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|---|----------------------------------|--------|------|------|---------|---|------|---------|---------------------|
| | | | | | 903.02 | 2 | 3.29 | 121-129 | GVNVSALSR |
| | | | | | 1317.52 | 2 | 3.10 | 221-232 | LPANHPLLTGQR |
| | | | | | 1051.16 | 2 | 2.45 | 281-289 | GNEM*SEVLR |
| | | | | | 1397.53 | 2 | 2.25 | 290-301 | DFPELTM*EVDGK |
| | | | | | 1532.75 | 2 | 4.18 | 309-323 | TALVANTSNM*PVAAR |
| | | | | | 1799.00 | 2 | 3.81 | 365-381 | LAEM*PADSGYPAYLGAR |
| | | | | | 1869.18 | 2 | 3.94 | 537-552 | TVGM*LSNM*IAFYDM*AR |
| | | | | | 1248.41 | 2 | 2.11 | 586-596 | FKDPLKDGEAK |
| | | | | | 1817.96 | 2 | 3.68 | 599-613 | SDYAQLLEDM*QNAFR |
| 2 | Lamin B2 | Q03252 | 67.7 | 5.29 | 17.67 | | | | |
| | | | | | 1427.67 | 2 | 3.18 | 46-57 | ALELENDRLLLK |
| | | | | | 1192.30 | 2 | 2.94 | 58-67 | ISEKEEVTR |
| | | | | | 1238.33 | 2 | 3.58 | 74-84 | ALYESELADAR |
| | | | | | 1089.18 | 2 | 2.77 | 152-161 | GLESVAELR |
| | | | | | 1434.50 | 2 | 3.60 | 271-284 | LSSDQNDKAASAAR |
| | | | | | 1770.05 | 2 | 3.50 | 292-306 | M*RLESLSYQLSGLQK |
| | | | | | 1453.69 | 2 | 2.67 | 362-373 | LALDM*EINAYRK |
| | | | | | 975.04 | 2 | 2.10 | 374-381 | LLEGEER |
| | | | | | 1520.69 | 2 | 4.09 | 542-555 | TVLVNADGEEVAM*R |
| 2 | Heat shock 70 kDa protein 1 | P08107 | 70.1 | 5.48 | 16.54 | | | | |
| | | | | | 1488.58 | 2 | 2.96 | 37-49 | TTPSYVAFTDTER |
| | | | | | 1659.83 | 2 | 4.00 | 57-71 | NQVALNPQNTVFDK |
| | | | | | 1688.91 | 2 | 4.24 | 172-187 | IINEPTAAAAYGLDR |
| | | | | | 1676.68 | 2 | 3.22 | 221-236 | ATAGDTHLGGEDFDNR |
| | | | | | 1110.25 | 2 | 2.57 | 349-357 | LLQDFNGR |
| | | | | | 1018.15 | 2 | 2.43 | 501-509 | ITITNDKGR |
| | | | | | 1004.12 | 2 | 2.44 | 510-517 | LSKEEIER |
| | | | | | 1142.31 | 2 | 2.30 | 518-526 | M*VQEAKEYK |
| | | | | | 1304.46 | 2 | 2.81 | 540-550 | NALESYAFNM*K |
| 2 | Stress-70 protein, mitochondrial | P38646 | 73.7 | 5.87 | 9.57 | | | | |
| | | | | | 1570.88 | 2 | 3.07 | 160-173 | LYSPSQIGAFVLM*K |
| | | | | | 1243.40 | 2 | 3.54 | 207-218 | DAGQISGLNVL |
| | | | | | 1646.87 | 2 | 4.48 | 219-234 | VINFPTAAAIAYGI DK |

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|---|----------------------------------|--------|------|------|-------|---------|---|------|---------|-------------------|
| 3 | Stress-70 protein, mitochondrial | P38646 | 73.7 | 5.87 | 8.25 | 1291.44 | 2 | 3.38 | 395-405 | VQQTVDLFR |
| | | | | | | 1243.40 | 2 | 2.60 | 207-218 | DAGQISGLNVL |
| | | | | | | 1646.87 | 2 | 4.44 | 219-234 | VINEPTAAALAYGLDK |
| | | | | | | 1291.44 | 2 | 2.51 | 395-405 | VQQTVDLFR |
| 3 | Serum albumin | P02768 | 69.4 | 5.92 | 6.90 | 1809.96 | 2 | 2.32 | 469-485 | SQVFSTAADGQTQVEIK |
| | | | | | | 1150.31 | 2 | 2.76 | 66-75 | LVNEVTEFAK |
| | | | | | | 961.14 | 2 | 2.44 | 427-434 | FQNALLVR |
| | | | | | | 1512.73 | 2 | 2.34 | 439-452 | VPOVSTPTLVEVSR |
| 4 | Serum albumin | P02768 | 69.4 | 5.92 | 6.90 | 1129.38 | 2 | 2.83 | 549-558 | KQTALVELVK |
| | | | | | | 1651.88 | 2 | 3.32 | 250-264 | AEFAEVSKLVTDLTK |
| | | | | | | 1640.88 | 2 | 2.71 | 348-360 | DVFLGM*FLYEYAR |
| | | | | | | 1512.73 | 2 | 2.82 | 439-452 | VPOVSTPTLVEVSR |
| 5 | Serum albumin | P02768 | 69.4 | 5.92 | 7.39 | 1150.31 | 2 | 2.70 | 66-75 | LVNEVTEFAK |
| | | | | | | 1658.78 | 2 | 3.62 | 414-426 | QNCLEFEQLGEYK |
| | | | | | | 1512.73 | 2 | 3.13 | 439-452 | VPOVSTPTLVEVSR |
| | | | | | | 1129.38 | 2 | 2.98 | 549-558 | KQTALVELVK |
| 6 | Serum albumin | P02768 | 69.4 | 5.92 | 3.94 | 1150.31 | 2 | 2.55 | 66-75 | LVNEVTEFAK |
| | | | | | | 1512.73 | 2 | 2.78 | 439-452 | VPOVSTPTLVEVSR |
| 7 | Serotransferrin | P02787 | 77.1 | 6.81 | 3.72 | 1274.41 | 2 | 2.88 | 226-236 | HSTIFENLANK |
| | | | | | | 1883.00 | 2 | 3.38 | 237-251 | ADRDQYELLCLDNTR |
| 8 | Neurofilament triplet L protein | P07196 | 61.4 | 4.64 | 23.99 | 1073.14 | 2 | 2.30 | 91-99 | AQLQDLNDR |
| | | | | | | 1125.22 | 2 | 2.35 | 107-115 | VHELEQQNK |
| | | | | | | 1155.41 | 2 | 3.43 | 116-125 | VLEAELLVLR |
| | | | | | | 1062.11 | 2 | 2.99 | 147-156 | LAAEDATNEK |
| | | | | | | 1025.09 | 2 | 2.90 | 177-184 | YEEEVLSR |
| | | | | | | 1002.11 | 2 | 2.53 | 196-205 | KGADEAALAR |

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|----|--|--------|------|------|-------|---------|---|------|---------|-------------------|
| | | | | | | 1092.14 | 2 | 2.73 | 299-308 | AAKDEVSESR |
| | | | | | | 992.10 | 2 | 2.54 | 315-322 | TLEIEACR |
| | | | | | | 1565.69 | 2 | 3.25 | 339-352 | QNADISAM*QDTINK |
| | | | | | | 1526.76 | 2 | 3.70 | 367-378 | YLKEYQDLLNVK |
| | | | | | | 1410.67 | 2 | 3.13 | 379-390 | M*ALDIEIAAYRK |
| | | | | | | 1075.20 | 2 | 2.60 | 390-398 | KLLEGEETR |
| 9 | Calreticulin | P27797 | 48.1 | 4.29 | 15.59 | | | | | |
| | | | | | | 1411.46 | 2 | 2.15 | 25-36 | EQFLDGDGWTSR |
| | | | | | | 1131.17 | 2 | 2.25 | 56-64 | FYGDEEKDK |
| | | | | | | 1608.78 | 2 | 4.37 | 74-87 | FYALSASFEPFSNK |
| | | | | | | 1477.55 | 2 | 3.88 | 99-111 | HEQNIDCGGGYVK |
| | | | | | | 1020.21 | 2 | 2.19 | 144-151 | VHVIFNYK |
| | | | | | | 1085.28 | 2 | 2.15 | 154-162 | NVLINKDIR |
| 10 | Protein disulfide-isomerase | P07237 | 57.1 | 4.76 | 5.12 | | | | | |
| | | | | | | 1781.86 | 2 | 4.53 | 82-97 | VDATEESDLAQQYGVR |
| | | | | | | 1223.42 | 2 | 2.17 | 317-326 | LITTLEEM*TK |
| 11 | 60 kDa heat shock protein, mitochondrial | P10809 | 61.1 | 5.70 | 15.36 | | | | | |
| | | | | | | 913.14 | 2 | 3.36 | 293-301 | VGLQVVAVK |
| | | | | | | 962.05 | 2 | 2.05 | 302-310 | APGFGDNRK |
| | | | | | | 1647.96 | 2 | 3.35 | 345-359 | VGEVIVTKDDAM*LLK |
| | | | | | | 902.07 | 2 | 3.18 | 397-405 | LSDGVAVLK |
| | | | | | | 1362.47 | 2 | 4.04 | 406-418 | VGGTSDVEVNEKK |
| | | | | | | 961.06 | 2 | 3.53 | 421-429 | VTDALNATR |
| | | | | | | 1772.93 | 2 | 3.83 | 447-462 | CIPALDSLTPANEDQK |
| | | | | | | 942.18 | 2 | 2.79 | 463-470 | IGIEIIR |
| 11 | Pyruvate kinase, isozymes M1/M2 | P14618 | 57.8 | 7.95 | 3.58 | | | | | |
| | | | | | | 1214.37 | 2 | 2.21 | 141-150 | ITLDNAYM*EK |
| | | | | | | 996.17 | 2 | 2.76 | 489-497 | VNFAM*NVGK |
| 12 | Vimentin | P08670 | 53.5 | 5.06 | 39.57 | | | | | |
| | | | | | | 1429.56 | 2 | 2.47 | 50-63 | SLYASSPGGVYATR |
| | | | | | | 1588.70 | 2 | 3.43 | 100-112 | TNEKVELQELNDR |
| | | | | | | 1126.29 | 2 | 2.94 | 113-121 | FANYIDKVR |
| | | | | | | 1540.83 | 2 | 3.46 | 129-142 | IIIAFI FOI KGQGGK |

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| | | | | | 1217.32 | 2 | 2.63 | 158-167 | RQVDQLTNDK |
| | | | | | 1320.50 | 2 | 2.23 | 186-195 | EKLQEEM*LQR |
| | | | | | 1324.38 | 2 | 2.76 | 196-206 | EEAENTLQSFR |
| | | | | | 1089.14 | 2 | 2.48 | 207-216 | QDVNASLAR |
| | | | | | 1662.95 | 3 | 4.29 | 222-235 | KVESLQEEIAFLKK |
| | | | | | 1094.16 | 2 | 3.09 | 294-303 | FADLSEANR |
| | | | | | 1491.66 | 2 | 2.61 | 321-333 | QVQSLTCEVDALK |
| | | | | | 1767.97 | 2 | 2.28 | 364-377 | LQDEIQNM*KEEM*AR |
| | | | | | 1312.52 | 2 | 3.56 | 390-400 | M*ALDIEIATYR |
| | | | | | 933.00 | 2 | 2.14 | 402-409 | LLEGEESR |
| 13 | Vacuolar ATP synthase subunit B, brain isoform | P21281 | 56.5 | 5.57 | 5.09 | | | | |
| | | | | | 1091.20 | 2 | 2.52 | 83-93 | SGQVLEVSGSK |
| | | | | | 1521.70 | 2 | 4.88 | 94-108 | AVVQVFEGTSGIDAK |
| 14 | Vacuolar ATP synthase subunit B, brain isoform | P21281 | 56.5 | 5.57 | 7.24 | | | | |
| | | | | | 1091.20 | 2 | 2.67 | 83-93 | SGQVLEVSGSK |
| | | | | | 1521.70 | 2 | 4.13 | 94-108 | AVVQVFEGTSGIDAK |
| | | | | | 1309.41 | 2 | 2.86 | 461-471 | NFIAQGPYENR |
| 15 | Tubulin alpha-3 chain | Q71U36 | 50.1 | 4.94 | 17.29 | | | | |
| | | | | | 1702.93 | 2 | 3.77 | 65-79 | AVFVDLEPTVIDEVR |
| | | | | | 1086.26 | 2 | 2.29 | 113-121 | EIIDLVDR |
| | | | | | 910.05 | 2 | 2.17 | 157-164 | LSVDYGKK |
| | | | | | 979.07 | 2 | 2.46 | 222-229 | PTYTNLNR |
| | | | | | 1016.17 | 2 | 2.82 | 327-336 | DVNAAIATIK |
| | | | | | 1882.12 | 2 | 4.28 | 374-390 | AVCM*LSNTTAAIEAWAR |
| | | | | | 1397.63 | 2 | 2.64 | 391-401 | LDHKFDLM*YAK |
| 15 | Tubulin alpha-1 chain | P68366 | 49.9 | 4.95 | 14.96 | | | | |
| | | | | | 910.05 | 2 | 2.17 | 157-164 | LSVDYGKK |
| | | | | | 979.07 | 2 | 2.46 | 222-229 | PTYTNLNR |
| | | | | | 986.15 | 2 | 3.24 | 327-336 | DVNAAIAAIK |
| | | | | | 1585.78 | 2 | 3.77 | 340-352 | SIQFVDWCPTGFK |
| | | | | | 1882.12 | 2 | 4.28 | 374-390 | AVCM*LSNTTAAIEAWAR |
| | | | | | 1397.63 | 2 | 2.64 | 391-401 | LDHKFDLM*YAK |
| 16 | S-arrestin | P10523 | 45.1 | 6.14 | 3.70 | | | | |

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|----|-----------------------|--------|------|------|-------|---------|---|------|---------|------------------|
| 17 | S-arrestin | P10523 | 45.1 | 6.14 | 19.01 | | | | | |
| | | | | | | 1199.38 | 2 | 2.50 | 10-19 | SEPNHVIFKK |
| | | | | | | 1358.60 | 2 | 3.20 | 60-70 | KVYVTLTCAFR |
| | | | | | | 957.07 | 2 | 3.00 | 85-91 | RDLYFSR |
| | | | | | | 959.17 | 2 | 2.37 | 107-114 | LQESLLKK |
| | | | | | | 1339.61 | 2 | 3.45 | 281-292 | TLTLLPLLANNR |
| | | | | | | 1670.89 | 2 | 3.05 | 303-317 | IKHEDTNLASSTIHK |
| | | | | | | 1554.65 | 2 | 3.27 | 385-398 | HNLKDAGEAEEGKR |
| 18 | S-arrestin | P10523 | 45.1 | 6.14 | 22.96 | | | | | |
| | | | | | | 1199.38 | 2 | 2.63 | 10-19 | SEPNHVIFKK |
| | | | | | | 1358.60 | 2 | 3.76 | 60-70 | KVYVTLTCAFR |
| | | | | | | 957.07 | 2 | 2.78 | 85-91 | RDLYFSR |
| | | | | | | 1515.74 | 2 | 2.57 | 92-106 | VQVYPPVGAASPTK |
| | | | | | | 1339.61 | 2 | 3.24 | 281-292 | TLTLLPLLANNR |
| | | | | | | 1670.89 | 2 | 3.10 | 303-317 | IKHEDTNLASSTIHK |
| | | | | | | 1334.63 | 2 | 2.54 | 323-334 | TVLGILVSYQIK |
| | | | | | | 1279.45 | 2 | 2.29 | 359-369 | LM*HPQPEDPAK |
| 19 | Tubulin beta-2C chain | P68371 | 49.8 | 4.79 | 19.55 | | | | | |
| | | | | | | 1618.84 | 2 | 2.97 | 63-77 | AVLVDLEPGTM*DSVR |
| | | | | | | 1078.16 | 2 | 2.41 | 155-162 | IREEYPDR |
| | | | | | | 1336.58 | 2 | 3.03 | 163-174 | IM*NTFSVVPSPK |
| | | | | | | 1131.27 | 2 | 2.70 | 242-251 | FPGQLNADLR |
| | | | | | | 1288.59 | 2 | 2.62 | 252-262 | KLAVNM*VPFPR |
| | | | | | | 1463.60 | 2 | 3.53 | 325-336 | EVDEQM*LVNQNK |
| | | | | | | 1029.16 | 2 | 2.09 | 351-359 | TAVCDIPPR |
| | | | | | | 1246.42 | 2 | 3.46 | 381-390 | ISEQFTAM*FR |
| 19 | Tubulin beta-2 chain | P07437 | 49.7 | 4.78 | 18.92 | | | | | |
| | | | | | | 1302.42 | 2 | 2.32 | 47-58 | ISVYYNEATGGK |
| | | | | | | 1078.16 | 2 | 2.41 | 155-162 | IREEYPDR |
| | | | | | | 1336.58 | 2 | 3.03 | 163-174 | IM*NTFSVVPSPK |
| | | | | | | 1131.27 | 2 | 2.70 | 242-251 | FPGQLNADLR |
| | | | | | | 1288.59 | 2 | 2.62 | 252-262 | KLAVNM*VPFPR |
| | | | | | | 1463.60 | 2 | 3.53 | 325-336 | EVDEQM*LVNQNK |

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|---------|------------------------------------|--------|---------|------------------|-------|---------|--|--------|---------|---------------------|
| 19 | Tubulin beta-3 chain | Q13509 | 50.4 | 4.83 | 16.89 | 1246.42 | 2 | 3.46 | 381-390 | ISEQFTAM*FR |
| | | | | | | 1336.58 | 2 | 3.03 | 163-174 | IM*NTFSVVPSPK |
| | | | | | | 1131.27 | 2 | 2.70 | 242-251 | FPGQLNADLR |
| | | | | | | 1288.59 | 2 | 2.62 | 252-262 | KLAVNM*VPFPR |
| | | | | | | 1917.22 | 2 | 3.49 | 321-336 | M*SM*KEVDEQM*LAIQSK |
| | | | | | | 1407.57 | 2 | 3.39 | 325-336 | EVDEQM*LAIQSK |
| | | | | | | 1891.14 | 2 | 2.86 | 363-379 | M*SSTFIGNSTAIQELFK |
| 19 | Tubulin beta-6 chain | Q9BUF5 | 49.9 | 4.77 | 11.88 | 1246.42 | 2 | 3.46 | 381-390 | ISEQFTAM*FR |
| | | | | | | 1062.16 | 2 | 2.43 | 155-162 | IREEFPDR |
| | | | | | | 1384.65 | 2 | 3.19 | 163-174 | IM*NTFSVM*PSPK |
| | | | | | | 1131.27 | 2 | 2.70 | 242-251 | FPGQLNADLR |
| | | | | | | 1288.59 | 2 | 2.62 | 252-262 | KLAVNM*VPFPR |
| | | | | | | 1407.57 | 2 | 3.39 | 325-336 | EVDEQM*LAIQSK |
| | | | | | | 20 | ATP synthase beta chain, mitochondrial | P06576 | 56.6 | 5.26 |
| 1279.45 | 2 | 2.74 | 110-121 | TIAM*DGTEGLVR | | | | | | |
| 976.15 | 2 | 2.62 | 202-212 | IGLFGGAGVGK | | | | | | |
| 1474.79 | 2 | 3.98 | 213-225 | TVLIM*ELINNVAK | | | | | | |
| 1407.52 | 2 | 3.29 | 226-239 | AHGGYSVFAGVGER | | | | | | |
| 1618.84 | 2 | 3.08 | 265-279 | VALVYQOM*NEPPGAR | | | | | | |
| 1440.67 | 2 | 3.12 | 282-294 | VALTGLTVAEYFR | | | | | | |
| 1436.60 | 2 | 3.73 | 311-324 | FTQAGSEVSALLGR | | | | | | |
| 21 | Gamma-enolase | P09104 | 47.1 | 4.91 | 12.47 | 1131.31 | 2 | 2.83 | 183-192 | LGAEVYHTLK |
| | | | | | | 1225.33 | 2 | 2.44 | 228-238 | EAIDKAGYTEK |
| | | | | | | 992.18 | 2 | 2.73 | 335-342 | ACNCLLLK |
| | | | | | | 1618.81 | 2 | 3.76 | 343-357 | VNQIGSVTEAIQACK |
| | | | | | | 1161.20 | 2 | 2.78 | 412-421 | IEEELGDEAR |
| 22 | Eukaryotic initiation factor 4A-II | Q14240 | 46.4 | 5.33 | 16.22 | 1829.05 | 2 | 2.85 | 47-62 | GIYAYGFEKPSAIQQR |
| | | | | | | 1545.77 | 2 | 3.71 | 148-162 | LQAEAPHIVGTPGR |

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| | | | | | 1516.72 | 2 | 3.22 | 192-203 | GFKDQIYEIFQK |
| | | | | | 1160.34 | 2 | 2.84 | 239-248 | KEELTLEGIK |
| 22 | Eukaryotic initiation factor 4A-I | P60842 | 46.2 | 5.32 | 12.56 | | | | |
| | | | | | 1829.05 | 2 | 2.85 | 46-61 | GIYAYGF EKPSAIQQR |
| | | | | | 1588.79 | 2 | 4.36 | 178-190 | M*FVLDEADEM*LSR |
| | | | | | 1502.70 | 2 | 3.72 | 191-202 | GFKDQIYDIFQK |
| | | | | | 1188.36 | 2 | 2.70 | 238-247 | KEELTLEGIR |
| 23 | Alpha-enolase | P06733 | 47.0 | 6.99 | 31.41 | | | | |
| | | | | | 1407.55 | 2 | 3.63 | 15-27 | GNPTVEVDLFTSK |
| | | | | | 1806.01 | 2 | 3.98 | 32-49 | AAVPSGASTGIYEALRLR |
| | | | | | 1445.64 | 2 | 4.12 | 80-91 | KLNVTEQEKIDK |
| | | | | | 1669.90 | 2 | 3.20 | 89-102 | IDKLM*IEM*DG TENK |
| | | | | | 1144.31 | 2 | 2.75 | 183-192 | IGAEVYHNLK |
| | | | | | 1962.06 | 2 | 4.92 | 202-220 | DATNVGDEGGFAPNILENK |
| | | | | | 1557.80 | 2 | 3.78 | 239-252 | VWIGM*DVAASEFFR |
| | | | | | 1827.93 | 2 | 4.17 | 253-268 | SGKYDLDFKSPDDPSR |
| | | | | | 1426.60 | 2 | 2.90 | 269-280 | YISPDQLADLYK |
| 24 | Alpha-enolase | P06733 | 47.0 | 6.99 | 24.71 | | | | |
| | | | | | 1407.55 | 2 | 3.36 | 15-27 | GNPTVEVDLFTSK |
| | | | | | 1445.64 | 2 | 3.59 | 80-91 | KLNVTEQEKIDK |
| | | | | | 1669.90 | 2 | 3.48 | 89-102 | IDKLM*IEM*DG TENK |
| | | | | | 1528.73 | 2 | 2.17 | 92-104 | LM*IEM*DG TENKSK |
| | | | | | 1941.31 | 2 | 4.48 | 162-178 | LAM*QEFM*ILPVGAANFR |
| | | | | | 1144.31 | 2 | 3.10 | 183-192 | IGAEVYHNLK |
| | | | | | 1827.93 | 2 | 3.90 | 253-268 | SGKYDLDFKSPDDPSR |
| | | | | | 1426.60 | 2 | 3.30 | 269-280 | YISPDQLADLYK |
| | | | | | 1542.75 | 2 | 3.03 | 358-371 | LAQANGWGVM*VSHR |
| 25 | Alpha-enolase | P06733 | 47.0 | 6.99 | 14.32 | | | | |
| | | | | | 1445.64 | 2 | 4.73 | 80-91 | KLNVTEQEKIDK |
| | | | | | 1669.90 | 2 | 3.19 | 89-102 | IDKLM*IEM*DG TENK |
| | | | | | 1144.31 | 2 | 3.34 | 183-192 | IGAEVYHNLK |
| | | | | | 1073.18 | 2 | 2.89 | 253-261 | SGKYDLDFK |
| | | | | | 1426.60 | 2 | 2.46 | 269-280 | YISPDQLADLYK |

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| 26 | Alpha-enolase | P06733 | 47.0 | 6.99 | 22.86 | 1407.55 | 2 | 2.80 | 15-27 | GNPTVEVDLFTSK | | | | | | |
| | | | | | | 1806.01 | 2 | 3.94 | 32-49 | AAVPSGASTGIYEALRL | | | | | | |
| | | | | | | 1445.64 | 2 | 3.15 | 80-91 | KLNVTEQEKIDK | | | | | | |
| | | | | | | 1669.90 | 2 | 3.45 | 89-102 | IDKLM*IEM*DG TENK | | | | | | |
| | | | | | | 1144.31 | 2 | 2.85 | 183-192 | IGAEVYHNLK | | | | | | |
| | | | | | | 1557.80 | 2 | 3.19 | 239-252 | VVIGM*DVAASEFFR | | | | | | |
| | | | | | | 1073.18 | 2 | 2.98 | 253-261 | SGKYDLDFK | | | | | | |
| 27 | Actin, cytoplasmic 1 | P60709 | 41.7 | 5.29 | 16.53 | 1426.60 | 2 | 2.89 | 269-280 | YISPDQLADLYK | | | | | | |
| | | | | | | 977.01 | 2 | 2.03 | 19-28 | AGFAGDDAPR | | | | | | |
| | | | | | | 1955.24 | 2 | 3.09 | 96-113 | VAPEEHPVLLTEAPLNPK | | | | | | |
| | | | | | | 1015.16 | 2 | 2.03 | 184-191 | DLTDYLM*K | | | | | | |
| | | | | | | 1133.19 | 2 | 2.38 | 197-206 | GYSFTTTAER | | | | | | |
| | | | | | | 1791.94 | 2 | 3.81 | 239-254 | SYELPDGQVITIGNER | | | | | | |
| | | | | | | 27 | Actin, cytoplasmic 2 | P63261 | 41.8 | 5.31 | 16.53 | 977.01 | 2 | 2.03 | 19-28 | AGFAGDDAPR |
| 1955.24 | 2 | 3.09 | 96-113 | VAPEEHPVLLTEAPLNPK | | | | | | | | | | | | |
| 1015.16 | 2 | 2.03 | 184-191 | DLTDYLM*K | | | | | | | | | | | | |
| 1133.19 | 2 | 2.38 | 197-206 | GYSFTTTAER | | | | | | | | | | | | |
| 1791.94 | 2 | 3.81 | 239-254 | SYELPDGQVITIGNER | | | | | | | | | | | | |
| 27 | Actin, gamma-enteric smooth muscle | P63267 | 41.9 | 5.31 | 11.70 | | | | | | | 977.01 | 2 | 2.03 | 20-29 | AGFAGDDAPR |
| | | | | | | | | | | | | 1015.16 | 2 | 2.03 | 185-192 | DLTDYLM*K |
| | | | | | | 1131.22 | 2 | 3.13 | 198-207 | GYSFVTTAER | | | | | | |
| | | | | | | 1791.94 | 2 | 3.81 | 240-255 | SYELPDGQVITIGNER | | | | | | |
| | | | | | | 27 | Actin, aortic smooth muscle | P62736 | 42.0 | 5.24 | 11.67 | 977.01 | 2 | 2.03 | 21-30 | AGFAGDDAPR |
| | | | | | | | | | | | | 1015.16 | 2 | 2.03 | 186-193 | DLTDYLM*K |
| | | | | | | | | | | | | 1131.22 | 2 | 3.13 | 199-208 | GYSFVTTAER |
| 1791.94 | 2 | 3.81 | 241-256 | SYELPDGQVITIGNER | | | | | | | | | | | | |
| 28 | Creatine kinase B-type | P12277 | 42.6 | 5.34 | 14.17 | | | | | | | 1587.76 | 2 | 4.07 | 157-172 | LAVEALSSLDGDLAGR |

| | | | | | | | | | |
|----|---------------------------------|--------|------|------|---------|---|------|---------|---------------------|
| | | | | | 1866.17 | 2 | 4.78 | 342-358 | LGFSEVELVQM*VVDGVK |
| | | | | | 1048.24 | 2 | 2.56 | 359-366 | LLIEM*EQR |
| 29 | Glutamine synthetase | P15104 | 41.9 | 6.42 | 6.45 | | | | |
| | | | | | 957.07 | 2 | 3.34 | 106-113 | RPAETNLR |
| | | | | | 1003.09 | 2 | 2.36 | 173-180 | DIVEAHYR |
| | | | | | 995.11 | 2 | 2.24 | 268-275 | YIEEAIEK |
| 30 | Glutamine synthetase | P15104 | 41.9 | 6.42 | 24.73 | | | | |
| | | | | | 1826.07 | 2 | 3.81 | 25-40 | VQAM*YIWIDGTGEGLR |
| | | | | | 957.07 | 2 | 3.16 | 106-113 | RPAETNLR |
| | | | | | 1003.09 | 2 | 2.66 | 173-180 | DIVEAHYR |
| | | | | | 1064.20 | 2 | 2.03 | 259-267 | AM*REENGLK |
| | | | | | 1323.52 | 2 | 2.40 | 268-278 | YIEEAIEKLSK |
| | | | | | 914.99 | 2 | 2.42 | 333-339 | KGYFEDR |
| | | | | | 1934.14 | 2 | 3.36 | 340-356 | RPSANCDPFSVTEALIR |
| | | | | | 1930.05 | 2 | 3.96 | 357-372 | TCLLNETGDEPFQYKN |
| 31 | Glutamine synthetase | P15104 | 41.9 | 6.42 | 6.45 | | | | |
| | | | | | 957.07 | 2 | 2.95 | 106-113 | RPAETNLR |
| | | | | | 1930.05 | 2 | 4.01 | 357-372 | TCLLNETGDEPFQYKN |
| 32 | L-lactate dehydrogenase B chain | P07195 | 36.5 | 5.72 | 7.51 | | | | |
| | | | | | 1511.66 | 2 | 2.81 | 77-90 | IVADKDYSVTANSK |
| | | | | | 1284.51 | 2 | 2.51 | 233-243 | M*VVESAYEVIK |
| 33 | L-lactate dehydrogenase B chain | P07195 | 36.5 | 5.72 | 27.03 | | | | |
| | | | | | 1953.18 | 2 | 3.39 | 5-22 | EKLIAPVAEEEEATVPNNK |
| | | | | | 1630.82 | 2 | 4.75 | 43-57 | SLADELALVDVLEDK |
| | | | | | 1511.66 | 2 | 3.21 | 77-90 | IVADKDYSVTANSK |
| | | | | | 914.13 | 2 | 2.61 | 91-99 | IVVVTAGVR |
| | | | | | 1249.35 | 2 | 3.70 | 158-169 | VIGSGCNLDSAR |
| | | | | | 1284.51 | 2 | 3.38 | 233-243 | M*VVESAYEVIK |
| | | | | | 1287.49 | 2 | 3.76 | 308-318 | LKDDEVAQLKK |
| 34 | L-lactate dehydrogenase B chain | P07195 | 36.5 | 5.72 | 39.04 | | | | |
| | | | | | 1953.18 | 2 | 4.08 | 5-22 | EKLIAPVAEEEEATVPNNK |
| | | | | | 1630.82 | 2 | 4.80 | 43-57 | SLADELALVDVLEDK |
| | | | | | 1965.24 | 2 | 3.41 | 60-76 | GEM*M*DLQHGSFLQTPK |

| | | | | | | | | | | |
|----|--|--------|------|------|-------|---------|---|------|---------|------------------|
| | | | | | | 914.13 | 2 | 2.82 | 91-99 | IVVVTAGVR |
| | | | | | | 720.84 | 1 | 1.94 | 113-118 | NVNVFK |
| | | | | | | 958.22 | 1 | 1.64 | 119-126 | FIIPQIVK |
| | | | | | | 1249.35 | 2 | 2.59 | 158-169 | VIGSGCNLDSAR |
| | | | | | | 1284.51 | 2 | 3.41 | 233-243 | M*VVESAYEVIK |
| | | | | | | 960.11 | 2 | 2.08 | 299-307 | GLTSVINQK |
| | | | | | | 1287.49 | 2 | 4.09 | 308-318 | LKDDEVAQLKK |
| 35 | Cellular retinaldehyde-binding protein | P12271 | 36.3 | 4.98 | 22.15 | | | | | |
| | | | | | | 1032.17 | 2 | 2.70 | 19-27 | AQLEQLTTK |
| | | | | | | 975.04 | 2 | 2.79 | 47-54 | AKDELNER |
| | | | | | | 1326.48 | 2 | 2.64 | 87-97 | VQEKDSGFLLR |
| | | | | | | 1865.08 | 2 | 4.39 | 121-136 | LQYPELFDLSPEAVR |
| | | | | | | 1510.67 | 2 | 3.92 | 137-150 | CTIEAGYPGVLSSR |
| | | | | | | 1442.65 | 2 | 3.39 | 222-233 | M*VDM*LQDSFPAR |
| 36 | Inorganic pyrophosphatase | Q15181 | 32.7 | 5.54 | 11.76 | | | | | |
| | | | | | | 1486.76 | 2 | 3.04 | 58-70 | M*EIATKDPLNPIK |
| | | | | | | 1267.46 | 2 | 2.46 | 64-74 | DPLNPIKQDVK |
| | | | | | | 1178.36 | 2 | 3.16 | 212-221 | DKDFAIDIIK |
| 36 | Guanine nucleotide-binding protein G(I)/G(S)/G(T) beta subunit 1 | P62873 | 37.2 | 5.60 | 6.49 | | | | | |
| | | | | | | 1018.15 | 2 | 2.72 | 68-77 | LLVSASQDGK |
| | | | | | | 1226.35 | 2 | 3.33 | 197-208 | LFVSGACDASAK |
| 37 | Inorganic pyrophosphatase | Q15181 | 32.7 | 5.54 | 14.88 | | | | | |
| | | | | | | 1486.76 | 2 | 3.02 | 58-70 | M*EIATKDPLNPIK |
| | | | | | | 1267.46 | 2 | 2.30 | 64-74 | DPLNPIKQDVK |
| | | | | | | 1807.06 | 2 | 4.83 | 140-155 | VLGILAM*DEGETDWK |
| | | | | | | 1178.36 | 2 | 3.34 | 212-221 | DKDFAIDIIK |
| 37 | Guanine nucleotide-binding protein G(I)/G(S)/G(T) beta subunit 1 | P62873 | 37.2 | 5.60 | 11.50 | | | | | |
| | | | | | | 1018.15 | 2 | 2.65 | 68-77 | LLVSASQDGK |
| | | | | | | 805.99 | 1 | 1.98 | 89-95 | VHAIPLR |
| | | | | | | 1226.35 | 2 | 3.55 | 197-208 | LFVSGACDASAK |
| | | | | | | 1010.09 | 2 | 2.25 | 304-313 | AGVLAGHDNR |
| 38 | Malate dehydrogenase, mitochondrial | P40926 | 35.5 | 8.92 | 19.82 | | | | | |
| | | | | | | 993.14 | 2 | 2.46 | 177-185 | ANTFVAELK |

| | | | | | | | | | | |
|----|--|--------|------|------|-------|---------|---|------|---------|-------------------|
| | | | | | | 1471.62 | 2 | 3.51 | 242-257 | AGAGSATLSM*AYAGAR |
| | | | | | | 1344.56 | 2 | 2.72 | 258-269 | FVFLVDAM*NGK |
| | | | | | | 1154.29 | 2 | 2.44 | 270-279 | EGVVECSFVK |
| | | | | | | 1133.34 | 2 | 2.78 | 315-324 | M*ISDAIPELK |
| 38 | Glyceraldehyde-3-phosphate dehydrogenase | P04406 | 35.9 | 8.58 | 10.78 | | | | | |
| | | | | | | 910.01 | 2 | 2.38 | 107-116 | AGAHLOGGAK |
| | | | | | | 1764.88 | 2 | 3.62 | 309-322 | LISWYDNEFGYSNR |
| | | | | | | 1363.59 | 2 | 2.93 | 323-334 | VVDLM*AHM*ASKE |
| 39 | 14-3-3 protein epsilon | P62258 | 29.2 | 4.63 | 14.51 | | | | | |
| | | | | | | 1464.63 | 2 | 2.39 | 30-42 | VAGM*DVELTVEER |
| | | | | | | 1418.58 | 2 | 2.48 | 62-73 | IISIEQKEENK |
| | | | | | | 1385.51 | 2 | 2.67 | 131-142 | YLAEFATGNDRK |
| 40 | 14-3-3 protein zeta/delta | P63104 | 27.7 | 4.73 | 14.69 | | | | | |
| | | | | | | 1549.58 | 2 | 3.39 | 28-41 | SVTEQGAELSNEER |
| | | | | | | 1280.41 | 2 | 3.05 | 128-139 | YLAEVAAGDDKK |
| | | | | | | 1206.44 | 2 | 2.96 | 213-222 | DSTLIM*QLLR |
| 40 | 14-3-3 protein theta | P27348 | 27.8 | 4.68 | 14.69 | | | | | |
| | | | | | | 1533.58 | 2 | 3.62 | 28-41 | AVTEQGAELSNEER |
| | | | | | | 1321.46 | 2 | 2.66 | 104-115 | YLIANATNPESK |
| | | | | | | 1206.44 | 2 | 2.96 | 213-222 | DSTLIM*QLLR |
| 40 | 14-3-3 protein gamma | P61981 | 28.2 | 4.80 | 13.82 | | | | | |
| | | | | | | 1644.72 | 2 | 3.64 | 28-41 | NVTELNEPLSNEER |
| | | | | | | 1081.20 | 2 | 2.67 | 132-141 | YLAEVATGEK |
| | | | | | | 1206.44 | 2 | 2.96 | 217-226 | DSTLIM*QLLR |
| 41 | Recoverin | P35243 | 23.0 | 5.06 | 10.05 | | | | | |
| | | | | | | 1455.64 | 2 | 3.18 | 43-54 | ITQQQFQSIYAK |
| | | | | | | 949.11 | 2 | 2.47 | 131-138 | M*ITPEDVK |
| 42 | Alpha crystallin A chain | P02489 | 19.9 | 5.77 | 16.76 | | | | | |
| | | | | | | 981.21 | 2 | 2.09 | 71-78 | FVIFLDVK |
| | | | | | | 1173.30 | 2 | 2.45 | 79-88 | HFSPEDLTVK |
| | | | | | | 1287.40 | 2 | 3.22 | 89-99 | VQDDFVEIHGK |
| 43 | Nucleoside diphosphate kinase A | P15531 | 17.1 | 5.83 | 18.42 | | | | | |
| | | | | | | 985.21 | 2 | 2.11 | 19-27 | GI VGFIIKR |

| | | | | | | | | | | |
|----|--------------------------|--------|------|------|-------|---------|---|------|---------|-----------------|
| 44 | Hemoglobin beta subunit | P68871 | 15.9 | 6.81 | 22.60 | 1052.16 | 2 | 2.22 | 106-114 | GDFCIQVGR |
| | | | | | | 953.08 | 2 | 2.67 | 1-8 | VHLTPEEK |
| | | | | | | 1315.42 | 2 | 3.36 | 18-30 | VNVDEVGGEALGR |
| | | | | | | 1150.36 | 2 | 3.22 | 133-144 | VVAGVANALAHK |
| 45 | Hemoglobin beta subunit | P68871 | 15.9 | 6.81 | 22.60 | 953.08 | 2 | 2.26 | 1-8 | VHLTPEEK |
| | | | | | | 1315.42 | 2 | 2.52 | 18-30 | VNVDEVGGEALGR |
| | | | | | | 1150.36 | 2 | 2.94 | 133-144 | VVAGVANALAHK |
| | | | | | | 1530.62 | 2 | 3.16 | 17-31 | VGAHAGEYGAEALER |
| 46 | Hemoglobin alpha subunit | P69905 | 15.1 | 8.73 | 23.40 | 1088.30 | 2 | 2.11 | 32-40 | M*FLSFPTTK |
| | | | | | | 1088.29 | 2 | 2.68 | 91-99 | LRVDPVNFK |

Table 2

Proteins identified from spots detected only macular retina.

Proteins from macular unique spots by LC-MS/MS and listed.

^(a)Spot ID corresponds to the numbers on gel images in figure 1 - 4.

^(b)Accession no. corresponds to UniProtKB/Swiss-Prot database (Release 48.8).

^(c)MW and pI are theoretical scores by Bioworks ver.3.1.

*Oxidation of methionine.

| Spot no. ^(a) | Protein name | Database Accession no. ^(b) | MW (kDa) ^(c) | pI ^(d) | Sequence coverage (%) | Precursor ion MH+ | Charge | XC | Residue | Sequence |
|-------------------------|--|---------------------------------------|-------------------------|-------------------|-----------------------|-------------------|--------|------|---------|--------------------|
| M1 | Pyruvate kinase, isozymes M1/M2 | P14618 | 32.7 | 4.69 | 18.11 | 1198.35 | 2 | 3.10 | 32-42 | LDIDSPPTAR |
| | | | | | | 1360.53 | 2 | 4.43 | 43-55 | NTGIICTIGPASR |
| | | | | | | 1194.43 | 2 | 2.70 | 56-65 | SVETLKEM*IK |
| | | | | | | 914.08 | 2 | 2.50 | 106-114 | PVAVALDTK |
| | | | | | | 1119.25 | 2 | 2.86 | 125-135 | GSGTAEVELKK |
| | | | | | | 1463.70 | 2 | 4.32 | 173-185 | IYVDDGLISLQVK |
| | | | | | | 1780.91 | 2 | 4.61 | 188-205 | GADFLVTEVENGGSLGSK |
| | | | | | | 1142.28 | 2 | 2.96 | 294-304 | GDLGIEIPA EK |
| M2 | Tropomyosin 1 alpha chain | P09493 | 32.7 | 4.69 | 13.73 | 1400.56 | 2 | 2.95 | 91-101 | RIQLVEEELDR |
| | | | | | | 1728.89 | 2 | 3.24 | 92-105 | IQLVEEELDRAQER |
| | | | | | | 1315.54 | 2 | 3.69 | 168-178 | KLVIIESDLER |
| | | | | | | 1672.86 | 2 | 2.58 | 169-182 | LVIIIESDLERAEER |
| | | | | | | 1121.21 | 2 | 2.35 | 190-198 | CAELEEEELK |
| M2 | Heterogeneous nuclear ribonucleoproteins C1/C2 | P07910 | 33.7 | 4.95 | 16.67 | 1317.60 | 2 | 4.08 | 18-29 | VFIGNLNLTLVVK |
| | | | | | | 1330.47 | 2 | 4.35 | 51-61 | GFAFVQYVNER |
| | | | | | | 1700.00 | 2 | 4.50 | 74-89 | M*IAGQVLDINLAAEPK |
| | | | | | | 1416.60 | 2 | 3.49 | 205-216 | QKVDSLLENLEK |
| M3 | Transaldolase | P37837 | 37.5 | 6.36 | 16.62 | 1051.20 | 2 | 2.82 | 11-19 | M*ESALDQLK |
| | | | | | | 1792.15 | 2 | 4.16 | 82-97 | NAIDKLFVLFGA EILK |
| | | | | | | 1269.45 | 2 | 2.86 | 111-121 | LSFDKDAM*VAR |
| | | | | | | 1234.34 | 2 | 2.50 | 205-215 | SYEPLDPGVK |
| | | | | | | 998.18 | 2 | 2.78 | 231-239 | TIVM*GASFR |
| M3 | 3'(2'),5'-bisphosphate nucleotidase 1 | O95861 | 33.4 | 5.46 | 10.06 | 1151.34 | 2 | 3.98 | 11-21 | LVASAYSIAQK |
| | | | | | | 1243.43 | 2 | 4.16 | 29-40 | VIAEGDLGIVEK |
| | | | | | | 914.13 | 2 | 2.84 | 225-232 | IIQLIEGK |
| M4 | Poly(rC)-binding protein 1 | Q15365 | 37.5 | 6.66 | 16.85 | 1289.37 | 2 | 3.24 | 47-57 | INISEGNCPER |
| | | | | | | 925.13 | 2 | 2.25 | 71-78 | AFAM*IIDK |

| | | | | | | | | | | |
|-----|---|--------|------|------|-------|---------|---|------|---------|---------------------|
| M5 | Crk-like protein | P46109 | 33.8 | 6.26 | 7.59 | 1087.17 | 2 | 2.54 | 315-325 | IANPVEGSSGR |
| | | | | | | 1229.45 | 2 | 3.50 | 254-265 | TALALEVGDIVK |
| | | | | | | 1318.33 | 2 | 2.79 | 293-303 | IFDPQNPENE |
| M6 | Heterogeneous nuclear ribonucleoproteins A2/B1 | P22626 | 37.4 | 8.97 | 4.53 | 1800.00 | 2 | 4.85 | 23-38 | LFIGGLSFETTEESLR |
| | | | | | | 1928.18 | 2 | 4.47 | 22-38 | KLFIGGLSFETTEESLR |
| M7 | Heterogeneous nuclear ribonucleoproteins A2/B1 | P22626 | 37.4 | 8.97 | 11.90 | 1189.34 | 2 | 3.72 | 138-147 | IDTIEITDR |
| | | | | | | 1696.80 | 2 | 3.17 | 154-168 | GFGFVTFDHDPVVK |
| | | | | | | 941.03 | 2 | 2.25 | 193-200 | NNFAVGYR |
| M8 | Voltage-dependent anion-selective channel protein 2 | P45880 | 38.1 | 6.32 | 9.80 | 1722.92 | 2 | 3.22 | 263-278 | VNSSLIGVGYTQTLR |
| | | | | | | 1017.20 | 2 | 2.81 | 283-292 | LTLSALVDGK |
| | | | | | | 1415.52 | 2 | 2.03 | 224-235 | YQIDPDACFSAK |
| M9 | Voltage-dependent anion-selective channel protein 1 | P21796 | 30.6 | 8.63 | 7.80 | 1031.23 | 2 | 3.29 | 256-265 | LTLSALLDGK |
| | | | | | | 1960.99 | 2 | 5.74 | 34-52 | SENGLEFTSSGSANTETTK |
| M10 | Voltage-dependent anion-selective channel protein 1 | P21796 | 30.6 | 8.63 | 15.60 | 1529.68 | 2 | 3.53 | 96-109 | LTFDSSFSPNTGKK |
| | | | | | | 1214.35 | 2 | 3.32 | 163-173 | VTQSNFAVGKY |
| | | | | | | 1325.54 | 2 | 2.88 | 37-48 | GALPLDTVTFYK |
| M11 | Endoplasmic reticulum protein ERp29 | P30040 | 29.0 | 6.77 | 27.59 | 1248.32 | 2 | 2.61 | 60-69 | FDTQYPYGEK |
| | | | | | | 1321.51 | 2 | 2.43 | 113-122 | ESYPVYLFYR |
| | | | | | | 1609.72 | 2 | 3.64 | 123-137 | DGDFENPVYTGAVK |
| | | | | | | 1725.86 | 2 | 4.72 | 209-223 | ILDQGEDFPASEM*TR |
| | | | | | | 1135.34 | 2 | 3.65 | 244-253 | SLNILTAFAQK |
| | | | | | | 1069.24 | 2 | 2.84 | 5-16 | PVLSGSPGAGK |
| M12 | Guanylate kinase | Q16774 | 21.6 | 6.11 | 13.27 | 1675.78 | 2 | 3.85 | 44-57 | PGEENGKDYFVTR |
| | | | | | | 1069.24 | 2 | 3.39 | 5-16 | PVLSGSPGAGK |
| M13 | Guanylate kinase | Q16774 | 21.6 | 6.11 | 19.39 | 1675.78 | 2 | 4.23 | 44-57 | PGEENGKDYFVTR |
| | | | | | | 1387.60 | 2 | 3.71 | 96-107 | ICVLDVLDGVR |

| | | | | | | | | | | |
|-----|--|--------|------|------|-------|---------|---|------|---------|----------------------|
| M15 | Fatty acid-binding protein, epidermal | Q01469 | 15.0 | 6.80 | 21.64 | 1674.84 | 2 | 4.65 | 81-96 | TVEEAENIAVTSGVVR |
| | | | | | | 928.11 | 2 | 2.22 | 24-32 | ELGVGIALR |
| | | | | | | 1272.38 | 2 | 2.94 | 61-71 | TTQFSCTLGEK |
| | | | | | | 1026.04 | 2 | 2.25 | 72-80 | FEETTADGR |
| M16 | Arrestin-C | P36575 | 42.8 | 5.53 | 14.95 | 1402.72 | 2 | 3.74 | 48-58 | KLFVM*LTCAFR |
| | | | | | | 1654.85 | 2 | 4.47 | 59-72 | YGRDDLEVIQLTFR |
| | | | | | | 1654.75 | 2 | 3.41 | 145-158 | SFCAENPEETVSKR |
| | | | | | | 1952.20 | 2 | 4.11 | 167-185 | KVQFAPPEAGPGPSAQTIR |
| M17 | Arrestin-C | P36575 | 42.8 | 5.53 | 4.64 | 1824.03 | 2 | 4.66 | 168-185 | VQFAPPEAGPGPSAQTIR |
| M18 | Isocitrate dehydrogenase [NAD] subunit alpha | P50213 | 39.6 | 6.46 | 22.40 | 1607.90 | 2 | 2.90 | 101-115 | TPIAAGHPSM*NLLLR |
| | | | | | | 1392.58 | 2 | 3.70 | 135-146 | TPYTDVNIIVTIR |
| | | | | | | 975.13 | 2 | 2.74 | 170-178 | LITEGASKR |
| | | | | | | 1217.36 | 2 | 3.94 | 179-188 | IAEFAFEYAR |
| | | | | | | 1055.23 | 2 | 2.38 | 206-214 | M*SDGLFLQK |
| | | | | | | 1896.29 | 2 | 4.58 | 300-316 | DM*ANPTALLLSAVM*M*LR |
| | | | | | | 1124.30 | 2 | 3.03 | 327-336 | IEAACFATIK |
| M18 | Transaldolase | P37837 | 37.5 | 6.36 | 15.73 | 1051.20 | 2 | 2.54 | 11-19 | M*ESALDQLK |
| | | | | | | 1250.55 | 2 | 2.65 | 87-97 | LFVLFGAEILK |
| | | | | | | 1234.34 | 2 | 2.34 | 205-215 | SYEPLEDPGVK |
| | | | | | | 998.18 | 2 | 2.35 | 231-239 | TIVM*GASFR |
| | | | | | | 1393.60 | 2 | 3.77 | 246-258 | ALAGCDFLTISPK |
| M19 | Tropomyosin 1 alpha chain | P09493 | 32.7 | 4.69 | 14.79 | 1885.07 | 3 | 4.05 | 91-105 | RIQLVEEELDRAQER |
| | | | | | | 1977.23 | 3 | 5.13 | 134-149 | AQKDEEKM*EIQEIQLK |
| | | | | | | 1315.54 | 2 | 3.66 | 168-178 | KLVIIESDLR |
| M19 | Heterogeneous nuclear ribonucleoproteins C1/C2 | P07910 | 33.7 | 4.95 | 12.75 | 1317.60 | 2 | 3.87 | 18-29 | VFIGNLNLTLVK |
| | | | | | | 1330.47 | 2 | 3.69 | 51-61 | GFAFVQYVNER |
| | | | | | | 1700.00 | 2 | 5.06 | 74-89 | M*IAGQVLDINLAAEPK |
| M20 | Pyruvate dehydrogenase E1 component beta subunit | P11177 | 39.2 | 6.20 | 31.75 | | | | | |

| | | | | | | | | | | |
|-----|---|--------|------|------|-------|---------|---|------|---------|---------------------|
| | | | | | | 1803.01 | 2 | 3.07 | 53-68 | VFLGEEVAQYDGAYK |
| | | | | | | 1845.16 | 2 | 4.59 | 130-145 | TYYM*SGGLQPPIVFR |
| | | | | | | 1352.49 | 2 | 2.48 | 259-269 | EGVECEVINM*R |
| | | | | | | 1901.22 | 2 | 3.37 | 270-285 | TIRPM*DM*ETIEASVM*K |
| | | | | | | 1765.03 | 2 | 4.39 | 309-324 | IM*EGPAFNFLDAPAVR |
| | | | | | | 1265.46 | 2 | 3.43 | 325-336 | VTGADVPM*PYAK |
| | | | | | | 1256.43 | 2 | 3.25 | 337-347 | ILEDNSIPQVK |
| M21 | Glucose-6-phosphate 1-dehydrogenase | P11413 | 59.1 | 6.44 | 5.84 | | | | | |
| | | | | | | 1174.34 | 2 | 2.75 | 182-191 | LSNHISLFR |
| | | | | | | 1265.53 | 2 | 2.37 | 205-214 | EM*VQNLN*VLR |
| | | | | | | 1192.30 | 2 | 2.39 | 498-507 | VGFAQYEGTYK |
| M22 | Glucose-6-phosphate 1-dehydrogenase | P11413 | 59.1 | 6.44 | 9.73 | | | | | |
| | | | | | | 1139.33 | 2 | 2.58 | 95-103 | LKLEDFAR |
| | | | | | | 1174.34 | 2 | 3.07 | 182-191 | LSNHISLFR |
| | | | | | | 1265.53 | 2 | 2.35 | 205-214 | EM*VQNLN*VLR |
| | | | | | | 1274.41 | 2 | 3.75 | 246-256 | GGYFDEFIIR |
| | | | | | | 1192.30 | 2 | 2.42 | 498-507 | VGFAQYEGTYK |
| M23 | Glucose-6-phosphate 1-dehydrogenase | P11413 | 59.1 | 6.44 | 12.65 | | | | | |
| | | | | | | 1011.16 | 2 | 2.36 | 81-88 | KQSEPFK |
| | | | | | | 1174.34 | 2 | 2.91 | 182-191 | LSNHISLFR |
| | | | | | | 1265.53 | 2 | 2.24 | 205-214 | EM*VQNLN*VLR |
| | | | | | | 1274.41 | 2 | 3.44 | 246-256 | GGYFDEFIIR |
| | | | | | | 1944.13 | 3 | 3.81 | 370-385 | LQFHDVAGDIFHQCK |
| | | | | | | 1192.30 | 2 | 2.72 | 498-507 | VGFAQYEGTYK |
| M24 | 26S proteasome non-ATPase regulatory subunit 11 | O00231 | 47.3 | 6.09 | 23.04 | | | | | |
| | | | | | | 1517.58 | 2 | 4.24 | 33-45 | DIQENDEEAVQVK |
| | | | | | | 1401.63 | 2 | 3.41 | 46-58 | EQSILELGSLAK |
| | | | | | | 1158.33 | 2 | 3.13 | 59-70 | TGQAAELGLLK |
| | | | | | | 1324.55 | 2 | 3.14 | 71-81 | YVRPFLNSISK |
| | | | | | | 1086.26 | 2 | 2.30 | 132-140 | LVSLYFDTK |
| | | | | | | 1342.61 | 2 | 3.28 | 163-174 | ALLVEVQLLESK |
| | | | | | | 1731.99 | 2 | 4.86 | 258-273 | IM*LNTPEVDVQALVSGK |
| | | | | | | 1267.50 | 2 | 3.15 | 344-354 | VQIEHISLIK |
| M25 | Elongation factor Tu | P49411 | 49.5 | 7.26 | 10.62 | | | | | |
| | | | | | | 1674.84 | 2 | 4.58 | 105-120 | GITINAAHVFYSTAAR |

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|-----|---|--------|------|------|-------|---------|---|------|---------|---------------------------------|
| | | | | | | 1186.30 | 2 | 3.31 | 316-327 | AEAGDNLGALVR |
| | | | | | | 1150.35 | 2 | 3.50 | 352-361 | VEAQVYILSK |
| M26 | Elongation factor Tu | P49411 | 49.5 | 7.26 | 4.87 | | | | | |
| | | | | | | 1186.30 | 2 | 3.66 | 316-327 | AEAGDNLGALVR |
| | | | | | | 1150.35 | 2 | 3.14 | 352-361 | VEAQVYILSK |
| M27 | Alpha-centractin | P61163 | 42.6 | 6.19 | 8.78 | | | | | |
| | | | | | | 1868.04 | 2 | 4.98 | 239-255 | AQYYLPDGSTIEIGPSR |
| | | | | | | 1684.96 | 2 | 3.94 | 293-308 | TLFSNIVLGGSTLFLK |
| M28 | Heterogeneous nuclear ribonucleoproteins C1/C2 | P07910 | 33.7 | 4.95 | 16.01 | | | | | |
| | | | | | | 1317.60 | 2 | 3.56 | 18-29 | VFIGNLNTLVVK |
| | | | | | | 1124.27 | 2 | 3.16 | 30-39 | KSDVEAIFSK |
| | | | | | | 1330.47 | 2 | 4.23 | 51-61 | GFAFVQYVNER |
| | | | | | | 1700.00 | 2 | 4.11 | 74-89 | M* ¹ IAGQVLDINLAAEPK |
| M29 | Heterogeneous nuclear ribonucleoproteins C1/C2 | P07910 | 33.7 | 4.95 | 22.55 | | | | | |
| | | | | | | 1317.60 | 2 | 3.72 | 18-29 | VFIGNLNTLVVK |
| | | | | | | 996.10 | 2 | 2.73 | 31-39 | SDVEAIFSK |
| | | | | | | 1330.47 | 2 | 4.45 | 51-61 | GFAFVQYVNER |
| | | | | | | 1700.00 | 2 | 5.44 | 74-89 | M* ¹ IAGQVLDINLAAEPK |
| | | | | | | 1229.45 | 2 | 3.27 | 188-198 | LKGDDLQAIKK |
| | | | | | | 1160.30 | 2 | 3.51 | 207-216 | VDSLLENLEK |
| M30 | Heterogeneous nuclear ribonucleoprotein H3 | P31942 | 36.9 | 6.37 | 11.27 | | | | | |
| | | | | | | 1272.39 | 2 | 3.88 | 56-67 | STGEAFVQFASK |
| | | | | | | 1920.12 | 2 | 4.95 | 206-222 | ATENDIANFFSPLNPIR |
| | | | | | | 1053.15 | 2 | 2.76 | 223-232 | VHIDIGADGR |
| M31 | Voltage-dependent anion-selective channel protein 1 | P21796 | 30.6 | 8.63 | 19.50 | | | | | |
| | | | | | | 1960.99 | 2 | 4.52 | 34-52 | SENGLEFTSSGSANTETTK |
| | | | | | | 1401.50 | 2 | 4.13 | 96-108 | LTFDSSFSPNTGK |
| | | | | | | 1214.35 | 2 | 3.33 | 163-173 | VTQSNFAVGYK |
| | | | | | | 1415.52 | 2 | 3.13 | 224-235 | YQIDPDACFSAK |
| M31 | Esterase D | P10768 | 31.5 | 6.54 | 4.61 | | | | | |
| | | | | | | 1402.53 | 2 | 4.63 | 186-198 | KAFSGYLGTDQSK |
| M32 | Pyruvate kinase, isozymes M1/M2 | P14618 | 57.8 | 7.95 | 33.21 | | | | | |
| | | | | | | 1198.35 | 2 | 3.32 | 32-42 | LDIDSPPIAR |
| | | | | | | 1360.53 | 2 | 3.86 | 43-55 | NTGIICTIGPASR |
| | | | | | | 1885.03 | 3 | 4.35 | 73-88 | LNFSHGTHEYHAETIK |

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|-----|--|--------|------|------|-------|---------|---|------|---------|--------------------|
| | | | | | | 914.08 | 2 | 2.85 | 106-114 | PVAVALDTK |
| | | | | | | 1214.37 | 2 | 2.87 | 141-150 | ITLDNAYM*EK |
| | | | | | | 1463.70 | 2 | 4.50 | 173-185 | IYVDDGLISLQVK |
| | | | | | | 1780.91 | 2 | 6.10 | 188-205 | GADFLVTEVENGGSLGSK |
| | | | | | | 1766.03 | 2 | 4.67 | 206-223 | KGVNLPGAAVDLPVSEK |
| | | | | | | 1682.88 | 2 | 4.25 | 279-293 | FDEILEASDGIM*VAR |
| | | | | | | 1142.28 | 2 | 3.10 | 294-304 | GDLGIEIPA EK |
| | | | | | | 1020.12 | 2 | 2.56 | 367-375 | GDYPLEAVR |
| | | | | | | 996.17 | 2 | 2.76 | 489-497 | VNFAM*NVGK |
| | | | | | | 1084.19 | 2 | 3.01 | 516-525 | PGSGFTNTM*R |
| M33 | Pyruvate kinase, isozymes M1/M2 | P14618 | 57.8 | 7.95 | 29.43 | | | | | |
| | | | | | | 1360.53 | 2 | 4.10 | 43-55 | NTGIICTIGPASR |
| | | | | | | 1571.71 | 2 | 4.07 | 92-105 | TATESFASDPILYR |
| | | | | | | 914.08 | 2 | 2.69 | 106-114 | PVAVALDTK |
| | | | | | | 1214.37 | 2 | 3.10 | 141-150 | ITLDNAYM*EK |
| | | | | | | 1463.70 | 2 | 4.43 | 173-185 | IYVDDGLISLQVK |
| | | | | | | 1780.91 | 2 | 5.94 | 188-205 | GADFLVTEVENGGSLGSK |
| | | | | | | 1637.86 | 2 | 4.16 | 207-223 | GVNLPGAAVDLPVSEK |
| | | | | | | 954.02 | 2 | 2.69 | 270-277 | IENHEGVR |
| | | | | | | 1682.88 | 2 | 3.17 | 279-293 | FDEILEASDGIM*VAR |
| | | | | | | 1142.28 | 2 | 3.04 | 294-304 | GDLGIEIPA EK |
| | | | | | | 1020.12 | 2 | 2.57 | 367-375 | GDYPLEAVR |
| | | | | | | 996.17 | 2 | 2.90 | 489-497 | VNFAM*NVGK |
| | | | | | | 1084.19 | 2 | 2.89 | 516-525 | PGSGFTNTM*R |
| M34 | Aspartate aminotransferase | P17174 | 46.1 | 6.57 | 8.74 | | | | | |
| | | | | | | 1357.54 | 2 | 3.39 | 86-98 | LALGDDSPALKEK |
| | | | | | | 1428.62 | 2 | 4.00 | 99-113 | RVGGVQSLGGTGALR |
| | | | | | | 1013.09 | 2 | 2.45 | 259-266 | NFGLYNER |
| M35 | Heterogeneous nuclear ribonucleoproteins A2/B1 | P22626 | 37.4 | 8.97 | 9.92 | | | | | |
| | | | | | | 1058.21 | 2 | 2.21 | 4-12 | TLETVPLER |
| | | | | | | 1800.00 | 2 | 4.67 | 23-38 | LFIGGLSFETTEESLR |
| | | | | | | 1189.34 | 2 | 2.67 | 138-147 | IDTIEITDR |
| M36 | Heterogeneous nuclear ribonucleoproteins A2/B1 | P22626 | 37.4 | 8.97 | 9.92 | | | | | |
| | | | | | | 1058.21 | 2 | 2.28 | 4-12 | TLETVPLER |
| | | | | | | 1800.00 | 2 | 4.67 | 23-38 | LFIGGLSFETTEESLR |

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|-----|--|--------|------|------|-------|---------|---|------|---------|------------------|
| M37 | Heterogeneous nuclear ribonucleoproteins A2/B1 | P22626 | 37.4 | 8.97 | 7.37 | 1800.00 | 2 | 4.40 | 23-38 | LFIGGLSFETTEESLR |
| | | | | | | 1189.34 | 2 | 2.81 | 138-147 | IDTIEITDR |
| M38 | Heterogeneous nuclear ribonucleoproteins A2/B1 | P22626 | 37.4 | 8.97 | 7.37 | 1800.00 | 2 | 4.06 | 23-38 | LFIGGLSFETTEESLR |
| | | | | | | 1189.34 | 2 | 2.99 | 138-147 | IDTIEITDR |
| M39 | Phosphoglycerate mutase 1 | P18669 | 28.7 | 6.75 | 8.30 | 1060.19 | 2 | 2.48 | 90-99 | HYGGLTGLNK |
| | | | | | | 1151.34 | 2 | 3.16 | 180-190 | VLIAAHGNSLR |
| M40 | Superoxide dismutase [Mn] | P04179 | 24.7 | 8.35 | 10.36 | 1425.66 | 2 | 3.68 | 76-89 | GDVTAQIALQPALK |
| | | | | | | 1029.22 | 2 | 2.59 | 115-123 | GELLEAIKR |