APPENDIX

Investigation of platinum drug mode of action and resistance using yeast and human neuroblastoma cells as model systems

2016

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A thesis submitted to the University of Kent for the degree of Doctor of Cell Biology

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APPENDIX contents

A. Members of the transcription regulator library of gene deletion yeast strains, their names and role descriptions, and their positions in a total of three 96-well plates for the initial screening. Names and roles were taken from their locus overview in the Saccharomyces Gene Database (SGD) (http://www.yeastgenome.org/). Purple – non-transcriptional regulators. It should be noted that for the cisplatin screening only, copies of strains YLR278C, UME6, ARR1, AFT1, AZF1 and SLA1 were inoculated into wells H7-H12 respectively of library plate 2.

Plate	Position	Standard Name	Systematic Name	Name description	Description
1	A1	-	CWG424	Wild type BY4741	Wild type BY4741
1	A2	-	CWG424	Wild type BY4741	Wild type BY4741
1	A3	-	CWG424	Wild type BY4741	Wild type BY4741
1	A4	-	CWG424	Wild type BY4741	Wild type BY4741
1	A5	-	CWG424	Wild type BY4741	Wild type BY4741
1	A6	-	CWG424	Wild type BY4741	Wild type BY4741
1	A7	-	CWG424	Wild type BY4741	Wild type BY4741
1	A8	-	CWG424	Wild type BY4741	Wild type BY4741
1	A9	-	CWG424	Wild type BY4741	Wild type BY4741
1	A10	-	CWG424	Wild type BY4741	Wild type BY4741
1	A11	-	CWG424	Wild type BY4741	Wild type BY4741
1	A12	-	CWG424	Wild type BY4741	Wild type BY4741
1	B1	OAF1	YAL051W	Oleate-Activated transcription Factor	Oleate-activated transcription factor; subunit of a heterodimeric complex with Pip2p, which binds to oleate-response elements (ORE) in the promoter of genes involved in beta-oxidation of fatty acids, peroxisome organization and biogenesis, activating transcription in the presence of oleate; regulates chromatin silencing at telomeres; involved in diauxic shift; OAF1 has a paralog, PIP2, that arose from the whole genome duplication
1	B2	-	YLL056C	-	Putative protein of unknown function; transcription is activated by paralogous transcription factors Yrm1p and Yrr1p and genes involved in pleiotropic drug resistance (PDR); expression is induced in cells treated with the mycotoxin patulin
1	B3	GAT3	YLR013W	-	Protein containing GATA family zinc finger motifs; involved in spore wall assembly; sequence similarity to GAT4, and the double mutant gat3 gat4 exhibits reduced dityrosine fluorescence relative to the single mutants
1	B4	PPR1	YLR014C	Pyrimidine Pathway Regulation	Zinc finger transcription factor; contains a Zn(2)-Cys(6) binuclear cluster domain, positively regulates transcription of URA1, URA3, URA4, and URA10, which are involved in de novo pyrimidine biosynthesis, in response to pyrimidine starvation; activity may be modulated by interaction with Tup1p
1	B5	-	YLR046C	-	Putative membrane protein; member of the fungal lipid-translocating exporter (LTE) family of proteins; transcription is activated by paralogous transcription factors Yrm1p and Yrr1p along with genes involved in multidrug resistance; YLR046C has a paralog, RTA1, that arose from the whole genome duplication

Plate	Position	Standard Name	Systematic Name	Name description	Description
1	B6	CHA4	YLR098C	Catabolism of Hydroxy Amino acids	DNA binding transcriptional activator; mediates serine/threonine activation of the catabolic L-serine (L-threonine) deaminase (CHA1); Zinc-finger protein with Zn[2]-Cys[6] fungal-type binuclear cluster domain
1	B7	HOG1	YLR113W	High Osmolarity Glycerol response	Mitogen-activated protein kinase involved in osmoregulation; controls global reallocation of RNAPII in osmotic shock; activates CDC28 by stimulating antisense RNA transcription; mediates recruitment/activation of RNAPII at Hot1p-dependent promoters; with Mrc1p defines novel S-phase checkpoint that prevent conflicts between DNA replication and transcription; nuclear form represses pseudohyphal growth; autophosphorylates; protein abundance increases under DNA replication stress
1	B8	GAL80	YML051W	GALactose metabolism	Transcriptional regulator involved in the repression of GAL genes; involved in the repression of GAL genes in the absence of galactose; inhibits transcriptional activation by Gal4p; inhibition relieved by Gal3p or Gal1p binding
1	B9	TDA9	YML081W	Topoisomerase I Damage Affected	Transcription factor that regulates acetate production; green fluorescent protein (GFP)-fusion protein localizes to the nucleus; null mutant is sensitive to expression of the top1-T722A allele; not an essential gene; TDA9 has a paralog, RSF2, that arose from the whole genome duplication
1	B10	YAP1	YML007W	Yeast AP-1	Basic leucine zipper (bZIP) transcription factor; required for oxidative stress tolerance; activated by H2O2 through the multistep formation of disulfide bonds and transit from the cytoplasm to the nucleus; Yap1p is degraded in the nucleus after the oxidative stress has passed; mediates resistance to cadmium; relative distribution to the nucleus increases upon DNA replication stress; YAP1 has a paralog, CAD1, that arose from the whole genome duplication
1	B11	SOK2	YMR016C	Suppressor Of Kinase	Nuclear protein that negatively regulates pseudohyphal differentiation; plays a regulatory role in the cyclic AMP (cAMP)-dependent protein kinase (PKA) signal transduction pathway; relocalizes to the cytosol in response to hypoxia; SOK2 has a paralog, PHD1, that arose from the whole genome duplication
1	B12	STB4	YMR019W	Sin Three Binding protein	Putative transcription factor; contains a Zn(II)2Cys6 zinc finger domain characteristic of DNA-binding proteins; computational analysis suggests a role in regulation of expression of genes encoding transporters; binds Sin3p in a two-hybrid assay
1	C1	MAC1	YMR021C	Metal binding ACtivator	Copper-sensing transcription factor; involved in regulation of genes required for high affinity copper transport; required for regulation of yeast copper genes in response to DNA-damaging agents; undergoes changes in redox state in response to changing levels of copper or MMS
1	C2	ARG80	YMR042W	ARGinine requiring	Transcription factor involved in regulating arginine-responsive genes; acts with Arg81p and Arg82p
1	C3	MSS11	YMR164C	Multicopy Suppressor of STA genes	Transcription factor; involved in regulation of invasive growth and starch degradation; controls the activation of FLO11 and STA2 in response to nutritional signals; forms a heterodimer with Flo8p that interacts with the Swi/Snf complex during transcriptional activation of FLO1, FLO11, and STA1
1	C4	RGM1	YMR182C	-	Putative zinc finger DNA binding transcription factor; contains two N-terminal C2H2 zinc fingers and C-terminal proline

Plate	Position	Standard Name	Systematic Name	Name description	Description
					rich domain; overproduction impairs cell growth and induces expression of genes involved in monosaccharide catabolism and aldehyde metabolism; regulates expression of of Y' telomeric elements and subtelomeric COS genes; relocalizes to the cytosol in response to hypoxia; RGM1 has a paralog, USV1, that arose from the whole genome duplication
1	C5	DAL82	YNL314W	Degradation of Allantoin	Positive regulator of allophanate inducible genes; binds a dodecanucleotide sequence upstream of all genes that are induced by allophanate; contains an UISALL DNA-binding, a transcriptional activation, and a coiled-coil domain
1	C6	STB1	YNL309W	Sin Three Binding protein	Protein with role in regulation of MBF-specific transcription at Start; phosphorylated by Cln-Cdc28p kinases in vitro; unphosphorylated form binds Swi6p, which is required for Stb1p function; expression is cell-cycle regulated; STB1 has a paralog, YOL131W, that arose from the whole genome duplication
1	C7	SIP3	YNL257C	SNF1-Interacting Protein	Transcription cofactor; acts through interaction with DNA-bound Snf1p; C-terminal region has a putative leucine zipper motif; potential Cdc28p substrate; SIP3 has a paralog, YSP1, that arose from the whole genome duplication
1	C8	HMS1	YOR032C	High-copy Mep Suppressor	bHLH protein with similarity to myc-family transcription factors; overexpression confers hyperfilamentous growth and suppresses the pseudohyphal filamentation defect of a diploid mep1 mep2 homozygous null mutant
1	C9	CIN5	YOR028C	Chromosome INstability	Basic leucine zipper (bZIP) transcription factor of the yAP-1 family; physically interacts with the Tup1-Cyc8 complex and recruits Tup1p to its targets; mediates pleiotropic drug resistance and salt tolerance; nuclearly localized under oxidative stress and sequestered in the cytoplasm by Lot6p under reducing conditions; CIN5 has a paralog, YAP6, that arose from the whole genome duplication
1	C10	HIR2	YOR038C	HIstone Regulation	Subunit of HIR nucleosome assembly complex; involved in regulation of histone gene transcription; recruits Swi-Snf complexes to histone gene promoters; promotes heterochromatic gene silencing with Asf1p; relocalizes to the cytosol in response to hypoxia
1	C11	**RAD27**	**YKL113C**	RADiation sensitive	5' to 3' exonuclease, 5' flap endonuclease; required for Okazaki fragment processing and maturation, for long-patch base-excision repair and large loop repair (LLR), ribonucleotide excision repair; member of the S. pombe RAD2/FEN1 family; relocalizes to the cytosol in response to hypoxia
1	C12	TYE7	YOR344C	Ty1-mediated Expression	Serine-rich protein that contains a bHLH DNA binding motif; binds E-boxes of glycolytic genes and contributes to their activation; may function as a transcriptional activator in Ty1-mediated gene expression; bHLH stands for basic-helix-loop-helix
1	D1	HAP5	YOR358W	Heme Activator Protein	Subunit of the Hap2p/3p/4p/5p CCAAT-binding complex; complex is heme-activated and glucose repressed; complex is a transcriptional activator and global regulator of respiratory gene expression; required for assembly and DNA binding activity of the complex
1	D2	PIP2	YOR363C	Peroxisome Induction Pathway	Autoregulatory, oleate-activated transcription factor; subunit of a heterodimeric complex with Oaf1p, which binds to oleate-response elements (ORE) in the promoter of genes involved in beta-oxidation of fatty acids, peroxisome organization and biogenesis, activating transcription in the presence of oleate; PIP2 has a paralog, OAF1, that arose

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					from the whole genome duplication
1	D3	RDR1	YOR380W	Repressor of Drug Resistance	Transcriptional repressor involved in regulating multidrug resistance; negatively regulates expression of the PDR5 gene; member of the Gal4p family of zinc cluster proteins
1	D4	YAP7	YOL028C	Yeast AP-1	Putative basic leucine zipper (bZIP) transcription factor; YAP7 has a paralog, YAP5, that arose from the whole genome duplication
1	D5	RTG1	YOL067C	ReTroGrade regulation	Transcription factor (bHLH) involved in interorganelle communication; contributes to communication between mitochondria, peroxisomes, and nucleus; target of Hog1p; activated in stochastic pulses of nuclear localization
1	D6	BUD29	YOL072W	Tho2/Hpr1 Phenotype	Nuclear pore-associated protein; component of TREX-2 complex (Sac3p-Thp1p-Sus1p-Cdc31p) involved in transcription elongation and mRNA export from the nucleus; involved in post-transcriptional tethering of active genes to the nuclear periphery and to non-nascent mRNP; contains a PAM domain implicated in protein-protein binding
1	D7	GAL4	YPL248C	GALactose metabolism	DNA-binding transcription factor required for activating GAL genes; responds to galactose; repressed by Gal80p and activated by Gal3p
1	D8	AFT2	YPL202C	Activator of Fe (iron) Transcription	Iron-regulated transcriptional activator; activates genes involved in intracellular iron use and required for iron homeostasis and resistance to oxidative stress; AFT2 has a paralog, AFT1, that arose from the whole genome duplication
1	D9	USV1	YPL230W	Up in StarVation	Putative transcription factor containing a C2H2 zinc finger; mutation affects transcriptional regulation of genes involved in growth on non-fermentable carbon sources, response to salt stress and cell wall biosynthesis; USV1 has a paralog, RGM1, that arose from the whole genome duplication
1	D10	SMP1	YBR182C	Second MEF2-like Protein 1	MADS-box transcription factor involved in osmotic stress response; SMP1 has a paralog, RLM1, that arose from the whole genome duplication
1	D11	ERT1	YBR239C	Ethanol Regulated Transcription factor	Transcriptional regulator; involved in regulation of gluconeogenesis and fermentable carbon utilization; GFP-fusion protein localizes to cytoplasm, nucleus; null mutation affects periodicity of transcriptional and metabolic oscillation; plays role in restricting Ty1 transposition; member of the zinc cluster family of proteins, similar to Rds2p
1	D12	THI2	YBR240C	THIamine metabolism	Transcriptional activator of thiamine biosynthetic genes; interacts with regulatory factor Thi3p to control expression of thiamine biosynthetic genes with respect to thiamine availability; acts together with Pdc2p to respond to thiaminediphosphate demand, possibly as related to carbon source availability; zinc finger protein of the Zn(II)2Cys6 type
1	E1	REI1	YBR267W	REquired for Isotropic bud growth	Cytoplasmic pre-60S factor; required for the correct recycling of shuttling factors Alb1, Arx1 and Tif6 at the end of the ribosomal large subunit biogenesis; involved in bud growth in the mitotic signaling network
1	E2	VMS1	YDR049W	VCP/Cdc48-	Component of a Cdc48p-complex involved in protein quality control; exhibits cytosolic and ER-membrane localization,

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				associated Mitochondrial Stress-responsive	with Cdc48p, during normal growth, and contributes to ER-associated degradation (ERAD) of specific substrates at a step after their ubiquitination; forms a mitochondrially-associated complex with Cdc48p and Npl4p under oxidative stress that is required for ubiquitin-mediated mitochondria-associated protein degradation (MAD); conserved in C. elegans and humans **1 2 3**
1	E3	GIS1	YDR096W	GIg1-2 Suppressor	Histone demethylase and transcription factor; regulates genes during nutrient limitation; activity modulated by proteasome-mediated proteolysis; has JmjC and JmjN domain in N-terminus that interact, promoting stability and proper transcriptional activity; contains two transactivating domains downstream of Jmj domains and a C-terminal DNA binding domain; relocalizes to the cytosol in response to hypoxia; GIS1 has a paralog, RPH1, that arose from the whole genome duplication
1	E4	INO2	YDR123C	INOsitol requiring	Transcription factor; component of the heteromeric Ino2p/Ino4p basic helix-loop-helix transcription activator that binds inositol/choline-responsive elements (ICREs), required for derepression of phospholipid biosynthetic genes in response to inositol depletion; involved in diauxic shift
1	E5	SWF1	YDR126W	Spore Wall Formation	Palmitoyltransferase that acts on transmembrane proteins; including the SNAREs Snc1p, Syn8p, Tlg1p and likely all SNAREs; contains an Asp-His-His-Cys-cysteine rich (DHHC-CRD) domain; may have a role in vacuole fusion
1	E6	SWI5	YDR146C	SWItching deficient	Transcription factor that recruits Mediator and Swi/Snf complexes; activates transcription of genes expressed at the M/G1 phase boundary and in G1 phase; required for expression of the HO gene controlling mating type switching; localization to nucleus occurs during G1 and appears to be regulated by phosphorylation by Cdc28p kinase; SWI5 has a paralog, ACE2, that arose from the whole genome duplication
1	E7	ARO80	YDR421W	AROmatic amino acid requiring	Zinc finger transcriptional activator of the Zn2Cys6 family; activates transcription of aromatic amino acid catabolic genes in the presence of aromatic amino acids
1	E8	GCN4	YEL009C	General Control Nonderepressible	bZIP transcriptional activator of amino acid biosynthetic genes; activator responds to amino acid starvation; expression is tightly regulated at both the transcriptional and translational levels
1	E9	SIP1	YDR422C	SNF1-Interacting Protein	Alternate beta-subunit of the Snf1p kinase complex; may confer substrate specificity; vacuolar protein containing KIS (Kinase-Interacting Sequence) and ASC (Association with Snf1 kinase Complex) domains involved in protein interactions
1	E10	GLN3	YER040W	GLutamiNe metabolism	Transcriptional activator of genes regulated by nitrogen catabolite repression; localization and activity regulated by quality of nitrogen source and Ure2p
1	E11	ACA1	YER045C	ATF/CREB Activator	ATF/CREB family basic leucine zipper (bZIP) transcription factor; binds as a homodimer to the ATF/CREB consensus sequence TGACGTCA; important for carbon source utilization; target genes include GRE2 and COS8; ACA1 has a paralog, CST6, that arose from the whole genome duplication
1	E12	**RAD52**	**YML032C**	RADiation sensitive	Protein that stimulates strand exchange; stimulates strand exchange by facilitating Rad51p binding to single-stranded DNA; anneals complementary single-stranded DNA; involved in the repair of double-strand breaks in DNA during vegetative growth and meiosis and UV induced sister chromatid recombination

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1	F1	MOT2	YER068W	Modulator Of Transcription	Ubiquitin-protein ligase subunit of the CCR4-NOT complex; with Ubc4p, ubiquitinates nascent polypeptide-associated complex subunits and histone demethyase Jhd2p; CCR4-NOT has roles in transcription regulation, mRNA degradation, and post-transcriptional modifications; regulates levels of DNA Polymerase-{alpha} to promote efficient and accurate DNA replication
1	F2	ECL1	YGR146C	Extends Chronological Lifespan	Protein of unknown function; mitochondrial-dependent role in the extension of chronological lifespan; overexpression increases oxygen consumption and respiratory activity while deletion results in reduced oxygen consumption under conditions of caloric restriction; induced by iron homeostasis transcription factor Aft2p; multicopy suppressor of temperature sensitive hsf1 mutant; induced by treatment with 8-methoxypsoralen and UVA irradiation
1	F3	GUT1	YHL032C	Glycerol UTilization	Glycerol kinase; converts glycerol to glycerol-3-phosphate; glucose repression of expression is mediated by Adr1p and Ino2p-Ino4p; derepression of expression on non-fermentable carbon sources is mediated by Opi1p and Rsf1p
1	F4	RIM101	YHL027W	Regulator of IME2	Cys2His2 zinc-finger transcriptional repressor; involved in alkaline responsive gene repression as part of adaptation to alkaline conditions; involved in cell wall assembly; required for alkaline pH-stimulated haploid invasive growth and sporulation; activated by alkaline-dependent proteolytic processing which results in removal of the C-terminal tail; similar to A. nidulans PacC
1	F5	YAP3	YHL009C	Yeast AP-1	Basic leucine zipper (bZIP) transcription factor
1	F6	NDT80	YHR124W	Non-DiTyrosine	Meiosis-specific transcription factor; required for exit from pachytene and for full meiotic recombination; activates middle sporulation genes; competes with Sum1p for binding to promoters containing middle sporulation elements (MSE)
1	F7	STB5	YHR178W	Sin Three Binding protein	Transcription factor; involved in regulating multidrug resistance and oxidative stress response; forms a heterodimer with Pdr1p; contains a Zn(II)2Cys6 zinc finger domain that interacts with a pleiotropic drug resistance element in vitro
1	F8	KAR4	YCL055W	KARyogamy	Transcription factor required for response to pheromones; also required during meiosis; exists in two forms, a slower-migrating form more abundant during vegetative growth and a faster-migrating form induced by pheromone
1	F9	SKN7	YHR206W	Suppressor of Kre Null	Nuclear response regulator and transcription factor; physically interacts with the Tup1-Cyc8 complex and recruits Tup1p to its targets; part of a branched two-component signaling system; required for optimal induction of heat-shock genes in response to oxidative stress; involved in osmoregulation; relocalizes to the cytosol in response to hypoxia; SKN7 has a paralog, HMS2, that arose from the whole genome duplication
1	F10	LEU3	YLR451W	LEUcine biosynthesis	Zinc-knuckle transcription factor, repressor and activator; regulates genes involved in branched chain amino acid biosynthesis and ammonia assimilation; acts as a repressor in leucine-replete conditions and as an activator in the presence of alpha-isopropylmalate, an intermediate in leucine biosynthesis that accumulates during leucine starvation
1	F11	ACE2	YLR131C	Activator of CUP1 Expression	Transcription factor required for septum destruction after cytokinesis; phosphorylation by Cbk1p blocks nuclear exit during M/G1 transition, causing localization to daughter cell nuclei, and also increases Ace2p activity; phosphorylation by Cdc28p and Pho85p prevents nuclear import during cell cycle phases other than cytokinesis; part of RAM network

Plate	Position	Standard Name	Systematic Name	Name description	Description
					that regulates cellular polarity and morphogenesis; ACE2 has a paralog, SWI5, that arose from the whole genome duplication
1	F12	RFX1	YLR176C	-	Major transcriptional repressor of DNA-damage-regulated genes; recruits repressors Tup1p and Cyc8p to their promoters; involved in DNA damage and replication checkpoint pathway; similar to a family of mammalian DNA binding RFX1-4 proteins
1	G1	SWI6	YLR182W	SWItching deficient	Transcription cofactor; forms complexes with Swi4p and Mbp1p to regulate transcription at the G1/S transition; involved in meiotic gene expression; also binds Stb1p to regulate transcription at START; cell wall stress induces phosphorylation by Mpk1p, which regulates Swi6p localization; required for the unfolded protein response, independently of its known transcriptional coactivators
1	G2	TOS4	YLR183C	Target Of Sbf	Putative transcription factor, contains Forkhead Associated domain; found associated with chromatin; target of SBF transcription factor; expression is periodic and peaks in G1; involved in DNA replication checkpoint response; interacts with Rpd3 and Set3 histone deacetylase (HDAC) complexes; APCC(Cdh1) substrate; relative distribution to the nucleus increases upon DNA replication stress; TOS4 has a paralog, PLM2, that arose from the whole genome duplication
1	G3	**-**	**CWG424**	Wild type BY4741	-
1	G4	SPT23	YKL020C	SuPpressor of Ty	ER membrane protein involved in regulation of OLE1 transcription; inactive ER form dimerizes and one subunit is then activated by ubiquitin/proteasome-dependent processing followed by nuclear targeting; SPT23 has a paralog, MGA2, that arose from the whole genome duplication
1	G5	IXR1	YKL032C	Intrastrand cross (X)-link Recognition	Transcriptional repressor that regulates hypoxic genes during normoxia; involved in the aerobic repression of genes such as COX5b, TIR1, and HEM13; binds DNA intrastrand cross-links formed by cisplatin; HMG (high mobility group box) domain containing protein which binds and bends cisplatin-modified DNA, blocking excision repair; IXR1 has a paralog, ABF2, that arose from the whole genome duplication
1	G6	RGT1	YKL038W	Restores Glucose Transport	Glucose-responsive transcription factor; regulates expression of several glucose transporter (HXT) genes in response to glucose; binds to promoters and acts both as a transcriptional activator and repressor; recruits Tup1p/Cyc8p to target gene promoters; RGT1 has a paralog, EDS1, that arose from the whole genome duplication
1	G7	PHD1	YKL043W	PseudoHyphal Determinant	Transcriptional activator that enhances pseudohyphal growth; physically interacts with the Tup1-Cyc8 complex and recruits Tup1p to its targets; regulates expression of FLO11, an adhesin required for pseudohyphal filament formation; similar to StuA, an A. nidulans developmental regulator; potential Cdc28p substrate; PHD1 has a paralog, SOK2, that arose from the whole genome duplication
1	G8	STB6	YKL072W	Sin Three Binding protein	Protein that binds Sin3p in a two-hybrid assay; STB6 has a paralog, STB2, that arose from the whole genome duplication
1	G9	MSN4	YKL062W	Multicopy suppressor of	Stress-responsive transcriptional activator; activated in stochastic pulses of nuclear localization in response to various stress conditions; binds DNA at stress response elements of responsive genes, inducing gene expression; involved in

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				SNF1 mutation	diauxic shift
1	G10	HAP4	YKL109W	Heme Activator Protein	Transcription factor; subunit of the heme-activated, glucose-repressed Hap2p/3p/4p/5p CCAAT-binding complex, a transcriptional activator and global regulator of respiratory gene expression; provides the principal activation function of the complex; involved in diauxic shift
1	G11	ASH1	YKL185W	Asymmetric Synthesis of HO	Component of the Rpd3L histone deacetylase complex; zinc-finger inhibitor of HO transcription; mRNA is localized and translated in the distal tip of anaphase cells, resulting in accumulation of Ash1p in daughter cell nuclei and inhibition of HO expression; potential Cdc28p substrate
1	G12	-	YGR035C	-	Putative protein of unknown function, potential Cdc28p substrate; transcription is activated by paralogous transcription factors Yrm1p and Yrr1p along with genes involved in multidrug resistance; YGR035C has a paralog, YLR346C, that arose from the whole genome duplication
1	H1	-	CWG424	Wild type BY4741	-
1	H2	-	CWG424	Wild type BY4741	-
1	H3	-	CWG424	Wild type BY4741	-
1	H4	-	CWG424	Wild type BY4741	-
1	H5	-	CWG424	Wild type BY4741	-
1	H6	-	CWG424	Wild type BY4741	-
1	H7	-	CWG424	Wild type BY4741	-
1	H8	-	CWG424	Wild type BY4741	-
1	H9	-	CWG424	Wild type BY4741	-
1	H10	-	CWG424	Wild type BY4741	-
1	H11	-	CWG424	Wild type BY4741	-
1	H12	-	CWG424	Wild type BY4741	-
2	A1	-	CWG424	Wild type BY4741	-
2	A2	-	CWG424	Wild type BY4741	-
2	A3	-	CWG424	Wild type BY4741	-
2	A4	-	CWG424	Wild type BY4741	-
2	A5	-	CWG424	Wild type BY4741	-
2	A6	-	CWG424	Wild type BY4741	-
2	A7	-	CWG424	Wild type BY4741	-
2	A8	-	CWG424	Wild type BY4741	-

Plate	Position	Standard Name	Systematic Name	Name description	Description
2	A9	-	CWG424	Wild type BY4741	-
2	A10	-	CWG424	Wild type BY4741	-
2	A11	-	CWG424	Wild type BY4741	-
2	A12	-	CWG424	Wild type BY4741	-
2	B1	RME1	YGR044C	Regulator of MEiosis	Zinc finger protein involved in control of meiosis; prevents meiosis by repressing IME1 expression and promotes mitosis by activating CLN2 expression; directly repressed by a1-alpha2 regulator; mediates cell type control of sporulation; relocalizes from nucleus to cytoplasm upon DNA replication stress
2	B2	-	YGR067C	-	Putative protein of unknown function; contains a zinc finger motif similar to that of Adr1p
2	B3	ASK10	YGR097W	Activator of SKn7	Component of RNA polymerase II holoenzyme; phosphorylated in response to oxidative stress; has a role in destruction of Ssn8p; proposed to function in activation of the glycerol channel Fps1p; ASK10 has a paralog, RGC1, that arose from the whole genome duplication
2	B4	AZF1	YOR113W	Asparagine-rich Zinc-Finger	Zinc-finger transcription factor; involved in diauxic shift; in the presence of glucose, activates transcription of genes involved in growth and carbon metabolism; in nonfermentable carbon sources, activates transcription of genes involved in maintenance of cell wall integrity; relocalizes to the cytosol in response to hypoxia
2	B5	SFL1	YOR140W	Suppressor gene for FLocculation	Transcriptional repressor and activator; involved in repression of flocculation-related genes, and activation of stress responsive genes; negatively regulated by cAMP-dependent protein kinase A subunit Tpk2p; premature stop codon (C1430T, Q477-stop) in SK1 background is linked to the aggressively invasive phenotype of SK1 relative to BY4741 (S288C)
2	B6	YRR1	YOR162C	Yeast Reveromycin-A Resistant	Zn2-Cys6 zinc-finger transcription factor; activates genes involved in multidrug resistance; paralog of Yrm1p, acting on an overlapping set of target genes; YRR1 has a paralog, PDR8, that arose from the whole genome duplication
2	B7	YRM1	YOR172W	Yeast Reveromycin resistance Modulator	Zinc finger transcription factor involved in multidrug resistance; Zn(2)-Cys(6) zinc finger transcription factor; activates genes involved in multidrug resistance; paralog of Yrr1p, acting on an overlapping set of target genes
2	B8	WTM2	YOR229W	WD repeat containing Transcriptional Modulator	Transcriptional modulator; involved in regulation of meiosis, silencing, and expression of RNR genes; involved in response to replication stress; contains WD repeats; relocalizes to the cytosol in response to hypoxia; WTM2 has a paralog, UME1, that arose from the whole genome duplication
2	B9	WTM1	YOR230W	WD repeat containing Transcriptional	Transcriptional modulator; involved in regulation of meiosis, silencing, and expression of RNR genes; required for nuclear localization of the ribonucleotide reductase small subunit Rnr2p and Rnr4p; contains WD repeats

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				Modulator	
2	B10	-	YJL206C	-	Putative protein of unknown function; similar to transcriptional regulators from the Zn[2]-Cys[6] binuclear cluster protein family; mRNA is weakly cell cycle regulated, peaking in S phase; induced rapidly upon MMS treatment
2	B11	ECM22	YLR228C	ExtraCellular Mutant	Sterol regulatory element binding protein; regulates transcription of sterol biosynthetic genes; contains Zn[2]-Cys[6] binuclear cluster; relocates from intracellular membranes to perinuclear foci on sterol depletion; ECM22 has a paralog, UPC2, that arose from the whole genome duplication
2	B12	PDR8	YLR266C	Pleiotropic Drug Resistance	Transcription factor; targets include ATP-binding cassette (ABC) transporters, major facilitator superfamily transporters, and other genes involved in the pleiotropic drug resistance (PDR) phenomenon; PDR8 has a paralog, YRR1, that arose from the whole genome duplication
2	C1	-	YLR278C	-	Zinc-cluster protein; GFP-fusion protein localizes to the nucleus; mutant shows moderate growth defect on caffeine; has a prion-domain like fragment that increases frequency of [URE3]; YLR278C is not an essential gene
2	C2	UME6	YDR207C	Unscheduled Meiotic gene Expression	Rpd3L histone deacetylase complex subunit; key transcriptional regulator of early meiotic genes; involved in chromatin remodeling and transcriptional repression via DNA looping; binds URS1 upstream regulatory sequence, couples metabolic responses to nutritional cues with initiation and progression of meiosis, forms complex with Ime1p
2	C3	UPC2	YDR213W	UPtake Control	Sterol regulatory element binding protein; induces transcription of sterol biosynthetic genes and of DAN/TIR gene products; relocates from intracellular membranes to perinuclear foci on sterol depletion; UPC2 has a paralog, ECM22, that arose from the whole genome duplication
2	C4	MDS3	YGL197W	Mck1 Dosage Suppressor	Putative component of the TOR regulatory pathway; negative regulator of early meiotic gene expression; required, with Pmd1p, for growth under alkaline conditions; has an N-terminal kelch-like domain; MDS3 has a paralog, PMD1, that arose from the whole genome duplication
2	C5	MIG2	YGL209W	Multicopy Inhibitor of GAL gene expression	Zinc finger transcriptional repressor; cooperates with Mig1p in glucose-induced gene repression; under low glucose conditions relocalizes to mitochondrion, where it interacts with Ups1p, antagonizes mitochondrial fission factor Dnm1p, indicative of a role in mitochondrial fusion or regulating morphology; regulates filamentous growth in response to glucose depletion; activated in stochastic pulses of nuclear localization in response to low glucose
2	C6	HAP2	YGL237C	Heme Activator Protein	Subunit of the Hap2p/3p/4p/5p CCAAT-binding complex; complex is heme-activated and glucose-repressed; complex is a transcriptional activator and global regulator of respiratory gene expression; contains sequences sufficient for both complex assembly and DNA binding
2	C7	FZF1	YGL254W	Five Zinc Fingers	Transcription factor involved in sulfite metabolism; sole identified regulatory target is SSU1; overexpression suppresses sulfite-sensitivity of many unrelated mutants due to hyperactivation of SSU1, contains five zinc fingers; protein abundance increases in response to DNA replication stress
2	C8	RLM1	YPL089C	Resistance to Lethality of	MADS-box transcription factor; component of the protein kinase C-mediated MAP kinase pathway involved in the maintenance of cell integrity; phosphorylated and activated by the MAP-kinase Slt2p; RLM1 has a paralog, SMP1, that

Plate	Position	Standard Name	Systematic Name	Name description	Description
				MKK1P386 overexpression	arose from the whole genome duplication
2	C9	-	YPL088W	-	Putative aryl alcohol dehydrogenase; transcription is activated by paralogous transcription factors Yrm1p and Yrr1p along with genes involved in multidrug resistance
2	C10	DIG1	YPL049C	Down-regulator of Invasive Growth	MAP kinase-responsive inhibitor of the Ste12p transcription factor; involved in the regulation of mating-specific genes and the invasive growth pathway; related regulators Dig1p and Dig2p bind to Ste12p; DIG1 has a paralog, DIG2, that arose from the whole genome duplication
2	C11	MET31	YPL038W	METhionine requiring	Zinc-finger DNA-binding transcription factor; targets strong transcriptional activator Met4p to promoters of sulfur metabolic genes; involved in transcriptional regulation of the methionine biosynthetic genes; feedforward loop controlling expression of MET32 and the lack of such a loop for MET31 may account for the differential actions of Met31p and Met32p; MET31 has a paralog, MET32, that arose from the whole genome duplication
2	C12	ECM23	YPL021W	ExtraCellular Mutant	Non-essential protein of unconfirmed function; affects pre-rRNA processing, may act as a negative regulator of the transcription of genes involved in pseudohyphal growth; homologous to Srd1p
2	D1	-	YPR127W	-	Putative pyridoxine 4-dehydrogenase; differentially expressed during alcoholic fermentation; expression activated by transcription factor YRM1/YOR172W; green fluorescent protein (GFP)-fusion protein localizes to both the cytoplasm and the nucleus
2	D2	-	YPR196W	-	Putative maltose-responsive transcription factor
2	D3	ARR1	YPR199C	ARsenicals Resistance	Transcriptional activator of the basic leucine zipper (bZIP) family; required for transcription of genes involved in resistance to arsenic compounds
2	D4	RDS1	YCR106W	Regulator of Drug Sensitivity	Putative zinc cluster transcription factor; involved in conferring resistance to cycloheximide
2	D5	RDS1	YCR106W	Regulator of Drug Sensitivity	Putative zinc cluster transcription factor; involved in conferring resistance to cycloheximide
2	D6	PHO4	YFR034C	PHOsphate metabolism	Basic helix-loop-helix (bHLH) transcription factor of the myc-family; activates transcription cooperatively with Pho2p in response to phosphate limitation; binding to 'CACGTG' motif is regulated by chromatin restriction, competitive binding of Cbf1p to the same DNA binding motif and cooperation with Pho2p; function is regulated by phosphorylation at multiple sites and by phosphate availability
2	D7	MGA1	YGR249W	-	Protein similar to heat shock transcription factor; multicopy suppressor of pseudohyphal growth defects of ammonium permease mutants
2	D8	PDR3	YBL005W	Pleiotropic Drug Resistance	Transcriptional activator of the pleiotropic drug resistance network; regulates expression of ATP-binding cassette (ABC) transporters through binding to cis-acting PDRE sites (PDR responsive elements); has a role in response to drugs and organic solvents; post-translationally up-regulated in cells lacking functional mitochondrial genome; involved in diauxic

Plate	Position	Standard Name	Systematic Name	Name description	Description
					shift; relative distribution to nucleus increases upon DNA replication stress; APCC(Cdh1) substrate
2	D9	SLA1	YBL007C	Synthetic Lethal with ABP1	Cytoskeletal protein binding protein; required for assembly of the cortical actin cytoskeleton; interacts with proteins regulating actin dynamics and proteins required for endocytosis; found in the nucleus and cell cortex; has 3 SH3 domains
2	D10	HAP3	YBL021C	Heme Activator Protein	Subunit of the Hap2p/3p/4p/5p CCAAT-binding complex; complex is heme-activated and glucose-repressed; complex is a transcriptional activator and global regulator of respiratory gene expression; contains sequences contributing to both complex assembly and DNA binding
2	D11	TOD6	YBL054W	Twin Of Dot6p	PAC motif binding protein involved in rRNA and ribosome biogenesis; subunit of the RPD3L histone deacetylase complex; Myb-like HTH transcription factor; hypophosphorylated by rapamycin treatment in a Sch9p-dependent manner; activated in stochastic pulses of nuclear localization
2	D12	SEF1	YBL066C	Suppressor of Essential Function	Putative transcription factor; has homolog in Kluyveromyces lactis
2	E1	PDR1	YGL013C	Pleiotropic Drug Resistance	Transcription factor that regulates the pleiotropic drug response; zinc cluster protein that is a master regulator involved in recruiting other zinc cluster proteins to pleiotropic drug response elements (PDREs) to fine tune the regulation of multidrug resistance genes; relocalizes to the cytosol in response to hypoxia; PDR1 has a paralog, PDR3, that arose from the whole genome duplication
2	E2	MIG1	YGL035C	Multicopy Inhibitor of GAL gene expression	Transcription factor involved in glucose repression; sequence specific DNA binding protein containing two Cys2His2 zinc finger motifs; regulated by the SNF1 kinase and the GLC7 phosphatase; regulates filamentous growth along with Mig2p in response to glucose depletion; activated in stochastic pulses of nuclear localization, shuttling between cytosol and nucleus depending on external glucose levels and its phosphorylation state
2	E3	AFT1	YGL071W	Activator of Ferrous Transport	Transcription factor involved in iron utilization and homeostasis; binds consensus site PyPuCACCCPu and activates transcription in response to changes in iron availability; in iron-replete conditions localization is regulated by Grx3p, Grx4p, and Fra2p, and promoter binding is negatively regulated via Grx3p-Grx4p binding; AFT1 has a paralog, AFT2, that arose from the whole genome duplication; relative distribution to the nucleus increases upon DNA replication stress
2	E4	TOS8	YGL096W	Target Of Sbf	Homeodomain-containing protein and putative transcription factor; found associated with chromatin; target of SBF transcription factor; induced during meiosis and under cell-damaging conditions; TOS8 has a paralog, CUP9, that arose from the whole genome duplication
2	E5	GCR2	YNL199C	GlyColysis Regulation	Transcriptional activator of genes involved in glycolysis; interacts and functions with the DNA-binding protein Gcr1p
2	E6	SKO1	YNL167C	Suppressor of Kinase	Basic leucine zipper transcription factor of the ATF/CREB family; forms a complex with Tup1p and Cyc8p to both activate and repress transcription; cytosolic and nuclear protein involved in osmotic and oxidative stress responses

Plate	Position	Standard Name	Systematic Name	Name description	Description
				Overexpression	
2	E7	-	YKL222C	-	Protein of unknown function; may interact with ribosomes, based on co-purification experiments; similar to transcriptional regulators from the zinc cluster (binuclear cluster) family; null mutant is sensitive to caffeine
2	E8	MET32	YDR253C	METhionine requiring	Zinc-finger DNA-binding transcription factor; involved in transcriptional regulation of the methionine biosynthetic genes; targets strong transcriptional activator Met4p to promoters of sulfur metabolic genes; feedforward loop exists in the regulation of genes controlled by Met4p and Met32p; lack of such a loop for MET31 may account for the differential actions of Met32p and Met31p; MET32 has a paralog, MET31, that arose from the whole genome duplication
2	E9	YAP6	YDR259C	Yeast homolog of AP-1	Basic leucine zipper (bZIP) transcription factor; physically interacts with the Tup1-Cyc8 complex and recruits Tup1p to its targets; overexpression increases sodium and lithium tolerance; computational analysis suggests a role in regulation of expression of genes involved in carbohydrate metabolism; YAP6 has a paralog, CIN5, that arose from the whole genome duplication
2	E10	OAF3	YKR064W	Oleate Activated transcription Factor	Putative transcriptional repressor with Zn(2)-Cys(6) finger; negatively regulates transcription in response to oleate levels, based on mutant phenotype and localization to oleate-responsive promoters; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies; forms nuclear foci upon DNA replication stress
2	E11	HEL2	YDR266C	Histone E3 Ligase	RING finger ubiquitin ligase (E3); involved in ubiquitylation and degradation of excess histones; interacts with Ubc4p and Rad53p; null mutant sensitive to hydroxyurea (HU); green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; computational analysis suggests a role as a transcription factor
2	E12	MTH1	YDR277C	MSN Three Homolog	Negative regulator of the glucose-sensing signal transduction pathway; required for repression of transcription by Rgt1p; interacts with Rgt1p and the Snf3p and Rgt2p glucose sensors; phosphorylated by Yck1p, triggering Mth1p degradation; MTH1 has a paralog, STD1, that arose from the whole genome duplication
2	F1	SUM1	YDR310C	SUppresor of Mar1-1	Transcriptional repressor that regulates middle-sporulation genes; required for mitotic repression of middle sporulation-specific genes; also acts as general replication initiation factor; involved in telomere maintenance, chromatin silencing; regulated by pachytene checkpoint
2	F2	CST6	YIL036W	Chromosome STability	Basic leucine zipper (bZIP) transcription factor, in ATF/CREB family; mediates transcriptional activation of NCE103 (encoding carbonic anhydrase) in response to low CO2 levels such as in the ambient air; proposed to be a regulator of oleate responsive genes; involved in utilization of non-optimal carbon sources and chromosome stability; relocalizes to the cytosol in response to hypoxia; CST6 has a paralog, ACA1, that arose from the whole genome duplication
2	F3	GAT1	YFL021W (YKR067W)	-	Transcriptional activator of nitrogen catabolite repression genes; contains a GATA-1-type zinc finger DNA-binding motif; activity and localization regulated by nitrogen limitation and Ure2p; different translational starts produce two major and two minor isoforms that are differentially regulated and localized
2	F4	HAC1	YFL031W	Homologous to	Basic leucine zipper (bZIP) transcription factor (ATF/CREB1 homolog); regulates the unfolded protein response, via

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				Atf/Creb1	UPRE binding, and membrane biogenesis; ER stress-induced splicing pathway facilitates efficient Hac1p synthesis; protein abundance increases in response to DNA replication stress
2	F5	OTU1	YFL044C	Ovarian TUmor	Deubiquitylation enzyme that binds to the chaperone-ATPase Cdc48p; may contribute to regulation of protein degradation by deubiquitylating substrates that have been ubiquitylated by Ufd2p; member of the Ovarian Tumor (OTU) family; protein abundance increases in response to DNA replication stress
2	F6	ZNF1	YFL052W	ZiNc Finger protein	Zinc cluster transcription factor that regulates respiratory growth; binds to promoters of genes involved in respiration, gluconeogenesis, and the glyoxylate shunt; required for normal carbon source utilization and stress response
2	F7	MAL13	YGR288W	MALtose fermentation	MAL-activator protein; part of complex locus MAL1; nonfunctional in genomic reference strain S288C
2	F8	MET28	YIR017C	METhionine	bZIP transcriptional activator in the Cbf1p-Met4p-Met28p complex; participates in the regulation of sulfur metabolism
2	F9	YAP5	YIR018W	Yeast AP-1	Basic leucine zipper (bZIP) iron-sensing transcription factor; involved in diauxic shift; YAP5 has a paralog, YAP7, that arose from the whole genome duplication
2	F10	MSA2	YKR077W	Mbf and Sbf Associated	Putative transcriptional activator; interacts with G1-specific transcription factor MBF and G1-specific promoters; MSA2 has a paralog, MSA1, that arose from the whole genome duplication
2	F11	MOT3	YMR070W	Modifier of Transcription	Transcriptional repressor and activator with two C2-H2 zinc fingers; involved in repression of a subset of hypoxic genes by Rox1p, repression of several DAN/TIR genes during aerobic growth and ergosterol biosynthetic genes in response to hyperosmotic stress; contributes to recruitment of Tup1p-Cyc8p general repressor to promoters; involved in positive transcriptional regulation of CWP2 and other genes; relocalizes to the cytosol in response to hypoxia; can form [MOT3+] prion
2	F12	X	X	X	-
2	G1	HAL9	YOL089C	HALotolerance	Putative transcription factor containing a zinc finger; overexpression increases salt tolerance through increased expression of the ENA1 (Na+/Li+ extrusion pump) gene while gene disruption decreases both salt tolerance and ENA1 expression; HAL9 has a paralog, TBS1, that arose from the whole genome duplication
2	G2	INO4	YOL108C	INOsitol requiring	Transcription factor involved in phospholipid synthesis; required for derepression of inositol-choline-regulated genes involved in phospholipid synthesis; forms a complex, with Ino2p, that binds the inositol-choline-responsive element through a basic helix-loop-helix domain
2	G3	MSN1	YOL116W	Multicopy suppressor of SNF1 mutation	Transcriptional activator; involved in regulation of invertase and glucoamylase expression, invasive growth and pseudohyphal differentiation, iron uptake, chromium accumulation, and response to osmotic stress; localizes to the nucleus; relative distribution to the nucleus increases upon DNA replication stress
2	G4	DOT6	YER088C	Disruptor Of Telomeric silencing	Protein involved in rRNA and ribosome biogenesis; activated in stochastic pulses of nuclear localization; binds polymerase A and C motif; subunit of the RPD3L histone deacetylase complex; has chromatin specific SANT domain; involved in telomeric gene silencing and filamentation; relative distribution to the nucleus increases upon DNA

Plate	Position	Standard Name	Systematic Name	Name description	Description
					replication stress
2	G5	AFB1	YLR040C	A-Factor Barrier	MATalpha-specific a-factor blocker; contributes to mating efficiency under certain conditions; localizes to the cell wall; predicted to be a GPI-attached protein; upregulated by Mcm1p-Alpha1p transcription factor; partially overlaps the dubious ORF YLR041W
2	G6	ARG81	YML099C	ARGinine requiring	Zinc finger transcription factor involved in arginine-responsive genes; Zn(2)-Cys(6) binuclear cluster domain type; involved in the regulation of arginine-responsive genes; acts with Arg80p and Arg82p
2	G7	DAT1	YML113W	DATin	DNA binding protein that recognizes oligo(dA).oligo(dT) tracts; Arg side chain in its N-terminal pentad Gly-Arg-Lys-Pro-Gly repeat is required for DNA-binding; relocalizes to the cytosol in response to hypoxia; not essential for viability
2	G8	-	YMR102C	-	Protein of unknown function; transcription is activated by paralogous transcription factors Yrm1p and Yrr1p along with genes involved in multidrug resistance; mutant shows increased resistance to azoles; not an essential gene; YMR102C has a paralog, DGR2, that arose from the whole genome duplication
2	G9	SUT2	YPR009W	Sterol UpTake	Putative transcription factor of the Zn2Cys6 family; regulates sterol uptake under anaerobic conditions along with SUT1; multicopy suppressor of mutations that cause low activity of the cAMP/protein kinase A pathway; positively regulates mating along with SUT1 by repressing the expression of genes (PRR2, NCE102 and RHO5) which function as mating inhibitors; SUT2 has a paralog, SUT1, that arose from the whole genome duplication
2	G10	SMK1	YPR054W	-	Middle sporulation-specific mitogen-activated protein kinase (MAPK); required for production of the outer spore wall layers; negatively regulates activity of the glucan synthase subunit Gsc2p
2	G11	ROX1	YPR065W	Regulation by OXygen	Heme-dependent repressor of hypoxic genes; mediates aerobic transcriptional repression of hypoxia induced genes such as COX5b and CYC7; repressor function regulated through decreased promoter occupancy in response to oxidative stress; contains an HMG domain that is responsible for DNA bending activity; involved in the hyperosmotic stress resistance
2	G12	SPT10	YJL127C	SuPpressor of Ty	Putative histone acetylase with a role in transcriptional silencing; sequence-specific activator of histone genes, binds specifically and cooperatively to pairs of UAS elements in core histone promoters, functions at or near the TATA box
2	H1	**-**	**CWG424**	Wild type BY4741	
2	H2	**-**	**CWG424**	Wild type BY4741	
2	H3	**RAD27**	**YKL113C**	RADiation sensitive	5' to 3' exonuclease, 5' flap endonuclease; required for Okazaki fragment processing and maturation, for long-patch base-excision repair and large loop repair (LLR), ribonucleotide excision repair; member of the S. pombe RAD2/FEN1 family; relocalizes to the cytosol in response to hypoxia
2	H4	**RAD27**	**YKL113C**	RADiation sensitive	5' to 3' exonuclease, 5' flap endonuclease; required for Okazaki fragment processing and maturation, for long-patch base-excision repair and large loop repair (LLR), ribonucleotide excision repair; member of the S. pombe RAD2/FEN1 family; relocalizes to the cytosol in response to hypoxia
2	H5	**RAD52**	**YML032C**	RADiation	Protein that stimulates strand exchange; stimulates strand exchange by facilitating Rad51p binding to single-stranded

Plate	Position	Standard Name	Systematic Name	Name description	Description
				sensitive	DNA; anneals complementary single-stranded DNA; involved in the repair of double-strand breaks in DNA during vegetative growth and meiosis and UV induced sister chromatid recombination
2	H6	**RAD52**	**YML032C**	RADiation sensitive	Protein that stimulates strand exchange; stimulates strand exchange by facilitating Rad51p binding to single-stranded DNA; anneals complementary single-stranded DNA; involved in the repair of double-strand breaks in DNA during vegetative growth and meiosis and UV induced sister chromatid recombination
2	H7	X	X	X	-
2	H8	X	X	X	-
2	H9	X	X	X	-
2	H10	X	X	X	-
2	H11	X	X	X	-
2	H12	X	X	X	-
3	A1	-	CWG424	Wild type BY4741	-
3	A2	-	CWG424	Wild type BY4741	-
3	A3	-	CWG424	Wild type BY4741	-
3	A4	-	CWG424	Wild type BY4741	-
3	A5	X	X	X	-
3	A6	X	X	X	-
3	A7	X	X	X	-
3	A8	X	X	X	-
3	A9	X	X	X	-
3	A10	X	X	X	-
3	A11	X	X	X	-
3	A12	X	X	X	-
3	B1	GZF3	YJL110C	Gata Zinc Finger protein	GATA zinc finger protein; negatively regulates nitrogen catabolic gene expression by competing with Gat1p for GATA site binding; function requires a repressive carbon source; dimerizes with Dal80p and binds to Tor1p; GZF3 has a paralog, DAL80, that arose from the whole genome duplication
3	B2	SIP4	YJL089W	SNF1-Interacting Protein	C6 zinc cluster transcriptional activator; binds to the carbon source-responsive element (CSRE) of gluconeogenic genes; involved in the positive regulation of gluconeogenesis; regulated by Snf1p protein kinase; localized to the nucleus
3	B3	ZAP1	YJL056C	Zinc-responsive Activator Protein	Zinc-regulated transcription factor; binds to zinc-responsive promoters to induce transcription of certain genes in presence of zinc, represses other genes in low zinc; regulates its own transcription; contains seven zinc-finger domains
3	B4	STP2	YHR006W	protein with	Transcription factor; activated by proteolytic processing in response to signals from the SPS sensor system for external

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				similarity to Stp1p	amino acids; activates transcription of amino acid permease genes; STP2 has a paralog, STP1, that arose from the whole genome duplication
3	B5	RSF2	YJR127C	ReSpiration Factor	Zinc-finger protein; involved in transcriptional control of both nuclear and mitochondrial genes, many of which specify products required for glycerol-based growth, respiration, and other functions; RSF2 has a paralog, TDA9, that arose from the whole genome duplication; relocalizes from nucleus to cytoplasm upon DNA replication stress
3	B6	BAS1	YKR099W	BASal	Myb-related transcription factor; involved in regulating basal and induced expression of genes of the purine and histidine biosynthesis pathways; also involved in regulation of meiotic recombination at specific genes
3	B7	-	YNR063W	-	Putative zinc-cluster protein of unknown function
3	B8	IME1	YJR094C	Inducer of MEiosis	Master regulator of meiosis that is active only during meiotic events; activates transcription of early meiotic genes through interaction with Ume6p; degraded by the 26S proteasome following phosphorylation by Ime2p; transcription is negatively regulated in cis by the IRT1 long noncoding antisense RNA
3	B9	HIR3	YJR140C	HIstone Regulation	Subunit of the HIR complex; a nucleosome assembly complex involved in regulation of histone gene transcription; involved in position-dependent gene silencing and nucleosome reassembly; ortholog of human CABIN1 protein
3	B10	BYE1	YKL005C	BYpass of ESS1	Negative regulator of transcription elongation; contains a TFIIS-like domain that associates with chromatin and a PHD domain that interacts with H3K4me3; multicopy suppressor of temperature-sensitive ess1 mutations, binds RNA polymerase II large subunit
3	B11	HOT1	YMR172W	High-Osmolarity-induced Transcription	Transcription factor for glycerol biosynthetic genes; required for the transient induction of glycerol biosynthetic genes GPD1 and GPP2 in response to high osmolarity; targets Hog1p to osmostress responsive promoters; has similarity to Msn1p and Gcr1p
3	B12	GAL3	YDR009W	GALactose metabolism	Transcriptional regulator; involved in activation of the GAL genes in response to galactose; forms a complex with Gal80p to relieve Gal80p inhibition of Gal4p; binds galactose and ATP but does not have galactokinase activity; GAL3 has a paralog, GAL1, that arose from the whole genome duplication
3	C1	NSI1	YDR026C	NTS1 SIlencing protein 1	RNA polymerase I termination factor; binds to rDNA terminator element, required for efficient Pol I termination; required for rDNA silencing at NTS1; facilities association of Sir2p with NTS1, contributes to rDNA stability and cell longevity; interacts physically with Fob1p and RENT subunits, Sir2p and Net1p; may interact with ribosomes, based on co-purification experiments; Myb-like DNA-binding protein; NSI1 has a paralog, REB1, that arose from the whole genome duplication
3	C2	NRG1	YDR043C	Negative Regulator of Glucose-repressed genes	Transcriptional repressor; recruits the Cyc8p-Tup1p complex to promoters; mediates glucose repression and negatively regulates a variety of processes including filamentous growth and alkaline pH response; activated in stochastic pulses of nuclear localization in response to low glucose
3	C3	MAL33	YBR297W	MALtose	MAL-activator protein; part of complex locus MAL3; nonfunctional in genomic reference strain S288C

Plate	Position	Standard Name	Systematic Name	Name description	Description
				fermentation	
3	C4	HCM1	YCR065W	High-Copy suppressor of Calmodulin	Forkhead transcription factor; drives S-phase specific expression of genes involved in chromosome segregation, spindle dynamics, and budding; suppressor of calmodulin mutants with specific SPB assembly defects; telomere maintenance role; regulates replicative lifespan; ortholog of C. elegans lifespan regulator PHA-4
3	C5	CBF1	YJR060W	Centromere Binding Factor	Basic helix-loop-helix (bHLH) protein; forms homodimer to bind E-box consensus sequence CACGTG present at MET gene promoters and centromere DNA element I (CDEI); affects nucleosome positioning at this motif; associates with other transcription factors such as Met4p and Isw1p to mediate transcriptional activation or repression; associates with kinetochore proteins, required for chromosome segregation; protein abundance increases in response to DNA replication stress
3	C6	PHO2	YDL106C	PHOsphate metabolism	Homeobox transcription factor; regulatory targets include genes involved in phosphate metabolism; binds cooperatively with Pho4p to the PHO5 promoter; phosphorylation of Pho2p facilitates interaction with Pho4p; relocalizes to the cytosol in response to hypoxia
3	C7	UGA3	YDL170W	Utilization of GAba	Transcriptional activator for GABA-dependent induction of GABA genes; binds to DNA elements found in the promoters of target genes and increases their expression in the presence of GABA (gamma-aminobutyrate); zinc finger transcription factor of the Zn(2)-Cys(6) binuclear cluster domain type; localized to the nucleus; examples of GABA genes include UGA1, UGA2, and UGA4
3	C8	CRZ1	YNL027W	Calcineurin-Responsive Zinc finger	Transcription factor, activates transcription of stress response genes; nuclear localization is positively regulated by calcineurin-mediated dephosphorylation; rapidly localizes to the nucleus under blue light stress; can be activated in stochastic pulses of nuclear localization in response to calcium
3	C9	RTG3	YBL103C	ReTroGrade regulation	bHLH/Zip transcription factor for retrograde (RTG) and TOR pathways; forms a complex with another bHLH/Zip protein, Rtg1p, to activate the pathways; target of **Hog1p**
3	C10	EDS1	YBR033W	Expression Dependent on Slt2	Putative zinc cluster protein, predicted to be a transcription factor; not an essential gene; EDS1 has a paralog, RGT1, that arose from the whole genome duplication
3	C11	THO2	YNL139C	suppressor of the Transcriptional defect of Hpr1 by Overexpression	Subunit of the THO complex; THO is required for efficient transcription elongation and involved in transcriptional elongation-associated recombination; required for LacZ RNA expression from certain plasmids
3	C12	XBP1	YIL101C	XhoI site-Binding Protein	Transcriptional repressor; binds promoter sequences of cyclin genes, CYS3, and SMF2; not expressed during log phase of growth, but induced by stress or starvation during mitosis, and late in meiosis; represses 15% of all yeast genes as cells transition to quiescence; important for maintaining G1 arrest and for longevity of quiescent cells; member of Swi4p/Mbp1p family; phosphorylated by Cdc28p; relative distribution to nucleus increases upon DNA replication stress

Plate	Position	Standard Name	Systematic Name	Name description	Description
3	D1	RPI1	YIL119C	Ras-cAMP Pathway Inhibitor	Transcription factor, allelic differences between S288C and Sigma1278b; mediates fermentation stress tolerance by modulating cell wall integrity; overexpression suppresses heat shock sensitivity of wild-type RAS2 overexpression and also suppresses cell lysis defect of mpk1 mutation; allele from S288c can confer fMAPK pathway independent transcription of FLO11; S288C and Sigma1278b alleles differ in number of tandem repeats within ORF
3	D2	MET18	YIL128W	METhionine requiring	Component of cytosolic iron-sulfur protein assembly (CIA) machinery; acts at a late step of Fe-S cluster assembly; forms the CIA targeting complex with Cia1p and Cia2p that directs Fe-S cluster incorporation into a subset of proteins involved in methionine biosynthesis, DNA replication and repair, transcription, and telomere maintenance; ortholog of human MMS19
3	D3	FKH2	YNL068C	ForK head Homolog	Forkhead family transcription factor; plays a major role in the expression of G2/M phase genes; positively regulates transcriptional elongation; facilitates clustering and activation of early-firing replication origins; negative role in chromatin silencing at HML and HMR; substrate of the Cdc28p/Clb5p kinase; relocalizes to the cytosol in response to hypoxia; FKH2 has a paralog, FKH1, that arose from the whole genome duplication
3	D4	KSS1	YGR040W	Kinase Suppressor of Sst2 mutations	Mitogen-activated protein kinase (MAPK); involved in signal transduction pathways that control filamentous growth and pheromone response; the KSS1 gene is nonfunctional in S288C strains and functional in W303 strains
3	D5	NNF2	YGR089W	-	Protein that exhibits physical and genetic interactions with Rpb8p; Rpb8p is a subunit of RNA polymerases I, II, and III; computational analysis of large-scale protein-protein interaction data suggests a role in chromosome segregation
3	D6	-	YJL175W	-	Dubious open reading frame unlikely to encode a functional protein; deletion confers resistance to cisplatin, hypersensitivity to 5-fluorouracil, and growth defect at high pH with high calcium; overlaps gene for SWI3 transcription factor
3	D7	DAL80	YKR034W	Degradation of Allantoin	Negative regulator of genes in multiple nitrogen degradation pathways; expression is regulated by nitrogen levels and by Gln3p; member of the GATA-binding family, forms homodimers and heterodimers with Gzf3p; DAL80 has a paralog, GZF3, that arose from the whole genome duplication
3	D8	TEC1	YBR083W	Transposon Enhancement Control	Transcription factor targeting filamentation genes and Ty1 expression; Ste12p activation of most filamentation gene promoters depends on Tec1p and Tec1p transcriptional activity is dependent on its association with Ste12p; binds to TCS elements upstream of filamentation genes, which are regulated by Tec1p/Ste12p/Dig1p complex; competes with Dig2p for binding to Ste12p/Dig1p; positive regulator of chronological life span; TEA/ATTS DNA-binding domain family member
3	D9	TBS1	YBR150C	ThiaBendazole Sensitive	Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies; TBS1 has a paralog, HAL9, that arose from the whole genome duplication
3	D10	CIS1 reserved	YLR346C	CItrinin Sensitive knockout	Putative protein of unknown function found in mitochondria; expression is regulated by transcription factors involved in pleiotropic drug resistance, Pdr1p and Yrr1p; not an essential gene; YLR346C has a paralog, YGR035C, that arose

Plate	Position	Standard Name	Systematic Name	Name description	Description
		name			from the whole genome duplication
3	D11	YOX1	YML027W	Yeast homeobOX	Homeobox transcriptional repressor; binds to Mcm1p and to early cell cycle boxes (ECBs) in the promoters of cell cycle-regulated genes expressed in M/G1 phase; expression is cell cycle-regulated; phosphorylated by Cdc28p; relocalizes from nucleus to cytoplasm upon DNA replication stress; YOX1 has a paralog, YHP1, that arose from the whole genome duplication
3	D12	WAR1	YML076C	Weak Acid Resistance	Homodimeric Zn2Cys6 zinc finger transcription factor; binds to a weak acid response element to induce transcription of PDR12 and FUN34, encoding an acid transporter and a putative ammonia transporter, respectively
3	E1	MBF1	YOR298C-A	Multiprotein Bridging Factor	Transcriptional coactivator; bridges the DNA-binding region of Gcn4p and TATA-binding protein Spt15p; suppressor of frameshift mutations; protein abundance increases in response to DNA replication stress
3	E2	DAL81	YIR023W	Degradation of Allantoin	Positive regulator of genes in multiple nitrogen degradation pathways; contains DNA binding domain but does not appear to bind the dodecanucleotide sequence present in the promoter region of many genes involved in allantoin catabolism
3	E3	PCC1	YKR095W-A	Polarized growth Chromatin-associated Controller	Component of the EKC/KEOPS protein complex; EKC/KEOPS complex is required for t6A tRNA modification and telomeric TG1-3 recombination; may have role in transcription; other complex members are Kae1p, Gon7p, Bud32p, and Cgi121p
3	E4	MSN2	YMR037C	Multicopy suppressor of SNF1 mutation	Stress-responsive transcriptional activator; activated in stochastic pulses of nuclear localization in response to various stress conditions; binds DNA at stress response elements of responsive genes; relative distribution to nucleus increases upon DNA replication stress
3	E5	HAA1	YPR008W	Homolog of Ace1 Activator	Transcriptional activator involved in adaptation to weak acid stress; activates transcription of TPO2, YRO2, and other genes encoding membrane stress proteins; HAA1 has a paralog, CUP2, that arose from the whole genome duplication; relocalizes from cytoplasm to nucleus upon DNA replication stress
3	E6	-	YPR022C	-	Putative transcription factor, as suggested by computational analysis; green fluorescent protein (GFP)-fusion protein localizes to both the cytoplasm and the nucleus and is induced in response to the DNA-damaging agent MMS
3	E7	RPN4	YDL020C	Regulatory Particle Non-ATPase	Transcription factor that stimulates expression of proteasome genes; Rpn4p levels are in turn regulated by the 26S proteasome in a negative feedback control mechanism; RPN4 is transcriptionally regulated by various stress responses; relative distribution to the nucleus increases upon DNA replication stress
3	E8	STP4	YDL048C	protein with similarity to Stp1p	Protein containing a Kruppel-type zinc-finger domain; similar to Stp1p, Stp2p; predicted transcription factor; relative distribution to the nucleus increases upon DNA replication stress; STP4 has a paralog, STP3, that arose from the whole genome duplication
3	E9	CBS1	YDL069C	Cytochrome B Synthesis	Mitochondrial translational activator of the COB mRNA; membrane protein that interacts with translating ribosomes, acts on the COB mRNA 5'-untranslated leader

Plate	Position	Standard Name	Systematic Name	Name description	Description
3	E10	BDF2	YDL070W	BromoDomain Factor	Protein involved in transcription initiation; acts at TATA-containing promoters; associates with the basal transcription factor TFIID; contains two bromodomains; corresponds to the C-terminal region of mammalian TAF1; redundant with Bdf1p; protein abundance increases in response to DNA replication stress; BDF2 has a paralog, BDF1, that arose from the whole genome duplication
3	E11	X	X	X	-
3	E12	STP1	YDR463W	Species-specific tRNA Processing	Transcription factor; contains a N-terminal regulatory motif (RI) that acts as a cytoplasmic retention determinant and as an Asi dependent degron in the nucleus; undergoes proteolytic processing by SPS (Ssy1p-Ptr3p-Ssy5p)-sensor component Ssy5p in response to extracellular amino acids; activates transcription of amino acid permease genes and may have a role in tRNA processing; STP1 has a paralog, STP2, that arose from the whole genome duplication
3	F1	PLM2	YDR501W	PLasmid Maintenance	Putative transcription factor, contains Forkhead Associated domain; found associated with chromatin; target of SBF transcription factor; induced in response to DNA damaging agents and deletion of telomerase; PLM2 has a paralog, TOS4, that arose from the whole genome duplication
3	F2	EMI1	YDR512C	Early Meiotic Induction	Non-essential protein of unknown function; required for transcriptional induction of the early meiotic-specific transcription factor IME1, also required for sporulation; contains twin cysteine-x9-cysteine motifs
3	F3	EMI2	YDR516C	Early Meiotic Induction	Non-essential protein of unknown function; required for transcriptional induction of the early meiotic-specific transcription factor IME1; required for sporulation; expression regulated by glucose-repression transcription factors Mig1/2p; EMI2 has a paralog, GLK1, that arose from the whole genome duplication; protein abundance increases in response to DNA replication stress
3	F4	URC2	YDR520C	URacil Catabolism	Putative Zn(II)2Cys6 motif containing transcription factor; non-essential gene identified in a screen for mutants with increased levels of rDNA transcription; similar to S. kluyveri Urc2p involved in uracil catabolism
3	F5	SNT2	YGL131C	-	Subunit of Snt2C complex, RING finger ubiquitin ligase (E3); physically associates with Ecm5p and Rpd3p; along with Ecm5p, recruits Rpd3p to small number of promoters; colocalizes with Ecm5p, independently of Rpd3p, to promoters of stress response genes upon oxidative stress; involved in ubiquitylation, degradation of excess histones; interacts with Ubc4p; role in regulating genes encoding amine transporters; relocalizes from nucleus to cytoplasm upon DNA replication stress
3	F6	SUT1	YGL162W	Sterol UpTake	Transcription factor of the Zn(II)2Cys6 family; positively regulates genes involved in sterol uptake under anaerobic conditions; involved in hypoxic gene expression; represses filamentation-inducing genes during non-starvation conditions; positively regulates mating with SUT2 by repressing expression of genes which act as mating inhibitors; relocalizes from nucleus to cytoplasm upon DNA replication stress; SUT1 has a paralog, SUT2, that arose from the whole genome duplication
3	F7	CUP9	YGL166W	-	Copper-binding transcription factor; activates transcription of the metallothionein genes CUP1-1 and CUP1-2 in response to elevated copper concentrations; required for regulation of copper genes in response to DNA-damaging

Plate	Position	Standard Name	Systematic Name	Name description	Description
					reagents; CUP2 has a paralog, HAA1, that arose from the whole genome duplication
3	F8	GTS1	YGL181W	Glycine Threonine Serine repeat protein	Protein involved in Arf3p regulation and in transcription regulation; localizes to the nucleus and to endocytic patches; contains an N-terminal Zn-finger and ArfGAP homology domain, a C-terminal glutamine-rich region, and a UBA (ubiquitin associated) domain; gts1 mutations affect budding, cell size, heat tolerance, sporulation, life span, ultradian rhythms, endocytosis; expression oscillates in a pattern similar to metabolic oscillations
3	F9	FLO8	YER109C	FLOcculation	Transcription factor; required for flocculation, diploid filamentous growth, and haploid invasive growth; forms a heterodimer with Mss1p that interacts with the Swi/Snf complex during transcriptional activation of FLO1, FLO11, and STA1; S. cerevisiae genome reference strain S288C contains an internal in-frame stop at codon 142, which in other strains encodes tryptophan
3	F10	SWI4	YER111C	SWItching deficient	DNA binding component of the SBF complex (Swi4p-Swi6p); a transcriptional activator that in concert with MBF (Mbp1-Swi6p) regulates late G1-specific transcription of targets including cyclins and genes required for DNA synthesis and repair; Slt2p-independent regulator of cold growth; acetylation at two sites, K1016 and K1066, regulates interaction with Swi6p
3	F11	YHP1	YDR451C	Yeast Homeo-Protein	Homeobox transcriptional repressor; binds Mcm1p and early cell cycle box (ECB) elements of cell cycle regulated genes, thereby restricting ECB-mediated transcription to the M/G1 interval; YHP1 has a paralog, YOX1, that arose from the whole genome duplication
3	F12	RPH1	YER169W	Regulator of PHR1	JmjC domain-containing histone demethylase; specifically demethylates H3K36 tri- and dimethyl modification states; associates with actively transcribed (RNAP II) regions in vivo and specifically targets H3K36 in its trimethylation state as its substrate; transcriptional repressor of PHR1; Rph1p phosphorylation during DNA damage is under control of the MEC1-RAD53 pathway; target of stess-induced hormesis; RPH1 has a paralog, GIS1, that arose from the whole genome duplication
3	G1	TOG1	YER184C	Transcriptional regulator of Oleate utilization Genes	Transcriptional activator of oleate genes; regulates genes involved in fatty acid utilization; zinc cluster protein; deletion confers sensitivity to Calcufluor white, and prevents growth on glycerol or lactate as sole carbon source
3	G2	STB2	YMR053C	Sin Three Binding protein	Protein that interacts with Sin3p in a two-hybrid assay; part of a large protein complex with Sin3p and Stb1p; STB2 has a paralog, STB6, that arose from the whole genome duplication
3	G3	FKH1	YIL131C	ForK head Homolog	Forkhead family transcription factor; minor role in expression of G2/M phase genes; negatively regulates transcription elongation; positive role in chromatin silencing at HML, HMR; facilitates clustering and activation of early-firing replication origins; binds to recombination enhancer near HML, regulates donor preference during mating-type switching; relocalizes to cytosol in response to hypoxia; FKH1 has a paralog, FKH2, that arose from the whole genome duplication

Plate	Position	Standard Name	Systematic Name	Name description	Description
3	G4	SNF1	YDR477W	Sucrose NonFermenting	AMP-activated serine/threonine protein kinase; found in a complex containing Snf4p and members of the Sip1p/Sip2p/Gal83p family; required for transcription of glucose-repressed genes, thermotolerance, sporulation, and peroxisome biogenesis; involved in regulation of the nucleocytoplasmic shuttling of Hxk2p; regulates filamentous growth in response to starvation; SUMOylation by Mms21p inhibits its function and targets Snf1p for destruction via the Slx5-Slx8 Ubiquitin ligase
3	G5	MIG3	YER028C	Multicopy Inhibitor of Growth	Transcriptional regulator; partially nonfunctional in S288C strains but has a major role in catabolite repression and ethanol response in some other strains; involved in response to toxic agents; phosphorylation by Snf1p or the Mec1p pathway inactivates Mig3p, allowing induction of damage response genesenvironment
3	G6	BDF1	YLR399C	BromoDomain Factor	Protein involved in transcription initiation; functions at TATA-containing promoters; associates with the basal transcription factor TFIID; contains two bromodomains; corresponds to the C-terminal region of mammalian TAF1; redundant with Bdf2p; BDF1 has a paralog, BDF2, that arose from the whole genome duplication
3	G7	SFP1	YLR403W	Split Finger Protein	Regulates transcription of ribosomal protein and biogenesis genes; regulates response to nutrients and stress, G2/M transitions during mitotic cell cycle and DNA-damage response, and modulates cell size; regulated by TORC1 and Mrs6p; sequence of zinc finger, ChIP localization data, and protein-binding microarray (PBM) data, and computational analyses suggest it binds DNA directly at highly active RP genes and indirectly through Rap1p at others; can form the [ISP+] prion
3	G8	IME4	YGL192W	Inducer of MEiosis	mRNA N6-adenosine methyltransferase required for entry into meiosis; mediates N6-adenosine methylation of bulk mRNA during the induction of sporulation which includes the meiotic regulators IME1, IME2 and IME4 itself; repressed in haploids via production of antisense IME4 transcripts; transcribed in diploid cells where antisense transcription is repressed; orthologous to human METTL3 (MT-A70)
3	G9	RCO1	YMR075W	-	Essential component of the Rpd3S histone deacetylase complex; interacts with Eaf3p
3	G10	PUT3	YKL015W	Proline UTilization	Transcriptional activator; binds specific gene recruitment sequences and is required for DNA zip code-mediated targeting of genes to nuclear periphery; regulates proline utilization genes, constitutively binds PUT1 and PUT2 promoters as a dimer, undergoes conformational change to form active state; binds other promoters only under activating conditions; differentially phosphorylated in presence of different nitrogen sources; has a Zn(2)-Cys(6) binuclear cluster domain
3	G11	COM2	YER130C	Cousin of Msn2	Transcription factor that binds IME1 Upstream Activation Signal (UAS)ru; COM2 transcription is regulated by Haa1p, Sok2p and Zap1p transcriptional activators; may bind the IME1 promoter under all growth conditions to negatively regulate its transcription in the absence of a positive regulator that binds more effectively; repressor activity may depend on phosphorylation by PKA; C. albicans homolog (MNL1) plays a role in adaptation to stress
3	G12	X	X	X	-
3	H1	X	X	X	-

Plate	Position	Standard Name	Systematic Name	Name description	Description
3	H2	X	X	X	-
3	H3	X	X	X	-
3	H4	X	X	X	-
3	H5	X	X	X	-
3	H6	X	X	X	-
3	H7	**-**	**CWG424**	Wild type BY4741	-
3	H8	**-**	**CWG424**	Wild type BY4741	-
3	H9	**RAD27**	**YKL113C**	RADiation sensitive	5' to 3' exonuclease, 5' flap endonuclease; required for Okazaki fragment processing and maturation, for long-patch base-excision repair and large loop repair (LLR), ribonucleotide excision repair; member of the S. pombe RAD2/FEN1 family; relocalizes to the cytosol in response to hypoxia
3	H10	**RAD27**	**YKL113C**	RADiation sensitive	5' to 3' exonuclease, 5' flap endonuclease; required for Okazaki fragment processing and maturation, for long-patch base-excision repair and large loop repair (LLR), ribonucleotide excision repair; member of the S. pombe RAD2/FEN1 family; relocalizes to the cytosol in response to hypoxia
3	H11	**RAD52**	**YML032C**	RADiation sensitive	Protein that stimulates strand exchange; stimulates strand exchange by facilitating Rad51p binding to single-stranded DNA; anneals complementary single-stranded DNA; involved in the repair of double-strand breaks in DNA during vegetative growth and meiosis and UV induced sister chromatid recombination
3	H12	**RAD52**	**YML032C**	RADiation sensitive	Protein that stimulates strand exchange; stimulates strand exchange by facilitating Rad51p binding to single-stranded DNA; anneals complementary single-stranded DNA; involved in the repair of double-strand breaks in DNA during vegetative growth and meiosis and UV induced sister chromatid recombination

B Hit yeast gene deletion strains, their names and role descriptions, and their positions in the 96-well glycerol stock plate for the conformation screening. names and roles were taken from their locus overview in the Saccharomyces Gene Database (SGD) (http://www.yeastgenome.org/). Purple – non-transcriptional regulators.

Plate	Position	Standard Name	Systematic Name	Name description	Description
1	A1	X	X	X	-
1	A2	X	X	X	-
1	A3	X	X	X	-
1	A4	X	X	X	-
1	A5	X	X	X	-
1	A6	X	X	X	-
1	A7	X	X	X	-
1	A8	X	X	X	-
1	A9	X	X	X	-
1	A10	X	X	X	-
1	A11	X	X	X	-
1	A12	X	X	X	-
1	B1	SWI5	YDR146C	SWItching deficient	Transcription factor that recruits Mediator and Swi/Snf complexes; activates transcription of genes expressed at the M/G1 phase boundary and in G1 phase; required for expression of the HO gene controlling mating type switching; localization to nucleus occurs during G1 and appears to be regulated by phosphorylation by Cdc28p kinase; SWI5 has a paralog, ACE2, that arose from the whole genome duplication
1	B2	NDT80	YHR124W	Non-DiTyrosine	Meiosis-specific transcription factor; required for exit from pachytene and for full meiotic recombination; activates middle sporulation genes; competes with Sum1p for binding to promoters containing middle sporulation elements (MSE)
1	B3	MET18	YIL128W	METhionine requiring	Component of cytosolic iron-sulfur protein assembly (CIA) machinery; acts at a late step of Fe-S cluster assembly; forms the CIA targeting complex with Cia1p and Cia2p that directs Fe-S cluster incorporation into a subset of proteins involved in methionine biosynthesis, DNA replication and repair, transcription, and telomere maintenance; ortholog of human MMS19
1	B4	EMI1	YDR512C	Early Meiotic Induction	Non-essential protein of unknown function; required for transcriptional induction of the early meiotic-specific transcription factor IME1, also required for sporulation; contains twin cysteine-x9-cysteine motifs
1	B5	ADR1	YDR216W	Alcohol Dehydrogenase Regulator	Carbon source-responsive zinc-finger transcription factor; required for transcription of the glucose-repressed gene ADH2, of peroxisomal protein genes, and of genes required for ethanol, glycerol, and fatty acid utilization
1	B6	HAP5	YOR358W	Heme Activator	Subunit of the Hap2p/3p/4p/5p CCAAT-binding complex; complex is heme-activated and glucose repressed; complex is a

Plate	Position	Standard Name	Systematic Name	Name description	Description
				Protein	transcriptional activator and global regulator of respiratory gene expression; required for assembly and DNA binding activity of the complex
1	B7	X	X	X	-
1	B8	X	X	X	-
1	B9	X	X	X	-
1	B10	X	X	X	-
1	B11	X	X	X	-
1	B12	X	X	X	-
1	C1	SFP1	YLR403W	Split Finger Protein	Regulates transcription of ribosomal protein and biogenesis genes; regulates response to nutrients and stress, G2/M transitions during mitotic cell cycle and DNA-damage response, and modulates cell size; regulated by TORC1 and Mrs6p; sequence of zinc finger, ChIP localization data, and protein-binding microarray (PBM) data, and computational analyses suggest it binds DNA directly at highly active RP genes and indirectly through Rap1p at others; can form the [ISP+] prion
1	C2	CIN5	YOR028C	Chromosome INstability	Basic leucine zipper (bZIP) transcription factor of the yAP-1 family; physically interacts with the Tup1-Cyc8 complex and recruits Tup1p to its targets; mediates pleiotropic drug resistance and salt tolerance; nuclearly localized under oxidative stress and sequestered in the cytoplasm by Lot6p under reducing conditions; CIN5 has a paralog, YAP6, that arose from the whole genome duplication
1	C3	**RAD27**	**YKL113C**	RADiation sensitive	5' to 3' exonuclease, 5' flap endonuclease; required for Okazaki fragment processing and maturation, for long-patch base-excision repair and large loop repair (LLR), ribonucleotide excision repair; member of the S. pombe RAD2/FEN1 family; relocalizes to the cytosol in response to hypoxia
1	C4	ZAP1	YJL056C	Zinc-responsive Activator Protein	Zinc-regulated transcription factor; binds to zinc-responsive promoters to induce transcription of certain genes in presence of zinc, represses other genes in low zinc; regulates its own transcription; contains seven zinc-finger domains
1	C5	SUM1	YDR310C	SUppresor of Mar1-1	Transcriptional repressor that regulates middle-sporulation genes; required for mitotic repression of middle sporulation-specific genes; also acts as general replication initiation factor; involved in telomere maintenance, chromatin silencing; regulated by pachytene checkpoint
1	C6	SKN7	YHR206W	Suppressor of Kre Null	Nuclear response regulator and transcription factor; physically interacts with the Tup1-Cyc8 complex and recruits Tup1p to its targets; part of a branched two-component signaling system; required for optimal induction of heat-shock genes in response to oxidative stress; involved in osmoregulation; relocalizes to the cytosol in response to hypoxia; SKN7 has a paralog, HMS2, that arose from the whole genome duplication
1	C7	X	X	X	-
1	C8	X	X	X	-

Plate	Position	Standard Name	Systematic Name	Name description	Description
1	C9	X	X	X	-
1	C10	X	X	X	-
1	C11	X	X	X	-
1	C12	X	X	X	-
1	D1	USV1	YPL230W	Up in StarVation	Putative transcription factor containing a C2H2 zinc finger; mutation affects transcriptional regulation of genes involved in growth on non-fermentable carbon sources, response to salt stress and cell wall biosynthesis; USV1 has a paralog, RGM1, that arose from the whole genome duplication
1	D2	SOK2	YMR016C	Suppressor Of Kinase	Nuclear protein that negatively regulates pseudohyphal differentiation; plays a regulatory role in the cyclic AMP (cAMP)-dependent protein kinase (PKA) signal transduction pathway; relocalizes to the cytosol in response to hypoxia; SOK2 has a paralog, PHD1, that arose from the whole genome duplication
1	D3	RIM101	YHL027W	Regulator of IME2	Cys2His2 zinc-finger transcriptional repressor; involved in alkaline responsive gene repression as part of adaptation to alkaline conditions; involved in cell wall assembly; required for alkaline pH-stimulated haploid invasive growth and sporulation; activated by alkaline-dependent proteolytic processing which results in removal of the C-terminal tail; similar to A. nidulans PacC
1	D4	SWI4	YER111C	SWItching deficient	DNA binding component of the SBF complex (Swi4p-Swi6p); a transcriptional activator that in concert with MBF (Mbp1-Swi6p) regulates late G1-specific transcription of targets including cyclins and genes required for DNA synthesis and repair; Slt2p-independent regulator of cold growth; acetylation at two sites, K1016 and K1066, regulates interaction with Swi6p
1	D5	GCR2	YNL199C	GlyColysis Regulation	Transcriptional activator of genes involved in glycolysis; interacts and functions with the DNA-binding protein Gcr1p
1	D6	BDF1	YLR399C	BromoDomain Factor	Protein involved in transcription initiation; functions at TATA-containing promoters; associates with the basal transcription factor TFIID; contains two bromodomains; corresponds to the C-terminal region of mammalian TAF1; redundant with Bdf2p; BDF1 has a paralog, BDF2, that arose from the whole genome duplication
1	D7	X	X	X	-
1	D8	X	X	X	-
1	D9	X	X	X	-
1	D10	X	X	X	-
1	D11	X	X	X	-
1	D12	X	X	X	-
1	E1	**RAD52**	**YML032C**	RADiation sensitive	Protein that stimulates strand exchange; stimulates strand exchange by facilitating Rad51p binding to single-stranded DNA; anneals complementary single-stranded DNA; involved in the repair of double-strand breaks in DNA during

Plate	Position	Standard Name	Systematic Name	Name description	Description
					vegetative growth and meiosis and UV induced sister chromatid recombination
1	E2	MAC1	YMR021C	Metal binding ACtivator	Copper-sensing transcription factor; involved in regulation of genes required for high affinity copper transport; required for regulation of yeast copper genes in response to DNA-damaging agents; undergoes changes in redox state in response to changing levels of copper or MMS
1	E3	UME6	YDR207C	Unscheduled Meiotic gene Expression	Rpd3L histone deacetylase complex subunit; key transcriptional regulator of early meiotic genes; involved in chromatin remodeling and transcriptional repression via DNA looping; binds URS1 upstream regulatory sequence, couples metabolic responses to nutritional cues with initiation and progression of meiosis, forms complex with Ime1p
1	E4	HIR1	YBL008W	HIstone Regulation	Subunit of the HIR complex; HIR is a nucleosome assembly complex involved in regulation of histone gene transcription; contributes to nucleosome formation, heterochromatic gene silencing, and formation of functional kinetochores
1	E5	AFT1	YGL071W	Activator of Ferrous Transport	Transcription factor involved in iron utilization and homeostasis; binds consensus site PyPuCACCCPu and activates transcription in response to changes in iron availability; in iron-replete conditions localization is regulated by Grx3p, Grx4p, and Fra2p, and promoter binding is negatively regulated via Grx3p-Grx4p binding; AFT1 has a paralog, AFT2, that arose from the whole genome duplication; relative distribution to the nucleus increases upon DNA replication stress
1	E6	SWI6	YLR182W	SWItching deficient	Transcription cofactor; forms complexes with Swi4p and Mbp1p to regulate transcription at the G1/S transition; involved in meiotic gene expression; also binds Stb1p to regulate transcription at START; cell wall stress induces phosphorylation by Mpk1p, which regulates Swi6p localization; required for the unfolded protein response, independently of its known transcriptional coactivators
1	E7	X	X	X	-
1	E8	X	X	X	-
1	E9	X	X	X	-
1	E10	X	X	X	-
1	E11	X	X	X	-
1	E12	X	X	X	-
1	F1	SLA1	YBL007C	Synthetic Lethal with ABP1	Cytoskeletal protein binding protein; required for assembly of the cortical actin cytoskeleton; interacts with proteins regulating actin dynamics and proteins required for endocytosis; found in the nucleus and cell cortex; has 3 SH3 domains
1	F2	SWF1	YDR126W	Spore Wall Formation	Palmitoyltransferase that acts on transmembrane proteins; including the SNAREs Snc1p, Syn8p, Tlg1p and likely all SNAREs; contains an Asp-His-His-Cys-cysteine rich (DHHC-CRD) domain; may have a role in vacuole fusion
1	F3	HMS1	YOR032C	High-copy Mep Suppressor	bHLH protein with similarity to myc-family transcription factors; overexpression confers hyperfilamentous growth and suppresses the pseudohyphal filamentation defect of a diploid mep1 mep2 homozygous null mutant
1	F4	KAR4	YCL055W	KARyogamy	Transcription factor required for response to pheromones; also required during meiosis; exists in two forms, a slower-

Plate	Position	Standard Name	Systematic Name	Name description	Description
					migrating form more abundant during vegetative growth and a faster-migrating form induced by pheromone
1	F5	AFT2	YPL202C	Activator of Fe (iron) Transcription	Iron-regulated transcriptional activator; activates genes involved in intracellular iron use and required for iron homeostasis and resistance to oxidative stress; AFT2 has a paralog, AFT1, that arose from the whole genome duplication
1	F6	-	**CWG424**	Wild type BY4741	-
1	F7	X	X	X	-
1	F8	X	X	X	-
1	F9	X	X	X	-
1	F10	X	X	X	-
1	F11	X	X	X	-
1	F12	X	X	X	-
1	G1	X	X	X	-
1	G2	X	X	X	-
1	G3	X	X	X	-
1	G4	X	X	X	-
1	G5	X	X	X	-
1	G6	X	X	X	-
1	G7	X	X	X	-
1	G8	X	X	X	-
1	G9	X	X	X	-
1	G10	X	X	X	-
1	G11	X	X	X	-
1	G12	X	X	X	-
1	H1	X	X	X	-
1	H2	X	X	X	-
1	H3	X	X	X	-
1	H4	X	X	X	-
1	H5	X	X	X	-
1	H6	X	X	X	-

Plate	Position	Standard Name	Systematic Name	Name description	Description
1	H7	X	X	X	-
1	H8	X	X	X	-
1	H9	X	X	X	-
1	H10	X	X	X	-
1	H11	X	X	X	-
1	H12	X	X	X	-

C. Yeast Fitness Database: cisplatin, carboplatin and oxaliplatin gene hits from the Yeast Fitness database with a p value <0.01, analysed using Gene Ontology (GO) Slim Mapper analysis via the Saccharomyces Gene Database (SGD) (http://www.yeastgenome.org/) using the Yeast GO-slim term '**function**'. Fold enrichment for each function is the % Frequency/% Genome Frequency. Note that for cisplatin, 17 genes were invalid nomenclature and not included for analysis, for carboplatin this was 5, and oxaliplatin 8.

Functions of all cisplatin hits	Frequency	Genome Frequency	Fold enrichment
histone binding	19 out of 1639 genes, 1.2%	41 of 6338 genes, 0.6%	2.0
hydrolase activity, acting on glycosyl bonds	21 out of 1639 genes, 1.3%	47 of 6338 genes, 0.7%	1.9
signal transducer activity	13 out of 1639 genes, 0.8%	34 of 6338 genes, 0.5%	1.6
methyltransferase activity	35 out of 1639 genes, 2.1%	90 of 6338 genes, 1.4%	1.5
phosphatase activity	32 out of 1639 genes, 2%	94 of 6338 genes, 1.5%	1.3
protein binding, bridging	19 out of 1639 genes, 1.2%	60 of 6338 genes, 0.9%	1.3
molecular function unknown	611 out of 1639 genes, 37.3%	1863 of 6338 genes, 29.4%	1.3
kinase activity	63 out of 1639 genes, 3.8%	195 of 6338 genes, 3.1%	1.2
DNA binding	119 out of 1639 genes, 7.3%	380 of 6338 genes, 6%	1.2
unfolded protein binding	22 out of 1639 genes, 1.3%	70 of 6338 genes, 1.1%	1.2
enzyme regulator activity	69 out of 1639 genes, 4.2%	227 of 6338 genes, 3.6%	1.2
lipid binding	30 out of 1639 genes, 1.8%	101 of 6338 genes, 1.6%	1.1
nucleic acid binding transcription factor activity	47 out of 1639 genes, 2.9%	162 of 6338 genes, 2.6%	1.1
enzyme binding	18 out of 1639 genes, 1.1%	64 of 6338 genes, 1.0%	1.1
lyase activity	24 out of 1639 genes, 1.5%	90 of 6338 genes, 1.4%	1.1

Functions of all carboplatin hits	Frequency	Genome Frequency	Fold enrichment
hydrolase activity, acting on glycosyl bonds	7 out of 577 genes, 1.2%	47 of 6338 genes, 0.7%	1.7
protein binding, bridging	8 out of 577 genes, 1.4%	60 of 6338 genes, 0.9%	1.6
methyltransferase activity	12 out of 577 genes, 2.1%	90 of 6338 genes, 1.4%	1.5
transmembrane transporter activity	40 out of 577 genes, 6.9%	317 of 6338 genes, 5.0%	1.4
molecular function unknown	219 out of 577 genes, 38%	1863 of 6338 genes, 29.4%	1.3
nucleic acid binding transcription factor activity	19 out of 577 genes, 3.3%	162 of 6338 genes, 2.6%	1.3
DNA binding	44 out of 577 genes, 7.6%	380 of 6338 genes, 6%	1.3
enzyme regulator activity	26 out of 577 genes, 4.5%	227 of 6338 genes, 3.6%	1.3
enzyme binding	7 out of 577 genes, 1.2%	64 of 6338 genes, 1.0%	1.2
ATPase activity	27 out of 577 genes, 4.7%	263 of 6338 genes, 4.1%	1.1
isomerase activity	6 out of 577 genes, 1.0%	59 of 6338 genes, 0.9%	1.1

Functions of all oxaliplatin hits	Frequency	Genome Frequency	Fold enrichment
ubiquitin-like protein binding	12 out of 649 genes, 1.8%	43 of 6338 genes, 0.7%	2.6
lipid binding	22 out of 649 genes, 3.4%	101 of 6338 genes, 1.6%	2.1
guanyl-nucleotide exchange factor activity	9 out of 649 genes, 1.4%	45 of 6338 genes, 0.7%	2.0
histone binding	8 out of 649 genes, 1.2%	41 of 6338 genes, 0.6%	2.0
ion binding	35 out of 649 genes, 5.4%	177 of 6338 genes, 2.8%	1.9
protein transporter activity	9 out of 649 genes, 1.4%	52 of 6338 genes, 0.8%	1.8
signal transducer activity	5 out of 649 genes, 0.8%	34 of 6338 genes, 0.5%	1.6
chromatin binding	16 out of 649 genes, 2.5%	103 of 6338 genes, 1.6%	1.6
cytoskeletal protein binding	11 out of 649 genes, 1.7%	67 of 6338 genes, 1.1%	1.5
unfolded protein binding	11 out of 649 genes, 1.7%	70 of 6338 genes, 1.1%	1.5
enzyme binding	10 out of 649 genes, 1.5%	64 of 6338 genes, 1.0%	1.5
GTPase activity	10 out of 649 genes, 1.5%	62 of 6338 genes, 1%	1.5
enzyme regulator activity	32 out of 649 genes, 4.9%	227 of 6338 genes, 3.6%	1.4
kinase activity	27 out of 649 genes, 4.2%	195 of 6338 genes, 3.1%	1.4
ATPase activity	36 out of 649 genes, 5.5%	263 of 6338 genes, 4.1%	1.3
phosphatase activity	13 out of 649 genes, 2.0%	94 of 6338 genes, 1.5%	1.3
protein binding, bridging	8 out of 649 genes, 1.2%	60 of 6338 genes, 0.9%	1.3
DNA binding	51 out of 649 genes, 7.9%	380 of 6338 genes, 6%	1.3
hydrolase activity, acting on glycosyl bonds	6 out of 649 genes, 0.9%	47 of 6338 genes, 0.7%	1.3
molecular function unknown	233 out of 649 genes, 35.9%	1863 of 6338 genes, 29.4%	1.2
hydrolase activity	103 out of 649 genes, 15.9%	867 of 6338 genes, 13.7%	1.2

D. Yeast Fitness Database: cisplatin, carboplatin and oxaliplatin gene hits from the Yeast Fitness database with a p value <0.01, analysed using Gene Ontology (GO) Slim analysis via the Saccharomyces Gene Database (SGD) (http://www.yeastgenome.org/) using the Yeast GO-slim term '**process**'. Fold enrichment for each process is the % Frequency/% Genome Frequency. Note that for cisplatin, 17 genes were invalid nomenclature and not included for analysis, for carboplatin this was 5, and oxaliplatin 8.

Processes of all cisplatin hits	Frequency	Genome Frequency	Fold enrichment
response to osmotic stress	41 out of 1639 genes, 2.5%	89 of 6338 genes, 1.4%	1.8
protein alkylation	23 out of 1639 genes, 1.4%	49 of 6338 genes, 0.8%	1.8
membrane invagination	19 out of 1639 genes, 1.2%	43 of 6338 genes, 0.7%	1.7
peroxisome organization	28 out of 1639 genes, 1.7%	69 of 6338 genes, 1.1%	1.5
sporulation	50 out of 1639 genes, 3.1%	133 of 6338 genes, 2.1%	1.5
regulation of transport	31 out of 1639 genes, 1.9%	82 of 6338 genes, 1.3%	1.5
organelle fission	110 out of 1639 genes, 6.7%	291 of 6338 genes, 4.6%	1.5
regulation of DNA metabolic process	37 out of 1639 genes, 2.3%	102 of 6338 genes, 1.6%	1.4
meiotic cell cycle	103 out of 1639 genes, 6.3%	278 of 6338 genes, 4.4%	1.4
cellular response to DNA damage stimulus	109 out of 1639 genes, 6.7%	297 of 6338 genes, 4.7%	1.4
telomere organization	28 out of 1639 genes, 1.7%	77 of 6338 genes, 1.2%	1.4
cell wall organization or biogenesis	74 out of 1639 genes, 4.5%	201 of 6338 genes, 3.2%	1.4
protein folding	35 out of 1639 genes, 2.1%	94 of 6338 genes, 1.5%	1.4
regulation of cell cycle	75 out of 1639 genes, 4.6%	206 of 6338 genes, 3.3%	1.4
histone modification	41 out of 1639 genes, 2.5%	112 of 6338 genes, 1.8%	1.4
DNA repair	88 out of 1639 genes, 5.4%	245 of 6338 genes, 3.9%	1.4
biological process unknown	380 out of 1639 genes, 23.2%	1066 of 6338 genes, 16.8%	1.4
peptidyl-amino acid modification	48 out of 1639 genes, 2.9%	136 of 6338 genes, 2.1%	1.4
protein dephosphorylation	18 out of 1639 genes, 1.1%	49 of 6338 genes, 0.8%	1.4
chromatin organization	91 out of 1639 genes, 5.6%	261 of 6338 genes, 4.1%	1.4
response to heat	24 out of 1639 genes, 1.5%	68 of 6338 genes, 1.1%	1.4
conjugation	44 out of 1639 genes, 2.7%	125 of 6338 genes, 2%	1.4
response to chemical	152 out of 1639 genes, 9.3%	437 of 6338 genes, 6.9%	1.3
endocytosis	33 out of 1639 genes, 2.0%	96 of 6338 genes, 1.5%	1.3
cytokinesis	27 out of 1639 genes, 1.6%	79 of 6338 genes, 1.2%	1.3
vacuole organization	26 out of 1639 genes, 1.6%	79 of 6338 genes, 1.2%	1.3
pseudohyphal growth	26 out of 1639 genes, 1.6%	75 of 6338 genes, 1.2%	1.3
lipid transport	21 out of 1639 genes, 1.3%	63 of 6338 genes, 1%	1.3
protein phosphorylation	66 out of 1639 genes, 4.0%	194 of 6338 genes, 3.1%	1.3
signaling	77 out of 1639 genes, 4.7%	237 of 6338 genes, 3.7%	1.3
DNA recombination	57 out of 1639 genes, 3.5%	175 of 6338 genes, 2.8%	1.3
regulation of organelle organization	91 out of 1639 genes, 5.6%	288 of 6338 genes, 4.5%	1.2
cell budding	18 out of 1639 genes, 1.1%	59 of 6338 genes, 0.9%	1.2
cell morphogenesis	10 out of 1639 genes, 0.6%	29 of 6338 genes, 0.5%	1.2
regulation of protein modification process	41 out of 1639 genes, 2.5%	133 of 6338 genes, 2.1%	1.2
Golgi vesicle transport	58 out of 1639 genes, 3.5%	189 of 6338 genes, 3%	1.2
mitotic cell cycle	98 out of 1639 genes, 6%	327 of 6338 genes, 5.2%	1.2
ion transport	69 out of 1639 genes, 4.2%	236 of 6338 genes, 3.7%	1.1
protein modification by small protein conjugation or removal	55 out of 1639 genes, 3.4%	193 of 6338 genes, 3.0%	1.1
DNA-templated transcription, elongation	28 out of 1639 genes, 1.7%	92 of 6338 genes, 1.5%	1.1
organelle inheritance	16 out of 1639 genes, 1%	58 of 6338 genes, 0.9%	1.1
invasive growth in response to glucose limitation	16 out of 1639 genes, 1%	60 of 6338 genes, 0.9%	1.1
proteolysis involved in cellular protein catabolic process	67 out of 1639 genes, 4.1%	237 of 6338 genes, 3.7%	1.1
cytoskeleton organization	69 out of 1639 genes, 4.2%	243 of 6338 genes, 3.8%	1.1
protein glycosylation	18 out of 1639 genes, 1.1%	62 of 6338 genes, 1%	1.1
protein acylation	18 out of 1639 genes, 1.1%	66 of 6338 genes, 1.0%	1.1
carbohydrate metabolic process	73 out of 1639 genes, 4.5%	258 of 6338 genes, 4.1%	1.1
DNA replication	43 out of 1639 genes, 2.6%	154 of 6338 genes, 2.4%	1.1
transmembrane transport	66 out of 1639 genes, 4.0%	235 of 6338 genes, 3.7%	1.1
transcription from RNA polymerase II promoter	132 out of 1639 genes, 8.1%	478 of 6338 genes, 7.5%	1.1
cellular respiration	23 out of 1639 genes, 1.4%	84 of 6338 genes, 1.3%	1.1
endosomal transport	25 out of 1639 genes, 1.5%	88 of 6338 genes, 1.4%	1.1
response to oxidative stress	28 out of 1639 genes, 1.7%	101 of 6338 genes, 1.6%	1.1
response to starvation	33 out of 1639 genes, 2.0%	119 of 6338 genes, 1.9%	1.1
cellular ion homeostasis	35 out of 1639 genes, 2.1%	124 of 6338 genes, 2%	1.1

D. continued

Processes of all carboplatin hits	Frequency	Genome Frequency	Fold enrichment
amino acid transport	8 out of 577 genes, 1.4%	40 of 6338 genes, 0.6%	2.3
DNA repair	41 out of 577 genes, 7.1%	245 of 6338 genes, 3.9%	1.8
invasive growth in response to glucose limitation	9 out of 577 genes, 1.6%	60 of 6338 genes, 0.9%	1.8
cellular response to DNA damage stimulus	48 out of 577 genes, 8.3%	297 of 6338 genes, 4.7%	1.8
pseudohyphal growth	12 out of 577 genes, 2.1%	75 of 6338 genes, 1.2%	1.8
protein dephosphorylation	8 out of 577 genes, 1.4%	49 of 6338 genes, 0.8%	1.8
meiotic cell cycle	44 out of 577 genes, 7.6%	278 of 6338 genes, 4.4%	1.7
regulation of DNA metabolic process	15 out of 577 genes, 2.6%	102 of 6338 genes, 1.6%	1.6
endocytosis	14 out of 577 genes, 2.4%	96 of 6338 genes, 1.5%	1.6
protein acylation	9 out of 577 genes, 1.6%	66 of 6338 genes, 1.0%	1.6
ion transport	33 out of 577 genes, 5.7%	236 of 6338 genes, 3.7%	1.5
cell wall organization or biogenesis	28 out of 577 genes, 4.9%	201 of 6338 genes, 3.2%	1.5
organelle fission	40 out of 577 genes, 6.9%	291 of 6338 genes, 4.6%	1.5
protein maturation	7 out of 577 genes, 1.2%	48 of 6338 genes, 0.8%	1.5
sporulation	18 out of 577 genes, 3.1%	133 of 6338 genes, 2.1%	1.5
biological process unknown	139 out of 577 genes, 24.1%	1066 of 6338 genes, 16.8%	1.4
DNA recombination	23 out of 577 genes, 4%	175 of 6338 genes, 2.8%	1.4
membrane invagination	6 out of 577 genes, 1.0%	43 of 6338 genes, 0.7%	1.4
telomere organization	9 out of 577 genes, 1.6%	77 of 6338 genes, 1.2%	1.3
regulation of transport	10 out of 577 genes, 1.7%	82 of 6338 genes, 1.3%	1.3
response to chemical	52 out of 577 genes, 9.0%	437 of 6338 genes, 6.9%	1.3
regulation of cell cycle	25 out of 577 genes, 4.3%	206 of 6338 genes, 3.3%	1.3
proteolysis involved in cellular protein catabolic process	27 out of 577 genes, 4.7%	237 of 6338 genes, 3.7%	1.3
protein folding	11 out of 577 genes, 1.9%	94 of 6338 genes, 1.5%	1.3
response to starvation	14 out of 577 genes, 2.4%	119 of 6338 genes, 1.9%	1.3
signaling	26 out of 577 genes, 4.5%	237 of 6338 genes, 3.7%	1.2
endosomal transport	10 out of 577 genes, 1.7%	88 of 6338 genes, 1.4%	1.2
lipid transport	7 out of 577 genes, 1.2%	63 of 6338 genes, 1%	1.2
DNA replication	16 out of 577 genes, 2.8%	154 of 6338 genes, 2.4%	1.2
vacuole organization	8 out of 577 genes, 1.4%	79 of 6338 genes, 1.2%	1.2
transmembrane transport	25 out of 577 genes, 4.3%	235 of 6338 genes, 3.7%	1.2
regulation of organelle organization	30 out of 577 genes, 5.2%	288 of 6338 genes, 4.5%	1.2
response to osmotic stress	9 out of 577 genes, 1.6%	89 of 6338 genes, 1.4%	1.1
cofactor metabolic process	16 out of 577 genes, 2.8%	159 of 6338 genes, 2.5%	1.1
tRNA processing	11 out of 577 genes, 1.9%	106 of 6338 genes, 1.7%	1.1
monocarboxylic acid metabolic process	13 out of 577 genes, 2.3%	133 of 6338 genes, 2.1%	1.1
response to oxidative stress	10 out of 577 genes, 1.7%	101 of 6338 genes, 1.6%	1.1

D. continued

Processes of all oxaliplatin hits	Frequency	Genome Frequency	Fold enrichment
endosomal transport	34 out of 649 genes, 5.2%	88 of 6338 genes, 1.4%	3.7
membrane invagination	15 out of 649 genes, 2.3%	43 of 6338 genes, 0.7%	3.3
endocytosis	32 out of 649 genes, 4.9%	96 of 6338 genes, 1.5%	3.3
vacuole organization	24 out of 649 genes, 3.7%	79 of 6338 genes, 1.2%	3.1
protein dephosphorylation	14 out of 649 genes, 2.2%	49 of 6338 genes, 0.8%	2.8
vesicle organization	19 out of 649 genes, 2.9%	72 of 6338 genes, 1.1%	2.6
Golgi vesicle transport	49 out of 649 genes, 7.6%	189 of 6338 genes, 3%	2.5
regulation of DNA metabolic process	26 out of 649 genes, 4.0%	102 of 6338 genes, 1.6%	2.5
cell budding	14 out of 649 genes, 2.2%	59 of 6338 genes, 0.9%	2.4
regulation of transport	20 out of 649 genes, 3.1%	82 of 6338 genes, 1.3%	2.4
cytokinesis	18 out of 649 genes, 2.8%	79 of 6338 genes, 1.2%	2.3
telomere organization	18 out of 649 genes, 2.8%	77 of 6338 genes, 1.2%	2.3
membrane fusion	18 out of 649 genes, 2.8%	76 of 6338 genes, 1.2%	2.3
DNA repair	57 out of 649 genes, 8.8%	245 of 6338 genes, 3.9%	2.3
exocytosis	12 out of 649 genes, 1.8%	48 of 6338 genes, 0.8%	2.3
protein acylation	14 out of 649 genes, 2.2%	66 of 6338 genes, 1.0%	2.2
cellular response to DNA damage stimulus	67 out of 649 genes, 10.3%	297 of 6338 genes, 4.7%	2.2
protein targeting	56 out of 649 genes, 8.6%	285 of 6338 genes, 4.5%	1.9
organelle inheritance	11 out of 649 genes, 1.7%	58 of 6338 genes, 0.9%	1.9
organelle fusion	17 out of 649 genes, 2.6%	88 of 6338 genes, 1.4%	1.9
organelle fission	55 out of 649 genes, 8.5%	291 of 6338 genes, 4.6%	1.8
meiotic cell cycle	51 out of 649 genes, 7.9%	278 of 6338 genes, 4.4%	1.8
response to starvation	22 out of 649 genes, 3.4%	119 of 6338 genes, 1.9%	1.8
response to osmotic stress	16 out of 649 genes, 2.5%	89 of 6338 genes, 1.4%	1.8
proteolysis involved in cellular protein catabolic process	43 out of 649 genes, 6.6%	237 of 6338 genes, 3.7%	1.8
mitotic cell cycle	60 out of 649 genes, 9.2%	327 of 6338 genes, 5.2%	1.8
sporulation	24 out of 649 genes, 3.7%	133 of 6338 genes, 2.1%	1.8
DNA recombination	32 out of 649 genes, 4.9%	175 of 6338 genes, 2.8%	1.8
regulation of cell cycle	37 out of 649 genes, 5.7%	206 of 6338 genes, 3.3%	1.7
response to chemical	76 out of 649 genes, 11.7%	437 of 6338 genes, 6.9%	1.7
signaling	40 out of 649 genes, 6.2%	237 of 6338 genes, 3.7%	1.7
DNA replication	26 out of 649 genes, 4.0%	154 of 6338 genes, 2.4%	1.7
DNA-templated transcription, elongation	16 out of 649 genes, 2.5%	92 of 6338 genes, 1.5%	1.7
chromatin organization	44 out of 649 genes, 6.8%	261 of 6338 genes, 4.1%	1.7
histone modification	19 out of 649 genes, 2.9%	112 of 6338 genes, 1.8%	1.6
cellular ion homeostasis	21 out of 649 genes, 3.2%	124 of 6338 genes, 2%	1.6
carbohydrate transport	5 out of 649 genes, 0.8%	33 of 6338 genes, 0.5%	1.6
conjugation	20 out of 649 genes, 3.1%	125 of 6338 genes, 2%	1.6
cell wall organization or biogenesis	31 out of 649 genes, 4.8%	201 of 6338 genes, 3.2%	1.5
protein glycosylation	10 out of 649 genes, 1.5%	62 of 6338 genes, 1%	1.5
protein phosphorylation	30 out of 649 genes, 4.6%	194 of 6338 genes, 3.1%	1.5
regulation of organelle organization	43 out of 649 genes, 6.6%	288 of 6338 genes, 4.5%	1.5
protein folding	14 out of 649 genes, 2.2%	94 of 6338 genes, 1.5%	1.5
cytoskeleton organization	36 out of 649 genes, 5.5%	243 of 6338 genes, 3.8%	1.4
protein modification by small protein conjugation or removal	27 out of 649 genes, 4.2%	193 of 6338 genes, 3.0%	1.4
peptidyl-amino acid modification	19 out of 649 genes, 2.9%	136 of 6338 genes, 2.1%	1.4
protein alkylation	7 out of 649 genes, 1.1%	49 of 6338 genes, 0.8%	1.4
protein maturation	7 out of 649 genes, 1.1%	48 of 6338 genes, 0.8%	1.4
regulation of protein modification process	18 out of 649 genes, 2.8%	133 of 6338 genes, 2.1%	1.3
response to oxidative stress	13 out of 649 genes, 2.0%	101 of 6338 genes, 1.6%	1.3
pseudohyphal growth	10 out of 649 genes, 1.5%	75 of 6338 genes, 1.2%	1.3
chromosome segregation	24 out of 649 genes, 3.7%	193 of 6338 genes, 3.0%	1.2
invasive growth in response to glucose limitation	7 out of 649 genes, 1.1%	60 of 6338 genes, 0.9%	1.2
cell morphogenesis	4 out of 649 genes, 0.6%	29 of 6338 genes, 0.5%	1.2
transcription from RNA polymerase II promoter	55 out of 649 genes, 8.5%	478 of 6338 genes, 7.5%	1.1
carbohydrate metabolic process	29 out of 649 genes, 4.5%	258 of 6338 genes, 4.1%	1.1
protein complex biogenesis	36 out of 649 genes, 5.5%	326 of 6338 genes, 5.1%	1.1
biological process unknown	116 out of 649 genes, 17.9%	1066 of 6338 genes, 16.8%	1.1

E. Initial screen: all cisplatin, carboplatin and oxaliplatin gene hits from the initial screening of the transcriptional regulator library, that grew less than 50 % over 4 days growth on YPD agar containing cisplatin, carboplatin and oxaliplatin compared to on YPD agar containing no drug, analysed using Gene Ontology (GO) Slim analysis via the Saccharomyces Gene Database (SGD) (http://www.yeastgenome.org/) using the Yeast GO-slim term '**function**'. Fold enrichment for each function is the % Frequency/% Genome Frequency. Note wild type strain CWG424 is not included and RAD52 did not map to a function.

Functions of all cisplatin hits	Frequency	Genome Frequency	Fold enrichment
nucleic acid binding transcription factor activity	19 out of 47 genes, 40.4%	162 of 6338 genes, 2.6%	15.5
transcription factor binding	7 out of 47 genes, 14.9%	69 of 6338 genes, 1.1%	13.5
transcription factor activity, protein binding	11 out of 47 genes, 23.4%	124 of 6338 genes, 2%	11.7
DNA binding	29 out of 47 genes, 61.7%	380 of 6338 genes, 6%	10.3
chromatin binding	3 out of 47 genes, 6.4%	103 of 6338 genes, 1.6%	4.0
histone binding	1 out of 47 genes, 2.1%	41 of 6338 genes, 0.6%	3.5
guanyl-nucleotide exchange factor activity	1 out of 47 genes, 2.1%	45 of 6338 genes, 0.7%	3.0
ubiquitin-like protein binding	1 out of 47 genes, 2.1%	43 of 6338 genes, 0.7%	3.0
protein binding, bridging	1 out of 47 genes, 2.1%	60 of 6338 genes, 0.9%	2.3

Functions of all carboplatin hits	Frequency	Genome Frequency	Fold enrichment
nucleic acid binding transcription factor activity	10 out of 24 genes, 41.7%	162 of 6338 genes, 2.6%	16.0
transcription factor binding	4 out of 24 genes, 16.7%	69 of 6338 genes, 1.1%	15.2
transcription factor activity, protein binding	4 out of 24 genes, 16.7%	124 of 6338 genes, 2%	8.4
DNA binding	11 out of 24 genes, 45.8%	380 of 6338 genes, 6%	7.6
histone binding	1 out of 24 genes, 4.2%	41 of 6338 genes, 0.6%	7.0
ubiquitin-like protein binding	1 out of 24 genes, 4.2%	43 of 6338 genes, 0.7%	6.0
protein binding, bridging	1 out of 24 genes, 4.2%	60 of 6338 genes, 0.9%	4.7
chromatin binding	1 out of 24 genes, 4.2%	103 of 6338 genes, 1.6%	2.6
nuclease activity	1 out of 24 genes, 4.2%	136 of 6338 genes, 2.1%	2.0

Functions of all oxaliplatin hits	Frequency	Genome Frequency	Fold enrichment
nucleic acid binding transcription factor activity	27 out of 56 genes, 48.2%	162 of 6338 genes, 2.6%	18.5
transcription factor binding	8 out of 56 genes, 14.3%	69 of 6338 genes, 1.1%	13.0
DNA binding	36 out of 56 genes, 64.3%	380 of 6338 genes, 6%	10.7
transcription factor activity, protein binding	10 out of 56 genes, 17.9%	124 of 6338 genes, 2%	9.0
signal transducer activity	2 out of 56 genes, 3.6%	34 of 6338 genes, 0.5%	7.2
chromatin binding	3 out of 56 genes, 5.4%	103 of 6338 genes, 1.6%	3.4
histone binding	1 out of 56 genes, 1.8%	41 of 6338 genes, 0.6%	3.0
ubiquitin-like protein binding	1 out of 56 genes, 1.8%	43 of 6338 genes, 0.7%	2.6
protein binding, bridging	1 out of 56 genes, 1.8%	60 of 6338 genes, 0.9%	2.0
methyltransferase activity	1 out of 56 genes, 1.8%	90 of 6338 genes, 1.4%	1.3
kinase activity	2 out of 56 genes, 3.6%	195 of 6338 genes, 3.1%	1.2

F. Initial screen: all cisplatin, carboplatin and oxaliplatin gene hits from the initial screening of the transcriptional regulator library, that grew less than 50 % over 4 days growth on YPD agar containing cisplatin, carboplatin and oxaliplatin compared to on YPD agar containing no drug, analysed using Gene Ontology (GO) Slim analysis via the Saccharomyces Gene Database (SGD) (http://www.yeastgenome.org/) using the Yeast GO-slim term ‘**process**’. Fold enrichment for each function is the % Frequency/% Genome Frequency. Note wild type strain CWG424 is not included. MET18 was the only hit (cisplatin) that did not match to a process.

Processes of all cisplatin hits	Frequency	Genome Frequency	Fold enrichment
pseudohyphal growth	6 out of 47 genes, 12.8%	75 of 6338 genes, 1.2%	10.7
transcription from RNA polymerase II promoter	32 out of 47 genes, 68.1%	478 of 6338 genes, 7.5%	9.1
regulation of transport	5 out of 47 genes, 10.6%	82 of 6338 genes, 1.3%	8.2
regulation of DNA metabolic process	6 out of 47 genes, 12.8%	102 of 6338 genes, 1.6%	8.0
protein acylation	3 out of 47 genes, 6.4%	66 of 6338 genes, 1.0%	6.4
cellular respiration	3 out of 47 genes, 6.4%	84 of 6338 genes, 1.3%	4.9
invasive growth in response to glucose limitation	2 out of 47 genes, 4.3%	60 of 6338 genes, 0.9%	4.8
mitotic cell cycle	11 out of 47 genes, 23.4%	327 of 6338 genes, 5.2%	4.5
response to starvation	4 out of 47 genes, 8.5%	119 of 6338 genes, 1.9%	4.5
meiotic cell cycle	9 out of 47 genes, 19.1%	278 of 6338 genes, 4.4%	4.3
response to chemical	14 out of 47 genes, 29.8%	437 of 6338 genes, 6.9%	4.3
lipid transport	2 out of 47 genes, 4.3%	63 of 6338 genes, 1%	4.3
DNA-templated transcription, elongation	3 out of 47 genes, 6.4%	92 of 6338 genes, 1.5%	4.3
sporulation	4 out of 47 genes, 8.5%	133 of 6338 genes, 2.1%	4.0
response to heat	2 out of 47 genes, 4.3%	68 of 6338 genes, 1.1%	3.9
chromatin organization	7 out of 47 genes, 14.9%	261 of 6338 genes, 4.1%	3.6
histone modification	3 out of 47 genes, 6.4%	112 of 6338 genes, 1.8%	3.6
cell wall organization or biogenesis	5 out of 47 genes, 10.6%	201 of 6338 genes, 3.2%	3.3
organelle fission	7 out of 47 genes, 14.9%	291 of 6338 genes, 4.6%	3.2
DNA-templated transcription, termination	1 out of 47 genes, 2.1%	43 of 6338 genes, 0.7%	3.0
protein lipidation	1 out of 47 genes, 2.1%	45 of 6338 genes, 0.7%	3.0
generation of precursor metabolites and energy	3 out of 47 genes, 6.4%	154 of 6338 genes, 2.4%	2.7
exocytosis	1 out of 47 genes, 2.1%	48 of 6338 genes, 0.8%	2.6
regulation of organelle organization	5 out of 47 genes, 10.6%	288 of 6338 genes, 4.5%	2.4
DNA recombination	3 out of 47 genes, 6.4%	175 of 6338 genes, 2.8%	2.3
cellular response to DNA damage stimulus	5 out of 47 genes, 10.6%	297 of 6338 genes, 4.7%	2.3
DNA repair	4 out of 47 genes, 8.5%	245 of 6338 genes, 3.9%	2.2
protein modification by small protein conjugation or removal	3 out of 47 genes, 6.4%	193 of 6338 genes, 3.0%	2.1
carbohydrate metabolic process	4 out of 47 genes, 8.5%	258 of 6338 genes, 4.1%	2.1
RNA catabolic process	2 out of 47 genes, 4.3%	132 of 6338 genes, 2.1%	2.0
peptidyl-amino acid modification	2 out of 47 genes, 4.3%	136 of 6338 genes, 2.1%	2.0
regulation of cell cycle	3 out of 47 genes, 6.4%	206 of 6338 genes, 3.3%	1.9
cellular amino acid metabolic process	3 out of 47 genes, 6.4%	211 of 6338 genes, 3.3%	1.9
DNA replication	2 out of 47 genes, 4.3%	154 of 6338 genes, 2.4%	1.8
cytokinesis	1 out of 47 genes, 2.1%	79 of 6338 genes, 1.2%	1.8
vacuole organization	1 out of 47 genes, 2.1%	79 of 6338 genes, 1.2%	1.8
telomere organization	1 out of 47 genes, 2.1%	77 of 6338 genes, 1.2%	1.8
membrane fusion	1 out of 47 genes, 2.1%	76 of 6338 genes, 1.2%	1.8
response to osmotic stress	1 out of 47 genes, 2.1%	89 of 6338 genes, 1.4%	1.5
organelle fusion	1 out of 47 genes, 2.1%	88 of 6338 genes, 1.4%	1.5
lipid metabolic process	3 out of 47 genes, 6.4%	281 of 6338 genes, 4.4%	1.5
chromosome segregation	2 out of 47 genes, 4.3%	193 of 6338 genes, 3.0%	1.4
endocytosis	1 out of 47 genes, 2.1%	96 of 6338 genes, 1.5%	1.4
response to oxidative stress	1 out of 47 genes, 2.1%	101 of 6338 genes, 1.6%	1.3
regulation of translation	1 out of 47 genes, 2.1%	101 of 6338 genes, 1.6%	1.3
transmembrane transport	2 out of 47 genes, 4.3%	235 of 6338 genes, 3.7%	1.2
ion transport	2 out of 47 genes, 4.3%	236 of 6338 genes, 3.7%	1.2
cytoskeleton organization	2 out of 47 genes, 4.3%	243 of 6338 genes, 3.8%	1.1
conjugation	1 out of 47 genes, 2.1%	125 of 6338 genes, 2%	1.1
cellular ion homeostasis	1 out of 47 genes, 2.1%	124 of 6338 genes, 2%	1.1

F. continued

Processes of all carboplatin hits	Frequency	Genome Frequency	Fold enrichment
regulation of transport	3 out of 24 genes, 12.5%	82 of 6338 genes, 1.3%	9.6
transcription from RNA polymerase II promoter	16 out of 24 genes, 66.7%	478 of 6338 genes, 7.5%	8.9
regulation of DNA metabolic process	3 out of 24 genes, 12.5%	102 of 6338 genes, 1.6%	7.8
response to heat	2 out of 24 genes, 8.3%	68 of 6338 genes, 1.1%	7.5
cytokinesis	2 out of 24 genes, 8.3%	79 of 6338 genes, 1.2%	6.9
meiotic cell cycle	7 out of 24 genes, 29.2%	278 of 6338 genes, 4.4%	6.6
mitotic cell cycle	8 out of 24 genes, 33.3%	327 of 6338 genes, 5.2%	6.4
organelle fission	7 out of 24 genes, 29.2%	291 of 6338 genes, 4.6%	6.3
protein lipidation	1 out of 24 genes, 4.2%	45 of 6338 genes, 0.7%	6.0
RNA catabolic process	3 out of 24 genes, 12.5%	132 of 6338 genes, 2.1%	6.0
DNA-templated transcription, elongation	2 out of 24 genes, 8.3%	92 of 6338 genes, 1.5%	5.5
exocytosis	1 out of 24 genes, 4.2%	48 of 6338 genes, 0.8%	5.3
DNA recombination	3 out of 24 genes, 12.5%	175 of 6338 genes, 2.8%	4.5
DNA repair	4 out of 24 genes, 16.7%	245 of 6338 genes, 3.9%	4.3
lipid transport	1 out of 24 genes, 4.2%	63 of 6338 genes, 1%	4.2
protein acylation	1 out of 24 genes, 4.2%	66 of 6338 genes, 1.0%	4.2
chromatin organization	4 out of 24 genes, 16.7%	261 of 6338 genes, 4.1%	4.1
sporulation	2 out of 24 genes, 8.3%	133 of 6338 genes, 2.1%	4.0
monocarboxylic acid metabolic process	2 out of 24 genes, 8.3%	133 of 6338 genes, 2.1%	4.0
cell wall organization or biogenesis	3 out of 24 genes, 12.5%	201 of 6338 genes, 3.2%	3.9
cellular amino acid metabolic process	3 out of 24 genes, 12.5%	211 of 6338 genes, 3.3%	3.8
regulation of organelle organization	4 out of 24 genes, 16.7%	288 of 6338 genes, 4.5%	3.7
cellular response to DNA damage stimulus	4 out of 24 genes, 16.7%	297 of 6338 genes, 4.7%	3.6
vacuole organization	1 out of 24 genes, 4.2%	79 of 6338 genes, 1.2%	3.5
pseudohyphal growth	1 out of 24 genes, 4.2%	75 of 6338 genes, 1.2%	3.5
telomere organization	1 out of 24 genes, 4.2%	77 of 6338 genes, 1.2%	3.5
membrane fusion	1 out of 24 genes, 4.2%	76 of 6338 genes, 1.2%	3.5
DNA replication	2 out of 24 genes, 8.3%	154 of 6338 genes, 2.4%	3.5
carbohydrate metabolic process	3 out of 24 genes, 12.5%	258 of 6338 genes, 4.1%	3.0
response to chemical	5 out of 24 genes, 20.8%	437 of 6338 genes, 6.9%	3.0
organelle fusion	1 out of 24 genes, 4.2%	88 of 6338 genes, 1.4%	3.0
endocytosis	1 out of 24 genes, 4.2%	96 of 6338 genes, 1.5%	2.8
protein modification by small protein conjugation or removal	2 out of 24 genes, 8.3%	193 of 6338 genes, 3.0%	2.8
regulation of cell cycle	2 out of 24 genes, 8.3%	206 of 6338 genes, 3.3%	2.5
histone modification	1 out of 24 genes, 4.2%	112 of 6338 genes, 1.8%	2.3
response to starvation	1 out of 24 genes, 4.2%	119 of 6338 genes, 1.9%	2.2
cytoskeleton organization	2 out of 24 genes, 8.3%	243 of 6338 genes, 3.8%	2.2
nucleobase-containing compound transport	1 out of 24 genes, 4.2%	124 of 6338 genes, 2%	2.1
cellular ion homeostasis	1 out of 24 genes, 4.2%	124 of 6338 genes, 2%	2.1
lipid metabolic process	2 out of 24 genes, 8.3%	281 of 6338 genes, 4.4%	1.9
generation of precursor metabolites and energy	1 out of 24 genes, 4.2%	154 of 6338 genes, 2.4%	1.8
cofactor metabolic process	1 out of 24 genes, 4.2%	159 of 6338 genes, 2.5%	1.7
mRNA processing	1 out of 24 genes, 4.2%	175 of 6338 genes, 2.8%	1.5
nuclear transport	1 out of 24 genes, 4.2%	178 of 6338 genes, 2.8%	1.5
chromosome segregation	1 out of 24 genes, 4.2%	193 of 6338 genes, 3.0%	1.4
nucleobase-containing small molecule metabolic process	1 out of 24 genes, 4.2%	201 of 6338 genes, 3.2%	1.3
transmembrane transport	1 out of 24 genes, 4.2%	235 of 6338 genes, 3.7%	1.1
proteolysis involved in cellular protein catabolic process	1 out of 24 genes, 4.2%	237 of 6338 genes, 3.7%	1.1
ion transport	1 out of 24 genes, 4.2%	236 of 6338 genes, 3.7%	1.1

F. continued

Processes of all oxaliplatin hits	Frequency	Genome Frequency	Fold enrichment
pseudohyphal growth	7 out of 56 genes, 12.5%	75 of 6338 genes, 1.2%	10.4
transcription from RNA polymerase II promoter	39 out of 56 genes, 69.6%	478 of 6338 genes, 7.5%	9.3
response to osmotic stress	6 out of 56 genes, 10.7%	89 of 6338 genes, 1.4%	7.6
invasive growth in response to glucose limitation	3 out of 56 genes, 5.4%	60 of 6338 genes, 0.9%	6.0
response to heat	3 out of 56 genes, 5.4%	68 of 6338 genes, 1.1%	4.9
response to starvation	5 out of 56 genes, 8.9%	119 of 6338 genes, 1.9%	4.7
response to oxidative stress	4 out of 56 genes, 7.1%	101 of 6338 genes, 1.6%	4.4
response to chemical	16 out of 56 genes, 28.6%	437 of 6338 genes, 6.9%	4.1
lipid transport	2 out of 56 genes, 3.6%	63 of 6338 genes, 1%	3.6
carbohydrate transport	1 out of 56 genes, 1.8%	33 of 6338 genes, 0.5%	3.6
regulation of DNA metabolic process	3 out of 56 genes, 5.4%	102 of 6338 genes, 1.6%	3.4
meiotic cell cycle	7 out of 56 genes, 12.5%	278 of 6338 genes, 4.4%	2.8
regulation of transport	2 out of 56 genes, 3.6%	82 of 6338 genes, 1.3%	2.8
organelle fission	7 out of 56 genes, 12.5%	291 of 6338 genes, 4.6%	2.7
carbohydrate metabolic process	6 out of 56 genes, 10.7%	258 of 6338 genes, 4.1%	2.6
monocarboxylic acid metabolic process	3 out of 56 genes, 5.4%	133 of 6338 genes, 2.1%	2.6
mitotic cell cycle	7 out of 56 genes, 12.5%	327 of 6338 genes, 5.2%	2.4
DNA-templated transcription, elongation	2 out of 56 genes, 3.6%	92 of 6338 genes, 1.5%	2.4
chromatin organization	5 out of 56 genes, 8.9%	261 of 6338 genes, 4.1%	2.2
regulation of organelle organization	5 out of 56 genes, 8.9%	288 of 6338 genes, 4.5%	2.0
DNA recombination	3 out of 56 genes, 5.4%	175 of 6338 genes, 2.8%	1.9
DNA repair	4 out of 56 genes, 7.1%	245 of 6338 genes, 3.9%	1.8
cellular ion homeostasis	2 out of 56 genes, 3.6%	124 of 6338 genes, 2%	1.8
protein acylation	1 out of 56 genes, 1.8%	66 of 6338 genes, 1.0%	1.8
RNA catabolic process	2 out of 56 genes, 3.6%	132 of 6338 genes, 2.1%	1.7
regulation of cell cycle	3 out of 56 genes, 5.4%	206 of 6338 genes, 3.3%	1.6
DNA-templated transcription, initiation	1 out of 56 genes, 1.8%	71 of 6338 genes, 1.1%	1.6
cellular response to DNA damage stimulus	4 out of 56 genes, 7.1%	297 of 6338 genes, 4.7%	1.5
DNA replication	2 out of 56 genes, 3.6%	154 of 6338 genes, 2.4%	1.5
telomere organization	1 out of 56 genes, 1.8%	77 of 6338 genes, 1.2%	1.5
protein complex biogenesis	4 out of 56 genes, 7.1%	326 of 6338 genes, 5.1%	1.4
lipid metabolic process	3 out of 56 genes, 5.4%	281 of 6338 genes, 4.4%	1.2
endocytosis	1 out of 56 genes, 1.8%	96 of 6338 genes, 1.5%	1.2
protein phosphorylation	2 out of 56 genes, 3.6%	194 of 6338 genes, 3.1%	1.2
cell wall organization or biogenesis	2 out of 56 genes, 3.6%	201 of 6338 genes, 3.2%	1.1
transposition	1 out of 56 genes, 1.8%	109 of 6338 genes, 1.7%	1.1

G. Initial screen: all cisplatin, carboplatin and oxaliplatin gene hits from the initial screening of the transcriptional regulator library, that grew less than 30 % over 4 days growth on YPD agar containing cisplatin, carboplatin and oxaliplatin compared to on YPD agar containing no drug, analysed using Gene Ontology (GO) Slim analysis the Saccharomyces Gene Database (SGD) (http://www.yeastgenome.org/) using the Yeast GO-slim term '**function**'. Fold enrichment for each function is the % Frequency/% Genome Frequency. Note wild type strain CWG424 is not included for oxaliplatin and RAD52 did not map to a function.

Functions of all cisplatin hits	Frequency	Genome Frequency	Fold enrichment	Gene(s)
DNA binding	5 out of 12 genes, 41.7%	380 of 6338 genes, 6%	7.0	SWI5,AFT1,NDT80,BDF1,HAP5
nucleic acid binding transcription factor activity	4 out of 12 genes, 33.3%	162 of 6338 genes, 2.6%	12.8	SWI5,AFT1,NDT80,HAP5
transcription factor activity, protein binding	3 out of 12 genes, 25%	124 of 6338 genes, 2%	12.5	SWI5,SWI6,SFP1
molecular function unknown	2 out of 12 genes, 16.7%	1863 of 6338 genes, 29.4%	0.6	EMI1,MET18
protein binding, bridging	1 out of 12 genes, 8.3%	60 of 6338 genes, 0.9%	9.2	SLA1
chromatin binding	1 out of 12 genes, 8.3%	103 of 6338 genes, 1.6%	5.2	BDF1
transcription factor binding	1 out of 12 genes, 8.3%	69 of 6338 genes, 1.1%	7.5	BDF1
histone binding	1 out of 12 genes, 8.3%	41 of 6338 genes, 0.6%	13.8	BDF1
ubiquitin-like protein binding	1 out of 12 genes, 8.3%	43 of 6338 genes, 0.7%	11.9	SLA1
transferase activity	1 out of 12 genes, 8.3%	832 of 6338 genes, 13.1%	0.6	SWF1

Functions of all carboplatin hits	Frequency	Genome Frequency	Fold enrichment	Gene(s)
DNA binding	5 out of 8 genes, 62.5%	380 of 6338 genes, 6%	10.4	UME6,SWI4,AFT1,RIM101,MAC1
nucleic acid binding transcription factor activity	5 out of 8 genes, 62.5%	162 of 6338 genes, 2.6%	24.0	UME6,SWI4,AFT1,RIM101,MAC1
transcription factor activity, protein binding	3 out of 8 genes, 37.5%	124 of 6338 genes, 2%	18.8	UME6,SWI6,GCR2
transcription factor binding	2 out of 8 genes, 25%	69 of 6338 genes, 1.1%	22.7	UME6,GCR2
protein binding, bridging	1 out of 8 genes, 12.5%	60 of 6338 genes, 0.9%	13.9	SLA1
ubiquitin-like protein binding	1 out of 8 genes, 12.5%	43 of 6338 genes, 0.7%	17.9	SLA1

Functions of all oxaliplatin hits	Frequency	Genome Frequency	Fold enrichment	Gene(s)
DNA binding	10 out of 13 genes, 76.9%	380 of 6338 genes, 6%	12.8	UME6,SUM1,AFT1,SKN7,ZAP1,BDF1,SOK2,MAC1,CIN5,USV1
nucleic acid binding transcription factor activity	7 out of 13 genes, 53.8%	162 of 6338 genes, 2.6%	20.7	UME6,SUM1,AFT1,SKN7,ZAP1,SOK2,MAC1
transcription factor binding	3 out of 13 genes, 23.1%	69 of 6338 genes, 1.1%	21.0	UME6,BDF1,CIN5
transcription factor activity, protein binding	2 out of 13 genes, 15.4%	124 of 6338 genes, 2%	7.7	UME6,SWI6
chromatin binding	1 out of 13 genes, 7.7%	103 of 6338 genes, 1.6%	4.8	BDF1
signal transducer activity	1 out of 13 genes, 7.7%	34 of 6338 genes, 0.5%	15.4	SKN7
histone binding	1 out of 13 genes, 7.7%	41 of 6338 genes, 0.6%	12.8	BDF1
ion binding	1 out of 13 genes, 7.7%	177 of 6338 genes, 2.8%	2.8	ZAP1
hydrolase activity	1 out of 13 genes, 7.7%	867 of 6338 genes, 13.7%	0.6	RAD27
nuclease activity	1 out of 13 genes, 7.7%	136 of 6338 genes, 2.1%	3.7	RAD27

H. Initial screen: All cisplatin, carboplatin and oxaliplatin gene hits from the initial screening of the transcriptional regulator library, that grew less than 30 % over 4 days growth on YPD agar containing cisplatin, carboplatin and oxaliplatin compared to on YPD agar containing no drug, analysed using Gene Ontology (GO) Slim analysis via the Saccharomyces Gene Database (SGD) (http://www.yeastgenome.org/) using the Yeast GO-slim term '**process**'. Fold enrichment for each function is the % Frequency/% Genome Frequency. Note wild type strain CWG424 is not included for oxaliplatin and MET18 was the only hit (cisplatin) that did not match to a process.

Processes of all cisplatin hits	Frequency	Genome Frequency	Fold enrichment	Gene(s)
transcription from RNA polymerase II promoter	7 out of 12 genes, 58.3%	478 of 6338 genes, 7.5%	7.8	SWI5,EMI1,AFT1,NDT80,SWI6,SFP1,HAP5
meiotic cell cycle	6 out of 12 genes, 50%	278 of 6338 genes, 4.4%	11.4	SWF1,EMI1,AFT1,NDT80,SWI6,RAD52
organelle fission	5 out of 12 genes, 41.7%	291 of 6338 genes, 4.6%	9.1	SWI5,AFT1,NDT80,SWI6,RAD52
regulation of DNA metabolic process	3 out of 12 genes, 25%	102 of 6338 genes, 1.6%	15.6	SWI5,SWI6,BDF1
mitotic cell cycle	3 out of 12 genes, 25%	327 of 6338 genes, 5.2%	4.8	SWI5,AFT1,SWI6
cell wall organization or biogenesis	2 out of 12 genes, 16.7%	201 of 6338 genes, 3.2%	5.2	SLA1,SWF1
cytoskeleton organization	2 out of 12 genes, 16.7%	243 of 6338 genes, 3.8%	4.4	SLA1,SWF1
regulation of transport	2 out of 12 genes, 16.7%	82 of 6338 genes, 1.3%	12.8	SWF1,AFT1
cellular response to DNA damage stimulus	2 out of 12 genes, 16.7%	297 of 6338 genes, 4.7%	3.6	BDF1,RAD52
DNA recombination	2 out of 12 genes, 16.7%	175 of 6338 genes, 2.8%	6.0	SWI6,RAD52
sporulation	2 out of 12 genes, 16.7%	133 of 6338 genes, 2.1%	8.0	SWF1,EMI1
regulation of organelle organization	2 out of 12 genes, 16.7%	288 of 6338 genes, 4.5%	3.7	SWI6,BDF1
DNA repair	2 out of 12 genes, 16.7%	245 of 6338 genes, 3.9%	4.3	BDF1,RAD52
cellular respiration	1 out of 12 genes, 8.3%	84 of 6338 genes, 1.3%	6.4	HAP5
vacuole organization	1 out of 12 genes, 8.3%	79 of 6338 genes, 1.2%	6.9	SWF1
protein acylation	1 out of 12 genes, 8.3%	66 of 6338 genes, 1.0%	8.3	SWF1
generation of precursor metabolites and energy	1 out of 12 genes, 8.3%	154 of 6338 genes, 2.4%	3.5	HAP5
regulation of cell cycle	1 out of 12 genes, 8.3%	206 of 6338 genes, 3.3%	2.5	SWI6
protein complex biogenesis	1 out of 12 genes, 8.3%	326 of 6338 genes, 5.1%	1.6	SLA1
response to chemical	1 out of 12 genes, 8.3%	437 of 6338 genes, 6.9%	1.2	HAP5
chromosome segregation	1 out of 12 genes, 8.3%	189 of 6338 genes, 3%	2.8	AFT1
response to heat	1 out of 12 genes, 8.3%	68 of 6338 genes, 1.1%	7.5	SWI6
mitochondrion organization	1 out of 12 genes, 8.3%	418 of 6338 genes, 6.6%	1.3	EMI1
endocytosis	1 out of 12 genes, 8.3%	96 of 6338 genes, 1.5%	5.5	SLA1
protein lipidation	1 out of 12 genes, 8.3%	45 of 6338 genes, 0.7%	11.9	SWF1
exocytosis	1 out of 12 genes, 8.3%	48 of 6338 genes, 0.8%	10.4	SWF1
telomere organization	1 out of 12 genes, 8.3%	77 of 6338 genes, 1.2%	6.9	RAD52
response to starvation	1 out of 12 genes, 8.3%	119 of 6338 genes, 1.9%	4.4	AFT1
organelle fusion	1 out of 12 genes, 8.3%	88 of 6338 genes, 1.4%	5.9	SWF1
membrane fusion	1 out of 12 genes, 8.3%	76 of 6338 genes, 1.2%	6.9	SWF1
chromatin organization	1 out of 12 genes, 8.3%	261 of 6338 genes, 4.1%	2.0	BDF1
ion transport	1 out of 12 genes, 8.3%	236 of 6338 genes, 3.7%	2.2	AFT1

H. continued

Processes of all carboplatin hits	Frequency	Genome Frequency	Fold enrichment	Gene(s)
transcription from RNA polymerase II promoter	7 out of 8 genes, 87.5%	478 of 6338 genes, 7.5%	11.7	UME6,SWI4,AFT1,RIM101,SWI6,MAC1,GCR2
mitotic cell cycle	5 out of 8 genes, 62.5%	327 of 6338 genes, 5.2%	12.0	UME6,SWI4,AFT1,RIM101,SWI6
organelle fission	4 out of 8 genes, 50%	291 of 6338 genes, 4.6%	10.9	UME6,AFT1,RIM101,SWI6
meiotic cell cycle	4 out of 8 genes, 50%	278 of 6338 genes, 4.4%	11.4	UME6,AFT1,RIM101,SWI6
cell wall organization or biogenesis	2 out of 8 genes, 25%	201 of 6338 genes, 3.2%	7.8	SLA1,RIM101
carbohydrate metabolic process	2 out of 8 genes, 25%	258 of 6338 genes, 4.1%	6.1	UME6,GCR2
regulation of cell cycle	2 out of 8 genes, 25%	206 of 6338 genes, 3.3%	7.6	UME6,SWI6
response to chemical	2 out of 8 genes, 25%	437 of 6338 genes, 6.9%	3.6	UME6,RIM101
response to heat	2 out of 8 genes, 25%	68 of 6338 genes, 1.1%	22.7	SWI4,SWI6
regulation of organelle organization	2 out of 8 genes, 25%	288 of 6338 genes, 4.5%	5.6	UME6,SWI6
cytokinesis	1 out of 8 genes, 12.5%	79 of 6338 genes, 1.2%	10.4	RIM101
pseudohyphal growth	1 out of 8 genes, 12.5%	75 of 6338 genes, 1.2%	10.4	UME6
cytoskeleton organization	1 out of 8 genes, 12.5%	243 of 6338 genes, 3.8%	3.3	SLA1
regulation of transport	1 out of 8 genes, 12.5%	82 of 6338 genes, 1.3%	9.6	AFT1
cellular amino acid metabolic process	1 out of 8 genes, 12.5%	211 of 6338 genes, 3.3%	3.8	UME6
lipid metabolic process	1 out of 8 genes, 12.5%	281 of 6338 genes, 4.4%	2.8	UME6
nucleobase-containing small molecule metabolic process	1 out of 8 genes, 12.5%	201 of 6338 genes, 3.2%	3.9	GCR2
generation of precursor metabolites and energy	1 out of 8 genes, 12.5%	154 of 6338 genes, 2.4%	5.2	GCR2
DNA recombination	1 out of 8 genes, 12.5%	175 of 6338 genes, 2.8%	4.5	SWI6
protein complex biogenesis	1 out of 8 genes, 12.5%	326 of 6338 genes, 5.1%	2.5	SLA1
regulation of DNA metabolic process	1 out of 8 genes, 12.5%	102 of 6338 genes, 1.6%	7.8	SWI6
chromosome segregation	1 out of 8 genes, 12.5%	189 of 6338 genes, 3%	4.2	AFT1
sporulation	1 out of 8 genes, 12.5%	133 of 6338 genes, 2.1%	6.0	RIM101
endocytosis	1 out of 8 genes, 12.5%	96 of 6338 genes, 1.5%	8.3	SLA1
cellular ion homeostasis	1 out of 8 genes, 12.5%	124 of 6338 genes, 2%	6.3	MAC1
monocarboxylic acid metabolic process	1 out of 8 genes, 12.5%	133 of 6338 genes, 2.1%	6.0	GCR2
response to starvation	1 out of 8 genes, 12.5%	119 of 6338 genes, 1.9%	6.6	AFT1
chromatin organization	1 out of 8 genes, 12.5%	261 of 6338 genes, 4.1%	3.0	UME6
cofactor metabolic process	1 out of 8 genes, 12.5%	159 of 6338 genes, 2.5%	5.0	GCR2
ion transport	1 out of 8 genes, 12.5%	236 of 6338 genes, 3.7%	3.4	AFT1

H. continued

Processes of all oxaliplatin hits	Frequency	Genome Frequency	Fold enrichment	Gene(s)
transcription from RNA polymerase II promoter	9 out of 13 genes, 69.2%	478 of 6338 genes, 7.5%	9.2	UME6,SUM1,AFT1,SKN7,ZAP1,SWI6,MAC1,CIN5,USV1
organelle fission	5 out of 13 genes, 38.5%	291 of 6338 genes, 4.6%	8.4	UME6,SUM1,AFT1,SWI6,RAD52
response to chemical	4 out of 13 genes, 30.8%	437 of 6338 genes, 6.9%	4.5	UME6,SKN7,CIN5,USV1
meiotic cell cycle	4 out of 13 genes, 30.8%	278 of 6338 genes, 4.4%	7.0	UME6,AFT1,SWI6,RAD52
mitotic cell cycle	4 out of 13 genes, 30.8%	327 of 6338 genes, 5.2%	5.9	UME6,SUM1,AFT1,SWI6
cellular response to DNA damage stimulus	3 out of 13 genes, 23.1%	297 of 6338 genes, 4.7%	4.9	RAD27,BDF1,RAD52
DNA recombination	3 out of 13 genes, 23.1%	175 of 6338 genes, 2.8%	8.3	RAD27,SWI6,RAD52
regulation of DNA metabolic process	3 out of 13 genes, 23.1%	102 of 6338 genes, 1.6%	14.4	SUM1,SWI6,BDF1
regulation of organelle organization	3 out of 13 genes, 23.1%	288 of 6338 genes, 4.5%	5.1	UME6,SWI6,BDF1
DNA repair	3 out of 13 genes, 23.1%	245 of 6338 genes, 3.9%	5.9	RAD27,BDF1,RAD52
response to osmotic stress	3 out of 13 genes, 23.1%	89 of 6338 genes, 1.4%	16.5	SKN7,CIN5,USV1
pseudohyphal growth	2 out of 13 genes, 15.4%	75 of 6338 genes, 1.2%	12.8	UME6,SOK2
DNA replication	2 out of 13 genes, 15.4%	154 of 6338 genes, 2.4%	6.4	SUM1,RAD27
regulation of cell cycle	2 out of 13 genes, 15.4%	206 of 6338 genes, 3.3%	4.7	UME6,SWI6
response to starvation	2 out of 13 genes, 15.4%	119 of 6338 genes, 1.9%	8.1	AFT1,ZAP1
chromatin organization	2 out of 13 genes, 15.4%	261 of 6338 genes, 4.1%	3.8	UME6,BDF1
regulation of transport	1 out of 13 genes, 7.7%	82 of 6338 genes, 1.3%	5.9	AFT1
cellular amino acid metabolic process	1 out of 13 genes, 7.7%	211 of 6338 genes, 3.3%	2.3	UME6
lipid metabolic process	1 out of 13 genes, 7.7%	281 of 6338 genes, 4.4%	1.8	UME6
RNA catabolic process	1 out of 13 genes, 7.7%	132 of 6338 genes, 2.1%	3.7	RAD27
carbohydrate metabolic process	1 out of 13 genes, 7.7%	258 of 6338 genes, 4.1%	1.9	UME6
chromosome segregation	1 out of 13 genes, 7.7%	189 of 6338 genes, 3%	2.6	AFT1
response to oxidative stress	1 out of 13 genes, 7.7%	101 of 6338 genes, 1.6%	4.8	SKN7
response to heat	1 out of 13 genes, 7.7%	68 of 6338 genes, 1.1%	7.0	SWI6
cellular ion homeostasis	1 out of 13 genes, 7.7%	124 of 6338 genes, 2%	3.9	MAC1
telomere organization	1 out of 13 genes, 7.7%	77 of 6338 genes, 1.2%	6.4	RAD52
ion transport	1 out of 13 genes, 7.7%	236 of 6338 genes, 3.7%	2.1	AFT1

I. A colour coded, simplified and unbiased representation, as a table, of all the MALDI-TOF MS and MALDI-TOF-TOF MS/MS identification results for the twenty definitely identified proteins (in numerical order of spot number) from the MASCOT human protein Swiss-Prot (http://www.uniprot.org/) and NCBInr (http://www.ncbi.nlm.nih.gov/refseq/) database searches for the UKF-NB-3 proteomics study.

Matched protein results passing the score cut-offs for both database searches were entered into this table and colour coded according to whether or not the expectation value was above or below 1 x 10^{-5}, resulting in a simplified and unbiased representation of all the data together. An expect value cut-off of 1 x 10^{-5} was taken as this represents a 1 in 100,000 chance that the match is random; we apply this strict criteria as for single spots from a 2D gel there is no reliable mechanism for measuring a false detection rate (http://www.matrixscience.com/). The NCBInr database is not as highly curated as the Swissprot database, so more likely for NCBInr many hits are frequently generated for a single query, and a single protein hit often consists of a list of proteins rather than a single protein (as for Swissprot) representing matches to, for example, different isoforms, partial sequences or subunits of the same protein. In Mascot MS data reports, proteins that match the same set or a sub-set of mass values are grouped into a single hit (listed in order of decreasing scores and expect values). For our MS data, the top scoring protein in the list for each hit was transferred into this table. However, if a protein was unnamed, then the next named protein in the list for that hit was also transferred (if there was one). In Mascot MS/MS data reports, proteins matching the same set of peptides (therefore having the same score and expect values) are grouped as hits, so in this instance, the first protein in the list for each hit was transferred into this table, and if that protein was unnamed, then the next named protein in the list for that hit was also transferred (if there was one). A second protein in a list for an MS/MS hit was sometimes transferred too if its name made more sense relating to the names of corresponding MS hits.

Colour coding was as follows. For the MS data, matches with an expect value <1 x 10^{-5} were colour coded green (strong match), and matches with an expect value >1 x 10^{-5} were colour coded orange (weak match). For the MS/MS data, matches were colour coded green (strong match) if 1. at least one of the five peptides passed the score cut-off (which gives a p value <0.05) as well as having a strong expect value <1 x 10^{-5}, 2. two or more of the five peptides passed the score cut-off (which gives a p value <0.05) but had weaker expect values (>1 x 10^{-5}), 3. just one of the five peptides passed the score cut-off (which gives a p value <0.05) with a weak expect value (>1 x 10^{-5}) but accompanied by another one or more of the five peptides having (a) score (s) near to the score cut-off and weak expect value(s) (>1 x 10^{-5}). An orange colour for the MS/MS data indicated a weaker match, and this was for when just a single peptide passed the score cut-off (which gives a p value <0.05) with a weak expect value (>1 x 10^{-5}). Generally speaking, spots were classed as definite identifications if each of the duplicates had strong identical identification in both databases, with more weighting given to MS/MS hits because MS/MS matches actual peptide sequences rather than masses.

I. continued

Spot #	SwissProt MS (cut off = 56 for all)	SwissProt MS/MS cut off	SwissProt MS/MS	NCBInr MS (cut off = 67 for all)	NCBInr MS/MS cut off	NCBInr MS/MS
NB3 1.449	ATPB_HUMAN Mass: 56525 Score: 186 Expect: 5.1e-015 Matches: 30 ATP synthase subunit beta, mitochondrial OS=Homo sapiens GN=ATP5B PE=1 SV=3	28	ATPB_HUMAN Mass: 56525 Score: 398 Matches: 5(5) Sequences: 5(5) ATP synthase subunit beta, mitochondrial OS=Homo sapiens GN=ATP5B PE=1 SV=3	gi|32189394 Mass: 56525 Score: 186 Expect: 6.8e-014 Matches: 30 ATP synthase subunit beta, mitochondrial precursor [Homo sapiens]	37	gi|28940 Mass: 57976 Score: 510 Matches: 5(5) Sequences: 5(5) unnamed protein product [Homo sapiens] gi|32189394 Mass: 56525 Score: 510 Matches: 5(5) Sequences: 5(5) ATP synthase subunit beta, mitochondrial precursor [Homo sapiens]
NB3 2.449	ATPB_HUMAN Mass: 56525 Score: 154 Expect: 8.1e-012 Matches: 23 ATP synthase subunit beta, mitochondrial OS=Homo sapiens GN=ATP5B PE=1 SV=3	28	ATPB_HUMAN Mass: 56525 Score: 361 Matches: 5(5) Sequences: 5(5) ATP synthase subunit beta, mitochondrial OS=Homo sapiens GN=ATP5B PE=1 SV=3	gi|89574029 Mass: 48083 Score: 162 Expect: 1.7e-011 Matches: 23 mitochondrial ATP synthase, H+ transporting F1 complex beta subunit [Homo sapiens]	37	gi|28940 Mass: 57976 Score: 468 Matches: 5(5) Sequences: 5(5) unnamed protein product [Homo sapiens] gi|32189394 Mass: 56525 Score: 468 Matches: 5(5) Sequences: 5(5) ATP synthase subunit beta, mitochondrial precursor [Homo sapiens]
NB3 1.635	ESTD_HUMAN Mass: 31956 Score: 89 Expect: 2.4e-005 Matches: 11 S-formylglutathione hydrolase OS=Homo sapiens GN=ESD PE=1 SV=2	28	ESTD_HUMAN Mass: 31956 Score: 114 Matches: 1(1) Sequences: 1(1) S-formylglutathione hydrolase OS=Homo sapiens GN=ESD PE=1 SV=2	gi|119629172 Mass: 29161 Score: 93 Expect: 0.00015 Matches: 11 esterase D/formylglutathione hydrolase, isoform CRA_a [Homo sapiens] gi|182265 Mass: 34181 Score: 86 Expect: 0.00073 Matches: 11 esterase D, partial [Homo sapiens]	37	gi|33413400 Mass: 31956 Score: 114 Matches: 1(1) Sequences: 1(1) S-formylglutathione hydrolase [Homo sapiens]
NB3 2.635	X *41 for CA167_HUMAN, Uncharacterized protein C1orf167 OS=Homo sapiens GN=C1orf167 PE=2 SV=2*	28	X	X *49 for gi|34534771, unnamed protein product [Homo sapiens]*	37	X
NB3 3.635 recut	X *52 for ESTD_HUMAN, S-formylglutathione hydrolase OS=Homo sapiens GN=ESD PE=1 SV=2*	28	ESTD_HUMAN Mass: 31956 Score: 105 Matches: 2(2) Sequences: 2(2) S-formylglutathione hydrolase OS=Homo sapiens GN=ESD PE=1 SV=2	X Note ESTD in list score 45 *62 for gi|530362280, PREDICTED: microtubule-actin cross-linking factor 1 isoform X7 [Homo sapiens]*	38	gi|33413400 Mass: 31956 Score: 127 Matches: 2(1) Sequences: 2(1) S-formylglutathione hydrolase [Homo sapiens]
NB3 1.637	VDAC2_HUMAN Mass: 32060 Score: 190 Expect: 2e-015 Matches: 17 Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 AP1M2_HUMAN Mass: 48192 Score: 62 Expect: 0.014 Matches: 9 AP-1 complex subunit mu-2 OS=Homo sapiens GN=AP1M2 PE=1 SV=4	28	VDAC2_HUMAN Mass: 32060 Score: 252 Matches: 3(3) Sequences: 3(3) Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 VDAC1_HUMAN Mass: 30868 Score: 40 Matches: 1(1) Sequences: 1(1) Voltage-dependent anion-selective channel protein 1 OS=Homo sapiens GN=VDAC1 PE=1 SV=2	gi|42476281 Mass: 32060 Score: 190 Expect: 2.7e-014 Matches: 17 voltage-dependent anion-selective channel protein 2 isoform 2 [Homo sapiens] gi|296317337 Mass: 33864 Score: 167 Expect: 5.4e-012 Matches: 16 voltage-dependent anion-selective channel protein 2 isoform 1 [Homo sapiens]	37	gi|190200 Mass: 38639 Score: 308 Matches: 3(3) Sequences: 3(3) porin, partial [Homo sapiens] gi|42476281 Mass: 32060 Score: 308 Matches: 3(3) Sequences: 3(3) voltage-dependent anion-selective channel protein 2 isoform 2 [Homo sapiens] gi|238427 Mass: 30737 Score: 40 Matches: 1(1) Sequences: 1(1) Porin 31HM [human, skeletal muscle membranes, Peptide, 282 aa] gi|119582688 Mass: 16691 Score: 40 Matches: 1(1) Sequences: 1(1) voltage-dependent anion channel 1, isoform CRA_b [Homo sapiens]
NB3 2.637	VDAC2_HUMAN Mass: 32060 Score: 157 Expect: 4e-012 Matches: 14 Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2	37	VDAC2_HUMAN Mass: 32060 Score: 305 Matches: 4(4) Sequences: 4(4) Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 VDAC1_HUMAN Mass: 30868 Score: 37 Matches: 1(1) Sequences: 1(1) Voltage-dependent anion-selective channel protein 1 OS=Homo sapiens GN=VDAC1 PE=1 SV=2	gi|42476281 Mass: 32060 Score: 157 Expect: 5.4e-011 Matches: 14 voltage-dependent anion-selective channel protein 2 isoform 2 [Homo sapiens] gi|296317337 Mass: 33864 Score: 154 Expect: 1.1e-010 Matches: 14 voltage-dependent anion-selective channel protein 2 isoform 1 [Homo sapiens]	37	gi|190200 Mass: 38639 Score: 381 Matches: 4(4) Sequences: 4(4) porin, partial [Homo sapiens] gi|42476281 Mass: 32060 Score: 381 Matches: 4(4) Sequences: 4(4) voltage-dependent anion-selective channel protein 2 isoform 2 [Homo sapiens] gi|238427 Mass: 30737 Score: 37 Matches: 1(1) Sequences: 1(1) Porin 31HM [human, skeletal muscle membranes, Peptide, 282 aa] gi|4507879 Mass: 30868 Score: 37 Matches: 1(1) Sequences: 1(1) voltage-dependent anion-selective channel protein 1 [Homo sapiens]
NB3 1.709	HSPB1_HUMAN Mass: 22826 Score: 153 Expect: 1e-011 Matches: 14 Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2	28	HSPB1_HUMAN Mass: 22826 Score: 162 Matches: 3(3) Sequences: 3(3) Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2	gi|662841 Mass: 22427 Score: 154 Expect: 1.1e-010 Matches: 14 heat shock protein 27 [Homo sapiens] gi|15126735 Mass: 22812 Score: 107 Expect: 5.4e-006 Matches: 12 Heat shock 27kDa protein 1 [Homo sapiens]	38	gi|662841 Mass: 22427 Score: 217 Matches: 3(2) Sequences: 3(2) heat shock protein 27 [Homo sapiens]
NB3 2.709	HSPB1_HUMAN Mass: 22826 Score: 156 Expect: 5.1e-012 Matches: 13 Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2	28	HSPB1_HUMAN Mass: 22826 Score: 180 Matches: 2(2) Sequences: 2(2) Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2	gi|662841 Mass: 22427 Score: 157 Expect: 5.4e-011 Matches: 12 heat shock protein 27 [Homo sapiens] gi|4504517 Mass: 22826 Score: 156 Expect: 6.8e-011 Matches: 13 heat shock protein beta-1 [Homo sapiens] gi|15126735 Mass: 22812 Score: 120 Expect: 2.7e-007 Matches: 12 Heat shock 27kDa protein 1 [Homo sapiens]	37	gi|662841 Mass: 22427 Score: 208 Matches: 2(2) Sequences: 2(2) heat shock protein 27 [Homo sapiens]
NB3 1.749	PRDX2_HUMAN Mass: 22049 Score: 138 Expect: 3.2e-010 Matches: 12 Peroxiredoxin-2 OS=Homo sapiens GN=PRDX2 PE=1 SV=5	27	PRDX2_HUMAN Mass: 22049 Score: 337 Matches: 5(5) Sequences: 5(5) Peroxiredoxin-2 OS=Homo sapiens GN=PRDX2 PE=1 SV=5	gi|530415124 Mass: 20209 Score: 142 Expect: 1.7e-009 Matches: 12 PREDICTED: peroxiredoxin-2 isoform X1 [Homo sapiens]	37	gi|9955007 Mass: 21909 Score: 447 Matches: 5(5) Sequences: 5(5) Chain A, Thioredoxin Peroxidase B From Red Blood Cells gi|32189392 Mass: 22049 Score: 447 Matches: 5(5) Sequences: 5(5) peroxiredoxin-2 [Homo sapiens] gi|28279049 Mass: 32742 Score: 42 Matches: 1(1) Sequences: 1(1) C7orf57 protein [Homo sapiens]
NB3 2.749	PRDX2_HUMAN Mass: 22049 Score: 169 Expect: 2.6e-013 Matches: 12 Peroxiredoxin-2 OS=Homo sapiens GN=PRDX2 PE=1 SV=5	28	PRDX2_HUMAN Mass: 22049 Score: 408 Matches: 5(5) Sequences: 5(5) Peroxiredoxin-2 OS=Homo sapiens GN=PRDX2 PE=1 SV=5	gi|530415124 Mass: 20209 Score: 172 Expect: 1.7e-012 Matches: 12 PREDICTED: peroxiredoxin-2 isoform X1 [Homo sapiens]	37	gi|9955007 Mass: 21909 Score: 517 Matches: 5(5) Sequences: 5(5) Chain A, Thioredoxin Peroxidase B From Red Blood Cells gi|32189392 Mass: 22049 Score: 517 Matches: 5(5) Sequences: 5(5) peroxiredoxin-2 [Homo sapiens]
NB3 1.792	STMN1_HUMAN Mass: 17292 Score: 71 Expect: 0.0016 Matches: 9 Stathmin OS=Homo sapiens GN=STMN1 PE=1 SV=3	27	STMN1_HUMAN Mass: 17292 Score: 73 Matches: 1(1) Sequences: 1(1) Stathmin OS=Homo sapiens GN=STMN1 PE=1 SV=3	gi|5031851 Mass: 17292 Score: 71 Expect: 0.022 Matches: 9 stathmin isoform a [Homo sapiens]	37	gi|5031851 Mass: 17292 Score: 73 Matches: 1(1) Sequences: 1(1) stathmin isoform a [Homo sapiens]
NB3 2.792	STMN1_HUMAN Mass: 17292 Score: 91 Expect: 1.7e-005 Matches: 10 Stathmin OS=Homo sapiens GN=STMN1 PE=1 SV=3 SYTM_HUMAN Mass: 81841 Score: 56 Expect: 0.057 Matches: 10 Threonine--tRNA ligase, mitochondrial OS=Homo sapiens GN=TARS2 PE=1 SV=1	28	STMN1_HUMAN Mass: 17292 Score: 76 Matches: 1(1) Sequences: 1(1) Stathmin OS=Homo sapiens GN=STMN1 PE=1 SV=3	gi|5031851 Mass: 17292 Score: 91 Expect: 0.00023 Matches: 10 stathmin isoform a [Homo sapiens]	37	gi|5031851 Mass: 17292 Score: 76 Matches: 1(1) Sequences: 1(1) stathmin isoform a [Homo sapiens]
NB3 1.901	CH60_HUMAN Mass: 61187 Score: 272 Expect: 1.3e-023 Matches: 34 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2	29	CH60_HUMAN Mass: 61187 Score: 289 Matches: 4(4) Sequences: 4(4) emPAI: 0.40 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2	gi|31542947 Mass: 61187 Score: 272 Expect: 1.7e-022 Matches: 34 60 kDa heat shock protein, mitochondrial [Homo sapiens] gi|221042312 Mass: 60181 Score: 245 Expect: 8.6e-020 Matches: 32 unnamed protein product [Homo sapiens] gi|221042182 Mass: 26726 Score: 103 Expect: 1.4e-005 Matches: 14 unnamed protein product [Homo sapiens]	38	gi|221042312 Mass: 60181 Score: 390 Matches: 5(4) Sequences: 5(4) emPAI: 0.41 unnamed protein product [Homo sapiens]
NB3 2.901	CH60_HUMAN Mass: 61187 Score: 255 Expect: 6.4e-022 Matches: 32 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2	28	CH60_HUMAN Mass: 61187 Score: 200 Matches: 3(3) Sequences: 3(3) 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2	gi|31542947 Mass: 61187 Score: 255 Expect: 8.6e-021 Matches: 32 60 kDa heat shock protein, mitochondrial [Homo sapiens] gi|221042312 Mass: 60181 Score: 232 Expect: 1.7e-018 Matches: 29 unnamed protein product [Homo sapiens] gi|221042182 Mass: 26726 Score: 101 Expect: 2.2e-005 Matches: 13 unnamed protein product [Homo sapiens]	38	gi|221042312 Mass: 60181 Score: 270 Matches: 4(3) Sequences: 4(3) unnamed protein product [Homo sapiens]

I. continued

Spot #	SwissProt MS (cut off = 56 for all)	SwissProt MS/MS cut off	SwissProt MS/MS	NCBInr MS (cut off = 67 for all)	NCBInr MS/MS cut off	NCBInr MS/MS
NB3 1.978	x *54 for TTC34_HUMAN, Tetratricopeptide repeat protein 34 OS=Homo sapiens GN=TTC34 PE=2 SV=2*	29	DPYL5_HUMAN Mass: 61952 Score: 44 Matches: 1(1) Sequences: 1(1) Dihydropyrimidinase-related protein 5 OS=Homo sapiens GN=DPYSL5 PE=1 SV=1 K2C1_HUMAN Mass: 66170 Score: 30 Matches: 1(1) Sequences: 1(1) Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6	x *54 for gi|336455091, tetratricopeptide repeat protein 34 [Homo sapiens]*	37	gi|8671168 Mass: 61925 Score: 44 Matches: 1(1) Sequences: 1(1) hypothetical protein [Homo sapiens] gi|8886025 Mass: 61990 Score: 44 Matches: 1(1) Sequences: 1(1) collapsin response mediator protein-5 [Homo sapiens]
NB3 2.978	DPYL5_HUMAN Mass: 61952 Score: 175 Expect: 6.4e-014 Matches: 26 Dihydropyrimidinase-related protein 5 OS=Homo sapiens GN=DPYSL5 PE=1 SV=1	28	DPYL5_HUMAN Mass: 61952 Score: 94 Matches: 2(2) Sequences: 2(2) Dihydropyrimidinase-related protein 5 OS=Homo sapiens GN=DPYSL5 PE=1 SV=1	gi|19923821 Mass: 61952 Score: 175 Expect: 8.6e-013 Matches: 26 dihydropyrimidinase-related protein 5 [Homo sapiens]	37	gi|8671168 Mass: 61925 Score: 122 Matches: 2(2) Sequences: 2(2) hypothetical protein [Homo sapiens] gi|8886025 Mass: 61990 Score: 122 Matches: 2(2) Sequences: 2(2) collapsin response mediator protein-5 [Homo sapiens]
NB3 1.1002	EF2_HUMAN Mass: 96246 Score: 205 Expect: 6.4e-017 Matches: 29 Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4	29	EF2_HUMAN Mass: 96246 Score: 112 Matches: 4(4) Sequences: 4(4) Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4	gi|4503483 Mass: 96246 Score: 205 Expect: 8.6e-016 Matches: 29 elongation factor 2 [Homo sapiens] **Mixture 1 Total score: 139 Expect:** 3.4e-009 **Matches:** 29 Components (only one family member shown for each component): gi|181969 Mass: 40264 Score: 109 Expect: 3.4e-006 Matches: 14 elongation factor 2, partial [Homo sapiens] gi|33869643 Mass: 65366 Score: 84 Expect: 0.001 Matches: 15 EEF2 protein, partial [Homo sapiens]	38	gi|4503483 Mass: 96246 Score: 190 Matches: 4(4) Sequences: 4(4) elongation factor 2 [Homo sapiens]
NB3 2.1002	EF2_HUMAN Mass: 96246 Score: 180 Expect: 2e-014 Matches: 24 Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4	28	EF2_HUMAN Mass: 96246 Score: 72 Matches: 4(3) Sequences: 4(3) Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4	gi|4503483 Mass: 96246 Score: 180 Expect: 2.7e-013 Matches: 24 elongation factor 2 [Homo sapiens] **Mixture 1 Total score: 116 Expect:** 6.8e-007 **Matches:** 24 Components (only one family member shown for each component): gi|33869643 Mass: 65366 Score: 90 Expect: 0.00024 Matches: 14 EEF2 protein, partial [Homo sapiens] gi|181969 Mass: 40264 Score: 74 Expect: 0.011 Matches: 10 elongation factor 2, partial [Homo sapiens]	38	gi|4503483 Mass: 96246 Score: 137 Matches: 4(1) Sequences: 4(1) elongation factor 2 [Homo sapiens]
NB3 1.1084	RUVB2_HUMAN Mass: 51296 Score: 124 Expect: 8.1e-009 Matches: 15 RuvB-like 2 OS=Homo sapiens GN=RUVBL2 PE=1 SV=3	29	RUVB2_HUMAN Mass: 51296 Score: 42 Matches: 3(2) Sequences: 3(2) RuvB-like 2 OS=Homo sapiens GN=RUVBL2 PE=1 SV=3 GRIP1_HUMAN Mass: 123202 Score: 39 Matches: 1(1) Sequences: 1(1) Glutamate receptor-interacting protein 1 OS=Homo sapiens GN=GRIP1 PE=1 SV=3	gi|5730023 Mass: 51296 Score: 124 Expect: 1.1e-007 Matches: 15 ruvB-like 2 [Homo sapiens] gi|395751504 Mass: 46448 Score: 100 Expect: 2.7e-005 Matches: 12 PREDICTED: ruvB-like 2 isoform 1 [Pongo abelii]	39	gi|5730023 Mass: 51296 Score: 78 Matches: 3(0) Sequences: 3(0) ruvB-like 2 [Homo sapiens] gi|119617574 Mass: 88446 Score: 39 Matches: 1(1) Sequences: 1(1) hCG1774522, isoform CRA_a [Homo sapiens]
NB3 2.1084	RUVB2_HUMAN Mass: 51296 Score: 106 Expect: 5.1e-007 Matches: 12 RuvB-like 2 OS=Homo sapiens GN=RUVBL2 PE=1 SV=3	29	RUVB2_HUMAN Mass: 51296 Score: 52 Matches: 3(2) Sequences: 3(2) RuvB-like 2 OS=Homo sapiens GN=RUVBL2 PE=1 SV=3	gi|5730023 Mass: 51296 Score: 106 Expect: 6.8e-006 Matches: 12 ruvB-like 2 [Homo sapiens] gi|395751504 Mass: 46448 Score: 82 Expect: 0.0017 Matches: 10 PREDICTED: ruvB-like 2 isoform 1 [Pongo abelii]	38	gi|5730023 Mass: 51296 Score: 94 Matches: 3(1) Sequences: 3(1) ruvB-like 2 [Homo sapiens]
NB3 3.1121	SERA_HUMAN Mass: 57356 Score: 102 Expect: 1.3e-006 Matches: 13 D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=4	28	SERA_HUMAN Mass: 57356 Score: 77 Matches: 4(2) Sequences: 4(2) D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=4	gi|23308577 Mass: 57356 Score: 102 Expect: 1.7e-005 Matches: 13 D-3-phosphoglycerate dehydrogenase [Homo sapiens]	38	gi|23308577 Mass: 57356 Score: 148 Matches: 4(2) Sequences: 4(2) D-3-phosphoglycerate dehydrogenase [Homo sapiens]
NB3 4.1121	SERA_HUMAN Mass: 57356 Score: 122 Expect: 1.3e-008 Matches: 14 D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=4	29	SERA_HUMAN Mass: 57356 Score: 72 Matches: 5(2) Sequences: 5(2) D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=4	gi|23308577 Mass: 57356 Score: 122 Expect: 1.7e-007 Matches: 14 D-3-phosphoglycerate dehydrogenase [Homo sapiens]	38	gi|23308577 Mass: 57356 Score: 167 Matches: 5(2) Sequences: 5(2) D-3-phosphoglycerate dehydrogenase [Homo sapiens]

I. continued

Spot #	SwissProt MS (cut off = 56 for all)	SwissProt MS/MS cut off	SwissProt MS/MS	NCBInr MS (cut off = 67 for all)	NCBInr MS/MS cut off	NCBInr MS/MS
NB3 1.1252	PRS10_HUMAN Mass: 44430 Score: 152 Expect: 1.3e-011 Matches: 21 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1	28	PRS10_HUMAN Mass: 44430 Score: 60 Matches: 4(1) Sequences: 4(1) 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1	gi|195539395 Mass: 46053 Score: 160 Expect: 2.7e-011 Matches: 21 26S protease regulatory subunit 10B [Homo sapiens]	38	gi|1526426 Mass: 44418 Score: 122 Matches: 4(1) Sequences: 4(1) proteasome subunit p42 [Homo sapiens] gi|27754103 Mass: 44430 Score: 122 Matches: 4(1) Sequences: 4(1) 26S protease regulatory subunit 10B [Mus musculus]
NB3 3.1252	**Mixture 1 Total score: 309 Expect:** 2.6e-027 **Matches:** 63 Components (only one family member shown for each component): K2C1_HUMAN Mass: 66170 Score: 172 Expect: 1.3e-013 Matches: 26 Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6 K1C9_HUMAN Mass: 62255 Score: 110 Expect: 2e-007 Matches: 21 Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3 PRS10_HUMAN Mass: 44430 Score: 101 Expect: 1.6e-006 Matches: 20 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 K2C1_HUMAN Mass: 66170 Score: 172 Expect: 1.3e-013 Matches: 26 Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6 K1C9_HUMAN Mass: 62255 Score: 110 Expect: 2e-007 Matches: 21 Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3 PRS10_HUMAN Mass: 44430 Score: 101 Expect: 1.6e-006 Matches: 20 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1	28	PRS10_HUMAN Mass: 44430 Score: 65 Matches: 1(1) Sequences: 1(1) emPAI: 0.12 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 K1C9_HUMAN Mass: 62255 Score: 45 Matches: 1(1) Sequences: 1(1) emPAI: 0.08 Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3 K2C1_HUMAN Mass: 66170 Score: 32 Matches: 2(2) Sequences: 2(2) emPAI: 0.17 Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6 GFAP_HUMAN Mass: 49907 Score: 31 Matches: 1(1) Sequences: 1(1) emPAI: 0.11 Glial fibrillary acidic protein OS=Homo sapiens GN=GFAP PE=1 SV=1	**Mixture 1 Total score: 305 Expect:** 8.6e-026 **Matches:** 63 Components (only one family member shown for each component): gi|7331218 Mass: 66149 Score: 162 Expect: 1.7e-011 Matches: 25 keratin 1 [Homo sapiens] gi|119581148 Mass: 57754 Score: 121 Expect: 2.2e-007 Matches: 21 keratin 9 (epidermolytic palmoplantar keratoderma) [Homo sapiens] gi|1526426 Mass: 44418 Score: 101 Expect: 2.2e-005 Matches: 20 proteasome subunit p42 [Homo sapiens] **Mixture 2 Total score: 293 Expect:** 1.4e-024 **Matches:** 63 Components (only one family member shown for each component): gi|7331218 Mass: 66149 Score: 162 Expect: 1.7e-011 Matches: 25 keratin 1 [Homo sapiens] gi|55956899 Mass: 62255 Score: 110 Expect: 2.7e-006 Matches: 21 keratin, type I cytoskeletal 9 [Homo sapiens] gi|1526426 Mass: 44418 Score: 101 Expect: 2.2e-005 Matches: 20 proteasome subunit p42 [Homo sapiens] **Mixture 3 Total score: 241 Expect:** 2.2e-019 **Matches:** 58 Components (only one family member shown for each component): gi|119581148 Mass: 57754 Score: 121 Expect: 2.2e-007 Matches: 21 keratin 9 (epidermolytic palmoplantar keratoderma) [Homo sapiens] gi|386854 Mass: 52928 Score: 105 Expect: 8.6e-006 Matches: 20 type II keratin subunit protein, partial [Homo sapiens] gi|1526426 Mass: 44418 Score: 101 Expect: 2.2e-005 Matches: 20 proteasome subunit p42 [Homo sapiens] **Mixture 4 Total score: 231 Expect:** 2.2e-018 **Matches:** 58 Components (only one family member shown for each component): gi|55956899 Mass: 62255 Score: 110 Expect: 2.7e-006 Matches: 21 keratin, type I cytoskeletal 9 [Homo sapiens] gi|386854 Mass: 52928 Score: 105 Expect: 8.6e-006 Matches: 20 type II keratin subunit protein, partial [Homo sapiens] gi|1526426 Mass: 44418 Score: 101 Expect: 2.2e-005 Matches: 20 proteasome subunit p42 [Homo sapiens] gi|119395750 Mass: 66170 Score: 172 Expect: 1.7e-012 Matches: 26 keratin, type II cytoskeletal 1 [Homo sapiens] gi|119581148 Mass: 57754 Score: 121 Expect: 2.2e-007 Matches: 21 keratin 9 (epidermolytic palmoplantar keratoderma) [Homo sapiens] gi|195539395 Mass: 46053 Score: 117 Expect: 5.4e-007 Matches: 21 26S protease regulatory subunit 10B [Homo sapiens] gi|435476 Mass: 62320 Score: 110 Expect: 2.7e-006 Matches: 21 cytokeratin 9 [Homo sapiens] gi|55956899 Mass: 62255 Score: 110 Expect: 2.7e-006 Matches: 21 keratin, type I cytoskeletal 9 [Homo sapiens] gi|386854 Mass: 52928 Score: 105 Expect: 8.6e-006 Matches: 20 type II keratin subunit protein, partial [Homo sapiens]	38	gi|1526426 Mass: 44418 Score: 65 Matches: 1(1) Sequences: 1(1) emPAI: 0.12 proteasome subunit p42 [Homo sapiens] gi|27754103 Mass: 44430 Score: 65 Matches: 1(1) Sequences: 1(1) 26S protease regulatory subunit 10B [Mus musculus] gi|386854 Mass: 52928 Score: 59 Matches: 2(0) Sequences: 2(0) emPAI: 0.10 type II keratin subunit protein, partial [Homo sapiens] gi|435476 Mass: 62320 Score: 45 Matches: 1(1) Sequences: 1(1) emPAI: 0.08 cytokeratin 9 [Homo sapiens]
NB3 1.1276	NPM_HUMAN Mass: 32726 Score: 80 Expect: 0.00022 Matches: 11 Nucleophosmin OS=Homo sapiens GN=NPM1 PE=1 SV=2	28	NPM_HUMAN Mass: 32726 Score: 118 Matches: 2(2) Sequences: 2(2) Nucleophosmin OS=Homo sapiens GN=NPM1 PE=1 SV=2	gi|10835063 Mass: 32726 Score: 80 Expect: 0.003 Matches: 11 nucleophosmin isoform 1 [Homo sapiens]	37	gi|609342 Mass: 76121 Score: 144 Matches: 2(2) Sequences: 2(2) nucleophosmin-anaplastic lymphoma kinase fusion protein [Homo sapiens] gi|825671 Mass: 31090 Score: 144 Matches: 2(2) Sequences: 2(2) B23 nucleophosmin (280 AA) [Homo sapiens]
NB3 2.1276	NPM_HUMAN Mass: 32726 Score: 72 Expect: 0.0013 Matches: 14 Nucleophosmin OS=Homo sapiens GN=NPM1 PE=1 SV=2 SRCN1_HUMAN Mass: 112670 Score: 56 Expect: 0.055 Matches: 19 SRC kinase signaling inhibitor 1 OS=Homo sapiens GN=SRCIN1 PE=1 SV=3	28	NPM_HUMAN Mass: 32726 Score: 142 Matches: 2(2) Sequences: 2(2) Nucleophosmin OS=Homo sapiens GN=NPM1 PE=1 SV=2	gi|12697913 Mass: 81605 Score: 82 Expect: 0.0018 Matches: 17 KIAA1684 protein [Homo sapiens] gi|193785204 Mass: 98500 Score: 78 Expect: 0.0045 Matches: 19 unnamed protein product [Homo sapiens] gi|21739272 Mass: 87609 Score: 68 Expect: 0.038 Matches: 17 hypothetical protein [Homo sapiens] NOTE: NUCLEOPHOSMIN SCORE 64	38	gi|609342 Mass: 76121 Score: 169 Matches: 2(2) Sequences: 2(2) nucleophosmin-anaplastic lymphoma kinase fusion protein [Homo sapiens] gi|825671 Mass: 31090 Score: 169 Matches: 2(2) Sequences: 2(2) B23 nucleophosmin (280 AA) [Homo sapiens]

I. continued

Spot #	SwissProt MS (cut off = 56 for all)	SwissProt MS/MS cut off	SwissProt MS/MS	NCBInr MS (cut off = 67 for all)	NCBInr MS/MS cut off	NCBInr MS/MS
NB3 1.1284	GBLP_HUMAN Mass: 35511 Score: 178 Expect: 3.2e-014 Matches: 20 Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Homo sapiens GN=GNB2L1 PE=1 SV=3	28	GBLP_HUMAN Mass: 35511 Score: 306 Matches: 4(4) Sequences: 4(4) Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Homo sapiens GN=GNB2L1 PE=1 SV=3	gi|5174447 Mass: 35511 Score: 178 Expect: 4.3e-013 Matches: 20 guanine nucleotide-binding protein subunit beta-2-like 1 [Homo sapiens] gi|119574079 Mass: 43547 Score: 163 Expect: 1.4e-011 Matches: 21 guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1, isoform CRA_c [Homo sapiens] gi|119574084 Mass: 40193 Score: 155 Expect: 8.6e-011 Matches: 19 guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1, isoform CRA_h [Homo sapiens] gi|194375063 Mass: 24703 Score: 107 Expect: 5.4e-006 Matches: 14 unnamed protein product [Homo sapiens]	37	gi|5174447 Mass: 35511 Score: 389 Matches: 4(4) Sequences: 4(4) guanine nucleotide-binding protein subunit beta-2-like 1 [Homo sapiens]
NB3 2.1284	GBLP_HUMAN Mass: 35511 Score: 144 Expect: 8.1e-011 Matches: 17 Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Homo sapiens GN=GNB2L1 PE=1 SV=3	28	GBLP_HUMAN Mass: 35511 Score: 196 Matches: 4(4) Sequences: 4(4) Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Homo sapiens GN=GNB2L1 PE=1 SV=3	gi|119574084 Mass: 40193 Score: 153 Expect: 1.4e-010 Matches: 18 guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1, isoform CRA_h [Homo sapiens] gi|62896535 Mass: 35545 Score: 144 Expect: 1.1e-009 Matches: 16 guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1 variant [Homo sapiens] gi|5174447 Mass: 35511 Score: 144 Expect: 1.1e-009 Matches: 17 guanine nucleotide-binding protein subunit beta-2-like 1 [Homo sapiens] gi|119574079 Mass: 43547 Score: 133 Expect: 1.4e-008 Matches: 19 guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1, isoform CRA_c [Homo sapiens] gi|194375063 Mass: 24703 Score: 108 Expect: 4.3e-006 Matches: 13 unnamed protein product [Homo sapiens]	38	gi|5174447 Mass: 35511 Score: 269 Matches: 4(4) Sequences: 4(4) guanine nucleotide-binding protein subunit beta-2-like 1 [Homo sapiens]
NB3 1.1369	PEBP1_HUMAN Mass: 21158 Score: 123 Expect: 1e-008 Matches: 11 Phosphatidylethanolamine-binding protein 1 OS=Homo sapiens GN=PEBP1 PE=1 SV=3	28	PEBP1_HUMAN Mass: 21158 Score: 255 Matches: 3(3) Sequences: 3(3) Phosphatidylethanolamine-binding protein 1 OS=Homo sapiens GN=PEBP1 PE=1 SV=3	gi|913159 Mass: 21027 Score: 123 Expect: 1.4e-007 Matches: 11 neuropolypeptide h3 [human, brain, Peptide, 186 aa]	38	gi|913159 Mass: 21027 Score: 306 Matches: 3(2) Sequences: 3(2) neuropolypeptide h3 [human, brain, Peptide, 186 aa]
NB3 2.1369	**Mixture 1 Total score: 146 Expect:** 5.1e-011 **Matches:** 20 Components (only one family member shown for each component): PEBP1_HUMAN Mass: 21158 Score: 128 Expect: 3.2e-009 Matches: 12 Phosphatidylethanolamine-binding protein 1 OS=Homo sapiens GN=PEBP1 PE=1 SV=3 CNBP_HUMAN Mass: 20704 Score: 60 Expect: 0.018 Matches: 8 Cellular nucleic acid-binding protein OS=Homo sapiens GN=CNBP PE=1 SV=1	28	PEBP1_HUMAN Mass: 21158 Score: 298 Matches: 3(3) Sequences: 3(3) Phosphatidylethanolamine-binding protein 1 OS=Homo sapiens GN=PEBP1 PE=1 SV=3	gi|913159 Mass: 21027 Score: 138 Expect: 4.3e-009 Matches: 12 neuropolypeptide h3 [human, brain, Peptide, 186 aa]	38	gi|913159 Mass: 21027 Score: 348 Matches: 3(3) Sequences: 3(3) neuropolypeptide h3 [human, brain, Peptide, 186 aa]
NB3 1.1571	**Mixture 1 Total score: 163 Expect:** 1e-012 **Matches:** 25 Components (only one family member shown for each component): IF4A3_HUMAN Mass: 47126 Score: 138 Expect: 3.2e-010 Matches: 17 Eukaryotic initiation factor 4A-III OS=Homo sapiens GN=EIF4A3 PE=1 SV=4 B4GT2_HUMAN Mass: 42345 Score: 51 Expect: 0.16 Matches: 8 Beta-1,4-galactosyltransferase 2 OS=Homo sapiens GN=B4GALT2 PE=1 SV=1	28	IF4A3_HUMAN Mass: 47126 Score: 154 Matches: 5(5) Sequences: 5(5) Eukaryotic initiation factor 4A-III OS=Homo sapiens GN=EIF4A3 PE=1 SV=4	**Mixture 1 Total score: 164 Expect:** 1.1e-011 **Matches:** 25 Components (only one family member shown for each component): gi|114794619 Mass: 45019 Score: 146 Expect: 6.8e-010 Matches: 17 Chain A, Crystal Structure Of Human Apo-Eif4aiii gi|193786644 Mass: 30157 Score: 57 Expect: 0.52 Matches: 8 unnamed protein product [Homo sapiens] gi|114794619 Mass: 45019 Score: 146 Expect: 6.8e-010 Matches: 17 Chain A, Crystal Structure Of Human Apo-Eif4aiii	37	gi|496902 Mass: 47088 Score: 257 Matches: 5(4) Sequences: 5(4) translation initiation factor [Homo sapiens]
NB3 2.1571	IF4A3_HUMAN Mass: 47126 Score: 93 Expect: 9.7e-006 Matches: 13 Eukaryotic initiation factor 4A-III OS=Homo sapiens GN=EIF4A3 PE=1 SV=4 ATPB_HUMAN Mass: 56525 Score: 60 Expect: 0.018 Matches: 9 ATP synthase subunit beta, mitochondrial OS=Homo sapiens GN=ATP5B PE=1 SV=3	28	IF4A3_HUMAN Mass: 47126 Score: 87 Matches: 3(3) Sequences: 3(3) Eukaryotic initiation factor 4A-III OS=Homo sapiens GN=EIF4A3 PE=1 SV=4	gi|114794619 Mass: 45019 Score: 101 Expect: 2.2e-005 Matches: 13 Chain A, Crystal Structure Of Human Apo-Eif4aiii gi|28940 Mass: 57976 Score: 70 Expect: 0.025 Matches: 10 unnamed protein product [Homo sapiens] gi|89574029 Mass: 48083 Score: 66 Expect: 0.061 Matches: 9 mitochondrial ATP synthase, H+ transporting F1 complex beta subunit [Homo sapiens]	38	gi|496902 Mass: 47088 Score: 135 Matches: 3(3) Sequences: 3(3) translation initiation factor [Homo sapiens]
NB3 1.1576	PRS8_HUMAN Mass: 45768 Score: 197 Expect: 4e-016 Matches: 29 26S protease regulatory subunit 8 OS=Homo sapiens GN=PSMC5 PE=1 SV=1	28	PRS8_HUMAN Mass: 45768 Score: 153 Matches: 4(4) Sequences: 4(4) 26S protease regulatory subunit 8 OS=Homo sapiens GN=PSMC5 PE=1 SV=1	gi|312596881 Mass: 44927 Score: 201 Expect: 2.2e-015 Matches: 29 26S protease regulatory subunit 8 isoform 2 [Homo sapiens] gi|2661071 Mass: 31298 Score: 133 Expect: 1.4e-008 Matches: 22 similar to 26S proteasome subunit p45 [Homo sapiens]	38	gi|695370 Mass: 45785 Score: 228 Matches: 4(3) Sequences: 4(3) thyroid receptor interactor [Homo sapiens] gi|976227 Mass: 45795 Score: 228 Matches: 4(3) Sequences: 4(3) 26S proteasome subunit p45 [Homo sapiens] gi|281500993 Mass: 8685 Score: 47 Matches: 1(1) Sequences: 1(1) Chain A, Crystal Structure Of A Domain Of 26s Proteasome Regulatory Subunit 8 From Homo Sapiens. Northeast Structural Genomics Consortium Target Id Hr3102a
NB3 3.1576	PRS8_HUMAN Mass: 45768 Score: 103 Expect: 1e-006 Matches: 16 26S protease regulatory subunit 8 OS=Homo sapiens GN=PSMC5 PE=1 SV=1	28	PRS8_HUMAN Mass: 45768 Score: 34 Matches: 4(2) Sequences: 4(2) 26S protease regulatory subunit 8 OS=Homo sapiens GN=PSMC5 PE=1 SV=1	gi|312596881 Mass: 44927 Score: 104 Expect: 1.1e-005 Matches: 16 26S protease regulatory subunit 8 isoform 2 [Homo sapiens]	38	X
NB3 2.1583	PGK1_HUMAN Mass: 44985 Score: 254 Expect: 8.1e-022 Matches: 36 Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3 MACF1_HUMAN Mass: 843033 Score: 65 Expect: 0.0067 Matches: 53 Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5 OS=Homo sapiens GN=MACF1 PE=1 SV=4	28	PGK1_HUMAN Mass: 44985 Score: 314 Matches: 4(4) Sequences: 4(4) emPAI: 0.62 Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3	gi|315583375 Mass: 44797 Score: 260 Expect: 2.7e-021 Matches: 36 Chain A, The Catalytically Active Fully Closed Conformation Of Human Phosphoglycerate Kinase K219a Mutant In Complex With Amp-Pcp And 3pg **Mixture 1 Total score: 167 Expect:** 5.4e-012 **Matches:** 36 Components (only one family member shown for each component): gi|119619009 Mass: 28014 Score: 151 Expect: 2.2e-010 Matches: 24 phosphoglycerate kinase 1, isoform CRA_b [Homo sapiens] gi|194379670 Mass: 25888 Score: 116 Expect: 6.8e-007 Matches: 17 unnamed protein product [Homo sapiens] gi|530362276 Mass: 871869 Score: 69 Expect: 0.036 Matches: 55 PREDICTED: microtubule-actin cross-linking factor 1 isoform X5 [Homo sapiens]	37	gi|4505763 Mass: 44985 Score: 393 Matches: 4(4) Sequences: 4(4) emPAI: 0.62 phosphoglycerate kinase 1 [Homo sapiens] gi|530422076 Mass: 35251 Score: 266 Matches: 3(2) Sequences: 3(2) emPAI: 0.36 PREDICTED: phosphoglycerate kinase 1 isoform X2 [Homo sapiens]
NB3 3.1583	PGK1_HUMAN Mass: 44985 Score: 193 Expect: 1e-015 Matches: 30 Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3 MACF1_HUMAN Mass: 843033 Score: 90 Expect: 2.2e-005 Matches: 60 Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5 OS=Homo sapiens GN=MACF1 PE=1 SV=4	28	PGK1_HUMAN Mass: 44985 Score: 322 Matches: 4(4) Sequences: 4(4) emPAI: 0.62 Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3	gi|315583375 Mass: 44797 Score: 198 Expect: 4.3e-015 Matches: 30 Chain A, The Catalytically Active Fully Closed Conformation Of Human Phosphoglycerate Kinase K219a Mutant In Complex With Amp-Pcp And 3pg gi|530362276 Mass: 871869 Score: 95 Expect: 7.9e-005 Matches: 63 PREDICTED: microtubule-actin cross-linking factor 1 isoform X5 [Homo sapiens]	37	gi|4505763 Mass: 44985 Score: 397 Matches: 4(4) Sequences: 4(4) emPAI: 0.62 phosphoglycerate kinase 1 [Homo sapiens] gi|530422076 Mass: 35251 Score: 272 Matches: 3(3) Sequences: 3(3) emPAI: 0.58 PREDICTED: phosphoglycerate kinase 1 isoform X2 [Homo sapiens]

I. continued

Spot #	SwissProt MS (cut off = 56 for all)	SwissProt MS/MS cut off	SwissProt MS/MS	NCBInr MS (cut off = 67 for all)	NCBInr MS/MS cut off	NCBInr MS/MS
NB3 1.1659	HSPB1_HUMAN Mass: 22826 Score: 103 Expect: 1e-006 Matches: 9 Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2	28	HSPB1_HUMAN Mass: 22826 Score: 136 Matches: 3(2) Sequences: 3(2) Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2	gi|4504517 Mass: 22826 Score: 103 Expect: 1.4e-005 Matches: 9 heat shock protein beta-1 [Homo sapiens] gi|15126735 Mass: 22812 Score: 73 Expect: 0.015 Matches: 8 Heat shock 27kDa protein 1 [Homo sapiens] gi|5542491 Mass: 37260 Score: 69 Expect: 0.034 Matches: 8 Chain A, Autoinhibited Serine Kinase Domain Of The Giant Muscle Protein Titin	38	gi|662841 Mass: 22427 Score: 185 Matches: 3(2) Sequences: 3(2) heat shock protein 27 [Homo sapiens]
NB3 2.1659	HSPB1_HUMAN Mass: 22826 Score: 102 Expect: 1.3e-006 Matches: 9 Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2	28	HSPB1_HUMAN Mass: 22826 Score: 160 Matches: 3(2) Sequences: 3(2) Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2	gi|4504517 Mass: 22826 Score: 102 Expect: 1.7e-005 Matches: 9 heat shock protein beta-1 [Homo sapiens] gi|15126735 Mass: 22812 Score: 73 Expect: 0.015 Matches: 7 Heat shock 27kDa protein 1 [Homo sapiens]	37	gi|662841 Mass: 22427 Score: 202 Matches: 3(2) Sequences: 3(2) heat shock protein 27 [Homo sapiens]
NB3 1.1719	LDHA_HUMAN Mass: 36950 Score: 111 Expect: 1.6e-007 Matches: 14 L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2	29	LDHA_HUMAN Mass: 36950 Score: 162 Matches: 3(3) Sequences: 3(3) L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2	gi|62897717 Mass: 36951 Score: 113 Expect: 1.4e-006 Matches: 14 lactate dehydrogenase A variant [Homo sapiens]	38	gi|5031857 Mass: 36950 Score: 220 Matches: 3(3) Sequences: 3(3) L-lactate dehydrogenase A chain isoform 1 [Homo sapiens]
NB3 2.1719	LDHA_HUMAN Mass: 36950 Score: 149 Expect: 2.6e-011 Matches: 18 L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2	29	LDHA_HUMAN Mass: 36950 Score: 210 Matches: 3(3) Sequences: 3(3) L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2	gi|62897717 Mass: 36951 Score: 151 Expect: 2.2e-010 Matches: 18 lactate dehydrogenase A variant [Homo sapiens]	38	gi|5031857 Mass: 36950 Score: 268 Matches: 3(3) Sequences: 3(3) L-lactate dehydrogenase A chain isoform 1 [Homo sapiens]

J. A colour coded, simplified and unbiased representation, as a table, of all the MALDI-TOF MS and MALDI-TOF-TOF MS/MS identification results for the fourteen definitely identified proteins (in numerical order of spot number) from the MASCOT human protein Swiss-Prot (http://www.uniprot.org/) and NCBInr (http://www.ncbi.nlm.nih.gov/refseq/) database searches for the UKF-NB-6 proteomics study.

Matched protein results passing the score cut-offs for both database searches were entered into this table and colour coded according to whether or not the expectation value was above or below 1 x 10^{-5}, resulting in a simplified and unbiased representation of all the data together. An expect value cut-off of 1 x 10^{-5} was taken as this represents a 1 in 100,000 chance that the match is random; we apply this strict criteria as for single spots from a 2D gel there is no reliable mechanism for measuring a false detection rate (http://www.matrixscience.com/). The NCBInr database is not as highly curated as the Swissprot database, so more likely for NCBInr many hits are frequently generated for a single query, and a single protein hit often consists of a list of proteins rather than a single protein (as for Swissprot) representing matches to, for example, different isoforms, partial sequences or subunits of the same protein. In Mascot MS data reports, proteins that match the same set or a sub-set of mass values are grouped into a single hit (listed in order of decreasing scores and expect values). For our MS data, the top scoring protein in the list for each hit was transferred into this table. However, if a protein was unnamed, then the next named protein in the list for that hit was also transferred (if there was one). In Mascot MS/MS data reports, proteins matching the same set of peptides (therefore having the same score and expect values) are grouped as hits, so in this instance, the first protein in the list for each hit was transferred into this table, and if that protein was unnamed, then the next named protein in the list for that hit was also transferred (if there was one). A second protein in a list for an MS/MS hit was sometimes transferred too if its name made more sense relating to the names of corresponding MS hits.

Colour coding was as follows. For the MS data, matches with an expect value <1 x 10^{-5} were colour coded green (strong match), and matches with an expect value >1 x 10^{-5} were colour coded orange (weak match). For the MS/MS data, matches were colour coded green (strong match) if 1. at least one of the five peptides passed the score cut-off (which gives a p value <0.05) as well as having a strong expect value <1 x 10^{-5}, 2. two or more of the five peptides passed the score cut-off (which gives a p value <0.05) but had weaker expect values (>1 x 10^{-5}), 3. just one of the five peptides passed the score cut-off (which gives a p value <0.05) with a weak expect value (>1 x 10^{-5}) but accompanied by another one or more of the five peptides having (a) score (s) near to the score cut-off and weak expect value(s) (>1 x 10^{-5}). An orange colour for the MS/MS data indicated a weaker match, and this was for when just a single peptide passed the score cut-off (which gives a p value <0.05) with a weak expect value (>1 x 10^{-5}). Generally speaking, spots were classed as definite identifications if each of the duplicates had strong identical identification in both databases, with more weighting given to MS/MS hits because MS/MS matches actual peptide sequences rather than masses.

J. continued

Spot #	SwissProt MS (cut off = 56 for all)	SwissProt MS/MS cut off	SwissProt MS/MS	NCBInr MS (cut off = 67 for all)	NCBInr MS/MS cut off	NCBInr MS/MS
NB6 1.163	ENPL_HUMAN Mass: 92696 Score: 173 Expect: 1e-013 Matches: 25 Endoplasmin OS=Homo sapiens GN=HSP90B1 PE=1 SV=1	28	ENPL_HUMAN Mass: 92696 Score: 68 Matches: 2(1) Sequences: 2(1) Endoplasmin OS=Homo sapiens GN=HSP90B1 PE=1 SV=1	gi|61656607 Mass: 92567 Score: 173 Expect: 1.4e-012 Matches: 25 tumor rejection antigen (gp96) 1 [Homo sapiens]	37	gi|4507677 Mass: 92696 Score: 91 Matches: 2(1) Sequences: 2(1) endoplasmin precursor [Homo sapiens]
NB6 2.163	ENPL_HUMAN Mass: 92696 Score: 168 Expect: 3.2e-013 Matches: 24 Endoplasmin OS=Homo sapiens GN=HSP90B1 PE=1 SV=1	29	ENPL_HUMAN Mass: 92696 Score: 102 Matches: 5(3) Sequences: 5(3) Endoplasmin OS=Homo sapiens GN=HSP90B1 PE=1 SV=1	gi|15010550 Mass: 90309 Score: 175 Expect: 8.6e-013 Matches: 24 heat shock protein gp96 precursor [Homo sapiens] **Mixture 1 Total score: 136 Expect:** 6.8e-009 **Matches:** 24 Components (only one family member shown for each component): gi|530400801 Mass: 54657 Score: 120 Expect: 2.7e-007 Matches: 17 PREDICTED: endoplasmin isoform X1 [Homo sapiens] gi|194386550 Mass: 18712 Score: 64 Expect: 0.097 Matches: 7 unnamed protein product [Homo sapiens]	38	gi|4507677 Mass: 92696 Score: 184 Matches: 5(2) Sequences: 5(2) endoplasmin precursor [Homo sapiens]
NB6 1.278	GRP78_HUMAN Mass: 72402 Score: 290 Expect: 2e-025 Matches: 36 78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2 CRY1_HUMAN Mass: 67151 Score: 57 Expect: 0.037 Matches: 13 Cryptochrome-1 OS=Homo sapiens GN=CRY1 PE=1 SV=1	28	GRP78_HUMAN Mass: 72402 Score: 312 Matches: 5(5) Sequences: 5(5) 78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2 HSP76_HUMAN Mass: 71440 Score: 50 Matches: 1(1) Sequences: 1(1) Heat shock 70 kDa protein 6 OS=Homo sapiens GN=HSPA6 PE=1 SV=2	gi|16507237 Mass: 72402 Score: 290 Expect: 2.7e-024 Matches: 36 78 kDa glucose-regulated protein precursor [Homo sapiens] gi|254540166 Mass: 72492 Score: 259 Expect: 3.4e-021 Matches: 35 78 kDa glucose-regulated protein precursor [Mus musculus] **Mixture 1 Total score: 214 Expect:** 1.1e-016 **Matches:** 36 Components (only one family member shown for each component): gi|119608027 Mass: 51197 Score: 173 Expect: 1.4e-012 Matches: 24 heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa), isoform CRA_b [Homo sapiens] gi|194374345 Mass: 30458 Score: 109 Expect: 3.4e-006 Matches: 14 unnamed protein product [Homo sapiens]	38	gi|386758 Mass: 72185 Score: 424 Matches: 5(5) Sequences: 5(5) GRP78 precursor, partial [Homo sapiens] gi|35222 Mass: 71209 Score: 50 Matches: 1(1) Sequences: 1(1) unnamed protein product [Homo sapiens] gi|184414 Mass: 27004 Score: 50 Matches: 1(1) Sequences: 1(1) 70 kDa heat shock protein, partial [Homo sapiens]
NB6 2.278	GRP78_HUMAN Mass: 72402 Score: 333 Expect: 1e-029 Matches: 43 78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2	28	GRP78_HUMAN Mass: 72402 Score: 345 Matches: 5(5) Sequences: 5(5) 78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2	gi|16507237 Mass: 72402 Score: 333 Expect: 1.4e-028 Matches: 43 78 kDa glucose-regulated protein precursor [Homo sapiens] **Mixture 1 Total score: 263 Expect:** 1.4e-021 **Matches:** 43 Components (only one family member shown for each component): gi|119608027 Mass: 51197 Score: 208 Expect: 4.3e-016 Matches: 28 heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa), isoform CRA_b [Homo sapiens] gi|194374345 Mass: 30458 Score: 129 Expect: 3.4e-008 Matches: 18 unnamed protein product [Homo sapiens]	37	gi|386758 Mass: 72185 Score: 452 Matches: 5(5) Sequences: 5(5) GRP78 precursor, partial [Homo sapiens]
NB6 1.323	DPYL2_HUMAN Mass: 62711 Score: 211 Expect: 1.6e-017 Matches: 28 Dihydropyrimidinase-related protein 2 OS=Homo sapiens GN=DPYSL2 PE=1 SV=1	28	DPYL2_HUMAN Mass: 62711 Score: 396 Matches: 5(5) Sequences: 5(5) Dihydropyrimidinase-related protein 2 OS=Homo sapiens GN=DPYSL2 PE=1 SV=1	gi|62087970 Mass: 68598 Score: 217 Expect: 5.4e-017 Matches: 29 dihydropyrimidinase-like 2 variant [Homo sapiens] **Mixture 1 Total score: 108 Expect:** 4.3e-006 **Matches:** 27 Components (only one family member shown for each component): gi|30582727 Mass: 67545 Score: 87 Expect: 0.00052 Matches: 18 dihydropyrimidinase-like 2 [Homo sapiens] gi|21750956 Mass: 21515 Score: 86 Expect: 0.00072 Matches: 12 unnamed protein product [Homo sapiens] gi|30582727 Mass: 67545 Score: 87 Expect: 0.00052 Matches: 18 dihydropyrimidinase-like 2 [Homo sapiens]	37	gi|4503377 Mass: 62711 Score: 498 Matches: 5(5) Sequences: 5(5) dihydropyrimidinase-related protein 2 isoform 2 [Homo sapiens]
NB6 2.323	DPYL2_HUMAN Mass: 62711 Score: 203 Expect: 1e-016 Matches: 25 Dihydropyrimidinase-related protein 2 OS=Homo sapiens GN=DPYSL2 PE=1 SV=1	28	DPYL2_HUMAN Mass: 62711 Score: 182 Matches: 5(4) Sequences: 5(4) Dihydropyrimidinase-related protein 2 OS=Homo sapiens GN=DPYSL2 PE=1 SV=1	gi|62087970 Mass: 68598 Score: 212 Expect: 1.7e-016 Matches: 26 dihydropyrimidinase-like 2 variant [Homo sapiens] **Mixture 1 Total score: 103 Expect:** 1.4e-005 **Matches:** 23 Components (only one family member shown for each component): gi|21750956 Mass: 21515 Score: 85 Expect: 0.00086 Matches: 11 unnamed protein product [Homo sapiens] gi|30582727 Mass: 67545 Score: 83 Expect: 0.0015 Matches: 14 dihydropyrimidinase-like 2 [Homo sapiens]	37	gi|4503377 Mass: 62711 Score: 286 Matches: 5(3) Sequences: 5(3) dihydropyrimidinase-related protein 2 isoform 2 [Homo sapiens]
NB6 1.679	**Mixture 1 Total score: 91 Expect:** 1.5e-005 **Matches:** 26 Components (only one family member shown for each component): K1C10_HUMAN Mass: 59020 Score: 78 Expect: 0.00034 Matches: 17 Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6 HSPB1_HUMAN Mass: 22826 Score: 60 Expect: 0.022 Matches: 9 Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2 K1C10_HUMAN Mass: 59020 Score: 78 Expect: 0.00034 Matches: 17 Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6 HSPB1_HUMAN Mass: 22826 Score: 60 Expect: 0.022 Matches: 9 Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2	28	HSPB1_HUMAN Mass: 22826 Score: 136 Matches: 2(2) Sequences: 2(2) emPAI: 0.58 Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2 K1C10_HUMAN Mass: 59020 Score: 76 Matches: 2(2) Sequences: 2(2) emPAI: 0.20 Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6	gi|21961605 Mass: 59020 Score: 78 Expect: 0.0046 Matches: 17 Keratin 10 [Homo sapiens] gi|307086 Mass: 46473 Score: 70 Expect: 0.025 Matches: 15 keratin-10 [Homo sapiens]	38	gi|662841 Mass: 22427 Score: 161 Matches: 2(2) Sequences: 2(2) emPAI: 0.59 heat shock protein 27 [Homo sapiens] gi|28317 Mass: 59720 Score: 103 Matches: 2(1) Sequences: 2(1) emPAI: 0.19 unnamed protein product [Homo sapiens] gi|21961605 Mass: 59020 Score: 103 Matches: 2(1) Sequences: 2(1) Keratin 10 [Homo sapiens]
NB6 2.679	HSPB1_HUMAN Mass: 22826 Score: 89 Expect: 2.4e-005 Matches: 8 Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2	28	HSPB1_HUMAN Mass: 22826 Score: 102 Matches: 4(2) Sequences: 4(2) Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2	gi|662841 Mass: 22427 Score: 90 Expect: 0.00027 Matches: 8 heat shock protein 27 [Homo sapiens]	38	gi|662841 Mass: 22427 Score: 143 Matches: 4(2) Sequences: 4(2) heat shock protein 27 [Homo sapiens]

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Spot #	SwissProt MS (cut off = 56 for all)	SwissProt MS/MS cut off	SwissProt MS/MS	NCBInr MS (cut off = 67 for all)	NCBInr MS/MS cut off	NCBInr MS/MS
NB6 1.682	PSA6_HUMAN Mass: 27838 Score: 123 Expect: 1e-008 Matches: 13 Proteasome subunit alpha type-6 OS=Homo sapiens GN=PSMA6 PE=1 SV=1	28	PSA6_HUMAN Mass: 27838 Score: 108 Matches: 3(3) Sequences: 3(3) Proteasome subunit alpha type-6 OS=Homo sapiens GN=PSMA6 PE=1 SV=1	gi|8394076 Mass: 27838 Score: 123 Expect: 1.4e-007 Matches: 13 proteasome subunit alpha type-6 [Rattus norvegicus] gi|296736 Mass: 25078 Score: 110 Expect: 2.7e-006 Matches: 11 macropain subunit iota [Homo sapiens]	37	gi|296736 Mass: 25078 Score: 159 Matches: 3(2) Sequences: 3(2) macropain subunit iota [Homo sapiens]
NB6 2.682	PSA6_HUMAN Mass: 27838 Score: 113 Expect: 1e-007 Matches: 13 Proteasome subunit alpha type-6 OS=Homo sapiens GN=PSMA6 PE=1 SV=1	28	PSA6_HUMAN Mass: 27838 Score: 130 Matches: 4(4) Sequences: 4(4) Proteasome subunit alpha type-6 OS=Homo sapiens GN=PSMA6 PE=1 SV=1	gi|8394076 Mass: 27838 Score: 113 Expect: 1.4e-006 Matches: 13 proteasome subunit alpha type-6 [Rattus norvegicus] gi|532691774 Mass: 25730 Score: 87 Expect: 0.00053 Matches: 11 proteasome subunit alpha type-6 isoform c [Homo sapiens]	38	gi|296736 Mass: 25078 Score: 203 Matches: 4(4) Sequences: 4(4) macropain subunit iota [Homo sapiens]
NB6 1.722	GSTP1_HUMAN Mass: 23569 Score: 79 Expect: 0.00025 Matches: 12 Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2	29	GSTP1_HUMAN Mass: 23569 Score: 180 Matches: 2(2) Sequences: 2(2) emPAI: 0.56 Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2	gi|20664358 Mass: 23430 Score: 87 Expect: 0.00051 Matches: 11 Chain A, Crystal Structure Of A Recombinant Glutathione Transferase, Created By Replacing The Last Seven Residues Of Each Subunit Of The Human Class Pi Isoenzyme With The Additional C-Terminal Helix Of Human Class Alpha Isoenzyme gi|4504183 Mass: 23569 Score: 73 Expect: 0.014 Matches: 12 glutathione S-transferase P [Homo sapiens]	38	gi|494066 Mass: 23438 Score: 209 Matches: 2(2) Sequences: 2(2) emPAI: 0.56 Chain A, Three-Dimensional Structure Of Class Pi Glutathione S-Transferase From Human Placenta In Complex With S-Hexylglutathione At 2.8 Angstroms Resolution
NB6 2.722	GSTP1_HUMAN Mass: 23569 Score: 95 Expect: 6e-006 Matches: 14 Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2	28	GSTP1_HUMAN Mass: 23569 Score: 214 Matches: 3(3) Sequences: 3(3) Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2	gi|20664358 Mass: 23430 Score: 95 Expect: 8e-005 Matches: 12 Chain A, Crystal Structure Of A Recombinant Glutathione Transferase, Created By Replacing The Last Seven Residues Of Each Subunit Of The Human Class Pi Isoenzyme With The Additional C-Terminal Helix Of Human Class Alpha Isoenzyme gi|4504183 Mass: 23569 Score: 95 Expect: 8e-005 Matches: 14 glutathione S-transferase P [Homo sapiens] gi|726098 Mass: 23583 Score: 81 Expect: 0.0022 Matches: 14 glutathione S-transferase-P1c [Homo sapiens] gi|11514448 Mass: 23325 Score: 69 Expect: 0.035 Matches: 12 Chain A, Crystal Structure Of Pi Class Glutathione Transferase	38	gi|494066 Mass: 23438 Score: 268 Matches: 3(3) Sequences: 3(3) Chain A, Three-Dimensional Structure Of Class Pi Glutathione S-Transferase From Human Placenta In Complex With S-Hexylglutathione At 2.8 Angstroms Resolution
NB6 1.779	STMN1_HUMAN Mass: 17292 Score: 190 Expect: 2e-015 Matches: 19 Stathmin OS=Homo sapiens GN=STMN1 PE=1 SV=3	29	STMN1_HUMAN Mass: 17292 Score: 217 Matches: 4(4) Sequences: 4(4) Stathmin OS=Homo sapiens GN=STMN1 PE=1 SV=3	gi|5031851 Mass: 17292 Score: 190 Expect: 2.7e-014 Matches: 19 stathmin isoform a [Homo sapiens]	38	gi|5031851 Mass: 17292 Score: 301 Matches: 4(4) Sequences: 4(4) stathmin isoform a [Homo sapiens]
NB6 2.779	STMN1_HUMAN Mass: 17292 Score: 102 Expect: 1.3e-006 Matches: 12 Stathmin OS=Homo sapiens GN=STMN1 PE=1 SV=3	28	STMN1_HUMAN Mass: 17292 Score: 54 Matches: 3(2) Sequences: 3(2) Stathmin OS=Homo sapiens GN=STMN1 PE=1 SV=3	gi|5031851 Mass: 17292 Score: 102 Expect: 1.7e-005 Matches: 12 stathmin isoform a [Homo sapiens]	38	gi|5031851 Mass: 17292 Score: 100 Matches: 3(1) Sequences: 3(1) stathmin isoform a [Homo sapiens]
NB6 1.950	HSP7C_HUMAN Mass: 71082 Score: 317 Expect: 4e-028 Matches: 41 Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1	28	HSP7C_HUMAN Mass: 71082 Score: 332 Matches: 4(3) Sequences: 4(3) emPAI: 0.24 Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1	gi|5729877 Mass: 71082 Score: 317 Expect: 5.4e-027 Matches: 41 heat shock cognate 71 kDa protein isoform 1 [Homo sapiens] **Mixture 1 Total score: 249 Expect:** 3.4e-020 **Matches:** 41 Components (only one family member shown for each component): gi|530398063 Mass: 55146 Score: 182 Expect: 1.7e-013 Matches: 26 PREDICTED: heat shock cognate 71 kDa protein isoform X3 [Homo sapiens] gi|194390750 Mass: 23238 Score: 154 Expect: 1.1e-010 Matches: 20 unnamed protein product [Homo sapiens]	37	gi|5729877 Mass: 71082 Score: 401 Matches: 4(3) Sequences: 4(3) emPAI: 0.24 heat shock cognate 71 kDa protein isoform 1 [Homo sapiens]
NB6 2.950	HSP7C_HUMAN Mass: 71082 Score: 293 Expect: 1e-025 Matches: 39 Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1 HSP72_HUMAN Mass: 70263 Score: 60 Expect: 0.02 Matches: 13 Heat shock-related 70 kDa protein 2 OS=Homo sapiens GN=HSPA2 PE=1 SV=1	28	HSP7C_HUMAN Mass: 71082 Score: 294 Matches: 4(3) Sequences: 4(3) emPAI: 0.24 Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1	gi|5729877 Mass: 71082 Score: 293 Expect: 1.4e-024 Matches: 39 heat shock cognate 71 kDa protein isoform 1 [Homo sapiens] **Mixture 1 Total score: 228 Expect:** 4.3e-018 **Matches:** 39 Components (only one family member shown for each component): gi|530398063 Mass: 55146 Score: 198 Expect: 4.3e-015 Matches: 26 PREDICTED: heat shock cognate 71 kDa protein isoform X3 [Homo sapiens] gi|194390750 Mass: 23238 Score: 123 Expect: 1.4e-007 Matches: 17 unnamed protein product [Homo sapiens] gi|254575046 Mass: 44527 Score: 70 Expect: 0.029 Matches: 10 Chain A, Crystal Structure Of The Human 70kda Heat Shock Protein 2 (Hsp70-2) Atpase Domain In Complex With Adp And Inorganic Phosphate	37	gi|5729877 Mass: 71082 Score: 355 Matches: 4(3) Sequences: 4(3) emPAI: 0.24 heat shock cognate 71 kDa protein isoform 1 [Homo sapiens]
NB6 1.1104	PRDX4_HUMAN Mass: 30749 Score: 98 Expect: 3.3e-006 Matches: 9 Peroxiredoxin-4 OS=Homo sapiens GN=PRDX4 PE=1 SV=1	28	PRDX4_HUMAN Mass: 30749 Score: 115 Matches: 4(4) Sequences: 4(4) Peroxiredoxin-4 OS=Homo sapiens GN=PRDX4 PE=1 SV=1	gi|349587814 Mass: 28181 Score: 101 Expect: 2.2e-005 Matches: 9 Chain A, Crystal Structure Of Full-Length Human Peroxiredoxin 4 In The Reduced Form	38	gi|5453549 Mass: 30749 Score: 194 Matches: 4(3) Sequences: 4(3) peroxiredoxin-4 precursor [Homo sapiens]
NB6 2.1104	PRDX4_HUMAN Mass: 30749 Score: 90 Expect: 1.9e-005 Matches: 9 Peroxiredoxin-4 OS=Homo sapiens GN=PRDX4 PE=1 SV=1	28	PRDX4_HUMAN Mass: 30749 Score: 194 Matches: 4(4) Sequences: 4(4) Peroxiredoxin-4 OS=Homo sapiens GN=PRDX4 PE=1 SV=1	gi|349587814 Mass: 28181 Score: 94 Expect: 0.00011 Matches: 9 Chain A, Crystal Structure Of Full-Length Human Peroxiredoxin 4 In The Reduced Form	38	gi|5453549 Mass: 30749 Score: 273 Matches: 4(4) Sequences: 4(4) peroxiredoxin-4 precursor [Homo sapiens]
NB6 1.1403	VDAC2_HUMAN Mass: 32060 Score: 146 Expect: 5.1e-011 Matches: 13 Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2	28	VDAC2_HUMAN Mass: 32060 Score: 306 Matches: 4(4) Sequences: 4(4) Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 VDAC1_HUMAN Mass: 30868 Score: 47 Matches: 1(1) Sequences: 1(1) Voltage-dependent anion-selective channel protein 1 OS=Homo sapiens GN=VDAC1 PE=1 SV=2	gi|340201 Mass: 32088 Score: 161 Expect: 2.2e-011 Matches: 14 voltage-dependent anion channel [Homo sapiens] gi|296317337 Mass: 33864 Score: 143 Expect: 1.4e-009 Matches: 13 voltage-dependent anion-selective channel protein 2 isoform 1 [Homo sapiens]	37	gi|190200 Mass: 38639 Score: 386 Matches: 4(4) Sequences: 4(4) porin, partial [Homo sapiens] gi|42476281 Mass: 32060 Score: 386 Matches: 4(4) Sequences: 4(4) voltage-dependent anion-selective channel protein 2 isoform 2 [Homo sapiens] gi|238427 Mass: 30737 Score: 47 Matches: 1(1) Sequences: 1(1) Porin 31HM [human, skeletal muscle membranes, Peptide, 282 aa] gi|4507879 Mass: 30868 Score: 47 Matches: 1(1) Sequences: 1(1) voltage-dependent anion-selective channel protein 1 [Homo sapiens]
NB6 2.1403	VDAC2_HUMAN Mass: 32060 Score: 142 Expect: 1.3e-010 Matches: 14 Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2	28	VDAC2_HUMAN Mass: 32060 Score: 223 Matches: 3(3) Sequences: 3(3) Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 VDAC1_HUMAN Mass: 30868 Score: 32 Matches: 1(1) Sequences: 1(1) Voltage-dependent anion-selective channel protein 1 OS=Homo sapiens GN=VDAC1 PE=1 SV=2	gi|42476281 Mass: 32060 Score: 142 Expect: 1.7e-009 Matches: 14 voltage-dependent anion-selective channel protein 2 isoform 2 [Homo sapiens] gi|296317337 Mass: 33864 Score: 139 Expect: 3.4e-009 Matches: 13 voltage-dependent anion-selective channel protein 2 isoform 1 [Homo sapiens]	37	gi|190200 Mass: 38639 Score: 275 Matches: 3(3) Sequences: 3(3) porin, partial [Homo sapiens] gi|42476281 Mass: 32060 Score: 275 Matches: 3(3) Sequences: 3(3) voltage-dependent anion-selective channel protein 2 isoform 2 [Homo sapiens]

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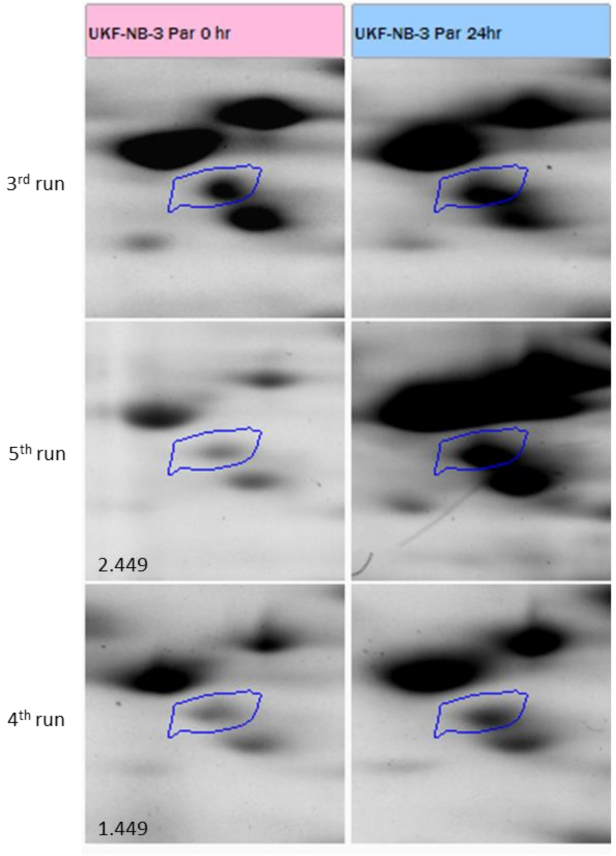
Spot #	SwissProt MS (cut off = 56 for all)	SwissProt MS/MS cut off	SwissProt MS/MS	NCBInr MS (cut off = 67 for all)	NCBInr MS/MS cut off	NCBInr MS/MS
NB6 1.1441	PRS8_HUMAN Mass: 45768 Score: 79 Expect: 0.00025 Matches: 19 26S protease regulatory subunit 8 OS=Homo sapiens GN=PSMC5 PE=1 SV=1	28	PRS8_HUMAN Mass: 45768 Score: 78 Matches: 5(3) Sequences: 4(3) emPAI: 0.39 26S protease regulatory subunit 8 OS=Homo sapiens GN=PSMC5 PE=1 SV=1	gi|312596881 Mass: 44927 Score: 82 Expect: 0.0019 Matches: 19 26S protease regulatory subunit 8 isoform 2 [Homo sapiens] gi|695370 Mass: 45785 Score: 73 Expect: 0.015 Matches: 19 thyroid receptor interactor [Homo sapiens]	38	gi|695370 Mass: 45785 Score: 142 Matches: 5(1) Sequences: 4(1) emPAI: 0.24 thyroid receptor interactor [Homo sapiens]
NB6 2.1441	**Mixture 1 Total score: 239 Expect:** 2.6e-020 **Matches:** 46 Components (only one family member shown for each component): PRS8_HUMAN Mass: 45768 Score: 193 Expect: 1e-015 Matches: 31 26S protease regulatory subunit 8 OS=Homo sapiens GN=PSMC5 PE=1 SV=1 RBMX_HUMAN Mass: 42306 Score: 76 Expect: 0.0005 Matches: 16 RNA-binding motif protein, X chromosome OS=Homo sapiens GN=RBMX PE=1 SV=3 **Mixture 2 Total score: 210 Expect:** 2e-017 **Matches:** 43 Components (only one family member shown for each component): PRS8_HUMAN Mass: 45768 Score: 193 Expect: 1e-015 Matches: 31 26S protease regulatory subunit 8 OS=Homo sapiens GN=PSMC5 PE=1 SV=1 RMXL1_HUMAN Mass: 42173 Score: 72 Expect: 0.0013 Matches: 15 RNA binding motif protein, X-linked-like-1 OS=Homo sapiens GN=RBMXL1 PE=1 SV=1 PRS8_HUMAN Mass: 45768 Score: 193 Expect: 1e-015 Matches: 31 26S protease regulatory subunit 8 OS=Homo sapiens GN=PSMC5 PE=1 SV=1 RBMX_HUMAN Mass: 42306 Score: 76 Expect: 0.0005 Matches: 16 RNA-binding motif protein, X chromosome OS=Homo sapiens GN=RBMX PE=1 SV=3 RMXL1_HUMAN Mass: 42173 Score: 72 Expect: 0.0013 Matches: 15 RNA binding motif protein, X-linked-like-1 OS=Homo sapiens GN=RBMXL1 PE=1 SV=1 NOP14_HUMAN Mass: 98292 Score: 59 Expect: 0.024 Matches: 18 Nucleolar protein 14 OS=Homo sapiens GN=NOP14 PE=1 SV=3	28	PRS8_HUMAN Mass: 45768 Score: 109 Matches: 5(2) Sequences: 4(2) 26S protease regulatory subunit 8 OS=Homo sapiens GN=PSMC5 PE=1 SV=1	**Mixture 1 Total score: 239 Expect:** 3.4e-019 **Matches:** 47 Components (only one family member shown for each component): gi|312596881 Mass: 44927 Score: 197 Expect: 5.4e-015 Matches: 31 26S protease regulatory subunit 8 isoform 2 [Homo sapiens] gi|542850 Mass: 47419 Score: 83 Expect: 0.0014 Matches: 17 heterogeneous nuclear ribonucleoprotein G - human gi|312596881 Mass: 44927 Score: 197 Expect: 5.4e-015 Matches: 31 26S protease regulatory subunit 8 isoform 2 [Homo sapiens] **Mixture 2 Total score: 173 Expect:** 1.4e-012 **Matches:** 37 Components (only one family member shown for each component): gi|62087652 Mass: 38907 Score: 155 Expect: 8.6e-011 Matches: 23 proteasome 26S ATPase subunit 5 variant [Homo sapiens] gi|82802769 Mass: 41497 Score: 72 Expect: 0.015 Matches: 15 RBM1 [Homo sapiens] gi|2661071 Mass: 31298 Score: 127 Expect: 5.4e-008 Matches: 23 similar to 26S proteasome subunit p45 [Homo sapiens] gi|542850 Mass: 47419 Score: 83 Expect: 0.0014 Matches: 17 heterogeneous nuclear ribonucleoprotein G - human gi|82802769 Mass: 41497 Score: 72 Expect: 0.015 Matches: 15 RBM1 [Homo sapiens]		**FATAL ERROR NO MS/MS DATA**
NB6 1.1539	ACON_HUMAN Mass: 86113 Score: 97 Expect: 4e-006 Matches: 19 Aconitate hydratase, mitochondrial OS=Homo sapiens GN=ACO2 PE=1 SV=2	28	ACON_HUMAN Mass: 86113 Score: 108 Matches: 4(3) Sequences: 4(3) Aconitate hydratase, mitochondrial OS=Homo sapiens GN=ACO2 PE=1 SV=2	gi|194380306 Mass: 84102 Score: 99 Expect: 3.8e-005 Matches: 19 unnamed protein product [Homo sapiens] gi|20072188 Mass: 86252 Score: 97 Expect: 5.3e-005 Matches: 19 Aconitase 2, mitochondrial [Homo sapiens]	38	gi|1718502 Mass: 86346 Score: 183 Matches: 4(3) Sequences: 4(3) mitochondrial aconitase [Homo sapiens]
NB6 2.1539	**Mixture 1 Total score: 144 Expect:** 8.1e-011 **Matches:** 36 Components (only one family member shown for each component): ACON_HUMAN Mass: 86113 Score: 121 Expect: 1.6e-008 Matches: 21 Aconitate hydratase, mitochondrial OS=Homo sapiens GN=ACO2 PE=1 SV=2 DDX1_HUMAN Mass: 83349 Score: 86 Expect: 5.2e-005 Matches: 19 ATP-dependent RNA helicase DDX1 OS=Homo sapiens GN=DDX1 PE=1 SV=2 ACON_HUMAN Mass: 86113 Score: 121 Expect: 1.6e-008 Matches: 21 Aconitate hydratase, mitochondrial OS=Homo sapiens GN=ACO2 PE=1 SV=2 DDX1_HUMAN Mass: 83349 Score: 86 Expect: 5.2e-005 Matches: 19 ATP-dependent RNA helicase DDX1 OS=Homo sapiens GN=DDX1 PE=1 SV=2	28	ACON_HUMAN Mass: 86113 Score: 185 Matches: 5(5) Sequences: 5(5) Aconitate hydratase, mitochondrial OS=Homo sapiens GN=ACO2 PE=1 SV=2	**Mixture 1 Total score: 141 Expect:** 2.2e-009 **Matches:** 36 Components (only one family member shown for each component): gi|194380306 Mass: 84102 Score: 124 Expect: 1.1e-007 Matches: 21 unnamed protein product [Homo sapiens] gi|326205203 Mass: 74838 Score: 92 Expect: 0.00019 Matches: 19 ATP-dependent RNA helicase DDX1 [Homo sapiens] **Mixture 2 Total score: 128 Expect:** 4.3e-008 **Matches:** 34 Components (only one family member shown for each component): gi|194386264 Mass: 73816 Score: 93 Expect: 0.00015 Matches: 17 unnamed protein product [Homo sapiens] gi|326205203 Mass: 74838 Score: 92 Expect: 0.00019 Matches: 19 ATP-dependent RNA helicase DDX1 [Homo sapiens] gi|194380306 Mass: 84102 Score: 124 Expect: 1.1e-007 Matches: 21 unnamed protein product [Homo sapiens] gi|4501867 Mass: 86113 Score: 121 Expect: 2.2e-007 Matches: 21 aconitate hydratase, mitochondrial precursor [Homo sapiens] gi|194386264 Mass: 73816 Score: 93 Expect: 0.00015 Matches: 17 unnamed protein product [Homo sapiens] gi|326205203 Mass: 74838 Score: 92 Expect: 0.00019 Matches: 19 ATP-dependent RNA helicase DDX1 [Homo sapiens] gi|194389932 Mass: 59900 Score: 86 Expect: 0.00072 Matches: 17 unnamed protein product [Homo sapiens]	38	gi|4501867 Mass: 86113 Score: 288 Matches: 5(5) Sequences: 5(5) aconitate hydratase, mitochondrial precursor [Homo sapiens]
NB6 1.1548	KPYM_HUMAN Mass: 58470 Score: 216 Expect: 5.1e-018 Matches: 23 Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4	29	KPYM_HUMAN Mass: 58470 Score: 192 Matches: 3(3) Sequences: 3(3) Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4 KHDR3_HUMAN Mass: 38776 Score: 42 Matches: 1(1) Sequences: 1(1) KH domain-containing, RNA-binding, signal transduction-associated protein 3 OS=Homo sapiens GN=KHDRBS3 PE=1 SV=1	gi|408536017 Mass: 57114 Score: 223 Expect: 1.4e-017 Matches: 23 Chain A, Pkm2 In Complex With An Activator	38	gi|35505 Mass: 58411 Score: 245 Matches: 3(3) Sequences: 3(3) pyruvate kinase [Homo sapiens] gi|4091776 Mass: 29398 Score: 42 Matches: 1(1) Sequences: 1(1) Sam68-like phosphotyrosine protein beta, partial [Homo sapiens]
NB6 3.1548	KPYM_HUMAN Mass: 58470 Score: 163 Expect: 1e-012 Matches: 22 Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4	26	KPYM_HUMAN Mass: 58470 Score: 75 Matches: 1(1) Sequences: 1(1) Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4 KHDR3_HUMAN Mass: 38776 Score: 35 Matches: 1(1) Sequences: 1(1) KH domain-containing, RNA-binding, signal transduction-associated protein 3 OS=Homo sapiens GN=KHDRBS3 PE=1 SV=1	gi|408536017 Mass: 57114 Score: 168 Expect: 4.3e-012 Matches: 22 Chain A, Pkm2 In Complex With An Activator gi|224510884 Mass: 58690 Score: 162 Expect: 1.7e-011 Matches: 23 Chain A, S437y Mutant Of Human Muscle Pyruvate Kinase, Isoform M2	35	gi|35505 Mass: 58411 Score: 75 Matches: 1(1) Sequences: 1(1) pyruvate kinase [Homo sapiens] gi|4091776 Mass: 29398 Score: 35 Matches: 1(0) Sequences: 1(0) Sam68-like phosphotyrosine protein beta, partial [Homo sapiens]

J. continued

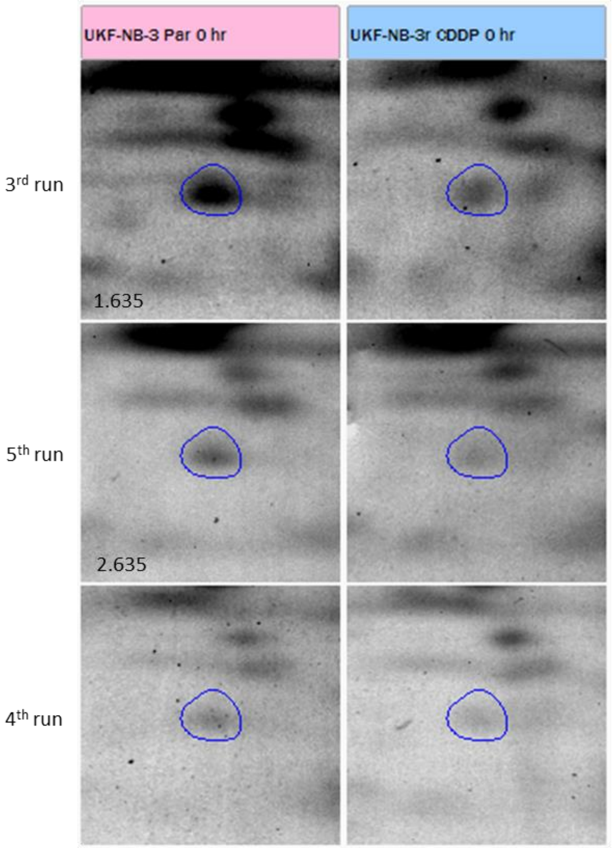
Spot #	SwissProt MS (cut off = 56 for all)	SwissProt MS/MS cut off	SwissProt MS/MS	NCBInr MS (cut off = 67 for all)	NCBInr MS/MS cut off	NCBInr MS/MS
NB6 1.1652	ACTB_HUMAN Mass: 42052 Score: 218 Expect: 3.2e-018 Matches: 22	28	ACTB_HUMAN Mass: 42052 Score: 317 Matches: 5(4) Sequences: 5(4)	gi|194388064 Mass: 40116 Score: 223 Expect: 1.4e-017 Matches: 22	38	gi|4501885 Mass: 42052 Score: 415 Matches: 5(4) Sequences: 5(4)
	Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1		Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1	unnamed protein product [Homo sapiens]		actin, cytoplasmic 1 [Homo sapiens]
	ACTH_HUMAN Mass: 42249 Score: 96 Expect: 5.1e-006 Matches: 12		ACTBL_HUMAN Mass: 42318 Score: 152 Matches: 2(2) Sequences: 2(2)	gi|15277503 Mass: 40536 Score: 223 Expect: 1.4e-017 Matches: 22		gi|63055057 Mass: 42318 Score: 179 Matches: 2(2) Sequences: 2(2)
	Actin, gamma-enteric smooth muscle OS=Homo sapiens GN=ACTG2 PE=1 SV=1		Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 PE=1 SV=2	ACTB protein, partial [Homo sapiens]		beta-actin-like protein 2 [Homo sapiens]
				Mixture 1 Total score: 181 Expect: 2.2e-013 **Matches:** 23		
				Components (only one family member shown for each component):		
				gi|354468985 Mass: 28478 Score: 134 Expect: 1.1e-008 Matches: 15		
				PREDICTED: actin, cytoplasmic 2-like [Cricetulus griseus]		
				gi|118505325 Mass: 13588 Score: 94 Expect: 0.00011 Matches: 8		
				beta-actin [Mus musculus]		
				gi|4501889 Mass: 42249 Score: 96 Expect: 6.8e-005 Matches: 12		
				actin, gamma-enteric smooth muscle isoform 1 precursor [Homo sapiens]		
				gi|118505325 Mass: 13588 Score: 94 Expect: 0.00011 Matches: 8		
				beta-actin [Mus musculus]		
NB6 2.1652	ACTB_HUMAN Mass: 42052 Score: 187 Expect: 4e-015 Matches: 25	28	ACTB_HUMAN Mass: 42052 Score: 302 Matches: 4(4) Sequences: 4(4)	gi|194388064 Mass: 40116 Score: 190 Expect: 2.7e-014 Matches: 25	38	gi|28336 Mass: 42128 Score: 385 Matches: 4(4) Sequences: 4(4)
	Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1		Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1	unnamed protein product [Homo sapiens]		mutant beta-actin (beta'-actin) [Homo sapiens]
	ACTH_HUMAN Mass: 42249 Score: 66 Expect: 0.0046 Matches: 15		ACTBL_HUMAN Mass: 42318 Score: 114 Matches: 2(2) Sequences: 2(2)	gi|15277503 Mass: 40536 Score: 190 Expect: 2.7e-014 Matches: 25		gi|63055057 Mass: 42318 Score: 141 Matches: 2(2) Sequences: 2(2)
	Actin, gamma-enteric smooth muscle OS=Homo sapiens GN=ACTG2 PE=1 SV=1		Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 PE=1 SV=2	ACTB protein, partial [Homo sapiens]		beta-actin-like protein 2 [Homo sapiens]
				Mixture 1 Total score: 133 Expect: 1.4e-008 **Matches:** 25		
				Components (only one family member shown for each component):		
				gi|354468985 Mass: 28478 Score: 114 Expect: 1.1e-006 Matches: 16		
				PREDICTED: actin, cytoplasmic 2-like [Cricetulus griseus]		
				gi|297281875 Mass: 38142 Score: 68 Expect: 0.046 Matches: 14		
				PREDICTED: actin, alpha skeletal muscle-like isoform 3 [Macaca mulatta]		
				gi|297281875 Mass: 38142 Score: 68 Expect: 0.046 Matches: 14		
				PREDICTED: actin, alpha skeletal muscle-like isoform 3 [Macaca mulatta]		

K. Progenesis Samespots software images of all spots, in numerical order, for the twenty UKF-NB-3 study proteins that were definitely identified, in each experiment comparison that they were a hit. Spot numbers are added to spot images to show where they were excised from, the number prefixing the spot number is the cut number. Spots were identified by mass spectroscopy method and searches against the human protein SwissProt (http://www.uniprot.org/) and NCBInr (http://www.ncbi.nlm.nih.gov/refseq/) databases.

449

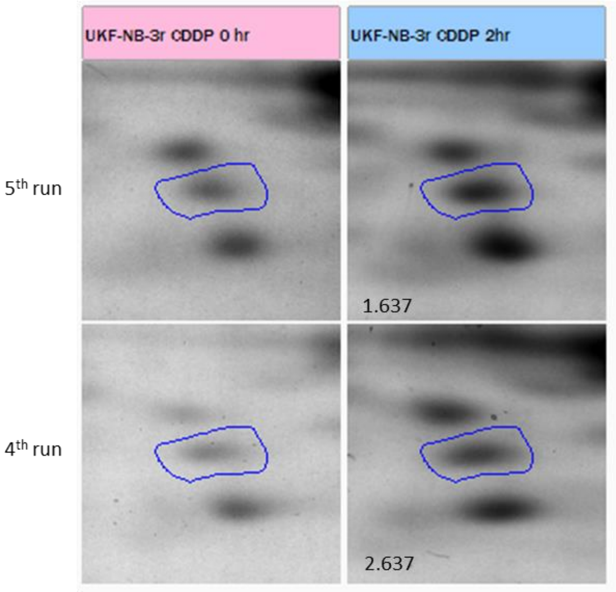


635

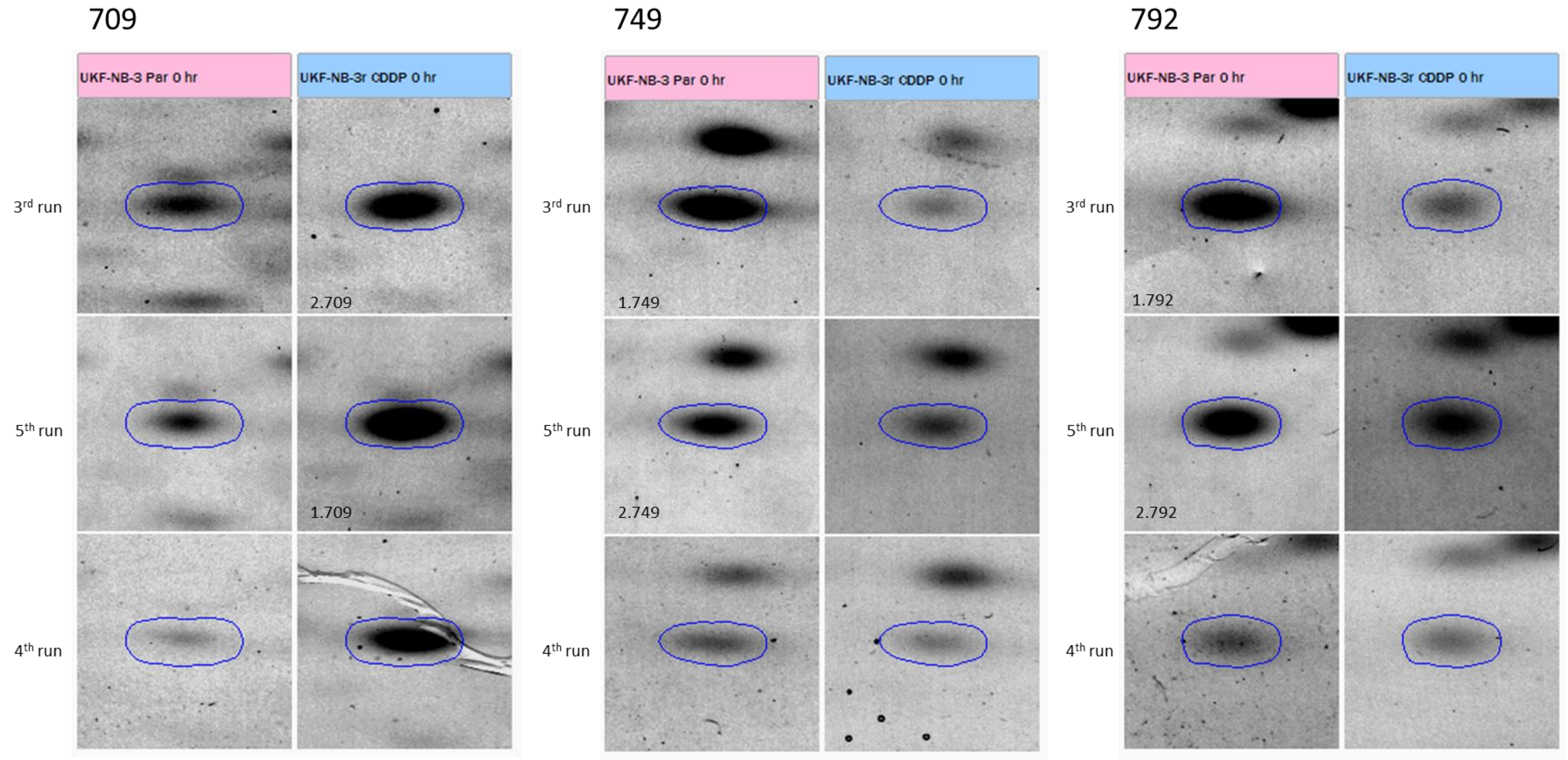


3.635 recut was taken from UKF-NB-3 Par 8hr 3rd run

637

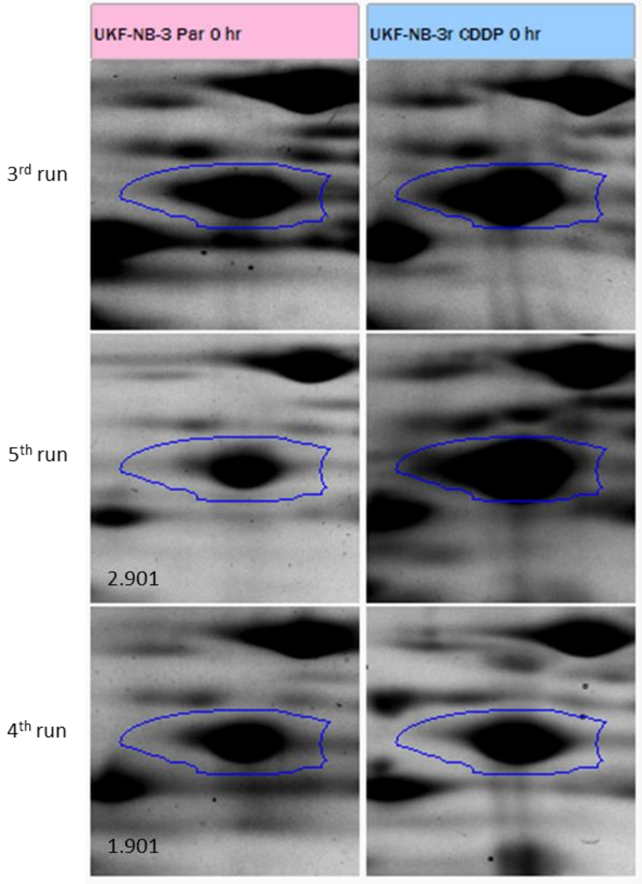


K. continued

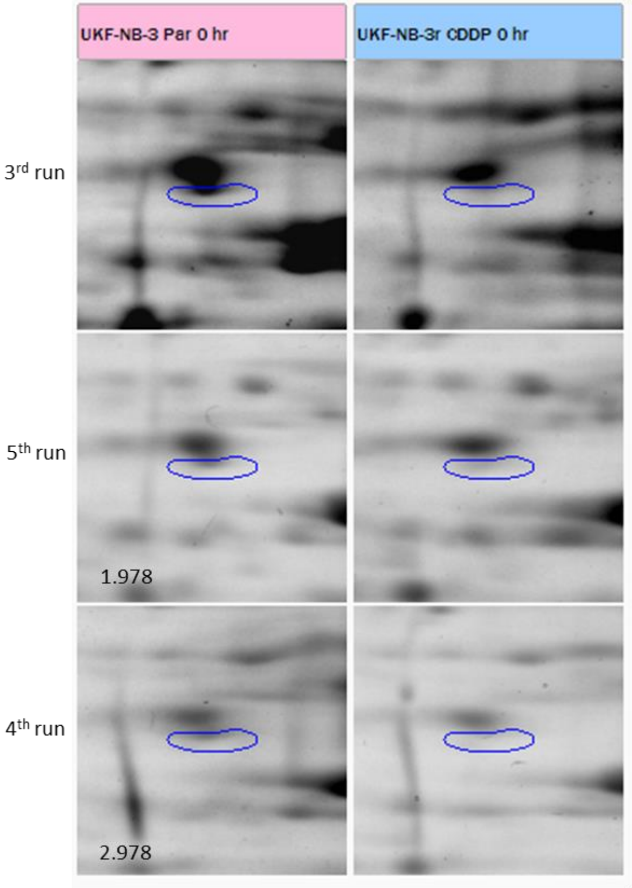

709
749
792
UKF-NB-3 Par 0 hr
UKF-NB-3r CDDP 0 hr
3rd run
5th run
4th run
2.709
1.709
1.749
2.749
1.792
2.792

K. continued

901



978



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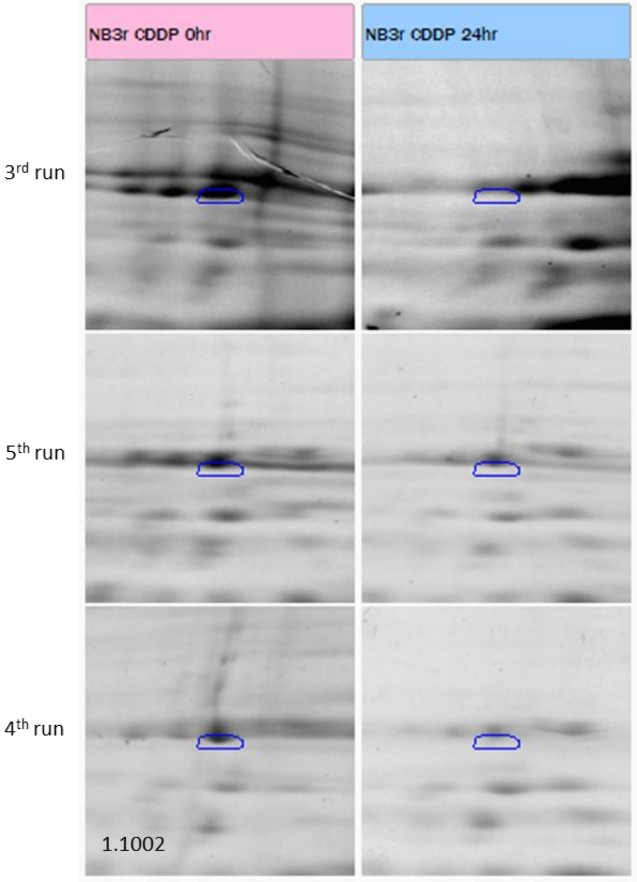
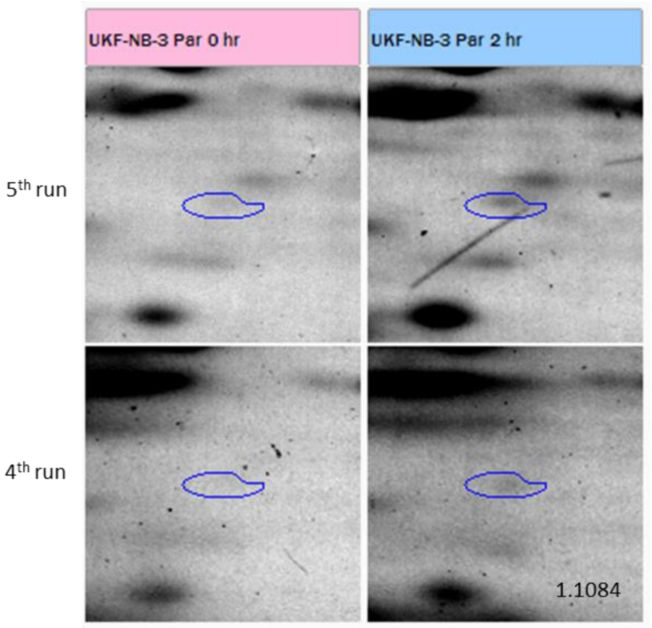


2.1002 was cut from NB3r CDDP 8hr 4th run

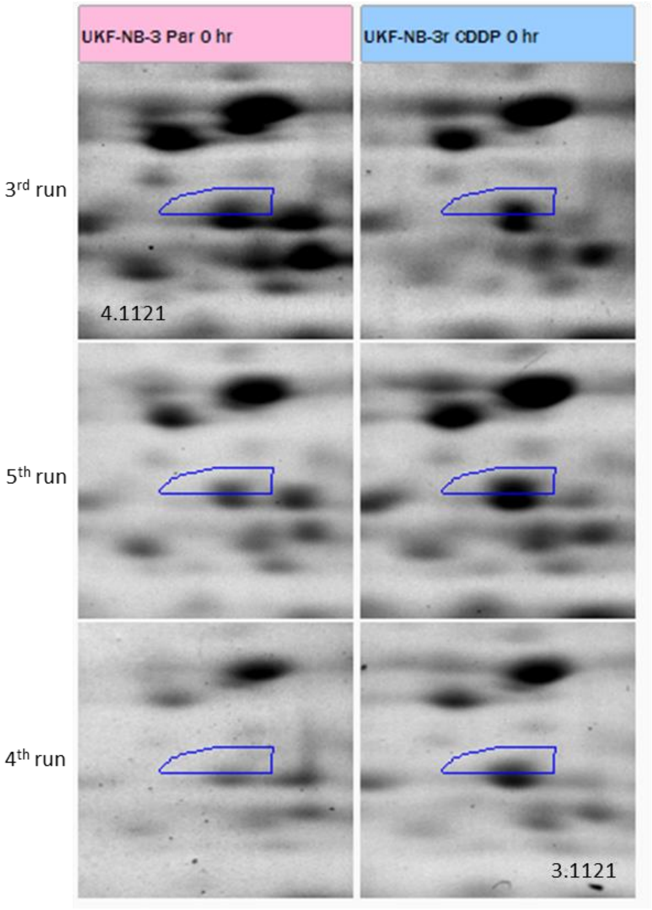
K. continued

1084

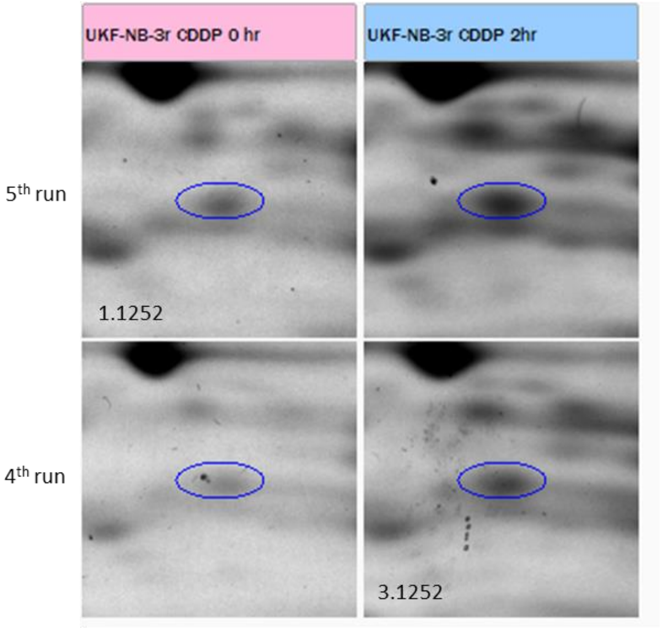


2.1084 was cut from UKF-NB-3 Par 8hr 3rd run

1121

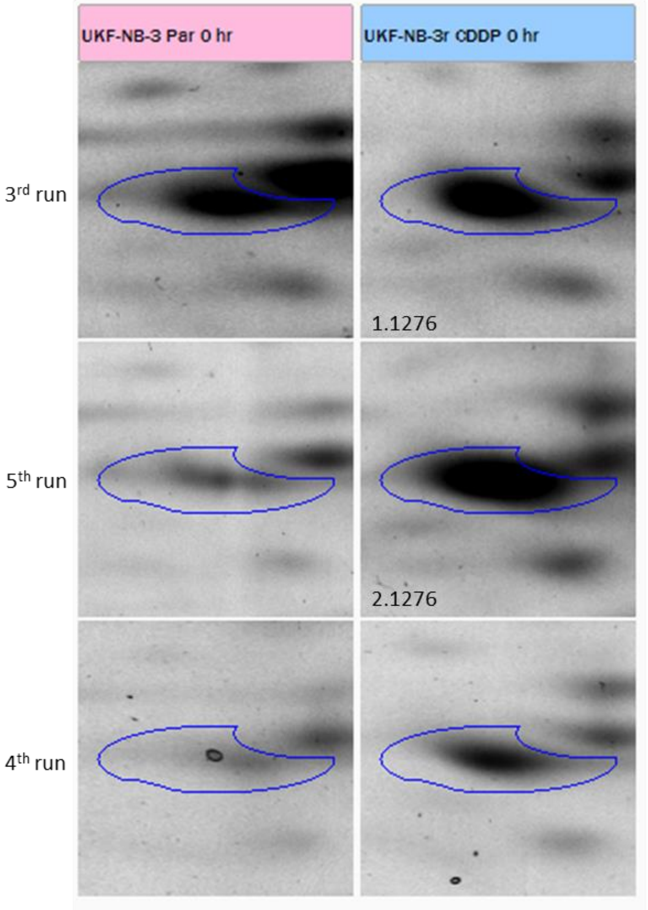


1252

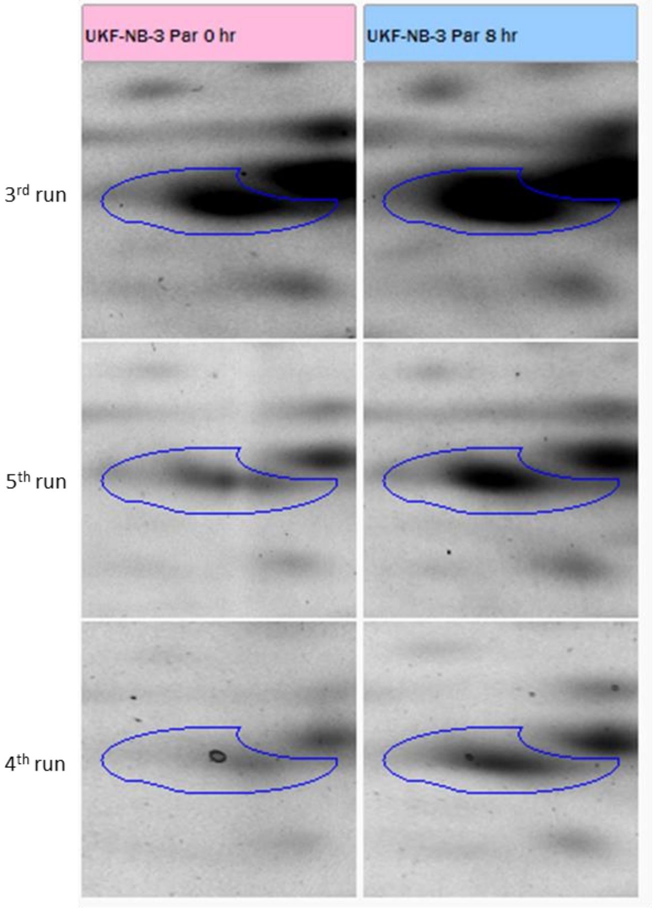


K. continued

1276



1276



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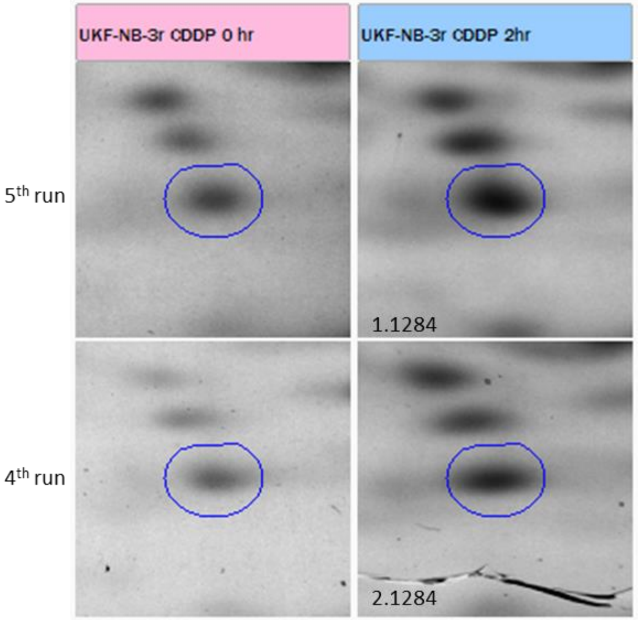
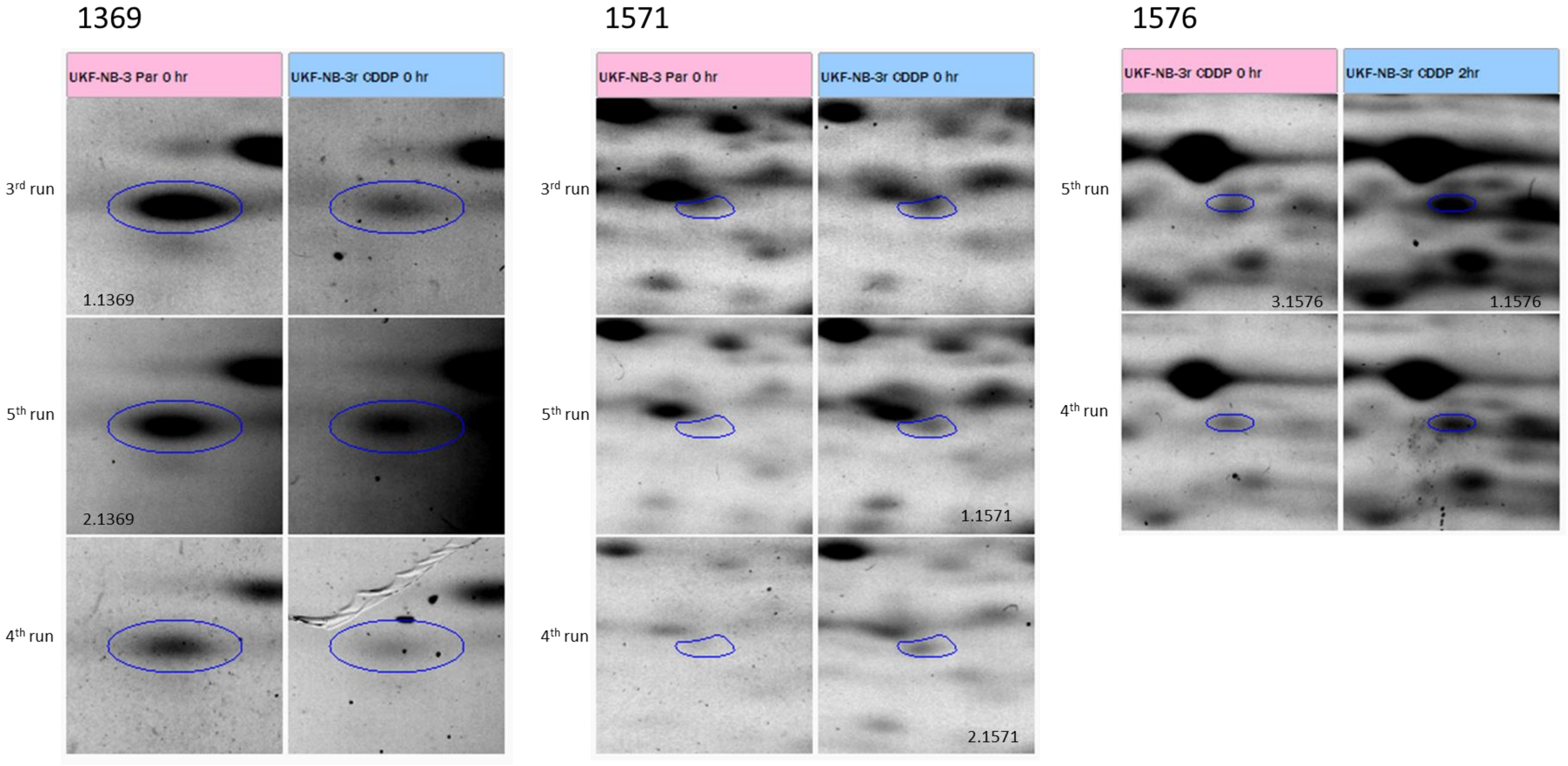
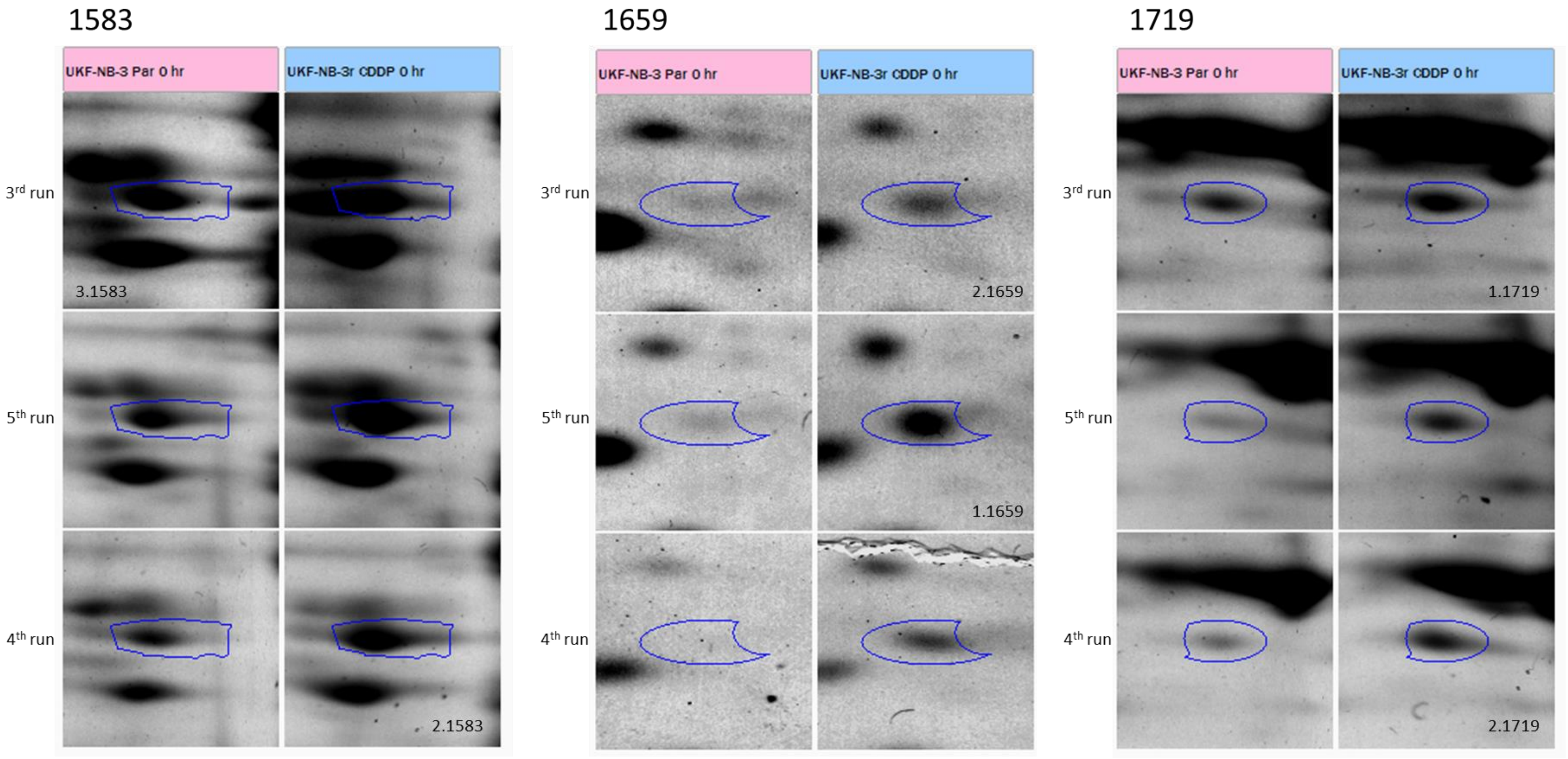


K. continued

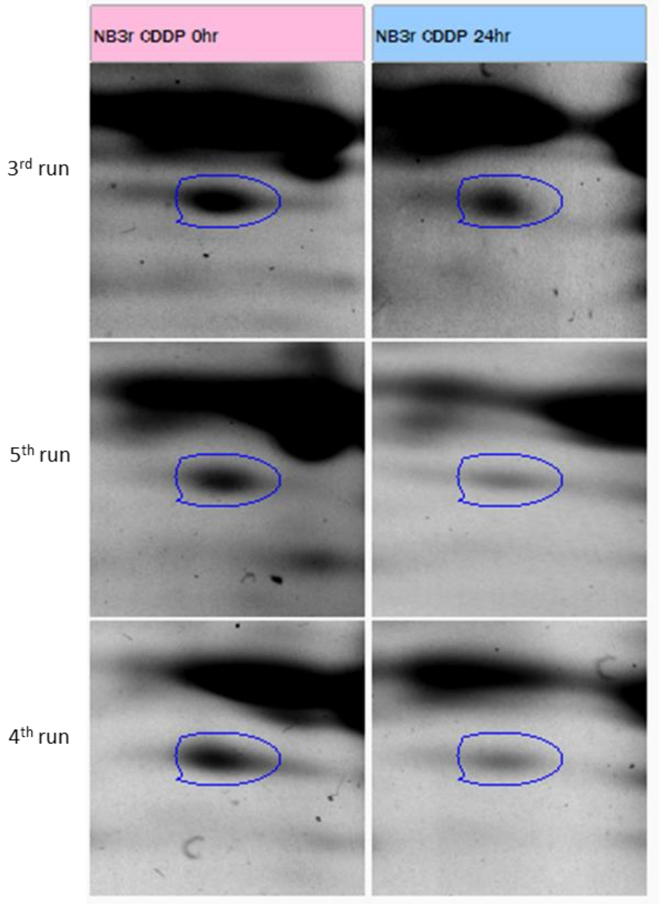

1369
UKF-NB-3 Par 0 hr
UKF-NB-3r CDDP 0 hr
3rd run
1.1369
5th run
2.1369
4th run
1571
UKF-NB-3 Par 0 hr
UKF-NB-3r CDDP 0 hr
3rd run
5th run
1.1571
4th run
2.1571
1576
UKF-NB-3r CDDP 0 hr
UKF-NB-3r CDDP 2hr
5th run
3.1576
1.1576
4th run

K. continued


1583
UKF-NB-3 Par 0 hr
UKF-NB-3r CDDP 0 hr
3rd run
5th run
4th run
3.1583
2.1583
1659
UKF-NB-3 Par 0 hr
UKF-NB-3r CDDP 0 hr
3rd run
5th run
4th run
2.1659
1.1659
1719
UKF-NB-3 Par 0 hr
UKF-NB-3r CDDP 0 hr
3rd run
5th run
4th run
1.1719
2.1719

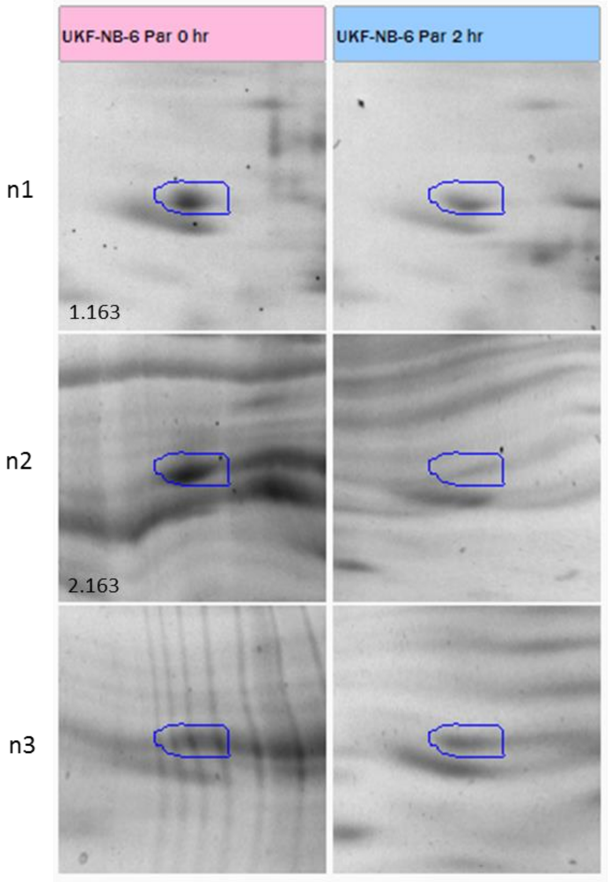
K. continued

1719

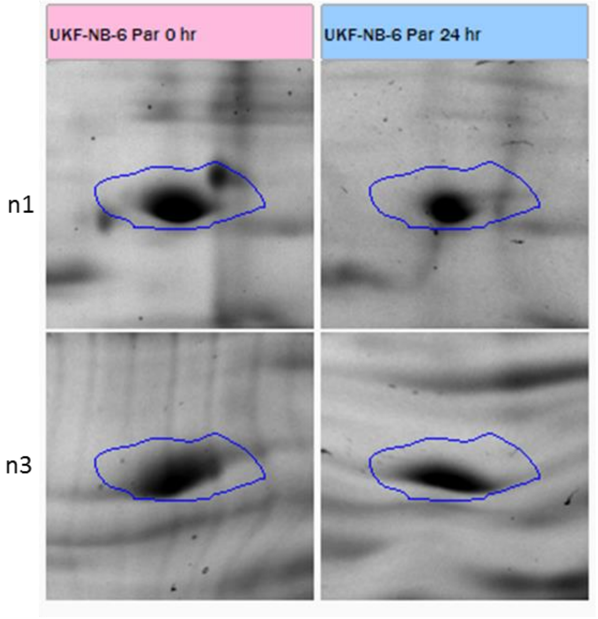


L. Progenesis Samespots software images of all spots, in numerical order, of the fourteen UKF-NB-6 study proteins that were definitely identified, in each experiment comparison that they were a hit. Spot numbers are added to spot images to show where they were excised from, the number prefixing the spot number is the cut number. Spots were identified by mass spectroscopy method and searches against the human protein SwissProt (http://www.uniprot.org/) and NCBInr (http://www.ncbi.nlm.nih.gov/refseq/) databases.

163



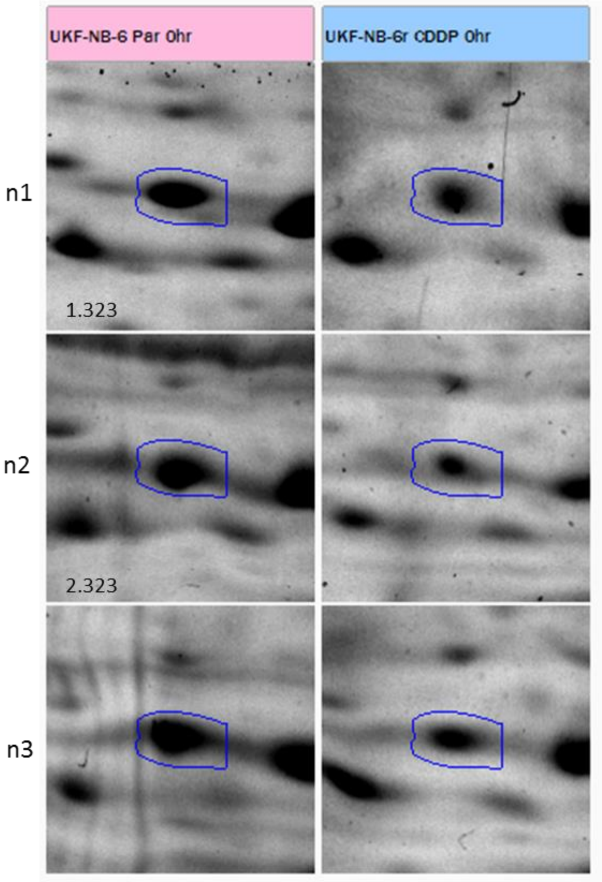
278



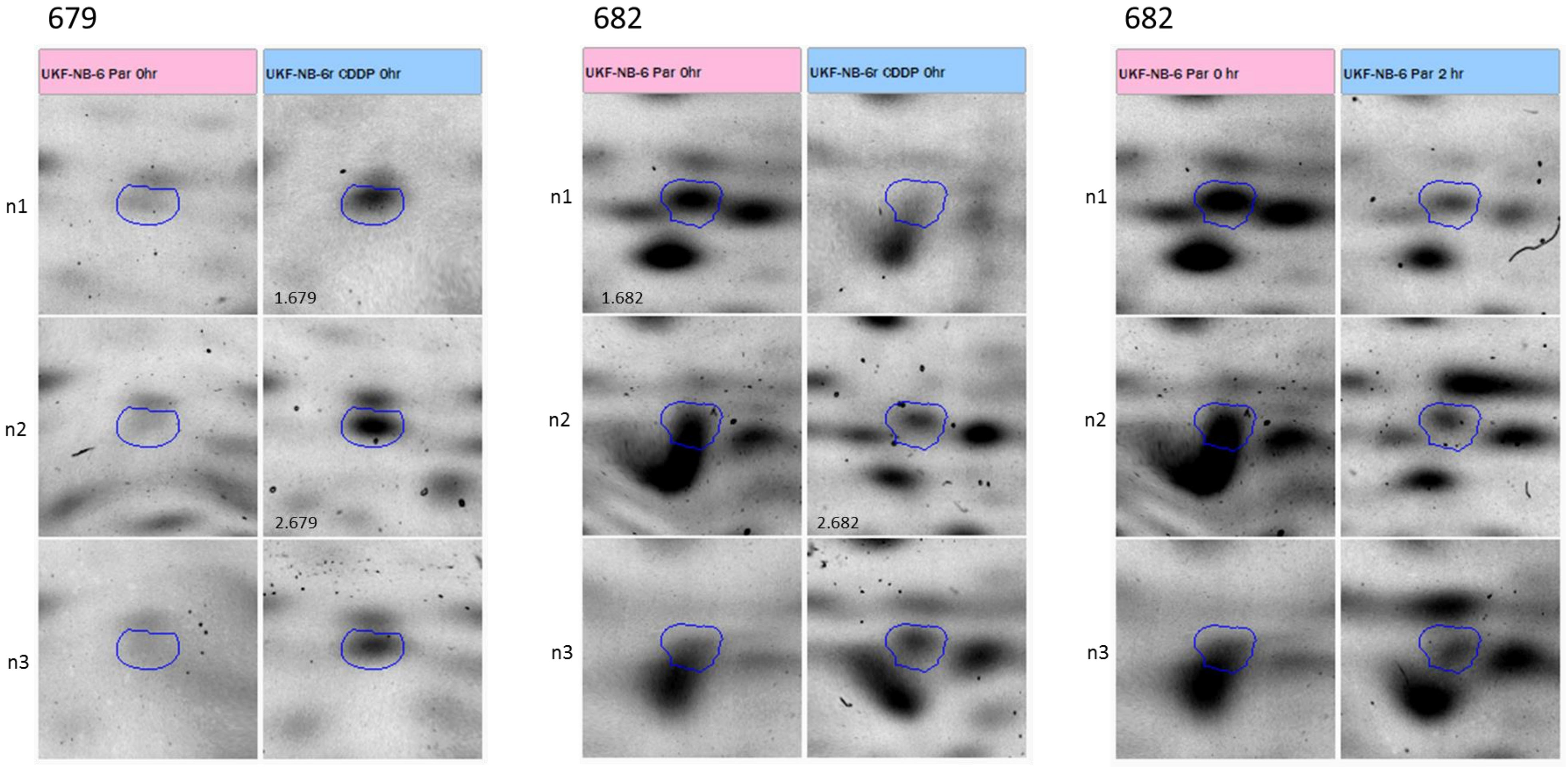
1.278 was cut out of UKF-NB-6r CDDP 0hr n2

2.278 was cut out of UKF-NB-6r CDDP 0hr n3

323

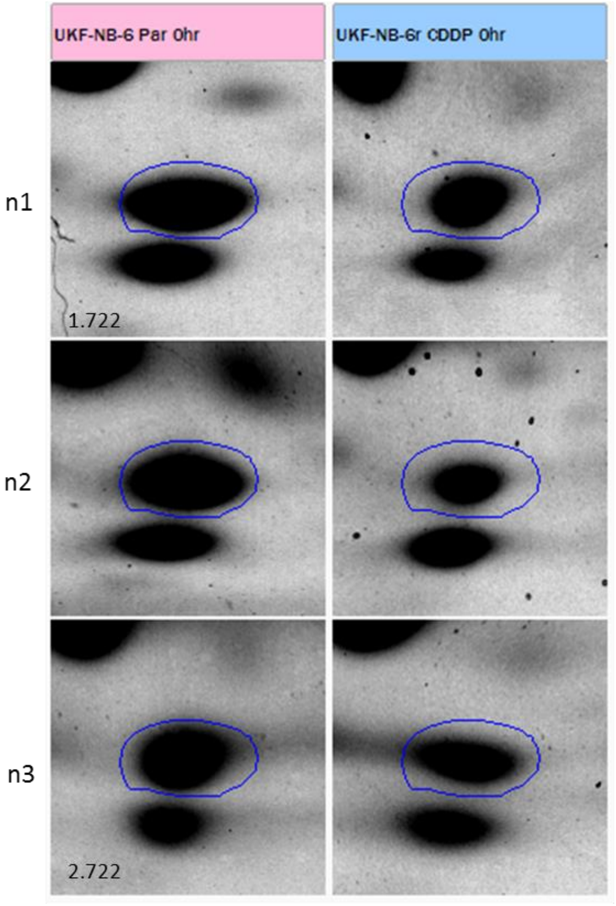


L. continued

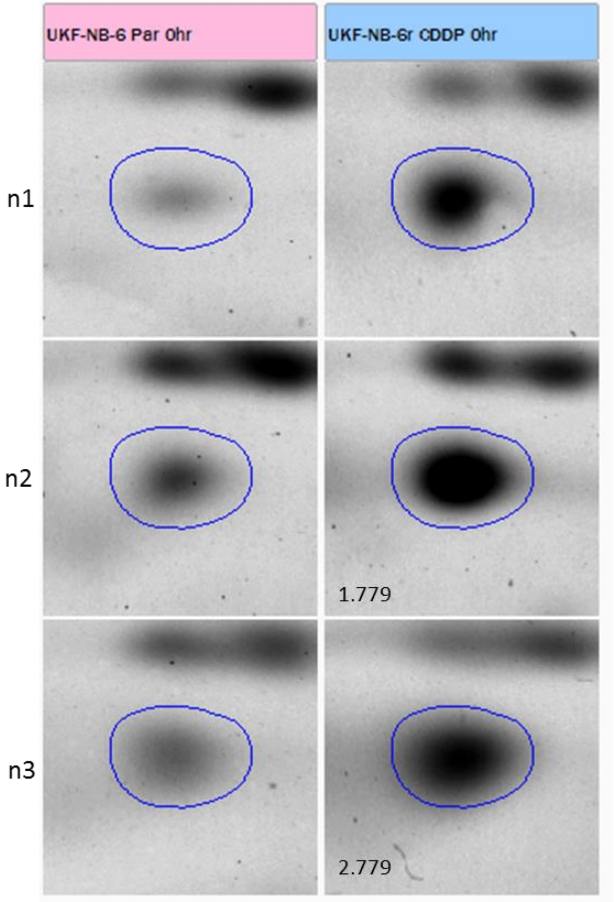

679
UKF-NB-6 Par 0hr
UKF-NB-6r CDDP 0hr
n1
n2
n3
1.679
2.679
682
UKF-NB-6 Par 0hr
UKF-NB-6r CDDP 0hr
n1
n2
n3
1.682
2.682
682
UKF-NB-6 Par 0 hr
UKF-NB-6 Par 2 hr
n1
n2
n3

L. continued

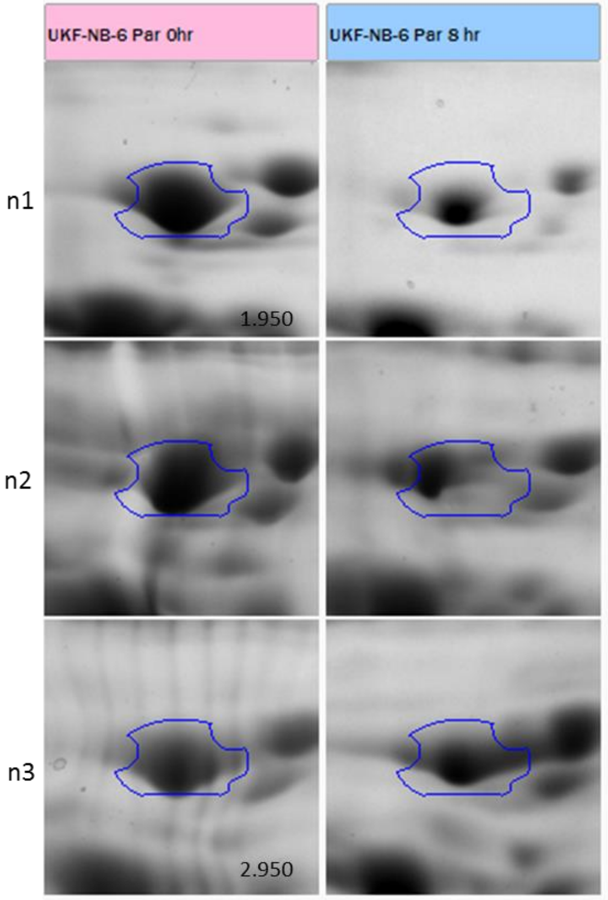
722



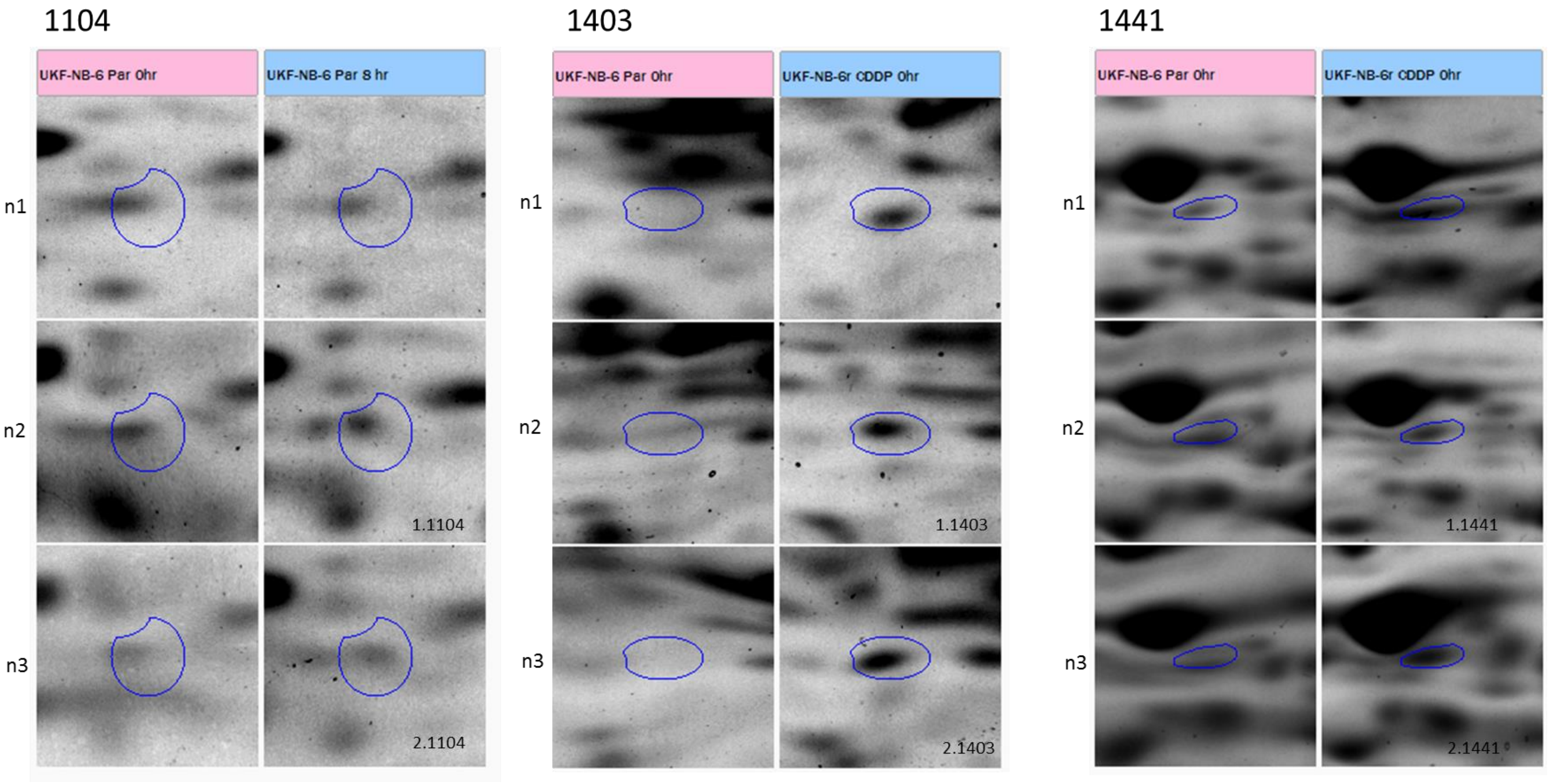
779



950

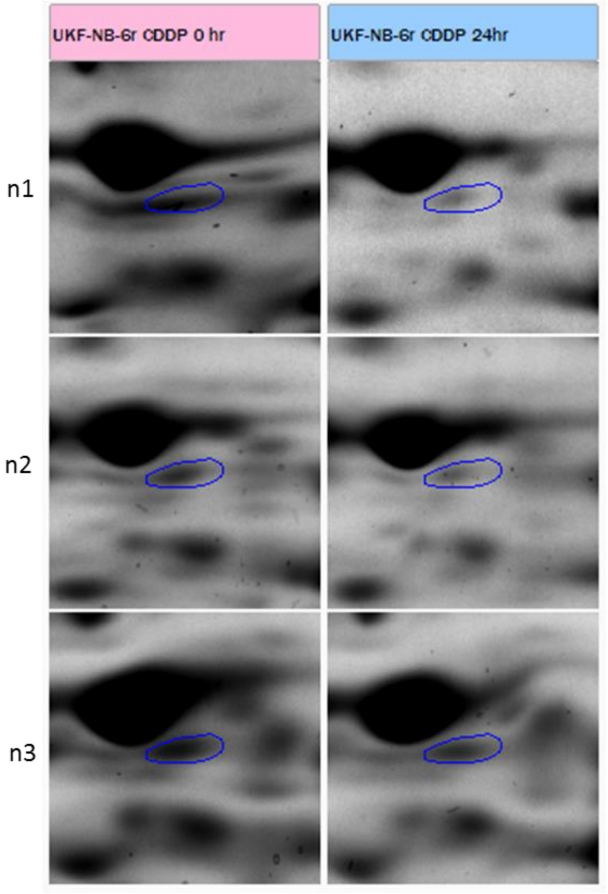


L. continued

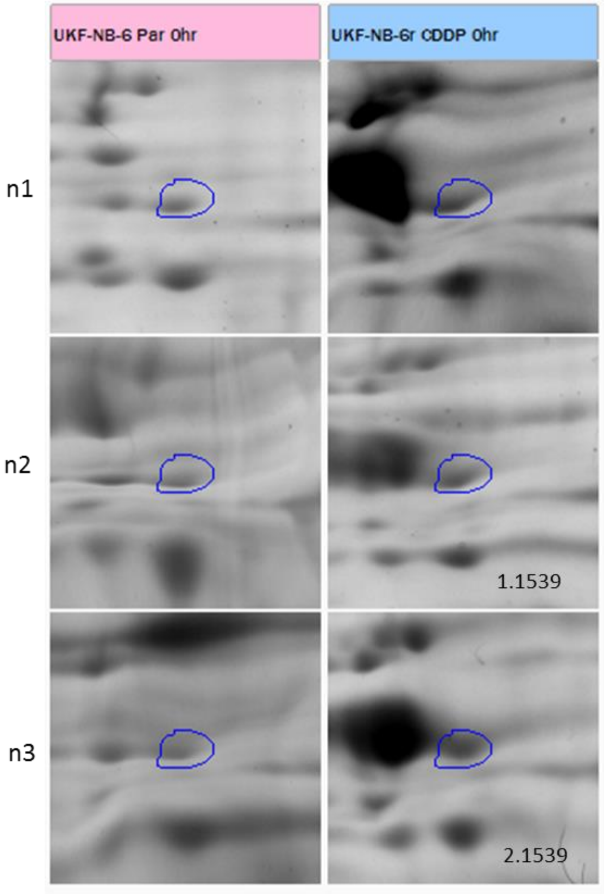

1104
UKF-NB-6 Par 0hr
UKF-NB-6 Par 8 hr
n1
n2
n3
1.1104
2.1104
1403
UKF-NB-6 Par 0hr
UKF-NB-6r CDDP 0hr
n1
n2
n3
1.1403
2.1403
1441
UKF-NB-6 Par 0hr
UKF-NB-6r CDDP 0hr
n1
n2
n3
1.1441
2.1441

L. continued

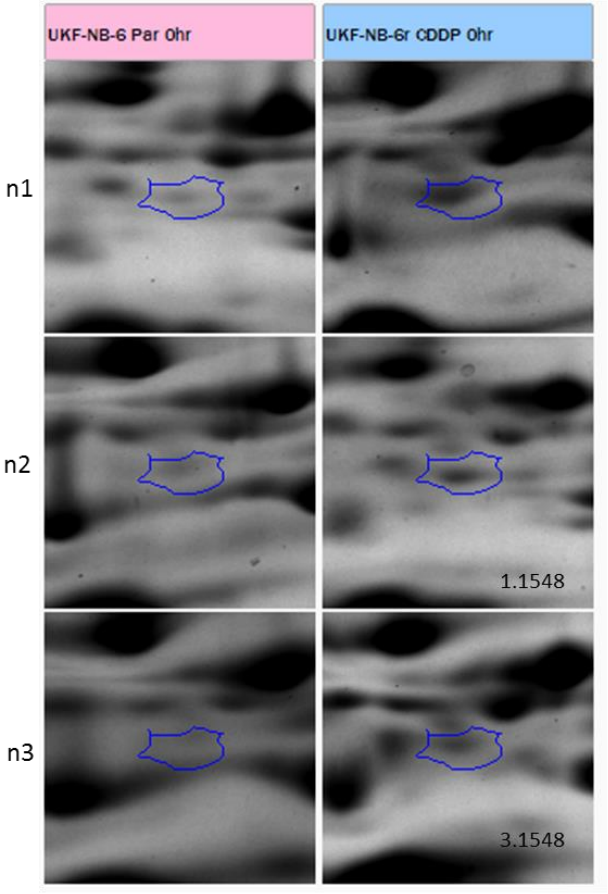
1441



1539

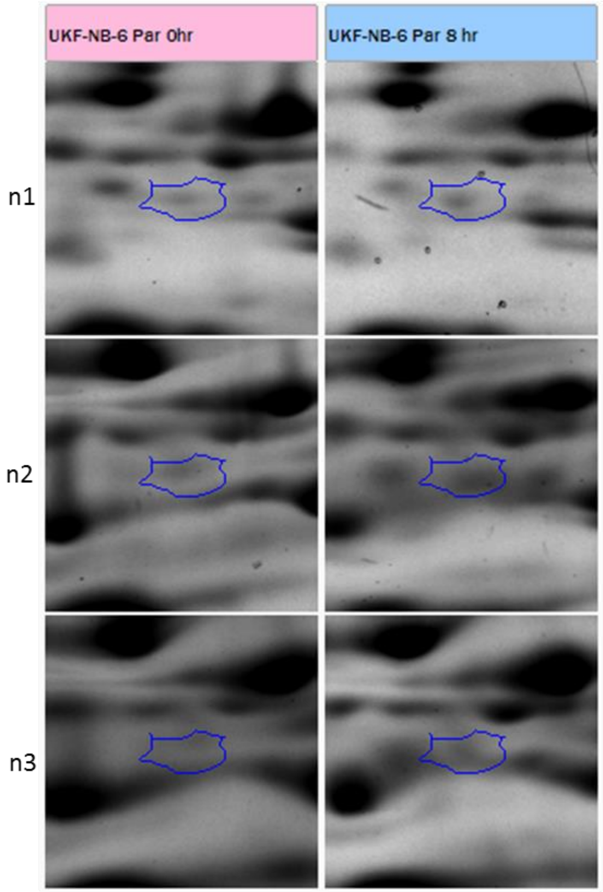


1548



L. continued

1548



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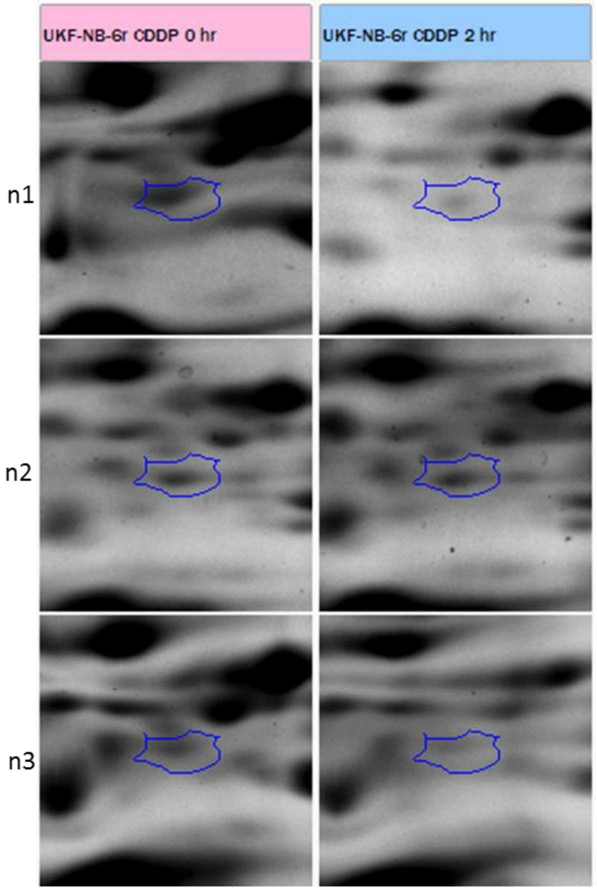
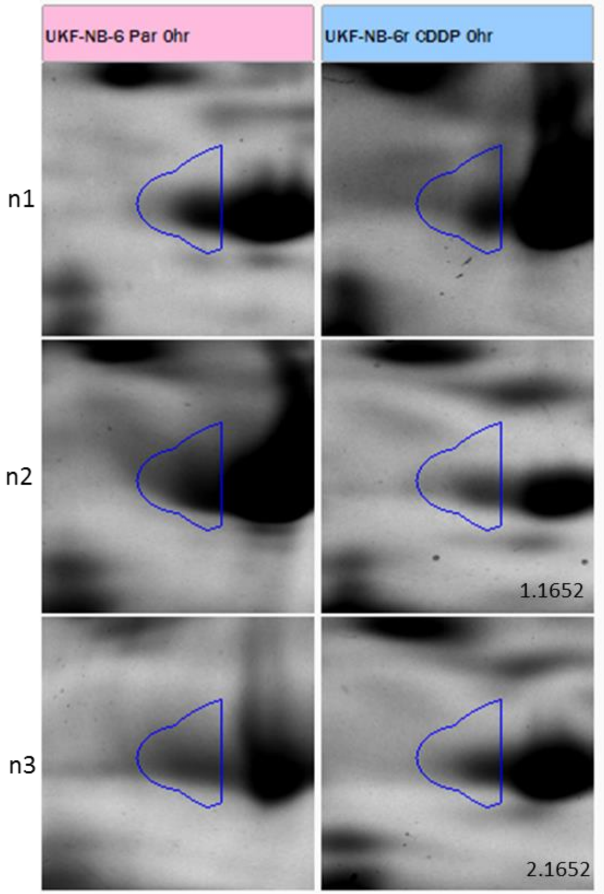


1652



M. Table of normalised spot volumes (to complement Table 15 of the thesis) generated by the Progenesis Samespots software for the twenty UKF-NB-3 study spots that were definitely identified, in each experiment comparison that they were a hit. Individual values are shown along with corresponding means and standard deviations (red text). When the Progenesis Samespots software produces a Fold value it is the highest mean normalised spot volume of the comparison over the lowest mean normalised spot volume, so a fold increase. Here fold change ratios of expression have been calculated (blue text) of both the mean normalised spot volume of the parental lines over that of the cisplatin resistant lines (a/b) and vice versa (b/a). However for our purposes we focussed on the fold change ratios of the mean normalised spot volume of the cisplatin resistant lines over that of the parental lines.

Normalized Spot Volumes											
UKF-NB-3 Parentals 0hr					UKF-NB-3^{r}CDDP^{1000} 0hr					Fold change ratio (a/b)	Fold change ratio (b/a)
3rd run	5th run	4th run	Mean^{a}	STDEV	3rd run	5th run	4th run	Mean^{b}	STDEV		
68149	63585	43583	58439	13067	26865	28354	30698	28639	1932	2.04	0.49
100667	126999	88802	105489	19550	51656	72282	47451	57129	13290	1.85	0.54
62206	91158	49975	67780	21150	36427	43046	38257	39243	3418	1.73	0.58
24357	21478	27186	24340	2854	14508	14527	13658	14231	496	1.71	0.58
17998	16446	13011	15819	2552	12273	7776	8311	9453	2456	1.67	0.60
38175	51220	30743	40046	10366	86835	119597	120876	109103	19295	0.37	2.72
12046	18911	20283	17080	4413	31175	47232	36438	38282	8186	0.45	2.24
38030	33155	40131	37105	3579	75884	56928	97644	76819	20374	0.48	2.07
155512	112007	100694	122738	28942	259116	305397	205112	256542	50192	0.48	2.09
9673	6367	4933	6991	2431	14886	12468	13177	13510	1243	0.52	1.93
119303	136005	131231	128846	8603	207256	227442	230020	221573	12466	0.58	1.72
206209	229257	324218	253228	62550	384095	383340	371874	379770	6849	0.67	1.50
21739	22971	18259	20990	2443	29613	37989	28648	32083	5137	0.65	1.53
UKF-NB-3 Parentals 0hr					UKF-NB-3 Parentals 2hr						
-	3721	3505	3613	153	-	6055	5981	6018	53	0.60	1.67
UKF-NB-3 Parentals 0hr					UKF-NB-3 Parentals 8hr						
155512	112007	100694	122738	28942	207684	178753	204874	197104	15954	0.62	1.61
UKF-NB-3 Parentals 0hr					UKF-NB-3 Parentals 24hr						
54556	43557	60624	52912	8652	91292	70821	79016	80376	10303	0.66	1.52
UKF-NB-3^{r}CDDP^{1000} 0hr					UKF-NB-3^{r}CDDP^{1000} 2hr						
-	8141	7504	7823	450	-	11690	13092	12391	992	0.63	1.58
-	35487	33016	34252	1747	-	50868	59391	55129	6027	0.62	1.61
-	46937	56250	51593	6585	-	78238	81365	79801	2211	0.65	1.55
-	23870	23058	23464	574	-	37193	35286	36239	1348	0.65	1.54
UKF-NB-3^{r}CDDP^{1000} 0hr					UKF-NB-3^{r}CDDP^{1000} 24hr						
25755	15159	17340	19418	5595	6107	10018	8041	8055	1956	2.41	0.41
75884	56928	97644	76819	20374	49161	31823	41391	40792	8684	1.88	0.53

N. Table of normalised spot volumes (to complement Table 16 of the thesis) generated by the Progenesis Samespots software for the fourteen UKF-NB-6 study spots that were definitely identified, in each experiment comparison that they were a hit. Individual values are shown along with corresponding means and standard deviations (red text). When the Progenesis Samespots software produces a Fold value it is the highest mean normalised spot volume of the comparison over the lowest mean normalised spot volume, so a fold increase. Here fold change ratios of expression have been calculated (blue text) of both the mean normalised spot volume of the parental lines over that of the cisplatin resistant lines (a/b) and vice versa (b/a). However for our purposes we focussed on the fold change ratios of the mean normalised spot volume of the cisplatin resistant lines over that of the parental lines.

	Normalized Spot Volumes											
	UKF-NB-6 Parentals 0hr					UKF-NB-6^{r}CDDP^{2000} 0hr					Fold change ratio (a/b)	Fold change ratio (b/a)
Spot #	n1	n2	n3	Mean^a	STDEV	n1	n2	n3	Mean^b	STDEV		
323	61638	52256	68005	60633	7922	32963	31542	38132	34212	3468	1.77	0.56
722	196231	161075	138728	165345	28988	114944	79458	93249	95884	17889	1.72	0.58
682	31078	32731	26310	30040	3334	18339	20377	19301	19339	1020	1.55	0.64
1652	100838	121427	120562	114276	11645	89207	66431	72181	75940	11844	1.50	0.66
679	11757	7946	10960	10221	2010	21354	27900	22669	23974	3463	0.43	2.35
779	50977	91476	103350	81934	27459	143880	231029	176793	183901	44007	0.45	2.24
1403	14331	12788	13577	13566	772	25373	27020	27877	26757	1273	0.51	1.97
1441	14955	15459	10572	13662	2688	24669	21671	26388	24243	2387	0.56	1.77
1548	11621	12941	12206	12256	661	29806	17835	19612	22418	6460	0.55	1.83
1539	19135	24643	26884	23554	3988	36853	37944	39727	38175	1450	0.62	1.62
	UKF-NB-6 Parentals 0hr					UKF-NB-6 Parentals 2hr						
163	23388	27219	33248	27952	4971	20321	12070	16979	16457	4150	1.70	0.59
682	31078	32731	26310	30040	3334	22932	21494	17686	20704	2711	1.45	0.69
	UKF-NB-6 Parentals 0hr					UKF-NB-6 Parentals 8hr						
950	316476	320236	303689	313467	8674	206188	161580	218936	195568	30117	1.60	0.62
1104	26166	27842	27867	27292	975	22270	18120	15360	18583	3478	1.47	0.68
1548	11621	12941	12206	12256	661	17536	19204	17304	18015	1036	0.68	1.47
	UKF-NB-6 Parentals 0hr					UKF-NB-6 Parentals 24hr						
278	178822	-	180287	179555	1036	123525	-	113167	118346	7324	1.52	0.66
	UKF-NB-6^{r}CDDP^{2000} 0hr					UKF-NB-6^{r}CDDP^{2000} 2hr						
1548	29806	17835	19612	22418	6460	12971	12695	10560	12075	1319	1.86	0.54
	UKF-NB-6^{r}CDDP^{2000} 0hr					UKF-NB-6^{r}CDDP^{2000} 24hr						
1441	24669	21671	26388	24243	2387	17093	13624	19361	16693	2889	1.45	0.69

O. Table of the roles of the twenty identified spots/protein (in the order of appearance in Table 15 of the thesis) for the UKF-NB-3 study, and also the Gene Ontology (GO) molecular function, biological process and cellular component terms that they are matched to (excluding those inferred by electronic annotation). All of this information was taken from the UniProt website (www.uniprot.org) on 10/02/16. Spots were identified by mass spectroscopy methods and searches against the human protein SwissProt (http://www.uniprot.org/) and NCBInr (http://www.ncbi.nlm.nih.gov/refseq/) databases.

Spot	Protein name	Role	GO - Molecular functions	GO - Biological processes	GO - Cellular components
749	Peroxiredoxin-2	Involved in redox regulation of the cell. Reduces peroxides with reducing equivalents provided through the thioredoxin system. It is not able to receive electrons from glutaredoxin. May play an important role in eliminating peroxides generated during metabolism. Might participate in the signaling cascades of growth factors and tumor necrosis factor-alpha by regulating the intracellular concentrations of $H2O2$. Catalytic activity: 2 R'-SH + ROOH = R'-S-S-R' + $H2O$ + ROH.	antioxidant activity, thioredoxin peroxidase activity	cellular response to oxidative stress, gene expression, hydrogen peroxide catabolic process, negative regulation of apoptotic process, regulation of apoptotic process, removal of superoxide radicals, response to oxidative stress, response to reactive oxygen species, transcription initiation from RNA polymerase II promoter	cytoplasm, cytosol, extracellular exosome
1369	Phosphatidylethanolamine-binding protein 1 / Neuropolypeptide h3	Binds ATP, opioids and phosphatidylethanolamine. Has lower affinity for phosphatidylinositol and phosphatidylcholine. Serine protease inhibitor which inhibits thrombin, neuropsin and chymotrypsin but not trypsin, tissue type plasminogen activator and elastase. Inhibits the kinase activity of RAF1 by inhibiting its activation and by dissociating the RAF1/MEK complex and acting as a competitive inhibitor of MEK phosphorylation. HCNP (by sequence similarity) may be involved in the function of the presynaptic cholinergic neurons of the central nervous system. HCNP increases the production of choline acetyltransferase but not acetylcholinesterase. Seems to be mediated by a specific receptor.	enzyme binding, phosphatidylethanolamine binding, poly(A) RNA binding, protein kinase binding	activation of MAPKK activity, axon guidance, epidermal growth factor receptor signaling pathway, Fc-epsilon receptor signaling pathway, fibroblast growth factor receptor signaling pathway, innate immune response, insulin receptor signaling pathway, MAPK cascade, neurotrophin TRK receptor signaling pathway, Ras protein signal transduction, small GTPase mediated signal transduction, vascular endothelial growth factor receptor signaling pathway	cytosol, extracellular exosome, nucleus
792	Stathmin	Involved in the regulation of the microtubule (MT) filament system by destabilizing microtubules. Prevents assembly and promotes disassembly of microtubules. Phosphorylation at Ser-16 may be required for axon formation during neurogenesis. Involved in the control of the learned and innate fear.	signal transducer activity, tubulin binding	intracellular signal transduction , microtubule depolymerization, mitotic spindle organization, neuron projection development, regulation of cytoskeleton organization, response to virus, signal transduction	cytoplasm, extracellular exosome, intracellular, neuron projection
978	Dihydropyrimidinase-related protein 5/Collapsin response mediator protein-5	May have a function in neuronal differentiation and/or axon growth.	-	axon guidance, nervous system development, signal transduction	cytosol

Spot	Protein name	Role	GO - Molecular functions	GO - Biological processes	GO - Cellular components
635	S-formylglutathione hydrolase /Esterase D	Serine hydrolase involved in the detoxification of formaldehyde. Catalytic activity; S-formylglutathione + H2O = glutathione + formate. Also, 4-methylumbelliferyl acetate + H2O = 4-methylumbelliferone + acetate.	carboxylic ester hydrolase activity, hydrolase activity, acting on ester bonds, S-formylglutathione hydrolase activity	glutathione derivative biosynthetic process, small molecule metabolic process, xenobiotic metabolic process	endoplasmic reticulum lumen, extracellular exosome
709 and 1659	Heat shock protein 27/Heat shock protein beta-1	Involved in stress resistance and actin organization.	identical protein binding, poly(A) RNA binding, protein kinase binding, protein kinase C binding, protein kinase C inhibitor activity, ubiquitin binding	cellular response to vascular endothelial growth factor stimulus, gene expression, intracellular signal transduction, movement of cell or subcellular component, negative regulation of apoptotic process, negative regulation of oxidative stress-induced intrinsic apoptotic signaling pathway, negative regulation of protein kinase activity, platelet aggregation, positive regulation of angiogenesis, positive regulation of blood vessel endothelial cell migration, positive regulation of endothelial cell chemotaxis, positive regulation of endothelial cell chemotaxis by VEGF-activated vascular endothelial growth factor receptor signaling pathway, positive regulation of interleukin-1 beta production, positive regulation of tumor necrosis factor biosynthetic process, regulation of I-kappaB kinase/NF-kappaB signaling, regulation of mRNA stability, regulation of translational initiation, response to unfolded protein, response to virus, retina homeostasis, vascular endothelial growth factor receptor signaling pathway	cytoplasm, cytoskeleton, cytosol, extracellular exosome, extracellular space, focal adhesion, nucleus, proteasome complex
1719	Lactate dehydrogenase	Catalytic activity -(S)-lactate + NAD+ = pyruvate + NADH. Pathway: pyruvate fermentation to lactate. This protein is involved in step 1 of the subpathway that synthesizes (S)-lactate from pyruvate. This subpathway is part of the pathway pyruvate fermentation to lactate, which is itself part of Fermentation.	L-lactate dehydrogenase activity	cellular metabolic process, glycolytic process, pyruvate metabolic process, small molecule metabolic process, substantia nigra development	cytosol, extracellular exosome, membrane, nucleus

Spot	Protein name	Role	GO - Molecular functions	GO - Biological processes	GO - Cellular components
1276	Nucleophosmin	Involved in diverse cellular processes such as ribosome biogenesis, centrosome duplication, protein chaperoning, histone assembly, cell proliferation, and regulation of tumor suppressors p53/TP53 and ARF. Binds ribosome presumably to drive ribosome nuclear export. Associated with nucleolar ribonucleoprotein structures and bind single-stranded nucleic acids. Acts as a chaperonin for the core histones H3, H2B and H4. Stimulates APEX1 endonuclease activity on apurinic/apyrimidinic (AP) double-stranded DNA but inhibits APEX1 endonuclease activity on AP single-stranded RNA. May exert a control of APEX1 endonuclease activity within nucleoli devoted to repair AP on rDNA and the removal of oxidized rRNA molecules. In concert with BRCA2, regulates centrosome duplication. Regulates centriole duplication: phosphorylation by PLK2 is able to trigger centriole replication. Negatively regulates the activation of EIF2AK2/PKR and suppresses apoptosis through inhibition of EIF2AK2/PKR autophosphorylation. Antagonizes the inhibitory effect of ATF5 on cell proliferation and relieves ATF5-induced G2/M blockade.	histone binding, NF-kappaB binding, poly(A) RNA binding, protein heterodimerization activity, protein homodimerization activity, protein kinase binding, protein kinase inhibitor activity, ribosomal large subunit binding, ribosomal small subunit binding, RNA binding, Tat protein binding, transcription coactivator activity, unfolded protein binding	cell aging, CENP-A containing nucleosome assembly, centrosome cycle, DNA repair, intracellular protein transport, negative regulation of apoptotic process, negative regulation of cell proliferation, negative regulation of centrosome duplication, negative regulation of cyclin-dependent protein kinase activity, negative regulation of protein kinase activity by regulation of protein phosphorylation, nucleocytoplasmic transport, nucleosome assembly, positive regulation of cell cycle G2/M phase transition, positive regulation of cell proliferation, positive regulation of NF-kappaB transcription factor activity, positive regulation of transcription, DNA-templated, positive regulation of translation, protein localization, protein oligomerization, regulation of centriole replication, regulation of eIF2 alpha phosphorylation by dsRNA, regulation of endodeoxyribonuclease activity, regulation of endoribonuclease activity, response to stress, ribosome assembly, signal transduction, viral process	centrosome, cytoplasm, cytosol, focal adhesion, membrane, nucleolus, nucleoplasm, nucleus, ribonucleoprotein complex, spindle pole centrosome

Spot	Protein name	Role	GO - Molecular functions	GO - Biological processes	GO - Cellular components
1571	Eukaryotic initiation factor 4A-III/Translation initiation factor	ATP-dependent RNA helicase. Core component of the splicing-dependent multiprotein exon junction complex (EJC) deposited at splice junctions on mRNAs. The EJC is a dynamic structure consisting of core proteins and several peripheral nuclear and cytoplasmic associated factors that join the complex only transiently either during EJC assembly or during subsequent mRNA metabolism. The EJC marks the position of the exon-exon junction in the mature mRNA for the gene expression machinery and the core components remain bound to spliced mRNAs throughout all stages of mRNA metabolism thereby influencing downstream processes including nuclear mRNA export, subcellular mRNA localization, translation efficiency and nonsense-mediated mRNA decay (NMD). Its RNA-dependent ATPase and RNA-helicase activities are induced by CASC3, but abolished in presence of the MAGOH-RBM8A heterodimer, thereby trapping the ATP-bound EJC core onto spliced mRNA in a stable conformation. The inhibition of ATPase activity by the MAGOH-RBM8A heterodimer increases the RNA-binding affinity of the EJC. Involved in translational enhancement of spliced mRNAs after formation of the 80S ribosome complex. Binds spliced mRNA in sequence-independent manner, 20-24 nucleotides upstream of mRNA exon-exon junctions. Shows higher affinity for single-stranded RNA in an ATP-bound core EJC complex than after the ATP is hydrolyzed. Involved in the splicing modulation of BCL2L1/Bcl-X (and probably other apoptotic genes); specifically inhibits formation of proapoptotic isoforms such as Bcl-X(S); the function is different from the established EJC assembly. Involved in craniofacial development. Catalytic activity; ATP + H2O = ADP + phosphate. Enzyme regulation; The ATPase activity is increased some 4-fold in the presence of RNA.	ATP binding, ATP-dependent RNA helicase activity, mRNA binding, poly(A) binding, poly(A) RNA binding	cytokine-mediated signaling pathway, embryonic cranial skeleton morphogenesis, gene expression, mRNA splicing, via spliceosome, negative regulation of translation, nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay, nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, nuclear-transcribed mRNA poly(A) tail shortening, positive regulation of translation, RNA secondary structure unwinding, RNA splicing	catalytic step 2 spliceosome, cytoplasm, cytosol, exon-exon junction complex, membrane, nucleoplasm
1583	Phosphoglycerate kinase 1	In addition to its role as a glycolytic enzyme, it seems that PGK-1 acts as a polymerase alpha cofactor protein (primer recognition protein).Catalytic activity: ATP + 3-phospho-D-glycerate = ADP + 3-phospho-D-glyceroyl phosphate. Pathway: glycolysis This protein is involved in step 2 of the subpathway that synthesizes pyruvate from D-glyceraldehyde 3-phosphate.	ATP binding, phosphoglycerate kinase activity	canonical glycolysis, carbohydrate metabolic process, epithelial cell differentiation, gluconeogenesis, glucose metabolic process, phosphorylation, small molecule metabolic process	cytosol, extracellular exosome, membrane, membrane raft

Spot	Protein name	Role	GO - Molecular functions	GO - Biological processes	GO - Cellular components
901	60 kDa heat shock protein, mitochondrial	Implicated in mitochondrial protein import and macromolecular assembly. May facilitate the correct folding of imported proteins. May also prevent misfolding and promote the refolding and proper assembly of unfolded polypeptides generated under stress conditions in the mitochondrial matrix.	ATPase activity, chaperone binding, DNA replication origin binding, double-stranded RNA binding, lipopolysaccharide binding, p53 binding, poly(A) RNA binding, single-stranded DNA binding, ubiquitin protein ligase binding, unfolded protein binding	'de novo' protein folding, activation of cysteine-type endopeptidase activity involved in apoptotic process, B cell activation, B cell cytokine production, B cell proliferation, chaperone-mediated protein complex assembly, isotype switching to IgG isotypes, MyD88-dependent toll-like receptor signaling pathway, negative regulation of apoptotic process, positive regulation of apoptotic process, positive regulation of interferon-alpha production, positive regulation of interferon-gamma production, positive regulation of interleukin-10 production, positive regulation of interleukin-12 production, positive regulation of interleukin-6 productionL, positive regulation of macrophage activation, positive regulation of T cell activation, positive regulation of T cell mediated immune response to tumor cell, protein maturation, protein refolding, protein stabilization, response to cold, response to unfolded protein, T cell activation	cell surface, coated pit, coated vesicle, cytoplasm, cytosol, early endosome, extracellular exosome, extracellular space, lipopolysaccharide receptor complex, membrane, mitochondrial inner membrane, mitochondrial matrix, mitochondrion, protein complex, secretory granule
1121	D-3-phosphoglycerate dehydrogenase	Catalytic activity: 3-phospho-D-glycerate + NAD+ = 3-phosphonooxypyruvate + NADH. Also 2-hydroxyglutarate + NAD+ = 2-oxoglutarate + NADH Pathway: L-serine biosynthesis; This protein is involved in step 1 of the subpathway that synthesizes L-serine from 3-phospho-D-glycerate.	electron carrier activity, phosphoglycerate dehydrogenase activity	brain development, cellular amino acid biosynthetic process, cellular nitrogen compound metabolic process, L-serine biosynthetic process, serine family amino acid biosynthetic process, small molecule metabolic process	cytosol, extracellular exosome

Spot	Protein name	Role	GO - Molecular functions	GO - Biological processes	GO - Cellular components
1084	RuvB-like 2	Possesses single-stranded DNA-stimulated ATPase and ATP-dependent DNA helicase (5' to 3') activity; hexamerization is thought to be critical for ATP hydrolysis and adjacent subunits in the ring-like structure contribute to the ATPase activity. Component of the NuA4 histone acetyltransferase complex which is involved in transcriptional activation of select genes principally by acetylation of nucleosomal histones H4 and H2A. This modification may both alter nucleosome - DNA interactions and promote interaction of the modified histones with other proteins which positively regulate transcription. This complex may be required for the activation of transcriptional programs associated with oncogene and proto-oncogene mediated growth induction, tumor suppressor mediated growth arrest and replicative senescence, apoptosis, and DNA repair. The NuA4 complex ATPase and helicase activities seem to be, at least in part, contributed by the association of RUVBL1 and RUVBL2 with EP400. NuA4 may also play a direct role in DNA repair when recruited to sites of DNA damage. Component of a SWR1-like complex that specifically mediates the removal of histone H2A.Z/H2AFZ from the nucleosome. Proposed core component of the chromatin remodeling INO80 complex which is involved in transcriptional regulation, DNA replication and probably DNA repair. Plays an essential role in oncogenic transformation by MYC and also modulates transcriptional activation by the LEF1/TCF1-CTNNB1 complex. May also inhibit the transcriptional activity of ATF2. Involved in the endoplasmic reticulum (ER)-associated degradation (ERAD) pathway where it negatively regulates expression of ER stress response genes. Catalytic activity; ATP + H2O = ADP + phosphate.	ATP-dependent DNA helicase activity, chromatin DNA binding, DNA helicase activity, identical protein binding, RNA polymerase II core promoter sequence-specific DNA binding, RNA polymerase II distal enhancer sequence-specific DNA binding, unfolded protein binding	cellular response to estradiol stimulus, cellular response to UV, chromatin organization, chromatin remodeling, DNA duplex unwinding, DNA recombination, DNA repair, establishment of protein localization to chromatin, histone H2A acetylation, histone H4 acetylation, negative regulation of estrogen receptor binding, positive regulation of histone acetylation, positive regulation of transcription from RNA polymerase II promoter, protein folding, transcriptional activation by promoter-enhancer looping	cytoplasm, extracellular exosome, Ino80 complex, intracellular, MLL1 complex, NuA4 histone acetyltransferase complex, nuclear euchromatin, nucleoplasm, nucleus, Swr1 complex
449	ATP synthase subunit beta, mitochondrial (ATPB) (56000)	Mitochondrial membrane ATP synthase (F1F0 ATP synthase or Complex V) produces ATP from ADP in the presence of a proton gradient across the membrane which is generated by electron transport complexes of the respiratory chain. F-type ATPases consist of two structural domains, F1 - containing the extramembraneous catalytic core, and F0 - containing the membrane proton channel, linked together by a central stalk and a peripheral stalk. During catalysis, ATP synthesis in the catalytic domain of F1 is coupled via a rotary mechanism of the central stalk subunits to proton translocation. Subunits alpha and beta form the catalytic core in F1. Rotation of the central stalk against the surrounding alpha3beta3 subunits leads to hydrolysis of ATP in three separate catalytic sites on the beta subunits. Catalytic activity ATP + H2O + H+(In) = ADP + phosphate + H+(Out).	MHC class I protein binding proton-transporting ATPase activity, rotational mechanism transmembrane transporter activity transporter activity	angiogenesis, ATP biosynthetic process, cellular metabolic process, generation of precursor metabolites and energy, mitochondrial ATP synthesis coupled proton transport, mitochondrion organization, organelle organization, osteoblast differentiation, proton transport, regulation of intracellular pH, respiratory electron transport chain, small molecule metabolic process	cell surface, extracellular exosome, membrane, mitochondrial matrix, mitochondrial membrane, mitochondrial nucleoid, mitochondrial proton-transporting ATP synthase, catalytic core, mitochondrial proton-transporting ATP synthase complex, mitochondrion, nucleus, plasma membrane

Spot	Protein name	Role	GO - Molecular functions	GO - Biological processes	GO - Cellular components
1576	26S protease regulatory subunit 8 isoform 2/Thyroid receptor interactor	The 26S protease is involved in the ATP-dependent degradation of ubiquitinated proteins. The regulatory (or ATPase) complex confers ATP dependency and substrate specificity to the 26S complex.	ATPase activity, proteasome-activating ATPase activity, TBP-class protein binding, thyrotropin-releasing hormone receptor binding, transcription cofactor activity, transcription factor binding	activation of MAPKK activity, anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process, antigen processing and presentation of exogenous peptide antigen via MHC class I, antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent, antigen processing and presentation of peptide antigen via MHC class I, apoptotic process, axon guidance, cellular nitrogen compound metabolic process, DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest, epidermal growth factor receptor signaling pathway, ER-associated ubiquitin-dependent protein catabolic process, Fc-epsilon receptor signaling pathway, fibroblast growth factor receptor signaling pathway, G1/S transition of mitotic cell cycle, gene expression, innate immune response, insulin receptor signaling pathway, MAPK cascade, mitotic cell cycle, negative regulation of apoptotic process, negative regulation of canonical Wnt signaling pathway, negative regulation of programmed cell death, negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle, neurotrophin TRK receptor signaling pathway, NIK/NF-kappaB signaling, polyamine metabolic process, positive regulation of canonical Wnt signaling pathway, positive regulation of proteasomal protein catabolic process, positive regulation of RNA polymerase II transcriptional preinitiation complex assembly, positive regulation of transcription, DNA-templated, positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle transition, programmed cell death, proteasome-mediated ubiquitin-dependent protein catabolic process, protein polyubiquitination, Ras protein signal transduction, regulation of apoptotic process, regulation of cellular amino acid metabolic process, regulation of mRNA stability, regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle, small GTPase mediated signal transduction, small molecule metabolic process, stimulatory C-type lectin receptor signaling pathway, T cell receptor signaling pathway, transcription from RNA polymerase II promoter, tumor necrosis factor-mediated signaling pathway, vascular endothelial growth factor receptor signaling pathway, viral process	blood microparticle, cytoplasm, cytoplasmic vesicle, cytosol, cytosolic proteasome complex, extracellular exosome, membrane, nuclear proteasome complex, nucleoplasm, nucleus, proteasome accessory complex, proteasome complex, proteasome regulatory particle, base subcomplex

Spot	Protein name	Role	GO - Molecular functions	GO - Biological processes	GO - Cellular components
637	Voltage-dependent anion-selective channel protein 2	Forms a channel through the mitochondrial outer membrane that allows diffusion of small hydrophilic molecules. The channel adopts an open conformation at low or zero membrane potential and a closed conformation at potentials above 30-40 mV. The open state has a weak anion selectivity whereas the closed state is cation-selective.	voltage-gated anion channel activity	anion transport, regulation of anion transmembrane transport	extracellular exosome, membrane raft, mitochondrial nucleoid, mitochondrion, nucleus
1284	Guanine nucleotide-binding protein subunit beta-2-like 1	Involved in the recruitment, assembly and/or regulation of a variety of signaling molecules. Interacts with a wide variety of proteins and plays a role in many cellular processes. Component of the 40S ribosomal subunit involved in translational repression. Binds to and stabilizes activated protein kinase C (PKC), increasing PKC-mediated phosphorylation. May recruit activated PKC to the ribosome, leading to phosphorylation of EIF6. Inhibits the activity of SRC kinases including SRC, LCK and YES1. Inhibits cell growth by prolonging the G0/G1 phase of the cell cycle. Enhances phosphorylation of BMAL1 by PRKCA and inhibits transcriptional activity of the BMAL1-CLOCK heterodimer. Facilitates ligand-independent nuclear translocation of AR following PKC activation, represses AR transactivation activity and is required for phosphorylation of AR by SRC. Modulates IGF1R-dependent integrin signaling and promotes cell spreading and contact with the extracellular matrix. Involved in PKC-dependent translocation of ADAM12 to the cell membrane. Promotes the ubiquitination and proteasome-mediated degradation of proteins such as CLEC1B and HIF1A. Required for VANGL2 membrane localization, inhibits Wnt signaling, and regulates cellular polarization and oriented cell division during gastrulation. Required for PTK2/FAK1 phosphorylation and dephosphorylation. Regulates internalization of the muscarinic receptor CHRM2. Promotes apoptosis by increasing oligomerization of BAX and disrupting the interaction of BAX with the anti-apoptotic factor BCL2L. Inhibits TRPM6 channel activity. Regulates cell surface expression of some GPCRs such as TBXA2R. Plays a role in regulation of FLT1-mediated cell migration. Involved in the transport of ABCB4 from the Golgi to the apical bile canalicular membrane (PubMed:19674157). Binds to Y.pseudotuberculosis yopK which leads to inhibition of phagocytosis and survival of bacteria following infection of host cells. Enhances phosphorylation of HIV-1 Nef by PKCs. Promotes migration of breast carcinoma cells by binding to and activating RHOA	cysteine-type endopeptidase activator activity involved in apoptotic process, enzyme binding, ion channel inhibitor activity, poly(A) RNA binding, protein complex scaffold, protein homodimerization activity, protein kinase C binding, protein phosphatase binding, protein tyrosine kinase inhibitor activity, receptor binding, receptor tyrosine kinase binding, SH2 domain binding, signaling adaptor activity	activation of cysteine-type endopeptidase activity involved in apoptotic process, cell surface receptor signaling pathway, cellular response to glucose stimulus, cellular response to growth factor stimulus, negative regulation of cell growth, negative regulation of endoplasmic reticulum unfolded protein response, negative regulation of gene expression, negative regulation of hydrogen peroxide-induced neuron death, negative regulation of peptidyl-serine phosphorylation, negative regulation of phagocytosis, negative regulation of protein kinase B signaling, negative regulation of protein tyrosine kinase activity, negative regulation of translation, negative regulation of Wnt signaling pathway, positive regulation of apoptotic process, positive regulation of cAMP catabolic process, positive regulation of cell migration, positive regulation of ceramide biosynthetic process, positive regulation of cyclic-nucleotide phosphodiesterase activity, positive regulation of gastrulation, positive regulation of Golgi to plasma membrane protein transport, positive regulation of GTPase activity, positive regulation of intrinsic apoptotic signaling pathway, positive regulation of mitochondrial depolarization, positive regulation of proteasomal ubiquitin-dependent protein catabolic process, positive regulation of protein homooligomerization, positive regulation of protein phosphorylation, regulation of cell cycle, regulation of cell division, regulation of establishment of cell polarity, regulation of protein localization, regulation of tumor necrosis factor-mediated signaling pathway, tumor necrosis factor-mediated signaling pathway	cytoplasm, cytosol, dendrite, extracellular exosome, IRE1-RACK1-PP2A complex, midbody, mitochondrion, neuronal cell body, nucleus, perinuclear region of cytoplasm, phagocytic cup, small ribosomal subunit

Spot	Protein name	Role	GO - Molecular functions	GO - Biological processes	GO - Cellular components
1252	26S protease regulatory subunit 10B /Proteasome subunit p42	The 26S protease is involved in the ATP-dependent degradation of ubiquitinated proteins. The regulatory (or ATPase) complex confers ATP dependency and substrate specificity to the 26S complex.	ATPase activity, proteasome-activating ATPase activity, protein binding, bridging, TBP-class protein binding	activation of MAPKK activity, anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process, antigen processing and presentation of exogenous peptide antigen via MHC class I, antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent, antigen processing and presentation of peptide antigen via MHC class I, apoptotic process, axon guidance, cellular nitrogen compound metabolic process, DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest, epidermal growth factor receptor signaling pathway, ER-associated ubiquitin-dependent protein catabolic process, Fc-epsilon receptor signaling pathway, fibroblast growth factor receptor signaling pathway, G1/S transition of mitotic cell cycle, gene expression, innate immune response, insulin receptor signaling pathway, MAPK cascade, mitotic cell cycle, negative regulation of apoptotic process, negative regulation of canonical Wnt signaling pathway, negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle, neurotrophin TRK receptor signaling pathway, NIK/NF-kappaB signaling, polyamine metabolic process, positive regulation of canonical Wnt signaling pathway, positive regulation of proteasomal protein catabolic process, positive regulation of RNA polymerase II transcriptional preinitiation complex assembly, positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle transition, programmed cell death, protein polyubiquitination, Ras protein signal transduction, regulation of apoptotic process, regulation of cellular amino acid metabolic process, regulation of mRNA stability, regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle, small GTPase mediated signal transduction, small molecule metabolic process, stimulatory C-type lectin receptor signaling pathway, T cell receptor signaling pathway, tumor necrosis factor-mediated signaling pathway, ubiquitin-dependent protein catabolic process, vascular endothelial growth factor receptor signaling pathway, viral process	cytosol, cytosolic proteasome complex, extracellular exosome, membrane, nuclear proteasome complex, nucleoplasm, nucleus, proteasome accessory complex, proteasome complex, proteasome regulatory particle, base subcomplex
1002	Elongation factor 2	Catalyzes the GTP-dependent ribosomal translocation step during translation elongation. During this step, the ribosome changes from the pre-translocational (PRE) to the post-translocational (POST) state as the newly formed A-site-bound peptidyl-tRNA and P-site-bound deacylated tRNA move to the P and E sites, respectively. Catalyzes the coordinated movement of the two tRNA molecules, the mRNA and conformational changes in the ribosome.	GTPase activity, poly(A) RNA binding, protein kinase binding, translation elongation factor activity	cellular protein metabolic process, gene expression, peptidyl-diphthamide biosynthetic process from peptidyl-histidine, positive regulation of translation, post-translational protein modification, translation, translational elongation	aggresome, cytoplasm, cytosol, extracellular exosome, membrane, nucleus, plasma membrane, ribonucleoprotein complex

P. Table of the roles of the fourteen identified spots/protein (in the order of appearance in Table 16 of the thesis) for the UKF-NB-6 study, and also the Gene Ontology (GO) molecular function, biological process and cellular component terms that they are matched to (excluding those inferred by electronic annotation). All of this information was taken from the UniProt website (www.uniprot.org) on 10/02/16. Spots were identified by mass spectroscopy methods and searches against the human protein SwissProt (http://www.uniprot.org/) and NCBInr (http://www.ncbi.nlm.nih.gov/refseq/) databases.

Spot	Protein name	Role	GO - Molecular functions	GO - Biological processes	GO - Cellular components
323	Dihydropyrimidinase-related protein 2	Plays a role in neuronal development and polarity, as well as in axon growth and guidance, neuronal growth cone collapse and cell migration. Necessary for signaling by class 3 semaphorins and subsequent remodeling of the cytoskeleton. May play a role in endocytosis.	dihydropyrimidinase activity	axon guidance, cytoskeleton organization, endocytosis, nervous system development, nucleobase-containing compound metabolic process, signal transduction	cytosol, extracellular exosome
722	Glutathione S-transferase P	Conjugation of reduced glutathione to a wide number of exogenous and endogenous hydrophobic electrophiles. Regulates negatively CDK5 activity via p25/p35 translocation to prevent neurodegeneration. Catalytic activity; RX + glutathione = HX + R-S-glutathione.	dinitrosyl-iron complex binding, glutathione transferase activity, JUN kinase binding, kinase regulator activity, nitric oxide binding, S-nitrosoglutathione binding	cellular response to lipopolysaccharide, central nervous system development, common myeloid progenitor cell proliferation, glutathione derivative biosynthetic process, glutathione metabolic process, negative regulation of acute inflammatory response, negative regulation of apoptotic process, negative regulation of biosynthetic process, negative regulation of ERK1 and ERK2 cascade, negative regulation of extrinsic apoptotic signaling pathway, negative regulation of fibroblast proliferation, negative regulation of I-kappaB kinase/NF-kappaB signaling, negative regulation of interleukin-1 beta production, negative regulation of JUN kinase activity, negative regulation of leukocyte proliferation, negative regulation of MAPK cascade, negative regulation of MAP kinase activity, negative regulation of monocyte chemotactic protein-1 production, negative regulation of nitric-oxide synthase biosynthetic process, negative regulation of protein kinase activity, negative regulation of stress-activated MAPK cascade, negative regulation of tumor necrosis factor-mediated signaling pathway, negative regulation of tumor necrosis factor production, nitric oxide storage, positive regulation of superoxide anion generation, regulation of ERK1 and ERK2 cascade, regulation of stress-activated MAPK cascade, response to reactive oxygen species, small molecule metabolic process, xenobiotic metabolic process	cytoplasm, cytosol, extracellular exosome, extracellular space, intracellular, mitochondrion, TRAF2-GSTP1 complex, vesicle

Spot	Protein name	Role	GO - Molecular functions	GO - Biological processes	GO - Cellular components
682	Proteasome subunit alpha type-6/Macropain subunit iota	The proteasome is a multicatalytic proteinase complex which is characterized by its ability to cleave peptides with Arg, Phe, Tyr, Leu, and Glu adjacent to the leaving group at neutral or slightly basic pH. The proteasome has an ATP-dependent proteolytic activity. Catalytic activity; Cleavage of peptide bonds with very broad specificity.	endopeptidase activity, NF-kappaB binding, purine ribonucleoside triphosphate binding, RNA binding	activation of MAPKK activity, anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process, antigen processing and presentation of exogenous peptide antigen via MHC class I, antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent, iron ion binding, apoptotic process, axon guidance, cellular nitrogen compound metabolic process, DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest, epidermal growth factor receptor signaling pathway, Fc-epsilon receptor signaling pathway, fibroblast growth factor receptor signaling pathway, G1/S transition of mitotic cell cycle, gene expression, innate immune response, insulin receptor signaling pathway, MAPK cascade, mitotic cell cycle, negative regulation of apoptotic process, negative regulation of canonical Wnt signaling pathway, negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle, neurotrophin TRK receptor signaling pathway, NIK/NF-kappaB signaling, polyamine metabolic process, positive regulation of canonical Wnt signaling pathway, positive regulation of NF-kappaB transcription factor activity, positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle transition, programmed cell death, proteasomal ubiquitin-independent protein catabolic process, proteasome-mediated ubiquitin-dependent protein catabolic process, protein polyubiquitination, proteolysis involved in cellular protein catabolic process, Ras protein signal transduction, regulation of apoptotic process, regulation of cellular amino acid metabolic process, regulation of inflammatory response, regulation of mRNA stability, regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle, small GTPase mediated signal transduction, small molecule metabolic process, stimulatory C-type lectin receptor signaling pathway, T cell receptor signaling pathway, tumor necrosis factor-mediated signaling pathway, vascular endothelial growth factor receptor signaling pathway, viral process	cytoplasm, cytoplasmic mRNA processing body, cytosol, extracellular exosome, myofibril, nuclear matrix, nucleoplasm, nucleus, polysome, proteasome complex, proteasome core complex, proteasome core complex, alpha-subunit complex, sarcomere

Spot	Protein name	Role	GO - Molecular functions	GO - Biological processes	GO - Cellular components
1652	Actin cytoplasmic 1	Actins are highly conserved proteins that are involved in various types of cell motility and are ubiquitously expressed in all eukaryotic cells.	identical protein binding, kinesin binding, nitric-oxide synthase binding, structural constituent of cytoskeleton, Tat protein binding	'de novo' posttranslational protein folding, adherens junction organization, ATP-dependent chromatin remodeling, axon guidance, blood coagulation, cell-cell junction organization, cell junction assembly, cellular protein metabolic process, chromatin organization, ephrin receptor signaling pathway, Fc-gamma receptor signaling pathway involved in phagocytosis, innate immune response, membrane organization, movement of cell or subcellular component, platelet aggregation, protein folding, retina homeostasis, small GTPase mediated signal transduction, substantia nigra development, vascular endothelial growth factor receptor signaling pathway	blood microparticle, cytoplasm, cytoplasmic ribonucleoprotein granule, cytoskeleton, cytosol, dense body, extracellular exosome, extracellular space, focal adhesion, membrane, MLL5-L complex, NuA4 histone acetyltransferase complex, nuclear chromatin, nucleoplasm, plasma membrane, protein complex, ribonucleoprotein complex
679	Heat shock protein beta-1 /heat shock protein 27	Involved in stress resistance and actin organization.	identical protein binding, poly(A) RNA binding, protein kinase binding, protein kinase C binding, protein kinase C inhibitor activity, ubiquitin binding	cellular response to vascular endothelial growth factor stimulus, gene expression, intracellular signal transduction, movement of cell or subcellular component, negative regulation of apoptotic process, negative regulation of oxidative stress-induced intrinsic apoptotic signaling pathway, negative regulation of protein kinase activity, platelet aggregation, positive regulation of angiogenesis, positive regulation of blood vessel endothelial cell migration, positive regulation of endothelial cell chemotaxis, positive regulation of endothelial cell chemotaxis by VEGF-activated vascular endothelial growth factor receptor signaling pathway, positive regulation of interleukin-1 beta production, positive regulation of tumor necrosis factor biosynthetic process, regulation of I-kappaB kinase/NF-kappaB signaling, regulation of mRNA stability, regulation of translational initiation, response to unfolded protein, response to virus, retina homeostasis, vascular endothelial growth factor receptor signaling pathway	cytoplasm, cytoskeleton, cytosol, extracellular exosome, extracellular space, focal adhesion, nucleus, proteasome complex
779	Stathmin	Involved in the regulation of the microtubule (MT) filament system by destabilizing microtubules. Prevents assembly and promotes disassembly of microtubules. Phosphorylation at Ser-16 may be required for axon formation during neurogenesis. Involved in the control of the learned and innate fear.	signal transducer activity, tubulin binding	intracellular signal transduction , microtubule depolymerization, mitotic spindle organization, neuron projection development, regulation of cytoskeleton organization, response to virus, signal transduction	cytoplasm, extracellular exosome, intracellular, neuron projection

Spot	Protein name	Role	GO - Molecular functions	GO - Biological processes	GO - Cellular components
1403	Voltage-dependent anion-selective channel protein 2 (VDAC2)	Forms a channel through the mitochondrial outer membrane that allows diffusion of small hydrophilic molecules. The channel adopts an open conformation at low or zero membrane potential and a closed conformation at potentials above 30-40 mV. The open state has a weak anion selectivity whereas the closed state is cation-selective.	voltage-gated anion chanel activity	anion transport, regulation of anion transmembrane transport	extracellular exosome, membrane raft, mitochondrial nucleoid, mitochondrial outer membrane, mitochondrion, nucleus

Spot	Protein name	Role	GO - Molecular functions	GO - Biological processes	GO - Cellular components
1441	26S protease regulatory subunit 8 /Thyroid receptor interactor	The 26S protease is involved in the ATP-dependent degradation of ubiquitinated proteins. The regulatory (or ATPase) complex confers ATP dependency and substrate specificity to the 26S complex.	ATPase activity, proteasome-activating ATPase activity, TBP-class protein binding, thyrotropin-releasing hormone receptor binding, transcription cofactor activity, transcription factor binding	activation of MAPKK activity, anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process, antigen processing and presentation of exogenous peptide antigen via MHC class I, antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent, antigen processing and presentation of peptide antigen via MHC class I, apoptotic process, axon guidance, cellular nitrogen compound metabolic process, DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest, epidermal growth factor receptor signaling pathway, ER-associated ubiquitin-dependent protein catabolic process, Fc-epsilon receptor signaling pathway, fibroblast growth factor receptor signaling pathway, G1/S transition of mitotic cell cycle, gene expression, innate immune response, insulin receptor signaling pathway, MAPK cascade, mitotic cell cycle, negative regulation of apoptotic process, negative regulation of canonical Wnt signaling pathway, negative regulation of programmed cell death, negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle, neurotrophin TRK receptor signaling pathway, NIK/NF-kappaB signaling, polyamine metabolic process, positive regulation of canonical Wnt signaling pathway, positive regulation of proteasomal protein catabolic process, positive regulation of RNA polymerase II transcriptional preinitiation complex assembly, positive regulation of transcription, DNA-templated, positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle transition, programmed cell death, proteasome-mediated ubiquitin-dependent protein catabolic process, protein polyubiquitination, Ras protein signal transduction, regulation of apoptotic process, regulation of cellular amino acid metabolic process, regulation of mRNA stability, regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle, small GTPase mediated signal transduction, small molecule metabolic process, stimulatory C-type lectin receptor signaling pathway, T cell receptor signaling pathway, transcription from RNA polymerase II promoter, tumor necrosis factor-mediated signaling pathway, vascular endothelial growth factor receptor signaling pathway, viral process	blood microparticle, cytoplasm, cytoplasmic vesicle, cytosol, cytosolic proteasome complex, extracellular exosome, membrane, nuclear proteasome complex, nucleoplasm, nucleus, proteasome accessory complex, proteasome complex, proteasome regulatory particle, base subcomplex

Spot	Protein name	Role	GO - Molecular functions	GO - Biological processes	GO - Cellular components
1548	Pyruvate kinase (PKM)	Glycolytic enzyme that catalyzes the transfer of a phosphoryl group from phosphoenolpyruvate (PEP) to ADP, generating ATP. Stimulates POU5F1-mediated transcriptional activation. Plays a general role in caspase independent cell death of tumor cells. The ratio betwween the highly active tetrameric form and nearly inactive dimeric form determines whether glucose carbons are channeled to biosynthetic processes or used for glycolytic ATP production. The transition between the 2 forms contributes to the control of glycolysis and is important for tumor cell proliferation and survival. Catalytic activity; ATP + pyruvate = ADP + phosphoenolpyruvate. Cofactor; Protein has several cofactor binding sites: Mg2+ and K+. Enzyme regulation; Isoform M2 is allosterically activated by D-fructose 1,6-bisphosphate (FBP). Inhibited by oxalate and 3,3',5-triiodo-L-thyronine (T3). The activity of the tetrameric form is inhibited by PML. Selective binding to tyrosine-phosphorylated peptides releases the allosteric activator FBP, leading to inhibition of PKM enzymatic activity, this diverts glucose metabolites from energy production to anabolic processes when cells are stimulated by certain growth factors. Glycolytic flux are highly dependent on de novo biosynthesis of serine and glycine, and serine is a natural ligand and allosteric activator of isoform M2. Pathway: glycolysis; This protein is involved in step 5 of the subpathway that synthesizes pyruvate from D-glyceraldehyde 3-phosphate. This subpathway is part of the pathway glycolysis, which is itself part of Carbohydrate degradation.	MHC class II protein complex binding, poly(A) RNA binding, pyruvate kinase activity	canonical glycolysis, carbohydrate metabolic process, glucose metabolic process, programmed cell death, small molecule metabolic process	cytoplasm, cytosol, extracellular exosome, extracellular matrix, extracellular vesicle, mitochondrion, nucleus, plasma membrane, vesicle
1539	Aconitate hydratase, mitochondrial	Catalyzes the isomerization of citrate to isocitrate via cis-aconitate. Catalytic activity; Citrate = isocitrate. Cofactor; [4Fe-4S] clusterBy similarityNote: Binds 1 [4Fe-4S] cluster per subunit. Binding of a [3Fe-4S] cluster leads to an inactive enzyme. Pathway: tricarboxylic acid cycle. This protein is involved in step 2 of the subpathway that synthesizes isocitrate from oxaloacetate - step 1 - Citrate synthase, mitochondrial (CS) , tep 2 - Aconitate hydratase, mitochondrial (ACO2). This subpathway is part of the pathway tricarboxylic acidhich is itself part of Carbohydrate metabolism.	iron ion binding	cellular metabolic process, citrate metabolic process, generation of precursor metabolites and energy, small molecule metabolic process, tricarboxylic acid cycle	mitochondrial matrix, mitochondrion, nucleus

Spot	Protein name	Role	GO - Molecular functions	GO - Biological processes	GO - Cellular components
163	Endoplasmin	Molecular chaperone that functions in the processing and transport of secreted proteins. When associated with CNPY3, required for proper folding of Toll-like receptors. Functions in endoplasmic reticulum associated degradation (ERAD). Has ATPase activity.	calcium ion binding, low-density lipoprotein particle receptor binding, protein phosphatase binding, RNA binding, virion binding	actin rod assembly, ATF6-mediated unfolded protein response, cellular protein metabolic process, cellular response to ATP, endoplasmic reticulum unfolded protein response, ER-associated ubiquitin-dependent protein catabolic process, innate immune response, negative regulation of apoptotic process, protein folding in endoplasmic reticulum, protein transport, receptor-mediated endocytosis, regulation of phosphoprotein phosphatase activity, response to endoplasmic reticulum stress, response to hypoxia, retrograde protein transport, ER to cytosol, sequestering of calcium ion, toll-like receptor signaling pathway	cytosol, endocytic vesicle lumen, endoplasmic reticulum, endoplasmic reticulum lumen, endoplasmic reticulum membrane, extracellular exosome, extracellular matrix, extracellular region, focal adhesion, membrane, midbody, nucleus, perinuclear region of cytoplasm
950	Heat shock cognate 71 kDa protein	Acts as a repressor of transcriptional activation. Inhibits the transcriptional coactivator activity of CITED1 on Smad-mediated transcription. Chaperone. Component of the PRP19-CDC5L complex that forms an integral part of the spliceosome and is required for activating pre-mRNA splicing. May have a scaffolding role in the spliceosome assembly as it contacts all other components of the core complex. Binds bacterial lipopolysaccharide (LPS) et mediates LPS-induced inflammatory response, including TNF secretion by monocytes. Participates in the ER-associated degradation (ERAD) quality control pathway in conjunction with J domain-containing co-chaperones and the E3 ligase CHIP.	ATPase activity, ATPase activity, coupled, ATP binding, C3HC4-type RING finger domain binding, enzyme binding, G-protein coupled receptor binding, heat shock protein binding, MHC class II protein complex binding, poly(A) RNA binding, ubiquitin protein ligase binding, unfolded protein binding	ATP metabolic process, axon guidance, cellular response to heat, chaperone-mediated autophagy, chaperone-mediated autophagy translocation complex disassembly, chaperone-mediated protein transport involved in chaperone-mediated autophagy, gene expression, membrane organization, mRNA splicing, via spliceosome, negative regulation of fibril organization, negative regulation of transcription, DNA-templated, neurotransmitter secretion, post-Golgi vesicle-mediated transport, protein folding, protein refolding, protein targeting to lysosome, protein targeting to lysosome involved in chaperone-mediated autophagy, regulation of cellular response to heat, regulation of mRNA stability, regulation of protein complex assembly, regulation of protein complex stability, regulation of protein import, regulation of protein stability, response to unfolded protein, RNA splicing, synaptic transmission	blood microparticle, clathrin-sculpted gamma-aminobutyric acid transport vesicle membrane, cytosol, extracellular exosome, extracellular space, focal adhesion, intracellular, lumenal side of lysosomal membrane, lysosomal lumen, lysosomal membrane, membrane, nucleoplasm, nucleus, plasma membrane, Prp19 complex, ribonucleoprotein complex
1104	Peroxiredoxin-4	Probably involved in redox regulation of the cell. Regulates the activation of NF-kappa-B in the cytosol by a modulation of I-kappa-B-alpha phosphorylation. Catalytic activity; 2 R'-SH + ROOH = R'-S-S-R' + H2O + ROH.	thioredoxin peroxidase activity	I-kappaB phosphorylation	extracellular exosome, nucleus

Spot	Protein name	Role	GO - Molecular functions	GO - Biological processes	GO - Cellular components
278	78 kDa glucose-regulated protein (GRP78)	Probably plays a role in facilitating the assembly of multimeric protein complexes inside the endoplasmic reticulum. Involved in the correct folding of proteins and degradation of misfolded proteins via its interaction with DNAJC10, probably to facilitate the release of DNAJC10 from its substrate.	ATPase activity, calcium ion binding, chaperone binding, enzyme binding, glycoprotein binding, misfolded protein binding, protein domain specific binding, ubiquitin protein ligase binding, unfolded protein binding	ATF6-mediated unfolded protein response, blood coagulation, cellular protein metabolic process, cellular response to glucose starvation, endoplasmic reticulum unfolded protein response, ER-associated ubiquitin-dependent protein catabolic process, IRE1-mediated unfolded protein response, maintenance of protein localization in endoplasmic reticulum, negative regulation of apoptotic process, negative regulation of protein homodimerization activity, PERK-mediated unfolded protein response, platelet activation, platelet degranulation, positive regulation of cell migration, positive regulation of transcription from RNA polymerase II promoter in response to endoplasmic reticulum stress, protein folding in endoplasmic reticulum, regulation of ATF6-mediated unfolded protein response, regulation of IRE1-mediated unfolded protein response, regulation of PERK-mediated unfolded protein response, regulation of protein folding in endoplasmic reticulum, substantia nigra development	endoplasmic reticulum, endoplasmic reticulum chaperone complex, endoplasmic reticulum-Golgi intermediate compartment, endoplasmic reticulum lumen, endoplasmic reticulum membrane, extracellular exosome, focal adhesion, integral component of endoplasmic reticulum membrane, membrane, midbody, nucleus