

AA-I	TAILS Peptide		pos'n	# of Genes	Annotated ATG context			Signal Peptide Annotation	Peptide AA1 context (if different)		Notes			
	AA1	site in CDS			xAxk-ATG	cA(ac)(acg)-ATG			xAxk-AA1	cA(ac)(acg)-AA1				
#M#R	M	1	175	112	64	60	34	10	6		<i>N-terminal tagging supports existing annotation; not cleaved by aminopeptidase (89/175 Met-Glu/Asp)</i>			
R	M	1	15	14	93			1	7		<i>N-terminal tagging supports existing annotation; not cleaved by aminopeptidase (8/15 Met-Glu/Asp); or could be Arg cleavage product from sample prep, but upstream context is usually AG (A@-3) rather than</i>			
M	any	2	242	180	74	85	35	20	8	242	100	<i>N-terminal tagging supports existing annotation; cleaved by aminopeptidase (197/242 Met-Ala/Ser)</i>		
#M#R	M	>2	48	12	25	0	0	8	17	31	65	17	35	<i>N-terminal tagging suggests probable alternative gene models; mapped peptide ATG context is more likely to be translated than annotated ATG context; not cleaved by aminopeptidase (19/48 Met-Glu/Asp)</i>
R	M	>2	17	11	65	6	35	6	35	6	35			<i>N-terminal tagging suggests possible alternative gene models; although annotated ATG context is more likely to be translated than mapped peptide ATG context; not cleaved by aminopeptidase (4/17 Met-Glu/)</i>
M	any	>2	65	19	29	5	8	15	23	65	100			<i>N-terminal tagging suggests probable alternative gene models; mapped peptide ATG context is more likely to be translated than annotated ATG context; cleaved by aminopeptidase (57/65 Met-Ala/Ser)</i>
#M#R	#M	>2	317	188	59	87	27	145	46	46	15	8	3	<i>N-terminal tagging identifies probable internal proteolytic cleavage sites; supported by ATG context & high prevalence of signal peptide predictions</i>
R	#M	>2	260	169	65	89	34	68	26	54	21			<i>Likely experimental artefacts, attributable to incomplete removal of experimental proteolytic cleavage products</i>
any	M	1	8244	4433	54	1702	21	1939	24	Entire Annotated Genome				
			2264	<i>N-terminally-tagged peptides (from all experiments)</i>										
			1911	<i>Distinct peptides (excluding 353 exact duplicates)</i>										
			1606	<i>Unique peptides (excluding 305 overlapping peptides)</i>										
			1139	<i>Number of genes (excluding 467 downstream peptides)</i>										