|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Spot** | **Entry UniProt** | **Name** | **MWt/MWe** | **pIt/pIe** | **Coverage** | **Protein score** | **Peptide sequence** |
| **10** | C0H6F9 | Putative cuticle protein | 28335/36000 | 4.63/4.3 | 49.6% | 545 | WQALDALKTVADVEASAKAADLAQAAADKSIATQPPVEEVKTAEAQLDGAVASQAVQLAKAVVNTNLAQEQAVDGVWAVEDKKSAVGAAPYVVAPVFPVVYPGIASPAIKTSAVESDAQTSGVLGAGHISTIQGAIATK |
| **31** | C0H6F9 | Putative cuticle protein | 28335/36000 | 4.63/4.5 | 59.6% | 1733 | WQALDALKTVADVEASAKAADLAQAAADKKWQALDALKSIATQPPVEEVKVEGNTDSVAVEAKAIAINEQNAENYNVKTAEAQLDGAVASQAVQLAKAVVNTNLAQEQAVDGVWAVEDKSAVGAAPYVVAPVFPVVYPGIASPAIKTSAVESDAQTSGVLGAGHISTIQGAIATK |
| **32** | B9VTR5 | 32 kDa apolipoprotein | 32299/34000 | 4.79/4.6 | 51.2% | 1625 | FFTVSELGSRQIIDEVVQERLMEGSLQMIGRFLGTWYEAEREKEPVEDSDSVKCVTTNYVSTPEGREKEPVEDSDSVKKIIVSNEIVNSLTGMKRERLPSLMAMQNAYAVLDRTNQADCTILPDPVAIPIEAKSAVPEISFEPKPVPVPEMILTENEK |
| **39** | Q8T8B2 | Tubulin beta chain | 50638/52000 | 4.75/4.8 | 33.8% | 1414 | YLTVAAIFRFPGQLNADLRLAVNMVPFPRISEQFTAMFRFPGQLNADLRKKLAVNMVPFPRINVYYNEASGGKIMNTYSVVPSPKEVDEQMLNIQNKAILVDLEPGTMDSVRLHFFMPGFAPLTSRLHFFMPGFAPLTSRALTVPELTQQMFDAKNSSYFVEWIPNNVKEIVHIQAGQCGNQIGAK |
| Q8I9N4 | Masquerade-like serine proteinase homolog | 46764/52000 | 4,96/4,8 | 40% | 633 | ERAPAGVRNPDGVAFRVDVPVVDRCFATGWGKNTCQSQLRTTGDVDGETKKVDVPVVDREIYPYQDRTWIDDKVAGKAGEWDTQNTKNTCQSQLRREIVIHKDFNKFGEFPWMVAILKVEPVDDNEPEGQKGDGGSPLVCPIDYEK |
| **49** | B9VTR5 | 32 kDa apolipoprotein | 32299/22000 | 4.79/4.9 | 27.4% | 1981 | FFTVSELGSRLMEGSLQMIGRFLGTWYEAERRLMEGSLQMIGRCVTTNYVSTPEGRIIVSNEIVNSLTGMKLPSLMAMQNAYAVLDRERLPSLMAMQNAYAVLDR |
| **54** | Q8T113 | 27 kDa glycoprotein | 25571/23000 | 5.12/5.1 | 56.4% | 1387 | TCFLNLKGLVDLNVLKDSPCHTALPKVDEMTSCIVKNNAEDKVPEVEAALRIALFIAEGGPECFQQKQSFPTVESANNLSLVEKTEIEEAKPNGALDEVFKKSLEECSTPTPANMAESLIK |
| **67** | Q03383 | Antichymotrypsin-1 | 44715/40000 | 5.21/5 | 29.5% | 458 | LADAFSRNAADIINRNDQVVVSRAFQEAFVKDIELEIPKIYVSDQYKSGLDLNTILPKSEVDNINFSAPKGLLEDVFNLSPAGRMIELPYKEPGFRDIELEIPKFEIRMVVVLPDKIDGLPAVLEK |
| **81** | H9JP12 | Sex-specific storage-protein 1 | 88007/82000 | 5.28/5 | 22.5% | 689 | EGILTGKTVDAVVRDFDVFMRDLGMSNTSKDLGMSNTSKFADVMIYREQFSFPGVKSEDIENLARTSDMTFMARVIHLTNLMKEPMVNLDMKVIHLTNLMKEPMVNLDMKLPSGDEMPVRVCNIFTVFKIRLPSGDEMPVRLVLGGLEIVGDDAKSCDKYMNVDVVKRGEIMMYANQQLLARSSMDMQGFIPEYLSTR |
| **90** | H9IXK0 | Antichymotrypsin-1 | 41893/45000 | 5.14/5.2 | 60.2% | 2417 | LGDAIDKTPVSEDKLADAFSRFLTVANKYAEFDPKNAADIINRDFHVDEKMIELPYKMVVVLPDKNDQVVVSRAFQEAFVKDIELEIPKTRLGDAIDKILFAGTHTHIYVSDQYKESYNLADDKIDGLPAVLEKLGDAIDKTSLKIFQEPAPGIVKWADEQTQGHIKGLLEDVFNLSPAGRMIELPYKEPGFRDIELEIPKFEIRVDHPFLFLILHEDKLLQSLFYTENEELGAKMVVVLPDKIDGLPAVLEKIFQEPAPGIVKNDQVVVSREILGGGEAQESSHTYGLLNQRVDHPFLFLILHEDKILFAGTHTH |
| **95** | C4PAW6 | Hemolin | 45335/50000 | 5.12/5.2 | 80.2% | 4911 | SDFGVASTREAPAEVLFRDGVNVDNTYKTYIETPAFEEKVTVVEGKPFELRDGVNVDNTYKDRASDEGEYQCFAKTYIETPAFEEKKRTYIETPAFEEKKVTVVEGKPFELRTLATQGEDVTIPCKRTYIETPAFEEKKRTLATQGEDVTIPCKHHDEDGSTENFMDRHHDEDGSTENFMDRRCPVPGGYPKPTISWMRLECATEGDDSGVEYSWRLECATEGDDSGVEYSWRKEVWAEDAGTYTCDVDNQAGRLQHTITFSVVSAPTFTTKPEKEVWAEDAGTYTCDVDNQAGRRRLQHTITFSVVSAPTFTTKPEKLQHTITFSVVSAPTFTTKPEKRVGDLTYLYCIYGGTPLAHPSWSKLVIKEVWAEDAGTYTCDVDNQAGRDGMHFSVGQDTLTTIDAGSLVFTQTKSNQGYYGCTASNEHGAEYAETALQVALVIKEVWAEDAGTYTCDVDNQAGRRKDGMHFSVGQDTLTTIDAGSLVFTQTKATGIPSPLVSWTYNGEPVTEGVTGDGLVIKLVCMASSPAADEGVPIVTYYITQVTPASEPTYGELIPQYLSDHVVAK |
| **98** | Q9GQC4 | Chitinase | 61886/65000 | 5.01/5.2 | 41% | 1270 | SVVDFLKKWDEFGKSVVDFLKKYSHMVAQKLVVGIPFYGRGLCGEENPLIKHMSTYTVPPARGTQWVGYEDPRRPHDQWAYEKFMVAVGGWAEGGSKLNVNDGLNLWEEKGWELTAAVPLANFRGNWAGFADVHSPLYKSSEVLIIDPELDVDKADRGWELTAAVPLANFRSFTLSAGNNNYGLGTYINKIVCYFSNWAVYRPGVGRGGSFSDKDEFLYFVQELKKYDFDGLDLDWEYPGAADRGGSFSDKDEFLYFVQELKR |
| **100** | I6XKQ0 | Heat shock protein 70-5 | 75536/80000 | 5.84/5.7 | 22.5% | 623 | NTTIPTKDQGIDIRLFEQAYKAAEQFAAADKALQDAEVQRDAGQISGLNVLRTATGQLQQASLKVQQTVQEIFGRSKLESLVGDLIRSDIGEVLLVGGMTRVYSPSQIGAFVLIKMKETAEAYLNTSVKVEVANQAEAVLHDTDTK |
| H9IXK0 | Heat shock cognate protein | 71359/80000 | 5,33/5,7 | 17.4% | 354 | NTTIPTKLLQDFFNGKDAGTISGLNVLRVEIIANDQGNRAQIHDIVLVGGSTRARFEELNADLFRTTPSYVAFTDTERIINEPTAAAIAYGLDKKTVQNAVITVPAYFNDSQR |
| **103** | Q8WR52 | Chitinase | 64280/65000 | 5.14/5.2 | 31.4% | 576 | SVVDFLKKWDEFGKLVVGIPFYGRFLYFVQELKGLCGEENPLIKHMSTYTVPPARRPHDQWAYEKFLYFVQELKRLNVNDGLNLWEEKGWELTAAVPLANFRGNWAGFADVHSPLYKSSEVLIIDPELDVDKSFTLSAGNNNYGLGTYINKIVCYFSNWAVYRPGVGRKYDFDGLDLDWEYPGAADR |
| **111** | Q2QEH2 | Cellular retinoic acid binding protein | 14963/65000 | 5.66/5.2 | 76.5% | 1760 | TIGVGLITREFGPEEMKTIGVGLITRKAPDGLEVTYVRAANAVTPTVELRSVCTFEGNTLKAANAVTPTVELRKKAANAVTPTVELRFKPGEEFEEDRMTSSENFDEFMKKAANAVTPTVELRKDGDEYNLVTSSTFKQVQKAPDGLEVTYVRKDGDEYNLVTSSTFKYKMTSSENFDEFMKFKPGEEFEEDRADGAK |
| **124** | Q27309 | Vitellogenin | 203725/40000 | 6.85/6 | 10.5% | 1087 | ELPVDLKEQQQGLFRTQEQQLIGRYQPTPNIDKVFEIEIDGGRVIHDSQNNYDRFANEQDPVEVTKGLISALQLDTSAHRTLAHLQEGPSSGSAFKAETTSTVHVHPHLYGKLENPQHGNFNEQLPDPRVAYHFGVPVGAEWTGTAHKIVSLDFPTSVPVPQENLIKYQPTPNIDKVFEIEIDGGRFSSQSQSTGGQTYPSPWQVGKVIHDSQNNYDREQQQGLFR |
| **126** | H9IXK0 | Antichymotrypsin-1 | 41893/45000 | 5.14/5.1 | 57.6% | 2062 | LGDAIDKTPVSEDKLADAFSRFLTVANKYAEFDPKNAADIINRMVVVLPDKMIELPYKNDQVVVSRAFQEAFVKDIELEIPKTRLGDAIDKILFAGTHTHIYVSDQYKESYNLADDKIDGLPAVLEKLGDAIDKTSLKIFQEPAPGIVKWADEQTQGHIKGLLEDVFNLSPAGRMIELPYKEPGFRDIELEIPKFEIRLLQSLFYTENEELGAKMVVVLPDKIDGLPAVLEKIFQEPAPGIVKNDQVVVSREILGGGEAQESSHTYGLLNQREEIREILGGGEAQESSHTYGLLNQR |
| **135** | Q2F5Y9 | Mitochondrial aldehyde dehydrogenase | 53127/54000 | 5.57/5.7 | 31.1% | 696 | VLNYIVAGKADIDLAVAAAKLAELLESQSRTYVQSGIYDKFETFDEVVDRIILGAASAVNLKREEIFGPVQSILKSPLVVFNDADVEKLFINNEWVDAVSKELGEDGISQYLETKLFINNEWVDAVSKKIAREEIFGPVQSILKYLAELETLDCGKPVKILGNTIPSDGEVLTFTMK |
| **141** | P49010 | Chitooligosaccharidolytic beta-N-acetylglucosaminidase | 68968/60000 | 5.17/5.7 | 39.3% | 1871 | AAAFAERLGAYSPTKNNLLIVRGILLDTARGNSFFGVRTLVSSSVPKTIDAMAAVKWTCENNRLWNYFQKDRPVYPYRNFYSIDSIKEPVLSLEACKSDDLLTAAADRWNLDKSSFLKNFYSIDSIKRINMNTIDIQITKSDDLLTAAADRFKVYGNSPAVMALSYRMWAEPSTAWQDAEHRNEPENKEPVLSLEACKIRNEPENKEPVLSLEACKRLPLILWTSTLTDYTHVEKLNTFHWHITDSQSFPLVLQKVLPEFDAPAHVGEGWQDTGLTVCFK |
| H9J8Q7 | Beta-hexosaminidase | 61914/60000 | 5.33/5.3 | 44.5% | 1836 | AAAFAERLGAYSPTKNNLLIVRGILLDTARGNSFFGVRTLVSSSVPKTIDAMAAVKLWNYFQKDRPVYPYRNFYSIDSIKSDDLLTAAADRWNLDKSSFLKNFYSIDSIKRINMNTIDIQITKSDDLLTAAADRFKVYGNSPAVMALSYRSVTVYLVNDNPYIRMWAEPSTAWQDAEHRHGLETLSQLIVYDDIRLPLILWTSTLTDYTHVEKRLPLILWTSTLTDYTHVEKLNTFHWHITDSQSFPLVLQKVLPEFDAPAHVGEGWQDTGLTVCFKWTCENNR |
| **144** | Q1HPP4 | Arylphorin | 83569/80000 | 5.7/6 | 53.9% | 1925 | LTNGLGKLTAGQNKAVEEFLKLYFDGVKSYEVFARIDFHDPKVPNMYFKFLDTYEKITDVKVDKDFETFYKTFVQFLQKNVDAVFVEKENDYFVYKDHFEAFGQKNSNEFVIFKIVEYIVEFKVLGAAPMPFDKTGYYPLMLTKNLEFSVFYDKDIFIYHEGEREDSVPMTEIMKQYLKPYTQDKDPAFYQLYNRRVLGAAPMPFDKMFMNMEVLQKFFELDWFTTKIPEFSWYSPIKFNIPSYDTQSNVVPKDIFIYHEGERFPYKDYDIEMNMDNYTNKKYDDNGIPLTLEDNWMKSDCHGFVVPAPYEVYPKIGKDYDIEMNMDNYTNKKILSFFQDVSQLNTDDEYYKNSNEFVIFKEDSVPMTEIMKAINFVGNYWQDNADLYGEEVTKFTPFAQRPDYYNLHTEENYER |
| H9JP12 | Sex-specific storage-protein 1 | 88007/80000 | 6.78/6 | 43.9% | 2164 | EGILTGKTVDAVVRLMSVNDKDGTVISLKDFDVFMRDGTVISLKKYMNVDVVKDLGMSNTSKQFMEMYKQNNMVVATKAAKDPVLWKFADVMIYREQFSFPGVKSEDIENLARTSDMTFMARVIHLTNLMKLPSGDEMPVREPMVNLDMKVCNIFTVFKFADVMIYRKDPVFWMIMKKSEDIENLARIRLPSGDEMPVRMLSYGQYNMDKEQFSFPGVKVEKLVLGGLEIVGDDAKQMMDDVEMMIRLDMFELDSFMYKRLDMFELDSFMYKRGEIMMYANQQLLARLLDHILQPTMFEDIKLNHHPFQVSIDVMSDKSSMDMQGFIPEYLSTRGETFVHTNELQMEEAVKLLDHILQPTMFEDIKEIAK |
| P20613 | Sex-specific storage-protein 2 | 83698/80000 | 6.04/6 | 48.4% | 1785 | LTNGLGKLTAGQNKAVEEFLKLYFDGVKSYEVFARIDFHDPKFLDTYEKITDVKVDKDFETFYKTFVQFLQKNVDAVFVEKENDYFVYKDHFEAFGQKNSNEFVIFKIVEYIVEFKVLGAAPMPFDKTGYYPLMLTKSKNVDAVFVEKNLEFSVFYDKMFMNMEVLQKEDSVPMTEIMKQYLKPYTQDKDPAFYQLYNRRVLGAAPMPFDKFFELDWFTTKIPEFSWYSPIKMQHGLINPEAAAKDYDIEMNMDNYTNKKYDDNGIPLTLEDNWMKIGKDYDIEMNMDNYTNKKILSFFQDVSQLNTDDEYYKNSNEFVIFKEDSVPMTEIMKAINFVGNYWQDNADLYGEEVTKFTPFAQRPDYYNLHTEENYER |
| **152** | Q1HPP5 | Actin-depolymerizing factor 1 | 17227/18000 | 6.17/6 | 81.8% | 1219 | SLVGVQKGGTGECRKSLVGVQKTTYEEIKYVVFYIRTTYEEIKKQIDVETVGERMLYSSSFDALKYVVFYIRDEKMLYSSSFDALKKLFLMSWCPDTAKKMLYSSSFDALKKNAEYEQFLEDLQKYIQATDLSEASQEAVEEKYIQATDLSEASQEAVEEKLRYGLFDFEYTHQCQGTSEASKYGLFDFEYTHQCQGTSEASKK |
| **157** | Q5CCJ4 | Glutathione S-transferase sigma | 23382/23000 | 5.85/6.2 | 71.1% | 1237 | ALGESQRLNEILTKAYVDAAPRNNGHIALGKFYYFPVKYPFFFEKASAASVHYEKKPIEAVLAIPKQYAQSTAICRAMLQKPDLEQKISSENWPEFKPKTPFGQMPVLEIDGKASAASVHYEKDEAVKLLLAYGGQEFEDNRAELEETKYPFFFEKKAELEETKYPFFFEKAMLQKPDLEQKYPAFR |
| **158** | Q5CCJ4 | Glutathione S-transferase sigma | 23382/23000 | 5.85/5.8 | 67.2% | 1177 | ALGESQRLNEILTKNNGHIALGKFYYFPVKYPFFFEKASAASVHYEKKPIEAVLAIPKQYAQSTAICRAMLQKPDLEQKISSENWPEFKPKTPFGQMPVLEIDGKASAASVHYEKDEAVKLLLAYGGQEFEDNRAELEETKYPFFFEKKAELEETKYPFFFEKAMLQKPDLEQKYPAFR |
| **167** | Q2F5T5 | Arginine kinase | 40308/40000 | 5.87/5.9 | 60.6% | 1841 | LQGSDSKLEAGFSKLEEVASKEVFDSLKKLEEVASKGIYHNENKFLQAANACRLVSAVNEIEKMGLTEYDAVKKIPFSHHDRGTFYPLTGMSKLVSAVNEIEKKEMYDGIAELIKVSGTLSSLEGELKGEHTEAEGGVYDISNKIISMQMGGDLQQVYKTFLVWCNEEDHLRETQQQLIDDHFLFKLGFLTFCPTNLGTTVRIISMQMGGDLQQVYKREMEDKVSGTLSSLEGELKGTRGEHTEAEGGVYDISNKNWGDVDTLGNLDPAGEFVVSTRMGLTEYDAVKEMYDGIAELIK |
| **172** | Q27309\* | Vitellogenin(light chain) | 40203/40000 | 6.85/6.3 | 65.6% | 3021 | ELPVDLKEQQQGLFRTQEQQLIGRYQPTPNIDKVFEIEIDGGRSTNYGHCHHRVIHDSQNNYDRFANEQDPVEVTKGLISALQLDTSAHRTLAHLQEGPSSGSAFKAETTSTVHVHPHLYGKELPKFANEQDPVEVTKLENPQHGNFNEQLPDPRVAYHFGVPVGAEWTGTAHKIVSLDFPTSVPVPQENLIKYQPTPNIDKVFEIEIDGGRFSSQSQSTGGQTYPSPWQVGKVIHDSQNNYDREQQQGLFREGPIYKAETTSTVHVHPHLYGKMETDVTGDCETLYTVSPVASEWRKMETDVTGDCETLYTVSPVASEWRKMETDVTGDCETLYTVSPVASEWRR |
| **173** | Q27309\* | Vitellogenin (light chain) | 40203/40000 | 6.85/6.3 | 71.3% | 2861 | ELPVDLKEQQQGLFRTQEQQLIGRYQPTPNIDKVFEIEIDGGRSTNYGHCHHRVIHDSQNNYDRFANEQDPVEVTKGLISALQLDTSAHRTLAHLQEGPSSGSAFKAETTSTVHVHPHLYGKELPKFANEQDPVEVTKLENPQHGNFNEQLPDPRVAYHFGVPVGAEWTGTAHKIVSLDFPTSVPVPQENLIKYQPTPNIDKVFEIEIDGGRFSSQSQSTGGQTYPSPWQVGKVIHDSQNNYDREQQQGLFRMETDVTGDCETLYTVSPVASEWRAEVYSHVHMELISVDQDSGAEWPRKMETDVTGDCETLYTVSPVASEWRKMETDVTGDCETLYTVSPVASEWRRQKAEVYSHVHMELISVDQDSGAEWPR |
| **180** | H9J859 | Fascin | 57239/55000 | 6.25/6.5 | 39.3% | 967 | YLNAGGKINANGTSLKCEQGFVGPKGYFLGSSSDKYALHTCNNKYLTAETFGFKANYETIQVVRDGSGAYLAPIGSKGWWTIGLINSRFHISVSDDNSGRLADADLASATHWEYGYFLGSSSDKLTCTAKYYFYLINRPILVLKDELFSLEDSLPQAAFVAALNDKYLAVDSFGNVTCESEEKEPGSKLQDTCTSECLFSAEYHAGALALR |
| **181** | H9JLS3 | Dynein heavy chain 2, axonemal-like | 386433/60000 | 6.42/6.5 | 6% | 759 | TPSTAPKTLLSEVERESNLEAERLAAFDLGLKGSVLAYLSRDLGNDCYKNLNMEDERLLESGLIALHKGSVLAYLSRILQGMQQPSKTVSLNPNWSKEFDNAITHYEKAENYEAALEDAEKLEPTNQQLAQGLRGNDALVNQNFDEAIKALELDPSNAEALEGYRKGNDALVNQNFDEAIKLAAFDLGLKDCEQCCKAMSDPEVQQILRDPAMRAYIDPVKAEQEKELGNEYFK |
| **186** | H9JGR2 | Chitinase precursor | 61037/58000 | 5.58/5.9 | 66.4% | 4098 | QANTGLKIQVVNYKDRFVASVKDFLQTWKGANPDLGSPKLVVGVAMYGRYLLTQGVQPKGNFGQLMQLKDGDVYVQLMKGLSSWNEPYKKLVVGVAMYGRETYTTDFGIREIEGSFQALQRGTWQDGVVDYRQMLDELAAETGREVWSGAGSATSAAFKTYELTSAISAGWDKFVASVKDFLQTWKVVGAYFVEWGVYPRYMDHIFVMSYDFKVSIHDPWAALQKPQKFFDGVDIDWEFPGGKELRQMLDELAAETGRDRFVASVKDFLQTWKEIVNGITSGTWQYFYDKGANPDLGSPKDGDVYVQLMKTFAIVEVNQAATAYNQLVTKEAQKYMDHIFVMSYDFKEDFKVSIHDPWAALQKPQKVLPSIGGWTLADPFFFFTDKGLSSWNEPYKGNFGQLMQLKTFAIVEVNQAATAYNQLVTKKTYELTSAISAGWDKIQVVNYKVAQAPYVWNPTTGDLVTYDDARGWTGVHDYNDDIPFTGVANGPVKVPVPNLTHLLYGFIPICGGDGINDSLK |
| **190** | Q17219 | Egg-specific protein | 63545/60000 | 6.14/6.3 | 71.2% | 3745 | MIAPTSKIPPTHQTRLQENLPNVKYNYGAETNMKTWDHFTDDAKNTFHDAISETQRQYGQNVASHDFREVDINHGDSVVWKVYGASEPPSYDLSKFYQYIHDQVGHGAFEPGKSLAYMLSDAGYDVWLGNVRVSAPVNLYHSHDAWLAHPKQSFEVPEQQHFTDLDFQFSKKKPVALLMHGLLGSADDWLLMGPSKFSNDEIALHDLPAIIDHVLDISGQERNIEMASGPNSPVQTEQDIEDIFGDSLKAPDTVYQKKAPDTVYQKHPALNDFWKHHSPVYSVIMKHLIETFGGAACRTWDHFTDDAKKDVEKLQENLPNVKKNTFHDAISETQRIVSMHALSPIVYMNYVRQSFEVPEQQHFTDLDFQFSKHQYPVEEHTVATDDGYHLTVLRKHQYPVEEHTVATDDGYHLTVLRLHYIGHSQGATTFFALMSEQPSYNEKHVCNNLNYVISGINVYNQDADIVPVVMAHLPAGTSAR |
| **191** | Q17219 | Egg-specific protein | 63545/60000 | 6.14/6.2 | 78.5% | 4668 | APDTVYQKHPALNDFWKHHSPVYSVIMKHLIETFGGAACRTWDHFTDDAKKNTFHDAISETQREVDINHGDSVVWKDVEKLQENLPNVKKNTFHDAISETQRVMKQYGQNVASHDFRSLAYMLSDAGYDVWLGNVRHQYPVEEHTVATDDGYHLTVLRKHQYPVEEHTVATDDGYHLTVLRKKPVALLMHGLLGSADDWLLMGPSKFSNDEIALHDLPAIIDHVLDISGQERNIEMASGPNSPVQTEQDIEDIFGDSLKLHYIGHSQGATTFFALMSEQPSYNEKFYQYIHDQVGHGAFEPGKHLIETFGGAACRHVCNNLNYVISGINVYNQDADIVPVVMAHLPAGTSARMIAPTSKIPPTHQTRKAPDTVYQKLQENLPNVKLMENMQNNSYNYGAETNMKTWDHFTDDAKKYNYGAETNMKQYGQNVASHDFRVYGTSEPPSYDLSKQYGQNVASHDFRKSHVSKHPALNDFWKIVSMHALSPIVYMNYVRFYQYIHDQVGHGAFEPGKVSAPVNLYHSHDAWLAHPKQSFEVPEQQHFTDLDFQFSKKPVALLMHGLLGSADDWLLMGPSKVSAPVNLYHSHDAWLAHPKDVEKQHSQDDIIQHPLDYVEQQIHQQK |
| **195** | Q1HPP4 | Arylphorin | 83569/80000 | 5.7/6.5 | 74.1% | 3186 | LTNGLGKLTAGQNKAVEEFLKLYFDGVKIDFHDPKSYEVFARVPNMYFKFLDTYEKITDVKVDKDFETFYKKAVEEFLKTFVQFLQKNVDAVFVEKENDYFVYKDHFEAFGQKNSNEFVIFKIVEYIVEFKVLGAAPMPFDKTGYYPLMLTKTKNVDAVFVEKNLEFSVFYDKDIFIYHEGEREDSVPMTEIMKQYLKPYTQDKDPAFYQLYNRRVLGAAPMPFDKMFMNMEVLQKFFELDWFTTKMQDGLINPEAAAKIPEFSWYSPIKEEIKNNHVHDVKYGIHKENDYFVYKDEAIALFHLFYYAKFNIPSYDTQSNVVPKDIFIYHEGERFPYKDYDIEMNMDNYTNKKYDDNGIPLTLEDNWMKRGEVYFYFYQQLLARSDCHGFVVPAPYEVYPKMRDEAIALFHLFYYAKIGKDYDIEMNMDNYTNKTFVQFLQKDHFEAFGQKIGKDYDIEMNMDNYTNKKGTEGGFPFQLFVFVYPFDNKILSFFQDVSQLNTDDEYYKNSNEFVIFKEDSVPMTEIMKMLDEGKVPFDMSEEFCYMPKKILSFFQDVSQLNTDDEYYKLNHSPFNVNIEVDSNVASDAVVKMLDEGKVPFDMSEEFCYMPKAINFVGNYWQDNADLYGEEVTKFTPFAQRPDYYNLHTEENYERAINFVGNYWQDNADLYGEEVTKDYQRDLAPFESFVLDNKPLGFPLDRPVVDALFKGKDLAPFESFVLDNKPLGFPLDRPVVDALFK |
| P09179 | Sex-specific storage-protein 1 | 87890/80000 | 6.78/6.5 | 67.3% | 5231 | EGILTGKTVDAVVRLMSVNDKDGTVISLKDFDVFMRDGTVISLKKLMSVNDKRDLGMSNTSKQFMEMYKYMNVDVVKQNNMVVATKAAKDPVLWKFADVMIYREQFSFPGVKSEDIENLARMKELCIMKVIHLTNLMKTSDMTFMAREPMVNLDMKLPSGDEMPVRVCNIFTVFKFADVMIYRKDPVFWMIMKKSEDIENLARVIHLTNLMKKTVDTSEMVMMKMLSYGQYNMDKIRLPSGDEMPVREQFSFPGVKVEKQMMDDVEMMIRLVLGGLEIVGDDAKSCDKYMNVDVVKKMLSYGQYNMDKDDLTYLDSDMLVKLDMFELDSFMYKTGMLLPTLDMTMMKVLYYAKDFDVFMRMKQMMDDVEMMIRRLDMFELDSFMYKLLDHILQPTMFEDIKRGEIMMYANQQLLARVMESEMMPSGDGQTMVKLNHHPFQVSIDVMSDKTGMLLPTLDMTMMKDRSSMDMQGFIPEYLSTRGETFVHTNELQMEEAVKINGGMFVYAFTAACFHRRVMESEMMPSGDGQTMVKSSMDMQGFIPEYLSTRRRLNHHPFQVSIDVMSDKLLDHILQPTMFEDIKEIAKMCDVKPMMWNEPLETGYWPKLMLPLGTIGGLEMQMYVIVSPVRLNHHPFQVSIDVMSDKTVDAVVRGLYLPAPYEIYPYFFVDSHVISKTVDTSEMVMMKDDLTYLDSDMLVKWSSCISTMPLGYPFDRPIDMASFFTSNMK |
| P20613 | Sex-specific storage-protein 2 | 83698/80000 | 6.04/6.5 | 58.1% | 2619 | LTNGLGKAVEEFLKLYFDGVKIDFHDPKSYEVFARFLDTYEKITDVKVDKDFETFYKKAVEEFLKTFVQFLQKNVDAVFVEKENDYFVYKDHFEAFGQKNSNEFVIFKIVEYIVEFKVLGAAPMPFDKTGYYPLMLTKSKNVDAVFVEKNLEFSVFYDKEDSVPMTEIMKQYLKPYTQDKDPAFYQLYNRRVLGAAPMPFDKMFMNMEVLQKFFELDWFTTKIPEFSWYSPIKMQHGLINPEAAAKYGIHKENDYFVYKDYDIEMNMDNYTNKKYDDNGIPLTLEDNWMKRGEVYFYFYQQLLARIGKDYDIEMNMDNYTNKTFVQFLQKDHFEAFGQKIGKDYDIEMNMDNYTNKKGTEGGFPFQLFVFVYPFDNKILSFFQDVSQLNTDDEYYKNSNEFVIFKEDSVPMTEIMKKILSFFQDVSQLNTDDEYYKLNHSPFNVNIEVDSNVASDAVVKMLDEGKVPFDMSEEFCYMPKAINFVGNYWQDNADLYGEEVTKFTPFAQRPDYYNLHTEENYERAINFVGNYWQDNADLYGEEVTKDYQR |
| **197** | Q1HPP4 | Arylphorin | 83569/80000 | 5.7/6.5 | 74.1% | 3186 | LTNGLGKLTAGQNKAVEEFLKLYFDGVKIDFHDPKSYEVFARVPNMYFKFLDTYEKITDVKVDKDFETFYKKAVEEFLKTFVQFLQKNVDAVFVEKENDYFVYKDHFEAFGQKNSNEFVIFKIVEYIVEFKVLGAAPMPFDKTGYYPLMLTKTKNVDAVFVEKNLEFSVFYDKDIFIYHEGEREDSVPMTEIMKQYLKPYTQDKDPAFYQLYNRRVLGAAPMPFDKMFMNMEVLQKFFELDWFTTKMQDGLINPEAAAKIPEFSWYSPIKEEIKNNHVHDVKYGIHKENDYFVYKDEAIALFHLFYYAKFNIPSYDTQSNVVPKDIFIYHEGERFPYKDYDIEMNMDNYTNKKYDDNGIPLTLEDNWMKRGEVYFYFYQQLLARSDCHGFVVPAPYEVYPKMRDEAIALFHLFYYAKIGKDYDIEMNMDNYTNKTFVQFLQKDHFEAFGQKIGKDYDIEMNMDNYTNKKGTEGGFPFQLFVFVYPFDNKILSFFQDVSQLNTDDEYYKNSNEFVIFKEDSVPMTEIMKMLDEGKVPFDMSEEFCYMPKKILSFFQDVSQLNTDDEYYKLNHSPFNVNIEVDSNVASDAVVKMLDEGKVPFDMSEEFCYMPKAINFVGNYWQDNADLYGEEVTKFTPFAQRPDYYNLHTEENYERAINFVGNYWQDNADLYGEEVTKDYQRDLAPFESFVLDNKPLGFPLDRPVVDALFKGKDLAPFESFVLDNKPLGFPLDRPVVDALFK |
| P09179 | Sex-specific storage-protein 1 | 87890/80000 | 6.78/6.5 | 67.3% | 5231 | EGILTGKTVDAVVRLMSVNDKDGTVISLKDFDVFMRDGTVISLKKLMSVNDKRDLGMSNTSKQFMEMYKYMNVDVVKQNNMVVATKAAKDPVLWKFADVMIYREQFSFPGVKSEDIENLARMKELCIMKVIHLTNLMKTSDMTFMAREPMVNLDMKLPSGDEMPVRVCNIFTVFKFADVMIYRKDPVFWMIMKKSEDIENLARVIHLTNLMKKTVDTSEMVMMKMLSYGQYNMDKIRLPSGDEMPVREQFSFPGVKVEKQMMDDVEMMIRLVLGGLEIVGDDAKSCDKYMNVDVVKKMLSYGQYNMDKDDLTYLDSDMLVKLDMFELDSFMYKTGMLLPTLDMTMMKVLYYAKDFDVFMRMKQMMDDVEMMIRRLDMFELDSFMYKLLDHILQPTMFEDIKRGEIMMYANQQLLARVMESEMMPSGDGQTMVKLNHHPFQVSIDVMSDKTGMLLPTLDMTMMKDRSSMDMQGFIPEYLSTRGETFVHTNELQMEEAVKINGGMFVYAFTAACFHRRVMESEMMPSGDGQTMVKSSMDMQGFIPEYLSTRRRLNHHPFQVSIDVMSDKLLDHILQPTMFEDIKEIAKMCDVKPMMWNEPLETGYWPKLMLPLGTIGGLEMQMYVIVSPVRLNHHPFQVSIDVMSDKTVDAVVRGLYLPAPYEIYPYFFVDSHVISKTVDTSEMVMMKDDLTYLDSDMLVKWSSCISTMPLGYPFDRPIDMASFFTSNMK |
| P20613 | Sex-specific storage-protein 2 | 83698/80000 | 6.04/6.5 | 58.1% | 2619 | LTNGLGKAVEEFLKLYFDGVKIDFHDPKSYEVFARFLDTYEKITDVKVDKDFETFYKKAVEEFLKTFVQFLQKNVDAVFVEKENDYFVYKDHFEAFGQKNSNEFVIFKIVEYIVEFKVLGAAPMPFDKTGYYPLMLTKSKNVDAVFVEKNLEFSVFYDKEDSVPMTEIMKQYLKPYTQDKDPAFYQLYNRRVLGAAPMPFDKMFMNMEVLQKFFELDWFTTKIPEFSWYSPIKMQHGLINPEAAAKYGIHKENDYFVYKDYDIEMNMDNYTNKKYDDNGIPLTLEDNWMKRGEVYFYFYQQLLARIGKDYDIEMNMDNYTNKTFVQFLQKDHFEAFGQKIGKDYDIEMNMDNYTNKKGTEGGFPFQLFVFVYPFDNKILSFFQDVSQLNTDDEYYKNSNEFVIFKEDSVPMTEIMKKILSFFQDVSQLNTDDEYYKLNHSPFNVNIEVDSNVASDAVVKMLDEGKVPFDMSEEFCYMPKAINFVGNYWQDNADLYGEEVTKFTPFAQRPDYYNLHTEENYERAINFVGNYWQDNADLYGEEVTKDYQR |
| **198** | H9JTA2 | Uncharacterized protein | 74049/73000 | 6.31/6.4 | 30.5% | 498 | FGSDAGRSISLDGKFAGSFLRVSNAISNRLIFPDIRLMIELDKVETYSDFRLIDIFMDTKEVTSVVPTGARKVETYSDFRIFIAPTLDENKIDISELEIWRSVDSSVTVPFERAIEDMAVILPNGRMPIVIPSNYTASDAEPEQRIFIAPTLDENKRPLNFDEQR |
| Q27451 | Phenoloxidase subunit 1 | 79305/73000 | 6.25/6.4 | 26% | 402 | FGSDAGRFAGTTIRVSNAIGNRGMDFTPRLDSTVASRLDFPNIRLMIELDKLTPYGNDREVSSVVPSGARLIDIFMGMRAAIEEGYFPKSDVSELETWRSIDSSVTIPYERFLQAIENMSVMLPNGRMPIVIPSNYTASDTEPEQRIFIAPTVDESGKPFSFDEQR |
| **225** | Q27309 | Vitellogenin | 203725/40000 | 6.85/6.5 | 17.6% | 2198 | ELPVDLKEQQQGLFRTQEQQLIGRYQPTPNIDKVFEIEIDGGRSTNYGHCHHRFANEQDPVEVTKGLISALQLDTSAHRTLAHLQEGPSSGSAFKAETTSTVHVHPHLYGKELPKFANEQDPVEVTKLENPQHGNFNEQLPDPRVAYHFGVPVGAEWTGTAHKYQPTPNIDKVFEIEIDGGRFSSQSQSTGGQTYPSPWQVGKVIHDSQNNYDREQQQGLFRMRDMPIATMAPGALSFYQPLKEGPIYKAETTSTVHVHPHLYGKAEVYSHVHMELISVDQDSGAEWPRKMETDVTGDCETLYTVSPVASEWRIDFSYFDRTYTVDIASPSGEARMR |
| **226** | Q27309\* | Vitellogenin (light chain) | 40203/40000 | 6.85/6.8 | 62.3% | 1779 | ELPVDLKEQQQGLFRTQEQQLIGRYQPTPNIDKVFEIEIDGGRSTNYGHCHHRVIHDSQNNYDRFANEQDPVEVTKGLISALQLDTSAHRTLAHLQEGPSSGSAFKAETTSTVHVHPHLYGKLENPQHGNFNEQLPDPRVAYHFGVPVGAEWTGTAHKIVSLDFPTSVPVPQENLIKYQPTPNIDKVFEIEIDGGRFSSQSQSTGGQTYPSPWQVGKVIHDSQNNYDREQQQGLFRMETDVTGDCETLYTVSPVASEWR |
| **237** | H9JP12 | Sex-specific storage-protein 1 | 88007/80000 | 6.78/6.8 | 44.08% | 1728 | EGILTGKTVDAVVRLMSVNDKDGTVISLKDFDVFMRDGTVISLKKDLGMSNTSKFADVMIYREQFSFPGVKSEDIENLARMKELCIMKVIHLTNLMKTSDMTFMAREPMVNLDMKLPSGDEMPVRVCNIFTVFKKSEDIENLARMLSYGQYNMDKIRLPSGDEMPVREQFSFPGVKVEKLVLGGLEIVGDDAKLDMFELDSFMYKRLDMFELDSFMYKRGEIMMYANQQLLARLLDHILQPTMFEDIKLNHHPFQVSIDVMSDKSSMDMQGFIPEYLSTRINGGMFVYAFTAACFHRGETFVHTNELQMEEAVKLLDHILQPTMFEDIKEIAKGLYLPAPYEIYPYFFVDSHVISK |
| **239** | O97158 | Transferrin | 77156/80000 | 6.89/7 | 39.4% | 1032 | VLGLSDKAIDYLNKALSTFFTKYLCVDGSKIPLTMLMKAMSVFAFSRVTLDCIPARTPNYAVAVVKLCVTSNVALAKTDEEPDAPFRNNNVIFNNAAKSIHDVISSCGIAIHYVADNIPIKDLPIDNLDQLKACQDMVDIPTKGLATVENLDFEKIPNQDFVVFQEYRYVLHPVFHEVYGEKSVQDNGSDLASVDDMRDTLSNYPTCNIAMAPSRKFFGLPVGTTPASPSNENPDEYR |
| **242** | Q27309\*\* | Vitellogenin (heavy chain) | 161327/160000 | 6.85/6.8 | 26.8% | 2062 | VESGAEKVSGSFDRVFSVDSKTSNNIIKLVSAGINKAIYDGQRYGQSGEIRAVLFSILRVEISTYLRLQFNIPFKSYEYPLSRVFAPYLEGKYYEANMIKNTAEPYPVRIDFSYFDRVQGMLFAGTKSDMWMIFRNDLSPNSETRQIQSWIENKFVVFTQDYRDQQEIYISYKGNWHELAILSRDGVTQAGTLPAFKGQNPEVSGIPSVKNTIEASFSSAERDSLVAISQDPATKSAILSAAELQHPRQIMTQFFNFARYTTELENHPLAKKGQNPEVSGIPSVKTYTVDIASPSGEARAQVYIQAIGNLGHRALATQQAYYPEYKLIASMSTEQLSQTSRYLVTNEEFGYQHSFKILQDIAQQLQNPNNMPKDMPIATMAPGALSFYQPLK |
| **243** | Q27309\*\* | Vitellogenin (heavy chain) | 161327/160000 | 6.85/7 | 24.1% | 1921 | VSGSFDRTSNNIIKLVSAGINKAIYDGQRYGQSGEIRAVLFSILRVEISTYLRDSVFAPHPKLQFNIPFKSYEYPLSRVFAPYLEGKYYEANMIKNTAEPYPVRYYEANMIKVQGMLFAGTKIDFSYFDRVQGMLFAGTKSDMWMIFRNDLSPNSETRFVVFTQDYRDQQEIYISYKGNWHELAILSRDGVTQAGTLPAFKNTIEASFSSAERGQNPEVSGIPSVKDSLVAISQDPATKSAILSAAELQHPRKGQNPEVSGIPSVKYKEPAVIHFQSKTYTVDIASPSGEARALATQQAYYPEYKLIASMSTEQLSQTSRYLVTNEEFGYQHSFKILQDIAQQLQNPNNMPKDMPIATMAPGALSFYQPLK |
| **244** | Q27309\*\* | Vitellogenin (heavy chain) | 161327/160000 | 6.85/7.1 | 27.1% | 1835 | VSGSFDRTSNNIIKLVSAGINKAIYDGQRYGQSGEIRAVLFSILRAPFGMHFKVEISTYLRDSVFAPHPKLQFNIPFKSYEYPLSRVFAPYLEGKNTAEPYPVRYYEANMIKVQGMLFAGTKIDFSYFDRSDMWMIFRQIQSWIENKFVVFTQDYRDQQEIYISYKGNWHELAILSRDGVTQAGTLPAFKNTIEASFSSAERGQNPEVSGIPSVKDSLVAISQDPATKSAILSAAELQHPRYTTELENHPLAKQIMTQFFNFARYKEPAVIHFQSKTYTVDIASPSGEARAQVYIQAIGNLGHRALATQQAYYPEYKLIASMSTEQLSQTSRYLVTNEEFGYQHSFKILQDIAQQLQNPNNMPKDMPIATMAPGALSFYQPLK |
| **245** | Q27309\*\* | Vitellogenin (heavy chain) | 161327/160000 | 6.85/6.8 | 30.7% | 2323 | VSGSFDRVFSVDSKTSNNIIKVPVTCQPLVSAGINKAIYDGQRYGQSGEIRAVLFSILRVEISTYLRLQFNIPFKSYEYPLSRVFAPYLEGKYYEANMIKNTAEPYPVRVQGMLFAGTKIDFSYFDRSDMWMIFRIQHVQVTCKQIQSWIENKFVVFTQDYRDQQEIYISYKGNWHELAILSRDGVTQAGTLPAFKNTIEASFSSAERGQNPEVSGIPSVKDSLVAISQDPATKSAILSAAELQHPRYTTELENHPLAKQIMTQFFNFARKGQNPEVSGIPSVKYKEPAVIHFQSKTYTVDIASPSGEARAQVYIQAIGNLGHRALATQQAYYPEYKLIASMSTEQLSQTSRYLVTNEEFGYQHSFKILQDIAQQLQNPNNMPKHDAFVLEEILPTLAADLKLYEYLGYWYTEANPLKFIDDSYDEDNDIGTFVISHIGSEDSLLPK |
| **247** | Q1HPS1 | ML-domain containing secreted protein | 17360/17000 | 6.28/7.2 | 27.9% | 324 | SVPELSKAGTNYIYKIHTEDDQKNTDQHIVIKFTPEKDVLDLK |
| **250** | Q1HQ02 | Ferritin | 26245/25000 | 6.75/7 | 49.8% | 843 | ALASLYLKFITENNGKLSDDSWEKSLAGHTSDLKALASLYLKRKLSDDSWEKDNHVVANELKMDFSSHTTLKSLAGHTSDLKRTLSLPHCSAYYGQFKDLSLAVYLFDEYLQKNSDLLHDAEITQYIEEEFVSQQADTIR |
| **259** | Q1HPN7 | Fructose-bisphosphate aldolase | 39971/40000 | 8.38/7.7 | 46.4% | 1376 | ATVTALLRALQASVLRIAQAIVAPAKTYTPNDVARYASICQSQRVTEVVLAAVYKYVAGSIPSLAASKADDGTPLVSLLEKGILAADESTGTMGKRPWVLTFSYGRTENILAGQQELIKLQDIGVENTEENRTENILAGQQELIKRNTPSYQAIQENANVLARIVPIVEPEVLPDGEHDLDR |
| **263** | H9ITY5 | Probable medium-chain specific acyl-CoA dehydrogenase. mitochondrial isoform X2 | 46461/45000 | 5.91/7.5 | 44.1% | 856 | ALQELARTFGVPIARIAMGAFDKNTVMASVAKGITFEDVRNTVMASVAKAFTGFIVEREILTAATQTNTGEYPWPVVKENVLIGEGAGFKDEIIPVAGQYDKTRPPVAAGATGLAQRIYQIYEGTSQIQRHQAVAFMLADMAIGVETARAATDAVQVFGGNGFNTEYPVEKLIDEPLVAAYGVTEPGAGSDVAGIK |
| **266** | A7BEX9 | Imaginal disk growth factor | 48362/50000 | 7.64/7.2 | 52.8% | 1734 | FGTYAFREGFTALVRLINPNQQKVLCYYDSRIVLSIATFGRTFGTTPVDEKSTWGSLWHGIKYNLLLESQQARGLCTGDKYPILRLVSLNENLDIDRTEGLLSYPEVCGKESEHREGFTALVREADYTAPIYTPQNRNLGGVAIVDLSLDDFRLVSLNENLDIDRTHDNYRNPLQNADAAVTYWLTSGAPSQKLPDDNGEGGIWVSYEDPDTAGQKLDADSEIAGVPPIHTDGPGEAGPYVKTFGTTPVDEKESEHREGFTALVR |
| **269** | Q68AP5 | Catalase | 57092/55000 | 8.11/8.2 | 67.5% | 2149 | SGAPVGIKGIPDGYRVFESIGKTAIQTVGKVAAGLAPYKQVFDDAAKDLYNSIAKVFESIGKRVAVSNYQRLVLDRNPKDSPGFITTKFNPFDLTKYNVGGDVDRVAAGLAPYKKDAAAFIQERAIANIVDHLKLFAYSDTHRDPATDQLINYKHMNGYGSHTFKTLKDSPGFITTKLVNSQGVGYWVKIFSQVHPELGNKDPATDQLINYKKFSTVGGESGSADTVRAGELASTDPDYSIRDPTLFPSFIHTQKIWPHAEYPLIPVGKDPTLFPSFIHTQKRGAGAFGYFEVTHDITKLGANYLQIPVNCPYKFSTVGGESGSADTVRDPRNGPALLQDVNFLDEMSSFDRERYNVGGDVDRYDSGQTEDNFSQATALYKDGPQAIHNQDDCPNYFPNSFSGPQECPR |
| **270** | H9IYX7 | Bifunctional purine biosynthesis protein | 64577/60000 | 7.19/7.8 | 49.6% | 1977 | TGLLSLAKITAELFKAPEMLGGRDLPSNAVRGGNYCVLKAALWWLRHPSVLAMRIALAHTNLRDLIVATIALKRHPSVLAMRTIFGLTLEQKEALSLPAAASFKTIFGLTLEQKRLSDSDQEDMKRYTQSNSVCFARLSDSDQEDMKRVALASDAFFPFRTLHPAVHAGILARQYSPGQAQLTLRDGQVIGIGAGQQSRNAGLTVQDVSDITRKQYSPGQAQLTLRIDPTYEPSLMEQKELKEALSLPAAASFKVTVVCDPADYDAVVKEVSDGVIAPGYSPEALKYGMNPHQKPAQVFTTRVALASDAFFPFRDNIDRSLSECGLQLIASGGTATALRAFTHTSDYDLAISDYFRAFTHTSDYDLAISDYFRK |
| **275** | H9IYX7 | Bifunctional purine biosynthesis protein | 64577/62000 | 7.19/7.5 | 49.2% | 1193 | TGLLSLAKITAELFKAPEMLGGRDLPSNAVRGGNYCVLKAALWWLRIALAHTNLRDLIVATIALKTIFGLTLEQKEALSLPAAASFKYTQSNSVCFARVALASDAFFPFRTLHPAVHAGILARDGQVIGIGAGQQSRNAGLTVQDVSDITRIDPTYEPSLMEQKELKEALSLPAAASFKVTVVCDPADYDAVVKEVSDGVIAPGYSPEALKYGMNPHQKPAQVFTTRVALASDAFFPFRDNIDRSLSECGLQLIASGGTATALRAFTHTSDYDLAISDYFRNAGLTVQDVSDITRAPEMLGGRMSSFGDFVALSDPCDVSTATIISR |
| **276** | H9IZ23 | Pyruvate kinase | 68697/55000 | 9/7.2 | 27.8% | 941 | SAHLLSKNVAVLEKNGAALHEIRQGSGFTNTVREAEAVIWHRGDLGIEIPPEKLTTSSDYQEKMMETGMNVARNITNVVKPGNRGNADTIYVDYKLSGIICTIGPASRLGSPFSLAIALDTKGFVHPGDNAVVVTGWKGVNLPGIPVDLPAVSEKKGVNLPGIPVDLPAVSEKGVLPIVYQEPTASDWLK |
| Q68AP5 | Catalase | 57092/55000 | 8.11/7.2 | 22% | 362 | GIPDGYRVFESIGKDLYNSIAKVAVSNYQRFNPFDLTKLVNSQGVGYWVKAGELASTDPDYSIRIWPHAEYPLIPVGKGAGAFGYFEVTHDITKFSTVGGESGSADTVRDPR |
| H9J8X4 | Glucose-6-phosphate 1-dehydrogenase | 56942/55000 | 6.86/7.2 | 28% | 288 | VFTPILKEPFGTEGRDNLLPHNTKIDYEFLNRVQPGEALYLKEMVQNLMTIRGGYFDDFGIIRIYPTIWYLYRLILDVFTGTQMHFVRLSNHLAGLFIEEQIYRDLEDNHIKPVPYVYGSR |
| **279** | O97158 | Transferrin | 77156/80000 | 6.89/7.5 | 71.8% | 4089 | VLGLSDKMVDIPTKAIDYLNKALSTFFTKSCHTGVNRYLCVDGSKIPLTMLMKAMSVFAFSRGHGAPELVVRMNDHSISPKVTLDCIPARTPNYAVAVVKYEAVIVIHKIIKPDQCIKIPLTMLMKRQCGSDSSPWKLCVTSNVALAKTDEEPDAPFRKTPNYAVAVVKNNNVIFNNAAKSIHDVISSCGIASKVTLDCIPARDLPINNLDQLKIHYVADNIPIKGTSFNKMEDLRLCSMCEHPERGLATVENLDFEKMECLNYVQQRKGTSFNKMEDLRCLAHNNGQVAFTKTDLFNIYGEFLKDRMECLNYVQQRIPNQDFVVFQEYRSVQDNGSDLASVDDMRYVLHPVFHEVYGEKCDYPDEFSGYVGALKQLADAGSSNQPEWFTKKYVLHPVFHEVYGEKQADFVPVDPEDMYVAAKDTLSNYPTCNIAMAPSRDTLSNYPTCNIAMAPSRTDEEPDAPFRYEAVIVIHKDIRPILDCVQEASETDCLKACSWAARPWQGLIGHNDVLAKFFGLPVGTTPASPSNENPDEYRDFLSDVSIAHTPLSLAQLLDTRSCHSSYGTFSGLDAPLYYLINKKFFGLPVGTTPASPSNENPDEYRSCHSSYGTFSGLDAPLYYLINKRNFGDFFSGGSCLPGVDKPENNPSGDDVSSLKK |
| **283** | Q27309\*\* | Vitellogenin (heavy chain) | 161327/160000 | 6.85/7.3 | 47.7% | 3470 | VSGSFDRTSNNIIKVPVTCQPLVSAGINKAIYDGQRYGQSGEIRAVLFSILRAPFGMHFKVEISTYLRSKVFSVDSKDSVFAPHPKLQFNIPFKSYEYPLSRVFAPYLEGKYYEANMIKNTAEPYPVRIDFSYFDRVQGMLFAGTKFSFPSKDNKIQHVQVTCKSDMWMIFRNDLSPNSETRQIQSWIENKFVVFTQDYRQFKVPVTCQPQIQSWIENKKDQQEIYISYKGNWHELAILSRDGVTQAGTLPAFKGQNPEVSGIPSVKNTIEASFSSAERDSLVAISQDPATKSAILSAAELQHPRYTTELENHPLAKQIMTQFFNFARKGQNPEVSGIPSVKYKEPAVIHFQSKTYTVDIASPSGEARKDSLVAISQDPATKAQVYIQAIGNLGHRALATQQAYYPEYKSWHVVMQDESTQRDGVLVINIEDDRIRLIASMSTEQLSQTSRYLVTNEEFGYQHSFKILQDIAQQLQNPNNMPKHDAFVLEEILPTLAADLKLYEYLGYWYTEANPLKDMPIATMAPGALSFYQPLKMRDMPIATMAPGALSFYQPLKSESGQDLEIEIQPASGDSAYQVKYGQSTHAVIYAQGYTYSSDWRLTHKHDAFVLEEILPTLAADLKVYNQDQVSIMFPVASGMPFIFKAYELVANYFTGHQYQPYCSIDGTRFRVEPLHPDQDQTLVHYSVWPYSASQKFIDDSYDEDNDIGTFVISHIGSEDSLLPK |
| **284** | Q27309\*\* | Vitellogenin (heavy chain) | 161327/160000 | 6.85/7.4 | 51.4% | 4638 | VSGSFDRVFSVDSKTSNNIIKVPVTCQPLVSAGINKAIYDGQRYGQSGEIRAVLFSILRAPFGMHFKVEISTYLRSKVFSVDSKDSVFAPHPKLQFNIPFKSYEYPLSRVFAPYLEGKNTAEPYPVRYYEANMIKVQGMLFAGTKIDFSYFDRFSFPSKDNKSDMWMIFRIQHVQVTCKVPSCQSHCRNDLSPNSETRQIQSWIENKFVVFTQDYRGKFSFPSKDNKDQQEIYISYKGNWHELAILSRDGVTQAGTLPAFKGQNPEVSGIPSVKNTIEASFSSAERGQNPEVSGIPSVKDSLVAISQDPATKSAILSAAELQHPRQIMTQFFNFARYTTELENHPLAKEQPFLQYHTHKKGQNPEVSGIPSVKYKEPAVIHFQSKTYTVDIASPSGEARKDSLVAISQDPATKAQVYIQAIGNLGHRKYTTELENHPLAKALATQQAYYPEYKSWHVVMQDESTQRDGVLVINIEDDRIRLIASMSTEQLSQTSRFLDYLRDSVFAPHPKYLVTNEEFGYQHSFKILQDIAQQLQNPNNMPKHDAFVLEEILPTLAADLKLYEYLGYWYTEANPLKDMPIATMAPGALSFYQPLKMRDMPIATMAPGALSFYQPLKSESGQDLEIEIQPASGDSAYQVKYGQSTHAVIYAQGYTYSSDWRLTHKHDAFVLEEILPTLAADLKVYNQDQVSIMFPVASGMPFIFKLFSFSESDLQQLSQYISEYMKLFSFSESDLQQLSQYISEYMKKAYELVANYFTGHQYQPYCSIDGTRFRVEPLHPDQDQTLVHYSVWPYSASQKFIDDSYDEDNDIGTFVISHIGSEDSLLPKVAAIQSIFISHPTGEMMQAMAEMTHNDPSVEVR |
| **286** | Q27309\*\* | Vitellogenin (heavy chain) | 161327/160000 | 6.85/7.5 | 40.6% | 3175 | VSGSFDRVFSVDSKTSNNIIKVPVTCQPLVSAGINKAIYDGQRYGQSGEIRAVLFSILRAPFGMHFKVEISTYLRDSVFAPHPKLQFNIPFKSYEYPLSRVFAPYLEGKNTAEPYPVRYYEANMIKVQGMLFAGTKIDFSYFDRFSFPSKDNKSDMWMIFRQIQSWIENKFVVFTQDYRDQQEIYISYKGNWHELAILSRDGVTQAGTLPAFKGQNPEVSGIPSVKNTIEASFSSAERDSLVAISQDPATKSAILSAAELQHPRQIMTQFFNFARYTTELENHPLAKKGQNPEVSGIPSVKYKEPAVIHFQSKTYTVDIASPSGEARKDSLVAISQDPATKAQVYIQAIGNLGHRALATQQAYYPEYKSWHVVMQDESTQRLIASMSTEQLSQTSRYLVTNEEFGYQHSFKILQDIAQQLQNPNNMPKLYEYLGYWYTEANPLKDMPIATMAPGALSFYQPLKMRDMPIATMAPGALSFYQPLKSESGQDLEIEIQPASGDSAYQVKYGQSTHAVIYAQGYTYSSDWRVYNQDQVSIMFPVASGMPFIFKAYELVANYFTGHQYQPYCSIDGTRAIVMAHAPDHVEFSVSFQDMSPQYRFRVEPLHPDQDQTLVHYSVWPYSASQK |
| **292** | Q69FX2 | Promoting protein | 17625/16000 | 8.37/8.8 | 68.8% | 863 | TGLFGLKIDPCVNSRLKTGLFGLKLPTGNFEFKKLPTGNFEFKTQTLDFSLHIGKEVDASACTVNEVRVSFDFTPQFSTTKLWNEDNESQMCCYRNGAEIPFDALYNADACTLTSCPTEAGK |
| **295** | Q60GK5 | Glutathione S-transferase delta | 24269/23000 | 7.61/8.3 | 91.2% | 2143 | AVLLTAKGLVNSMLKGLVNSMLKKALNLNLNLKAIITYLVNKGSSLYPEDPKVQEALQLLDKSTAPGYQEANEKGSSLYPEDPKARLYFDIGTLYQRAIITYLVNKYAKTIDLYYVPGSAPCRVQEALQLLDKFLEGQKLVDLHHGEQLKPEYLKFSDYFYPQVFAGAPADKSTAPGYQEANEKGLEAFKFSDYFYPQVFAGAPADKAKNEKVQEALQLLDKFLEGQKLNPQHTVPTLVDDGLSIWESRYVAGPNLTVADLSLIASVSSLEASDIDFKK |
| **309** | Q68AP5 | Catalase | 57092/55000 | 8.11/8 | 58.6% | 1430 | AGELASTDPDYSIRAIANIVDHLKDAAAFIQERDLYNSIAKDPTLFPSFIHTQKDSPGFITTKFNPFDLTKFSTVGGESGSADTVRDPRGAGAFGYFEVTHDITKGIPDGYRHMNGYGSHTFKIWPHAEYPLIPVGKLFAYSDTHRLGANYLQIPVNCPYKLVNSQGVGYWVKNGPALLQDVNFLDEMSSFDRNYFAEVEQIAFSPSNLVPGIEPSPDKQVFDDAAKSGAPVGIKTAIQTVGKTLKDSPGFITTKVAAGLAPYKVAVSNYQRVFESIGKYNVGGDVDRYDSGQTEDNFSQATALYK |
| **312** | G1UIS8 | Apolipophorin protein | 371420/73000 | 7.94/9 | 7.8% | 1511 | ISLDILKFGYQDGKVINGVPEKQLDSEIRLSISGPDGKHVNNDALKKISLDILKVFLDALLRADGVVAISQKVLEHFLGPKHLENSLIEKNDHACLGAVKRVFLDALLRTEEDTVVAVLKAAAGLLDLPNLPKSKTEEDTVVAVLKTESPQAIYDSLVKSDIIISNVNPNAGVKDVYLGAGALAGAYCRIQPQICAEEDDTRDMQVLQSTLNVESKAAVLEAFHADPCSPKSVTNNVGANSASSFAQLVREQGKSDIIISNVNPNAGVK |
| **325** | C6L8Q2 | Putative acetyl transferase | 41580/40000 | 8.91/9.3 | 59.3% | 1082 | GIFIVGAKTANDAGVFKLGAQFGITRTPFGTFGGVFRITAHLVHELRAEIEPVSLTIKRTPFGTFGGVFRAGIPQEKPVLGINRDEVDNYALQSQQKNTSATELQTIATVGALKISVAGGVENMSQAPFAVRLNVNGGATALGHPLGASGSRLCGSGFQSIVNSAQDILTGAAKLGAQFGITRDEVDNYALQSQQKEGLVTAGTASGISDGAGALVLVSEEAAKLTLNDVDLIEINEAFVAQTLSCAK |
| A0A0A0QY84 | Elongation factor 1-alpha | 50626/40000 | 9.24/9.3 | 41.7% | 1013 | GYVAGDSKEAQEMGKEVSSYIKQLIVGVNKTIEKFEKRGYVAGDSKLPLQDVYKIGGIGTVPVGRSTTTGHLIYKEHALLAFTLGVKYYVTIIDAPGHRMDSTEPPYSEPRTHINIVVIGHVDSGKVETGVLKPGTIVVFAPANITTEVKSVEMHHEALQEAVPGDNVGFNVKIGYNPAAVAFVPISGWHGDNMLEPSTKKIGYNPAAVAFVPISGWHGDNMLEPSTK |
| **328** | Q2F5T3 | ATP synthase subunit alpha | 59792/55000 | 9.21/9 | 51.2% | 1447 | APGIIPRVGSAAQTKELIIGDRSTVAQIVKADLEETGRLELAQYREPMQTGIKVLSIGDGIARAVDSLVPIGRGHLDKLDPSKVVDALGNPIDGKAAEISTILEERHALIIYDDLSKLYCIYVAIGQKVSVREPMQTGIKGIRPAINVGLSVSRTALAIDTIINQQRIVTDFLATFTQSQDGQITPESDASLKKEAYPGDVFYLHSRITAFEKEFTQHIKQVAGSMKLELAQYRTGAIVDVPVGEQILGRVVDALGNPIDGKGPIDTKGMALNLEPDNVGVVVFGNDKEVAAFAQFGSDLDAATQQLLNR |
| **332** | H9JP12 | Sex-specific storage-protein 1 | 88007/80000 | 6.78/9.3 | 20.02% | 679 | EGILTGKTVDAVVRLMSVNDKDFDVFMRDLGMSNTSKQFMEMYKFADVMIYREQFSFPGVKSEDIENLARVIHLTNLMKEPMVNLDMKLPSGDEMPVRVCNIFTVFKMLSYGQYNMDKIRLPSGDEMPVRLVLGGLEIVGDDAKGETFVHTNELQMEEAVK |
| Q1HPP4 | Arylphorin | 83569/80000 | 5.7/9.3 | 26.3% | 476 | AVEEFLKSYEVFARFLDTYEKDFETFYKTFVQFLQKNVDAVFVEKENDYFVYKDHFEAFGQKIVEYIVEFKVLGAAPMPFDKTGYYPLMLTKNLEFSVFYDKMFMNMEVLQKFFELDWFTTKMQDGLINPEAAAKIPEFSWYSPIKFNIPSYDTQSNVVPKSDCHGFVVPAPYEVYPK |