Supplemental table S1. Tryptic peptide counts of all secretory medium proteins identified by QTOF in YNB-S, pH 7.4 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	1[c]	nd	nd	2
Als3[d]	77-92	FTTSQTSVDLTAHGVK	1156 aa	2	nd	nd	nd	1	nd
	306-311	APFTLR			nd	2	nd	2	nd
Bgl2	19-29	MGDLAFNLGVK	308 aa	9	nd	nd	1	1	nd
	106-112	ISVSTIK			2	1	2	2	2
	124-134	EDLTASELASK			1	1	nd	nd	nd
	289-297	HWGVWQSDK			1	nd	nd	nd	nd
Cht2[d]	99-121	TVLLSLGGGVGDYGFSDVASATK	583 aa	11	nd	nd	nd	2	nd
	178-200	NYFLSAAPQCPYPDASLGDLLSK			nd	nd	1	nd	nd
	240-258	LFVGVPATSNIAGYVDTSK			nd	nd	nd	nd	1
Cht3	21-39	SNSNVAVYWGQNSGGSQQR	567 aa	20	1	3	3	nd	3
	100-121	TILLSLGGAAGSYSGFSDDATAK			3	1	1	1	1
	122-135	QFAHTLWDLFGNSK			2	nd	3	3	1
	182-203	NYYLGAAPQCPYPDASVGPLLK			2	1	3	nd	3
	246-255	LFVGVPASSR			2	nd	nd	nd	nd
	256-279	AAGSGYNDPSAVSQYLTSDILNSK			nd	1	1	nd	2
Coi1	20-27	FNLLHDDK (n-term.)	191 aa	34	nd	nd	nd	nd	2
	28-43	GFAILPPTNIVLDHLK			3	1	1	nd	nd
	49-61	AVTTHYDVLNTIK			2	1	3	nd	3
	103-110	TIEDSSLK			nd	nd	nd	3	nd
	160-171	LKDMDDVPAQVR			1	2	3	2	3
	182-191	AEVVGGACAK (C-term)			1	1	nd	nd	3
Crh11[d]	29-45	SSDCSPVPALGSSFLEK	453 aa	6	nd	1	nd	nd	nd
	77-84 [78-84][e]	FDNPSFK [RFDNPSFK][f]			nd	1	nd	nd	nd
Dag7	185-198 [185-199]	SVGNNPNHNPLCNK [SVGNNPNHNPLCNKK]	251 aa	17	nd	3	nd	nd	nd
	208-216	SVDVTVVDR			1	2	2	nd	nd
	217-234	CEGCAYNDLDFSPAAFDK			nd	nd	1	nd	nd
Ecm33[d]	171-202	VFNVNNNDNIDTIDSGLQEVTDTIDISYNAEK	423 aa	17	nd	nd	nd	1	nd
	246-262	VELAELTSIGNSLTINK			nd	2	nd	nd	nd
	276-290	TIGGALQISDNSELR			1	nd	1	nd	3
	322-329	VSGGFILK			nd	nd	1	nd	1
Eng1	430-442	AIDTNAPPTVFAR	1145 aa	12	nd	nd	nd	nd	2
	703-710	FSYTTAGK			1	nd	nd	2	3
	711-746	SSSNNPIVFALPHHMDSLTGSALDALTGITVTSTTK			nd	nd	nd	1	nd
	798-807	ELAANIAATVK			nd	nd	nd	1	1
	808-817	NMNSNYFSGK			nd	nd	nd	nd	1
	858-867	QYYPLMYDTK			nd	nd	nd	nd	1
	914-923	LGGTWAQSNK			nd	nd	nd	nd	2
	924-931	DWVNSLVR			1	nd	nd	nd	nd
	1030-1038	VSGIFFENK			nd	nd	nd	nd	2
	1082-1100	DQIAGFIDNVDSGWTGILR			nd	nd	nd	nd	1
Fgr41[d]	30-36	GNVVVVK	250 aa	3	nd	nd	1	nd	nd
Gca1	108-132	LNVHIEPTDLTDVFVLPEELVVKPK	946 aa	3	nd	nd	nd	nd	2
Hex1	363-378	LTMWDDVLLSDVSADK	562 aa	3	1	nd	nd	nd	nd
Mp65	128-141	GITYSPYSDNGGCK	378 aa	30	3	1	3	nd	3
	142-160	SESQIASEIAQLSGFDVIR			2	nd	3	nd	nd
	161-174	LYGVDCDQVSAVLK			1	1	2	nd	3
	234-240 [234-241]	AYVDEGR [AYVDEGRK]			3	nd	3	3	3
	302-309	VWTACSGK			3	nd	3	nd	3
	311-322 [311-333]	NVLITETGWPSK [NVLITETGWPSKGDSNGVAVPSK]			nd	nd	3	3	1
	334-344	SNQQAAISSIK			2	nd	2	2	2
	363-371 [363-378]	ADGPYNAEK [ADGPYNAEKYGIYSN] (C-term)			3	2	nd	3	nd
Msb2	1212-1219	SLQNVSVR	1409 aa	5	nd	nd	1	2	3
	1223-1237	ALGSFITTPGSAIYR			nd	nd	nd	1	1
	1238-1253	NPDSVLQALASLIDSR			nd	nd	nd	1	nd
	1254-1290	IPLTGLVTDDQQVSGSSSDSNPSTNSYGSMDIVSNTK			nd	nd	nd	1	nd

Pga4[d]	99-116	AGIYVILDVNTPHSSITR	451 aa	4	nd	nd	nd	2	2
Pga45[d]	86-98	DANTEQTIEGILK	462 aa	6	1	nd	nd	nd	nd
	351-364	YSGALSQILQDLEK			nd	1	nd	nd	nd
Phr1[d]	438-452	LSYVLNQYYLDQDKK	548 aa	3	nd	nd	nd	1	nd
Pir1	249-266	ACSSANNLEMTLHDSVLK	346 aa	5	3	nd	1	nd	2
Pra1	152-165	YLSQLCSGGYTVSK	299 aa	5	nd	1	nd	nd	nd
Rbe1	149-169	LAEYAQDYANTGFDCSNLNLK	271 aa	14	1	1	nd	nd	1
	221-229	STTQVGCAK			1	1	nd	nd	nd
	230-237	MMCSTAWR			nd	nd	nd	nd	3
Rbt1	199-220	VNAVSNAIGTFDASALFNAQVK	721 aa	3	nd	nd	nd	nd	1
Rbt4	208-221	DTQFAQQILDAHNK	358 aa	12	nd	nd	nd	2	nd
	286-307	DGLSYSYGSSSVYNHFTQVVWK			nd	nd	nd	1	nd
	312-317	LGCAYK			nd	1	nd	nd	nd
Rbt5[d]	61-92	QSTSSTPCPYWDTGCLCVMPQFAGAVGNCVAK	241 aa	13	2	nd	1	nd	nd
Sap5	334-347	TSGTIDFQFGNNLK	418 aa	3	nd	1	nd	nd	nd
Scw11	267-275	SDIQLINSK	506 aa	21	2	nd	2	1	2
	282-298	SYGTDCGSLTTVLETCR			2	nd	3	nd	nd
	366-376	SQLQSAGYNGK			nd	1	nd	1	nd
	377-388	VTTSEPPATYLK			3	2	3	1	3
	417-436	DAGSYIVHQQQQVAEICGGK			3	1	2	nd	3
	437-448	SVLITETGYPSK			2	nd	2	2	3
	449-471	GSTLGVNVPSPENQEIAISSIIK			3	nd	3	nd	3
Sim1	162-176	DGYYCSYACQAGMSK	372 aa	28	nd	nd	2	nd	nd
	177-196	TQWPSEQPSNGMSIGGLYCK			nd	nd	1	nd	nd
	203-216	SNTDNDYLCEWGSK			3	1	3	nd	3
	217-232	DVNFVSEISEDVAICR			2	nd	nd	nd	1
	233-252	TDYPGSENMNIPTLLSAGGK			3	nd	3	1	nd
	326-333	DKPNYNNIK			1	2	3	nd	3
	334-344	IVGDDVNGDCK			nd	3	nd	nd	nd
Sod4[d]	105-117	TPAALELGDLSGR	232 aa	6	1	nd	nd	nd	nd
Ssr1[d]	41-54	CSGLNDLSCICTTK	234 aa	13	nd	1	2	nd	1
	64-79	EICPNGDADTAISAFK			nd	2	nd	nd	nd
Sun41	204-218	EGSYCSYACQSGMSK	418 aa	25	2	3	3	nd	2
	219-238	TQWPEDQPSNGVSIGGLLCK			3	nd	3	nd	3
	249-258 [249-259]	SNYLCEWGVK [SNYLCEWGVKK]			1	nd	2	nd	nd
	259-264 [258-264]	ANVVNK [KANVVNK]			1	nd	nd	nd	nd
	266-274	LSETVAICR			3	3	3	nd	3
	275-309	TDYPGTENMVIPTVVGGGSTSVITVVDQSTYYTWR			1	nd	nd	nd	nd
	368-373	DSLNFK			3	nd	3	1	3
Tos1	22-36	GCSFEGGNYYCSETK	468 aa	34	nd	nd	1	nd	nd
	42-61	GIGFSGSYMDVTNMDENTGK			2	3	nd	3	1
	231-259	DSYYTPGSTDNCVFLNYHGGSGSGVWSAK			3	2	1	nd	1
	260-287	FGNSLSYANADNSGGSSTPVPLEETTIK			2	1	nd	nd	1
	288-299	SGEEYIIFSGSK			2	nd	nd	nd	1
	300-310	CGSSSDCGYYR			3	nd	3	nd	3
	311-320 [310-320]	GTVAYHGFK [KGTVAYHGFK]			3	nd	3	3	3
	358-370	TLQYGEATCSCWK			nd	1	nd	nd	nd
	371-388	TGCGELDLFEVLSSGSNK			3	nd	1	1	1
Utr2[d]	75-85	MSTFQESFDSK	470 aa	14	nd	1	nd	nd	nd
	245-253	YDYPQTPSR			1	nd	3	3	nd
	246-268	IQFSLWPGGDSSNAK			nd	1	nd	nd	2
	288-296	YGYYYAHIK			nd	nd	nd	nd	2
	297-310	EIYATAYDIPNDVK			1	nd	nd	nd	3
Xog1	39-54	GGGHNVAWDYDNNVIR	438 aa	40	3	1	3	3	2

	108-119	HWSTWITEQDFK			nd	nd	1	1	nd
	120-130	QISNLGLNFVR			3	nd	1	nd	1
	168-189	VWIDLHGAPGSQNGFDNSGLR			1	2	nd	3	1
	243-253	QFFLDGYNSLR			nd	nd	nd	1	nd
	304-320	NINDHISVACNWGWDAK			2	nd	1	nd	3
	322-340	ESHWNVAGEWSAALTDCAK			1	nd	1	nd	1
	341-347	WLNGVNR			3	nd	nd	nd	3
	351-378	YEGAYDNAPYIGSCQPLLDISQWSDEHK			nd	nd	1	nd	nd
	405-429	TENAPEWSFQTLTYNGLFPQPVTDR			nd	nd	3	nd	nd
	430-438	QFPNQCGFH			1	1	2	nd	nd
Ywp1[d]	87-93	VINVPAR	533 aa	7	3	2	nd	nd	2
	94-110	NLYGAGAVPFFQVHLEK			3	nd	1	1	1
	329-339	VITVVACDEHK			nd	3	1	nd	1

nd = not detected   average protein coverage % 13

[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	140-157	ILGSQINTGNTHFNYTQR	nd	2	nd	nd	nd
	179-192	LGPVLATGSTTVLK	nd	3	nd	nd	nd
	362-373	SQGATVVTGGAR	nd	1	nd	nd	nd
Cdc54	862-868	FNDLSVK	1	nd	nd	nd	nd
Cyp1	124-138	HVVFGEVTDGLDIVK	nd	1	nd	nd	nd
Cyp5[g]	156-171	WLDGAHVVFGEVLDGK	1	nd	nd	nd	nd
Eno1	34-51	SIVPSGASTGVHEALELR	nd	nd	nd	nd	1
	225-236	EALDLIMDAIDK	nd	nd	2	nd	nd
	260-265	YDLDFK	nd	1	nd	nd	nd
	319-333	IQIVGDDLTVTNPTR	nd	nd	3	nd	nd
	341-349	KAANALLLK	nd	1	nd	nd	nd
Hsp90	90-101	ADLVNNLGTIAK	nd	1	nd	nd	nd
Met15	311-332	NPNVESVSYLGLPSHESHELSK	nd	1	nd	nd	nd
Mnt1[g]	201-210	IIYGHSESYR	nd	nd	nd	1	nd
	259-270	DYAFTISLPEYK	nd	nd	nd	1	nd
Pdi1[g]	134-144	EAAGIADYMIK	nd	nd	nd	1	nd
	222-231	KPSYLVVQPK	nd	nd	1	1	nd
	321-345	HAEVINMDPEVVPLFAIHHISDNKK	nd	nd	nd	1	nd
	498-507	ELDTLIEFIK	nd	nd	1	nd	nd
Pup3	50-65	TFLGLTGLATDVISLK	nd	1	nd	nd	nd
	199-204	RVLKTR	nd	1	nd	nd	nd
Tdh3	234-247	VPTTDVSVVDLTVR	nd	1	nd	nd	nd
Tef1	254-264	IGGIGTVPVGR	nd	1	nd	nd	nd
	272-288	AGMVVTFAPAGVTTEVK	nd	1	nd	nd	nd
Ubi3[g]	49-53	TLTGK	nd	1	nd	nd	nd
	106-114	ESTLHLVLR	nd	2	nd	nd	nd

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