# RI NSF/EPSCoR Proteomics Facility
# Mass Spectrometry Report
# Protein Groups and Peptide-Spectrum Matches (PSMs)

Sample: Ctr 30
Researcher: Djuro Josic
Data collected: 24 Aug 2011
Results filtering: Unique PSMs; MOWSE Score > 47.1

MS data file: Ctr_30_082511_190846.raw
Instrument type: ESI-FTICR
Search engine: Mascot
Parameter file: N/D
Search database: N/D (269577 entries)
Enzyme specificity: Trypsin (2 missed cleavages allowed)
MS mass tolerance: 20 ppm; MS/MS tolerance 0.5 Da
Fixed modifications: Carbamidomethyl (C)
Var. modifications: [1] Oxidation (M)
Number of spectra: 4434
Input PSMs: 145 'Target'; 2 'Decoy'; 1.4% FDR
Output PSMs: 145

## UniProt Human Protein IDs

| *Grp Nr.* | *Accession Number* | *Protein Name* | *Protein Score* | *Unique PSMs* | *PSM Serial Nrs.* | *Other Grp.* | *% Seq. Cover.* |
|---|---|---|---|---|---|---|---|
| 1 | Q53H26 | Transferrin variant (Fragment) OS=Homo sapiens PE=2 SV=1 | 1059.30 | 16 | 23 33 38 41 42 47 68 74 80 97 102 111 132 136 138 142 | | *43.3* |
| | Q06AH7 | Transferrin OS=Homo sapiens GN=TF PE=2 SV=1 | 1059.30 | 16 | 23 33 38 41 42 47 68 74 80 97 102 111 132 136 138 142 | | *43.3* |
| | P02787 | Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3 | 1059.30 | 16 | 23 33 38 41 42 47 68 74 80 97 102 111 132 136 138 142 | | *43.3* |
| 2 | P04264 | Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6 | 699.14 | 11 | 3 5 26 44 61 69 85 107 113 120 126 | | *24.5* |

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|---|---|---|---|---|---|---|---|
| | H6VRG3 | Keratin 1 OS=Homo sapiens GN=KRT1 PE=3 SV=1 | 699.14 | 11 | 3 5 26 44 61 69 85 107 113 120 126 | | *24.5* |
| | H6VRG2 | Keratin 1 OS=Homo sapiens GN=KRT1 PE=3 SV=1 | 699.14 | 11 | 3 5 26 44 61 69 85 107 113 120 126 | | *24.5* |
| | H6VRG1 | Keratin 1 OS=Homo sapiens GN=KRT1 PE=2 SV=1 | 699.14 | 11 | 3 5 26 44 61 69 85 107 113 120 126 | | *24.5* |
| | H6VRG0 | Keratin 1 OS=Homo sapiens GN=KRT1 PE=3 SV=1 | 699.14 | 11 | 3 5 26 44 61 69 85 107 113 120 126 | | *24.5* |
| | H6VRF9 | Keratin 1 OS=Homo sapiens GN=KRT1 PE=3 SV=1 | 699.14 | 11 | 3 5 26 44 61 69 85 107 113 120 126 | | *24.5* |
| | H6VRF8 | Keratin 1 OS=Homo sapiens GN=KRT1 PE=3 SV=1 | 699.14 | 11 | 3 5 26 44 61 69 85 107 113 120 126 | | *24.5* |
| 3 | P35527 | Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3 | 531.98 | 6 | 25 32 79 98 104 109 | | *21.7* |
| 4 | P13645 | Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6 | 486.54 | 7 | 35 48 49 78 95 108 110 | | *18.7* |
| 5 | Q5TCU3 | Tropomyosin beta chain OS=Homo sapiens GN=TPM2 PE=2 SV=1 | 381.37 | 5 | 12 75 125 127 131 | | *27.5* |
| 6 | P02533 | Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4 | 373.13 | 6 | 28 86 89 116 140 143 | | *19.7* |
| 7 | P35908 | Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2 | 307.43 | 4 | 1 7 55 103 | | *17.7* |
| 8 | Q5T8M8 | Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=4 SV=1 | 299.37 | 4 | 34 36 67 101 | | *25.8* |
| | P68133 | Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1 | 299.37 | 4 | 34 36 67 101 | | *25.8* |
| | P68032 | Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1 | 299.37 | 4 | 34 36 67 101 | | *25.8* |
| | B7Z6P1 | cDNA FLJ53662, highly similar to Actin, alpha skeletal muscle OS=Homo sapiens PE=2 SV=1 | 299.37 | 4 | 34 36 67 101 | | *25.8* |
| | A8K3K1 | cDNA FLJ78096, highly similar to Homo sapiens actin, alpha, cardiac muscle (ACTC), mRNA OS=Homo sapiens PE=2 SV=1 | 299.37 | 4 | 34 36 67 101 | | *25.8* |
| | A6NL76 | Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=2 SV=2 | 299.37 | 4 | 34 36 67 101 | | *25.8* |
| 9 | Q5RKT7 | Ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=2 SV=1 | 212.50 | 4 | 17 45 87 139 | | *34.0* |
| | P62979 | Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=1 SV=2 | 212.50 | 4 | 17 45 87 139 | | *34.0* |
| | B2RDW1 | Ribosomal protein S27a, isoform CRA_c OS=Homo sapiens GN=RPS27A PE=2 SV=1 | 212.50 | 4 | 17 45 87 139 | | *34.0* |
| 10 | P11021 | 78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2 | 200.02 | 3 | 18 77 90 | | *12.7* |
| 11 | Q5JQ13 | Vinculin (Fragment) OS=Homo sapiens GN=VCL PE=2 SV=1 | 199.90 | 3 | 11 30 84 | | *7.4* |
| | P18206 | Vinculin OS=Homo sapiens GN=VCL PE=1 SV=4 | 199.90 | 3 | 11 30 84 | | *7.4* |
| | B4E3Q9 | cDNA FLJ59659, highly similar to Vinculin OS=Homo sapiens PE=2 SV=1 | 199.90 | 3 | 11 30 84 | | *7.4* |
| | B3KXA2 | cDNA FLJ45031 fis, clone BRAWH3018548, highly similar to Vinculin OS=Homo sapiens PE=2 SV=1 | 199.90 | 3 | 11 30 84 | | *7.4* |
| 12 | Q53GZ6 | Heat shock 70kDa protein 8 isoform 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1 | 198.62 | 3 | 19 63 114 | | *11.1* |
| | P11142 | Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1 | 198.62 | 3 | 19 63 114 | | *11.1* |
| | E9PKE3 | Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=2 SV=1 | 198.62 | 3 | 19 63 114 | | *11.1* |
| | B3KTV0 | cDNA FLJ38781 fis, clone LIVER2000216, highly similar to HEAT SHOCK COGNATE 71 kDa PROTEIN OS=Homo sapiens PE=2 SV=1 | 198.62 | 3 | 19 63 114 | | *11.1* |
| 13 | Q53HU8 | Vimentin variant (Fragment) OS=Homo sapiens PE=2 SV=1 | 183.47 | 3 | 56 66 70 | | *18.8* |
| | P08670 | Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4 | 183.47 | 3 | 56 66 70 | | *18.8* |
| | B3KRK8 | cDNA FLJ34494 fis, clone HLUNG2005030, highly similar to VIMENTIN OS=Homo sapiens PE=2 SV=1 | 183.47 | 3 | 56 66 70 | | *18.8* |
| | B0YJC4 | Vimentin OS=Homo sapiens GN=VIM PE=3 SV=1 | 183.47 | 3 | 56 66 70 | | *18.8* |
| 14 | P08779 | Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4 | 175.13 | 3 | 2 93 144 | | *19.9* |
| 15 | Q6ZN40 | Tropomyosin 1 (Alpha), isoform CRA_f OS=Homo sapiens GN=TPM1 PE=2 SV=1 | 173.88 | 3 | 73 92 129 | | *21.8* |

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|---|---|---|---|---|---|---|---|
| 16 | P13647 | Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3 | 172.65 | 3 | 6 39 112 | | 11.5 |
| 17 | Q56G89 | Serum albumin OS=Homo sapiens PE=2 SV=1 | 151.45 | 2 | 50 100 | | 12.2 |
| | P02768 | Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2 | 151.45 | 2 | 50 100 | | 12.2 |
| | F6KPG5 | Albumin (Fragment) OS=Homo sapiens PE=2 SV=1 | 151.45 | 2 | 50 100 | | 12.2 |
| | B2RBS8 | cDNA, FLJ95666, highly similar to Homo sapiens albumin (ALB), mRNA OS=Homo sapiens PE=2 SV=1 | 151.45 | 2 | 50 100 | | 12.2 |
| 18 | Q5VU66 | Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=4 SV=1 | 148.17 | 2 | 40 118 | | 27.4 |
| | B2RDE1 | cDNA, FLJ96568, highly similar to Homo sapiens tropomyosin 3 (TPM3), mRNA OS=Homo sapiens PE=2 SV=1 | 148.17 | 2 | 40 118 | | 27.4 |
| 19 | Q6FI52 | TAGLN protein OS=Homo sapiens GN=TAGLN PE=2 SV=1 | 127.85 | 2 | 51 60 | | 21.9 |
| | Q5U0D2 | Putative uncharacterized protein DKFZp686P11128 OS=Homo sapiens GN=TAGLN PE=2 SV=1 | 127.85 | 2 | 51 60 | | 21.9 |
| | Q53GC9 | Transgelin variant (Fragment) OS=Homo sapiens PE=2 SV=1 | 127.85 | 2 | 51 60 | | 21.9 |
| | Q01995 | Transgelin OS=Homo sapiens GN=TAGLN PE=1 SV=4 | 127.85 | 2 | 51 60 | | 21.9 |
| 20 | P04075 | Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2 | 126.08 | 2 | 58 64 | | 12.2 |
| | J3KPS3 | Fructose-bisphosphate aldolase OS=Homo sapiens GN=ALDOA PE=3 SV=1 | 126.08 | 2 | 58 64 | | 12.2 |
| | H3BUH7 | Fructose-bisphosphate aldolase A (Fragment) OS=Homo sapiens GN=ALDOA PE=2 SV=1 | 126.08 | 2 | 58 64 | | 12.2 |
| | H3BQN4 | Fructose-bisphosphate aldolase OS=Homo sapiens GN=ALDOA PE=2 SV=1 | 126.08 | 2 | 58 64 | | 12.2 |
| | H3BPS8 | Fructose-bisphosphate aldolase A (Fragment) OS=Homo sapiens GN=ALDOA PE=2 SV=1 | 126.08 | 2 | 58 64 | | 12.2 |
| 21 | P63104 | 14-3-3 protein zeta/delta OS=Homo sapiens GN=YWHAZ PE=1 SV=1 | 104.31 | 1 | 81 | | 12.2 |
| | E7EX29 | 14-3-3 protein zeta/delta (Fragment) OS=Homo sapiens GN=YWHAZ PE=2 SV=1 | 104.31 | 1 | 81 | | 12.2 |
| | E7ESK7 | 14-3-3 protein zeta/delta (Fragment) OS=Homo sapiens GN=YWHAZ PE=2 SV=1 | 104.31 | 1 | 81 | | 12.2 |
| | D0PNI1 | Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein zeta polypeptide OS=Homo sapiens GN=YWHAZ PE=2 SV=1 | 104.31 | 1 | 81 | | 12.2 |
| 22 | P17540 | Creatine kinase S-type, mitochondrial OS=Homo sapiens GN=CKMT2 PE=1 SV=2 | 103.55 | 2 | 16 46 | | 10.7 |
| | B3KVA7 | cDNA FLJ16309 fis, clone SKMUS2007816, highly similar to Creatine kinase, sarcomeric mitochondrial (EC 2.7.3.2) OS=Homo sapiens PE=2 SV=1 | 103.55 | 2 | 16 46 | | 10.7 |
| | B2R8A3 | cDNA, FLJ93805, highly similar to Homo sapiens creatine kinase, mitochondrial 2 (sarcomeric) (CKMT2), nuclear gene encoding mitochondrial protein, mRNA OS=Homo sapiens PE=2 SV=1 | 103.55 | 2 | 16 46 | | 10.7 |
| 23 | Q6FHV6 | ENO2 protein OS=Homo sapiens GN=ENO2 PE=2 SV=1 | 98.20 | 2 | 9 133 | | 9.7 |
| | P09104 | Gamma-enolase OS=Homo sapiens GN=ENO2 PE=1 SV=3 | 98.20 | 2 | 9 133 | | 9.7 |
| | B7Z2X9 | Enolase OS=Homo sapiens GN=ENO2 PE=2 SV=1 | 98.20 | 2 | 9 133 | | 9.7 |
| 24 | Q9UNM1 | Chaperonin 10-related protein (Fragment) OS=Homo sapiens GN=EPFP1 PE=2 SV=1 | 92.98 | 1 | 119 | | 13.9 |
| | P61604 | 10 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPE1 PE=1 SV=2 | 92.98 | 1 | 119 | | 13.9 |
| | B8ZZL8 | 10 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPE1 PE=3 SV=1 | 92.98 | 1 | 119 | | 13.9 |
| 25 | P00441 | Superoxide dismutase [Cu-Zn] OS=Homo sapiens GN=SOD1 PE=1 SV=2 | 90.13 | 1 | 62 | | 8.9 |
| | H7BYH4 | Superoxide dismutase [Cu-Zn] OS=Homo sapiens GN=SOD1 PE=2 SV=1 | 90.13 | 1 | 62 | | 8.9 |
| 26 | P12883 | Myosin-7 OS=Homo sapiens GN=MYH7 PE=1 SV=5 | 88.18 | 1 | 15 | | 4.1 |
| | A5YM51 | MYH7 protein (Fragment) OS=Homo sapiens GN=MYH7 PE=2 SV=1 | 88.18 | 1 | 15 | | 4.1 |
| 27 | B4E3P1 | cDNA FLJ57036, highly similar to Homo sapiens tropomyosin 2 (beta) (TPM2), transcript variant 2, mRNA OS=Homo sapiens PE=2 SV=1 | 83.27 | 1 | 72 | | 20.8 |
| 28 | P30086 | Phosphatidylethanolamine-binding protein 1 OS=Homo sapiens GN=PEBP1 PE=1 SV=3 | 79.86 | 1 | 83 | | 16.0 |
| | D9IAI1 | Phosphatidylethanolamine-binding protein 1 OS=Homo sapiens PE=2 SV=1 | 79.86 | 1 | 83 | | 16.0 |

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|---|---|---|---|---|---|---|---|
| 29 | Q5I6Y6 | Lamin A/C transcript variant 1 OS=Homo sapiens GN=LMNA PE=2 SV=1 | 76.53 | 1 | 130 | | *1.6* |
| | Q5I6Y4 | Lamin A/C transcript variant 1 OS=Homo sapiens GN=LMNA PE=2 SV=1 | 76.53 | 1 | 130 | | *21.8* |
| | P02545 | Prelamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1 | 76.53 | 1 | 130 | | *1.6* |
| 30 | Q8TCD0 | Putative uncharacterized protein OS=Homo sapiens PE=2 SV=1 | 74.67 | 1 | 21 | | *9.1* |
| | Q7Z3Y4 | Putative uncharacterized protein OS=Homo sapiens PE=1 SV=1 | 74.67 | 1 | 21 | | *9.1* |
| | Q6PJF2 | IGK@ protein OS=Homo sapiens GN=IGK@ PE=1 SV=1 | 74.67 | 1 | 21 | | *9.1* |
| | Q6PIL8 | IGK@ protein OS=Homo sapiens GN=IGK@ PE=1 SV=1 | 74.67 | 1 | 21 | | *9.1* |
| | Q6P5S8 | IGK@ protein OS=Homo sapiens GN=IGK@ PE=1 SV=1 | 74.67 | 1 | 21 | | *9.1* |
| | Q6GMX0 | Putative uncharacterized protein OS=Homo sapiens PE=2 SV=1 | 74.67 | 1 | 21 | | *9.1* |
| | Q5EFE6 | Anti-RhD monoclonal T125 kappa light chain (Precursor) OS=Homo sapiens PE=2 SV=1 | 74.67 | 1 | 21 | | *9.1* |
| | Q0KKI6 | Immunoblobulin light chain (Fragment) OS=Homo sapiens PE=2 SV=1 | 74.67 | 1 | 21 | | *9.1* |
| | P01834 | Ig kappa chain C region OS=Homo sapiens GN=IGKC PE=1 SV=1 | 74.67 | 1 | 21 | | *9.1* |
| 31 | Q9Y490 | Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3 | 73.83 | 1 | 141 | | *0.6* |
| | Q5TCU6 | Talin-1 OS=Homo sapiens GN=TLN1 PE=2 SV=1 | 73.83 | 1 | 141 | | *0.6* |
| 32 | H0YNC7 | Tropomyosin alpha-1 chain (Fragment) OS=Homo sapiens GN=TPM1 PE=3 SV=1 | 72.91 | 1 | 88 | | *22.9* |
| 33 | P27348 | 14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1 | 68.62 | 1 | 22 | | *12.8* |
| | E9PG15 | 14-3-3 protein theta (Fragment) OS=Homo sapiens GN=YWHAQ PE=2 SV=1 | 68.62 | 1 | 22 | | *12.8* |

# UniProt Human Protein IDs, *cont.*

| *Grp Nr.* | *Accession Number* | *Protein Name* | *Protein Score* | *Unique PSMs* | *PSM Serial Nrs.* | *Other Grp.* | *% Seq. Cover.* |
|---|---|---|---|---|---|---|---|
| 34 | Q8N1C8 | HSPA9 protein (Fragment) OS=Homo sapiens GN=HSPA9 PE=2 SV=1 | 65.84 | 1 | 122 | | *3.4* |
| | P38646 | Stress-70 protein, mitochondrial OS=Homo sapiens GN=HSPA9 PE=1 SV=2 | 65.84 | 1 | 122 | | *3.4* |
| | B7Z4V2 | cDNA FLJ51907, highly similar to Stress-70 protein, mitochondrial OS=Homo sapiens PE=2 SV=1 | 65.84 | 1 | 122 | | *3.4* |
| | B7Z4T3 | cDNA FLJ51903, highly similar to Stress-70 protein, mitochondrial OS=Homo sapiens PE=2 SV=1 | 65.84 | 1 | 122 | | *3.4* |
| | A1XP52 | Catecholamine-regulated protein 40 OS=Homo sapiens PE=2 SV=1 | 65.84 | 1 | 122 | | *3.4* |
| 35 | P16870 | Carboxypeptidase E OS=Homo sapiens GN=CPE PE=1 SV=1 | 65.49 | 1 | 124 | | *2.4* |
| | D6RF88 | Carboxypeptidase E (Fragment) OS=Homo sapiens GN=CPE PE=2 SV=1 | 65.49 | 1 | 124 | | *2.4* |
| | D6R930 | Carboxypeptidase E (Fragment) OS=Homo sapiens GN=CPE PE=2 SV=1 | 65.49 | 1 | 124 | | *2.4* |
| | C9JE88 | Carboxypeptidase E (Fragment) OS=Homo sapiens GN=CPE PE=2 SV=2 | 65.49 | 1 | 124 | | *2.4* |
| | B3KXD3 | cDNA FLJ45230 fis, clone BRCAN2021325, highly similar to Carboxypeptidase E (EC 3.4.17.10) OS=Homo sapiens PE=2 SV=1 | 65.49 | 1 | 124 | | *2.4* |
| 36 | Q6FH91 | TNNC1 protein OS=Homo sapiens GN=TNNC1 PE=2 SV=1 | 64.57 | 1 | 135 | | *11.2* |
| | P63316 | Troponin C, slow skeletal and cardiac muscles OS=Homo sapiens GN=TNNC1 PE=1 SV=1 | 64.57 | 1 | 135 | | *11.2* |
| 37 | J3KN67 | Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=3 SV=1 | 64.23 | 1 | 94 | | *19.3* |
| 38 | B4DUW4 | Small ubiquitin-related modifier 3 OS=Homo sapiens GN=SUMO3 PE=2 SV=1 | 63.89 | 1 | 29 | | *22.0* |
| 39 | Q59GX5 | L-plastin variant (Fragment) OS=Homo sapiens PE=2 SV=1 | 63.71 | 1 | 128 | | *1.6* |

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|---|---|---|---|---|---|---|---|
| | Q53FI1 | L-plastin variant (Fragment) OS=Homo sapiens PE=2 SV=1 | 63.71 | 1 | 128 | | 1.6 |
| | P13796 | Plastin-2 OS=Homo sapiens GN=LCP1 PE=1 SV=6 | 63.71 | 1 | 128 | | 1.6 |
| 40 | Q53FC7 | Heat shock 70kDa protein 6 (HSP70B~) variant (Fragment) OS=Homo sapiens PE=2 SV=1 | 63.20 | 1 | 137 | | 6.4 |
| | P17066 | Heat shock 70 kDa protein 6 OS=Homo sapiens GN=HSPA6 PE=1 SV=2 | 63.20 | 1 | 137 | | 6.4 |
| | B3KSM6 | cDNA FLJ36606 fis, clone TRACH2015654, highly similar to HEAT SHOCK 70 kDa PROTEIN 6 OS=Homo sapiens PE=2 SV=1 | 63.20 | 1 | 137 | | 6.4 |
| | B2R6X5 | cDNA, FLJ93166, highly similar to Homo sapiens heat shock 70kDa protein 6 (HSP70B~) (HSPA6), mRNA OS=Homo sapiens PE=2 SV=1 | 63.20 | 1 | 137 | | 6.4 |
| 41 | Q9BZ93 | Prosomal P27K protein (Fragment) OS=Homo sapiens GN=PSMA6 PE=2 SV=1 | 62.76 | 1 | 91 | | 6.4 |
| | P60900 | Proteasome subunit alpha type-6 OS=Homo sapiens GN=PSMA6 PE=1 SV=1 | 62.76 | 1 | 91 | | 6.4 |
| | G3V5Z7 | Proteasome subunit alpha type OS=Homo sapiens GN=PSMA6 PE=2 SV=1 | 62.76 | 1 | 91 | | 6.4 |
| | G3V3U4 | Proteasome subunit alpha type OS=Homo sapiens GN=PSMA6 PE=2 SV=1 | 62.76 | 1 | 91 | | 6.4 |
| | G3V3I1 | Proteasome subunit alpha type OS=Homo sapiens GN=PSMA6 PE=2 SV=1 | 62.76 | 1 | 91 | | 6.4 |
| | G3V295 | Proteasome subunit alpha type OS=Homo sapiens GN=PSMA6 PE=2 SV=1 | 62.76 | 1 | 91 | | 6.4 |
| | B4DXJ9 | Proteasome (Prosome, macropain) subunit, alpha type, 6, isoform CRA_a OS=Homo sapiens GN=PSMA6 PE=2 SV=1 | 62.76 | 1 | 91 | | 6.4 |
| 42 | H0YN42 | Annexin (Fragment) OS=Homo sapiens GN=ANXA2 PE=2 SV=1 | 62.34 | 1 | 52 | | 21.9 |
| 43 | Q86Z22 | Putative uncharacterized protein OS=Homo sapiens PE=2 SV=1 | 61.51 | 1 | 31 | | 3.9 |
| | D3DPK5 | SH3 domain binding glutamic acid-rich protein like 3, isoform CRA_a (Fragment) OS=Homo sapiens GN=SH3BGRL3 PE=2 SV=1 | 61.51 | 1 | 31 | | 3.9 |
| 44 | P02790 | Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2 | 61.47 | 1 | 57 | | 12.6 |
| 45 | Q53GD8 | Peptidyl-prolyl cis-trans isomerase (Fragment) OS=Homo sapiens PE=2 SV=1 | 59.79 | 1 | 37 | | 4.9 |
| | Q00688 | Peptidyl-prolyl cis-trans isomerase FKBP3 OS=Homo sapiens GN=FKBP3 PE=1 SV=1 | 59.79 | 1 | 37 | | 4.9 |
| 46 | P22626 | Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 PE=1 SV=2 | 59.73 | 1 | 76 | | 27.5 |
| 47 | Q53GX6 | Nucleobindin 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1 | 58.84 | 1 | 121 | | 8.8 |
| | Q02818 | Nucleobindin-1 OS=Homo sapiens GN=NUCB1 PE=1 SV=4 | 58.84 | 1 | 121 | | 8.8 |
| | B4DZX0 | cDNA FLJ52898, highly similar to Nucleobindin-1 OS=Homo sapiens PE=2 SV=1 | 58.84 | 1 | 121 | | 8.8 |
| | A8K7Q1 | cDNA FLJ77770, highly similar to Homo sapiens nucleobindin 1 (NUCB1), mRNA OS=Homo sapiens PE=2 SV=1 | 58.84 | 1 | 121 | | 8.8 |
| 48 | P19013 | Keratin, type II cytoskeletal 4 OS=Homo sapiens GN=KRT4 PE=1 SV=4 | 58.15 | 1 | 13 | | 4.1 |
| | F5H8K9 | Keratin, type II cytoskeletal 4 OS=Homo sapiens GN=KRT4 PE=2 SV=1 | 58.15 | 1 | 13 | | 4.1 |
| | B4DRW1 | cDNA FLJ55805, highly similar to Keratin, type II cytoskeletal 4 OS=Homo sapiens PE=2 SV=1 | 58.15 | 1 | 13 | | 4.1 |
| | B4DRS2 | cDNA FLJ58275, highly similar to Keratin, type II cytoskeletal 4 OS=Homo sapiens PE=2 SV=1 | 58.15 | 1 | 13 | | 4.1 |
| | B4DRR7 | cDNA FLJ59399, highly similar to Keratin, type II cytoskeletal 4 OS=Homo sapiens PE=2 SV=1 | 58.15 | 1 | 13 | | 4.1 |
| | B4DKJ0 | cDNA FLJ58539, highly similar to Keratin, type II cytoskeletal 4 OS=Homo sapiens PE=2 SV=1 | 58.15 | 1 | 13 | | 4.1 |
| 49 | B7Z722 | Tropomyosin 1 (Alpha), isoform CRA_i OS=Homo sapiens GN=TPM1 PE=2 SV=1 | 58.08 | 1 | 59 | | 24.2 |
| 50 | Q0QEN7 | ATP synthase subunit beta (Fragment) OS=Homo sapiens GN=ATP5B PE=2 SV=1 | 57.82 | 1 | 54 | | 5.4 |
| | P06576 | ATP synthase subunit beta, mitochondrial OS=Homo sapiens GN=ATP5B PE=1 SV=3 | 57.82 | 1 | 54 | | 5.4 |
| | F8W079 | ATP synthase subunit beta, mitochondrial (Fragment) OS=Homo sapiens GN=ATP5B PE=2 SV=1 | 57.82 | 1 | 54 | | 5.4 |

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|---|---|---|---|---|---|---|---|
| | F8VQY0 | ATP synthase subunit beta, mitochondrial (Fragment) OS=Homo sapiens GN=ATP5B PE=2 SV=1 | 57.82 | 1 | 54 | | *5.4* |
| | F8VPV9 | ATP synthase subunit beta OS=Homo sapiens GN=ATP5B PE=2 SV=1 | 57.82 | 1 | 54 | | *5.4* |
| 51 | P13646 | Keratin, type I cytoskeletal 13 OS=Homo sapiens GN=KRT13 PE=1 SV=4 | 56.24 | 1 | 117 | | *8.7* |
| | K7ERE3 | Keratin, type I cytoskeletal 13 OS=Homo sapiens GN=KRT13 PE=3 SV=1 | 56.24 | 1 | 117 | | *8.7* |
| | A8K2H9 | cDNA FLJ78503, highly similar to Homo sapiens keratin 13 (KRT13), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1 | 56.24 | 1 | 117 | | *8.7* |
| | A1A4E9 | Keratin 13 OS=Homo sapiens GN=KRT13 PE=2 SV=1 | 56.24 | 1 | 117 | | *8.7* |
| 52 | Q8N1A0 | Keratin-like protein KRT222 OS=Homo sapiens GN=KRT222 PE=2 SV=1 | 56.24 | 1 | 115 | | *11.1* |
| 53 | Q6IBN1 | HNRPK protein OS=Homo sapiens GN=HNRPK PE=2 SV=1 | 56.21 | 1 | 71 | | *4.9* |
| | Q5T6W5 | Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=2 SV=1 | 56.21 | 1 | 71 | | *4.9* |
| | Q5EC54 | Heterogeneous nuclear ribonucleoprotein K transcript variant OS=Homo sapiens GN=HNRPK PE=2 SV=1 | 56.21 | 1 | 71 | | *4.9* |
| | P61978 | Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 SV=1 | 56.21 | 1 | 71 | | *4.9* |
| | B4DUQ1 | cDNA FLJ54552, highly similar to Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens PE=2 SV=1 | 56.21 | 1 | 71 | | *4.9* |
| | B4DFF1 | cDNA FLJ53312, highly similar to Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens PE=2 SV=1 | 56.21 | 1 | 71 | | *4.9* |
| | B3KU16 | cDNA FLJ39066 fis, clone NT2RP7014743, highly similar to HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN K OS=Homo sapiens PE=2 SV=1 | 56.21 | 1 | 71 | | *4.9* |
| 54 | P62258 | 14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1 | 55.68 | 1 | 65 | | *16.7* |
| | G9K389 | YWHAE/FAM22B fusion protein (Fragment) OS=Homo sapiens GN=YWHAE/FAM22B fusion PE=2 SV=1 | 55.68 | 1 | 65 | | *16.7* |
| | G9K388 | YWHAE/FAM22A fusion protein (Fragment) OS=Homo sapiens GN=YWHAE/FAM22A fusion PE=2 SV=1 | 55.68 | 1 | 65 | | *16.7* |
| | B7ZA86 | cDNA, FLJ79100, highly similar to 14-3-3 protein epsilon (14-3-3E) OS=Homo sapiens PE=2 SV=1 | 55.68 | 1 | 65 | | *16.7* |
| 55 | P10809 | 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 | 55.61 | 1 | 134 | | *9.0* |
| | B7Z5E7 | cDNA FLJ51046, highly similar to 60 kDa heat shock protein, mitochondrial OS=Homo sapiens PE=2 SV=1 | 55.61 | 1 | 134 | | *9.0* |
| | B7Z597 | cDNA FLJ54373, highly similar to 60 kDa heat shock protein, mitochondrial OS=Homo sapiens PE=2 SV=1 | 55.61 | 1 | 134 | | *9.0* |
| | B7Z4F6 | cDNA FLJ54912, highly similar to 60 kDa heat shock protein, mitochondrial OS=Homo sapiens PE=2 SV=1 | 55.61 | 1 | 134 | | *9.0* |
| | B3GQS7 | Mitochondrial heat shock 60kD protein 1 variant 1 OS=Homo sapiens GN=HSPD1 PE=2 SV=1 | 55.61 | 1 | 134 | | *9.0* |
| 56 | P81605 | Dermcidin OS=Homo sapiens GN=DCD PE=1 SV=2 | 54.27 | 1 | 105 | | *20.0* |
| 57 | J3KN62 | Cadherin-13 OS=Homo sapiens GN=CDH13 PE=4 SV=1 | 53.12 | 1 | 43 | | *43.3* |
| | B7Z9B1 | cDNA FLJ52398, highly similar to Cadherin-13 OS=Homo sapiens PE=2 SV=1 | 53.12 | 1 | 43 | | *43.3* |
| 58 | Q13162 | Peroxiredoxin-4 OS=Homo sapiens GN=PRDX4 PE=1 SV=1 | 52.94 | 1 | 24 | | *18.0* |
| | H7C3T4 | Peroxiredoxin-4 (Fragment) OS=Homo sapiens GN=PRDX4 PE=4 SV=1 | 52.94 | 1 | 24 | | *18.0* |
| 59 | Q9NX34 | cDNA FLJ20465 fis, clone KAT06236 OS=Homo sapiens PE=2 SV=1 | 52.37 | 1 | 4 | | *3.3* |
| | Q9BTI9 | NPM1 protein (Fragment) OS=Homo sapiens GN=NPM1 PE=2 SV=2 | 52.37 | 1 | 4 | | *3.3* |
| | P06748 | Nucleophosmin OS=Homo sapiens GN=NPM1 PE=1 SV=2 | 52.37 | 1 | 4 | | *3.3* |
| | A4ZU86 | Truncated nucleolar phosphoprotein B23 OS=Homo sapiens GN=NPM1 PE=2 SV=1 | 52.37 | 1 | 4 | | *3.3* |
| 60 | Q1JUQ4 | FK506 binding protein12 OS=Homo sapiens GN=FKBP12-Exip3 PE=4 SV=1 | 52.08 | 1 | 8 | | *35.1* |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| | Q1JUQ3 | FK506 binding protein12 OS=Homo sapiens GN=FKBP12-Exin PE=4 SV=1 | 52.08 | 1 | 8 | | *35.1* |
| | P62942 | Peptidyl-prolyl cis-trans isomerase FKBP1A OS=Homo sapiens GN=FKBP1A PE=1 SV=2 | 52.08 | 1 | 8 | | *35.1* |
| 61 | P13521 | Secretogranin-2 OS=Homo sapiens GN=SCG2 PE=1 SV=2 | 51.56 | 1 | 82 | | *7.1* |
| | B4DQJ6 | cDNA FLJ51276, highly similar to Secretogranin-2 OS=Homo sapiens PE=2 SV=1 | 51.56 | 1 | 82 | | *7.1* |
| 62 | Q96K68 | cDNA FLJ14473 fis, clone MAMMA1001080, highly similar to Homo sapiens SNC73 protein (SNC73) mRNA OS=Homo sapiens PE=2 SV=1 | 51.20 | 1 | 27 | | *24.5* |
| | Q6ZW64 | cDNA FLJ41552 fis, clone COLON2004478, highly similar to Protein Tro alpha1 H,myeloma OS=Homo sapiens PE=1 SV=1 | 51.20 | 1 | 27 | | *24.5* |
| | Q6N092 | Putative uncharacterized protein DKFZp686K18196 (Fragment) OS=Homo sapiens GN=DKFZp686K18196 PE=1 SV=1 | 51.20 | 1 | 27 | | *24.5* |
| 63 | Q9UEW6 | Vasopressin-neurophysin (Fragment) OS=Homo sapiens PE=2 SV=1 | 50.42 | 1 | 14 | | *20.5* |
| | P01185 | Vasopressin-neurophysin 2-copeptin OS=Homo sapiens GN=AVP PE=1 SV=2 | 50.42 | 1 | 14 | | *20.5* |
| 64 | P67936 | Tropomyosin alpha-4 chain OS=Homo sapiens GN=TPM4 PE=1 SV=3 | 50.37 | 1 | 123 | | *21.0* |
| | B4DVY2 | cDNA FLJ54184, highly similar to Tropomyosin alpha-4 chain OS=Homo sapiens PE=2 SV=1 | 50.37 | 1 | 123 | | *21.0* |
| 65 | P02748 | Complement component C9 OS=Homo sapiens GN=C9 PE=1 SV=2 | 49.79 | 1 | 145 | | *1.6* |
| 66 | Q9HCJ6 | Synaptic vesicle membrane protein VAT-1 homolog-like OS=Homo sapiens GN=VAT1L PE=1 SV=2 | 49.59 | 1 | 20 | | *2.1* |
| | Q8NDE0 | Putative uncharacterized protein DKFZp547P162 (Fragment) OS=Homo sapiens GN=DKFZp547P162 PE=2 SV=1 | 49.59 | 1 | 20 | | *2.1* |
| | A8K288 | cDNA FLJ76322 OS=Homo sapiens PE=2 SV=1 | 49.59 | 1 | 20 | | *2.1* |
| 67 | P69905 | Hemoglobin subunit alpha OS=Homo sapiens GN=HBA1 PE=1 SV=2 | 48.51 | 1 | 106 | | *34.5* |
| | I1VZV6 | Hemoglobin alpha 1 OS=Homo sapiens GN=HBA1 PE=3 SV=1 | 48.51 | 1 | 106 | | *34.5* |
| | E9M4D4 | Hemoglobin alpha-1 globin chain (Fragment) OS=Homo sapiens GN=HBA1 PE=3 SV=1 | 48.51 | 1 | 106 | | *34.5* |
| | D1MGQ2 | Alpha-2 globin chain OS=Homo sapiens GN=HBA2 PE=2 SV=1 | 48.51 | 1 | 106 | | *34.5* |
| 68 | P16615 | Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Homo sapiens GN=ATP2A2 PE=1 SV=1 | 48.13 | 1 | 96 | | *4.1* |
| | H7C5W9 | Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 (Fragment) OS=Homo sapiens GN=ATP2A2 PE=3 SV=1 | 48.13 | 1 | 96 | | *4.1* |
| 69 | P68036 | Ubiquitin-conjugating enzyme E2 L3 OS=Homo sapiens GN=UBE2L3 PE=1 SV=1 | 47.93 | 1 | 10 | | *4.2* |
| | E7EWS7 | Ubiquitin-conjugating enzyme E2 L3 OS=Homo sapiens GN=UBE2L3 PE=2 SV=1 | 47.93 | 1 | 10 | | *4.2* |
| | B4DSZ4 | cDNA FLJ59750, highly similar to Ubiquitin-conjugating enzyme E2 L3 (EC 6.3.2.19) OS=Homo sapiens PE=2 SV=1 | 47.93 | 1 | 10 | | *4.2* |
| | A8K4W8 | cDNA FLJ77917, highly similar to Homo sapiens ubiquitin-conjugating enzyme E2L 3 (UBE2L3), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1 | 47.93 | 1 | 10 | | *4.2* |
| 70 | Q06830 | Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 | 47.38 | 1 | 99 | | *23.6* |
| | B2R4P2 | cDNA, FLJ92164, highly similar to Homo sapiens peroxiredoxin 1 (PRDX1), mRNA OS=Homo sapiens PE=2 SV=1 | 47.38 | 1 | 99 | | *23.6* |
| 71 | Q53SS8 | Poly(RC) binding protein 1 OS=Homo sapiens GN=PCBP1 PE=2 SV=1 | 47.17 | 1 | 53 | | *3.1* |
| | Q15365 | Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 | 47.17 | 1 | 53 | | *3.1* |

*Group Nr.*

By the rule of parsimony, we have gathered all proteins sharing the same identified peptides into a single group.
*Accession Nr.*

The accession number from the searched database (DB).

*Protein Name*

The protein name in the DB.
*Protein Score*

Sum of the contributing peptide scores.

NOTE: This score can only be used to support the identification of **one** protein per group.
*Unique PSMs.*

The number of unique peptide-spectrum matches that contribute to the protein assignment.
*PSM Serial Nrs.*

Sequential number of assigned peptide (in the following table.)
*Other Grp.*

If the protein is assigned to another group, that (those) group number(s).
*% Seq. Cover.*

Percent sequence coverage of this protein.

## Assigned Peptides

| *#* | *Sequence* | *PTM Site* | *Nr. Scans* | *Mascot Score* | *Expectation* | *Isolated Mass* | *Delta Mass* | *Charge State* | *Matched Ions* | *Scan Nr.* |
|---|---|---|---|---|---|---|---|---|---|---|
| 1 | K.NVQDAIADAEQR.G | | 1 | 55.380 | 0.00031 | 665.32 | 0.9 | 2 | '9/22 | 3188 |
| 2 | R.DAETWFLSK.T | | 1 | 47.970 | 0.0016 | 548.77 | 0.4 | 2 | '5/16 | 4962 |
| 3 | K.LNDLEDALQQAK.E | | 1 | 70.190 | 1.6e-005 | 679.35 | -1.6 | 2 | '9/22 | 4076 |
| 4 | K.GPSSVEDIK.A | | 4 | 52.370 | 0.00088 | 466.24 | 0.6 | 2 | '7/16 | 1588 |
| 5 | K.SLNNQFASFIDK.V | | 1 | 65.290 | 3.7e-005 | 692.35 | 0.2 | 2 | '7/22 | 4836 |
| 6 | R.ISISTSGGSFR.N | | 1 | 52.360 | 0.0007 | 556.29 | 4.6 | 2 | '10/20 | 2984 |
| 7 | R.GSSSGGGYSSGSSSYGSGGR.Q | | 1 | 133.370 | 3e-013 | 870.86 | -1.2 | 2 | '13/38 | 1191 |
| 8 | M.GVQVETISPGDGR.T | | 1 | 52.080 | 0.00078 | 657.84 | 0.9 | 2 | '8/24 | 2462 |
| 9 | R.IEEELGDEAR.F | | 1 | 50.770 | 0.00055 | 580.77 | -0.6 | 2 | '13/18 | 1960 |
| 10 | R.ADLAEEYSK.D | | 1 | 47.930 | 0.0012 | 513.24 | -0.8 | 2 | '8/16 | 1978 |
| 11 | R.ALASQLQDSLK.D | | 1 | 61.450 | 0.00022 | 587.33 | 1.9 | 2 | '8/20 | 3490 |
| 12 | K.TIDDLEETLASAK.E | | 1 | 94.540 | 4.9e-008 | 703.36 | -1.6 | 2 | '11/24 | 4690 |
| 13 | R.AQYEEIAQR.S | | 1 | 58.150 | 0.0002 | 554.27 | -1.5 | 2 | '6/16 | 1884 |
| 14 | R.AMSDLELR.- | 0.01000000.0 | 1 | 50.420 | 0.0013 | 475.73 | -1.2 | 2 | '7/14 | 2137 |
| 15 | R.ELEEISERLEEAGGATSVQIEMNK.K | 0.000000000000000000000100.0 | 5 | 88.180 | 1.6e-007 | 893.43 | 0.4 | 3 | '21/46 | 4943 |
| 16 | R.SEVELVQIVIDGVNYLVDCEK.K | | 1 | 48.570 | 0.0026 | 807.74 | -1.7 | 3 | '17/40 | 7233 |
| 17 | K.ESTLHLVLR.L | | 4 | 48.530 | 0.0011 | 534.31 | -2.6 | 2 | '7/16 | 3979 |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 18 | K.NQLTSNPENTVFDAK.R | | 1 | 87.050 | 3.8e-007 | 839.41 | -1.0 | 2 | '9/28 | 3425 |
| 19 | K.VEIIANDQGNR.T | | 2 | 63.200 | 6.3e-005 | 614.82 | -0.2 | 2 | '8/20 | 2002 |
| 20 | R.NADYVQEVK.R | | 1 | 49.590 | 0.0015 | 533.26 | -1.4 | 2 | '13/16 | 1944 |
| 21 | K.VDNALQSGNSQESVTEQDSK.D | | 2 | 74.670 | 2.2e-006 | 1068.49 | -0.3 | 2 | '14/38 | 1874 |
| 22 | K.AVTEQGAELSNEER.N | | 1 | 68.620 | 1.4e-005 | 766.86 | 0.8 | 2 | '10/26 | 1830 |
| 23 | K.SVIPSDGPSVACVK.K | | 2 | 61.870 | 7.7e-005 | 708.36 | 0.4 | 2 | '7/26 | 3111 |
| 24 | R.QITLNDLPVGR.S | | 1 | 52.940 | 0.00043 | 613.35 | 0.7 | 2 | '8/20 | 4113 |
| 25 | R.QVLDNLTMEK.S | 0.0000000100.0 | 1 | 49.760 | 0.0017 | 603.81 | 3.1 | 2 | '8/18 | 2969 |
| 26 | K.SKAEAESLYQSK.Y | | 2 | 67.560 | 4.2e-005 | 670.84 | -0.1 | 2 | '10/22 | 2083 |
| 27 | R.WLQGSQELPR.E | | 2 | 51.200 | 0.0009 | 607.32 | -0.9 | 2 | '9/18 | 3445 |
| 28 | K.DAEEWFFTK.T | | 1 | 50.060 | 0.0012 | 586.77 | -2.0 | 2 | '6/16 | 5233 |
| 29 | K.VAGQDGSVVQFK.I | | 1 | 63.890 | 7.5e-005 | 617.82 | -0.9 | 2 | '10/22 | 2759 |
| 30 | K.STVEGIQASVK.T | | 1 | 57.820 | 0.00029 | 559.81 | 0.6 | 2 | '8/20 | 2215 |
| 31 | R.VYSTSVTGSR.E | | 1 | 61.510 | 7.3e-005 | 528.77 | 0.2 | 2 | '7/18 | 1378 |
| 32 | R.QGVDADINGLR.Q | | 1 | 52.690 | 0.00063 | 579.30 | -1.6 | 2 | '8/20 | 2979 |
| 33 | K.SASDLTWDNLK.G | | 10 | 67.900 | 2.3e-005 | 625.31 | -1.0 | 2 | '7/20 | 3607 |
| 34 | K.LCYVALDFENEMATAASSSSLEK.S | 0.00000000000100000000000.0 | 7 | 86.360 | 1.6e-007 | 851.39 | 2.3 | 3 | '25/44 | 4998 |
| 35 | R.SQYEQLAEQNR.K | | 2 | 78.810 | 1.3e-006 | 683.32 | 0.7 | 2 | '8/20 | 2049 |
| 36 | K.AGFAGDDAPR.A | | 3 | 74.790 | 2.1e-006 | 488.73 | -0.4 | 2 | '9/18 | 1732 |
| 37 | K.SEETLDEGPPK.Y | | 1 | 59.790 | 8.3e-005 | 601.28 | 3.6 | 2 | '7/20 | 1640 |
| 38 | R.KPVEEYANCHLAR.A | | 2 | 57.420 | 0.00024 | 529.60 | 1.1 | 3 | '11/24 | 3133 |
| 39 | K.AQYEEIANR.S | | 1 | 57.800 | 0.00025 | 547.27 | 0.5 | 2 | '6/16 | 1845 |
| 40 | K.IQVLQQQADDAEER.A | | 1 | 82.010 | 8.6e-007 | 821.90 | -1.8 | 2 | '11/26 | 2721 |
| 41 | K.DSGFQMNQLR.G | 0.0000010000.0 | 2 | 56.650 | 9.9e-005 | 606.28 | -0.3 | 2 | '9/18 | 2135 |
| 42 | K.MYLGYEYVTAIR.N | 0.100000000000.0 | 1 | 79.300 | 1.7e-006 | 747.87 | 1.9 | 2 | '10/22 | 4794 |
| 43 | R.INENTGSVSVTR.T | | 1 | 53.120 | 0.00066 | 638.82 | -17.2 | 2 | '10/22 | 1641 |
| 44 | K.YEELQITAGR.H | | 2 | 63.400 | 7.3e-005 | 590.31 | 4.8 | 2 | '8/18 | 3032 |
| 45 | K.IQDKEGIPPDQQR.L | | 14 | 56.020 | 0.00041 | 762.40 | 4.5 | 2 | '10/24 | 1787 |
| 46 | K.TVGMVAGDEESYEVFADLFDPVIK.L | 0.000100000000000000000000.0 | 2 | 54.980 | 0.00035 | 883.09 | 1.2 | 3 | '24/46 | 6396 |
| 47 | K.KSASDLTWDNLK.G | | 4 | 78.740 | 2.3e-006 | 689.35 | -0.4 | 2 | '8/22 | 3562 |
| 48 | R.SLLEGEGSSGGGGR.G | | 1 | 59.310 | 0.00011 | 631.80 | -0.3 | 2 | '17/26 | 2184 |
| 49 | R.QSVEADINGLR.R | | 2 | 58.210 | 0.00022 | 601.31 | -0.4 | 2 | '10/20 | 3293 |
| 50 | K.KVPQVSTPTLVEVSR.N | | 10 | 80.430 | 5.7e-007 | 820.47 | -0.4 | 2 | '9/28 | 3720 |
| 51 | K.KYDEELEER.L | | 2 | 65.320 | 2.2e-005 | 605.78 | -0.7 | 2 | '8/16 | 2006 |
| 52 | R.TNQELQEINR.V | | 1 | 62.340 | 8.4e-005 | 622.82 | -0.2 | 2 | '7/18 | 2004 |
| 53 | K.IANPVEGSSGR.Q | | 1 | 47.170 | 0.0025 | 543.78 | 0.6 | 2 | '7/20 | 1719 |
| 54 | K.SLQDIIAILGMDELSEEDKLTVSR.A | 0.000000000010000000000000.0 | 1 | 57.820 | 0.00022 | 897.80 | 2.8 | 3 | '20/46 | 6410 |
| 55 | K.AQYEEIAQR.S | | 3 | 58.150 | 0.0002 | 554.27 | -1.5 | 2 | '6/16 | 1884 |
| 56 | K.ILLAELEQLK.G | | 1 | 50.880 | 0.00038 | 585.36 | -0.3 | 2 | '9/18 | 5416 |
| 57 | K.GGYTLVSGYPK.R | | 2 | 61.470 | 8.6e-005 | 571.30 | -1.5 | 2 | '8/20 | 3374 |
| 58 | K.GILAADESTGSIAK.R | | 1 | 57.440 | 0.00035 | 666.85 | -1.6 | 2 | '16/26 | 3060 |
| 59 | R.SLQEQADAAEER.A | | 1 | 58.080 | 0.0001 | 673.81 | 1.2 | 2 | '9/22 | 1829 |
| 60 | R.EFTESQLQEGK.H | | 1 | 62.530 | 5.3e-005 | 648.31 | 0.7 | 2 | '8/20 | 2292 |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| 61 | R.TNAENEFVTIK.K | | 2 | 52.890 | 0.00079 | 633.32 | 1.3 | 2 | '8/20 | 3184 |
| 62 | R.HVGDLGNVTADK.D | | 1 | 90.130 | 1.1e-007 | 613.31 | -3.1 | 2 | '19/22 | 2430 |
| 63 | K.DAGTIAGLNVLR.I | | 2 | 73.130 | 9.3e-006 | 600.34 | -2.3 | 2 | '10/22 | 4709 |
| 64 | R.LQSIGTENTEENR.R | | 1 | 68.640 | 1.4e-005 | 745.86 | 1.0 | 2 | '10/24 | 1734 |
| 65 | K.EAAENSLVAYK.A | | 1 | 55.680 | 0.00039 | 597.80 | 2.0 | 2 | '7/20 | 2539 |
| 66 | K.FADLSEAANR.N | | 1 | 61.930 | 9.7e-005 | 547.27 | 2.2 | 2 | '9/18 | 2661 |
| 67 | K.LCYVALDFENEMATAASSSSLEK.S | | 3 | 83.650 | 3.2e-007 | 1268.58 | 0.2 | 2 | '15/44 | 5827 |
| 68 | R.WCAVSEHEATK.C | | 6 | 50.200 | 0.00044 | 659.30 | -3.8 | 2 | '9/20 | 2153 |
| 69 | R.DYQELMNTK.L | 0.000001000.0 | 1 | 50.160 | 0.00044 | 579.26 | 0.5 | 2 | '7/16 | 1765 |
| 70 | R.QDVDNASLAR.L | | 1 | 70.660 | 1e-005 | 544.77 | -3.3 | 2 | '9/18 | 1423 |
| 71 | K.IDEPLEGSEDR.I | | 1 | 56.210 | 0.00012 | 630.29 | -0.8 | 2 | '14/20 | 2248 |
| 72 | K.ATDAEADVASLNR.G | | 1 | 83.270 | 5.2e-007 | 666.82 | 1.3 | 2 | '9/24 | 2546 |
| 73 | K.QLEEDIAAK.E | | 2 | 50.580 | 0.0013 | 508.77 | -0.3 | 2 | '7/16 | 1991 |
| 74 | K.HSTIFENLANKADR.D | | 4 | 77.490 | 2.9e-006 | 539.28 | -0.7 | 3 | '11/26 | 4722 |
| 75 | K.ATDAEADVASLNR.R | | 3 | 83.270 | 5.2e-007 | 666.82 | 1.3 | 2 | '9/24 | 2546 |
| 76 | K.IDTIEIITDR.Q | | 1 | 59.730 | 0.00021 | 594.83 | -1.4 | 2 | '7/18 | 4449 |
| 77 | K.ELEEIVQPIISK.L | | 1 | 49.770 | 0.00092 | 699.40 | 2.2 | 2 | '14/22 | 4644 |
| 78 | R.ALEESNYELEGK.I | | 1 | 87.230 | 3e-007 | 691.33 | -0.3 | 2 | '9/22 | 2608 |
| 79 | R.SGGGGGGGLGSGGSIR.S | | 1 | 114.910 | 3.8e-010 | 616.80 | -1.0 | 2 | '15/30 | 1982 |
| 80 | K.CDEWSVNSVGK.I | | 1 | 72.970 | 1.6e-006 | 640.78 | -4.1 | 2 | '9/20 | 2933 |
| 81 | K.SVTEQGAELSNEER.N | | 1 | 104.310 | 3e-009 | 774.86 | 0.3 | 2 | '10/26 | 1942 |
| 82 | K.VLEYLNQEK.A | | 1 | 51.560 | 0.003 | 568.30 | -0.2 | 2 | '6/16 | 3048 |
| 83 | K.LYTLVLTDPDAPSR.K | | 1 | 79.860 | 1.7e-006 | 780.92 | 0.1 | 2 | '11/26 | 4756 |
| 84 | K.QVATALQNLQTK.T | | 1 | 80.630 | 1.5e-006 | 657.87 | 0.0 | 2 | '10/22 | 3030 |
| 85 | K.QISNLQQSISDAEQR.G | | 2 | 100.000 | 1.4e-008 | 858.93 | -0.5 | 2 | '12/28 | 3557 |
| 86 | K.ASLENSLEETK.G | | 2 | 59.330 | 0.0002 | 610.80 | -0.2 | 2 | '8/20 | 2612 |
| 87 | R.TLSDYNIQK.E | | 2 | 49.300 | 0.0016 | 541.28 | -0.1 | 2 | '12/16 | 2305 |
| 88 | K.AEADVASLNR.R | | 2 | 72.910 | 7.9e-006 | 523.27 | -0.2 | 2 | '9/18 | 1811 |
| 89 | R.ALEEANADLEVK.I | | 4 | 63.010 | 7.4e-005 | 651.33 | 0.2 | 2 | '9/22 | 2798 |
| 90 | R.VEIIANDQGNR.I | | 1 | 63.200 | 6.3e-005 | 614.82 | -0.2 | 2 | '8/20 | 2002 |
| 91 | K.AINQGGLTSVAVR.G | | 1 | 62.760 | 6.4e-005 | 643.37 | 4.7 | 2 | '9/24 | 3024 |
| 92 | R.KLVIIESDLER.A | | 4 | 67.100 | 2.6e-005 | 657.88 | -1.7 | 2 | '7/20 | 4438 |
| 93 | K.EVASNSELVQSSR.S | | 1 | 69.300 | 1.7e-005 | 703.35 | 3.9 | 2 | '9/24 | 1814 |
| 94 | K.AADAEAEVASLNR.R | | 1 | 64.230 | 4.5e-005 | 658.83 | 2.0 | 2 | '8/24 | 2418 |
| 95 | K.QSLEASLAETEGR.Y | | 1 | 101.350 | 1.2e-008 | 695.84 | 0.4 | 2 | '10/24 | 3394 |
| 96 | K.TASEMVLADDNFSTIVAAVEEGR.A | 0.00001000000000000000000.0 | 2 | 48.130 | 0.0019 | 814.39 | 0.1 | 3 | '15/44 | 5963 |
| 97 | K.HSTIFENLANK.A | | 12 | 77.010 | 3.7e-006 | 637.33 | 1.3 | 2 | '9/20 | 4410 |
| 98 | R.GGSGGSYGGGGSGGGYGGGSGSR.G | | 2 | 133.450 | 4.2e-013 | 896.37 | -0.1 | 2 | '15/44 | 1496 |
| 99 | R.LVQAFQFTDK.H | | 1 | 47.380 | 0.0024 | 598.82 | -1.2 | 2 | '8/18 | 4096 |
| 100 | K.VPQVSTPTLVEVSR.N | | 1 | 71.020 | 7.4e-006 | 756.42 | 0.0 | 2 | '11/26 | 3876 |
| 101 | K.DSYVGDEAQSK.R | | 2 | 54.570 | 0.00016 | 599.76 | -0.3 | 2 | '14/20 | 1278 |
| 102 | K.DGAGDVAFVK.H | | 12 | 71.570 | 1.1e-005 | 489.75 | 0.2 | 2 | '9/18 | 3019 |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| 103 | R.TAAENDFVTLK.K | | 1 | 60.530 | 0.00016 | 604.81 | -0.1 | 2 | '9/20 | 3310 |
| 104 | R.FSSSSGYGGGSSR.V | | 1 | 78.730 | 3.2e-007 | 618.27 | 0.0 | 2 | '11/24 | 1287 |
| 105 | K.DAVEDLESVGK.G | | 1 | 54.270 | 0.00042 | 581.28 | -2.2 | 2 | '14/20 | 3836 |
| 106 | K.VGAHAGEYGAEALER.M | | 2 | 48.510 | 0.0014 | 510.58 | -0.5 | 3 | '8/28 | 3684 |
| 107 | K.NMQDMVEDYR.N | 0.0100100000.0 | 1 | 50.020 | 7.9e-005 | 666.76 | -0.3 | 2 | '6/18 | 1782 |
| 108 | K.YENEVALR.Q | | 1 | 48.940 | 0.0021 | 497.25 | -0.5 | 2 | '7/14 | 2124 |
| 109 | K.VQALEEANNDLENK.I | | 1 | 102.440 | 6.8e-009 | 793.89 | -0.8 | 2 | '10/26 | 2816 |
| 110 | R.LENEIQTYR.S | | 1 | 52.690 | 0.0013 | 583.30 | 1.2 | 2 | '11/16 | 2363 |
| 111 | K.EFQLFSSPHGK.D | | 6 | 52.820 | 0.00084 | 638.82 | 0.3 | 2 | '8/20 | 4217 |
| 112 | K.YEELQQTAGR.H | | 1 | 62.490 | 6.4e-005 | 597.79 | 0.2 | 2 | '8/18 | 1678 |
| 113 | R.FLEQQNQVLQTK.W | | 2 | 71.100 | 1.5e-005 | 738.40 | 5.6 | 2 | '8/22 | 3134 |
| 114 | R.TTPSYVAFTDTER.L | | 3 | 62.290 | 5.6e-005 | 744.35 | 0.7 | 2 | '10/24 | 3511 |
| 115 | R.LEQEIATYR.H | | 1 | 56.240 | 0.00046 | 561.79 | -0.4 | 2 | '6/16 | 2455 |
| 116 | R.LEQEIATYR.R | | 3 | 56.240 | 0.00046 | 561.79 | -0.4 | 2 | '6/16 | 2455 |
| 117 | R.LEQEIATYR.S | | 1 | 56.240 | 0.00046 | 561.79 | -0.4 | 2 | '6/16 | 2455 |
| 118 | R.EQAEAEVASLNR.R | | 1 | 66.160 | 2.9e-005 | 658.83 | 2.0 | 2 | '8/22 | 2418 |
| 119 | K.VLQATVVAVGSGSK.G | | 1 | 92.980 | 5.2e-008 | 658.38 | -0.1 | 2 | '20/26 | 2945 |
| 120 | R.TLLEGEESR.M | | 1 | 50.840 | 0.0013 | 517.26 | 0.2 | 2 | '6/16 | 2145 |
| 121 | R.LSQETEALGR.S | | 1 | 58.840 | 0.00023 | 552.29 | 0.2 | 2 | '7/18 | 1806 |
| 122 | R.QAASSLQQASLK.L | | 1 | 65.840 | 4.6e-005 | 616.34 | -0.6 | 2 | '9/22 | 1946 |
| 123 | R.KLVILEGELER.A | | 2 | 50.370 | 0.00072 | 649.89 | -0.8 | 2 | '6/20 | 4860 |
| 124 | R.SNAQGIDLNR.N | | 1 | 65.490 | 3.7e-005 | 544.28 | -0.6 | 2 | '8/18 | 1906 |
| 125 | R.IQLVEEELDR.A | | 9 | 69.010 | 1.9e-005 | 622.33 | 3.0 | 2 | '8/18 | 3884 |
| 126 | K.AEAESLYQSK.Y | | 1 | 57.690 | 0.00016 | 563.27 | -0.2 | 2 | '8/18 | 1696 |
| 127 | R.KLVILEGELER.S | | 6 | 50.370 | 0.00072 | 649.89 | -0.8 | 2 | '6/20 | 4860 |
| 128 | R.QFVTATDVVR.G | | 1 | 63.710 | 0.00017 | 568.31 | -0.3 | 2 | '9/18 | 3207 |
| 129 | K.CAELEEELK.T | | 3 | 56.200 | 0.00022 | 560.76 | -0.4 | 2 | '6/16 | 2767 |
| 130 | R.ITESEEVVSR.E | | 1 | 76.530 | 3.6e-006 | 574.79 | 0.3 | 2 | '8/18 | 1646 |
| 131 | K.QLEEEQQALQK.K | | 3 | 84.180 | 5.2e-007 | 672.34 | 0.3 | 2 | '9/20 | 1926 |
| 132 | R.APNHAVVTR.K | | 4 | 54.370 | 0.00042 | 482.77 | 1.5 | 2 | '7/16 | 1457 |
| 133 | R.SGETEDTFIADLVVGLCTGQIK.T | | 2 | 47.430 | 0.0026 | 785.06 | -1.6 | 3 | '7/42 | 6553 |
| 134 | K.VGGTSDVEVNEK.K | | 1 | 55.610 | 0.00032 | 617.30 | -1.9 | 2 | '7/22 | 1346 |
| 135 | K.AAFDIFVLGAEDGCISTK.E | | 1 | 64.570 | 4.4e-005 | 957.47 | 0.0 | 2 | '14/34 | 5873 |
| 136 | K.EGYYGYTGAFR.C | | 5 | 55.140 | 0.00014 | 642.29 | -2.2 | 2 | '8/20 | 3928 |
| 137 | R.VEILANDQGNR.T | | 1 | 63.200 | 6.3e-005 | 614.82 | -0.2 | 2 | '8/20 | 2002 |
| 138 | K.SKEFQLFSSPHGK.D | | 8 | 75.740 | 5.8e-006 | 746.38 | -0.5 | 2 | '8/24 | 4232 |
| 139 | K.TITLEVEPSDTIENVK.A | | 2 | 58.650 | 0.00022 | 894.46 | -2.7 | 2 | '16/30 | 4330 |
| 140 | R.VLDELTLAR.A | | 2 | 57.860 | 0.00029 | 515.30 | -2.0 | 2 | '6/16 | 3999 |
| 141 | K.ADAEGESDLENSR.K | | 1 | 73.830 | 8e-007 | 696.79 | -5.0 | 2 | '10/24 | 1437 |
| 142 | K.EDPQTFYYAVAVVK.K | | 4 | 70.110 | 5.1e-005 | 815.41 | 1.1 | 2 | '11/26 | 5076 |
| 143 | R.EVATNSELVQSGK.S | | 2 | 86.630 | 3.7e-007 | 681.35 | 1.2 | 2 | '9/24 | 1791 |
| 144 | R.VLDELTLAR.T | | 2 | 57.860 | 0.00029 | 515.30 | -2.0 | 2 | '6/16 | 3999 |
| 145 | R.VVEESELAR.T | | 1 | 49.790 | 0.0019 | 516.27 | 2.9 | 2 | '8/16 | 1772 |

#

Serial (sequential) number for peptide.
*Sequence*

Assigned peptide sequence. Periods (".") delimit the sequence for internal peptides.
*PTM Site*

Location of the post-translational modification (PTM) in the peptide.

Modification codes: [1] Oxidation (M)
*Nr. Scans*

The number of MS/MS scans that were matched to this peptide.
*Mascot Score*

Score given to this peptide/spectrum match by Mascot.
*Expectation*

The number of matches with equal or better scores that are expected to occur by chance alone.
*Isolated Mass*

"Mass" in the Orbitrap analyzer.
*Delta Mass*

Difference between the observed and theoretical masses, in ppm.
*Charge State*

Inferred ionic state of the peptide.
*Matched Ions*

Number of matched MS/MS ions, as reported by Mascot.
*Scan Nr.*

MS/MS scan number in the original Xcalibur RAW file.