

A Protein was classified as identified if at least 2 high or 3 medium (at least) confident peptides were counted

Filtering: Peptides high and medium confident, Rank 1

Grouping: no Protein or Peptide Grouping applied

Proteins Ido1.msf

| Accession | Description | Σ Coverage | Σ # Proteins | Σ # Unique Peptides | Σ # Peptides | Σ # PSMs | Score A3 |
|-----------|---------------------------------------------------------------------------------------------------------------|-------------------|---------------------|----------------------------|---------------------|-----------------|------------|
| P42704 | Leucine-rich PPR motif-containing protein, mitochondrial OS=Homo sapiens GN=LRPPRC PE=1 SV=3 - [LRPPRC_HUMAN] | 38.95 | 1 | 11 | 47 | 162 | 493.265287 |
| Q9Y5B9 | FACT complex subunit SPT16 OS=Homo sapiens GN=SUPT16H PE=1 SV=1 - [SP16H_HUMAN] | 15.19 | 1 | 10 | 14 | 41 | 118.72624 |
| P04264 | Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6 - [K2C1_HUMAN] | 17.55 | 1 | 10 | 12 | 38 | 113.71954 |
| P13645 | Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6 - [K1C10_HUMAN] | 11.64 | 1 | 6 | 7 | 13 | 37.1180353 |
| Q08211 | ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4 - [DHX9_HUMAN] | 18.58 | 1 | 3 | 20 | 51 | 150.121027 |
| P35527 | Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3 - [K1C9_HUMAN] | 5.14 | 1 | 3 | 3 | 5 | 15.0945359 |
| P35908 | Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2 - [K22E_HUMAN] | 11.89 | 1 | 2 | 6 | 20 | 60.0736578 |
| Q9Y2W1 | Thyroid hormone receptor-associated protein 3 OS=Homo sapiens GN=THRAP3 PE=1 SV=2 - [TR150_HUMAN] | 3.25 | 1 | 2 | 3 | 4 | 9.59124613 |
| Q9Y2H6 | Fibronectin type-III domain-containing protein 3A OS=Homo sapiens GN=FNDC3A PE=1 SV=4 - [FND3A_HUMAN] | 1.84 | 1 | 2 | 2 | 3 | 9.13725853 |
| P08779 | Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4 - [K1C16_HUMAN] | 23.04 | 1 | 1 | 9 | 26 | 75.3197753 |
| P02533 | Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4 - [K1C14_HUMAN] | 19.49 | 1 | 1 | 8 | 25 | 74.2519693 |
| Q15393 | Splicing factor 3B subunit 3 OS=Homo sapiens GN=SF3B3 PE=1 SV=4 - [SF3B3_HUMAN] | 6.16 | 1 | 1 | 6 | 10 | 26.9986374 |
| Q29RF7 | Sister chromatid cohesion protein PDS5 homolog A OS=Homo sapiens GN=PDS5A PE=1 SV=1 - [PDS5A_HUMAN] | 2.92 | 1 | 1 | 3 | 7 | 20.386085 |
| O75533 | Splicing factor 3B subunit 1 OS=Homo sapiens GN=SF3B1 PE=1 | 1.84 | 1 | 1 | 2 | 4 | 11.851424 |

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| | SV=3 - [SF3B1_HUMAN] | | | | | | |
| B4DSR0 | cDNA FLJ60080, highly similar to 130 kDa leucine-rich protein (LRP 130) (Fragment) OS=Homo sapiens PE=2 SV=1 - [B4DSR0_HUMAN] | 32.01 | 1 | 0 | 32 | 116 | 347.283659 |
| B4E0E1 | cDNA FLJ53442, highly similar to Poly (ADP-ribose) polymerase 1 (EC 2.4.2.30) OS=Homo sapiens PE=2 SV=1 - [B4E0E1_HUMAN] | 25.28 | 1 | 0 | 20 | 54 | 159.558493 |
| P09874 | Poly [ADP-ribose] polymerase 1 OS=Homo sapiens GN=PARP1 PE=1 SV=4 - [PARP1_HUMAN] | 24.75 | 1 | 0 | 20 | 54 | 159.558493 |
| B2R5W3 | cDNA, FLJ92658, highly similar to Homo sapiens poly (ADP-ribose) polymerase family, member 1 (PARP1), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R5W3_HUMAN] | 23.08 | 1 | 0 | 19 | 53 | 154.729016 |
| B8ZZ38 | Uncharacterized protein OS=Homo sapiens GN=LRPPRC PE=4 SV=1 - [B8ZZ38_HUMAN] | 32.74 | 1 | 0 | 15 | 48 | 159.493713 |
| C9JCA9 | Uncharacterized protein OS=Homo sapiens GN=LRPPRC PE=4 SV=1 - [C9JCA9_HUMAN] | 43.18 | 1 | 0 | 14 | 47 | 157.232792 |
| B3KX72 | cDNA FLJ44920 fis, clone BRAMY3011501, highly similar to Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens PE=2 SV=1 - [B3KX72_HUMAN] | 19.07 | 1 | 0 | 12 | 42 | 124.937752 |
| B4DLR3 | cDNA FLJ54020, highly similar to Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens PE=2 SV=1 - [B4DLR3_HUMAN] | 18.24 | 1 | 0 | 12 | 42 | 124.937752 |
| Q00839 | Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6 - [HNRNPU_HUMAN] | 17.33 | 1 | 0 | 12 | 42 | 124.937752 |
| B4DRR0 | cDNA FLJ53910, highly similar to Keratin, type II cytoskeletal 6A OS=Homo sapiens PE=2 SV=1 - [B4DRR0_HUMAN] | 20.93 | 1 | 0 | 12 | 29 | 76.95767 |
| B4DRU6 | cDNA FLJ54657, highly similar to Keratin, type II cytoskeletal 6A OS=Homo sapiens PE=2 SV=1 - [B4DRU6_HUMAN] | 20.4 | 1 | 0 | 12 | 29 | 76.95767 |
| P02538 | Keratin, type II cytoskeletal 6A OS=Homo sapiens GN=KRT6A PE=1 SV=3 - [K2C6A_HUMAN] | 19.86 | 1 | 0 | 12 | 29 | 76.95767 |
| A8K2I0 | cDNA FLJ78504, highly similar to Homo sapiens keratin 6A (KRT6A), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K2I0_HUMAN] | 19.86 | 1 | 0 | 12 | 29 | 76.95767 |
| B4DWU6 | cDNA FLJ51361, highly similar to Keratin, type II cytoskeletal 6A | 19.62 | 1 | 0 | 11 | 27 | 71.4421184 |

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| | OS=Homo sapiens PE=2 SV=1 - [B4DWU6_HUMAN] | | | | | | |
| P48668 | Keratin, type II cytoskeletal 6C OS=Homo sapiens GN=KRT6C PE=1 SV=3 - [K2C6C_HUMAN] | 18.09 | 1 | 0 | 11 | 27 | 71.4421184 |
| Q05CI5 | DHX9 protein (Fragment) OS=Homo sapiens GN=DHX9 PE=2 SV=1 - [Q05CI5_HUMAN] | 19.73 | 1 | 0 | 11 | 25 | 70.4537067 |
| Q58F26 | DHX9 protein (Fragment) OS=Homo sapiens GN=DHX9 PE=2 SV=1 - [Q58F26_HUMAN] | 19.63 | 1 | 0 | 11 | 25 | 70.4537067 |
| Q6PJK6 | DHX9 protein (Fragment) OS=Homo sapiens GN=DHX9 PE=2 SV=1 - [Q6PJK6_HUMAN] | 19.53 | 1 | 0 | 11 | 25 | 70.4537067 |
| C9JC37 | Uncharacterized protein OS=Homo sapiens GN=DHX30 PE=4 SV=1 - [C9JC37_HUMAN] | 10.21 | 1 | 0 | 11 | 22 | 56.9982493 |
| Q7L2E3 | Putative ATP-dependent RNA helicase DHX30 OS=Homo sapiens GN=DHX30 PE=1 SV=1 - [DHX30_HUMAN] | 9.97 | 1 | 0 | 11 | 22 | 56.9982493 |
| Q96BA7 | HNRPU protein OS=Homo sapiens PE=2 SV=1 - [Q96BA7_HUMAN] | 18.42 | 1 | 0 | 10 | 38 | 112.918967 |
| Q5RI17 | Heterogeneous nuclear ribonucleoprotein U (Scaffold attachment factor A) (Fragment) OS=Homo sapiens GN=HNRNPU PE=2 SV=1 - [Q5RI17_HUMAN] | 18.4 | 1 | 0 | 10 | 38 | 112.918967 |
| B4DZC0 | cDNA FLJ51771, highly similar to SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5 (EC 3.6.1.-) OS=Homo sapiens PE=2 SV=1 - [B4DZC0_HUMAN] | 11.26 | 1 | 0 | 10 | 30 | 79.1457472 |
| B7ZAX9 | cDNA, FLJ79343, highly similar to SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5 (EC 3.6.1.-) OS=Homo sapiens PE=2 SV=1 - [B7ZAX9_HUMAN] | 11.26 | 1 | 0 | 10 | 30 | 79.1457472 |
| O60264 | SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5 OS=Homo sapiens GN=SMARCA5 PE=1 SV=1 - [SMCA5_HUMAN] | 10.65 | 1 | 0 | 10 | 30 | 79.1457472 |
| P04259 | Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5 - [K2C6B_HUMAN] | 16.49 | 1 | 0 | 10 | 27 | 70.4482784 |
| Q499G6 | General transcription factor II, i OS=Homo sapiens GN=GTF2I PE=2 SV=1 - [Q499G6_HUMAN] | 13.63 | 1 | 0 | 10 | 26 | 73.5153756 |
| A8K9W7 | cDNA FLJ77440, highly similar to Homo sapiens general | 13.6 | 1 | 0 | 10 | 26 | 73.5153756 |

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| | transcription factor II, i (GTF2I), transcript variant 2, mRNA OS=Homo sapiens PE=2 SV=1 - [A8K9W7_HUMAN] | | | | | | |
| B4DH52 | cDNA FLJ55916, highly similar to General transcription factor II-I OS=Homo sapiens PE=2 SV=1 - [B4DH52_HUMAN] | 13.39 | 1 | 0 | 10 | 26 | 73.5153756 |
| P78347 | General transcription factor II-I OS=Homo sapiens GN=GTF2I PE=1 SV=2 - [GTF2I_HUMAN] | 13.33 | 1 | 0 | 10 | 26 | 73.5153756 |
| B4DRY0 | cDNA FLJ54379, highly similar to Keratin, type II cytoskeletal 6E OS=Homo sapiens PE=2 SV=1 - [B4DRY0_HUMAN] | 17 | 1 | 0 | 10 | 25 | 66.7205281 |
| B2R853 | cDNA, FLJ93744, highly similar to Homo sapiens keratin 6E (KRT6E), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R853_HUMAN] | 16.49 | 1 | 0 | 10 | 25 | 66.7205281 |
| B4DKV4 | cDNA FLJ60647, highly similar to Keratin, type II cytoskeletal 6B OS=Homo sapiens PE=2 SV=1 - [B4DKV4_HUMAN] | 17.11 | 1 | 0 | 9 | 23 | 59.7493434 |
| Q9UQE7 | Structural maintenance of chromosomes protein 3 OS=Homo sapiens GN=SMC3 PE=1 SV=2 - [SMC3_HUMAN] | 9.12 | 1 | 0 | 9 | 16 | 44.9258223 |
| B0AZQ4 | cDNA, FLJ79494, highly similar to Structural maintenance of chromosome 3 OS=Homo sapiens PE=2 SV=1 - [B0AZQ4_HUMAN] | 9.12 | 1 | 0 | 9 | 16 | 44.9258223 |
| Q86VX4 | Structural maintenance of chromosomes 3 OS=Homo sapiens GN=SMC3 PE=2 SV=1 - [Q86VX4_HUMAN] | 9.12 | 1 | 0 | 9 | 16 | 44.9258223 |
| Q7Z4Q5 | Heterogeneous nuclear ribonucleoprotein U (Scaffold attachment factor A), isoform CRA_a OS=Homo sapiens GN=HNRPU PE=2 SV=1 - [Q7Z4Q5_HUMAN] | 19.88 | 1 | 0 | 8 | 26 | 76.1465623 |
| Q5RI19 | Heterogeneous nuclear ribonucleoprotein U (Scaffold attachment factor A) OS=Homo sapiens GN=HNRNPU PE=2 SV=1 - [Q5RI19_HUMAN] | 18.58 | 1 | 0 | 8 | 26 | 76.1465623 |
| A2BEY0 | Valyl-tRNA synthetase (Fragment) OS=Homo sapiens GN=VARS PE=3 SV=1 - [A2BEY0_HUMAN] | 9.39 | 1 | 0 | 8 | 18 | 59.0810394 |
| P26640 | Valyl-tRNA synthetase OS=Homo sapiens GN=VARS PE=1 SV=4 - [SYVC_HUMAN] | 8.78 | 1 | 0 | 8 | 18 | 59.0810394 |
| B0V043 | Valyl-tRNA synthetase OS=Homo sapiens GN=VARS PE=3 SV=1 - [B0V043_HUMAN] | 8.78 | 1 | 0 | 8 | 18 | 59.0810394 |
| B7Z2N4 | cDNA FLJ56074, highly similar to 150 kDa oxygen-regulated protein (Orp150) OS=Homo sapiens PE=2 SV=1 - | 8.56 | 1 | 0 | 7 | 18 | 53.6937654 |

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| | [B7Z2N4_HUMAN] | | | | | | |
| Q9Y4L1 | Hypoxia up-regulated protein 1 OS=Homo sapiens GN=HYOU1 PE=1 SV=1 - [HYOU1_HUMAN] | 8.41 | 1 | 0 | 7 | 18 | 53.6937654 |
| B4DRA9 | cDNA FLJ61347, highly similar to General transcription factor II-I OS=Homo sapiens PE=2 SV=1 - [B4DRA9_HUMAN] | 16.79 | 1 | 0 | 7 | 17 | 48.8051691 |
| B4DJT7 | cDNA FLJ56511, highly similar to Neurofilament triplet M protein OS=Homo sapiens PE=2 SV=1 - [B4DJT7_HUMAN] | 10.17 | 1 | 0 | 7 | 13 | 35.303158 |
| A5YM63 | NEFM protein OS=Homo sapiens GN=NEFM PE=2 SV=1 - [A5YM63_HUMAN] | 8.1 | 1 | 0 | 7 | 13 | 35.303158 |
| P07197 | Neurofilament medium polypeptide OS=Homo sapiens GN=NEFM PE=1 SV=3 - [NFM_HUMAN] | 7.75 | 1 | 0 | 7 | 13 | 35.303158 |
| B3KU66 | cDNA FLJ39263 fis, clone OCBBF2009571, highly similar to ATP-dependent RNA helicase A (EC 3.6.1.-) OS=Homo sapiens PE=2 SV=1 - [B3KU66_HUMAN] | 15.85 | 1 | 0 | 6 | 18 | 60.0372725 |
| B7Z766 | cDNA FLJ54564, highly similar to 150 kDa oxygen-regulated protein (Orp150) OS=Homo sapiens PE=2 SV=1 - [B7Z766_HUMAN] | 8.02 | 1 | 0 | 6 | 16 | 46.541353 |
| B3KXH0 | cDNA FLJ45395 fis, clone BRHIP3027191, highly similar to 150 kDa oxygen-regulated protein (Orp150) OS=Homo sapiens PE=2 SV=1 - [B3KXH0_HUMAN] | 6.86 | 1 | 0 | 6 | 16 | 46.541353 |
| Q15155 | Nodal modulator 1 OS=Homo sapiens GN=NOMO1 PE=1 SV=5 - [NOMO1_HUMAN] | 6.71 | 1 | 0 | 6 | 15 | 43.8505869 |
| P69849 | Nodal modulator 3 OS=Homo sapiens GN=NOMO3 PE=2 SV=2 - [NOMO3_HUMAN] | 6.71 | 1 | 0 | 6 | 15 | 43.8505869 |
| Q5JPE7 | Nodal modulator 2 OS=Homo sapiens GN=NOMO2 PE=1 SV=1 - [NOMO2_HUMAN] | 6.47 | 1 | 0 | 6 | 15 | 43.8505869 |
| B4E2P9 | cDNA FLJ56708, highly similar to Keratin, type I cytoskeletal 17 OS=Homo sapiens PE=2 SV=1 - [B4E2P9_HUMAN] | 22.09 | 1 | 0 | 5 | 15 | 27.9421244 |
| Q05D33 | PARP1 protein (Fragment) OS=Homo sapiens GN=PARP1 PE=2 SV=1 - [Q05D33_HUMAN] | 29.74 | 1 | 0 | 5 | 14 | 44.216289 |
| Q6PJL0 | PARP1 protein (Fragment) OS=Homo sapiens GN=PARP1 PE=2 SV=1 - [Q6PJL0_HUMAN] | 27.6 | 1 | 0 | 5 | 14 | 44.216289 |
| Q1LZN2 | NOMO3 protein (Fragment) OS=Homo sapiens GN=NOMO3 PE=2 SV=1 - [Q1LZN2_HUMAN] | 8.43 | 1 | 0 | 5 | 13 | 37.4618847 |

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| Q4G177 | NOMO2 protein OS=Homo sapiens GN=NOMO2 PE=2 SV=1 - [Q4G177_HUMAN] | 6.18 | 1 | 0 | 5 | 13 | 37.4618847 |
| B7Z602 | cDNA FLJ59408, highly similar to 150 kDa oxygen-regulated protein (Orp150) OS=Homo sapiens PE=2 SV=1 - [B7Z602_HUMAN] | 9.76 | 1 | 0 | 5 | 12 | 39.9326749 |
| B4E1T1 | cDNA FLJ54081, highly similar to Keratin, type II cytoskeletal 5 OS=Homo sapiens PE=2 SV=1 - [B4E1T1_HUMAN] | 8.11 | 1 | 0 | 5 | 12 | 30.615799 |
| P13647 | Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3 - [K2C5_HUMAN] | 7.63 | 1 | 0 | 5 | 12 | 30.615799 |
| A8K6V3 | cDNA FLJ78677, highly similar to Homo sapiens splicing factor 3b, subunit 3, 130kDa (SF3B3), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K6V3_HUMAN] | 5.42 | 1 | 0 | 5 | 9 | 24.7939765 |
| Q0VGA3 | SUPT16H protein (Fragment) OS=Homo sapiens GN=SUPT16H PE=2 SV=1 - [Q0VGA3_HUMAN] | 8.04 | 1 | 0 | 4 | 13 | 36.2141337 |
| Q32Q22 | DHX9 protein (Fragment) OS=Homo sapiens GN=DHX9 PE=2 SV=1 - [Q32Q22_HUMAN] | 13.09 | 1 | 0 | 4 | 12 | 38.1625383 |
| Q5RI18 | Heterogeneous nuclear ribonucleoprotein U (Scaffold attachment factor A) (Fragment) OS=Homo sapiens GN=HNRNPU PE=2 SV=1 - [Q5RI18_HUMAN] | 22.73 | 1 | 0 | 4 | 11 | 33.2770281 |
| B4E091 | cDNA FLJ55438, highly similar to Splicing factor 3 subunit 1 OS=Homo sapiens PE=2 SV=1 - [B4E091_HUMAN] | 9.13 | 1 | 0 | 4 | 9 | 29.5671911 |
| Q15459 | Splicing factor 3A subunit 1 OS=Homo sapiens GN=SF3A1 PE=1 SV=1 - [SF3A1_HUMAN] | 7.94 | 1 | 0 | 4 | 9 | 29.5671911 |
| Q5SP20 | Valyl-tRNA synthetase (Fragment) OS=Homo sapiens GN=VARS PE=4 SV=1 - [Q5SP20_HUMAN] | 17.49 | 1 | 0 | 4 | 8 | 26.4099331 |
| B3KQH1 | cDNA FLJ90452 fis, clone NT2RP3001475, highly similar to Splicing factor 3B subunit 3 OS=Homo sapiens PE=2 SV=1 - [B3KQH1_HUMAN] | 6.47 | 1 | 0 | 4 | 8 | 22.0791998 |
| C9JDC4 | Uncharacterized protein OS=Homo sapiens GN=DHX30 PE=4 SV=1 - [C9JDC4_HUMAN] | 12.98 | 1 | 0 | 4 | 7 | 18.0113943 |
| P12035 | Keratin, type II cytoskeletal 3 OS=Homo sapiens GN=KRT3 PE=1 SV=3 - [K2C3_HUMAN] | 4.78 | 1 | 0 | 4 | 7 | 18.9879749 |
| Q16195 | Keratin (Fragment) OS=Homo sapiens GN=keratin PE=2 SV=1 - [Q16195_HUMAN] | 17.21 | 1 | 0 | 4 | 7 | 13.9744183 |

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| B7Z2A1 | cDNA FLJ56068, highly similar to DNA damage-binding protein 1 OS=Homo sapiens PE=2 SV=1 - [B7Z2A1_HUMAN] | 5.68 | 1 | 0 | 4 | 6 | 18.5237398 |
| Q16531 | DNA damage-binding protein 1 OS=Homo sapiens GN=DDB1 PE=1 SV=1 - [DDB1_HUMAN] | 5.44 | 1 | 0 | 4 | 6 | 18.5237398 |
| B4E3Q9 | cDNA FLJ59659, highly similar to Vinculin OS=Homo sapiens PE=2 SV=1 - [B4E3Q9_HUMAN] | 4.64 | 1 | 0 | 4 | 5 | 12.8222017 |
| B3KXA2 | cDNA FLJ45031 fis, clone BRAWH3018548, highly similar to Vinculin OS=Homo sapiens PE=2 SV=1 - [B3KXA2_HUMAN] | 4.27 | 1 | 0 | 4 | 5 | 12.8222017 |
| P18206 | Vinculin OS=Homo sapiens GN=VCL PE=1 SV=4 - [VINC_HUMAN] | 3.79 | 1 | 0 | 4 | 5 | 12.8222017 |
| B4DJ10 | cDNA FLJ58533, highly similar to Leucyl-tRNA synthetase, cytoplasmic (EC 6.1.1.4) OS=Homo sapiens PE=2 SV=1 - [B4DJ10_HUMAN] | 4.1 | 1 | 0 | 4 | 5 | 12.1183436 |
| B4E266 | cDNA FLJ58466, highly similar to Leucyl-tRNA synthetase, cytoplasmic (EC 6.1.1.4) OS=Homo sapiens PE=2 SV=1 - [B4E266_HUMAN] | 4.07 | 1 | 0 | 4 | 5 | 12.1183436 |
| B4DER1 | cDNA FLJ58157, highly similar to Leucyl-tRNA synthetase, cytoplasmic (EC 6.1.1.4) OS=Homo sapiens PE=2 SV=1 - [B4DER1_HUMAN] | 4 | 1 | 0 | 4 | 5 | 12.1183436 |
| Q9P2J5 | Leucyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=LARS PE=1 SV=2 - [SYLC_HUMAN] | 3.91 | 1 | 0 | 4 | 5 | 12.1183436 |
| B2RCM2 | cDNA, FLJ96156, highly similar to Homo sapiens leucyl-tRNA synthetase (LARS), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RCM2_HUMAN] | 3.91 | 1 | 0 | 4 | 5 | 12.1183436 |
| Q96C32 | UBC protein OS=Homo sapiens PE=2 SV=1 - [Q96C32_HUMAN] | 49.84 | 1 | 0 | 3 | 16 | 50.9694574 |
| P0CG47 | Polyubiquitin-B OS=Homo sapiens GN=UBB PE=1 SV=1 - [UBB_HUMAN] | 49.78 | 1 | 0 | 3 | 16 | 50.9694574 |
| Q5PY61 | Ubiquitin C splice variant OS=Homo sapiens GN=UBC PE=2 SV=1 - [Q5PY61_HUMAN] | 49.78 | 1 | 0 | 3 | 16 | 50.9694574 |
| Q5UGI3 | Ubiquitin C splice variant OS=Homo sapiens GN=UBC PE=2 SV=1 - [Q5UGI3_HUMAN] | 49.67 | 1 | 0 | 3 | 16 | 50.9694574 |
| B4DV12 | cDNA FLJ51326, highly similar to Homo sapiens ubiquitin B (UBB), mRNA OS=Homo sapiens PE=2 SV=1 - [B4DV12_HUMAN] | 49.67 | 1 | 0 | 3 | 16 | 50.9694574 |

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| Q59EM9 | Ubiquitin C variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59EM9_HUMAN] | 49.35 | 1 | 0 | 3 | 16 | 50.9694574 |
| Q66K58 | Putative uncharacterized protein (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q66K58_HUMAN] | 49 | 1 | 0 | 3 | 16 | 50.9694574 |
| Q96H31 | UBC protein (Fragment) OS=Homo sapiens GN=UBC PE=2 SV=2 - [Q96H31_HUMAN] | 48.72 | 1 | 0 | 3 | 16 | 50.9694574 |
| P0CG48 | Polyubiquitin-C OS=Homo sapiens GN=UBC PE=1 SV=2 - [UBC_HUMAN] | 48.03 | 1 | 0 | 3 | 16 | 50.9694574 |
| Q9UFQ0 | Putative uncharacterized protein DKFZp434K0435 (Fragment) OS=Homo sapiens GN=DKFZp434K0435 PE=2 SV=1 - [Q9UFQ0_HUMAN] | 47.7 | 1 | 0 | 3 | 16 | 50.9694574 |
| A8K674 | cDNA FLJ75516, highly similar to Xenopus tropicalis ubiquitin C, mRNA OS=Homo sapiens PE=2 SV=1 - [A8K674_HUMAN] | 47.29 | 1 | 0 | 3 | 16 | 50.9694574 |
| Q96MH4 | cDNA FLJ32377 fis, clone SKMUS1000014, highly similar to Polyubiquitin 9 OS=Homo sapiens PE=2 SV=1 - [Q96MH4_HUMAN] | 45.88 | 1 | 0 | 3 | 16 | 50.9694574 |
| P62987 | Ubiquitin-60S ribosomal protein L40 OS=Homo sapiens GN=UBA52 PE=1 SV=2 - [RL40_HUMAN] | 29.69 | 1 | 0 | 3 | 16 | 50.9694574 |
| P62979 | Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=1 SV=2 - [RS27A_HUMAN] | 24.36 | 1 | 0 | 3 | 16 | 50.9694574 |
| Q5RKT7 | Ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=2 SV=1 - [Q5RKT7_HUMAN] | 24.36 | 1 | 0 | 3 | 16 | 50.9694574 |
| B4E204 | cDNA FLJ58872, highly similar to Keratin, type I cytoskeletal 15 OS=Homo sapiens PE=2 SV=1 - [B4E204_HUMAN] | 11.97 | 1 | 0 | 3 | 16 | 34.4543213 |
| C9JM50 | Uncharacterized protein OS=Homo sapiens GN=KRT19 PE=4 SV=1 - [C9JM50_HUMAN] | 13.27 | 1 | 0 | 3 | 11 | 19.6733164 |
| P08727 | Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=4 - [K1C19_HUMAN] | 6.5 | 1 | 0 | 3 | 11 | 19.6733164 |
| B5MDB6 | Uncharacterized protein OS=Homo sapiens GN=NLRC3 PE=4 SV=2 - [B5MDB6_HUMAN] | 3.67 | 1 | 0 | 3 | 10 | 27.239696 |
| Q7RTR2 | Protein NLRC3 OS=Homo sapiens GN=NLRC3 PE=2 SV=2 - [NLRC3_HUMAN] | 3.57 | 1 | 0 | 3 | 10 | 27.239696 |
| C9JW09 | Uncharacterized protein OS=Homo sapiens GN=NLRC3 PE=4 SV=1 - [C9JW09_HUMAN] | 3.57 | 1 | 0 | 3 | 10 | 27.239696 |

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|--------|-----------------------------------------------------------------------------------------------------------------|-------|---|---|---|----|------------|
| C9JLH9 | Uncharacterized protein OS=Homo sapiens GN=NLRC3 PE=4 SV=1 - [C9JLH9_HUMAN] | 3.42 | 1 | 0 | 3 | 10 | 27.239696 |
| B4DWU0 | cDNA FLJ56791, highly similar to Keratin, type I cytoskeletal 16 OS=Homo sapiens PE=2 SV=1 - [B4DWU0_HUMAN] | 28.15 | 1 | 0 | 3 | 9 | 24.7203991 |
| Q01546 | Keratin, type II cytoskeletal 2 oral OS=Homo sapiens GN=KRT76 PE=1 SV=2 - [K22O_HUMAN] | 4.23 | 1 | 0 | 3 | 9 | 21.6266592 |
| B4DG00 | cDNA FLJ52436, highly similar to DNA damage-binding protein 1 OS=Homo sapiens PE=2 SV=1 - [B4DG00_HUMAN] | 5.76 | 1 | 0 | 3 | 9 | 17.8252127 |
| Q12803 | ATP-dependent RNA helicase A OS=Homo sapiens GN=LKP PE=1 SV=1 - [Q12803_HUMAN] | 17.87 | 1 | 0 | 3 | 8 | 22.847188 |
| Q05D91 | HYOU1 protein (Fragment) OS=Homo sapiens GN=HYOU1 PE=2 SV=1 - [Q05D91_HUMAN] | 5.48 | 1 | 0 | 3 | 8 | 20.9135029 |
| Q6IN67 | HYOU1 protein OS=Homo sapiens GN=HYOU1 PE=2 SV=1 - [Q6IN67_HUMAN] | 5.31 | 1 | 0 | 3 | 8 | 20.9135029 |
| B4DJM5 | cDNA FLJ61294, highly similar to Keratin, type I cytoskeletal 17 OS=Homo sapiens PE=2 SV=1 - [B4DJM5_HUMAN] | 12.99 | 1 | 0 | 3 | 7 | 12.7046026 |
| A2BEY1 | Valyl-tRNA synthetase (Fragment) OS=Homo sapiens GN=VARS PE=4 SV=1 - [A2BEY1_HUMAN] | 54.26 | 1 | 0 | 3 | 6 | 21.6376209 |
| B0V044 | Valyl-tRNA synthetase (Fragment) OS=Homo sapiens GN=VARS PE=4 SV=1 - [B0V044_HUMAN] | 29.31 | 1 | 0 | 3 | 6 | 21.6376209 |
| A2ABF4 | Valyl-tRNA synthetase (Fragment) OS=Homo sapiens GN=VARS PE=4 SV=1 - [A2ABF4_HUMAN] | 29.31 | 1 | 0 | 3 | 6 | 21.6376209 |
| Q04695 | Keratin, type I cytoskeletal 17 OS=Homo sapiens GN=KRT17 PE=1 SV=2 - [K1C17_HUMAN] | 6.94 | 1 | 0 | 3 | 6 | 16.0688987 |
| B4DZJ6 | cDNA FLJ54706, highly similar to Ubiquitin-associated protein 2-like OS=Homo sapiens PE=2 SV=1 - [B4DZJ6_HUMAN] | 5.46 | 1 | 0 | 3 | 6 | 16.2502239 |
| O95678 | Keratin, type II cytoskeletal 75 OS=Homo sapiens GN=KRT75 PE=1 SV=2 - [K2C75_HUMAN] | 5.26 | 1 | 0 | 3 | 6 | 16.1943338 |
| B4DYY5 | cDNA FLJ55671, highly similar to Ubiquitin-associated protein 2-like OS=Homo sapiens PE=2 SV=1 - [B4DYY5_HUMAN] | 4.55 | 1 | 0 | 3 | 6 | 16.2502239 |
| Q14157 | Ubiquitin-associated protein 2-like OS=Homo sapiens GN=UBAP2L PE=1 SV=2 - [UBP2L_HUMAN] | 4.51 | 1 | 0 | 3 | 6 | 16.2502239 |
| Q05BV1 | SMC2 protein (Fragment) OS=Homo sapiens GN=SMC2 PE=2 SV=1 - [Q05BV1_HUMAN] | 4.35 | 1 | 0 | 3 | 5 | 13.3650858 |

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|--------|-----------------------------------------------------------------------------------------------------------------------------------------------------------|------|---|---|---|---|------------|
| O95347 | Structural maintenance of chromosomes protein 2 OS=Homo sapiens GN=SMC2 PE=1 SV=2 - [SMC2_HUMAN] | 2.84 | 1 | 0 | 3 | 5 | 13.3650858 |
| B3KMB1 | cDNA FLJ10623 fis, clone NT2RP2005520, highly similar to Structural maintenance of chromosome 2-like 1 protein OS=Homo sapiens PE=2 SV=1 - [B3KMB1_HUMAN] | 2.84 | 1 | 0 | 3 | 5 | 13.3650858 |
| A8K984 | cDNA FLJ78259 OS=Homo sapiens PE=2 SV=1 - [A8K984_HUMAN] | 2.84 | 1 | 0 | 3 | 5 | 13.3650858 |
| B7ZLZ7 | SMC2 protein OS=Homo sapiens GN=SMC2 PE=2 SV=1 - [B7ZLZ7_HUMAN] | 2.84 | 1 | 0 | 3 | 5 | 13.3650858 |
| B4DFD5 | cDNA FLJ58528, highly similar to N-acetyltransferase 10 (EC 2.3.1.-) OS=Homo sapiens PE=2 SV=1 - [B4DFD5_HUMAN] | 3.46 | 1 | 0 | 3 | 5 | 11.3712509 |
| Q9H0A0 | N-acetyltransferase 10 OS=Homo sapiens GN=NAT10 PE=1 SV=2 - [NAT10_HUMAN] | 3.22 | 1 | 0 | 3 | 5 | 11.3712509 |
| B4DZP5 | cDNA FLJ51165, highly similar to DNA damage-binding protein 1 OS=Homo sapiens PE=2 SV=1 - [B4DZP5_HUMAN] | 6.17 | 1 | 0 | 3 | 4 | 13.132762 |
| Q7Z3K9 | Putative uncharacterized protein DKFZp781L0540 (Fragment) OS=Homo sapiens GN=DKFZp781L0540 PE=1 SV=1 - [Q7Z3K9_HUMAN] | 4.76 | 1 | 0 | 3 | 4 | 10.7700143 |
| B3KXZ4 | cDNA FLJ46429 fis, clone THYMU3014372, highly similar to DNA replication licensing factor MCM2 OS=Homo sapiens PE=2 SV=1 - [B3KXZ4_HUMAN] | 4.46 | 1 | 0 | 3 | 4 | 9.69437504 |
| Q13435 | Splicing factor 3B subunit 2 OS=Homo sapiens GN=SF3B2 PE=1 SV=2 - [SF3B2_HUMAN] | 4.25 | 1 | 0 | 3 | 4 | 10.7700143 |
| Q5JQ13 | Vinculin (Fragment) OS=Homo sapiens GN=VCL PE=2 SV=1 - [Q5JQ13_HUMAN] | 4.22 | 1 | 0 | 3 | 4 | 9.98726988 |
| P49736 | DNA replication licensing factor MCM2 OS=Homo sapiens GN=MCM2 PE=1 SV=4 - [MCM2_HUMAN] | 3.98 | 1 | 0 | 3 | 4 | 9.69437504 |
| B7Z8Z6 | cDNA FLJ53276, moderately similar to DNA replication licensing factor MCM2 OS=Homo sapiens PE=2 SV=1 - [B7Z8Z6_HUMAN] | 3.77 | 1 | 0 | 3 | 4 | 9.69437504 |
| B4DLT2 | cDNA FLJ56637, highly similar to Nuclear pore complex protein Nup155 OS=Homo sapiens PE=2 SV=1 - [B4DLT2_HUMAN] | 3.25 | 1 | 0 | 3 | 4 | 12.1687031 |
| O75694 | Nuclear pore complex protein Nup155 OS=Homo sapiens GN=NUP155 PE=1 SV=1 - [NU155_HUMAN] | 3.16 | 1 | 0 | 3 | 4 | 12.1687031 |
| B4DGN2 | cDNA FLJ58361, highly similar to Neurofilament triplet M | 7.04 | 1 | 0 | 3 | 4 | 7.89556003 |

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|--------|---------------------------------------------------------------------------------------------------------------------------------------------------|-------|---|---|---|----|------------|
| | protein OS=Homo sapiens PE=2 SV=1 - [B4DGN2_HUMAN] | | | | | | |
| B3KMG3 | cDNA FLJ10929 fis, clone OVARC1000479, highly similar to Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens PE=2 SV=1 - [B3KMG3_HUMAN] | 6.99 | 1 | 0 | 3 | 4 | 8.68950045 |
| A8K1R6 | cDNA FLJ77026, highly similar to Homo sapiens ataxin 2-like (ATXN2L), transcript variant E, mRNA OS=Homo sapiens PE=2 SV=1 - [A8K1R6_HUMAN] | 2.59 | 1 | 0 | 3 | 4 | 8.44911051 |
| Q63ZY4 | ATXN2L protein OS=Homo sapiens GN=ATXN2L PE=2 SV=1 - [Q63ZY4_HUMAN] | 2.54 | 1 | 0 | 3 | 4 | 8.44911051 |
| Q8WWM7 | Ataxin-2-like protein OS=Homo sapiens GN=ATXN2L PE=1 SV=2 - [ATX2L_HUMAN] | 2.51 | 1 | 0 | 3 | 4 | 8.44911051 |
| Q49A90 | RPS27A protein OS=Homo sapiens GN=RPS27A PE=4 SV=1 - [Q49A90_HUMAN] | 30.53 | 1 | 0 | 2 | 14 | 45.69134 |
| Q4W5H1 | Putative uncharacterized protein SMARCA5 (Fragment) OS=Homo sapiens GN=SMARCA5 PE=2 SV=1 - [Q4W5H1_HUMAN] | 6.54 | 1 | 0 | 2 | 11 | 28.6389418 |
| Q7Z794 | Keratin, type II cytoskeletal 1b OS=Homo sapiens GN=KRT77 PE=1 SV=3 - [K2C1B_HUMAN] | 3.63 | 1 | 0 | 2 | 8 | 23.1684144 |
| Q0IIN1 | Keratin 77 OS=Homo sapiens GN=KRT77 PE=1 SV=1 - [Q0IIN1_HUMAN] | 3.63 | 1 | 0 | 2 | 8 | 23.1684144 |
| B4E2J5 | cDNA FLJ53570, highly similar to Keratin, type I cytoskeletal 16 OS=Homo sapiens PE=2 SV=1 - [B4E2J5_HUMAN] | 16.49 | 1 | 0 | 2 | 7 | 19.8214006 |
| E0CX14 | Uncharacterized protein OS=Homo sapiens GN=KRT15 PE=4 SV=1 - [E0CX14_HUMAN] | 4.84 | 1 | 0 | 2 | 7 | 19.2182055 |
| P19012 | Keratin, type I cytoskeletal 15 OS=Homo sapiens GN=KRT15 PE=1 SV=3 - [K1C15_HUMAN] | 4.82 | 1 | 0 | 2 | 7 | 19.2182055 |
| B3KVF5 | cDNA FLJ16494 fis, clone CTONG3004576, highly similar to Keratin, type I cytoskeletal 15 OS=Homo sapiens PE=2 SV=1 - [B3KVF5_HUMAN] | 4.82 | 1 | 0 | 2 | 7 | 19.2182055 |
| P51610 | Host cell factor 1 OS=Homo sapiens GN=HCFC1 PE=1 SV=2 - [HCFC1_HUMAN] | 1.23 | 1 | 0 | 2 | 7 | 18.7293379 |
| A6NEM2 | Uncharacterized protein OS=Homo sapiens GN=HCFC1 PE=4 SV=2 - [A6NEM2_HUMAN] | 1.2 | 1 | 0 | 2 | 7 | 18.7293379 |

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|--------|--------------------------------------------------------------------------------------------------------------------------------------------------------|-------|---|---|---|---|------------|
| Q68D25 | Putative uncharacterized protein DKFZp686N08236 (Fragment) OS=Homo sapiens GN=DKFZp686N08236 PE=2 SV=1 - [Q68D25_HUMAN] | 25.83 | 1 | 0 | 2 | 6 | 17.9810698 |
| Q4W5G3 | Putative uncharacterized protein SMARCA5 (Fragment) OS=Homo sapiens GN=SMARCA5 PE=2 SV=1 - [Q4W5G3_HUMAN] | 10.14 | 1 | 0 | 2 | 6 | 15.4541583 |
| B3KM77 | cDNA FLJ10435 fis, clone NT2RP1000493, highly similar to Splicing factor 3B subunit 3 OS=Homo sapiens PE=2 SV=1 - [B3KM77_HUMAN] | 6.56 | 1 | 0 | 2 | 6 | 16.4334221 |
| Q8NF06 | FLJ00398 protein (Fragment) OS=Homo sapiens GN=FLJ00398 PE=2 SV=1 - [Q8NF06_HUMAN] | 3.79 | 1 | 0 | 2 | 6 | 15.2007811 |
| B7Z909 | cDNA FLJ54708, highly similar to 150 kDa oxygen-regulated protein (Orp150) OS=Homo sapiens PE=2 SV=1 - [B7Z909_HUMAN] | 3.58 | 1 | 0 | 2 | 6 | 13.7610905 |
| Q5XKE5 | Keratin, type II cytoskeletal 79 OS=Homo sapiens GN=KRT79 PE=1 SV=2 - [K2C79_HUMAN] | 3.18 | 1 | 0 | 2 | 6 | 14.8294494 |
| Q96P95 | Poly(ADP-ribose) polymerase (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q96P95_HUMAN] | 57.14 | 1 | 0 | 2 | 5 | 20.7933173 |
| B4DZ61 | cDNA FLJ50305, highly similar to Valyl-tRNA synthetase (EC 6.1.1.9) OS=Homo sapiens PE=2 SV=1 - [B4DZ61_HUMAN] | 9.09 | 1 | 0 | 2 | 5 | 18.3250248 |
| B3KMN2 | cDNA FLJ11695 fis, clone HEMBA1005019, highly similar to Homo sapiens SCC-112 protein (SCC-112), mRNA OS=Homo sapiens PE=2 SV=1 - [B3KMN2_HUMAN] | 9.01 | 1 | 0 | 2 | 5 | 15.5696888 |
| Q96DB6 | PDS5A protein (Fragment) OS=Homo sapiens GN=PDS5A PE=2 SV=2 - [Q96DB6_HUMAN] | 7.94 | 1 | 0 | 2 | 5 | 15.5696888 |
| C9JH30 | Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [C9JH30_HUMAN] | 4.62 | 1 | 0 | 2 | 5 | 13.8502984 |
| A8MW45 | Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [A8MW45_HUMAN] | 4.54 | 1 | 0 | 2 | 5 | 13.8502984 |
| B4DT32 | cDNA FLJ54383, highly similar to Valyl-tRNA synthetase (EC 6.1.1.9) OS=Homo sapiens PE=2 SV=1 - [B4DT32_HUMAN] | 2.96 | 1 | 0 | 2 | 5 | 14.3460815 |
| B3KY56 | cDNA FLJ46898 fis, clone UTERU3022168, highly similar to Protein FAM62A OS=Homo sapiens PE=2 SV=1 - [B3KY56_HUMAN] | 2.27 | 1 | 0 | 2 | 5 | 13.2772295 |

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| Q9BSJ8 | Extended synaptotagmin-1 OS=Homo sapiens GN=ESYT1 PE=1 SV=1 - [ESYT1_HUMAN] | 2.17 | 1 | 0 | 2 | 5 | 13.2772295 |
| B3KMV5 | cDNA FLJ12728 fis, clone NT2RP2000040, highly similar to Protein FAM62A OS=Homo sapiens PE=2 SV=1 - [B3KMV5_HUMAN] | 2.17 | 1 | 0 | 2 | 5 | 13.2772295 |
| Q14666 | Radiated keratinocyte mRNA 266 (keratin-related protein) (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q14666_HUMAN] | 8.65 | 1 | 0 | 2 | 4 | 11.1699002 |
| Q9UEL2 | p120 (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q9UEL2_HUMAN] | 5.24 | 1 | 0 | 2 | 4 | 12.018785 |
| B3KM27 | cDNA FLJ10093 fis, clone HEMBA1002363, highly similar to Structural maintenance of chromosome 2-like 1 protein (Fragment) OS=Homo sapiens PE=2 SV=1 - [B3KM27_HUMAN] | 3.89 | 1 | 0 | 2 | 4 | 9.96798253 |
| D7EZH4 | SNF2LT OS=Homo sapiens PE=2 SV=1 - [D7EZH4_HUMAN] | 2.58 | 1 | 0 | 2 | 4 | 10.3525639 |
| Q86UA8 | SMARCA1 protein (Fragment) OS=Homo sapiens GN=SMARCA1 PE=2 SV=2 - [Q86UA8_HUMAN] | 2.07 | 1 | 0 | 2 | 4 | 10.3525639 |
| B1ALF5 | SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (Fragment) OS=Homo sapiens GN=SMARCA1 PE=4 SV=1 - [B1ALF5_HUMAN] | 1.99 | 1 | 0 | 2 | 4 | 10.3525639 |
| P28370 | Probable global transcription activator SNF2L1 OS=Homo sapiens GN=SMARCA1 PE=1 SV=2 - [SMCA1_HUMAN] | 1.9 | 1 | 0 | 2 | 4 | 10.3525639 |
| B7ZLQ5 | SMARCA1 protein OS=Homo sapiens GN=SMARCA1 PE=2 SV=1 - [B7ZLQ5_HUMAN] | 1.87 | 1 | 0 | 2 | 4 | 10.3525639 |
| Q86U51 | General transcription factor II, i OS=Homo sapiens GN=GTF2I PE=2 SV=1 - [Q86U51_HUMAN] | 9.85 | 1 | 0 | 2 | 3 | 8.05656123 |
| B4DL32 | cDNA FLJ59922, highly similar to Keratin, type II cytoskeletal 5 OS=Homo sapiens PE=2 SV=1 - [B4DL32_HUMAN] | 8.12 | 1 | 0 | 2 | 3 | 8.03494859 |
| A8K849 | cDNA FLJ75527, highly similar to Homo sapiens zinc finger RNA binding protein (ZFR), mRNA (Fragment) OS=Homo sapiens PE=2 SV=1 - [A8K849_HUMAN] | 4.44 | 1 | 0 | 2 | 3 | 9.51038909 |
| Q59FC4 | Presynaptic protein SAP97 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59FC4_HUMAN] | 3.49 | 1 | 0 | 2 | 3 | 7.6226573 |
| P43243 | Matrin-3 OS=Homo sapiens GN=MATR3 PE=1 SV=2 - [MATR3_HUMAN] | 3.42 | 1 | 0 | 2 | 3 | 7.80963349 |

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| Q68D11 | Putative uncharacterized protein DKFZp686K23100 OS=Homo sapiens GN=DKFZp686K23100 PE=2 SV=1 - [Q68D11_HUMAN] | 3.42 | 1 | 0 | 2 | 3 | 7.80963349 |
| A8MXP9 | Uncharacterized protein OS=Homo sapiens GN=MATR3 PE=4 SV=1 - [A8MXP9_HUMAN] | 3.24 | 1 | 0 | 2 | 3 | 7.80963349 |
| Q2KQ72 | Chromosome-associated protein E OS=Homo sapiens PE=2 SV=1 - [Q2KQ72_HUMAN] | 3.16 | 1 | 0 | 2 | 3 | 7.87564754 |
| B4DGZ8 | cDNA FLJ50509, highly similar to Disks large homolog 1 OS=Homo sapiens PE=2 SV=1 - [B4DGZ8_HUMAN] | 3.05 | 1 | 0 | 2 | 3 | 7.6226573 |
| B4DGU1 | cDNA FLJ50502, highly similar to Disks large homolog 1 OS=Homo sapiens PE=2 SV=1 - [B4DGU1_HUMAN] | 3 | 1 | 0 | 2 | 3 | 7.6226573 |
| B4DSV5 | cDNA FLJ55651, highly similar to DNA replication licensing factor MCM2 OS=Homo sapiens PE=2 SV=1 - [B4DSV5_HUMAN] | 2.97 | 1 | 0 | 2 | 3 | 7.3793695 |
| Q8IXJ3 | Small nuclear ribonucleoprotein component OS=Homo sapiens GN=SNRP116 PE=2 SV=1 - [Q8IXJ3_HUMAN] | 2.94 | 1 | 0 | 2 | 3 | 9.00532699 |
| Q86VP6 | Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens GN=CAND1 PE=1 SV=2 - [CAND1_HUMAN] | 2.76 | 1 | 0 | 2 | 3 | 8.53037691 |
| A8K8U1 | cDNA FLJ77762, highly similar to Homo sapiens cullin-associated and neddylation-dissociated 1 (CAND1), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K8U1_HUMAN] | 2.76 | 1 | 0 | 2 | 3 | 8.53037691 |
| B4DZB1 | cDNA FLJ59645, highly similar to 116 kDa U5 small nuclear ribonucleoprotein component OS=Homo sapiens PE=2 SV=1 - [B4DZB1_HUMAN] | 2.71 | 1 | 0 | 2 | 3 | 9.00532699 |
| B4DK30 | cDNA FLJ59627, highly similar to 116 kDa U5 small nuclear ribonucleoprotein component OS=Homo sapiens PE=2 SV=1 - [B4DK30_HUMAN] | 2.67 | 1 | 0 | 2 | 3 | 9.00532699 |
| Q12959 | Disks large homolog 1 OS=Homo sapiens GN=DLG1 PE=1 SV=2 - [DLG1_HUMAN] | 2.65 | 1 | 0 | 2 | 3 | 7.6226573 |
| B5MEH6 | Uncharacterized protein OS=Homo sapiens GN=ZFR PE=4 SV=1 - [B5MEH6_HUMAN] | 2.65 | 1 | 0 | 2 | 3 | 9.51038909 |
| Q96KR1 | Zinc finger RNA-binding protein OS=Homo sapiens GN=ZFR PE=1 SV=2 - [ZFR_HUMAN] | 2.61 | 1 | 0 | 2 | 3 | 9.51038909 |
| B2RNR6 | Zinc finger RNA binding protein OS=Homo sapiens GN=ZFR PE=2 SV=1 - [B2RNR6_HUMAN] | 2.61 | 1 | 0 | 2 | 3 | 9.51038909 |
| B3KX19 | cDNA FLJ44500 fis, clone UTERU3000828, highly similar to 116 | 2.6 | 1 | 0 | 2 | 3 | 9.00532699 |

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| | kDa U5 small nuclear ribonucleoprotein component OS=Homo sapiens PE=2 SV=1 - [B3KX19_HUMAN] | | | | | | |
| B4DMC0 | cDNA FLJ55341, highly similar to 116 kDa U5 small nuclear ribonucleoprotein component OS=Homo sapiens PE=2 SV=1 - [B4DMC0_HUMAN] | 2.6 | 1 | 0 | 2 | 3 | 9.00532699 |
| Q15029 | 116 kDa U5 small nuclear ribonucleoprotein component OS=Homo sapiens GN=EFTUD2 PE=1 SV=1 - [U5S1_HUMAN] | 2.57 | 1 | 0 | 2 | 3 | 9.00532699 |
| Q6IBM8 | U5-116KD protein OS=Homo sapiens GN=U5-116KD PE=2 SV=1 - [Q6IBM8_HUMAN] | 2.57 | 1 | 0 | 2 | 3 | 9.00532699 |
| A8KAP3 | cDNA FLJ78483, highly similar to Homo sapiens elongation factor Tu GTP binding domain containing 2 (EFTUD2), mRNA OS=Homo sapiens PE=2 SV=1 - [A8KAP3_HUMAN] | 2.57 | 1 | 0 | 2 | 3 | 9.00532699 |
| B4DSA8 | cDNA FLJ51067, highly similar to DNA damage-binding protein 1 OS=Homo sapiens PE=2 SV=1 - [B4DSA8_HUMAN] | 2.08 | 1 | 0 | 2 | 3 | 7.79844141 |
| Q7L576 | Cytoplasmic FMR1-interacting protein 1 OS=Homo sapiens GN=CYFIP1 PE=1 SV=1 - [CYFP1_HUMAN] | 1.84 | 1 | 0 | 2 | 3 | 8.44002008 |
| B3KVV6 | cDNA FLJ43948 fis, clone TESTI4014924, highly similar to Homo sapiens cytoplasmic FMR1 interacting protein 1 (CYFIP1), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1 - [B3KVV6_HUMAN] | 1.83 | 1 | 0 | 2 | 3 | 8.44002008 |
| B4DTM7 | cDNA FLJ53006, highly similar to Vinculin OS=Homo sapiens PE=2 SV=1 - [B4DTM7_HUMAN] | 7.03 | 1 | 0 | 2 | 2 | 4.53847075 |
| B4DKC9 | cDNA FLJ55698, highly similar to Vinculin OS=Homo sapiens PE=2 SV=1 - [B4DKC9_HUMAN] | 4.68 | 1 | 0 | 2 | 2 | 4.53847075 |
| B7Z5E7 | cDNA FLJ51046, highly similar to 60 kDa heat shock protein, mitochondrial OS=Homo sapiens PE=2 SV=1 - [B7Z5E7_HUMAN] | 4.06 | 1 | 0 | 2 | 2 | 5.02819633 |
| B7Z4F6 | cDNA FLJ54912, highly similar to 60 kDa heat shock protein, mitochondrial OS=Homo sapiens PE=2 SV=1 - [B7Z4F6_HUMAN] | 3.82 | 1 | 0 | 2 | 2 | 5.02819633 |
| B7Z597 | cDNA FLJ54373, highly similar to 60 kDa heat shock protein, mitochondrial OS=Homo sapiens PE=2 SV=1 - [B7Z597_HUMAN] | 3.72 | 1 | 0 | 2 | 2 | 5.02819633 |
| B3GQS7 | Mitochondrial heat shock 60kD protein 1 variant 1 OS=Homo sapiens GN=HSPD1 PE=2 SV=1 - [B3GQS7_HUMAN] | 3.69 | 1 | 0 | 2 | 2 | 5.02819633 |

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| P10809 | 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 - [CH60_HUMAN] | 3.66 | 1 | 0 | 2 | 2 | 5.02819633 |
| Q6DCA8 | BCLAF1 protein (Fragment) OS=Homo sapiens GN=BCLAF1 PE=2 SV=1 - [Q6DCA8_HUMAN] | 3.38 | 1 | 0 | 2 | 2 | 4.50842094 |
| Q9NYF8 | Bcl-2-associated transcription factor 1 OS=Homo sapiens GN=BCLAF1 PE=1 SV=2 - [BCLF1_HUMAN] | 2.5 | 1 | 0 | 2 | 2 | 4.50842094 |

Proteins ID02.msf

| Accession | Description | Σ Coverage | Σ # Proteins | Σ # Unique Peptides | Σ # Peptides | Σ # PSMs | Score A3 |
|-----------|--------------------------------------------------------------------------------------------------------------------------------------|-------------------|---------------------|----------------------------|---------------------|-----------------|------------|
| P49327 | Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 - [FAS_HUMAN] | 21.27 | 1 | 30 | 41 | 80 | 263.227102 |
| Q8TEM1 | Nuclear pore membrane glycoprotein 210 OS=Homo sapiens GN=NUP210 PE=1 SV=3 - [PO210_HUMAN] | 13.51 | 1 | 20 | 20 | 34 | 105.755519 |
| Q14008 | Cytoskeleton-associated protein 5 OS=Homo sapiens GN=CKAP5 PE=1 SV=3 - [CKAP5_HUMAN] | 22.24 | 1 | 19 | 35 | 70 | 238.902539 |
| Q6P2Q9 | Pre-mRNA-processing-splicing factor 8 OS=Homo sapiens GN=PRPF8 PE=1 SV=2 - [PRP8_HUMAN] | 20.13 | 1 | 16 | 33 | 65 | 208.147331 |
| P13645 | Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6 - [K1C10_HUMAN] | 27.57 | 1 | 10 | 11 | 19 | 63.1830347 |
| A6NHR9 | Structural maintenance of chromosomes flexible hinge domain-containing protein 1 OS=Homo sapiens GN=SMCHD1 PE=1 SV=2 - [SMHD1_HUMAN] | 6.73 | 1 | 10 | 10 | 19 | 58.8048689 |
| Q14160 | Protein scribble homolog OS=Homo sapiens GN=SCRIB PE=1 SV=4 - [SCRIB_HUMAN] | 14.72 | 1 | 9 | 17 | 32 | 106.116722 |
| P78527 | DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3 - [PRKDC_HUMAN] | 4.34 | 1 | 9 | 13 | 23 | 77.619642 |
| Q14204 | Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5 - [DYHC1_HUMAN] | 2.76 | 1 | 9 | 9 | 12 | 37.6121943 |
| P04264 | Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6 - [K2C1_HUMAN] | 14.6 | 1 | 7 | 10 | 22 | 69.390785 |
| Q92621 | Nuclear pore complex protein Nup205 OS=Homo sapiens GN=NUP205 PE=1 SV=3 - [NU205_HUMAN] | 8.05 | 1 | 6 | 13 | 19 | 56.1781037 |
| O14646 | Chromodomain-helicase-DNA-binding protein 1 OS=Homo sapiens GN=CHD1 PE=1 SV=2 - [CHD1_HUMAN] | 4.97 | 1 | 5 | 6 | 9 | 25.4241133 |
| P35527 | Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3 - [K1C9_HUMAN] | 16.85 | 1 | 5 | 5 | 8 | 34.6602659 |
| P35579 | Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4 - [MYH9_HUMAN] | 49.69 | 1 | 4 | 96 | 262 | 957.561561 |

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|--------|------------------------------------------------------------------------------------------------------------------------------------------------|-------|---|---|----|-----|------------|
| Q14690 | Protein RRP5 homolog OS=Homo sapiens GN=PDCD11 PE=1 SV=3 - [RRP5_HUMAN] | 8.18 | 1 | 4 | 10 | 14 | 47.7700963 |
| Q8N3C0 | Activating signal cointegrator 1 complex subunit 3 OS=Homo sapiens GN=ASCC3 PE=1 SV=3 - [HELC1_HUMAN] | 2.72 | 1 | 4 | 5 | 6 | 18.7750919 |
| Q7KZ85 | Transcription elongation factor SPT6 OS=Homo sapiens GN=SUPT6H PE=1 SV=2 - [SPT6H_HUMAN] | 3.07 | 1 | 4 | 4 | 6 | 19.3219683 |
| A5YKK6 | CCR4-NOT transcription complex subunit 1 OS=Homo sapiens GN=CNOT1 PE=1 SV=2 - [CNOT1_HUMAN] | 11.24 | 1 | 3 | 20 | 35 | 111.870018 |
| P27816 | Microtubule-associated protein 4 OS=Homo sapiens GN=MAP4 PE=1 SV=3 - [MAP4_HUMAN] | 46.88 | 1 | 2 | 40 | 85 | 313.603896 |
| Q13428 | Treacle protein OS=Homo sapiens GN=TCOF1 PE=1 SV=3 - [TCOF_HUMAN] | 19.56 | 1 | 2 | 22 | 49 | 163.375848 |
| Q9H1A4 | Anaphase-promoting complex subunit 1 OS=Homo sapiens GN=ANAPC1 PE=1 SV=1 - [APC1_HUMAN] | 1.65 | 1 | 2 | 2 | 4 | 12.4358902 |
| Q5JRA6 | Melanoma inhibitory activity protein 3 OS=Homo sapiens GN=MIA3 PE=1 SV=1 - [MIA3_HUMAN] | 1.78 | 1 | 2 | 2 | 2 | 5.95845652 |
| P46013 | Antigen KI-67 OS=Homo sapiens GN=MKI67 PE=1 SV=2 - [KI67_HUMAN] | 1.35 | 1 | 2 | 2 | 2 | 6.63481712 |
| E1NZA1 | Peroxisome proliferator activated receptor interacting complex protein OS=Homo sapiens GN=PRIC295 PE=2 SV=1 - [E1NZA1_HUMAN] | 10.71 | 1 | 1 | 19 | 38 | 123.996264 |
| B4DZC9 | cDNA FLJ61681, highly similar to STE20-like serine/threonine-protein kinase (EC2.7.11.1) (Fragment) OS=Homo sapiens PE=2 SV=1 - [B4DZC9_HUMAN] | 11.55 | 1 | 1 | 11 | 18 | 51.3186715 |
| Q9H2G2 | STE20-like serine/threonine-protein kinase OS=Homo sapiens GN=SLK PE=1 SV=1 - [SLK_HUMAN] | 9.8 | 1 | 1 | 11 | 18 | 50.7079961 |
| P35908 | Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2 - [K22E_HUMAN] | 8.29 | 1 | 1 | 5 | 9 | 25.8249438 |
| P58107 | Epiplakin OS=Homo sapiens GN=EPPK1 PE=1 SV=2 - [EPIPL_HUMAN] | 3.83 | 1 | 1 | 2 | 4 | 17.3479407 |
| B4E106 | cDNA FLJ53399, highly similar to Monocarboxylate transporter 1 OS=Homo sapiens PE=2 SV=1 - [B4E106_HUMAN] | 8.54 | 1 | 1 | 2 | 3 | 10.981164 |
| P35580 | Myosin-10 OS=Homo sapiens GN=MYH10 PE=1 SV=3 - [MYH10_HUMAN] | 41.85 | 1 | 0 | 80 | 193 | 695.156039 |

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|--------|--------------------------------------------------------------------------------------------------------------------------------|-------|---|---|----|-----|------------|
| B2RWP9 | MYH10 protein OS=Homo sapiens GN=MYH10 PE=2 SV=1 - [B2RWP9_HUMAN] | 41.16 | 1 | 0 | 79 | 192 | 692.889815 |
| Q4LE45 | MYH10 variant protein (Fragment) OS=Homo sapiens GN=MYH10 variant protein PE=2 SV=1 - [Q4LE45_HUMAN] | 40.49 | 1 | 0 | 79 | 192 | 692.889815 |
| Q149N4 | Myosin, heavy chain 10, non-muscle OS=Homo sapiens GN=MYH10 PE=2 SV=1 - [Q149N4_HUMAN] | 41.04 | 1 | 0 | 79 | 191 | 686.703715 |
| Q14980 | Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 PE=1 SV=2 - [NUMA1_HUMAN] | 35.93 | 1 | 0 | 58 | 130 | 481.402889 |
| Q4LE64 | NUMA1 variant protein (Fragment) OS=Homo sapiens GN=NUMA1 variant protein PE=2 SV=1 - [Q4LE64_HUMAN] | 35.83 | 1 | 0 | 58 | 130 | 481.402889 |
| Q86XU5 | MYH9 protein (Fragment) OS=Homo sapiens GN=MYH9 PE=2 SV=1 - [Q86XU5_HUMAN] | 43.52 | 1 | 0 | 57 | 150 | 536.896182 |
| D3DTS1 | Myosin, heavy polypeptide 10, non-muscle, isoform CRA_a OS=Homo sapiens GN=MYH10 PE=4 SV=1 - [D3DTS1_HUMAN] | 51.87 | 1 | 0 | 54 | 139 | 523.571034 |
| Q59HB8 | Nuclear mitotic apparatus protein 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59HB8_HUMAN] | 38.04 | 1 | 0 | 48 | 112 | 410.393434 |
| B4DSI9 | cDNA FLJ56483, highly similar to Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens PE=2 SV=1 - [B4DSI9_HUMAN] | 30.42 | 1 | 0 | 40 | 93 | 290.675779 |
| B4DGF1 | cDNA FLJ56479, highly similar to Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens PE=2 SV=1 - [B4DGF1_HUMAN] | 29.37 | 1 | 0 | 40 | 93 | 290.675779 |
| D3DNT2 | Eukaryotic translation initiation factor 4 gamma, 1, isoform CRA_c OS=Homo sapiens GN=EIF4G1 PE=4 SV=1 - [D3DNT2_HUMAN] | 28.81 | 1 | 0 | 40 | 93 | 291.403928 |
| Q04637 | Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=4 - [IF4G1_HUMAN] | 28.77 | 1 | 0 | 40 | 93 | 290.675779 |
| B2RU06 | EIF4G1 protein OS=Homo sapiens GN=EIF4G1 PE=2 SV=1 - [B2RU06_HUMAN] | 28.64 | 1 | 0 | 40 | 93 | 290.675779 |
| B2RU10 | EIF4G1 protein OS=Homo sapiens GN=EIF4G1 PE=2 SV=1 - [B2RU10_HUMAN] | 28.64 | 1 | 0 | 40 | 93 | 290.675779 |
| Q4LE58 | EIF4G1 variant protein (Fragment) OS=Homo sapiens GN=EIF4G1 variant protein PE=2 SV=1 - [Q4LE58_HUMAN] | 28.33 | 1 | 0 | 40 | 93 | 290.675779 |
| Q7Z757 | NUMA1 protein OS=Homo sapiens PE=2 SV=1 - | 36.8 | 1 | 0 | 34 | 82 | 295.534184 |

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|--------|----------------------------------------------------------------------------------------------------------------------------------------------------------|-------|---|---|----|----|------------|
| | [Q7Z757_HUMAN] | | | | | | |
| O75643 | U5 small nuclear ribonucleoprotein 200 kDa helicase OS=Homo sapiens GN=SNRNP200 PE=1 SV=2 - [U520_HUMAN] | 20.93 | 1 | 0 | 34 | 75 | 256.45002 |
| A8K6E4 | cDNA FLJ77145, highly similar to Homo sapiens myosin, heavy polypeptide 9, non-muscle (MYH9), mRNA (Fragment) OS=Homo sapiens PE=2 SV=1 - [A8K6E4_HUMAN] | 36.17 | 1 | 0 | 33 | 86 | 291.090019 |
| P27708 | CAD protein OS=Homo sapiens GN=CAD PE=1 SV=3 - [PYR1_HUMAN] | 21.03 | 1 | 0 | 33 | 60 | 205.459403 |
| Q53SY7 | Putative uncharacterized protein CAD (Fragment) OS=Homo sapiens GN=CAD PE=2 SV=1 - [Q53SY7_HUMAN] | 20.22 | 1 | 0 | 32 | 58 | 198.743053 |
| Q6ZNL4 | FLJ00279 protein (Fragment) OS=Homo sapiens GN=FLJ00279 PE=2 SV=1 - [Q6ZNL4_HUMAN] | 50.62 | 1 | 0 | 31 | 90 | 344.73665 |
| A4FU77 | SNRNP200 protein (Fragment) OS=Homo sapiens GN=SNRNP200 PE=2 SV=1 - [A4FU77_HUMAN] | 21.62 | 1 | 0 | 31 | 70 | 240.165901 |
| B4E3S1 | cDNA FLJ57040, highly similar to Myosin-9 OS=Homo sapiens PE=2 SV=1 - [B4E3S1_HUMAN] | 35.06 | 1 | 0 | 30 | 77 | 247.312132 |
| Q60FE6 | Filamin A OS=Homo sapiens GN=FLNA PE=2 SV=1 - [Q60FE6_HUMAN] | 17.5 | 1 | 0 | 29 | 60 | 219.359272 |
| Q60FE5 | Filamin A OS=Homo sapiens GN=FLNA PE=2 SV=1 - [Q60FE5_HUMAN] | 17.44 | 1 | 0 | 29 | 60 | 219.359272 |
| P21333 | Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4 - [FLNA_HUMAN] | 17.26 | 1 | 0 | 29 | 60 | 219.359272 |
| Q5HY54 | Filamin A, alpha (Actin binding protein 280) OS=Homo sapiens GN=FLNA PE=2 SV=1 - [Q5HY54_HUMAN] | 16.46 | 1 | 0 | 28 | 58 | 208.833544 |
| Q96HN5 | Putative uncharacterized protein (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q96HN5_HUMAN] | 38.21 | 1 | 0 | 27 | 67 | 245.512174 |
| Q9BTE9 | NUMA1 protein OS=Homo sapiens GN=NUMA1 PE=2 SV=1 - [Q9BTE9_HUMAN] | 38.51 | 1 | 0 | 27 | 65 | 244.93939 |
| B2ZZ80 | Filamin A OS=Homo sapiens GN=FLNA PE=2 SV=1 - [B2ZZ80_HUMAN] | 17.88 | 1 | 0 | 27 | 56 | 203.442343 |
| A6NDY9 | Uncharacterized protein OS=Homo sapiens GN=FLNA PE=4 SV=3 - [A6NDY9_HUMAN] | 17.88 | 1 | 0 | 27 | 56 | 203.442343 |
| Q9BWG0 | MYH10 protein (Fragment) OS=Homo sapiens GN=MYH10 PE=2 SV=1 - [Q9BWG0_HUMAN] | 50.11 | 1 | 0 | 25 | 60 | 222.994843 |

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|--------|-------------------------------------------------------------------------------------------------------------------------------------------------------|-------|---|---|----|----|------------|
| B4DM10 | cDNA FLJ58263, highly similar to Microtubule-associated protein 4 OS=Homo sapiens PE=2 SV=1 - [B4DM10_HUMAN] | 45.27 | 1 | 0 | 25 | 51 | 188.667021 |
| Q96I65 | EIF4G1 protein OS=Homo sapiens GN=EIF4G1 PE=2 SV=1 - [Q96I65_HUMAN] | 36.74 | 1 | 0 | 22 | 54 | 163.742556 |
| A8K394 | cDNA FLJ76708, highly similar to Homo sapiens nuclear mitotic apparatus protein 1 (NUMA1), mRNA (Fragment) OS=Homo sapiens PE=2 SV=1 - [A8K394_HUMAN] | 32.98 | 1 | 0 | 21 | 39 | 151.995281 |
| B2RWN5 | HEAT repeat containing 1 OS=Homo sapiens GN=HEATR1 PE=2 SV=1 - [B2RWN5_HUMAN] | 11.89 | 1 | 0 | 19 | 33 | 105.217399 |
| C9JF13 | Uncharacterized protein OS=Homo sapiens GN=EIF4G1 PE=4 SV=1 - [C9JF13_HUMAN] | 24.7 | 1 | 0 | 18 | 39 | 126.933223 |
| Q92616 | Translational activator GCN1 OS=Homo sapiens GN=GCN1L1 PE=1 SV=6 - [GCN1L_HUMAN] | 10.3 | 1 | 0 | 18 | 37 | 121.706929 |
| Q8TES4 | FLJ00119 protein (Fragment) OS=Homo sapiens GN=FLJ00119 PE=2 SV=1 - [Q8TES4_HUMAN] | 19.66 | 1 | 0 | 18 | 35 | 127.633117 |
| Q3SYK8 | NUMA1 protein (Fragment) OS=Homo sapiens GN=NUMA1 PE=2 SV=1 - [Q3SYK8_HUMAN] | 34.73 | 1 | 0 | 18 | 34 | 134.692203 |
| B4DK16 | cDNA FLJ57882, highly similar to Pre-mRNA-processing-splicing factor 8 OS=Homo sapiens PE=2 SV=1 - [B4DK16_HUMAN] | 20.56 | 1 | 0 | 17 | 36 | 112.395033 |
| C9J6B6 | Uncharacterized protein OS=Homo sapiens GN=EIF4G1 PE=4 SV=1 - [C9J6B6_HUMAN] | 27.74 | 1 | 0 | 17 | 35 | 113.0304 |
| Q5T3Q7 | HEAT repeat containing 1 OS=Homo sapiens GN=HEATR1 PE=2 SV=1 - [Q5T3Q7_HUMAN] | 10.71 | 1 | 0 | 17 | 29 | 91.1974053 |
| Q9H583 | HEAT repeat-containing protein 1 OS=Homo sapiens GN=HEATR1 PE=1 SV=3 - [HEAT1_HUMAN] | 10.31 | 1 | 0 | 17 | 29 | 91.1974053 |
| C9JFC3 | Uncharacterized protein OS=Homo sapiens GN=MAP4 PE=4 SV=1 - [C9JFC3_HUMAN] | 26.42 | 1 | 0 | 16 | 37 | 133.061309 |
| Q96CK3 | CAD protein (Fragment) OS=Homo sapiens GN=CAD PE=2 SV=2 - [Q96CK3_HUMAN] | 23.15 | 1 | 0 | 15 | 24 | 76.9076107 |
| Q86Y04 | MAP4 protein (Fragment) OS=Homo sapiens GN=MAP4 PE=1 SV=1 - [Q86Y04_HUMAN] | 21.12 | 1 | 0 | 14 | 31 | 108.997135 |
| C9K073 | Uncharacterized protein OS=Homo sapiens GN=EIF4G1 PE=4 SV=1 - [C9K073_HUMAN] | 21.17 | 1 | 0 | 14 | 30 | 99.5489452 |
| P55196 | Afadin OS=Homo sapiens GN=MLLT4 PE=1 SV=3 - | 10.36 | 1 | 0 | 14 | 26 | 88.4765475 |

| | [AFAD_HUMAN] | | | | | | |
|--------|-----------------------------------------------------------------------------------------------------------------------------------------------|-------|---|---|----|----|------------|
| A8MQ02 | Uncharacterized protein OS=Homo sapiens GN=MLLT4 PE=4 SV=1 - [A8MQ02_HUMAN] | 10.36 | 1 | 0 | 14 | 26 | 88.4765475 |
| C9J2Z7 | Uncharacterized protein OS=Homo sapiens GN=EIF4G1 PE=4 SV=1 - [C9J2Z7_HUMAN] | 20.38 | 1 | 0 | 13 | 28 | 91.1899664 |
| D6RHJ4 | Uncharacterized protein OS=Homo sapiens GN=TCOF1 PE=4 SV=1 - [D6RHJ4_HUMAN] | 20 | 1 | 0 | 13 | 28 | 94.5483923 |
| P48634 | Large proline-rich protein BAT2 OS=Homo sapiens GN=BAT2 PE=1 SV=3 - [BAT2_HUMAN] | 10.11 | 1 | 0 | 13 | 22 | 76.1633565 |
| Q6MZU1 | Putative uncharacterized protein DKFZp686A1195 OS=Homo sapiens GN=DKFZp686A1195 PE=1 SV=1 - [Q6MZU1_HUMAN] | 10.76 | 1 | 0 | 13 | 20 | 65.0486507 |
| Q07157 | Tight junction protein ZO-1 OS=Homo sapiens GN=TJP1 PE=1 SV=3 - [ZO1_HUMAN] | 10.41 | 1 | 0 | 13 | 20 | 65.0486507 |
| A9CQZ8 | Tight junction protein ZO-1 (Fragment) OS=Homo sapiens GN=TJP1 PE=2 SV=1 - [A9CQZ8_HUMAN] | 10.34 | 1 | 0 | 13 | 20 | 65.0486507 |
| Q9H8B9 | cDNA FLJ13778 fis, clone PLACE4000431, highly similar to H.sapiens U5 snRNP-specific 200kD protein OS=Homo sapiens PE=2 SV=1 - [Q9H8B9_HUMAN] | 20.67 | 1 | 0 | 12 | 32 | 109.717393 |
| Q6NX68 | MAP4 protein (Fragment) OS=Homo sapiens GN=MAP4 PE=2 SV=1 - [Q6NX68_HUMAN] | 31.91 | 1 | 0 | 12 | 28 | 96.2756135 |
| C9JX92 | Uncharacterized protein OS=Homo sapiens GN=MLLT4 PE=4 SV=1 - [C9JX92_HUMAN] | 8.95 | 1 | 0 | 12 | 23 | 79.2618616 |
| Q05D06 | MAP4 protein (Fragment) OS=Homo sapiens GN=MAP4 PE=2 SV=1 - [Q05D06_HUMAN] | 34.55 | 1 | 0 | 11 | 26 | 88.619585 |
| Q59FZ2 | TCOF1 protein variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59FZ2_HUMAN] | 20.37 | 1 | 0 | 11 | 26 | 84.374465 |
| C9JAQ9 | Uncharacterized protein OS=Homo sapiens GN=SNRNP200 PE=4 SV=1 - [C9JAQ9_HUMAN] | 20.8 | 1 | 0 | 11 | 24 | 78.1342988 |
| Q6PJJ3 | FASN protein (Fragment) OS=Homo sapiens GN=FASN PE=2 SV=1 - [Q6PJJ3_HUMAN] | 17.83 | 1 | 0 | 11 | 23 | 75.2905929 |
| Q6PK16 | MYH10 protein (Fragment) OS=Homo sapiens GN=MYH10 PE=2 SV=1 - [Q6PK16_HUMAN] | 39.04 | 1 | 0 | 11 | 22 | 77.2333972 |
| Q59FP0 | Afadin variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59FP0_HUMAN] | 8.85 | 1 | 0 | 11 | 22 | 76.7689896 |

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|--------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------|---|---|----|----|------------|
| C9IYT9 | Uncharacterized protein OS=Homo sapiens GN=MLLT4 PE=4 SV=1 - [C9IYT9_HUMAN] | 8.73 | 1 | 0 | 11 | 22 | 76.7689896 |
| Q5TIG5 | Myeloid/lymphoid or mixed-lineage leukemia (Trithorax homolog, Drosophila); translocated to, 4 OS=Homo sapiens GN=MLLT4 PE=2 SV=1 - [Q5TIG5_HUMAN] | 8.71 | 1 | 0 | 11 | 22 | 76.7689896 |
| B4DRA2 | cDNA FLJ57828, highly similar to Treacle protein (Fragment) OS=Homo sapiens PE=2 SV=1 - [B4DRA2_HUMAN] | 15.49 | 1 | 0 | 11 | 21 | 63.7212579 |
| B4DYL7 | cDNA FLJ58490, highly similar to Homo sapiens CCR4-NOT transcription complex, subunit 1 (CNOT1), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1 - [B4DYL7_HUMAN] | 11.65 | 1 | 0 | 11 | 20 | 60.564482 |
| B9EGQ8 | SMARCA4 protein OS=Homo sapiens GN=SMARCA4 PE=2 SV=1 - [B9EGQ8_HUMAN] | 8.51 | 1 | 0 | 11 | 20 | 64.5350688 |
| B1A8Z7 | SMARCA4 isoform 1 OS=Homo sapiens GN=SMARCA4 PE=2 SV=1 - [B1A8Z7_HUMAN] | 8.18 | 1 | 0 | 11 | 20 | 64.5350688 |
| B1A8Z4 | SMARCA4 isoform 3 OS=Homo sapiens PE=2 SV=1 - [B1A8Z4_HUMAN] | 8.18 | 1 | 0 | 11 | 20 | 64.5350688 |
| B1A8Z6 | SMARCA4 isoform 4 OS=Homo sapiens PE=2 SV=1 - [B1A8Z6_HUMAN] | 8.17 | 1 | 0 | 11 | 20 | 64.5350688 |
| B1A8Z5 | SMARCA4 isoform 2 OS=Homo sapiens PE=2 SV=1 - [B1A8Z5_HUMAN] | 8.16 | 1 | 0 | 11 | 20 | 64.5350688 |
| P51532 | Transcription activator BRG1 OS=Homo sapiens GN=SMARCA4 PE=1 SV=2 - [SMCA4_HUMAN] | 8.01 | 1 | 0 | 11 | 20 | 64.5350688 |
| Q9HBD4 | SMARCA4 isoform 2 OS=Homo sapiens GN=SMARCA4 PE=2 SV=1 - [Q9HBD4_HUMAN] | 7.86 | 1 | 0 | 11 | 20 | 64.5350688 |
| B4E263 | cDNA FLJ53502, highly similar to HEAT repeat-containing protein 1 OS=Homo sapiens PE=2 SV=1 - [B4E263_HUMAN] | 14.03 | 1 | 0 | 11 | 19 | 61.8593881 |
| A2VDI1 | HEATR1 protein (Fragment) OS=Homo sapiens GN=HEATR1 PE=2 SV=1 - [A2VDI1_HUMAN] | 10.65 | 1 | 0 | 11 | 19 | 60.3980827 |
| B9ZVR1 | Uncharacterized protein OS=Homo sapiens GN=MAP4 PE=4 SV=2 - [B9ZVR1_HUMAN] | 15.79 | 1 | 0 | 10 | 23 | 82.3449843 |
| B4DQZ7 | cDNA FLJ50838, highly similar to Apoptotic chromatin condensation inducer in the nucleus (Fragment) OS=Homo sapiens PE=2 SV=1 - [B4DQZ7_HUMAN] | 11.59 | 1 | 0 | 10 | 23 | 80.5024834 |
| Q9UKV3 | Apoptotic chromatin condensation inducer in the nucleus | 9.47 | 1 | 0 | 10 | 23 | 80.5024834 |

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|--------|---------------------------------------------------------------------------------------------------------------------------------------------------------------|-------|---|---|----|----|------------|
| | OS=Homo sapiens GN=ACIN1 PE=1 SV=2 - [ACINU_HUMAN] | | | | | | |
| Q5JPV5 | Myeloid/lymphoid or mixed-lineage leukemia (Trithorax homolog, Drosophila); translocated to, 4 (Fragment) OS=Homo sapiens GN=MLLT4 PE=2 SV=1 - [Q5JPV5_HUMAN] | 8.66 | 1 | 0 | 10 | 18 | 58.2216523 |
| Q8N7L7 | cDNA FLJ40893 fis, clone UTERU2001607 OS=Homo sapiens PE=2 SV=1 - [Q8N7L7_HUMAN] | 15.94 | 1 | 0 | 10 | 17 | 55.2711213 |
| C9JB33 | Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [C9JB33_HUMAN] | 8.19 | 1 | 0 | 10 | 17 | 57.9059381 |
| C9J9U2 | Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [C9J9U2_HUMAN] | 8.19 | 1 | 0 | 10 | 17 | 57.9059381 |
| C9J1F6 | Uncharacterized protein OS=Homo sapiens GN=PRRC2A PE=4 SV=1 - [C9J1F6_HUMAN] | 8.19 | 1 | 0 | 10 | 17 | 57.9059381 |
| C9JTM3 | Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [C9JTM3_HUMAN] | 8.19 | 1 | 0 | 10 | 17 | 57.9059381 |
| C9JI26 | Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [C9JI26_HUMAN] | 8.14 | 1 | 0 | 10 | 17 | 57.9059381 |
| C9JD87 | Uncharacterized protein OS=Homo sapiens GN=PRRC2A PE=4 SV=1 - [C9JD87_HUMAN] | 8.14 | 1 | 0 | 10 | 17 | 57.9059381 |
| C9JXZ3 | Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [C9JXZ3_HUMAN] | 8.14 | 1 | 0 | 10 | 17 | 57.9059381 |
| C9JI93 | Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [C9JI93_HUMAN] | 8.14 | 1 | 0 | 10 | 17 | 57.9059381 |
| Q5TCU6 | Talin 1 OS=Homo sapiens GN=TLN1 PE=2 SV=1 - [Q5TCU6_HUMAN] | 7.12 | 1 | 0 | 10 | 15 | 58.8865337 |
| Q9Y490 | Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3 - [TLN1_HUMAN] | 6.81 | 1 | 0 | 10 | 15 | 58.8865337 |
| B4E150 | cDNA FLJ55548, highly similar to U5 small nuclear ribonucleoprotein 200 kDa helicase (EC 3.6.1.-) OS=Homo sapiens PE=2 SV=1 - [B4E150_HUMAN] | 17.27 | 1 | 0 | 9 | 22 | 78.36601 |
| B5MEG9 | Uncharacterized protein OS=Homo sapiens GN=MAP4 PE=4 SV=2 - [B5MEG9_HUMAN] | 15.73 | 1 | 0 | 9 | 22 | 77.5826545 |
| B2RTT4 | ACIN1 protein OS=Homo sapiens GN=ACIN1 PE=2 SV=1 - [B2RTT4_HUMAN] | 8.89 | 1 | 0 | 9 | 21 | 75.1963956 |

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|--------|----------------------------------------------------------------------------------------------------------------------------------------------|-------|---|---|---|----|------------|
| Q8IYN5 | CKAP5 protein OS=Homo sapiens GN=CKAP5 PE=2 SV=1 - [Q8IYN5_HUMAN] | 12.8 | 1 | 0 | 9 | 17 | 55.0123808 |
| B7ZAU8 | cDNA, FLJ79312, highly similar to HEAT repeat-containing protein 1 OS=Homo sapiens PE=2 SV=1 - [B7ZAU8_HUMAN] | 11.01 | 1 | 0 | 9 | 15 | 47.8393946 |
| B3KWS1 | cDNA FLJ43675 fis, clone SYNOV4008440, highly similar to HEAT repeat-containing protein 1 OS=Homo sapiens PE=2 SV=1 - [B3KWS1_HUMAN] | 10.09 | 1 | 0 | 9 | 15 | 47.8393946 |
| C9J6L0 | Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [C9J6L0_HUMAN] | 6.92 | 1 | 0 | 9 | 15 | 51.0052395 |
| C9JTL3 | Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [C9JTL3_HUMAN] | 6.89 | 1 | 0 | 9 | 15 | 51.0052395 |
| D6W5C0 | Spectrin, beta, non-erythrocytic 1, isoform CRA_b OS=Homo sapiens GN=SPTBN1 PE=4 SV=1 - [D6W5C0_HUMAN] | 4.61 | 1 | 0 | 9 | 15 | 43.8785849 |
| Q01082 | Spectrin beta chain, brain 1 OS=Homo sapiens GN=SPTBN1 PE=1 SV=2 - [SPTB2_HUMAN] | 4.44 | 1 | 0 | 9 | 15 | 43.8785849 |
| Q9UNL7 | Nuclear mitotic apparatus protein 1 (Fragment) OS=Homo sapiens GN=NUMA1 PE=2 SV=1 - [Q9UNL7_HUMAN] | 40.14 | 1 | 0 | 8 | 24 | 81.0819287 |
| Q99529 | Non-muscle myosin heavy chain (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q99529_HUMAN] | 43.75 | 1 | 0 | 8 | 22 | 91.1093595 |
| Q9UNV9 | Putative RNA helicase OS=Homo sapiens PE=2 SV=1 - [Q9UNV9_HUMAN] | 18.82 | 1 | 0 | 8 | 20 | 72.5863838 |
| B4E0P5 | cDNA FLJ56901, highly similar to U5 small nuclear ribonucleoprotein 200 kDa helicase (EC 3.6.1.-) OS=Homo sapiens PE=2 SV=1 - [B4E0P5_HUMAN] | 18.82 | 1 | 0 | 8 | 20 | 72.9388535 |
| A2RRQ7 | SNRNP200 protein OS=Homo sapiens GN=SNRNP200 PE=2 SV=1 - [A2RRQ7_HUMAN] | 18.82 | 1 | 0 | 8 | 20 | 72.5863838 |
| Q3MIV8 | Myosin, heavy chain 11, smooth muscle OS=Homo sapiens GN=MYH11 PE=2 SV=1 - [Q3MIV8_HUMAN] | 4.13 | 1 | 0 | 8 | 19 | 61.4064033 |
| Q3MNF0 | Myosin, heavy chain 11, smooth muscle OS=Homo sapiens GN=MYH11 PE=2 SV=1 - [Q3MNF0_HUMAN] | 4.11 | 1 | 0 | 8 | 19 | 61.4064033 |
| P35749 | Myosin-11 OS=Homo sapiens GN=MYH11 PE=1 SV=3 - [MYH11_HUMAN] | 4.06 | 1 | 0 | 8 | 19 | 61.4064033 |
| Q3MNF1 | Smooth muscle myosin heavy chain isoform SM1 OS=Homo sapiens GN=MYH11 PE=2 SV=1 - [Q3MNF1_HUMAN] | 4.04 | 1 | 0 | 8 | 19 | 61.4064033 |

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|--------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------|---|---|---|----|------------|
| B1PS43 | Myosin heavy chain 11 smooth muscle isoform OS=Homo sapiens GN=MYH11 PE=2 SV=1 - [B1PS43_HUMAN] | 3.94 | 1 | 0 | 8 | 19 | 61.4064033 |
| Q59FZ6 | SWI/SNF-related matrix-associated actin-dependent regulator of chromatin a4 variant (Fragment) OS=Homo sapiens PE=2 SV=2 - [Q59FZ6_HUMAN] | 8.5 | 1 | 0 | 8 | 17 | 57.1578002 |
| C9JAS0 | Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [C9JAS0_HUMAN] | 7.22 | 1 | 0 | 8 | 13 | 45.81043 |
| C9J8K3 | Uncharacterized protein OS=Homo sapiens GN=PRRC2A PE=4 SV=1 - [C9J8K3_HUMAN] | 7.22 | 1 | 0 | 8 | 13 | 45.81043 |
| A6NG23 | Uncharacterized protein OS=Homo sapiens PE=4 SV=3 - [A6NG23_HUMAN] | 7.22 | 1 | 0 | 8 | 13 | 45.81043 |
| C9JM53 | Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [C9JM53_HUMAN] | 7.22 | 1 | 0 | 8 | 13 | 45.81043 |
| Q9P172 | PRO2281 OS=Homo sapiens PE=2 SV=1 - [Q9P172_HUMAN] | 29.18 | 1 | 0 | 7 | 16 | 56.7068114 |
| Q7L5W4 | SNRNP200 protein (Fragment) OS=Homo sapiens GN=SNRNP200 PE=2 SV=1 - [Q7L5W4_HUMAN] | 19.43 | 1 | 0 | 7 | 16 | 56.7068114 |
| B4DSQ1 | cDNA FLJ58279, highly similar to Microtubule-associated protein 4 OS=Homo sapiens PE=2 SV=1 - [B4DSQ1_HUMAN] | 33.73 | 1 | 0 | 7 | 15 | 54.8593705 |
| A5D6X0 | SMARCA4 protein (Fragment) OS=Homo sapiens GN=SMARCA4 PE=2 SV=1 - [A5D6X0_HUMAN] | 14.73 | 1 | 0 | 7 | 15 | 49.1882763 |
| Q8NAH3 | cDNA FLJ35359 fis, clone SALGL1000107, highly similar to CH-TOG PROTEIN OS=Homo sapiens PE=2 SV=1 - [Q8NAH3_HUMAN] | 28.15 | 1 | 0 | 7 | 12 | 37.1929491 |
| B4DLB1 | cDNA FLJ58017, moderately similar to Treacle protein OS=Homo sapiens PE=2 SV=1 - [B4DLB1_HUMAN] | 14.39 | 1 | 0 | 7 | 12 | 39.3275943 |
| B3KPW6 | cDNA FLJ32365 fis, clone PUAEN1000161, highly similar to Homo sapiens CCR4-NOT transcription complex, subunit 1 (CNOT1), transcript variant 2, mRNA OS=Homo sapiens PE=2 SV=1 - [B3KPW6_HUMAN] | 9.16 | 1 | 0 | 7 | 11 | 39.3680315 |
| B4DLY2 | cDNA FLJ56600, highly similar to Large proline-rich protein BAT2 OS=Homo sapiens PE=2 SV=1 - [B4DLY2_HUMAN] | 8.68 | 1 | 0 | 7 | 11 | 40.0964966 |
| C9JI89 | Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [C9JI89_HUMAN] | 5.96 | 1 | 0 | 7 | 11 | 38.9097314 |

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|--------|-----------------------------------------------------------------------------------------------------------------|-------|---|---|---|----|------------|
| Q13085 | Acetyl-CoA carboxylase 1 OS=Homo sapiens GN=ACACA PE=1 SV=2 - [ACACA_HUMAN] | 4.52 | 1 | 0 | 7 | 11 | 35.6702731 |
| Q8N201 | Integrator complex subunit 1 OS=Homo sapiens GN=INTS1 PE=1 SV=2 - [INT1_HUMAN] | 3.88 | 1 | 0 | 7 | 10 | 28.8517389 |
| A4D212 | DKFZP586J0619 protein OS=Homo sapiens GN=DKFZP586J0619 PE=1 SV=1 - [A4D212_HUMAN] | 3.55 | 1 | 0 | 7 | 10 | 28.8517389 |
| A4D213 | DKFZP586J0619 protein OS=Homo sapiens GN=DKFZP586J0619 PE=4 SV=1 - [A4D213_HUMAN] | 3.53 | 1 | 0 | 7 | 10 | 28.8517389 |
| B4DE72 | cDNA FLJ50078, highly similar to Nuclear pore complex protein Nup205 OS=Homo sapiens PE=2 SV=1 - [B4DE72_HUMAN] | 8.69 | 1 | 0 | 7 | 8 | 23.168643 |
| Q7Z406 | Myosin-14 OS=Homo sapiens GN=MYH14 PE=1 SV=1 - [MYH14_HUMAN] | 2.66 | 1 | 0 | 6 | 14 | 44.6828442 |
| B0I1S2 | MYH14 variant protein OS=Homo sapiens PE=2 SV=1 - [B0I1S2_HUMAN] | 2.6 | 1 | 0 | 6 | 14 | 44.6828442 |
| Q9UPG3 | Nuclear mitotic apparatus protein (Fragment) OS=Homo sapiens GN=NuMA PE=2 SV=1 - [Q9UPG3_HUMAN] | 34.68 | 1 | 0 | 6 | 13 | 43.5255704 |
| Q9UE82 | Nonmuscle myosin heavy chain IIB (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q9UE82_HUMAN] | 60.49 | 1 | 0 | 6 | 12 | 33.6998873 |
| Q53GM6 | U5 snRNP-specific protein variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53GM6_HUMAN] | 20.1 | 1 | 0 | 6 | 12 | 35.6907163 |
| Q6NXF2 | FLNA protein (Fragment) OS=Homo sapiens GN=FLNA PE=2 SV=1 - [Q6NXF2_HUMAN] | 11.5 | 1 | 0 | 6 | 11 | 44.1554866 |
| C9JAP8 | Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [C9JAP8_HUMAN] | 6.39 | 1 | 0 | 6 | 11 | 36.06686 |
| A0PJK8 | SCRIB protein (Fragment) OS=Homo sapiens GN=SCRIB PE=2 SV=1 - [A0PJK8_HUMAN] | 14.66 | 1 | 0 | 6 | 9 | 28.0870085 |
| Q68DX9 | Putative uncharacterized protein DKFZp686M05161 OS=Homo sapiens GN=DKFZp686M05161 PE=2 SV=1 - [Q68DX9_HUMAN] | 7.42 | 1 | 0 | 6 | 9 | 32.3058109 |
| Q6P486 | NUP205 protein (Fragment) OS=Homo sapiens GN=NUP205 PE=2 SV=1 - [Q6P486_HUMAN] | 11.02 | 1 | 0 | 6 | 7 | 20.906678 |
| Q96C32 | UBC protein OS=Homo sapiens PE=2 SV=1 - [Q96C32_HUMAN] | 64.26 | 1 | 0 | 5 | 15 | 48.5218687 |
| POCG47 | Polyubiquitin-B OS=Homo sapiens GN=UBB PE=1 SV=1 - [UBB_HUMAN] | 64.19 | 1 | 0 | 5 | 15 | 48.5218687 |

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|--------|-----------------------------------------------------------------------------------------------------------------------|-------|---|---|---|----|------------|
| Q5PY61 | Ubiquitin C splice variant OS=Homo sapiens GN=UBC PE=2 SV=1 - [Q5PY61_HUMAN] | 64.19 | 1 | 0 | 5 | 15 | 48.5218687 |
| B4DV12 | cDNA FLJ51326, highly similar to Homo sapiens ubiquitin B (UBB), mRNA OS=Homo sapiens PE=2 SV=1 - [B4DV12_HUMAN] | 64.05 | 1 | 0 | 5 | 15 | 48.5218687 |
| Q59EM9 | Ubiquitin C variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59EM9_HUMAN] | 63.64 | 1 | 0 | 5 | 15 | 48.5218687 |
| Q66K58 | Putative uncharacterized protein (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q66K58_HUMAN] | 63.18 | 1 | 0 | 5 | 15 | 48.5218687 |
| Q96H31 | UBC protein (Fragment) OS=Homo sapiens GN=UBC PE=2 SV=2 - [Q96H31_HUMAN] | 62.82 | 1 | 0 | 5 | 15 | 48.5218687 |
| P0CG48 | Polyubiquitin-C OS=Homo sapiens GN=UBC PE=1 SV=2 - [UBC_HUMAN] | 62.19 | 1 | 0 | 5 | 15 | 48.5218687 |
| A8K674 | cDNA FLJ75516, highly similar to Xenopus tropicalis ubiquitin C, mRNA OS=Homo sapiens PE=2 SV=1 - [A8K674_HUMAN] | 61.74 | 1 | 0 | 5 | 15 | 48.5218687 |
| Q9UFQ0 | Putative uncharacterized protein DKFZp434K0435 (Fragment) OS=Homo sapiens GN=DKFZp434K0435 PE=2 SV=1 - [Q9UFQ0_HUMAN] | 61.51 | 1 | 0 | 5 | 15 | 48.5218687 |
| Q96MH4 | cDNA FLJ32377 fis, clone SKMUS1000014, highly similar to Polyubiquitin 9 OS=Homo sapiens PE=2 SV=1 - [Q96MH4_HUMAN] | 60.57 | 1 | 0 | 5 | 15 | 48.5218687 |
| Q5UGI3 | Ubiquitin C splice variant OS=Homo sapiens GN=UBC PE=2 SV=1 - [Q5UGI3_HUMAN] | 58.17 | 1 | 0 | 5 | 15 | 48.5218687 |
| P62987 | Ubiquitin-60S ribosomal protein L40 OS=Homo sapiens GN=UBA52 PE=1 SV=2 - [RL40_HUMAN] | 38.28 | 1 | 0 | 5 | 15 | 48.5218687 |
| P62979 | Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=1 SV=2 - [RS27A_HUMAN] | 31.41 | 1 | 0 | 5 | 15 | 48.5218687 |
| Q5RKT7 | Ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=2 SV=1 - [Q5RKT7_HUMAN] | 31.41 | 1 | 0 | 5 | 15 | 48.5218687 |
| Q5BKV1 | MYH9 protein OS=Homo sapiens GN=MYH9 PE=2 SV=1 - [Q5BKV1_HUMAN] | 27.98 | 1 | 0 | 5 | 12 | 40.2615542 |
| Q8NDS5 | Putative uncharacterized protein DKFZp547H1810 (Fragment) OS=Homo sapiens GN=DKFZp547H1810 PE=2 SV=1 - [Q8NDS5_HUMAN] | 34.76 | 1 | 0 | 5 | 9 | 30.2042148 |
| B4DZ56 | cDNA FLJ56810, highly similar to Large proline-rich protein BAT2 | 13.66 | 1 | 0 | 5 | 9 | 27.4325984 |

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| | OS=Homo sapiens PE=2 SV=1 - [B4DZ56_HUMAN] | | | | | | |
| Q6JH03 | Apoptosis-regulated protein 2 (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q6JH03_HUMAN] | 11.9 | 1 | 0 | 5 | 9 | 26.0045044 |
| Q59FY4 | Acetyl-Coenzyme A carboxylase alpha isoform 2 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59FY4_HUMAN] | 7.01 | 1 | 0 | 5 | 9 | 28.5232482 |
| Q9P2E9 | Ribosome-binding protein 1 OS=Homo sapiens GN=RRBP1 PE=1 SV=4 - [RRBP1_HUMAN] | 4.61 | 1 | 0 | 5 | 8 | 27.0633402 |
| A7BI36 | p180/ribosome receptor OS=Homo sapiens GN=RRBP1 PE=2 SV=1 - [A7BI36_HUMAN] | 4.22 | 1 | 0 | 5 | 8 | 27.0633402 |
| Q14669 | Probable E3 ubiquitin-protein ligase TRIP12 OS=Homo sapiens GN=TRIP12 PE=1 SV=1 - [TRIPC_HUMAN] | 3.11 | 1 | 0 | 5 | 7 | 20.7429669 |
| D4HL82 | ULF OS=Homo sapiens PE=2 SV=1 - [D4HL82_HUMAN] | 3.06 | 1 | 0 | 5 | 7 | 20.7429669 |
| Q14CA3 | TRIP12 protein OS=Homo sapiens GN=TRIP12 PE=2 SV=1 - [Q14CA3_HUMAN] | 3.04 | 1 | 0 | 5 | 7 | 20.7429669 |
| B4DH82 | cDNA FLJ54437, highly similar to RRP5 protein homolog (Fragment) OS=Homo sapiens PE=2 SV=1 - [B4DH82_HUMAN] | 6.16 | 1 | 0 | 5 | 6 | 19.9248917 |
| Q49A90 | RPS27A protein OS=Homo sapiens GN=RPS27A PE=4 SV=1 - [Q49A90_HUMAN] | 42.11 | 1 | 0 | 4 | 13 | 43.3513389 |
| B4DM32 | cDNA FLJ54481, highly similar to GCN1-like protein 1 (Fragment) OS=Homo sapiens PE=2 SV=1 - [B4DM32_HUMAN] | 8.73 | 1 | 0 | 4 | 10 | 36.8137643 |
| Q5HY89 | Filamin A, alpha (Actin binding protein 280) (Fragment) OS=Homo sapiens GN=FLNA PE=2 SV=1 - [Q5HY89_HUMAN] | 35.93 | 1 | 0 | 4 | 8 | 33.1048632 |
| D6RC21 | Uncharacterized protein OS=Homo sapiens GN=TCOF1 PE=4 SV=1 - [D6RC21_HUMAN] | 13.15 | 1 | 0 | 4 | 8 | 22.9743674 |
| Q6JH02 | Apoptosis-regulated protein 1 (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q6JH02_HUMAN] | 10.32 | 1 | 0 | 4 | 8 | 23.7676666 |
| B4DZE1 | cDNA FLJ53944, highly similar to Eukaryotic translation initiation factor 4 gamma 3 OS=Homo sapiens PE=2 SV=1 - [B4DZE1_HUMAN] | 5.21 | 1 | 0 | 4 | 8 | 23.3665078 |
| B4DH17 | cDNA FLJ59298, highly similar to Eukaryotic translation initiation factor 4 gamma 3 OS=Homo sapiens PE=2 SV=1 - [B4DH17_HUMAN] | 4.71 | 1 | 0 | 4 | 8 | 23.3665078 |
| Q504Z1 | EIF4G3 protein OS=Homo sapiens GN=EIF4G3 PE=2 SV=1 - | 4.29 | 1 | 0 | 4 | 8 | 23.3665078 |

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| | [Q504Z1_HUMAN] | | | | | | |
| Q8WWQ0 | PH-interacting protein OS=Homo sapiens GN=PHIP PE=1 SV=2 - [PHIP_HUMAN] | 3.68 | 1 | 0 | 4 | 8 | 29.2364476 |
| A7J992 | Pleckstrin homology domain-interacting protein variant 1 OS=Homo sapiens GN=PHIP PE=2 SV=1 - [A7J992_HUMAN] | 3.68 | 1 | 0 | 4 | 8 | 29.2364476 |
| O43432 | Eukaryotic translation initiation factor 4 gamma 3 OS=Homo sapiens GN=EIF4G3 PE=1 SV=2 - [IF4G3_HUMAN] | 3.53 | 1 | 0 | 4 | 8 | 23.3665078 |
| B9EGQ7 | EIF4G3 protein OS=Homo sapiens GN=EIF4G3 PE=2 SV=1 - [B9EGQ7_HUMAN] | 3.52 | 1 | 0 | 4 | 8 | 23.3665078 |
| Q59GJ0 | Eukaryotic translation initiation factor 4 gamma, 3 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59GJ0_HUMAN] | 3.15 | 1 | 0 | 4 | 8 | 23.3665078 |
| Q7Z7R0 | Smooth muscle myosin heavy chain (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q7Z7R0_HUMAN] | 2.66 | 1 | 0 | 4 | 8 | 25.2715189 |
| B4DTD5 | cDNA FLJ57890, highly similar to Filamin-A OS=Homo sapiens PE=2 SV=1 - [B4DTD5_HUMAN] | 11.21 | 1 | 0 | 4 | 7 | 27.4638336 |
| Q96C61 | FLNA protein OS=Homo sapiens PE=2 SV=1 - [Q96C61_HUMAN] | 9.07 | 1 | 0 | 4 | 7 | 27.4638336 |
| C9JXK4 | Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [C9JXK4_HUMAN] | 8.74 | 1 | 0 | 4 | 7 | 20.5318997 |
| Q7Z5W8 | ACACA protein (Fragment) OS=Homo sapiens GN=ACACA PE=2 SV=1 - [Q7Z5W8_HUMAN] | 8.55 | 1 | 0 | 4 | 7 | 22.3311272 |
| Q69YJ6 | Putative uncharacterized protein DKFZp667N107 (Fragment) OS=Homo sapiens GN=DKFZp667N107 PE=2 SV=1 - [Q69YJ6_HUMAN] | 5.59 | 1 | 0 | 4 | 7 | 25.3305514 |
| B4DL41 | cDNA FLJ57825, highly similar to DNA-dependent protein kinase catalytic subunit (EC 2.7.11.1) OS=Homo sapiens PE=2 SV=1 - [B4DL41_HUMAN] | 4.07 | 1 | 0 | 4 | 7 | 23.5805891 |
| Q6W2J9 | BCL-6 corepressor OS=Homo sapiens GN=BCOR PE=1 SV=1 - [BCOR_HUMAN] | 3.19 | 1 | 0 | 4 | 7 | 26.4121296 |
| B4E3V7 | cDNA FLJ61585, highly similar to DNA-directed RNA polymerase II largest subunit (EC 2.7.7.6) OS=Homo sapiens PE=2 SV=1 - [B4E3V7_HUMAN] | 2.58 | 1 | 0 | 4 | 7 | 22.7830842 |
| P24928 | DNA-directed RNA polymerase II subunit RPB1 OS=Homo sapiens GN=POLR2A PE=1 SV=2 - [RPB1_HUMAN] | 2.54 | 1 | 0 | 4 | 7 | 22.7830842 |

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| A1A5C5 | RRBP1 protein OS=Homo sapiens GN=RRBP1 PE=2 SV=1 - [A1A5C5_HUMAN] | 6.26 | 1 | 0 | 4 | 6 | 19.6707127 |
| A1A5C4 | RRBP1 protein OS=Homo sapiens GN=RRBP1 PE=2 SV=1 - [A1A5C4_HUMAN] | 5.03 | 1 | 0 | 4 | 6 | 19.6707127 |
| P51531 | Probable global transcription activator SNF2L2 OS=Homo sapiens GN=SMARCA2 PE=1 SV=2 - [SMCA2_HUMAN] | 2.64 | 1 | 0 | 4 | 6 | 18.4366918 |
| Q4LE79 | DSP variant protein (Fragment) OS=Homo sapiens GN=DSP variant protein PE=2 SV=1 - [Q4LE79_HUMAN] | 2.63 | 1 | 0 | 4 | 6 | 20.7129636 |
| D7RX09 | Desmoplakin la OS=Homo sapiens PE=2 SV=1 - [D7RX09_HUMAN] | 2.51 | 1 | 0 | 4 | 6 | 20.7129636 |
| P15924 | Desmoplakin OS=Homo sapiens GN=DSP PE=1 SV=3 - [DESP_HUMAN] | 2.12 | 1 | 0 | 4 | 6 | 20.7129636 |
| B4DES7 | cDNA FLJ61218, highly similar to RRP5 protein homolog OS=Homo sapiens PE=2 SV=1 - [B4DES7_HUMAN] | 7.78 | 1 | 0 | 4 | 5 | 17.8834388 |
| B3KNW7 | cDNA FLJ30606 fis, clone CTONG2000330, highly similar to Probable global transcription activator SNF2L4 (EC 3.6.1.-) OS=Homo sapiens PE=2 SV=1 - [B3KNW7_HUMAN] | 6.24 | 1 | 0 | 4 | 5 | 15.3467925 |
| B4E0F1 | cDNA FLJ60382, highly similar to Probable global transcription activator SNF2L4(EC 3.6.1.-) OS=Homo sapiens PE=2 SV=1 - [B4E0F1_HUMAN] | 5.52 | 1 | 0 | 4 | 5 | 15.3467925 |
| B4DSI8 | cDNA FLJ60344, highly similar to Probable global transcription activator SNF2L4 (EC 3.6.1.-) OS=Homo sapiens PE=2 SV=1 - [B4DSI8_HUMAN] | 5.31 | 1 | 0 | 4 | 5 | 15.3467925 |
| Q86V26 | Microtubule-associated protein 4 OS=Homo sapiens GN=MAP4 PE=2 SV=1 - [Q86V26_HUMAN] | 40.4 | 1 | 0 | 3 | 8 | 29.2918773 |
| B1AH99 | Myosin, heavy chain 9, non-muscle (Fragment) OS=Homo sapiens GN=MYH9 PE=4 SV=1 - [B1AH99_HUMAN] | 33.01 | 1 | 0 | 3 | 7 | 23.4560165 |
| Q96C95 | MLLT4 protein (Fragment) OS=Homo sapiens GN=MLLT4 PE=2 SV=1 - [Q96C95_HUMAN] | 10.82 | 1 | 0 | 3 | 7 | 24.0152094 |
| O14729 | Smooth muscle myosin heavy chain SM2 (Fragment) OS=Homo sapiens PE=2 SV=1 - [O14729_HUMAN] | 4.59 | 1 | 0 | 3 | 7 | 24.1884134 |
| O14794 | Smooth muscle myosin heavy chain SM1 (Fragment) OS=Homo sapiens PE=2 SV=1 - [O14794_HUMAN] | 4.34 | 1 | 0 | 3 | 7 | 24.1884134 |
| B4E2F9 | cDNA FLJ57038, highly similar to Filamin-A OS=Homo sapiens | 7.69 | 1 | 0 | 3 | 6 | 23.5137639 |

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| | PE=2 SV=1 - [B4E2F9_HUMAN] | | | | | | |
| Q9NWP3 | cDNA FLJ20705 fis, clone KAIA1571 OS=Homo sapiens PE=2 SV=1 - [Q9NWP3_HUMAN] | 6.08 | 1 | 0 | 3 | 6 | 21.3215797 |
| P04259 | Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5 - [K2C6B_HUMAN] | 5.5 | 1 | 0 | 3 | 6 | 16.2246702 |
| E3UVQ2 | BCL6 corepressor/retinoic acid receptor alpha fusion protein OS=Homo sapiens GN=BCOR-RARA PE=2 SV=1 - [E3UVQ2_HUMAN] | 2.28 | 1 | 0 | 3 | 6 | 23.4003191 |
| D3YHM4 | Tenascin-C isoform 14/AD1/16 OS=Homo sapiens PE=2 SV=1 - [D3YHM4_HUMAN] | 1.9 | 1 | 0 | 3 | 6 | 18.4197268 |
| Q96N67 | Dedicator of cytokinesis protein 7 OS=Homo sapiens GN=DOCK7 PE=1 SV=4 - [DOCK7_HUMAN] | 1.82 | 1 | 0 | 3 | 6 | 20.9990411 |
| A7MBN2 | TNC protein OS=Homo sapiens GN=TNC PE=2 SV=1 - [A7MBN2_HUMAN] | 1.82 | 1 | 0 | 3 | 6 | 18.4197268 |
| P24821 | Tenascin OS=Homo sapiens GN=TNC PE=1 SV=3 - [TENA_HUMAN] | 1.59 | 1 | 0 | 3 | 6 | 18.4197268 |
| Q4LE33 | TNC variant protein (Fragment) OS=Homo sapiens GN=TNC variant protein PE=2 SV=1 - [Q4LE33_HUMAN] | 1.57 | 1 | 0 | 3 | 6 | 18.4197268 |
| Q6P664 | HEAT repeat containing 1 OS=Homo sapiens GN=HEATR1 PE=2 SV=1 - [Q6P664_HUMAN] | 20 | 1 | 0 | 3 | 5 | 15.0305026 |
| B4DIG6 | cDNA FLJ52591, highly similar to Acetyl-CoA carboxylase 1 (EC 6.4.1.2) OS=Homo sapiens PE=2 SV=1 - [B4DIG6_HUMAN] | 11.72 | 1 | 0 | 3 | 5 | 14.844075 |
| B4DIW1 | cDNA FLJ50410, highly similar to Acetyl-CoA carboxylase 1 (EC 6.4.1.2) OS=Homo sapiens PE=2 SV=1 - [B4DIW1_HUMAN] | 10.98 | 1 | 0 | 3 | 5 | 14.844075 |
| B4DWK9 | cDNA FLJ50718, highly similar to Acetyl-CoA carboxylase 1 (EC 6.4.1.2) OS=Homo sapiens PE=2 SV=1 - [B4DWK9_HUMAN] | 10.11 | 1 | 0 | 3 | 5 | 14.844075 |
| B4DIR2 | cDNA FLJ52592, highly similar to Acetyl-CoA carboxylase 1 (EC 6.4.1.2) OS=Homo sapiens PE=2 SV=1 - [B4DIR2_HUMAN] | 9.53 | 1 | 0 | 3 | 5 | 14.844075 |
| B4DK35 | cDNA FLJ61591, highly similar to Probable global transcription activator SNF2L2 (EC 3.6.1.-) (Fragment) OS=Homo sapiens PE=2 SV=1 - [B4DK35_HUMAN] | 3.33 | 1 | 0 | 3 | 5 | 15.9915159 |
| Q14CF1 | TRIP12 protein OS=Homo sapiens GN=TRIP12 PE=2 SV=1 - [Q14CF1_HUMAN] | 2.26 | 1 | 0 | 3 | 5 | 14.1993666 |

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|--------|---------------------------------------------------------------------------------------------------------------------------------------------------------------|-------|---|---|---|---|------------|
| A6H8X9 | Centrosomal protein 170kDa OS=Homo sapiens GN=CEP170 PE=2 SV=1 - [A6H8X9_HUMAN] | 1.99 | 1 | 0 | 3 | 5 | 14.3982406 |
| B2RTS4 | Centrosomal protein 170kDa OS=Homo sapiens GN=CEP170 PE=2 SV=1 - [B2RTS4_HUMAN] | 1.95 | 1 | 0 | 3 | 5 | 14.3982406 |
| Q5SW79 | Centrosomal protein of 170 kDa OS=Homo sapiens GN=CEP170 PE=1 SV=1 - [CE170_HUMAN] | 1.83 | 1 | 0 | 3 | 5 | 14.3982406 |
| Q4VBX7 | NUP205 protein (Fragment) OS=Homo sapiens GN=NUP205 PE=2 SV=1 - [Q4VBX7_HUMAN] | 11.64 | 1 | 0 | 3 | 4 | 13.5277443 |
| Q6DKH1 | NUP205 protein (Fragment) OS=Homo sapiens GN=NUP205 PE=2 SV=1 - [Q6DKH1_HUMAN] | 8.97 | 1 | 0 | 3 | 4 | 13.5277443 |
| Q53TE7 | Putative uncharacterized protein TRIP12 (Fragment) OS=Homo sapiens GN=TRIP12 PE=2 SV=1 - [Q53TE7_HUMAN] | 6.79 | 1 | 0 | 3 | 4 | 12.7423258 |
| B4DZK4 | cDNA FLJ50931, highly similar to Tight junction protein ZO-1 OS=Homo sapiens PE=2 SV=1 - [B4DZK4_HUMAN] | 6.34 | 1 | 0 | 3 | 4 | 12.5346682 |
| B7Z3U6 | ATPase, Na+/K+ transporting, alpha 1 polypeptide, isoform CRA_a OS=Homo sapiens GN=ATP1A1 PE=2 SV=1 - [B7Z3U6_HUMAN] | 4.74 | 1 | 0 | 3 | 4 | 13.684025 |
| B7Z3V1 | cDNA FLJ60077, highly similar to Sodium/potassium- transporting ATPase alpha-1 chain (EC 3.6.3.9) (Fragment) OS=Homo sapiens PE=2 SV=1 - [B7Z3V1_HUMAN] | 4.61 | 1 | 0 | 3 | 4 | 13.684025 |
| P05023 | Sodium/potassium-transporting ATPase subunit alpha-1 OS=Homo sapiens GN=ATP1A1 PE=1 SV=1 - [AT1A1_HUMAN] | 4.59 | 1 | 0 | 3 | 4 | 13.684025 |
| B7Z2T5 | cDNA FLJ55427, highly similar to Sodium/potassium- transporting ATPase alpha-1 chain (EC 3.6.3.9) OS=Homo sapiens PE=2 SV=1 - [B7Z2T5_HUMAN] | 4.59 | 1 | 0 | 3 | 4 | 13.684025 |
| B4DSC8 | cDNA FLJ53181, highly similar to Probable global transcription activator SNF2L2 (EC 3.6.1.-) (Fragment) OS=Homo sapiens PE=2 SV=1 - [B4DSC8_HUMAN] | 4.34 | 1 | 0 | 3 | 4 | 12.6762738 |
| Q14839 | Chromodomain-helicase-DNA-binding protein 4 OS=Homo sapiens GN=CHD4 PE=1 SV=2 - [CHD4_HUMAN] | 2.35 | 1 | 0 | 3 | 4 | 11.5730836 |
| Q2PS10 | Non-muscle myosin heavy chain (Fragment) OS=Homo sapiens GN=MYH9 PE=2 SV=1 - [Q2PS10_HUMAN] | 38.03 | 1 | 0 | 2 | 7 | 23.5772877 |
| Q5T0G3 | Leucine rich repeat containing 1 OS=Homo sapiens GN=LRR1 PE=2 SV=1 - [Q5T0G3_HUMAN] | 14.94 | 1 | 0 | 2 | 5 | 16.1317964 |

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| Q9BTT6 | Leucine-rich repeat-containing protein 1 OS=Homo sapiens GN=LRRRC1 PE=1 SV=1 - [LRRRC1_HUMAN] | 4.39 | 1 | 0 | 2 | 5 | 16.1317964 |
| A8K883 | cDNA FLJ77590, highly similar to Homo sapiens leucine rich repeat containing 1, mRNA OS=Homo sapiens PE=2 SV=1 - [A8K883_HUMAN] | 4.39 | 1 | 0 | 2 | 5 | 16.1317964 |
| Q14222 | EEF1A protein (Fragment) OS=Homo sapiens GN=EEF1A PE=1 SV=1 - [Q14222_HUMAN] | 15.42 | 1 | 0 | 2 | 4 | 15.8832026 |
| Q96C29 | Putative uncharacterized protein (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q96C29_HUMAN] | 14.11 | 1 | 0 | 2 | 4 | 15.8832026 |
| Q8TBL1 | Putative uncharacterized protein (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q8TBL1_HUMAN] | 14 | 1 | 0 | 2 | 4 | 15.8832026 |
| Q6P082 | EEF1A1 protein (Fragment) OS=Homo sapiens GN=EEF1A1 PE=2 SV=1 - [Q6P082_HUMAN] | 13.94 | 1 | 0 | 2 | 4 | 15.8832026 |
| C9JHW9 | Uncharacterized protein OS=Homo sapiens GN=EIF4G1 PE=4 SV=1 - [C9JHW9_HUMAN] | 12.5 | 1 | 0 | 2 | 4 | 12.8800144 |
| Q96CD8 | Putative uncharacterized protein (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q96CD8_HUMAN] | 12.2 | 1 | 0 | 2 | 4 | 15.8832026 |
| Q6P4C9 | EEF1A1 protein (Fragment) OS=Homo sapiens GN=EEF1A1 PE=2 SV=1 - [Q6P4C9_HUMAN] | 12.07 | 1 | 0 | 2 | 4 | 15.8832026 |
| Q504Z0 | EEF1A1 protein OS=Homo sapiens GN=EEF1A1 PE=2 SV=1 - [Q504Z0_HUMAN] | 11.36 | 1 | 0 | 2 | 4 | 15.8832026 |
| B4E2C5 | cDNA FLJ54032, highly similar to Elongation factor 1-alpha 1 OS=Homo sapiens PE=2 SV=1 - [B4E2C5_HUMAN] | 11.36 | 1 | 0 | 2 | 4 | 15.8832026 |
| Q8IUB0 | CTCL tumor antigen HD-CL-08 OS=Homo sapiens PE=2 SV=1 - [Q8IUB0_HUMAN] | 9.7 | 1 | 0 | 2 | 4 | 15.8832026 |
| B4DNE0 | cDNA FLJ52573, highly similar to Elongation factor 1-alpha 1 OS=Homo sapiens PE=2 SV=1 - [B4DNE0_HUMAN] | 8.86 | 1 | 0 | 2 | 4 | 15.8832026 |
| Q96RE1 | Translation elongation factor 1 alpha 1-like 14 OS=Homo sapiens GN=EEF1A1L14 PE=2 SV=1 - [Q96RE1_HUMAN] | 8.79 | 1 | 0 | 2 | 4 | 15.8832026 |
| O95065 | Eucaryotic translation initiation factor 4G isoform 1 (Fragment) OS=Homo sapiens PE=2 SV=1 - [O95065_HUMAN] | 8.7 | 1 | 0 | 2 | 4 | 12.8800144 |
| Q9NZS6 | Glucocorticoid receptor AF-1 specific elongation factor (Fragment) OS=Homo sapiens PE=1 SV=1 - [Q9NZS6_HUMAN] | 8.22 | 1 | 0 | 2 | 4 | 15.8832026 |
| Q53G89 | Eukaryotic translation elongation factor 1 alpha 1 variant | 8.08 | 1 | 0 | 2 | 4 | 15.8832026 |

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|--------|------------------------------------------------------------------------------------------------------------------------------------------------------------|------|---|---|---|---|------------|
| | (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53G89_HUMAN] | | | | | | |
| Q6IQ15 | EEF1A1 protein OS=Homo sapiens GN=EEF1A1 PE=2 SV=1 - [Q6IQ15_HUMAN] | 7.94 | 1 | 0 | 2 | 4 | 15.8832026 |
| Q68D89 | Putative uncharacterized protein DKFZp686D10126 (Fragment) OS=Homo sapiens GN=DKFZp686D10126 PE=2 SV=1 - [Q68D89_HUMAN] | 7.81 | 1 | 0 | 2 | 4 | 12.7950292 |
| B5MEB1 | Uncharacterized protein OS=Homo sapiens GN=PHIP PE=4 SV=1 - [B5MEB1_HUMAN] | 7.79 | 1 | 0 | 2 | 4 | 14.8611021 |
| P68104 | Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 - [EF1A1_HUMAN] | 7.58 | 1 | 0 | 2 | 4 | 15.8832026 |
| Q5VTE0 | Putative elongation factor 1-alpha-like 3 OS=Homo sapiens GN=EEF1A3 PE=5 SV=1 - [EF1A3_HUMAN] | 7.58 | 1 | 0 | 2 | 4 | 15.8832026 |
| Q53HM9 | Eukaryotic translation elongation factor 1 alpha 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53HM9_HUMAN] | 7.58 | 1 | 0 | 2 | 4 | 15.8832026 |
| Q6IPT9 | Eukaryotic translation elongation factor 1 alpha 1 OS=Homo sapiens GN=EEF1A1 PE=2 SV=1 - [Q6IPT9_HUMAN] | 7.58 | 1 | 0 | 2 | 4 | 15.8832026 |
| Q6IPN6 | Eukaryotic translation elongation factor 1 alpha 1 OS=Homo sapiens GN=EEF1A1 PE=2 SV=1 - [Q6IPN6_HUMAN] | 7.58 | 1 | 0 | 2 | 4 | 15.8832026 |
| Q53HR5 | Eukaryotic translation elongation factor 1 alpha 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53HR5_HUMAN] | 7.58 | 1 | 0 | 2 | 4 | 15.8832026 |
| Q53GE9 | Eukaryotic translation elongation factor 1 alpha 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53GE9_HUMAN] | 7.58 | 1 | 0 | 2 | 4 | 15.8832026 |
| Q53HQ7 | Eukaryotic translation elongation factor 1 alpha 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53HQ7_HUMAN] | 7.58 | 1 | 0 | 2 | 4 | 15.8832026 |
| A8K9C4 | cDNA FLJ76726, highly similar to Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K9C4_HUMAN] | 7.58 | 1 | 0 | 2 | 4 | 15.8832026 |
| Q53G85 | Eukaryotic translation elongation factor 1 alpha 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53G85_HUMAN] | 7.58 | 1 | 0 | 2 | 4 | 15.8832026 |
| Q96ES5 | HEATR1 protein OS=Homo sapiens GN=HEATR1 PE=2 SV=1 - [Q96ES5_HUMAN] | 7.16 | 1 | 0 | 2 | 4 | 12.7084 |
| Q6NX41 | POLR2A protein OS=Homo sapiens GN=POLR2A PE=2 SV=1 - [Q6NX41_HUMAN] | 5.12 | 1 | 0 | 2 | 4 | 12.8323083 |

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|--------|---------------------------------------------------------------------------------------------------------------------------|------|---|---|---|---|------------|
| Q96HX3 | Similar to ribophorin I (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q96HX3_HUMAN] | 4.75 | 1 | 0 | 2 | 4 | 12.6898828 |
| P04843 | Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Homo sapiens GN=RPN1 PE=1 SV=1 - [RPN1_HUMAN] | 4.45 | 1 | 0 | 2 | 4 | 12.6898828 |
| Q53EP4 | Ribophorin I variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53EP4_HUMAN] | 4.45 | 1 | 0 | 2 | 4 | 12.6898828 |
| Q6IBR0 | RPN1 protein OS=Homo sapiens GN=RPN1 PE=2 SV=1 - [Q6IBR0_HUMAN] | 4.45 | 1 | 0 | 2 | 4 | 12.6898828 |
| B4DWU6 | cDNA FLJ51361, highly similar to Keratin, type II cytoskeletal 6A OS=Homo sapiens PE=2 SV=1 - [B4DWU6_HUMAN] | 4.04 | 1 | 0 | 2 | 4 | 10.6616945 |
| B4DKV4 | cDNA FLJ60647, highly similar to Keratin, type II cytoskeletal 6B OS=Homo sapiens PE=2 SV=1 - [B4DKV4_HUMAN] | 3.99 | 1 | 0 | 2 | 4 | 10.6616945 |
| Q96NI0 | Dedicator of cytokinesis 7 OS=Homo sapiens GN=DOCK7 PE=2 SV=1 - [Q96NI0_HUMAN] | 3.96 | 1 | 0 | 2 | 4 | 12.2581811 |
| B4DRR0 | cDNA FLJ53910, highly similar to Keratin, type II cytoskeletal 6A OS=Homo sapiens PE=2 SV=1 - [B4DRR0_HUMAN] | 3.93 | 1 | 0 | 2 | 4 | 10.6616945 |
| B4DRY0 | cDNA FLJ54379, highly similar to Keratin, type II cytoskeletal 6E OS=Homo sapiens PE=2 SV=1 - [B4DRY0_HUMAN] | 3.84 | 1 | 0 | 2 | 4 | 10.6616945 |
| B4DRU6 | cDNA FLJ54657, highly similar to Keratin, type II cytoskeletal 6A OS=Homo sapiens PE=2 SV=1 - [B4DRU6_HUMAN] | 3.83 | 1 | 0 | 2 | 4 | 10.6616945 |
| P02538 | Keratin, type II cytoskeletal 6A OS=Homo sapiens GN=KRT6A PE=1 SV=3 - [K2C6A_HUMAN] | 3.72 | 1 | 0 | 2 | 4 | 10.6616945 |
| P48668 | Keratin, type II cytoskeletal 6C OS=Homo sapiens GN=KRT6C PE=1 SV=3 - [K2C6C_HUMAN] | 3.72 | 1 | 0 | 2 | 4 | 10.6616945 |
| B2R853 | cDNA, FLJ93744, highly similar to Homo sapiens keratin 6E (KRT6E), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R853_HUMAN] | 3.72 | 1 | 0 | 2 | 4 | 10.6616945 |
| A8K2I0 | cDNA FLJ78504, highly similar to Homo sapiens keratin 6A (KRT6A), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K2I0_HUMAN] | 3.72 | 1 | 0 | 2 | 4 | 10.6616945 |
| B3KWH4 | cDNA FLJ43092 fis, clone COLON2002520, highly similar to Myosin-14 (Fragment) OS=Homo sapiens PE=2 SV=1 - [B3KWH4_HUMAN] | 2.54 | 1 | 0 | 2 | 4 | 10.8033421 |

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|--------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------|---|---|---|---|------------|
| B5MDH9 | Uncharacterized protein OS=Homo sapiens GN=GAPVD1 PE=4 SV=2 - [B5MDH9_HUMAN] | 2.41 | 1 | 0 | 2 | 4 | 19.116605 |
| Q14C86 | GTPase-activating protein and VPS9 domain-containing protein 1 OS=Homo sapiens GN=GAPVD1 PE=1 SV=2 - [GAPD1_HUMAN] | 2.3 | 1 | 0 | 2 | 4 | 19.116605 |
| B4E177 | cDNA FLJ56368, highly similar to Myosin-14 OS=Homo sapiens PE=2 SV=1 - [B4E177_HUMAN] | 1.57 | 1 | 0 | 2 | 4 | 12.7950292 |
| A1L2Z2 | MYH14 protein OS=Homo sapiens GN=MYH14 PE=2 SV=1 - [A1L2Z2_HUMAN] | 1.57 | 1 | 0 | 2 | 4 | 12.7950292 |
| B1ARM6 | Centrosomal protein 170kDa (Fragment) OS=Homo sapiens GN=CEP170 PE=4 SV=1 - [B1ARM6_HUMAN] | 1.22 | 1 | 0 | 2 | 4 | 11.4109232 |
| Q8WYN9 | Ribosomal protein S27A (Fragment) OS=Homo sapiens GN=RPS27A PE=2 SV=1 - [Q8WYN9_HUMAN] | 14.88 | 1 | 0 | 2 | 3 | 7.58704782 |
| Q5TIH1 | Myeloid/lymphoid or mixed-lineage leukemia (Trithorax homolog, Drosophila); translocated to, 4 (Fragment) OS=Homo sapiens GN=MLLT4 PE=2 SV=1 - [Q5TIH1_HUMAN] | 14.13 | 1 | 0 | 2 | 3 | 10.2433152 |
| Q5TIH0 | Myeloid/lymphoid or mixed-lineage leukemia (Trithorax homolog, Drosophila); translocated to, 4 (Fragment) OS=Homo sapiens GN=MLLT4 PE=2 SV=1 - [Q5TIH0_HUMAN] | 10.66 | 1 | 0 | 2 | 3 | 10.2433152 |
| Q96SQ4 | cDNA FLJ14711 fis, clone NT2RP3000661 OS=Homo sapiens PE=2 SV=1 - [Q96SQ4_HUMAN] | 9.19 | 1 | 0 | 2 | 3 | 7.69168258 |
| B7Z1N5 | cDNA FLJ53830, highly similar to Sodium/potassium-transporting ATPase alpha-1 chain (EC 3.6.3.9) OS=Homo sapiens PE=2 SV=1 - [B7Z1N5_HUMAN] | 8.4 | 1 | 0 | 2 | 3 | 10.3250129 |
| B3KNQ8 | cDNA FLJ30174 fis, clone BRACE2000975, highly similar to Sodium/potassium-transporting ATPase alpha-3 chain (EC 3.6.3.9) OS=Homo sapiens PE=2 SV=1 - [B3KNQ8_HUMAN] | 7.82 | 1 | 0 | 2 | 3 | 10.3250129 |
| B3KS60 | cDNA FLJ35566 fis, clone SPLEN2005474, highly similar to Homo sapiens CCR4-NOT transcription complex, subunit 1 (CNOT1), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1 - [B3KS60_HUMAN] | 6.05 | 1 | 0 | 2 | 3 | 8.16602278 |
| B5MDN3 | Uncharacterized protein OS=Homo sapiens GN=CNOT1 PE=4 SV=1 - [B5MDN3_HUMAN] | 6.03 | 1 | 0 | 2 | 3 | 8.16602278 |
| B3KSY7 | cDNA FLJ37309 fis, clone BRAMY2016611, highly similar to Sodium/potassium-transporting ATPase alpha-3 chain (EC | 5.33 | 1 | 0 | 2 | 3 | 10.3250129 |

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| | 3.6.3.9) OS=Homo sapiens PE=2 SV=1 - [B3KSY7_HUMAN] | | | | | | |
| B7Z6X2 | cDNA FLJ61738, highly similar to Homo sapiens CCR4-NOT transcription complex, subunit 1 (CNOT1), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1 - [B7Z6X2_HUMAN] | 4.99 | 1 | 0 | 2 | 3 | 8.16602278 |
| B3KV59 | cDNA FLJ16157 fis, clone BRAWH2006479, highly similar to Sodium/potassium-transporting ATPase alpha-3 chain (EC 3.6.3.9) OS=Homo sapiens PE=2 SV=1 - [B3KV59_HUMAN] | 4.99 | 1 | 0 | 2 | 3 | 10.3250129 |
| A6NE70 | Uncharacterized protein OS=Homo sapiens GN=BCOR PE=4 SV=1 - [A6NE70_HUMAN] | 4.66 | 1 | 0 | 2 | 3 | 11.2587578 |
| Q8NBP1 | cDNA PSEC0075 fis, clone NT2RP2003227 OS=Homo sapiens PE=2 SV=1 - [Q8NBP1_HUMAN] | 4.11 | 1 | 0 | 2 | 3 | 7.69168258 |
| B3KTC2 | cDNA FLJ38041 fis, clone CTONG2013986, highly similar to BCoR protein OS=Homo sapiens PE=2 SV=1 - [B3KTC2_HUMAN] | 4.07 | 1 | 0 | 2 | 3 | 11.2587578 |
| B7Z1Q9 | cDNA FLJ59485, highly similar to Sodium/potassium-transporting ATPase alpha-3 chain (EC 3.6.3.9) OS=Homo sapiens PE=2 SV=1 - [B7Z1Q9_HUMAN] | 3.73 | 1 | 0 | 2 | 3 | 10.3250129 |
| B4DKX6 | cDNA FLJ53584, highly similar to Desmoplakin (Fragment) OS=Homo sapiens PE=2 SV=1 - [B4DKX6_HUMAN] | 3.67 | 1 | 0 | 2 | 3 | 13.2679031 |
| B7Z3F8 | cDNA FLJ59543, highly similar to Sodium/potassium-transporting ATPase alpha-3 chain (EC 3.6.3.9) OS=Homo sapiens PE=2 SV=1 - [B7Z3F8_HUMAN] | 3.46 | 1 | 0 | 2 | 3 | 10.3250129 |
| P13637 | Sodium/potassium-transporting ATPase subunit alpha-3 OS=Homo sapiens GN=ATP1A3 PE=1 SV=3 - [AT1A3_HUMAN] | 3.36 | 1 | 0 | 2 | 3 | 10.3250129 |
| Q53ES0 | Na ⁺ /K ⁺ -ATPase alpha 3 subunit variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53ES0_HUMAN] | 3.36 | 1 | 0 | 2 | 3 | 10.3250129 |
| B7Z401 | cDNA FLJ54717, highly similar to Sodium/potassium-transporting ATPase alpha-3 chain (EC 3.6.3.9) OS=Homo sapiens PE=2 SV=1 - [B7Z401_HUMAN] | 3.32 | 1 | 0 | 2 | 3 | 10.3250129 |
| B7Z9V4 | cDNA, FLJ78968, highly similar to Sodium/potassium-transporting ATPase alpha-3 chain (EC 3.6.3.9) OS=Homo sapiens PE=2 SV=1 - [B7Z9V4_HUMAN] | 3.31 | 1 | 0 | 2 | 3 | 10.3250129 |
| B7Z2T0 | cDNA FLJ59513, highly similar to Sodium/potassium-transporting ATPase alpha-3 chain (EC 3.6.3.9) OS=Homo sapiens PE=2 SV=1 - [B7Z2T0_HUMAN] | 3.31 | 1 | 0 | 2 | 3 | 10.3250129 |

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| B4E0E1 | cDNA FLJ53442, highly similar to Poly (ADP-ribose) polymerase 1 (EC 2.4.2.30) OS=Homo sapiens PE=2 SV=1 - [B4E0E1_HUMAN] | 2.62 | 1 | 0 | 2 | 3 | 8.33165383 |
| B4E2A0 | cDNA FLJ61543, highly similar to Desmoplakin OS=Homo sapiens PE=2 SV=1 - [B4E2A0_HUMAN] | 2.59 | 1 | 0 | 2 | 3 | 13.2679031 |
| P09874 | Poly [ADP-ribose] polymerase 1 OS=Homo sapiens GN=PARP1 PE=1 SV=4 - [PARP1_HUMAN] | 2.56 | 1 | 0 | 2 | 3 | 8.33165383 |
| B2R5W3 | cDNA, FLJ92658, highly similar to Homo sapiens poly (ADP-ribose) polymerase family, member 1 (PARP1), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R5W3_HUMAN] | 2.56 | 1 | 0 | 2 | 3 | 8.33165383 |
| B4DL23 | cDNA FLJ53512, highly similar to Homo sapiens centrosomal protein 170 kDa (CEP170), transcript variant alpha, mRNA (Fragment) OS=Homo sapiens PE=2 SV=1 - [B4DL23_HUMAN] | 2.31 | 1 | 0 | 2 | 3 | 9.454813 |
| Q53R87 | Putative uncharacterized protein TRIP12 (Fragment) OS=Homo sapiens GN=TRIP12 PE=2 SV=1 - [Q53R87_HUMAN] | 1.85 | 1 | 0 | 2 | 3 | 8.00064111 |
| Q68CP9 | AT-rich interactive domain-containing protein 2 OS=Homo sapiens GN=ARID2 PE=1 SV=2 - [ARID2_HUMAN] | 1.42 | 1 | 0 | 2 | 3 | 7.69168258 |
| B3KY63 | cDNA FLJ16830 fis, clone UTERU3022536, highly similar to Chromodomain helicase-DNA-binding protein 4 (EC 3.6.1.-) OS=Homo sapiens PE=2 SV=1 - [B3KY63_HUMAN] | 1.38 | 1 | 0 | 2 | 3 | 8.74486327 |
| B4DKS0 | cDNA FLJ53381, highly similar to Monocarboxylate transporter 1 OS=Homo sapiens PE=2 SV=1 - [B4DKS0_HUMAN] | 8.54 | 1 | 0 | 2 | 2 | 8.0501008 |
| P53985 | Monocarboxylate transporter 1 OS=Homo sapiens GN=SLC16A1 PE=1 SV=3 - [MOT1_HUMAN] | 8.2 | 1 | 0 | 2 | 2 | 8.0501008 |
| B4DYJ6 | cDNA FLJ52804, highly similar to Thyroid receptor-interacting protein 12 OS=Homo sapiens PE=2 SV=1 - [B4DYJ6_HUMAN] | 6.65 | 1 | 0 | 2 | 2 | 6.54360032 |
| B3KSG1 | cDNA FLJ36146 fis, clone TESTI2025117, highly similar to Ribosome-binding protein 1 OS=Homo sapiens PE=2 SV=1 - [B3KSG1_HUMAN] | 6.36 | 1 | 0 | 2 | 2 | 5.10908747 |
| Q5QD01 | SP-A receptor subunit SP-R210 alphaS OS=Homo sapiens GN=MYO18A PE=2 SV=1 - [Q5QD01_HUMAN] | 2.02 | 1 | 0 | 2 | 2 | 8.05322599 |
| B4DYM1 | cDNA FLJ60372, highly similar to Myosin-18A OS=Homo sapiens PE=2 SV=1 - [B4DYM1_HUMAN] | 1.95 | 1 | 0 | 2 | 2 | 8.05322599 |
| A8MRT3 | Uncharacterized protein OS=Homo sapiens GN=GTF3C1 PE=4 | 1.6 | 1 | 0 | 2 | 2 | 5.80041456 |

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|--------|-----------------------------------------------------------------------------------------------------------------------|------|---|---|---|---|------------|
| | SV=2 - [A8MRT3_HUMAN] | | | | | | |
| Q92614 | Myosin-XVIIIa OS=Homo sapiens GN=MYO18A PE=1 SV=3 - [MY18A_HUMAN] | 1.56 | 1 | 0 | 2 | 2 | 8.05322599 |
| O00763 | Acetyl-CoA carboxylase 2 OS=Homo sapiens GN=ACACB PE=1 SV=3 - [ACACB_HUMAN] | 1.46 | 1 | 0 | 2 | 2 | 7.14702487 |
| A6NLM9 | Uncharacterized protein OS=Homo sapiens GN=ACACB PE=4 SV=3 - [A6NLM9_HUMAN] | 1.45 | 1 | 0 | 2 | 2 | 7.14702487 |
| Q96HP0 | Dedicator of cytokinesis protein 6 OS=Homo sapiens GN=DOCK6 PE=1 SV=3 - [DOCK6_HUMAN] | 1.32 | 1 | 0 | 2 | 2 | 6.05850959 |
| C9IZV6 | Uncharacterized protein OS=Homo sapiens GN=DOCK6 PE=4 SV=1 - [C9IZV6_HUMAN] | 1.32 | 1 | 0 | 2 | 2 | 6.05850959 |
| Q12789 | General transcription factor 3C polypeptide 1 OS=Homo sapiens GN=GTF3C1 PE=1 SV=4 - [TF3C1_HUMAN] | 1.28 | 1 | 0 | 2 | 2 | 5.80041456 |
| Q6AWA4 | Putative uncharacterized protein DKFZp686O0870 (Fragment) OS=Homo sapiens GN=DKFZp686O0870 PE=2 SV=1 - [Q6AWA4_HUMAN] | 1.28 | 1 | 0 | 2 | 2 | 5.80041456 |
| Q6AHZ7 | Putative uncharacterized protein DKFZp686A111 OS=Homo sapiens GN=DKFZp686A111 PE=2 SV=1 - [Q6AHZ7_HUMAN] | 1.28 | 1 | 0 | 2 | 2 | 5.80041456 |

Proteins ID03.msf

| Accession | Description | Σ Coverage | Σ # Proteins | Σ # Unique Peptides | Σ # Peptides | Σ # PSMs | Score A3 |
|-----------|----------------------------------------------------------------------------------------------------------|-------------------|---------------------|----------------------------|---------------------|-----------------|------------|
| P49327 | Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 - [FAS_HUMAN] | 32.18 | 1 | 45 | 65 | 146 | 474.471259 |
| P78527 | DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3 - [PRKDC_HUMAN] | 11.34 | 1 | 29 | 39 | 79 | 236.935424 |
| Q14204 | Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5 - [DYHC1_HUMAN] | 7.55 | 1 | 25 | 27 | 47 | 133.674908 |
| Q5JRA6 | Melanoma inhibitory activity protein 3 OS=Homo sapiens GN=MIA3 PE=1 SV=1 - [MIA3_HUMAN] | 15.42 | 1 | 19 | 21 | 38 | 122.273765 |
| P46013 | Antigen KI-67 OS=Homo sapiens GN=MKI67 PE=1 SV=2 - [KI67_HUMAN] | 8.91 | 1 | 17 | 17 | 31 | 93.4159536 |
| Q9BTC0 | Death-inducer obliterator 1 OS=Homo sapiens GN=DIDO1 PE=1 SV=5 - [DIDO1_HUMAN] | 5.67 | 1 | 10 | 10 | 17 | 47.9439771 |
| P13645 | Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6 - [K1C10_HUMAN] | 24.83 | 1 | 9 | 13 | 31 | 95.0218493 |
| P04264 | Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6 - [K2C1_HUMAN] | 17.86 | 1 | 8 | 11 | 23 | 69.0359232 |
| P15924 | Desmoplakin OS=Homo sapiens GN=DSP PE=1 SV=3 - [DESP_HUMAN] | 11.04 | 1 | 6 | 26 | 47 | 132.655014 |
| P35527 | Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3 - [K1C9_HUMAN] | 16.37 | 1 | 6 | 7 | 14 | 45.5132624 |
| O75691 | Small subunit processome component 20 homolog OS=Homo sapiens GN=UTP20 PE=1 SV=3 - [UTP20_HUMAN] | 3.73 | 1 | 5 | 10 | 12 | 27.1543701 |
| Q09666 | Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2 - [AHNK_HUMAN] | 10.49 | 1 | 4 | 16 | 18 | 55.1782134 |
| P35908 | Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2 - [K22E_HUMAN] | 15.49 | 1 | 4 | 8 | 14 | 42.5653112 |
| Q9UIF9 | Bromodomain adjacent to zinc finger domain protein 2A OS=Homo sapiens GN=BAZ2A PE=1 SV=4 - [BAZ2A_HUMAN] | 2.62 | 1 | 4 | 4 | 5 | 15.1617864 |
| P58107 | Epiplakin OS=Homo sapiens GN=EPPK1 PE=1 SV=2 - | 8.82 | 1 | 3 | 6 | 12 | 46.730613 |

| | [EPIPL_HUMAN] | | | | | | |
|--------|------------------------------------------------------------------------------------------------------------------------------|-------|---|---|----|-----|------------|
| Q5UIP0 | Telomere-associated protein RIF1 OS=Homo sapiens GN=RIF1 PE=1 SV=2 - [RIF1_HUMAN] | 1.7 | 1 | 3 | 3 | 5 | 14.6003082 |
| Q9Y490 | Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3 - [TLN1_HUMAN] | 21.41 | 1 | 2 | 32 | 65 | 245.531878 |
| Q9HCK8 | Chromodomain-helicase-DNA-binding protein 8 OS=Homo sapiens GN=CHD8 PE=1 SV=5 - [CHD8_HUMAN] | 0.77 | 1 | 2 | 2 | 4 | 8.58366752 |
| Q01082 | Spectrin beta chain, brain 1 OS=Homo sapiens GN=SPTBN1 PE=1 SV=2 - [SPTB2_HUMAN] | 34.69 | 1 | 1 | 70 | 146 | 439.517465 |
| E1NZA1 | Peroxisome proliferator activated receptor interacting complex protein OS=Homo sapiens GN=PRIC295 PE=2 SV=1 - [E1NZA1_HUMAN] | 25.5 | 1 | 1 | 51 | 109 | 341.312945 |
| Q14839 | Chromodomain-helicase-DNA-binding protein 4 OS=Homo sapiens GN=CHD4 PE=1 SV=2 - [CHD4_HUMAN] | 27.2 | 1 | 1 | 47 | 116 | 366.218757 |
| P12270 | Nucleoprotein TPR OS=Homo sapiens GN=TPR PE=1 SV=3 - [TPR_HUMAN] | 16.12 | 1 | 1 | 31 | 62 | 197.407273 |
| Q14676 | Mediator of DNA damage checkpoint protein 1 OS=Homo sapiens GN=MDC1 PE=1 SV=3 - [MDC1_HUMAN] | 22.69 | 1 | 1 | 22 | 40 | 157.647305 |
| Q8WYP5 | Protein ELYS OS=Homo sapiens GN=AHCTF1 PE=1 SV=3 - [ELYS_HUMAN] | 12.89 | 1 | 1 | 18 | 29 | 101.371489 |
| Q4LE33 | TNC variant protein (Fragment) OS=Homo sapiens GN=TNC variant protein PE=2 SV=1 - [Q4LE33_HUMAN] | 11.69 | 1 | 1 | 17 | 26 | 84.4136858 |
| Q13428 | Treacle protein OS=Homo sapiens GN=TCOF1 PE=1 SV=3 - [TCOF_HUMAN] | 13.31 | 1 | 1 | 15 | 25 | 71.8048794 |
| Q14315 | Filamin-C OS=Homo sapiens GN=FLNC PE=1 SV=3 - [FLNC_HUMAN] | 4.73 | 1 | 1 | 14 | 32 | 85.1124289 |
| O14497 | AT-rich interactive domain-containing protein 1A OS=Homo sapiens GN=ARID1A PE=1 SV=3 - [ARI1A_HUMAN] | 4.9 | 1 | 1 | 8 | 14 | 45.5672979 |
| Q92576 | PHD finger protein 3 OS=Homo sapiens GN=PHF3 PE=1 SV=3 - [PHF3_HUMAN] | 3.58 | 1 | 1 | 6 | 8 | 19.8424623 |
| Q8NFD5 | AT-rich interactive domain-containing protein 1B OS=Homo sapiens GN=ARID1B PE=1 SV=2 - [ARI1B_HUMAN] | 1.57 | 1 | 1 | 2 | 4 | 12.9139745 |
| Q9C0C2 | 182 kDa tankyrase-1-binding protein OS=Homo sapiens GN=TNKS1BP1 PE=1 SV=4 - [TB182_HUMAN] | 1.39 | 1 | 1 | 2 | 4 | 12.3758061 |

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|--------|--------------------------------------------------------------------------------------------------------------------------------------------------------------|-------|---|---|-----|-----|------------|
| P21333 | Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4 - [FLNA_HUMAN] | 57.08 | 1 | 0 | 123 | 390 | 1366.09093 |
| Q5HY54 | Filamin A, alpha (Actin binding protein 280) OS=Homo sapiens GN=FLNA PE=2 SV=1 - [Q5HY54_HUMAN] | 56.89 | 1 | 0 | 122 | 384 | 1339.86909 |
| Q60FE5 | Filamin A OS=Homo sapiens GN=FLNA PE=2 SV=1 - [Q60FE5_HUMAN] | 56.68 | 1 | 0 | 121 | 385 | 1344.69115 |
| Q60FE6 | Filamin A OS=Homo sapiens GN=FLNA PE=2 SV=1 - [Q60FE6_HUMAN] | 56.85 | 1 | 0 | 121 | 385 | 1344.69115 |
| B2ZZ80 | Filamin A OS=Homo sapiens GN=FLNA PE=2 SV=1 - [B2ZZ80_HUMAN] | 53.56 | 1 | 0 | 103 | 338 | 1164.21126 |
| A6NDY9 | Uncharacterized protein OS=Homo sapiens GN=FLNA PE=4 SV=3 - [A6NDY9_HUMAN] | 53.56 | 1 | 0 | 103 | 338 | 1164.21126 |
| Q13813 | Spectrin alpha chain, brain OS=Homo sapiens GN=SPTAN1 PE=1 SV=3 - [SPTA2_HUMAN] | 32.4 | 1 | 0 | 67 | 152 | 516.075348 |
| D6W5C0 | Spectrin, beta, non-erythrocytic 1, isoform CRA_b OS=Homo sapiens GN=SPTBN1 PE=4 SV=1 - [D6W5C0_HUMAN] | 34.59 | 1 | 0 | 67 | 141 | 426.514831 |
| A6NG51 | Uncharacterized protein OS=Homo sapiens GN=SPTAN1 PE=4 SV=2 - [A6NG51_HUMAN] | 31.61 | 1 | 0 | 66 | 150 | 508.560888 |
| O75369 | Filamin-B OS=Homo sapiens GN=FLNB PE=1 SV=2 - [FLNB_HUMAN] | 33.51 | 1 | 0 | 65 | 142 | 453.130561 |
| Q60FE7 | Filamin B OS=Homo sapiens GN=FLNB PE=2 SV=1 - [Q60FE7_HUMAN] | 33.65 | 1 | 0 | 65 | 142 | 453.130561 |
| B2ZZ83 | Filamin B OS=Homo sapiens GN=FLNB PE=2 SV=1 - [B2ZZ83_HUMAN] | 33.12 | 1 | 0 | 65 | 142 | 453.130561 |
| Q8TES4 | FLJ00119 protein (Fragment) OS=Homo sapiens GN=FLJ00119 PE=2 SV=1 - [Q8TES4_HUMAN] | 54.5 | 1 | 0 | 58 | 188 | 689.122908 |
| Q68CT4 | Putative uncharacterized protein DKFZp686A1668 OS=Homo sapiens GN=DKFZp686A1668 PE=2 SV=1 - [Q68CT4_HUMAN] | 31.67 | 1 | 0 | 53 | 112 | 366.337561 |
| Q92616 | Translational activator GCN1 OS=Homo sapiens GN=GCN1L1 PE=1 SV=6 - [GCN1L_HUMAN] | 25.08 | 1 | 0 | 50 | 107 | 336.111163 |
| B3KY63 | cDNA FLJ16830 fis, clone UTERU3022536, highly similar to Chromodomain helicase-DNA-binding protein 4 (EC 3.6.1.-) OS=Homo sapiens PE=2 SV=1 - [B3KY63_HUMAN] | 26.3 | 1 | 0 | 45 | 107 | 337.07052 |
| Q6NXF2 | FLNA protein (Fragment) OS=Homo sapiens GN=FLNA PE=2 SV=1 | 54.43 | 1 | 0 | 40 | 118 | 435.273651 |

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|--------|-----------------------------------------------------------------------------------------------------------------------------|-------|---|---|----|-----|------------|
| | - [Q6NXF2_HUMAN] | | | | | | |
| B4DGT1 | cDNA FLJ59116, highly similar to Spectrin alpha chain, brain OS=Homo sapiens PE=2 SV=1 - [B4DGT1_HUMAN] | 34.53 | 1 | 0 | 40 | 89 | 288.22146 |
| Q96C61 | FLNA protein OS=Homo sapiens PE=2 SV=1 - [Q96C61_HUMAN] | 58.71 | 1 | 0 | 37 | 109 | 401.021236 |
| B4DTV8 | cDNA FLJ61399, highly similar to Spectrin alpha chain, brain OS=Homo sapiens PE=2 SV=1 - [B4DTV8_HUMAN] | 34.52 | 1 | 0 | 36 | 81 | 260.7319 |
| B4E2F9 | cDNA FLJ57038, highly similar to Filamin-A OS=Homo sapiens PE=2 SV=1 - [B4E2F9_HUMAN] | 57.56 | 1 | 0 | 33 | 100 | 364.75156 |
| Q9UG16 | Putative uncharacterized protein DKFZp564P0562 (Fragment) OS=Homo sapiens GN=DKFZp564P0562 PE=2 SV=1 - [Q9UG16_HUMAN] | 31.4 | 1 | 0 | 33 | 77 | 275.804817 |
| Q5TCU6 | Talin 1 OS=Homo sapiens GN=TLN1 PE=2 SV=1 - [Q5TCU6_HUMAN] | 21.2 | 1 | 0 | 30 | 61 | 231.512275 |
| Q99968 | Tpr OS=Homo sapiens GN=tpr PE=2 SV=1 - [Q99968_HUMAN] | 15.83 | 1 | 0 | 30 | 60 | 193.838305 |
| B4DTD5 | cDNA FLJ57890, highly similar to Filamin-A OS=Homo sapiens PE=2 SV=1 - [B4DTD5_HUMAN] | 55.16 | 1 | 0 | 28 | 78 | 291.412294 |
| P11717 | Cation-independent mannose-6-phosphate receptor OS=Homo sapiens GN=IGF2R PE=1 SV=3 - [MPRI_HUMAN] | 12.85 | 1 | 0 | 26 | 49 | 139.322935 |
| Q59EZ3 | Insulin-like growth factor 2 receptor variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59EZ3_HUMAN] | 13.26 | 1 | 0 | 26 | 49 | 139.322935 |
| Q6PJJ3 | FASN protein (Fragment) OS=Homo sapiens GN=FASN PE=2 SV=1 - [Q6PJJ3_HUMAN] | 26.74 | 1 | 0 | 20 | 44 | 139.414572 |
| D7RX09 | Desmoplakin la OS=Homo sapiens PE=2 SV=1 - [D7RX09_HUMAN] | 10.17 | 1 | 0 | 20 | 36 | 101.559236 |
| B4DYH4 | cDNA FLJ51571, moderately similar to Mediator of DNA damage checkpoint protein 1 OS=Homo sapiens PE=2 SV=1 - [B4DYH4_HUMAN] | 25.26 | 1 | 0 | 19 | 34 | 136.989107 |
| Q4LE79 | DSP variant protein (Fragment) OS=Homo sapiens GN=DSP variant protein PE=2 SV=1 - [Q4LE79_HUMAN] | 9.83 | 1 | 0 | 18 | 30 | 85.5109639 |
| Q12789 | General transcription factor 3C polypeptide 1 OS=Homo sapiens GN=GTF3C1 PE=1 SV=4 - [TF3C1_HUMAN] | 8.2 | 1 | 0 | 17 | 32 | 86.6009059 |
| A8MRT3 | Uncharacterized protein OS=Homo sapiens GN=GTF3C1 PE=4 SV=2 - [A8MRT3_HUMAN] | 10.27 | 1 | 0 | 17 | 32 | 86.6009059 |

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|--------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------|---|---|----|----|------------|
| Q6AWA4 | Putative uncharacterized protein DKFZp686O0870 (Fragment) OS=Homo sapiens GN=DKFZp686O0870 PE=2 SV=1 - [Q6AWA4_HUMAN] | 8.19 | 1 | 0 | 17 | 32 | 86.6009059 |
| Q6AHZ7 | Putative uncharacterized protein DKFZp686A111 OS=Homo sapiens GN=DKFZp686A111 PE=2 SV=1 - [Q6AHZ7_HUMAN] | 8.2 | 1 | 0 | 17 | 32 | 86.6009059 |
| P24821 | Tenascin OS=Homo sapiens GN=TNC PE=1 SV=3 - [TENA_HUMAN] | 11.36 | 1 | 0 | 16 | 24 | 78.7222812 |
| Q5HY90 | Filamin A, alpha (Actin binding protein 280) (Fragment) OS=Homo sapiens GN=FLNA PE=2 SV=2 - [Q5HY90_HUMAN] | 73.31 | 1 | 0 | 15 | 40 | 160.886604 |
| P27708 | CAD protein OS=Homo sapiens GN=CAD PE=1 SV=3 - [PYR1_HUMAN] | 8.58 | 1 | 0 | 15 | 25 | 68.6965386 |
| Q53SY7 | Putative uncharacterized protein CAD (Fragment) OS=Homo sapiens GN=CAD PE=2 SV=1 - [Q53SY7_HUMAN] | 8.88 | 1 | 0 | 15 | 25 | 68.6965386 |
| B3KVE5 | cDNA FLJ16456 fis, clone BRAWH3009013, highly similar to AT- hook-containing transcription factor 1 (Fragment) OS=Homo sapiens PE=2 SV=1 - [B3KVE5_HUMAN] | 18 | 1 | 0 | 15 | 24 | 83.7774789 |
| Q14966 | Zinc finger protein 638 OS=Homo sapiens GN=ZNF638 PE=1 SV=2 - [ZN638_HUMAN] | 8.65 | 1 | 0 | 14 | 27 | 74.6709239 |
| A7MBN2 | TNC protein OS=Homo sapiens GN=TNC PE=2 SV=1 - [A7MBN2_HUMAN] | 11.42 | 1 | 0 | 14 | 22 | 72.1724207 |
| Q2VP91 | FLNA protein (Fragment) OS=Homo sapiens GN=FLNA PE=2 SV=3 - [Q2VP91_HUMAN] | 53.09 | 1 | 0 | 13 | 40 | 148.083773 |
| B4DM32 | cDNA FLJ54481, highly similar to GCN1-like protein 1 (Fragment) OS=Homo sapiens PE=2 SV=1 - [B4DM32_HUMAN] | 22.51 | 1 | 0 | 13 | 30 | 99.2966959 |
| Q8TDI0 | Chromodomain-helicase-DNA-binding protein 5 OS=Homo sapiens GN=CHD5 PE=1 SV=1 - [CHD5_HUMAN] | 6.09 | 1 | 0 | 12 | 27 | 76.0514243 |
| A8K583 | cDNA FLJ77126, highly similar to Homo sapiens zinc finger protein 638 (ZNF638), transcript variant 1, mRNA (Fragment) OS=Homo sapiens PE=2 SV=1 - [A8K583_HUMAN] | 7.98 | 1 | 0 | 12 | 23 | 59.337548 |
| B3KTD2 | cDNA FLJ38079 fis, clone CTONG2016056, highly similar to AT- hook-containing transcription factor 1 (Fragment) OS=Homo sapiens PE=2 SV=1 - [B3KTD2_HUMAN] | 20.97 | 1 | 0 | 12 | 20 | 68.855927 |
| B3KRDO | cDNA FLJ34045 fis, clone FCBBF2007095, highly similar to AT- hook-containing transcription factor 1 (Fragment) OS=Homo | 26.8 | 1 | 0 | 12 | 19 | 67.0640721 |

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|--------|------------------------------------------------------------------------------------------------------------------------------------------|-------|---|---|----|----|------------|
| | sapiens PE=2 SV=1 - [B3KRD0_HUMAN] | | | | | | |
| D3YHM4 | Tenascin-C isoform 14/AD1/16 OS=Homo sapiens PE=2 SV=1 - [D3YHM4_HUMAN] | 10.33 | 1 | 0 | 12 | 19 | 59.8704038 |
| Q93008 | Probable ubiquitin carboxyl-terminal hydrolase FAF-X OS=Homo sapiens GN=USP9X PE=1 SV=3 - [USP9X_HUMAN] | 5.64 | 1 | 0 | 11 | 22 | 63.7560817 |
| D3DWB6 | Ubiquitin specific peptidase 9, X-linked, isoform CRA_b OS=Homo sapiens GN=USP9X PE=4 SV=1 - [D3DWB6_HUMAN] | 6.09 | 1 | 0 | 11 | 22 | 63.7560817 |
| C9JCC2 | Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [C9JCC2_HUMAN] | 32.13 | 1 | 0 | 11 | 22 | 90.5312312 |
| A6NN88 | Uncharacterized protein OS=Homo sapiens GN=SPTAN1 PE=4 SV=2 - [A6NN88_HUMAN] | 28.54 | 1 | 0 | 10 | 25 | 90.8259292 |
| Q12873 | Chromodomain-helicase-DNA-binding protein 3 OS=Homo sapiens GN=CHD3 PE=1 SV=3 - [CHD3_HUMAN] | 5.05 | 1 | 0 | 10 | 21 | 59.4851214 |
| D6W5H1 | Zinc finger protein 638, isoform CRA_c OS=Homo sapiens GN=ZNF638 PE=4 SV=1 - [D6W5H1_HUMAN] | 8.21 | 1 | 0 | 10 | 20 | 53.6735539 |
| B4DL41 | cDNA FLJ57825, highly similar to DNA-dependent protein kinase catalytic subunit (EC 2.7.11.1) OS=Homo sapiens PE=2 SV=1 - [B4DL41_HUMAN] | 9.65 | 1 | 0 | 10 | 19 | 54.7800536 |
| B4E2A0 | cDNA FLJ61543, highly similar to Desmoplakin OS=Homo sapiens PE=2 SV=1 - [B4E2A0_HUMAN] | 8.15 | 1 | 0 | 10 | 14 | 37.3483456 |
| B5MEH8 | Uncharacterized protein OS=Homo sapiens GN=AHNAK PE=4 SV=1 - [B5MEH8_HUMAN] | 5.24 | 1 | 0 | 10 | 12 | 33.745533 |
| B1AK51 | Chromodomain helicase DNA binding protein 5 OS=Homo sapiens GN=CHD5 PE=4 SV=1 - [B1AK51_HUMAN] | 8.03 | 1 | 0 | 9 | 21 | 57.8608441 |
| Q14917 | SPTAN1 protein (Fragment) OS=Homo sapiens GN=SPTAN1 PE=2 SV=1 - [Q14917_HUMAN] | 26.53 | 1 | 0 | 9 | 21 | 73.9153671 |
| Q15624 | Tpr protein OS=Homo sapiens GN=Tpr PE=2 SV=1 - [Q15624_HUMAN] | 15.29 | 1 | 0 | 9 | 18 | 60.0189536 |
| O15020 | Spectrin beta chain, brain 2 OS=Homo sapiens GN=SPTBN2 PE=1 SV=3 - [SPTN2_HUMAN] | 4.39 | 1 | 0 | 9 | 15 | 43.3730757 |
| Q86TQ3 | Similar to filamin C, gamma (Actin binding protein 280) (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q86TQ3_HUMAN] | 58.76 | 1 | 0 | 8 | 27 | 92.4783061 |
| B3KRD4 | cDNA FLJ34067 fis, clone FCBBF3001914, highly similar to Chromodomain helicase-DNA-binding protein 5 (EC 3.6.1.-) | 7.87 | 1 | 0 | 8 | 20 | 53.0950499 |

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| | OS=Homo sapiens PE=2 SV=1 - [B3KRD4_HUMAN] | | | | | | |
| B4DIF8 | Spectrin, beta, non-erythrocytic 1, isoform CRA_c OS=Homo sapiens GN=SPTBN1 PE=2 SV=1 - [B4DIF8_HUMAN] | 29.1 | 1 | 0 | 8 | 19 | 59.5100062 |
| Q659F1 | Putative uncharacterized protein DKFZp434K213 (Fragment) OS=Homo sapiens GN=DKFZp434K213 PE=2 SV=1 - [Q659F1_HUMAN] | 8.22 | 1 | 0 | 8 | 19 | 54.212706 |
| Q659D0 | Putative uncharacterized protein DKFZp434P202 (Fragment) OS=Homo sapiens GN=DKFZp434P202 PE=2 SV=1 - [Q659D0_HUMAN] | 8.2 | 1 | 0 | 8 | 19 | 54.212706 |
| Q58F23 | TPR protein (Fragment) OS=Homo sapiens GN=TPR PE=2 SV=1 - [Q58F23_HUMAN] | 14.7 | 1 | 0 | 8 | 16 | 54.0082231 |
| Q504U6 | TPR protein (Fragment) OS=Homo sapiens GN=TPR PE=2 SV=1 - [Q504U6_HUMAN] | 14.6 | 1 | 0 | 8 | 16 | 54.0082231 |
| B4DRA2 | cDNA FLJ57828, highly similar to Treacle protein (Fragment) OS=Homo sapiens PE=2 SV=1 - [B4DRA2_HUMAN] | 9.97 | 1 | 0 | 8 | 15 | 43.5793293 |
| A4QPE4 | SPTBN2 protein OS=Homo sapiens GN=SPTBN2 PE=2 SV=1 - [A4QPE4_HUMAN] | 10.17 | 1 | 0 | 8 | 14 | 40.7913351 |
| D6RHJ4 | Uncharacterized protein OS=Homo sapiens GN=TCOF1 PE=4 SV=1 - [D6RHJ4_HUMAN] | 12.76 | 1 | 0 | 8 | 13 | 38.0887291 |
| Q6ZQN2 | cDNA FLJ46846 fis, clone UTERU3004635, moderately similar to Neuroblast differentiation associated protein AHNAK (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q6ZQN2_HUMAN] | 8.17 | 1 | 0 | 8 | 9 | 24.9243183 |
| Q5HY89 | Filamin A, alpha (Actin binding protein 280) (Fragment) OS=Homo sapiens GN=FLNA PE=2 SV=1 - [Q5HY89_HUMAN] | 44.59 | 1 | 0 | 7 | 24 | 84.9090695 |
| B4E187 | cDNA FLJ60083, highly similar to Zinc finger protein 638 (Fragment) OS=Homo sapiens PE=2 SV=1 - [B4E187_HUMAN] | 8.98 | 1 | 0 | 7 | 16 | 43.7836621 |
| Q5TG85 | Chromodomain helicase DNA binding protein 5 OS=Homo sapiens GN=CHD5 PE=2 SV=1 - [Q5TG85_HUMAN] | 8.91 | 1 | 0 | 7 | 14 | 42.6844273 |
| Q59FZ2 | TCOF1 protein variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59FZ2_HUMAN] | 12.5 | 1 | 0 | 7 | 14 | 42.5665798 |
| B4DF54 | cDNA FLJ60235, highly similar to Zinc finger protein 638 OS=Homo sapiens PE=2 SV=1 - [B4DF54_HUMAN] | 6.84 | 1 | 0 | 7 | 14 | 35.7181456 |
| C9JBI6 | Uncharacterized protein OS=Homo sapiens GN=ZNF638 PE=4 SV=1 - [C9JBI6_HUMAN] | 7.63 | 1 | 0 | 7 | 14 | 35.7181456 |

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|--------|-----------------------------------------------------------------------------------------------------------------------------------------------------|-------|---|---|---|----|------------|
| Q6KC79 | Nipped-B-like protein OS=Homo sapiens GN=NIPBL PE=1 SV=2 - [NIPBL_HUMAN] | 3 | 1 | 0 | 7 | 11 | 31.6493373 |
| Q6IEH8 | Transcriptional regulator OS=Homo sapiens GN=NIPBL PE=2 SV=1 - [Q6IEH8_HUMAN] | 3 | 1 | 0 | 7 | 11 | 31.6493373 |
| P62987 | Ubiquitin-60S ribosomal protein L40 OS=Homo sapiens GN=UBA52 PE=1 SV=2 - [RL40_HUMAN] | 42.97 | 1 | 0 | 6 | 21 | 65.2230117 |
| P62979 | Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=1 SV=2 - [RS27A_HUMAN] | 35.26 | 1 | 0 | 6 | 21 | 65.2230117 |
| P0CG47 | Polyubiquitin-B OS=Homo sapiens GN=UBB PE=1 SV=1 - [UBB_HUMAN] | 72.05 | 1 | 0 | 6 | 21 | 65.2230117 |
| P0CG48 | Polyubiquitin-C OS=Homo sapiens GN=UBC PE=1 SV=2 - [UBC_HUMAN] | 70.36 | 1 | 0 | 6 | 21 | 65.2230117 |
| Q5PY61 | Ubiquitin C splice variant OS=Homo sapiens GN=UBC PE=2 SV=1 - [Q5PY61_HUMAN] | 72.05 | 1 | 0 | 6 | 21 | 65.2230117 |
| Q96C32 | UBC protein OS=Homo sapiens PE=2 SV=1 - [Q96C32_HUMAN] | 72.13 | 1 | 0 | 6 | 21 | 65.2230117 |
| Q5UGI3 | Ubiquitin C splice variant OS=Homo sapiens GN=UBC PE=2 SV=1 - [Q5UGI3_HUMAN] | 66.01 | 1 | 0 | 6 | 21 | 65.2230117 |
| Q5RKT7 | Ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=2 SV=1 - [Q5RKT7_HUMAN] | 35.26 | 1 | 0 | 6 | 21 | 65.2230117 |
| B4DV12 | cDNA FLJ51326, highly similar to Homo sapiens ubiquitin B (UBB), mRNA OS=Homo sapiens PE=2 SV=1 - [B4DV12_HUMAN] | 71.9 | 1 | 0 | 6 | 21 | 65.2230117 |
| Q96MH4 | cDNA FLJ32377 fis, clone SKMUS1000014, highly similar to Polyubiquitin 9 OS=Homo sapiens PE=2 SV=1 - [Q96MH4_HUMAN] | 65.72 | 1 | 0 | 6 | 21 | 65.2230117 |
| A8K674 | cDNA FLJ75516, highly similar to Xenopus tropicalis ubiquitin C, mRNA OS=Homo sapiens PE=2 SV=1 - [A8K674_HUMAN] | 69.29 | 1 | 0 | 6 | 21 | 65.2230117 |
| Q6ZU36 | cDNA FLJ44024 fis, clone TESTI4026524, moderately similar to Chromodomain helicase-DNA-binding protein 4 OS=Homo sapiens PE=2 SV=1 - [Q6ZU36_HUMAN] | 9.54 | 1 | 0 | 6 | 12 | 37.832721 |
| Q96CK3 | CAD protein (Fragment) OS=Homo sapiens GN=CAD PE=2 SV=2 - [Q96CK3_HUMAN] | 9.17 | 1 | 0 | 6 | 8 | 19.9983447 |
| B4DKX6 | cDNA FLJ53584, highly similar to Desmoplakin (Fragment) OS=Homo sapiens PE=2 SV=1 - [B4DKX6_HUMAN] | 7.44 | 1 | 0 | 6 | 7 | 18.7004367 |

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| Q49A90 | RPS27A protein OS=Homo sapiens GN=RPS27A PE=4 SV=1 - [Q49A90_HUMAN] | 48.42 | 1 | 0 | 5 | 20 | 62.6425517 |
| Q66K58 | Putative uncharacterized protein (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q66K58_HUMAN] | 63.18 | 1 | 0 | 5 | 19 | 61.4113294 |
| Q59EM9 | Ubiquitin C variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59EM9_HUMAN] | 63.64 | 1 | 0 | 5 | 19 | 61.4113294 |
| Q9UFQ0 | Putative uncharacterized protein DKFZp434K0435 (Fragment) OS=Homo sapiens GN=DKFZp434K0435 PE=2 SV=1 - [Q9UFQ0_HUMAN] | 61.51 | 1 | 0 | 5 | 19 | 61.4113294 |
| Q96H31 | UBC protein (Fragment) OS=Homo sapiens GN=UBC PE=2 SV=2 - [Q96H31_HUMAN] | 62.82 | 1 | 0 | 5 | 19 | 61.4113294 |
| Q05CG6 | CHD4 protein (Fragment) OS=Homo sapiens GN=CHD4 PE=2 SV=1 - [Q05CG6_HUMAN] | 19.72 | 1 | 0 | 5 | 14 | 53.7489012 |
| P48634 | Large proline-rich protein BAT2 OS=Homo sapiens GN=BAT2 PE=1 SV=3 - [BAT2_HUMAN] | 4.08 | 1 | 0 | 5 | 9 | 21.6801852 |
| B4DLC6 | cDNA FLJ59330, highly similar to Chromodomain helicase-DNA-binding protein 3 (EC 3.6.1.-) OS=Homo sapiens PE=2 SV=1 - [B4DLC6_HUMAN] | 4.49 | 1 | 0 | 5 | 9 | 25.0427443 |
| C9JXZ3 | Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [C9JXZ3_HUMAN] | 4.09 | 1 | 0 | 5 | 9 | 21.6801852 |
| Q57Z90 | Putative uncharacterized protein NP220 (Fragment) OS=Homo sapiens GN=NP220 PE=2 SV=1 - [Q57Z90_HUMAN] | 9 | 1 | 0 | 5 | 9 | 27.5422325 |
| C9JTM3 | Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [C9JTM3_HUMAN] | 4.12 | 1 | 0 | 5 | 9 | 21.6801852 |
| B4E1W8 | cDNA FLJ60213, highly similar to Tenascin OS=Homo sapiens PE=2 SV=1 - [B4E1W8_HUMAN] | 7.5 | 1 | 0 | 5 | 8 | 23.1710873 |
| B4DWT7 | cDNA FLJ51487, highly similar to Desmoplakin (Fragment) OS=Homo sapiens PE=2 SV=1 - [B4DWT7_HUMAN] | 10.19 | 1 | 0 | 5 | 6 | 16.6125449 |
| B4DN27 | cDNA FLJ57057, highly similar to Small subunit processome component 20 homolog OS=Homo sapiens PE=2 SV=1 - [B4DN27_HUMAN] | 10.72 | 1 | 0 | 5 | 6 | 14.3468022 |
| Q6ZSZ4 | cDNA FLJ45103 fis, clone BRAWH3032571, moderately similar to Chromodomain helicase-DNA-binding protein 4 OS=Homo sapiens PE=2 SV=1 - [Q6ZSZ4_HUMAN] | 3.35 | 1 | 0 | 4 | 11 | 29.7020332 |

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|--------|---------------------------------------------------------------------------------------------------------------------|-------|---|---|---|---|------------|
| P49750 | YLP motif-containing protein 1 OS=Homo sapiens GN=YLPM1 PE=1 SV=3 - [YLPM1_HUMAN] | 2.77 | 1 | 0 | 4 | 9 | 25.6923064 |
| P02533 | Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4 - [K1C14_HUMAN] | 5.3 | 1 | 0 | 4 | 8 | 18.2667096 |
| P08779 | Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4 - [K1C16_HUMAN] | 5.29 | 1 | 0 | 4 | 8 | 18.2667096 |
| C9JB33 | Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [C9JB33_HUMAN] | 3.04 | 1 | 0 | 4 | 8 | 18.7642013 |
| C9JI26 | Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [C9JI26_HUMAN] | 3.02 | 1 | 0 | 4 | 8 | 18.7642013 |
| C9JD87 | Uncharacterized protein OS=Homo sapiens GN=PRRC2A PE=4 SV=1 - [C9JD87_HUMAN] | 3.02 | 1 | 0 | 4 | 8 | 18.7642013 |
| C9J6L0 | Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [C9J6L0_HUMAN] | 3.04 | 1 | 0 | 4 | 8 | 18.7642013 |
| C9JTL3 | Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [C9JTL3_HUMAN] | 3.02 | 1 | 0 | 4 | 8 | 18.7642013 |
| C9J9U2 | Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [C9J9U2_HUMAN] | 3.04 | 1 | 0 | 4 | 8 | 18.7642013 |
| Q8NC65 | cDNA FLJ90459 fis, clone NT2RP3001754 OS=Homo sapiens PE=2 SV=1 - [Q8NC65_HUMAN] | 7.96 | 1 | 0 | 4 | 8 | 27.5353525 |
| C9J1F6 | Uncharacterized protein OS=Homo sapiens GN=PRRC2A PE=4 SV=1 - [C9J1F6_HUMAN] | 3.04 | 1 | 0 | 4 | 8 | 18.7642013 |
| C9JI93 | Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [C9JI93_HUMAN] | 3.02 | 1 | 0 | 4 | 8 | 18.7642013 |
| A6NG23 | Uncharacterized protein OS=Homo sapiens PE=4 SV=3 - [A6NG23_HUMAN] | 3.73 | 1 | 0 | 4 | 7 | 15.6984907 |
| B4DLB1 | cDNA FLJ58017, moderately similar to Treacle protein OS=Homo sapiens PE=2 SV=1 - [B4DLB1_HUMAN] | 8.3 | 1 | 0 | 4 | 7 | 18.1730137 |
| Q6ZP16 | CDNA FLJ26719 fis, clone PNC03379 OS=Homo sapiens PE=2 SV=1 - [Q6ZP16_HUMAN] | 21.08 | 1 | 0 | 4 | 7 | 18.6479089 |
| Q4LE49 | ARID1A variant protein (Fragment) OS=Homo sapiens GN=ARID1A variant protein PE=2 SV=1 - [Q4LE49_HUMAN] | 3.86 | 1 | 0 | 4 | 6 | 20.2900407 |
| Q8N274 | cDNA FLJ33834 fis, clone CTONG2004264, moderately similar to NEUROBLAST DIFFERENTIATION ASSOCIATED PROTEIN AHNAK | 10.37 | 1 | 0 | 4 | 5 | 15.6464322 |

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| | OS=Homo sapiens PE=2 SV=1 - [Q8N274_HUMAN] | | | | | | |
| Q8NF45 | FLJ00353 protein (Fragment) OS=Homo sapiens GN=FLJ00353 PE=2 SV=1 - [Q8NF45_HUMAN] | 2.32 | 1 | 0 | 3 | 7 | 19.7285632 |
| Q9NSU9 | Putative uncharacterized protein DKFz434G0719 (Fragment) OS=Homo sapiens GN=DKFz434G0719 PE=2 SV=1 - [Q9NSU9_HUMAN] | 10.67 | 1 | 0 | 3 | 7 | 26.97349 |
| P19012 | Keratin, type I cytoskeletal 15 OS=Homo sapiens GN=KRT15 PE=1 SV=3 - [K1C15_HUMAN] | 3.51 | 1 | 0 | 3 | 6 | 13.0362864 |
| Q04695 | Keratin, type I cytoskeletal 17 OS=Homo sapiens GN=KRT17 PE=1 SV=2 - [K1C17_HUMAN] | 3.7 | 1 | 0 | 3 | 6 | 13.0362864 |
| P08727 | Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=4 - [K1C19_HUMAN] | 4 | 1 | 0 | 3 | 6 | 13.0362864 |
| P04259 | Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5 - [K2C6B_HUMAN] | 5.5 | 1 | 0 | 3 | 6 | 16.9252946 |
| P11277 | Spectrin beta chain, erythrocyte OS=Homo sapiens GN=SPTB PE=1 SV=5 - [SPTB1_HUMAN] | 1.22 | 1 | 0 | 3 | 6 | 14.4214525 |
| Q9Y4G6 | Talin-2 OS=Homo sapiens GN=TLN2 PE=1 SV=4 - [TLN2_HUMAN] | 1.18 | 1 | 0 | 3 | 6 | 16.0109884 |
| C9JAS0 | Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [C9JAS0_HUMAN] | 2.66 | 1 | 0 | 3 | 6 | 12.7825068 |
| B2RMN7 | Spectrin, beta, erythrocytic OS=Homo sapiens GN=SPTB PE=2 SV=1 - [B2RMN7_HUMAN] | 1.22 | 1 | 0 | 3 | 6 | 14.4214525 |
| E0CX14 | Uncharacterized protein OS=Homo sapiens GN=KRT15 PE=4 SV=1 - [E0CX14_HUMAN] | 3.52 | 1 | 0 | 3 | 6 | 13.0362864 |
| Q96SM7 | cDNA FLJ14749 fis, clone NT2RP3002876, weakly similar to Drosophila melanogaster eyelid (eld) mRNA OS=Homo sapiens PE=2 SV=1 - [Q96SM7_HUMAN] | 6.36 | 1 | 0 | 3 | 6 | 16.9204824 |
| B4DWU0 | cDNA FLJ56791, highly similar to Keratin, type I cytoskeletal 16 OS=Homo sapiens PE=2 SV=1 - [B4DWU0_HUMAN] | 11.85 | 1 | 0 | 3 | 6 | 13.0362864 |
| B4DLY2 | cDNA FLJ56600, highly similar to Large proline-rich protein BAT2 OS=Homo sapiens PE=2 SV=1 - [B4DLY2_HUMAN] | 4.12 | 1 | 0 | 3 | 6 | 12.7825068 |
| C9J8K3 | Uncharacterized protein OS=Homo sapiens GN=PRRC2A PE=4 SV=1 - [C9J8K3_HUMAN] | 2.66 | 1 | 0 | 3 | 6 | 12.7825068 |
| B4E2J5 | cDNA FLJ53570, highly similar to Keratin, type I cytoskeletal 16 | 8.51 | 1 | 0 | 3 | 6 | 13.0362864 |

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| | OS=Homo sapiens PE=2 SV=1 - [B4E2J5_HUMAN] | | | | | | |
| C9JM53 | Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [C9JM53_HUMAN] | 2.66 | 1 | 0 | 3 | 6 | 12.7825068 |
| Q96T01 | cDNA FLJ14536 fis, clone NT2RM2001105, weakly similar to Drosophila melanogaster eyelid (eld) mRNA OS=Homo sapiens PE=2 SV=1 - [Q96T01_HUMAN] | 7.4 | 1 | 0 | 3 | 6 | 16.9204824 |
| A0PJC9 | TPR protein (Fragment) OS=Homo sapiens GN=TPR PE=2 SV=1 - [A0PJC9_HUMAN] | 11.04 | 1 | 0 | 3 | 6 | 26.8050354 |
| B4E2P9 | cDNA FLJ56708, highly similar to Keratin, type I cytoskeletal 17 OS=Homo sapiens PE=2 SV=1 - [B4E2P9_HUMAN] | 9.3 | 1 | 0 | 3 | 6 | 13.0362864 |
| Q59FP5 | Spectrin, beta, erythrocytic (Includes spherocytosis, clinical type I) variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59FP5_HUMAN] | 1.11 | 1 | 0 | 3 | 6 | 14.4214525 |
| C9JM50 | Uncharacterized protein OS=Homo sapiens GN=KRT19 PE=4 SV=1 - [C9JM50_HUMAN] | 8.16 | 1 | 0 | 3 | 6 | 13.0362864 |
| C9JI89 | Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [C9JI89_HUMAN] | 2.66 | 1 | 0 | 3 | 6 | 12.7825068 |
| B4E204 | cDNA FLJ58872, highly similar to Keratin, type I cytoskeletal 15 OS=Homo sapiens PE=2 SV=1 - [B4E204_HUMAN] | 6.84 | 1 | 0 | 3 | 6 | 13.0362864 |
| B4DKV1 | cDNA FLJ58804, highly similar to Chromodomain helicase-DNA-binding protein 3 (EC 3.6.1.-) OS=Homo sapiens PE=2 SV=1 - [B4DKV1_HUMAN] | 3.81 | 1 | 0 | 3 | 6 | 16.6125358 |
| Q9Y520 | Protein BAT2-like 2 OS=Homo sapiens GN=BAT2L2 PE=1 SV=3 - [BA2L2_HUMAN] | 1.31 | 1 | 0 | 3 | 5 | 9.90001202 |
| Q2TAZ1 | CHD3 protein (Fragment) OS=Homo sapiens GN=CHD3 PE=2 SV=1 - [Q2TAZ1_HUMAN] | 4.08 | 1 | 0 | 3 | 5 | 16.5428998 |
| B7WNZ6 | Uncharacterized protein OS=Homo sapiens GN=PRRC2C PE=4 SV=2 - [B7WNZ6_HUMAN] | 1.38 | 1 | 0 | 3 | 5 | 9.90001202 |
| A8MUW8 | Uncharacterized protein OS=Homo sapiens GN=DSP PE=4 SV=2 - [A8MUW8_HUMAN] | 15.14 | 1 | 0 | 3 | 5 | 11.3365186 |
| Q6ZQV0 | cDNA FLJ46873 fis, clone UTERU3013302, highly similar to Homo sapiens NP220 nuclear protein (NP220) OS=Homo sapiens PE=2 SV=1 - [Q6ZQV0_HUMAN] | 5.8 | 1 | 0 | 3 | 5 | 12.2088566 |

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| Q6P468 | USP9X protein (Fragment) OS=Homo sapiens GN=USP9X PE=2 SV=1 - [Q6P468_HUMAN] | 4.9 | 1 | 0 | 3 | 5 | 13.4464203 |
| D6RC21 | Uncharacterized protein OS=Homo sapiens GN=TCOF1 PE=4 SV=1 - [D6RC21_HUMAN] | 8.77 | 1 | 0 | 3 | 5 | 11.2817202 |
| D3YTG2 | Uncharacterized protein OS=Homo sapiens GN=DSP PE=4 SV=1 - [D3YTG2_HUMAN] | 15.14 | 1 | 0 | 3 | 5 | 11.3365186 |
| O75179 | Ankyrin repeat domain-containing protein 17 OS=Homo sapiens GN=ANKRD17 PE=1 SV=3 - [ANR17_HUMAN] | 1.73 | 1 | 0 | 3 | 4 | 13.386847 |
| P05023 | Sodium/potassium-transporting ATPase subunit alpha-1 OS=Homo sapiens GN=ATP1A1 PE=1 SV=1 - [AT1A1_HUMAN] | 5.28 | 1 | 0 | 3 | 4 | 15.1077921 |
| Q15154 | Pericentriolar material 1 protein OS=Homo sapiens GN=PCM1 PE=1 SV=4 - [PCM1_HUMAN] | 1.58 | 1 | 0 | 3 | 4 | 10.183213 |
| B7Z3U6 | ATPase, Na+/K+ transporting, alpha 1 polypeptide, isoform CRA_a OS=Homo sapiens GN=ATP1A1 PE=2 SV=1 - [B7Z3U6_HUMAN] | 5.44 | 1 | 0 | 3 | 4 | 15.1077921 |
| D3DSQ0 | Pericentriolar material 1, isoform CRA_a OS=Homo sapiens GN=PCM1 PE=4 SV=1 - [D3DSQ0_HUMAN] | 1.58 | 1 | 0 | 3 | 4 | 10.183213 |
| A2RUU9 | PCM1 protein OS=Homo sapiens GN=PCM1 PE=2 SV=1 - [A2RUU9_HUMAN] | 1.72 | 1 | 0 | 3 | 4 | 10.183213 |
| C9JGS5 | Uncharacterized protein OS=Homo sapiens GN=PCM1 PE=4 SV=1 - [C9JGS5_HUMAN] | 1.81 | 1 | 0 | 3 | 4 | 10.183213 |
| A8K376 | cDNA FLJ76657, highly similar to Homo sapiens PHD finger protein 3 (PHF3), mRNA (Fragment) OS=Homo sapiens PE=2 SV=1 - [A8K376_HUMAN] | 4.95 | 1 | 0 | 3 | 4 | 10.8383408 |
| A6NNN6 | Uncharacterized protein OS=Homo sapiens GN=PCM1 PE=4 SV=3 - [A6NNN6_HUMAN] | 1.63 | 1 | 0 | 3 | 4 | 10.183213 |
| B7Z3V1 | cDNA FLJ60077, highly similar to Sodium/potassium-transporting ATPase alpha-1 chain (EC 3.6.3.9) (Fragment) OS=Homo sapiens PE=2 SV=1 - [B7Z3V1_HUMAN] | 5.29 | 1 | 0 | 3 | 4 | 15.1077921 |
| B3KP41 | cDNA FLJ31116 fis, clone IMR322000604, highly similar to PHD finger protein 3 (Fragment) OS=Homo sapiens PE=2 SV=1 - [B3KP41_HUMAN] | 5.23 | 1 | 0 | 3 | 4 | 10.8383408 |
| BOAZS7 | cDNA, FLJ79517, highly similar to PHD finger protein 3 (Fragment) OS=Homo sapiens PE=2 SV=1 - [BOAZS7_HUMAN] | 6.01 | 1 | 0 | 3 | 4 | 10.8383408 |

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| B4DTV0 | cDNA FLJ57801, highly similar to Homo sapiens AHNAK nucleoprotein (desmoyokin) (AHNAK), transcript variant 1, mRNA (Fragment) OS=Homo sapiens PE=2 SV=1 - [B4DTV0_HUMAN] | 4.63 | 1 | 0 | 3 | 4 | 10.8214886 |
| B9EIS5 | PCM1 protein OS=Homo sapiens GN=PCM1 PE=2 SV=1 - [B9EIS5_HUMAN] | 1.59 | 1 | 0 | 3 | 4 | 10.183213 |
| Q96TA9 | SWI related protein OS=Homo sapiens PE=2 SV=1 - [Q96TA9_HUMAN] | 2.65 | 1 | 0 | 3 | 4 | 9.67517066 |
| B7Z2T5 | cDNA FLJ55427, highly similar to Sodium/potassium-transporting ATPase alpha-1 chain (EC 3.6.3.9) OS=Homo sapiens PE=2 SV=1 - [B7Z2T5_HUMAN] | 5.28 | 1 | 0 | 3 | 4 | 15.1077921 |
| Q9ULT8 | E3 ubiquitin-protein ligase HECTD1 OS=Homo sapiens GN=HECTD1 PE=1 SV=3 - [HECD1_HUMAN] | 1.57 | 1 | 0 | 3 | 3 | 7.3383379 |
| D3DS86 | HECT domain containing 1, isoform CRA_a OS=Homo sapiens GN=HECTD1 PE=4 SV=1 - [D3DS86_HUMAN] | 1.57 | 1 | 0 | 3 | 3 | 7.3383379 |
| B4DQ09 | cDNA FLJ55896, highly similar to PHD finger protein 3 (Fragment) OS=Homo sapiens PE=2 SV=1 - [B4DQ09_HUMAN] | 3.48 | 1 | 0 | 3 | 3 | 7.25063968 |
| O00507 | Probable ubiquitin carboxyl-terminal hydrolase FAF-Y OS=Homo sapiens GN=USP9Y PE=1 SV=2 - [USP9Y_HUMAN] | 0.9 | 1 | 0 | 2 | 6 | 13.7401662 |
| Q15758 | Neutral amino acid transporter B(0) OS=Homo sapiens GN=SLC1A5 PE=1 SV=2 - [AAAT_HUMAN] | 5.55 | 1 | 0 | 2 | 4 | 10.8885784 |
| Q99456 | Keratin, type I cytoskeletal 12 OS=Homo sapiens GN=KRT12 PE=1 SV=1 - [K1C12_HUMAN] | 1.82 | 1 | 0 | 2 | 4 | 9.15412545 |
| Q7Z3Y7 | Keratin, type I cytoskeletal 28 OS=Homo sapiens GN=KRT28 PE=1 SV=2 - [K1C28_HUMAN] | 3.45 | 1 | 0 | 2 | 4 | 9.11258411 |
| P02538 | Keratin, type II cytoskeletal 6A OS=Homo sapiens GN=KRT6A PE=1 SV=3 - [K2C6A_HUMAN] | 3.72 | 1 | 0 | 2 | 4 | 11.2878392 |
| P48668 | Keratin, type II cytoskeletal 6C OS=Homo sapiens GN=KRT6C PE=1 SV=3 - [K2C6C_HUMAN] | 3.72 | 1 | 0 | 2 | 4 | 11.2878392 |
| A2AB05 | Mediator of DNA damage checkpoint 1 (Fragment) OS=Homo sapiens GN=MDC1 PE=4 SV=1 - [A2AB05_HUMAN] | 11.73 | 1 | 0 | 2 | 4 | 10.6318016 |
| A1Z5I7 | Mediator of DNA damage checkpoint 1 variant 3 (Fragment) OS=Homo sapiens GN=MDC1 PE=2 SV=1 - [A1Z5I7_HUMAN] | 7.76 | 1 | 0 | 2 | 4 | 10.6318016 |
| Q59H94 | Gamma filamin variant (Fragment) OS=Homo sapiens PE=1 SV=1 | 1.79 | 1 | 0 | 2 | 4 | 11.2731748 |

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| | - [Q59H94_HUMAN] | | | | | | |
| C9JH30 | Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [C9JH30_HUMAN] | 2.08 | 1 | 0 | 2 | 4 | 9.15412545 |
| B3KVV4 | cDNA FLJ43940 fis, clone TESTI4014175, highly similar to Chromodomain helicase-DNA-binding protein 3 (EC 3.6.1.-) OS=Homo sapiens PE=2 SV=1 - [B3KVV4_HUMAN] | 2.43 | 1 | 0 | 2 | 4 | 12.9643977 |
| Q71UA6 | Neutral amino acid transporter OS=Homo sapiens GN=SLC1A5 PE=2 SV=1 - [Q71UA6_HUMAN] | 5.55 | 1 | 0 | 2 | 4 | 10.8885784 |
| B2R853 | cDNA, FLJ93744, highly similar to Homo sapiens keratin 6E (KRT6E), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R853_HUMAN] | 3.72 | 1 | 0 | 2 | 4 | 11.2878392 |
| A8K2IO | cDNA FLJ78504, highly similar to Homo sapiens keratin 6A (KRT6A), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K2IO_HUMAN] | 3.72 | 1 | 0 | 2 | 4 | 11.2878392 |
| B4DRY0 | cDNA FLJ54379, highly similar to Keratin, type II cytoskeletal 6E OS=Homo sapiens PE=2 SV=1 - [B4DRY0_HUMAN] | 3.84 | 1 | 0 | 2 | 4 | 11.2878392 |
| B7ZB81 | cDNA, FLJ79445, highly similar to Neutral amino acid transporter B(0) OS=Homo sapiens PE=2 SV=1 - [B7ZB81_HUMAN] | 8.85 | 1 | 0 | 2 | 4 | 10.8885784 |
| A1Z5I6 | Mediator of DNA damage checkpoint 1 variant 2 (Fragment) OS=Homo sapiens GN=MDC1 PE=2 SV=1 - [A1Z5I6_HUMAN] | 7.76 | 1 | 0 | 2 | 4 | 10.6318016 |
| B4DRU6 | cDNA FLJ54657, highly similar to Keratin, type II cytoskeletal 6A OS=Homo sapiens PE=2 SV=1 - [B4DRU6_HUMAN] | 3.83 | 1 | 0 | 2 | 4 | 11.2878392 |
| B4DRR0 | cDNA FLJ53910, highly similar to Keratin, type II cytoskeletal 6A OS=Homo sapiens PE=2 SV=1 - [B4DRR0_HUMAN] | 3.93 | 1 | 0 | 2 | 4 | 11.2878392 |
| B4DWS4 | cDNA FLJ57638, highly similar to Neutral amino acid transporter B(0) OS=Homo sapiens PE=2 SV=1 - [B4DWS4_HUMAN] | 9.58 | 1 | 0 | 2 | 4 | 10.8885784 |
| B4DJM5 | cDNA FLJ61294, highly similar to Keratin, type I cytoskeletal 17 OS=Homo sapiens PE=2 SV=1 - [B4DJM5_HUMAN] | 5.08 | 1 | 0 | 2 | 4 | 9.15412545 |
| A8MW45 | Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [A8MW45_HUMAN] | 2.04 | 1 | 0 | 2 | 4 | 9.15412545 |
| B4DKV4 | cDNA FLJ60647, highly similar to Keratin, type II cytoskeletal 6B OS=Homo sapiens PE=2 SV=1 - [B4DKV4_HUMAN] | 3.99 | 1 | 0 | 2 | 4 | 11.2878392 |
| B4DWU6 | cDNA FLJ51361, highly similar to Keratin, type II cytoskeletal 6A OS=Homo sapiens PE=2 SV=1 - [B4DWU6_HUMAN] | 4.04 | 1 | 0 | 2 | 4 | 11.2878392 |

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|--------|-----------------------------------------------------------------------------------------------------------------------------------------------|-------|---|---|---|---|------------|
| Q96SY8 | cDNA FLJ14561 fis, clone NT2RM2002091, weakly similar to Drosophila melanogaster eyelid (eld) mRNA OS=Homo sapiens PE=2 SV=1 - [Q96SY8_HUMAN] | 7.2 | 1 | 0 | 2 | 4 | 12.0955653 |
| P05141 | ADP/ATP translocase 2 OS=Homo sapiens GN=SLC25A5 PE=1 SV=7 - [ADT2_HUMAN] | 7.38 | 1 | 0 | 2 | 3 | 6.59685302 |
| Q8IWZ3 | Ankyrin repeat and KH domain-containing protein 1 OS=Homo sapiens GN=ANKHD1 PE=1 SV=1 - [ANKH1_HUMAN] | 1.3 | 1 | 0 | 2 | 3 | 11.0707855 |
| Q04637 | Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=4 - [IF4G1_HUMAN] | 1.13 | 1 | 0 | 2 | 3 | 7.52250767 |
| P27816 | Microtubule-associated protein 4 OS=Homo sapiens GN=MAP4 PE=1 SV=3 - [MAP4_HUMAN] | 3.47 | 1 | 0 | 2 | 3 | 10.0962777 |
| P35579 | Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4 - [MYH9_HUMAN] | 1.22 | 1 | 0 | 2 | 3 | 6.50368929 |
| Q15149 | Plectin OS=Homo sapiens GN=PLEC PE=1 SV=3 - [PLEC_HUMAN] | 0.47 | 1 | 0 | 2 | 3 | 8.64297843 |
| Q9H254 | Spectrin beta chain, brain 3 OS=Homo sapiens GN=SPTBN4 PE=1 SV=2 - [SPTN4_HUMAN] | 0.78 | 1 | 0 | 2 | 3 | 8.36487246 |
| Q96I65 | EIF4G1 protein OS=Homo sapiens GN=EIF4G1 PE=2 SV=1 - [Q96I65_HUMAN] | 2.79 | 1 | 0 | 2 | 3 | 7.52250767 |
| Q8IWZ2 | HCG2045902, isoform CRA_b OS=Homo sapiens GN=hCG_2045902 PE=2 SV=1 - [Q8IWZ2_HUMAN] | 1.26 | 1 | 0 | 2 | 3 | 11.0707855 |
| C9JAP8 | Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [C9JAP8_HUMAN] | 1.3 | 1 | 0 | 2 | 3 | 7.76356936 |
| D3DNT2 | Eukaryotic translation initiation factor 4 gamma, 1, isoform CRA_c OS=Homo sapiens GN=EIF4G1 PE=4 SV=1 - [D3DNT2_HUMAN] | 1.13 | 1 | 0 | 2 | 3 | 7.52250767 |
| D3DWL0 | Plectin 1, intermediate filament binding protein 500kDa, isoform CRA_b OS=Homo sapiens GN=PLEC1 PE=4 SV=1 - [D3DWL0_HUMAN] | 1.05 | 1 | 0 | 2 | 3 | 8.64297843 |
| Q8WYN9 | Ribosomal protein S27A (Fragment) OS=Homo sapiens GN=RPS27A PE=2 SV=1 - [Q8WYN9_HUMAN] | 14.88 | 1 | 0 | 2 | 3 | 6.71955633 |
| Q6NVC0 | SLC25A5 protein (Fragment) OS=Homo sapiens GN=SLC25A5 PE=2 SV=1 - [Q6NVC0_HUMAN] | 6.81 | 1 | 0 | 2 | 3 | 6.59685302 |
| B7ZCV9 | Mediator of DNA damage checkpoint 1 (Fragment) OS=Homo sapiens GN=MDC1 PE=4 SV=1 - [B7ZCV9_HUMAN] | 20.98 | 1 | 0 | 2 | 3 | 10.5876608 |

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| Q86XU5 | MYH9 protein (Fragment) OS=Homo sapiens GN=MYH9 PE=2 SV=1 - [Q86XU5_HUMAN] | 1.75 | 1 | 0 | 2 | 3 | 6.50368929 |
| Q4LE58 | EIF4G1 variant protein (Fragment) OS=Homo sapiens GN=EIF4G1 variant protein PE=2 SV=1 - [Q4LE58_HUMAN] | 1.11 | 1 | 0 | 2 | 3 | 7.52250767 |
| B2RU06 | EIF4G1 protein OS=Homo sapiens GN=EIF4G1 PE=2 SV=1 - [B2RU06_HUMAN] | 1.12 | 1 | 0 | 2 | 3 | 7.52250767 |
| A8K2T2 | cDNA FLJ75519 (Fragment) OS=Homo sapiens PE=2 SV=1 - [A8K2T2_HUMAN] | 2.39 | 1 | 0 | 2 | 3 | 7.88819003 |
| C9JRP8 | Uncharacterized protein OS=Homo sapiens GN=SPTBN4 PE=4 SV=1 - [C9JRP8_HUMAN] | 1.53 | 1 | 0 | 2 | 3 | 8.36487246 |
| D6R9X2 | Uncharacterized protein OS=Homo sapiens GN=PHF3 PE=4 SV=1 - [D6R9X2_HUMAN] | 4.76 | 1 | 0 | 2 | 3 | 8.40200686 |
| B4DGF1 | cDNA FLJ56479, highly similar to Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens PE=2 SV=1 - [B4DGF1_HUMAN] | 1.15 | 1 | 0 | 2 | 3 | 7.52250767 |
| Q71S06 | Beta spectrin IV OS=Homo sapiens PE=2 SV=1 - [Q71S06_HUMAN] | 1 | 1 | 0 | 2 | 3 | 8.36487246 |
| Q59EZ5 | USP9X protein variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59EZ5_HUMAN] | 4.38 | 1 | 0 | 2 | 3 | 9.74116325 |
| B4DM10 | cDNA FLJ58263, highly similar to Microtubule-associated protein 4 OS=Homo sapiens PE=2 SV=1 - [B4DM10_HUMAN] | 5.41 | 1 | 0 | 2 | 3 | 10.0962777 |
| B4DSI9 | cDNA FLJ56483, highly similar to Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens PE=2 SV=1 - [B4DSI9_HUMAN] | 1.19 | 1 | 0 | 2 | 3 | 7.52250767 |
| Q8TEF1 | FLJ00246 protein (Fragment) OS=Homo sapiens GN=FLJ00246 PE=2 SV=1 - [Q8TEF1_HUMAN] | 2.22 | 1 | 0 | 2 | 3 | 11.0707855 |
| Q71S07 | Non-erythrocytic beta-spectrin 4 OS=Homo sapiens GN=SPNB4 PE=2 SV=1 - [Q71S07_HUMAN] | 0.78 | 1 | 0 | 2 | 3 | 8.36487246 |
| B4DTP3 | cDNA FLJ57343, highly similar to Homo sapiens ankyrin repeat domain 17 (ANKRD17), transcript variant 1, mRNA (Fragment) OS=Homo sapiens PE=2 SV=1 - [B4DTP3_HUMAN] | 2.54 | 1 | 0 | 2 | 3 | 11.0707855 |
| Q13727 | AHNAK-related protein (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q13727_HUMAN] | 9.74 | 1 | 0 | 2 | 3 | 7.18127728 |
| A6QL62 | NIPBL protein (Fragment) OS=Homo sapiens GN=NIPBL PE=2 | 2.38 | 1 | 0 | 2 | 3 | 7.88819003 |

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| | SV=1 - [A6QL62_HUMAN] | | | | | | |
| C9IYG5 | Uncharacterized protein OS=Homo sapiens GN=MIA3 PE=4 SV=1 - [C9IYG5_HUMAN] | 20.97 | 1 | 0 | 2 | 3 | 8.63859749 |
| Q92862 | Dynein heavy chain (Fragment) OS=Homo sapiens GN=Dnchc1 PE=2 SV=1 - [Q92862_HUMAN] | 27.27 | 1 | 0 | 2 | 3 | 8.62631798 |
| B2RU10 | EIF4G1 protein OS=Homo sapiens GN=EIF4G1 PE=2 SV=1 - [B2RU10_HUMAN] | 1.12 | 1 | 0 | 2 | 3 | 7.52250767 |
| B4E3S1 | cDNA FLJ57040, highly similar to Myosin-9 OS=Homo sapiens PE=2 SV=1 - [B4E3S1_HUMAN] | 2.49 | 1 | 0 | 2 | 3 | 6.50368929 |
| A8K6E4 | cDNA FLJ77145, highly similar to Homo sapiens myosin, heavy polypeptide 9, non-muscle (MYH9), mRNA (Fragment) OS=Homo sapiens PE=2 SV=1 - [A8K6E4_HUMAN] | 2.38 | 1 | 0 | 2 | 3 | 6.50368929 |
| B2RCV1 | cDNA, FLJ96310, highly similar to Homo sapiens solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 (SLC25A5), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RCV1_HUMAN] | 7.38 | 1 | 0 | 2 | 3 | 6.59685302 |
| Q86YA8 | YLPM1 protein (Fragment) OS=Homo sapiens GN=YLPM1 PE=2 SV=1 - [Q86YA8_HUMAN] | 4.62 | 1 | 0 | 2 | 3 | 7.90132797 |
| Q9UE33 | TPR protein (Fragment) OS=Homo sapiens GN=TPR PE=2 SV=1 - [Q9UE33_HUMAN] | 24.71 | 1 | 0 | 2 | 3 | 8.0734551 |
| B4DM27 | cDNA FLJ54637, highly similar to Homo sapiens BAT2 domain containing 1 (BAT2D1), mRNA (Fragment) OS=Homo sapiens PE=2 SV=1 - [B4DM27_HUMAN] | 3.22 | 1 | 0 | 2 | 3 | 3.91831756 |
| P12236 | ADP/ATP translocase 3 OS=Homo sapiens GN=SLC25A6 PE=1 SV=4 - [ADT3_HUMAN] | 7.38 | 1 | 0 | 2 | 2 | 5.21125627 |
| P50993 | Sodium/potassium-transporting ATPase subunit alpha-2 OS=Homo sapiens GN=ATP1A2 PE=1 SV=1 - [AT1A2_HUMAN] | 4.02 | 1 | 0 | 2 | 2 | 8.05736423 |
| P13637 | Sodium/potassium-transporting ATPase subunit alpha-3 OS=Homo sapiens GN=ATP1A3 PE=1 SV=3 - [AT1A3_HUMAN] | 4.05 | 1 | 0 | 2 | 2 | 8.05736423 |
| P35658 | Nuclear pore complex protein Nup214 OS=Homo sapiens GN=NUP214 PE=1 SV=2 - [NU214_HUMAN] | 1.29 | 1 | 0 | 2 | 2 | 6.54241514 |
| P24928 | DNA-directed RNA polymerase II subunit RPB1 OS=Homo sapiens GN=POLR2A PE=1 SV=2 - [RPB1_HUMAN] | 1.47 | 1 | 0 | 2 | 2 | 7.10114741 |

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| B4E3V7 | cDNA FLJ61585, highly similar to DNA-directed RNA polymerase II largest subunit (EC 2.7.7.6) OS=Homo sapiens PE=2 SV=1 - [B4E3V7_HUMAN] | 1.5 | 1 | 0 | 2 | 2 | 7.10114741 |
| B7Z3F8 | cDNA FLJ59543, highly similar to Sodium/potassium-transporting ATPase alpha-3 chain (EC 3.6.3.9) OS=Homo sapiens PE=2 SV=1 - [B7Z3F8_HUMAN] | 4.17 | 1 | 0 | 2 | 2 | 8.05736423 |
| B3KRI1 | cDNA FLJ34298 fis, clone FEBRA2006357, highly similar to Sodium/potassium-transporting ATPase alpha-2 chain (EC 3.6.3.9) OS=Homo sapiens PE=2 SV=1 - [B3KRI1_HUMAN] | 4.33 | 1 | 0 | 2 | 2 | 8.05736423 |
| B3KV59 | cDNA FLJ16157 fis, clone BRAWH2006479, highly similar to Sodium/potassium-transporting ATPase alpha-3 chain (EC 3.6.3.9) OS=Homo sapiens PE=2 SV=1 - [B3KV59_HUMAN] | 6.01 | 1 | 0 | 2 | 2 | 8.05736423 |
| B3KX35 | cDNA FLJ44610 fis, clone BRACE2012317, highly similar to Sodium/potassium-transporting ATPase alpha-2 chain (EC 3.6.3.9) OS=Homo sapiens PE=2 SV=1 - [B3KX35_HUMAN] | 6.26 | 1 | 0 | 2 | 2 | 8.05736423 |
| Q2KQ74 | HECTD1 (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q2KQ74_HUMAN] | 2.04 | 1 | 0 | 2 | 2 | 4.78491068 |
| B2RAQ4 | cDNA, FLJ95053, highly similar to Homo sapiens ATPase, Na+/K+ transporting, alpha 2 (+) polypeptide(ATP1A2), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RAQ4_HUMAN] | 4.02 | 1 | 0 | 2 | 2 | 8.05736423 |
| B3KNQ8 | cDNA FLJ30174 fis, clone BRACE2000975, highly similar to Sodium/potassium-transporting ATPase alpha-3 chain (EC 3.6.3.9) OS=Homo sapiens PE=2 SV=1 - [B3KNQ8_HUMAN] | 9.43 | 1 | 0 | 2 | 2 | 8.05736423 |
| B1AKZ0 | ATPase, Na+/K+ transporting, alpha 2 (+) polypeptide (Fragment) OS=Homo sapiens GN=ATP1A2 PE=1 SV=1 - [B1AKZ0_HUMAN] | 5.75 | 1 | 0 | 2 | 2 | 8.05736423 |
| B7Z1N5 | cDNA FLJ53830, highly similar to Sodium/potassium-transporting ATPase alpha-1 chain (EC 3.6.3.9) OS=Homo sapiens PE=2 SV=1 - [B7Z1N5_HUMAN] | 10.12 | 1 | 0 | 2 | 2 | 8.05736423 |
| Q5JUP9 | Nucleoporin 214kDa (Fragment) OS=Homo sapiens GN=NUP214 PE=2 SV=1 - [Q5JUP9_HUMAN] | 1.6 | 1 | 0 | 2 | 2 | 6.54241514 |
| B3KW93 | cDNA FLJ42590 fis, clone BRACE3009708, highly similar to Sodium/potassium-transporting ATPase alpha-2chain (EC 3.6.3.9) OS=Homo sapiens PE=2 SV=1 - [B3KW93_HUMAN] | 4.46 | 1 | 0 | 2 | 2 | 8.05736423 |

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| B7Z1Q9 | cDNA FLJ59485, highly similar to Sodium/potassium-transporting ATPase alpha-3 chain (EC 3.6.3.9) OS=Homo sapiens PE=2 SV=1 - [B7Z1Q9_HUMAN] | 4.5 | 1 | 0 | 2 | 2 | 8.05736423 |
| C9JBL6 | Uncharacterized protein OS=Homo sapiens GN=PCM1 PE=4 SV=1 - [C9JBL6_HUMAN] | 3.97 | 1 | 0 | 2 | 2 | 4.7709322 |
| E5RGQ4 | Uncharacterized protein OS=Homo sapiens GN=PCM1 PE=4 SV=1 - [E5RGQ4_HUMAN] | 5.15 | 1 | 0 | 2 | 2 | 4.7709322 |
| B7Z401 | cDNA FLJ54717, highly similar to Sodium/potassium-transporting ATPase alpha-3 chain (EC 3.6.3.9) OS=Homo sapiens PE=2 SV=1 - [B7Z401_HUMAN] | 4 | 1 | 0 | 2 | 2 | 8.05736423 |
| Q59EI9 | ADP,ATP carrier protein, liver isoform T2 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59EI9_HUMAN] | 6.81 | 1 | 0 | 2 | 2 | 5.21125627 |
| B4DIQ8 | cDNA FLJ56089, highly similar to Sodium/potassium-transporting ATPase alpha-2 chain (EC 3.6.3.9) OS=Homo sapiens PE=2 SV=1 - [B4DIQ8_HUMAN] | 5.67 | 1 | 0 | 2 | 2 | 8.05736423 |
| Q53ES0 | Na ⁺ /K ⁺ -ATPase alpha 3 subunit variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53ES0_HUMAN] | 4.05 | 1 | 0 | 2 | 2 | 8.05736423 |
| B7Z9V4 | cDNA, FLJ78968, highly similar to Sodium/potassium-transporting ATPase alpha-3 chain (EC 3.6.3.9) OS=Homo sapiens PE=2 SV=1 - [B7Z9V4_HUMAN] | 4 | 1 | 0 | 2 | 2 | 8.05736423 |
| Q7Z3C4 | Putative uncharacterized protein DKFZp686J0330 OS=Homo sapiens GN=DKFZp686J0330 PE=2 SV=1 - [Q7Z3C4_HUMAN] | 1.78 | 1 | 0 | 2 | 2 | 6.54241514 |
| B1AKY9 | ATPase, Na ⁺ /K ⁺ transporting, alpha 2 (+) polypeptide OS=Homo sapiens GN=ATP1A2 PE=4 SV=1 - [B1AKY9_HUMAN] | 4.06 | 1 | 0 | 2 | 2 | 8.05736423 |
| B7Z2T0 | cDNA FLJ59513, highly similar to Sodium/potassium-transporting ATPase alpha-3 chain (EC 3.6.3.9) OS=Homo sapiens PE=2 SV=1 - [B7Z2T0_HUMAN] | 4 | 1 | 0 | 2 | 2 | 8.05736423 |

Proteins ID04.msf

| Accession | Description | Σ Coverage | Σ # Proteins | Σ # Unique Peptides | Σ # Peptides | Σ # PSMs | Score A3 |
|-----------|-------------------------------------------------------------------------------------------------------|-------------------|---------------------|----------------------------|---------------------|-----------------|------------|
| Q14204 | Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5 - [DYHC1_HUMAN] | 35.79 | 1 | 120 | 135 | 305 | 1017.33021 |
| P78527 | DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3 - [PRKDC_HUMAN] | 30.5 | 1 | 70 | 103 | 231 | 782.060258 |
| Q15149 | Plectin OS=Homo sapiens GN=PLEC PE=1 SV=3 - [PLEC_HUMAN] | 19.34 | 1 | 40 | 76 | 138 | 433.456006 |
| Q09666 | Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2 - [AHNK_HUMAN] | 45.72 | 1 | 27 | 129 | 244 | 810.183429 |
| P46013 | Antigen KI-67 OS=Homo sapiens GN=MKI67 PE=1 SV=2 - [KI67_HUMAN] | 13.76 | 1 | 26 | 27 | 47 | 157.81365 |
| P58107 | Epiplakin OS=Homo sapiens GN=EPPK1 PE=1 SV=2 - [EPIPL_HUMAN] | 25.09 | 1 | 19 | 26 | 58 | 206.90641 |
| P04264 | Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6 - [K2C1_HUMAN] | 40.68 | 1 | 19 | 24 | 61 | 221.172907 |
| P35527 | Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3 - [K1C9_HUMAN] | 51.04 | 1 | 19 | 19 | 43 | 176.782397 |
| P13645 | Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6 - [K1C10_HUMAN] | 39.21 | 1 | 18 | 21 | 43 | 151.517243 |
| Q5UIP0 | Telomere-associated protein RIF1 OS=Homo sapiens GN=RIF1 PE=1 SV=2 - [RIF1_HUMAN] | 15.05 | 1 | 13 | 25 | 47 | 162.619357 |
| Q9NU22 | Midasin OS=Homo sapiens GN=MDN1 PE=1 SV=2 - [MDN1_HUMAN] | 4.82 | 1 | 10 | 19 | 33 | 101.635284 |
| P35908 | Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2 - [K22E_HUMAN] | 30.67 | 1 | 9 | 16 | 29 | 97.5802865 |
| Q96T58 | Msx2-interacting protein OS=Homo sapiens GN=SPEN PE=1 SV=1 - [MINT_HUMAN] | 2.92 | 1 | 8 | 8 | 11 | 32.4291575 |
| P49792 | E3 SUMO-protein ligase RanBP2 OS=Homo sapiens GN=RANBP2 PE=1 SV=2 - [RBP2_HUMAN] | 6.95 | 1 | 6 | 14 | 24 | 76.5331867 |
| P46939 | Utrophin OS=Homo sapiens GN=UTRN PE=1 SV=2 - [UTRO_HUMAN] | 3.32 | 1 | 4 | 7 | 11 | 36.71717 |

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|--------|---------------------------------------------------------------------------------------------------------------------------------|-------|---|---|----|----|------------|
| Q6ZRS2 | Helicase SRCAP OS=Homo sapiens GN=SRCAP PE=1 SV=3 - [SRCAP_HUMAN] | 2.11 | 1 | 4 | 5 | 8 | 24.2276888 |
| P02533 | Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4 - [K1C14_HUMAN] | 17.58 | 1 | 3 | 7 | 17 | 57.042079 |
| Q12830 | Nucleosome-remodeling factor subunit BPTF OS=Homo sapiens GN=BPTF PE=1 SV=3 - [BPTF_HUMAN] | 2.13 | 1 | 3 | 5 | 8 | 25.8385119 |
| P49454 | Centromere protein F OS=Homo sapiens GN=CENPF PE=1 SV=2 - [CENPF_HUMAN] | 1.12 | 1 | 3 | 3 | 4 | 11.4101927 |
| P16615 | Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Homo sapiens GN=ATP2A2 PE=1 SV=1 - [AT2A2_HUMAN] | 5.37 | 1 | 2 | 3 | 4 | 15.4979656 |
| Q8NFC6 | Biorientation of chromosomes in cell division protein 1-like OS=Homo sapiens GN=BOD1L PE=1 SV=2 - [BOD1L_HUMAN] | 0.75 | 1 | 2 | 2 | 4 | 10.6519868 |
| Q5T4S7 | E3 ubiquitin-protein ligase UBR4 OS=Homo sapiens GN=UBR4 PE=1 SV=1 - [UBR4_HUMAN] | 0.73 | 1 | 2 | 2 | 3 | 10.5157354 |
| Q14676 | Mediator of DNA damage checkpoint protein 1 OS=Homo sapiens GN=MDC1 PE=1 SV=3 - [MDC1_HUMAN] | 14.31 | 1 | 1 | 14 | 23 | 91.2194078 |
| B7WNZ6 | Uncharacterized protein OS=Homo sapiens GN=PRRC2C PE=4 SV=2 - [B7WNZ6_HUMAN] | 6.29 | 1 | 1 | 14 | 21 | 68.7387388 |
| Q7Z6Z7 | E3 ubiquitin-protein ligase HUWE1 OS=Homo sapiens GN=HUWE1 PE=1 SV=3 - [HUWE1_HUMAN] | 4.3 | 1 | 1 | 12 | 21 | 76.1134436 |
| Q5CZB5 | Putative uncharacterized protein DKFZp686M0430 OS=Homo sapiens GN=DKFZp686M0430 PE=2 SV=1 - [Q5CZB5_HUMAN] | 13.74 | 1 | 1 | 10 | 21 | 86.0408802 |
| P13647 | Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3 - [K2C5_HUMAN] | 15.08 | 1 | 1 | 10 | 20 | 56.3212869 |
| P46977 | Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A OS=Homo sapiens GN=STT3A PE=1 SV=2 - [STT3A_HUMAN] | 6.52 | 1 | 1 | 5 | 7 | 17.2943408 |
| P50851 | Lipopolysaccharide-responsive and beige-like anchor protein OS=Homo sapiens GN=LRBA PE=1 SV=4 - [LRBA_HUMAN] | 2.24 | 1 | 1 | 4 | 5 | 16.1958549 |
| B4E106 | cDNA FLJ53399, highly similar to Monocarboxylate transporter 1 OS=Homo sapiens PE=2 SV=1 - [B4E106_HUMAN] | 11.04 | 1 | 1 | 3 | 8 | 29.2185481 |
| Q9P035 | 3-hydroxyacyl-CoA dehydratase 3 OS=Homo sapiens GN=PTPLAD1 PE=1 SV=2 - [HACD3_HUMAN] | 11.88 | 1 | 1 | 3 | 5 | 20.0018325 |
| P61956 | Small ubiquitin-related modifier 2 OS=Homo sapiens | 23.16 | 1 | 1 | 2 | 3 | 9.58589101 |

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| | GN=SUMO2 PE=1 SV=2 - [SUMO2_HUMAN] | | | | | | |
| B5MEH8 | Uncharacterized protein OS=Homo sapiens GN=AHNAK PE=4 SV=1 - [B5MEH8_HUMAN] | 38.31 | 1 | 0 | 76 | 146 | 472.302005 |
| Q6ZQN2 | cDNA FLJ46846 fis, clone UTERU3004635, moderately similar to Neuroblast differentiation associated protein AHNAK (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q6ZQN2_HUMAN] | 41.89 | 1 | 0 | 46 | 92 | 294.842401 |
| D3DWL0 | Plectin 1, intermediate filament binding protein 500kDa, isoform CRA_b OS=Homo sapiens GN=PLEC1 PE=4 SV=1 - [D3DWL0_HUMAN] | 22.23 | 1 | 0 | 36 | 65 | 206.23895 |
| B4DL41 | cDNA FLJ57825, highly similar to DNA-dependent protein kinase catalytic subunit (EC 2.7.11.1) OS=Homo sapiens PE=2 SV=1 - [B4DL41_HUMAN] | 30.97 | 1 | 0 | 33 | 68 | 201.189955 |
| B4DTV0 | cDNA FLJ57801, highly similar to Homo sapiens AHNAK nucleoprotein (desmoyokin) (AHNAK), transcript variant 1, mRNA (Fragment) OS=Homo sapiens PE=2 SV=1 - [B4DTV0_HUMAN] | 36.52 | 1 | 0 | 28 | 51 | 170.514961 |
| P46821 | Microtubule-associated protein 1B OS=Homo sapiens GN=MAP1B PE=1 SV=2 - [MAP1B_HUMAN] | 18.11 | 1 | 0 | 27 | 53 | 193.619276 |
| A2BDK6 | Microtubule-associated protein 1B OS=Homo sapiens GN=MAP1B PE=2 SV=1 - [A2BDK6_HUMAN] | 17.68 | 1 | 0 | 25 | 49 | 179.013644 |
| Q13727 | AHNAK-related protein (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q13727_HUMAN] | 56.37 | 1 | 0 | 21 | 45 | 143.735242 |
| Q8N274 | cDNA FLJ33834 fis, clone CTONG2004264, moderately similar to NEUROBLAST DIFFERENTIATION ASSOCIATED PROTEIN AHNAK OS=Homo sapiens PE=2 SV=1 - [Q8N274_HUMAN] | 41.85 | 1 | 0 | 18 | 39 | 125.802517 |
| Q96IE3 | Similar to plectin 1, intermediate filament binding protein, 500kD (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q96IE3_HUMAN] | 20.8 | 1 | 0 | 17 | 26 | 77.0779867 |
| Q5H9P1 | Putative uncharacterized protein DKFZp686F1345 (Fragment) OS=Homo sapiens GN=DKFZp686F1345 PE=2 SV=1 - [Q5H9P1_HUMAN] | 15.12 | 1 | 0 | 16 | 31 | 118.622315 |
| A6NEC7 | Uncharacterized protein OS=Homo sapiens GN=AKAP12 PE=4 SV=2 - [A6NEC7_HUMAN] | 13.48 | 1 | 0 | 15 | 30 | 116.770886 |
| Q02952 | A-kinase anchor protein 12 OS=Homo sapiens GN=AKAP12 PE=1 | 12.74 | 1 | 0 | 15 | 30 | 116.770886 |

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| | SV=4 - [AKA12_HUMAN] | | | | | | |
| Q9UQ35 | Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2 - [SRRM2_HUMAN] | 7.34 | 1 | 0 | 14 | 25 | 83.0221159 |
| O60382 | KIAA0324 (Fragment) OS=Homo sapiens GN=KIAA0324 PE=2 SV=1 - [O60382_HUMAN] | 10.33 | 1 | 0 | 13 | 23 | 78.2332432 |
| B4DYH4 | cDNA FLJ51571, moderately similar to Mediator of DNA damage checkpoint protein 1 OS=Homo sapiens PE=2 SV=1 - [B4DYH4_HUMAN] | 16.31 | 1 | 0 | 13 | 21 | 82.7344778 |
| Q9Y520 | Protein BAT2-like 2 OS=Homo sapiens GN=BAT2L2 PE=1 SV=3 - [BA2L2_HUMAN] | 5.63 | 1 | 0 | 13 | 20 | 66.3854761 |
| B4DRJ4 | cDNA FLJ55392, highly similar to Telomere-associated protein RIF1 (Fragment) OS=Homo sapiens PE=2 SV=1 - [B4DRJ4_HUMAN] | 18.07 | 1 | 0 | 12 | 20 | 66.5217929 |
| Q05BW8 | MAP1B protein (Fragment) OS=Homo sapiens GN=MAP1B PE=2 SV=1 - [Q05BW8_HUMAN] | 23.73 | 1 | 0 | 11 | 22 | 76.0131497 |
| Q32NB7 | MAP1B protein (Fragment) OS=Homo sapiens GN=MAP1B PE=2 SV=1 - [Q32NB7_HUMAN] | 23.21 | 1 | 0 | 11 | 22 | 76.0131497 |
| Q6PJD3 | MAP1B protein (Fragment) OS=Homo sapiens GN=MAP1B PE=2 SV=1 - [Q6PJD3_HUMAN] | 22.94 | 1 | 0 | 11 | 22 | 76.0131497 |
| A5D6X1 | MAP1B protein (Fragment) OS=Homo sapiens GN=MAP1B PE=2 SV=1 - [A5D6X1_HUMAN] | 21.9 | 1 | 0 | 11 | 22 | 76.0131497 |
| Q4VBY4 | MAP1B protein (Fragment) OS=Homo sapiens GN=MAP1B PE=2 SV=1 - [Q4VBY4_HUMAN] | 21.87 | 1 | 0 | 11 | 22 | 76.0131497 |
| D6RA32 | Uncharacterized protein OS=Homo sapiens GN=MAP1B PE=4 SV=2 - [D6RA32_HUMAN] | 21.49 | 1 | 0 | 10 | 21 | 72.7071378 |
| Q86X89 | MAP1B protein (Fragment) OS=Homo sapiens GN=MAP1B PE=2 SV=1 - [Q86X89_HUMAN] | 21.02 | 1 | 0 | 10 | 21 | 72.7071378 |
| B7Z3U6 | ATPase, Na ⁺ /K ⁺ transporting, alpha 1 polypeptide, isoform CRA_a OS=Homo sapiens GN=ATP1A1 PE=2 SV=1 - [B7Z3U6_HUMAN] | 14.31 | 1 | 0 | 10 | 17 | 57.5450501 |
| P05023 | Sodium/potassium-transporting ATPase subunit alpha-1 OS=Homo sapiens GN=ATP1A1 PE=1 SV=1 - [AT1A1_HUMAN] | 13.88 | 1 | 0 | 10 | 17 | 57.5450501 |
| B7Z2T5 | cDNA FLJ55427, highly similar to Sodium/potassium-transporting ATPase alpha-1 chain (EC 3.6.3.9) OS=Homo | 13.88 | 1 | 0 | 10 | 17 | 57.5450501 |

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| | sapiens PE=2 SV=1 - [B7Z2T5_HUMAN] | | | | | | |
| B1ANR3 | Microtubule-actin crosslinking factor 1 (Fragment) OS=Homo sapiens GN=MACF1 PE=4 SV=1 - [B1ANR3_HUMAN] | 2.82 | 1 | 0 | 10 | 17 | 54.1608379 |
| Q9UPN3 | Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5 OS=Homo sapiens GN=MACF1 PE=1 SV=3 - [MACF1_HUMAN] | 2.3 | 1 | 0 | 10 | 17 | 54.1608379 |
| Q96PK2 | Microtubule-actin cross-linking factor 1, isoform 4 OS=Homo sapiens GN=MACF1 PE=1 SV=2 - [MACF4_HUMAN] | 2.11 | 1 | 0 | 10 | 17 | 54.1608379 |
| P04259 | Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5 - [K2C6B_HUMAN] | 14.18 | 1 | 0 | 9 | 19 | 55.8452284 |
| B4E1T1 | cDNA FLJ54081, highly similar to Keratin, type II cytoskeletal 5 OS=Homo sapiens PE=2 SV=1 - [B4E1T1_HUMAN] | 14.05 | 1 | 0 | 9 | 18 | 51.2134073 |
| Q5H924 | HECT, UBA and WWE domain containing 1 (Fragment) OS=Homo sapiens GN=HUWE1 PE=2 SV=1 - [Q5H924_HUMAN] | 4.05 | 1 | 0 | 9 | 17 | 60.982971 |
| B7Z3V1 | cDNA FLJ60077, highly similar to Sodium/potassium-transporting ATPase alpha-1 chain (EC 3.6.3.9) (Fragment) OS=Homo sapiens PE=2 SV=1 - [B7Z3V1_HUMAN] | 12.25 | 1 | 0 | 9 | 15 | 48.4905562 |
| A5D8X6 | MAP1B protein (Fragment) OS=Homo sapiens GN=MAP1B PE=2 SV=1 - [A5D8X6_HUMAN] | 19.44 | 1 | 0 | 8 | 17 | 58.1015058 |
| B4DWU6 | cDNA FLJ51361, highly similar to Keratin, type II cytoskeletal 6A OS=Homo sapiens PE=2 SV=1 - [B4DWU6_HUMAN] | 13.46 | 1 | 0 | 8 | 17 | 50.0504258 |
| B4DRR0 | cDNA FLJ53910, highly similar to Keratin, type II cytoskeletal 6A OS=Homo sapiens PE=2 SV=1 - [B4DRR0_HUMAN] | 13.08 | 1 | 0 | 8 | 17 | 50.0504258 |
| P02538 | Keratin, type II cytoskeletal 6A OS=Homo sapiens GN=KRT6A PE=1 SV=3 - [K2C6A_HUMAN] | 12.41 | 1 | 0 | 8 | 17 | 50.0504258 |
| P48668 | Keratin, type II cytoskeletal 6C OS=Homo sapiens GN=KRT6C PE=1 SV=3 - [K2C6C_HUMAN] | 12.41 | 1 | 0 | 8 | 17 | 50.0504258 |
| A8K2I0 | cDNA FLJ78504, highly similar to Homo sapiens keratin 6A (KRT6A), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K2I0_HUMAN] | 12.41 | 1 | 0 | 8 | 17 | 50.0504258 |
| Q5HY54 | Filamin A, alpha (Actin binding protein 280) OS=Homo sapiens GN=FLNA PE=2 SV=1 - [Q5HY54_HUMAN] | 4.83 | 1 | 0 | 8 | 9 | 27.3606062 |
| Q60FE6 | Filamin A OS=Homo sapiens GN=FLNA PE=2 SV=1 - [Q60FE6_HUMAN] | 4.82 | 1 | 0 | 8 | 9 | 27.3606062 |

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| Q60FE5 | Filamin A OS=Homo sapiens GN=FLNA PE=2 SV=1 - [Q60FE5_HUMAN] | 4.81 | 1 | 0 | 8 | 9 | 27.3606062 |
| P21333 | Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4 - [FLNA_HUMAN] | 4.76 | 1 | 0 | 8 | 9 | 27.3606062 |
| Q9NSU9 | Putative uncharacterized protein DKFZp434G0719 (Fragment) OS=Homo sapiens GN=DKFZp434G0719 PE=2 SV=1 - [Q9NSU9_HUMAN] | 23.73 | 1 | 0 | 7 | 21 | 69.2125695 |
| D6RA40 | Uncharacterized protein OS=Homo sapiens GN=MAP1B PE=4 SV=1 - [D6RA40_HUMAN] | 16.87 | 1 | 0 | 7 | 16 | 54.7954938 |
| B2R853 | cDNA, FLJ93744, highly similar to Homo sapiens keratin 6E (KRT6E), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R853_HUMAN] | 10.82 | 1 | 0 | 7 | 15 | 44.2767832 |
| B4DRU6 | cDNA FLJ54657, highly similar to Keratin, type II cytoskeletal 6A OS=Homo sapiens PE=2 SV=1 - [B4DRU6_HUMAN] | 10.56 | 1 | 0 | 7 | 15 | 43.4498584 |
| C9JCC2 | Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [C9JCC2_HUMAN] | 19.92 | 1 | 0 | 7 | 12 | 46.1495705 |
| B2ZZ80 | Filamin A OS=Homo sapiens GN=FLNA PE=2 SV=1 - [B2ZZ80_HUMAN] | 4.19 | 1 | 0 | 7 | 8 | 23.0425153 |
| A6NDY9 | Uncharacterized protein OS=Homo sapiens GN=FLNA PE=4 SV=3 - [A6NDY9_HUMAN] | 4.19 | 1 | 0 | 7 | 8 | 23.0425153 |
| B4DSR6 | cDNA FLJ52684, highly similar to Dynein heavy chain, cytosolic OS=Homo sapiens PE=2 SV=1 - [B4DSR6_HUMAN] | 23.74 | 1 | 0 | 5 | 16 | 58.4649191 |
| Q6P2H7 | DYNC1H1 protein OS=Homo sapiens GN=DYNC1H1 PE=2 SV=1 - [Q6P2H7_HUMAN] | 29.95 | 1 | 0 | 5 | 12 | 47.2854211 |
| B4DL32 | cDNA FLJ59922, highly similar to Keratin, type II cytoskeletal 5 OS=Homo sapiens PE=2 SV=1 - [B4DL32_HUMAN] | 17.52 | 1 | 0 | 5 | 11 | 32.1645985 |
| B7Z3F8 | cDNA FLJ59543, highly similar to Sodium/potassium- transporting ATPase alpha-3 chain (EC 3.6.3.9) OS=Homo sapiens PE=2 SV=1 - [B7Z3F8_HUMAN] | 8.44 | 1 | 0 | 5 | 10 | 33.3079638 |
| P13637 | Sodium/potassium-transporting ATPase subunit alpha-3 OS=Homo sapiens GN=ATP1A3 PE=1 SV=3 - [AT1A3_HUMAN] | 8.19 | 1 | 0 | 5 | 10 | 33.3079638 |
| Q53ES0 | Na+/K+-ATPase alpha 3 subunit variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53ES0_HUMAN] | 8.19 | 1 | 0 | 5 | 10 | 33.3079638 |
| B7Z401 | cDNA FLJ54717, highly similar to Sodium/potassium- | 8.11 | 1 | 0 | 5 | 10 | 33.3079638 |

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| | transporting ATPase alpha-3 chain (EC 3.6.3.9) OS=Homo sapiens PE=2 SV=1 - [B7Z401_HUMAN] | | | | | | |
| B7Z9V4 | cDNA FLJ78968, highly similar to Sodium/potassium-transporting ATPase alpha-3 chain (EC 3.6.3.9) OS=Homo sapiens PE=2 SV=1 - [B7Z9V4_HUMAN] | 8.09 | 1 | 0 | 5 | 10 | 33.3079638 |
| B7Z2T0 | cDNA FLJ59513, highly similar to Sodium/potassium-transporting ATPase alpha-3 chain (EC 3.6.3.9) OS=Homo sapiens PE=2 SV=1 - [B7Z2T0_HUMAN] | 8.09 | 1 | 0 | 5 | 10 | 33.3079638 |
| Q6AI22 | Putative uncharacterized protein DKFZp686H16106 (Fragment) OS=Homo sapiens GN=DKFZp686H16106 PE=2 SV=1 - [Q6AI22_HUMAN] | 2.38 | 1 | 0 | 5 | 10 | 33.3562987 |
| B4DS49 | cDNA FLJ60845, highly similar to Telomere-associated protein RIF1 OS=Homo sapiens PE=2 SV=1 - [B4DS49_HUMAN] | 26.39 | 1 | 0 | 5 | 9 | 29.6763268 |
| B4DRY0 | cDNA FLJ54379, highly similar to Keratin, type II cytoskeletal 6E OS=Homo sapiens PE=2 SV=1 - [B4DRY0_HUMAN] | 9.32 | 1 | 0 | 5 | 9 | 25.0872738 |
| B4DKV4 | cDNA FLJ60647, highly similar to Keratin, type II cytoskeletal 6B OS=Homo sapiens PE=2 SV=1 - [B4DKV4_HUMAN] | 9.13 | 1 | 0 | 5 | 9 | 24.260349 |
| A0AUK8 | SRRM2 protein (Fragment) OS=Homo sapiens GN=SRRM2 PE=2 SV=1 - [A0AUK8_HUMAN] | 33.19 | 1 | 0 | 5 | 8 | 28.3739176 |
| B8ZZM4 | Uncharacterized protein OS=Homo sapiens GN=RGPD3 PE=4 SV=1 - [B8ZZM4_HUMAN] | 3.53 | 1 | 0 | 5 | 8 | 23.0912948 |
| A6NKT7 | RanBP2-like and GRIP domain-containing protein 3 OS=Homo sapiens GN=RGPD3 PE=2 SV=1 - [RGPD3_HUMAN] | 3.51 | 1 | 0 | 5 | 8 | 23.0912948 |
| D3DX73 | HCG1994636, isoform CRA_b OS=Homo sapiens GN=hCG_1994636 PE=4 SV=1 - [D3DX73_HUMAN] | 8.85 | 1 | 0 | 5 | 7 | 20.4393241 |
| Q01546 | Keratin, type II cytoskeletal 2 oral OS=Homo sapiens GN=KRT76 PE=1 SV=2 - [K22O_HUMAN] | 4.23 | 1 | 0 | 4 | 10 | 30.0003772 |
| Q15758 | Neutral amino acid transporter B(0) OS=Homo sapiens GN=SLC1A5 PE=1 SV=2 - [AAAT_HUMAN] | 9.98 | 1 | 0 | 4 | 9 | 29.2593777 |
| Q71UA6 | Neutral amino acid transporter OS=Homo sapiens GN=SLC1A5 PE=2 SV=1 - [Q71UA6_HUMAN] | 9.98 | 1 | 0 | 4 | 9 | 29.2593777 |
| P08779 | Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4 - [K1C16_HUMAN] | 9.73 | 1 | 0 | 4 | 9 | 26.2765002 |
| B7Z1Q9 | cDNA FLJ59485, highly similar to Sodium/potassium- | 7.89 | 1 | 0 | 4 | 8 | 28.6604528 |

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| | transporting ATPase alpha-3 chain (EC 3.6.3.9) OS=Homo sapiens PE=2 SV=1 - [B7Z1Q9_HUMAN] | | | | | | |
| Q96HX3 | Similar to ribophorin I (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q96HX3_HUMAN] | 7.75 | 1 | 0 | 4 | 8 | 21.9585204 |
| Q6ZVV6 | cDNA FLJ42031 fis, clone SPLEN2037194, weakly similar to NORQ PROTEIN OS=Homo sapiens PE=2 SV=1 - [Q6ZVV6_HUMAN] | 7.68 | 1 | 0 | 4 | 8 | 22.2305603 |
| B4DL99 | cDNA FLJ51740, highly similar to Dolichyl-diphosphooligosaccharide--proteinglycosyltransferase 67 kDa subunit (EC 2.4.1.119) OS=Homo sapiens PE=2 SV=1 - [B4DL99_HUMAN] | 7.57 | 1 | 0 | 4 | 8 | 21.9585204 |
| P04843 | Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Homo sapiens GN=RPN1 PE=1 SV=1 - [RPN1_HUMAN] | 7.25 | 1 | 0 | 4 | 8 | 21.9585204 |
| Q53EP4 | Ribophorin I variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53EP4_HUMAN] | 7.25 | 1 | 0 | 4 | 8 | 21.9585204 |
| Q6IBRO | RPN1 protein OS=Homo sapiens GN=RPN1 PE=2 SV=1 - [Q6IBRO_HUMAN] | 7.25 | 1 | 0 | 4 | 8 | 21.9585204 |
| B3KRI1 | cDNA FLJ34298 fis, clone FEBRA2006357, highly similar to Sodium/potassium-transporting ATPase alpha-2 chain (EC 3.6.3.9) OS=Homo sapiens PE=2 SV=1 - [B3KRI1_HUMAN] | 7.07 | 1 | 0 | 4 | 8 | 25.8344443 |
| B1AKY9 | ATPase, Na+/K+ transporting, alpha 2 (+) polypeptide OS=Homo sapiens GN=ATP1A2 PE=4 SV=1 - [B1AKY9_HUMAN] | 6.64 | 1 | 0 | 4 | 8 | 25.8344443 |
| P50993 | Sodium/potassium-transporting ATPase subunit alpha-2 OS=Homo sapiens GN=ATP1A2 PE=1 SV=1 - [AT1A2_HUMAN] | 6.57 | 1 | 0 | 4 | 8 | 25.8344443 |
| B2RAQ4 | cDNA, FLJ95053, highly similar to Homo sapiens ATPase, Na+/K+ transporting, alpha 2 (+) polypeptide(ATP1A2), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RAQ4_HUMAN] | 6.57 | 1 | 0 | 4 | 8 | 25.8344443 |
| P12270 | Nucleoprotein TPR OS=Homo sapiens GN=TPR PE=1 SV=3 - [TPR_HUMAN] | 2.37 | 1 | 0 | 4 | 8 | 29.057956 |
| Q99968 | Tpr OS=Homo sapiens GN=tpr PE=2 SV=1 - [Q99968_HUMAN] | 2.37 | 1 | 0 | 4 | 8 | 29.057956 |
| B4DQN8 | cDNA FLJ50056, highly similar to Homo sapiens BAT2 domain containing 1 (BAT2D1), mRNA (Fragment) OS=Homo sapiens PE=2 SV=1 - [B4DQN8_HUMAN] | 4.77 | 1 | 0 | 4 | 7 | 21.3237827 |

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| B4DGF6 | cDNA FLJ59294, highly similar to HECT, UBA and WWE domain-containing protein 1 (EC 6.3.2.-) (Fragment) OS=Homo sapiens PE=2 SV=1 - [B4DGF6_HUMAN] | 4.39 | 1 | 0 | 4 | 7 | 24.4923768 |
| Q5H962 | HECT, UBA and WWE domain containing 1 OS=Homo sapiens GN=HUWE1 PE=2 SV=1 - [Q5H962_HUMAN] | 3.53 | 1 | 0 | 4 | 7 | 24.4923768 |
| B4DJ24 | cDNA FLJ58575, highly similar to Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A (EC 2.4.1.119) OS=Homo sapiens PE=2 SV=1 - [B4DJ24_HUMAN] | 6.04 | 1 | 0 | 4 | 6 | 15.0120957 |
| B4DZH4 | cDNA FLJ59078, highly similar to Ran-binding protein 2-like 6 OS=Homo sapiens PE=2 SV=1 - [B4DZH4_HUMAN] | 4.71 | 1 | 0 | 4 | 6 | 18.3122966 |
| B9A029 | Uncharacterized protein OS=Homo sapiens GN=RGPD4 PE=4 SV=1 - [B9A029_HUMAN] | 3.01 | 1 | 0 | 4 | 6 | 18.3122966 |
| Q7Z3J3 | RanBP2-like and GRIP domain-containing protein 4 OS=Homo sapiens GN=RGPD4 PE=2 SV=2 - [RGPD4_HUMAN] | 3 | 1 | 0 | 4 | 6 | 18.3122966 |
| Q96C32 | UBC protein OS=Homo sapiens PE=2 SV=1 - [Q96C32_HUMAN] | 49.84 | 1 | 0 | 3 | 12 | 41.9395463 |
| P0CG47 | Polyubiquitin-B OS=Homo sapiens GN=UBB PE=1 SV=1 - [UBB_HUMAN] | 49.78 | 1 | 0 | 3 | 12 | 41.9395463 |
| Q5PY61 | Ubiquitin C splice variant OS=Homo sapiens GN=UBC PE=2 SV=1 - [Q5PY61_HUMAN] | 49.78 | 1 | 0 | 3 | 12 | 41.9395463 |
| Q5UGI3 | Ubiquitin C splice variant OS=Homo sapiens GN=UBC PE=2 SV=1 - [Q5UGI3_HUMAN] | 49.67 | 1 | 0 | 3 | 12 | 41.9395463 |
| B4DV12 | cDNA FLJ51326, highly similar to Homo sapiens ubiquitin B (UBB), mRNA OS=Homo sapiens PE=2 SV=1 - [B4DV12_HUMAN] | 49.67 | 1 | 0 | 3 | 12 | 41.9395463 |
| Q59EM9 | Ubiquitin C variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59EM9_HUMAN] | 49.35 | 1 | 0 | 3 | 12 | 41.9395463 |
| Q66K58 | Putative uncharacterized protein (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q66K58_HUMAN] | 49 | 1 | 0 | 3 | 12 | 41.9395463 |
| Q96H31 | UBC protein (Fragment) OS=Homo sapiens GN=UBC PE=2 SV=2 - [Q96H31_HUMAN] | 48.72 | 1 | 0 | 3 | 12 | 41.9395463 |
| P0CG48 | Polyubiquitin-C OS=Homo sapiens GN=UBC PE=1 SV=2 - [UBC_HUMAN] | 48.03 | 1 | 0 | 3 | 12 | 41.9395463 |
| Q9UFQ0 | Putative uncharacterized protein DKFZp434K0435 (Fragment) OS=Homo sapiens GN=DKFZp434K0435 PE=2 SV=1 - | 47.7 | 1 | 0 | 3 | 12 | 41.9395463 |

| | [Q9UFQ0_HUMAN] | | | | | | |
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| A8K674 | cDNA FLJ75516, highly similar to Xenopus tropicalis ubiquitin C, mRNA OS=Homo sapiens PE=2 SV=1 - [A8K674_HUMAN] | 47.29 | 1 | 0 | 3 | 12 | 41.9395463 |
| Q96MH4 | cDNA FLJ32377 fis, clone SKMUS1000014, highly similar to Polyubiquitin 9 OS=Homo sapiens PE=2 SV=1 - [Q96MH4_HUMAN] | 45.88 | 1 | 0 | 3 | 12 | 41.9395463 |
| P62987 | Ubiquitin-60S ribosomal protein L40 OS=Homo sapiens GN=UBA52 PE=1 SV=2 - [RL40_HUMAN] | 29.69 | 1 | 0 | 3 | 12 | 41.9395463 |
| P62979 | Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=1 SV=2 - [RS27A_HUMAN] | 24.36 | 1 | 0 | 3 | 12 | 41.9395463 |
| Q5RKT7 | Ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=2 SV=1 - [Q5RKT7_HUMAN] | 24.36 | 1 | 0 | 3 | 12 | 41.9395463 |
| P05787 | Keratin, type II cytoskeletal 8 OS=Homo sapiens GN=KRT8 PE=1 SV=7 - [K2C8_HUMAN] | 3.93 | 1 | 0 | 3 | 8 | 24.9631519 |
| P12035 | Keratin, type II cytoskeletal 3 OS=Homo sapiens GN=KRT3 PE=1 SV=3 - [K2C3_HUMAN] | 2.87 | 1 | 0 | 3 | 8 | 24.9143629 |
| B4E2P9 | cDNA FLJ56708, highly similar to Keratin, type I cytoskeletal 17 OS=Homo sapiens PE=2 SV=1 - [B4E2P9_HUMAN] | 9.3 | 1 | 0 | 3 | 8 | 18.0140378 |
| B4E204 | cDNA FLJ58872, highly similar to Keratin, type I cytoskeletal 15 OS=Homo sapiens PE=2 SV=1 - [B4E204_HUMAN] | 6.84 | 1 | 0 | 3 | 8 | 18.0140378 |
| B4DWU0 | cDNA FLJ56791, highly similar to Keratin, type I cytoskeletal 16 OS=Homo sapiens PE=2 SV=1 - [B4DWU0_HUMAN] | 27.41 | 1 | 0 | 3 | 7 | 21.0153501 |
| B4E2J5 | cDNA FLJ53570, highly similar to Keratin, type I cytoskeletal 16 OS=Homo sapiens PE=2 SV=1 - [B4E2J5_HUMAN] | 19.68 | 1 | 0 | 3 | 7 | 21.0153501 |
| Q04695 | Keratin, type I cytoskeletal 17 OS=Homo sapiens GN=KRT17 PE=1 SV=2 - [K1C17_HUMAN] | 7.18 | 1 | 0 | 3 | 7 | 20.8577507 |
| C9JH30 | Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [C9JH30_HUMAN] | 7.16 | 1 | 0 | 3 | 7 | 20.8577507 |
| A8MW45 | Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [A8MW45_HUMAN] | 7.03 | 1 | 0 | 3 | 7 | 20.8577507 |
| B7Z1N5 | cDNA FLJ53830, highly similar to Sodium/potassium-transporting ATPase alpha-1 chain (EC 3.6.3.9) OS=Homo sapiens PE=2 SV=1 - [B7Z1N5_HUMAN] | 14.07 | 1 | 0 | 3 | 6 | 21.3356061 |

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|--------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------|---|---|---|---|------------|
| B4DKS0 | cDNA FLJ53381, highly similar to Monocarboxylate transporter 1 OS=Homo sapiens PE=2 SV=1 - [B4DKS0_HUMAN] | 11.04 | 1 | 0 | 3 | 6 | 24.2570176 |
| P05141 | ADP/ATP translocase 2 OS=Homo sapiens GN=SLC25A5 PE=1 SV=7 - [ADT2_HUMAN] | 10.74 | 1 | 0 | 3 | 6 | 14.7733452 |
| P12236 | ADP/ATP translocase 3 OS=Homo sapiens GN=SLC25A6 PE=1 SV=4 - [ADT3_HUMAN] | 10.74 | 1 | 0 | 3 | 6 | 15.2830768 |
| P53985 | Monocarboxylate transporter 1 OS=Homo sapiens GN=SLC16A1 PE=1 SV=3 - [MOT1_HUMAN] | 10.6 | 1 | 0 | 3 | 6 | 24.2570176 |
| Q6NVC0 | SLC25A5 protein (Fragment) OS=Homo sapiens GN=SLC25A5 PE=2 SV=1 - [Q6NVC0_HUMAN] | 9.91 | 1 | 0 | 3 | 6 | 14.7733452 |
| Q59EI9 | ADP,ATP carrier protein, liver isoform T2 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59EI9_HUMAN] | 9.91 | 1 | 0 | 3 | 6 | 15.2830768 |
| B3KV59 | cDNA FLJ16157 fis, clone BRAWH2006479, highly similar to Sodium/potassium-transporting ATPase alpha-3 chain (EC 3.6.3.9) OS=Homo sapiens PE=2 SV=1 - [B3KV59_HUMAN] | 8.36 | 1 | 0 | 3 | 6 | 21.3356061 |
| B7Z4L4 | cDNA FLJ50809, highly similar to Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 67 kDa subunit (EC 2.4.1.119) OS=Homo sapiens PE=2 SV=1 - [B7Z4L4_HUMAN] | 7.82 | 1 | 0 | 3 | 6 | 16.8765197 |
| B3KW93 | cDNA FLJ42590 fis, clone BRACE3009708, highly similar to Sodium/potassium-transporting ATPase alpha-2chain (EC 3.6.3.9) OS=Homo sapiens PE=2 SV=1 - [B3KW93_HUMAN] | 5.65 | 1 | 0 | 3 | 6 | 18.5095975 |
| Q7Z794 | Keratin, type II cytoskeletal 1b OS=Homo sapiens GN=KRT77 PE=1 SV=3 - [K2C1B_HUMAN] | 5.02 | 1 | 0 | 3 | 6 | 17.8000367 |
| Q0IIN1 | Keratin 77 OS=Homo sapiens GN=KRT77 PE=1 SV=1 - [Q0IIN1_HUMAN] | 5.02 | 1 | 0 | 3 | 6 | 17.8000367 |
| A8K8Z1 | cDNA FLJ77189, highly similar to Homo sapiens utrophin (homologous to dystrophin) (UTRN), mRNA (Fragment) OS=Homo sapiens PE=2 SV=1 - [A8K8Z1_HUMAN] | 3.57 | 1 | 0 | 3 | 6 | 20.3039098 |
| Q5T795 | MDN1, midasin homolog (Yeast) (Fragment) OS=Homo sapiens GN=MDN1 PE=2 SV=1 - [Q5T795_HUMAN] | 3.13 | 1 | 0 | 3 | 6 | 17.5290296 |
| Q9NRC3 | Cytoplasmic dynein heavy chain (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q9NRC3_HUMAN] | 30 | 1 | 0 | 3 | 5 | 19.2401061 |
| Q59ES3 | Solute carrier family 1 (Neutral amino acid transporter), member | 6.2 | 1 | 0 | 3 | 5 | 14.7427344 |

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| | 5 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59ES3_HUMAN] | | | | | | |
| Q5XKE5 | Keratin, type II cytoskeletal 79 OS=Homo sapiens GN=KRT79 PE=1 SV=2 - [K2C79_HUMAN] | 5.42 | 1 | 0 | 3 | 5 | 13.6873446 |
| O95678 | Keratin, type II cytoskeletal 75 OS=Homo sapiens GN=KRT75 PE=1 SV=2 - [K2C75_HUMAN] | 5.26 | 1 | 0 | 3 | 5 | 13.2452998 |
| Q5H935 | HECT, UBA and WWE domain containing 1 (Fragment) OS=Homo sapiens GN=HUWE1 PE=2 SV=1 - [Q5H935_HUMAN] | 3.18 | 1 | 0 | 3 | 5 | 16.2906911 |
| D3DSF6 | SON DNA binding protein, isoform CRA_g OS=Homo sapiens GN=SON PE=4 SV=1 - [D3DSF6_HUMAN] | 2.18 | 1 | 0 | 3 | 5 | 16.4963994 |
| D3DSF5 | SON DNA binding protein, isoform CRA_a OS=Homo sapiens GN=SON PE=4 SV=1 - [D3DSF5_HUMAN] | 1.98 | 1 | 0 | 3 | 5 | 16.4963994 |
| P18583 | Protein SON OS=Homo sapiens GN=SON PE=1 SV=4 - [SON_HUMAN] | 1.9 | 1 | 0 | 3 | 5 | 16.4963994 |
| B4DM27 | cDNA FLJ54637, highly similar to Homo sapiens BAT2 domain containing 1 (BAT2D1), mRNA (Fragment) OS=Homo sapiens PE=2 SV=1 - [B4DM27_HUMAN] | 4.18 | 1 | 0 | 3 | 4 | 12.6523547 |
| Q8TES4 | FLJ00119 protein (Fragment) OS=Homo sapiens GN=FLJ00119 PE=2 SV=1 - [Q8TES4_HUMAN] | 3.37 | 1 | 0 | 3 | 4 | 12.009727 |
| Q59HC1 | Beige-like protein variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59HC1_HUMAN] | 2.46 | 1 | 0 | 3 | 4 | 11.6571934 |
| Q49A90 | RPS27A protein OS=Homo sapiens GN=RPS27A PE=4 SV=1 - [Q49A90_HUMAN] | 30.53 | 1 | 0 | 2 | 9 | 34.1691415 |
| Q969I0 | KRT8 protein (Fragment) OS=Homo sapiens GN=KRT8 PE=2 SV=2 - [Q969I0_HUMAN] | 2.74 | 1 | 0 | 2 | 6 | 19.1895094 |
| B4DWS4 | cDNA FLJ57638, highly similar to Neutral amino acid transporter B(0) OS=Homo sapiens PE=2 SV=1 - [B4DWS4_HUMAN] | 9.58 | 1 | 0 | 2 | 5 | 16.8142698 |
| C9JM50 | Uncharacterized protein OS=Homo sapiens GN=KRT19 PE=4 SV=1 - [C9JM50_HUMAN] | 9.18 | 1 | 0 | 2 | 5 | 13.3569396 |
| B7ZB81 | cDNA, FLJ79445, highly similar to Neutral amino acid transporter B(0) OS=Homo sapiens PE=2 SV=1 - [B7ZB81_HUMAN] | 8.85 | 1 | 0 | 2 | 5 | 16.8142698 |
| P08727 | Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=4 - [K1C19_HUMAN] | 4.5 | 1 | 0 | 2 | 5 | 13.3569396 |
| EOCX14 | Uncharacterized protein OS=Homo sapiens GN=KRT15 PE=4 | 3.96 | 1 | 0 | 2 | 5 | 13.3569396 |

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| | SV=1 - [E0CX14_HUMAN] | | | | | | |
| P19012 | Keratin, type I cytoskeletal 15 OS=Homo sapiens GN=KRT15 PE=1 SV=3 - [K1C15_HUMAN] | 3.95 | 1 | 0 | 2 | 5 | 13.3569396 |
| Q92862 | Dynein heavy chain (Fragment) OS=Homo sapiens GN=Dnchc1 PE=2 SV=1 - [Q92862_HUMAN] | 27.27 | 1 | 0 | 2 | 4 | 12.2723207 |
| D6RCL2 | Uncharacterized protein OS=Homo sapiens GN=MAP1B PE=4 SV=2 - [D6RCL2_HUMAN] | 25.24 | 1 | 0 | 2 | 4 | 13.5650978 |
| D6RGJ3 | Uncharacterized protein OS=Homo sapiens GN=MAP1B PE=4 SV=1 - [D6RGJ3_HUMAN] | 21.31 | 1 | 0 | 2 | 4 | 13.5650978 |
| Q14222 | EEF1A protein (Fragment) OS=Homo sapiens GN=EEF1A PE=1 SV=1 - [Q14222_HUMAN] | 15.42 | 1 | 0 | 2 | 4 | 15.778218 |
| Q96C29 | Putative uncharacterized protein (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q96C29_HUMAN] | 14.11 | 1 | 0 | 2 | 4 | 15.778218 |
| Q8TBL1 | Putative uncharacterized protein (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q8TBL1_HUMAN] | 14 | 1 | 0 | 2 | 4 | 15.778218 |
| Q6P082 | EEF1A1 protein (Fragment) OS=Homo sapiens GN=EEF1A1 PE=2 SV=1 - [Q6P082_HUMAN] | 13.94 | 1 | 0 | 2 | 4 | 15.778218 |
| A2AB05 | Mediator of DNA damage checkpoint 1 (Fragment) OS=Homo sapiens GN=MDC1 PE=4 SV=1 - [A2AB05_HUMAN] | 12.35 | 1 | 0 | 2 | 4 | 11.9240119 |
| Q96CD8 | Putative uncharacterized protein (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q96CD8_HUMAN] | 12.2 | 1 | 0 | 2 | 4 | 15.778218 |
| Q6P4C9 | EEF1A1 protein (Fragment) OS=Homo sapiens GN=EEF1A1 PE=2 SV=1 - [Q6P4C9_HUMAN] | 12.07 | 1 | 0 | 2 | 4 | 15.778218 |
| B4DRF4 | cDNA FLJ54138, highly similar to Homo sapiens butyrate- induced transcript 1 (HSPC121), mRNA OS=Homo sapiens PE=2 SV=1 - [B4DRF4_HUMAN] | 11.4 | 1 | 0 | 2 | 4 | 17.5438693 |
| Q504Z0 | EEF1A1 protein OS=Homo sapiens GN=EEF1A1 PE=2 SV=1 - [Q504Z0_HUMAN] | 11.36 | 1 | 0 | 2 | 4 | 15.778218 |
| B4E2C5 | cDNA FLJ54032, highly similar to Elongation factor 1-alpha 1 OS=Homo sapiens PE=2 SV=1 - [B4E2C5_HUMAN] | 11.36 | 1 | 0 | 2 | 4 | 15.778218 |
| Q8IUB0 | CTCL tumor antigen HD-CL-08 OS=Homo sapiens PE=2 SV=1 - [Q8IUB0_HUMAN] | 9.7 | 1 | 0 | 2 | 4 | 15.778218 |
| B4DHD7 | cDNA FLJ53737, highly similar to Sodium/potassium- transporting ATPase alpha-2 chain (EC 3.6.3.9) OS=Homo | 9.56 | 1 | 0 | 2 | 4 | 11.9723577 |

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| | sapiens PE=2 SV=1 - [B4DHD7_HUMAN] | | | | | | |
| B3KNQ8 | cDNA FLJ30174 fis, clone BRACE2000975, highly similar to Sodium/potassium-transporting ATPase alpha-3 chain (EC 3.6.3.9) OS=Homo sapiens PE=2 SV=1 - [B3KNQ8_HUMAN] | 9.43 | 1 | 0 | 2 | 4 | 13.8620865 |
| B4DNE0 | cDNA FLJ52573, highly similar to Elongation factor 1-alpha 1 OS=Homo sapiens PE=2 SV=1 - [B4DNE0_HUMAN] | 8.86 | 1 | 0 | 2 | 4 | 15.778218 |
| Q96RE1 | Translation elongation factor 1 alpha 1-like 14 OS=Homo sapiens GN=EEF1A1L14 PE=2 SV=1 - [Q96RE1_HUMAN] | 8.79 | 1 | 0 | 2 | 4 | 15.778218 |
| Q14666 | Radiated keratinocyte mRNA 266 (keratin-related protein) (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q14666_HUMAN] | 8.27 | 1 | 0 | 2 | 4 | 12.9991722 |
| Q9NZS6 | Glucocorticoid receptor AF-1 specific elongation factor (Fragment) OS=Homo sapiens PE=1 SV=1 - [Q9NZS6_HUMAN] | 8.22 | 1 | 0 | 2 | 4 | 15.778218 |
| A1Z5I7 | Mediator of DNA damage checkpoint 1 variant 3 (Fragment) OS=Homo sapiens GN=MDC1 PE=2 SV=1 - [A1Z5I7_HUMAN] | 8.16 | 1 | 0 | 2 | 4 | 11.9240119 |
| A1Z5I6 | Mediator of DNA damage checkpoint 1 variant 2 (Fragment) OS=Homo sapiens GN=MDC1 PE=2 SV=1 - [A1Z5I6_HUMAN] | 8.16 | 1 | 0 | 2 | 4 | 11.9240119 |
| Q53G89 | Eukaryotic translation elongation factor 1 alpha 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53G89_HUMAN] | 8.08 | 1 | 0 | 2 | 4 | 15.778218 |
| Q6IQ15 | EEF1A1 protein OS=Homo sapiens GN=EEF1A1 PE=2 SV=1 - [Q6IQ15_HUMAN] | 7.94 | 1 | 0 | 2 | 4 | 15.778218 |
| P68104 | Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 - [EF1A1_HUMAN] | 7.58 | 1 | 0 | 2 | 4 | 15.778218 |
| Q5VTE0 | Putative elongation factor 1-alpha-like 3 OS=Homo sapiens GN=EEF1A1L3 PE=5 SV=1 - [EF1A3_HUMAN] | 7.58 | 1 | 0 | 2 | 4 | 15.778218 |
| Q53HM9 | Eukaryotic translation elongation factor 1 alpha 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53HM9_HUMAN] | 7.58 | 1 | 0 | 2 | 4 | 15.778218 |
| Q6IPT9 | Eukaryotic translation elongation factor 1 alpha 1 OS=Homo sapiens GN=EEF1A1 PE=2 SV=1 - [Q6IPT9_HUMAN] | 7.58 | 1 | 0 | 2 | 4 | 15.778218 |
| Q6IPN6 | Eukaryotic translation elongation factor 1 alpha 1 OS=Homo sapiens GN=EEF1A1 PE=2 SV=1 - [Q6IPN6_HUMAN] | 7.58 | 1 | 0 | 2 | 4 | 15.778218 |
| Q53HR5 | Eukaryotic translation elongation factor 1 alpha 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53HR5_HUMAN] | 7.58 | 1 | 0 | 2 | 4 | 15.778218 |
| Q53GE9 | Eukaryotic translation elongation factor 1 alpha 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53GE9_HUMAN] | 7.58 | 1 | 0 | 2 | 4 | 15.778218 |

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| Q53HQ7 | Eukaryotic translation elongation factor 1 alpha 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53HQ7_HUMAN] | 7.58 | 1 | 0 | 2 | 4 | 15.778218 |
| A8K9C4 | cDNA FLJ76726, highly similar to Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K9C4_HUMAN] | 7.58 | 1 | 0 | 2 | 4 | 15.778218 |
| Q53G85 | Eukaryotic translation elongation factor 1 alpha 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53G85_HUMAN] | 7.58 | 1 | 0 | 2 | 4 | 15.778218 |
| B2RCV1 | cDNA, FLJ96310, highly similar to Homo sapiens solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 (SLC25A5), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RCV1_HUMAN] | 7.38 | 1 | 0 | 2 | 4 | 9.98579311 |
| B2R6A5 | cDNA, FLJ92862, highly similar to Homo sapiens solute carrier family 16 (monocarboxylic acid transporters), member 1 (SLC16A1), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R6A5_HUMAN] | 6.6 | 1 | 0 | 2 | 4 | 13.0921607 |
| B3KX35 | cDNA FLJ44610 fis, clone BRACE2012317, highly similar to Sodium/potassium-transporting ATPase alpha-2 chain (EC 3.6.3.9) OS=Homo sapiens PE=2 SV=1 - [B3KX35_HUMAN] | 6.26 | 1 | 0 | 2 | 4 | 13.8620865 |
| B1AKZ0 | ATPase, Na ⁺ /K ⁺ transporting, alpha 2 (+) polypeptide (Fragment) OS=Homo sapiens GN=ATP1A2 PE=1 SV=1 - [B1AKZ0_HUMAN] | 5.75 | 1 | 0 | 2 | 4 | 13.8620865 |
| B4DIQ8 | cDNA FLJ56089, highly similar to Sodium/potassium-transporting ATPase alpha-2 chain (EC 3.6.3.9) OS=Homo sapiens PE=2 SV=1 - [B4DIQ8_HUMAN] | 5.67 | 1 | 0 | 2 | 4 | 13.8620865 |
| D3DSF7 | SON DNA binding protein, isoform CRA_b OS=Homo sapiens GN=SON PE=4 SV=1 - [D3DSF7_HUMAN] | 4.64 | 1 | 0 | 2 | 4 | 13.6496329 |
| Q7Z3Z0 | Keratin, type I cytoskeletal 25 OS=Homo sapiens GN=KRT25 PE=1 SV=1 - [K1C25_HUMAN] | 4 | 1 | 0 | 2 | 4 | 10.4741163 |
| Q7Z3Y8 | Keratin, type I cytoskeletal 27 OS=Homo sapiens GN=KRT27 PE=1 SV=2 - [K1C27_HUMAN] | 3.92 | 1 | 0 | 2 | 4 | 10.4741163 |
| Q7Z3Y7 | Keratin, type I cytoskeletal 28 OS=Homo sapiens GN=KRT28 PE=1 SV=2 - [K1C28_HUMAN] | 3.88 | 1 | 0 | 2 | 4 | 10.4741163 |
| B3KSY7 | cDNA FLJ37309 fis, clone BRAMY2016611, highly similar to Sodium/potassium-transporting ATPase alpha-3 chain (EC | 6.11 | 1 | 0 | 2 | 3 | 11.2896755 |

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| | 3.6.3.9) OS=Homo sapiens PE=2 SV=1 - [B3KSY7_HUMAN] | | | | | | |
| B4DRW1 | cdDNA FLJ55805, highly similar to Keratin, type II cytoskeletal 4 OS=Homo sapiens PE=2 SV=1 - [B4DRW1_HUMAN] | 4.01 | 1 | 0 | 2 | 3 | 7.34120798 |
| B4DRR7 | cdDNA FLJ59399, highly similar to Keratin, type II cytoskeletal 4 OS=Homo sapiens PE=2 SV=1 - [B4DRR7_HUMAN] | 3.79 | 1 | 0 | 2 | 3 | 7.34120798 |
| B4DKJ0 | cdDNA FLJ58539, highly similar to Keratin, type II cytoskeletal 4 OS=Homo sapiens PE=2 SV=1 - [B4DKJ0_HUMAN] | 3.73 | 1 | 0 | 2 | 3 | 7.34120798 |
| B4DRS2 | cdDNA FLJ58275, highly similar to Keratin, type II cytoskeletal 4 OS=Homo sapiens PE=2 SV=1 - [B4DRS2_HUMAN] | 3.65 | 1 | 0 | 2 | 3 | 7.34120798 |
| P19013 | Keratin, type II cytoskeletal 4 OS=Homo sapiens GN=KRT4 PE=1 SV=4 - [K2C4_HUMAN] | 3.56 | 1 | 0 | 2 | 3 | 7.34120798 |
| Q13733 | Sodium/potassium-transporting ATPase subunit alpha-4 OS=Homo sapiens GN=ATP1A4 PE=1 SV=3 - [AT1A4_HUMAN] | 3.3 | 1 | 0 | 2 | 3 | 8.46366692 |
| C9J8M9 | Uncharacterized protein OS=Homo sapiens GN=RGPD8 PE=4 SV=1 - [C9J8M9_HUMAN] | 2.54 | 1 | 0 | 2 | 3 | 8.65850425 |
| Q99666 | RANBP2-like and GRIP domain-containing protein 5/6 OS=Homo sapiens GN=RGPD5 PE=1 SV=3 - [RGPD5_HUMAN] | 1.3 | 1 | 0 | 2 | 3 | 8.65850425 |
| O14715 | RANBP2-like and GRIP domain-containing protein 8 OS=Homo sapiens GN=RGPD8 PE=1 SV=2 - [RGPD8_HUMAN] | 1.3 | 1 | 0 | 2 | 3 | 8.65850425 |
| C9JIQ8 | Uncharacterized protein OS=Homo sapiens GN=EP400 PE=4 SV=1 - [C9JIQ8_HUMAN] | 1.07 | 1 | 0 | 2 | 3 | 9.53273821 |
| A6NJX1 | Uncharacterized protein OS=Homo sapiens GN=EP400 PE=4 SV=2 - [A6NJX1_HUMAN] | 1.06 | 1 | 0 | 2 | 3 | 9.53273821 |
| A8MSW4 | Uncharacterized protein OS=Homo sapiens GN=EP400 PE=4 SV=1 - [A8MSW4_HUMAN] | 1.06 | 1 | 0 | 2 | 3 | 9.53273821 |
| Q96L91 | E1A-binding protein p400 OS=Homo sapiens GN=EP400 PE=1 SV=4 - [EP400_HUMAN] | 1.04 | 1 | 0 | 2 | 3 | 9.53273821 |
| Q96KK5 | Histone H2A type 1-H OS=Homo sapiens GN=HIST1H2AH PE=1 SV=3 - [H2A1H_HUMAN] | 21.88 | 1 | 0 | 2 | 2 | 5.12635374 |
| Q99878 | Histone H2A type 1-J OS=Homo sapiens GN=HIST1H2AJ PE=1 SV=3 - [H2A1J_HUMAN] | 21.88 | 1 | 0 | 2 | 2 | 5.12635374 |
| Q16777 | Histone H2A type 2-C OS=Homo sapiens GN=HIST2H2AC PE=1 SV=4 - [H2A2C_HUMAN] | 21.71 | 1 | 0 | 2 | 2 | 5.12635374 |

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| Q9BTM1 | Histone H2A.J OS=Homo sapiens GN=H2AFJ PE=1 SV=1 - [H2AJ_HUMAN] | 21.71 | 1 | 0 | 2 | 2 | 5.12635374 |
| P0C0S8 | Histone H2A type 1 OS=Homo sapiens GN=HIST1H2AG PE=1 SV=2 - [H2A1_HUMAN] | 21.54 | 1 | 0 | 2 | 2 | 5.12635374 |
| Q7L7L0 | Histone H2A type 3 OS=Homo sapiens GN=HIST3H2A PE=1 SV=3 - [H2A3_HUMAN] | 21.54 | 1 | 0 | 2 | 2 | 5.12635374 |
| P04908 | Histone H2A type 1-B/E OS=Homo sapiens GN=HIST1H2AB PE=1 SV=2 - [H2A1B_HUMAN] | 21.54 | 1 | 0 | 2 | 2 | 5.12635374 |
| Q93077 | Histone H2A type 1-C OS=Homo sapiens GN=HIST1H2AC PE=1 SV=3 - [H2A1C_HUMAN] | 21.54 | 1 | 0 | 2 | 2 | 5.12635374 |
| P20671 | Histone H2A type 1-D OS=Homo sapiens GN=HIST1H2AD PE=1 SV=2 - [H2A1D_HUMAN] | 21.54 | 1 | 0 | 2 | 2 | 5.12635374 |
| Q6FI13 | Histone H2A type 2-A OS=Homo sapiens GN=HIST2H2AA3 PE=1 SV=3 - [H2A2A_HUMAN] | 21.54 | 1 | 0 | 2 | 2 | 5.12635374 |
| B2R5B3 | cDNA, FLJ92406, highly similar to Homo sapiens histone 1, H2ag (HIST1H2AG), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R5B3_HUMAN] | 21.54 | 1 | 0 | 2 | 2 | 5.12635374 |
| Q5HY89 | Filamin A, alpha (Actin binding protein 280) (Fragment) OS=Homo sapiens GN=FLNA PE=2 SV=1 - [Q5HY89_HUMAN] | 16.45 | 1 | 0 | 2 | 2 | 7.28127456 |
| Q6NXF2 | FLNA protein (Fragment) OS=Homo sapiens GN=FLNA PE=2 SV=1 - [Q6NXF2_HUMAN] | 3.87 | 1 | 0 | 2 | 2 | 7.28127456 |
| B7Z3E7 | cDNA FLJ56510, highly similar to Tumor suppressor p53-binding protein 1 OS=Homo sapiens PE=2 SV=1 - [B7Z3E7_HUMAN] | 2.33 | 1 | 0 | 2 | 2 | 6.59569573 |
| A6NNK5 | Uncharacterized protein OS=Homo sapiens GN=TP53BP1 PE=4 SV=2 - [A6NNK5_HUMAN] | 2.13 | 1 | 0 | 2 | 2 | 6.59569573 |
| Q12888 | Tumor suppressor p53-binding protein 1 OS=Homo sapiens GN=TP53BP1 PE=1 SV=2 - [TP53B_HUMAN] | 2.08 | 1 | 0 | 2 | 2 | 6.59569573 |
| Q59FH1 | Transformation/transcription domain-associated protein variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59FH1_HUMAN] | 1.06 | 1 | 0 | 2 | 2 | 6.12586331 |
| Q9Y4A5 | Transformation/transcription domain-associated protein OS=Homo sapiens GN=TRRAP PE=1 SV=3 - [TRRAP_HUMAN] | 0.98 | 1 | 0 | 2 | 2 | 6.12586331 |
| Q14789 | Golgin subfamily B member 1 OS=Homo sapiens GN=GOLGB1 PE=1 SV=2 - [G0GB1_HUMAN] | 0.8 | 1 | 0 | 2 | 2 | 5.58100152 |
| B2ZZ91 | Golgin B1 OS=Homo sapiens GN=GOLGB1 PE=2 SV=1 - | 0.8 | 1 | 0 | 2 | 2 | 5.58100152 |

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|--|----------------|--|--|--|--|--|--|
| | [B2ZZ91_HUMAN] | | | | | | |
|--|----------------|--|--|--|--|--|--|

Protein ID05.msf

| Accession | Description | Σ Coverage | Σ # Proteins | Σ # Unique Peptides | Σ # Peptides | Σ # PSMs | Score A3 |
|-----------|---------------------------------------------------------------------------------------------------|-------------------|---------------------|----------------------------|---------------------|-----------------|------------|
| P04264 | Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6 - [K2C1_HUMAN] | 44.72 | 1 | 25 | 27 | 96 | 383.313886 |
| P13645 | Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6 - [K1C10_HUMAN] | 52.23 | 1 | 21 | 23 | 71 | 282.793497 |
| P35527 | Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3 - [K1C9_HUMAN] | 42.54 | 1 | 13 | 13 | 30 | 130.36068 |
| P35908 | Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2 - [K22E_HUMAN] | 41.63 | 1 | 12 | 17 | 32 | 122.643323 |
| P02533 | Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4 - [K1C14_HUMAN] | 12.5 | 1 | 2 | 4 | 6 | 19.9560161 |
| P07339 | Cathepsin D OS=Homo sapiens GN=CTSD PE=1 SV=1 - [CATD_HUMAN] | 7.28 | 1 | 2 | 3 | 5 | 12.7856759 |
| P78527 | DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3 - [PRKDC_HUMAN] | 0.94 | 1 | 2 | 3 | 3 | 8.71859932 |
| P13647 | Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3 - [K2C5_HUMAN] | 12.03 | 1 | 1 | 7 | 10 | 31.7739744 |
| Q60FE6 | Filamin A OS=Homo sapiens GN=FLNA PE=2 SV=1 - [Q60FE6_HUMAN] | 4.79 | 1 | 0 | 8 | 13 | 47.9343114 |
| Q5HY54 | Filamin A, alpha (Actin binding protein 280) OS=Homo sapiens GN=FLNA PE=2 SV=1 - [Q5HY54_HUMAN] | 4.79 | 1 | 0 | 8 | 13 | 47.9343114 |
| Q60FE5 | Filamin A OS=Homo sapiens GN=FLNA PE=2 SV=1 - [Q60FE5_HUMAN] | 4.77 | 1 | 0 | 8 | 13 | 47.9343114 |
| P21333 | Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4 - [FLNA_HUMAN] | 4.72 | 1 | 0 | 8 | 13 | 47.9343114 |
| P08779 | Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4 - [K1C16_HUMAN] | 12.05 | 1 | 0 | 7 | 14 | 33.8673677 |
| B2ZZ80 | Filamin A OS=Homo sapiens GN=FLNA PE=2 SV=1 - [B2ZZ80_HUMAN] | 4.79 | 1 | 0 | 7 | 11 | 41.6355247 |
| A6NDY9 | Uncharacterized protein OS=Homo sapiens GN=FLNA PE=4 SV=3 | 4.79 | 1 | 0 | 7 | 11 | 41.6355247 |

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|--------|--------------------------------------------------------------------------------------------------------------------|-------|---|---|---|----|------------|
| | - [A6NDY9_HUMAN] | | | | | | |
| B4DRR0 | cDNA FLJ53910, highly similar to Keratin, type II cytoskeletal 6A OS=Homo sapiens PE=2 SV=1 - [B4DRR0_HUMAN] | 11.59 | 1 | 0 | 6 | 10 | 32.5541446 |
| P02538 | Keratin, type II cytoskeletal 6A OS=Homo sapiens GN=KRT6A PE=1 SV=3 - [K2C6A_HUMAN] | 10.99 | 1 | 0 | 6 | 10 | 32.5541446 |
| P04259 | Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5 - [K2C6B_HUMAN] | 10.99 | 1 | 0 | 6 | 10 | 32.5541446 |
| P48668 | Keratin, type II cytoskeletal 6C OS=Homo sapiens GN=KRT6C PE=1 SV=3 - [K2C6C_HUMAN] | 10.99 | 1 | 0 | 6 | 10 | 32.5541446 |
| B2R853 | cDNA, FLJ93744, highly similar to Homo sapiens keratin 6E (KRT6E), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R853_HUMAN] | 10.99 | 1 | 0 | 6 | 10 | 32.5541446 |
| A8K2I0 | cDNA FLJ78504, highly similar to Homo sapiens keratin 6A (KRT6A), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K2I0_HUMAN] | 10.99 | 1 | 0 | 6 | 10 | 32.5541446 |
| B4E1T1 | cDNA FLJ54081, highly similar to Keratin, type II cytoskeletal 5 OS=Homo sapiens PE=2 SV=1 - [B4E1T1_HUMAN] | 10.81 | 1 | 0 | 6 | 9 | 28.7219062 |
| B4DWU0 | cDNA FLJ56791, highly similar to Keratin, type I cytoskeletal 16 OS=Homo sapiens PE=2 SV=1 - [B4DWU0_HUMAN] | 27.41 | 1 | 0 | 5 | 12 | 29.084065 |
| B4E2J5 | cDNA FLJ53570, highly similar to Keratin, type I cytoskeletal 16 OS=Homo sapiens PE=2 SV=1 - [B4E2J5_HUMAN] | 19.68 | 1 | 0 | 5 | 12 | 29.084065 |
| E0CX14 | Uncharacterized protein OS=Homo sapiens GN=KRT15 PE=4 SV=1 - [E0CX14_HUMAN] | 8.13 | 1 | 0 | 5 | 12 | 29.084065 |
| P19012 | Keratin, type I cytoskeletal 15 OS=Homo sapiens GN=KRT15 PE=1 SV=3 - [K1C15_HUMAN] | 8.11 | 1 | 0 | 5 | 12 | 29.084065 |
| B4E2P9 | cDNA FLJ56708, highly similar to Keratin, type I cytoskeletal 17 OS=Homo sapiens PE=2 SV=1 - [B4E2P9_HUMAN] | 27.33 | 1 | 0 | 5 | 10 | 23.214287 |
| B4DWU6 | cDNA FLJ51361, highly similar to Keratin, type II cytoskeletal 6A OS=Homo sapiens PE=2 SV=1 - [B4DWU6_HUMAN] | 10.19 | 1 | 0 | 5 | 9 | 29.5758414 |
| B4DL32 | cDNA FLJ59922, highly similar to Keratin, type II cytoskeletal 5 OS=Homo sapiens PE=2 SV=1 - [B4DL32_HUMAN] | 22.22 | 1 | 0 | 5 | 8 | 25.6429708 |
| B4DRU6 | cDNA FLJ54657, highly similar to Keratin, type II cytoskeletal 6A OS=Homo sapiens PE=2 SV=1 - [B4DRU6_HUMAN] | 9.11 | 1 | 0 | 5 | 8 | 25.6537664 |

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|--------|-----------------------------------------------------------------------------------------------------------------------------------------|-------|---|---|---|----|------------|
| Q8TES4 | FLJ00119 protein (Fragment) OS=Homo sapiens GN=FLJ00119 PE=2 SV=1 - [Q8TES4_HUMAN] | 5.5 | 1 | 0 | 5 | 8 | 29.0116401 |
| B4DRY0 | cDNA FLJ54379, highly similar to Keratin, type II cytoskeletal 6E OS=Homo sapiens PE=2 SV=1 - [B4DRY0_HUMAN] | 9.51 | 1 | 0 | 5 | 7 | 22.8154421 |
| C9JM50 | Uncharacterized protein OS=Homo sapiens GN=KRT19 PE=4 SV=1 - [C9JM50_HUMAN] | 12.76 | 1 | 0 | 4 | 10 | 22.7874494 |
| B4E204 | cDNA FLJ58872, highly similar to Keratin, type I cytoskeletal 15 OS=Homo sapiens PE=2 SV=1 - [B4E204_HUMAN] | 11.97 | 1 | 0 | 4 | 10 | 23.7526751 |
| C9JH30 | Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [C9JH30_HUMAN] | 7.16 | 1 | 0 | 4 | 10 | 25.4765577 |
| A8MW45 | Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [A8MW45_HUMAN] | 7.03 | 1 | 0 | 4 | 10 | 25.4765577 |
| P08727 | Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=4 - [K1C19_HUMAN] | 6.25 | 1 | 0 | 4 | 10 | 22.7874494 |
| B4DKV4 | cDNA FLJ60647, highly similar to Keratin, type II cytoskeletal 6B OS=Homo sapiens PE=2 SV=1 - [B4DKV4_HUMAN] | 7.6 | 1 | 0 | 4 | 5 | 15.9150639 |
| Q7RTS7 | Keratin, type II cytoskeletal 74 OS=Homo sapiens GN=KRT74 PE=1 SV=2 - [K2C74_HUMAN] | 5.67 | 1 | 0 | 3 | 9 | 21.7720134 |
| Q86Y46 | Keratin, type II cytoskeletal 73 OS=Homo sapiens GN=KRT73 PE=1 SV=1 - [K2C73_HUMAN] | 5.56 | 1 | 0 | 3 | 9 | 21.7720134 |
| C9JA77 | Uncharacterized protein OS=Homo sapiens GN=KRT13 PE=4 SV=1 - [C9JA77_HUMAN] | 6.76 | 1 | 0 | 3 | 6 | 19.4722464 |
| P13646 | Keratin, type I cytoskeletal 13 OS=Homo sapiens GN=KRT13 PE=1 SV=4 - [K1C13_HUMAN] | 5.24 | 1 | 0 | 3 | 6 | 19.4722464 |
| A1A4E9 | Keratin 13 OS=Homo sapiens GN=KRT13 PE=2 SV=1 - [A1A4E9_HUMAN] | 5.24 | 1 | 0 | 3 | 6 | 19.4722464 |
| A8K2H9 | cDNA FLJ78503, highly similar to Homo sapiens keratin 13 (KRT13), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1 - [A8K2H9_HUMAN] | 5.24 | 1 | 0 | 3 | 6 | 19.4722464 |
| Q86YZ3 | Hornerin OS=Homo sapiens GN=HRNR PE=1 SV=2 - [HORN_HUMAN] | 4.98 | 1 | 0 | 3 | 6 | 22.2381661 |
| Q5DT20 | Hornerin OS=Homo sapiens GN=HRNR PE=2 SV=1 - [Q5DT20_HUMAN] | 4.98 | 1 | 0 | 3 | 6 | 22.2381661 |
| P27816 | Microtubule-associated protein 4 OS=Homo sapiens GN=MAP4 | 3.39 | 1 | 0 | 3 | 6 | 20.1557591 |

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|--------|-------------------------------------------------------------------------------------------------------------------------------------|-------|---|---|---|---|------------|
| | PE=1 SV=3 - [MAP4_HUMAN] | | | | | | |
| Q14666 | Radiated keratinocyte mRNA 266 (keratin-related protein) (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q14666_HUMAN] | 11.28 | 1 | 0 | 3 | 6 | 15.9497607 |
| B3KVF5 | cDNA FLJ16494 fis, clone CTONG3004576, highly similar to Keratin, type I cytoskeletal 15 OS=Homo sapiens PE=2 SV=1 - [B3KVF5_HUMAN] | 6.14 | 1 | 0 | 3 | 6 | 15.5444925 |
| Q7Z3Y7 | Keratin, type I cytoskeletal 28 OS=Homo sapiens GN=KRT28 PE=1 SV=2 - [K1C28_HUMAN] | 5.39 | 1 | 0 | 3 | 6 | 13.6443207 |
| Q01546 | Keratin, type II cytoskeletal 2 oral OS=Homo sapiens GN=KRT76 PE=1 SV=2 - [K22O_HUMAN] | 4.55 | 1 | 0 | 3 | 5 | 16.3589897 |
| B4DSI9 | cDNA FLJ56483, highly similar to Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens PE=2 SV=1 - [B4DSI9_HUMAN] | 1.79 | 1 | 0 | 3 | 5 | 10.55547 |
| B4DGF1 | cDNA FLJ56479, highly similar to Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens PE=2 SV=1 - [B4DGF1_HUMAN] | 1.72 | 1 | 0 | 3 | 5 | 10.55547 |
| Q04637 | Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=4 - [IF4G1_HUMAN] | 1.69 | 1 | 0 | 3 | 5 | 10.55547 |
| D3DNT2 | Eukaryotic translation initiation factor 4 gamma, 1, isoform CRA_c OS=Homo sapiens GN=EIF4G1 PE=4 SV=1 - [D3DNT2_HUMAN] | 1.69 | 1 | 0 | 3 | 5 | 10.55547 |
| B2RU06 | EIF4G1 protein OS=Homo sapiens GN=EIF4G1 PE=2 SV=1 - [B2RU06_HUMAN] | 1.68 | 1 | 0 | 3 | 5 | 10.55547 |
| B2RU10 | EIF4G1 protein OS=Homo sapiens GN=EIF4G1 PE=2 SV=1 - [B2RU10_HUMAN] | 1.68 | 1 | 0 | 3 | 5 | 10.55547 |
| Q4LE58 | EIF4G1 variant protein (Fragment) OS=Homo sapiens GN=EIF4G1 variant protein PE=2 SV=1 - [Q4LE58_HUMAN] | 1.66 | 1 | 0 | 3 | 5 | 10.55547 |
| O95678 | Keratin, type II cytoskeletal 75 OS=Homo sapiens GN=KRT75 PE=1 SV=2 - [K2C75_HUMAN] | 5.81 | 1 | 0 | 3 | 4 | 12.8361285 |
| Q5XKE5 | Keratin, type II cytoskeletal 79 OS=Homo sapiens GN=KRT79 PE=1 SV=2 - [K2C79_HUMAN] | 5.79 | 1 | 0 | 3 | 4 | 12.9367607 |
| P06702 | Protein S100-A9 OS=Homo sapiens GN=S100A9 PE=1 SV=1 - [S10A9_HUMAN] | 31.58 | 1 | 0 | 3 | 4 | 9.88064504 |

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|---------|----------------------------------------------------------------------------------------------------------------------------------------------------------|-------|---|---|---|---|------------|
| B2R4M6 | cDNA, FLJ92148, highly similar to Homo sapiens S100 calcium binding protein A9 (calgranulin B) (S100A9), mRNA OS=Homo sapiens PE=4 SV=1 - [B2R4M6_HUMAN] | 31.58 | 1 | 0 | 3 | 4 | 9.88064504 |
| B4DM10 | cDNA FLJ58263, highly similar to Microtubule-associated protein 4 OS=Homo sapiens PE=2 SV=1 - [B4DM10_HUMAN] | 5.27 | 1 | 0 | 3 | 4 | 11.9650292 |
| Q6NXF2 | FLNA protein (Fragment) OS=Homo sapiens GN=FLNA PE=2 SV=1 - [Q6NXF2_HUMAN] | 3.97 | 1 | 0 | 3 | 4 | 11.5994151 |
| Q8IUUK7 | ALB protein OS=Homo sapiens PE=2 SV=1 - [Q8IUUK7_HUMAN] | 3.79 | 1 | 0 | 2 | 6 | 21.8046372 |
| C9JKR2 | Albumin, isoform CRA_k OS=Homo sapiens GN=ALB PE=4 SV=1 - [C9JKR2_HUMAN] | 3.6 | 1 | 0 | 2 | 6 | 21.8046372 |
| D6RHD5 | Uncharacterized protein OS=Homo sapiens GN=ALB PE=4 SV=1 - [D6RHD5_HUMAN] | 3.27 | 1 | 0 | 2 | 6 | 21.8046372 |
| B7WNR0 | Uncharacterized protein OS=Homo sapiens GN=ALB PE=4 SV=1 - [B7WNR0_HUMAN] | 3.04 | 1 | 0 | 2 | 6 | 21.8046372 |
| B4DPR2 | cDNA FLJ50830, highly similar to Serum albumin OS=Homo sapiens PE=2 SV=1 - [B4DPR2_HUMAN] | 2.87 | 1 | 0 | 2 | 6 | 21.8046372 |
| A8K9P0 | cDNA FLJ78413, highly similar to Homo sapiens albumin, mRNA OS=Homo sapiens PE=2 SV=1 - [A8K9P0_HUMAN] | 2.47 | 1 | 0 | 2 | 6 | 21.8046372 |
| P02768 | Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2 - [ALBU_HUMAN] | 2.46 | 1 | 0 | 2 | 6 | 21.8046372 |
| Q56G89 | Serum albumin OS=Homo sapiens PE=2 SV=1 - [Q56G89_HUMAN] | 2.46 | 1 | 0 | 2 | 6 | 21.8046372 |
| B2RBS8 | cDNA, FLJ95666, highly similar to Homo sapiens albumin (ALB), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RBS8_HUMAN] | 2.46 | 1 | 0 | 2 | 6 | 21.8046372 |
| B4DPP6 | cDNA FLJ54371, highly similar to Serum albumin OS=Homo sapiens PE=2 SV=1 - [B4DPP6_HUMAN] | 2.43 | 1 | 0 | 2 | 6 | 21.8046372 |
| A6NBZ8 | Uncharacterized protein OS=Homo sapiens GN=ALB PE=4 SV=2 - [A6NBZ8_HUMAN] | 2.39 | 1 | 0 | 2 | 6 | 21.8046372 |
| Q96C32 | UBC protein OS=Homo sapiens PE=2 SV=1 - [Q96C32_HUMAN] | 38.03 | 1 | 0 | 2 | 4 | 14.8975017 |
| P0CG47 | Polyubiquitin-B OS=Homo sapiens GN=UBB PE=1 SV=1 - [UBB_HUMAN] | 37.99 | 1 | 0 | 2 | 4 | 14.8975017 |
| Q5PY61 | Ubiquitin C splice variant OS=Homo sapiens GN=UBC PE=2 SV=1 - [Q5PY61_HUMAN] | 37.99 | 1 | 0 | 2 | 4 | 14.8975017 |

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|--------|-----------------------------------------------------------------------------------------------------------------------|-------|---|---|---|---|------------|
| Q5UGI3 | Ubiquitin C splice variant OS=Homo sapiens GN=UBC PE=2 SV=1 - [Q5UGI3_HUMAN] | 37.91 | 1 | 0 | 2 | 4 | 14.8975017 |
| B4DV12 | cDNA FLJ51326, highly similar to Homo sapiens ubiquitin B (UBB), mRNA OS=Homo sapiens PE=2 SV=1 - [B4DV12_HUMAN] | 37.91 | 1 | 0 | 2 | 4 | 14.8975017 |
| Q59EM9 | Ubiquitin C variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59EM9_HUMAN] | 37.66 | 1 | 0 | 2 | 4 | 14.8975017 |
| Q66K58 | Putative uncharacterized protein (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q66K58_HUMAN] | 37.39 | 1 | 0 | 2 | 4 | 14.8975017 |
| Q96H31 | UBC protein (Fragment) OS=Homo sapiens GN=UBC PE=2 SV=2 - [Q96H31_HUMAN] | 37.18 | 1 | 0 | 2 | 4 | 14.8975017 |
| Q96MH4 | cDNA FLJ32377 fis, clone SKMUS1000014, highly similar to Polyubiquitin 9 OS=Homo sapiens PE=2 SV=1 - [Q96MH4_HUMAN] | 36.6 | 1 | 0 | 2 | 4 | 14.8975017 |
| Q9UFQ0 | Putative uncharacterized protein DKFZp434K0435 (Fragment) OS=Homo sapiens GN=DKFZp434K0435 PE=2 SV=1 - [Q9UFQ0_HUMAN] | 36.4 | 1 | 0 | 2 | 4 | 14.8975017 |
| P0CG48 | Polyubiquitin-C OS=Homo sapiens GN=UBC PE=1 SV=2 - [UBC_HUMAN] | 36.2 | 1 | 0 | 2 | 4 | 14.8975017 |
| A8K674 | cDNA FLJ75516, highly similar to Xenopus tropicalis ubiquitin C, mRNA OS=Homo sapiens PE=2 SV=1 - [A8K674_HUMAN] | 35.47 | 1 | 0 | 2 | 4 | 14.8975017 |
| Q49A90 | RPS27A protein OS=Homo sapiens GN=RPS27A PE=4 SV=1 - [Q49A90_HUMAN] | 30.53 | 1 | 0 | 2 | 4 | 14.8975017 |
| P62987 | Ubiquitin-60S ribosomal protein L40 OS=Homo sapiens GN=UBA52 PE=1 SV=2 - [RL40_HUMAN] | 22.66 | 1 | 0 | 2 | 4 | 14.8975017 |
| P62979 | Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=1 SV=2 - [RS27A_HUMAN] | 18.59 | 1 | 0 | 2 | 4 | 14.8975017 |
| Q5RKT7 | Ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=2 SV=1 - [Q5RKT7_HUMAN] | 18.59 | 1 | 0 | 2 | 4 | 14.8975017 |
| B5MEG9 | Uncharacterized protein OS=Homo sapiens GN=MAP4 PE=4 SV=2 - [B5MEG9_HUMAN] | 3.65 | 1 | 0 | 2 | 4 | 12.4896595 |
| C9JFC3 | Uncharacterized protein OS=Homo sapiens GN=MAP4 PE=4 SV=1 - [C9JFC3_HUMAN] | 3.21 | 1 | 0 | 2 | 4 | 12.4896595 |
| P12035 | Keratin, type II cytoskeletal 3 OS=Homo sapiens GN=KRT3 PE=1 SV=3 - [K2C3_HUMAN] | 3.18 | 1 | 0 | 2 | 4 | 13.3806865 |

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|--------|------------------------------------------------------------------------------------|------|---|---|---|---|------------|
| B9ZVR1 | Uncharacterized protein OS=Homo sapiens GN=MAP4 PE=4 SV=2 - [B9ZVR1_HUMAN] | 3.18 | 1 | 0 | 2 | 4 | 12.4896595 |
| Q86Y04 | MAP4 protein (Fragment) OS=Homo sapiens GN=MAP4 PE=1 SV=1 - [Q86Y04_HUMAN] | 3.03 | 1 | 0 | 2 | 4 | 12.4896595 |
| Q04695 | Keratin, type I cytoskeletal 17 OS=Homo sapiens GN=KRT17 PE=1 SV=2 - [K1C17_HUMAN] | 7.41 | 1 | 0 | 2 | 3 | 9.77840018 |

Protein ID06.msf

| Accession | Description | Σ Coverage | Σ # Proteins | Σ # Unique Peptides | Σ # Peptides | Σ # PSMs | Score A3 |
|-----------|-------------------------------------------------------------------------------------------------------------------|-------------------|---------------------|----------------------------|---------------------|-----------------|------------|
| P04264 | Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6 - [K2C1_HUMAN] | 33.39 | 1 | 14 | 15 | 33 | 142.653161 |
| P13645 | Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6 - [K1C10_HUMAN] | 35.27 | 1 | 12 | 12 | 31 | 127.176213 |
| P35527 | Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3 - [K1C9_HUMAN] | 33.55 | 1 | 9 | 9 | 19 | 85.1466668 |
| P35908 | Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2 - [K22E_HUMAN] | 27.07 | 1 | 8 | 8 | 18 | 82.4768212 |
| P13647 | Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3 - [K2C5_HUMAN] | 24.92 | 1 | 3 | 14 | 30 | 78.7870923 |
| P02533 | Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4 - [K1C14_HUMAN] | 9.96 | 1 | 2 | 3 | 8 | 30.1062145 |
| B4E1T1 | cDNA FLJ54081, highly similar to Keratin, type II cytoskeletal 5 OS=Homo sapiens PE=2 SV=1 - [B4E1T1_HUMAN] | 20 | 1 | 0 | 11 | 25 | 65.5137757 |
| B4DRR0 | cDNA FLJ53910, highly similar to Keratin, type II cytoskeletal 6A OS=Homo sapiens PE=2 SV=1 - [B4DRR0_HUMAN] | 18.88 | 1 | 0 | 10 | 24 | 64.2256237 |
| P02538 | Keratin, type II cytoskeletal 6A OS=Homo sapiens GN=KRT6A PE=1 SV=3 - [K2C6A_HUMAN] | 17.91 | 1 | 0 | 10 | 24 | 64.2256237 |
| A8K2I0 | cDNA FLJ78504, highly similar to Homo sapiens keratin 6A (KRT6A), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K2I0_HUMAN] | 17.91 | 1 | 0 | 10 | 24 | 64.2256237 |
| P04259 | Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5 - [K2C6B_HUMAN] | 16.31 | 1 | 0 | 9 | 24 | 65.262967 |
| B4DRU6 | cDNA FLJ54657, highly similar to Keratin, type II cytoskeletal 6A OS=Homo sapiens PE=2 SV=1 - [B4DRU6_HUMAN] | 16.21 | 1 | 0 | 9 | 22 | 57.8662928 |
| P48668 | Keratin, type II cytoskeletal 6C OS=Homo sapiens GN=KRT6C PE=1 SV=3 - [K2C6C_HUMAN] | 16.13 | 1 | 0 | 9 | 22 | 59.160499 |
| B4DWU6 | cDNA FLJ51361, highly similar to Keratin, type II cytoskeletal 6A OS=Homo sapiens PE=2 SV=1 - [B4DWU6_HUMAN] | 15.77 | 1 | 0 | 8 | 20 | 53.510918 |

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|--------|--------------------------------------------------------------------------------------------------------------------|-------|---|---|---|----|------------|
| B2R853 | cDNA, FLJ93744, highly similar to Homo sapiens keratin 6E (KRT6E), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R853_HUMAN] | 14.54 | 1 | 0 | 8 | 20 | 54.0616361 |
| B4DRY0 | cDNA FLJ54379, highly similar to Keratin, type II cytoskeletal 6E OS=Homo sapiens PE=2 SV=1 - [B4DRY0_HUMAN] | 13.16 | 1 | 0 | 7 | 15 | 40.3831033 |
| B4DKV4 | cDNA FLJ60647, highly similar to Keratin, type II cytoskeletal 6B OS=Homo sapiens PE=2 SV=1 - [B4DKV4_HUMAN] | 13.12 | 1 | 0 | 7 | 15 | 39.1226352 |
| B4DL32 | cDNA FLJ59922, highly similar to Keratin, type II cytoskeletal 5 OS=Homo sapiens PE=2 SV=1 - [B4DL32_HUMAN] | 26.07 | 1 | 0 | 6 | 16 | 42.4307858 |
| Q04695 | Keratin, type I cytoskeletal 17 OS=Homo sapiens GN=KRT17 PE=1 SV=2 - [K1C17_HUMAN] | 10.65 | 1 | 0 | 6 | 12 | 29.5411743 |
| P08779 | Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4 - [K1C16_HUMAN] | 12.47 | 1 | 0 | 6 | 11 | 27.5197226 |
| Q01546 | Keratin, type II cytoskeletal 2 oral OS=Homo sapiens GN=KRT76 PE=1 SV=2 - [K22O_HUMAN] | 7.37 | 1 | 0 | 5 | 15 | 39.9623477 |
| B4DWU0 | cDNA FLJ56791, highly similar to Keratin, type I cytoskeletal 16 OS=Homo sapiens PE=2 SV=1 - [B4DWU0_HUMAN] | 32.59 | 1 | 0 | 5 | 9 | 21.4071709 |
| B4E2J5 | cDNA FLJ53570, highly similar to Keratin, type I cytoskeletal 16 OS=Homo sapiens PE=2 SV=1 - [B4E2J5_HUMAN] | 23.4 | 1 | 0 | 5 | 9 | 21.4071709 |
| O95678 | Keratin, type II cytoskeletal 75 OS=Homo sapiens GN=KRT75 PE=1 SV=2 - [K2C75_HUMAN] | 7.44 | 1 | 0 | 4 | 9 | 23.0164608 |
| C9JM50 | Uncharacterized protein OS=Homo sapiens GN=KRT19 PE=4 SV=1 - [C9JM50_HUMAN] | 12.76 | 1 | 0 | 4 | 8 | 18.5573884 |
| C9JH30 | Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [C9JH30_HUMAN] | 7.16 | 1 | 0 | 4 | 8 | 21.3515708 |
| A8MW45 | Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [A8MW45_HUMAN] | 7.03 | 1 | 0 | 4 | 8 | 21.3515708 |
| P08727 | Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=4 - [K1C19_HUMAN] | 6.25 | 1 | 0 | 4 | 8 | 18.5573884 |
| B4DJT7 | cDNA FLJ56511, highly similar to Neurofilament triplet M protein OS=Homo sapiens PE=2 SV=1 - [B4DJT7_HUMAN] | 5.73 | 1 | 0 | 4 | 8 | 21.9463549 |
| E0CX14 | Uncharacterized protein OS=Homo sapiens GN=KRT15 PE=4 SV=1 - [E0CX14_HUMAN] | 5.49 | 1 | 0 | 4 | 8 | 18.5573884 |
| P19012 | Keratin, type I cytoskeletal 15 OS=Homo sapiens GN=KRT15 | 5.48 | 1 | 0 | 4 | 8 | 18.5573884 |

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|---------|----------------------------------------------------------------------------------------------------------------|-------|---|---|---|----|------------|
| | PE=1 SV=3 - [K1C15_HUMAN] | | | | | | |
| A5YM63 | NEFM protein OS=Homo sapiens GN=NEFM PE=2 SV=1 - [A5YM63_HUMAN] | 4.56 | 1 | 0 | 4 | 8 | 21.9463549 |
| P07197 | Neurofilament medium polypeptide OS=Homo sapiens GN=NEFM PE=1 SV=3 - [NFM_HUMAN] | 4.37 | 1 | 0 | 4 | 8 | 21.9463549 |
| P12035 | Keratin, type II cytoskeletal 3 OS=Homo sapiens GN=KRT3 PE=1 SV=3 - [K2C3_HUMAN] | 4.62 | 1 | 0 | 3 | 11 | 29.1209409 |
| Q5XKE5 | Keratin, type II cytoskeletal 79 OS=Homo sapiens GN=KRT79 PE=1 SV=2 - [K2C79_HUMAN] | 5.98 | 1 | 0 | 3 | 7 | 17.3668798 |
| P81605 | Dermcidin OS=Homo sapiens GN=DCD PE=1 SV=2 - [DCD_HUMAN] | 22.73 | 1 | 0 | 3 | 6 | 17.7037059 |
| A5JHP3 | Dermcidin isoform 2 OS=Homo sapiens GN=DCD PE=2 SV=1 - [A5JHP3_HUMAN] | 20.66 | 1 | 0 | 3 | 6 | 17.7037059 |
| Q14666 | Radiated keratinocyte mRNA 266 (keratin-related protein) (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q14666_HUMAN] | 11.28 | 1 | 0 | 3 | 6 | 16.0178442 |
| B4E2P9 | cDNA FLJ56708, highly similar to Keratin, type I cytoskeletal 17 OS=Homo sapiens PE=2 SV=1 - [B4E2P9_HUMAN] | 9.3 | 1 | 0 | 3 | 6 | 13.5233301 |
| B4E204 | cDNA FLJ58872, highly similar to Keratin, type I cytoskeletal 15 OS=Homo sapiens PE=2 SV=1 - [B4E204_HUMAN] | 6.84 | 1 | 0 | 3 | 6 | 13.5233301 |
| Q8IUUK7 | ALB protein OS=Homo sapiens PE=2 SV=1 - [Q8IUUK7_HUMAN] | 3.79 | 1 | 0 | 2 | 8 | 28.8103862 |
| C9JKR2 | Albumin, isoform CRA_k OS=Homo sapiens GN=ALB PE=4 SV=1 - [C9JKR2_HUMAN] | 3.6 | 1 | 0 | 2 | 8 | 28.8103862 |
| D6RHD5 | Uncharacterized protein OS=Homo sapiens GN=ALB PE=4 SV=1 - [D6RHD5_HUMAN] | 3.27 | 1 | 0 | 2 | 8 | 28.8103862 |
| B7WNRO | Uncharacterized protein OS=Homo sapiens GN=ALB PE=4 SV=1 - [B7WNRO_HUMAN] | 3.04 | 1 | 0 | 2 | 8 | 28.8103862 |
| B4DPR2 | cDNA FLJ50830, highly similar to Serum albumin OS=Homo sapiens PE=2 SV=1 - [B4DPR2_HUMAN] | 2.87 | 1 | 0 | 2 | 8 | 28.8103862 |
| A8K9P0 | cDNA FLJ78413, highly similar to Homo sapiens albumin, mRNA OS=Homo sapiens PE=2 SV=1 - [A8K9P0_HUMAN] | 2.47 | 1 | 0 | 2 | 8 | 28.8103862 |
| P02768 | Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2 - [ALBU_HUMAN] | 2.46 | 1 | 0 | 2 | 8 | 28.8103862 |
| Q56G89 | Serum albumin OS=Homo sapiens PE=2 SV=1 - | 2.46 | 1 | 0 | 2 | 8 | 28.8103862 |

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|--------|---------------------------------------------------------------------------------------------------------------|------|---|---|---|---|------------|
| | [Q56G89_HUMAN] | | | | | | |
| B2RBS8 | cDNA, FLJ95666, highly similar to Homo sapiens albumin (ALB), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RBS8_HUMAN] | 2.46 | 1 | 0 | 2 | 8 | 28.8103862 |
| B4DPP6 | cDNA FLJ54371, highly similar to Serum albumin OS=Homo sapiens PE=2 SV=1 - [B4DPP6_HUMAN] | 2.43 | 1 | 0 | 2 | 8 | 28.8103862 |
| A6NBZ8 | Uncharacterized protein OS=Homo sapiens GN=ALB PE=4 SV=2 - [A6NBZ8_HUMAN] | 2.39 | 1 | 0 | 2 | 8 | 28.8103862 |

Protein ID07.msf

| Accession | Description | Σ Coverage | Σ # Proteins | Σ # Unique Peptides | Σ # Peptides | Σ # PSMs | Score A3 |
|-----------|----------------------------------------------------------------------------------------------------------|-------------------|---------------------|----------------------------|---------------------|-----------------|------------|
| P04264 | Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6 - [K2C1_HUMAN] | 36.8 | 1 | 16 | 17 | 69 | 311.033462 |
| P13645 | Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6 - [K1C10_HUMAN] | 42.47 | 1 | 15 | 15 | 65 | 294.899292 |
| P35908 | Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2 - [K22E_HUMAN] | 33.18 | 1 | 11 | 11 | 37 | 174.587055 |
| P35527 | Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3 - [K1C9_HUMAN] | 32.58 | 1 | 10 | 10 | 35 | 166.07112 |
| P47929 | Galectin-7 OS=Homo sapiens GN=LGALS7 PE=1 SV=2 - [LEG7_HUMAN] | 40.44 | 1 | 4 | 4 | 10 | 24.1358395 |
| P15924 | Desmoplakin OS=Homo sapiens GN=DSP PE=1 SV=3 - [DESP_HUMAN] | 3.27 | 1 | 3 | 8 | 13 | 25.5856175 |
| P14923 | Junction plakoglobin OS=Homo sapiens GN=JUP PE=1 SV=3 - [PLAK_HUMAN] | 4.16 | 1 | 3 | 3 | 5 | 11.978369 |
| P02533 | Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4 - [K1C14_HUMAN] | 24.15 | 1 | 2 | 7 | 13 | 55.1580346 |
| P06733 | Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2 - [ENOA_HUMAN] | 13.13 | 1 | 1 | 4 | 7 | 22.5920208 |
| O95678 | Keratin, type II cytoskeletal 75 OS=Homo sapiens GN=KRT75 PE=1 SV=2 - [K2C75_HUMAN] | 16.33 | 1 | 0 | 12 | 44 | 121.423209 |
| P29508 | Serpin B3 OS=Homo sapiens GN=SERPINB3 PE=1 SV=2 - [SPB3_HUMAN] | 29.49 | 1 | 0 | 11 | 15 | 38.2219901 |
| B3W5Y6 | Squamous cell carcinoma antigen-1 isoform SCCA-PD OS=Homo sapiens GN=SERPINB3 PE=2 SV=1 - [B3W5Y6_HUMAN] | 29.49 | 1 | 0 | 11 | 15 | 38.2219901 |
| Q5K634 | SCCA2/SCCA1 fusion protein isoform 1 OS=Homo sapiens PE=2 SV=1 - [Q5K634_HUMAN] | 25.9 | 1 | 0 | 10 | 16 | 43.8044407 |
| Q01546 | Keratin, type II cytoskeletal 2 oral OS=Homo sapiens GN=KRT76 PE=1 SV=2 - [K22O_HUMAN] | 8.78 | 1 | 0 | 9 | 45 | 124.605325 |
| P12035 | Keratin, type II cytoskeletal 3 OS=Homo sapiens GN=KRT3 PE=1 | 8.12 | 1 | 0 | 9 | 43 | 120.905483 |

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|--------|-------------------------------------------------------------------------------------------------------------|-------|---|---|---|----|------------|
| | SV=3 - [K2C3_HUMAN] | | | | | | |
| B4E2P9 | cDNA FLJ56708, highly similar to Keratin, type I cytoskeletal 17 OS=Homo sapiens PE=2 SV=1 - [B4E2P9_HUMAN] | 45.35 | 1 | 0 | 9 | 24 | 59.9210515 |
| C9JH30 | Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [C9JH30_HUMAN] | 15.94 | 1 | 0 | 9 | 21 | 54.8045726 |
| A8MW45 | Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [A8MW45_HUMAN] | 15.65 | 1 | 0 | 9 | 21 | 54.8045726 |
| Q5K684 | SCCA1/SCCA2 fusion protein OS=Homo sapiens PE=2 SV=1 - [Q5K684_HUMAN] | 25.13 | 1 | 0 | 9 | 10 | 27.0119979 |
| B4DVQ0 | cDNA FLJ58286, highly similar to Actin, cytoplasmic 2 OS=Homo sapiens PE=2 SV=1 - [B4DVQ0_HUMAN] | 25.53 | 1 | 0 | 8 | 16 | 42.0281571 |
| B4E335 | cDNA FLJ52842, highly similar to Actin, cytoplasmic 1 OS=Homo sapiens PE=2 SV=1 - [B4E335_HUMAN] | 24.22 | 1 | 0 | 8 | 16 | 42.0281571 |
| B4E3A4 | cDNA FLJ57283, highly similar to Actin, cytoplasmic 2 OS=Homo sapiens PE=2 SV=1 - [B4E3A4_HUMAN] | 23.88 | 1 | 0 | 8 | 16 | 42.0281571 |
| Q8WVW5 | Putative uncharacterized protein (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q8WVW5_HUMAN] | 23.42 | 1 | 0 | 8 | 16 | 42.0281571 |
| P60709 | Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN] | 22.67 | 1 | 0 | 8 | 16 | 42.0281571 |
| P63261 | Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 - [ACTG_HUMAN] | 22.67 | 1 | 0 | 8 | 16 | 42.0281571 |
| Q53G99 | Beta actin variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53G99_HUMAN] | 22.67 | 1 | 0 | 8 | 16 | 42.0281571 |
| Q53GK6 | Beta actin variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53GK6_HUMAN] | 22.67 | 1 | 0 | 8 | 16 | 42.0281571 |
| Q53G76 | Beta actin variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53G76_HUMAN] | 22.67 | 1 | 0 | 8 | 16 | 42.0281571 |
| Q9BYF7 | SCCA2b OS=Homo sapiens GN=SCCA2 PE=2 SV=1 - [Q9BYF7_HUMAN] | 22.76 | 1 | 0 | 8 | 11 | 32.5944486 |
| P48594 | Serpin B4 OS=Homo sapiens GN=SERPINB4 PE=1 SV=2 - [SPB4_HUMAN] | 21.54 | 1 | 0 | 8 | 11 | 32.5944486 |
| Q5K633 | SCCA2/SCCA1 fusion protein isoform 2 OS=Homo sapiens PE=2 SV=1 - [Q5K633_HUMAN] | 21.54 | 1 | 0 | 8 | 11 | 32.5944486 |

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|--------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------|---|---|---|----|------------|
| A8K847 | cDNA FLJ75229, highly similar to Homo sapiens serpin peptidase inhibitor, clade B (ovalbumin), member 4 (SERPINB4), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K847_HUMAN] | 21.54 | 1 | 0 | 8 | 11 | 32.5944486 |
| Q86W03 | Squamous cell carcinoma antigen 2 OS=Homo sapiens GN=SERPINB4 PE=2 SV=1 - [Q86W03_HUMAN] | 21.54 | 1 | 0 | 8 | 11 | 32.5944486 |
| Q86W05 | Squamous cell carcinoma antigen 2 OS=Homo sapiens GN=SERPINB4 PE=2 SV=1 - [Q86W05_HUMAN] | 21.54 | 1 | 0 | 8 | 11 | 32.5944486 |
| Q5XKE5 | Keratin, type II cytoskeletal 79 OS=Homo sapiens GN=KRT79 PE=1 SV=2 - [K2C79_HUMAN] | 9.35 | 1 | 0 | 7 | 35 | 94.577338 |
| B4DWU0 | cDNA FLJ56791, highly similar to Keratin, type I cytoskeletal 16 OS=Homo sapiens PE=2 SV=1 - [B4DWU0_HUMAN] | 46.67 | 1 | 0 | 7 | 24 | 62.6195915 |
| E0CX14 | Uncharacterized protein OS=Homo sapiens GN=KRT15 PE=4 SV=1 - [E0CX14_HUMAN] | 10.55 | 1 | 0 | 7 | 23 | 58.8988881 |
| P19012 | Keratin, type I cytoskeletal 15 OS=Homo sapiens GN=KRT15 PE=1 SV=3 - [K1C15_HUMAN] | 10.53 | 1 | 0 | 7 | 23 | 58.8988881 |
| B4DW52 | cDNA FLJ55253, highly similar to Actin, cytoplasmic 1 OS=Homo sapiens PE=2 SV=1 - [B4DW52_HUMAN] | 21.04 | 1 | 0 | 7 | 14 | 36.8942047 |
| B4E2J5 | cDNA FLJ53570, highly similar to Keratin, type I cytoskeletal 16 OS=Homo sapiens PE=2 SV=1 - [B4E2J5_HUMAN] | 29.79 | 1 | 0 | 6 | 23 | 59.792491 |
| P08727 | Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=4 - [K1C19_HUMAN] | 11 | 1 | 0 | 6 | 21 | 49.6313334 |
| P13646 | Keratin, type I cytoskeletal 13 OS=Homo sapiens GN=KRT13 PE=1 SV=4 - [K1C13_HUMAN] | 9.17 | 1 | 0 | 6 | 15 | 43.650661 |
| P48668 | Keratin, type II cytoskeletal 6C OS=Homo sapiens GN=KRT6C PE=1 SV=3 - [K2C6C_HUMAN] | 15.25 | 1 | 0 | 6 | 14 | 56.9913461 |
| B2R853 | cDNA, FLJ93744, highly similar to Homo sapiens keratin 6E (KRT6E), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R853_HUMAN] | 15.25 | 1 | 0 | 6 | 14 | 56.9913461 |
| P13647 | Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3 - [K2C5_HUMAN] | 15.08 | 1 | 0 | 6 | 13 | 53.8853548 |
| Q5T8M8 | Actin, alpha 1, skeletal muscle OS=Homo sapiens GN=ACTA1 PE=2 SV=1 - [Q5T8M8_HUMAN] | 19.86 | 1 | 0 | 6 | 10 | 18.7639343 |
| A6NL76 | Uncharacterized protein OS=Homo sapiens GN=ACTA1 PE=4 SV=2 - [A6NL76_HUMAN] | 19.72 | 1 | 0 | 6 | 10 | 18.7639343 |

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|--------|----------------------------------------------------------------------------------------------------------------------------------------|-------|---|---|---|----|------------|
| Q5T8M7 | Actin, alpha 1, skeletal muscle OS=Homo sapiens GN=ACTA1 PE=2 SV=1 - [Q5T8M7_HUMAN] | 16.67 | 1 | 0 | 6 | 10 | 18.7639343 |
| B3KUD3 | cDNA FLJ39583 fis, clone SKMUS2004897, highly similar to ACTIN, ALPHA SKELETAL MUSCLE OS=Homo sapiens PE=2 SV=1 - [B3KUD3_HUMAN] | 16.67 | 1 | 0 | 6 | 10 | 18.7639343 |
| B7Z6P1 | cDNA FLJ53662, highly similar to Actin, alpha skeletal muscle OS=Homo sapiens PE=2 SV=1 - [B7Z6P1_HUMAN] | 16.62 | 1 | 0 | 6 | 10 | 18.7639343 |
| P63267 | Actin, gamma-enteric smooth muscle OS=Homo sapiens GN=ACTG2 PE=1 SV=1 - [ACTH_HUMAN] | 15.16 | 1 | 0 | 6 | 10 | 18.7639343 |
| B3KW67 | cDNA FLJ42347 fis, clone UTERU2003399, highly similar to Actin, gamma-enteric smooth muscle OS=Homo sapiens PE=2 SV=1 - [B3KW67_HUMAN] | 15.16 | 1 | 0 | 6 | 10 | 18.7639343 |
| P62736 | Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1 - [ACTA_HUMAN] | 15.12 | 1 | 0 | 6 | 10 | 18.7639343 |
| P68032 | Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1 - [ACTC_HUMAN] | 15.12 | 1 | 0 | 6 | 10 | 18.7639343 |
| P68133 | Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1 - [ACTS_HUMAN] | 15.12 | 1 | 0 | 6 | 10 | 18.7639343 |
| C9JM50 | Uncharacterized protein OS=Homo sapiens GN=KRT19 PE=4 SV=1 - [C9JM50_HUMAN] | 17.86 | 1 | 0 | 5 | 19 | 43.72721 |
| B4DJM5 | cDNA FLJ61294, highly similar to Keratin, type I cytoskeletal 17 OS=Homo sapiens PE=2 SV=1 - [B4DJM5_HUMAN] | 18.08 | 1 | 0 | 5 | 15 | 35.5729957 |
| B4DWU6 | cDNA FLJ51361, highly similar to Keratin, type II cytoskeletal 6A OS=Homo sapiens PE=2 SV=1 - [B4DWU6_HUMAN] | 13.65 | 1 | 0 | 5 | 13 | 53.1831014 |
| B4DRR0 | cDNA FLJ53910, highly similar to Keratin, type II cytoskeletal 6A OS=Homo sapiens PE=2 SV=1 - [B4DRR0_HUMAN] | 13.27 | 1 | 0 | 5 | 13 | 53.1831014 |
| B4DRU6 | cDNA FLJ54657, highly similar to Keratin, type II cytoskeletal 6A OS=Homo sapiens PE=2 SV=1 - [B4DRU6_HUMAN] | 12.93 | 1 | 0 | 5 | 13 | 53.1831014 |
| P02538 | Keratin, type II cytoskeletal 6A OS=Homo sapiens GN=KRT6A PE=1 SV=3 - [K2C6A_HUMAN] | 12.59 | 1 | 0 | 5 | 13 | 53.1831014 |
| A8K2I0 | cDNA FLJ78504, highly similar to Homo sapiens keratin 6A (KRT6A), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K2I0_HUMAN] | 12.59 | 1 | 0 | 5 | 13 | 53.1831014 |
| B4E1T1 | cDNA FLJ54081, highly similar to Keratin, type II cytoskeletal 5 | 13.33 | 1 | 0 | 5 | 12 | 50.0771101 |

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|--------|-----------------------------------------------------------------------------------------------------------------------------------------|-------|---|---|---|----|------------|--|
| | OS=Homo sapiens PE=2 SV=1 - [B4E1T1_HUMAN] | | | | | | | |
| P04259 | Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5 - [K2C6B_HUMAN] | 12.23 | 1 | 0 | 5 | 12 | 48.3981655 | |
| B3KVF5 | cDNA FLJ16494 fis, clone CTONG3004576, highly similar to Keratin, type I cytoskeletal 15 OS=Homo sapiens PE=2 SV=1 - [B3KVF5_HUMAN] | 8.55 | 1 | 0 | 5 | 11 | 30.2403133 | |
| A1A4E9 | Keratin 13 OS=Homo sapiens GN=KRT13 PE=2 SV=1 - [A1A4E9_HUMAN] | 7.64 | 1 | 0 | 5 | 11 | 35.8503222 | |
| A8K2H9 | cDNA FLJ78503, highly similar to Homo sapiens keratin 13 (KRT13), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1 - [A8K2H9_HUMAN] | 7.64 | 1 | 0 | 5 | 11 | 35.8503222 | |
| B4DRY0 | cDNA FLJ54379, highly similar to Keratin, type II cytoskeletal 6E OS=Homo sapiens PE=2 SV=1 - [B4DRY0_HUMAN] | 13.89 | 1 | 0 | 5 | 10 | 40.5800288 | |
| P08779 | Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4 - [K1C16_HUMAN] | 16.28 | 1 | 0 | 5 | 8 | 33.3182721 | |
| Q7Z7J6 | Actin alpha 1 skeletal muscle protein OS=Homo sapiens GN=ACTA1 PE=2 SV=1 - [Q7Z7J6_HUMAN] | 16.14 | 1 | 0 | 5 | 8 | 13.3602804 | |
| A8K3K1 | cDNA FLJ78096, highly similar to Homo sapiens actin, alpha, cardiac muscle (ACTC), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K3K1_HUMAN] | 14.85 | 1 | 0 | 5 | 8 | 18.7639343 | |
| B4E315 | cDNA FLJ51195, highly similar to Actin, gamma-enteric smooth muscle OS=Homo sapiens PE=2 SV=1 - [B4E315_HUMAN] | 13.51 | 1 | 0 | 5 | 8 | 13.6299819 | |
| D7RX09 | Desmoplakin Ia OS=Homo sapiens PE=2 SV=1 - [D7RX09_HUMAN] | 2.18 | 1 | 0 | 5 | 7 | 14.5593973 | |
| P05787 | Keratin, type II cytoskeletal 8 OS=Homo sapiens GN=KRT8 PE=1 SV=7 - [K2C8_HUMAN] | 3.93 | 1 | 0 | 4 | 25 | 69.4429059 | |
| Q7Z794 | Keratin, type II cytoskeletal 1b OS=Homo sapiens GN=KRT77 PE=1 SV=3 - [K2C1B_HUMAN] | 5.02 | 1 | 0 | 4 | 24 | 62.5702953 | |
| Q0IIN1 | Keratin 77 OS=Homo sapiens GN=KRT77 PE=1 SV=1 - [Q0IIN1_HUMAN] | 5.02 | 1 | 0 | 4 | 24 | 62.5702953 | |
| B4E204 | cDNA FLJ58872, highly similar to Keratin, type I cytoskeletal 15 OS=Homo sapiens PE=2 SV=1 - [B4E204_HUMAN] | 11.97 | 1 | 0 | 4 | 18 | 42.5326896 | |
| C9JA77 | Uncharacterized protein OS=Homo sapiens GN=KRT13 PE=4 SV=1 - [C9JA77_HUMAN] | 8.73 | 1 | 0 | 4 | 11 | 29.8875253 | |

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|--------|--------------------------------------------------------------------------------------------------------------------------|-------|---|---|---|---|------------|
| C9JKR2 | Albumin, isoform CRA_k OS=Homo sapiens GN=ALB PE=4 SV=1 - [C9JKR2_HUMAN] | 8.15 | 1 | 0 | 4 | 9 | 26.1340802 |
| D6RHD5 | Uncharacterized protein OS=Homo sapiens GN=ALB PE=4 SV=1 - [D6RHD5_HUMAN] | 7.41 | 1 | 0 | 4 | 9 | 26.1340802 |
| B7WNR0 | Uncharacterized protein OS=Homo sapiens GN=ALB PE=4 SV=1 - [B7WNR0_HUMAN] | 6.88 | 1 | 0 | 4 | 9 | 26.1340802 |
| B4DPR2 | cDNA FLJ50830, highly similar to Serum albumin OS=Homo sapiens PE=2 SV=1 - [B4DPR2_HUMAN] | 6.5 | 1 | 0 | 4 | 9 | 26.1340802 |
| B4DE59 | cDNA FLJ60424, highly similar to Junction plakoglobin OS=Homo sapiens PE=2 SV=1 - [B4DE59_HUMAN] | 6.22 | 1 | 0 | 4 | 9 | 20.9727585 |
| A8K9P0 | cDNA FLJ78413, highly similar to Homo sapiens albumin, mRNA OS=Homo sapiens PE=2 SV=1 - [A8K9P0_HUMAN] | 5.59 | 1 | 0 | 4 | 9 | 26.1340802 |
| P02768 | Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2 - [ALBU_HUMAN] | 5.58 | 1 | 0 | 4 | 9 | 26.1340802 |
| Q56G89 | Serum albumin OS=Homo sapiens PE=2 SV=1 - [Q56G89_HUMAN] | 5.58 | 1 | 0 | 4 | 9 | 26.1340802 |
| B2RBS8 | cDNA, FLJ95666, highly similar to Homo sapiens albumin (ALB), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RBS8_HUMAN] | 5.58 | 1 | 0 | 4 | 9 | 26.1340802 |
| B4DPP6 | cDNA FLJ54371, highly similar to Serum albumin OS=Homo sapiens PE=2 SV=1 - [B4DPP6_HUMAN] | 5.5 | 1 | 0 | 4 | 9 | 26.1340802 |
| A6NBZ8 | Uncharacterized protein OS=Homo sapiens GN=ALB PE=4 SV=2 - [A6NBZ8_HUMAN] | 5.42 | 1 | 0 | 4 | 9 | 26.1340802 |
| B4DKV4 | cDNA FLJ60647, highly similar to Keratin, type II cytoskeletal 6B OS=Homo sapiens PE=2 SV=1 - [B4DKV4_HUMAN] | 11.22 | 1 | 0 | 4 | 8 | 31.9868481 |
| A1E282 | Beta-actin (Fragment) OS=Homo sapiens PE=2 SV=1 - [A1E282_HUMAN] | 42.15 | 1 | 0 | 4 | 8 | 27.6840477 |
| B3KWQ3 | cDNA FLJ43573 fis, clone RECTM2001691, highly similar to Actin, cytoplasmic 2 OS=Homo sapiens PE=2 SV=1 - [B3KWQ3_HUMAN] | 13.44 | 1 | 0 | 4 | 8 | 14.3441094 |
| Q6PJ43 | ACTG1 protein (Fragment) OS=Homo sapiens GN=ACTG1 PE=2 SV=1 - [Q6PJ43_HUMAN] | 12.93 | 1 | 0 | 4 | 8 | 14.3441094 |
| B7ZAP6 | cDNA, FLJ79260, highly similar to Actin, cytoplasmic 2 OS=Homo sapiens PE=2 SV=1 - [B7ZAP6_HUMAN] | 11.56 | 1 | 0 | 4 | 8 | 14.3441094 |
| B4DUI8 | cDNA FLJ52761, highly similar to Actin, aortic smooth muscle | 10.84 | 1 | 0 | 4 | 8 | 14.5219673 |

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| | OS=Homo sapiens PE=2 SV=1 - [B4DUI8_HUMAN] | | | | | | | |
| B3KTVO | cDNA FLJ38781 fis, clone LIVER2000216, highly similar to HEAT SHOCK COGNATE 71 kDa PROTEIN OS=Homo sapiens PE=2 SV=1 - [B3KTVO_HUMAN] | 7.57 | 1 | 0 | 4 | 7 | 18.724715 | |
| P11142 | Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1 - [HSP7C_HUMAN] | 7.28 | 1 | 0 | 4 | 7 | 18.724715 | |
| B4E2A0 | cDNA FLJ61543, highly similar to Desmoplakin OS=Homo sapiens PE=2 SV=1 - [B4E2A0_HUMAN] | 3.11 | 1 | 0 | 4 | 5 | 10.3555049 | |
| Q4LE79 | DSP variant protein (Fragment) OS=Homo sapiens GN=DSP variant protein PE=2 SV=1 - [Q4LE79_HUMAN] | 1.81 | 1 | 0 | 4 | 5 | 10.3555049 | |
| Q7RTS7 | Keratin, type II cytoskeletal 74 OS=Homo sapiens GN=KRT74 PE=1 SV=2 - [K2C74_HUMAN] | 3.4 | 1 | 0 | 3 | 17 | 42.4516473 | |
| Q86Y46 | Keratin, type II cytoskeletal 73 OS=Homo sapiens GN=KRT73 PE=1 SV=1 - [K2C73_HUMAN] | 3.33 | 1 | 0 | 3 | 17 | 42.4516473 | |
| Q9NSB2 | Keratin, type II cuticular Hb4 OS=Homo sapiens GN=KRT84 PE=1 SV=2 - [KRT84_HUMAN] | 3.33 | 1 | 0 | 3 | 17 | 43.0279384 | |
| B3KY79 | cDNA FLJ46620 fis, clone TLUNG2000654, highly similar to Keratin, type II cytoskeletal 7 OS=Homo sapiens PE=2 SV=1 - [B3KY79_HUMAN] | 4.04 | 1 | 0 | 3 | 16 | 38.623203 | |
| P08729 | Keratin, type II cytoskeletal 7 OS=Homo sapiens GN=KRT7 PE=1 SV=5 - [K2C7_HUMAN] | 3.84 | 1 | 0 | 3 | 16 | 38.623203 | |
| Q7Z3Y7 | Keratin, type I cytoskeletal 28 OS=Homo sapiens GN=KRT28 PE=1 SV=2 - [K1C28_HUMAN] | 5.39 | 1 | 0 | 3 | 10 | 22.2152305 | |
| B4DL32 | cDNA FLJ59922, highly similar to Keratin, type II cytoskeletal 5 OS=Homo sapiens PE=2 SV=1 - [B4DL32_HUMAN] | 17.95 | 1 | 0 | 3 | 7 | 30.1991146 | |
| B4DRW1 | cDNA FLJ55805, highly similar to Keratin, type II cytoskeletal 4 OS=Homo sapiens PE=2 SV=1 - [B4DRW1_HUMAN] | 5.49 | 1 | 0 | 3 | 7 | 16.3891444 | |
| B4DRR7 | cDNA FLJ59399, highly similar to Keratin, type II cytoskeletal 4 OS=Homo sapiens PE=2 SV=1 - [B4DRR7_HUMAN] | 5.19 | 1 | 0 | 3 | 7 | 16.3891444 | |
| B4DKJO | cDNA FLJ58539, highly similar to Keratin, type II cytoskeletal 4 OS=Homo sapiens PE=2 SV=1 - [B4DKJO_HUMAN] | 5.11 | 1 | 0 | 3 | 7 | 16.3891444 | |
| B4DRS2 | cDNA FLJ58275, highly similar to Keratin, type II cytoskeletal 4 OS=Homo sapiens PE=2 SV=1 - [B4DRS2_HUMAN] | 5 | 1 | 0 | 3 | 7 | 16.3891444 | |

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| P19013 | Keratin, type II cytoskeletal 4 OS=Homo sapiens GN=KRT4 PE=1 SV=4 - [K2C4_HUMAN] | 4.87 | 1 | 0 | 3 | 7 | 16.3891444 |
| A4UCT3 | Beta-actin (Fragment) OS=Homo sapiens PE=2 SV=1 - [A4UCT3_HUMAN] | 18.18 | 1 | 0 | 3 | 6 | 9.38801491 |
| A5GZ75 | Beta-actin (Fragment) OS=Homo sapiens PE=2 SV=1 - [A5GZ75_HUMAN] | 15.89 | 1 | 0 | 3 | 6 | 9.38801491 |
| Q96DE1 | Putative uncharacterized protein (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q96DE1_HUMAN] | 15.09 | 1 | 0 | 3 | 6 | 9.38801491 |
| Q96FU6 | ACTG1 protein (Fragment) OS=Homo sapiens GN=ACTG1 PE=2 SV=2 - [Q96FU6_HUMAN] | 14.55 | 1 | 0 | 3 | 6 | 9.38801491 |
| B3KPP5 | cDNA FLJ32030 fis, clone NTONG2000040, highly similar to Actin, alpha cardiac OS=Homo sapiens PE=2 SV=1 - [B3KPP5_HUMAN] | 12.9 | 1 | 0 | 3 | 6 | 9.38801491 |
| P04406 | Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3 - [G3P_HUMAN] | 12.84 | 1 | 0 | 3 | 6 | 20.9001091 |
| Q2TSD0 | Aging-associated gene 9 protein OS=Homo sapiens PE=2 SV=1 - [Q2TSD0_HUMAN] | 12.84 | 1 | 0 | 3 | 6 | 20.9001091 |
| A6NMY6 | Putative annexin A2-like protein OS=Homo sapiens GN=ANXA2P2 PE=5 SV=2 - [AXA2L_HUMAN] | 10.91 | 1 | 0 | 3 | 6 | 21.9897211 |
| B4DL17 | cDNA FLJ52558, highly similar to Keratin, type I cytoskeletal 13 OS=Homo sapiens PE=2 SV=1 - [B4DL17_HUMAN] | 7.47 | 1 | 0 | 3 | 6 | 19.8369117 |
| Q562R1 | Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 PE=1 SV=2 - [ACTBL_HUMAN] | 6.38 | 1 | 0 | 3 | 6 | 9.38801491 |
| P17066 | Heat shock 70 kDa protein 6 OS=Homo sapiens GN=HSPA6 PE=1 SV=2 - [HSP76_HUMAN] | 5.13 | 1 | 0 | 3 | 6 | 16.2639534 |
| B2R6X5 | cDNA, FLJ93166, highly similar to Homo sapiens heat shock 70kDa protein 6 (HSP70B') (HSPA6), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R6X5_HUMAN] | 5.13 | 1 | 0 | 3 | 6 | 16.2639534 |
| Q53FC7 | Heat shock 70kDa protein 6 (HSP70B') variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53FC7_HUMAN] | 5.13 | 1 | 0 | 3 | 6 | 16.2639534 |
| B3KSM6 | cDNA FLJ36606 fis, clone TRACH2015654, highly similar to HEAT SHOCK 70 kDa PROTEIN 6 OS=Homo sapiens PE=2 SV=1 - [B3KSM6_HUMAN] | 5.13 | 1 | 0 | 3 | 6 | 16.2639534 |
| Q53GZ6 | Heat shock 70kDa protein 8 isoform 1 variant (Fragment) | 4.64 | 1 | 0 | 3 | 6 | 15.1152527 |

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| | OS=Homo sapiens PE=2 SV=1 - [Q53GZ6_HUMAN] | | | | | | |
| Q13092 | Epidermal type I keratin (Fragment) OS=Homo sapiens GN=K14 PE=1 SV=1 - [Q13092_HUMAN] | 29.3 | 1 | 0 | 3 | 5 | 20.4158685 |
| Q04695 | Keratin, type I cytoskeletal 17 OS=Homo sapiens GN=KRT17 PE=1 SV=2 - [K1C17_HUMAN] | 11.34 | 1 | 0 | 3 | 5 | 21.8056176 |
| P62805 | Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2 - [H4_HUMAN] | 27.18 | 1 | 0 | 3 | 5 | 12.2180681 |
| Q0VAS5 | HIST1H4H protein OS=Homo sapiens GN=HIST1H4H PE=2 SV=1 - [Q0VAS5_HUMAN] | 27.18 | 1 | 0 | 3 | 5 | 12.2180681 |
| C9JZ65 | Uncharacterized protein OS=Homo sapiens GN=SERPINB4 PE=4 SV=1 - [C9JZ65_HUMAN] | 18.96 | 1 | 0 | 3 | 5 | 16.4371009 |
| Q9BT62 | ENO1 protein (Fragment) OS=Homo sapiens GN=ENO1 PE=2 SV=1 - [Q9BT62_HUMAN] | 16.18 | 1 | 0 | 3 | 5 | 16.1073756 |
| E2DRY6 | C-myc promoter-binding protein 1 OS=Homo sapiens PE=2 SV=1 - [E2DRY6_HUMAN] | 13.02 | 1 | 0 | 3 | 5 | 16.1073756 |
| B3KRA2 | cDNA FLJ33920 fis, clone CTONG2016904, highly similar to KERATIN, TYPE I CYTOSKELETAL 15 OS=Homo sapiens PE=2 SV=1 - [B3KRA2_HUMAN] | 7.97 | 1 | 0 | 3 | 5 | 16.3661985 |
| A8MT21 | Uncharacterized protein OS=Homo sapiens GN=KRT15 PE=4 SV=1 - [A8MT21_HUMAN] | 6.87 | 1 | 0 | 3 | 5 | 16.3661985 |
| B4E1Q1 | cDNA FLJ55485, highly similar to Heat shock cognate 71 kDa protein OS=Homo sapiens PE=2 SV=1 - [B4E1Q1_HUMAN] | 6.79 | 1 | 0 | 3 | 5 | 12.5124793 |
| P54652 | Heat shock-related 70 kDa protein 2 OS=Homo sapiens GN=HSPA2 PE=1 SV=1 - [HSP72_HUMAN] | 6.1 | 1 | 0 | 3 | 5 | 14.2468781 |
| Q96IS6 | HSPA8 protein (Fragment) OS=Homo sapiens GN=HSPA8 PE=2 SV=2 - [Q96IS6_HUMAN] | 5.79 | 1 | 0 | 3 | 5 | 12.5124793 |
| C9JTX5 | Uncharacterized protein OS=Homo sapiens GN=ACTB PE=4 SV=1 - [C9JTX5_HUMAN] | 41.25 | 1 | 0 | 3 | 4 | 9.37591934 |
| C9JUM1 | Uncharacterized protein OS=Homo sapiens GN=ACTB PE=4 SV=1 - [C9JUM1_HUMAN] | 33.33 | 1 | 0 | 3 | 4 | 9.37591934 |
| C9JZR7 | Uncharacterized protein OS=Homo sapiens GN=ACTB PE=4 SV=1 - [C9JZR7_HUMAN] | 32.04 | 1 | 0 | 3 | 4 | 9.37591934 |
| B8ZZJ2 | Uncharacterized protein OS=Homo sapiens GN=ACTG2 PE=4 SV=1 - [B8ZZJ2_HUMAN] | 27.73 | 1 | 0 | 3 | 4 | 9.37591934 |

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| C9JFL5 | Uncharacterized protein OS=Homo sapiens GN=ACTG2 PE=4 SV=1 - [C9JFL5_HUMAN] | 22.76 | 1 | 0 | 3 | 4 | 9.37591934 |
| Q5T9N7 | Actin, alpha 2, smooth muscle, aorta (Fragment) OS=Homo sapiens GN=ACTA2 PE=2 SV=1 - [Q5T9N7_HUMAN] | 21.85 | 1 | 0 | 3 | 4 | 9.37591934 |
| B8ZZK2 | Uncharacterized protein OS=Homo sapiens GN=GGCT PE=4 SV=1 - [B8ZZK2_HUMAN] | 21.69 | 1 | 0 | 3 | 4 | 12.1379504 |
| B7Z611 | cDNA FLJ52755, highly similar to Actin, aortic smooth muscle OS=Homo sapiens PE=2 SV=1 - [B7Z611_HUMAN] | 21.43 | 1 | 0 | 3 | 4 | 9.37591934 |
| O75223 | Gamma-glutamylcyclotransferase OS=Homo sapiens GN=GGCT PE=1 SV=1 - [GGCT_HUMAN] | 19.15 | 1 | 0 | 3 | 4 | 12.1379504 |
| Q13707 | ACTA2 protein (Fragment) OS=Homo sapiens GN=ACTA2 PE=2 SV=1 - [Q13707_HUMAN] | 11.21 | 1 | 0 | 3 | 4 | 9.64562082 |
| B4DHH2 | cDNA FLJ59325, highly similar to C-jun-amino-terminal kinase-interacting protein 4 OS=Homo sapiens PE=2 SV=1 - [B4DHH2_HUMAN] | 4.33 | 1 | 0 | 3 | 4 | 11.814522 |
| D6RC32 | Uncharacterized protein OS=Homo sapiens GN=SPAG9 PE=4 SV=1 - [D6RC32_HUMAN] | 3.89 | 1 | 0 | 3 | 4 | 11.814522 |
| O60271 | C-Jun-amino-terminal kinase-interacting protein 4 OS=Homo sapiens GN=SPAG9 PE=1 SV=4 - [JIP4_HUMAN] | 3.86 | 1 | 0 | 3 | 4 | 11.814522 |
| D6RDV3 | Uncharacterized protein OS=Homo sapiens GN=SPAG9 PE=4 SV=1 - [D6RDV3_HUMAN] | 3.86 | 1 | 0 | 3 | 4 | 11.814522 |
| B4DKX6 | cDNA FLJ53584, highly similar to Desmoplakin (Fragment) OS=Homo sapiens PE=2 SV=1 - [B4DKX6_HUMAN] | 3.46 | 1 | 0 | 3 | 4 | 7.64538038 |
| Q6S8J3 | POTE ankyrin domain family member E OS=Homo sapiens GN=POTEE PE=1 SV=3 - [POTEE_HUMAN] | 3.44 | 1 | 0 | 3 | 4 | 9.64562082 |
| A5A3E0 | POTE ankyrin domain family member F OS=Homo sapiens GN=POTEF PE=1 SV=2 - [POTEF_HUMAN] | 3.44 | 1 | 0 | 3 | 4 | 9.64562082 |
| Q08188 | Protein-glutamine gamma-glutamyltransferase E OS=Homo sapiens GN=TGM3 PE=1 SV=4 - [TGM3_HUMAN] | 6.49 | 1 | 0 | 3 | 3 | 9.03920174 |
| D3DVX1 | Transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase), isoform CRA_a OS=Homo sapiens GN=TGM3 PE=4 SV=1 - [D3DVX1_HUMAN] | 6.49 | 1 | 0 | 3 | 3 | 9.03920174 |
| C9J1H1 | Uncharacterized protein OS=Homo sapiens GN=S100A9 PE=4 SV=1 - [C9J1H1_HUMAN] | 35.44 | 1 | 0 | 2 | 5 | 20.0921381 |

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| P06702 | Protein S100-A9 OS=Homo sapiens GN=S100A9 PE=1 SV=1 - [S10A9_HUMAN] | 24.56 | 1 | 0 | 2 | 5 | 20.0921381 |
| B2R4M6 | cDNA, FLJ92148, highly similar to Homo sapiens S100 calcium binding protein A9 (calgranulin B) (S100A9), mRNA OS=Homo sapiens PE=4 SV=1 - [B2R4M6_HUMAN] | 24.56 | 1 | 0 | 2 | 5 | 20.0921381 |
| B4DNH8 | cDNA FLJ59138, highly similar to Annexin A2 OS=Homo sapiens PE=2 SV=1 - [B4DNH8_HUMAN] | 15.46 | 1 | 0 | 2 | 3 | 12.1486752 |
| Q16195 | Keratin (Fragment) OS=Homo sapiens GN=keratin PE=2 SV=1 - [Q16195_HUMAN] | 13.11 | 1 | 0 | 2 | 3 | 14.1663532 |
| Q14666 | Radiated keratinocyte mRNA 266 (keratin-related protein) (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q14666_HUMAN] | 11.28 | 1 | 0 | 2 | 3 | 13.239198 |
| P07355 | Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2 - [ANXA2_HUMAN] | 8.85 | 1 | 0 | 2 | 3 | 12.1486752 |
| Q96C32 | UBC protein OS=Homo sapiens PE=2 SV=1 - [Q96C32_HUMAN] | 38.03 | 1 | 0 | 2 | 2 | 8.07130599 |
| P0CG47 | Polyubiquitin-B OS=Homo sapiens GN=UBB PE=1 SV=1 - [UBB_HUMAN] | 37.99 | 1 | 0 | 2 | 2 | 8.07130599 |
| Q5PY61 | Ubiquitin C splice variant OS=Homo sapiens GN=UBC PE=2 SV=1 - [Q5PY61_HUMAN] | 37.99 | 1 | 0 | 2 | 2 | 8.07130599 |
| Q5UGI3 | Ubiquitin C splice variant OS=Homo sapiens GN=UBC PE=2 SV=1 - [Q5UGI3_HUMAN] | 37.91 | 1 | 0 | 2 | 2 | 8.07130599 |
| B4DV12 | cDNA FLJ51326, highly similar to Homo sapiens ubiquitin B (UBB), mRNA OS=Homo sapiens PE=2 SV=1 - [B4DV12_HUMAN] | 37.91 | 1 | 0 | 2 | 2 | 8.07130599 |
| Q59EM9 | Ubiquitin C variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59EM9_HUMAN] | 37.66 | 1 | 0 | 2 | 2 | 8.07130599 |
| Q66K58 | Putative uncharacterized protein (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q66K58_HUMAN] | 37.39 | 1 | 0 | 2 | 2 | 8.07130599 |
| Q96H31 | UBC protein (Fragment) OS=Homo sapiens GN=UBC PE=2 SV=2 - [Q96H31_HUMAN] | 37.18 | 1 | 0 | 2 | 2 | 8.07130599 |
| Q96MH4 | cDNA FLJ32377 fis, clone SKMUS1000014, highly similar to Polyubiquitin 9 OS=Homo sapiens PE=2 SV=1 - [Q96MH4_HUMAN] | 36.6 | 1 | 0 | 2 | 2 | 8.07130599 |
| Q9UFQ0 | Putative uncharacterized protein DKFZp434K0435 (Fragment) OS=Homo sapiens GN=DKFZp434K0435 PE=2 SV=1 - [Q9UFQ0_HUMAN] | 36.4 | 1 | 0 | 2 | 2 | 8.07130599 |

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| P0CG48 | Polyubiquitin-C OS=Homo sapiens GN=UBC PE=1 SV=2 - [UBC_HUMAN] | 36.2 | 1 | 0 | 2 | 2 | 8.07130599 |
| A8K674 | cDNA FLJ75516, highly similar to Xenopus tropicalis ubiquitin C, mRNA OS=Homo sapiens PE=2 SV=1 - [A8K674_HUMAN] | 35.47 | 1 | 0 | 2 | 2 | 8.07130599 |
| Q49A90 | RPS27A protein OS=Homo sapiens GN=RPS27A PE=4 SV=1 - [Q49A90_HUMAN] | 30.53 | 1 | 0 | 2 | 2 | 8.07130599 |
| P62987 | Ubiquitin-60S ribosomal protein L40 OS=Homo sapiens GN=UBA52 PE=1 SV=2 - [RL40_HUMAN] | 22.66 | 1 | 0 | 2 | 2 | 8.07130599 |
| P62979 | Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=1 SV=2 - [RS27A_HUMAN] | 18.59 | 1 | 0 | 2 | 2 | 8.07130599 |
| Q5RKT7 | Ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=2 SV=1 - [Q5RKT7_HUMAN] | 18.59 | 1 | 0 | 2 | 2 | 8.07130599 |

Protein ID08.msf

| Accession | Description | Σ Coverage | Σ # Proteins | Σ # Unique Peptides | Σ # Peptides | Σ # PSMs | Score A3 |
|-----------|--------------------------------------------------------------------------------------------------------------------|-------------------|---------------------|----------------------------|---------------------|-----------------|------------|
| P13645 | Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6 - [K1C10_HUMAN] | 44.69 | 1 | 20 | 24 | 90 | 293.111529 |
| P04264 | Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6 - [K2C1_HUMAN] | 32.14 | 1 | 16 | 20 | 110 | 345.940815 |
| P35527 | Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3 - [K1C9_HUMAN] | 44.3 | 1 | 15 | 15 | 37 | 127.657821 |
| P35908 | Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2 - [K22E_HUMAN] | 43.35 | 1 | 14 | 21 | 60 | 190.236341 |
| P13647 | Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3 - [K2C5_HUMAN] | 16.78 | 1 | 1 | 10 | 24 | 64.343142 |
| P02533 | Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4 - [K1C14_HUMAN] | 12.71 | 1 | 1 | 5 | 10 | 30.377795 |
| B4E1T1 | cDNA FLJ54081, highly similar to Keratin, type II cytoskeletal 5 OS=Homo sapiens PE=2 SV=1 - [B4E1T1_HUMAN] | 15.86 | 1 | 0 | 9 | 22 | 58.942924 |
| B4DRR0 | cDNA FLJ53910, highly similar to Keratin, type II cytoskeletal 6A OS=Homo sapiens PE=2 SV=1 - [B4DRR0_HUMAN] | 16.45 | 1 | 0 | 9 | 21 | 56.1005869 |
| B4DRU6 | cDNA FLJ54657, highly similar to Keratin, type II cytoskeletal 6A OS=Homo sapiens PE=2 SV=1 - [B4DRU6_HUMAN] | 16.03 | 1 | 0 | 9 | 21 | 56.1005869 |
| P02538 | Keratin, type II cytoskeletal 6A OS=Homo sapiens GN=KRT6A PE=1 SV=3 - [K2C6A_HUMAN] | 15.6 | 1 | 0 | 9 | 21 | 56.1005869 |
| P48668 | Keratin, type II cytoskeletal 6C OS=Homo sapiens GN=KRT6C PE=1 SV=3 - [K2C6C_HUMAN] | 15.6 | 1 | 0 | 9 | 21 | 56.1005869 |
| B2R853 | cDNA, FLJ93744, highly similar to Homo sapiens keratin 6E (KRT6E), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R853_HUMAN] | 15.6 | 1 | 0 | 9 | 21 | 56.1005869 |
| A8K2I0 | cDNA FLJ78504, highly similar to Homo sapiens keratin 6A (KRT6A), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K2I0_HUMAN] | 15.6 | 1 | 0 | 9 | 21 | 56.1005869 |
| P04259 | Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B | 14.01 | 1 | 0 | 8 | 29 | 78.8138964 |

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| | PE=1 SV=5 - [K2C6B_HUMAN] | | | | | | |
| B4DWU6 | cDNA FLJ51361, highly similar to Keratin, type II cytoskeletal 6A OS=Homo sapiens PE=2 SV=1 - [B4DWU6_HUMAN] | 15.19 | 1 | 0 | 8 | 19 | 50.6582992 |
| B4DKV4 | cDNA FLJ60647, highly similar to Keratin, type II cytoskeletal 6B OS=Homo sapiens PE=2 SV=1 - [B4DKV4_HUMAN] | 14.83 | 1 | 0 | 8 | 17 | 44.7465608 |
| B4DRY0 | cDNA FLJ54379, highly similar to Keratin, type II cytoskeletal 6E OS=Homo sapiens PE=2 SV=1 - [B4DRY0_HUMAN] | 14.26 | 1 | 0 | 8 | 17 | 44.7465608 |
| B4DL32 | cDNA FLJ59922, highly similar to Keratin, type II cytoskeletal 5 OS=Homo sapiens PE=2 SV=1 - [B4DL32_HUMAN] | 26.07 | 1 | 0 | 6 | 16 | 42.8586349 |
| Q01546 | Keratin, type II cytoskeletal 2 oral OS=Homo sapiens GN=KRT76 PE=1 SV=2 - [K220_HUMAN] | 5.96 | 1 | 0 | 4 | 12 | 31.4810386 |
| O95678 | Keratin, type II cytoskeletal 75 OS=Homo sapiens GN=KRT75 PE=1 SV=2 - [K2C75_HUMAN] | 7.62 | 1 | 0 | 4 | 9 | 23.5444474 |
| Q5XKE5 | Keratin, type II cytoskeletal 79 OS=Homo sapiens GN=KRT79 PE=1 SV=2 - [K2C79_HUMAN] | 5.79 | 1 | 0 | 3 | 8 | 20.9764688 |
| B4E2P9 | cDNA FLJ56708, highly similar to Keratin, type I cytoskeletal 17 OS=Homo sapiens PE=2 SV=1 - [B4E2P9_HUMAN] | 9.3 | 1 | 0 | 3 | 7 | 15.1173663 |
| C9JM50 | Uncharacterized protein OS=Homo sapiens GN=KRT19 PE=4 SV=1 - [C9JM50_HUMAN] | 8.16 | 1 | 0 | 3 | 7 | 15.1173663 |
| P08727 | Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=4 - [K1C19_HUMAN] | 4 | 1 | 0 | 3 | 7 | 15.1173663 |
| P08779 | Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4 - [K1C16_HUMAN] | 6.77 | 1 | 0 | 3 | 6 | 15.7290297 |
| C9JA77 | Uncharacterized protein OS=Homo sapiens GN=KRT13 PE=4 SV=1 - [C9JA77_HUMAN] | 6.76 | 1 | 0 | 3 | 6 | 17.3322215 |
| P13646 | Keratin, type I cytoskeletal 13 OS=Homo sapiens GN=KRT13 PE=1 SV=4 - [K1C13_HUMAN] | 5.24 | 1 | 0 | 3 | 6 | 17.3322215 |
| A1A4E9 | Keratin 13 OS=Homo sapiens GN=KRT13 PE=2 SV=1 - [A1A4E9_HUMAN] | 5.24 | 1 | 0 | 3 | 6 | 17.3322215 |
| A8K2H9 | cDNA FLJ78503, highly similar to Homo sapiens keratin 13 (KRT13), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1 - [A8K2H9_HUMAN] | 5.24 | 1 | 0 | 3 | 6 | 17.3322215 |
| Q14666 | Radiated keratinocyte mRNA 266 (keratin-related protein) (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q14666_HUMAN] | 12.03 | 1 | 0 | 3 | 5 | 12.2301992 |

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|--------|-------------------------------------------------------------------------------------------------------------|-------|---|---|---|---|------------|
| P12035 | Keratin, type II cytoskeletal 3 OS=Homo sapiens GN=KRT3 PE=1 SV=3 - [K2C3_HUMAN] | 3.18 | 1 | 0 | 2 | 8 | 20.9209266 |
| Q86YZ3 | Hornerin OS=Homo sapiens GN=HRNR PE=1 SV=2 - [HORN_HUMAN] | 4.49 | 1 | 0 | 2 | 5 | 14.4908164 |
| Q5DT20 | Hornerin OS=Homo sapiens GN=HRNR PE=2 SV=1 - [Q5DT20_HUMAN] | 4.49 | 1 | 0 | 2 | 5 | 14.4908164 |
| B4DWU0 | cDNA FLJ56791, highly similar to Keratin, type I cytoskeletal 16 OS=Homo sapiens PE=2 SV=1 - [B4DWU0_HUMAN] | 15.56 | 1 | 0 | 2 | 4 | 10.8632162 |
| B4E2J5 | cDNA FLJ53570, highly similar to Keratin, type I cytoskeletal 16 OS=Homo sapiens PE=2 SV=1 - [B4E2J5_HUMAN] | 11.17 | 1 | 0 | 2 | 4 | 10.8632162 |
| B4E204 | cDNA FLJ58872, highly similar to Keratin, type I cytoskeletal 15 OS=Homo sapiens PE=2 SV=1 - [B4E204_HUMAN] | 8.97 | 1 | 0 | 2 | 4 | 10.8632162 |
| Q04695 | Keratin, type I cytoskeletal 17 OS=Homo sapiens GN=KRT17 PE=1 SV=2 - [K1C17_HUMAN] | 5.09 | 1 | 0 | 2 | 4 | 11.5265803 |
| C9JH30 | Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [C9JH30_HUMAN] | 5.08 | 1 | 0 | 2 | 4 | 11.5265803 |
| A8MW45 | Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [A8MW45_HUMAN] | 4.99 | 1 | 0 | 2 | 4 | 11.5265803 |
| E0CX14 | Uncharacterized protein OS=Homo sapiens GN=KRT15 PE=4 SV=1 - [E0CX14_HUMAN] | 4.62 | 1 | 0 | 2 | 4 | 10.8632162 |
| P19012 | Keratin, type I cytoskeletal 15 OS=Homo sapiens GN=KRT15 PE=1 SV=3 - [K1C15_HUMAN] | 4.61 | 1 | 0 | 2 | 4 | 10.8632162 |
| P81605 | Dermcidin OS=Homo sapiens GN=DCD PE=1 SV=2 - [DCD_HUMAN] | 22.73 | 1 | 0 | 2 | 3 | 8.60801697 |
| A5JHP3 | Dermcidin isoform 2 OS=Homo sapiens GN=DCD PE=2 SV=1 - [A5JHP3_HUMAN] | 20.66 | 1 | 0 | 2 | 3 | 8.60801697 |

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| Accession | Description | Σ Coverage | Σ # Proteins | Σ # Unique Peptides | Σ # Peptides | Σ # PSMs | Score A3 |
|-----------|---------------------------------------------------------------------------------------------------------|-------------------|---------------------|----------------------------|---------------------|-----------------|------------|
| P13645 | Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6 - [K1C10_HUMAN] | 59.42 | 1 | 22 | 28 | 81 | 294.048095 |
| P04264 | Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6 - [K2C1_HUMAN] | 46.74 | 1 | 21 | 26 | 97 | 344.178274 |
| P35908 | Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2 - [K22E_HUMAN] | 39.91 | 1 | 16 | 25 | 65 | 208.494367 |
| Q5JTZ9 | Alanyl-tRNA synthetase, mitochondrial OS=Homo sapiens GN=AARS2 PE=1 SV=1 - [SYAM_HUMAN] | 27.51 | 1 | 16 | 17 | 30 | 100.640332 |
| P35527 | Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3 - [K1C9_HUMAN] | 41.89 | 1 | 15 | 15 | 43 | 171.528032 |
| Q9NR30 | Nucleolar RNA helicase 2 OS=Homo sapiens GN=DDX21 PE=1 SV=5 - [DDX21_HUMAN] | 32.82 | 1 | 14 | 21 | 54 | 189.642886 |
| P16615 | Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Homo sapiens GN=ATP2A2 PE=1 SV=1 - [AT2A2_HUMAN] | 31.96 | 1 | 13 | 23 | 50 | 171.926918 |
| Q15031 | Probable leucyl-tRNA synthetase, mitochondrial OS=Homo sapiens GN=LARS2 PE=1 SV=2 - [SYLM_HUMAN] | 10.3 | 1 | 5 | 7 | 12 | 28.8135047 |
| P53618 | Coatomer subunit beta OS=Homo sapiens GN=COPB1 PE=1 SV=3 - [COPB_HUMAN] | 6.72 | 1 | 5 | 5 | 8 | 24.350127 |
| Q15269 | Periodic tryptophan protein 2 homolog OS=Homo sapiens GN=PWP2 PE=1 SV=2 - [PWP2_HUMAN] | 7.4 | 1 | 4 | 4 | 8 | 24.94996 |
| P22314 | Ubiquitin-like modifier-activating enzyme 1 OS=Homo sapiens GN=UBA1 PE=1 SV=3 - [UBA1_HUMAN] | 18.53 | 1 | 3 | 12 | 30 | 115.34727 |
| P05556 | Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2 - [ITB1_HUMAN] | 7.39 | 1 | 3 | 5 | 9 | 23.8414454 |
| Q9Y5Q9 | General transcription factor 3C polypeptide 3 OS=Homo sapiens GN=GTF3C3 PE=1 SV=1 - [TF3C3_HUMAN] | 5.19 | 1 | 3 | 4 | 7 | 23.5051773 |
| P13647 | Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3 - [K2C5_HUMAN] | 22.54 | 1 | 2 | 14 | 28 | 78.3950579 |
| P11586 | C-1-tetrahydrofolate synthase, cytoplasmic OS=Homo sapiens | 32.94 | 1 | 1 | 25 | 67 | 214.697333 |

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|--------|-------------------------------------------------------------------------------------------------------------------------------------------------------|-------|---|---|----|-----|------------|
| | GN=MTHFD1 PE=1 SV=3 - [C1TC_HUMAN] | | | | | | |
| B3KPH8 | cDNA FLJ31804 fis, clone NT2RI2009103, highly similar to Lon protease homolog, mitochondrial (EC 3.4.21.-) OS=Homo sapiens PE=2 SV=1 - [B3KPH8_HUMAN] | 39.32 | 1 | 1 | 22 | 53 | 188.217451 |
| P55072 | Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4 - [TERA_HUMAN] | 30.02 | 1 | 1 | 18 | 52 | 176.968776 |
| Q9NSE4 | Isoleucyl-tRNA synthetase, mitochondrial OS=Homo sapiens GN=IARS2 PE=1 SV=2 - [SYIM_HUMAN] | 14.72 | 1 | 1 | 14 | 31 | 90.3237684 |
| O14980 | Exportin-1 OS=Homo sapiens GN=XPO1 PE=1 SV=1 - [XPO1_HUMAN] | 14.75 | 1 | 1 | 11 | 26 | 83.2243299 |
| Q12906 | Interleukin enhancer-binding factor 3 OS=Homo sapiens GN=ILF3 PE=1 SV=3 - [ILF3_HUMAN] | 11.07 | 1 | 1 | 10 | 16 | 41.4711795 |
| P57740 | Nuclear pore complex protein Nup107 OS=Homo sapiens GN=NUP107 PE=1 SV=1 - [NU107_HUMAN] | 8.11 | 1 | 1 | 5 | 5 | 15.0709338 |
| Q53FM3 | ATPase, H+/K+ exchanging, alpha polypeptide variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53FM3_HUMAN] | 3.57 | 1 | 1 | 3 | 7 | 23.6796434 |
| P13639 | Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 - [EF2_HUMAN] | 63.05 | 1 | 0 | 43 | 177 | 644.024065 |
| Q5CAQ5 | Tumor rejection antigen (Gp96) 1 OS=Homo sapiens GN=TRA1 PE=2 SV=1 - [Q5CAQ5_HUMAN] | 55.24 | 1 | 0 | 38 | 144 | 470.852964 |
| P14625 | Endoplasmin OS=Homo sapiens GN=HSP90B1 PE=1 SV=1 - [ENPL_HUMAN] | 55.17 | 1 | 0 | 38 | 144 | 470.852964 |
| Q6PK56 | EEF2 protein (Fragment) OS=Homo sapiens GN=EEF2 PE=2 SV=1 - [Q6PK56_HUMAN] | 62.26 | 1 | 0 | 29 | 106 | 360.622913 |
| B4DPU3 | cDNA FLJ56548, highly similar to Elongation factor 2 OS=Homo sapiens PE=2 SV=1 - [B4DPU3_HUMAN] | 62.01 | 1 | 0 | 27 | 118 | 460.087384 |
| B7Z3U6 | ATPase, Na+/K+ transporting, alpha 1 polypeptide, isoform CRA_a OS=Homo sapiens GN=ATP1A1 PE=2 SV=1 - [B7Z3U6_HUMAN] | 33.77 | 1 | 0 | 27 | 62 | 214.260098 |
| P05023 | Sodium/potassium-transporting ATPase subunit alpha-1 OS=Homo sapiens GN=ATP1A1 PE=1 SV=1 - [AT1A1_HUMAN] | 32.75 | 1 | 0 | 27 | 62 | 214.260098 |
| B7Z2T5 | cDNA FLJ55427, highly similar to Sodium/potassium-transporting ATPase alpha-1 chain (EC 3.6.3.9) OS=Homo sapiens PE=2 SV=1 - [B7Z2T5_HUMAN] | 32.75 | 1 | 0 | 27 | 62 | 214.260098 |

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|--------|--------------------------------------------------------------------------------------------------------------------------------------------------------|-------|---|---|----|-----|------------|
| Q8TA90 | Similar to Elongation factor 2b (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q8TA90_HUMAN] | 64.99 | 1 | 0 | 26 | 119 | 433.174151 |
| P19338 | Nucleolin OS=Homo sapiens GN=NCL PE=1 SV=3 - [NUCL_HUMAN] | 34.37 | 1 | 0 | 26 | 102 | 383.628721 |
| Q59FC6 | Tumor rejection antigen (Gp96) 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59FC6_HUMAN] | 54.34 | 1 | 0 | 25 | 108 | 355.90626 |
| B4DHT9 | cDNA FLJ58812, highly similar to Endoplasmin (Heat shock protein 90kDa beta member 1) OS=Homo sapiens PE=2 SV=1 - [B4DHT9_HUMAN] | 57.91 | 1 | 0 | 25 | 78 | 241.664337 |
| B4DU71 | cDNA FLJ58626, highly similar to Endoplasmin (Heat shock protein 90 kDa beta member 1) OS=Homo sapiens PE=2 SV=1 - [B4DU71_HUMAN] | 49.09 | 1 | 0 | 25 | 78 | 241.664337 |
| B7Z3V1 | cDNA FLJ60077, highly similar to Sodium/potassium-transporting ATPase alpha-1 chain (EC 3.6.3.9) (Fragment) OS=Homo sapiens PE=2 SV=1 - [B7Z3V1_HUMAN] | 29.71 | 1 | 0 | 25 | 56 | 188.090765 |
| B3KTP9 | cDNA FLJ38578 fis, clone HCHON2007674, highly similar to NUCLEOLIN OS=Homo sapiens PE=2 SV=1 - [B3KTP9_HUMAN] | 35.7 | 1 | 0 | 24 | 99 | 376.545188 |
| B4DRE8 | cDNA FLJ58164, highly similar to Elongation factor 2 OS=Homo sapiens PE=2 SV=1 - [B4DRE8_HUMAN] | 60.2 | 1 | 0 | 24 | 92 | 321.562764 |
| Q14697 | Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB PE=1 SV=3 - [GANAB_HUMAN] | 30.61 | 1 | 0 | 24 | 67 | 234.830107 |
| B4DJ30 | cDNA FLJ61290, highly similar to Neutral alpha-glucosidase AB OS=Homo sapiens PE=2 SV=1 - [B4DJ30_HUMAN] | 29.05 | 1 | 0 | 24 | 67 | 234.830107 |
| B7Z809 | cDNA FLJ56016, highly similar to C-1-tetrahydrofolate synthase, cytoplasmic OS=Homo sapiens PE=2 SV=1 - [B7Z809_HUMAN] | 28.04 | 1 | 0 | 24 | 60 | 187.911042 |
| B4DSM6 | cDNA FLJ54057, highly similar to Neutral alpha-glucosidase AB OS=Homo sapiens PE=2 SV=1 - [B4DSM6_HUMAN] | 32.94 | 1 | 0 | 23 | 63 | 221.063423 |
| Q2VPA0 | LONP1 protein (Fragment) OS=Homo sapiens GN=LONP1 PE=2 SV=1 - [Q2VPA0_HUMAN] | 36.67 | 1 | 0 | 23 | 56 | 195.47181 |
| Q8N8K8 | cDNA FLJ39307 fis, clone OCBBF2013208, highly similar to MITOCHONDRIAL LON PROTEASE (EC 3.4.21.-) OS=Homo sapiens PE=2 SV=1 - [Q8N8K8_HUMAN] | 34.75 | 1 | 0 | 23 | 56 | 195.47181 |
| B3KXS5 | cDNA FLJ45970 fis, clone PLACE7016526, highly similar to Lon protease homolog, mitochondrial (EC 3.4.21.-) OS=Homo | 33.69 | 1 | 0 | 23 | 56 | 195.47181 |

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|--------|-------------------------------------------------------------------------------------------------------------------------------------------------------------|-------|---|---|----|----|------------|
| | sapiens PE=2 SV=1 - [B3KXS5_HUMAN] | | | | | | |
| P36776 | Lon protease homolog, mitochondrial OS=Homo sapiens GN=LONP1 PE=1 SV=2 - [LONM_HUMAN] | 32.43 | 1 | 0 | 23 | 56 | 195.47181 |
| E5KMI6 | Mitochondrial lon protease-like protein OS=Homo sapiens PE=4 SV=1 - [E5KMI6_HUMAN] | 32.43 | 1 | 0 | 23 | 56 | 195.47181 |
| B3KM80 | Nucleolin, isoform CRA_c OS=Homo sapiens GN=NCL PE=2 SV=1 - [B3KM80_HUMAN] | 40.49 | 1 | 0 | 22 | 95 | 367.626421 |
| Q6ZS99 | cDNA FLJ45706 fis, clone FEBRA2028457, highly similar to Nucleolin OS=Homo sapiens PE=2 SV=1 - [Q6ZS99_HUMAN] | 35.99 | 1 | 0 | 22 | 95 | 367.626421 |
| B3KU28 | cDNA FLJ39114 fis, clone NTONG2006099, highly similar to Lon protease homolog, mitochondrial (EC 3.4.21.-) OS=Homo sapiens PE=2 SV=1 - [B3KU28_HUMAN] | 35.86 | 1 | 0 | 22 | 54 | 190.568534 |
| E5KMH8 | Mitochondrial lon protease-like protein OS=Homo sapiens PE=4 SV=1 - [E5KMH8_HUMAN] | 30.97 | 1 | 0 | 22 | 54 | 188.590087 |
| B4DPX0 | cDNA FLJ56219, highly similar to Lon protease homolog, mitochondrial (EC 3.4.21.-) OS=Homo sapiens PE=2 SV=1 - [B4DPX0_HUMAN] | 33.03 | 1 | 0 | 21 | 52 | 179.965696 |
| B4DMC6 | cDNA FLJ60696, highly similar to Elongation factor 2 OS=Homo sapiens PE=2 SV=1 - [B4DMC6_HUMAN] | 64.34 | 1 | 0 | 20 | 68 | 244.932186 |
| Q13263 | Transcription intermediary factor 1-beta OS=Homo sapiens GN=TRIM28 PE=1 SV=5 - [TIF1B_HUMAN] | 34.25 | 1 | 0 | 19 | 49 | 159.545086 |
| B2R8R5 | cDNA, FLJ94025, highly similar to Homo sapiens tripartite motif- containing 28 (TRIM28), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R8R5_HUMAN] | 34.25 | 1 | 0 | 19 | 49 | 159.545086 |
| B4DIW2 | cDNA FLJ54035, highly similar to Neutral alpha-glucosidase AB OS=Homo sapiens PE=2 SV=1 - [B4DIW2_HUMAN] | 30.72 | 1 | 0 | 19 | 44 | 165.806548 |
| Q9BSV4 | SFPQ protein (Fragment) OS=Homo sapiens GN=SFPQ PE=2 SV=2 - [Q9BSV4_HUMAN] | 27.29 | 1 | 0 | 17 | 49 | 156.884649 |
| P23246 | Splicing factor, proline- and glutamine-rich OS=Homo sapiens GN=SFPQ PE=1 SV=2 - [SFPQ_HUMAN] | 24.47 | 1 | 0 | 17 | 49 | 156.884649 |
| Q86VG2 | Splicing factor proline/glutamine-rich (Polypyrimidine tract binding protein associated) OS=Homo sapiens GN=SFPQ PE=2 SV=1 - [Q86VG2_HUMAN] | 24.47 | 1 | 0 | 17 | 49 | 156.884649 |

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|--------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------|---|---|----|----|------------|
| O43707 | Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2 - [ACTN4_HUMAN] | 24.48 | 1 | 0 | 17 | 36 | 119.104118 |
| Q9BQ02 | NCL protein OS=Homo sapiens PE=2 SV=1 - [Q9BQ02_HUMAN] | 32.99 | 1 | 0 | 16 | 56 | 198.336739 |
| B4DZ53 | cDNA FLJ59643, highly similar to Neutral alpha-glucosidase AB OS=Homo sapiens PE=2 SV=1 - [B4DZ53_HUMAN] | 24.88 | 1 | 0 | 16 | 35 | 121.847822 |
| P55060 | Exportin-2 OS=Homo sapiens GN=CSE1L PE=1 SV=3 - [XPO2_HUMAN] | 23.07 | 1 | 0 | 16 | 35 | 116.044626 |
| B4E0E1 | cDNA FLJ53442, highly similar to Poly (ADP-ribose) polymerase 1 (EC 2.4.2.30) OS=Homo sapiens PE=2 SV=1 - [B4E0E1_HUMAN] | 24.37 | 1 | 0 | 16 | 31 | 104.535754 |
| P09874 | Poly [ADP-ribose] polymerase 1 OS=Homo sapiens GN=PARP1 PE=1 SV=4 - [PARP1_HUMAN] | 23.87 | 1 | 0 | 16 | 31 | 104.535754 |
| B2R5W3 | cDNA, FLJ92658, highly similar to Homo sapiens poly (ADP-ribose) polymerase family, member 1 (PARP1), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R5W3_HUMAN] | 23.87 | 1 | 0 | 16 | 31 | 104.535754 |
| P43246 | DNA mismatch repair protein Msh2 OS=Homo sapiens GN=MSH2 PE=1 SV=1 - [MSH2_HUMAN] | 22.91 | 1 | 0 | 16 | 30 | 93.7093418 |
| P25205 | DNA replication licensing factor MCM3 OS=Homo sapiens GN=MCM3 PE=1 SV=3 - [MCM3_HUMAN] | 23.89 | 1 | 0 | 16 | 27 | 89.6501238 |
| Q53HJ4 | Minichromosome maintenance protein 3 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53HJ4_HUMAN] | 23.89 | 1 | 0 | 16 | 27 | 89.6501238 |
| B2R7C5 | cDNA, FLJ93378, highly similar to Homo sapiens MCM3 minichromosome maintenance deficient 3 (<i>S. cerevisiae</i>) (MCM3), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R7C5_HUMAN] | 23.89 | 1 | 0 | 16 | 27 | 89.6501238 |
| B4DWW4 | MCM3 minichromosome maintenance deficient 3 (<i>S. cerevisiae</i>), isoform CRA_b OS=Homo sapiens GN=MCM3 PE=2 SV=1 - [B4DWW4_HUMAN] | 22.63 | 1 | 0 | 16 | 27 | 89.6501238 |
| Q96IF9 | VCP protein (Fragment) OS=Homo sapiens GN=VCP PE=2 SV=2 - [Q96IF9_HUMAN] | 31.06 | 1 | 0 | 15 | 45 | 153.195307 |
| A3RLL6 | Cellular apoptosis susceptibility protein variant 2 OS=Homo sapiens GN=CSE1L-2 PE=2 SV=1 - [A3RLL6_HUMAN] | 22.62 | 1 | 0 | 15 | 29 | 90.2169228 |
| Q53GS1 | MutS homolog 2 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53GS1_HUMAN] | 23.12 | 1 | 0 | 15 | 28 | 86.8261209 |

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|--------|-------------------------------------------------------------------------------------------------------------------------------------------|-------|---|---|----|----|------------|
| Q53FK0 | MutS homolog 2 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53FK0_HUMAN] | 23.12 | 1 | 0 | 15 | 28 | 86.8261209 |
| Q6PIX2 | SFPQ protein (Fragment) OS=Homo sapiens GN=SFPQ PE=2 SV=1 - [Q6PIX2_HUMAN] | 25.71 | 1 | 0 | 14 | 43 | 137.58832 |
| B4E2Z2 | cDNA FLJ51193, highly similar to DNA mismatch repair protein Msh2 OS=Homo sapiens PE=2 SV=1 - [B4E2Z2_HUMAN] | 21.31 | 1 | 0 | 14 | 27 | 85.6778727 |
| Q8NHX6 | Cervical cancer proto-oncogene 5 OS=Homo sapiens GN=HCC5 PE=2 SV=1 - [Q8NHX6_HUMAN] | 25.74 | 1 | 0 | 14 | 23 | 78.585042 |
| Q96GW1 | HSP90B1 protein OS=Homo sapiens GN=HSP90B1 PE=2 SV=1 - [Q96GW1_HUMAN] | 54.6 | 1 | 0 | 13 | 66 | 229.188627 |
| Q14974 | Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2 - [IMB1_HUMAN] | 21.69 | 1 | 0 | 13 | 38 | 136.704844 |
| B2RBR9 | cDNA, FLJ95650, highly similar to Homo sapiens karyopherin (importin) beta 1 (KPNB1), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RBR9_HUMAN] | 21.69 | 1 | 0 | 13 | 38 | 136.704844 |
| A8K5W7 | cDNA FLJ75180, highly similar to Homo sapiens mitochondrial isoleucine tRNA synthetase, mRNA OS=Homo sapiens PE=2 SV=1 - [A8K5W7_HUMAN] | 14.26 | 1 | 0 | 13 | 29 | 85.3369877 |
| B4DRRO | cDNA FLJ53910, highly similar to Keratin, type II cytoskeletal 6A OS=Homo sapiens PE=2 SV=1 - [B4DRRO_HUMAN] | 23.18 | 1 | 0 | 13 | 27 | 82.7441678 |
| P02538 | Keratin, type II cytoskeletal 6A OS=Homo sapiens GN=KRT6A PE=1 SV=3 - [K2C6A_HUMAN] | 21.99 | 1 | 0 | 13 | 27 | 82.7441678 |
| P48668 | Keratin, type II cytoskeletal 6C OS=Homo sapiens GN=KRT6C PE=1 SV=3 - [K2C6C_HUMAN] | 21.99 | 1 | 0 | 13 | 27 | 82.6378176 |
| B2R853 | cDNA, FLJ93744, highly similar to Homo sapiens keratin 6E (KRT6E), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R853_HUMAN] | 21.99 | 1 | 0 | 13 | 27 | 82.6378176 |
| B4DLA6 | cDNA FLJ54365, highly similar to DNA replication licensing factor MCM4 OS=Homo sapiens PE=2 SV=1 - [B4DLA6_HUMAN] | 22.84 | 1 | 0 | 13 | 26 | 80.3747735 |
| P33991 | DNA replication licensing factor MCM4 OS=Homo sapiens GN=MCM4 PE=1 SV=5 - [MCM4_HUMAN] | 21.78 | 1 | 0 | 13 | 26 | 80.3747735 |
| B3KMX0 | cDNA FLJ12837 fis, clone NT2RP2003228, highly similar to DNA replication licensing factor MCM4 OS=Homo sapiens PE=2 SV=1 - [B3KMX0_HUMAN] | 21.78 | 1 | 0 | 13 | 26 | 80.3747735 |

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|--------|----------------------------------------------------------------------------------------------------------------------------------------------|-------|---|---|----|----|------------|
| Q53RU4 | Putative uncharacterized protein MSH2 (Fragment) OS=Homo sapiens GN=MSH2 PE=2 SV=1 - [Q53RU4_HUMAN] | 29.86 | 1 | 0 | 13 | 25 | 77.4077992 |
| B4DM31 | cDNA FLJ54022, highly similar to Exportin-2 OS=Homo sapiens PE=2 SV=1 - [B4DM31_HUMAN] | 23.23 | 1 | 0 | 13 | 25 | 78.2652807 |
| B4DUQ9 | cDNA FLJ50873, highly similar to DNA replication licensing factor MCM3 OS=Homo sapiens PE=2 SV=1 - [B4DUQ9_HUMAN] | 20.6 | 1 | 0 | 13 | 22 | 76.4279275 |
| P13637 | Sodium/potassium-transporting ATPase subunit alpha-3 OS=Homo sapiens GN=ATP1A3 PE=1 SV=3 - [AT1A3_HUMAN] | 14.22 | 1 | 0 | 12 | 31 | 116.221705 |
| Q53ES0 | Na ⁺ /K ⁺ -ATPase alpha 3 subunit variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53ES0_HUMAN] | 14.22 | 1 | 0 | 12 | 31 | 116.221705 |
| B7Z401 | cDNA FLJ54717, highly similar to Sodium/potassium-transporting ATPase alpha-3 chain (EC 3.6.3.9) OS=Homo sapiens PE=2 SV=1 - [B7Z401_HUMAN] | 14.06 | 1 | 0 | 12 | 31 | 116.221705 |
| B7Z9V4 | cDNA, FLJ78968, highly similar to Sodium/potassium-transporting ATPase alpha-3 chain (EC 3.6.3.9) OS=Homo sapiens PE=2 SV=1 - [B7Z9V4_HUMAN] | 14.04 | 1 | 0 | 12 | 31 | 116.221705 |
| B7Z2T0 | cDNA FLJ59513, highly similar to Sodium/potassium-transporting ATPase alpha-3 chain (EC 3.6.3.9) OS=Homo sapiens PE=2 SV=1 - [B7Z2T0_HUMAN] | 14.04 | 1 | 0 | 12 | 31 | 116.221705 |
| P04259 | Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5 - [K2C6B_HUMAN] | 18.97 | 1 | 0 | 12 | 27 | 75.0736806 |
| B4DRU6 | cDNA FLJ54657, highly similar to Keratin, type II cytoskeletal 6A OS=Homo sapiens PE=2 SV=1 - [B4DRU6_HUMAN] | 20.4 | 1 | 0 | 12 | 25 | 76.8968399 |
| B4E1T1 | cDNA FLJ54081, highly similar to Keratin, type II cytoskeletal 5 OS=Homo sapiens PE=2 SV=1 - [B4E1T1_HUMAN] | 19.28 | 1 | 0 | 12 | 24 | 65.7711346 |
| P11387 | DNA topoisomerase 1 OS=Homo sapiens GN=TOP1 PE=1 SV=2 - [TOP1_HUMAN] | 17.25 | 1 | 0 | 12 | 21 | 67.6685972 |
| B7Z1Q9 | cDNA FLJ59485, highly similar to Sodium/potassium-transporting ATPase alpha-3 chain (EC 3.6.3.9) OS=Homo sapiens PE=2 SV=1 - [B7Z1Q9_HUMAN] | 14.58 | 1 | 0 | 11 | 29 | 110.97701 |
| B7Z1N5 | cDNA FLJ53830, highly similar to Sodium/potassium-transporting ATPase alpha-1 chain (EC 3.6.3.9) OS=Homo sapiens PE=2 SV=1 - [B7Z1N5_HUMAN] | 32.1 | 1 | 0 | 11 | 28 | 106.233739 |
| B4DUC5 | cDNA FLJ53202, highly similar to Exportin-2 OS=Homo sapiens | 20.16 | 1 | 0 | 11 | 26 | 86.3488405 |

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|--------|-------------------------------------------------------------------------------------------------------------------|-------|---|---|----|----|------------|
| | PE=2 SV=1 - [B4DUC5_HUMAN] | | | | | | |
| B7ZM99 | MTHFD1L protein OS=Homo sapiens GN=MTHFD1L PE=2 SV=1 - [B7ZM99_HUMAN] | 14.61 | 1 | 0 | 11 | 25 | 78.1189141 |
| A4VCH6 | LONP1 protein (Fragment) OS=Homo sapiens GN=LONP1 PE=2 SV=1 - [A4VCH6_HUMAN] | 45.12 | 1 | 0 | 11 | 24 | 81.1615319 |
| B4DWU6 | cDNA FLJ51361, highly similar to Keratin, type II cytoskeletal 6A OS=Homo sapiens PE=2 SV=1 - [B4DWU6_HUMAN] | 20.38 | 1 | 0 | 11 | 23 | 72.8643601 |
| A8K2IO | cDNA FLJ78504, highly similar to Homo sapiens keratin 6A (KRT6A), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K2IO_HUMAN] | 17.2 | 1 | 0 | 11 | 23 | 64.1805139 |
| B4DRY0 | cDNA FLJ54379, highly similar to Keratin, type II cytoskeletal 6E OS=Homo sapiens PE=2 SV=1 - [B4DRY0_HUMAN] | 20.84 | 1 | 0 | 11 | 21 | 64.019021 |
| Q59GF8 | Heat shock 70kDa protein 4 isoform a variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59GF8_HUMAN] | 17.01 | 1 | 0 | 11 | 20 | 62.839021 |
| B7Z565 | cDNA FLJ54739, highly similar to Alpha-actinin-1 OS=Homo sapiens PE=2 SV=1 - [B7Z565_HUMAN] | 16.06 | 1 | 0 | 11 | 20 | 61.7479656 |
| P34932 | Heat shock 70 kDa protein 4 OS=Homo sapiens GN=HSPA4 PE=1 SV=4 - [HSP74_HUMAN] | 15.83 | 1 | 0 | 11 | 20 | 62.839021 |
| B4DH02 | cDNA FLJ50510, highly similar to Heat shock 70 kDa protein 4 OS=Homo sapiens PE=2 SV=1 - [B4DH02_HUMAN] | 15.83 | 1 | 0 | 11 | 20 | 62.839021 |
| B3V8S3 | Actinin 1 smooth muscle variant OS=Homo sapiens GN=ACTN1 PE=2 SV=1 - [B3V8S3_HUMAN] | 14.88 | 1 | 0 | 11 | 20 | 61.7479656 |
| B4DHH3 | cDNA FLJ59209, highly similar to Alpha-actinin-1 OS=Homo sapiens PE=2 SV=1 - [B4DHH3_HUMAN] | 14.88 | 1 | 0 | 11 | 20 | 61.7479656 |
| P12814 | Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=1 SV=2 - [ACTN1_HUMAN] | 14.8 | 1 | 0 | 11 | 20 | 61.7479656 |
| Q1HE25 | Actinin alpha 1 isoform b OS=Homo sapiens GN=ACTN1 PE=2 SV=1 - [Q1HE25_HUMAN] | 14.44 | 1 | 0 | 11 | 20 | 61.7479656 |
| B7TY16 | Actinin alpha 1 isoform 3 OS=Homo sapiens GN=ACTN1 PE=2 SV=1 - [B7TY16_HUMAN] | 14.19 | 1 | 0 | 11 | 20 | 61.7479656 |
| B4DS46 | cDNA FLJ55751, highly similar to DNA replication licensing factor MCM3 OS=Homo sapiens PE=2 SV=1 - [B4DS46_HUMAN] | 16.42 | 1 | 0 | 11 | 19 | 63.740701 |
| B9EG90 | Topoisomerase (DNA) I OS=Homo sapiens GN=TOP1 PE=2 SV=1 - [B9EG90_HUMAN] | 15.56 | 1 | 0 | 11 | 19 | 60.4037614 |

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| Q96T88 | E3 ubiquitin-protein ligase UHRF1 OS=Homo sapiens GN=UHRF1 PE=1 SV=1 - [UHRF1_HUMAN] | 17.02 | 1 | 0 | 11 | 18 | 58.0402369 |
| B2RBA9 | cDNA FLJ95411, highly similar to Homo sapiens ubiquitin-like, containing PHD and RING finger domains, 1 (UHRF1), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RBA9_HUMAN] | 17.02 | 1 | 0 | 11 | 18 | 58.0402369 |
| A8K024 | cDNA FLJ78091, highly similar to Homo sapiens ubiquitin-like, containing PHD and RING finger domains, 1 (UHRF1), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K024_HUMAN] | 17.02 | 1 | 0 | 11 | 18 | 58.0402369 |
| Q2HIX7 | Ubiquitin-like with PHD and ring finger domains 1 OS=Homo sapiens GN=UHRF1 PE=2 SV=2 - [Q2HIX7_HUMAN] | 16.75 | 1 | 0 | 11 | 18 | 58.0402369 |
| B3KV59 | cDNA FLJ16157 fis, clone BRAWH2006479, highly similar to Sodium/potassium-transporting ATPase alpha-3 chain (EC 3.6.3.9) OS=Homo sapiens PE=2 SV=1 - [B3KV59_HUMAN] | 17.3 | 1 | 0 | 10 | 27 | 103.149702 |
| B7Z3F8 | cDNA FLJ59543, highly similar to Sodium/potassium-transporting ATPase alpha-3 chain (EC 3.6.3.9) OS=Homo sapiens PE=2 SV=1 - [B7Z3F8_HUMAN] | 12.72 | 1 | 0 | 10 | 27 | 97.0715361 |
| Q6UB35 | Monofunctional C1-tetrahydrofolate synthase, mitochondrial OS=Homo sapiens GN=MTHFD1L PE=1 SV=1 - [C1TM_HUMAN] | 13.6 | 1 | 0 | 10 | 24 | 75.6756306 |
| Q96BG6 | ACTN4 protein (Fragment) OS=Homo sapiens GN=ACTN4 PE=2 SV=2 - [Q96BG6_HUMAN] | 20.98 | 1 | 0 | 10 | 23 | 75.0758963 |
| D6PXX4 | Alpha actinin 4 short isoform OS=Homo sapiens GN=ACTN4 PE=2 SV=1 - [D6PXX4_HUMAN] | 19.22 | 1 | 0 | 10 | 23 | 75.0758963 |
| B4DPS6 | cDNA FLJ59371, highly similar to Exportin-2 OS=Homo sapiens PE=2 SV=1 - [B4DPS6_HUMAN] | 21.29 | 1 | 0 | 10 | 20 | 60.521137 |
| B3KX72 | cDNA FLJ44920 fis, clone BRAMY3011501, highly similar to Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens PE=2 SV=1 - [B3KX72_HUMAN] | 15.6 | 1 | 0 | 10 | 18 | 52.7273927 |
| Q00839 | Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6 - [HNRPU_HUMAN] | 14.18 | 1 | 0 | 10 | 18 | 52.7273927 |
| Q0IIN5 | VCP protein OS=Homo sapiens GN=VCP PE=2 SV=1 - [Q0IIN5_HUMAN] | 26.53 | 1 | 0 | 9 | 25 | 90.1246629 |
| B3KSY7 | cDNA FLJ37309 fis, clone BRAMY2016611, highly similar to Sodium/potassium-transporting ATPase alpha-3 chain (EC 3.6.3.9) OS=Homo sapiens PE=2 SV=1 - [B3KSY7_HUMAN] | 15.67 | 1 | 0 | 9 | 25 | 94.6812975 |

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| B2RD24 | cDNA, FLJ96424 OS=Homo sapiens PE=2 SV=1 - [B2RD24_HUMAN] | 16.51 | 1 | 0 | 9 | 23 | 73.3914411 |
| B4DS32 | cDNA FLJ56236, highly similar to Exportin-2 OS=Homo sapiens PE=2 SV=1 - [B4DS32_HUMAN] | 21.79 | 1 | 0 | 9 | 22 | 74.0175369 |
| B3KRI1 | cDNA FLJ34298 fis, clone FEBRA2006357, highly similar to Sodium/potassium-transporting ATPase alpha-2 chain (EC 3.6.3.9) OS=Homo sapiens PE=2 SV=1 - [B3KRI1_HUMAN] | 12.25 | 1 | 0 | 9 | 21 | 79.3322155 |
| B1AKY9 | ATPase, Na+/K+ transporting, alpha 2 (+) polypeptide OS=Homo sapiens GN=ATP1A2 PE=4 SV=1 - [B1AKY9_HUMAN] | 11.5 | 1 | 0 | 9 | 21 | 79.3322155 |
| P50993 | Sodium/potassium-transporting ATPase subunit alpha-2 OS=Homo sapiens GN=ATP1A2 PE=1 SV=1 - [AT1A2_HUMAN] | 11.37 | 1 | 0 | 9 | 21 | 79.3322155 |
| B2RAQ4 | cDNA, FLJ95053, highly similar to Homo sapiens ATPase, Na+/K+ transporting, alpha 2 (+) polypeptide(ATP1A2), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RAQ4_HUMAN] | 11.37 | 1 | 0 | 9 | 21 | 79.3322155 |
| B4DL39 | cDNA FLJ57316, highly similar to DNA mismatch repair protein Msh2 OS=Homo sapiens PE=2 SV=1 - [B4DL39_HUMAN] | 17.3 | 1 | 0 | 9 | 19 | 60.9825525 |
| O14992 | HS24/P52 OS=Homo sapiens GN=HS24/p52 PE=2 SV=1 - [O14992_HUMAN] | 24.68 | 1 | 0 | 9 | 17 | 55.7288001 |
| P56192 | Methionyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=MARS PE=1 SV=2 - [SYMC_HUMAN] | 14.89 | 1 | 0 | 9 | 17 | 59.9909949 |
| A8K492 | cDNA FLJ76789, highly similar to Homo sapiens methionine-tRNA synthetase (MARS), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K492_HUMAN] | 14.89 | 1 | 0 | 9 | 17 | 59.9909949 |
| Q96BA7 | HNRPU protein OS=Homo sapiens PE=2 SV=1 - [Q96BA7_HUMAN] | 14.82 | 1 | 0 | 9 | 17 | 49.7077951 |
| Q5RI17 | Heterogeneous nuclear ribonucleoprotein U (Scaffold attachment factor A) (Fragment) OS=Homo sapiens GN=HNRNPU PE=2 SV=1 - [Q5RI17_HUMAN] | 14.8 | 1 | 0 | 9 | 17 | 49.7077951 |
| B4DN49 | cDNA FLJ50998, highly similar to DNA mismatch repair protein Msh2 OS=Homo sapiens PE=2 SV=1 - [B4DN49_HUMAN] | 13.99 | 1 | 0 | 9 | 17 | 55.1845455 |
| B4E337 | cDNA FLJ58087, highly similar to Alpha-actinin-4 OS=Homo sapiens PE=2 SV=1 - [B4E337_HUMAN] | 20.28 | 1 | 0 | 9 | 16 | 52.5617502 |
| A8K590 | cDNA FLJ77456, highly similar to Homo sapiens interleukin enhancer binding factor 3, 90kDa (ILF3), transcript variant 2, | 12.54 | 1 | 0 | 9 | 14 | 36.3453374 |

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|--------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------|---|---|---|----|------------|
| | mRNA OS=Homo sapiens PE=2 SV=1 - [A8K590_HUMAN] | | | | | | |
| Q9BXJ9 | N-alpha-acetyltransferase 15, NatA auxiliary subunit OS=Homo sapiens GN=NAA15 PE=1 SV=1 - [NAA15_HUMAN] | 12.12 | 1 | 0 | 9 | 14 | 39.0858116 |
| B2RBE5 | cDNA, FLJ95468, highly similar to Homo sapiens transcriptional coactivator tubedown-100 (TBDN100), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1 - [B2RBE5_HUMAN] | 12.12 | 1 | 0 | 9 | 14 | 39.0858116 |
| C9JFV5 | Uncharacterized protein OS=Homo sapiens GN=ILF3 PE=4 SV=1 - [C9JFV5_HUMAN] | 11.52 | 1 | 0 | 9 | 14 | 36.3453374 |
| Q9NTC4 | Putative uncharacterized protein DKFZp434K0126 (Fragment) OS=Homo sapiens GN=DKFZp434K0126 PE=2 SV=1 - [Q9NTC4_HUMAN] | 26.45 | 1 | 0 | 8 | 23 | 84.0930359 |
| A4K467 | Actinin alpha4 isoform OS=Homo sapiens GN=ACTN4 PE=2 SV=1 - [A4K467_HUMAN] | 20.92 | 1 | 0 | 8 | 20 | 66.5423677 |
| B4DM22 | cDNA FLJ53357, highly similar to 26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens PE=2 SV=1 - [B4DM22_HUMAN] | 11.89 | 1 | 0 | 8 | 18 | 61.0785487 |
| Q13200 | 26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 PE=1 SV=3 - [PSMD2_HUMAN] | 11.78 | 1 | 0 | 8 | 18 | 61.0785487 |
| Q53XQ4 | Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 2 OS=Homo sapiens PE=2 SV=1 - [Q53XQ4_HUMAN] | 11.78 | 1 | 0 | 8 | 18 | 61.0785487 |
| Q59EG8 | Proteasome 26S non-ATPase subunit 2 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59EG8_HUMAN] | 11.72 | 1 | 0 | 8 | 18 | 61.0785487 |
| B4DSB9 | cDNA FLJ51069, highly similar to DNA mismatch repair protein Msh2 OS=Homo sapiens PE=2 SV=1 - [B4DSB9_HUMAN] | 13.06 | 1 | 0 | 8 | 17 | 51.5923691 |
| B4DKV4 | cDNA FLJ60647, highly similar to Keratin, type II cytoskeletal 6B OS=Homo sapiens PE=2 SV=1 - [B4DKV4_HUMAN] | 14.26 | 1 | 0 | 8 | 15 | 39.6080391 |
| B4DLR3 | cDNA FLJ54020, highly similar to Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens PE=2 SV=1 - [B4DLR3_HUMAN] | 11.86 | 1 | 0 | 8 | 15 | 44.1574543 |
| P46087 | Putative ribosomal RNA methyltransferase NOP2 OS=Homo sapiens GN=NOP2 PE=1 SV=2 - [NOP2_HUMAN] | 11.33 | 1 | 0 | 8 | 12 | 34.9711926 |
| Q3KQS4 | NOP2 protein OS=Homo sapiens GN=NOP2 PE=2 SV=1 - [Q3KQS4_HUMAN] | 10.89 | 1 | 0 | 8 | 12 | 34.9711926 |

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| B7Z4B2 | cDNA FLJ56108, highly similar to Puromycin-sensitive aminopeptidase (EC 3.4.11.-) OS=Homo sapiens PE=2 SV=1 - [B7Z4B2_HUMAN] | 10.18 | 1 | 0 | 8 | 11 | 31.0696051 |
| B7Z463 | cDNA FLJ53354, highly similar to Puromycin-sensitive aminopeptidase (EC 3.4.11.-) OS=Homo sapiens PE=2 SV=1 - [B7Z463_HUMAN] | 10.01 | 1 | 0 | 8 | 11 | 31.0696051 |
| B7Z899 | cDNA FLJ55506, highly similar to Puromycin-sensitive aminopeptidase (EC3.4.11.-) OS=Homo sapiens PE=2 SV=1 - [B7Z899_HUMAN] | 9.18 | 1 | 0 | 8 | 11 | 31.0696051 |
| P55786 | Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS PE=1 SV=2 - [PSA_HUMAN] | 9.14 | 1 | 0 | 8 | 11 | 31.0696051 |
| B4DQX3 | cDNA FLJ58927, highly similar to Endoplasmic (Heat shock protein 90 kDa beta member 1) OS=Homo sapiens PE=2 SV=1 - [B4DQX3_HUMAN] | 49.69 | 1 | 0 | 7 | 54 | 189.822133 |
| Q9HAP1 | Valosin-containing protein (Fragment) OS=Homo sapiens GN=VCP PE=2 SV=1 - [Q9HAP1_HUMAN] | 28.66 | 1 | 0 | 7 | 22 | 69.2421803 |
| B3KNQ8 | cDNA FLJ30174 fis, clone BRACE2000975, highly similar to Sodium/potassium-transporting ATPase alpha-3 chain (EC 3.6.3.9) OS=Homo sapiens PE=2 SV=1 - [B3KNQ8_HUMAN] | 21.38 | 1 | 0 | 7 | 20 | 75.8636401 |
| B4DDE4 | cDNA FLJ54582, highly similar to Ubiquitin-activating enzyme E1 OS=Homo sapiens PE=2 SV=1 - [B4DDE4_HUMAN] | 19.82 | 1 | 0 | 7 | 20 | 75.6818192 |
| B4DMA2 | cDNA FLJ54023, highly similar to Heat shock protein HSP 90-beta OS=Homo sapiens PE=2 SV=1 - [B4DMA2_HUMAN] | 10.2 | 1 | 0 | 7 | 20 | 65.2714179 |
| B4DGL0 | cDNA FLJ53619, highly similar to Heat shock protein HSP 90-beta OS=Homo sapiens PE=2 SV=1 - [B4DGL0_HUMAN] | 9.8 | 1 | 0 | 7 | 20 | 65.2714179 |
| P08238 | Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4 - [HS90B_HUMAN] | 9.67 | 1 | 0 | 7 | 20 | 65.2714179 |
| B4DM67 | cDNA FLJ59343, highly similar to Exportin-2 OS=Homo sapiens PE=2 SV=1 - [B4DM67_HUMAN] | 18.2 | 1 | 0 | 7 | 18 | 64.069226 |
| P08779 | Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4 - [K1C16_HUMAN] | 18.82 | 1 | 0 | 7 | 17 | 52.5209467 |
| B7ZAV6 | cDNA, FLJ79320, highly similar to Importin beta-1 subunit OS=Homo sapiens PE=2 SV=1 - [B7ZAV6_HUMAN] | 16.55 | 1 | 0 | 7 | 17 | 63.5569177 |
| B3KX35 | cDNA FLJ44610 fis, clone BRACE2012317, highly similar to | 13.74 | 1 | 0 | 7 | 17 | 66.2602119 |

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| | Sodium/potassium-transporting ATPase alpha-2 chain (EC 3.6.3.9) OS=Homo sapiens PE=2 SV=1 - [B3KX35_HUMAN] | | | | | | |
| Q8N3X5 | Similar to ATPase, Ca++ transporting, cardiac muscle, fast twitch 1 (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q8N3X5_HUMAN] | 13.27 | 1 | 0 | 7 | 17 | 67.8220484 |
| B1AKZ0 | ATPase, Na+/K+ transporting, alpha 2 (+) polypeptide (Fragment) OS=Homo sapiens GN=ATP1A2 PE=1 SV=1 - [B1AKZ0_HUMAN] | 12.62 | 1 | 0 | 7 | 17 | 66.2602119 |
| B4DIQ8 | cDNA FLJ56089, highly similar to Sodium/potassium-transporting ATPase alpha-2 chain (EC 3.6.3.9) OS=Homo sapiens PE=2 SV=1 - [B4DIQ8_HUMAN] | 12.45 | 1 | 0 | 7 | 17 | 66.2602119 |
| Q7Z675 | Putative uncharacterized protein DKFZp779O2152 OS=Homo sapiens GN=DKFZp779O2152 PE=2 SV=1 - [Q7Z675_HUMAN] | 11.27 | 1 | 0 | 7 | 17 | 67.8220484 |
| O14983 | Sarcoplasmic/endoplasmic reticulum calcium ATPase 1 OS=Homo sapiens GN=ATP2A1 PE=1 SV=1 - [AT2A1_HUMAN] | 11.19 | 1 | 0 | 7 | 17 | 67.8220484 |
| B4DXY1 | cDNA FLJ55045, highly similar to 26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens PE=2 SV=1 - [B4DXY1_HUMAN] | 12.42 | 1 | 0 | 7 | 16 | 55.6324894 |
| B4DX07 | cDNA FLJ54077, highly similar to 26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens PE=2 SV=1 - [B4DX07_HUMAN] | 11.95 | 1 | 0 | 7 | 16 | 55.6324894 |
| B4DR01 | cDNA FLJ55480, highly similar to Exportin-1 OS=Homo sapiens PE=2 SV=1 - [B4DR01_HUMAN] | 12.8 | 1 | 0 | 7 | 15 | 48.6039917 |
| B7ZB16 | cDNA, FLJ79380, highly similar to Exportin-1 OS=Homo sapiens PE=2 SV=1 - [B7ZB16_HUMAN] | 12.8 | 1 | 0 | 7 | 15 | 48.6039917 |
| E1P648 | Adaptor-related protein complex 2, beta 1 subunit, isoform CRA_c OS=Homo sapiens GN=AP2B1 PE=4 SV=1 - [E1P648_HUMAN] | 9.85 | 1 | 0 | 7 | 15 | 48.4624915 |
| E1P647 | Adaptor-related protein complex 2, beta 1 subunit, isoform CRA_b OS=Homo sapiens GN=AP2B1 PE=4 SV=1 - [E1P647_HUMAN] | 9.84 | 1 | 0 | 7 | 15 | 48.4624915 |
| P63010 | AP-2 complex subunit beta OS=Homo sapiens GN=AP2B1 PE=1 SV=1 - [AP2B1_HUMAN] | 9.82 | 1 | 0 | 7 | 15 | 48.4624915 |
| E1P646 | Adaptor-related protein complex 2, beta 1 subunit, isoform CRA_d OS=Homo sapiens GN=AP2B1 PE=4 SV=1 - | 9.69 | 1 | 0 | 7 | 15 | 48.4624915 |

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| | [E1P646_HUMAN] | | | | | | |
| A8K916 | cDNA FLJ78481, highly similar to Homo sapiens adaptor-related protein complex 2, beta 1 subunit, mRNA OS=Homo sapiens PE=2 SV=1 - [A8K916_HUMAN] | 9.67 | 1 | 0 | 7 | 15 | 48.4624915 |
| A8K0G3 | cDNA FLJ78733, highly similar to Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1 - [A8K0G3_HUMAN] | 9.67 | 1 | 0 | 7 | 15 | 48.4624915 |
| Q4ZG57 | Putative uncharacterized protein MCM6 (Fragment) OS=Homo sapiens GN=MCM6 PE=2 SV=1 - [Q4ZG57_HUMAN] | 7.9 | 1 | 0 | 7 | 15 | 51.4135878 |
| Q14566 | DNA replication licensing factor MCM6 OS=Homo sapiens GN=MCM6 PE=1 SV=1 - [MCM6_HUMAN] | 7.55 | 1 | 0 | 7 | 15 | 51.4135878 |
| B4DSX0 | cDNA FLJ61380, highly similar to Alpha-actinin-4 OS=Homo sapiens PE=2 SV=1 - [B4DSX0_HUMAN] | 21.63 | 1 | 0 | 7 | 13 | 44.0282216 |
| B4DG62 | cDNA FLJ56506, highly similar to Hexokinase-1 (EC 2.7.1.1) OS=Homo sapiens PE=2 SV=1 - [B4DG62_HUMAN] | 8.31 | 1 | 0 | 7 | 13 | 35.3957806 |
| P19367 | Hexokinase-1 OS=Homo sapiens GN=HK1 PE=1 SV=3 - [HXK1_HUMAN] | 8.29 | 1 | 0 | 7 | 13 | 35.3957806 |
| A8K7J7 | cDNA FLJ78173, highly similar to Homo sapiens hexokinase 1 (HK1) mRNA OS=Homo sapiens PE=2 SV=1 - [A8K7J7_HUMAN] | 8.29 | 1 | 0 | 7 | 13 | 35.3957806 |
| Q59FD4 | Hexokinase 1 isoform HK1 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59FD4_HUMAN] | 8.01 | 1 | 0 | 7 | 13 | 35.3957806 |
| B3KXY9 | cDNA FLJ46359 fis, clone TESTI4049786, highly similar to Hexokinase-1 (EC 2.7.1.1) OS=Homo sapiens PE=2 SV=1 - [B3KXY9_HUMAN] | 7.98 | 1 | 0 | 7 | 13 | 35.3957806 |
| B4E2G8 | cDNA FLJ54047, highly similar to Alpha-1 catenin (Cadherin-associated protein) OS=Homo sapiens PE=2 SV=1 - [B4E2G8_HUMAN] | 14.37 | 1 | 0 | 7 | 12 | 47.7035728 |
| P35221 | Catenin alpha-1 OS=Homo sapiens GN=CTNNA1 PE=1 SV=1 - [CTNA1_HUMAN] | 14.13 | 1 | 0 | 7 | 12 | 47.7035728 |
| B4DQW2 | NOL1/NOP2/Sun domain family, member 2, isoform CRA_a OS=Homo sapiens GN=NSUN2 PE=2 SV=1 - [B4DQW2_HUMAN] | 12.16 | 1 | 0 | 7 | 12 | 36.7545776 |
| Q08J23 | tRNA (cytosine-5-)-methyltransferase NSUN2 OS=Homo sapiens GN=NSUN2 PE=1 SV=2 - [NSUN2_HUMAN] | 11.6 | 1 | 0 | 7 | 12 | 36.7545776 |

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| A8K529 | cDNA FLJ76184, highly similar to Homo sapiens NOL1/NOP2/Sun domain family, member 2 (NSUN2), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K529_HUMAN] | 11.6 | 1 | 0 | 7 | 12 | 36.7545776 |
| B4DIZ3 | cDNA FLJ52593, highly similar to Heat shock 70 kDa protein 4 OS=Homo sapiens PE=2 SV=1 - [B4DIZ3_HUMAN] | 11.37 | 1 | 0 | 7 | 12 | 37.8642035 |
| B4DUS3 | cDNA FLJ50691, highly similar to Heat shock 70 kDa protein 4 OS=Homo sapiens PE=2 SV=1 - [B4DUS3_HUMAN] | 11.16 | 1 | 0 | 7 | 12 | 37.8642035 |
| O95757 | Heat shock 70 kDa protein 4L OS=Homo sapiens GN=HSPA4L PE=1 SV=3 - [HS74L_HUMAN] | 11.8 | 1 | 0 | 7 | 11 | 34.9507172 |
| Q53ZP9 | Heat shock protein apg-1 OS=Homo sapiens PE=2 SV=1 - [Q53ZP9_HUMAN] | 11.8 | 1 | 0 | 7 | 11 | 34.9507172 |
| A8MQ38 | Uncharacterized protein OS=Homo sapiens GN=NOP2 PE=4 SV=1 - [A8MQ38_HUMAN] | 9.48 | 1 | 0 | 7 | 11 | 32.6880565 |
| B7Z1V9 | cDNA FLJ53310, highly similar to Puromycin-sensitive aminopeptidase (EC 3.4.11.-) OS=Homo sapiens PE=2 SV=1 - [B7Z1V9_HUMAN] | 15.43 | 1 | 0 | 7 | 9 | 25.0092673 |
| B7Z1H4 | cDNA FLJ56052, highly similar to Puromycin-sensitive aminopeptidase (EC 3.4.11.-) OS=Homo sapiens PE=2 SV=1 - [B7Z1H4_HUMAN] | 12.13 | 1 | 0 | 7 | 9 | 25.0092673 |
| Q6W6M8 | Antigen MLAA-42 (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q6W6M8_HUMAN] | 47.68 | 1 | 0 | 6 | 29 | 143.279075 |
| Q6PK50 | HSP90AB1 protein (Fragment) OS=Homo sapiens GN=HSP90AB1 PE=2 SV=1 - [Q6PK50_HUMAN] | 18.23 | 1 | 0 | 6 | 18 | 60.9784122 |
| B4DL67 | cDNA FLJ53392, highly similar to Ubiquitin-activating enzyme E1 OS=Homo sapiens PE=2 SV=1 - [B4DL67_HUMAN] | 14.93 | 1 | 0 | 6 | 17 | 63.199723 |
| Q7Z6E5 | Putative uncharacterized protein DKFZp779G2251 (Fragment) OS=Homo sapiens GN=DKFZp779G2251 PE=2 SV=1 - [Q7Z6E5_HUMAN] | 9.77 | 1 | 0 | 6 | 16 | 65.7133403 |
| B4DL32 | cDNA FLJ59922, highly similar to Keratin, type II cytoskeletal 5 OS=Homo sapiens PE=2 SV=1 - [B4DL32_HUMAN] | 21.37 | 1 | 0 | 6 | 15 | 41.9009368 |
| B7Z752 | cDNA FLJ50715, highly similar to Importin beta-1 subunit OS=Homo sapiens PE=2 SV=1 - [B7Z752_HUMAN] | 14.36 | 1 | 0 | 6 | 15 | 56.7323415 |
| B3KY17 | cDNA FLJ46599 fis, clone THYMU3047115, highly similar to Sarcoplasmic/endoplasmic reticulum calcium ATPase 1 (EC | 10.82 | 1 | 0 | 6 | 15 | 61.1917646 |

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| | 3.6.3.8) OS=Homo sapiens PE=2 SV=1 - [B3KY17_HUMAN] | | | | | | |
| B3KW93 | cDNA FLJ42590 fis, clone BRACE3009708, highly similar to Sodium/potassium-transporting ATPase alpha-2chain (EC 3.6.3.9) OS=Homo sapiens PE=2 SV=1 - [B3KW93_HUMAN] | 8.8 | 1 | 0 | 6 | 15 | 52.3547382 |
| Q68DI0 | Putative uncharacterized protein DKFZp781K0743 OS=Homo sapiens GN=DKFZp781K0743 PE=2 SV=1 - [Q68DI0_HUMAN] | 8.83 | 1 | 0 | 6 | 14 | 46.0427341 |
| B7Z5M1 | cDNA FLJ50625, highly similar to Importin beta-1 subunit OS=Homo sapiens PE=2 SV=1 - [B7Z5M1_HUMAN] | 15.91 | 1 | 0 | 6 | 13 | 48.5896692 |
| B4DFY0 | cDNA FLJ53313, highly similar to Alpha-actinin-1 OS=Homo sapiens PE=2 SV=1 - [B4DFY0_HUMAN] | 13.48 | 1 | 0 | 6 | 13 | 41.8031871 |
| B3KWD0 | cDNA FLJ42779 fis, clone BRAWH3005300, highly similar to Exportin-1 OS=Homo sapiens PE=2 SV=1 - [B3KWD0_HUMAN] | 12.53 | 1 | 0 | 6 | 13 | 43.7634895 |
| B4E261 | cDNA FLJ55646, highly similar to Adapter-relatedprotein complex 2 beta-1 subunit OS=Homo sapiens PE=2 SV=1 - [B4E261_HUMAN] | 12.21 | 1 | 0 | 6 | 13 | 42.7337773 |
| Q7Z451 | Adaptor-related protein complex 2, beta 1 subunit, isoform CRA_f OS=Homo sapiens GN=AP2B1 PE=2 SV=1 - [Q7Z451_HUMAN] | 9.55 | 1 | 0 | 6 | 13 | 42.7337773 |
| B4DWG4 | cDNA FLJ53223, highly similar to Adapter-relatedprotein complex 2 beta-1 subunit OS=Homo sapiens PE=2 SV=1 - [B4DWG4_HUMAN] | 8.65 | 1 | 0 | 6 | 13 | 43.5891728 |
| B4DKT9 | cDNA FLJ54052, highly similar to Alpha-1 catenin (Cadherin-associated protein) OS=Homo sapiens PE=2 SV=1 - [B4DKT9_HUMAN] | 14.05 | 1 | 0 | 6 | 11 | 44.608927 |
| B4DU00 | cDNA FLJ54547, highly similar to Alpha-1 catenin (Cadherin-associated protein) OS=Homo sapiens PE=2 SV=1 - [B4DU00_HUMAN] | 13.7 | 1 | 0 | 6 | 11 | 44.608927 |
| B4E354 | cDNA FLJ55293, highly similar to Heat shock 70 kDa protein 4 OS=Homo sapiens PE=2 SV=1 - [B4E354_HUMAN] | 11.29 | 1 | 0 | 6 | 11 | 35.6404486 |
| B4DT47 | cDNA FLJ54507, highly similar to Heat shock 70 kDa protein 4 OS=Homo sapiens PE=2 SV=1 - [B4DT47_HUMAN] | 10.53 | 1 | 0 | 6 | 11 | 35.6404486 |
| B3KP09 | cDNA FLJ30894 fis, clone FEBRA2005416, highly similar to Homo sapiens NOL1/NOP2/Sun domain family, member 2 (NSUN2), mRNA OS=Homo sapiens PE=2 SV=1 - [B3KP09_HUMAN] | 13.18 | 1 | 0 | 6 | 10 | 29.7261355 |

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| Q7Z4Q5 | Heterogeneous nuclear ribonucleoprotein U (Scaffold attachment factor A), isoform CRA_a OS=Homo sapiens GN=HNRPU PE=2 SV=1 - [Q7Z4Q5_HUMAN] | 12.67 | 1 | 0 | 6 | 10 | 29.3526623 |
| A8K1B6 | cDNA FLJ78533, highly similar to Homo sapiens dynamin 2 (DNM2), transcript variant 4, mRNA OS=Homo sapiens PE=2 SV=1 - [A8K1B6_HUMAN] | 12.47 | 1 | 0 | 6 | 10 | 32.8480334 |
| P50570 | Dynamin-2 OS=Homo sapiens GN=DNM2 PE=1 SV=2 - [DYN2_HUMAN] | 12.41 | 1 | 0 | 6 | 10 | 32.8480334 |
| Q5RI19 | Heterogeneous nuclear ribonucleoprotein U (Scaffold attachment factor A) OS=Homo sapiens GN=HNRNPU PE=2 SV=1 - [Q5RI19_HUMAN] | 11.84 | 1 | 0 | 6 | 10 | 29.3526623 |
| C9JMP9 | Uncharacterized protein OS=Homo sapiens GN=CTNNA1 PE=4 SV=1 - [C9JMP9_HUMAN] | 10.98 | 1 | 0 | 6 | 10 | 34.7239466 |
| B4DXT2 | cDNA FLJ59635, highly similar to Heat shock 70 kDa protein 4L OS=Homo sapiens PE=2 SV=1 - [B4DXT2_HUMAN] | 10.46 | 1 | 0 | 6 | 10 | 31.6130738 |
| B4DFG4 | cDNA FLJ58801, highly similar to Interleukin enhancer-binding factor 3 OS=Homo sapiens PE=2 SV=1 - [B4DFG4_HUMAN] | 10.08 | 1 | 0 | 6 | 10 | 24.0267339 |
| B4DZI8 | Coatomer protein complex, subunit beta 2 (Beta prime), isoform CRA_b OS=Homo sapiens GN=COPB2 PE=2 SV=1 - [B4DZI8_HUMAN] | 7.75 | 1 | 0 | 6 | 10 | 28.2636318 |
| P35606 | Coatomer subunit beta' OS=Homo sapiens GN=COPB2 PE=1 SV=2 - [COPB2_HUMAN] | 7.51 | 1 | 0 | 6 | 10 | 28.2636318 |
| Q01546 | Keratin, type II cytoskeletal 2 oral OS=Homo sapiens GN=KRT76 PE=1 SV=2 - [K22O_HUMAN] | 6.9 | 1 | 0 | 6 | 10 | 26.8235495 |
| D6RJ96 | Uncharacterized protein OS=Homo sapiens GN=HSPA4L PE=4 SV=1 - [D6RJ96_HUMAN] | 16.76 | 1 | 0 | 6 | 9 | 29.6492519 |
| B3KNM0 | cDNA FLJ14916 fis, clone PLACE1006958, highly similar to Heat shock 70 kDa protein 4L (Fragment) OS=Homo sapiens PE=2 SV=1 - [B3KNM0_HUMAN] | 15.56 | 1 | 0 | 6 | 9 | 29.6492519 |
| Q59GP7 | Interleukin enhancer binding factor 3 isoform c variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59GP7_HUMAN] | 13.11 | 1 | 0 | 6 | 9 | 24.2519813 |
| B4E2T6 | cDNA FLJ58231, highly similar to NMDA receptor-regulated protein 1 OS=Homo sapiens PE=2 SV=1 - [B4E2T6_HUMAN] | 10 | 1 | 0 | 6 | 9 | 25.841136 |
| Q86TX4 | Full-length cDNA clone CS0DB009YA03 of Neuroblastoma of | 13.32 | 1 | 0 | 6 | 8 | 22.5579009 |

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| | Homo sapiens (human) (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q86TX4_HUMAN] | | | | | | |
| B3KU93 | cDNA FLJ39390 fis, clone PLACE6004219, highly similar to Puromycin-sensitive aminopeptidase OS=Homo sapiens PE=2 SV=1 - [B3KU93_HUMAN] | 8.2 | 1 | 0 | 6 | 8 | 21.3964725 |
| B7Z3E5 | cDNA FLJ53573, highly similar to Myosin Ic OS=Homo sapiens PE=2 SV=1 - [B7Z3E5_HUMAN] | 6.83 | 1 | 0 | 6 | 8 | 21.7562573 |
| O00159 | Myosin-Ic OS=Homo sapiens GN=MYO1C PE=1 SV=4 - [MYO1C_HUMAN] | 6.68 | 1 | 0 | 6 | 8 | 21.7562573 |
| Q9HAP0 | Valosin-containing protein (Fragment) OS=Homo sapiens GN=VCP PE=2 SV=1 - [Q9HAP0_HUMAN] | 25.9 | 1 | 0 | 5 | 13 | 52.8084118 |
| Q13041 | P67 OS=Homo sapiens PE=2 SV=1 - [Q13041_HUMAN] | 9.98 | 1 | 0 | 5 | 13 | 45.4703038 |
| B3KUX9 | cDNA FLJ40884 fis, clone UTERU2000607, highly similar to Alpha-actinin-1 OS=Homo sapiens PE=2 SV=1 - [B3KUX9_HUMAN] | 12.92 | 1 | 0 | 5 | 12 | 39.1900647 |
| P02533 | Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4 - [K1C14_HUMAN] | 10.59 | 1 | 0 | 5 | 12 | 34.07388 |
| Q14444 | Caprin-1 OS=Homo sapiens GN=CAPRIN1 PE=1 SV=2 - [CAPR1_HUMAN] | 7.76 | 1 | 0 | 5 | 11 | 29.4774566 |
| O95678 | Keratin, type II cytoskeletal 75 OS=Homo sapiens GN=KRT75 PE=1 SV=2 - [K2C75_HUMAN] | 8.35 | 1 | 0 | 5 | 10 | 25.8655918 |
| Q9BVT2 | Putative uncharacterized protein (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q9BVT2_HUMAN] | 30.68 | 1 | 0 | 5 | 9 | 27.7901967 |
| Q7KYNO | HS24/P52 protein (Fragment) OS=Homo sapiens GN=HS24/P52 PE=2 SV=1 - [Q7KYNO_HUMAN] | 22.56 | 1 | 0 | 5 | 9 | 26.7269061 |
| B3KVK7 | cDNA FLJ16674 fis, clone THYMU3008136, highly similar to Methionyl-tRNA synthetase (EC 6.1.1.10) OS=Homo sapiens PE=2 SV=1 - [B3KVK7_HUMAN] | 15.2 | 1 | 0 | 5 | 9 | 32.662185 |
| B4DF61 | cDNA FLJ53309, highly similar to Methionyl-tRNA synthetase (EC 6.1.1.10) OS=Homo sapiens PE=2 SV=1 - [B4DF61_HUMAN] | 11.02 | 1 | 0 | 5 | 9 | 28.7520583 |
| B4E0H6 | cDNA FLJ52584, highly similar to Heat shock 70 kDa protein 4 OS=Homo sapiens PE=2 SV=1 - [B4E0H6_HUMAN] | 10.46 | 1 | 0 | 5 | 9 | 28.8659971 |
| B2R5U1 | cDNA, FLJ92620, highly similar to Homo sapiens staphylococcal nuclease domain containing 1 (SND1),mRNA OS=Homo sapiens | 6.89 | 1 | 0 | 5 | 9 | 26.4448998 |

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| | PE=2 SV=1 - [B2R5U1_HUMAN] | | | | | | |
| B3KU67 | cDNA FLJ39264 fis, clone OCBBF2009603, highly similar to Staphylococcal nuclease domain-containing protein 1 OS=Homo sapiens PE=2 SV=1 - [B3KU67_HUMAN] | 6.78 | 1 | 0 | 5 | 9 | 26.4448998 |
| Q7KZF4 | Staphylococcal nuclease domain-containing protein 1 OS=Homo sapiens GN=SND1 PE=1 SV=1 - [SND1_HUMAN] | 6.7 | 1 | 0 | 5 | 9 | 26.4448998 |
| Q59FF0 | EBNA-2 co-activator variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59FF0_HUMAN] | 6.33 | 1 | 0 | 5 | 9 | 26.4448998 |
| C9J809 | Uncharacterized protein OS=Homo sapiens GN=MSH2 PE=4 SV=1 - [C9J809_HUMAN] | 47.86 | 1 | 0 | 5 | 8 | 24.6953201 |
| Q5TC01 | ATPase, Na+/K+ transporting, alpha 1 polypeptide (Fragment) OS=Homo sapiens GN=ATP1A1 PE=2 SV=1 - [Q5TC01_HUMAN] | 35.42 | 1 | 0 | 5 | 8 | 21.3503797 |
| B4DIL5 | cDNA FLJ54516, highly similar to Adapter-related protein complex 2 beta-1 subunit OS=Homo sapiens PE=2 SV=1 - [B4DIL5_HUMAN] | 18.53 | 1 | 0 | 5 | 8 | 20.8024557 |
| Q58F05 | NARG1 protein (Fragment) OS=Homo sapiens GN=NARG1 PE=2 SV=1 - [Q58F05_HUMAN] | 10.26 | 1 | 0 | 5 | 8 | 22.3952217 |
| B4DZR0 | cDNA FLJ55529, highly similar to Heat shock 70 kDa protein 4L OS=Homo sapiens PE=2 SV=1 - [B4DZR0_HUMAN] | 8.06 | 1 | 0 | 5 | 8 | 26.6811495 |
| Q8WUM4 | Programmed cell death 6-interacting protein OS=Homo sapiens GN=PDCD6IP PE=1 SV=1 - [PDC6I_HUMAN] | 6.91 | 1 | 0 | 5 | 8 | 24.8636003 |
| Q4W4Y1 | Dopamine receptor interacting protein 4 OS=Homo sapiens GN=DRIP4 PE=2 SV=1 - [Q4W4Y1_HUMAN] | 6.91 | 1 | 0 | 5 | 8 | 24.8636003 |
| Q6NUS1 | PDCD6IP protein OS=Homo sapiens GN=PDCD6IP PE=1 SV=1 - [Q6NUS1_HUMAN] | 6.87 | 1 | 0 | 5 | 8 | 24.8636003 |
| Q86X54 | AP1B1 protein OS=Homo sapiens PE=1 SV=1 - [Q86X54_HUMAN] | 6.64 | 1 | 0 | 5 | 8 | 24.1710756 |
| Q10567 | AP-1 complex subunit beta-1 OS=Homo sapiens GN=AP1B1 PE=1 SV=2 - [AP1B1_HUMAN] | 6.43 | 1 | 0 | 5 | 8 | 24.1710756 |
| B4DU52 | cDNA FLJ50221, highly similar to RNA-binding protein 28 OS=Homo sapiens PE=2 SV=1 - [B4DU52_HUMAN] | 11.33 | 1 | 0 | 5 | 7 | 18.5456429 |
| Q9NW13 | RNA-binding protein 28 OS=Homo sapiens GN=RBM28 PE=1 SV=3 - [RBM28_HUMAN] | 9.22 | 1 | 0 | 5 | 7 | 18.5456429 |

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| D3DTH7 | Myosin IC, isoform CRA_a OS=Homo sapiens GN=MYO1C PE=4 SV=1 - [D3DTH7_HUMAN] | 6.5 | 1 | 0 | 5 | 6 | 14.8542333 |
| B7Z2W3 | cDNA FLJ54432, highly similar to Alpha-actinin-1 OS=Homo sapiens PE=2 SV=1 - [B7Z2W3_HUMAN] | 7.54 | 1 | 0 | 4 | 11 | 36.0790362 |
| Q13733 | Sodium/potassium-transporting ATPase subunit alpha-4 OS=Homo sapiens GN=ATP1A4 PE=1 SV=3 - [AT1A4_HUMAN] | 5.25 | 1 | 0 | 4 | 11 | 39.6976602 |
| A1L0V1 | ACTN1 protein (Fragment) OS=Homo sapiens GN=ACTN1 PE=2 SV=1 - [A1L0V1_HUMAN] | 16.5 | 1 | 0 | 4 | 10 | 34.2371178 |
| E5RG31 | Uncharacterized protein OS=Homo sapiens GN=MCM4 PE=4 SV=1 - [E5RG31_HUMAN] | 16.13 | 1 | 0 | 4 | 10 | 26.4819012 |
| B4DWU0 | cDNA FLJ56791, highly similar to Keratin, type I cytoskeletal 16 OS=Homo sapiens PE=2 SV=1 - [B4DWU0_HUMAN] | 36.3 | 1 | 0 | 4 | 9 | 25.2498825 |
| B4E2J5 | cDNA FLJ53570, highly similar to Keratin, type I cytoskeletal 16 OS=Homo sapiens PE=2 SV=1 - [B4E2J5_HUMAN] | 26.06 | 1 | 0 | 4 | 9 | 25.2498825 |
| B4E2Z3 | cDNA FLJ54090, highly similar to 4F2 cell-surface antigen heavy chain OS=Homo sapiens PE=2 SV=1 - [B4E2Z3_HUMAN] | 10.96 | 1 | 0 | 4 | 9 | 28.1157072 |
| P08195 | 4F2 cell-surface antigen heavy chain OS=Homo sapiens GN=SLC3A2 PE=1 SV=3 - [4F2_HUMAN] | 8.89 | 1 | 0 | 4 | 9 | 28.1157072 |
| B3KXU8 | cDNA FLJ46087 fis, clone TESTI2009497, highly similar to GPI-anchored protein p137 OS=Homo sapiens PE=2 SV=1 - [B3KXU8_HUMAN] | 7.32 | 1 | 0 | 4 | 9 | 24.6756973 |
| B4DRF6 | cDNA FLJ51591, highly similar to DNA replication licensing factor MCM6 (Fragment) OS=Homo sapiens PE=2 SV=1 - [B4DRF6_HUMAN] | 7.27 | 1 | 0 | 4 | 9 | 34.8844621 |
| B4DUB7 | cDNA FLJ50225, highly similar to Glycogen phosphorylase, liver form (EC 2.4.1.1) OS=Homo sapiens PE=2 SV=1 - [B4DUB7_HUMAN] | 6.64 | 1 | 0 | 4 | 9 | 24.4496214 |
| P06737 | Glycogen phosphorylase, liver form OS=Homo sapiens GN=PYGL PE=1 SV=4 - [PYGL_HUMAN] | 6.38 | 1 | 0 | 4 | 9 | 24.4496214 |
| B2R825 | cDNA, FLJ93707, highly similar to Homo sapiens phosphorylase, glycogen; liver (Hers disease, glycogenstorage disease type VI) (PYGL), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R825_HUMAN] | 6.38 | 1 | 0 | 4 | 9 | 24.4496214 |
| Q9BUK9 | Heat shock 70kDa protein 4 OS=Homo sapiens GN=HSPA4 PE=2 SV=1 - [Q9BUK9_HUMAN] | 34.46 | 1 | 0 | 4 | 8 | 24.9748175 |

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| B4DSF8 | cDNA FLJ57278 OS=Homo sapiens PE=2 SV=1 - [B4DSF8_HUMAN] | 11.56 | 1 | 0 | 4 | 8 | 22.7799335 |
| B3KRA9 | cDNA FLJ33948 fis, clone CTONG2018379, highly similar to Hexokinase-1 (EC 2.7.1.1) OS=Homo sapiens PE=2 SV=1 - [B3KRA9_HUMAN] | 7.42 | 1 | 0 | 4 | 8 | 22.2412953 |
| Q8TDD1 | ATP-dependent RNA helicase DDX54 OS=Homo sapiens GN=DDX54 PE=1 SV=2 - [DDX54_HUMAN] | 7.15 | 1 | 0 | 4 | 8 | 27.0269845 |
| B9ZVP3 | DEAD (Asp-Glu-Ala-Asp) box polypeptide 54, isoform CRA_a OS=Homo sapiens GN=DDX54 PE=4 SV=2 - [B9ZVP3_HUMAN] | 7.14 | 1 | 0 | 4 | 8 | 27.0269845 |
| P49588 | Alanyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=AARS PE=1 SV=2 - [SYAC_HUMAN] | 4.86 | 1 | 0 | 4 | 8 | 20.6304705 |
| B4DR45 | cDNA FLJ61339, highly similar to Alanyl-tRNA synthetase (EC 6.1.1.7) OS=Homo sapiens PE=2 SV=1 - [B4DR45_HUMAN] | 4.74 | 1 | 0 | 4 | 8 | 20.6304705 |
| C9JYW2 | Uncharacterized protein OS=Homo sapiens GN=NCL PE=4 SV=1 - [C9JYW2_HUMAN] | 19.15 | 1 | 0 | 4 | 7 | 16.0023003 |
| C9JLB1 | Uncharacterized protein OS=Homo sapiens GN=NCL PE=4 SV=1 - [C9JLB1_HUMAN] | 17.88 | 1 | 0 | 4 | 7 | 16.0023003 |
| B4E0E9 | cDNA FLJ55046, highly similar to Methionyl-tRNA synthetase (EC 6.1.1.10) OS=Homo sapiens PE=2 SV=1 - [B4E0E9_HUMAN] | 16.98 | 1 | 0 | 4 | 7 | 25.0657735 |
| C9J1H7 | Uncharacterized protein OS=Homo sapiens GN=NCL PE=4 SV=1 - [C9J1H7_HUMAN] | 16.27 | 1 | 0 | 4 | 7 | 16.0023003 |
| C9JWL1 | Uncharacterized protein OS=Homo sapiens GN=NCL PE=4 SV=1 - [C9JWL1_HUMAN] | 15.88 | 1 | 0 | 4 | 7 | 16.0023003 |
| Q8N1C0 | CTNNA1 protein OS=Homo sapiens GN=CTNNA1 PE=2 SV=1 - [Q8N1C0_HUMAN] | 15.67 | 1 | 0 | 4 | 7 | 31.0326817 |
| B3KSR8 | cDNA FLJ36832 fis, clone ASTRO2010799, highly similar to ALPHA-1 CATENIN OS=Homo sapiens PE=2 SV=1 - [B3KSR8_HUMAN] | 14.29 | 1 | 0 | 4 | 7 | 31.0326817 |
| Q14137 | Ribosome biogenesis protein BOP1 OS=Homo sapiens GN=BOP1 PE=1 SV=2 - [BOP1_HUMAN] | 7.64 | 1 | 0 | 4 | 7 | 21.0326707 |
| A8K3R2 | cDNA FLJ78061, highly similar to Homo sapiens block of proliferation 1, mRNA OS=Homo sapiens PE=2 SV=1 - [A8K3R2_HUMAN] | 7.64 | 1 | 0 | 4 | 7 | 21.0326707 |
| Q2VPJ6 | HSP90AA1 protein (Fragment) OS=Homo sapiens GN=HSP90AA1 | 7.35 | 1 | 0 | 4 | 7 | 20.3998361 |

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| | PE=2 SV=1 - [Q2VPJ6_HUMAN] | | | | | | |
| Q5XKE5 | Keratin, type II cytoskeletal 79 OS=Homo sapiens GN=KRT79 PE=1 SV=2 - [K2C79_HUMAN] | 7.1 | 1 | 0 | 4 | 7 | 19.1623275 |
| Q8TBA7 | HSP90AA1 protein (Fragment) OS=Homo sapiens GN=HSP90AA1 PE=2 SV=2 - [Q8TBA7_HUMAN] | 6.74 | 1 | 0 | 4 | 7 | 20.3998361 |
| A8K9K1 | cDNA FLJ77199, highly similar to Homo sapiens ATPase, Ca++ transporting, ubiquitous (ATP2A3), transcript variant 6, mRNA OS=Homo sapiens PE=2 SV=1 - [A8K9K1_HUMAN] | 6.21 | 1 | 0 | 4 | 7 | 28.0284574 |
| Q93084 | Sarcoplasmic/endoplasmic reticulum calcium ATPase 3 OS=Homo sapiens GN=ATP2A3 PE=1 SV=2 - [AT2A3_HUMAN] | 5.94 | 1 | 0 | 4 | 7 | 28.0284574 |
| A8MYK9 | Uncharacterized protein OS=Homo sapiens GN=ATP2A3 PE=4 SV=1 - [A8MYK9_HUMAN] | 5.89 | 1 | 0 | 4 | 7 | 28.0284574 |
| P07900 | Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5 - [HS90A_HUMAN] | 5.87 | 1 | 0 | 4 | 7 | 20.3998361 |
| P78344 | Eukaryotic translation initiation factor 4 gamma 2 OS=Homo sapiens GN=EIF4G2 PE=1 SV=1 - [IF4G2_HUMAN] | 5.4 | 1 | 0 | 4 | 7 | 21.8435223 |
| D3DQV9 | Eukaryotic translation initiation factor 4 gamma, 2, isoform CRA_b (Fragment) OS=Homo sapiens GN=EIF4G2 PE=4 SV=1 - [D3DQV9_HUMAN] | 5.4 | 1 | 0 | 4 | 7 | 21.8435223 |
| B4E299 | cDNA FLJ54574, highly similar to Staphylococcal nuclease domain-containing protein 1 OS=Homo sapiens PE=2 SV=1 - [B4E299_HUMAN] | 5.4 | 1 | 0 | 4 | 7 | 20.1989379 |
| Q59G42 | Eukaryotic translation initiation factor 4 gamma, 2 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59G42_HUMAN] | 5.21 | 1 | 0 | 4 | 7 | 21.8435223 |
| B4DZF2 | cDNA FLJ59571, highly similar to Eukaryotic translation initiation factor 4gamma 2 OS=Homo sapiens PE=2 SV=1 - [B4DZF2_HUMAN] | 5 | 1 | 0 | 4 | 7 | 21.8435223 |
| Q5TC02 | ATPase, Na+/K+ transporting, alpha 1 polypeptide (Fragment) OS=Homo sapiens GN=ATP1A1 PE=2 SV=1 - [Q5TC02_HUMAN] | 37.74 | 1 | 0 | 4 | 6 | 16.105684 |
| B4DRP5 | cDNA FLJ54718, highly similar to Alpha-actinin-1 OS=Homo sapiens PE=2 SV=1 - [B4DRP5_HUMAN] | 18.43 | 1 | 0 | 4 | 6 | 17.7335746 |
| Q96EL6 | Putative uncharacterized protein (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q96EL6_HUMAN] | 9.89 | 1 | 0 | 4 | 6 | 15.0737414 |

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| B1AHB1 | MCM5 minichromosome maintenance deficient 5, cell division cycle 46 (<i>S. cerevisiae</i>), isoform CRA_c OS=Homo sapiens GN=MCM5 PE=4 SV=1 - [B1AHB1_HUMAN] | 9.41 | 1 | 0 | 4 | 6 | 17.5971508 |
| B3KVF0 | cDNA FLJ16474 fis, clone BRSSN2012254, highly similar to DNA replication licensing factor MCM5 OS=Homo sapiens PE=2 SV=1 - [B3KVF0_HUMAN] | 9.41 | 1 | 0 | 4 | 6 | 17.5971508 |
| P33992 | DNA replication licensing factor MCM5 OS=Homo sapiens GN=MCM5 PE=1 SV=5 - [MCM5_HUMAN] | 8.86 | 1 | 0 | 4 | 6 | 17.5971508 |
| A8K521 | cDNA FLJ78580, highly similar to Homo sapiens MCM5 minichromosome maintenance deficient 5, cell division cycle 46 (MCM5), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K521_HUMAN] | 8.86 | 1 | 0 | 4 | 6 | 17.5971508 |
| Q53FG5 | Minichromosome maintenance deficient protein 5 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53FG5_HUMAN] | 8.86 | 1 | 0 | 4 | 6 | 17.5971508 |
| B7Z5C1 | cDNA FLJ56126, highly similar to Programmed cell death 6-interacting protein OS=Homo sapiens PE=2 SV=1 - [B7Z5C1_HUMAN] | 7.4 | 1 | 0 | 4 | 6 | 19.3791971 |
| B4DHD2 | cDNA FLJ55458, highly similar to Programmed cell death 6-interacting protein OS=Homo sapiens PE=2 SV=1 - [B4DHD2_HUMAN] | 7.17 | 1 | 0 | 4 | 6 | 20.4948049 |
| B4DPL9 | cDNA FLJ59369, highly similar to Zinc phosphodiesterase ELAC protein 2 (EC 3.1.26.11) OS=Homo sapiens PE=2 SV=1 - [B4DPL9_HUMAN] | 6.87 | 1 | 0 | 4 | 6 | 21.2712319 |
| Q05BA7 | NOP2 protein OS=Homo sapiens GN=NOP2 PE=2 SV=1 - [Q05BA7_HUMAN] | 6.85 | 1 | 0 | 4 | 6 | 17.9365771 |
| B3KT00 | cDNA FLJ37368 fis, clone BRAMY2024530, highly similar to Zinc phosphodiesterase ELAC protein 2 (EC 3.1.26.11) OS=Homo sapiens PE=2 SV=1 - [B3KT00_HUMAN] | 6.69 | 1 | 0 | 4 | 6 | 21.2712319 |
| B4DT15 | cDNA FLJ56150, highly similar to Zinc phosphodiesterase ELAC protein 2 (EC 3.1.26.11) OS=Homo sapiens PE=2 SV=1 - [B4DT15_HUMAN] | 6.66 | 1 | 0 | 4 | 6 | 21.2712319 |
| P02786 | Transferrin receptor protein 1 OS=Homo sapiens GN=TFRC PE=1 SV=2 - [TFR1_HUMAN] | 6.58 | 1 | 0 | 4 | 6 | 15.8529944 |
| A8K6Q8 | cDNA FLJ75881, highly similar to Homo sapiens transferrin | 6.58 | 1 | 0 | 4 | 6 | 15.8529944 |

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| | receptor (p90, CD71) (TFRC), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K6Q8_HUMAN] | | | | | | |
| Q9BQ52 | Zinc phosphodiesterase ELAC protein 2 OS=Homo sapiens GN=ELAC2 PE=1 SV=2 - [RNZ2_HUMAN] | 6.54 | 1 | 0 | 4 | 6 | 21.2712319 |
| P12035 | Keratin, type II cytoskeletal 3 OS=Homo sapiens GN=KRT3 PE=1 SV=3 - [K2C3_HUMAN] | 4.3 | 1 | 0 | 4 | 6 | 17.2977595 |
| Q0ZAJ2 | MSH2-Ex3 isoform (Fragment) OS=Homo sapiens GN=MSH2 PE=2 SV=1 - [Q0ZAJ2_HUMAN] | 19.62 | 1 | 0 | 4 | 5 | 11.7407873 |
| B4E0F9 | cDNA FLJ60383, highly similar to Ubiquitin-like PHD and RING fingerdomain-containing protein 1 (EC 6.3.2.-) OS=Homo sapiens PE=2 SV=1 - [B4E0F9_HUMAN] | 13.24 | 1 | 0 | 4 | 5 | 15.9034522 |
| B3KMC6 | cDNA FLJ10692 fis, clone NT2RP3000361, highly similar to Pre-mRNA-processing factor 6 homolog OS=Homo sapiens PE=2 SV=1 - [B3KMC6_HUMAN] | 5.11 | 1 | 0 | 4 | 5 | 13.4029973 |
| O94906 | Pre-mRNA-processing factor 6 OS=Homo sapiens GN=PRPF6 PE=1 SV=1 - [PRP6_HUMAN] | 4.89 | 1 | 0 | 4 | 5 | 13.4029973 |
| B2RAR5 | cDNA, FLJ95067 OS=Homo sapiens PE=2 SV=1 - [B2RAR5_HUMAN] | 4.89 | 1 | 0 | 4 | 5 | 13.4029973 |
| B3KMK0 | cDNA FLJ11217 fis, clone PLACE1008044, highly similar to NUCLEAR PORE COMPLEX PROTEIN NUP107 OS=Homo sapiens PE=2 SV=1 - [B3KMK0_HUMAN] | 10.62 | 1 | 0 | 4 | 4 | 12.238143 |
| B4DZ67 | cDNA FLJ58739, highly similar to Nuclear pore complex protein Nup107 OS=Homo sapiens PE=2 SV=1 - [B4DZ67_HUMAN] | 7.03 | 1 | 0 | 4 | 4 | 12.238143 |
| Q96C32 | UBC protein OS=Homo sapiens PE=2 SV=1 - [Q96C32_HUMAN] | 49.84 | 1 | 0 | 3 | 11 | 39.2796974 |
| P0CG47 | Polyubiquitin-B OS=Homo sapiens GN=UBB PE=1 SV=1 - [UBB_HUMAN] | 49.78 | 1 | 0 | 3 | 11 | 39.2796974 |
| Q5PY61 | Ubiquitin C splice variant OS=Homo sapiens GN=UBC PE=2 SV=1 - [Q5PY61_HUMAN] | 49.78 | 1 | 0 | 3 | 11 | 39.2796974 |
| Q5UGI3 | Ubiquitin C splice variant OS=Homo sapiens GN=UBC PE=2 SV=1 - [Q5UGI3_HUMAN] | 49.67 | 1 | 0 | 3 | 11 | 39.2796974 |
| B4DV12 | cDNA FLJ51326, highly similar to Homo sapiens ubiquitin B (UBB), mRNA OS=Homo sapiens PE=2 SV=1 - [B4DV12_HUMAN] | 49.67 | 1 | 0 | 3 | 11 | 39.2796974 |
| Q59EM9 | Ubiquitin C variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59EM9_HUMAN] | 49.35 | 1 | 0 | 3 | 11 | 39.2796974 |

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| Q66K58 | Putative uncharacterized protein (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q66K58_HUMAN] | 49 | 1 | 0 | 3 | 11 | 39.2796974 |
| Q96H31 | UBC protein (Fragment) OS=Homo sapiens GN=UBC PE=2 SV=2 - [Q96H31_HUMAN] | 48.72 | 1 | 0 | 3 | 11 | 39.2796974 |
| P0CG48 | Polyubiquitin-C OS=Homo sapiens GN=UBC PE=1 SV=2 - [UBC_HUMAN] | 48.03 | 1 | 0 | 3 | 11 | 39.2796974 |
| Q9UFQ0 | Putative uncharacterized protein DKFZp434K0435 (Fragment) OS=Homo sapiens GN=DKFZp434K0435 PE=2 SV=1 - [Q9UFQ0_HUMAN] | 47.7 | 1 | 0 | 3 | 11 | 39.2796974 |
| A8K674 | cDNA FLJ75516, highly similar to Xenopus tropicalis ubiquitin C, mRNA OS=Homo sapiens PE=2 SV=1 - [A8K674_HUMAN] | 47.29 | 1 | 0 | 3 | 11 | 39.2796974 |
| Q96MH4 | cDNA FLJ32377 fis, clone SKMUS1000014, highly similar to Polyubiquitin 9 OS=Homo sapiens PE=2 SV=1 - [Q96MH4_HUMAN] | 45.88 | 1 | 0 | 3 | 11 | 39.2796974 |
| P62987 | Ubiquitin-60S ribosomal protein L40 OS=Homo sapiens GN=UBA52 PE=1 SV=2 - [RL40_HUMAN] | 29.69 | 1 | 0 | 3 | 11 | 39.2796974 |
| P62979 | Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=1 SV=2 - [RS27A_HUMAN] | 24.36 | 1 | 0 | 3 | 11 | 39.2796974 |
| Q5RKT7 | Ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=2 SV=1 - [Q5RKT7_HUMAN] | 24.36 | 1 | 0 | 3 | 11 | 39.2796974 |
| Q5JRR6 | Ubiquitin-like modifier activating enzyme 1 OS=Homo sapiens GN=UBA1 PE=2 SV=1 - [Q5JRR6_HUMAN] | 8.7 | 1 | 0 | 3 | 11 | 40.263335 |
| B3KUJ2 | cDNA FLJ40024 fis, clone STOMA2007745, highly similar to UBIQUITIN-ACTIVATING ENZYME E1 OS=Homo sapiens PE=2 SV=1 - [B3KUJ2_HUMAN] | 8.7 | 1 | 0 | 3 | 11 | 40.263335 |
| Q9BS14 | GANAB protein (Fragment) OS=Homo sapiens GN=GANAB PE=2 SV=1 - [Q9BS14_HUMAN] | 16.93 | 1 | 0 | 3 | 10 | 43.1748049 |
| Q7Z794 | Keratin, type II cytoskeletal 1b OS=Homo sapiens GN=KRT77 PE=1 SV=3 - [K2C1B_HUMAN] | 4.67 | 1 | 0 | 3 | 10 | 30.6013603 |
| Q0IIN1 | Keratin 77 OS=Homo sapiens GN=KRT77 PE=1 SV=1 - [Q0IIN1_HUMAN] | 4.67 | 1 | 0 | 3 | 10 | 30.6013603 |
| Q3SWU7 | DDX21 protein (Fragment) OS=Homo sapiens GN=DDX21 PE=2 SV=1 - [Q3SWU7_HUMAN] | 37.8 | 1 | 0 | 3 | 8 | 31.2770195 |
| C9JKM9 | Uncharacterized protein OS=Homo sapiens GN=XPO1 PE=4 SV=1 | 22.35 | 1 | 0 | 3 | 8 | 24.6921754 |

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| | - [C9JKM9_HUMAN] | | | | | | |
| E0CX14 | Uncharacterized protein OS=Homo sapiens GN=KRT15 PE=4 SV=1 - [E0CX14_HUMAN] | 6.59 | 1 | 0 | 3 | 8 | 21.8856215 |
| P19012 | Keratin, type I cytoskeletal 15 OS=Homo sapiens GN=KRT15 PE=1 SV=3 - [K1C15_HUMAN] | 6.58 | 1 | 0 | 3 | 8 | 21.8856215 |
| Q5JYA8 | Methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like (Fragment) OS=Homo sapiens GN=MTHFD1L PE=2 SV=1 - [Q5JYA8_HUMAN] | 35.43 | 1 | 0 | 3 | 7 | 23.18483 |
| C9JA77 | Uncharacterized protein OS=Homo sapiens GN=KRT13 PE=4 SV=1 - [C9JA77_HUMAN] | 6.76 | 1 | 0 | 3 | 7 | 20.320987 |
| B4E3E9 | cDNA FLJ59657, highly similar to 2-oxoglutarate dehydrogenase E1 component, mitochondrial (EC 1.2.4.2) OS=Homo sapiens PE=2 SV=1 - [B4E3E9_HUMAN] | 5.26 | 1 | 0 | 3 | 7 | 20.9945602 |
| P13646 | Keratin, type I cytoskeletal 13 OS=Homo sapiens GN=KRT13 PE=1 SV=4 - [K1C13_HUMAN] | 5.24 | 1 | 0 | 3 | 7 | 20.320987 |
| A1A4E9 | Keratin 13 OS=Homo sapiens GN=KRT13 PE=2 SV=1 - [A1A4E9_HUMAN] | 5.24 | 1 | 0 | 3 | 7 | 20.320987 |
| A8K2H9 | cDNA FLJ78503, highly similar to Homo sapiens keratin 13 (KRT13), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1 - [A8K2H9_HUMAN] | 5.24 | 1 | 0 | 3 | 7 | 20.320987 |
| B4DK55 | cDNA FLJ59557, highly similar to 2-oxoglutarate dehydrogenase E1 component, mitochondrial (EC 1.2.4.2) OS=Homo sapiens PE=2 SV=1 - [B4DK55_HUMAN] | 4.93 | 1 | 0 | 3 | 7 | 20.9945602 |
| B4DF00 | cDNA FLJ53308, highly similar to 2-oxoglutarate dehydrogenase E1 component, mitochondrial (EC 1.2.4.2) OS=Homo sapiens PE=2 SV=1 - [B4DF00_HUMAN] | 4.41 | 1 | 0 | 3 | 7 | 20.9945602 |
| B4E2U9 | cDNA FLJ54748, highly similar to 2-oxoglutarate dehydrogenase E1 component, mitochondrial (EC 1.2.4.2) OS=Homo sapiens PE=2 SV=1 - [B4E2U9_HUMAN] | 4.22 | 1 | 0 | 3 | 7 | 20.9945602 |
| Q02218 | 2-oxoglutarate dehydrogenase, mitochondrial OS=Homo sapiens GN=OGDH PE=1 SV=3 - [ODO1_HUMAN] | 4.2 | 1 | 0 | 3 | 7 | 20.9945602 |
| P05787 | Keratin, type II cytoskeletal 8 OS=Homo sapiens GN=KRT8 PE=1 SV=7 - [K2C8_HUMAN] | 3.52 | 1 | 0 | 3 | 7 | 20.7351141 |
| O14942 | Heat shock protein beta (Fragment) OS=Homo sapiens PE=4 | 26.92 | 1 | 0 | 3 | 6 | 17.4705 |

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| | SV=1 - [O14942_HUMAN] | | | | | | |
| B4DI39 | cDNA FLJ54328, highly similar to Heat shock 70 kDa protein 1 OS=Homo sapiens PE=2 SV=1 - [B4DI39_HUMAN] | 6.31 | 1 | 0 | 3 | 6 | 19.7929699 |
| P17066 | Heat shock 70 kDa protein 6 OS=Homo sapiens GN=HSPA6 PE=1 SV=2 - [HSP76_HUMAN] | 6.22 | 1 | 0 | 3 | 6 | 20.8066006 |
| B2R6X5 | cDNA, FLJ93166, highly similar to Homo sapiens heat shock 70kDa protein 6 (HSP70B') (HSPA6), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R6X5_HUMAN] | 6.22 | 1 | 0 | 3 | 6 | 20.8066006 |
| Q53FC7 | Heat shock 70kDa protein 6 (HSP70B') variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53FC7_HUMAN] | 6.22 | 1 | 0 | 3 | 6 | 20.8066006 |
| B3KSM6 | cDNA FLJ36606 fis, clone TRACH2015654, highly similar to HEAT SHOCK 70 kDa PROTEIN 6 OS=Homo sapiens PE=2 SV=1 - [B3KSM6_HUMAN] | 6.22 | 1 | 0 | 3 | 6 | 20.8066006 |
| P08107 | Heat shock 70 kDa protein 1A/1B OS=Homo sapiens GN=HSPA1A PE=1 SV=5 - [HSP71_HUMAN] | 6.08 | 1 | 0 | 3 | 6 | 19.7929699 |
| P27824 | Calnexin OS=Homo sapiens GN=CANX PE=1 SV=2 - [CALX_HUMAN] | 5.91 | 1 | 0 | 3 | 6 | 18.6782527 |
| Q9NSM5 | Putative uncharacterized protein DKFZp564A2282 (Fragment) OS=Homo sapiens GN=DKFZp564A2282 PE=2 SV=2 - [Q9NSM5_HUMAN] | 5.85 | 1 | 0 | 3 | 6 | 18.4292514 |
| B4DGP8 | cDNA FLJ55574, highly similar to Calnexin OS=Homo sapiens PE=2 SV=1 - [B4DGP8_HUMAN] | 5.58 | 1 | 0 | 3 | 6 | 18.6782527 |
| Q68E02 | Putative uncharacterized protein DKFZp686I1650 (Fragment) OS=Homo sapiens GN=DKFZp686I1650 PE=2 SV=1 - [Q68E02_HUMAN] | 5.49 | 1 | 0 | 3 | 6 | 15.5884218 |
| B4DY72 | cDNA FLJ52360, highly similar to Heat-shock protein 105 kDa OS=Homo sapiens PE=2 SV=1 - [B4DY72_HUMAN] | 5.47 | 1 | 0 | 3 | 6 | 18.3719819 |
| B4DF68 | cDNA FLJ55325, highly similar to Heat-shock protein 105 kDa OS=Homo sapiens PE=2 SV=1 - [B4DF68_HUMAN] | 4.9 | 1 | 0 | 3 | 6 | 18.3719819 |
| B2RDN4 | cDNA, FLJ96693, highly similar to Homo sapiens block of proliferation 1 (BOP1), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RDN4_HUMAN] | 4.83 | 1 | 0 | 3 | 6 | 17.2971358 |
| Q92598 | Heat shock protein 105 kDa OS=Homo sapiens GN=HSPH1 PE=1 SV=1 - [HS105_HUMAN] | 4.31 | 1 | 0 | 3 | 6 | 18.3719819 |

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| B4DYH1 | Heat shock 105kDa/110kDa protein 1, isoform CRA_b OS=Homo sapiens GN=HSPH1 PE=2 SV=1 - [B4DYH1_HUMAN] | 4.3 | 1 | 0 | 3 | 6 | 18.3719819 |
| Q8NI36 | WD repeat-containing protein 36 OS=Homo sapiens GN=WDR36 PE=1 SV=1 - [WDR36_HUMAN] | 4.1 | 1 | 0 | 3 | 6 | 15.5884218 |
| D6RAY5 | Uncharacterized protein OS=Homo sapiens GN=WDR36 PE=4 SV=1 - [D6RAY5_HUMAN] | 4.1 | 1 | 0 | 3 | 6 | 15.5884218 |
| B4DSH1 | cDNA FLJ51295, highly similar to Cell division cycle 5-like protein OS=Homo sapiens PE=2 SV=1 - [B4DSH1_HUMAN] | 4 | 1 | 0 | 3 | 6 | 16.055656 |
| Q99459 | Cell division cycle 5-like protein OS=Homo sapiens GN=CDC5L PE=1 SV=2 - [CDC5L_HUMAN] | 3.87 | 1 | 0 | 3 | 6 | 16.055656 |
| B3KY60 | cDNA FLJ16777 fis, clone BRHIP2029567, highly similar to Cell division cycle 5-like protein OS=Homo sapiens PE=2 SV=1 - [B3KY60_HUMAN] | 3.87 | 1 | 0 | 3 | 6 | 16.055656 |
| D3DV75 | Adenosine deaminase, RNA-specific, isoform CRA_b OS=Homo sapiens GN=ADAR PE=4 SV=1 - [D3DV75_HUMAN] | 3.84 | 1 | 0 | 3 | 6 | 14.7964687 |
| B7Z8Y3 | cDNA FLJ61696, highly similar to Double-stranded RNA-specific adenosine deaminase (EC 3.5.4.-) OS=Homo sapiens PE=2 SV=1 - [B7Z8Y3_HUMAN] | 3.51 | 1 | 0 | 3 | 6 | 14.7964687 |
| P55265 | Double-stranded RNA-specific adenosine deaminase OS=Homo sapiens GN=ADAR PE=1 SV=4 - [DSRAD_HUMAN] | 2.77 | 1 | 0 | 3 | 6 | 14.7964687 |
| Q59EC0 | Adenosine deaminase, RNA-specific isoform ADAR-a variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59EC0_HUMAN] | 2.73 | 1 | 0 | 3 | 6 | 14.7964687 |
| B3GQE6 | DEAD box polypeptide 27 OS=Homo sapiens GN=DDX27 PE=2 SV=1 - [B3GQE6_HUMAN] | 4.44 | 1 | 0 | 3 | 6 | 11.7817069 |
| B7Z6D5 | cDNA FLJ61659, highly similar to Probable ATP-dependent RNA helicase DDX27 (EC 3.6.1.-) OS=Homo sapiens PE=2 SV=1 - [B7Z6D5_HUMAN] | 4.44 | 1 | 0 | 3 | 6 | 11.7817069 |
| Q96GQ7 | Probable ATP-dependent RNA helicase DDX27 OS=Homo sapiens GN=DDX27 PE=1 SV=2 - [DDX27_HUMAN] | 4.27 | 1 | 0 | 3 | 6 | 11.7817069 |
| E5RK04 | Uncharacterized protein OS=Homo sapiens GN=MCM4 PE=4 SV=1 - [E5RK04_HUMAN] | 45.83 | 1 | 0 | 3 | 5 | 16.9389055 |
| E5RHP5 | Uncharacterized protein OS=Homo sapiens GN=MCM4 PE=4 SV=1 - [E5RHP5_HUMAN] | 42.31 | 1 | 0 | 3 | 5 | 16.9389055 |
| Q59G96 | Dynamin 2 isoform 4 variant (Fragment) OS=Homo sapiens PE=2 | 11.5 | 1 | 0 | 3 | 5 | 16.8827925 |

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| | SV=1 - [Q59G96_HUMAN] | | | | | | |
| B4DDF3 | cDNA FLJ58050, highly similar to Interleukin enhancer-binding factor 3 OS=Homo sapiens PE=2 SV=1 - [B4DDF3_HUMAN] | 10.07 | 1 | 0 | 3 | 5 | 12.0933561 |
| Q7Z6P5 | Minichromosome maintenance complex component 3 (Fragment) OS=Homo sapiens GN=MCM3 PE=2 SV=1 - [Q7Z6P5_HUMAN] | 9.76 | 1 | 0 | 3 | 5 | 23.4782436 |
| B4DQ39 | cDNA FLJ55743, highly similar to DNA replication licensing factor MCM5 OS=Homo sapiens PE=2 SV=1 - [B4DQ39_HUMAN] | 9.02 | 1 | 0 | 3 | 5 | 15.3002491 |
| Q86U12 | Full-length cDNA clone CS0CAP007YF18 of Thymus of Homo sapiens (human) OS=Homo sapiens PE=2 SV=1 - [Q86U12_HUMAN] | 7.51 | 1 | 0 | 3 | 5 | 14.1946259 |
| Q58FF2 | Heat shock protein 94c OS=Homo sapiens GN=GRP94c PE=2 SV=1 - [Q58FF2_HUMAN] | 6.62 | 1 | 0 | 3 | 5 | 12.8618672 |
| C9J1E7 | Uncharacterized protein OS=Homo sapiens GN=AP1B1 PE=4 SV=1 - [C9J1E7_HUMAN] | 6.4 | 1 | 0 | 3 | 5 | 16.6406977 |
| B4DLG2 | cDNA FLJ58196, highly similar to Zinc finger CCCH domain-containing protein 11A OS=Homo sapiens PE=2 SV=1 - [B4DLG2_HUMAN] | 6.35 | 1 | 0 | 3 | 5 | 21.2131338 |
| Q96FS1 | CTNND1 protein (Fragment) OS=Homo sapiens GN=CTNND1 PE=2 SV=2 - [Q96FS1_HUMAN] | 6.14 | 1 | 0 | 3 | 5 | 17.1372099 |
| O75152 | Zinc finger CCCH domain-containing protein 11A OS=Homo sapiens GN=ZC3H11A PE=1 SV=3 - [ZC11A_HUMAN] | 5.93 | 1 | 0 | 3 | 5 | 21.2131338 |
| O75322 | Hsp89-alpha-delta-N OS=Homo sapiens PE=2 SV=1 - [O75322_HUMAN] | 5.75 | 1 | 0 | 3 | 5 | 14.1946259 |
| C9JZR2 | Uncharacterized protein OS=Homo sapiens GN=CTNND1 PE=4 SV=1 - [C9JZR2_HUMAN] | 5.55 | 1 | 0 | 3 | 5 | 17.1372099 |
| B4DRW1 | cDNA FLJ55805, highly similar to Keratin, type II cytoskeletal 4 OS=Homo sapiens PE=2 SV=1 - [B4DRW1_HUMAN] | 5.49 | 1 | 0 | 3 | 5 | 11.8151057 |
| Q68DU0 | Putative uncharacterized protein DKFZp781O2021 OS=Homo sapiens GN=DKFZp781O2021 PE=2 SV=1 - [Q68DU0_HUMAN] | 5.44 | 1 | 0 | 3 | 5 | 17.1372099 |
| C9JKX3 | Uncharacterized protein OS=Homo sapiens GN=CTNND1 PE=4 SV=1 - [C9JKX3_HUMAN] | 5.38 | 1 | 0 | 3 | 5 | 17.1372099 |
| O60716 | Catenin delta-1 OS=Homo sapiens GN=CTNND1 PE=1 SV=1 - [CTND1_HUMAN] | 5.27 | 1 | 0 | 3 | 5 | 17.1372099 |

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| B4DRR7 | cDNA FLJ59399, highly similar to Keratin, type II cytoskeletal 4 OS=Homo sapiens PE=2 SV=1 - [B4DRR7_HUMAN] | 5.19 | 1 | 0 | 3 | 5 | 11.8151057 |
| B4DKJ0 | cDNA FLJ58539, highly similar to Keratin, type II cytoskeletal 4 OS=Homo sapiens PE=2 SV=1 - [B4DKJ0_HUMAN] | 5.11 | 1 | 0 | 3 | 5 | 11.8151057 |
| B4DRS2 | cDNA FLJ58275, highly similar to Keratin, type II cytoskeletal 4 OS=Homo sapiens PE=2 SV=1 - [B4DRS2_HUMAN] | 5 | 1 | 0 | 3 | 5 | 11.8151057 |
| B3KRS1 | cDNA FLJ34794 fis, clone NT2NE2005676, highly similar to Gamma-tubulin complex component 2 OS=Homo sapiens PE=2 SV=1 - [B3KRS1_HUMAN] | 4.99 | 1 | 0 | 3 | 5 | 13.1520669 |
| P19013 | Keratin, type II cytoskeletal 4 OS=Homo sapiens GN=KRT4 PE=1 SV=4 - [K2C4_HUMAN] | 4.87 | 1 | 0 | 3 | 5 | 11.8151057 |
| A8K6F7 | Unc-45 homolog A (C. elegans), isoform CRA_a OS=Homo sapiens GN=UNC45A PE=2 SV=1 - [A8K6F7_HUMAN] | 4.84 | 1 | 0 | 3 | 5 | 16.441402 |
| Q9H3U1 | Protein unc-45 homolog A OS=Homo sapiens GN=UNC45A PE=1 SV=1 - [UN45A_HUMAN] | 4.77 | 1 | 0 | 3 | 5 | 16.441402 |
| Q7Z3Y7 | Keratin, type I cytoskeletal 28 OS=Homo sapiens GN=KRT28 PE=1 SV=2 - [K1C28_HUMAN] | 4.09 | 1 | 0 | 3 | 5 | 13.3801398 |
| Q53EQ3 | Tubulin, gamma complex associated protein 2 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53EQ3_HUMAN] | 4 | 1 | 0 | 3 | 5 | 13.1520669 |
| Q9BSJ2 | Gamma-tubulin complex component 2 OS=Homo sapiens GN=TUBGCP2 PE=1 SV=2 - [GCP2_HUMAN] | 3.99 | 1 | 0 | 3 | 5 | 13.1520669 |
| B7ZKL8 | TUBGCP2 protein OS=Homo sapiens GN=TUBGCP2 PE=2 SV=1 - [B7ZKL8_HUMAN] | 3.87 | 1 | 0 | 3 | 5 | 13.1520669 |
| Q6N069 | N-alpha-acetyltransferase 16, NatA auxiliary subunit OS=Homo sapiens GN=NAA16 PE=1 SV=2 - [NAA16_HUMAN] | 3.59 | 1 | 0 | 3 | 5 | 13.2446756 |
| Q08043 | Alpha-actinin-3 OS=Homo sapiens GN=ACTN3 PE=1 SV=2 - [ACTN3_HUMAN] | 3.44 | 1 | 0 | 3 | 5 | 13.9166198 |
| B2R8Y4 | cDNA, FLJ94117, highly similar to Homo sapiens actinin, alpha 3 (ACTN3), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R8Y4_HUMAN] | 3.44 | 1 | 0 | 3 | 5 | 13.9166198 |
| B4DZQ2 | cDNA FLJ58651, highly similar to Alpha-actinin-3 OS=Homo sapiens PE=2 SV=1 - [B4DZQ2_HUMAN] | 3.28 | 1 | 0 | 3 | 5 | 13.9166198 |
| E5KLB6 | DNA ligase 3 OS=Homo sapiens GN=LIG3 PE=4 SV=1 - [E5KLB6_HUMAN] | 3.06 | 1 | 0 | 3 | 5 | 11.0565702 |

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| Q5JYA1 | Methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like (Fragment) OS=Homo sapiens GN=MTHFD1L PE=2 SV=1 - [Q5JYA1_HUMAN] | 11.18 | 1 | 0 | 3 | 4 | 10.4071245 |
| B3KSU9 | cDNA FLJ37014 fis, clone BRACE2010203, highly similar to Zinc phosphodiesterase ELAC protein 2 (EC 3.1.26.11) OS=Homo sapiens PE=2 SV=1 - [B3KSU9_HUMAN] | 7.85 | 1 | 0 | 3 | 4 | 15.2739618 |
| B7Z9E8 | cDNA, FLJ78812, highly similar to DNA topoisomerase I, mitochondrial (EC 5.99.1.2) OS=Homo sapiens PE=2 SV=1 - [B7Z9E8_HUMAN] | 4.97 | 1 | 0 | 3 | 4 | 10.9502604 |
| B7ZAR5 | cDNA, FLJ79279, highly similar to DNA topoisomerase I, mitochondrial(EC 5.99.1.2) OS=Homo sapiens PE=2 SV=1 - [B7ZAR5_HUMAN] | 4.97 | 1 | 0 | 3 | 4 | 10.9502604 |
| B4DYD2 | cDNA FLJ50294, highly similar to DNA topoisomerase I, mitochondrial (EC 5.99.1.2) OS=Homo sapiens PE=2 SV=1 - [B4DYD2_HUMAN] | 4.97 | 1 | 0 | 3 | 4 | 10.9502604 |
| B7Z9C0 | cDNA FLJ52405, highly similar to Myosin Ic OS=Homo sapiens PE=2 SV=1 - [B7Z9C0_HUMAN] | 4.35 | 1 | 0 | 3 | 4 | 11.7901015 |
| B7Z2N5 | cDNA FLJ51840, highly similar to Alpha-actinin-2 OS=Homo sapiens PE=2 SV=1 - [B7Z2N5_HUMAN] | 4.23 | 1 | 0 | 3 | 4 | 12.0316832 |
| Q969P6 | DNA topoisomerase I, mitochondrial OS=Homo sapiens GN=TOP1MT PE=2 SV=1 - [TOP1M_HUMAN] | 4.16 | 1 | 0 | 3 | 4 | 10.9502604 |
| E5KMK6 | Mitochondrial DNA topoisomerase I OS=Homo sapiens PE=4 SV=1 - [E5KMK6_HUMAN] | 4.16 | 1 | 0 | 3 | 4 | 10.9502604 |
| E5KMK5 | Mitochondrial DNA topoisomerase I OS=Homo sapiens PE=4 SV=1 - [E5KMK5_HUMAN] | 4.16 | 1 | 0 | 3 | 4 | 10.9502604 |
| Q6I7N8 | Lymphoid specific helicase variant9 OS=Homo sapiens GN=HELLS PE=2 SV=1 - [Q6I7N8_HUMAN] | 3.83 | 1 | 0 | 3 | 4 | 10.0025411 |
| P35609 | Alpha-actinin-2 OS=Homo sapiens GN=ACTN2 PE=1 SV=1 - [ACTN2_HUMAN] | 3.8 | 1 | 0 | 3 | 4 | 12.0316832 |
| B2RCS5 | Actinin, alpha 2, isoform CRA_b OS=Homo sapiens GN=ACTN2 PE=2 SV=1 - [B2RCS5_HUMAN] | 3.8 | 1 | 0 | 3 | 4 | 12.0316832 |
| Q9NRZ9 | Lymphoid-specific helicase OS=Homo sapiens GN=HELLS PE=1 SV=1 - [HELLS_HUMAN] | 3.7 | 1 | 0 | 3 | 4 | 10.0025411 |
| A8KA17 | cDNA FLJ77211, highly similar to Homo sapiens nucleoporin | 3.74 | 1 | 0 | 3 | 4 | 8.47805917 |

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| | 98kDa (NUP98), transcript variant 3, mRNA OS=Homo sapiens PE=2 SV=1 - [A8KA17_HUMAN] | | | | | | |
| P52948 | Nuclear pore complex protein Nup98-Nup96 OS=Homo sapiens GN=NUP98 PE=1 SV=4 - [NUP98_HUMAN] | 1.93 | 1 | 0 | 3 | 4 | 8.47805917 |
| Q6PJE1 | NUP107 protein OS=Homo sapiens GN=NUP107 PE=2 SV=1 - [Q6PJE1_HUMAN] | 7.58 | 1 | 0 | 3 | 3 | 9.98323894 |
| P78316 | Nucleolar protein 14 OS=Homo sapiens GN=NOP14 PE=1 SV=3 - [NOP14_HUMAN] | 3.38 | 1 | 0 | 3 | 3 | 7.15553761 |
| A8KA74 | cDNA FLJ76065 OS=Homo sapiens PE=2 SV=1 - [A8KA74_HUMAN] | 3.38 | 1 | 0 | 3 | 3 | 7.15553761 |
| Q5T9W8 | Heat shock protein 90kDa alpha (Cytosolic), class B member 1 (Fragment) OS=Homo sapiens GN=HSP90AB1 PE=2 SV=1 - [Q5T9W8_HUMAN] | 8.33 | 1 | 0 | 2 | 10 | 36.2822082 |
| Q49A90 | RPS27A protein OS=Homo sapiens GN=RPS27A PE=4 SV=1 - [Q49A90_HUMAN] | 30.53 | 1 | 0 | 2 | 9 | 34.0128989 |
| B3KS35 | cDNA FLJ35372 fis, clone SKMUS2001742, highly similar to Sarcoplasmic/endoplasmic reticulum calcium ATPase 1 (EC 3.6.3.8) OS=Homo sapiens PE=2 SV=1 - [B3KS35_HUMAN] | 13.22 | 1 | 0 | 2 | 9 | 42.804462 |
| B1AKZ1 | ATPase, Na+/K+ transporting, alpha 4 polypeptide (Fragment) OS=Homo sapiens GN=ATP1A4 PE=4 SV=1 - [B1AKZ1_HUMAN] | 7.68 | 1 | 0 | 2 | 8 | 32.1780889 |
| Q5ZEZ4 | Alpha-actinin 1 (Fragment) OS=Homo sapiens GN=ACTN1 PE=2 SV=1 - [Q5ZEZ4_HUMAN] | 27.91 | 1 | 0 | 2 | 7 | 23.6422057 |
| C9IZS4 | Uncharacterized protein OS=Homo sapiens GN=XPO1 PE=4 SV=1 - [C9IZS4_HUMAN] | 27.66 | 1 | 0 | 2 | 6 | 17.7773435 |
| C9JQ02 | Uncharacterized protein OS=Homo sapiens GN=XPO1 PE=4 SV=1 - [C9JQ02_HUMAN] | 27.37 | 1 | 0 | 2 | 6 | 17.7773435 |
| C9JV99 | Uncharacterized protein OS=Homo sapiens GN=XPO1 PE=4 SV=1 - [C9JV99_HUMAN] | 26 | 1 | 0 | 2 | 6 | 17.7773435 |
| Q4VXM0 | Methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like (Fragment) OS=Homo sapiens GN=MTHFD1L PE=2 SV=1 - [Q4VXM0_HUMAN] | 22.83 | 1 | 0 | 2 | 6 | 16.3136752 |
| Q0ZAJ1 | MSH2-Ex5 isoform (Fragment) OS=Homo sapiens GN=MSH2 PE=2 SV=1 - [Q0ZAJ1_HUMAN] | 22.77 | 1 | 0 | 2 | 6 | 17.6197152 |
| C9J673 | Uncharacterized protein OS=Homo sapiens GN=XPO1 PE=4 SV=1 | 19.7 | 1 | 0 | 2 | 6 | 17.7773435 |

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| | - [C9J673_HUMAN] | | | | | | |
| C9JM50 | Uncharacterized protein OS=Homo sapiens GN=KRT19 PE=4 SV=1 - [C9JM50_HUMAN] | 9.18 | 1 | 0 | 2 | 6 | 15.4326241 |
| B4E204 | cDNA FLJ58872, highly similar to Keratin, type I cytoskeletal 15 OS=Homo sapiens PE=2 SV=1 - [B4E204_HUMAN] | 8.97 | 1 | 0 | 2 | 6 | 16.2681868 |
| P08727 | Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=4 - [K1C19_HUMAN] | 4.5 | 1 | 0 | 2 | 6 | 15.4326241 |
| Q04695 | Keratin, type I cytoskeletal 17 OS=Homo sapiens GN=KRT17 PE=1 SV=2 - [K1C17_HUMAN] | 4.17 | 1 | 0 | 2 | 6 | 15.4326241 |
| C9JH30 | Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [C9JH30_HUMAN] | 4.16 | 1 | 0 | 2 | 6 | 15.4326241 |
| A8MW45 | Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [A8MW45_HUMAN] | 4.08 | 1 | 0 | 2 | 6 | 15.4326241 |
| Q658V6 | Putative uncharacterized protein DKFZp666G172 (Fragment) OS=Homo sapiens GN=DKFZp666G172 PE=2 SV=1 - [Q658V6_HUMAN] | 2.79 | 1 | 0 | 2 | 6 | 21.3717017 |
| Q969I0 | KRT8 protein (Fragment) OS=Homo sapiens GN=KRT8 PE=2 SV=2 - [Q969I0_HUMAN] | 2.74 | 1 | 0 | 2 | 6 | 18.6187966 |
| P20648 | Potassium-transporting ATPase alpha chain 1 OS=Homo sapiens GN=ATP4A PE=2 SV=5 - [ATP4A_HUMAN] | 2.71 | 1 | 0 | 2 | 6 | 21.3717017 |
| Q53FI9 | Nucleolar protein GU2 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53FI9_HUMAN] | 7.44 | 1 | 0 | 2 | 5 | 16.7850842 |
| B4DED6 | cDNA FLJ56545, highly similar to ATP-dependent RNA helicase DDX50 (EC 3.6.1.-) OS=Homo sapiens PE=2 SV=1 - [B4DED6_HUMAN] | 4.2 | 1 | 0 | 2 | 5 | 16.7850842 |
| B4DW97 | cDNA FLJ61430, highly similar to ATP-dependent RNA helicase DDX50 (EC 3.6.1.-) OS=Homo sapiens PE=2 SV=1 - [B4DW97_HUMAN] | 3.8 | 1 | 0 | 2 | 5 | 16.7850842 |
| Q9BQ39 | ATP-dependent RNA helicase DDX50 OS=Homo sapiens GN=DDX50 PE=1 SV=1 - [DDX50_HUMAN] | 3.66 | 1 | 0 | 2 | 5 | 16.7850842 |
| B4DH65 | cDNA FLJ53323, highly similar to 2-oxoglutarate dehydrogenase E1 component, mitochondrial (EC 1.2.4.2) OS=Homo sapiens PE=2 SV=1 - [B4DH65_HUMAN] | 3.62 | 1 | 0 | 2 | 5 | 15.5374613 |

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| C9JPK5 | Uncharacterized protein OS=Homo sapiens GN=ITGB1 PE=4 SV=1 - [C9JPK5_HUMAN] | 27.55 | 1 | 0 | 2 | 4 | 12.0452187 |
| D6RAQ8 | Uncharacterized protein OS=Homo sapiens GN=CANX PE=4 SV=1 - [D6RAQ8_HUMAN] | 24.3 | 1 | 0 | 2 | 4 | 13.1988614 |
| Q8NI92 | DEAD/H(Asp-Glu-Ala-Asp/His)box polypeptide 21 OS=Homo sapiens GN=OK/SW-cl.65 PE=2 SV=1 - [Q8NI92_HUMAN] | 23.45 | 1 | 0 | 2 | 4 | 14.1809709 |
| Q5T3E6 | Integrin, beta 1 (Fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12) (Fragment) OS=Homo sapiens GN=ITGB1 PE=2 SV=1 - [Q5T3E6_HUMAN] | 19.85 | 1 | 0 | 2 | 4 | 12.0452187 |
| D6RAU8 | Uncharacterized protein OS=Homo sapiens GN=CANX PE=4 SV=1 - [D6RAU8_HUMAN] | 19.4 | 1 | 0 | 2 | 4 | 13.1988614 |
| C9JUP7 | Uncharacterized protein OS=Homo sapiens GN=VCP PE=4 SV=1 - [C9JUP7_HUMAN] | 19.13 | 1 | 0 | 2 | 4 | 11.7968817 |
| D6RB85 | Uncharacterized protein OS=Homo sapiens GN=CANX PE=4 SV=1 - [D6RB85_HUMAN] | 18.06 | 1 | 0 | 2 | 4 | 13.1988614 |
| Q9UQC1 | Heat shock protein 72 (Fragment) OS=Homo sapiens GN=HSP70-1 PE=4 SV=1 - [Q9UQC1_HUMAN] | 17.22 | 1 | 0 | 2 | 4 | 13.2573786 |
| D6RDP7 | Uncharacterized protein OS=Homo sapiens GN=CANX PE=4 SV=1 - [D6RDP7_HUMAN] | 15.48 | 1 | 0 | 2 | 4 | 13.1988614 |
| C9IZA5 | Uncharacterized protein OS=Homo sapiens GN=VCP PE=4 SV=1 - [C9IZA5_HUMAN] | 13.75 | 1 | 0 | 2 | 4 | 11.7968817 |
| P81605 | Dermcidin OS=Homo sapiens GN=DCD PE=1 SV=2 - [DCD_HUMAN] | 12.73 | 1 | 0 | 2 | 4 | 13.3550215 |
| C9JCM4 | Uncharacterized protein OS=Homo sapiens GN=HSPA1B PE=4 SV=1 - [C9JCM4_HUMAN] | 12.5 | 1 | 0 | 2 | 4 | 15.0118282 |
| C9IYE6 | Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [C9IYE6_HUMAN] | 12.18 | 1 | 0 | 2 | 4 | 15.0118282 |
| A5JHP3 | Dermcidin isoform 2 OS=Homo sapiens GN=DCD PE=2 SV=1 - [A5JHP3_HUMAN] | 11.57 | 1 | 0 | 2 | 4 | 13.3550215 |
| Q9UPH5 | Dynammin II (AA 474-866) [Homo sapiens] (Fragment) OS=Homo sapiens GN=DNM2 PE=2 SV=1 - [Q9UPH5_HUMAN] | 10.43 | 1 | 0 | 2 | 4 | 13.8748055 |
| B3KV39 | cDNA FLJ16099 fis, clone TESTI2008278, highly similar to Homo sapiens forkhead box K1 (FOXK1), mRNA OS=Homo sapiens PE=2 SV=1 - [B3KV39_HUMAN] | 9.63 | 1 | 0 | 2 | 4 | 18.121254 |

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| B4DHD7 | cDNA FLJ53737, highly similar to Sodium/potassium-transporting ATPase alpha-2 chain (EC 3.6.3.9) OS=Homo sapiens PE=2 SV=1 - [B4DHD7_HUMAN] | 9.56 | 1 | 0 | 2 | 4 | 13.0720036 |
| Q16094 | Calnexin (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q16094_HUMAN] | 9.56 | 1 | 0 | 2 | 4 | 13.1988614 |
| Q8N1K8 | cDNA FLJ40556 fis, clone THYMU2002583, highly similar to DYNAMIN 2 OS=Homo sapiens PE=2 SV=1 - [Q8N1K8_HUMAN] | 8.84 | 1 | 0 | 2 | 4 | 13.8748055 |
| B4DJ53 | cDNA FLJ56447, highly similar to Dynamin-2 (EC 3.6.5.5) OS=Homo sapiens PE=2 SV=1 - [B4DJ53_HUMAN] | 6.86 | 1 | 0 | 2 | 4 | 13.8748055 |
| B3KUU8 | cDNA FLJ40670 fis, clone THYMU2020959, highly similar to Dynamin-2 OS=Homo sapiens PE=2 SV=1 - [B3KUU8_HUMAN] | 6.59 | 1 | 0 | 2 | 4 | 13.8748055 |
| P48741 | Putative heat shock 70 kDa protein 7 OS=Homo sapiens GN=HSPA7 PE=5 SV=2 - [HSP77_HUMAN] | 6.54 | 1 | 0 | 2 | 4 | 12.3303638 |
| P85037 | Forkhead box protein K1 OS=Homo sapiens GN=FOXK1 PE=1 SV=1 - [FOXK1_HUMAN] | 6.41 | 1 | 0 | 2 | 4 | 18.121254 |
| B4DVK5 | cDNA FLJ54759, highly similar to DNA replication licensing factor MCM5 OS=Homo sapiens PE=2 SV=1 - [B4DVK5_HUMAN] | 6.31 | 1 | 0 | 2 | 4 | 11.1948371 |
| B4DFN9 | cDNA FLJ54303, highly similar to Heat shock 70 kDa protein 1 OS=Homo sapiens PE=2 SV=1 - [B4DFN9_HUMAN] | 5.07 | 1 | 0 | 2 | 4 | 15.0118282 |
| B4E3B6 | cDNA FLJ54408, highly similar to Heat shock 70 kDa protein 1 OS=Homo sapiens PE=2 SV=1 - [B4E3B6_HUMAN] | 4.95 | 1 | 0 | 2 | 4 | 15.0118282 |
| B4DXJ6 | cDNA FLJ61453, highly similar to Adapter-related protein complex 2 alpha-1 subunit OS=Homo sapiens PE=2 SV=1 - [B4DXJ6_HUMAN] | 4.86 | 1 | 0 | 2 | 4 | 10.234982 |
| B4DYM8 | cDNA FLJ60373, highly similar to Zinc finger CCCH domain-containing protein 11A OS=Homo sapiens PE=2 SV=1 - [B4DYM8_HUMAN] | 4.84 | 1 | 0 | 2 | 4 | 19.0600309 |
| B4DWK5 | cDNA FLJ54392, highly similar to Heat shock 70 kDa protein 1 OS=Homo sapiens PE=2 SV=1 - [B4DWK5_HUMAN] | 4.65 | 1 | 0 | 2 | 4 | 15.0118282 |
| B3KVF5 | cDNA FLJ16494 fis, clone CTONG3004576, highly similar to Keratin, type I cytoskeletal 15 OS=Homo sapiens PE=2 SV=1 - [B3KVF5_HUMAN] | 4.61 | 1 | 0 | 2 | 4 | 12.0704322 |
| B3KRY3 | cDNA FLJ35079 fis, clone PLACE6005283, highly similar to Lysosome-associated membrane glycoprotein 1 OS=Homo | 4.3 | 1 | 0 | 2 | 4 | 9.56365466 |

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| | sapiens PE=2 SV=1 - [B3KRY3_HUMAN] | | | | | | |
| Q59EJ3 | Heat shock 70kDa protein 1A variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59EJ3_HUMAN] | 4.09 | 1 | 0 | 2 | 4 | 15.0118282 |
| P11279 | Lysosome-associated membrane glycoprotein 1 OS=Homo sapiens GN=LAMP1 PE=1 SV=3 - [LAMP1_HUMAN] | 4.08 | 1 | 0 | 2 | 4 | 9.56365466 |
| Q7Z3Z0 | Keratin, type I cytoskeletal 25 OS=Homo sapiens GN=KRT25 PE=1 SV=1 - [K1C25_HUMAN] | 4 | 1 | 0 | 2 | 4 | 10.5578294 |
| Q7Z3Y8 | Keratin, type I cytoskeletal 27 OS=Homo sapiens GN=KRT27 PE=1 SV=2 - [K1C27_HUMAN] | 3.92 | 1 | 0 | 2 | 4 | 10.5578294 |
| Q96HX7 | HSP90AA1 protein (Fragment) OS=Homo sapiens GN=HSP90AA1 PE=2 SV=2 - [Q96HX7_HUMAN] | 3.79 | 1 | 0 | 2 | 4 | 10.1360173 |
| B4DHG3 | cDNA FLJ55329, highly similar to Procollagen-lysine,2-oxoglutarate5-dioxygenase 2 (EC 1.14.11.4) OS=Homo sapiens PE=2 SV=1 - [B4DHG3_HUMAN] | 3.7 | 1 | 0 | 2 | 4 | 13.0918639 |
| B4E029 | cDNA FLJ57693, highly similar to POU domain, class 2, transcription factor 1 OS=Homo sapiens PE=2 SV=1 - [B4E029_HUMAN] | 3.7 | 1 | 0 | 2 | 4 | 11.993973 |
| P26232 | Catenin alpha-2 OS=Homo sapiens GN=CTNNA2 PE=1 SV=5 - [CTNA2_HUMAN] | 3.67 | 1 | 0 | 2 | 4 | 16.4999111 |
| B4DZ95 | cDNA FLJ54570, highly similar to 2-oxoglutarate dehydrogenase E1 component, mitochondrial (EC 1.2.4.2) OS=Homo sapiens PE=2 SV=1 - [B4DZ95_HUMAN] | 3.57 | 1 | 0 | 2 | 4 | 12.4325225 |
| O00469 | Procollagen-lysine,2-oxoglutarate 5-dioxygenase 2 OS=Homo sapiens GN=PLOD2 PE=1 SV=2 - [PLOD2_HUMAN] | 3.53 | 1 | 0 | 2 | 4 | 13.0918639 |
| B3KRE9 | cDNA FLJ34119 fis, clone FCBBF3009464, highly similar to POU domain, class 2, transcription factor 1 OS=Homo sapiens PE=2 SV=1 - [B3KRE9_HUMAN] | 3.51 | 1 | 0 | 2 | 4 | 11.993973 |
| P14859 | POU domain, class 2, transcription factor 1 OS=Homo sapiens GN=POU2F1 PE=1 SV=2 - [PO2F1_HUMAN] | 3.5 | 1 | 0 | 2 | 4 | 11.993973 |
| B4DS45 | cDNA FLJ58259, highly similar to Gamma-tubulin complex component 2 OS=Homo sapiens PE=2 SV=1 - [B4DS45_HUMAN] | 3.36 | 1 | 0 | 2 | 4 | 10.5895655 |
| B7Z6I3 | cDNA FLJ61710, highly similar to DNA ligase 3 (EC 6.5.1.1) OS=Homo sapiens PE=2 SV=1 - [B7Z6I3_HUMAN] | 3.25 | 1 | 0 | 2 | 4 | 10.9076047 |

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| B4DM18 | cDNA FLJ58511, highly similar to Gamma-tubulin complex component 2 OS=Homo sapiens PE=2 SV=1 - [B4DM18_HUMAN] | 3.24 | 1 | 0 | 2 | 4 | 10.5895655 |
| Q7Z2W4 | Zinc finger CCCH-type antiviral protein 1 OS=Homo sapiens GN=ZC3HAV1 PE=1 SV=3 - [ZCCHV_HUMAN] | 3.1 | 1 | 0 | 2 | 4 | 12.8727705 |
| A8K9U6 | cDNA FLJ76121, highly similar to Homo sapiens zinc finger CCCH-type, antiviral 1 (ZC3HAV1), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1 - [A8K9U6_HUMAN] | 3.1 | 1 | 0 | 2 | 4 | 12.8727705 |
| C9J6P4 | Uncharacterized protein OS=Homo sapiens GN=ZC3HAV1 PE=4 SV=1 - [C9J6P4_HUMAN] | 2.73 | 1 | 0 | 2 | 4 | 12.8727705 |
| B4DSW9 | cDNA FLJ59415, highly similar to Beta-catenin OS=Homo sapiens PE=2 SV=1 - [B4DSW9_HUMAN] | 2.68 | 1 | 0 | 2 | 4 | 10.2832019 |
| B4DL06 | cDNA FLJ59565, highly similar to Beta-catenin OS=Homo sapiens PE=2 SV=1 - [B4DL06_HUMAN] | 2.57 | 1 | 0 | 2 | 4 | 10.2832019 |
| O95782 | AP-2 complex subunit alpha-1 OS=Homo sapiens GN=AP2A1 PE=1 SV=3 - [AP2A1_HUMAN] | 2.46 | 1 | 0 | 2 | 4 | 10.234982 |
| B4DGU4 | cDNA FLJ57878, highly similar to Beta-catenin OS=Homo sapiens PE=2 SV=1 - [B4DGU4_HUMAN] | 2.45 | 1 | 0 | 2 | 4 | 10.2832019 |
| P35222 | Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=1 SV=1 - [CTNB1_HUMAN] | 2.43 | 1 | 0 | 2 | 4 | 10.2832019 |
| B5BU28 | Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=2 SV=1 - [B5BU28_HUMAN] | 2.43 | 1 | 0 | 2 | 4 | 10.2832019 |
| P49916 | DNA ligase 3 OS=Homo sapiens GN=LIG3 PE=1 SV=2 - [DNLI3_HUMAN] | 2.38 | 1 | 0 | 2 | 4 | 10.9076047 |
| Q7Z3N6 | Putative uncharacterized protein DKFZp686A01173 (Fragment) OS=Homo sapiens GN=DKFZp686A01173 PE=2 SV=1 - [Q7Z3N6_HUMAN] | 2.07 | 1 | 0 | 2 | 4 | 9.60237765 |
| O94832 | Myosin-Id OS=Homo sapiens GN=MYO1D PE=1 SV=2 - [MYO1D_HUMAN] | 1.89 | 1 | 0 | 2 | 4 | 9.60237765 |
| E5RFJ8 | Uncharacterized protein OS=Homo sapiens GN=MCM4 PE=4 SV=1 - [E5RFJ8_HUMAN] | 23.58 | 1 | 0 | 2 | 3 | 14.6090989 |
| E5RIC3 | Uncharacterized protein OS=Homo sapiens GN=CTNNA1 PE=4 SV=1 - [E5RIC3_HUMAN] | 17.03 | 1 | 0 | 2 | 3 | 9.67565227 |
| Q14222 | EEF1A protein (Fragment) OS=Homo sapiens GN=EEF1A PE=1 | 15.42 | 1 | 0 | 2 | 3 | 11.0109358 |

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|--------|------------------------------------------------------------------------------------------------------------------------------|-------|---|---|---|---|------------|
| | SV=1 - [Q14222_HUMAN] | | | | | | |
| E5RIB1 | Uncharacterized protein OS=Homo sapiens GN=CTNNA1 PE=4 SV=1 - [E5RIB1_HUMAN] | 14.42 | 1 | 0 | 2 | 3 | 9.67565227 |
| Q96C29 | Putative uncharacterized protein (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q96C29_HUMAN] | 14.11 | 1 | 0 | 2 | 3 | 11.0109358 |
| Q8TBL1 | Putative uncharacterized protein (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q8TBL1_HUMAN] | 14 | 1 | 0 | 2 | 3 | 11.0109358 |
| Q6P082 | EEF1A1 protein (Fragment) OS=Homo sapiens GN=EEF1A1 PE=2 SV=1 - [Q6P082_HUMAN] | 13.94 | 1 | 0 | 2 | 3 | 11.0109358 |
| Q7Z3M8 | Putative uncharacterized protein DKFZp686A01208 OS=Homo sapiens GN=DKFZp686A01208 PE=2 SV=1 - [Q7Z3M8_HUMAN] | 13.33 | 1 | 0 | 2 | 3 | 7.53037786 |
| Q96CD8 | Putative uncharacterized protein (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q96CD8_HUMAN] | 12.2 | 1 | 0 | 2 | 3 | 11.0109358 |
| Q6P4C9 | EEF1A1 protein (Fragment) OS=Homo sapiens GN=EEF1A1 PE=2 SV=1 - [Q6P4C9_HUMAN] | 12.07 | 1 | 0 | 2 | 3 | 11.0109358 |
| Q504Z0 | EEF1A1 protein OS=Homo sapiens GN=EEF1A1 PE=2 SV=1 - [Q504Z0_HUMAN] | 11.36 | 1 | 0 | 2 | 3 | 11.0109358 |
| B4E2C5 | cDNA FLJ54032, highly similar to Elongation factor 1-alpha 1 OS=Homo sapiens PE=2 SV=1 - [B4E2C5_HUMAN] | 11.36 | 1 | 0 | 2 | 3 | 11.0109358 |
| Q8IUB0 | CTCL tumor antigen HD-CL-08 OS=Homo sapiens PE=2 SV=1 - [Q8IUB0_HUMAN] | 9.7 | 1 | 0 | 2 | 3 | 11.0109358 |
| B4DNE0 | cDNA FLJ52573, highly similar to Elongation factor 1-alpha 1 OS=Homo sapiens PE=2 SV=1 - [B4DNE0_HUMAN] | 8.86 | 1 | 0 | 2 | 3 | 11.0109358 |
| Q6DKJ9 | BOP1 protein (Fragment) OS=Homo sapiens GN=BOP1 PE=2 SV=1 - [Q6DKJ9_HUMAN] | 8.83 | 1 | 0 | 2 | 3 | 10.3858471 |
| Q96RE1 | Translation elongation factor 1 alpha 1-like 14 OS=Homo sapiens GN=EEF1A1L14 PE=2 SV=1 - [Q96RE1_HUMAN] | 8.79 | 1 | 0 | 2 | 3 | 11.0109358 |
| B4DKH5 | cDNA FLJ58495, highly similar to Adapter-related protein complex 1 beta-1 subunit OS=Homo sapiens PE=2 SV=1 - [B4DKH5_HUMAN] | 8.36 | 1 | 0 | 2 | 3 | 7.53037786 |
| Q9NZS6 | Glucocorticoid receptor AF-1 specific elongation factor (Fragment) OS=Homo sapiens PE=1 SV=1 - [Q9NZS6_HUMAN] | 8.22 | 1 | 0 | 2 | 3 | 11.0109358 |
| Q4G0D9 | BOP1 protein (Fragment) OS=Homo sapiens GN=BOP1 PE=2 SV=1 - [Q4G0D9_HUMAN] | 8.11 | 1 | 0 | 2 | 3 | 10.3858471 |

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|--------|------------------------------------------------------------------------------------------------------------------------------------------------------------|------|---|---|---|---|------------|
| B7Z4V1 | cDNA FLJ55401, highly similar to Alpha-actinin-2 OS=Homo sapiens PE=2 SV=1 - [B7Z4V1_HUMAN] | 8.1 | 1 | 0 | 2 | 3 | 9.41856074 |
| Q53G89 | Eukaryotic translation elongation factor 1 alpha 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53G89_HUMAN] | 8.08 | 1 | 0 | 2 | 3 | 11.0109358 |
| Q6IQ15 | EEF1A1 protein OS=Homo sapiens GN=EEF1A1 PE=2 SV=1 - [Q6IQ15_HUMAN] | 7.94 | 1 | 0 | 2 | 3 | 11.0109358 |
| P68104 | Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 - [EF1A1_HUMAN] | 7.58 | 1 | 0 | 2 | 3 | 11.0109358 |
| Q5VTE0 | Putative elongation factor 1-alpha-like 3 OS=Homo sapiens GN=EEF1AL3 PE=5 SV=1 - [EF1A3_HUMAN] | 7.58 | 1 | 0 | 2 | 3 | 11.0109358 |
| Q53HM9 | Eukaryotic translation elongation factor 1 alpha 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53HM9_HUMAN] | 7.58 | 1 | 0 | 2 | 3 | 11.0109358 |
| Q6IPT9 | Eukaryotic translation elongation factor 1 alpha 1 OS=Homo sapiens GN=EEF1A1 PE=2 SV=1 - [Q6IPT9_HUMAN] | 7.58 | 1 | 0 | 2 | 3 | 11.0109358 |
| Q6IPN6 | Eukaryotic translation elongation factor 1 alpha 1 OS=Homo sapiens GN=EEF1A1 PE=2 SV=1 - [Q6IPN6_HUMAN] | 7.58 | 1 | 0 | 2 | 3 | 11.0109358 |
| Q53HR5 | Eukaryotic translation elongation factor 1 alpha 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53HR5_HUMAN] | 7.58 | 1 | 0 | 2 | 3 | 11.0109358 |
| Q53GE9 | Eukaryotic translation elongation factor 1 alpha 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53GE9_HUMAN] | 7.58 | 1 | 0 | 2 | 3 | 11.0109358 |
| Q53HQ7 | Eukaryotic translation elongation factor 1 alpha 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53HQ7_HUMAN] | 7.58 | 1 | 0 | 2 | 3 | 11.0109358 |
| A8K9C4 | cDNA FLJ76726, highly similar to Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K9C4_HUMAN] | 7.58 | 1 | 0 | 2 | 3 | 11.0109358 |
| Q53G85 | Eukaryotic translation elongation factor 1 alpha 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53G85_HUMAN] | 7.58 | 1 | 0 | 2 | 3 | 11.0109358 |
| B0AZS1 | cDNA, FLJ79511, highly similar to Heat shock 70 kDa protein 4 OS=Homo sapiens PE=2 SV=1 - [B0AZS1_HUMAN] | 7.51 | 1 | 0 | 2 | 3 | 7.11022091 |
| Q96Q25 | KM-PA-2 protein OS=Homo sapiens GN=KM-PA-2 PE=2 SV=1 - [Q96Q25_HUMAN] | 7.26 | 1 | 0 | 2 | 3 | 10.3858471 |
| B4DEN9 | cDNA FLJ56617, highly similar to Ribosome biogenesis protein BOP1 OS=Homo sapiens PE=2 SV=1 - [B4DEN9_HUMAN] | 7.26 | 1 | 0 | 2 | 3 | 10.3858471 |
| Q6PEK6 | OPA1 protein OS=Homo sapiens PE=2 SV=1 - [Q6PEK6_HUMAN] | 7.25 | 1 | 0 | 2 | 3 | 7.50717878 |

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|--------|----------------------------------------------------------------------------------------------------------------------------------|------|---|---|---|---|------------|
| Q9NW36 | Helicase, lymphoid-specific OS=Homo sapiens GN=HELLS PE=2 SV=1 - [Q9NW36_HUMAN] | 6.77 | 1 | 0 | 2 | 3 | 7.91242719 |
| D3DWJ7 | Topoisomerase (DNA) I, mitochondrial, isoform CRA_a OS=Homo sapiens GN=TOP1MT PE=4 SV=1 - [D3DWJ7_HUMAN] | 6.19 | 1 | 0 | 2 | 3 | 8.85394287 |
| B7Z5E7 | cDNA FLJ51046, highly similar to 60 kDa heat shock protein, mitochondrial OS=Homo sapiens PE=2 SV=1 - [B7Z5E7_HUMAN] | 5.8 | 1 | 0 | 2 | 3 | 9.14200544 |
| E5RIC7 | Uncharacterized protein OS=Homo sapiens GN=TOP1MT PE=4 SV=1 - [E5RIC7_HUMAN] | 5.49 | 1 | 0 | 2 | 3 | 8.85394287 |
| B0AZU6 | cDNA, FLJ79536, highly similar to Heat shock 70 kDa protein 4 OS=Homo sapiens PE=2 SV=1 - [B0AZU6_HUMAN] | 5.48 | 1 | 0 | 2 | 3 | 7.11022091 |
| B7Z2I6 | cDNA FLJ57106, highly similar to Transferrin receptor protein 1 OS=Homo sapiens PE=2 SV=1 - [B7Z2I6_HUMAN] | 5.44 | 1 | 0 | 2 | 3 | 8.40977764 |
| B7Z597 | cDNA FLJ54373, highly similar to 60 kDa heat shock protein, mitochondrial OS=Homo sapiens PE=2 SV=1 - [B7Z597_HUMAN] | 5.32 | 1 | 0 | 2 | 3 | 9.14200544 |
| B3GQS7 | Mitochondrial heat shock 60kD protein 1 variant 1 OS=Homo sapiens GN=HSPD1 PE=2 SV=1 - [B3GQS7_HUMAN] | 5.27 | 1 | 0 | 2 | 3 | 9.14200544 |
| P10809 | 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 - [CH60_HUMAN] | 5.24 | 1 | 0 | 2 | 3 | 9.14200544 |
| Q58FF3 | Putative endoplasmic-like protein OS=Homo sapiens GN=HSP90B2P PE=5 SV=1 - [ENPLL_HUMAN] | 5.01 | 1 | 0 | 2 | 3 | 8.4930687 |
| B4DS79 | cDNA FLJ56828, highly similar to Adapter-relatedprotein complex 1 beta-1 subunit OS=Homo sapiens PE=2 SV=1 - [B4DS79_HUMAN] | 4.81 | 1 | 0 | 2 | 3 | 7.53037786 |
| B4DG47 | cDNA FLJ56967, highly similar to Adapter-relatedprotein complex 1 beta-1 subunit OS=Homo sapiens PE=2 SV=1 - [B4DG47_HUMAN] | 4.78 | 1 | 0 | 2 | 3 | 7.53037786 |
| Q05BX4 | PSMD1 protein (Fragment) OS=Homo sapiens GN=PSMD1 PE=2 SV=1 - [Q05BX4_HUMAN] | 4.61 | 1 | 0 | 2 | 3 | 13.6282349 |
| Q05CW6 | PSMD1 protein (Fragment) OS=Homo sapiens GN=PSMD1 PE=2 SV=1 - [Q05CW6_HUMAN] | 4.44 | 1 | 0 | 2 | 3 | 13.6282349 |
| B4E365 | cDNA FLJ56210, highly similar to Zinc phosphodiesterase ELAC protein 2 (EC 3.1.26.11) OS=Homo sapiens PE=2 SV=1 - [B4E365_HUMAN] | 4.01 | 1 | 0 | 2 | 3 | 9.51381421 |
| Q53QX9 | Putative uncharacterized protein HK2 (Fragment) OS=Homo | 4.01 | 1 | 0 | 2 | 3 | 8.98018646 |

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|--------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------|------|---|---|---|---|------------|
| | sapiens GN=HK2 PE=2 SV=1 - [Q53QX9_HUMAN] | | | | | | |
| Q99460 | 26S proteasome non-ATPase regulatory subunit 1 OS=Homo sapiens GN=PSMD1 PE=1 SV=2 - [PSMD1_HUMAN] | 3.99 | 1 | 0 | 2 | 3 | 13.6282349 |
| B2R6D0 | cDNA, FLJ92896, highly similar to Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 1 (PSMD1), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R6D0_HUMAN] | 3.99 | 1 | 0 | 2 | 3 | 13.6282349 |
| Q2TU89 | Aging-associated protein 1 OS=Homo sapiens GN=AAG1 PE=2 SV=1 - [Q2TU89_HUMAN] | 3.85 | 1 | 0 | 2 | 3 | 9.60749149 |
| B3KTP2 | cDNA FLJ38558 fis, clone HCHON2003327, highly similar to Puromycin-sensitive aminopeptidase OS=Homo sapiens PE=2 SV=1 - [B3KTP2_HUMAN] | 3.35 | 1 | 0 | 2 | 3 | 9.05323982 |
| Q9NSB2 | Keratin, type II cuticular Hb4 OS=Homo sapiens GN=KRT84 PE=1 SV=2 - [KRT84_HUMAN] | 3 | 1 | 0 | 2 | 3 | 8.82233119 |
| Q7RTS7 | Keratin, type II cytoskeletal 74 OS=Homo sapiens GN=KRT74 PE=1 SV=2 - [K2C74_HUMAN] | 2.84 | 1 | 0 | 2 | 3 | 6.5596633 |
| Q86Y46 | Keratin, type II cytoskeletal 73 OS=Homo sapiens GN=KRT73 PE=1 SV=1 - [K2C73_HUMAN] | 2.78 | 1 | 0 | 2 | 3 | 6.5596633 |
| Q68E10 | Putative uncharacterized protein DKFZp686M1669 OS=Homo sapiens GN=DKFZp686M1669 PE=2 SV=1 - [Q68E10_HUMAN] | 2.59 | 1 | 0 | 2 | 3 | 8.98018646 |
| P52789 | Hexokinase-2 OS=Homo sapiens GN=HK2 PE=1 SV=2 - [HXK2_HUMAN] | 2.51 | 1 | 0 | 2 | 3 | 8.98018646 |
| A8K2U2 | cDNA FLJ75392, highly similar to Homo sapiens hexokinase II (HKII) mRNA OS=Homo sapiens PE=2 SV=1 - [A8K2U2_HUMAN] | 2.51 | 1 | 0 | 2 | 3 | 8.98018646 |
| Q9UIA9 | Exportin-7 OS=Homo sapiens GN=XPO7 PE=1 SV=3 - [XPO7_HUMAN] | 2.39 | 1 | 0 | 2 | 3 | 8.95551014 |
| A8K607 | cDNA FLJ76855, highly similar to Homo sapiens exportin 7 (XPO7), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K607_HUMAN] | 2.39 | 1 | 0 | 2 | 3 | 8.95551014 |
| E5KLK2 | Mitochondrial dynamin-like 120 kDa protein OS=Homo sapiens GN=OPA1 PE=4 SV=1 - [E5KLK2_HUMAN] | 2.16 | 1 | 0 | 2 | 3 | 7.50717878 |
| E5KLK0 | Mitochondrial dynamin-like 120 kDa protein OS=Homo sapiens GN=OPA1 PE=4 SV=1 - [E5KLK0_HUMAN] | 2.12 | 1 | 0 | 2 | 3 | 7.50717878 |
| O60313 | Dynamin-like 120 kDa protein, mitochondrial OS=Homo sapiens GN=OPA1 PE=1 SV=3 - [OPA1_HUMAN] | 2.08 | 1 | 0 | 2 | 3 | 7.50717878 |

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|--------|-----------------------------------------------------------------------------------------------------------------------------------|-------|---|---|---|---|------------|
| E5KLM2 | Mitochondrial dynamin-like 120 kDa protein OS=Homo sapiens PE=4 SV=1 - [E5KLM2_HUMAN] | 2.08 | 1 | 0 | 2 | 3 | 7.50717878 |
| E5KLK1 | Mitochondrial dynamin-like 120 kDa protein OS=Homo sapiens GN=OPA1 PE=4 SV=1 - [E5KLK1_HUMAN] | 2.08 | 1 | 0 | 2 | 3 | 7.50717878 |
| E5KLJ6 | Mitochondrial dynamin-like 120 kDa protein OS=Homo sapiens GN=OPA1 PE=4 SV=1 - [E5KLJ6_HUMAN] | 2.04 | 1 | 0 | 2 | 3 | 7.50717878 |
| E5KLM0 | Mitochondrial dynamin-like 120 kDa protein OS=Homo sapiens PE=4 SV=1 - [E5KLM0_HUMAN] | 2.04 | 1 | 0 | 2 | 3 | 7.50717878 |
| E5KLJ9 | Mitochondrial dynamin-like 120 kDa protein OS=Homo sapiens GN=OPA1 PE=4 SV=1 - [E5KLJ9_HUMAN] | 2.04 | 1 | 0 | 2 | 3 | 7.50717878 |
| E5KLM1 | Mitochondrial dynamin-like 120 kDa protein OS=Homo sapiens PE=4 SV=1 - [E5KLM1_HUMAN] | 2.01 | 1 | 0 | 2 | 3 | 7.50717878 |
| E5KLJ7 | Mitochondrial dynamin-like 120 kDa protein OS=Homo sapiens GN=OPA1 PE=4 SV=1 - [E5KLJ7_HUMAN] | 2.01 | 1 | 0 | 2 | 3 | 7.50717878 |
| E5KLL9 | Mitochondrial dynamin-like 120 kDa protein OS=Homo sapiens PE=4 SV=1 - [E5KLL9_HUMAN] | 1.97 | 1 | 0 | 2 | 3 | 7.50717878 |
| E5KLJ5 | Mitochondrial dynamin-like 120 kDa protein OS=Homo sapiens GN=OPA1 PE=4 SV=1 - [E5KLJ5_HUMAN] | 1.97 | 1 | 0 | 2 | 3 | 7.50717878 |
| Q5JYA5 | Methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like (Fragment) OS=Homo sapiens GN=MTHFD1L PE=2 SV=1 - [Q5JYA5_HUMAN] | 18.33 | 1 | 0 | 2 | 2 | 4.72747302 |
| Q68CW0 | Putative uncharacterized protein DKFZp547C166 OS=Homo sapiens GN=DKFZp547C166 PE=2 SV=2 - [Q68CW0_HUMAN] | 10.33 | 1 | 0 | 2 | 2 | 5.67633367 |
| Q5JRR9 | Ubiquitin-like modifier activating enzyme 1 (Fragment) OS=Homo sapiens GN=UBA1 PE=2 SV=1 - [Q5JRR9_HUMAN] | 7.75 | 1 | 0 | 2 | 2 | 5.78997231 |
| Q5JRS0 | Ubiquitin-like modifier activating enzyme 1 (Fragment) OS=Homo sapiens GN=UBA1 PE=2 SV=1 - [Q5JRS0_HUMAN] | 7.39 | 1 | 0 | 2 | 2 | 5.78997231 |
| B3KMX1 | cDNA FLJ12848 fis, clone NT2RP2003391, highly similar to Transportin-3 OS=Homo sapiens PE=2 SV=1 - [B3KMX1_HUMAN] | 5 | 1 | 0 | 2 | 2 | 5.85115314 |
| B4DJ90 | cDNA FLJ51865, highly similar to RNA-binding protein 28 OS=Homo sapiens PE=2 SV=1 - [B4DJ90_HUMAN] | 4.91 | 1 | 0 | 2 | 2 | 5.18279648 |
| B3KM69 | cDNA FLJ10401 fis, clone NT2RM4000421, highly similar to Transportin-3 OS=Homo sapiens PE=2 SV=1 - | 4.59 | 1 | 0 | 2 | 2 | 5.85115314 |

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| | [B3KM69_HUMAN] | | | | | | |
| B4DXL4 | cDNA FLJ59781, highly similar to Nucleolar complex protein 3 homolog OS=Homo sapiens PE=2 SV=1 - [B4DXL4_HUMAN] | 4.39 | 1 | 0 | 2 | 2 | 5.68410993 |
| B3KM90 | cDNA FLJ10529 fis, clone NT2RP2000965, highly similar to Targeting protein for Xklp2 OS=Homo sapiens PE=2 SV=1 - [B3KM90_HUMAN] | 3.8 | 1 | 0 | 2 | 2 | 4.25025749 |
| B4DNM8 | cDNA FLJ53395, highly similar to Prolyl 3-hydroxylase 1 (EC 1.14.11.7) OS=Homo sapiens PE=2 SV=1 - [B4DNM8_HUMAN] | 3.66 | 1 | 0 | 2 | 2 | 5.67633367 |
| B0AZS5 | cDNA, FLJ79515, highly similar to Kinesin-like protein KIF2 OS=Homo sapiens PE=2 SV=1 - [B0AZS5_HUMAN] | 3.48 | 1 | 0 | 2 | 2 | 5.87805176 |
| B4E061 | cDNA FLJ51170, highly similar to DNA topoisomerase I, mitochondrial (EC 5.99.1.2) OS=Homo sapiens PE=2 SV=1 - [B4E061_HUMAN] | 3.35 | 1 | 0 | 2 | 2 | 4.41180563 |
| O00139 | Kinesin-like protein KIF2A OS=Homo sapiens GN=KIF2A PE=1 SV=3 - [KIF2A_HUMAN] | 3.26 | 1 | 0 | 2 | 2 | 5.87805176 |
| B4DM85 | cDNA FLJ56002, highly similar to Kinesin-like protein KIF2 OS=Homo sapiens PE=2 SV=1 - [B4DM85_HUMAN] | 3.09 | 1 | 0 | 2 | 2 | 5.87805176 |
| Q9ULW0 | Targeting protein for Xklp2 OS=Homo sapiens GN=TPX2 PE=1 SV=2 - [TPX2_HUMAN] | 3.08 | 1 | 0 | 2 | 2 | 4.25025749 |
| Q32P28 | Prolyl 3-hydroxylase 1 OS=Homo sapiens GN=LEPRE1 PE=1 SV=2 - [P3H1_HUMAN] | 2.99 | 1 | 0 | 2 | 2 | 5.67633367 |
| Q96RR5 | Hepatocellular carcinoma-associated antigen 90 OS=Homo sapiens GN=HCA90 PE=2 SV=1 - [Q96RR5_HUMAN] | 2.94 | 1 | 0 | 2 | 2 | 4.25025749 |
| Q8WTT2 | Nucleolar complex protein 3 homolog OS=Homo sapiens GN=NOC3L PE=1 SV=1 - [NOC3L_HUMAN] | 2.75 | 1 | 0 | 2 | 2 | 5.68410993 |
| A6NJZ9 | Uncharacterized protein OS=Homo sapiens GN=NOC3L PE=4 SV=1 - [A6NJZ9_HUMAN] | 2.75 | 1 | 0 | 2 | 2 | 5.68410993 |
| A8K905 | cDNA FLJ77615, highly similar to Homo sapiens nucleolar complex associated 3 homolog (<i>S. cerevisiae</i>) (NOC3L), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K905_HUMAN] | 2.75 | 1 | 0 | 2 | 2 | 5.68410993 |
| Q9Y5L0 | Transportin-3 OS=Homo sapiens GN=TNPO3 PE=1 SV=3 - [TNPO3_HUMAN] | 2.6 | 1 | 0 | 2 | 2 | 5.85115314 |
| B2R6H7 | cDNA, FLJ92955, highly similar to Homo sapiens transportin-SR (TRN-SR), mRNA OS=Homo sapiens PE=2 SV=1 - | 2.6 | 1 | 0 | 2 | 2 | 5.85115314 |

| | [B2R6H7_HUMAN] | | | | | | |
|--------|-----------------------------------------------------------------------------|------|---|---|---|---|------------|
| C9J7E5 | Uncharacterized protein OS=Homo sapiens GN=TNPO3 PE=4 SV=1 - [C9J7E5_HUMAN] | 2.51 | 1 | 0 | 2 | 2 | 5.85115314 |
| B5MD86 | Uncharacterized protein OS=Homo sapiens GN=TNPO3 PE=4 SV=2 - [B5MD86_HUMAN] | 2.48 | 1 | 0 | 2 | 2 | 5.85115314 |

Protein ID10.msf

| Accession | Description | Σ Coverage | Σ # Proteins | Σ # Unique Peptides | Σ # Peptides | Σ # PSMs | Score A3 |
|-----------|------------------------------------------------------------------------------------------------------------------|-------------------|---------------------|----------------------------|---------------------|-----------------|------------|
| P04264 | Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6 - [K2C1_HUMAN] | 39.91 | 1 | 17 | 18 | 82 | 378.299591 |
| P35527 | Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3 - [K1C9_HUMAN] | 47.99 | 1 | 15 | 15 | 52 | 256.317428 |
| P13645 | Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6 - [K1C10_HUMAN] | 36.13 | 1 | 13 | 13 | 48 | 222.689058 |
| P35908 | Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2 - [K22E_HUMAN] | 34.12 | 1 | 9 | 11 | 26 | 127.009608 |
| P02533 | Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4 - [K1C14_HUMAN] | 20.97 | 1 | 2 | 6 | 16 | 72.4583981 |
| P08779 | Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4 - [K1C16_HUMAN] | 17.76 | 1 | 1 | 5 | 10 | 42.4020312 |
| P13647 | Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3 - [K2C5_HUMAN] | 9.66 | 1 | 1 | 4 | 8 | 31.8519762 |
| P81605 | Dermcidin OS=Homo sapiens GN=DCD PE=1 SV=2 - [DCD_HUMAN] | 35.45 | 1 | 1 | 4 | 7 | 22.6413534 |
| Q16891 | Mitochondrial inner membrane protein OS=Homo sapiens GN=IMMT PE=1 SV=1 - [IMMT_HUMAN] | 37.99 | 1 | 0 | 19 | 59 | 286.521101 |
| B9A067 | Uncharacterized protein OS=Homo sapiens GN=IMMT PE=4 SV=2 - [B9A067_HUMAN] | 36.99 | 1 | 0 | 18 | 58 | 281.4249 |
| B4DQY2 | cDNA FLJ59388, highly similar to Mitochondrial inner membrane protein OS=Homo sapiens PE=2 SV=1 - [B4DQY2_HUMAN] | 36.99 | 1 | 0 | 18 | 58 | 281.4249 |
| B4DKR1 | cDNA FLJ51884, highly similar to Mitochondrial inner membrane protein OS=Homo sapiens PE=2 SV=1 - [B4DKR1_HUMAN] | 32.57 | 1 | 0 | 17 | 51 | 231.802927 |
| B4DS66 | cDNA FLJ54290, highly similar to Mitochondrial inner membrane protein OS=Homo sapiens PE=2 SV=1 - [B4DS66_HUMAN] | 37.88 | 1 | 0 | 17 | 50 | 246.412533 |
| C9J406 | Uncharacterized protein OS=Homo sapiens GN=IMMT PE=4 SV=1 - [C9J406_HUMAN] | 34.14 | 1 | 0 | 16 | 49 | 241.316331 |
| B8ZZQ7 | Uncharacterized protein OS=Homo sapiens GN=IMMT PE=4 | 33.23 | 1 | 0 | 14 | 47 | 235.04461 |

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|--------|------------------------------------------------------------------------------------------------------------------|-------|---|---|----|----|------------|
| | SV=2 - [B8ZZQ7_HUMAN] | | | | | | |
| B4DT20 | cDNA FLJ59418, highly similar to Mitochondrial inner membrane protein OS=Homo sapiens PE=2 SV=1 - [B4DT20_HUMAN] | 33.23 | 1 | 0 | 14 | 47 | 235.04461 |
| B4DL32 | cDNA FLJ59922, highly similar to Keratin, type II cytoskeletal 5 OS=Homo sapiens PE=2 SV=1 - [B4DL32_HUMAN] | 41.45 | 1 | 0 | 14 | 42 | 123.393643 |
| Q01546 | Keratin, type II cytoskeletal 2 oral OS=Homo sapiens GN=KRT76 PE=1 SV=2 - [K22O_HUMAN] | 8.78 | 1 | 0 | 10 | 34 | 91.2595078 |
| O95678 | Keratin, type II cytoskeletal 75 OS=Homo sapiens GN=KRT75 PE=1 SV=2 - [K2C75_HUMAN] | 12.89 | 1 | 0 | 10 | 30 | 81.1182485 |
| P12035 | Keratin, type II cytoskeletal 3 OS=Homo sapiens GN=KRT3 PE=1 SV=3 - [K2C3_HUMAN] | 7.96 | 1 | 0 | 8 | 29 | 78.7787703 |
| B4E2B5 | cDNA FLJ53959, highly similar to Mitochondrial inner membrane protein OS=Homo sapiens PE=2 SV=1 - [B4E2B5_HUMAN] | 26.49 | 1 | 0 | 7 | 25 | 131.119985 |
| Q5XKE5 | Keratin, type II cytoskeletal 79 OS=Homo sapiens GN=KRT79 PE=1 SV=2 - [K2C79_HUMAN] | 9.35 | 1 | 0 | 7 | 24 | 62.0418652 |
| B4E2P9 | cDNA FLJ56708, highly similar to Keratin, type I cytoskeletal 17 OS=Homo sapiens PE=2 SV=1 - [B4E2P9_HUMAN] | 38.37 | 1 | 0 | 7 | 23 | 60.4772937 |
| P08727 | Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=4 - [K1C19_HUMAN] | 14 | 1 | 0 | 7 | 23 | 54.3744937 |
| E0CX14 | Uncharacterized protein OS=Homo sapiens GN=KRT15 PE=4 SV=1 - [E0CX14_HUMAN] | 7.91 | 1 | 0 | 6 | 23 | 60.6414642 |
| P19012 | Keratin, type I cytoskeletal 15 OS=Homo sapiens GN=KRT15 PE=1 SV=3 - [K1C15_HUMAN] | 7.89 | 1 | 0 | 6 | 23 | 60.6414642 |
| C9JM50 | Uncharacterized protein OS=Homo sapiens GN=KRT19 PE=4 SV=1 - [C9JM50_HUMAN] | 23.98 | 1 | 0 | 6 | 21 | 48.5881487 |
| Q05DN3 | IMMT protein (Fragment) OS=Homo sapiens GN=IMMT PE=2 SV=1 - [Q05DN3_HUMAN] | 37.97 | 1 | 0 | 6 | 20 | 110.518679 |
| C9JH30 | Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [C9JH30_HUMAN] | 10.62 | 1 | 0 | 6 | 19 | 51.210521 |
| A8MW45 | Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [A8MW45_HUMAN] | 10.43 | 1 | 0 | 6 | 19 | 51.210521 |
| B4DWU0 | cDNA FLJ56791, highly similar to Keratin, type I cytoskeletal 16 OS=Homo sapiens PE=2 SV=1 - [B4DWU0_HUMAN] | 32.59 | 1 | 0 | 5 | 21 | 54.4655676 |

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|--------|---------------------------------------------------------------------------------------------------------------|-------|---|---|---|----|------------|
| B4E2J5 | cDNA FLJ53570, highly similar to Keratin, type I cytoskeletal 16 OS=Homo sapiens PE=2 SV=1 - [B4E2J5_HUMAN] | 23.4 | 1 | 0 | 5 | 21 | 54.4655676 |
| P13646 | Keratin, type I cytoskeletal 13 OS=Homo sapiens GN=KRT13 PE=1 SV=4 - [K1C13_HUMAN] | 6.55 | 1 | 0 | 5 | 15 | 44.6490991 |
| B7WJP1 | Uncharacterized protein OS=Homo sapiens GN=IMMT PE=4 SV=1 - [B7WJP1_HUMAN] | 26.54 | 1 | 0 | 5 | 13 | 58.1126447 |
| B4DE59 | cDNA FLJ60424, highly similar to Junction plakoglobin OS=Homo sapiens PE=2 SV=1 - [B4DE59_HUMAN] | 8.35 | 1 | 0 | 5 | 12 | 28.1323093 |
| B4DPR2 | cDNA FLJ50830, highly similar to Serum albumin OS=Homo sapiens PE=2 SV=1 - [B4DPR2_HUMAN] | 7.84 | 1 | 0 | 5 | 11 | 33.0369173 |
| A8K9P0 | cDNA FLJ78413, highly similar to Homo sapiens albumin, mRNA OS=Homo sapiens PE=2 SV=1 - [A8K9P0_HUMAN] | 6.74 | 1 | 0 | 5 | 11 | 33.0369173 |
| P02768 | Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2 - [ALBU_HUMAN] | 6.73 | 1 | 0 | 5 | 11 | 33.0369173 |
| Q56G89 | Serum albumin OS=Homo sapiens PE=2 SV=1 - [Q56G89_HUMAN] | 6.73 | 1 | 0 | 5 | 11 | 33.0369173 |
| B2RBS8 | cDNA, FLJ95666, highly similar to Homo sapiens albumin (ALB), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RBS8_HUMAN] | 6.73 | 1 | 0 | 5 | 11 | 33.0369173 |
| B4DPP6 | cDNA FLJ54371, highly similar to Serum albumin OS=Homo sapiens PE=2 SV=1 - [B4DPP6_HUMAN] | 6.63 | 1 | 0 | 5 | 11 | 33.0369173 |
| A6NBZ8 | Uncharacterized protein OS=Homo sapiens GN=ALB PE=4 SV=2 - [A6NBZ8_HUMAN] | 6.54 | 1 | 0 | 5 | 11 | 33.0369173 |
| B4DWU6 | cDNA FLJ51361, highly similar to Keratin, type II cytoskeletal 6A OS=Homo sapiens PE=2 SV=1 - [B4DWU6_HUMAN] | 15.38 | 1 | 0 | 5 | 9 | 37.4630854 |
| B4DRR0 | cDNA FLJ53910, highly similar to Keratin, type II cytoskeletal 6A OS=Homo sapiens PE=2 SV=1 - [B4DRR0_HUMAN] | 14.95 | 1 | 0 | 5 | 9 | 37.4630854 |
| B4DRU6 | cDNA FLJ54657, highly similar to Keratin, type II cytoskeletal 6A OS=Homo sapiens PE=2 SV=1 - [B4DRU6_HUMAN] | 14.57 | 1 | 0 | 5 | 9 | 37.4630854 |
| P02538 | Keratin, type II cytoskeletal 6A OS=Homo sapiens GN=KRT6A PE=1 SV=3 - [K2C6A_HUMAN] | 14.18 | 1 | 0 | 5 | 9 | 37.4630854 |
| P48668 | Keratin, type II cytoskeletal 6C OS=Homo sapiens GN=KRT6C PE=1 SV=3 - [K2C6C_HUMAN] | 14.18 | 1 | 0 | 5 | 9 | 37.4630854 |
| B2R853 | cDNA, FLJ93744, highly similar to Homo sapiens keratin 6E (KRT6E), mRNA OS=Homo sapiens PE=2 SV=1 - | 14.18 | 1 | 0 | 5 | 9 | 37.4630854 |

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| | [B2R853_HUMAN] | | | | | | |
| A8K2I0 | cDNA FLJ78504, highly similar to Homo sapiens keratin 6A (KRT6A), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K2I0_HUMAN] | 14.18 | 1 | 0 | 5 | 9 | 37.4630854 |
| P05787 | Keratin, type II cytoskeletal 8 OS=Homo sapiens GN=KRT8 PE=1 SV=7 - [K2C8_HUMAN] | 3.93 | 1 | 0 | 4 | 24 | 69.1263913 |
| Q7Z794 | Keratin, type II cytoskeletal 1b OS=Homo sapiens GN=KRT77 PE=1 SV=3 - [K2C1B_HUMAN] | 5.02 | 1 | 0 | 4 | 16 | 42.7372702 |
| Q0IIN1 | Keratin 77 OS=Homo sapiens GN=KRT77 PE=1 SV=1 - [Q0IIN1_HUMAN] | 5.02 | 1 | 0 | 4 | 16 | 42.7372702 |
| Q7RTS7 | Keratin, type II cytoskeletal 74 OS=Homo sapiens GN=KRT74 PE=1 SV=2 - [K2C74_HUMAN] | 3.4 | 1 | 0 | 4 | 15 | 37.8403541 |
| Q86Y46 | Keratin, type II cytoskeletal 73 OS=Homo sapiens GN=KRT73 PE=1 SV=1 - [K2C73_HUMAN] | 3.33 | 1 | 0 | 4 | 15 | 37.8403541 |
| Q3B7X4 | IMMT protein OS=Homo sapiens GN=IMMT PE=1 SV=1 - [Q3B7X4_HUMAN] | 19.89 | 1 | 0 | 4 | 12 | 53.0164428 |
| B3KVF5 | cDNA FLJ16494 fis, clone CTONG3004576, highly similar to Keratin, type I cytoskeletal 15 OS=Homo sapiens PE=2 SV=1 - [B3KVF5_HUMAN] | 5.92 | 1 | 0 | 4 | 12 | 34.3992798 |
| A1A4E9 | Keratin 13 OS=Homo sapiens GN=KRT13 PE=2 SV=1 - [A1A4E9_HUMAN] | 5.02 | 1 | 0 | 4 | 11 | 36.6629267 |
| A8K2H9 | cDNA FLJ78503, highly similar to Homo sapiens keratin 13 (KRT13), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1 - [A8K2H9_HUMAN] | 5.02 | 1 | 0 | 4 | 11 | 36.6629267 |
| C9JKR2 | Albumin, isoform CRA_k OS=Homo sapiens GN=ALB PE=4 SV=1 - [C9JKR2_HUMAN] | 8.15 | 1 | 0 | 4 | 10 | 31.1657865 |
| D6RHD5 | Uncharacterized protein OS=Homo sapiens GN=ALB PE=4 SV=1 - [D6RHD5_HUMAN] | 7.41 | 1 | 0 | 4 | 10 | 31.1657865 |
| B7WNRO | Uncharacterized protein OS=Homo sapiens GN=ALB PE=4 SV=1 - [B7WNRO_HUMAN] | 6.88 | 1 | 0 | 4 | 10 | 31.1657865 |
| P04259 | Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5 - [K2C6B_HUMAN] | 11.17 | 1 | 0 | 4 | 8 | 33.3008983 |
| B4DRY0 | cDNA FLJ54379, highly similar to Keratin, type II cytoskeletal 6E OS=Homo sapiens PE=2 SV=1 - [B4DRY0_HUMAN] | 12.8 | 1 | 0 | 4 | 6 | 25.4772844 |

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| P13639 | Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 - [EF2_HUMAN] | 11.19 | 1 | 0 | 4 | 6 | 29.7903006 |
| Q2VPJ6 | HSP90AA1 protein (Fragment) OS=Homo sapiens GN=HSP90AA1 PE=2 SV=1 - [Q2VPJ6_HUMAN] | 8.03 | 1 | 0 | 4 | 6 | 16.5230112 |
| Q8TBA7 | HSP90AA1 protein (Fragment) OS=Homo sapiens GN=HSP90AA1 PE=2 SV=2 - [Q8TBA7_HUMAN] | 7.37 | 1 | 0 | 4 | 6 | 16.5230112 |
| B4DI39 | cDNA FLJ54328, highly similar to Heat shock 70 kDa protein 1 OS=Homo sapiens PE=2 SV=1 - [B4DI39_HUMAN] | 7.12 | 1 | 0 | 4 | 6 | 16.4297874 |
| P08107 | Heat shock 70 kDa protein 1A/1B OS=Homo sapiens GN=HSPA1A PE=1 SV=5 - [HSP71_HUMAN] | 6.86 | 1 | 0 | 4 | 6 | 16.4297874 |
| P07900 | Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5 - [HS90A_HUMAN] | 6.42 | 1 | 0 | 4 | 6 | 16.5230112 |
| B4DMA2 | cDNA FLJ54023, highly similar to Heat shock protein HSP 90-beta OS=Homo sapiens PE=2 SV=1 - [B4DMA2_HUMAN] | 6.41 | 1 | 0 | 4 | 6 | 14.8639662 |
| B4DGL0 | cDNA FLJ53619, highly similar to Heat shock protein HSP 90-beta OS=Homo sapiens PE=2 SV=1 - [B4DGL0_HUMAN] | 6.16 | 1 | 0 | 4 | 6 | 14.8639662 |
| P08238 | Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4 - [HS90B_HUMAN] | 6.08 | 1 | 0 | 4 | 6 | 14.8639662 |
| B4E204 | cDNA FLJ58872, highly similar to Keratin, type I cytoskeletal 15 OS=Homo sapiens PE=2 SV=1 - [B4E204_HUMAN] | 6.84 | 1 | 0 | 3 | 15 | 34.2283568 |
| Q9NSB2 | Keratin, type II cuticular Hb4 OS=Homo sapiens GN=KRT84 PE=1 SV=2 - [KRT84_HUMAN] | 3.33 | 1 | 0 | 3 | 12 | 29.9360963 |
| Q7Z3Y7 | Keratin, type I cytoskeletal 28 OS=Homo sapiens GN=KRT28 PE=1 SV=2 - [K1C28_HUMAN] | 5.39 | 1 | 0 | 3 | 10 | 23.2395601 |
| C9JA77 | Uncharacterized protein OS=Homo sapiens GN=KRT13 PE=4 SV=1 - [C9JA77_HUMAN] | 5.35 | 1 | 0 | 3 | 10 | 25.8765848 |
| Q13092 | Epidermal type I keratin (Fragment) OS=Homo sapiens GN=K14 PE=1 SV=1 - [Q13092_HUMAN] | 29.3 | 1 | 0 | 3 | 9 | 40.31903 |
| B3KRA2 | cDNA FLJ33920 fis, clone CTONG2016904, highly similar to KERATIN, TYPE I CYTOSKELETAL 15 OS=Homo sapiens PE=2 SV=1 - [B3KRA2_HUMAN] | 7.97 | 1 | 0 | 3 | 8 | 26.4131074 |
| A8MT21 | Uncharacterized protein OS=Homo sapiens GN=KRT15 PE=4 SV=1 - [A8MT21_HUMAN] | 6.87 | 1 | 0 | 3 | 8 | 26.4131074 |
| Q86YZ3 | Hornerin OS=Homo sapiens GN=HRNR PE=1 SV=2 - | 5.16 | 1 | 0 | 3 | 7 | 25.2830136 |

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| | [HORN_HUMAN] | | | | | | |
| Q5DT20 | Hornerin OS=Homo sapiens GN=HRNR PE=2 SV=1 - [Q5DT20_HUMAN] | 5.16 | 1 | 0 | 3 | 7 | 25.2830136 |
| Q04695 | Keratin, type I cytoskeletal 17 OS=Homo sapiens GN=KRT17 PE=1 SV=2 - [K1C17_HUMAN] | 11.34 | 1 | 0 | 3 | 6 | 27.8325696 |
| B4E1T1 | cDNA FLJ54081, highly similar to Keratin, type II cytoskeletal 5 OS=Homo sapiens PE=2 SV=1 - [B4E1T1_HUMAN] | 7.57 | 1 | 0 | 3 | 6 | 23.935998 |
| A5JHP3 | Dermcidin isoform 2 OS=Homo sapiens GN=DCD PE=2 SV=1 - [A5JHP3_HUMAN] | 20.66 | 1 | 0 | 3 | 6 | 20.7727189 |
| P17066 | Heat shock 70 kDa protein 6 OS=Homo sapiens GN=HSPA6 PE=1 SV=2 - [HSP76_HUMAN] | 5.13 | 1 | 0 | 3 | 6 | 16.6153774 |
| B2R6X5 | cDNA, FLJ93166, highly similar to Homo sapiens heat shock 70kDa protein 6 (HSP70B') (HSPA6), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R6X5_HUMAN] | 5.13 | 1 | 0 | 3 | 6 | 16.6153774 |
| Q53FC7 | Heat shock 70kDa protein 6 (HSP70B') variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53FC7_HUMAN] | 5.13 | 1 | 0 | 3 | 6 | 16.6153774 |
| B3KSM6 | cDNA FLJ36606 fis, clone TRACH2015654, highly similar to HEAT SHOCK 70 kDa PROTEIN 6 OS=Homo sapiens PE=2 SV=1 - [B3KSM6_HUMAN] | 5.13 | 1 | 0 | 3 | 6 | 16.6153774 |
| P35900 | Keratin, type I cytoskeletal 20 OS=Homo sapiens GN=KRT20 PE=1 SV=1 - [K1C20_HUMAN] | 2.83 | 1 | 0 | 3 | 6 | 21.148231 |
| B4DRE8 | cDNA FLJ58164, highly similar to Elongation factor 2 OS=Homo sapiens PE=2 SV=1 - [B4DRE8_HUMAN] | 13.86 | 1 | 0 | 3 | 5 | 25.0940106 |
| B4DPU3 | cDNA FLJ56548, highly similar to Elongation factor 2 OS=Homo sapiens PE=2 SV=1 - [B4DPU3_HUMAN] | 12.54 | 1 | 0 | 3 | 5 | 24.7950203 |
| Q6PK56 | EEF2 protein (Fragment) OS=Homo sapiens GN=EEF2 PE=2 SV=1 - [Q6PK56_HUMAN] | 12.01 | 1 | 0 | 3 | 5 | 25.0940106 |
| B4DKV4 | cDNA FLJ60647, highly similar to Keratin, type II cytoskeletal 6B OS=Homo sapiens PE=2 SV=1 - [B4DKV4_HUMAN] | 10.08 | 1 | 0 | 3 | 5 | 21.3150973 |
| Q6PK50 | HSP90AB1 protein (Fragment) OS=Homo sapiens GN=HSP90AB1 PE=2 SV=1 - [Q6PK50_HUMAN] | 9.69 | 1 | 0 | 3 | 5 | 13.0514026 |
| B4DXY3 | cDNA FLJ56517, highly similar to Heat shock 70 kDa protein 1L OS=Homo sapiens PE=2 SV=1 - [B4DXY3_HUMAN] | 6.39 | 1 | 0 | 3 | 5 | 14.0896749 |

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| B4E3B6 | cDNA FLJ54408, highly similar to Heat shock 70 kDa protein 1 OS=Homo sapiens PE=2 SV=1 - [B4E3B6_HUMAN] | 5.8 | 1 | 0 | 3 | 5 | 14.0896749 |
| B4DWK5 | cDNA FLJ54392, highly similar to Heat shock 70 kDa protein 1 OS=Homo sapiens PE=2 SV=1 - [B4DWK5_HUMAN] | 5.46 | 1 | 0 | 3 | 5 | 14.0896749 |
| P34931 | Heat shock 70 kDa protein 1-like OS=Homo sapiens GN=HSPA1L PE=1 SV=2 - [HS71L_HUMAN] | 5.3 | 1 | 0 | 3 | 5 | 14.0896749 |
| Q53FA3 | Heat shock 70kDa protein 1-like (Fragment) OS=Homo sapiens GN=HSPA1L PE=2 SV=1 - [Q53FA3_HUMAN] | 5.3 | 1 | 0 | 3 | 5 | 14.0896749 |
| B2RCQ9 | cDNA, FLJ96225, highly similar to Homo sapiens heat shock 70kDa protein 1-like (HSPA1L), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RCQ9_HUMAN] | 5.3 | 1 | 0 | 3 | 5 | 14.0896749 |
| B4DI54 | cDNA FLJ56386, highly similar to Heat shock 70 kDa protein 1L OS=Homo sapiens PE=2 SV=1 - [B4DI54_HUMAN] | 4.82 | 1 | 0 | 3 | 5 | 14.0896749 |
| Q59EJ3 | Heat shock 70kDa protein 1A variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59EJ3_HUMAN] | 4.8 | 1 | 0 | 3 | 5 | 14.0896749 |
| Q86U12 | Full-length cDNA clone CS0CAP007YF18 of Thymus of Homo sapiens (human) OS=Homo sapiens PE=2 SV=1 - [Q86U12_HUMAN] | 8.47 | 1 | 0 | 3 | 4 | 10.6369812 |
| O75322 | Hsp89-alpha-delta-N OS=Homo sapiens PE=2 SV=1 - [O75322_HUMAN] | 6.49 | 1 | 0 | 3 | 4 | 10.6369812 |
| D6RAW4 | Uncharacterized protein OS=Homo sapiens GN=IMMT PE=4 SV=1 - [D6RAW4_HUMAN] | 25.85 | 1 | 0 | 2 | 9 | 40.1085689 |
| B4DMC6 | cDNA FLJ60696, highly similar to Elongation factor 2 OS=Homo sapiens PE=2 SV=1 - [B4DMC6_HUMAN] | 11.63 | 1 | 0 | 2 | 4 | 20.0987303 |
| Q14666 | Radiated keratinocyte mRNA 266 (keratin-related protein) (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q14666_HUMAN] | 11.28 | 1 | 0 | 2 | 4 | 18.7453194 |
| Q16195 | Keratin (Fragment) OS=Homo sapiens GN=keratin PE=2 SV=1 - [Q16195_HUMAN] | 13.11 | 1 | 0 | 2 | 3 | 13.0846841 |
| Q8TA90 | Similar to Elongation factor 2b (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q8TA90_HUMAN] | 9.86 | 1 | 0 | 2 | 2 | 9.69157028 |