Supplemental Materials

Molecular Biology of the Cell

Bode et al.

					Both Experiments				Experiment A				Experiment B			
Gene Name	Systematic Name	Molecular Weight [kDa]	Sequence Coverage [%]	PEP	Peptides	Unique Peptides	Ratio L/H	Ratio L/H Normalized	Peptides	Unique Peptides	Ratio L/H	Ratio L/H Normalized	Peptides	Unique Peptides	Ratio L/H	Ratio L/H Normalized
COX19	YLL018C-A	11.105	33.7	3.42E-09	3	3	35.42	20.17	2	2	36.08	20.72	2	2	19.84	14.39
COX11	YPL132W	34.044	18	1.06E-135	5	5	17.08	10.81	4	4	17.05	10.77	3	3	21.00	14.66
TEF2	YBR118W	50.032	2.4	5.59E-02	1	1	3.48	2.44	1	1	6.07	3.77	1	1	1.97	1.54
MCR1	YKL150W	34.137	57.3	9.12E-256	14	14	2.76	1.78	13	13	4.93	3.11	12	12	1.61	1.24
AIM9	YER080W	72.413	2.2	8.90E-11	1	1	3.00	1.77	1	1	2.67	1.57	1	1	16.49	11.78
IDP1	YDL066W	48.19	28.3	2.74E-98	9	7	2.59	1.76	8	6	3.65	2.16	9	7	1.75	1.28
RPL23A	YBL087C	14.473	5.8	1.78E-01	1	1	2.50	1.74	0	0	not found	not found	1	1	2.50	1.74
BBC1	YJL020C	128.29	16.9	0.00E+00	17	17	2.68	1.71	14	14	2.90	1.82	13	13	1.76	1.34
CCP1	YKR066C	40.352	21.9	3.29E-30	6	6	2.78	1.71	6	6	2.86	1.75	1	1	1.72	1.29
MYO3	YKL129C	142.45	2.2	1.41E-23	2	2	2.57	1.54	2	2	2.76	1.65	2	2	1.36	1.00
NPR1	YNL183C	85.989	3.7	6.96E-02	2	2	2.60	1.53	2	2	2.60	1.53	0	0	not found	not found
FSF1	YOR271C	35.414	9.8	3.46E-02	2	2	2.61	1.50	2	2	2.61	1.50	0	0	not found	not found
YMR31	YFR049W	13.689	7.3	8.07E-01	1	1	2.07	1.49	0	0	not found	not found	1	1	2.07	1.49
SPG1	YGR236C	10.545	13.7	9.41E-06	1	1	2.58	1.49	1	1	2.65	1.55	1	1	1.31	0.96
PRX1	YBL064C	29.495	50.2	1.73E-253	10	10	1.95	1.48	8	8	2.20	1.40	9	9	1.83	1.50
HSP10	YOR020C	11.372	10.4	1.73E-20	1	1	1.88	1.47	0	0	not found	not found	1	1	1.88	1.47
ACO1	YLR304C	85.367	33.9	6.10E-154	19	19	1.89	1.43	10	10	2.03	1.25	19	19	1.84	1.47
MRM1	YOR201C	46.387	10.9	9.29E-18	2	2	2.42	1.42	2	2	2.42	1.42	0	0	not found	not found
RPL32	YBL092W	14.771	23.8	6.81E-22	4	4	2.09	1.42	4	4	2.43	1.51	3	3	1.55	1.27
TIM17	YJL143W	16.584	15.2	8.78E-04	1	1	2.12	1.38	1	1	2.12	1.38	0	0	not found	not found
QCR10	YHR001W-A	8.5928	26	7.91E-15	2	2	1.88	1.38	2	2	1.84	1.16	2	2	1.95	1.57
MMF1	YIL051C	15.908	6.2	8.60E-07	1	1	1.99	1.38	1	1	1.95	1.12	1	1	2.11	1.75
YHM2	YMR241W	34.184	32.5	2.58E-301	8	8	2.19	1.38	8	8	2.28	1.41	5	5	1.51	1.16
CDC42	YLR229C	21.322	9.4	2.64E-09	2	2	2.02	1.36	1	1	2.02	1.23	2	2	2.01	1.44
PDA1	YER178W	46.343	2.6	6.38E-19	1	1	1.80	1.36	0	0	not found	not found	1	1	1.80	1.36
TDH1	YJL052W	35.75	61.4	0.00E+00	19	14	1.87	1.36	18	13	1.96	1.22	16	11	1.82	1.49
DIC1	YLR348C	32.991	5.7	3.06E-03	1	1	2.37	1.35	1	1	2.37	1.35	0	0	not found	not found
GLO4	YOR040W	32.338	7.4	7.81E-02	1	1	2.15	1.35	1	1	2.15	1.35	0	0	not found	not found
MDH1	YKL085W	35.65	56.3	1.31E-246	12	12	1.68	1.35	4	4	1.25	0.74	12	12	1.75	1.36
SEC1	YDR164C	83.479	2.2	1.08E-19	1	1	2.19	1.33	1	1	2.19	1.33	0	0	not found	not found

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Scer                MSGNPGSSLSALRPTPPERGSFPLDHDGECTKYMQEYLKCMQLVQNENAM  50
Klac                MSANPGNSLKALSPTPPERGSFPLDHDGDCTKQMQEYLSCIKLVKGENAP  50
Calb              MLFSFFIGGNFRTWTPTPPERGSFPLDHDGECKEYMTKYLTCMKFTENKNAP  52
Anid               MSFGSPGGGATNVKPTPPERGSFPLDHDGECKHLIQSYLRCLKLQRGVNDE  51
Anig               MGFGAPGGGAVPVKPTPPERGSFPLDHDGECKHLITDYLKCLKSRRGVNDD  51
Bcin              MSTFGSPGGRMVNNKPSPPERGSFPLDHDGECKSVMQSYLSCMKKVRGMNDP  52
Atha MITIKFDLNRYSRSWGAGGAFGGNRGLRPIPPEKGIFPLDHLHECDAEKKEYLGCLKSSAHKSE-  64
Pvul              MSAAGGAFGGNRGLRPVPPEKGIFPLDHMHLCDLEKAEYLNCLKTAGHQSE-  51
Dmel                 MTSQIYSQKKFVPTPPEKGSFPLDHEGLCKKQFLLYASCLRKNAQDTS-  48
Btau                MSTAMNFGSKSFQPRPPDKGSFPLDHFGECKSFKEKFMKCLRDNNFENA-  49
Hsap                MSTAMNFGTKSFQPRPPDKGSFPLDHLGECKSFKEKFMKCLHNNNFENA-  49

HsMia40                 41 GLILPNGNINWNCPCLGGMASGPCGEQFKSAFSCFHYSTEEIKG  84
ScMia40                284 AYNPDTGEINWDCPCLGGMAHGPCGEEFKSAFSCFVYSEAEPKG 327


Scer     NCRLLAKDYLRCRMDHQLMDYDEWSHLGLPEDAPGNNGKTIKDATDNK 98
Klac     NCRLLAKEYLKCRMDNKLMDRDDWKHLGLPSDKKEANDVTKETTPTSGQ 99
Calb     NCRILAKQYLKCRMDNQLMEKSDWDSLGLVNLPGENDVELDHHHHLNNNNTKADGKSG… 133
Anid     QCRRLAKGYLACRMDKNLMAPDDFRNLGLVFENDGDGSHAQAQAQTQVQTQSGSSSG 108
Anig     ECRKLAKSYLSCRMDHNLMAPDDFKNLGLIFEKDKATPSGGAEGAEKKE 100
Bcin     ECRDLAKSYLSCRMDRNLMAKDEFKNLGFADESSETKGADKKDVKEGGNDANKHKNELRW 112
Atha     QCRHLSKKYLQCRMAKNLMAKQDMAELGFSGVKELDSTEDKNTESIEH 112
Pvul     KCRQFSKKYLQCRMERNLMAKQDLAELGFKESNVETPGGKITDRVDNQDQ 101
Dmel     QCRQDAQNYLACRMDNNLMEKTEWSKLGFHDQSTKTDQKEPEVQKQ 94
Btau     LCRNESKEYLECRMERQLMAQEPLEKLGFGDLIDGKSDKN 89
Hsap     LCRKESKEYLECRMERKLMLQEPLEKLGFGDLTSGKSEAKK 90

HsMia40 SDCVDQFRAMQECMQKYPDLYPQEDEDEEEEREKKPAEQAEETAPIEATATKEEEGSS 142
ScMia40 IDCVEKFQHMQDCFRKYPEHYAEQLKETSDDEEPQDKVKVNTIESAPNVSSAKENAAKKA… 403
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                                  _________________________________Matrix/Cytosolic Domain_________________________ Transmembrane Domain__
S. cerevisiae   -----------------MIRICPIVRSKVPLLGTFLRSDSWLAPHALALRRAICKNVALRSYSVNSEQPKHTFDISKLTRNEIQQLRELKRARERKFKDRTVAFYFSSVAVLFLGLAYAA 103
K. lactis XP_453373.1  --------------------------MLKFFLRAALPASGIRTTINRTRFYRTTRLLRNNGTGNKFDLSKLTREEIKEIRDYKISAARRYKDRTVAFYFTSIAVLFLGLAYAA 88
C. albicans XP_711523.1.  ------------MNRLRIYTPIFRSTIVKPAVFRPYAFIVSRGIHTTGKLFQMQHQQQPSVPDQSSIEKQREWVDRLAREREERQKYRNRTATYYTASLGIFFLALAFSA 98
A. niger EHA22857.1  --------------------------------------------------------MFSRPISSWGRLPWSGPGLRPSTMTNTRCVDSGRRFFTRSSRYYAASLILGTVALAYGS 59
A. nidulans CBF69758.1  -------------------------------MFSRLTPPWGWSLSPGAGAARSVLSQAKGLAPGRRYFSRNSWLNQSPSAPFNTPQSQKRNASTMYYTISIILGTVSLAYGS 81
B. cinerea XP_001545817.1  ---------------------MNSIPRISRALSSKNANWICTSCAKAKRTNTPFFKPSINRSISNNSTPRGNVAPTMEQLRAPFSQKNSSTMYYTLSIILGTVAFSYGS 88
P. vulgaris XP_007163355.1  WSRLSRRTHLLPYVRAMQANSLESRFINPNTSFQHNFSYNIRVSKFNKESFYLSYRSSAFATQNVGKSSSMPGFRHFSSHASKEQKSQKMLLYLTGLVFAMVGCTYAA 110
A. thaliana AAG00893.1  ----------------------------------------------------------------------------MLDSAHRQYSTHSPSETKSQKMLYYLTAVVFGMVGLTYAA 40
H. sapiens NP_004366.1 MGGLWRPGWRCVPFCGWRWIHPGSPTRAAERVEPFLRPEWSGTGGAERGLRWLGTWKRCSLRARHPALQPPRRPKSSNPFTRAQEEERRRQNKTTLTYVAAVAVGMLGASYAA 113
B. taurus DAA19212.1   MGGLWCPAWRRVVFCGWSWSHLGRPTRAAERAEPCLRPGRSGPAGTEQGLRRLGTWRRPS-----PAEQPARRPKSTNPYTRSQEEDWRRRNKTVLTYMAAAAVGMLGASYAA 108
D. melanogaster NP_723086.1  ------------------------------------MMRSLCALRGQCQQLFRSSIRPQNSVHSQQFWRMKSTDSPEDAARKLRAKSTLYYITAGGVLIVGLSYAA 71
C. elegans NP_502547.2  --------------------------------MSLSRLWGPARSCYSFFATKSPLATLSSLQRNSNVISFQIARGFSKKPNRVVDKSADTRNYTYYVMSLVIVAIGCTFAA 79
Rickettsia prowazekii WP_014411674.1  -----------------------------------------------------------------------MSKKSNKNLAFSLLGLMMSMVLLSFAS 27
Brucella ovis YP_001258489.1  -------------------------------------------------------------------MTDQGENEKKQRRSNATIAVACLSFFVCMIGAAYAS 36
Paracoccus spec. WP_010392505.1  -----------------------------------------------------------------------MSGQEKRSNGRTVAILLGVAVLMGALSWAA 30

                _ ________________________________________Intermembrane Space/Periplasmic Domain__________________________________
Scer            VPLYRAICARTGFGGIPITDRRKFTD--------DKLIPVDTEKRIRISFTSEVSQILPWKFVPQQREVYVLPGETALAFYKAKNYSDKDIIGMATYSIAPGEAAQYFNKIQCFCFEEQK 215
Klac            VPLYRAICARTGYGGIPITDKRKFTD--------DKLIPVDSNKRIRISFTSEVSQILPWKFVPQQREVYVLPGETALAFYKAKNNSDKDIIGMATYSITPGESSPYFNKIQCFCFEEQK 200
Calb            VPIYRAICQRTGWGGIPITDSTKFTP--------DKLIPVDTNKRIRIQFTCQSSGILPWKFTPLQREVYVVPGETALAFYRAKNMSKEDIIGMATYSISPDNVAGYFNKIQCFCFEEQR 210
Anig            VPLYKMICQQTGWNGQPVLTHRGGDN-----DTSSRVTPVTDSRRLRITFNGSVSDVLPWKFTPQQREVRVLPGETALAFYTATNKGPTDIIGVATYSVTPGQVAPYFSKIQCFCFDEQK 174
Anid            VPLYKMICQQTGWNGQPVLTHRAGDG-----DTSSRVTPVTDSRRLRITFNGSVSDVLPWKFTPQQREVRVLPGETALAFYTATNKGPTDIIGVATYSVTPGQVAPYFSKIQCFCFEEQK 196
Bcin            VPMYKMICQTTGWGGQPIKAPGHGGSGVEGEDPSERLRPVTSAKRIRVTFNGSVSDVLPWKFTPQQREVRVLPGETALAFYTATNKSDEDIIGVATYSVTPGQVAPYFSKIQCFCFEEQR 208
Pvul            VPLYRRLCQATGYGGTVARRETVEEKI-----ARHDSNNTVSTREIVVQFNADIADGMQWKFVPAQREVRVKPGESALAFYTAENKSSTPITGVSTYNVTPMKAAVYFNKIQCFCFEEQR 225
Atha            VPLYRTFCQATGYGGTVQRKETVEEKI-----ARHSESGTVTEREIVVQFNADVADGMQWKFTPTQREVRVKPGESALAFYTAENKSSAPITGVSTYNVTPMKAGVYFNKIQCFCFEEQR 155
Hsap            VPLYRLYCQTTGLGGSAVAG-HASDKI--------ENMVPVKDRIIKISFNADVHASLQWNFRPQQTEIYVVPGETALAFYRAKNPTDKPVIGISTYNIVPFEAGQYFNKIQCFCFEEQR 224
Btau            VPLYRLYCQTTGLGGSAVAG-HASDQI--------ENMVPVKDRIIKITFNADVHASLQWNFRPQQTEIYVVPGETALAFYKAKNPTDKPVIGISTYNVVPFEAGQYFNKIQCFCFEEQR 219
Dmel            VPLYSIFCQAYSYGGTTTQG-HDAEKV--------EHMKKIEDRVLKIRFNADIGSSMRWNFKPQQYEIKVAPGETALAFYTARNPTDKPVIGISTYNVIPFEAGAYFNKIQCFCFEEQQ 182
Cele            IPAYRIFCEQTSFGGLTQVA-KDFDKI--------ANMKKCEDRLIRVQFNSDVPSSMRWEFKPQQHEIYVHPGETALAFYTARNPTDKPIIGISSYNLTPFQAAYYFNKIQCFCFEEQI 190
Rpro            VPIYNLFCKVTGYGGTTIKETVSVYS------------KVKGTKAIIIEFDANVDPNLPWRFIPRQKEVQIVPGQNTLVFYEAENLSNKDIIGTSIYNVTPNKAGKYFVKIHCFCFEEQL 135
Bovi            VPLYRIFCQVTGYGGTTQRVEQYSNT--------------ILDKTIKVRFDANIANGLPWDFKPMQREVTVRIGETTMIKYEAHNLFGEETYGRASFNVAPGRAGAYFNKVECFCFTDNT 142
Para            VPFYSWFCRVTGFAGTTNVAEAASDT--------------VLEEKIRVRFDANVDPNLGWTFRPMQREMELRIGENALAFYEAVNNTDEPITGTASYNVAPDAAGYFFNKIDCFCFTEQT 136

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Scer            LAAGEEIDMPVFFFIDPDFASDPAMRNIDDIILHYTFFRAHYGDGTAVSDSKKEPEMNADEKAASLANAAILSPEVIDTRKDNSN 300
Klac            LAAGEEVDMPVFFFIDPDFASDPSMRNIDDIILHYTFFKAHYADGSAVSDAAAKPEVITSQ 261
Calb            LSAGEEVDMPVFFFIDPDFAKDPAMRNIDDVVLHYSFFKAHYSDGELAAAPIGNMEMKASVVS 273
Anig            LNAGESVDMPVFFFIDPDFVKDPAMKGIDTITLSYTFFKARYDDNGVLKPLPSS 228
Anid            LNAGESVDMPVFFFIDPDFVTDPAMKGIDTITLSYTFFKARYDDNGVLKPIAGN 250
Bcin            LNAGETVDMPVFFYIDPDFVNDPNMRGIEQVTLSYTFFKARYDKNGHLKAMPVAVLRTVAGYLHMYLKSEE 279
Pvul            LLPGEQIDMPVFFYIDPEFETDPKMNGINNIVLSYTFFKVSEE 268
Atha            LLPGEQIDMPVFFYIDPEFETDPRMDGINNLILSYTFFKVSEENTTETVNNNNSVPVQETN 216
Hsap            LNPQEEVDMPVFFYIDPEFAEDPRMIKVDLITLSYTFFEAKEGHKLPVPGYN 276
Btau            LNPQEEVDMPVFFYIDPEFAEDPRMVNVDLITLSYTFFEAKEGHTLPVPGYNSNQQLSPASNL 282
Dmel            LNPHEEVDMPVFFYIDPEITADPALETCDTITLSYTFFEAKEGLKLNFPSYAKPHAASA 241
Cele            LNPGEQVDLPVFFYIDPDYVNDPALEYLDSILLSYTFFEAKSGLKLPDPFDPKNRPSIAPSPDKVPEATK 260
Rpro            LKAREKVLMPVTFYIDNDFERDPEMENIKVITLSYSFFKIREL 178
Bovi            LKPGEDLELPVVFFVDPEFVNDPDLKDVKTITLSYTFFPIDKPKPVVNAKAVGSTRNGG 201
Para            LQPGERVEMPVSFFVDADLVNDRDAGRIRDITLSYTFHRTGPPAPQQAALDHETEPTVN 195
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