**Figure S1:** Expression profiles were separated into clusters of expression patterns. (A) Each line represents the standardized abundance of a spot across all gels and belongs to treated for 24h compared to the control cluster generated by hierarchical cluster analysis. (B) Spots with decreased abundance indicate 12 downregulated proteins in treated MCF-7 after 24h when compared to the experimental control. Spots with decreased abundance indicated 15 downregulated proteins in treated MCF-7 cells after 48h when compared to the control. (C) Each line represents the standardized abundance of a spot across all gels and belongs treated for 48h compared to the control cluster generated by hierarchical cluster analysis, (D) Spots with increased abundance indicate the 33 proteins upregulated in treated MCF-7 after 24h compared to the experimental control. Spots with increased abundance indicated that the 16 proteins were upregulated with *E. faecalis* for 48h compared to the control (Progenesis Same Spots).

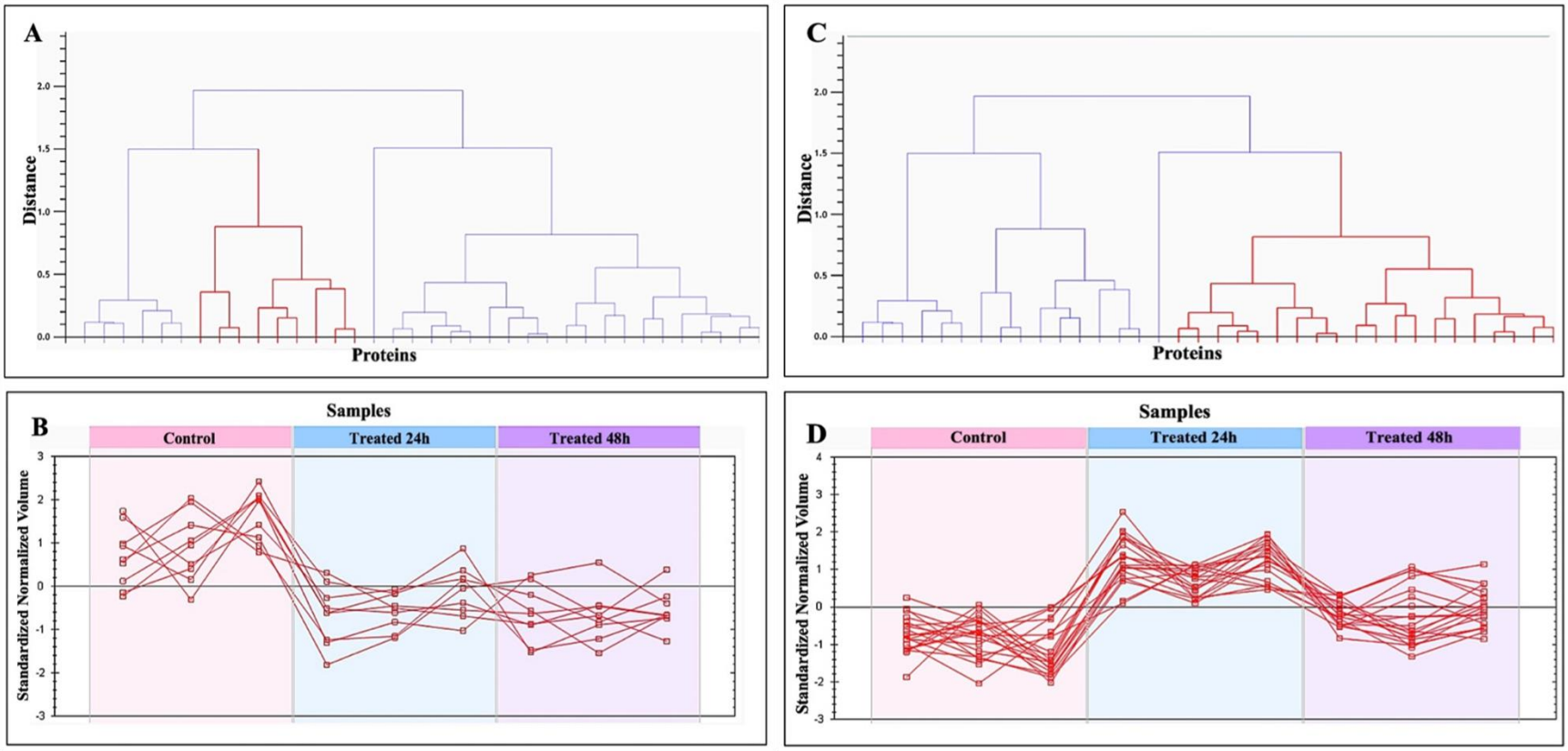

**Figure S2:** (A) 23 top canonical pathways identified using ingenuity pathway analysis (IPA) ranked by p-value after 24h, (B) 9 top canonical pathways identified using ingenuity pathway analysis (IPA) ranked by the P-values AFTER 48h.

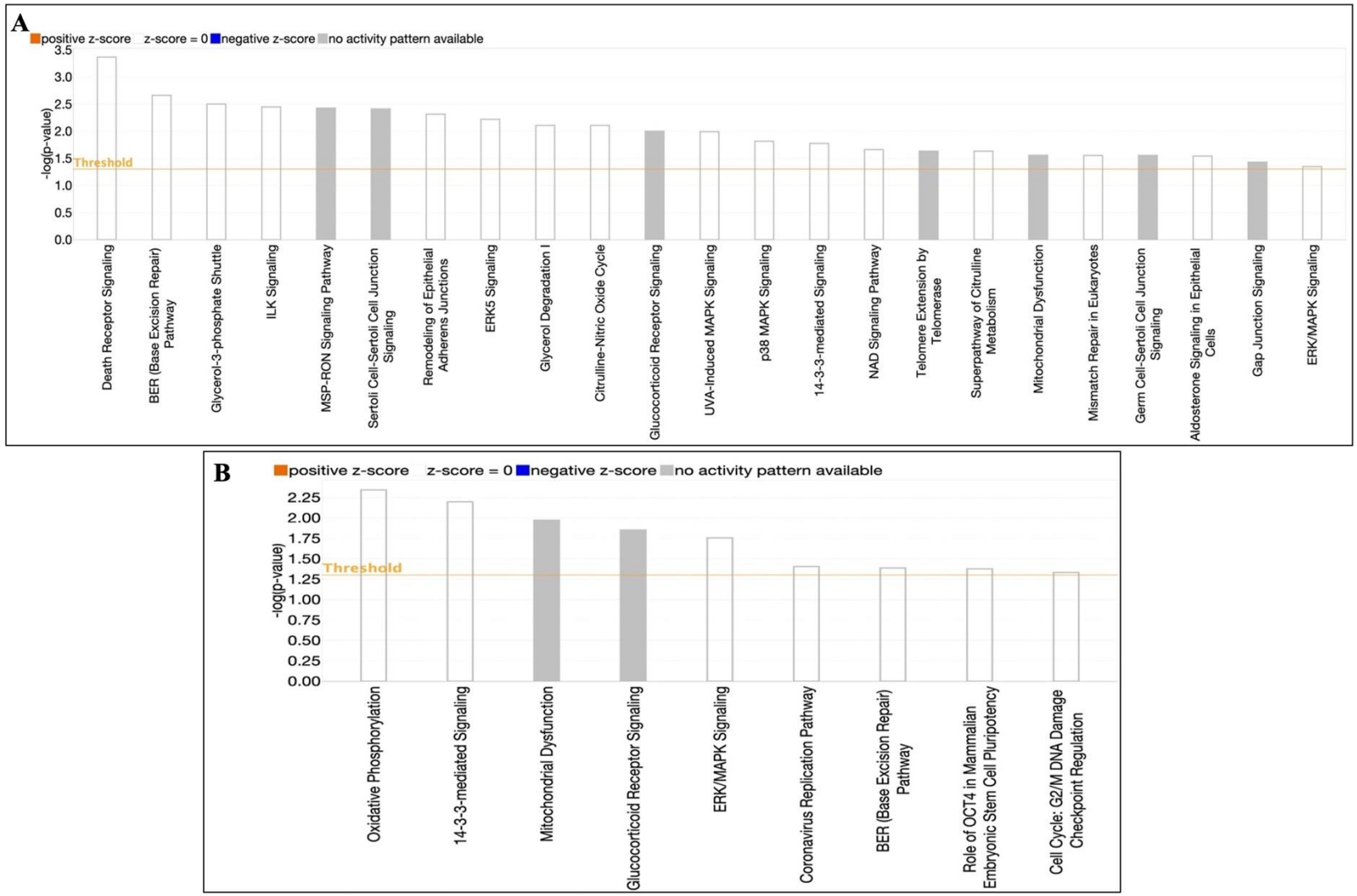

**Table S1:** Experimental design: 9 samples run on 5 2D-PAGE gels, samples were labeled randomly with Cy3 and Cy5, and a pooled sample was used as an internal standard and was stained with Cy2.

| Gel | Cy3 | Cy5 | Cy2 |
|---|---|---|---|
| 1 | N-1 | T24-1 | Pooled sample |
| 2 | T48-1 | N-2 | Pooled sample |
| 3 | N-3 | T24-2 | Pooled sample |
| 4 | T24-3 | T48-2 | Pooled sample |
| 5 | T48-3 B | - | Pooled sample |

N: NON-TREATED, T24: TREATED AT 24 TIME POINT, T48: TREATED AT 48 TIME POINT.

**Figure S3:** Study workflow

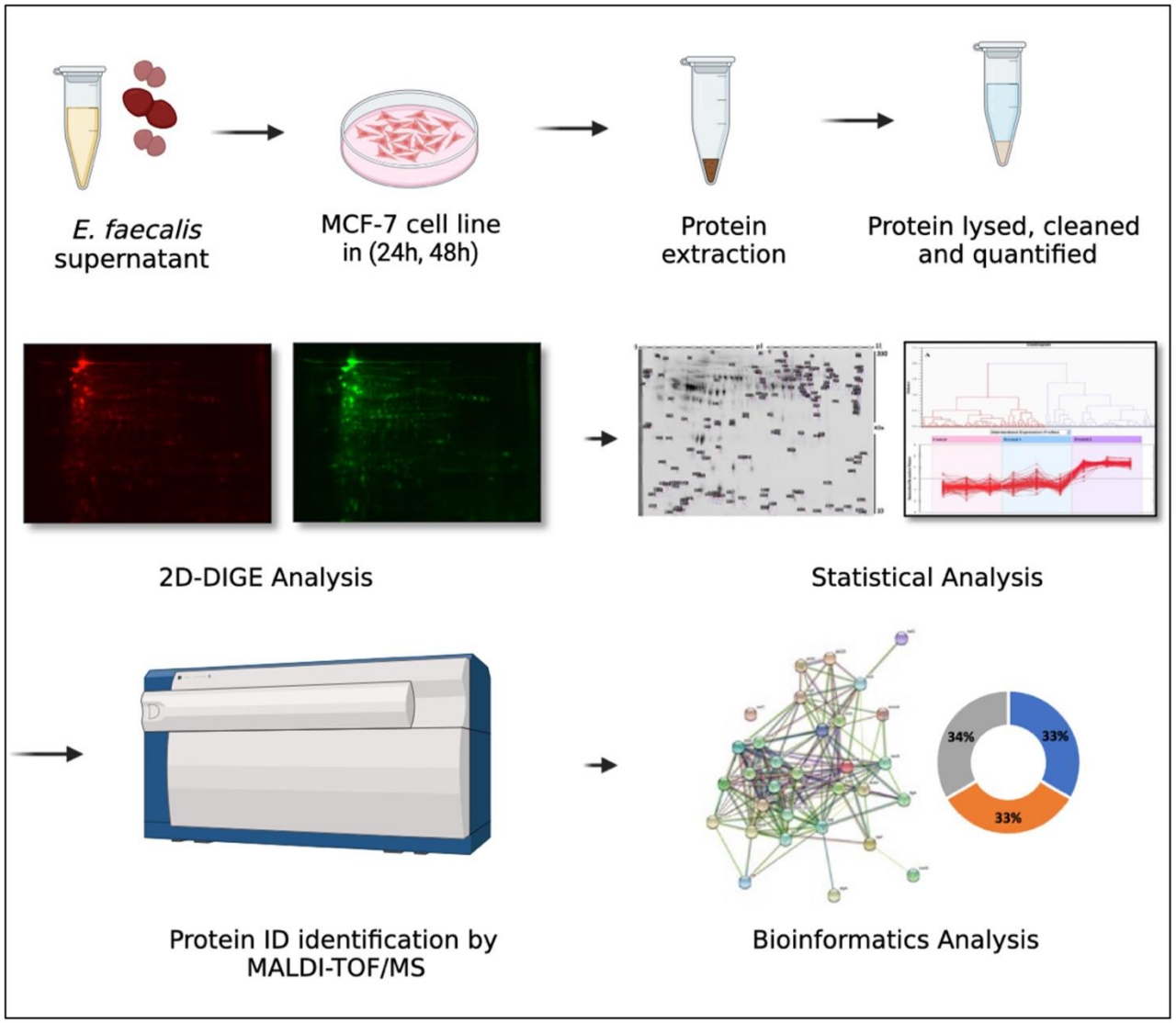

**Table S2:** Mass spectrometry list of significant differentially abundant proteins between liraglutide pre-treated and post –treated states identified in urine samples, using 2D-DIGE with. Protein name, accession number, Mascot score, MS % coverage, protein MW and pI values according to Uniprot database are listed. a Protein accession number for SWISSPROT Database.

| Sl no: | Spot No[a] | Accession No | Protein Name | MASCOT ID | Pi[b] | MW[C] | Cov%[d] | Score[e] |
|---|---|---|---|---|---|---|---|---|
| 1 | 309 | Q08AN1 | Zinc finger protein 616 | ZN616_HUMAN | 9.6 | 93066 | 22 | 63 |
| 2 | 641 | P35228 | Nitric oxide synthase, inducible | NOS2_HUMAN | 8.20 | 132573 | 19 | 57 |
| 3 | 652 | Q01995 | Transgelin | TAGL_HUMAN | 8.8 | 22653 | 46 | 65 |
| 4 | 644 | Q9UIF3 | Tektin-2 | TEKT2_HUMAN | 5.3 | 50155 | 30 | 57 |
| 5 | 827 | Q9GZT9 | Egl nine homolog 1 | EGLN1_HUMAN | 8.8 | 46847 | 34 | 85 |
| 6 | 682 | Q8IVF4 | Dynein axonemal heavy chain 10 | DYH10_HUMAN | 5.64 | 517677 | 14 | 57 |
| 7 | 828 | Q6IBS0 | Twinfilin-2 | TWF2_HUMAN | 6.3 | 39751 | 24 | 51 |
| 8 | 899 | Q9NRC6 | Spectrin beta chain, non-erythrocytic 5 | SPTN5_HUMAN | 6.2 | 419259 | 20 | 68 |
| 9 | 655 | P05783 | Keratin, type I cytoskeletal 18 | K1C18_HUMAN | 5.3 | 48029 | 69 | 184 |
| 10 | 896 | P20674 | Cytochrome c oxidase subunit 5A, mitochondrial | COX5A_HUMAN | 6.3 | 16923 | 66 | 85 |
| 11 | 365 | Q16891 | MICOS complex subunit MIC60 | MIC60_HUMAN | 6.08 | 84025 | 46 | 165 |
| 12 | 428 | A6NI56 | Coiled-coil domain-containing protein 154 | CC154_HUMAN | 8.62 | 76422 | 26 | 66 |
| 13 | 606 | Q15149 | Plectin | PLEC1_HUMAN | 5.74 | 533462 | 14 | 57 |
| 14 | 686 | Q6ZNG1 | Zinc finger protein 600 | ZN600_HUMAN | 9.4 | 85841 | 24 | 57 |
| 15 | 692 | Q8NAA6 | Putative uncharacterized protein encoded by LINC02694 | CO053_HUMAN | 9.9 | 20123 | 38 | 57 |
| 16 | 674 | O75665 | Centriole and centriolar satellite protein OFD1 | OFD1_HUMAN | 5.8 | 117055 | 12 | 58 |
| 17 | 696 | Q96JY0 | Protein maelstrom homolog | MAEL_HUMAN | 8.9 | 49872 | 29 | 59 |
| 18 | 786 | P35232 | Prohibitin 1 | PHB_HUMAN | 5.5 | 29843 | 83 | 131 |
| 19 | 603 | Q96JE9 | Microtubule-associated protein 6 | MAP6_HUMAN | 9.2 | 86680 | 31 | 57 |
| 20 | 767 | P21941 | Cartilage matrix protein | MATN1_HUMAN | 7.8 | 54465 | 27 | 58 |
| 21 | 581 | P06576 | ATP synthase subunit beta, mitochondrial | ATPB_HUMAN | 5.2 | 56525 | 72 | 241 |
| 22 | 779 | P13645 | Keratin, type I cytoskeletal 10 | K1C10_HUMAN | 5.13 | 59020 | 29 | 63 |
| 23 | 465 | P07437 | Tubulin beta chain | TBB5_HUMAN | 4.7 | 50095 | 60 | 185 |
| 24 | 605 | Q9H2K2 | Poly [ADP-ribose] polymerase tankyrase-2 | TNKS2_HUMAN | 6.6 | 128492 | 19 | 65 |
| 25 | 409 | P35251 | Replication factor C subunit 1 | RFC1_HUMAN | 9.3 | 128688 | 16 | 58 |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| 26 | 419 | P10809 | 60 kDa heat shock protein, mitochondrial | CH60_HUMAN | 5.7 | 61187 | 39 | 100 |
| 27 | 453 | Q9Y2G4 | Ankyrin repeat domain-containing protein 6 | ANKR6_HUMAN | 9.42 | 80763 | 20 | 58 |
| 28 | 695 | Q9H8U3 | AN1-type zinc finger protein 3 | ZFAN3_HUMAN | 7.4 | 26023 | 25 | 59 |
| 29 | 362 | Q9H8U3 | AN1-type zinc finger protein 3 | ZFAN3_HUMAN | 7.4 | 26023 | 38 | 73 |
| 30 | 637 | P63261 | Actin, cytoplasmic 2 | ACTG_HUMAN | 5.3 | 42108 | 74 | 178 |
| 31 | 791 | P63104 | 14-3-3 protein zeta/delta | 1433Z_HUMAN | 4.7 | 27899 | 56 | 93 |
| 32 | 678 | Q96HD9 | N-acyl-aromatic-L-amino acid amidohydrolase (carboxylate-forming) | ACY3_HUMAN | 5.5 | 35504 | 21 | 59 |
| 33 | 386 | Q9NYC9 | Dynein axonemal heavy chain 9 | DYH9_HUMAN | 5.6 | 515627 | 19 | 74 |
| 34 | 677 | B1AJZ9 | Forkhead-associated domain-containing protein 1 | FHAD1_HUMAN | 6.5 | 162659 | 20 | 72 |
| 35 | 847 | Q7Z3Y8 | Keratin, type I cytoskeletal 27 | K1C27_HUMAN | 5.06 | 50420 | 24 | 69 |
| 36 | 680 | Q99959 | Plakophilin-2 | PKP2_HUMAN | 9.3 | 97852 | 21 | 66 |
| 37 | 601 | O95243 | Methyl-CpG-binding domain protein 4 | MBD4_HUMAN | 9.01 | 66808 | 33 | 57 |
| 38 | 665 | Q9UK32 | Ribosomal protein S6 kinase alpha-6 | KS6A6_HUMAN | 5.9 | 84389 | 33 | 63 |
| 39 | 642 | P43304 | Glycerol-3-phosphate dehydrogenase, mitochondrial | GPDM_HUMAN | 7.5 | 81315 | 25 | 57 |
| 40 | 814 | P04792 | Heat shock protein beta-1 | HSPB1_HUMAN | 5.9 | 22826 | 72 | 152 |
| 41 | 612 | P63261 | Actin, cytoplasmic 2 | ACTG_HUMAN | 5.3 | 42108 | 80 | 197 |
| 42 | 691 | B2CW77 | Killin | KILIN_HUMAN | 11.2 | 20288 | 67 | 73 |
| 43 | 799 | Q9NZQ3 | NCK-interacting protein with SH3 domain | SPN90_HUMAN | 5.9 | 79651 | 21 | 57 |
| 44 | 449 | A2A3K4 | Protein tyrosine phosphatase domain-containing protein 1 | PTPC1_HUMAN | 7.3 | 85543 | 27 | 57 |
| 45 | 707 | Q8NBN7 | Retinol dehydrogenase 13 | RDH13_HUMAN | 8.2 | 36195 | 33 | 63 |
| 46 | 414 | O95613 | Pericentrin | PCNT_HUMAN | 5.39 | 380644 | 11 | 64 |
| 47 | 334 | O95171 | Sciellin | SCEL_HUMAN | 9.42 | 78018 | 20 | 66 |
| 48 | 423 | P07237 | Protein disulfide-isomerase | PDIA1_HUMAN | 4.7 | 57480 | 73 | 239 |
| 49 | 460 | P12883 | Myosin-7 | MYH7_HUMAN | 5.6 | 223757 | 24 | 57 |
| 50 | 804 | Q9Y3D5 | 28S ribosomal protein S18c, mitochondrial | RT18C_HUMAN | 9.6 | 16238 | 52 | 67 |
| 51 | 393 | P25705 | ATP synthase subunit alpha, mitochondrial | ATPA_HUMAN | 9.16 | 59828 | 55 | 126 |
| 52 | 438 | Q9H8U3 | AN1-type zinc finger protein 3 | ZFAN3_HUMAN | 7.4 | 26023 | 28 | 59 |
| 53 | 912 | O00571 | ATP-dependent RNA helicase DDX3X | DDX3X_HUMAN | 6.7 | 73597 | 29 | 59 |
| 54 | 547 | P10809 | 60 kDa heat shock protein, mitochondrial | CH60_HUMAN | 5.7 | 61187 | 38 | 70 |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| 55 | 790 | Q8IY21 | Probable ATP-dependent RNA helicase DDX60 | DDX60_HUMAN | 7.6 | 199680 | 14 | 57 |
| 56 | 792 | Q9UKX3 | Myosin-13 | MYH13_HUMAN | 5.5 | 224681 | 17 | 65 |
| 57 | 487 | P10809 | 60 kDa heat shock protein, mitochondrial | CH60_HUMAN | 5.7 | 61187 | 34 | 85 |
| 58 | 635 | Q9Y623 | Myosin-4 | MYH4_HUMAN | 5.6 | 223902 | 23 | 64 |

[a] Spot numbers
[b] Theoretical isoelectric point
[c] Theoretical relative mass
[d] MASCOT coverage
[e] MASCOT score