Supplemental table S2. Tryptic peptide counts of all secretory medium proteins identified by QTOF in YNB-S, pH 7.4 + 0.5 mg/L fluconazole at 37°C after 18 hours

Name	**Residues**	**Peptide**	Protein length	Coverage %	R1[a]	R2	R3	R4	R5
Als family[b]	237-254	GLNDWNYPVSSESFSYTK			nd	nd	nd	1[c]	nd
Bgl2	19-29	MGDLAFNLGVK	308 aa	40	nd	3	2	1	nd
	57-96	TYAVSDCNTLQNLGPAAEAEGFQIQLGIWPNDDAHFEAEK			nd	nd	nd	nd	1
	97-105	EALQNYLPK			1	2	nd	nd	nd
	106-112	ISVSTIK			3	1	3	1	3
	124-134	EDLTASELASK			3	nd	nd	nd	nd
	218-254	GSTDIEFWVGETGWPTDGSSYGDSVPSVENAADQWQK			nd	nd	nd	nd	1
	289-297	HWGVWQSDK			nd	nd	1	nd	1
Cfl2	60-77	CYCNQDPGFGTISDCLVR	738 aa	2	nd	nd	nd	1	nd
Cht1	230 - 253	LYLGLPGSSSSAGSGFVGLSTVQR	462 aa	5	nd	nd	nd	nd	2
Cht2[d]	99-121	TVLLSLGGGVGDYGFSDVASATK	583 aa	4	nd	nd	nd	nd	1
Cht3	21-39	SNSNVAVYWGQNSGGSQQR	567 aa	20	3	nd	nd	1	nd
	100-121	TILLSLGGAAGSYSGFSDDATAK			nd	nd	2	1	nd
	122-135	QFAHTLWDLFGNSK			1	1	2	nd	1
	182-203	NYYLGAAPQCPYPDASVGPLLK			2	2	2	3	3
	246-255	LFVGVPASSR			nd	nd	nd	nd	1
	256-279	AAGSGYNDPSAVSQYLTSDILNSK			nd	1	1	1	nd
Coi1	28-43	GFAILPPTNIVLDHLK	191 aa	31	nd	2	nd	nd	nd
	49-61	AVTTHYDVLNTIK			1	3	2	3	2
	144-152	YSCLLDVMK			nd	nd	1	nd	nd
	160-171	LKDMDDVPAQVR			3	3	3	nd	3
	182-191	AEVVGGACAK (C-term)			nd	3	nd	nd	nd
Crh11[d]	29-45	SSDCSPVPALGSSFLEK	453 aa	15	1	2	nd	1	nd
	77-84 [78-84][e]	FDNPSFK [RFDNPSFK][f]			nd	nd	nd	1	nd
	148-158	GGYHDIANPLK			nd	nd	nd	nd	1
	159-169	DYHTYVIDWTK			nd	1	nd	nd	nd
	170-182	DAVTWSVDGSVIR			1	1	nd	nd	nd
	271-279	YDQAQDDIK			nd	nd	nd	nd	3
Dag7	185-198 [185-199]	SVGNNPNHNPLCNK [SVGNNPNHNPLCNKK]	251 aa	26	3	3	nd	nd	2
	202-207	AFYEGK			nd	nd	nd	1	2
	208-216	SVDVTVVDR			2	3	3	nd	1
	217-234	CEGCAYNDLDFSPAAFDK			2	2	nd	nd	1
	235-242	LADESLGR			nd	nd	nd	1	nd
	243-251	IDITWEWLN			nd	nd	nd	nd	1
Ece1	177-193	LISNVFDGVSETVQQAK	271 aa	6	nd	1	nd	nd	nd
Ecm33[d]	139-168	TGLTAGITSAESVVISDTGLSSLTGINVFK	423 aa	16	3	1	nd	nd	1
	276-290	TIGGALQISDNSELR			nd	3	3	nd	1
	322-329	VSGGFILK			1	1	3	nd	nd
	342-349	LNTNGDIK			nd	nd	nd	2	1
	335-340	FQCEDR			nd	nd	nd	2	3
Eng1	914-923	LGGTWAQSNK	1145 aa	3	1	nd	nd	nd	nd
	1082-1100	DQIAGFIDNVDSGWTGILR			1	nd	nd	nd	nd
Gca1	108-132	LNVHIEPTDLTDVFVLPEELVVKPK	946 aa	7	nd	3	nd	nd	nd
	193-214	GHSITGLGESIHGSLNEPGVVK			nd	1	nd	nd	nd
	685-704	NHNVLGAIPQEPYVWEAVMK			nd	nd	1	nd	nd
Mp65	128-141	GITYSPYSDNGGCK	378 aa	30	1	3	2	2	2
	161-174	LYGVDCDQVSAVLK			2	1	1	nd	nd
	234-240 [234-241]	AYVDEGR [AYVDEGRK]			3	3	3	3	3
	302-309	VWTACSGK			3	3	3	nd	2
	311-322 [311-333]	NVLITETGWPSK [NVLITETGWPSKGDSNGVAVPSK]			nd	1	nd	nd	nd
	323-333	GDSNGLAVPSK			nd	nd	nd	1	nd
	334-344	SNQQAAISSIK			nd	3	3	1	2
	345-362	SSCGASALLFTAFNDLWK			nd	nd	nd	nd	nd
	363-371 [363-378]	ADGPYNAEK [ADGPYNAEKYGIYSN] (C-term)			nd	nd	1	1	2
Msb2	1223-1238	ALGSFITTPGSAIYR	1409 aa	2	1	nd	2	nd	nd
	1239-1253	NPDSVLQALASLIDSR			nd	nd	nd	nd	1
Op4	93-108	LTTDPSISSSLSNIIK	403 aa	9	nd	1	nd	nd	nd
	261-281	QSGLWDQALVYIQNNAGSWIK			nd	2	nd	nd	nd
Orf19.1239	67 - 79	ENQIVTDVLTAIK	328 aa	15	nd	1	nd	nd	nd
	80 - 89	NTNLSPGIIK			nd	3	nd	nd	nd
	135 - 148	DLINDCAFYAYIYK			nd	1	nd	nd	nd
	274 - 286	SVIVTALAAAFGK			nd	1	nd	nd	nd
Orf19.1765	158 - 174	LMELIQGQWSNEVGGVR	418 aa	4	nd	nd	nd	1	nd
Orf19.1766	172 - 191	VDSNYIASISTVEAALSAVK	401 aa	5	nd	2	nd	nd	nd
Orf19.3499	28 - 42	TFGYPPPQYPEVTGK	167 aa	15	nd	nd	nd	2	3
	132 - 141	NIDDPYNYSK			nd	nd	nd	1	nd
Orf19.6553	196 - 210	LFINELSQLIHLGEK	393 aa	4	nd	1	nd	nd	nd

Pbr1	90-101	TSYALTYSEDGK	175 aa	7	nd	nd	nd	1	1
Pga4[d]	42-65	GVDYQPGGSSELEDPLADTNVCER	451 aa	12	nd	nd	nd	1	nd
	99-116	AGIYVILDVNTPHSSITR			nd	2	nd	nd	2
	302-315	GDSVTTNDDFDNLK			nd	nd	nd	nd	3
Pga7[d]	14-27	ADYGNFGTYPKVPK	219 aa	26	nd	nd	nd	1	nd
	52-94	FSTSNTPCPYWDTGCFCVMPQWAGLVGQCVAQK			nd	nd	1	nd	nd
Pga46[d]	74-80	ESFIPRR	340 aa	4	nd	nd	nd	2	nd
	292-297	ELNKLK			nd	nd	nd	2	nd
Phr family	175-184/165-174	SNTDASAFVK			nd	1	2	nd	2
Phr1[d]	21-35	KFESSTPPVEVVGNK	548 aa	44	1	nd	1	nd	2
	49-70 [49-71]	GIAYQQDAAGSVSSGYDADPNR [GIAYQQDAAGSVSSGYDADPNRK]			2	2	nd	1	3
	99-113	VYAIDPDKDHEECMK			nd	3	3	2	2
	114-135	IFSDAGIYIVADLSEPTVSINR			1	2	2	nd	2
	136-146	NNPEWNLDLYK			1	nd	nd	nd	nd
	175-184	SNTDASAFVK			3	2	3	1	nd
	201-215	QIPVGYSSNDDEEIR			1	nd	2	1	1
	231-244	ADFFGINMYEWCGK			1	nd	nd	nd	nd
	245-253	STFETSGYK			nd	1	3	nd	nd
	254-260	DRTEEIK			nd	nd	nd	2	nd
	280-291	LFQEIGTLYSDK			nd	nd	1	nd	nd
	367-385	AATNLPPTPDESYCDCISK			nd	nd	nd	1	nd
	386-423	SLECVVADDVDKEDYGDLFGQVCGYIDCSAISADGSK			1	nd	nd	nd	nd
	424-435 [424-437]	GEYGVASFCSDK [GEYGVASFCSDKDR]			2	nd	nd	3	2
	438-452	LSYVLNQYYLDQDKK			nd	3	2	1	nd
Phr2[d]	89-126	VYALDTSQDHTECMQMLQDAGIYVIADLSQPDESINR	544 aa	16	nd	nd	nd	nd	1
	239-250	ASGYESATNDYK			nd	nd	nd	nd	3
	251-269	NLGIPIFFSEYGCNEVRPR			nd	nd	2	nd	nd
	384-399	VDSDDYSDLFSYICAK			nd	nd	1	nd	nd
Pir1	249-266	ACSSANNLEMTLHDSVLK	346 aa	5	2	1	3	nd	1
Plb3[d]	216-244	ALSHQFFPGLDDGGDALTWSTLQDVDVFK	632 aa	7	nd	nd	nd	nd	1
	295-308	NYEMPFPIVVADGR			nd	nd	nd	nd	1
Rbe1	136-148	ALHGVPALSWSNK	271 aa	59	1	2	1	1	nd
	149-169	LAEYAQDYANTGFDCSNLNLK			1	nd	1	nd	1
	221-229	STTQVGCAK			2	nd	nd	nd	nd
	230-237	MMCSTAWR			nd	nd	nd	nd	1
	238-347	QITVCEYLPR			nd	2	nd	nd	nd
Rbt4	208-221	DTQFAQQILDAHNK	358 aa	9	2	3	nd	nd	nd
	312-317	LGCAYK			1	3	nd	nd	nd
	348-358	SYMAENVLRPQ			nd	1	1	nd	nd
Rbt5[d]	61-92	QSTSSTPCPYWDTGCLCVMPQFAGAVGNCVAK	241 aa	13	nd	nd	3	nd	nd
Sap9[d]	244-256	SLYSLYLNTADAK	544 aa	7	nd	nd	1	nd	nd
	307-319	AGSILFGAIDHAK			nd	nd	1	nd	1
	332-341	TYSQISYPVR			1	nd	1	nd	nd
Scw11	267-275	SDIQLINSK	506 aa	18	nd	1	3	nd	nd
	282-298	SYGTDCGSLTTVLETCR			2	3	3	nd	nd
	377-388	VTTSEPPATYLK			nd	1	1	2	nd
	417-436	DAGSYIVHQQQQVAEICGGK			3	nd	2	1	2
	437-448	SVLITETGYPSK			2	2	1	1	2
	449-471	GSTLGVNVPSPENQEIAISSIIK			1	nd	1	nd	2
Sim1	162-176	DGYYCSYACQAGMSK	372 aa	20	nd	1	nd	nd	nd
	203-216	SNTDNDYLCEWGSK			nd	nd	1	nd	nd
	217-232	DVNFVSEISEDVAICR			1	3		nd	nd
	233-252	TDYPGSENMNIPTLLSAGGK			1	2	3	2	2
	326-333	DKPNYNNIK			3	3	3	nd	2
Sod4[d]	28-33 [26-33]	APLVAR [GKAPLVAR]	232 aa	9	nd	3	nd	nd	nd
	105-117	TPAALELGDLSGR			2	nd	nd	nd	1
Sod5[d]	103-117	AATPAAHEVGDLAGK	228 aa	7	1	nd	nd	nd	nd
Ssr1[d]	41-54	CSGLNDLSCICTTK	234 aa	13	1	nd	2	1	3
	64-79	EICPNGDADTAISAFK			nd	nd	nd	1	1
Sun41	204-218	EGSYCSYACQSGMSK	418 aa	29	3	3	3	3	3
	219-238	TQWPEDQPSNGVSIGGLLCK			3	3	1	nd	2
	249-258 [249-259]	SNYLCEWGVK [SNYLCEWGVKK]			nd	nd	1	nd	nd
	259-264 [258-264]	ANVVNK [KANVVNK]			3	nd	nd	nd	nd
	266-274	LSETVAICR			3	2	nd	nd	3
	275-309	TDYPGTENMVIPTVVGGGSTSVITVVDQSTYYTWR			nd	nd	nd	nd	nd
	368-373	DSLNFK			3	3	1	1	2
	376-394	IVGESGSTVSGSCSYANGK			1	nd	nd	nd	1
Sur7	66-93	ADYSNCLLGPAYPISPEDNFGTTADIPK	270 aa	16	1	nd	nd	nd	nd
	175-181	YAHIGAK			1	nd	nd	nd	nd
	246-254	DEENTGGIR			nd	nd	nd	1	nd

Tos1	22-36	GCSFEGGNYYCSETK	468 aa	41	nd	nd	nd	1	1
	42-61	GIGFSGSYMDVTNMDENTGK			nd	nd	nd	3	3
	62-85	CTQQLYSFSGNLSPLDEELSVHFR			nd	2	2	nd	1
	107-116	QIDDQDCNVK			nd	nd	nd	1	nd
	231-259	DSYYTPGSTDNCVFLNYHGGSGSGVWSAK			1	2	nd	1	2
	260-287	FGNSLSYANADNSGGSSTPVPLEETTIK			3	1	1	1	nd
	288-299	SGEEYIIFSGSK			1	1	1	nd	nd
	300-310	CGSSSDCGYYR			3	1	2	3	2
	311-320 [310-320]	GTVAYHGFK [KGTVAYHGFK]			3	3	2	nd	1
	358-370	TLQYGEATCSCWK			nd	2	nd	nd	nd
	371-388	TGCGELDLFEVLSSGSNK			2	1	nd	2	nd
Utr2[d]	137-142	YLWYGK	470 aa	15	nd	nd	nd	nd	2
	245-253	YDYPQTPSR			nd	1	2	1	nd
	254-268	IQFSLWPGGDSSNAK			nd	nd	1	nd	nd
	269-286	GTIEWAGGLINWDSEDIK			nd	nd	3	nd	nd
	288-296	YGYYYAHIK			nd	nd	nd	nd	1
	297-310	EIYATAYDIPNDVK			3	2	3	3	1
Xog1	39-54	GGGHNVAWDYDNNVIR	438 aa	53	3	2	2	nd	1
	108-119	HWSTWITEQDFK			2	3	3	1	1
	120-130	QISNLGLNFVR			2	1	nd	nd	nd
	168-189	VWIDLHGAPGSQNGFDNSGLR			nd	1	nd	2	1
	190-211	DSYNFQNGDNTQVTLNVLNTIFK			1	1	nd	nd	1
	212-240	YGGNEYSDVVIGIELLNEPLGPVLNMDK			nd	nd	nd	nd	1
	243-253	QFFLDGYNSLR			1	nd	nd	1	nd
	304-320	NINDHISVACNWGWDAK			1	2	3	1	2
	322-340	ESHWNVAGEWSAALTDCAK			2	nd	2	nd	2
	341-347	WLNGVNR			2	1	nd	1	nd
	351-378	YEGAYDNAPYIGSCQPLLDISQWSDEHK			1	nd	nd	nd	nd
	405-429	TENAPEWSFQTLTYNGLFPQPVTDR			1	nd	3	nd	1
	430-438	QFPNQCGFH			nd	nd	1	nd	nd
Ywp1[d]	87-93	VINVPAR	533 aa	7	nd	2	nd	2	3
	94-110	NLYGAGAVPFFQVHLEK			2	1	nd	1	1
	329-339	VITVVACDEHK			nd	nd	nd	1	3

nd = not detected — average protein coverage % 16

[a] Independent biological replicate
[b] Peptide common to at least two members of the protein family
[c] Number of peptides per biological replicate found in three technical replicates
[d] GPI-wall protein
[e] Residues in parentheses are from the miscleaved peptide
[f] The sequence of the miscleaved peptide is in parentheses

Proteins with predicted intracellular localization

Name	**Residues**	**Peptide**	**R1[a]**	**R2**	**R3**	**R4**	**R5**
Ald5	179 - 192	LGPVLATGSTTVLK	nd	1	nd	nd	nd
Arf2	128 - 142	QDLPNAMNAAEITEK	nd	nd	nd	nd	1
	143 - 149	LGLHSIR	nd	2	nd	nd	nd
Arf3	41 - 53	TVPTVGFNVETVK	nd	nd	nd	nd	1
Asc1	247 - 258	YWLAAATTSGIK	nd	1	nd	nd	nd
Atc1	1018 - 1035	ISAPFDPEEYFQVWVPTR	nd	nd	nd	nd	1
Cdc42	134 - 147	LSPITQEQGEKLAK	nd	nd	nd	1	nd
Cyp1	81 - 88	FADENFVK	nd	nd	nd	nd	1
Eno1	134 - 142	HIANISNAK	nd	3	nd	nd	nd
	225 - 236	EALDLIMDAIDK	nd	1	nd	nd	nd
	266 - 273	NPESDPSK	nd	nd	nd	nd	1
	319 - 333	IQIVGDDLTVTNPTR	nd	1	nd	nd	2
Fba1	55 - 72	APIILQTSQGGAAYFAGK	nd	2	nd	nd	nd
	95 - 113	AIAPTYGIPVVLHTDHCAK	nd	1	nd	nd	nd
	193 - 211	DALYTSPETVFAVYESLHK	nd	nd	2	nd	nd
Het1	37 - 50	LFDLLGSSAFTVVK	nd	3	nd	nd	nd
Kar2[g]	205 - 216	DAGTIAGLNVLR	nd	1	nd	nd	nd
Mnt1[g]	259 - 270	DYAFTISLPEYK	nd	nd	nd	nd	1
Orf19.1267	48 - 64	FQELGEAYGILSNPESR	nd	nd	nd	1	nd
Orf19.2204.	9 bis 19	LVIVGDGACGK	1	nd	nd	nd	nd
Orf19.251	22 - 37	TGVFVVEALHPFEVFR	nd	1	nd	nd	nd
	179 - 186	KGNLLTIK	nd	1	nd	nd	nd
	213 - 224	IVTGVNPQSAVK	nd	3	nd	nd	nd
Orf19.86	14 - 23	GEPYPFEQLK	nd	3	nd	nd	nd

	96 - 108	IEVNGDNTDPVYK	nd	nd	nd	nd	1
	115 - 122	SGVLGLTR	nd	3	nd	nd	nd
Pgi1	67 - 77	EILDQLVTLAK	nd	nd	1	nd	nd
Pst3	50 - 80	LLHAPAKPNYPIATNDTLTGYDAYLFGIPTR	nd	nd	nd	2	nd
	148 - 176	AFPLQTNLEEIHGGSPYGAGTFAGVDGSR	nd	nd	nd	1	nd
Rdi1	31 - 41	NLDAEDESLAK	nd	nd	nd	1	nd
	44 - 62	ASLGLTADTKPYPVKPGDK	2	1	1	nd	nd
	65 - 84	VVVTELALEFPEQPDLQPIR	nd	nd	nd	nd	1
	85 - 98	INLEDSDGNTIVDK	nd	nd	nd	1	3
	108 - 115	SIYQLVVK	1	2	nd	nd	nd
	128 - 133	YLHSVK	nd	1	nd	nd	nd
Rga2	327 - 333	SNSTSLR	nd	nd	nd	2	nd
	743 - 748	LNEQLK	nd	nd	nd	2	nd
Rho1	56 - 72	KVELALWDTAGQEDYDR	nd	nd	nd	3	3
	127 - 136	DDPHTIEALR	nd	nd	nd	1	nd
Sec14	35 - 41	TTLDIFR	nd	1	nd	nd	3
	106 - 113	MYPTYYHK	1	nd	1	nd	nd
	200 - 208	IGQDYYPER	nd	nd	1	nd	nd
	279 - 297	DVGPWRDPEFIGPEGECPR	nd	nd	nd	nd	1
Tdh3	234 - 247	VPTTDVSVVDLTVR	nd	2	1	nd	nd
Tef1	272 - 288	AGMVVTFAPAGVTTEVK	nd	1	nd	nd	nd
Ykt6	72 - 96	SEGISGIIITDKDYPVRPAYTLINK	nd	1	nd	nd	nd
Ynk1	88 - 104	AILGATNPLQSAPGTIR	nd	2	nd	nd	nd

[g] Predicted to be ER- or Golgi-associated proteins