Supplementary Table I. Proteins identified from Tick-derived vesicles.

LC-MS/MS analysis revealed a total of 20 protein groups including 287 proteins.

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Reference
FileScan
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tr|A0A1E1X3F6|A0A1E1X3F6_9ACAR Putative actin related protein 1 OS=Amblyomma aureolatum OX=18776
tr|A0A224YSP0|A0A224YSP0_9ACAR Actin OS=Rhipicephalus zambeziensis OX=60191 PE=3 SV=1
tr|A0A131XI67|A0A131XI67_9ACAR Putative actin-2 OS=Hyalomma excavatum OX=257692 PE=2 SV=1
tr|A0A023FZB7|A0A023FZB7_9ACAR Putative actin OS=Amblyomma parvum OX=251391 PE=2 SV=1
tr|A4UTU3|A4UTU3_DERVA Beta-actin OS=Dermacentor variabilis OX=34621 PE=2 SV=2
tr|Q5D579|Q5D579_IXORI Actin (Fragment) OS=Ixodes ricinus OX=34613 PE=2 SV=1
tr|A0A023FX30|A0A023FX30_9ACAR Putative actin OS=Amblyomma parvum OX=251391 PE=2 SV=1
tr|A0A131XSH9|A0A131XSH9_IXORI Putative actin OS=Ixodes ricinus OX=34613 PE=2 SV=1
tr|A0A2R5L7C1|A0A2R5L7C1_9ACAR Putative actin OS=Ornithodoros turicata OX=34597 PE=4 SV=1
tr|A0A2R5LJK9|A0A2R5LJK9_9ACAR Putative actin OS=Ornithodoros turicata OX=34597 PE=4 SV=1
tr|D9IFL5|D9IFL5_9ACAR Actin OS=Hyalomma asiaticum OX=266040 PE=2 SV=1
tr|A9ZT00|A9ZT00_IXOPE Actin OS=Ixodes persulcatus OX=34615 GN=act PE=2 SV=1
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tr|A0A023GJC4|A0A023GJC4_9ACAR Putative actin OS=Amblyomma triste OX=251400 PE=2 SV=1
tr|A0A097CK67|A0A097CK67_HAEFA Actin OS=Haemaphysalis flava OX=181088 PE=2 SV=1
tr|G3MLM7|G3MLM7_9ACAR Uncharacterized protein OS=Amblyomma maculatum OX=34609 PE=2 SV=1
tr|A0A131XNB9|A0A131XNB9_9ACAR Putative actin-related protein (Fragment) OS=Hyalomma excavatum O
tr|A0A293M032|A0A293M032_ORNER Actin (Fragment) OS=Ornithodoros erraticus OX=265619 PE=3 SV=1
tr|Q6QD58|Q6QD58_ORNMO Actin OS=Ornithodoros moubata OX=6938 PE=2 SV=1
tr|Q5CAR2|Q5CAR2_IXORI Actin OS=Ixodes ricinus OX=34613 GN=act PE=2 SV=1
tr|A0A023GJF8|A0A023GJF8_9ACAR Putative actin OS=Amblyomma triste OX=251400 PE=2 SV=1
tr|Q6X4V4|Q6X4V4_RHIMP Actin 1 OS=Rhipicephalus microplus OX=6941 PE=2 SV=1
tr|A0A293M9S1|A0A293M9S1_ORNER Actin (Fragment) OS=Ornithodoros erraticus OX=265619 PE=3 SV=1
tr|A0A293M4Q5|A0A293M4Q5_ORNER Actin (Fragment) OS=Ornithodoros erraticus OX=265619 PE=3 SV=1
tr|A0A293N6Y3|A0A293N6Y3_ORNER Uncharacterized protein (Fragment) OS=Ornithodoros erraticus OX=26
tr|Q3LGW2|Q3LGW2_ORNMO Actin OS=Ornithodoros moubata OX=6938 PE=2 SV=1
tr|Q6X4W2|Q6X4W2_RHIAP Actin OS=Rhipicephalus appendiculatus OX=34631 GN=Act1 PE=2 SV=1
tr|D9IFL4|D9IFL4_9ACAR Actin OS=Rhipicephalus haemaphysaloides OX=237073 PE=2 SV=1
tr|L7M8J7|L7M8J7_9ACAR Putative actin OS=Rhipicephalus pulchellus OX=72859 PE=2 SV=1
tr|A0A023FIL9|A0A023FIL9_9ACAR Putative actin OS=Amblyomma cajennense OX=34607 PE=2 SV=1
tr|A0A023FKT1|A0A023FKT1_9ACAR Putative actin OS=Amblyomma cajennense OX=34607 PE=2 SV=1
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R933,31105
R933,16143
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tr|A0A023GHR7|A0A023GHR7_9ACAR Histone H2B OS=Amblyomma triste OX=251400 PE=2 SV=1
tr|A0A131Y6E4|A0A131Y6E4_IXORI Histone H2B (Fragment) OS=Ixodes ricinus OX=34613 PE=2 SV=1
tr|A0A0K8RN92|A0A0K8RN92_IXORI Histone H2B (Fragment) OS=Ixodes ricinus OX=34613 PE=2 SV=1
tr|G3MN10|G3MN10_9ACAR Histone H2B OS=Amblyomma maculatum OX=34609 PE=2 SV=1
tr|A0A293MAR2|A0A293MAR2_ORNER Histone H2B (Fragment) OS=Ornithodoros erraticus OX=265619 PE=3
tr|A0A0C9RRX6|A0A0C9RRX6_AMBAM Histone H2B (Fragment) OS=Amblyomma americanum OX=6943 PE=2
tr|A0A1E1WXS4|A0A1E1WXS4_9ACAR Histone H2B (Fragment) OS=Amblyomma aureolatum OX=187763 PE=
tr|A0A131XRH5|A0A131XRH5_9ACAR Histone H2B OS=Hyalomma excavatum OX=257692 PE=2 SV=1
tr|A0A096XIA7|A0A096XIA7_9ACAR Histone H2B OS=Nuttalliella namaqua OX=1029659 PE=3 SV=1
tr|A0A023FWA6|A0A023FWA6_9ACAR Histone H2B OS=Amblyomma parvum OX=251391 PE=2 SV=1
tr|V5I1T0|V5I1T0_IXORI Histone H2B OS=Ixodes ricinus OX=34613 PE=2 SV=1

R933,30437
R933,31510
tr|A0A0K8RID7|A0A0K8RID7_IXORI Elongation factor 1-alpha OS=Ixodes ricinus OX=34613 PE=2 SV=1
tr|A0A1E1XHQ1|A0A1E1XHQ1_9ACAR Elongation factor 1-alpha OS=Amblyomma aureolatum OX=187763 PE
tr|F0J8I9|F0J8I9_AMBVA Elongation factor 1-alpha (Fragment) OS=Amblyomma variegatum OX=34610 PE=2
tr|A0A293N8J1|A0A293N8J1_ORNER Elongation factor 1-alpha (Fragment) OS=Ornithodoros erraticus OX=26
tr|A0A1Z5LG77|A0A1Z5LG77_ORNMO Elongation factor 1-alpha (Fragment) OS=Ornithodoros moubata OX=6
tr|A0A023FLP4|A0A023FLP4_9ACAR Elongation factor 1-alpha (Fragment) OS=Amblyomma cajennense OX=3
tr|B7Q349|B7Q349_IXOSC Elongation factor 1-alpha OS=Ixodes scapularis OX=6945 GN=8035179 PE=3 SV=1
tr|A0A034WYY9|A0A034WYY9_RHIMP Elongation factor 1-alpha OS=Rhipicephalus microplus OX=6941 PE=3
tr|A0A1E1XAX2|A0A1E1XAX2_9ACAR Elongation factor 1-alpha (Fragment) OS=Amblyomma aureolatum OX=
tr|A0A0K8R5B0|A0A0K8R5B0_IXORI Putative ptz00141 elongation factor 1-alpha OS=Ixodes ricinus OX=3461
tr|G3MGH3|G3MGH3_9ACAR Uncharacterized protein (Fragment) OS=Amblyomma maculatum OX=34609 PE
tr|A0A2R5LI30|A0A2R5LI30_9ACAR Putative translation elongation factor ef-1 alpha/tu OS=Ornithodoros turi
tr|A0A224YXN0|A0A224YXN0_9ACAR Elongation factor 1-alpha OS=Rhipicephalus zambeziensis OX=60191 PE
tr|A0A131Z5A0|A0A131Z5A0_RHIAP Elongation factor 1-alpha OS=Rhipicephalus appendiculatus OX=34631 P
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tr|A0A023FY92|A0A023FY92_9ACAR Putative translation elongation factor ef-1 alpha/tu OS=Amblyomma pa
R933,13646
R933,13647
tr|A0A0C9R2A0|A0A0C9R2A0_AMBAM Putative adp/atp translocase OS=Amblyomma americanum OX=6943
tr|A0A1E1XIT8|A0A1E1XIT8_9ACAR Putative adp/atp translocase (Fragment) OS=Amblyomma aureolatum OX
tr|A0A1Z5LG78|A0A1Z5LG78_ORNMO Uncharacterized protein (Fragment) OS=Ornithodoros moubata OX=6
tr|A0A131Y0U7|A0A131Y0U7_IXORI Putative mitochondrial adp/atp carrier OS=Ixodes ricinus OX=34613 PE=
tr|A0A0K8R6D7|A0A0K8R6D7_IXORI Putative mitochondrial adp/atp carrier OS=Ixodes ricinus OX=34613 PE=
tr|V5IFY7|V5IFY7_IXORI Putative mitochondrial adp/atp carrier OS=Ixodes ricinus OX=34613 PE=2 SV=1
tr|A0A1Z5L6M8|A0A1Z5L6M8_ORNMO Uncharacterized protein (Fragment) OS=Ornithodoros moubata OX=
tr|A0A224YZR0|A0A224YZR0_9ACAR Solute carrier family 25 (Mitochondrial adenine nucleotide translocator
tr|A0A023GL78|A0A023GL78_9ACAR Putative mitochondrial adp/atp carrier (Fragment) OS=Amblyomma tris
tr|A0A147BAB4|A0A147BAB4_9ACAR Adp atp translocase 1 (Fragment) OS=Carios mimon OX=360319 PE=3 S
tr|A0A1Z5LG51|A0A1Z5LG51_ORNMO ADP-ATP translocase 4 (Fragment) OS=Ornithodoros moubata OX=693
tr|G3MLP0|G3MLP0_9ACAR Uncharacterized protein OS=Amblyomma maculatum OX=34609 PE=2 SV=1
tr|F0JA23|F0JA23_AMBVA ADP/ATP translocase OS=Amblyomma variegatum OX=34610 PE=2 SV=1
tr|A0A1E1XIG3|A0A1E1XIG3_9ACAR Putative mitochondrial adp/atp carrier (Fragment) OS=Amblyomma aure
tr|A0A293MP87|A0A293MP87_ORNER ADP/ATP translocase 4 (Fragment) OS=Ornithodoros erraticus OX=26
tr|A0A131YNP5|A0A131YNP5_RHIAP Solute carrier family 25 (Mitochondrial adenine nucleotide translocator
tr|A0A147BVU8|A0A147BVU8_IXORI Putative mitochondrial adp/atp carrier OS=Ixodes ricinus OX=34613 PE=
tr|B5M782|B5M782_AMBAM ADP/ATP translocase (Fragment) OS=Amblyomma americanum OX=6943 PE=2
tr|A0A023FIQ0|A0A023FIQ0_9ACAR Putative mitochondrial adp/atp carrier OS=Amblyomma cajennense OX=
tr|A0A023FHC1|A0A023FHC1_9ACAR Putative mitochondrial adp/atp carrier OS=Amblyomma cajennense OX
tr|Q4PMB2|Q4PMB2_IXOSC ADP/ATP translocase OS=Ixodes scapularis OX=6945 PE=2 SV=1
R933,30778
tr|A0A0C9S156|A0A0C9S156_AMBAM Putative acyl-coa synthetase family member 4 (Fragment) OS=Amblyo
R933,31614
tr|A0A0C9SCJ0|A0A0C9SCJ0_AMBAM Putative 60 kDa chaperonin (Fragment) OS=Amblyomma americanum
R933,31558
tr|A0A0K8R692|A0A0K8R692_IXORI Uncharacterized protein OS=Ixodes ricinus OX=34613 PE=2 SV=1
R933,31037
tr|A0A131XCY7|A0A131XCY7_9ACAR Tubulin alpha chain (Fragment) OS=Hyalomma excavatum OX=257692 P
tr|A0A1E1XEP2|A0A1E1XEP2_9ACAR Tubulin alpha chain (Fragment) OS=Amblyomma aureolatum OX=18776

tr|A0A023FZA1|A0A023FZA1_9ACAR Tubulin alpha chain (Fragment) OS=Amblyomma parvum OX=251391 PE
tr|A0A2R5LH80|A0A2R5LH80_9ACAR Putative alpha-1 tubulin OS=Ornithodoros turicata OX=34597 PE=4 SV=
tr|A0A131XWB5|A0A131XWB5_IXORI Tubulin alpha chain (Fragment) OS=Ixodes ricinus OX=34613 PE=2 SV=
tr|B7PGI8|B7PGI8_IXOSC Tubulin alpha chain OS=Ixodes scapularis OX=6945 GN=8052898 PE=3 SV=1
tr|A0A224Z2L9|A0A224Z2L9_9ACAR Tubulin alpha chain OS=Rhipicephalus zambeziensis OX=60191 PE=3 SV=
tr|B7P872|B7P872_IXOSC Alpha tubulin, putative OS=Ixodes scapularis OX=6945 GN=8026030 PE=3 SV=1
tr|A0A131Z6B0|A0A131Z6B0_RHIAP Tubulin alpha chain OS=Rhipicephalus appendiculatus OX=34631 PE=3 S
tr|A0A023FHB8|A0A023FHB8_9ACAR Tubulin alpha chain (Fragment) OS=Amblyomma cajennense OX=34607
tr|A0A293M7T6|A0A293M7T6_ORNER Tubulin alpha chain (Fragment) OS=Ornithodoros erraticus OX=26561
tr|A0A224YJ96|A0A224YJ96_9ACAR Tubulin alpha chain (Fragment) OS=Rhipicephalus zambeziensis OX=6019
tr|A0A224ZBA7|A0A224ZBA7_9ACAR Tubulin alpha chain (Fragment) OS=Rhipicephalus zambeziensis OX=601
tr|G3MGN2|G3MGN2_9ACAR Tubulin alpha chain (Fragment) OS=Amblyomma maculatum OX=34609 PE=2 S
tr|A0A023GNK0|A0A023GNK0_9ACAR Tubulin alpha chain (Fragment) OS=Amblyomma triste OX=251400 PE=
tr|A0A1E1XUK0|A0A1E1XUK0_9ACAR Tubulin alpha chain (Fragment) OS=Amblyomma sculptum OX=158141
tr|A0A131ZCB2|A0A131ZCB2_RHIAP Tubulin alpha chain (Fragment) OS=Rhipicephalus appendiculatus OX=34
tr|A0A023FK91|A0A023FK91_9ACAR Tubulin alpha chain (Fragment) OS=Amblyomma cajennense OX=34607
tr|A0A131ZD36|A0A131ZD36_RHIAP Tubulin alpha chain (Fragment) OS=Rhipicephalus appendiculatus OX=3
tr|A0A131XG32|A0A131XG32_9ACAR Tubulin alpha chain (Fragment) OS=Hyalomma excavatum OX=257692
tr|L7MD37|L7MD37_9ACAR Tubulin alpha chain (Fragment) OS=Rhipicephalus pulchellus OX=72859 PE=2 SV=
tr|L7M1J3|L7M1J3_9ACAR Tubulin alpha chain OS=Rhipicephalus pulchellus OX=72859 PE=2 SV=1
R933,31402
tr|A0A131XHQ7|A0A131XHQ7_9ACAR Putative vacuolar atp synthase subunit e OS=Hyalomma excavatum O
tr|A0A0C9SBI7|A0A0C9SBI7_AMBAM Putative vacuolar atp synthase subunit e OS=Amblyomma americanum
tr|L7LZ11|L7LZ11_9ACAR Putative vacuolar h +-atpase 26kd e subunit OS=Rhipicephalus pulchellus OX=72859
tr|A0A224ZBE4|A0A224ZBE4_9ACAR V-type H+-transporting ATPase subunit E OS=Rhipicephalus zambeziensi
tr|A0A023GGF9|A0A023GGF9_9ACAR Putative vacuolar h+-atpase v1 sector subunit e (Fragment) OS=Ambly
tr|A0A023GGK7|A0A023GGK7_9ACAR Putative vacuolar h+-atpase v1 sector subunit e (Fragment) OS=Ambly
tr|A0A1E1X8S7|A0A1E1X8S7_9ACAR Putative vacuolar atp synthase subunit e OS=Amblyomma aureolatum O
tr|A0A023FH08|A0A023FH08_9ACAR Putative vacuolar h+-atpase v1 sector subunit e (Fragment) OS=Amblyo
tr|A0A023FVL5|A0A023FVL5_9ACAR Putative vacuolar h+-atpase v1 sector subunit e (Fragment) OS=Amblyo
tr|A0A131YQN0|A0A131YQN0_RHIAP V-type H+-transporting ATPase subunit E OS=Rhipicephalus appendicul
tr|A0A023FH56|A0A023FH56_9ACAR Putative vacuolar h+-atpase v1 sector subunit e (Fragment) OS=Amblyo
R933,31192
tr|A0A131XMT1|A0A131XMT1_9ACAR Proteinral transcription factor iif subunit (Fragment) OS=Hyalomma ex
R933,31381
tr|A0A131Y846|A0A131Y846_IXORI Putative vegetative cell wall protein gp1 (Fragment) OS=Ixodes ricinus OX
R933,31439
tr|A0A1E1WWD0|A0A1E1WWD0_9ACAR Putative ubiquitin/40s ribosomal protein s27a (Fragment) OS=Ambl
tr|A0A131XIP5|A0A131XIP5_9ACAR Putative ubiquitin c variant (Fragment) OS=Hyalomma excavatum OX=25
tr|A0A0C9SCH5|A0A0C9SCH5_AMBAM Putative 40s ribosomal protein s27a OS=Amblyomma americanum OX
tr|A0A1E1X272|A0A1E1X272_9ACAR Putative ubiquitin OS=Amblyomma aureolatum OX=187763 PE=2 SV=1
tr|A0A1Z5LGF2|A0A1Z5LGF2_ORNMO Ubiquitin-40S ribosomal protein S27a (Fragment) OS=Ornithodoros m
tr|A0A224ZBP0|A0A224ZBP0_9ACAR Ubiquitin/40s ribosomal protein s27a fusion OS=Rhipicephalus zambezi
tr|A0A131XPH6|A0A131XPH6_9ACAR Putative 40s ribosomal protein s27a OS=Hyalomma excavatum OX=257
tr|A0A1Z5LER6|A0A1Z5LER6_ORNMO Uncharacterized protein (Fragment) OS=Ornithodoros moubata OX=69
tr|A0A0C9S1S7|A0A0C9S1S7_AMBAM Putative polyubiquitin OS=Amblyomma americanum OX=6943 PE=2 SV
tr|A0A131Y7D2|A0A131Y7D2_IXORI Putative 40s ribosomal protein s27a (Fragment) OS=Ixodes ricinus OX=3
tr|A0A090X8K1|A0A090X8K1_IXORI Putative polyubiquitin (Fragment) OS=Ixodes ricinus OX=34613 PE=2 SV=
tr|A0A131XRZ5|A0A131XRZ5_IXORI Putative polyubiquitin (Fragment) OS=Ixodes ricinus OX=34613 PE=2 SV=
tr|V5I3A6|V5I3A6_IXORI Putative ubiquitin c isoform cra a ubiquitin c isoform cra a OS=Ixodes ricinus OX=346

tr|B2D284|B2D284_ORNCO Ubiquitin/40S ribosomal protein S27a (Fragment) OS=Ornithodoros coriaceus OX
tr|A0A0C9SDC7|A0A0C9SDC7_AMBAM Putative polyubiquitin OS=Amblyomma americanum OX=6943 PE=2 S
tr|V5I3F4|V5I3F4_IXORI Putative ubiquitin/40s ribosomal protein (Fragment) OS=Ixodes ricinus OX=34613 PE
tr|L7LX35|L7LX35_9ACAR Putative ubiquitin/40s ribosomal protein s27a fusion OS=Rhipicephalus pulchellus
tr|A0A224YY51|A0A224YY51_9ACAR Polyubiquitin (Fragment) OS=Rhipicephalus zambeziensis OX=60191 PE=
tr|A0A023GMC0|A0A023GMC0_9ACAR Uncharacterized protein (Fragment) OS=Amblyomma triste OX=2514
tr|A0A023G5B1|A0A023G5B1_9ACAR Putative ubiquitin/40s ribosomal protein s27a fusion OS=Amblyomma
tr|A0A2R5LB09|A0A2R5LB09_9ACAR Putative ubiquitin/40s ribosomal protein s27a (Fragment) OS=Ornithod
tr|A0A023GEE1|A0A023GEE1_9ACAR Putative ubiquitin-40s ribosomal protein s27a (Fragment) OS=Amblyom
tr|E2J6V0|E2J6V0_9ACAR Ubiquitin/ribosomal protein S27a fusion protein (Fragment) OS=Hyalomma rufipes
tr|Q09JW5|Q09JW5_ARGMO Ubiquitin/40S ribosomal protein S27a fusion protein OS=Argas monolakensis O
tr|F0J9P3|F0J9P3_AMBVA Ubiquitin (Fragment) OS=Amblyomma variegatum OX=34610 PE=2 SV=1
tr|A0A2R5LIV0|A0A2R5LIV0_9ACAR Putative ubiquitin/40s ribosomal protein s27a fusion OS=Ornithodoros tu
tr|B7SP62|B7SP62_DERVA Ubiquitin/ribosomal protein S27a fusion protein OS=Dermacentor variabilis OX=34
tr|A0A023FH61|A0A023FH61_9ACAR Putative ubiquitin/40s ribosomal protein s27a fusion OS=Amblyomma c
tr|G3MMT5|G3MMT5_9ACAR Uncharacterized protein OS=Amblyomma maculatum OX=34609 PE=2 SV=1
tr|G3MHK9|G3MHK9_9ACAR Uncharacterized protein (Fragment) OS=Amblyomma maculatum OX=34609 PE
tr|A0A224YW71|A0A224YW71_9ACAR Polyubiquitin-B (Fragment) OS=Rhipicephalus zambeziensis OX=60191
tr|E2J6Y2|E2J6Y2_9ACAR Ubiquitin (Fragment) OS=Hyalomma rufipes OX=72862 PE=2 SV=1
tr|F0J9K1|F0J9K1_AMBVA Ubiquitin (Fragment) OS=Amblyomma variegatum OX=34610 PE=2 SV=1
tr|Q4PM40|Q4PM40_IXOSC Ubiquitin/ribosomal protein S27a fusion protein OS=Ixodes scapularis OX=6945
tr|A0A0K8RRC3|A0A0K8RRC3_IXORI Putative ubiquitin/40s ribosomal protein s27a fusion (Fragment) OS=Ixo
tr|A0A293M9I9|A0A293M9I9_ORNER Uncharacterized protein (Fragment) OS=Ornithodoros erraticus OX=26
tr|M4GY12|M4GY12_ANTDE Polyubiquitin-B (Fragment) OS=Antricola delacruzi OX=480319 PE=2 SV=1
tr|A0A1E1XER6|A0A1E1XER6_9ACAR Putative ubiquitin c variant (Fragment) OS=Amblyomma aureolatum OX
tr|A0A1E1WWS9|A0A1E1WWS9_9ACAR Putative ubiquitin/ribosomal fusion protein (Fragment) OS=Amblyo
tr|A0A023FGV8|A0A023FGV8_9ACAR Putative ubiquitin/40s ribosomal protein s27a fusion OS=Amblyomma
tr|A6N9Z0|A6N9Z0_ORNPR Ubiquitin/40S ribosomal protein S27a OS=Ornithodoros parkeri OX=140564 PE=2
tr|A0A023FGJ7|A0A023FGJ7_9ACAR Uncharacterized protein (Fragment) OS=Amblyomma cajennense OX=34
tr|A0A023FDP0|A0A023FDP0_9ACAR Uncharacterized protein (Fragment) OS=Amblyomma cajennense OX=3
tr|A0A1E1WZ33|A0A1E1WZ33_9ACAR Putative 40s ribosomal protein s27a OS=Amblyomma aureolatum OX=
tr|B7P0U0|B7P0U0_IXOSC 40S ribosomal protein S27A, putative OS=Ixodes scapularis OX=6945 GN=8023181
tr|B7Q5Q7|B7Q5Q7_IXOSC Ubiquitin/40S ribosomal protein S27A fusion, putative OS=Ixodes scapularis OX=6
tr|A6NA05|A6NA05_ORNPR Ubiquitin/40S ribosomal protein S27a OS=Ornithodoros parkeri OX=140564 PE=
tr|A0A0K8R331|A0A0K8R331_IXORI Putative ubiquitin/40s ribosomal protein s27a fusion (Fragment) OS=Ixod
tr|A0A0K8RQA6|A0A0K8RQA6_IXORI Putative ubiquitin/40s ribosomal protein s27a fusion (Fragment) OS=Ixo
tr|V5HFB2|V5HFB2_IXORI Putative polyubiquitin-b (Fragment) OS=Ixodes ricinus OX=34613 PE=2 SV=1
tr|A0A090X8L8|A0A090X8L8_IXORI Putative polyubiquitin babesia bovis t2bo polyubiquitin (Fragment) OS=Ix
tr|A0A0K8RL79|A0A0K8RL79_IXORI Putative ubiquitin/40s ribosomal protein s27a fusion OS=Ixodes ricinus O
tr|A0A0K8RP30|A0A0K8RP30_IXORI Putative ubiquitin/40s ribosomal protein s27a fusion (Fragment) OS=Ixo
tr|A0A147BVN0|A0A147BVN0_IXORI Putative 40s ribosomal protein s27a (Fragment) OS=Ixodes ricinus OX=3
tr|A0A0K8R2I3|A0A0K8R2I3_IXORI Putative ubiquitin/40s ribosomal protein s27a (Fragment) OS=Ixodes ricin
tr|A0A131YQV0|A0A131YQV0_RHIAP Ubiquitin C OS=Rhipicephalus appendiculatus OX=34631 PE=4 SV=1
tr|A0A131Z6S6|A0A131Z6S6_RHIAP Ubiquitin C (Fragment) OS=Rhipicephalus appendiculatus OX=34631 PE=
tr|A0A1E1XVQ6|A0A1E1XVQ6_9ACAR Putative polyubiquitin-c-like isoform x2 (Fragment) OS=Amblyomma sc
tr|A0A0C9SCZ4|A0A0C9SCZ4_AMBAM Putative polyubiquitin (Fragment) OS=Amblyomma americanum OX=6
tr|A0A131ZAN1|A0A131ZAN1_RHIAP Small subunit ribosomal protein S27Ae (Fragment) OS=Rhipicephalus ap
tr|A0A1E1XUH5|A0A1E1XUH5_9ACAR Putative 40s ribosomal protein s27a OS=Amblyomma sculptum OX=15
tr|A0A1E1XQV0|A0A1E1XQV0_9ACAR Putative ubiquitin (Fragment) OS=Amblyomma sculptum OX=1581419
tr|A0A1E1XMY1|A0A1E1XMY1_9ACAR Putative ubiquitin/40s ribosomal protein s27a fusion (Fragment) OS=A

tr|A0A1E1XNF5|A0A1E1XNF5_9ACAR Putative ubiquitin/40s ribosomal protein s27a fusion (Fragment) OS=A
R933,31778
tr|A0A1E1WWN6|A0A1E1WWN6_9ACAR Histone H3 (Fragment) OS=Amblyomma aureolatum OX=187763 PE
tr|A0A131XI99|A0A131XI99_9ACAR Histone H3 (Fragment) OS=Hyalomma excavatum OX=257692 PE=2 SV=1
tr|A0A240EVR0|A0A240EVR0_9ACAR Histone H3 (Fragment) OS=Hyalomma anatolicum OX=176092 GN=H3 P
tr|A0A0C9SBM7|A0A0C9SBM7_AMBAM Putative histones h3 and h4 (Fragment) OS=Amblyomma americanu
tr|A0A2H4FVK3|A0A2H4FVK3_9ACAR Histone H3 (Fragment) OS=Hyalomma truncatum OX=72855 GN=H3 PE
tr|A0A131XII1|A0A131XII1_9ACAR Histone H3 OS=Hyalomma excavatum OX=257692 PE=2 SV=1
tr|A0A219XBT7|A0A219XBT7_9ACAR Histone H3 (Fragment) OS=Hyalomma kumari OX=1917744 GN=H3 PE=
tr|A0A240EVT5|A0A240EVT5_9ACAR Histone H3 (Fragment) OS=Hyalomma kumari OX=1917744 GN=H3 PE=
tr|G3MMX6|G3MMX6_9ACAR Histone H3 OS=Amblyomma maculatum OX=34609 PE=2 SV=1
tr|A0A240EVS2|A0A240EVS2_9ACAR Histone H3 (Fragment) OS=Hyalomma excavatum OX=257692 GN=H3 P
tr|A0A1Z5L7F9|A0A1Z5L7F9_ORNMO Histone H3 (Fragment) OS=Ornithodoros moubata OX=6938 PE=3 SV=1
tr|A0A0K8RN17|A0A0K8RN17_IXORI Putative histones h3 and h4 (Fragment) OS=Ixodes ricinus OX=34613 PE
tr|A0A131Y5N0|A0A131Y5N0_IXORI Putative histones h3 and h4 (Fragment) OS=Ixodes ricinus OX=34613 PE
tr|V5HHL8|V5HHL8_IXORI Histone H3 OS=Ixodes ricinus OX=34613 PE=2 SV=1
tr|A0A131YC02|A0A131YC02_IXORI Histone H3 (Fragment) OS=Ixodes ricinus OX=34613 PE=2 SV=1
tr|V5HRZ9|V5HRZ9_IXORI Putative histone h3.3 (Fragment) OS=Ixodes ricinus OX=34613 PE=2 SV=1
tr|A0A0K8RJJ6|A0A0K8RJJ6_IXORI Histone H3 OS=Ixodes ricinus OX=34613 PE=2 SV=1
tr|L7LVH9|L7LVH9_9ACAR Histone H3 OS=Rhipicephalus pulchellus OX=72859 PE=2 SV=1
tr|A0A2H4FVM6|A0A2H4FVM6_9ACAR Histone H3 (Fragment) OS=Hyalomma truncatum OX=72855 GN=H3 P
tr|L7M6B6|L7M6B6_9ACAR Histone H3 OS=Rhipicephalus pulchellus OX=72859 PE=2 SV=1
tr|V5HDU4|V5HDU4_IXORI Putative histone h3 (Fragment) OS=Ixodes ricinus OX=34613 PE=2 SV=1
tr|A0A219XBS4|A0A219XBS4_9ACAR Histone H3 (Fragment) OS=Hyalomma hussaini OX=139400 GN=H3 PE=
tr|A0A240EVU6|A0A240EVU6_9ACAR Histone H3 (Fragment) OS=Hyalomma rhipicephaloides OX=1917747 G
tr|A0A2R5LBF9|A0A2R5LBF9_9ACAR Putative histone H3.3 OS=Ornithodoros turicata OX=34597 PE=4 SV=1
tr|A0A240EVV7|A0A240EVV7_9ACAR Histone H3 (Fragment) OS=Hyalomma schulzei OX=1678209 GN=H3 PE
tr|A0A240EVR4|A0A240EVR4_9ACAR Histone H3 (Fragment) OS=Hyalomma asiaticum OX=266040 GN=H3 PE
tr|A0A240EVU0|A0A240EVU0_9ACAR Histone H3 (Fragment) OS=Hyalomma marginatum OX=34627 GN=H3
tr|A0A224YPP5|A0A224YPP5_9ACAR Histone H3 OS=Rhipicephalus zambeziensis OX=60191 PE=3 SV=1
tr|F0JA43|F0JA43_AMBVA Histone H3 OS=Amblyomma variegatum OX=34610 PE=2 SV=1
tr|A0A1E1XMN9|A0A1E1XMN9_9ACAR Putative histone H3.3-like isoform x2 OS=Amblyomma sculptum OX=
tr|A0A224Z0L1|A0A224Z0L1_9ACAR Histone H3 OS=Rhipicephalus zambeziensis OX=60191 PE=3 SV=1
tr|A0A0K8R3K9|A0A0K8R3K9_IXORI Histone H3 OS=Ixodes ricinus OX=34613 PE=2 SV=1
tr|A0A240EVT1|A0A240EVT1_9ACAR Histone H3 (Fragment) OS=Hyalomma impressum OX=947028 GN=H3 P
tr|A0A240EVW3|A0A240EVW3_9ACAR Histone H3 (Fragment) OS=Hyalomma somalicum OX=1917748 GN=H
tr|A0A240EVQ1|A0A240EVQ1_9ACAR Histone H3 (Fragment) OS=Nosomma monstrosum OX=72866 GN=H3
tr|A0A240EVQ6|A0A240EVQ6_9ACAR Histone H3 (Fragment) OS=Hyalomma albiparmatum OX=1917740 GN
tr|A0A240EVV2|A0A240EVV2_9ACAR Histone H3 (Fragment) OS=Hyalomma rufipes OX=72862 GN=H3 PE=3 S
tr|A0A219XBX5|A0A219XBX5_9ACAR Histone H3 (Fragment) OS=Hyalomma turanicum OX=1564501 GN=H3
tr|A0A240EVT7|A0A240EVT7_9ACAR Histone H3 (Fragment) OS=Hyalomma lusitanicum OX=49205 GN=H3 PE
tr|A0A240EVP9|A0A240EVP9_AMBVA Histone H3 (Fragment) OS=Amblyomma variegatum OX=34610 GN=H3
tr|A0A240EVT3|A0A240EVT3_9ACAR Histone H3 (Fragment) OS=Hyalomma isaaci OX=1917743 GN=H3 PE=3
tr|A0A240EVR1|A0A240EVR1_9ACAR Histone H3 (Fragment) OS=Hyalomma arabica OX=1917741 GN=H3 PE=
tr|A0A240EVW4|A0A240EVW4_9ACAR Histone H3 (Fragment) OS=Hyalomma truncatum OX=72855 GN=H3 P
tr|A0A2H4FZM2|A0A2H4FZM2_9ACAR Histone H3 (Fragment) OS=Hyalomma truncatum OX=72855 GN=H3 P
tr|A0A240EVS0|A0A240EVS0_9ACAR Histone H3 (Fragment) OS=Hyalomma excavatum OX=257692 GN=H3 P
tr|A0A240EVS8|A0A240EVS8_9ACAR Histone H3 (Fragment) OS=Hyalomma impeltatum OX=563069 GN=H3 P
tr|A0A240EVU1|A0A240EVU1_9ACAR Histone H3 (Fragment) OS=Hyalomma nitidum OX=1917745 GN=H3 PE
tr|A0A293LL03|A0A293LL03_ORNER Histone H3 (Fragment) OS=Ornithodoros erraticus OX=265619 PE=3 SV=

tr|A0A1Z5LBX3|A0A1Z5LBX3_ORNMO Histone H3 (Fragment) OS=Ornithodoros moubata OX=6938 PE=3 SV=
tr|A0A240EVQ5|A0A240EVQ5_9ACAR Histone H3 (Fragment) OS=Hyalomma aegyptium OX=72854 GN=H3 PE
tr|A0A240EVW1|A0A240EVW1_9ACAR Histone H3 (Fragment) OS=Hyalomma scupense OX=1260755 GN=H3
tr|A0A131YET8|A0A131YET8_RHIAP Histone H3 OS=Rhipicephalus appendiculatus OX=34631 PE=3 SV=1
tr|A0A096XIC3|A0A096XIC3_9ACAR Histone H3 OS=Nuttalliella namaqua OX=1029659 PE=3 SV=1
tr|A0A023FGI2|A0A023FGI2_9ACAR Histone H3 OS=Amblyomma cajennense OX=34607 PE=2 SV=1
tr|A0A219XBU5|A0A219XBU5_9ACAR Histone H3 (Fragment) OS=Hyalomma punt OX=1917746 GN=H3 PE=3
tr|A0A1E1X079|A0A1E1X079_9ACAR Histone H3 OS=Amblyomma aureolatum OX=187763 PE=2 SV=1
tr|A0A023GEV8|A0A023GEV8_9ACAR Histone H3 OS=Amblyomma triste OX=251400 PE=2 SV=1
tr|A0A240EVU5|A0A240EVU5_9ACAR Histone H3 (Fragment) OS=Hyalomma punt OX=1917746 GN=H3 PE=3
tr|B7PAJ2|B7PAJ2_IXOSC Histone H3 OS=Ixodes scapularis OX=6945 GN=8027010 PE=3 SV=1
tr|B7P7T4|B7P7T4_IXOSC Histone H3 OS=Ixodes scapularis OX=6945 GN=8025862 PE=3 SV=1
tr|A0A240EVS4|A0A240EVS4_9ACAR Histone H3 (Fragment) OS=Hyalomma glabrum OX=1917742 GN=H3 PE
tr|A0A219XBR4|A0A219XBR4_9ACAR Histone H3 (Fragment) OS=Hyalomma dromedarii OX=34626 GN=H3 PE
tr|A0A240EVQ3|A0A240EVQ3_9ACAR Histone H3 (Fragment) OS=Hyalomma aegyptium OX=72854 GN=H3 PE
tr|A0A240EVW2|A0A240EVW2_9ACAR Histone H3 (Fragment) OS=Hyalomma scupense OX=1260755 GN=H3
R933,31357
tr|A0A1E1XL25|A0A1E1XL25_9ACAR Putative receptor tyrosine phosphatase type r2b (Fragment) OS=Amblyo
tr|G3MT41|G3MT41_9ACAR ATP synthase subunit alpha OS=Amblyomma maculatum OX=34609 PE=2 SV=1
tr|A0A131YQY7|A0A131YQY7_RHIAP F-type H+-transporting ATPase subunit alpha OS=Rhipicephalus append
tr|A0A131Z614|A0A131Z614_RHIAP ATP synthase subunit alpha OS=Rhipicephalus appendiculatus OX=34631
tr|A0A023FL62|A0A023FL62_9ACAR Putative f0f1-type atp synthase alpha subunit (Fragment) OS=Amblyom
tr|A0A023FKR0|A0A023FKR0_9ACAR ATP synthase subunit alpha OS=Amblyomma cajennense OX=34607 PE=
tr|A0A0K8R485|A0A0K8R485_IXORI ATP synthase subunit alpha OS=Ixodes ricinus OX=34613 PE=2 SV=1
tr|A0A023FZX4|A0A023FZX4_9ACAR ATP synthase subunit alpha (Fragment) OS=Amblyomma parvum OX=25
tr|A0A0K8R3H6|A0A0K8R3H6_IXORI ATP synthase subunit alpha OS=Ixodes ricinus OX=34613 PE=2 SV=1
tr|A0A131Y060|A0A131Y060_IXORI ATP synthase subunit alpha OS=Ixodes ricinus OX=34613 PE=2 SV=1
tr|A0A023FMB4|A0A023FMB4_9ACAR Putative f0f1-type atp synthase alpha subunit (Fragment) OS=Amblyo
tr|A0A293MCV3|A0A293MCV3_ORNER ATP synthase subunit alpha (Fragment) OS=Ornithodoros erraticus O
tr|A0A293MXH8|A0A293MXH8_ORNER ATP synthase subunit alpha (Fragment) OS=Ornithodoros erraticus O
tr|B7QCK2|B7QCK2_IXOSC ATP synthase subunit alpha OS=Ixodes scapularis OX=6945 GN=8039213 PE=3 SV=
tr|A0A293MXB7|A0A293MXB7_ORNER ATP synthase subunit alpha (Fragment) OS=Ornithodoros erraticus O
tr|L7MAA0|L7MAA0_9ACAR ATP synthase subunit alpha OS=Rhipicephalus pulchellus OX=72859 PE=2 SV=1
tr|A0A224YYL3|A0A224YYL3_9ACAR ATP synthase subunit alpha OS=Rhipicephalus zambeziensis OX=60191 P
tr|A0A224YYR7|A0A224YYR7_9ACAR F0f1 type atp synthase alpha subunit OS=Rhipicephalus zambeziensis O
tr|L7MMY2|L7MMY2_9ACAR ATP synthase subunit alpha (Fragment) OS=Rhipicephalus pulchellus OX=72859
tr|A0A147B8M9|A0A147B8M9_9ACAR Mitochondrial h+ transporting atp synthase f1 complex alpha subunit
tr|A0A023GHE9|A0A023GHE9_9ACAR Putative f0f1-type atp synthase alpha subunit (Fragment) OS=Amblyom
tr|A0A023GLF5|A0A023GLF5_9ACAR ATP synthase subunit alpha OS=Amblyomma triste OX=251400 PE=2 SV
tr|A0A2R5LIG7|A0A2R5LIG7_9ACAR Putative f0f1-type atp synthase alpha subunit OS=Ornithodoros turicata
tr|A0A1D2AIJ3|A0A1D2AIJ3_ORNBR ATP synthase subunit alpha (Fragment) OS=Ornithodoros brasiliensis OX
tr|G3MGG7|G3MGG7_9ACAR ATP synthase subunit alpha (Fragment) OS=Amblyomma maculatum OX=34609
tr|A0A131XMH8|A0A131XMH8_9ACAR ATP synthase subunit alpha (Fragment) OS=Hyalomma excavatum OX
tr|A0A1Z5LEP7|A0A1Z5LEP7_ORNMO ATP synthase subunit alpha (Fragment) OS=Ornithodoros moubata OX
tr|A0A1E1X8X8|A0A1E1X8X8_9ACAR ATP synthase subunit alpha (Fragment) OS=Amblyomma aureolatum O
tr|A0A1E1X883|A0A1E1X883_9ACAR ATP synthase subunit alpha OS=Amblyomma aureolatum OX=187763 P
tr|A0A2R5LM05|A0A2R5LM05_9ACAR Putative f0f1-type atp synthase alpha subunit OS=Ornithodoros turica
tr|G3MT42|G3MT42_9ACAR ATP synthase subunit alpha OS=Amblyomma maculatum OX=34609 PE=2 SV=1
tr|A0A131XKB7|A0A131XKB7_9ACAR ATP synthase subunit alpha OS=Hyalomma excavatum OX=257692 PE=
tr|A0A224YWE5|A0A224YWE5_9ACAR ATP synthase subunit alpha OS=Rhipicephalus zambeziensis OX=6019

R933,30382
tr|A0A2R5LBL7|A0A2R5LBL7_9ACAR Uncharacterized protein (Fragment) OS=Ornithodoros turicata OX=3459
R933,24302
tr|B7PXQ7|B7PXQ7_IXOSC Ribosomal protein L8, putative (Fragment) (Fragment) OS=Ixodes scapularis OX=6
R933,30191
tr|B7Q040|B7Q040_IXOSC Uncharacterized protein (Fragment) (Fragment) OS=Ixodes scapularis OX=6945 GN
R933,7258
tr|B7QMG1|B7QMG1_IXOSC Sidestep protein, putative OS=Ixodes scapularis OX=6945 GN=8043461 PE=4 SV
R933,26303
tr|L7LU59|L7LU59_9ACAR Putative secreted mucin muc17 OS=Rhipicephalus pulchellus OX=72859 PE=2 SV=1
R933,25900
tr|V5I1U8|V5I1U8_IXORI Uncharacterized protein OS=Ixodes ricinus OX=34613 PE=2 SV=1
R933,30119

PepCount	UniquePep	CoverPerce	MW	PI				
Sequence	MH+	Diff(MH+)	Charge	Rank	Score	DeltaScore	ExpectValu	Ions
3	3	8.78%	41823.37	5.3				
3	3	8.78%	41777.35	5.29				
3	3	8.78%	41793.35	5.29				
3	3	8.78%	41779.32	5.29				
3	3	8.78%	41793.35	5.29				
3	3	8.78%	41823.37	5.3				
3	3	8.82%	41562.16	5.57				
3	3	8.78%	41823.37	5.3				
3	3	8.78%	41797.36	5.29				
3	3	8.78%	41793.35	5.29				
3	3	8.78%	41823.37	5.3				
3	3	8.78%	41807.33	5.29				
3	3	8.78%	41766.32	5.38				
3	3	8.78%	41823.37	5.3				
3	3	8.80%	41692.18	5.3				
3	3	8.78%	41823.37	5.3				
3	3	8.78%	41823.37	5.3				
3	3	8.78%	41793.35	5.29				
3	3	9.07%	40481.83	5.16				
3	3	8.25%	44149.07	5.39				
3	3	8.78%	41793.35	5.29				
3	3	8.78%	41823.37	5.3				
3	3	8.78%	41793.35	5.29				
3	3	8.78%	41823.37	5.3				
3	3	7.62%	48206.87	6.23				
3	3	8.78%	41793.35	5.29				
3	3	8.78%	41793.35	5.29				
3	3	8.78%	41837.4	5.3				
3	3	8.78%	41807.33	5.3				
3	3	8.78%	41823.37	5.3				
3	3	8.78%	41823.37	5.3				
3	3	8.78%	41793.35	5.29				
3	3	8.78%	41823.37	5.3				
K.AGFAGD	976.4483	-0.00024	2	1	61.94	0	8.05E-05	0|0
K.IIAPPER.K	795.4723	0.00066	2	1	39.71	0	1.12E-02	0|0
K.SYELPDG	1790.892	-0.00018	2	1	38.6	0	3.55E-02	0|0
2	2	12.90%	13861.96	10.52				
2	2	12.90%	13861.96	10.52				
2	2	10.74%	16740.32	10.62				
2	2	13.22%	13584.56	10.41				
2	2	12.90%	13861.96	10.52				
2	2	23.88%	7455.45	9.87				
2	2	14.04%	12767.7	10.53				
2	2	13.33%	13408.41	10.53				
2	2	12.90%	13861.96	10.52				
2	2	12.90%	13861.96	10.52				
2	2	12.90%	13861.96	10.52				
2	2	12.90%	13889.98	10.6				

R.EIQTAVR	816.4574	-0.00088	2	1	48.12	0	5.64E-03	0|0
R.LLLPGELA	953.603	0.00006	2	1	39.26	0	4.70E-03	0|0
2	1	3.35%	49167.28	9.14				
2	1	3.35%	49244.38	9.13				
2	1	3.84%	43146.05	8.52				
2	1	3.25%	50717.82	9.12				
2	1	3.25%	50686.85	9.12				
2	1	3.19%	51568.85	9.17				
2	1	3.25%	50752.89	9.13				
2	1	3.25%	50762.97	9.12				
2	1	3.20%	51435.73	9.17				
2	1	15.00%	11428.06	9.01				
2	1	2.99%	54820.78	9.35				
2	1	3.25%	50730.87	9.13				
2	1	3.25%	50762.97	9.12				
2	1	3.25%	50762.97	9.12				
2	1	3.25%	50569.69	9.18				
2	1	5.28%	31460.89	8.98				
K.THINIVVI	1588.881	-0.00016	3	1	55.84	0	5.60E-04	0|0
K.THINIVVI	1588.881	0.0005	2	1	44.82	0	7.12E-03	0|0
1	1	2.68%	33036.17	9.86				
1	1	2.60%	33859.09	9.9				
1	1	3.39%	25980.81	9.94				
1	1	2.68%	32734.7	9.93				
1	1	2.68%	32886.89	9.88				
1	1	2.45%	35514.84	10				
1	1	2.68%	33173.24	9.86				
1	1	2.68%	33075.2	9.84				
1	1	2.58%	34135.38	9.9				
1	1	4.79%	18204.93	10.09				
1	1	2.90%	30818.46	9.98				
1	1	2.45%	35790.22	9.88				
1	1	2.68%	32969.07	9.76				
1	1	2.78%	31609.53	9.94				
1	1	4.55%	19456.4	10.07				
1	1	2.68%	33045.11	9.84				
1	1	2.46%	35477.75	9.89				
1	1	4.37%	20036.99	9.63				
1	1	2.53%	34735.15	9.96				
1	1	2.68%	33010.13	9.89				
1	1	2.68%	32906.94	9.86				
K.TAVAPIE	856.4887	0.00021	2	1	35.3	0	3.91E-02	0|0
1	1	3.49%	19086.79	7.1				
R.ELPDHR.	766.3842	0.00159	2	1	48.05	0	2.47E-03	0|0
1	1	1.94%	49258.9	4.88				
R.VEDALHA	1011.522	0.00161	2	1	55.88	0	5.23E-04	0|0
1	1	7.59%	9533.89	10.54				
-.M*EKMP	807.3851	-0.00886	2	1	37.85	0	2.95E-02	0|0
1	1	3.30%	50680.97	5.26				
1	1	3.36%	49212.13	5.28				

1	1	3.86%	42765.34	6.92				
1	1	3.33%	50078.95	4.96				
1	1	3.31%	50310.31	4.95				
1	1	3.01%	54954.72	5.5				
1	1	3.34%	49974.09	5.2				
1	1	2.37%	70619.56	5.22				
1	1	3.34%	49960.07	5.2				
1	1	5.02%	32901.69	5.81				
1	1	3.34%	49905.98	4.99				
1	1	3.43%	48659.74	5.28				
1	1	6.61%	25133.95	5.21				
1	1	3.18%	52671.15	5.44				
1	1	3.13%	53529.14	5.27				
1	1	3.31%	50329.36	5				
1	1	6.17%	26701.9	5.98				
1	1	3.28%	50853.92	4.96				
1	1	7.43%	21903.59	5.97				
1	1	3.18%	52448.81	5.26				
1	1	3.14%	53100.59	5.38				
1	1	3.34%	49940.94	5.05				
R.AVFVDLE	1687.89	0.00269	2	1	46.22	0	6.32E-03	0|0
1	1	3.59%	26012.62	8.69				
1	1	3.60%	25785.43	8.48				
1	1	3.60%	25760.42	8.61				
1	1	3.60%	25774.4	8.62				
1	1	3.51%	26423.28	8.84				
1	1	3.38%	27604.54	8.75				
1	1	3.60%	25809.58	8.62				
1	1	3.65%	25281.87	8.22				
1	1	3.56%	26063.69	8.22				
1	1	3.60%	25815.46	8.62				
1	1	3.56%	26014.66	8.61				
R.LVAEQRL	956.5887	0.01123	2	1	41.75	0	1.05E-02	0|0
1	1	1.27%	62532.23	5.58				
K.AGEDDK	762.3628	0.00026	2	1	35.29	0	4.67E-02	0|0
1	1	0.77%	124918	8.6				
K.KDPEGGE	956.4683	0.00681	2	1	37.6	0	2.29E-02	0|0
1	1	8.18%	12399.03	5.66				
1	1	1.65%	61235.65	6.79				
1	1	5.77%	17948.74	9.71				
1	1	1.97%	51426.47	7.05				
1	1	5.77%	17978.76	9.71				
1	1	5.77%	17948.74	9.71				
1	1	5.77%	17950.67	9.65				
1	1	7.03%	14728.16	9.87				
1	1	3.93%	25820.32	6.86				
1	1	5.70%	18190.03	9.76				
1	1	3.54%	28477.12	9.67				
1	1	1.58%	64154.99	6.48				
1	1	4.71%	20497.77	7.66				

1	1	6.04%	17116.67	9.67
1	1	3.93%	25786.31	6.86
1	1	5.66%	17649.71	9.51
1	1	7.26%	14171.49	10.2
1	1	4.41%	22949.11	5.85
1	1	2.40%	41830.46	8.73
1	1	4.81%	21207.56	9.63
1	1	5.42%	19239.06	9.57
1	1	10.00%	10333.8	9.87
1	1	6.25%	16542.05	9.69
1	1	3.88%	26509.49	9.58
1	1	3.73%	27092.92	8.91
1	1	1.69%	59948.21	7.09
1	1	5.77%	17914.72	9.71
1	1	5.77%	17948.74	9.71
1	1	5.77%	17948.74	9.71
1	1	5.36%	18978.59	8.93
1	1	6.52%	15563.51	5.76
1	1	3.27%	31013.17	7.12
1	1	4.64%	21916.15	7.91
1	1	5.77%	17934.71	9.71
1	1	4.89%	20978.5	10.79
1	1	4.69%	22161.73	10.18
1	1	5.77%	17385.75	6.95
1	1	2.28%	44586.83	8.59
1	1	9.57%	10812.67	10.23
1	1	5.77%	17754.51	9.71
1	1	5.77%	17978.76	9.71
1	1	6.34%	15981.07	5.89
1	1	10.71%	9495.87	8.25
1	1	5.77%	17948.74	9.71
1	1	5.33%	19397.49	9.66
1	1	1.48%	68519.91	7.13
1	1	5.88%	17214.6	6.75
1	1	4.81%	21532.53	9.92
1	1	6.98%	14523.33	9.81
1	1	5.63%	18266.08	9.27
1	1	9.28%	10989.58	9.57
1	1	5.73%	17590.39	9.76
1	1	5.73%	17490.8	6.8
1	1	5.56%	18464.37	9.81
1	1	7.44%	13608.47	9.1
1	1	2.95%	34333.03	6.94
1	1	4.84%	20941.86	6.2
1	1	3.24%	31234.61	7.99
1	1	4.79%	21132.19	8.14
1	1	6.92%	15059.42	9.86
1	1	5.77%	17948.74	9.71
1	1	5.17%	19657.4	8.86
1	1	4.86%	20808.76	6.76

1	1	8.11%	12513.22	8.21				
K.ESTLHLVL	1067.621	-0.00069	2	1	37.73	0	1.74E-02	0|0
1	1	5.07%	15574.01	11.13				
1	1	4.93%	15914.38	11.13				
1	1	7.87%	9995.57	11.25				
1	1	7.69%	10527.16	10.11				
1	1	7.87%	9839.38	11.05				
1	1	5.15%	15327.72	11.27				
1	1	7.87%	9683.2	10.83				
1	1	7.87%	9995.57	11.25				
1	1	5.15%	15387.84	11.27				
1	1	7.87%	10023.62	11.25				
1	1	5.15%	15387.84	11.27				
1	1	4.22%	18442.49	11.11				
1	1	4.58%	17189.92	11				
1	1	5.11%	15413.88	11.12				
1	1	5.26%	14594.03	11.36				
1	1	8.14%	9938.46	9.88				
1	1	5.15%	15502.08	10.98				
1	1	5.15%	15387.84	11.27				
1	1	7.87%	9938.52	11.25				
1	1	5.15%	15327.72	11.27				
1	1	5.83%	13620.94	11.13				
1	1	7.87%	9995.57	11.25				
1	1	7.87%	9995.57	11.25				
1	1	5.15%	15327.72	11.27				
1	1	7.87%	9995.57	11.25				
1	1	7.87%	9995.57	11.25				
1	1	7.87%	9995.57	11.25				
1	1	5.15%	15327.72	11.27				
1	1	5.15%	15327.72	11.27				
1	1	5.15%	15031.36	11.26				
1	1	5.15%	15387.84	11.27				
1	1	5.15%	15327.72	11.27				
1	1	7.87%	9995.57	11.25				
1	1	7.87%	9995.57	11.25				
1	1	7.87%	9995.57	11.25				
1	1	7.87%	9995.57	11.25				
1	1	7.87%	9995.57	11.25				
1	1	7.87%	9995.57	11.25				
1	1	7.87%	9995.57	11.25				
1	1	7.87%	9995.57	11.25				
1	1	7.87%	9995.57	11.25				
1	1	7.87%	9995.57	11.25				
1	1	7.87%	9995.57	11.25				
1	1	7.87%	10004.58	11.25				
1	1	7.87%	9995.57	11.25				
1	1	7.87%	9995.57	11.25				
1	1	7.87%	9995.57	11.25				
1	1	5.15%	15387.84	11.27				

1	1	3.24%	24437.95	12.21				
1	1	7.87%	9839.38	11.05				
1	1	7.87%	9894.46	11.25				
1	1	5.15%	15327.72	11.27				
1	1	5.15%	15387.84	11.27				
1	1	5.15%	15327.72	11.27				
1	1	7.87%	9752.31	11.05				
1	1	5.15%	15327.72	11.27				
1	1	5.15%	15327.72	11.27				
1	1	7.87%	10064.68	11.41				
1	1	5.15%	15502.08	10.98				
1	1	5.15%	15327.72	11.27				
1	1	7.87%	9995.57	11.25				
1	1	7.87%	9995.57	11.25				
1	1	7.87%	9839.38	11.05				
1	1	7.87%	9995.57	11.25				
K.STELLIR.K	831.4934	0.0011	2	1	45	0	8.25E-03	0|0
1	1	1.09%	61095.64	8.19				
1	1	1.08%	60033.58	8.9				
1	1	1.64%	40039.51	8.8				
1	1	1.08%	59938.4	9.06				
1	1	1.60%	41249.06	9.05				
1	1	1.08%	59966.37	8.9				
1	1	1.08%	59857.41	9.09				
1	1	1.08%	59852.34	9.12				
1	1	1.08%	59972.48	8.86				
1	1	1.08%	59867.44	9.09				
1	1	1.40%	46848.62	9.4				
1	1	2.16%	30632.11	9.79				
1	1	1.08%	59901.48	9.12				
1	1	1.08%	59843.38	9.09				
1	1	1.07%	60723.43	9.07				
1	1	1.08%	59904.36	8.98				
1	1	1.08%	59925.34	9.12				
1	1	2.11%	31464.69	6.12				
1	1	1.08%	58829.21	9.44				
1	1	1.90%	34544.37	9.53				
1	1	2.23%	29515.56	8.86				
1	1	1.02%	63264.35	9.19				
1	1	1.08%	60434.11	9.2				
1	1	1.17%	56082.97	9.05				
1	1	1.04%	62042.77	9.14				
1	1	1.05%	61869.5	9.05				
1	1	1.08%	60546.18	9.2				
1	1	1.05%	61974.83	9.32				
1	1	1.08%	59900.35	8.9				
1	1	1.08%	59926.66	8.97				
1	1	1.08%	59998.56	9.12				
1	1	1.08%	59883.35	8.98				
1	1	1.08%	59822.26	9.12				

K.QAVAYR.	707.3835	-0.0007	2	1	39.33	0	2.65E-02	0|0
1	1	0.87%	114640.3	8.8				
K.SSISMSP	992.5193	0.01351	1	1	49.74	0	2.82E-03	0|0
1	1	3.35%	22785.8	9.9				
R.IEYDPNR	906.4316	-0.0006	2	1	40.93	0	1.61E-02	0|0
1	1	2.01%	32474.32	4.83				
K.TAEPER.R	702.3417	0.01147	1	1	30.75	0	4.59E-02	0|0
1	1	1.84%	46277.26	5.5				
R.DGEIQEG	903.4166	-0.00136	2	1	38.33	0	1.48E-02	0|0
1	1	0.11%	693904.5	6.34				
K.TTSSTSR.	739.3581	0.00013	2	1	36.96	0	2.08E-02	0|0
1	1	3.52%	30867.92	9.08				
M.ISSPEAV	1046.548	0.00053	2	1	48.22	0	4.83E-03	0|0

Reference	DIFF_MOD	PI	MissCleava	ModificatioMatchedTI	NumProteaEngine	Tag
tr|Q5CAR2|Q5CAR2_I		4.21	0	0	2	MASCOT
tr|Q5CAR2|Q5CAR2_I		6	0	0	2	MASCOT
tr|Q5CAR2|Q5CAR2_I		4.14	0	0	2	MASCOT

tr|A0A293MAR2|A0A	6.1	0		0	2 MASCOT
tr|A0A0K8RB64|A0A0	6	0		0	2 MASCOT
tr|B7Q349|B7Q349_IX	6.61	0		0	2 MASCOT
tr|B7Q349|B7Q349_IX	6.61	0		0	2 MASCOT
tr|A0A1E1XIG3|A0A1E	5.66	0		0	2 MASCOT
tr|A0A0C9S156|A0A0	5.32	0		0	2 MASCOT
tr|A0A0C9SCJ0|A0A0C	5.32	0		0	2 MASCOT
tr|A0A0K8R692|A0A0	8.5	1	15.994919	0	2 MASCOT

tr|B7P872|B7P872_IX	3.92	0	0	2	MASCOT
tr|A0A1E1X8S7|A0A1	8.75	1	0	2	MASCOT
tr|A0A131XMT1|A0A1	4.56	1	0	2	MASCOT
tr|A0A131Y846|A0A1	4.68	1	0	2	MASCOT

tr|B7P0U0|B7P0U0_IX	6.85	0	0	2	MASCOT

tr|A0A240EVT3|A0A2	5.72	0	0	2	MASCOT

tr|B7QCK2|B7QCK2_I	8.75	0	0	2	MASCOT
tr|A0A2R5LBL7|A0A2	11	1	0	2	MASCOT
tr|B7PXQ7|B7PXQ7_I	4.37	0	0	2	MASCOT
tr|B7Q040|B7Q040_IX	4.53	0	0	2	MASCOT
tr|B7QMG1|B7QMG1	4.14	0	0	2	MASCOT
tr|L7LU59|L7LU59_9A	9.41	0	0	2	MASCOT
tr|V5I1U8|V5I1U8_IX	6	0	0	2	MASCOT

Decoy

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