

Table 2: Impact of induced α -Syn expression on the relative amounts of phosphoprotein. The intensity of Pro-Q diamond stain or that of Sypro ruby stain was measured by densitometric analysis. Statistical analysis was based on 3 or more sets of experiments and unpaired two-tailed *t* test. SD: standard deviation.

Table 3: Characteristics of proteins differentially glycosylated between samples from the induced and non-induced cells.

Table 4: Impact of induced α -Syn expression on the relative amounts of glycoprotein. The intensity of Pro-Q emerald stain or that of Sypro ruby stain was measured by densitometric analysis. Statistical analysis was performed based on 3 or more sets of studies and unpaired two-tailed *t* test. SD: standard deviation.

Table 5: Biological functions of proteins differentially phosphorylated and glycosylated in samples from the cells with versus without induced expression of wild-type α -Syn.

Supplementary Figure 1: Sub-regions of the Pro-Q diamond stained gels from Figure 4. Spot numbers indicate phosphoproteins that show a greater than 2 fold difference between the induced and non-induced controls (S-14d versus S-14d, S+28d versus S-28d).

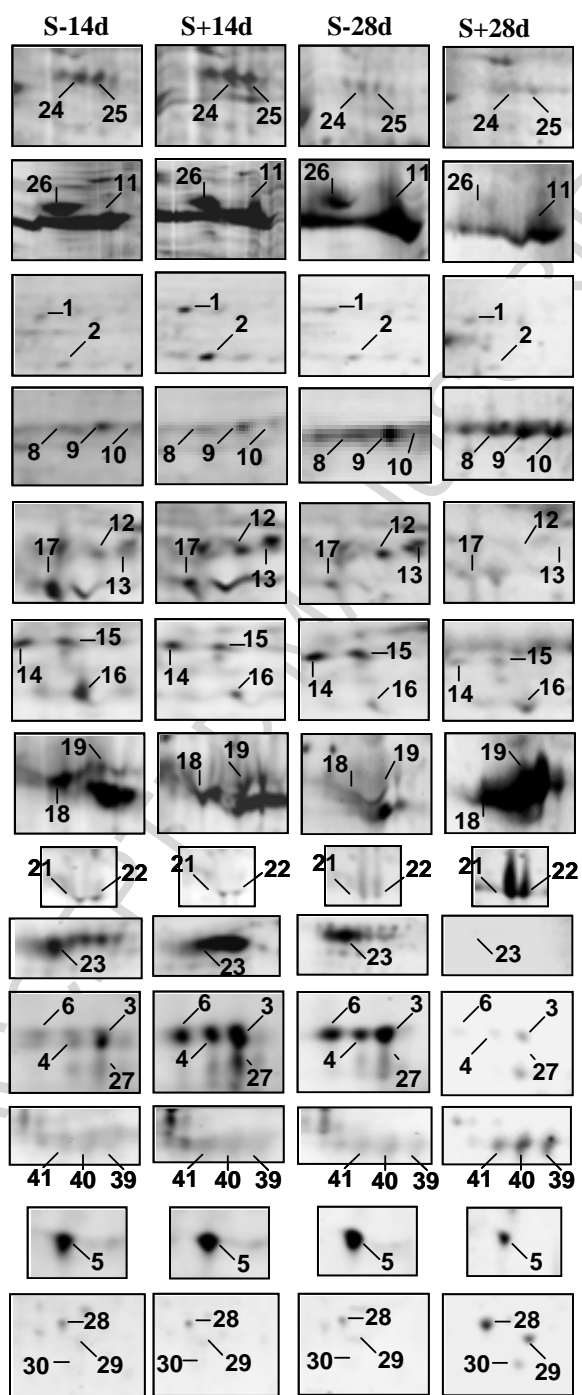
Supplementary Figure 2: Sub-regions of the Pro-Q emerald stained gels from Figure 6. Spot numbers indicate glycoproteins that show a greater than 2 fold changes between the TetOff induced and non-induced cells.

Supplementary table S1: Demographic data of human subjects.

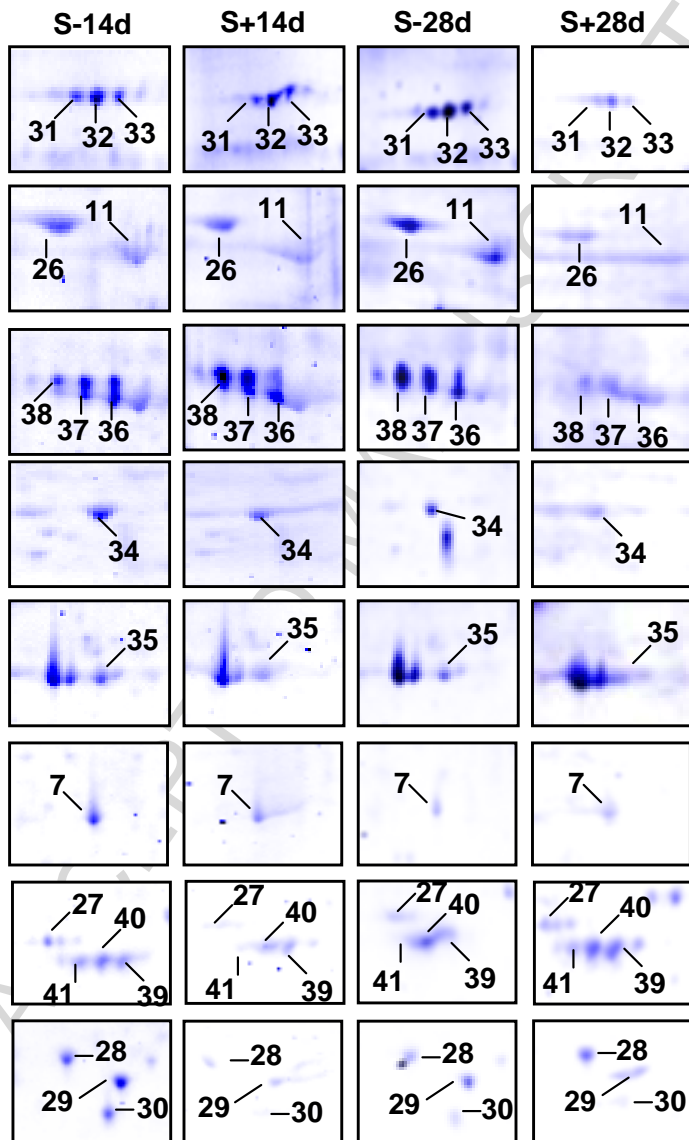
Supplementary table S2: List of proteins identified **a)** by MS/MS using LCQ-Deca XP
Plus **b)** by nanoLC-ESI-MS/MS using LTQ Orbitrap Hybrid Mass Spectrometer.

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Supplementary Fig. 1



Supplementary Fig. 2



Supplementary table S1: Demographic data of human subjects.

Case	Age (years)	Sex	Clinical Diagnosis	Pathological Diagnosis	Braak stage
1	88	M	Normal	Normal	2
2	90	F	Normal	Normal	1.5
3	81	F	Normal	Normal	2
4	85	M	PD	TLBD	2
5	86	M	PD	TLBD	3
6	82	F	PD	TLBD	3

TLBD: transitional Lewy Body disease

Spot #	Protein Name	P (protein)	Molecular Weight (Da)	Unique peptides	Protein coverage %
7	L-lactate dehydrogenase B chain (P07195) Sequence K.LIAPVAEEEEATVPNNK K.SLADELALVDVLEDK K.MVVESAYEVIK	4.55E-09	36507.1	3	12.61
11	Heatshock protein HSP 90-beta (P08238) Sequence R.TLTLVDTGIGMTK K.ADLINNLGTIAK K.HNDDEQYAWESSAGGSFTVR K.HSQFIGYPITLYLEK R.NPDDITQEEYGEFYK K.SLTNDWEDHLAVK K.HFSVEGQLEFR R.GVVDEDLPLNISR K.HLEINPDHPIVETLR	6.22E-10	83132.5	9	17.70
12	Heat shock cognate 71kDa protein (P11142) Sequence R.TTPSYVAFTDTER K.TVTNAVVTVPAYFNDSQR R.IINEPTAAAIAYGLDK K.SINPDEAVAYGAAVQAAILSGDK	2.08E-11	70897.6	4	10.84
13	Heat shock cognate 71kDa protein (P11142) Sequence K.VEIIANDQGNR R.TTPSYVAFTDTER K.NQVAMNPTNTVFDAK K.HWPFMVVNDAGRPK K.TVTNAVVTVPAYFNDSQR K.DAGTIAGLNVLR R.IINEPTAAAIAYGLDK R.FEELNADLFR K.SQIHDIVLVGGSTR K.LLQDFFNGK K.SINPDEAVAYGAAVQAAILSGDK K.NSLESYAFNMK	4.25E-12	70897.6	12	25.70
14	Heat shock cognate 71kDa protein (P11142) Sequence R.TTPSYVAFTDTER K.NQVAMNPTNTVFDAK R.IINEPTAAAIAYGLDK K.STAGDTHLGGEDFDNR	4.79E-07	70897.6	4	9.29

15	Heat shock 70kDa protein 1 (P08107)	8.24E-11	70051.8	8	17.63
	Sequence				
	R.TTPSYVAFTDTER				
	K.NQVALNPQNTVFDK				
	K.HWPFQVINDGDKPK				
	K.DAGVIAGLNVL				
	R.IINEPTAAAIAYGLDR				
	K.LLQDFN				
	K.SINPDEAVAYGAAVQAAILMGDK				
	K.NALESYAFNMK				
16	T-complex protein 1 subunit epsilon (P48643)	5.36E-11	59670.7	3	9.80
	Sequence				
	K.ISDSVLVDIKDTEPLIQTA				
	R.WWGGPEIELIAIATGGR				
	K.LGFAGLVQEISFGTTK				
17	60kDa heat shock protein, mitochondrial precursor (P10809)	7.96E-13	61054.2	4	14.31
	Sequence				
	K.LVQDVANNTNNEEAGDGTATVLR				
	K.ISSIQSIVPALEIANAHR				
	R.KPLVIAEDVDGEALSTLVNLR				
	R.IQEIIQLDVTTSEYEK				
21	Actin (gamma actin) (P63261)	6.11E-15	41792.6	11	41.87
	Sequence				
	K.AGFAGDDAPR				
	R.AVFPVIVGRPR				
	K.DSYVGDEAQSK				
	K.IWHHTFYNELR				
	R.VAPEEHPVLLTEAPLNPK				
	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR				
	R.DLTDYLMK				
	R.GYSFTTTAER				
	K.SYELPDGQVITIGNER				
	K.DLYANTVLSGGTTMYPGIADR				
	K.EITALAPSTMK				
22	Actin (beta actin) (P60709)	1.16E-11	41736.5	7	31.20
	Sequence				
	K.IWHHTFYNELR				
	R.VAPEEHPVLLTEAPLNPK				
	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR				
	R.GYSFTTTAER				
	K.SYELPDGQVITIGNER				
	K.DLYANTVLSGGTTMYPGIADR				
	K.EITALAPSTMK				
23	Nucleophosmin (P06748)	1.22E-06	32574.8	2	16.67
	Sequence				

	R.TVSLGAGAKDELHIVEAEAMNYEGSPIK K.MSVQPTVSLGGFEITPPVVL				
24	Transitional endoplasmic reticulum ATPase (P55072) Sequence R.LIVDEAINEDNSVVSLSQPK R.AVANETGAFFFLINGPEIMSK K.NAPAIIFIDELDAIPK R.IVSQLLTLM DGLK R.LDQLIYIPLPEK	2.02E-08	89190.1	5	10.43
25	Transitional endoplasmic reticulum ATPase (P55072) Sequence R.LIVDEAINEDNSVVSLSQPK R.IVSQLLTLM DGLK R.LDQLIYIPLPEK R.QTNPSAMEVEEDDPVPEIR	1.00E-08	89190.1	4	8.07
26	Endoplasmin precursor (HSP90 beta member) (P14625) Sequence R.TDDEVVQREEEAIQLDGLNASQIR K.FAFQAEVNR R.ELISNASDALDK R.LISLTDENALSGNEELTVK K.NLLHVTDGTGVMTR K.EEASDYLELDTIK K.SILFVPTSAPR K.GVVDSDDLPLNVS R.FQSSHPTDITSLDQYVER	1.33E-10	92468.2	9	16.81
27	14-3-3 protein epsilon (P62258) Sequence K.VAGMDVELTVEER R.LGLALNFSVFYIEILNSPDR K.AAFDDAIAELDTLSEESYK	2.41E-10	29173.7	3	20.39
28	Ubiquitin carboxy-terminal hydrolase isozyme (P09936) Sequence MQLKPMEINPEMLNK R.LGVAGQWR K.QIEELKGQEVSPK K.LGFEDGSVLK R.VDDKVNFFHILFNNVDGHL YELDGR K.VNFFHILFNNVDGHL YELDGR R.MFPFVNHGASSEDLLK	6.84E-14	24824.2	7	39.46
29	Glutathione S-transferase P (P09211) Sequence PPYTVVYFPVR K.FQDGLTLYQSNTILR	3.55E-15	23224.5	6	40.67

K.DQQAALVDMVNDGVEDLR
K.ALPGQLKPFETLLSQNQQGK
K.AFLASPEYVNLPIPINGNK
K.AFLASPEYVNLPIPINGNKQ

30	Peroxiredoxin-2 (P32119)	3.18E-11	21760.6	6	28.43
	Sequence				
	K.ATAVVDGAFK				
	R.KEGGLGPLNIPLLADVTR				
	K.EGGLGPLNIPLLADVTR				
	R.LSEDYGVLK				
	R.GLFIIDGK				
	R.QITVNDLPVGR				

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Spot #	Protein name	Protein molecular weight (Da)	Protein identification probability	Number of unique peptides	Percentage sequence coverage
3	Elongation factor 1-beta (P24534) sequence: AKKPALVAK GPADVEDTTGSGATDSK LAQYESK SIQADGLVWGSSK SPAGLQVLNDYLADK SSILLDVK SSILLDVKPWDEETDMAK SYIEGYVPSQADVAVF SYIEGYVPSQADVAVFEAVSSPPPADLCH VGTDMLEEQITAFEDYVQSM DVAAFNK VGTDMLEEQITAFEDYVQSM DVAAFNKI VVEDDKVGTDMLEEQITAFEDYVQSM DVAAFNK YGPADVEDTTGSGATDSK	24,746.20	100.00%	13	63.60%
4	Elongation factor 1-beta (P24534) sequence: AKKPALVAK GPADVEDTTGSGATDSK LAQYESK SIQADGLVWGSSK SPAGLQVLNDYLADK SSILLDVK SSILLDVKPWDEETDMAK SYIEGYVPSQADVAVF VGTDMLEEQITAFEDYVQSM DVAAFNK YGPADVEDTTGSGATD	24,746.20	100.00%	11	54.70%
5	Proteasome subunit alpha type-3 (P25788) sequence: AFELELSWVGELTNGR AVENSSTAIGIR	28,415.70	100.00%	15	50.20%

CKDGVVFGVEK
 DGVVFGVEK
 EEASNFR
 HVGMAVAGLLADAR
 IYIVHDEVK
 IYIVHDEVKDK
 LYEEGSNK
 LYEEGSNKR
 RLFNVDR
 SNFGYNIPLK
 TEIEKLQMK
 VFQVEYAMK
 YDLSASTFSPDGR

6	Elongation factor 1-beta (P24534) sequence:	24,746.20	100.00%	9	64.40%
	AKKPALVAK LAQYESK SIQADGLVWGSSK SPAGLQVLNDYLADK SSILLDVKPWDDETDMAK SYIEGYVPSQADVAVFEAVSSPPPADLCHALR VGTDMLEEQITAFEDYVQSMDVAAFNK VVEDDKVGTDMLEEQITAFEDYVQSMDVAAFNK YGPADVEDTTGSGATDSK				
31	Neutral alpha-glucosidase AB precursor (Q14697) sequence:	106,857.90	100.00%	59	60.30%
	AAETWVDISSNTAGK AEKDEPGAWEEETFK AFFAGSQR ALLDSLQLGPDSLTVHLLIHEVTK DENSVELTMAEGPYK DGDKPEETQGK DLGIFWLNAETWVDISSNTAGK DPAEGDGAQPEETPR DPAEGDGAQPEETPRD				

DPAEGDGAQPEETPRDGDKPEETQGK
DVHNIYGLYVHMATADGLR
FGAVWTGDNTAEWDHLK
FQHDPETSVLVLRL
FRIDELEPR
FSFSGNTLVSSADPEGHFETPIWIER
GAGKPAAVVLQTK
GLLEFEHQR
IDELEPR
IGAGKPAAVVLQTK
IIGAGKPAAVVLQTK
ISIPMCLSLGLVGLSFCGADVGGFFK
KLVAIVDPHIK
LGPDSLTVHLIHEVTK
LKVTEGGEPYR
LSFQHDPETSVLVLRL
LVAIVDPHIK
LYNLDFVQYELYNPM
LYNLDFVQYELYNPMALYGSVPVLLAHNPH
LYNLDFVQYELYNPMALYGSVPVLLAHNPHR
MMDYLQGSGETPQTDVR
NDMNEPSVFNNGPEVTMLK
NPEPELLVR
PAAVVLQTK
PAAVVLQTKGSPESR
PAEGDGAQPEETPR
PGLSPYR
PGSAGYPDFTNPTMR
PPLFSLGYHQSR
QYASLTGTQALPPLFSLGYHQSR
RFSFSGNTLVSSAD
SGGMERPFVLAR
SIRPGLSPYR
SLLLSVNAR
SYDNYEGSAPNLFVWVNDMNEPSVFNNGPEVTMLK
TCEESSFCK
TLVSSADPEGHFETPIWIER

VALSPQGT AQGELFLDDGHTFN YQTR
 VHEELR
 VIIGAGKPAAVVLQTK
 VLLVLELQGLQK
 VPDVLVADPPIAR
 VSQGSKDPAEGDGAQPEETPR
 VTEGGEPYR
 VVIIGAGKPAAVVLQTK
 WMSETGIIDVFLLLGPSISDVFR
 WYQMGAYQPFFR
 YFTWDPSR
 YRVPDVLVADPPIAR
 YSLLPFWYTL LYQAHR

32	Neutral alpha-glucosidase AB precursor (Q14697) sequence:	106,857.90	100.00%	76	63.20%
	AAETWVDISSNTAGK				
	AEKDEPGAWEEFK				
	AFFAGSQR				
	ALLDSLQLGPDSLTVH				
	ALLDSLQLGPDSLTVH LIHEVTK				
	ASLTGTQALPPLFSLGYHQSR				
	DENSVELTMAEGPYK				
	DGDKPEETQGK				
	DLGIFWL NAAETWVDISSNTAGK				
	DPAEGDGAQPEETPR				
	DPAEGDGAQPEETPRD				
	DVHNIYGLYVH				
	DVHNIYGLYVH MATADGLR				
	EPWLLPSQHNDIIR				
	FGAVWTGDNTAEWDHLK				
	FQHDPETSVLVLR				
	FRIDELEPR				
	FSFSGNTLVSSADPEGHFETPIWIER				
	GLLEFEHQK				
	HHGPQTL YLPVTLSSIPVFQR				
	IDELEPR				

IGAGKPAAVVLQTK
IIGAGKPAAVVLQTK
ISIPMCLSLGLVGLSFCGADVGGFFK
KLVAIVDPH
KLVAIVDPHIK
KPGINVASDWSIHLR
LFVWNDMNEPSVFNGPEVTK
LGPDSLTVHLIHEVTK
LKVTEGGEPYR
LLLGPSISDVFR
LSFQHPETSVLVLR
LVAIVDPHIK
LYNLDVFQYELYNPMALYGSVPVLLAHNPH
LYNLDVFQYELYNPMALYGSVPVLLAHNPHR
MMDYLQGSGETPQTDVR
NDMNEPSVFNGPEVTK
NIYGLYVHMATADGLR
NLGLYVK
NPEPELLVR
PAAVVLQTK
PAAVVLQTKGSPESR
PAEGDGAQPEETPR
PDSLTVHLIHEVTK
PFWYTLLYQAHR
PGLSPYR
PMALYGSVPVLLAHNPHR
PPLFSLGYHQSR
QYASLTGTQALPPLFSLGYHQSR
REPWLLPSQHNDIIR
RFSFGNTLVSSAD
SGGMERPFVLAR
SGNTLVSSADPEGHFETPIWIER
SIRPGLSPYR
SLLLSVNAR
SPQGTAQGELFLDDGHTFNYQTR
SYDNYEGSAPNLFVWNDMNEPSVFNGPEVTK
TLVSSADPEGHFETPIWIER

VALSPQGT AQGELFLDDGHTFNYQTR
 VIIGAGK PAAVVLQTK
 VLLVLELQGLQK
 VPDVLVADPPIAR
 VSQGSKDPAEGDGAQPEETPR
 VTEGGEPYR
 VVIIGAGK
 VVIIGAGK PAAVVLQTK
 WLNAETWVDISSNTAGK
 WMSETGIIDVFLLLGPSISDVFR
 WYQMGAYQPFFR
 YFTWDPSR
 YGLYVHMATADGLR
 YLPVTLSSIPVFQR
 YLQSGGETPQTDVDR
 YRVPDVLVADPPIAR
 YSLLPFWYTLLYQAH
 YSLLPFWYTLLYQAHR

33	Neutral alpha-glucosidase AB precursor (Q14697) sequence:	106,857.90	100.00%	49	55.20%
	AFFAGSQR				
	AHAHLDTGR				
	ALLDSLQLGPD SLTVHLIHEVTK				
	DENSVELTMAEGPYK				
	DGDKPEETQGK				
	DLGIFWLNAETWVDISSNTAGK				
	DPAEGDGAQPEETPR				
	DVHNIYGLYVHMATADGLR				
	FGAVWTGDNTAEWDHLK				
	FRIDELEPR				
	FSFSGNTLVSSADPEGHFETPIWIER				
	GLLEFEHQR				
	HHGPQTL YLPVTLSSIPVFQR				
	IDELEPR				
	IGAGK PAAVVLQTK				
	IIGAGK PAAVVLQTK				

ISIPMCLSLGLVGLSFCGADVGGFFK
 KLVAIVDPH
 KLVAIVDPHIK
 KPGINVASDWSIHLR
 LGPDSLTVHLIHEVTK
 LSFQHDPETSVLVR
 LVAIVDPHIK
 LYNLDVFQYELYNPMALYGSVPVLLAHNPHR
 MMDYLQGSGETPQTDVR
 NPEPELLVR
 PAAVVLQTK
 PAEGDGAQEETPR
 PDSLTVHLIHEVTK
 PGLSPYR
 PMALYGSVPVLLAHNPHR
 QYASLTGTQALPPLFSLGYHQSR
 REPWLLPSQHNDIIR
 RFSFSGNTLVSSSAD
 SGGMERPFVLAR
 SIRPGLSPYR
 SLLSVNAR
 VALSPQGTAQGELFLDDGHTFNYQTR
 VIIGAGKPAAVVLQTK
 VLLVLELQGLQK
 VPDVLVADPPIAR
 VSQGSKDPAEGDGAQEETPR
 VTEGGEPYR
 VVIIGAGK
 VVIIGAGKPAAVVLQTK
 WYQMGAYQPFFR
 YFTWDPSR
 YRVPDVLVADPPIAR
 YSLLPFWYTLLYQAHR

34	Protein disulfide-isomerase A3 precursor (P30101) sequence: DASIVGFFDDSFSEAH	56,766.60	100.00%	52	73.70%
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DASIVGFFDDSFSEAHSEFLK
DGEEAGAYDGPR
DLLIAYYDVYK
DPNIVIAK
DVLELTDDNFESR
EATNPPVIQEEK
EATNPPVIQEEKPK
EATNPPVIQEEKPKK
ELSDFGLESTAGEIPVVAIR
ELSDFISYLQR
FAHTNVESLVNEYDDNGEGILFR
FDDSFSEAHSEFLK
FFDDSFSEAHSEFLK
FIQENIFGICPHMTEDNKDLIQGK
FISDKDASIVGFFDDSFSEAH
FISDKDASIVGFFDDSFSEAHSEFLK
FLDAGHKLNFASR
FLQDYFDGNLK
FLQDYFDGNLKR
FVMQEEFSR
FVMQEEFSRDGK
GFFDDSFSEAHSEFLK
GFPTIYFSPANK
GFPTIYFSPANKK
ISDTGSAGLMLVEF
ISDTGSAGLMLVEFFAPWCGH
IVGFFDDSFSEAHSEFLK
KFLDAGHK
KQAGPASVPLR
LAPEYAAAATR
LNFAVASR
LSKDPNIVIAK
MDATANDVPSPYEVR
MTEDNKDLIQGK
PSHLTNK
PSHLTNKFEDK
QAGPASVPLR

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RLAPYEAAATR
 SDKDASIVGFFDDSFSEAHSEFLK
 SEPIPESNDGPVK
 SIVGFFDDSFSEAHSEFLK
 TADGIVSHLK
 TADGIVSHLKK
 TEEEFKK
 TFSHELSDFGLESTAGEIPVVAIR
 TVAYTEQK
 VDCTANTNTCNK
 VGFFDDSFSEAHSEFLK
 VLELTDDNFESR
 VVVAENFDEIVNNENK
 YGVSGYPTLK

35	Actin, cytoplasmic 1 (P84336)	41,784.90	100.00%	37	74.40%
	sequence:				
	AGFAGDDAPR				
	ANTVLSGGTTMYPGIADR				
	APEEHPVLLTEAPLNPK				
	AVFPSIVGR				
	AVFPSIVGRPR				
	CDVDIR				
	DLTDYLMK				
	DLTDYLMKILTER				
	DLYANTVLSGGTTMYPGIADR				
	DSYVGDEAQS				
	DSYVGDEAQS				
	DSYVGDEAQS				
	DSYVGDEAQS				
	EEHPVLLTEAPLNPK				
	EITALAPSTMK				
	EKMTQIMFETFNTPAMYVAIQAVLSLYASGR				
	ELPDGQVITIGNER				
	FEQEMATAASSSSLEK				
	GIHETTFNSIMK				
	GIVTNWDDMEK				
	GVTHTVPIYEGYALPHAILR				
	GYSFTTTAER				

HQGVMVGMGQK
 IIAPPERK
 IWHHTFYNELR
 KDLYANTVLSGGTTMYPGIADR
 LCYVALDFEQEMATAASSSSLEK
 LDFEQEMATAASSSSLEK
 NTPAMYVAIQAVLSLYASGR
 PEEHPVLLTEAPLNPK
 PIYEGYALPHAILR
 QEYDESGPSIVHR
 SYELPDGQVITIGNER
 TTGIVMDSGDGVTH
 TTGIVMDSGDGVTHTVPIYEGY
 TTGIVMDSGDGVTHTVPIYEGYALPH
 TTGIVMDSGDGVTHTVPIYEGYALPHAILR
 TVLSGGTTMYPGIADR
 VALDFEQEMATAASSSSLEK
 VAPEEHPVLLTEAPLNPK

36	Heat shock cognate 71 kDa protein (P19378) sequence:	70,881,80	100.00%	42	70.70%
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AGDTHLGGEDFDNR
 ARFEELNADLFR
 DAGTIAGLNVLR
 DNNLLGK
 EEFHQK
 FDDAVVQSDMK
 FEELNADLFR
 GAAVQAAILSGDK
 GDTHLGGEDFDNR
 GPAVGIDLGTTYSCVGVFQHGK
 GTLDPVEK
 GVPQIEVTFDIDANGILNVSVDK
 HWPFMVNDAGR
 HWPFMVNDAGRPK
 IINEPTAAAIAYGLDK
 LIGDAAKNQVAMNPTNTVFDK

LLQDFNKG
 LSKEDIER
 LYQSAGGMPGGMPGGFPGGGAPPSGGASSGPTIEEVD
 MKEIAEAYLGK
 MVNHFAEFK
 NEPTAAAIAYGLDK
 NEPTAAAIAYGLDKK
 NPDEAVAYGAAVQAAILSGDK
 NQTAEKEEFEHQK
 NQVAMNPTNTVFDAK
 NSLESYAFNMK
 NVLIFDLGGGTFDVSILTIEDGIFEVK
 PFMVVNDAGRPK
 QTQTFTTYSDNQPGVLIQVYGER
 RFDDAVVQSDMK
 SENVQDLLLDDVTPSLGIETAGGVMTVLIK
 SFYPEEVSSMVLTK
 SINPDEAVAYGAAVQAAILSGDK
 SLGIETAGGVMTVLIK
 SQIHDIVLVGGSTR
 STAGDTHLGGEDFD
 STAGDTHLGGEDFDNR
 TSSSTQASIEIDSLYEGIDFYTSITR
 TTPSYVAFTDTER
 TTYSDNQPGVLIQVYGER
 TVTNAVVTVPAYFNDSQR

37	Heat shock cognate 71 kDa protein (P19378) sequence:	70,881.80	100.00%	38	70.90%
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GPAVGIDLGTTYSCVGVFQHGK
 GTLDPVEK
 GVPQIEVTFDIDANGILNNSAVDK
 HWPFFMVNDAGRPK
 IINEPTAAAIAYGLDK
 IINEPTAAAIAYGLDKK
 KDISENKR
 LIGDAAKNQVAMNPTNTVFDK
 LLQDFFNGK
 LSKEDIER
 LYQSAGGMPGGMPGGFPGGGAPPSGGASSGPTIEEVD
 MKEIAEAYLGK
 MVNHFAEFK
 NEPTAAAIAYGLDKK
 NQTAEKEEFEHQK
 NQVAMNPTNTVFDK
 NSLESYAFNMK
 NVLIFDLGGGTFDVSILTIEDGIFEVK
 QTQTFTTYSDNQPGVLIQVYEGER
 RFDDAVVQSDMK
 SENVQDLLLDVTPSLGIETAGGVMTVLIK
 SFYPEEVSSMVLTK
 SINPDEAVAYGAAVQAAILSGDK
 SLGIETAGGVMTVLIK
 SQIHDIVLVGGSTR
 STAGDTHLGGEDFDNR
 TLSSSTQASIEIDSLYEGIDFYTSITR
 TTPSYVAFTDTER
 TTYSNQPGLIQVYEGER
 TVTNAVVTVPAYFNDSQR

38	Heat shock cognate 71 kDa protein (P19378) sequence: AGDTHLGGEDFDNR ARFEELNADLFR DAGTIAGLNVLR DNNLLGK	70,881.80	100.00%	44	72.60%
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EEFEHQK
EIAEAYLGK
FDDAVVQSDMK
FEELNADLFR
GAAVQAAILSGDK
GDTHLGGEDFDNR
GPAVGIDLGTTYSVGVFQHGK
GTLDPVEK
GVPQIEVTFDIDANGILNVSVDK
HWPFMVVNDAGRPK
IINEPTAAAIYGLDK
IINEPTAAAIYGLDKK
KDIENKR
LIGDAAKNQVAMNPTNTVFDK
LLQDFNGK
LYQSAGGMPGGMPGGFPGGGAPSGGASSGPTIEVD
MKEIAEAYLGK
MVNHFAEFK
NEPTAAAIYGLDK
NEPTAAAIYGLDKK
NPDEAVAYGAAVQAAILSGDK
NQTAKEEFEHQK
NQVAMNPTNTVFDK
NQVAMNPTNTVFDKR
NSLESYAFNMK
NVLIFDLGGGTFDVSILTIEDGIFEVK
PDEAVAYGAAVQAAILSGDK
QTQTFTTYSNQPGLIQVYGER
RFDDAVVQSDMK
SENVQDLLLDVTPLSLGIETAGGVMTVLIK
SFYPEEVSSMLTK
SINPDEAVAYGAAVQAAILSGDK
SINPDEAVAYGAAVQAAILSGDKSENVQDLLLDVTPL
SLGIETAGGVMTVLIK
SQIHDIVLVGGSTR
STAGDTHLGGEDFDNR
TLSSSTQASIEIDSLYEGIDFYTSITR

	TTPSYVAFTDTER				
	TTYSDNQPGVLIQVYEGER				
	TVTNAVVTVPAYFNDSQR				
	VEIANDQGNR				
39	14-3-3 protein zeta/delta (P63103)	27,727.90	100.00%	20	79.60%
	sequence:				
	DICNDVLSLLEK				
	DNLTLWTSDTQGDEAEAGEGGEN				
	DSTLIMQLLR				
	EMQPTHPIR				
	FLIPNASQAESK				
	GIVDQSQQAYQEAF				
	GIVDQSQQAYQEAFEISK				
	KEMQPTHPIR				
	KGIVDQSQQAYQEAFEISK				
	LAEQAER				
	LGLALNFSVFYIEILNSPEK				
	MDKNELVQK				
	MKGDYYR				
	NLLSVAYKNVVGAR				
	SQQAYQEAFEISK				
	SVTEQGAELSNEER				
	TAFDEAIAELDTLSEESYK				
	TSDTQGDEAEAGEGGEN				
	VVSSIEQK				
	YLAEVAAGDDK				
	YLAEVAAGDDKK				
40	14-3-3 protein zeta/delta (P63103)	27,727.90	100.00%	24	83.70%
	sequence:				
	DICNDVLSLLEK				
	DNLTLWTSDTQGDEAEAGEGGEN				
	DQSQQAYQEAFEISK				
	DSTLIMQLLR				
	EKIETELR				
	EMQPTHPIR				

FLIPNASQAESK
 GIVDQSQQAYQEAF
 GIVDQSQQAYQEA FEISK
 KEMQPTHPIR
 KGIVDQSQQAYQEA FEISK
 LAEQAER
 LGLALNFSVFYIEILNSPEK
 MDKNELVQK
 NLLSVAYK
 NLLSVAYKNVVGAR
 SQQAYQEA FEISK
 SVTEQGAELSNEER
 TAFDEAIAELDTLSEESYK
 TEQGAELSNEER
 TSDTQGDEAEAGEGGEN
 VVSSIEQK
 YDDMAACMK
 YLAEVAAGDDK
 YLAEVAAGDDKK

41	14-3-3 protein zeta/delta (P63103) sequence: DICNDVLSLLEK DNLTWTSQTGDEAEAGEGGEN DSTLIMQLLR EKIE TELR EMQPTHPIR FDEAIAELDTLSEESYK FLIPNASQAESK GIVDQSQQAYQEAF GIVDQSQQAYQEA FEISK IVDQSQQAYQEA FEISK KEMQPTHPIR KGIVDQSQQAYQEA FEISK LAEQAER LGLALNFSVFYIEILNSPEK MDKNELVQK	27,727.90	100.00%	26	82.90%
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MKGDYYR
NLLSVAYK
NLLSVAYKNVVGAR
SQQAYQEAFFISK
SVTEQGAELSNEER
TAFDEAIAELDTLSEESYK
TEQGAELSNEER
TSDTQGDEAEAGEGGEN
VDQSQQAYQEAFFISK
VVSSIEQK
YLAEVAAGDDK
YLAEVAAGDDKK

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