Table 1. Proteins aggregated upon DnaK and DnaJ depletion in a *secB* null background.

	Name/ Function[a]	Mw (kDa)	DnaK/DnaJ depleted (4)[b]	*secB* null (5)[c]	Localization	Swiss-Prot/TrEMBL entry
IbpB*	Chaperone	16	+	+	Cytoplasm	P0C059
IbpA*	Chaperone	16	+	+	Cytoplasm	P0C055
OmpX	Outer membrane protein X	19	-	+	Outer membrane	P0A919
S3	30S ribosomal protein	26	-	-	Cytoplasm	P0A7V5
OmpA	Outer membrane protein A	37	-	+	Outer membrane	P0A911
PhoE	Outer membrane protein E	39	-	-	Outer membrane	Q8CWC3
OmpC	Outer membrane protein C	40	-	-	Outer membrane	P06996
EF-Tu	Elongation factor Tu	43	+	-	Cytoplasm	P0A6N3
MurA	UDP-N-acetylglucosamine 1-carboxylvinyltransferase	45	+	-	Cytoplasm	Q8X9J9
ClpX*	Chaperone	47	+	-	Cytoplasm	P0A6H3
Rho	Transcriptional terminator	47	+	-	Cytoplasm	P0AG32
Gnd	Gluconate-6-phosphate dehydrogenase	48	+	-	Cytoplasm	Q5JBG2
HflX	GTP-binding protein	49	-	-	Cytoplasm	P25519
AtpD	ATP synthase subunit beta	50	-	-	Cytoplasm	P0ABB6
AccC	Biotin carboxylase	50	-	-	Cytoplasm	Q8X9B6
LpdA	Dihydrolipoamide dehydrogenase	51	+	-	Cytoplasm	P0A9P2
GroEL*	Chaperone	57	-	-	Cytoplasm	Q6UDB5
PyrG	CTP synthase	61	+	-	Cytoplasm	P0A7E7
TypA	GTP-binding protein	68	+	-	Cytoplasm	P0A3B2
NuoC	NADH-quinone oxidoreductase	69	-	-	Cytoplasm	P33599
FtsH*	ATP-dependent protease	71	-	-	Inner membrane	Q8X9L0
ThrS	Threonyl-tRNA synthase	75	+	-	Cytoplasm	Q8XE27
EF-G	Elongation factor G	78	+	-	Cytoplasm	P0A6N0
PflB	Formate acetyltransferase 1	85	+	-	Cytoplasm	P09373
Lon*	ATP-dependent protease	88	+	-	Cytoplasm	P0A9M1
YaeT	Outer membrane protein assembly factor	91	-	-	Outer membrane	P0A942
AdhE	Aldehyde–alcohol dehydrogenase	96	+	-	Cytoplasm	P0A9Q8
AceE	Pyruvate dehydrogenase E1 component	99	+	-	Cytoplasm	P0AFG9
TrcF	Transcription-repair coupling factor	130	+	-	Cytoplasm	P30958
NarG	Nitrate reductase	141	+	-	Cytoplasm	P09152
RpoB	RNA polymerase	151	+	-	Cytoplasm	P0A8V4
RpoC	RNA polymerase	156	+	-	Cytoplasm	Q8FB83

[a] Proteins found in the aggregated fraction after 3 h of DnaK and DnaJ depletion in the *secB* null strain background at 30°C (as presented in Fig. 4C, line 3). Proteins are listed according to their sizes in kDa. The protein bands present in the aggregates were excised from the Coomassie Blue-stained SDS-polyacrylamide gels and protein species were identified by peptide mass fingerprinting as described (6). Proteins marked with the symbol (*) are either chaperones or proteases which most likely co-aggregate with unfolded substrates (4).

[b] Aggregated proteins that were (+), or were not (-) previously identified upon DnaK and DnaJ depletion at 37°C in a $SecB^+$ background (4).

[c] Aggregated proteins that were (+), or were not (-) previously identified in a *secB* null mutant background at 37°C in the presence of endogenous DnaK and DnaJ (5).