**Supplementary file 1**

**Evaluation of female *Aedes aegypti* proteome *via* LC-ESI-MS/MS using two protein extraction methods**

Table 1: Top 20 proteins based on the highest -10lgp score TCA acetone precipitation extracted proteins replicate 1

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **SN** | **Accession** | **-10lgP** | **Coverage (%)** | **#Peptides** | **#Unique** | **Avg. Mass** | **Description** |
| 1. | tr|Q179E8|Q179E8\_AEDAE | 238.89 | 33 | 68 | 15 | 221462 | AAEL005656-PA OS=Aedes aegypti OX=7159 GN=AAEL005656 PE=3 SV=1 |
| 2. | tr|W0FUL2|W0FUL2\_AEDAE | 234.71 | 31 | 63 | 15 | 221323 | Myosin heavy chain OS=Aedes aegypti OX=7159 GN=myo-sex PE=2 SV=1 |
| 3. | tr|A0A1Q3G4T4|A0A1Q3G4T4\_CULTA | 230.61 | 24 | 51 | 15 | 224263 | Putative myosin class i heavy chain OS=Culex tarsalis OX=7177 PE=3 SV=1 |
| 4. | tr|Q178Y4|Q178Y4\_AEDAE | 229.19 | 24 | 50 | 15 | 224208 | AAEL005733-PB OS=Aedes aegypti OX=7159 GN=AAEL005733 PE=3 SV=1 |
| 5. | tr|Q178Y3|Q178Y3\_AEDAE | 229.19 | 24 | 50 | 15 | 222221 | AAEL005733-PA OS=Aedes aegypti OX=7159 GN=AAEL005733 PE=3 SV=1 |
| 6. | tr|B0W188|B0W188\_CULQU | 220.81 | 22 | 46 | 15 | 219420 | Myosin heavy chain OS=Culex quinquefasciatus OX=7176 GN=6031761 PE=3 SV=1 |
| 7. | tr|A0A1S4H419|A0A1S4H419\_ANOGA | 220.7 | 21 | 44 | 15 | 224088 | Myosin heavy chain OS=Anopheles gambiae OX=7165 PE=3 SV=1 |
| 8. | tr|A0A182XLF1|A0A182XLF1\_ANOQN | 220.7 | 18 | 44 | 15 | 253203 | Uncharacterized protein OS=Anopheles quadriannulatus OX=34691 PE=3 SV=1 |
| 9. | tr|A0A182V4B9|A0A182V4B9\_ANOME | 220.37 | 19 | 44 | 15 | 246591 | Uncharacterized protein OS=Anopheles merus OX=30066 PE=3 SV=1 |
| 10. | tr|A0A2M4CTP0|A0A2M4CTP0\_ANODA | 220.21 | 21 | 44 | 15 | 221726 | Putative myosin class i heavy chain OS=Anopheles darlingi OX=43151 PE=3 SV=1 |
| 11. | tr|A0A182HQV8|A0A182HQV8\_ANOAR | 218.41 | 18 | 42 | 15 | 254328 | Uncharacterized protein OS=Anopheles arabiensis OX=7173 PE=3 SV=1 |
| 12. | tr|A0A1S4H355|A0A1S4H355\_ANOGA | 218.41 | 20 | 42 | 15 | 223756 | Myosin heavy chain OS=Anopheles gambiae OX=7165 PE=3 SV=1 |
| 13. | tr|A0A1Q3G4C2|A0A1Q3G4C2\_CULTA | 218.22 | 20 | 42 | 15 | 221303 | Putative myosin class i heavy chain OS=Culex tarsalis OX=7177 PE=3 SV=1 |
| 14. | tr|A0A1Q3FI37|A0A1Q3FI37\_CULTA | 205.92 | 16 | 35 | 15 | 222981 | Putative myosin class i heavy chain OS=Culex tarsalis OX=7177 PE=3 SV=1 |
| 15. | tr|Q6QNY2|Q6QNY2\_AEDAE | 186.74 | 42 | 26 | 7 | 41582 | AAEL001951-PA OS=Aedes aegypti OX=7159 GN=5572985 PE=2 SV=1 |
| 16. | tr|A0A182H2T8|A0A182H2T8\_AEDAL | 186.74 | 42 | 26 | 7 | 41566 | Uncharacterized protein OS=Aedes albopictus OX=7160 GN=109412625 PE=3 SV=1 |
| 17. | tr|B0WZI4|B0WZI4\_CULQU | 178.1 | 38 | 22 | 7 | 41598 | Actin-5 OS=Culex quinquefasciatus OX=7176 GN=6045432 PE=3 SV=1 |
| 18. | tr|Q4JQ54|Q4JQ54\_CULPP | 176.89 | 38 | 22 | 7 | 41810 | Actin OS=Culex pipiens pipiens OX=38569 PE=2 SV=1 |
| 19. | tr|A0A182GF96|A0A182GF96\_AEDAL | 176.89 | 38 | 22 | 7 | 41643 | Uncharacterized protein OS=Aedes albopictus OX=7160 GN=109412623 PE=3 SV=1 |
| 20. | tr|A0A182XUG6|A0A182XUG6\_ANOQN | 176.89 | 38 | 22 | 6 | 41659 | Uncharacterized protein OS=Anopheles quadriannulatus OX=34691 PE=3 SV=1 |

Table 2: Top 20 proteins based on the highest -10lgp score TCA acetone precipitation extracted proteins replicate 2

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **SN** | **Accession** | **-10lgP** | **Coverage (%)** | **#Peptides** | **#Unique** | **Avg. Mass** | **Description** |
| 1. | tr|A0A3F2YYT0|A0A3F2YYT0\_ANOGA | 133.71 | 37 | 16 | 16 | 48804 | ATP synthase subunit beta OS=Anopheles gambiae OX=7165 PE=3 SV=1 |
| 2. | tr|A0A1S4H9B2|A0A1S4H9B2\_ANOGA | 133.71 | 34 | 16 | 16 | 53143 | ATP synthase subunit beta OS=Anopheles gambiae OX=7165 PE=3 SV=1 |
| 3. | tr|A0A1S4F4H1|A0A1S4F4H1\_AEDAE | 133.71 | 34 | 16 | 16 | 53988 | ATP synthase subunit beta OS=Aedes aegypti OX=7159 GN=5577999 PE=3 SV=1 |
| 4. | tr|A0A1S4H8F8|A0A1S4H8F8\_ANOGA | 133.71 | 34 | 16 | 16 | 54080 | ATP synthase subunit beta OS=Anopheles gambiae OX=7165 PE=3 SV=1 |
| 5. | tr|A0A182X065|A0A182X065\_ANOQN | 133.71 | 34 | 16 | 16 | 54022 | ATP synthase subunit beta OS=Anopheles quadriannulatus OX=34691 PE=3 SV=1 |
| 6. | tr|A0A1Q3FH39|A0A1Q3FH39\_CULTA | 133.71 | 34 | 16 | 16 | 53891 | ATP synthase subunit beta OS=Culex tarsalis OX=7177 PE=3 SV=1 |
| 7. | tr|A0A182RSV0|A0A182RSV0\_ANOFN | 133.71 | 34 | 16 | 16 | 53974 | ATP synthase subunit beta OS=Anopheles funestus OX=62324 PE=3 SV=1 |
| 8. | tr|A0A4Y0BGI4|A0A4Y0BGI4\_ANOFN | 133.71 | 34 | 16 | 16 | 53986 | ATP synthase subunit beta OS=Anopheles funestus OX=62324 PE=3 SV=1 |
| 9. | tr|A0A182HPL3|A0A182HPL3\_ANOAR | 133.71 | 34 | 16 | 16 | 54022 | ATP synthase subunit beta OS=Anopheles arabiensis OX=7173 PE=3 SV=1 |
| 10. | tr|Q17FL3|Q17FL3\_AEDAE | 133.71 | 34 | 16 | 16 | 53974 | ATP synthase subunit beta OS=Aedes aegypti OX=7159 GN=AAEL003393 PE=3 SV=1 |
| 11. | tr|A0A023ETB9|A0A023ETB9\_AEDAL | 133.71 | 34 | 16 | 16 | 54017 | ATP synthase subunit beta OS=Aedes albopictus OX=7160 PE=2 SV=1 |
| 12. | tr|Q17H12|Q17H12\_AEDAE | 133.71 | 34 | 16 | 16 | 53912 | ATP synthase subunit beta OS=Aedes aegypti OX=7159 GN=5576214 PE=3 SV=1 |
| 13. | tr|A0A182RAH9|A0A182RAH9\_ANOFN | 133.71 | 34 | 16 | 16 | 54018 | ATP synthase subunit beta OS=Anopheles funestus OX=62324 PE=3 SV=1 |
| 14. | tr|A0A023EUC8|A0A023EUC8\_AEDAL | 133.71 | 34 | 16 | 16 | 53912 | ATP synthase subunit beta OS=Aedes albopictus OX=7160 PE=2 SV=1 |
| 15. | tr|E3XEC7|E3XEC7\_ANODA | 133.71 | 34 | 16 | 16 | 53768 | ATP synthase subunit beta OS=Anopheles darlingi OX=43151 GN=AND\_006288 PE=3 SV=1 |
| 16. | tr|A0A182FTY5|A0A182FTY5\_ANOAL | 133.71 | 34 | 16 | 16 | 53774 | ATP synthase subunit beta OS=Anopheles albimanus OX=7167 PE=3 SV=1 |
| 17. | tr|T1DES1|T1DES1\_ANOAQ | 133.71 | 34 | 16 | 16 | 53790 | ATP synthase subunit beta OS=Anopheles aquasalis OX=42839 PE=2 SV=1 |
| 18. | tr|A0A182FTY6|A0A182FTY6\_ANOAL | 133.71 | 34 | 16 | 16 | 53768 | ATP synthase subunit beta OS=Anopheles albimanus OX=7167 PE=3 SV=1 |
| 19. | tr|A0A182UML8|A0A182UML8\_ANOME | 133.71 | 34 | 16 | 16 | 53727 | ATP synthase subunit beta OS=Anopheles merus OX=30066 PE=3 SV=1 |
| 20. | tr|A0A182X083|A0A182X083\_ANOQN | 133.71 | 34 | 16 | 16 | 53727 | ATP synthase subunit beta OS=Anopheles quadriannulatus OX=34691 PE=3 SV=1 |

Table 3: Top 20 proteins based on the highest -10lgp score TCA acetone precipitation extracted proteins replicate 3

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **SN** | **Accession** | **-10lgP** | **Coverage (%)** | **#Peptides** | **#Unique** | **Avg. Mass** | **Description** |
| 1. | tr|Q1HRQ7|Q1HRQ7\_AEDAE | 141.29 | 23 | 15 | 15 | 59392 | ATP synthase subunit alpha OS=Aedes aegypti OX=7159 GN=5575914 PE=2 SV=1 |
| 2. | tr|A0A023EUC8|A0A023EUC8\_AEDAL | 141.27 | 25 | 13 | 13 | 53912 | ATP synthase subunit beta OS=Aedes albopictus OX=7160 PE=2 SV=1 |
| 3. | tr|A0A3F2YYT0|A0A3F2YYT0\_ANOGA | 141.27 | 28 | 13 | 13 | 48804 | ATP synthase subunit beta OS=Anopheles gambiae OX=7165 PE=3 SV=1 |
| 4. | tr|Q1HR61|Q1HR61\_AEDAE | 141.27 | 25 | 13 | 13 | 53971 | ATP synthase subunit beta OS=Aedes aegypti OX=7159 PE=2 SV=1 |
| 5. | tr|B0WGW0|B0WGW0\_CULQU | 141.27 | 25 | 13 | 13 | 54589 | ATP synthase subunit beta OS=Culex quinquefasciatus OX=7176 GN=6038107 PE=3 SV=1 |
| 6. | tr|A0A182RAH9|A0A182RAH9\_ANOFN | 141.27 | 25 | 13 | 13 | 54018 | ATP synthase subunit beta OS=Anopheles funestus OX=62324 PE=3 SV=1 |
| 7. | tr|A0A023ETB9|A0A023ETB9\_AEDAL | 141.27 | 25 | 13 | 13 | 54017 | ATP synthase subunit beta OS=Aedes albopictus OX=7160 PE=2 SV=1 |
| 8. | tr|Q17FL3|Q17FL3\_AEDAE | 141.27 | 25 | 13 | 13 | 53974 | ATP synthase subunit beta OS=Aedes aegypti OX=7159 GN=AAEL003393 PE=3 SV=1 |
| 9. | tr|A0A4Y0BGI4|A0A4Y0BGI4\_ANOFN | 141.27 | 25 | 13 | 13 | 53986 | ATP synthase subunit beta OS=Anopheles funestus OX=62324 PE=3 SV=1 |
| 10. | tr|A0A182RSV0|A0A182RSV0\_ANOFN | 141.27 | 25 | 13 | 13 | 53974 | ATP synthase subunit beta OS=Anopheles funestus OX=62324 PE=3 SV=1 |
| 11. | tr|A0A1Q3FH39|A0A1Q3FH39\_CULTA | 141.27 | 25 | 13 | 13 | 53891 | ATP synthase subunit beta OS=Culex tarsalis OX=7177 PE=3 SV=1 |
| 12. | tr|A0A182X065|A0A182X065\_ANOQN | 141.27 | 25 | 13 | 13 | 54022 | ATP synthase subunit beta OS=Anopheles quadriannulatus OX=34691 PE=3 SV=1 |
| 13. | tr|A0A1S4F4H1|A0A1S4F4H1\_AEDAE | 141.27 | 25 | 13 | 13 | 53988 | ATP synthase subunit beta OS=Aedes aegypti OX=7159 GN=5577999 PE=3 SV=1 |
| 14. | tr|A0A182FTY5|A0A182FTY5\_ANOAL | 141.27 | 25 | 13 | 13 | 53774 | ATP synthase subunit beta OS=Anopheles albimanus OX=7167 PE=3 SV=1 |
| 15. | tr|E3XEC7|E3XEC7\_ANODA | 141.27 | 25 | 13 | 13 | 53768 | ATP synthase subunit beta OS=Anopheles darlingi OX=43151 GN=AND\_006288 PE=3 SV=1 |
| 16. | tr|A0A182X083|A0A182X083\_ANOQN | 141.27 | 25 | 13 | 13 | 53727 | ATP synthase subunit beta OS=Anopheles quadriannulatus OX=34691 PE=3 SV=1 |
| 17. | tr|A0A182UML8|A0A182UML8\_ANOME | 141.27 | 25 | 13 | 13 | 53727 | ATP synthase subunit beta OS=Anopheles merus OX=30066 PE=3 SV=1 |
| 18. | tr|A0A1S4H9B2|A0A1S4H9B2\_ANOGA | 141.27 | 26 | 13 | 13 | 53143 | ATP synthase subunit beta OS=Anopheles gambiae OX=7165 PE=3 SV=1 |
| 19. | tr|A0A084WIY6|A0A084WIY6\_ANOSI | 141.27 | 25 | 13 | 13 | 54048 | ATP synthase subunit beta OS=Anopheles sinensis OX=74873 GN=ZHAS\_00018244 PE=3 SV=1 |
| 20. | tr|A0A1S4FIY1|A0A1S4FIY1\_AEDAE | 94.37 | 19 | 8 | 8 | 35296 | Uncharacterized protein OS=Aedes aegypti OX=7159 GN=5570233 PE=3 SV=1 |

Table 4: Top 20 proteins based on the highest -10lgp score Cytobuster extracted proteins replicate 1

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **SN** | **Accession** | **-10lgP** | **Coverage (%)** | **#Peptides** | **#Unique** | **Avg. Mass** | **Description** |
| 1. | tr|Q1HR61|Q1HR61\_AEDAE | 202.23 | 58 | 35 | 27 | 53971 | ATP synthase subunit beta OS=Aedes aegypti OX=7159 PE=2 SV=1 |
| 2. | tr|A0A182FTY5|A0A182FTY5\_ANOAL | 202.23 | 58 | 35 | 27 | 53774 | ATP synthase subunit beta OS=Anopheles albimanus OX=7167 PE=3 SV=1 |
| 3. | tr|A0A1S4F4H1|A0A1S4F4H1\_AEDAE | 202.23 | 58 | 35 | 27 | 53988 | ATP synthase subunit beta OS=Aedes aegypti OX=7159 GN=5577999 PE=3 SV=1 |
| 4. | tr|A0A182X065|A0A182X065\_ANOQN | 202.23 | 58 | 35 | 27 | 54022 | ATP synthase subunit beta OS=Anopheles quadriannulatus OX=34691 PE=3 SV=1 |
| 5. | tr|A0A4Y0BGI4|A0A4Y0BGI4\_ANOFN | 202.23 | 58 | 35 | 27 | 53986 | ATP synthase subunit beta OS=Anopheles funestus OX=62324 PE=3 SV=1 |
| 6. | tr|Q17FL3|Q17FL3\_AEDAE | 202.23 | 58 | 35 | 27 | 53974 | ATP synthase subunit beta OS=Aedes aegypti OX=7159 GN=AAEL003393 PE=3 SV=1 |
| 7. | tr|A0A023ETB9|A0A023ETB9\_AEDAL | 202.23 | 58 | 35 | 27 | 54017 | ATP synthase subunit beta OS=Aedes albopictus OX=7160 PE=2 SV=1 |
| 8. | tr|A0A023EUC8|A0A023EUC8\_AEDAL | 202.23 | 58 | 35 | 27 | 53912 | ATP synthase subunit beta OS=Aedes albopictus OX=7160 PE=2 SV=1 |
| 9. | tr|A0A3F2YYT0|A0A3F2YYT0\_ANOGA | 202.23 | 64 | 35 | 27 | 48804 | ATP synthase subunit beta OS=Anopheles gambiae OX=7165 PE=3 SV=1 |
| 10. | tr|Q16KR4|Q16KR4\_AEDAE | 173.56 | 27 | 21 | 21 | 85724 | Aconitate hydratase mitochondrial OS=Aedes aegypti OX=7159 GN=5580315 PE=3 SV=1 |
| 11. | tr|Q17EL3|Q17EL3\_AEDAE | 173.56 | 27 | 21 | 21 | 87334 | Aconitate hydratase mitochondrial OS=Aedes aegypti OX=7159 GN=AAEL003734 PE=3 SV=1 |
| 12. | tr|Q172T4|Q172T4\_AEDAE | 170.17 | 20 | 19 | 19 | 103646 | AAEL007306-PA OS=Aedes aegypti OX=7159 GN=AAEL007306 PE=4 SV=1 |
| 13. | tr|A0A023EWA2|A0A023EWA2\_AEDAL | 170.17 | 20 | 19 | 19 | 103615 | Putative ca2+-binding actin-bundling protein OS=Aedes albopictus OX=7160 PE=2 SV=1 |
| 14. | tr|Q178U9|Q178U9\_AEDAE | 174.83 | 47 | 18 | 18 | 39120 | Fructose-bisphosphate aldolase OS=Aedes aegypti OX=7159 GN=5567031 PE=3 SV=1 |
| 15. | tr|A0A023EQM6|A0A023EQM6\_AEDAL | 174.83 | 47 | 18 | 18 | 39152 | Fructose-bisphosphate aldolase OS=Aedes albopictus OX=7160 PE=2 SV=1 |
| 16. | Q16P20|CISY2\_AEDAE | 167.65 | 23 | 15 | 15 | 51641 | Probable citrate synthase 2 mitochondrial OS=Aedes aegypti OX=7159 GN=AAEL011789 PE=3 SV=1 |
| 17. | Q17GM7|CISY1\_AEDAE | 167.65 | 23 | 15 | 15 | 51657 | Probable citrate synthase 1 mitochondrial OS=Aedes aegypti OX=7159 GN=AAEL002956 PE=3 SV=1 |
| 18. | tr|A0A023ESP1|A0A023ESP1\_AEDAL | 167.65 | 23 | 15 | 15 | 51576 | Citrate synthase OS=Aedes albopictus OX=7160 PE=2 SV=1 |
| 19. | tr|T1E2L3|T1E2L3\_9DIPT | 167.65 | 23 | 15 | 15 | 51646 | Citrate synthase OS=Psorophora albipes OX=869069 PE=2 SV=1 |
| 20. | tr|A0A182GKM3|A0A182GKM3\_AEDAL | 167.65 | 23 | 15 | 15 | 51502 | Citrate synthase OS=Aedes albopictus OX=7160 GN=RP20\_CCG011547 PE=3 SV=1 |

Table 5: Top 20 proteins based on the highest -10lgp Cytobuster extracted proteins replicate 2

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **SN** | **Accession** | **-10lgP** | **Coverage (%)** | **#Peptides** | **#Unique** | **Avg. Mass** | **Description** |
| 1. | tr|Q1HRQ7|Q1HRQ7\_AEDAE | 193.31 | 39 | 25 | 21 | 59392 | ATP synthase subunit alpha OS=Aedes aegypti OX=7159 GN=5575914 PE=2 SV=1 |
| 2. | tr|A0A023EWA2|A0A023EWA2\_AEDAL | 179.43 | 23 | 20 | 20 | 103615 | Putative ca2+-binding actin-bundling protein OS=Aedes albopictus OX=7160 PE=2 SV=1 |
| 3. | tr|Q172T4|Q172T4\_AEDAE | 179.43 | 23 | 20 | 20 | 103646 | AAEL007306-PA OS=Aedes aegypti OX=7159 GN=AAEL007306 PE=4 SV=1 |
| 4. | tr|T1E2L3|T1E2L3\_9DIPT | 162.66 | 27 | 17 | 17 | 51646 | Citrate synthase OS=Psorophora albipes OX=869069 PE=2 SV=1 |
| 5. | tr|A0A023ESP1|A0A023ESP1\_AEDAL | 162.66 | 27 | 17 | 17 | 51576 | Citrate synthase OS=Aedes albopictus OX=7160 PE=2 SV=1 |
| 6. | tr|A0A182GKM3|A0A182GKM3\_AEDAL | 162.66 | 27 | 17 | 17 | 51502 | Citrate synthase OS=Aedes albopictus OX=7160 GN=RP20\_CCG011547 PE=3 SV=1 |
| 7. | tr|A0A1S4EZ75|A0A1S4EZ75\_AEDAE | 148.94 | 29 | 13 | 13 | 40568 | Glycerol-3-phosphate dehydrogenase [NAD(+)] OS=Aedes aegypti OX=7159 GN=5571293 PE=3 SV=1 |
| 8. | tr|Q16F38|Q16F38\_AEDAE | 139.4 | 24 | 11 | 11 | 57457 | Pyruvate kinase OS=Aedes aegypti OX=7159 GN=5565629 PE=1 SV=1 |
| 9. | tr|Q16LP5|Q16LP5\_AEDAE | 139.4 | 24 | 11 | 11 | 56218 | Pyruvate kinase OS=Aedes aegypti OX=7159 GN=AAEL012576 PE=3 SV=1 |
| 10. | tr|Q17E81|Q17E81\_AEDAE | 131.57 | 17 | 11 | 11 | 80970 | Glycerol-3-phosphate dehydrogenase OS=Aedes aegypti OX=7159 GN=5579187 PE=3 SV=1 |
| 11. | tr|Q17E82|Q17E82\_AEDAE | 131.57 | 17 | 11 | 11 | 81269 | Glycerol-3-phosphate dehydrogenase OS=Aedes aegypti OX=7159 GN=5579187 PE=3 SV=1 |
| 12. | tr|Q17AK0|Q17AK0\_AEDAE | 139.81 | 23 | 10 | 10 | 45570 | AAEL005269-PA OS=Aedes aegypti OX=7159 GN=AAEL005269 PE=4 SV=1 |
| 13. | tr|A0A1S4EXR8|A0A1S4EXR8\_AEDAE | 96.36 | 18 | 10 | 10 | 68763 | Malic enzyme OS=Aedes aegypti OX=7159 PE=3 SV=1 |
| 14. | tr|Q17M99|Q17M99\_AEDAE | 96.36 | 17 | 10 | 10 | 72027 | Malic enzyme OS=Aedes aegypti OX=7159 GN=AAEL001091 PE=3 SV=1 |
| 15. | tr|Q1HR67|Q1HR67\_AEDAE | 206.18 | 60 | 25 | 9 | 39874 | AAEL009185-PA OS=Aedes aegypti OX=7159 GN=5571596 PE=2 SV=1 |
| 16. | tr|Q16XK3|Q16XK3\_AEDAE | 132.83 | 29 | 9 | 9 | 32751 | ATP synthase subunit gamma OS=Aedes aegypti OX=7159 GN=5571150 PE=3 SV=1 |
| 17. | tr|Q17A27|Q17A27\_AEDAE | 126.8 | 21 | 9 | 9 | 63275 | Multifunctional fusion protein OS=Aedes aegypti OX=7159 GN=5566485 PE=3 SV=1 |
| 18. | tr|A0A023ETA6|A0A023ETA6\_AEDAL | 121.08 | 27 | 9 | 9 | 46553 | Putative enolase OS=Aedes albopictus OX=7160 PE=2 SV=1 |
| 19. | tr|Q17KK5|Q17KK5\_AEDAE | 121.08 | 27 | 9 | 9 | 46621 | AAEL001668-PA OS=Aedes aegypti OX=7159 GN=AAEL001668 PE=3 SV=1 |
| 20. | tr|Q16KR4|Q16KR4\_AEDAE | 168.93 | 24 | 21 | 8 | 85724 | Aconitate hydratase mitochondrial OS=Aedes aegypti OX=7159 GN=5580315 PE=3 SV=1 |

Table 6: Top 20 proteins based on the highest -10lgp score Cytobuster extracted proteins replicate 3

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **SN** | **Accession** | **-10lgP** | **Coverage (%)** | **#Peptides** | **#Unique** | **Avg. Mass** | **Description** |
| 1. | tr|Q17EL3|Q17EL3\_AEDAE | 172.8 | 33 | 25 | 25 | 87334 | Aconitate hydratase mitochondrial OS=Aedes aegypti OX=7159 GN=AAEL003734 PE=3 SV=1 |
| 2. | tr|Q16KR4|Q16KR4\_AEDAE | 172.8 | 33 | 25 | 25 | 85724 | Aconitate hydratase mitochondrial OS=Aedes aegypti OX=7159 GN=5580315 PE=3 SV=1 |
| 3. | tr|Q1HR67|Q1HR67\_AEDAE | 184.28 | 52 | 22 | 22 | 39874 | AAEL009185-PA OS=Aedes aegypti OX=7159 GN=5571596 PE=2 SV=1 |
| 4. | tr|Q1HRQ7|Q1HRQ7\_AEDAE | 175.15 | 41 | 25 | 22 | 59392 | ATP synthase subunit alpha OS=Aedes aegypti OX=7159 GN=5575914 PE=2 SV=1 |
| 5. | tr|Q172T4|Q172T4\_AEDAE | 160.59 | 20 | 19 | 19 | 103646 | AAEL007306-PA OS=Aedes aegypti OX=7159 GN=AAEL007306 PE=4 SV=1 |
| 6. | tr|A0A023EWA2|A0A023EWA2\_AEDAL | 160.59 | 20 | 19 | 19 | 103615 | Putative ca2+-binding actin-bundling protein OS=Aedes albopictus OX=7160 PE=2 SV=1 |
| 7. | tr|Q17KS3|Q17KS3\_AEDAE | 141.91 | 33 | 13 | 13 | 38178 | Glycerol-3-phosphate dehydrogenase [NAD(+)] OS=Aedes aegypti OX=7159 GN=AAEL001593 PE=3 SV=1 |
| 8. | tr|Q17KS5|Q17KS5\_AEDAE | 141.91 | 32 | 13 | 13 | 38903 | Glycerol-3-phosphate dehydrogenase [NAD(+)] OS=Aedes aegypti OX=7159 GN=5571293 PE=3 SV=1 |
| 9. | tr|Q17KS4|Q17KS4\_AEDAE | 141.91 | 32 | 13 | 13 | 39292 | Glycerol-3-phosphate dehydrogenase [NAD(+)] OS=Aedes aegypti OX=7159 GN=5571293 PE=3 SV=1 |
| 10. | tr|A0A1S4EZ75|A0A1S4EZ75\_AEDAE | 141.91 | 31 | 13 | 13 | 40568 | Glycerol-3-phosphate dehydrogenase [NAD(+)] OS=Aedes aegypti OX=7159 GN=5571293 PE=3 SV=1 |
| 11. | tr|Q17NG8|Q17NG8\_AEDAE | 138.5 | 16 | 13 | 13 | 96956 | Alpha-1 4 glucan phosphorylase OS=Aedes aegypti OX=7159 GN=5565921 PE=3 SV=1 |
| 12. | tr|Q16ZI5|Q16ZI5\_AEDAE | 186.9 | 55 | 26 | 12 | 44274 | AAEL008166-PA OS=Aedes aegypti OX=7159 GN=AAEL008166 PE=4 SV=1 |
| 13. | tr|A0A1S4FIY1|A0A1S4FIY1\_AEDAE | 186.9 | 69 | 26 | 12 | 35296 | Uncharacterized protein OS=Aedes aegypti OX=7159 GN=5570233 PE=3 SV=1 |
| 14. | tr|J9HYM2|J9HYM2\_AEDAE | 143.81 | 45 | 11 | 11 | 35441 | Glyceraldehyde-3-phosphate dehydrogenase OS=Aedes aegypti OX=7159 GN=23687404 PE=3 SV=1 |
| 15. | tr|Q16LP5|Q16LP5\_AEDAE | 128.13 | 24 | 11 | 11 | 56218 | Pyruvate kinase OS=Aedes aegypti OX=7159 GN=AAEL012576 PE=3 SV=1 |
| 16. | tr|Q16F38|Q16F38\_AEDAE | 128.13 | 24 | 11 | 11 | 57457 | Pyruvate kinase OS=Aedes aegypti OX=7159 GN=5565629 PE=1 SV=1 |
| 17. | tr|A0A1S4EXR8|A0A1S4EXR8\_AEDAE | 111.42 | 21 | 11 | 11 | 68763 | Malic enzyme OS=Aedes aegypti OX=7159 PE=3 SV=1 |
| 18. | tr|Q17M99|Q17M99\_AEDAE | 111.42 | 21 | 11 | 11 | 72027 | Malic enzyme OS=Aedes aegypti OX=7159 GN=AAEL001091 PE=3 SV=1 |
| 19. | tr|Q17E82|Q17E82\_AEDAE | 144.47 | 15 | 10 | 10 | 81269 | Glycerol-3-phosphate dehydrogenase OS=Aedes aegypti OX=7159 GN=5579187 PE=3 SV=1 |
| 20. | tr|Q17E81|Q17E81\_AEDAE | 144.47 | 15 | 10 | 10 | 80970 | Glycerol-3-phosphate dehydrogenase OS=Aedes aegypti OX=7159 GN=5579187 PE=3 SV=1 |