|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| ***E.gracilis* subunits** | ***E.gracilis* subunit identifier** | **GenBank accession code** | **ORF MW [kDa]** | **previously identified in *E. gracilis*** | ***S. cerevisiae* gene nomenclature/name in previous identification** | **comments** | ***Euglena-Trypanosoma* BLAST E-value** |
| **α** | comp27580\_c0\_seq1 | GDJR01036292.1 | 61,84 | universally conserved | ATP1 | canonical F1 | - |
| **β** | comp30487\_c1\_seq1 | GDJR01048402.1 | 53,17 | universally conserved | ATP2 | canonical F1 | - |
| **γ** | EG\_transcript\_19235 | GEFR01019235.1 | 35,07 | universally conserved | ATP3 | canonical F1 | - |
| **δ** | comp8147\_c0\_seq1 | GDJR01108837.1 | 19,54 | universally conserved | ATP16 | canonical F1 | - |
| **ε** | comp36626\_c0\_seq1 | GDJR01100113.1 | 8,74 | universally conserved | ATP15 | canonical F1 | - |
| **p18** | comp36594\_c0\_seq1 | GDJR01100103.1 | 20,97 | Yadav et al, Perez et al | p18 | euglenozoa-specific F1 | - |
| **IF1** | EG\_transcript\_49190 | GEFR01049155.1 | 11.67 | universally conserved | INH1 | F1 inhibitor | - |
| **OSCP** | comp36635\_c0\_seq1 | GDJR01100117.1 | 29.53 | universally conserved | ATP5 | Fo yeast homolog | - |
| **subunit *a*** | sga\_contig\_684056 | - | 32.61 | newly identified | ATP6 | Fo yeast homolog | - |
| **subunit *b*** | comp8208\_c0\_seq1 | GDJR01108903.1 | 12.66 | newly identified | ATP4 | Fo yeast homolog | - |
| **subunit c** | EG\_transcript\_45706 | GEFR01045692.1 | 10.81 | universally conserved | ATP9 | Fo yeast homolog | - |
| **subunit *d*** | comp20520\_c0\_seq1 | GDJR01017994.1 | 53.87 | Yadav et al, Perez et al | ATP7/ATPTB2 | Fo yeast homolog | 0.19 |
| **subunit *f*** | VDSF\_6\_rev\_Run01\_Cp357\_MD1/ G11.esd | EC611052.1 | 11.18 | newly identified | ATP17 | Fo yeast homolog | - |
| **subunit *i/j*** | comp12674\_c0\_seq1 | GDJR01005239.1 | 12.51 | Yadav et al | ATP18/ATPTB10/ UP19  | Fo yeast homolog | 0.063 |
| **subunit *k*** | EG\_transcript\_55785 | GEFR01055688.1 | 12.73 | Yadav et al | ATP19/UP21  | Fo yeast homolog | - |
| **subunit 8** | sga\_contig\_684056 |  KT732265.1 | 7.01 | newly identified | ATP8 | Fo yeast homolog | - |
| **ATPTB1** | EG\_transcript\_7573 | GEFR01007572.1 | 55.93 | Yadav et al, Perez et al | ATPTB1 | Fo *Trypanosoma* homolog | 2E-6 |
| **ATPTB3** | EG\_transcript\_14428 | GEFR01014423.1 | 35.14 | Yadav et al, Perez et al | ATPTB3 | Fo *Trypanosoma* homolog/putative isocitrate dehydrogenase homolog | 8E-5 |
| **ATPTB4** | comp8167\_c0\_seq1 | GDJR01108860.1 | 18.81 | Yadav et al, Perez et al | ATPTB4 | Fo *Trypanosoma* homolog | 9E-24 |
| **ATPTB6** | EG\_transcript\_28774 | GEFR01028782.1 | 21.71 | Yadav et al, Perez et al | ATPTB6 | Fo *Trypanosoma* homolog | 7E-11 |
| **ATPTB12** | comp12685\_c0\_seq1 | GDJR01005257.1 | 11.35 | Yadav et al, Perez et al | ATPTB12 | Fo *Trypanosoma* homolog | 9E-8 |
| **ATPEG1** | comp12813\_c0\_seq1 | GDJR01005511.1 | 19.72 | Yadav et al | UP14 (comp51661\_c0\_seq2) | no homolog outside *Euglena* identified | - |
| **ATPEG2** | EG\_transcript\_33701 | GEFR01033662.1 | 16.18 | Yadav et al | UP15comp46683\_c0\_seq1\_cut | no homolog outside *Euglena* identified | - |
| **ATPEG3** | comp17420\_c0\_seq1 | GDJR01012366.1 | 13.79 | Yadav et al | UP18(gi | 109777597\_cut) | no homolog outside *Euglena* identified | 4E-6 |
| **ATPEG4** | EG\_transcript\_49361 | GEFR01049309.1 | 13.69 | Yadav et al | UP16 (comp48845\_c0\_seq1\_cut) | no homolog outside *Euglena* identified | - |
| **ATPEG5** | EG\_transcript\_70983 | GEFR01071033.1 | 10.81 | newly identified | -  | cytochrome c oxidase assembly factor 6, putative homolog | - |
| **ATPEG6** | comp30797\_c0\_seq1 | GDJR01049874.1 | 9.22 | newly identified | -  | no homolog outside *Euglena* identified | - |
| **ATPEG7** | comp8129\_c0\_seq1 | GDJR01108818.1 | 8.85 | newly identified | -  | no homolog outside *Euglena* identified | - |
| **ATPEG8** | comp8203\_c0\_seq1 | GDJR01108900.1 | 7.43 | newly identified | -  | no homolog outside *Euglena* identified | - |

**Table S3: Subunits of the *E. gracilis* ATP synthase dimer identified in this study.**