**Table S1A: MALDI-TOF/TOF identification of differential expressed proteins from 20 min curcumin time point using DIGE analysis**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Spot No** | **Uniprot ID** | **Name of the protein** | **M.W (kDa)** | **No. of peptides** | **Fold change** | **Score** | **Ion Score** | **Peptides** |
| **Down regulation** |
| D-1\* | P37809 | ATP synthase subunit beta  | 51.42 | 19 | -1.56 | 662 | 423 | EVQSTLQRYDHLPEDAFRVSQVLGPVVDVRFTQAGSEVSALLGRVALTGLTMAEHFRTAMVFGQMNEPPGARFEDGHLPEIYNAIKALAPEIVGEEHYAVARDVQGQDVLFFIDNIFRKLTEMGIYPAVDPLASTSRGMEAVDTGAPISVPVGDVTLGRVFNVLGENIDLNEPVPADAKTREGNDLFYEMSDSGVINKIQFFLSQNFHVAEQFTGQKMPSAVGYQPTLATEMGQLQERRIQFFLSQNFHVAEQFTGQKELQDIIAILGMDELGEEDKLVVHRTVLIQELINNIAQEHGGISVFAGVGERISQPAASENEVGIDLTLEVALHLGDDTVR |
| **D-2** | P80698 | Trigger factor  | 47.48 | 11 | -1.78 | 579 | 426 | AIDFLVENRQEGNEGVLTVEVDAETFKAVEEAGIEPVDRPEIDVEKASENAEIDVPQAMVDTELDRFGVEALYQDALDILLPVEYPKDVEVTFPEEYHAEDLAGKPAVFKLQMQGMNLELYTQFSGQDEAALKEEGAVEEGNTVVLDFEGFVDGEAFEGGKELPELDDEFAKDIDEEVETLAELTEKAENYSLEVGSGSFIPGFEDQLVGLEAGAEKLQMQGMNLELYTQFSGQDEAALKEQMK |
| **Up regulation** |
| U-1\* | P46336 | Protein IolS  | 35.17 | 13 | 1.85 | 167 | 104 | TFFPYTKKSVDESLKSEELIGEVLRRADQLIDNIKNEQEHFKGEREFNREDVVIATKSIGVSNFSLEQLKYTEDTTFPEGDLRNGVTMLDTAYIYGIGRTADVTLSQEDISFIDKDGLVDVLQGEYNLLNRQGNDFVFDNSPDFLKKEANKDGLVDVLQGEYNLLNR |
| **U-2** | O31605 | Oligoendopeptidase F homolog  | 77.07 | 4 | 1.78 | 109 | 85 | LYTYAHMRLYILNHMLEGFRQITHGNFINFLESENRVLELDEVHIYDLYTPLVK |

Table S1B: MALDI-TOF/TOF identification of differential expressed proteins from 60 min curcumin time point using DIGE analysis

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Spot No** | **Uniprot ID** | **Name of the protein** | **M.W (kDa)** | **No. of peptides** | **Fold change** | **Score** | **Ion Score** | **Peptides** |
| **Down regulation** |
| D-1\* | P37253 | Ketol-acid reductoisomerase  | 37.43 | 19 | -1.67 | 1240 | 1163 |

|  |
| --- |
| VYYNGDIK |
| ESGVDVIVGVR |
| SFTQAQEDGHK |
| EWIVENQVNRPR |
| VYEAEIKDELTAG |
| VYYNGDIKENVLAGKLIVDLMYEEGLAGMR |
| YSISDTAQWGDFVSGPR |
| TVAVIGYGSQGHAHALNLK |
| FNAINASENEHQIEVVGR |
| EAAAQAEIIMVLLPDEQQQK |
| YSISDTAQWGDFVSGPRVVDAK |
| TYEQGAGVPALFAIYQDVTGEAR |
| EETETDLFGEQAVLCGGLSALK |
| RTYEQGAGVPALFAIYQDVTGR |
| AGFETLTEAGYQPELAYFECLHEK |
| TVAVIGYGSQGHAHALNLKESGDVIVGVR |

SLVFAHGFNVHFHQIVPPADVDVFLVAPKAGVLETTFKEETETDLFGEQAVLCGGLSALVK |
| D-2\* | P42973 | Aryl-phospho-beta-D-glucosidase BglA | 54.84 | 18 | -1.69 | 266 | 229 | SHIEALKKYGMIYVDRGYYPSYALKYFFPDVQVRCLRTSIGWSRGPSVVDVMTAGAHGVPREGYNITFEDGDDEILRYGMIYVDRDNEGNGSMKEVMYQTAHHELVASALAVAKITDTIEENEFYPNHEAIDFYHRKITDTIEENEFYPNHEAIDFYHR |
| D-3# | O32114 | Diaminopimelate epimerase | 30.85 | 4 | -1.72 | 109 | 100 | YAYEHKIFNNDGSEGKCVAKYAYEHKVNVVTVDMGEPR |
| D-4\* | P20429 | DNA-directed RNA polymerase alpha chain | 34.77 | 13 | -1.95 | 245 | 200 | IEIEKPKSYNCLKRFVVEPLERLEELGLGLRGYTPADANKRVSYQVENTRGYGTTLGNSLRAKLEELGLGLRAGINTVQELANKFGKFVVEPLERVLEMTIEELDLSVRDDQPIGVIPIDSIYTPVSRRDDQPIGVIPIDSIYTPVSR |
| D-5\* | P22250 | Glutamate--tRNA ligase  | 55.72 | 36 | -2.23 | 783 | 648 | VIAFNDIVKEREEQIARNQGGKFIIRSPALFDMHKWVNNQYVKSPALFDMHKGEDHISNTPKDLTQEEQEKVYYEELLEKTALFNYLFAREQFIEIFDVNRHRDLTQEEQEKDESIIQFIEQYKLEELEEFTPDNIKYAPSPTGHLHIGNARNIEGGEQSQLNYLKVGTELSAEEQEWVRCYCTEEELEKERRDESIIQFIEQYKGEISFESDGIGDFVIVKAVLEEEQVPEVLSTFAAKKLDLDQVVELTLPHLQKDGTPTYNFAVAIDDYLMKVAVTGQTHGPELPQSIELIGK |
| **D-6** | Q07836 | Uncharacterized protein yxxG  | 16.43 | 4 | -2.72 | 274 | 207 | DFSAVLLESEYKIKDDCIELELTPRSNSNLFEINCNEEKLESFVTALKGNQDSISLETIEPFLFLSIDQENGNYR |
| **D-7** | P80868 | Elongation factor G  | 76.62 | 50 | -5.01 | 1120 | 889 | QATTYGVPRGRVEGMEARVMTDPYVGKILQMHANSRLAEEDPTFRNIGIMAHIDAGKCNPVLLEPIMKVEANVGAPQVAYRIGADFLYSVGTLRGTRPDTNEEIERGITITSAATTAQWKYLEGEEITIDELKHSSDEEPFSALAFKQATTYGVPRIVFVNKAMVPLAEMFGYATALREIPEEYKEQAEELREFKVEANVGAPQVAYREEISTVYAGDIAAAVGLKGTFTMHMDHYEEVPKGTLNVEFYPVLVGSAFKKGTLNVEFYPVLVGSAFKLFDGSYHDVDSNEMAFKVNIIDTPGHVDFTVEVERLTFFRVYSGTLDSGSYVKVEVVIPEEYMGDIMGDITSRGVQLVLDAVLDYLPAPTDVAAIKIGETHEGASQMDWMEQEQERDLVILESMEFPEPVIDVAIEPKVLDGAVAVLDAQSGVEPQTETVWRNKGVQLVLDAVLDYLPAPTDVAAIKTQTNPETGQTIISGMGELHLDIIVDREYIPAVQAGLEDALENGVLAGFPLIDIKGQFGHVWIEFEPNEEGAGFEFENAIVGGVVPR |
| **D-8** | P80868 | Elongation factor G  | 76.61 | 49 | -5.92 | 1090 | 884 | QATTYGVPRGRVEGMEARVMTDPYVGKSVAEEIIKKILQMHANSRLAEEDPTFRNIGIMAHIDAGKCNPVLLEPIMKVEANVGAPQVAYRIGADFLYSVGTLRGTRPDTNEEIERGITITSAATTAQWKYLEGEEITIDELKHSSDEEPFSALAFKQATTYGVPRIVFVNKAMVPLAEMFGYATALREIPEEYKEQAEELREFKVEANVGAPQVAYREEISTVYAGDIAAAVGLKGTFTMHMDHYEEVPKGTLNVEFYPVLVGSAFKNIGIMAHIDAGKTTTTERKGTLNVEFYPVLVGSAFKLFDGSYHDVDSNEMAFKVNIIDTPGHVDFTVEVERLTFFRVYSGTLDSGSYVKVEVVIPEEYMGDIMGDITSRIGETHEGASQMDWMEQEQERVLDGAVAVLDAQSGVEPQTETVWRTQTNPETGQTIISGMGELHLDIIVDREYIPAVQAGLEDALENGVLAGFPLIDIK |
| **Up regulation** |
| **U-1** | O32201 | Protein LiaH  | 25.69 | 31 | 17 | 788 | 663 | IEEMEIRIDSESAYRMRTLSLQKVMLNQYVRSAEAGTELTRVMLNQYVRDMESDIAKAKEHMNTTFDKQHTIAYQFKKYEEAAEVAGKQHTIAYQFKKEFADDVEAEIEKDMFVASVHEGLDKIENRIEEMEIRKEFADDVEAEIEKASYEQANSQLADLKQTIVKQHTIAYQFKIRDMFVASVHEGLDKNQAQLAFDAGEEELAKEHMNTTFDKIDSESAYRASYEQANSQLADLKEQLAALETK |
| U-2\* | P21464 | 30S ribosomal protein S2  | 27.96 | 15 | 4.22 | 601 | 534 | YIFTERRYIFTERSGMYYVNQRNGIYIIDLQKKVEEAYNFTKMQENGTFDVLPKDLPDALFIIDPRQLLEAGVHFGHQTRWLGGTLTNFETIQKDMKDLPDALFIIDPRWLGGTLTNFETIQKRDMKDLPDALFIIDPRYIFTERNGIYIIDLQKLNIPIIGIVDTNCDPDEIDVVIPANDDAIRKLNIPIIGIVDTNCDPDEIDVVIPANDDAIR |
| **U-3** | P49814 | Malate dehydrogenase  | 33.64 | 13 | 2.97 | 628 | 586 | IDAIVERSVTQEIVKDDLVSTNEKERIDAIVERVIGQSGVLDTARTFVAEELNLSVKYSYAGGIPLETLIPKALDMLEASPVQGFDAKVSVIGAGFTGATTAFLIAQKDVTGFVLGGHGDDMVPLVRELADVVLVDIPQLENPTKELADVVLVDIPQLENPTKGKITGTSNYEDTAGSDIVVITAGIAR |
| U-4\* | P80866 | Vegetative protein 296  | 29.03 | 9 | 2.95 | 110 | 96 | MAASTLTIKYLNEGFSGGEKGGEFHAVMGPNGTGKNEILQLMMIEPKEEGDEISLMKFIRSENFGCLMITHYQR |
| U-5\* | P17820 | Chaperone protein dnaK  | 66 | 29 | 2.79 | 1000 | 793 | VILVGGSTRNEFEEIKVIANAEGNRTTPSVVAFKIPAVQEAIKAQQAQGGANAEGKFQLTDIPPAPRSSSGLSDEEIERFEELSSHLVERTTPSVVAFKNGERAAIEKNEFEEIKSYAESYLGETVSKQSITNPNTIMSIKHMGTDYKVEIEGKAKFEELSSHLVERAVITVPAYFNDAERQSITNPNTIMSIKRIINEPTAAALAYGLDKKDELQTIVQELSMKDYTPQEVSAIILQHLKLGGDDFDQVIIDHLVSEFKGVPQIEVSFDIDKNGIVNVRVIGIDLGTTNSCVAVLEGGEPKLGGDDFDQVIIDHLVSEFKKGVNPDEVVALGAAIQGGVITGDVKADDNVVDAEYEEVNDDQNKKQALQDAGLSASEIDKVILVGGSTRDLSGVSSTQISLPFITAGEAGPLHLELTLTRSQVFSTAADNQTAVDIHVLQGERPMSADNK |
| **U-6** | P54550 | Probable NADH-dependent flavin oxidoreductase yqiM  | 37.58 | 14 | 2.33 | 513 | 463 | ADLIFIGRLFTPITIKIGIQLAHAGRVKETVQEFKQVWDGPLFVRTDEYGGSPENRLTEQVKEQGSKGLDIADHIGFAKELLRDPFFARLTPFHMAHYISRQLNTEIPAPVQYERIVMSPMCMYSSHEKAIGQVGLIIVEASAVNPQGRITDQDLGIWSDEHIEGFAK |
| **U-7** | P80864 | Probable thiol peroxidase  | 18.31 | 10 | 2.18 | 303 | 233 | RFNEEAAKWCGANGIDKSVFVLDENGKGGPVTLVGQEVKDMSFGEAFGVYIKWCGANGIDKVETLSDHRVGDQAPDFTVLTNSLEEKLGDVNVYTISADLPFAQARVTIISVIPSIDTGVCDAQTRVVYAEYVSEATNHPNYEKPIEAAK |
| **U-8** | P96611 | Thioredoxin-like protein ydbP | 12.43 | 5 | 2.11 | 120 | 102 | FYADWCPDCTRYQVMGIPSLLIFKTPEEVTEFLSEHISTPEEVTEFLSEHISITTNEQFNELIQSDKEIIVK |
| U-9\* | P49778 | Elongation factor P  | 20.47 | 7 | 2.07 | 203 | 175 | VVETEPGIKMISVNDFRVVDFQHVKPGKTGLTIEVDGGIWRVVETEPGIKGDTASGGTKPAKTETGLVVNVPFFVNEGDTLVVNTSDGSYVSR |
| U-10\* | P37809 | ATP synthase beta chain  | 51.42 | 29 | 1.96 | 1350 | 1192 | ETVQGFKIEEVVEKLVVHRAREVQSTLQRIGLFGGAGVGKVVDLLAPYIKTIAMASTDGVQRYDHLPEDAFRVSQVLGPVVDVRFTQAGSEVSALLGRVALTGLTMAEHFRGSYVPVKETVQGFKTAMVFGQMNEPPGARFEDGHLPEIYNAIKALAPEIVGEEHYAVAREGNDLFYEMSDSGVINKLTEMGIYPAVDPLASTSRDVQGQDVLFFIDNIFREGNDLFYEMSDSGVINKKLTEMGIYPAVDPLASTSRGMEAVDTGAPISVPVGDVTLGRVFNVLGENIDLNEPVPADAKTREGNDLFYEMSDSGVINKQAPSFDQLSTEVEILETGIKMPSAVGYQPTLATEMGQLQERRIQFFLSQNFHVAEQFTGQKELQDIIAILGMDELGEEDKLVVHRTVLIQELINNIAQEHGGISVFAGVGERISQPAASENEVGIDLTLEVALHLGDDTVR |
| **U-11** | O35022 | FMN-dependent NADH-azoreductase 1  | 22.98 | 17 | 1.78 | 436 | 391 | DMINGTFKENLPYLGRLYEAFLAAYKYTQEGPVGLMGGKAGQGMEMTEDEKKYTQEGPVGLMGGKKENNPNDEVVELDLHKAGVTFKYTQEGPVGLMGGKENNPNDEVVELDLHKENLPYLGR |
| **U-12** | P28599 | 10 kDa chaperonin  | 10.17 | 5 | 1.51 | 157 | 122 | MLKPLGDRTASGIVLPDSAKYEGTEYLILRVVIELVESEEKYAGTEVKYEGTEYLILR |

Table S1C: MALDI-TOF/TOF identification of differential expressed proteins from 120 min curcumin time point using DIGE analysis

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Spot No** | **Uniprot ID** | **Name of the protein** | **M.W (kDa)** | **No. of peptides** | **Fold change** | **Score** | **Ion Score** | **Peptides** |
| **Down regulation** |
| **D-1** | **P23630**  | Diaminopimelate decarboxylase  | 48.7 | 18 | -3.64 | 482 | 414 | AQVAYASKKLDEWRYEAAAANRDSYSFVSKQAFISAGLKIHFHGNNKETYEDIVKVLNLGGGFGIRETGHSIDVLLRFGFDLHNGQTERYGTPLYVYDVALIRSLVGDAGTTLYTVGSQKYTEDDEPLHATEYVEKIPRPAVVFVENGEAHLVVKQNQHGHLEIGGVDALYLAEKITPGVEAHTHDYITTGQEDSKQYVAVDGGMNDNIRPALYQAKIGCIVVDNFYEIALLEDLCK |
| **D-2** | P30950 | Delta-aminolevulinic acid dehydratase  | 36.2 | 4 | -3.57 | 146 | 102 | AMREMVKYSSEFYGPFRAGADIIAPSNMMDGFVTVIREAQSDVEEGADFLIVKPSLSYMDIMR |
| **D-3** | P32395 | Uroporphyrinogen decarboxylase  | 39.64 | 3 | -3.57 | 208 | 164 | ADHTPVWYMRAIQIFDSWVGALNQADYRYGLFEITHQPELCAYVTR |
| **D-4** | P54419 | S-adenosylmethionine synthetase  | 44 | 10 | -1.67 | 104 | 83 | HGGGAFSGKYFINPTGRQTAAYGHFGRHDVDLPWERIIVDTYGGYARKIIVDTYGGYAR NNFDLRPAGIIKFVIGGPQGDAGLTGRRLFTSESVTEGHPDKTQVTVEYDENNKPVR |
| D-5\* | P39121 | Deoxyribose-phosphate aldolase | 22.19 | 6 | -2.35 | 175 | 150 | EDIALMRDKEDDVVEADIRTKEDVDTMVEAGASRFASVCVNPTWVELAAKVIIETCLLTDEEKERSLANIIDHTALKPHTQK |
| **D-6** | P05654 | Aspartate carbamoyltransferase | 34.31 | 16 | -2.29 | 468 | 373 | SNAEVLTRFSFEVAEKGETLYDTIRFSFEVAEKKQMKNGVFIRRGEAAYVISHGLTVSIHGDIKYGLTVERAERTRFSFEVAEKHAIIMHPAPVNRFAANLFFEPSTRGVEIDDSLVESEKTLESIGVDVCVIRMAVIQRALQTNVKLGMNVLNLDGTSTSVQKKLGMNVLNLDGTSTSVQK |
| **D-7** | P52996 | 3-methyl-2-oxobutanoate hydroxymethyltransferase  | 30 | 3 | -1.94 | 328 | 284 | LEGGEGVFESIRIDETIETAISGYVQDVRADGQVLVYHDIIGHGVER |
| D-8\* | P21882 | Pyruvate dehydrogenase E1 component subunit beta  | 35.47 | 26 | -1.69 | 317 | 171 | GLLISAIRWTSPVTIRDGISAEVVDLRAILSLEAPVLRVVIPSTPYDAKSGGRWTSPVTIRDNDPVVFLEHMKATEGLQKEFGEDRQAGIAANVVAEINDRAQMTMIQAITDALRTVSPLDIDTIIASVEKAADELEKDGISAEVVDLRTVSPLDIDTIIASVEKTGRAQMTMIQAITDALRTELKSFRQEVPEEEYTIELGKEGTDLSIITYGAMVHESLKNDENVLVFGEDVGVNGGVFRREGTDLSIITYGAMVHESLKGLLISAIRDNDPVVFLEHMKVAAPDTVFPFSQAESVWLPNHKAIVVQEAQKQAGIAANVVAEINDRTELKNDENVLVFGEDVGVNGGVFRQAGIAANVVAEINDRAILSLEAPVLREGTDLSIITYGAMVHESLKAADELEKSPFGGGVHTPELHADSLEGLVAQQPGIKVAAPDTVFPFSQAESVWLPNHKDVLETAR |
| D-9\* | Q9KWU4 | Pyruvate carboxylase  | 127.9 | 30 | -2.75 | 315 | 188 | IRSHDLKKVNIPEQKACTELNIRVDVDQQPARGAEGLANWVKGMTLAIDAVRFLKEDPWKDAHQSLLATRIFDSLNWVKHIEVQVIGDKSVLLTDTTFRQGNVVHLFERTNIPFLENVAKVVYFELNGQPREKPAFDKPLGVKGNIGQPHGGFPEKAAFGNDEVYVEKDIFTIGYAIQSRLISIGEPQPDATRYKADEAYLVGEGKEVPNTLFQMLLRRCEEEGIVFIGPKLSTWALTFEQAAAKVIEVAPSVSLSPELRVAEAAICYTGDILDKGNIGQPHGGFPEKLQKSSNAVGYTNYPDNVIKVNDMFGDIVKVTPSSKVVGDMALYMVQNNLTEKGQEPITVRPGELLEPVSFEAIK |
| **D-10** | O32117 | NADH dehydrogenase-like protein yutJ  | 39.75 | 19 | -2.28 | 865 | 737 | QVLFQDRNPYHCLKVSFPEHPRSGLLWMYKWFEEHGVRGNLILSSFPERDDLNIILFDRDLDVEKDAQGRLVLIGGGYGNMRAGFGLVADRPLIGRKAGFGLVADRPLIGRESRDDLNIILFDRWNGEALPESMPQFKRWNGEALPESMPQFKLDVQYGDITSIDIVQKTEYYALAAGTISDHHIRLLPNQLPDDVSITLIDRYHNVPGAPEFTYSIQTIDQSRLNNLSANATVAIVGAGLSGVELASELR |
| **Up regulation** |
| **U-1** | P80244 | ATP-dependent Clp protease proteolytic subunit  | 21.6 | 5 | 1.63 | 323 | 241 | AYDIYSRTGQPLEVIERMNLIPTVIEQTNRMNLIPTVIEQTNRGERYALPNSEVMIHQPLGGAQGQATEIEIAAK |
| U-2\* | P21880 | Dihydrolipoyl dehydrogenase  | 49.7 | 20 | 1.67 | 996 | 929 | ALINAGHRFPFAANGRQMSSLVTRALSLNETDGFMKGEAYFVDSNSVRTVDADYVLITVGRALINAGHRYENAKVMDENSAQTYTFKATLGGVCLNVGCIPSKGVEERPDGVTVTFEVKNAIIATGSRPIELPNFKGEEKTVDADYVLITVGRVDVVKGEAYFVDSNSVRHSDDMGITAENVTVDFTKRPNTDELGLEQVGIEMTDRVTVVEKATLGGVCLNVGCIPSKGVEERPDGVTVTFEVKGEEKTNVPNIYAIGDIIEGPPLAHKVVGDFPIETDTLVIGAGPGGYVAAIRYENAKHSDDMGITAENVTVDFTK |
| U-3\* | P20429 | DNA-directed RNA polymerase alpha chain  | 34.77 | 13 | 2 | 245 | 200 | IEIEKPKSYNCLKRFVVEPLERLEELGLGLRGYTPADANKRVSYQVENTRGYGTTLGNSLRAKLEELGLGLRAGINTVQELANKFGKFVVEPLERVLEMTIEELDLSVRDDQPIGVIPIDSIYTPVSRRDDQPIGVIPIDSIYTPVSR |
| **U-4** | P81101 | Ribosome recycling factor | 20.62 | 10 | 2.56 | 346 | 273 | VAVRNVRTAIGDIEKANPSLLDKLTDEYVSKMLVITPYDKIAIPALTEERNGDITEDELRLEKNGDITEDELRADLGLTPTSDGNMIRVTVEYYGAQTPLNQLSSINVPEAR |
| **U-5** | O32259 | Lactate utilization protein C  | 26.27 | 2 | 2.58 | 223 | 199 | TGGVAVPEWAHQPQYKDWPSEGTPVWEWDADKGEENIK |
| U-6\* | P37487 | Manganese-dependent inorganic pyrophosphatase  | 34 | 7 | 2.6 | 379 | 283 | LGFNAEPVRIANFETAEPLYYRDIEEVQVLEVIDHHRELAEIAGVDAEEYGLNMLKLVETAANEVNGVILVDHNERQQSIKDIEEVQVLEVIDHHRILIFGHQNPDTDTICSAIAYADLK |
| **U-7** | P28598 | 60 kDa chaperonin | 57.25 | 25 | 2.84 | 1340 | 1224 | ALEEPIRAPGFGDRRGTFNAVAVKGVDALADAVKSTQIAQLGRIEDALNSTRNVTAGANPVGVRLRIEDALNSTRAQVEETTSEFDRGYASPYMVTDSDKFGSPLITNDGVTIAKEIELEDAFENMGAKKGMEQAVAVAIENLKAQVEETTSEFDREKQIAHNAGLEGSVIVERMEAVLDNPYILITDK GFTTELEVVEGMQFDRENTTIVEGAGETDKISARVAAVEAEGDAQTGINIVLRAAVEEGIVSGGGTALVNVYNKTNDVAGDGTTTATVLAQAMIRAMLEDIAVLTGGEVITEDLGLDLKLKNEEIGVGFNAATGEWVNMIEKTNDVAGDGTTTATVLAQAMIREGLKESIAQVAAISAADEEVGSLIAEAMER |
| **U-8** | P15874 | GrpE protein (HSP-70 cofactor)  | 21.53 | 6 | 3.98 | 186 | 167 | VQADFENYKSRLEMEASQKVQADFENYKRSLLQGMEMVHRALQVEADNEQTKSQNIVTDLLPALDSFER |
| U-9\* | P37869 | Enolase  | 46.42 | 8 | 5.86 | 75 | 49 | YNQLLRAGYTAVISHRPYIVDVYARMGAQIFHSLKLGANAILGVSMACARVQLVGDDLFVTNTKALVPSGASTGEYEAVELRGNPTVEVEVYTETGAFGR |
| U-10\* | P39121 | Deoxyribose-phosphate aldolase  | 23.47 | 13 | 1.72 | 611 | 524 | EDIALMRTVGPDIGVKIGASAGVSIVKLAVSAGADFVKTSTGFSTGGATKDKEDDVVEADIRGATEVDMVINIAALKTKEDVDTMVEAGASRGATEVDMVINIAALKDKVIIETCLLTDEEKERSLANIIDHTALKPHTQKTSTGFSTGGATKEDIALMRGTGVDVCTVIGFPLGANTTETK |
| **U-11** | P09339 | Aconitate hydratase | 99.61 | 28 | 4.13 | 789 | 664 | QVDGFVIKVLLESVLRDFNSYGSRGNHEVMMRTVIAESFERQTVTPELFRHGGILQMVLRRGNHEVMMRDIDVPFKPSRLPNGTTATDLALKNDLLITSVLSGNREYETVFDDNKRFDSEVEIDYYRSNLVFMGVLPLQFKDPEHIDVVEAYCRWNEIETTDEALYKEVIEVDVDETVRPRAINEDGNVTTFEAVVRGNHEVMMRGTFANIRFGDSVTTDHISPAGAIGKRPQDLIPLSAMQETFKFVEFFGPGIAELPLADRAGTEDALAVNMDLEFERRPQDLIPLSAMQETFKKLPNGTTATDLALKVTQVLRVILQDFTGVPAVVDLASLRRPQDLIPLSAMQETFKKLTGRDPEHIDVVEAYCR |

* # : Proteins unique in DIGE
* Bold : Same trend in both DIGE and iTRAQ
* \* No significant change in iTRAQ (less than 1.2 fold up and down)