**Supplementary information**

**Combination of podophyllotoxin and rutin modulate radiation induced alterations of jejunal proteome in mice**

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TABLE S1: Proteins Identified by MALDI TOF MS/MS with their peptide details:

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| SPOT ID | PROTEIN | MOWSE SCORE | SEQUENCE COVERAGE  (%) | Mr/pI  Theoretical | Mr/pI  observed | PEPTIDES  (MS/MS) | ION SCORE | RMS Error  (ppm) |
| 1 | Thioredoxin domain-containing protein 17 | 88 | 32% | 14.8/4.5 | 14.006/4.56 | K.TIFAYFSGSK.D  K.SWCPDCVEAEPVIR.E | 38  50 | 29 |
| 2 | Tropomyosin alpha-4 chain | 363 | 27% | 28.45/4.65 | 30/4.53 | R.KIQALQQQADDAEDR.A  K.IQALQQQADDAEDR.A  R.RIQLLEEELDR.A  R.IQLLEEELDR.A  R.AQEQLATALQNLEEAEK.A  R.KLVILEGELK.R  K.CGDLEEELKNVTNNLK.S | 54  49  24  47  96  40  54 | 47 |
| 3 | Complement component 1 Q subcomponent-binding protein | 96 | 8% | 30.9/4.8 | 32.35/4.3 | K.AFVEFLTDEIK.E  K.EVSFQATGDSEWR.D | 63  27 | 58 |
| 4 | Chymotrypsinogen B precursor | 711 | 45% | 27.8/4.91 | 26.73/4.7 | R.IVNGEDAIPGSWPWQVSLQDR.T  R.TGFHFCGGSLISENWVVTAAHCGVK.T  K.TTDVVVAGEFDQGSDEENVQVLK.I  K.FNSFTVR.N  K.TPDKLQQAALPIVSEAK.C  K.LQQAALPIVSEAK.C  K.DGVWTLAGIVSWGSGFCSTSTPAVYAR.V | 106  108  174  45  107  79  91 | 20 |
| 5 | Tropomyosin alpha-3 chain | 536 | 26% | 33.29/4.73 | 28.8/4.71 | K.AADAEAEVASLNR.R  R.RIQLVEEELDR.A  R.IQLVEEELDR.A  R.IQLVEEELDRAQER.L  K.HIAEEADR.K  R.KYEEVAR.K  R.KLVIIEGDLER.T  K.LVIIEGDLER.T  K.TIDDLEDKLK.C  K.CTKEEHLCTQR.  K.EEHLCTQR.M | 42  39  85  44  28  35  71  43  32  65  55 | 19 |
| 6 | Thioredoxin-dependent peroxide reductase | 654 | 47% | 28.109/7.15 | 23/6.45 | K.ANEFHDVNCEVVAVSVDSHFSHLAWINTPR.K  R.KNGGLGHMNITLLSDITK.Q  K.NGGLGHMNITLLSDITK.Q  R.DYGVLLESAGIALR.G  **R.GLFIIDPNGVVK.H**  K.HLSVNDLPVGR.S  R.SVEETLR.L  K.AFQFVETHGEVCPANWTPESPTIKPSPTASK.E | 110  87  98  124  50  51  30  104 | 12 |
| 7 | Ketohexokinase | 855 | 60% | 32.72/5.81 | 32.7/5.81 | R.GGNASNSCTVLSLLGAR.C  R.CAFMGSLAPGHVADFLVADFR.Q  R.CAFMGSLAPGHVADFLVADFR.Q  R.GVDVSQVTWQSQGDTPCSCCIVNNSNGSR.T  R.TIILYDTNLPDVSAK.D  K.WIHIEGR.N  R.VSVEIEKPREELFQLFSYGEVVFVSK.D  K.HLGFQSAVEALR.G  K.GATLVCAWAEEGADALGPDGQLLHSDAFPPPR.V  R.VVDTLGAGDTFNASVIFSLSK.G | 111  72  16  88  99  51  34  102  141  157 | 14 |
| 8 | Alcohol dehydrogenase 6A (class V) | 417 | 20% | 39.95/5.82 | 46/6.08 | K.NSPLSIEEVQVEPPK.S  K.VLILIIPQCR.E  K.IYHSFR.T  R.TSSFTEYTVVPEIAAVK.I  R.IIGVDINEEKFPR.A  R.DCIPQIVTDYLQNK.I | 53  51  35  83  109  86 | 14 |
| 9 | Gamma-actin | 486 | 29% | 40.9/5.56 | 39.1/5.78 | K.AGFAGDDAPR.A  R.AVFPSIVGRPR.H  K.IWHHTFYNELR.V  R.VAPEEHPVLLTEAPLNPK.A  R.GYSFTTTAER.E  K.SYELPDGQVITIGNER.F  K.DLYANTVLSGGTTMYPGIADR.M  K.QEYDESGPSIVHR.K | 33  39  47  103  63  103  22  78 | 12 |
| 10 | Endoplasmic reticulum resident protein 29 | 376 | 25% | 28.8/6.51 | 28.7/6.23 | K.FDTQYPYGEK.Q  K.ESYPVFYLFR.D  R.DGDLENPVLYNGAVK.V  K.WASQYLK.I  K.ILDQGEDFPASEMAR.I  K.ILDQGEDFPASEMAR.I  K.SLNILTAFR.K | 54  72  74  32  109  42  36 | 6 |
| 11 | Cofilin-1 | 353 | 21% | 18.54/8.22 | 17.8/6.8 | K.AVLFCLSEDKK.N  R.YALYDATYETK.E  K.HELQANCYEEVK.D  K.HELQANCYEEVKDR.C | 69  78  100  106 | 18 |
| 12 | PCNA | 67 | 5% | 28.76/4.66 | 36/4.6 | R.SEGFDTYR.C  R.YLNFFTK.A | 30  38 | 16 |
| 13 | Ribonuclease inhibitor | 1172 | 53% | 49.78/4.69 | 50/4.6 | R.WTELLPLIQQYEVVR.L  R.LDDCGLTEVR.C  R.CKDISSAVQANPALTELSLR.T  K.LSLQNCGLTEAGCGILPGMLR.S  K.LLCEGLQDPQCR.L  K.LQLEYCNLTATSCEPLASVLR.V  K.ELVLSNNDLHEPGVR.I  K.LENCGITAANCK.D  K.LGNAGIAALCPGLLLPSCK.L  K.ELSLASNELKDEGAR.L  R.LLCESLLEPGCQLESLWIK.T  K.TCSLTAASCPYFCSVLTK.S  K.ALSQPDTVLR.E  R.ELWLGDCDVTNSGCSSLANVLLANR.S  R.ALEEERPSLR.I | 45  69  26  119  77  131  100  83  108  92  15  82  25  170  35 | 16 |
| 14 | Myosin regulatory light chain | 594 | 51% | 19.8/4.8 | 15.6/4.63 | R.ATSNVFAMFDQSQIQEFK.E  R.ATSNVFAMFDQSQIQEFK.E  K.EAFNMIDQNR.D  R.DGFIDKEDLHDMLASLGK.N  R.DGFIDKEDLHDMLASLGK.N  R.NAFACFDEEASGFIHEDHLR.E  R.FTDEEVDEMYR.E  K.KGNFNYVEFTR.I  K.GNFNYVEFTR.I | 133  65  53  81  59  142  90  28  67 | 9 |
| 15 | Abhydrolase domain-containing protein 14B | 302 | 22% | 29.08/6.4 | 23/6.05 | R.AVAIDLPGLGR.S  R.FSVLLLHGIR.F  R.FSSETWQNLGTLQR.L  R.GFVPVAPICTDKINAVDYASVK.T  K.TPALIVYGDQDPMGSSSFQHLK.Q | 21  18  28  53  47 | 24 |
| 16 | Endoplasmic reticulum resident protein 29 | 371 | 25% | 28.8/5.90 | 28.7/6.23 | K.FDTQYPYGEK.Q  K.ESYPVFYLFR.D  K.ESYPVFYLFR.D  R.DGDLENPVLYNGAVK.V  K.WASQYLK.I  K.ILDQGEDFPASEMAR.I  K.ILDQGEDFPASEMAR.I  K.SLNILTAFR.K | 72  20  59  70  26  100  45  44 | 7 |
| 17 | Ornithine aminotransferase | 1517 | 56% | 49/6.2 | 48.3/6.19 | K.KTEQGPPSSEYIFER.E  K.TEQGPPSSEYIFER.E  K.YGAHNYHPLPVALER.G  K.GIYMWDVEGR.Q  K.GIYMWDVEGR.Q  R.QYFDFLSAYGAVSQGHCHPK.I  R.QYFDFLSAYGAVSQGHCHPK.I  R.AFYNNVLGEYEEYITK.L  K.VLPMNTGVEAGETACK.L  R.RWGYTVK.G  K.IVFADGNFWGR.T  R.ALQDPNVAAFMVEPIQGEAGVIVPDPGYLTGVR.E  R.HQVLFIADEIQTGLAR.T  R.WLAVDHENVRPDMVLLGK.A  R.IAIAALEVLEEENLAENADK.M  K.LPSDVVTSVR.G  K.GLLNAIVIR.E  R.LRDNGLLAKPTHGDIIR.L  R.LAPPLVIKEDEIR.E | 103  93  79  85  30  136  164  130  114  41  100  86  104  55  125  67  49  40  82 | 11 |
| 18 | Haloaciddehalogenase-like hydrolase domain-containing protein 3 | 568 | 38% | 28/6.31 | 31/6.75 | R.LLTWDVK.D  K.LRRPVGEEYASK.A  R.RPVGEEYASK.A  R.AHGVVVEDITVEQAFR.Q  R.AQSHNFPNYGLSR.G  K.DVVLHTFR.L  K.LAVVSNFDR.R  R.RLEDILTGLGLR.E  R.LEDILTGLGLR.E  R.EHFDFVLTSEAVGCPKPDPR.I | 47  20  34  118  78  54  45  58  66  48 | 4 |
| 19 | Eukaryotic translation initiation factor 4H | 333 | 38% | 35/6.6 | 27.32/6.67 | R.AYSSFGGGR.G  K.GFCYVEFDEVDSLK.E  K.EALTYDGALLGDR.S  R.DDFNSGYR.D  R.DDFNSGYRDDFLGGR.G  R.FRDGPPLR.G  R.GSNMDFREPTEEER.A  R.TVATPLNQVANPNSAIFGGARPR.E | 6  76  70  30  41  22  57  33 | 10 |
| 20 | Dopa/tyrosine sulfotransferase | 712 | 38% | 34.9/6.33 | 36/6.8 | R.IEEFQSTPGDIVITTYPK.S  K.VPMLELSVPGIR.I  K.VPMLELSVPGIR.I  K.THLPIDLLPK.S  K.SFWENK.C  K.FLAGNVAYGSWFDHVK.S  K.REEHPLLYLYYEELK.Q  R.EEHPLLYLYYEELK.Q  K.TLDEEALDR.I  R.IVHHTSFEMMK.E  R.IVHHTSFEMMK.E  K.ENPLVNYTHLPTAMMDHSK.S | 99  60  28  69  33  131  53  106  38  41  42  84 | 11 |
| 21 | 40S ribosomal protein SA | 518 | 49% | 47/4.7 | 32.8/4.80 | K.FLAAGTHLGGTNLDFQMEQYIYK.R  K.FLAAGTHLGGTNLDFQMEQYIYK.R  R.AIVAIENPADVSVISSR.N  K.FAAATGATPIAGR.F  R.FTPGTFTNQIQAAFR.E  R.FTPGTFTNQIQAAFREPR.L  R.LLVVTDPR.A  R.ADHQPLTEASYVNLPTIALCNTDSPLR.Y  R.YVDIAIPCNNK.G  K.GAHSVGLMWWMLAR.E  R.EHPWEVMPDLYFYR.D | 136  103  88  78  87  55  30  109  54  102  85 | 12 |
| 22 | Rho GDP-dissociation inhibitor 2 | 280 | 39% | 23/4.82 | 22.83/4.97 | K.TLLGDVPVVADPTVPNVTVTR.L  R.LSLVCDSAPGPITMDLTGDLEALKK.D  K.YVQHTYR.T  K.ATFMVGSYGPRPEEYEFLTPVEEAPK.G | 56  99  39  75 | 25 |
| 23 | Cytochrome c oxidase subunit Va preprotein | 252 | 18% | 11/5.25 | 16.02/6.08 | R.WVTYFNKPDIDAWELR.K  R.WVTYFNKPDIDAWELRK.G  R.RLNDFASAVR.I) | 126  69  35 | 21 |
| 24 | Apoptosis-associated speck-like protein containing a CARD | 906 | 67% | 21/5.5 | 21.4/5.26 | R.DAILDALENLSGDELKK.F  K.LVSYYLESYGLELTMTVLR.D  R.DMGLQELAEQLQTTK.E  K.EESGAVAAAASVPAQSTAR.T  R.TGHFVDQHR.Q  R.VTEVDGVLDALHGSVLTEGQYQAVR.A  R.KLFSFVPSWNLTCK.D  K.LFSFVPSWNLTCK.D  K.EIHPYLVMDLEQS  K.EIHPYLVMDLEQS. | 131  45  111  82  47  150  77  103  101  77 | 24 |
| 25 | Retinol-binding protein 2 | 284 | 40% | 15.6/6.14 | 14.2/6.4 | K.ALDIDFATR.K  R.NYDLDFTVGVEFDEHTK.G  K.TLVTWEGNTLVCVQK.G  K.LYLELTCGDQVCR.Q | 65  15  83  96 | 31 |
| 26 | aldehyde dehydrogenase | 630 | 19% | 59/6.6 | 56.02/7.53 | R.AAFQLGSPWR.R  K.TIPIDGDFFSYTR.H  K.VAEQTPLTALYVANLIK.E  R.TFVQENVYDEFVER.S  R.VVGNPFDSR.T  R.GYFIQPTVFGDVK.D  K.EEIFGPVMQILK.F  K.EEIFGPVMQILK.F  R.ELGEYGLQAYTEVK.T | 44  118  65  127  17  95  66  38  57 | 50 |
| 27 | Calreticulin | 674 | 26% | 42.1/4.57 | 45.8/4.48 | K.EQFLDGDAWTNR.W  K.EQFLDGDAWTNR.W  K.FEPFSNK.G  K.GQTLVVQFTVK.H  K.HEQNIDCGGGYVK.L  K.KVHVIFNYK.G  R.CKDDEFTHLYTLIVRPDNTYEVK.I  K.IDNSQVESGSLEDDWDFLPPKK.I  K.IKDPDAAKPEDWDER.A | 28  109  22  70  82  60  75  126  89 | 18 |
| 29 | Heat shock cognate 71 kDa protein | 241 | 7% | 52/4.8 | 70.8/5.28 | R.ARFEELNADLFR.G  R.FEELNADLFR.G  K.QTQTFTTYSDNQPGVLIQVYEGER.A  K.QTQTFTTYSDNQPGVLIQVYEGER.A  K.FELTGIPPAPR.G | 32  45  59  143  14 | 11 |
| 30 | Heterogeneous nuclear ribonucleoproteins C1/C2 | 76 | 3% | 46/5.7 | 34.36/4.92 | K.GFAFVQYVNER.N | 71 | 5 |
| 32 | Rho GDP dissociation inhibitor (GDI) alpha | 48 | 21% | 23.3/5.12 | 22.9/5.15 | R.LTLVCSTAPGPLELDLTGDLESFKK.Q  R.FTDDDKTDHLSWEWNLTIK.K | 26  21 | 43 |
| 34 | ATP synthase subunit d | 740 | 65% | 21/5.70 | 18.73/5.52 | K.SWNETFHAR.L  R.LASLSEKPPAIDWAYYR.A  R.ANVAKPGLVDDFEK.K  K.YTALVDQEEKEDVK.S  K.SCAEFVSGSQLR.I  R.IQEYEK.Q  R.NIIPFDQMTIDDLNEIFPETK.L  K.KYPYWPHQPIENL.  K.YPYWPHQPIENL. | 62  123  44  63  97  51  107  71  69 | 25 |
| 35 | GTP-specific succinyl-CoA synthetase beta subunit | 898 | 44% | 49/5.78 | 38.09/5.05 | K.GVFNSGLK.G  K.VVGELAQQMIGYNLATK.Q  K.VVGELAQQMIGYNLATK.  K.VMVAEALDISR.E  R.ETYLAILMDR.S  K.EQIDIFEGIK.D  K.EQIDIFEGIKDSQAQR.M  R.MAENLGFLGSLK.N  K.LYHLFLK.I  K.IDATQVEVNPFGETPEGQVVCFDAK.I  K.INFDDNAEFR.Q  K.DIFAMDDKSENEPIENEAAR.Y  K.EAQVYEAFK.L  R.LEGTNVQEAQNILK.S | 43  59  49  29  57  59  47  45  49  129  84  116  70  73 | 18 |
| 36 | UMP-CMP kinase | 869 | 62% | 22.15/5.68 | 22/6.05 | .MKPLVVFVLGGPGAGK.G  MKPLVVFVLGGPGAGK.G  K.YGYTHLSAGELLR.D  R.KNPDSQYGELIEK.Y  K.IVPVEITISLLK.R  K.FLIDGFPR.N  R.NQDNLQGWNK.T  K.ADVSFVLFFDCNNEICIER.C  K.RIQTYLESTKPIIDLYEEMGK.V  K.RIQTYLESTKPIIDLYEEMGK.V  R.IQTYLESTKPIIDLYEEMGK.V  R.IQTYLESTKPIIDLYEEMGK.V  K.SVDEVFGEVVK.I | 93  75  65  67  62  52  83  134  31  12  115  71  102 | 14 |
| 37 | Interferon-induced 35 kDa protein | 126 | 15% | 31.88/5.49 | 36/6 | K.IPFSVPEVPLVFQGQTK.Q  R.VLVSGFPAGLR.L  R.LSEEELLDKLEIFFGK.A | 59  24  39 | 22 |
| 38 | Purine nucleoside phosphorylase | 712 | 42% | 32.25/ 5.93 | 28/6.05 | K.EAQIFDYNEIPNFPQSTVQGHAGR.L  R.LVFGLLNGR.C  R.FHMYEGYSLSK.V  R.DHINLPGFCGQNPLR.G  R.FPAMSDAYDR.D  R.KLQEGTYVMLAGPNFETVAESR.L  K.MLGADAVGMSTVPEVIVAR.H  R.FVSILMESIPLPDR.G  R.FVSILMESIPLPDR.G | 164  39  100  83  69  128  15  68  50 | 41 |
| 39 | Proteasome subnuit MECL-1 | 503 | 40% | 29.10/6.40 | 26/6.25 | K.IYCCGAGVAADTEMTTR.M 2  R.YQGHVGASLVVGGVDLNGPQLYEVHPHGSYSR.L  R.LPFTALGSGQGAAVALLEDR.F  R.ALSTPTEPVQR.A  R.FAPGTTPVLTR.E  R.EVRPLTLELLEETVQAMEVE.  R.EVRPLTLELLEETVQAMEVE. | 110  88  116  58  45  79  45 | 28 |
| 40 | PDZ and LIM domain protein 1 | 946 | 49% | 35.75/6.38 | 38/6.75 | R.LVGGKDFEQPLAISR.V  K.DFEQPLAISR.V  K.IWSPLVTEEGKR.H  K.MNLASEPQEVLHIGSAHNR.S  K.MNLASEPQEVLHIGSAHNR.S  R.SAMPFTASPAPSTR.V  K.TSASGEEANSRPVVQPHPSGSLIIDKDSEVYK.M  K.QSTSFLVLQEILESDGKGDPNKPSGFR.S R.HPECYVCTDCGINLK.Q  K.GHFFVEDQIYCEK.H  R.VTPPEGYDVVTVFR.E  R.VTPPEGYDVVTVFRE. | 80  88  111  121  85  19  74  103  103  102  56  70 | 19 |
| 41 | Retinol-binding protein 2 | 742 | 68% | 15.6/6.14 | 14.9/6.8 | M.TKDQNGTWEMESNENFEGYMK.A  M.TKDQNGTWEMESNENFEGYMK.A  K.ALDIDFATR.K  K.IITQDGDNFK.T  R.NYDLDFTVGVEFDEHTK.G  K.TLVTWEGNTLVCVQK.G  K.QWVEGDKLYLELTCGDQVCR.Q  K.QWVEGDKLYLELTCGDQVCR.Q  K.LYLELTCGDQVCR.Q | 112  61  72  61  155  105  127  109  84 | 11 |
| 42 | Proteasome subunit beta | 665 | 38% | 22.94/6.15 | 22/6.6 | R.FGIQAQMVTTDFQK.I  R.FGIQAQMVTTDFQK.I  K.IFPMGDR.L  R.LYIGLAGLATDVQTVAQR.L  R.LNLYELK.E  R.FGPYYTEPVIAGLDPK.T  R.DAVSGMGVIVHVIEK.D  R.DAVSGMGVIVHVIEKDK.I | 132  76  46  137  42  75  107  64 | 9 |
| 43 | Thioredoxin-like protein 1 | 737 | 39% | 32.2/4.84 | 37/5.00 | M.VGVKPVGSDPDFQPELSGAGSR.L  R.GCGPCLR.I  R.IDQYQGADAVGLEEK.I  K.AGCECLNESDEHGFDNCLR.K  K.IFINLPR.S  R.SEPTQALELTEDDIKEDGIVPLR.Y  K.FQNVNSVTLFVQSNQGEEETTR.I | 96  21  107  100  32  165  174 | 17 |

TABLE S2: Cellular localization and classification of identified differentially expressed proteins on the basis of their function:

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Spot Id | Name of Protein | Cellular Localization | Functional Category | Functions |
| 1 | Thioredoxin domain-containing protein 17 | Endoplasmic reticulum | Post-translational modification, protein turnover, and chaperones | Apoptotic cell clearance, cell redox homeostasis and response to endoplasmic reticulum stress |
| 2 | Tropomyosin alpha-4 chain | Cytoplasm, Cytoskeleton | Cytoskeleton | Structural constituent of muscle, actin filament organization |
| 3 | Complement component 1 Q subcomponent-binding protein | Cell membrane, Cytoplasm, Mitochondrion, Nucleus, Secreted | Defense mechanisms | Involved in [Complement pathway](http://www.uniprot.org/keywords/KW-0180), inflammation, [apoptosis](http://www.uniprot.org/keywords/KW-0053), [Immunity](http://www.uniprot.org/keywords/KW-0391), [transcription](http://www.uniprot.org/keywords/KW-0804) |
| 4 | Chymotrypsinogen B precursor | Secreted | Post-translational modification, protein turnover, and chaperones | Involved in digestion and proteolysis |
| 5 | Tropomyosin alpha-3 chain | Cytoplasm, Cytoskeleton | Cytoskeleton | Actin filament organization, muscle contraction |
| 6 | Thioredoxin-dependent peroxide reductase | [Cytoplasm](http://www.ebi.ac.uk/QuickGO/GTerm?id=GO:0005737), [extracellular exosome](http://www.ebi.ac.uk/QuickGO/GTerm?id=GO:0070062), [mitochondrion](http://www.ebi.ac.uk/QuickGO/GTerm?id=GO:0005739) and [myelin sheat](http://www.ebi.ac.uk/QuickGO/GTerm?id=GO:0043209)h | Post-translational modification, protein turnover, and chaperones | Cellular response to oxidative stress, regulation of NF-kappaB transcription factor activity, regulation of mitochondrial membrane potential |
| 7 | Ketohexokinase | Secreted  extracellular exosome, nucleus and cytoplasm | Carbohydrate transport and metabolism | Fructose metabolic process and regulation of glycogen metabolic process |
| 8 | Alcohol dehydrogenase 6A (class V) | Cytoplasm | Metabolites biosynthesis, transport, and catabolism | Ethanol oxidation, retinol metabolic process |
| 9 | Gamma-actin | Cytoplasmic mRNP granules containing untranslated mRNAs | . Cytoskeleton | ATP-dependent chromatin remodeling, platelet aggregation and postsynaptic actin cytoskeleton organization |
| 10 | Endoplasmic reticulum resident protein 29 | Endoplasmic reticulum | Post-translational modification, protein turnover, and chaperones | chaperone binding and  regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway |
| 11 | Cofilin-1 | Cell membrane, Cell projection, Cytoplasm, Cytoskeleton, Nucleus | Cytoskeleton | Regulates actin cytoskeleton dynamics.  Important for normal progress through mitosis and normal cytokinesis. |
| 12 | Proliferating cell nuclear antigen | [Nucleus](http://www.uniprot.org/keywords/KW-0539) | Replication, recombination and repair | [DNA damage](http://www.uniprot.org/keywords/KW-0227),  [DNA repair](http://www.uniprot.org/keywords/KW-0234) and [replication](http://www.uniprot.org/keywords/KW-0235) |
| 13 | Ribonuclease inhibitor | Cytoplasm | Lipid transport and metabolism | Ribonuclease inhibitor activity.  May play a role in redox homeostasis |
| 14 | Myosin regulatory light chain | Cytoskeleton, Z disc | Cytoskeleton | Implicated in cytokinesis, receptor capping, and cell locomotion. |
| 15 | Abhydrolase domain-containing protein 14B | Cytoplasm, Nucleus | Function unknown | Hydrolase activity  May activate transcription |
| 16 | Endoplasmic reticulum resident protein 29 | Endoplasmic reticulum | Post-translational modification, protein turnover, and chaperones | Chaperone binding and  regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway. |
| 17 | Ornithine aminotransferase | Mitochondrion | Amino acid transport and metabolism | Amino acid synthesis and interconversion |
| 18 | Haloacid dehalogenase-like hydrolase domain-containing protein 3 | Mitochondrion | Post-translational modification, protein turnover, and chaperones | Hydrolase activity metabolic process |
| 19 | Eukaryotic translation initiation factor 4H | Cytoplasm | RNA processing and modification | Formation of translation preinitiation complex |
| 20 | Dopa/tyrosine sulfotransferase | Cytoplasm | Translation, ribosomal structure and biogenesis | Catalyzes sulfate conjugation of hormones, neurotransmitters and xenobiotic compounds |
| 21 | 40S ribosomal protein SA | Cell membrane, Cytoplasm, Nucleus | Translation, ribosomal structure and biogenesis | Cell surface receptor for laminin and cell-cell adhesion |
| 22 | Rho GDP | Cytosol | Signal transduction mechanisms | Cellular response to redox state,  regulation of actin cytoskeleton,  regulation of Rho protein signal transduction |
| 23 | Cytochrome c oxidase subunit Va preprotein | Mitochondrion inner membrane | Energy production and conversion | Part of mitochondrial electron transport chain, cytochrome c to oxygen |
| 24 | Apoptosis Speck like protein containing CARD | Cytoplasm, Endoplasmic reticulum, Mitochondrion, Nucleus | Signal transduction mechanisms | Promotes caspase-mediated apoptosis. It is also an integral adapter in the assembly of the inflammasome |
| 25 | Retinol-binding protein 2 | Cytoplasm | Lipid transport and metabolism. | Intracellular transport of retinol |
| 26 | Aldehyde dehydrogenase | Mitochondrion matrix | Energy production and conversion | Oxidoreductase, ethanol catabolic process |
| 27 | Calreticulin | Endoplasmic reticulum, Sarcoplasmic reticulum | Post-translational modification, protein turnover, and chaperones | Calcium-binding chaperone that promotes folding, oligomeric assembly and quality control in the endoplasmic reticulum (ER) via the calreticulin/calnexin cycle |
| 29 | Heat shock shock cognate 71 kDa protein | Cytoplasm, Nucleus | Post-translational modification, protein turnover, and chaperones | Temperature-dependent chaperone and stress response |
| 30 | Heterogeneous nuclear ribonucleoproteins C1/C2 | Nucleus, Spliceosome | RNA processing and modification | mRNA processing, ATP-dependent chromatin remodeling |
| 32 | Rho GDP dissociation inhibitor (GDI) alpha | Cytoplasm | Signal transduction mechanisms | Controls and regulates Rho proteins homeostasis |
| 34 | ATP synthase subunit d | CF(0), Mitochondrion inner membrane | Energy production and conversion | ATP synthesis coupled proton transport |
| 35 | GTP-specific succinyl-CoA synthetase beta subunit | Mitochondrion | Energy production and conversion | Succinyl-CoA metabolic process in TCA cycle |
| 36 | UMP-CMP kinase | Cytoplasm, Nucleus | Nucleotide transport and metabolism | de novo pyrimidine nucleotide biosynthesis |
| 37 | Interferon-induced 35 kDa protein | Nucleus | Function unknown | Induced by interferon gamma, interacts with B-ATF immune effector process |
| 38 | Purine nucleoside phosphorylase | Cytoskeleton | Nucleotide transport and metabolism | Catalyzes breakdown of N-glyosidic bond in DNA. Involved in intrinsic apoptotic pathway in response to DNA damage. |
| 39 | Proteasome subnuit MECL-1 | Proteasome core complex | Post-translational modification, protein turnover, and chaperones | Involved in immune system process, proteolysis and cellular protein catabolic process |
| 40 | PDZ and LIM domain protein 1 | Cytoskeleton,  Transcription factor complex | Signal transduction mechanisms and Cytoskeleton | Regulation of transcription,  Involved in assembly, disassembly and directioning of stress fibers in fibroblasts. Required for the localization of ACTN1 and PALLD to stress fibers. |
| 41 | Retinol-binding protein 2 | Cytoplasm | Lipid transport and metabolism. | Intracellular transport of retinol |
| 42 | Proteasome subunit beta | Cytoplasm, Nucleus, Proteasome | Post-translational modification, protein turnover, and chaperones | Component of the 20S core proteasome complex. Associated with two 19S regulatory particles, forms the 26S proteasome and thus participates in the ATP-dependent degradation of ubiquitinated proteins. The 26S proteasome plays a key role in the maintenance of protein homeostasis by removing misfolded or damaged proteins. Associated with the PA200 or PA28, the 20S proteasome mediates ubiquitin-independent protein degradation. |
| 43 | Thioredoxin-like protein 1 | Cytoplasm, Nucleus, Proteasome | Post-translational modification, protein turnover, and chaperones | It mains cell redox homeostasis, involved in cellular response to oxidative stress |

TABLE. S3: Differential expression of identified jejunal proteins after 9Gray irradiation and their modulation by G-003M pretreatment-2DE Analysis.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Spot ID | Uniprot ID | Gene name | Protein name | FOLD CHANGE | | | | | | | | | | | | | | | | |
| **Control vs G-003M onlya** | | | | | **Control vs 9 Gray irradiated onlyb** | | | | | **Control vs G-003M + 9Gray irradiatedc** | | | | | | |
| 1h | 24h | 72h | 120h | 216h | 1h | 24h | 72h | 120h | 216h | 1h | 24h | 72h | 120h | 216h | 360h | 840h |
| 1. | Q9CQM5 | Txndc17 | Thioredoxin domain-containing protein 17 | 1.31±0.13 | 1.47±0.18 | 1.52±0.33 | 1.23±0.42 | 1.08±0.16 | 1.1±0.11 | 0.91±0.08 | 1.2±0.12 | 1.08±0.15 | 1.01±0.27 | 1.01±0.16 | 1.43±0.16 | 2.63±0.47 | 1.37±0.21 | 0.92±0.09 | 0.95±0.07 | 0.98±0.1 |
| 2. | Q6IRU2 | Tmp4 | Tropomyosin alpha-4 chain | 1.11±0.09 | 1.2±0.1 | 1±0.18 | 1.28±0.22 | 0.97±0.19 | 1.1±0.15 | 0.8±0.04 | 0.88±0.07 | 0.76±0.14 | 0.65±0.1 | 1.36±0.07 | 1.4±0.14 | 1.2±0.21 | 1.53±0.19 | 1.15±0.17 | 1.19±0.23 | 1.04±0.08 |
| 3. | O35658 | C1qbp | Complement component 1 Q subcomponent-binding protein | 1±0.11 | 1.29±0.12 | 1.22±0.99 | 1.17±0.19 | 1±0.05 | 1.3±0.21 | 1.1±0.05 | 1.5±0.25 | 1.6±0.06 | 2.4±0.091 | 1.21±0.18 | 1.22±0.09 | 1.12±0.02 | 1.18±0.13 | 1.19±0.12 | 1.15±0.16 | 1.1±0.11 |
| 4. | Q9CR35 | Ctrb1 | Chymotrypsinogen B precursor | 1.1±0.09 | 1±0.20 | 1±0.1 | 0.99±0.09 | 1.03±0.15 | 1±0.02 | 1.08±0.08 | 0.79±0.06 | 0.37±0.02 | 0.17±0.09 | 1.05±0.1 | 1.26±0.16 | 1.24±0.21 | 0.48±0.2 | 0.3±0.07 | 0.51±0.09 | 0.6±0.15 |
| 5. | P21107 | Tpm3 | Tropomyosin alpha-3 chain | 1.12±0.04 | 1.11±0.11 | 1±0.02 | 0.98±0.05 | 1.01±0.13 | 0.96±0.07 | 0.94±0.08 | 0.72±0.09 | 0.66±0.1 | 0.58±0.06 | 0.94±0.04 | 1.1±0.1 | 1±0.1 | 0.95±0.17 | 1.2±0.13 | 1.1±0.08 | 0.83±0.11 |
| 6. | P20108 | Prdx3 | Thioredoxin-dependent peroxide reductase | 1.08±0.13 | 1.14±0.21 | 1.01±0.09 | 1.18±0.03 | 1.23±0.08 | 1.17±0.04 | 1.11±0.12 | 0.7±0.04 | 0.7±0.08 | 0.64±0.12 | 0.95±0.07 | 1±0.03 | 1±0.12 | 0.95±0.1 | 1.27±0.05 | 1.1±0.06 | 0.89±0.09 |
| 7. | P97328 | Khk | Ketohexokinase | 1±0.03 | 1.04±0.13 | 0.95±0.17 | 0.92±0.1 | 1.01±0.14 | 1.59±0.18 | 1.1±0.09 | 0.87±0.05 | 0.42±0.06 | 1.18±0.12 | 1.6±0.08 | 1.7±0.09 | 0.8±0.06 | 0.712±0.09 | 0.8±0.1 | 0.89±0.06 | 0.85±0.12 |
| 8. | E9Q5Z6 | Adh6a | Alcohol dehydrogenase 6A (class V) | 1.26±0.09 | 1.27±0.02 | 1.27±0.11 | 1.1±0.2 | 1.07±0.05 | 3.2±0.22 | 1.87±0.16 | 2.1±0.14 | 1.4±0.12 | 1.3±0.1 | 1.44±0.06 | 1.5±0.1 | 1.3±0.07 | 0.97±0.16 | 1±0.11 | 0.93±0.08 | 1.1±0.09 |
| 9. | P60710 | Actb | Gamma-actin | 1.1±0.4 | 1.2±0.06 | 1.1±0.9 | 0.92±0.07 | 0.98±0.06 | 0.75±0.03 | 1.38±0.13 | 1.23±0.12 | 1.4±0.15 | 0.49±0.08 | 0.728±0.09 | 0.78±0.09 | 0.8±0.08 | 0.66±0.09 | 0.69±0.11 | 1.1±0.09 | 1.2±0.08 |
| 10. | P57759 | Erp29 | Endoplasmic reticulum resident protein 29 precursor | 1.01±0.11 | 0.98±0.09 | 1±0.18 | 1.01±0.05 | 1.05±0.08 | 0.47±0.13 | 1.17±0.07 | 1.512±0.11 | 1.48±0.06 | 0.38±0.1 | 0.57±0.12 | 0.66±0.1 | 0.7±0.07 | 0.78±0.11 | 0.73±0.08 | 0.75±0.09 | 0.82±0.12 |
| 11. | P18760 | Cfl1 | Cofilin-1 | 0.92±0.1 | 0.98±0.07 | 0.88±0.04 | 0.89±0.08 | 0.91±0.12 | 0.22±0.03 | 0.42±0.04 | 0.52±0.04 | 0.19±0.09 | 0±0.01 | 0.32±0.08 | 0.61±0.1 | 0.58±0.06 | 0.57±0.13 | 0.63±0.07 | 0.73±0.08 | 0.88±0.1 |
| 12. | P17918 | Pcna | Proliferating cell nuclear antigen | 0.89±0.1 | 0.87±0.06 | 1.1±0.11 | 0.96±0.08 | 1.04±0.12 | 0.66±0.7 | 0.7±0.1 | 0.57±0.04 | 0.62±0.05 | 0.42±0.02 | 1.04±0.09 | 0.87±0.15 | 1.4±0.06 | 1.81±0.03 | 0.99±0.2 | 0.9±0.1 | 0.98±0.06 |
| 13. | Q91VI7 | Rnh1 | Ribonuclease inhibitor isoform a | 0.98±0.02 | 0.93±0.1 | 0.93±0.12 | 0.89±0.03 | 0.91±0.08 | 1.2±0.04 | 1.3±0.03 | 1.24±0.11 | 1.14±0.2 | 1.54±0.08 | 1±0.07 | 0.92±0.05 | 1.17±0.1 | 1.16±0.11 | 1.3±0.04 | 1.19±0.08 | 1.2±0.08 |
| 14. | Q9CQ19 | Myl9 | Myosin regulatory light polypeptide 9 | 1.2±0.09 | 1.21±0.04 | 1.06±0.02 | 1.1±0.11 | 1.1±0.09 | 1.27±0.04 | 1.51±0.05 | 1.03±0.1 | 0.78±0.98 | 0.66±0.3 | 1.22±0.21 | 0.98±0.08 | 1.3±0.04 | 0.97±0.15 | 0.81±0.06 | 1.24±0.11 | 1±0.01 |
| 15. | Q8VCR7 | Abhd14b | Abhydrolase domain-containing protein 14B | 1.04±0.02 | 1±0.09 | 0.98±0.12 | 0.96±0.16 | 0.99±0.07 | 1.03±0.05 | 0.59±0.05 | 0.65±0.03 | 0.9±0.12 | 1.96±0.11 | 0.79±0.14 | 0.5±0.03 | 0.55±0.09 | 0.67±0.12 | 0.78±0.2 | 1.25±0.11 | 0.75±0.07 |
| 16. | P57759 | Erp29 | Endoplasmic reticulum resident protein 29 | 1±0.02 | 1±0.12 | 1.1±0.1 | 0.98±0.05 | 1±0.09 | 0.59±0.24 | 1.3±0.21 | 1.57±0.17 | 1.49±0.17 | 0.64±0.11 | 0.79±0.12 | 0.76±0.07 | 0.77±0.09 | 0.94±0.04 | 0.77±0.02 | 0.83±0.1 | 1±0.1 |
| 17. | P29758 | Oat | Ornithine aminotransferase | 1.1±0.1 | 0.99±0.1 | 0.98±0.03 | 1.14±0.2 | 0.92±0.07 | 0.72±0.05 | 0.7±008 | 0.34±0.21 | 0.4±0.11 | 0.41±0.1 | 1.05±0.1 | 0.8±0.08 | 0.78±0.2 | 0.73±0.1 | 1.05±0.1 | 0.89±0.2 | 0.93±0.1 |
| 18. | Q9CYW4 | Hdhd3 | Haloaciddehalogenase-like hydrolase domain-containing protein 3 | 0.99±0.04 | 0.91±0.08 | 0.92±0.3 | 0.83±0.12 | 0.87±0.03 | 1.2±0.02 | 1.11±0.1 | 0.7±0.1 | 0.8±0.09 | 1.7±0.06 | 1.04±0.12 | 0.7±0.02 | 0.7±0.08 | 0.99±0.12 | 0.65±0.05 | 0.98±0.07 | 0.72±0.03 |
| 19. | Q9WUK2 | Eif4h | Eukaryotic translation initiation factor 4H | 0.56±0.08 | 0.7±0.03 | 0.71±0.12 | 0.78±0.08 | 0.82±0.09 | 2.7±0.091 | 1.56±0.12 | 1.26±0.11 | 1.11±0.08 | 1.13±0.05 | 0.61±0.14 | 0.89±0.1 | 0.8±0.09 | 0.77±0.1 | 0.71±0.21 | 0.86±0.05 | 0.98±0.09 |
| 20. | Q9QWG7 | Sult1b1 | dopa/tyrosine sulfotransferase | 1.25±0.21 | 1.29±0.18 | 1.31±0.11 | 1.09±0.09 | 0.93±0.15 | 1.8±0.12 | 0.99±0.09 | 0.86±0.08 | 0.7±0.2 | 1.58±0.09 | 0.78±0.11 | 0.82±0.12 | 0.82±0.09 | 0.68±0.04 | 0.81±0.05 | 0.63±0.07 | 0.58±0.03 |
| 21. | P14206 | Rpsa | Ribosomal protein SA | 1.09±0.13 | 1.1±0.16 | 1.01±0.088 | 0.92±0.21 | 0.96±0.09 | 0.98±0.16 | 0.806±0.05 | 1.2±0.09 | 1.1±0.12 | 1.56±0.04 | 0.94±0.2 | 1.14±0.06 | 0.99±0.09 | 1.18±0.11 | 1.12±0.08 | 1.03±0.12 | 0.88±0.07 |
| 22. | Q61599 | Arhgdib | Rho GDP-dissociation inhibitor 2 | 0.94±0.11 | 0.76±0.13 | 0.75±0.09 | 0.88±0.07 | 0.89±0.09 | 0.89±0.04 | 0.58±0.12 | 0.65±0.13 | 0.46±0.07 | 0.3±0.19 | 0.74±0.10 | 0.59±0.06 | 0.54±0.16 | 0.44±0.05 | 0.56±0.04 | 0.57±0.15 | 0.722±0.14 |
| 23. | P12787 | Cox5a | Cytochrome c oxidase subunit 5A | 1.1±0.16 | 1.21±0.08 | 0.98±0.15 | 0.89±0.21 | 0.97±0.1 | 1.51±0.14 | 0.92±0.09 | 0.72±0.03 | 0.5±0.04 | 0.52±0.03 | 0.91±0.17 | 0.95±0.1 | 0.74±0.05 | 0.8±0.16 | 1.12±0.1 | 1.04±0.18 | 0.78±0.09 |
| 24. | Q9EPB4 | Pycard | Apoptosis-associated speck-like protein containing a CARD | 1.1±0.11 | 1.02±0.21 | 1.08±0.09 | 0.95±0.06 | 0.97±0.1 | 1.1±0.05 | 0.67±0.13 | 1.27±0.05 | 1.3±0.09 | 1.56±0.46 | 0.91±0.21 | 0.78±0.17 | 0.69±0.06 | 0.81±0.17 | 1.1±0.15 | 0.96±0.08 | 0.89±0.09 |
| 25. | Q08652 | Rbp2 | Retinol-binding protein 2 | 1.09±0.18 | 1.19±0.06 | 1.21±0.08 | 1.1±0.12 | 0.98±0.09 | 2.56±0.08 | 1.1±0.04 | 1.27±0.05 | 0.78±0.07 | 0.67±0.06 | 2.24±0.27 | 1.2±0.12 | 1.5±0.18 | 1.25±0.15 | 1.38±0.11 | 1.25±0.08 | 0.8±0.1 |
| 26. | P47738 | Aldh2 | Aldehyde dehydrogenase | 1.26±0.11 | 1.44±0.13 | 1.1±0.15 | 1.08±0.17 | 0.99±0.06 | 1.4±0.05 | 1.15±0.08 | 1.07±0.06 | 0.76±0.18 | 1.04±0.19 | 2.46±0.11 | 1.38±0.13 | 0.87±0.07 | 0.8±0.03 | 0.8±0.09 | 1.08±0.1 | 1.2±0.13 |
| 27. | P14211 | CRP | Calreticulin | 1±0.06 | 0.92±0.12 | 0.83±0.3 | 0.85±0.07 | 0.99±0.1 | 1.23±0.14 | 0.96±0.07 | 1.25±0.16 | 1.65±0.1 | 1.58±0.22 | 0.86±0.19 | 0.92±0.11 | 1±0.08 | 0.82±0.06 | 0.86±0.1 | 0.96±0.21 | 0.88±0.14 |
| 29. | P63017 | Hspa8 | Heat shock cognate 71 kDa protein | 0.79±0.13 | 0.89±0.09 | 0.86±0.21 | 0.92±0.15 | 0.91±0.2 | 0.53±0.08 | 1.64±0.16 | 1.5±0.09 | 2.1±0.12 | 0.44±0.09 | 0.608±0.02 | 1.01±0.06 | 1.1±0.07 | 0.8±0.17 | 0.78±0.08 | 1.02±0.15 | 1.1±0.16 |
| 30. | Q9Z204 | Hnrnpc | Heterogeneous nuclear ribonucleoproteins C1/C2 | 1.23±0.14 | 1.18±0.18 | 1.31±0.16 | 1.21±0.09 | 1.09±0.16 | 2.05±0.07 | 0.94±0.09 | 1.1±0.08 | 0.69±0.12 | 0.59±0.09 | 1.1±0.12 | 1.49±0.21 | 1.7±1.11 | 1.46±0.09 | 1.27±0.08 | 1.33±0.09 | 1.06±0.12 |
| 32. | Q99PT1 | Arhgdia | Rho GDP dissociation inhibitor (GDI) alpha | 0.89±0.09 | 0.82±0.08 | 0.94±0.07 | 0.89±0.09 | 0.96±0.12 | 1.25±0.16 | 1.01±0.17 | 0.92±0.09 | 0.74±0.08 | 0.66±0.08 | 0.96±0.06 | 0.86±0.21 | 0.93±0.07 | 1.16±0.06 | 1.07±0.05 | 0.88±0.08 | 0.93±0.05 |
| 34. | Q9DCX2 | Atp5h | ATP synthase subunit d | 0.98±0.08 | 0.99±0.11 | 1.03±0.08 | 1±0.07 | 0.86±0.05 | 0.28±0.20 | 0.95±0.08 | 1±0.07 | 0.9±0.07 | 1.42±0.18 | 0.8±0.07 | 0.9±0.08 | 0.82±0.06 | 1.16±0.08 | 1.07±0.11 | 0.76±0.08 | 0.78±0.07 |
| 35. | Q9Z218 | Dpp6 | GTP-specific succinyl-CoA synthetase beta subunit | 1.12±0.17 | 1.21±0.81 | 1.2±0.13 | 1.09±0.06 | 0.96±0.08 | 0.99±0.20 | 0.94±0.08 | 0.66±0.07 | 0.54±0.08 | 0.68±0.15 | 1.03±0.09 | 1±0.1 | 0.86±0.087 | 0.86±0.13 | 0.93±0.09 | 0.73±0.15 | 0.74±0.03 |
| 36. | Q9DBP5 | Cmpk1 | UMP-CMP kinase | 1.03±0.09 | 1.1±0.11 | 1.09±0.08 | 1±0.09 | 1±0.07 | 1.6±0.2 | 0.91±0.08 | 0.97±0.05 | 1±0.06 | 1.24±0.08 | 0.95±0.09 | 0.89±0.05 | 0.83±0.1 | 1.12±0.17 | 1.17±0.09 | 0.89±0.05 | 0.91±0.04 |
| 37. | Q9D8C4 | Ifi35 | Interferon-induced 35 kDa protein | 0.92±0.04 | 0.96±0.07 | 0.7±0.05 | 0.63±1.09 | 0.69±0.11 | 1±0.21 | 0.86±0.06 | 0.8±0.07 | 0.8±0.08 | 0.92±0.1 | 0.95±0.16 | 0.88±0.09 | 1.1±0.08 | 0.53±1.1 | 0.58±0.12 | 0.78±0.095 | 1.07±1.2 |
| 38. | P23492 | Pnp | Purine nucleoside phosphorylase | 1±0.08 | 0.99±0.07 | 1.07±0.12 | 1±0.17 | 0.92±0.06 | 1±0.12 | 1.02±0.16 | 0.66±0.21 | 0.71±0.17 | 0.68±0.21 | 1.19±0.12 | 0.96±0.06 | 0.7±0.16 | 1.11±0.08 | 0.99±0.15 | 0.76±0.07 | 0.83±0.17 |
| 39. | Q91VC5 | MECL1 | Proteasome subnuit MECL-1 | 0.88±0.09 | 0.89±0.05 | 0.92±0.11 | 0.91±0.16 | 1±0.03 | 1.48±0.21 | 0.97±0.08 | 0.99±0.09 | 0.73±0.1 | 1.38±0.21 | 0.82±0.08 | 0.8±0.07 | 0.64±0.15 | 0.8±0.07 | 0.8±0.09 | 0.83±0.16 | 0.86±0.06 |
| 40. | O70400 | Pdlim1 | PDZ and LIM domain protein 1 | 1.13±0.09 | 1±0.11 | 0.98±0.08 | 1.02±0.06 | 1.02±0.11 | 1.68±0.23 | 0.97±0.17 | 1.1±0.08 | 1.3±0.14 | 1.25±0.18 | 0.91±0.05 | 0.82±0.17 | 1±0.09 | 1.83±0.17 | 1.44±0.16 | 1.28±0.15 | 1.18±0.06 |
| 41. | Q08652 | Rbp2 | Retinol-binding protein 2 | 1±0.07 | 0.98±0.14 | 0.95±0.08 | 0.99±0.04 | 1.1±0.1 | 3.0±1.4 | 1.7±0.18 | 0.9±0.07 | 0.8±0.06 | 0.66±0.12 | 1.3±0.02 | 1.2±0.19 | 1±0.07 | 1.3±0.14 | 1.43±0.23 | 1.36±0.16 | 0.8±0.08 |
| 42. | Q9R1P1 | Psmb3 | Proteasome subunit beta | 0.78±0.04 | 0.76±0.08 | 0.85±0.05 | 0.97±0.11 | 1.02±0.1 | 0.89±0.08 | 0.84±0.07 | 0.62±0.18 | 0.67±0.2 | 0.76±0.16 | 0.76±0.09 | 0.7±0.09 | 0.82±0.05 | 1.1±0.1 | 0.83±0.08 | 0.64±0.19 | 0.75±0.08 |
| 43. | Q8CDN6 | Txnl1 | Thioredoxin-like protein 1 | 1.05±0.12 | 1.1±0.16 | 1.16±0.21 | 1±0.08 | 1.11±0.13 | 1.3±0.08 | 0.88±0.07 | 1.06±0.12 | 0.66±0.26 | 0.61±0.17 | 0.84±0.05 | 0.8±0.07 | 1±0.1 | 0.96±0.08 | 1.54±0.14 | 1.04±0.12 | 0.83±0.07 |

a,b,c) fold changes in protein expression on 2DE gels with respect to controls along with their ±SD values.

TABLE S4: Predicted functional partners used in string network analysis .

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| S.No. | Uniprot ID | Gene name | Protein name | Biological functions |
| 1. | P99026 | Psmb4 | Proteasome subunit beta type-4 | These proteins are component of the 20S core proteasome complex involved in the proteolytic degradation of most intracellular proteins. This complex plays numerous essential roles within the cell by associating with different regulatory particles. These associates with two 19S regulatory particles to forms the 26S proteasome and thus participates in the ATP-dependent degradation of ubiquitinated proteins. The 26S proteasome plays a key role in the maintenance of protein homeostasis by removing misfolded or damaged proteins that could impair cellular functions, and by removing proteins whose functions are no longer required. Associated with the PA200 or PA28, the 20S proteasome mediates ubiquitin-independent protein degradation. |
| 2. | P70195 | Psmb7 | Proteasome subunit beta type-7 |
| 3. | Q9R1P3 | Psmb2 | Proteasome subunit beta type-2 |
| 4. | Q9Z2U0 | Psma7 | Proteasome subunit alpha type-7 |
| 5. | O09061 | Psmb1 | Proteasome subunit beta type-1 |
| 6. | P49722 | Psma2 | Proteasome subunit alpha type-2 |
| 7. | Q9R1P4 | Psma1 | Proteasome subunit alpha type-1 |
| 8. | Q9R1P0 | Psma4 | Proteasome subunit alpha type-4 |
| 9. | P08113 | Hsp90b1 | 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. It functions in endoplasmic reticulum associated degradation |
| 10. | P27773 | Pdia3 | Protein disulfide-isomerase A3 | An endoplasmic reticulum protein which activates in response to stress conditions and maintains cell redox homeostasis. |

Table 5: Histopathology parameters studied in jejunum tissue after 9Gray irradiation and G-003M pretreatment.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Parameters studied | Untreated | G-003M | **72 h** | | **216 h** | | **840 h** |
| 9 Gray | G-003M+9 Gray | 9 Gray | G-003M+9 Gray | G-003M+9 Gray |
| Villi height (µm) a | 499.48±29.36 | 472.7271±22.80 | 212.99±32.22 | 381.34±38.58 | 147.82±27.21 | 426.44±19.08 | 470.60±26.23 |
| Villi number b | 52.4±4.6 | 50.3±4.49 | 33.6±4.2 | 40.2±3.8 | 21.8±2.3 | 44.3±4.0 | 53.3±3.88 |
| Crypt number c | 100.8±4.41 | 100.3±3.16 | 43.6±5.8 | 70.5±6 | 23.1±3.3 | 83.8±4.2 | 91.0±11 |

a,b,c): The details of three different parameters which were studied in all experimental groups at three different time-points (early, mid and recovery) with their ±SD values.