

Supporting Information

Differential Phosphoproteomic Analysis of Recombinant Chinese Hamster Ovary Cells Following Temperature Shift

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Supplementary Figure S-2: CHO-specific sequence for ATF2 aligned against human ATF2 sequence showing conservation of the phosphorylation site (RED BOX) that was detected using the phospho-specific antibody to ATF2. (Page S4)

The following are supplied in an additional xlsx worksheet

Supplementary Table S-1: Full list of differentially expressed phosphopeptides from TiO₂ enrichment with increased expression at 31°C compared to 37°C. The table also includes associated MS data.

Supplementary Table S-2: Full list of differentially expressed phosphopeptides from TiO₂ enrichment with decreased expression at 31°C compared to 37°C. The table also includes associated MS data.

Supplementary Table S-3: Full list of differentially expressed phosphopeptides from Fe-NTA (IMAC) enrichment with increased expression at 31°C compared to 37°C. The table also includes associated MS data.

Supplementary Table S-4: Full list of differentially expressed phosphopeptides from Fe-NTA (IMAC) enrichment with decreased expression at 31°C compared to 37°C. The table also includes associated MS data.

Supplementary Table S-5: List of differentially expressed proteins from non-enriched whole cell lysates (WCL) with increased expression at 31°C compared to 37°C.

Supplementary Table S-6: List of differentially expressed proteins from non-enriched whole cell lysates (WCL) with decreased expression at 31°C compared to 37°C.

Supplementary Table S-7: MS data associated with Supplementary Tables S-5 and S-6.

Supplementary Table S-8: Overlapping differentially expressed proteins which contained peptides in common between the phosphoproteomic analysis and the whole cell lysate non-enriched proteomic analysis.

Supplementary Table S-9: Overlapping differentially expressed proteins which did not share common peptides between the phosphoproteomic analysis and the whole cell lysate non-enriched proteomic analysis.

Score	Expect	Method	Identities	Positives	Gaps
702 bits(1811)	0.0	Compositional matrix adjust.	340/388(88%)	351/388(90%)	20/388(5%)
Query 1	MSREMQDQVDLAEVKPLVEKGETITGLLQEFQDIETLHGSVHVTLCGTPKGNRPVIL				60
Sbjct 1	MSRE+ DVDLAEVKP ETITGLLQEFQDIETLHGS+HVTLCGTPKGNRPVIL				60
Query 61	TYHDIGMNHKTCYNPLFNIEDMQEITQHFVCHVDAPGQQDGAASFPAGYMYPSMDQLAE				120
Sbjct 61	TYHDIGMNHKTCYNPLFNIEDMQEITQHFVCHVDAPGQQDGA SFPAGYMYPSMDQLAE				120
Query 121	MLPGVLQQFGLKSIIGMTGAGAYILTRFALNNPEMVEGLVLINNVNCAEGWMDWAASKI				180
Sbjct 121	MLPGVL QFGLKS+IGMTGAGAYILTRFALNNPEMVEGLVL+NVNCAEGWMDWAASKI				180
Query 181	SGWTQALPDMVVSHLFGKEEQSNVEVVHTYRQHI+NDMNP NLHLFI+AYNSRRDLEIE				240
Sbjct 181	SGWTQALPDMVVSHLFGKEEIHNSVEVVHTYRQHILNDMNPSNLHLFISAYNSRRDLEIE				240
Query 241	RPMPGTHVTTLQCPALLVVGDS+SPAVDAVVECNKLDPTKTTLLKMADCGGLPQISQPAK				300
Sbjct 241	RPMPGTHVTTLQCPALLVVGDN+SPAVDAVVECNKLDPTKTTLLKMADCGGLS QISQPAK				300
Query 301	LAEAFKYFVQGMGYMPSASMTLRMSRTASGSSVTSLDGTRSRSHSEGT				360
Sbjct 301	LAEAFKYFVQGMGYMPSASMTLRMSRTASGSSVTS+G RSRSHSE R				351
Query 361	RRSHTSEGAHLDITPNSGAAGNSAGPK				388
Sbjct 352	-----LNITPNSGATGNNAGPN				368

Supplementary Figure S-1: CHO-specific sequence for NDRG1 aligned against human NDRG1 sequence showing conservation of the phosphorylation site (RED BOX) that was detected using the phospho-specific antibody to NDRG1.

Range 1: 1 to 388 [Graphics](#) ▼ Next Match ▲ Previous Match

Score	Expect	Method	Identities	Positives	Gaps	
722 bits(1864)	0.0	Compositional matrix adjust.	376/486(77%)	382/486(78%)	98/486(20%)	
Query 19	MSDDKPF	LCTAPGCGQ	RFTNEDHLAVHKHKHEMTLKFGPARND	SVIVAD	TRTPTRFLKN 78	
Sbjct 1	MSDDKPF	LCTAPGCGQ	RFTNEDHLAVHKHKHEMTLKFGPARND	SVIVAD	TRTPTRFLKN 60	
Query 79	CEEVGLF	NELASPFENE	FKKASEDDIKKMPDL	SPLATPIIRSKIEEPSV	VETTHQDSPL 138	
Sbjct 61	CEEVGLF	NELASPFENE	FKKASEDDIKKMPDL	SPLATPIIRSKIEEPSV	VETTHQDSPL 120	
Query 139	PHPESTT	SDEKEVPLAQ	TASIVRPASLQV	PNVLLTSSDSSV	IIQQAVPSPTSSTVI 198	
Sbjct 121	PHPESTT	-----	SD ++	-----	SDEKLV----- 133	
Query 199	TQAPSSNR	PVPGPFLL	LHLPNGQTM	PAIPASITSSNV	HVPAAPVLRPVTM	VPVSV 258
Sbjct 134	-----	RPV	-----	-----	-----MVPSV 142	
Query 259	PGIPGPSS	PQPVQSEAK	MRLKAALTQQHPP	VTNGDTVKGHGS	GLVRTQSEESR	PQSLQQP 318
Sbjct 143	PGIPGPSS	PQPVQSEAK	MRLKAALTQQHPP	VTNGDTVKGHGS	GLVRTQSEESR	PQSLQQP 202
Query 319	ATSTTTET	PASPAHTT	PQTQSTSGRRRA	ANEDPDEKRRK	FLERNRAAAS	RCRQKRKVWVQ 378
Sbjct 203	ATSTTTET	PASPAHTT	PQTQSTSGRRRA	ANEDPDEKRRK	FLERNRAAAS	RCRQKRKVWVQ 262
Query 379	SLEKKAED	LSSNLGQL	QSEVTLLRNEVA	QKQLLLAHKDC	PVTAHQKKSGY	HADKDDSS 438
Sbjct 263	SLEKKAED	LSSNLGQL	QSEVTLLRNEVA	QKQLLLAHKDC	PVTAHQKKSGY	HADKDDSS 322
Query 439	EDISVPSS	PHTEAIQHSS	VSTSNVSVSTSK	AEAVATSVLTQ	MADQSTEPALS	QIVMAPSS 498
Sbjct 323	EDISVPSS	PHTEAIQHSS	VSTSNVSVSTSK	AEAVATSVLTQ	MADQSTEPALS	QIVMAPSS 382
Query 499	QSQPSG	504				
Sbjct 383	QPQPSG	388				

Supplementary Figure S-2: CHO-specific sequence for ATF2 aligned against human ATF2 sequence showing conservation of the phosphorylation site (RED BOX) that was detected using the phospho-specific antibody to ATF2.