

TABLE 1. Selected degradation candidates during growth into the glucose-limited stationary phase identified by pulse-chase labeling and 2-D PAGE

Functional category and enzyme	Stability (% remaining protein after 8 h of pulse-chase labeling)				Functional category and enzyme	Stability (% remaining protein after 8 h of pulse-chase labeling)			
	Wild type	$\Delta clpP$	$\Delta clpC$	$\Delta clpX$		Wild type	$\Delta clpP$	$\Delta clpC$	$\Delta clpX$
Cell wall biosynthesis					RNA polymerase subunits				
GlmS	12	85	71	20	RpoB	35	84	>100	73
MurAA	22	49	75	16	Clp ATPase				
Amino acid biosynthesis					ClpC1	12	83	x	67
ArgB	38	54	80	100	ClpC2	22	95	x	98
AroA1	41	68	93	28	Cold shock				
CarB	6	97	71	22	F-CspB	10	59	11	38
IlvA	17	61	84	26	CspD	12	23	19	14
IlvB1	8	74	39	17	General stress response				
GltA1	11	80	82	64	Ctc	50	98	67	48
GltA2	22	91	>100	51	OsmC(YkrA)	21	61	23	9
LeuA1	19	71	30	47	Secretion				
LeuA2	20	56	27	83	SecA1	32	62	76	84
LeuC1	9	69	41	18	SecA2	39	82	93	>100
LeuC2	14	67	50	39	Chemotaxis				
LeuD	28	77	63	38	CheW	9	>100	ND	59
LysC α	31	91	76	22	Inactive glutamate dehydrogenase				
LysC β	21	79	73	20	GudB	2	28	18	18
MetE1	39	75	75	70	Methionine salvage pathway				
Nucleic acid biosynthesis					MtnK (YkrT)	19	93	45	22
NrdE	24	38	70	25	MtnS (YkrS)	41	64	60	37
PurB1	28	75	>100	>100	Sporulation				
PurB2	34	100	69	100	SpoVG	10	19	5	20
PurF	36	72	77	10	Unknown function				
PurL	30	95	61	17	YfhM	24	62	100	93
PurQ	19	44	>100	13	YhaM	40	75	99	65
PyrB	21	61	64	49	YhxA	11	65	90	72
Xpt	26	79	ND	21	YkqC	49	72	>100	100
Vitamin biosynthesis					YloV	47	>100	59	43
BioB	18	43	56	19	YugI	19	45	67	43
ThiC1	22	69	90	40	YurU1	18	31	10	20
ThiC2	28	62	>100	47	YvFW2	19	48	74	45
ThiD (YjbV)	39	57	74	52	Degradation candidates				
Aminoacyl-tRNA synthetases					D112	26	72	79	72
IleS	49	87	69	100	D116	42	100	56	26
ThrS	47	66	68	94	D12	26	100	51	54
ThrZ	27	65	>100	ND	D34	14	75	23	65
Glycolysis					D38	12	85	100	26
PycA1	10	45	50	56	D42	18	71	49	12
Ribosomal proteins					D43	8	>100	36	87
Efp	32	35	40	41	D50	22	82	49	>100
Tig	47	>100	96	78	D65	19	89	63	100
TufA	50	45	65	76	D74	28	54	>100	>100
DNA replication									
GyrA	24	89	90	>100					
GyrB	48	60	53	80					