

**Table S1. Candidate peptides containing misincorporated Leu/Ser at Gly (GGG) codon**

Type	Sequence <sup>a</sup>	Modification	Observed m/z	Mascot Score	Screening <sup>b</sup>	Retention time (min) <sup>c</sup>			Swiss-Prot AC #	Description	Source protein for identified peptide
						Candidate	Internal Standard	Δ time			
Gly-to-Leu	LNLIL EYK		471,3061	23.67	common	70.1	59.5	10.6	MADD_CAEEL	MAP kinase-activating death domain protein	
	QGEPPA <del>R</del> GKGLKK		550,3103	14.13	common	60.8	25.2	35.6	MEDI_CAEEL	Mediator of RNA polymerase II transcription subunit 1.1	
	TALAVGTRR		472,7859	23.00	common	38.3	27.6	10.7	NDUS7_CAEEL	Probable NADH dehydrogenase [ubiquinone] iron-sulfur protein 7 mitochondrial	
	ERGELLES <del>G</del> PK		607,8239	12.72	common	46.7	34.6	12.1	NGLY1_CAEEL	Peptide-N(4)-(N-acetyl-beta-glucosaminyl)asparagine amidase	
	QVLC <del>D</del> L		438,2366	17.49	common	ND	ND	-	PAFA_CAEEL	Platelet-activating factor acetylhydrolase homolog 2	
	FEEA <del>R</del> LR		524,7807	21.22	common	36.7	30.6	6.1	IFA2_CAEEL	Intermediate filament protein ifa-2	
	AFVLA <del>V</del> MR		485,7629	19.27	common	57.1	58.3	1.2	LE418_CAEEL	Protein let-418	
	RTDTL K		367,2139	12.70	common	ND	ND	-	RIM_CAEEL	Rab-3-interacting molecule unc-10	
	ALEMTSLK		452,7621	18.27	common	48.5	52.5	4.0	ACN1_CAEEL	Inactive angiotensin-converting enzyme-related protein	
	RDLEHNA <del>V</del> YL		623,3240	10.55	common	ND	54.9	-	CADH3_CAEEL	Cadherin-3	
	LAELNNLTITSL		713,9298	18.62	(a)	ND	ND	-	CLAP1_CAEEL	Protein CLASP-1	
	EDATSVK <del>V</del> ANLL		666,8645	31.15	(b)	72.8	57.4	15.4	CHITL_CAEEL	Chitinase-like protein C25A8.4	
	RSKDV <del>L</del> L		415,7591	23.69	(b)	40.8	31.2	9.6	SIR41_CAEEL	NAD-dependent protein deacetylase sir-2.2	
	TPSMK <del>V</del> TL		444,7649	25.66	(b)	68.9	53.5	15.4	NHR20_CAEEL	Nuclear hormone receptor family member nrh-20	
	SPASLDD <del>D</del> IK		530,7622	20.47	(b)	36.3	37.8	1.5	PS11A_CAEEL	Probable 26S proteasome regulatory subunit rpn-6-1	
	L <del>L</del> IEK		308,2075	31.40	(b)	ND	ND	-	SRRT_CAEEL	Serratia RNA effector molecule homolog	
	TL <del>D</del> IK		301,6973	25.82	(b)	ND	ND	-	CLH_CAEEL	Probable clathrin heavy chain 1	
Gly-to-Ser	LSEFAI <del>S</del> F		336,8471	15.16	common	35.2	59.9	24.7	DHTK1_CAEEL	Probable 2-oxoglutarate dehydrogenase E1 component DHKTD1 homolog mitochondrial	
	SGTIQATEL <del>S</del> R		587,8251	27.20	common	ND	45.1	-	U520_CAEEL	Putative U5 small nuclear ribonucleoprotein 200 kDa helicase	
	AERQV <del>S</del> LR		523,2858	22.76	common	34.1	27.0	7.1	HUTU_CAEEL	Probable uracinate hydratase	
	HSLIR		313,1930	24.63	(b)	ND	ND	-	GALT9_CAEEL	Probable N-acetyl-galactosaminyltransferase 9	
	MP <del>S</del> LFP <del>M</del> K	Oxidation@M:7	483,7424	23.90	(b)	50.6	58.5	7.9	DGK3_CAEEL	Probable diacylglycerol kinase 3	
	VT <del>S</del> OE <del>G</del> AR		424,2170	27.19	(b)	ND	22.6	-	SRB5_CAEEL	Serpentine receptor class beta-5	
	FIS <del>S</del> LPI <del>T</del> R		523,3242	26.38	(b)	73.9	58.8	15.1	SRE37_CAEEL	Serpentine receptor class epsilon-37	

<sup>a</sup> Amino acid residues arising from the decoding of Gly (GGG) codon are shown in red.

<sup>b</sup> Screening types of each mutant peptide candidate are shown (see Figure 3A).

<sup>c</sup> Chromatographic retention times of the targeted peptides are shown.