDPVDFGKGTQHDLSLAD- SISQSSSIKQRELNAAADKC
YBR298C	Mal31p	12	68	in	PETAGRTFIEINELFRLGVPARKFKSTKVPFAAAKAAAAEINVKD- PKEDLETSVVDEGRNTSSVVNK
YOL119C	Mch4p	12	13	in	SRHICVGAKLCKF
YGR121C	Mep1p	11	97	in	GYIPGMRLRISEEAEEAGMDEQIGEFAYDYVEVRRDYLLWGVDED- SQRSVDNHRVNNNAHLAAERSSSGTNSSSDNGEMIQSEKILPIHQED- PANR
YNL142W	Mep2p	11	85	in	MNAIFPLKLRLSADEEELGTDAQAIGFEITYEESTAYIEPIRSKT- SAQMPPPHENIDDKIVGNTDAEKNSTPSDASSTKNTDHIW
YPR138C	Mep3p	11	95	in	GKIPGVHLRVTEEAELGLDEDQIGEFAYDYVEVRRDYQWGVDT- DALHTTCNGANSASETNPTEDSQNSLSSATVSGQNEKSNPKLH- HAKA
YLL061W	Mmp1p	12	53	in	RRDWRHWYIKRMDIDLDSGHSLEDPEATKLERDEDKKYVSSKPLYRI- YRFFC
YKL064W	Mnr2p	2	7	in	TKRRFGF
YDL247W	Mph2p	12	64	in	PETAGKTFEINELFKLGVSAKFKSTKVPVFKPLKTSLITTPRE- ISKPLQRNSNVSHHL
YGR055W	Mup1p	12	62	in	QLLPRWGHYKLVSKDVLGEDGFWRVKIAKYVDDTIGDVTQEDGVI- ETNIIEHYKSEQEKSL
YHL036W	Mup3p	12	36	in	KFVLLPKFFHYKLLPKITYLHDGLIVTEWVKKPCLC
YLR138W	Nha1p	13	551	in	AII TLGRHLNITITLTKTFTTHTTNGDNGKSSWMQRLPSLDKAGRS- FSLHRMDTQMTLSGDEGEAEEGGRKGLAGGEDDEGLNNDQI- GSVATSGIPARPAGGMPRRRKLRSRKEKRLNRRQKLRNKGREIFSSR- SKNEMYDDELDNDLGRERLQKEKEARAATFALSTAVNTQRNEEIGMG- GDEEEDYTPKEYSNRYNNTPSFESSRSLLRGRTYVPRNRY- DGEETESEIESEDEMENESERSMASSEERRIRKMKKEEMKPGTAY- LDGNRMIIENKQGEILNQVDIEDRNEARDEVSVDSTAHSSTTT- MTNLSSSSGGRLKRILPTSLGKIHSVLDKGDKNKNSKYHAFKIDNLLI- IENEDGDVIKRYKINPHKSDDDKSKNRPNDVSVSRALTAVGLKSKAN- SGVPPPVEEKAIEGPRKGPMLKRTLPAPPRGVQDSDLDEEPS- SEEDLGDSDYNMDSSEYDDNAYESETEFERQRLNALGEMTAPADQD- DEELPPLPVEAQTGNDGPGTAEAGKKKQKSAAVKALSKTGLNKL
YDR456W	Nhx1p	11	154	in	AGMLEVLNIKTGEEDTSDEDFIEAPRAINLLNGSSIQDTL- GPYSNNSPDISIDQFAVSSNKLNPNNISTTGGNTFGGLNE- TENTSPNPARSSMDKRLNRDLKGTIFNSDSQWFQNFDEQVLKPVFLD- NVSPSLQDSATQSPADFSSQNH
YJL212C	Opt1p	13	42	out	VQYPGGKLSWGNVWKRTYDNDYKFFYLTKKGETFGYDKWW
YML123C	Pho84p	12	44	in	ETKRKTLLEEINELYHDEIPATLNFNRKNNDIESSSPSQLQHEA
YNR013C	Pho91p	13	4	out	VMGF
YGL006W	Pmc1p	10	56	in	RICPDEVAVKVFPAAFVQRFKYVFGLEFLRNKHTGKHDEEALLEES- DSPESTAFY
YKR093W	Ptr2p	12	49	in	RKYNDTEEEEMNAMYEEEDFDLNPISAPKANDIEILEPMESLRSTTKY
YOR348C	Put4p	12	49	in	TRTWQRQWWLPVSEIDVTTLGLVEIEEKSREIEEMLRPTGFKDKFLDALL
YIL120W	Qdr1p	12	31	in	KNGKQLSFDRIRANDKSAGRSVGVKNSKST
YIL121W	Qdr2p	12	18	in	RKGKELAFKRKKQELGVN
YBR043C	Qdr3p	12	20	in	KHGDYWRENYDLQLYDKID
YPL274W	Sam3p	12	53	in	RRDWKHFIYIKRSEIDLDTGCSVENLELFKAQKEAEEQLIASKPFYY- KIYRFWC
YPR198W	Sge1p	14	13	in	SSKTTTISAKKQQ
YEL065W	Sit1p	14	49	in	RNHKLTDSIALEGNDHLESKNTEFIEIEEESFLKNKFFHTFTSSKDRKD
YOL122C	Smf1p	11	11	out	VQLGMSHGDIS
YLR034C	Smf3p	11	11	out	ISYLLGADIHF

YDR160W	Ssy1p	12	47	in	GTSKIQRLDQLDMDSGRREMDRTDWEHSQYLGTYRERAKKLVTWLI
YBR069C	Tat1p	12	68	in	FKSWSFWIPAEEKIDLSHRNIFVSPSLTEIDKVDNDNDLKEYENSES- SENPNSSRSRKKFFKRMNTNFWC
YOL020W	Tat2p	12	56	in	YKQCTGKWWGVKALKDIDLETDRKDIDIEIVKQIEIAEKMYLDSRP- WYVRQFHFWC
YGR260W	Tna1p	12	38	in	KRENDKKKAIDRCNELGEPIDYDERLSDKNPEFKYMY
YJL129C	Trk1p	8	73	in	PYSLDRAILPSDRLEHIDHLEGMKLRQARTNTEDPMTEHFKRSFTD- VKHRWALGRKRTTHSRNPKRSSTL
YKR050W	Trk2p	8	65	in	NRGLPYTLDRAIMLPSDKLEQDRLQDMKAKGLLAKVGEDPMT- TYVKKRSHLKKIATKFWGKH
YDL210W	Uga4p	12	36	in	YKKKYYHGPNLSDDDYTEAVGADVITIMSKQEP
YMR088C	Vba1p	14	10	in	KHTYKRSSSS
YBR293W	Vba2p	13	10	in	DNLAKPKTRR
YCL069W	Vba3p	11	21	in	SNKKLIIPKDETPEDNLEDK
YDR119W	Vba4p	14	15	in	FNRIHCRSQNCLSL
YKR105C	Vba5p	14	19	in	KKLIIPKDDTPEDNLEDK
YDL128W	Vcx1p	11	10	out	KTLDISGNL
YBR235W	Vhc1p	13	339	out	RTHSLRVLFVEQEYHRTNETQRMKLLQVLRIDAEVLVSLDQ- FRVYNTIVKGDPIVFDYVNSKLADNEWKDLVEARDLTKPKRRF- STIEPQTIKQFTQSRKYTSQVQLGVFSMTNTRMPTNRIDTP- CESESDLDLTDLTSIRDAFSASTNISVSKDLTTKSKTGSDRTNLL- VKNLQSDVSTQSLRPVFSNTPRTRVVEDGTGEQPTLIPIAEPDL- SNGNGTSGSIGNGNKLKPVLPSPCCSKDLSVTAMQNLGFNDLP- STAQHLVNDVMTQMSKSSDLIFSTLVPALGTHEDHDASLQYV- EDLDIWLLEGLPPCMLINSQTMVTYAL
YGR065C	Vht1p	11	46	out	YKRNEKKHALGNLIYDSNKGEELEPEFVKKNMEERDGYYYLKRSS
YHL035C	Vmr1p	17	318	in	RLYSTFEMNMNSVERLKEYSSIEQENYLGHDEGRILLNNEPSWPK- DGEIEIENLSRYAPNLPVIRNVSFKVDPQSKIGIVGRTGAGKSTIIT- TALFRLEPITGCKIDGQDISKIDLVTLRRSITIIPODPILFAGTIKSN- VDPYDEYDEKIKFALSQVNLISSEHEFEVNLSEERFNSTHNKFLNLH- TEIAEGGLNLSQGERQLLFARSLLREPILLDEATSSIDYSDHLIQ- GIIRSEFNKSTILIAHRLRSVIDYDRIIIVMDAGEVKEYDRPSELLKDER- GIFYSMCRDSSGGLLELLKQJAKQSSKMMK
YNL321W	Vnx1p	15	2	out	SE
YLL048C	Ybt1p	17	328	in	LWLVRLYSEVEMNMNSVERVKEYMEIEQEPYNEHKEIPPPQWPQDG- KIEVNDLSRYAPNLPVIRNVSFSVDAQSKIGIVGRTGAGKSTIIT- FRLEPETGHKIDNIDISGVDLQRLRRSITIIPODPTLFSGTIKTNLD- PYDEFSDRQIFEALKRVNLISEEQQQGATRETSNEASSTNSENVNK- FLDLSSEISEGGSNLSQGRQLMCLARSLRSPKILLDEATASIDYS- SDAKIQETIRKEFGGSTILIAHRLRSVIDYDKILVMDAGEVKEYDH- PYSLLLKQSAFYSMCEHSGELDILIELAKKAFVEKLNKDD
YDR135C	Ycf1p	18	78	out	AAVDVETDKVVQETIRTAFKDRILTIAHRLNTIMSDRIIVLDNGK- VAEFDSPGQLSDNKSIFYSLCMEAGLVNEN
YLL055W	Yct1p	12	63	in	LKRRNNQRLKNYDENLQNYLDRIQIESENPSIEEGKVVTHENN- LAVFDLTDLENETFIYPL
YJL059W	Yhc3p	10	14	in	RHQJADDRPWCME
YOR291W	Ypk9p	11	26	in	KGWLKKKKSSKYYKLLIQEEMKLEV
YOR087W	Yvc1p	8	134	in	EARRIKYNRMKRLNDDANEYDTPWDLTDGVLDDDDGLFSDNRNSGM- RATQLKNRSRLKLRQTAEQEDVHFVKPKWYKVNKKSPPSEFYQDND- DTEDDAGEDKVEKELTKKVENLTAVIDLLEKLDIKDKKE
YMR243C	Zrc1p	6	156	in	SRRASRILLQATPSTISADQJREILAVPGVIIVHDFHVVNLTESIYASI- HVQIDCAPDKFMSSAKLIRKIFHQHGHISATVQPEFVSGDVNEDIRRRF- SIIAGGSPSSSQEAFDSHGNTHEGRKRSPTAYGATTASSNCIVD- DAVNCNTSNCL
YGL255W	Zrt1p	8	1	out	A

YLR130C	Zrt2p	8	1	out	A
YKL175W	Zrt3p	6	1	out	T
YMR279C		14	17	in	ENLWNRHRKSEDRSLEA
YBR241C		12	20	in	YKRVPETKGKTTYSEVWAGY
YCR023C		12	48	in	KIAPIDDNENELHQGSEDAYNSQSQSSDLRMAHRSSLSLSNQRCTT
YML018C		10	26	in	SSEEEHFENSITASNYESVEVPAANN

## Appendix 2

UniProtKB Acc	Organism	Predicted C-terminus
Q5AG77	<i>Candida albicans</i>	KRDWTLFIRAKDIDLDTGRINVDLQLLQEQEIAEKAQLAEKPFYRIYRIFWC
H8X557	<i>Candida orthopsilosis</i>	TRNWKLYRADEIDIDTGRDLDLQLLQEQEIAEERAILKAKPFYKRIYHFWC
H8X8Z7	<i>Candida orthopsilosis</i>	KIWKRNLKLYLKADEIDIDTGRANVDLQLLQEQEIAEKAELAEKPFYRYRIFWC
H8X8Z9	<i>Candida orthopsilosis</i>	KIWKRNLKLYLPIEIDVDVTGRADVDTLLKQEVLEEREALAEKPFYRCYRIFWC
C5MJG0	<i>Candida tropicalis</i>	WTRNWKLFIRAKDIDIDTGRRELDLVLKQEVAAEKAYASLPYRRVWHMWC
A5DY10	<i>Lodderomyces elongisporus</i>	KIYSRNWKIFYRAHEIDIDTGRAELDLVLRQEVAAEKAAALRASPFYKRFHFHC
Q6BUX4	<i>Debaryomyces hansenii</i>	WKNNWILCIRAKNIDVDVGRRETDLALKQELLEERAILRTKPLYRYRIFWC
Q6BIX2	<i>Debaryomyces hansenii</i>	KKDWTLFIRAKNLDIDTGRINIDVLQEQEIAEKAQLAEKPFYRIFKFWC
Q6BPX6	<i>Debaryomyces hansenii</i>	SRKLNIVPLDMDVDTGRRETIDIDKQELKEEKDIRSAYPMYRKYWNFLF
A5DQ23	<i>Meyerozyma guilliermondii</i>	WKKNWILFIRAADIDVDTGRRETDLALKKEELKEERAILATKPWYYRTYRIFWC
A5DJZ4	<i>Meyerozyma guilliermondii</i>	WARNFHVFHRAKDIDIDTGRRELDLVLKQEVAAEKAAHIAAKPFYRIYHFWC
A5DHV6	<i>Meyerozyma guilliermondii</i>	KVWKRQWRLYPIEELDIDTGRVHIDADLIRQEKEEEREQLSKRAFYYRIYKFWC
A5DQ62	<i>Meyerozyma guilliermondii</i>	YSRKLNTIVPLDMDLDTGRRNNDLVLKQENYKLAAYRAMPWYKVINFLV
G8YF74	<i>Pichia sorbitophila</i>	HKIWKKNWILCIPSRDIDVDVGRRETDLALKQEQEIAEKEIMKAPFYRILNFWC
G8YSS8	<i>Pichia sorbitophila</i>	TKNWRLYIKWQDIDIDTGRRELDLFLKQEQEIAEKAVIAKPFYRYRIFWC
G8Y1A0	<i>Pichia sorbitophila</i>	YTKNWLFYIKTEDLDIDTGRREIDLVLKQELAEAKVMASKPFYRYRWNFWC
G8Y1A1	<i>Pichia sorbitophila</i>	LYRRNWRLYLRSEHIDIDTGRRDVDLLELLKQEQEIAEKRLSSKPFYRILRYWC
G8YRZ6	<i>Pichia sorbitophila</i>	KMWKNQWKLFIKAEIDIDTGRANVDIDLKQELAEERANLQKNFFYRSYKFWC
G8YAL9	<i>Pichia sorbitophila</i>	SRKLNIVPLETMDLDSGRRETVDKLVQELKEEKESKRAAPWYKVLDFLV
A3GF84	<i>Scheffersomyces stipitis</i>	WRKNWILFIRAKDIDVDSGRREADIEALKEELAEERAILRSKPFYRYRIFWC
A3LNX9	<i>Scheffersomyces stipitis</i>	WKRTWRLYIPAKEIDIDTGRRELDLVLKQEQEIVEEKAYIASLPFYRYHFWC
A3LVM7	<i>Scheffersomyces stipitis</i>	WKKDWTLFIRAKDIDVDTGRANIDLVLQQTIAEESKLSKPFYRYRIFWC
A3LZA0	<i>Scheffersomyces stipitis</i>	RNWRFYVSLKDIDLITGRRDVDLIVRAIEIEDEKRVNKTCPFYIRVWNYWC
G3AEC4	<i>Spathaspora passalidarum</i>	WRKNWILFIRAKDIDIDSGRRETDLALKRELAEEERRVLQSKPWVFRILNYWC
G3AR68	<i>Spathaspora passalidarum</i>	YSRNWLYIRAKDIDIDTGRREMDLVLKQEVAAEKAYIASLPFYRYRIFWC
G3AR69	<i>Spathaspora passalidarum</i>	KIYTKNWKFFIRAKDIDVDTGRREMDLVLKQEVAAEKAYIASLPFYRYRIFWC
G3APH6	<i>Spathaspora passalidarum</i>	LFARNWILIRAKDIDVDGGKRETDIDLRLQEQEIEEKEHLKQPLYRYRIFWC
G3ANQ4	<i>Spathaspora passalidarum</i>	YTRNWRIYSSADIDLESGRRIVDVEVLQAEEMTEEKANRKPVIYRILNFWC
G3B310	<i>Candida tenuis</i>	WTKNWKLYFRASEIDIDTGRRELDLQLLQEQEIAEERAYIASKPLYRILYHFFC
G3B2Q4	<i>Candida tenuis</i>	WSGNWTLFIRAKDMDIDTGRGENDEALKAELAQERAVLQSKPLLYRIYHLLC
Q6C6E2	<i>Yarrowia lipolytica</i>	KRDGLFLLKDLIDTGRREPLDERVKAEMAERYALSQKNFYRYRIFWC
Q6CCF3	<i>Yarrowia lipolytica</i>	KRDGILKISEIDIDTGRREKLEKLAIEAQEYDLSQRFAYRYRIFWC

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Q6CE13	<i>Yarrowia lipolytica</i>	KVWKRPPFLKVSDDLDTGRRDLDLDRVRAETTAEREYIASRNFYRYVYKFWC
Q6CED5	<i>Yarrowia lipolytica</i>	KLWKRPSFVALKMDLDTGRRETDPELLMHEMDEEAAYASKPFYRYVYKFWC
C4XXU0	<i>Clavispora lusitanae</i>	WKKNRWYYPASEVDIDTGRRELDLCLKQEIIEKAYLASLPFYRYVYKFWC
C4Y8H1	<i>Clavispora lusitanae</i>	KRNWILQIPAKDLDTGRRPELLELRQEQKAILRSKPWYSRFYHLWC
C4Y9T4	<i>Clavispora lusitanae</i>	YSRKLNTIVPLETMDLDTGRRETDPEKLNQELAEKMAFRTLWPYKLYQLVLF
AOA061ANN9	<i>Cybertindnera fabianii</i>	KVWKRNLWILFIRAEDMDIDTGRKHVMDLCLKQEIIEKMAETPLYRYLYKTWC
AOA061ALK6	<i>Cybertindnera fabianii</i>	IWVRKIWEFLPLNEIPLDAGKAHPDLDLQEQEIAEKAIAAKPFYRYVYKFWC
AOA061B7H7	<i>Cybertindnera fabianii</i>	RAVTGKFVARLWTPLDQIDLDTGKRYPDVLLIQEQKQDRERLRSKPIYKYRFFC
AOA061AZD6	<i>Cybertindnera fabianii</i>	TKNWRFLIPADEIDLVKGRKIFDADVLAQEDAEDREKYRYAAWYVLFKFRIMC
FZQPS2	<i>Komagataella pastoris</i>	KIYKRNWAMYIRSEEMDLDTGRREMDLCLKQEQVAERELRLQKPFYRYVYKFWC
K0KEU3	<i>Wickerhamomyces ciferrii</i>	WKKNWTLFIRAKMDIDTGRKHIDMELLCLKQEIIEFKQLRANSPLYRYVYKFWC
K0KCB0	<i>Wickerhamomyces ciferrii</i>	WKKNWSLFVRIEDMIDSGRAERDLCLKQEIIEKAEKELATKPFIRLYRYVYKFWC
K0KGE7	<i>Wickerhamomyces ciferrii</i>	WTRKFWFEPLNQINLDSGRKDVDTDLRLQELDEEKIYKSRPFYRYVYKFWC
K0KZN6	<i>Wickerhamomyces ciferrii</i>	RLISKRFKPKYIPLNEIDLDTGKRYPIELKAKQKLDLAEIASKPLYRYVYKFWC
I2JRW8	<i>Brettanomyces bruxellensis</i>	KKDFLIYIKTKDLDTGRREMDLDRVKQEQVAEKAIAKSPFYRYVYKFWC
I2JVD4	<i>Brettanomyces bruxellensis</i>	KRDTHILPVDSDIDLDTGRRVVDIDLKQEQVAEKAIAKSPFYRYVYKFWC
W1QB26	<i>Ogataea parapolyomorpha</i>	KRKEYVLFIRSKDIDTGRRDLDLVLKAEIAEKAHLRSKPFYRYVYKFWC
AOA099NYK4	<i>Issatchenka orientalis</i>	KKDYKFFVRSADIDTGRREVDLCLKQEQVAEKAIAKSPFYRYVYKFWC
AOA099P6Z2	<i>Issatchenka orientalis</i>	KKNYTFFIKYSNIDLDTGRRVLDLVEVLKQEQVAEKAIAKSPFYRYVYKFWC
AOA099P546	<i>Issatchenka orientalis</i>	KKFKVTWLPVGEIDIVTGRRFVDLCLKQEQVAEKAIAKSPFYRYVYKFWC
AOA099P7C6	<i>Issatchenka orientalis</i>	KRFKVTWLPVSEIDIVTGRRYVDLVEVLKQEQVAEKAIAKSPFYRYVYKFWC
AOA099P5I0	<i>Issatchenka orientalis</i>	KRFKVTWIPIKEIDIDTGRRVVDLCLKQEQVAEKAIAKSPFYRYVYKFWC
AOA099P867	<i>Issatchenka orientalis</i>	KKFNVVFLVNLKDVDTGRRVVDLQJRIEAEKAIAKSPFYRYVYKFWC
Q753U5	<i>Ashbya gossypii</i>	IWSRNWFFIKAKEMDIDTGRRELDLLELKEELAEKALRAKPFYRYVYKFWC
Q755W3	<i>Ashbya gossypii</i>	YRRDWKTWLPARDLDTGRKPEDLEMMKHELIVSRARIASSPFWYRYVYKFWC
Q757P2	<i>Ashbya gossypii</i>	YRSTTGQWWKILPLAIEDLESGRKNIDIEVVKHEVAARKYISEQRWYRYVYKFWC
Q74Z84	<i>Ashbya gossypii</i>	YKRDWRLFIPAGQIDVDSGRALDIEELKEQLREQAETAKKPFYRYVYKFWC
Q750B9	<i>Ashbya gossypii</i>	YSRNWTLNPLDKMDLDTHRRVYDVEVLKQEQVEFKERMNRSPFWYVYKFWC
Q750B7	<i>Ashbya gossypii</i>	YHKDWRICIPASEVDLISHRQVFDEDELKQEDLEWKLKLSPIVYRYVYKFWC
Q751X7	<i>Ashbya gossypii</i>	NKDWRLFIRADQIDLVSHRRIFADVLLKQEDIEYRAKLRNSIWHRIANFWC
Q750B8	<i>Ashbya gossypii</i>	WKRDVRLVPSSEVDLISHRQVFDEEVLQEQVAEERKERLNRSTLFRKLLDFWC
G8JUJ8	<i>Eremothecium cymbalariae</i>	TKNWKLLIDPKYMDIDTGRRELDLLELKEELAEKALRAKPFYRYVYKFWC
G8JSP9	<i>Eremothecium cymbalariae</i>	YNKNWHTWFVRAKDIDLSTGKKAEDIELMKHEIMVSRAKIAASPLYRYVYKFWC
G8JPF4	<i>Eremothecium cymbalariae</i>	YFRITTGKWWGIKLSEVDLDTGRVNDIEIIEKVAERKFLRNKAWYTRYVYKFWC
G8JNU7	<i>Eremothecium cymbalariae</i>	TKNWTILNPLSSVDSHRRSYDVEVMKQEDLEKQKMKRSKYVYRYVYKFWC
G8JNU9	<i>Eremothecium cymbalariae</i>	YKDWRLCIPATEVDLNSHRKIFDEDELKQEDLDWKEKMRASIWYRYVYKFWC
G8JMA5	<i>Eremothecium cymbalariae</i>	YNKNWQLFIPAEKIDLDLHRKIFDADVLLKQEQVAEYRAKLRDSSMWHRIALWC
G8JNU8	<i>Eremothecium cymbalariae</i>	YREVQLLIPVDKIDLETHRQVFDEEVLQEQVEELERKERMKTASFQRKFIKFWC
G8JSS8	<i>Eremothecium cymbalariae</i>	KRNWSWMIRSNKIDVNTGRRMIDKEEKEKEKQEFNEYMARKSFIKLVNWLWC
H2AXD6	<i>Kazachstania africana</i>	CKGWKDWVFRAKDIDLDTGNSITDFEIKAEIEEKEKRIASPLYRYVYKFWC
H2APM2	<i>Kazachstania africana</i>	HKTYKKGWRSFLIPLKHIDLDTGRAVENLALFKQREQEKIIASKPFYRYVYKFWC
H2AVD9	<i>Kazachstania africana</i>	FARNWRLQIGAEEMDIDSGRKIIDLGLKQEQVEEKEKAMNSFLIKFVHWVWC
H2ARN5	<i>Kazachstania africana</i>	KRDFTFLKLEDIDLDAHRRYDPEFLRQEQVEERKEKIRNSFWIKMKYVYKFWC

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H2AMF1	<i>Kazachstania africana</i>	KRDFTLFSDLESVDLDYHRRIDPELVKQEDEEKEMLKNSPMWRMYFWC
H2AUL0	<i>Kazachstania africana</i>	KRDWKLFIKADIDLVSHRKYDGLIKQEEEEFKERLRNGPFWKVVAFWC
H2AUL2	<i>Kazachstania africana</i>	KKDWKLFIKADIDLVSHRKYDGLIKQEEEEFKERLRNGPFWKVVAFWC
H2AUL1	<i>Kazachstania africana</i>	RDWKLFIKADIDLVSHRKYDGLIKQEEEEFKERLRNGPFWKVVAFWC
H2ATJ7	<i>Kazachstania africana</i>	KIWNRDWRLFIRAKNIDLIHRHIYDPELLRQERKEMRERARNAPLWRKIYFWC
H2ATJ8	<i>Kazachstania africana</i>	WKRDWRLFIRAKDIDLVSHRHIHDPILRQEREYQEKLRNGPWRVYDFWC
H2ATJ9	<i>Kazachstania africana</i>	KKDWNLFIRAKDIDLVSHRHIYDEVDLQEKQNKYKLNKNSLWKIYAFWC
J7R3B9	<i>Kazachstania naganishii</i>	YKKNWKIFIKAEQMDIDTGRKDDDLRQVEAEERAVLATKPWWYRWVFWC
J7S8W6	<i>Kazachstania naganishii</i>	KLYIRKKRLIDVADMDLVSDRQVVDVEVCREEMRIEQLAKRSFFARFLHLWC
J7RPC6	<i>Kazachstania naganishii</i>	NKDFTFLLPLESIDLDFHRRVYDPEFIRQEREKIKLKNSSIWTRMYFWC
J7SAM4	<i>Kazachstania naganishii</i>	NKDYTFLNPLDKIDLHRRIDPELVKQEDMENKERVNRNGNIWTKLKWFWC
J7RI00	<i>Kazachstania naganishii</i>	KCYTKDWRLYIKSQDIDLVAHRQYDEDLRQEREETERLKNGPYKWRAYFWC
J7S706	<i>Kazachstania naganishii</i>	KRDWKFVIPAHRIDLVSHRKFVDEDLKQVEAEIEQEKLNLSGRKIQEFFF
Q6CXN2	<i>Kluyveromyces lactis</i>	GHKIWKKNWKLFIKASDIDISGRRETIEALKQEIIEEAFIASKPFYIRMYKFWC
Q6CX27	<i>Kluyveromyces lactis</i>	KIWKRNRLRYIKLSEVDVDSGRDTDAAATLKQEKAEALMKTQPFYIRLWVFWC
Q6CW55	<i>Kluyveromyces lactis</i>	YTGWNKSFVPLSGIDLDTGLSHSDVEIMKHELEIRVQLASKPLYRIFRWC
Q6CX68	<i>Kluyveromyces lactis</i>	YFKCSTGKWFDFKPLAEIDLETDRKNIDIEIVKQEVREEMYLASKPWIYRIFRWC
Q6CUX2	<i>Kluyveromyces lactis</i>	KKDWRLYIPASEIDLISHRKFDEEILKQDEEYKIKMKHASIWKLSNFWC
A0A090C5I2	<i>Kluyveromyces marxianus</i>	WKRNFVLNKLSEIDVDSGRVDIETLKKKEKAEADLLMKSQPFYIKFVFWC
A0A090CA47	<i>Kluyveromyces marxianus</i>	TKDFTFLVPLKEIDLSDYRKYDPEILRQEDLEHKEKVRSGWVWYLYDIWC
A0A090C2Y2	<i>Kluyveromyces marxianus</i>	YKDWRLVIPAEVDLVSHRKLFDVDLQVEDEEYKLRKLNKHSFVAKMQDFWC
W0T5C5	<i>Kluyveromyces marxianus</i>	WKRNVRLFIRAKDIDLDTGRRETIEALKVEIAEAKAWLASKPFYIRYRFFWC
W0T7S5	<i>Kluyveromyces marxianus</i>	YFRISTGKWFDFKPLTEIDLETDRKNIDIEIVKQEVREREFYLRSTRPWIYRIFRWC
Q875S6	<i>Lachancea kluveri</i>	HKDWRLCIPASEVDLSSHRNIDEEILRQEDYEWNEKMSNSSIIVRCLHFWC
Q875S5	<i>Lachancea kluveri</i>	YSKEWKLPLDEIDLNSHRHIFDKHILQDEDEHKEKLNKSGWVWVMAFWC
C5DIW2	<i>Lachancea thermotolerans</i>	YTRNWTFAKRAKDIDIDTGRRELDLDAKQEIIEEKLRLSTKPWWYRIVLHWC
C5DEC4	<i>Lachancea thermotolerans</i>	ANKSKRVLIPAQEIIDLDTGRKIKDLEQFKHEVLEDEKELASKPLYRIFRWC
C5E3G7	<i>Lachancea thermotolerans</i>	RISTGKWWGFKALRDIDLDMRVDTLSKHELHEKRVKLAQKPLIVRLYHQWC
C5DCD1	<i>Lachancea thermotolerans</i>	YTRSRLTPTKEIDLDSGRRVLDLMLKDEKRIEQAQRQKSLFARFVHWC
C5DK41	<i>Lachancea thermotolerans</i>	KRDWKLIPLEQIDLVSHRKFVDEDLKQEDAEEYIESIRNSGWSRVAHFWC
C5DK42	<i>Lachancea thermotolerans</i>	RDWRVIPAENEVDLVSHRKFDAEIMQSEQLKEEQLRHSWTKRAAEFWC
Q6FLI0	<i>Candida glabrata</i>	YARNWKLIPLSKLDIDTGRREMDLVLRQEIIEEQAQMMSTRPWWYRWYFWC
Q6FW85	<i>Candida glabrata</i>	YYRVSGKWWVDPKPLKIDLETGRKNVDIVIKAEIAERKMYLKKKPPWVRYHFWC
Q6FXR1	<i>Candida glabrata</i>	WKRDWRLVPLMEMDLDSGRVRLDAETREEELRVEREYLANASFFTRFLHWC
Q6FKY8	<i>Candida glabrata</i>	TRDFQLKPLDKIDLDFHRRIDPELMRQEDEESKERLRNGSFMRRMYHFWC
Q6FRI0	<i>Candida glabrata</i>	YKDFVTLTDLNQVDLNRKRYDPEFLRQEDLENKERLRNSSFLVYKIFRWC
Q6FMR8	<i>Candida glabrata</i>	WKRDWRLFIRAKDIDLVSYRQVFDEELLKQDEEYKELKNGPMWKRVDVFWC
Q6FX81	<i>Candida glabrata</i>	KKDWSLFIKADIDLVSHRKYDGLIKQEEEEFKERLRNGPFWKVVAFWC
GOVAE4	<i>Naumovozyma castellii</i>	YKRNWKLFIPLDMDIDTGRRETMELLKQEIIEEKAILASKPWIYRIFRWC
GOV7K2	<i>Naumovozyma castellii</i>	YRYKTGKWWVSMPLNKIDLETDRKNIDIEILKQEIIEERNLRSAPWYRIVHFWC
GOV721	<i>Naumovozyma castellii</i>	YVRKREFMVLADMDLDTGRRQVDLVRREELRREELAKQSFYKFLVHFWC
GOVDX8	<i>Naumovozyma castellii</i>	FKNWSWVVTLEEMDLDTGRKALDPLHRAEIVAEAAVAKMSFKRWFVHFWC
GOV828	<i>Naumovozyma castellii</i>	KRDFTFVPLDKIDLNFHRRIDPELIRQEDEENKEIKNNSVWVRFHFWC



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G0VJY7	<i>Naumovozyma castellii</i>	SRDFTFLDLKIDLNHRRLYDPELLRQEDEETKERIRNGGWTKQLNFWC
G0VAR5	<i>Naumovozyma castellii</i>	KIWKDWLRFIRAEDIDLVSREIFDEELLKQEDEEYRRLKRDGPMWRRVYDFWC
G0V566	<i>Naumovozyma castellii</i>	KKDWKLFIRAKNIDLISHRNIFDEELIKQEDEYRERLRTGPKWRRVYDFWC
G0W6Z4	<i>Naumovozyma dairenensis</i>	YKKNWKLFIKAEDMDIDTGRRETDLLELLKQEIIEEKALATKGWVYRQYQFWC
J7S4Q7	<i>Naumovozyma dairenensis</i>	HKVFYRYKTGKWWAIMDLKIDLETDRKNIDIDLKQEIERNRHLQASPWYVRWYHFWC
G0W9R9	<i>Naumovozyma dairenensis</i>	YYRKKQIVALEMDIDTGRQVDLTIRRQEMKEEQEHLAKSSFFARLHVWC
G0W844	<i>Naumovozyma dairenensis</i>	YVRNLQVLKLEMDLETGRKHIDAHEHRAEILAEKAALSQKSFIRFWHVWC
G0W4H9	<i>Naumovozyma dairenensis</i>	KRDFTILNPLEKIDLDFHRRYDPDFIKQEDEENKERLNKSSIWARIYHFWC
G0W515	<i>Naumovozyma dairenensis</i>	SRDFTFLPLDKIDLDFHRRYDPELLRQEDAETKERLRNSGWLARLRSFWC
G0WD96	<i>Naumovozyma dairenensis</i>	LYFGYKIYTKNWTIFIRAKDIDLVSHRNIFDEEIIKQEEEEEYREKLRNGPMWRRVYDFWC
G0W334	<i>Naumovozyma dairenensis</i>	KIYTKDWLRFIRAKDIDLINRDVFEELIRQEDEEYKEMRNAPIWQKIYEFWC
J8QB31	<i>Saccharomyces arboricola</i>	NRDFTLLPLDKIDLDFHRRYDPELMRQEDDENKERMRNASLMKKAYHFWC
Q876K8	<i>Saccharomyces bayanus</i>	NRDFTFLNPLDKIDLDFHRRYDPELMRQEDLENEERKRDMSLMRKYHFWC
P19145	<i>Saccharomyces cerevisiae</i>	YKRNWKLFIKAEKMDIDTGRREVDLCLKQEIIEEKAIMATKPRWYRIWVFWC
Q08986	<i>Saccharomyces cerevisiae</i>	YRRDWKHFYIKRSEIDLDTGCSVENLELFKAQKEAEQLIASKPFYKIRYFWC
Q12372	<i>Saccharomyces cerevisiae</i>	RIYRDRWHWYIKRMDIDLSGHSLEDFEATKLEDEDKKYVSSKPLYRIRFFC
P38967	<i>Saccharomyces cerevisiae</i>	YYKQCTGKWWGVKALKDIDLETDRKDIDIEIVKQEIIEEKMYLDSRPWYVRQFHWC
P06775	<i>Saccharomyces cerevisiae</i>	YTRNWTLMVKLEMDLDTGRKQVDTLRREEMRIERTLAKRSFVTRFLHFWC
P41815	<i>Saccharomyces cerevisiae</i>	KRDFTFLNPLDKIDLDFHRRYDPEIMRQEDDENKERLNKSSIFRVYKFWC
P38084	<i>Saccharomyces cerevisiae</i>	NRDFTLLNPLDKIDLDFHRRYDPELMRQEDDENKEKLRNMSLMRKYHFWC
C7GKU3	<i>Saccharomyces cerevisiae</i>	WKDWSLFIKADKVDLVSHRNIFDEELLKQEDEEYKERLRNGPYWKRVLDFWC
P48813	<i>Saccharomyces cerevisiae</i>	WKDWSLFIKADKVDLVSHRNIFDEELLKQEDEEYKERLRNGPYWKRVLDFWC
P25376	<i>Saccharomyces cerevisiae</i>	WHKDWLFIKADKIDLSHRQJFDEELIKQEDEEYRERLRNGPYWKRVAFWC
J6EKT3	<i>Saccharomyces kudriavzevii</i>	KRNWKLFIKAEKMDIDTGRREVDRDLKQEVAAERTHLAASWYRTWVFWC
J4U463	<i>Saccharomyces kudriavzevii</i>	NRDFTLLNPLDKIDLDFHRRYDPELIRQEDQENEEKTKNMSLMRKYHFWC
Q7LW70	<i>Saccharomyces pastorianus</i>	NRDFTFLNPLDKIDLDFHRRYDPELMRQEDLENKEKKHMLMKKAYHFWC
I2H0N4	<i>Tetrapisispora blattae</i>	YWRQTGKIWAFTPLAEIDLDEGRKNIDLVLKQEIHERKMYLKSHPWYIRFYHWC
I2GZP0	<i>Tetrapisispora blattae</i>	FFEGYLSPELLGCIYAHKVYFKNWRWYIPASKMDLHSGRQVDLEVVREELRLEKHLAQRS- FFYRFLHVWC
I2GW09	<i>Tetrapisispora blattae</i>	TPDANSFFSNYLAMPILIVFYFGYKIWKRDWRLFIRAKDIDLISHRTIYDEELLRQEDEEY- REKLRNGPKWKRVAFWC
I2GW10	<i>Tetrapisispora blattae</i>	RRDFRFLIRAKNIDLISHRIIFDEELLRQEDEEYKELRNGPKWKRVDVFWC
I2H906	<i>Tetrapisispora blattae</i>	KKDWVIWNPIESIDLDCRKYDPEQLKREDEENRERIRNAGFWARCRAFWC
G8BQJ4	<i>Tetrapisispora phaffii</i>	HKLWTKNWKIFIPLGQLDLDTGRKQLDLDLRQEVAAERATLAARPRWFRIYTFWCA
G8BWD8	<i>Tetrapisispora phaffii</i>	HRFYRKNWRDWYKSLDEIDLDTGCSYDDIELFKHQREQIKHKIQSKPLYKIRYFWC
G8BN55	<i>Tetrapisispora phaffii</i>	RYKTKKWEIPLKIDLDTGRKNIDIDIVKEEIKERKQYLATPKWYIRLMHHWC
G8BMI1	<i>Tetrapisispora phaffii</i>	FKNWRIMTLEEIDLLTGRKEVDIDLKEELKIEREALRQSSFMKRFLLIWC
G8C0I0	<i>Tetrapisispora phaffii</i>	YNKEWTILTDLSKIDLDAHRRYDPLIRQEDAENKEKLNKSPFVWRVYVFWC
G8BQ63	<i>Tetrapisispora phaffii</i>	YRDWKLYIKADKIDLISHRQJFIDENILKQEDEEYKELRNGPAWRRRIADFWC
G8BU77	<i>Tetrapisispora phaffii</i>	YKDWTLIIKAEIDLQSHRQJFDELLKEEDFEYRQLKNGPFWRVYVDFWC
G8BNJ4	<i>Tetrapisispora phaffii</i>	KDYTLNPLESIDLDHRRYDPEELKKEDLATKAEKRRGFHAQLVAFFC
G8ZR40	<i>Torulaspora delbrueckii</i>	WKRNVKLFIPKDLDTGRREVLDLRELEAEERAAARPFYRWSKFWC
G8ZNE8	<i>Torulaspora delbrueckii</i>	RFYRNDWGNWYIKRRNIDLDTGCSIENVELFRQREQEQEKISSRPFYRIRYFWC
G8ZW19	<i>Torulaspora delbrueckii</i>	HRNDWGNWYVYKRDMDLDTGCSIEDFELFQAQKEAEKRALASRPLYRVRVFWC

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G9A0B6	<i>Torulaspota delbrueckii</i>	RNDWKNWYVKRRDMDLDTGCSIENLELFQSQKESEKEDLACKPLYRYRFFWC
G8ZUH4	<i>Torulaspota delbrueckii</i>	RKDWSHWYIKAKDIDRDSGYTLAELDNIMRKEKDKAHIASRPFYKYRFFWC
G8ZQ3	<i>Torulaspota delbrueckii</i>	KKDWTLFIRAKDIDLHHRQJFDEDLRQDEEETKEKLRNGPLWKRLNFWC
R9XIH3	<i>Ashbya aceri</i>	WTRNWKFFIKAKDMDIDTGRRELDLELFKEEIAHEKAIMAQKPFIRVYRFFWC
A7THT3	<i>Vanderwaltozyma polyspora</i>	WKRNWKLLIPLKDIDIDTGRREDINLLKQIEAEKKAALAMPWWYRVYVFWCG
A7THT4	<i>Vanderwaltozyma polyspora</i>	HKLWKNWKFLEPLEVDIDTGRDIDVNLKQIEAEKKAALAMPWWYRVYVFWCA
A7TJK0	<i>Vanderwaltozyma polyspora</i>	RVTTGHWWYIALKDIDLDRKNVDIEIKQIEHEKMYLASKPWYRQFHWVC
A7TIH8	<i>Vanderwaltozyma polyspora</i>	KFYFKNWRLFTPYNEIDLDSGKRDIIDLELLREEKMEELAKLQILR
A7TL35	<i>Vanderwaltozyma polyspora</i>	NKDFTLSPDKIDLDSYRRIYDPELLIKQEDEENKLNKSRPLYKYRFFWC
A7TF99	<i>Vanderwaltozyma polyspora</i>	KRDWKLFIKAKDIDLDRHQJFDEENILRQDEEYKEKLRNGPMWRFLAFWC
A7TM27	<i>Vanderwaltozyma polyspora</i>	AKDFTFLNPESIDLDFHRIYDPEEMAEINRQEKEEYKNSIVGKIIYWLC
S6EA41	<i>Zygosaccharomyces bailii</i>	YRRDWNHWYIRRADIDLDTGCSMENLDMFKQQKEEERVIASKPIYRYRFFWC
W0W0M9	<i>Zygosaccharomyces bailii</i>	HKIWKKNWKFIRAEDMDIDTGRREMDLELLKQIEAEERAAALAKPWYRIFKIFC
W0W6L2	<i>Zygosaccharomyces bailii</i>	TRNWKLLVPPKEMDVQSGRKKVDIEHNRQEKQIEAELVAKPLWWRFTNFWC
W0W6G3	<i>Zygosaccharomyces bailii</i>	YRDFTLTPLDKIDLSYHRRFYDPELLRQDEENRQALKNAPFWVRMHAFFC
W0VRS2	<i>Zygosaccharomyces bailii</i>	KKDFRLFIRSKNIDLKGRQVFDEELLRQDEEYDQKAGPRWRRVAFWC
C5DV44	<i>Zygosaccharomyces rouxii</i>	KKNWKLFIKAEEDMDIDTGRRELDLRLRQVEEERAAALAKPMWYRIYKFFC
C5DWV7	<i>Zygosaccharomyces rouxii</i>	YRKDWTHWYIKRSDIDLDTGCSVENIELFKEQREEEKIYAATKPFYKYRFLC
C5E0F7	<i>Zygosaccharomyces rouxii</i>	TRDFTFLIPLNKVDLDSYRRIYDPELLRQDEEHHQAMKSASIWIKHSFFC
C5DZ15	<i>Zygosaccharomyces rouxii</i>	KKDFRIFIRSKDIDLDFKRQVFDEDLIKQEDEEYAEQMRNAPRWKVIKFLF