Table S1. List of BIAM reactive Cys containing peptides, identified in the LC-MS/MS analysis

LOCUS	DEFINITION	Sequence	SUBCELLULAR LOCATION	Source
ACO1	Mitochondrial aconitase	VGLIGSC#TNSSYEDMSR	cytoplasm\mitochondrial matrix	3,4
ACO1	Mitochondrial aconitase	VAC#QDATAQMA	cytoplasm\mitochondrial matrix	3,4
ACT1	Actin	IDNGSGMC#K	actin cable	3,4
ADE3	Cytoplasmic trifunctional enzyme C1-tetrahydrofolate synthase	C#VGDVEFNEAIK	cytoplasm\nucleus	1,2,3,4
ADE3	Cytoplasmic trifunctional enzyme C1-tetrahydrofolate synthase	AGQVLDGKAC#AQ	cytoplasm	1,2,3,4
ADE6	Formylglycinamidine-ribonucleotide (FGAM)-synthetase	C#QQVIDAC#	cytoplasm	1,3,4
ADE6	Formylglycinamidine-ribonucleotide (FGAM)-synthetase	GLDLC#PALGVAIPVGKDSMSMK	cytoplasm	1,3,4
ADE6	Formylglycinamidine-ribonucleotide (FGAM)-synthetase	YVLGVSPQDLSIFEEIC#KR	cytoplasm	1,3,4
ADH1/ADH2	alcohol dehydrogenase activity	C#CSDVFNQVVK	cytoplasm	1,2,4

ADH3	alcohol dehydrogenase activity	YSGVC#HTDLHAWHGDWPLPVK	cytoplasm	1
AHP1	Thiol-specific peroxiredoxin	FQYIAISQSDADSESC#K	cytoplasm	1,2,3
ALD4	aldehyde dehydrogenase (NAD) activity	AVQNIILGIYYNSGEVC#CAGSR	mitochondrion	1,2
ALD5	aldehyde dehydrogenase activity	SLFC#AR	mitochondrion	2
ALD6	Utilizes NADP+ as the preferred coenzyme	AQDGKTYPVEDPSTENTVC#EVSSA	cytoplasm	1,2,3,4
ALD6	Utilizes NADP+ as the preferred coenzyme	NAGQIC#SSGSR	cytoplasm	1,2,3,4
ALD6	Utilizes NADP+ as the preferred coenzyme	TTEDVEYAIEC#ADR	cytoplasm	1,2,3,4
APE3	Vacuolar aminopeptidase Y	C#YHQLC#DDVSNL	vacuole	3
APJ1	Putative chaperone of the HSP40 (DNAJ) family	LGLNRTRIC#SVCDGHGGLK	cytoplasm\nucleus	1
ARC40	structural constituent of cytoskeleton	FPFGC#LIR	cytoplasm	1
ARO4	3-deoxy-D-arabino-heptulosonate-7-phosphate (DAHP) synthase	VNDVVC#EQIANGENAITGV	cytoplasm\nucleus	3
ARO4	3-deoxy-D-arabino-heptulosonate-7-phosphate (DAHP) synthase	DAC#IGWETTEDVLR	cytoplasm\nucleus	3
ASC1	WD repeat protein (G-beta like protein) that interacts with the translational machinery	GQC#LATLLGHNDWVSQVR	cytoplasm	1
ASN1	Asparagine synthetase	NLHLADC#LR	cytoplasm	1,2,3
ASN1	Asparagine synthetase	ADWGC#AEDPSGR	cytoplasm	1,2,3

BAT1/2	branched-chain-amino-acid transaminase activity	LGANYAPC#ILPQLQAAK	mitochondrial matrix	2
BMH1/2	DNA Protein binding, RAS protein signal transduction	EKSEHQVELIC#SYR	cytoplasm	1
BNI5	Protein involved in organization of septins	LADQTPHDDNSENC#PNR	septin ring	1,2,3,4
CDC19	pyruvate kinase activity	NC#TPKPTSTTETVAAS	cytoplasm	1,2,3,4
CDC19	pyruvate kinase activity	AC#DDKIMYVDYK	cytoplasm	1,2,3,4
CDC19	pyruvate kinase activity	NAGKIC#SHK	cytoplasm	1,2,3,4
CDC19	pyruvate kinase activity	AEVSDVGNAILDGADC#VMLSGETAK	cytoplasm	1,2,3,4
CDC19	pyruvate kinase activity	SNLAGKPVIC#AT	cytoplasm	1,2,3,4
CDC55	Non-essential regulatory subunit B of protein phosphatase 2A	QNSLC#DNK	nucleus	2
CIS3	cik1 suppressor	NVAEQC#SAIHLE	bud tip	3,
CUP1-1/2	Metallothionein	SC#C#SGK	cytoplasm	1,2
CUP1-1/2	Metallothionein	QNEGHEC#QCQCGSCK	cytoplasm	1,2
CYR1	Required for START A of cell cycle,	QQRC#SGLEICR	plasma membrane	1
DAK1	putative dihydroxyacetone kinase	SEPHITELDNQVGDGDC#GYTLVAGVK	cytoplasm	2
DAP1	damage response protein	PC#IGTLIPEPGVNV	membrane	3
DED81	Cytosolic asparaginyl-tRNA synthetase	ILAWLC#DR	cytoplasm	1

DLD3	D-lactate dehydrogenase	C#DAGVVMR	cytoplasm	3
DRS1	Nucleolar DEAD-box protein required for ribosome assembly	KNLEVPVLIC#TD	nucleolus	4
DYS1	Deoxyhypusine synthase, catalyzes formation of deoxyhypusine	IGNLLVPNDNYC#K	cytoplasm	1,2,4
ECM33	GPI-anchored protein of unknown function	QSNGAIQGDSFVC#K	plasma membrane	3
ECM39	Alpha-1,6-mannosyltransferase localized to the ER	GIVGLTNGLSFIYLKNC#LQDMFDEITEKK	ER	1
EDE1	Key endocytic protein involved in a network of interactions with other endocytic proteins	C#NWDLEAATNFLLDSA	actin cortical patch\bud neck	3
EFT2	translation elongation factor eEF-2 - yeast	VTDGALVVVDTIEGVC#VQTETVLR	cytoplasm	1,2
EMI2	probable glucokinase	TPFQLC#SEVLSR	cytoplasm	1
ENO1/2	Enolase I, catalyzes the first common step of glycolysis and gluconeogenesis	IGLDC#ASSEFFK	cytoplasm	1,2,3
EPS1	Pdi1p (protein disulfide isomerase)-related protein	IESADLC#GDENIEYFPEIRL	endoplasmic reticulum membrane	3
ERG10	Acetyl-CoA C-acetyltransferase (acetoacetyl-CoA thiolase),	IGVAAIC#NGGGGASSIVIEKI	cytoplasm	1,2
ERG20	Farnesyl pyrophosphate synthetase	DVLIPLGEYFQIQDDYLDC#FGTPEQIGK	cytoplasm	3
FAS2	Alpha subunit of fatty acid synthetase	VGNC#SGSGMGGVSALR	fatty-acid synthase complex	1,3

FBA1	Fructose 1,6-bisphosphate adolase	HMLDLSEETDEENISTC#VK	cytoplasm	1,2,3,4
FBA1	Fructose 1,6-bisphosphate adolase	LDTDC#QYAYLTGIR	cytoplasm	1,2,3,4
FBA1	Fructose 1,6-bisphosphate adolase	GNC#HGLYAGDIA	cytoplasm	1,2,3,4
FBA1	Fructose 1,6-bisphosphate adolase	EQVGC#KEEKPLFL	cytoplasm	1,2,3,4
FMP12	The authentic, non-tagged protein	SMEESSKPVSVC#	mitochondrion	3
FPR1	Peptidyl-prolyl cis-trans isomerase (PPIase), binds to the drugs FK506 and rapamycin	GSPFQC#NIGVGQVIK	cytoplasm\nucleus	1,2
FRT1	Exhibits physical and genetic interactions with TCP1 and FRT2	NC#TLLPPSFPR	endoplasmic reticulum	1
GAS1	Beta-1.3-glucanosyltransferase	EYGC#NEVTPR	plasma membrane	3
GCN1	Positive regulator of the Gcn2p kinase	YC#IFQTTVK	cytoplasm	2
GCV2	P subunit of the mitochondrial glycine decarboxylase complex	LDDTYGDMNLIC#TC#PSVEEIANETE	mitochondrion	1,2,
GIS2	GIG3 suppressor	C#YTCGQAGHMSR	cytoplasm	3,4
GIS2	GIG3 suppressor	SEC#TVQR	cytoplasm	3,4
GIS2	GIG3 suppressor	NKPGHVQTDC#TMPR	cytoplasm	3,4
GLK1	glucokinase	AVDQIC#DDFEVTPEKLDELTAY	cytoplasm	3
GLY1	L-threonine aldolase	HPFDC#NGPTQIY	cytoplasm	1
GND1	6-phosphogluconate dehydrogenase	PEC#ASDNLPVDK	cytoplasm	1,2

GPX2	glutathione peroxidase activity	C#QLNYGVTFPIMK	cytoplasm	4
GRS1	glycine-tRNA ligase activity	HFILEEDMLEVDC#TMLTPYEVLK	cytoplasm\mitochondrion	1
GUA1	GMP synthase	AGLYNQISQAFAC#LLPVK	N\A	1
HAP1	Heme-responsive zinc finger transcription factor of the Zn(2)-Cys(6) binuclear cluster domain type	IPLSCTIC#R	nucleus	1
HEM13	coproporphyrinogen oxidase	C#DEYFYI	mitochondrial inner membrane	3
HIS1	ATP phosphoribosyltransferase, a hexameric enzyme,	IKFVSGSVEASC#ALGIGDAIVDLVESGETMR	cell	1,3
HIS4	Multifunctional enzyme containing phosphoribosyl-ATP pyrophosphatase	C#FGEFKHGLVGLESLLK	cell	3
HIS4	Multifunctional enzyme containing phosphoribosyl-ATP pyrophosphatase	QC#KEIVFASPPR	cell	3
HIS4	Multifunctional enzyme containing phosphoribosyl-ATP pyrophosphatase	C#LGLVYSSK	cell	3
HIS5	Histidinol-phosphate aminotransferase	C#LGVGSDESIDAIIRACCVPGKEK	cell	4
HOM2	Aspartic beta semi-aldehyde dehydrogenase,	HTEC#ISLR	cytoplasm\ nucleus	3
HXK1/2	Hexokinase isoenzyme 1	C#EYGSFDNEHLVLPR	cytoplasm	3,4
HXK2	Hexokinase isoenzyme 2	YDVC#SDIEKLQ	cytoplasm\nucleus	3,4

HYP2	Translation initiation factor eIF-5A	DAGSSATYPMQC#SALR	cytoplasm\ ribosome	3
HYR1	glutathione peroxidase activity	SKC#GFTPQYKELEALYKR	cytoplasm	3,4
IDI1	Isopentenyl diphosphate:dimethylallyl diphosphate isomerase	SSETSNDESGETC#FSGHDEEQIK	cytoplasm	1
IDP1	isocitrate dehydrogenase (NADP+) activity	RGELDNTPALC#K	mitochondrion	1
ILV5	Acetohydroxyacid reductoisomerase	C#LMGGIHGMF	mitochondrion	1,4
PDI1	protein disulfide-isomerase	KDVLVLYYAPWC#GHCK	cytoplasm	1,2
KRE11	molecular_function unknown	C#DLDGSNIEQLR	TRAPP	2
LYS7	copper chaperone for SOD1	QVC#AC#TGK	cytoplasm	1,2
MAP1	methionine aminopeptidase	TYC#GHGVGEFFHCSPNIPHYAK	cytosolic ribosome	1
MPD1	Disulfide isomerase related protein	APWC#GHCK	vacuole	1
MSL5	branchpoint bridging protein	KIPNIQGIVC#K	commitment complex	2
MSU1	Protein essential for mitochondrial biogenesis	ITSKC#SGK	mitochondrial matrix	1,2
NUP82	Subunit of the nuclear pore complex (NPC),	ACISPC#ERIIPSADR	nuclear pore	2
PDC1	pyruvate decarboxylase	VKDAKNPVILADAC#CSR	cytoplasm\nucleus	1,2,3
PDC1	pyruvate decarboxylase	DIATAPAEIDRC#IR	cytoplasm\nucleus	1,2,3
PDI1	formation and isomerization of disulfide bonds	FFAPWC#GHC#K	endoplasmic reticulum lumen	1,3,4

PDI1	formation and isomerization of disulfide bonds	QIDC#TENQDLC#MEHNIPGFPSLK	cytoplasm	1,3,4
PDX3	pyridoxine (pyridoxiamine) phosphate oxidase	KDAEDIPC#PDY	N\A	3
PET191	Protein required for assembly of cytochrome c oxidase	YDQQYENLC#K	mitochondrial inner membrane	2
PEX19	40 kDa farnesylated protein associated with peroxisomes	VPHQQMEQGC#SSLK	cytoplasm	1,2
PFK1	phosphofructokinase activity	QDSC#YGVAFR	cytoplasm	1,2,3,4
PFK1	phosphofructokinase activity	C#GGDGSLTGADLF	cytoplasm	1,2,3,4
PHO11/3/5/12	acid phosphatase activity	VAGTDFLKVC#	extracellular	1,3,4
PHO11/3/5/12	acid phosphatase activity	VINDAVVPIETC#	extracellular	3
PMI40	mannose-6-phosphate isomerase activity	TDFEGFC#GFKPL	cytoplasm\ nucleus	1,3,4
POL2	DNA polymerase II	AAPESIFSC#VRC#HK	epsilon DNA polymerase complex	1
PRO2	glutamate-5-semialdehyde dehydrogenase activity	HADGIC#SIYLDEDADLIKAK	cytoplasm\nucleas	1,2,3
PRO2	glutamate-5-semialdehyde dehydrogenase activity	LTEAIQC#K	cytoplasm\nucleas	1,2,3
PRX1	Mitochondrial peroxiredoxin	SHPADFTPVC#TTEVSAF	mitochondrion	3

PSA1	mannose-1-phosphate guanylyltransferase	STIVGWNSTVGQWC#R	cytoplasm	1,2,3,4
PSA1	mannose-1-phosphate guanylyltransferase	NSDVIC#EYPFKEL	cytoplasm	1,2,3,4
PSA1	mannose-1-phosphate guanylyltransferase activity	SVVLC#NSTIK	cytoplasm	1,2,3,4
PYC1/2	converts pyruvate to oxaloacetate	KLTC#RPGLELEPFDLEK	cytoplasm	1,2
QNS1	Glutamine-dependent NAD Synthetase	YDC#SSADINPIGGISK	cytoplasm\nucleas	2
QNS1	Glutamine-dependent NAD Synthetase	FDPTVC#PTK	cytoplasm\nucleas	2
RGR1	RNA polymerase II transcription mediator activity	TTNMNVNNC#IWALK	mediator complex	1
RPL10	Protein component of the large (60S) ribosomal subunit	ATVDEFPLC#VH	cytosolic large ribosomal subunit	4
RPL11	Protein component of the large (60S) ribosomal subunit	C#KGTVGNSHK	cytosolic large ribosomal subunit	4
RPL12A/B	Protein component of the large (60S) ribosomal subunit	TLASVTKEILGTAQSVGC#RVDF	cytosolic large ribosomal subunit	1,3
RPL15A	Protein component of the large (60S) ribosomal subunit	YNWIC#DPVHK	cytosolic large ribosomal subunit	1
RPL23A/B	Protein component of the large (60S) ribosomal subunit	TGPVGKEC#ADLWPR	cytosolic large ribosomal subunit	1,3
RPL3	Protein component of the large (60S)	GC#IPGNR	cytosolic large ribosomal subunit	2

RPL34A/B	Protein component of the large (60S) ribosomal subunit	C#ANCVK	cytosolic large ribosomal subunit	2
RPL37B	Protein component of the large (60S)	TC#SSCGYPSAK	cytosolic large ribosomal subunit	1,2
RPL40A/B	ribosomal chaperone activity	C#GHTNQLRPK	cytosolic large ribosomal subunit	2
RPL40A/B	ribosomal chaperone activity	ATNC#R	cytosolic large ribosomal subunit	2
RPL4A/B	N-terminally acetylated protein component of the large (60S) ribosomal subunit	SGQGAFGNMC#R	cytosolic large ribosomal subunit	1,2,4
RPS0A/B	Protein component of the small (40S) ribosomal subunit	TDLDSPSEFVDVAIPC#NNR	cytosolic small ribosomal subunit	1,4
RPS11A/B	Protein component of the small (40S) ribosomal subunit	VQVGDIVTVGQC#RPISK	cytosolic small ribosomal subunit	1
RPS11A/B	40S ribosomal protein S11 (S18) (YS12) (RP41).	C#PFTGLVSIR	cytosolic small ribosomal subunit	1
RPS17A/B	Ribosomal protein 51 (rp51) of the small (40s) subunit	LC#DEIATIQSK	cytosolic small ribosomal	1
RPS2	component of the small (40S) subunit	C#GSVTVR	cytosolic large ribosomal subunit	1
RPS21A/B	Protein component of the small (40S) ribosomal subunit	KC#SATNR	cytosolic small ribosomal subunit	2,3,4

RPS22A/B	Protein component of the small (40S) ribosomal subunit	C#GVISPR	cytosolic small ribosomal subunit	1
RPS27	Protein component of the small (40S) ribosomal subunit	C#TPTGGKAK	cytosolic small ribosomal subunit	3
RPS31	Fusion protein that is cleaved to yield a ribosomal protein of the small (40S) subunit	EC#SNPTCGAGVFLANHK	cytoplasm	1
RPS8A/B	Protein component of the small (40S) ribosomal subunit	C#DGYILEGEELAFYLRR	cytosolic small ribosomal subunit	1,3
SAM4	AdoMet-homocysteine methyltransferase	IIGGCC#R	cytoplasm\nucleus	1
SBP1	single stranded nucleic acid binding protein	NVAHEC#TEDDLKQL	nucleus	3
SHE3	mRNA binding	NSSAIEQSC#SEK	cytoplasm	2
SHM2	serine hydroxymethyltransferase	VLVAGTSAYC#R	cytoplasm	1
SHP1	Putative regulator of Glc7p (protein phosphatase I),	AINTEHVGGLC#PKPGSSQGSNEYLK	cytoplasm\ nucleus	2
SOD1	Cu, Zn superoxide dismutase	TGNAGPRPAC#GVIGLTN	cytoplasm\mitochondrial	2,3,4
SOD1	Cu, Zn superoxide dismutase	EFGDATNGC#VSAGPHFNPFKK	cytoplasm\ mitochondrial intermembrane space	2,3,4
SSA1	Stress-Seventy Subfamily B;	FEELC#ADLFR	cytoplasm	1,2,3,4
SSB1/SSB2	Stress-Seventy Subfamily B;	VNC#KENTLLGEFDLK	cytoplasm	1,2,3,4
SSE1	HSP70 family member	C#DPSGLHTIEEAYTIE	cytoplasm	3

STI1	Heat shock protein	FSDALNDANEC#VK	cytoplasm	3
STP1	transcription factor, activated by proteolytic processing in response to signals from the SPS sensor system	QADSC#INCK	nucleus	1
TDH3/1/2	Glyceraldehyde-3-phosphate dehydrogenase 3	SNASC#TTNC#	cytoplasm	1,3,4
TEF2	translation elongation factor eEF-1 alpha-A chain	NHPGQISAGYSPVLDC#HTAHIA	cytoplasm	1,2,3,4
TEF2	translation elongation factor eEF-1 alpha-A chain	C#RFDELLEKNDR	cytoplasm	1,2,3,4
TEF2	translation elongation factor eEF-1 alpha-A chain	FVPSKPMC#VEAFSEYPPLGR	cytoplasm	1,2,3,4
TEF2	translation elongation factor eEF-1 alpha-A chain	C#GGIDKR	cytoplasm	1,2,3,4
TEF2	translation elongation factor eEF-1 alpha-A chain	GNVC#GDAK	cytoplasm	1,2,3,4
TFP1	Encodes a protein with three regions (ABC)	LNLC#AEYK	hydrogen-transporting ATPase V1 domain	2
TFP1	hydrogen-transporting ATPase activity, rotational mechanism	VLDALFPC#VQGGTTCIPGAFGCGK	hydrogen-transporting ATPase V1 domain	1,2
THR4	threonine synthase	SVTGTFDNC#QDIVK	cytoplasm\nucleus	1,3
TPM2	Actin-binding protein	KC#EEFQSK	actin cable	2

TRR1	Thioredoxin reductase	GISAC#AVC#DGAVPIFR	cytoplasm	1,3
TRX1/3	thioredoxin	C#GPC#KM	cytoplasm	1,2,3,4
TRX2	thioredoxin	SASEYDSALASGDKLVVVDFFATWC#GPC#K	cytoplasm	1,4
TSA1	Thiol-specific antioxidant protein	AFTFVC#PTEIIAFSEAAK	cytoplasm	1,2,3,4
TSA1	Thiol-specific antioxidant protein	AFIPLAFTFVC#PTEIIAFSEAAK	cytoplasm	1,2,3,4
TTR1	glutaredoxin	TYC#PYC#K	cytoplasm	2,4
VAS1	mitochondrial and cytoplasmic valyl-tRNA synthetase	SSEAEYFHWLGNIQDWC#ISR	cytoplasm\ mitochondrion	1
VPS15	myristoylated protein kinase involved in vacuolar protein sorting	HGAVSSIC#IDEECCVLILGTTR	Golgi membrane	1
YAL049C	contains Dienelactone hydrolase family	C#C#FEGVCHDGTPK	cytoplasm	2
YAR1	200-amino-acid protein with two ANK repeat motifs	C#DEYEADPFIR	cytoplasm	3
YBR267W	Hypothetical ORF,zinc finger	IGLGNIC#IVCNYQGR	cytoplasm	1
YDR051C	contains Phosphoglycerate mutase domain	WTDC#EGDLTT	cytoplasm\nucleus	2
YDR051C	contains Phosphoglycerate mutase domain	IC#EDMR	cytoplasm\nucleus	2
YDR365W-A	TyA Gag protein	TEEC#EK	retrotransposon nucleocapsid	2
YJR119C	Hypothetical ORF	TILC#DSCDKPFHIYCLSPPLER	cytoplasm\nucleus	2

YKL215C	molecular_function unknown	NGERC#AFITTK	cytoplasm	2
YLR257W	Hypothetical ORF	GSTPC#LIGDSIR	cytoplasm	1,2
YMR031C	contains Chromosome segregation ATPase domain	C#EQDITEAR	cytoplasm	2
YNL134C	alcohol dehydrogenase (NADP+) activity	IGPQGALLGC#DAAGQIVK	cytoplasm	1
YNL247W	Protein required for cell viability	C#QPWNK	cytoplasm\colocalizes with ribosome	1
YOR220W	molecular_function unknown	C#LFASKPLGLTIDTSTR	cytoplasm	2
YSA1	phosphoribosyl-ATP diphosphatase activity	VC#IEMPAGLIDAGEDIDTA	cytoplasm\nucleus	3
ZPR1	binds to translation elongation factor eEF-1	NC#EIQPASQIQEK	cytoplasm\nucleus	2
ZTA1	quinone reductase	C#TIPEQQK	cytoplasm	2

detected reactive Cys; 1 = BIAM reactive Cys, regulated (reducible) by TCEP; 2 = BIAM reactive Cys, not regulated by reducing agents; 3 = BIAM reactive Cys, regulated by TRX1; 4 = BIAM reactive Cys, regulated by TTR1