**Supplementary material - The proteomics of the giant cedratvirus particles reveals unique and shared features with pitho-like viruses**

|  |
| --- |
| **Supplementary Table 1** Function and classification into functional categories for proteins found in the proteome of cedratvirus pambiensis. |
| **Gene ID** | **Function** | **Classification** |
| 12 | Ribonuclease H [Brazilian cedratvirus IHUMI] | Transcription and RNA processing |
| 13 | Ankyrin repeat-containing protein [Brazilian cedratvirus IHUMI] | Miscellaneous |
| 21 | F-box domain-containing protein [Brazilian cedratvirus IHUMI] | Signal transduction regulation |
| 30 | Serine/Threonine protein kinase [Cedratvirus Ce7-1] | Signal transduction regulation |
| 35 | hypothetical protein Ce0701\_0388 [Cedratvirus Ce7-1] | Hypothetical protein |
| 37 | Hypothetical protein BRZCDTV\_503 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 42 | Hypothetical protein BRZCDTV\_498 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 44 | GTP-binding protein [Cedratvirus Ce7-1] | Miscellaneous |
| 45 | Uncharacterized protein Ce0701\_0382 [Cedratvirus Ce7-1] | Uncharacterized |
| 50 | DNA-directed RNA polymerase subunit RPB2 [Brazilian cedratvirus IHUMI] | Transcription and RNA processing |
| 51 | Endoribonuclease L-PSP/chorismate mutase-like protein [Brazilian cedratvirus IHUMI] | Host-virus interaction |
| 58 | Hypothetical protein BRZCDTV\_486 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 59 | Ankyrin repeat-containing protein [Brazilian cedratvirus IHUMI] | Miscellaneous |
| 65 | SET domain-containing protein [Brazilian cedratvirus IHUMI] | Nucleotide metabolism |
| 68 | translation elongation factor [Cedratvirus A11] | Translation |
| 77 | ankyrin repeat-containing protein [Cedratvirus duvanny] | Miscellaneous |
| 83 | DNA-directed RNA polymerase subunit RPB2 [Brazilian cedratvirus IHUMI] | Transcription and RNA processing |
| 84 | Endoribonuclease L-PSP/chorismate mutase-like protein [Brazilian cedratvirus IHUMI] | Host-virus interaction |
| 92 | Ankyrin repeat-containing protein [Brazilian cedratvirus IHUMI] | Miscellaneous |
| 100 | Transmembrane domain-containing protein [Brazilian cedratvirus IHUMI] | Uncharacterized |
| 104 | Hypothetical protein BRZCDTV\_453 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 112 | Uncharacterized protein Ce0701\_0410 [Cedratvirus Ce7-1] | Uncharacterized |
| 116 | Hypothetical protein BRZCDTV\_442 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 127 | Hypothetical protein BRZCDTV\_433 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 129 | Uncharacterized protein Ce0201\_0281 [Cedratvirus Ce2-1] | Uncharacterized |
| 157 | NTF2-like domain-containing protein [Brazilian cedratvirus IHUMI] | Miscellaneous |
| 167 | AP-endonuclease [Brazilian cedratvirus IHUMI] | DNA replication, recombination and repair |
| 168 | F-box domain-containing protein [Cedratvirus Ce7-1] | Signal transduction regulation |
| 169 | Uncharacterized protein Ce0701\_0016 [Cedratvirus Ce7-1] | Uncharacterized |
| 176 | Hypothetical protein BRZCDTV\_403 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 181 | DNA-directed RNA polymerase subunit [Cedratvirus Ce7-1] | Transcription and RNA processing |
| 183 | Uncharacterized protein Ce0701\_0029 [Cedratvirus Ce7-1] | Uncharacterized |
| 185 | Uncharacterized protein Ce0201\_0068 [Cedratvirus Ce2-1] | Uncharacterized |
| 186 | Uncharacterized protein Ce0701\_0032 [Cedratvirus Ce7-1] | Uncharacterized |
| 191 | DNA-directed RNA polymerase subunit RPB1 [Brazilian cedratvirus IHUMI] | Transcription and RNA processing |
| 193 | Hypothetical protein BRZCDTV\_394 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 196 | Uncharacterized protein Ce0701\_0032 [Cedratvirus Ce7-1] | Uncharacterized |
| 197 | Hypothetical protein BRZCDTV\_389 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 199 | Ankyrin repeat-containing protein [Cedratvirus Ce7-1] | Miscellaneous |
| 201 | Ubiquitin ligase [Brazilian cedratvirus IHUMI] | Protein metabolism |
| 203 | Hypothetical protein BRZCDTV\_384 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 204 | Hypothetical protein BRZCDTV\_383 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 205 | Class 3 lipase [Brazilian cedratvirus IHUMI] | Lipid metabolism |
| 207 | Ankyrin repeat-containing protein [Cedratvirus Ce7-1] | Miscellaneous |
| 209 | Hypothetical protein BRZCDTV\_379 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 210 | Hypothetical protein BRZCDTV\_378 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 211 | Ankyrin repeat-containing protein [Cedratvirus Ce7-1] | Miscellaneous |
| 219 | F-box domain-containing protein [Cedratvirus Ce7-1] | Signal transduction regulation |
| 223 | F-box domain-containing protein [Cedratvirus Ce7-1] | Signal transduction regulation |
| 224 | F-box domain-containing protein [Cedratvirus Ce7-1] | Signal transduction regulation |
| 226 | hypothetical protein Cbor\_269 [Cedratvirus borely] | Hypothetical protein |
| 232 | Hypothetical protein BRZCDTV\_389 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 235 | Lectin domain-containing protein [Cedratvirus Ce7-1] | Uncharacterized |
| 237 | Hypothetical protein BRZCDTV\_384 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 238 | RRM domain-containing protein [Cedratvirus Ce7-1] | Transcription and RNA processing |
| 239 | Class 3 lipase [Brazilian cedratvirus IHUMI] | Lipid metabolism |
| 242 | Ankyrin repeat-containing protein [Cedratvirus Ce7-1] | Miscellaneous |
| 243 | Ankyrin repeat-containing protein [Cedratvirus Ce7-1] | Miscellaneous |
| 244 | Ankyrin repeat-containing protein [Cedratvirus Ce7-1] | Miscellaneous |
| 252 | Uncharacterized protein Ce0701\_0057 [Cedratvirus Ce7-1] | Uncharacterized |
| 253 | F-box domain-containing protein [Cedratvirus Ce7-1] | Signal transduction regulation |
| 255 | Uncharacterized protein Ce0701\_0065 [Cedratvirus Ce7-1] | Uncharacterized |
| 264 | RNAse III putative (Double-stranded ribonuclease) [Cedratvirus Ce7-1] | Transcription and RNA processing |
| 267 | Nucleotidyl transferase [Cedratvirus Ce7-1] | Nucleotide metabolism |
| 271 | Transmembrane domain-containing protein [Cedratvirus Ce7-1] | Uncharacterized |
| 272 | EGF-like domain-containing protein [Brazilian cedratvirus IHUMI] | Miscellaneous |
| 273 | Uncharacterized protein Ce0701\_0437 [Cedratvirus Ce7-1] | Uncharacterized |
| 274 | Transmembrane domain-containing protein [Cedratvirus Ce7-1] | Uncharacterized |
| 275 | Hypothetical protein BRZCDTV\_349 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 276 | Transmembrane domain-containing protein [Cedratvirus Ce7-1] | Uncharacterized |
| 278 | Uncharacterized protein Ce0701\_0433 [Cedratvirus Ce7-1] | Uncharacterized |
| 280 | Uncharacterized protein Ce0701\_0437 [Cedratvirus Ce7-1] | Uncharacterized |
| 282 | Hypothetical protein BRZCDTV\_349 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 284 | hypothetical protein Cplu\_202 [Cedratvirus plubellavi] | Hypothetical protein |
| 285 | Uncharacterized protein Ce0701\_0431 [Cedratvirus Ce7-1] | Uncharacterized |
| 286 | Ankyrin repeat-containing protein [Brazilian cedratvirus IHUMI] | Miscellaneous |
| 293 | DEAD/SNF2 DNA/RNA helicase [Brazilian cedratvirus IHUMI] | Transcription and RNA processing |
| 294 | DEAD/SNF2 DNA/RNA helicase [Cedratvirus Ce7-1] | Transcription and RNA processing |
| 295 | Hypothetical protein BRZCDTV\_336 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 296 | Protein kinase domain-containing protein [Cedratvirus Ce7-1] | Miscellaneous |
| 297 | Hypothetical protein BRZCDTV\_334 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 302 | Ribonuclease H-like protein [Brazilian cedratvirus IHUMI] | Transcription and RNA processing |
| 304 | Uncharacterized protein Ce0701\_0276 [Cedratvirus Ce7-1] | Uncharacterized |
| 305 | DEAD/SNF2 DNA/RNA helicase [Cedratvirus Ce7-1] | Transcription and RNA processing |
| 306 | Hypothetical protein BRZCDTV\_336 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 307 | Protein kinase domain-containing protein [Cedratvirus Ce7-1] | Miscellaneous |
| 310 | Ankyrin repeat-containing protein [Cedratvirus Ce7-1] | Miscellaneous |
| 311 | Ankyrin repeat-containing protein [Cedratvirus Ce7-1] | Miscellaneous |
| 312 | Uncharacterized protein Ce0701\_0280 [Cedratvirus Ce7-1] | Uncharacterized |
| 313 | Uncharacterized protein Ce0701\_0279 [Cedratvirus Ce7-1] | Uncharacterized |
| 317 | Hypothetical protein BRZCDTV\_326 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 318 | Uncharacterized protein Ce0701\_0276 [Cedratvirus Ce7-1] | Uncharacterized |
| 319 | Protein containing kinase domain [Brazilian cedratvirus IHUMI] | Miscellaneous |
| 323 | Hypothetical protein BRZCDTV\_321 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 325 | Uncharacterized protein Ce0701\_0269 [Cedratvirus Ce7-1] | Uncharacterized |
| 326 | Transmembrane domain-containing protein [Brazilian cedratvirus IHUMI] | Uncharacterized |
| 327 | Beta\_helix domain-containing protein [Cedratvirus Ce7-1] | Miscellaneous |
| 328 | Hypothetical protein BRZCDTV\_316 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 331 | Hypothetical protein BRZCDTV\_316 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 333 | DNA-directed RNA Pol II C-term-like phosphatase [Cedratvirus Ce7-1] | Transcription and RNA processing |
| 338 | Hypothetical protein BRZCDTV\_309 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 340 | DNA-directed RNA Pol II C-term-like phosphatase [Cedratvirus Ce7-1] | Transcription and RNA processing |
| 345 | Uncharacterized protein Ce0701\_0258 [Cedratvirus Ce7-1] | Uncharacterized |
| 353 | Helicase nuclease [Cedratvirus Ce7-1] | DNA replication, recombination and repair |
| 355 | Hypothetical protein BRZCDTV\_303 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 356 | Acyl-CoA N-acyltransferase [Brazilian cedratvirus IHUMI] | Other metabolic functions |
| 357 | Acyl-CoA N-acyltransferase [Cedratvirus Ce7-1] | Other metabolic functions |
| 358 | Hypothetical protein BRZCDTV\_300 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 359 | Acyl-CoA N-acyltransferase [Brazilian cedratvirus IHUMI] | Other metabolic functions |
| 360 | Acyl-CoA N-acyltransferase [Brazilian cedratvirus IHUMI] | Other metabolic functions |
| 361 | Hypothetical protein BRZCDTV\_300 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 362 | Transmembrane domain-containing protein [Cedratvirus Ce7-1] | Uncharacterized |
| 363 | Transmembrane domain-containing protein [Cedratvirus Ce7-1] | Uncharacterized |
| 364 | Hypothetical protein BQ3484\_129 [Cedratvirus A11] | Hypothetical protein |
| 365 | divergent major capsid protein [Cedratvirus lena] | Virion structure and morphogenesis |
| 368 | Transmembrane domain-containing protein [Cedratvirus Ce7-1] | Uncharacterized |
| 371 | Hypothetical protein BRZCDTV\_290 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 372 | Transmembrane domain-containing protein [Cedratvirus Ce7-1] | Uncharacterized |
| 373 | Hypothetical protein BRZCDTV\_297 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 375 | Divergent Major Capsid Protein [Cedratvirus Ce7-1] | Virion structure and morphogenesis |
| 377 | Transmembrane domain-containing protein [Cedratvirus Ce7-1] | Uncharacterized |
| 380 | Hypothetical protein BRZCDTV\_290 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 381 | Uncharacterized protein Ce0701\_0312 [Cedratvirus Ce7-1] | Uncharacterized |
| 382 | Uncharacterized protein Ce0701\_0312 [Cedratvirus Ce7-1] | Uncharacterized |
| 383 | Uncharacterized protein Ce0701\_0313 [Cedratvirus Ce7-1] | Uncharacterized |
| 385 | Hypothetical protein BRZCDTV\_286 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 386 | Hypothetical protein BRZCDTV\_285 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 387 | Patatin-like phospholipase [Cedratvirus Ce7-1] | Lipid metabolism |
| 388 | Uncharacterized protein Ce0701\_0318 [Cedratvirus Ce7-1] | Uncharacterized |
| 389 | Transmembrane domain-containing protein [Brazilian cedratvirus IHUMI] | Uncharacterized |
| 390 | Hypothetical protein BRZCDTV\_281 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 393 | Hypothetical protein BRZCDTV\_278 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 394 | Uncharacterized protein Ce0701\_0322 [Cedratvirus Ce7-1] | Uncharacterized |
| 398 | ADPrib\_exo\_Tox domain-containing protein [Cedratvirus Ce2-1] | DNA replication, recombination and repair |
| 404 | Hypothetical protein BRZCDTV\_272 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 405 | F-box domain-containing protein [Brazilian cedratvirus IHUMI] | Signal transduction regulation |
| 406 | VV D6-like helicase [Brazilian cedratvirus IHUMI] | Transcription and RNA processing |
| 407 | Uncharacterized protein Ce0701\_0429 [Cedratvirus Ce7-1] | Uncharacterized |
| 412 | Hypothetical protein BRZCDTV\_267 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 414 | TFIIS transcription elongation factor [Cedratvirus Ce7-1] | Transcription and RNA processing |
| 415 | Uncharacterized protein Ce0701\_0419 [Cedratvirus Ce7-1 | Uncharacterized |
| 416 | F-box domain-containing protein [Cedratvirus Ce7-1] | Signal transduction regulation |
| 417 | F-box domain-containing protein [Brazilian cedratvirus IHUMI] | Signal transduction regulation |
| 418 | RecD/TraA family helicase repair protein [Cedratvirus Ce7-1] | DNA replication, recombination and repair |
| 429 | Transmembrane domain-containing protein [Brazilian cedratvirus IHUMI] | Uncharacterized |
| 430 | Transmembrane domain-containing protein [Brazilian cedratvirus IHUMI] | Uncharacterized |
| 434 | F-box domain-containing protein [Brazilian cedratvirus IHUMI] | Signal transduction regulation |
| 439 | F-box domain-containing protein [Brazilian cedratvirus IHUMI] | Signal transduction regulation |
| 440 | RNA polymerase II RPB5 subunit [Cedratvirus Ce7-1] | Transcription and RNA processing |
| 442 | Hypothetical protein BRZCDTV\_246 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 447 | F-box domain-containing protein [Cedratvirus Ce7-1] | Signal transduction regulation |
| 448 | RNA polymerase II RPB5 subunit [Cedratvirus Ce7-1] | Transcription and RNA processing |
| 450 | Uncharacterized protein Ce0701\_0228 [Cedratvirus Ce7-1] | Uncharacterized |
| 451 | Uncharacterized protein Ce0701\_0228 [Cedratvirus Ce7-1] | Uncharacterized |
| 454 | Transmembrane domain-containing protein [Cedratvirus Ce7-1] | Uncharacterized |
| 463 | Transmembrane domain-containing protein [Brazilian cedratvirus IHUMI] | Uncharacterized |
| 464 | Hypothetical protein BRZCDTV\_235 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 468 | Transmembrane domain-containing protein [Brazilian cedratvirus IHUMI] | Uncharacterized |
| 469 | Hypothetical protein BRZCDTV\_235 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 472 | Glycosyltransferase family 2 [Brazilian cedratvirus IHUMI] | Carbohydrate metabolism |
| 476 | Uncharacterized protein Ce0201\_0148 [Cedratvirus Ce2-1] | Uncharacterized |
| 479 | Hypothetical protein BRZCDTV\_227 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 482 | Hypothetical protein BRZCDTV\_230 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 483 | Uncharacterized protein Ce0701\_0243 [Cedratvirus Ce7-1] | Uncharacterized |
| 493 | DNA-directed RNA polymerase RPB1 (Domain 5) [Cedratvirus Ce7-1] | Transcription and RNA processing |
| 497 | Hydrolase-like domain-containing protein [Cedratvirus Ce7-1] | Other metabolic functions |
| 507 | Uncharacterized protein Ce0701\_0181 [Cedratvirus Ce7-1] | Uncharacterized |
| 514 | Uncharacterized protein Ce0701\_0188 [Cedratvirus Ce7-1] | Uncharacterized |
| 515 | Serine/Threonine protein kinase [Cedratvirus Ce7-1] | Signal transduction regulation |
| 516 | hypothetical protein Cbor\_435 [Cedratvirus borely] | Hypothetical protein |
| 518 | Hypothetical protein ZAZAV\_583 [Cedratvirus Zaza IHUMI] | Hypothetical protein |
| 519 | hypothetical protein Cbor\_555 [Cedratvirus borely] | Hypothetical protein |
| 523 | Uncharacterized protein Ce0701\_0188 [Cedratvirus Ce7-1] | Uncharacterized |
| 527 | Uncharacterized protein Ce0701\_0191 [Cedratvirus Ce7-1] | Uncharacterized |
| 528 | Protein containing kinase domain [Brazilian cedratvirus IHUMI] | Miscellaneous |
| 537 | Protein containing kinase domain [Brazilian cedratvirus IHUMI] | Miscellaneous |
| 539 | TFIIB transcription initiation factor [Cedratvirus Ce7-1] | Transcription and RNA processing |
| 541 | Uncharacterized protein Ce0701\_0203 [Cedratvirus Ce7-1] | Uncharacterized |
| 542 | Hypothetical protein BRZCDTV\_180 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 550 | Hypothetical protein BRZCDTV\_181 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 552 | Hypothetical protein BRZCDTV\_180 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 556 | Hypothetical protein BRZCDTV\_176 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 557 | RNAse III [Cedratvirus Ce7-1] | Transcription and RNA processing |
| 558 | Hypothetical protein BQ3484\_556 [Cedratvirus A11] | Hypothetical protein |
| 563 | hypothetical protein [Cedratvirus kamchatka] | Hypothetical protein |
| 572 | Hypothetical protein BRZCDTV\_169 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 573 | DNA-directed RNA polymerase RPB10 [Brazilian cedratvirus IHUMI] | Transcription and RNA processing |
| 574 | Caspase-like protein [Brazilian cedratvirus IHUMI] | Protein metabolism |
| 582 | Hypothetical protein BRZCDTV\_169 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 584 | Caspase-like protein [Brazilian cedratvirus IHUMI] | Protein metabolism |
| 594 | Hypothetical protein BRZCDTV\_163 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 597 | Hypothetical protein BRZCDTV\_159 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 598 | Hypothetical protein BRZCDTV\_163 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 601 | Transmembrane domain-containing protein [Brazilian cedratvirus IHUMI] | Uncharacterized |
| 602 | Hypothetical protein BRZCDTV\_159 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 603 | Hypothetical protein BRZCDTV\_158 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 608 | Hypothetical protein BRZCDTV\_159 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 610 | Hypothetical protein BRZCDTV\_157 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 615 | ATP-dependent DNA ligase [Brazilian cedratvirus IHUMI] | DNA replication, recombination and repair |
| 621 | Hypothetical protein BRZCDTV\_149 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 624 | Transmembrane domain-containing protein [Brazilian cedratvirus IHUMI] | Uncharacterized |
| 625 | Hypothetical protein BRZCDTV\_145 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 626 | hypothetical protein Cduv\_22 [Cedratvirus duvanny] | Hypothetical protein |
| 636 | 7-methylguanosine mRNA capping enzyme [Brazilian cedratvirus IHUMI] | Transcription and RNA processing |
| 646 | Uncharacterized protein Ce0701\_0148 [Cedratvirus Ce7-1] | Uncharacterized |
| 651 | HMG box domain-containing protein [Cedratvirus Ce2-1] | DNA replication, recombination and repair |
| 652 | VETF-like early transcription factor large subunit [Cedratvirus Ce7-1] | Transcription and RNA processing |
| 654 | PolyA polymerase reg subunit [Cedratvirus Ce7-1] | Transcription and RNA processing |
| 657 | 5'-3' exoribonuclease [Brazilian cedratvirus IHUMI] | DNA replication, recombination and repair |
| 660 | Uncharacterized protein Ce0701\_0148 [Cedratvirus Ce7-1] | Uncharacterized |
| 665 | Hypothetical protein BRZCDTV\_123 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 666 | VETF-like early transcription factor large subunit [Cedratvirus Ce7-1] | Transcription and RNA processing |
| 670 | Cyclin dependent kinase [Cedratvirus Ce7-1] | Miscellaneous |
| 671 | 5'-3' exoribonuclease [Brazilian cedratvirus IHUMI] | DNA replication, recombination and repair |
| 672 | 5'-3' exoribonuclease [Brazilian cedratvirus IHUMI] | DNA replication, recombination and repair |
| 674 | Hypothetical protein BRZCDTV\_115 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 675 | Uncharacterized protein Ce0701\_0164 [Cedratvirus Ce7-1] | Uncharacterized |
| 677 | Uncharacterized protein Ce0701\_0166 [Cedratvirus Ce7-1] | Uncharacterized |
| 678 | Hypothetical protein BRZCDTV\_113 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 679 | Ankyrin repeat-containing protein [Cedratvirus Ce7-1] | Miscellaneous |
| 684 | Ankyrin repeat-containing protein [Cedratvirus Ce2-1] | Miscellaneous |
| 690 | Alpha/beta hydrolase [Cedratvirus Ce7-1] | Other metabolic functions |
| 692 | WD40 domain-containing protein [Cedratvirus Ce7-1] | Miscellaneous |
| 693 | Uncharacterized protein Ce0701\_0376 [Cedratvirus Ce7-1] | Uncharacterized |
| 695 | Mannosyl phosphorylinositol ceramide synthase [Cedratvirus Ce7-1] | Other metabolic functions |
| 700 | Lipocalin/cytosolic fatty-acid binding domain-containing protein [Cedratvirus Ce7-1] | Miscellaneous |
| 704 | Cyclin dependent kinase 2 [Brazilian cedratvirus IHUMI] | Miscellaneous |
| 706 | Serine/Threonine protein kinase [Brazilian cedratvirus IHUMI] | Signal transduction regulation |
| 708 | Hypothetical protein BRZCDTV\_84 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 714 | Hypothetical protein BRZCDTV\_78 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 720 | Uncharacterized protein Ce0701\_0333 [Cedratvirus Ce7-1] | Uncharacterized |
| 723 | Beta-1,3-N-acetylglucosaminyltransferase lunatic fringe-like [Brazilian cedratvirus IHUMI] | Carbohydrate metabolism |
| 724 | Hypothetical protein BRZCDTV\_68 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 725 | Lipocalin/cytosolic fatty-acid binding domain-containing protein [Cedratvirus Ce7-1] | Miscellaneous |
| 745 | Phosphoglycerate mutase [Cedratvirus Ce7-1] | Other metabolic functions |
| 747 | Uncharacterized protein Ce0201\_0009 [Cedratvirus Ce2-1] | Uncharacterized |
| 756 | Alpha/beta hydrolase [Brazilian cedratvirus IHUMI] | Other metabolic functions |
| 762 | alpha/beta hydrolase [Cedratvirus borely] | Other metabolic functions |
| 766 | Hypothetical protein BRZCDTV\_44 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 778 | Uncharacterized protein Ce0701\_0127 [Cedratvirus Ce7-1] | Uncharacterized |
| 779 | Hypothetical protein BRZCDTV\_37 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 780 | F-box domain-containing protein [Cedratvirus Ce2-1] | Signal transduction regulation |
| 781 | Methyltransferase [Cedratvirus Ce7-1] | Nucleotide metabolism |
| 782 | Uncharacterized protein Ce0701\_0122 [Cedratvirus Ce7-1] | Uncharacterized |
| 784 | Hypothetical protein BRZCDTV\_32 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 786 | PD-(D/E)XK nuclease [Cedratvirus Ce7-1] | Transcription and RNA processing |
| 787 | Uncharacterized protein Ce0701\_0118 [Cedratvirus Ce7-1] | Uncharacterized |
| 788 | Uncharacterized protein Ce0701\_0117 [Cedratvirus Ce7-1] | Uncharacterized |
| 789 | Hypothetical protein BRZCDTV\_27 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 792 | Uncharacterized protein Ce0701\_0114 [Cedratvirus Ce7-1] | Uncharacterized |
| 798 | Uncharacterized protein Ce0701\_0110 [Cedratvirus Ce7-1] | Uncharacterized |
| 799 | Hypothetical protein BRZCDTV\_18 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 800 | Hypothetical protein BRZCDTV\_17 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 801 | Transmembrane domain-containing protein [Brazilian cedratvirus IHUMI] | Uncharacterized |
| 802 | Uncharacterized protein Ce0701\_0108 [Cedratvirus Ce7-1] | Uncharacterized |
| 803 | Hypothetical protein BRZCDTV\_14 [Brazilian cedratvirus IHUMI] | Hypothetical protein |
| 804 | Ankyrin repeat-containing protein [Cedratvirus Ce7-1] | Miscellaneous |
| 806 | Deoxynucleoside monophosphate kinase [Cedratvirus Ce7-1] | Nucleotide metabolism |
| 807 | F-box domain-containing protein [Brazilian cedratvirus IHUMI] | Signal transduction regulation |
| 810 | Uncharacterized protein Ce0201\_0219 [Cedratvirus Ce2-1] | Uncharacterized |
| 817 | F-box domain-containing protein [Cedratvirus Ce7-1] | Signal transduction regulation |
| 824 | Ankyrin repeat-containing protein [Cedratvirus Ce7-1] | Miscellaneous |
| 828 | DNA topoisomerase IIA [Brazilian cedratvirus IHUMI] | DNA replication, recombination and repair |
| 838 | Uncharacterized protein Ce0701\_0091 [Cedratvirus Ce7-1] | Uncharacterized |
| 840 | hypothetical protein Cbor\_452 [Cedratvirus borely] | Hypothetical protein |
| 841 | Hypothetical protein BRZCDTV\_2 [Brazilian cedratvirus IHUMI] | Hypothetical protein |

|  |
| --- |
| **Supplementary Table 2** BLAST results performed for cedratvirus proteins against pithovirus proteins. Expect threshold: 0.001. |
| **Gene ID** | **Hits with Pithovirus (Expect threshold: 0.001)** | **Total Score** | **Query Cover** | **E-value** | **Per. Ident.** | **Information** |
| 12 | No significant similarity found | - | - | - | - | Exclusive |
| 13 | No significant similarity found | - | - | - | - | Exclusive |
| 21 | pv\_468 [protein=hypothetical protein] [protein\_id=AHH02034.1] | 59.3 | 32% | 5,00E-13 | 39.19% | 6 more hits |
| 30 | pv\_405 [protein=Ser/Thr protein kinase] [protein\_id=AHH01971.1]pv\_438 [protein=cyclin-dependent kinase] [protein\_id=AHH02004.1] | 58.257.8 | 62%50% | 2,00E-112,00E-11 | 25.89%25.00% |   |
| 35 | No significant similarity found | - | - | - | - | Exclusive |
| 37 | No significant similarity found | - | - | - | - | Exclusive |
| 42 | No significant similarity found | - | - | - | - | Exclusive |
| 44 | pv\_112 [protein=GTP-binding protein] [protein\_id=AHH01679.1] | 43.1 | 95% | 2,00E-08 | 25.83% |   |
| 45 | No significant similarity found | - | - | - | - | Exclusive |
| 50 | pv\_242 [protein=DNA-directed RNA polymerase subunit RPB2 [protein\_id=AHH01809.1] | 1500 | 99% | 0 | 58.23% |   |
| 51 | No significant similarity found | - | - | - | - | Exclusive |
| 58 | No significant similarity found | - | - | - | - | Exclusive |
| 59 | No significant similarity found | - | - | - | - | Exclusive |
| 65 | No significant similarity found | - | - | - | - | Exclusive |
| 68 | No significant similarity found | - | - | - | - | Exclusive |
| 77 | No significant similarity found | - | - | - | - | Exclusive |
| 83 | pv\_242 [protein=DNA-directed RNA polymerase subunit RPB2 | 1513 | 99% | 0 | 58.55% |   |
| 84 | No significant similarity found | - | - | - | - | Exclusive |
| 92 | No significant similarity found | - | - | - | - | Exclusive |
| 100 | No significant similarity found | - | - | - | - | Exclusive |
| 104 | No significant similarity found | - | - | - | - | Exclusive |
| 112 | No significant similarity found | - | - | - | - | Exclusive |
| 116 | No significant similarity found | - | - | - | - | Exclusive |
| 127 | No significant similarity found | - | - | - | - | Exclusive |
| 129 | No significant similarity found | - | - | - | - | Exclusive |
| 157 | pv\_384 [protein=hypothetical protein] [protein\_id=AHH01950.1] | 295 | 83% | 3,00E-105 | 77.14% |   |
| 167 | pv\_293 [protein=AP-endonuclease] [protein\_id=AHH01860.1] | 325 | 98% | 8,00E-110 | 38.75% |   |
| 168 | pv\_468 [protein=hypothetical protein] [protein\_id=AHH02034.1] | 52.8 | 46% | 1,00E-10 | 28.80% | 4 more hits |
| 169 | pv\_277 [protein=hypothetical protein] [protein\_id=AHH01844.1] | 246 | 97% | 4,00E-82 | 39.58% |   |
| 176 | pv\_265 [protein=hypothetical protein] [protein\_id=AHH01832.1]pv\_256 [protein=hypothetical protein] [protein\_id=AHH01823.1] | 10538.5 | 99%87% | 5,00E-308,00E-06 | 33.78%21.39% |   |
| 181 | pv\_366-368 [protein=DNA-directed RNA polymerase subunit RPB1 [protein\_id=AHH01933.1] | 1195 | 96% | 0 | 61.96% |   |
| 183 | pv\_383 [protein=hypothetical protein] [protein\_id=AHH01949.1] | 176 | 93% | 1,00E-55 | 36.12% |   |
| 185 | No significant similarity found | - | - | - | - | Exclusive |
| 186 | pv\_274 [protein=hypothetical protein] [protein\_id=AHH01841.1] | 155 | 75% | 3,00E-48 | 48.41% |   |
| 191 | pv\_366-368 [protein=DNA-directed RNA polymerase subunit RPB1 [protein\_id=AHH01933.1] | 1196 | 96% | 0 | 61.96% |   |
| 193 | pv\_383 [protein=hypothetical protein] [protein\_id=AHH01949.1] | 174 | 93% | 4,00E-55 | 35.36% |   |
| 196 | pv\_274 [protein=hypothetical protein] [protein\_id=AHH01841.1] | 211 | 81% | 1,00E-68 | 48.44% |   |
| 197 | No significant similarity found | - | - | - | - | Exclusive |
| 199 | No significant similarity found | - | - | - | - | Exclusive |
| 201 | No significant similarity found | - | - | - | - | Exclusive |
| 203 | pv\_106 [protein=hypothetical protein] [protein\_id=AHH01673.1] | 340 | 61% | 8,00E-114 | 51.38% |   |
| 204 | No significant similarity found | - | - | - | - | Exclusive |
| 205 | pv\_212 [protein=class 3 lipase] [protein\_id=AHH01779.1] | 191 | 98% | 2,00E-61 | 37.99% |   |
| 207 | pv\_224 [protein=hypothetical protein] [protein\_id=AHH01791.1] | 47.4 | 72% | 4,00E-08 | 21.90% | 13 more hits |
| 209 | pv\_224 [protein=hypothetical protein] [protein\_id=AHH01791.1] | 115 | 90% | 1,00E-30 | 30.00% | 20 more hits |
| 210 | pv\_224 [protein=hypothetical protein] [protein\_id=AHH01791.1] | 84 | 90% | 6,00E-20 | 25.74% | 21 more hits |
| 211 | pv\_202 [protein=hypothetical protein] [protein\_id=AHH01769.1] | 90.9 | 90% | 2,00E-22 | 27.84% | 17 more hits |
| 219 | pv\_468 [protein=hypothetical protein] [protein\_id=AHH02034.1] | 53.5 | 38% | 4,00E-11 | 37.18% | 6 more hits |
| 223 | pv\_468 [protein=hypothetical protein] [protein\_id=AHH02034.1] | 43.1 | 45% | 1,00E-07 | 28.40% | 5 more hits |
| 224 | pv\_468 [protein=hypothetical protein] [protein\_id=AHH02034.1] | 55.8 | 70% | 2,00E-12 | 35.51% | 5 more hits |
| 226 | pv\_222 [protein=hypothetical protein] [protein\_id=AHH01789.1] | 100 | 91% | 1,00E-25 | 25.89% | 19 more hits |
| 232 | pv\_98 [protein=hypothetical protein] [protein\_id=AHH01665.1] | 42 | 26% | 1,00E-06 | 29.67% |   |
| 235 | pv\_95 [protein=hypothetical protein] [protein\_id=AHH01662.1] | 221 | 95% | 3,00E-72 | 38.99% |   |
| 237 | pv\_106 [protein=hypothetical protein] [protein\_id=AHH01673.1] | 343 | 62% | 3,00E-115 | 52.00% |   |
| 238 | No significant similarity found | - | - | - | - | Exclusive |
| 239 | pv\_212 [protein=class 3 lipase] [protein\_id=AHH01779.1] | 192 | 97% | 9,00E-62 | 38.99% |   |
| 242 | pv\_224 [protein=hypothetical protein] [protein\_id=AHH01791.1] | 107 | 91% | 8,00E-28 | 29.41% | 19 more hits |
| 243 | pv\_224 [protein=hypothetical protein] [protein\_id=AHH01791.1] | 83.6 | 90% | 7,00E-20 | 25.80% | 23 more hits |
| 244 | pv\_202 [protein=hypothetical protein] [protein\_id=AHH01769.1] | 86.3 | 87% | 9,00E-21 | 26.08% | 17 more hits |
| 252 | pv\_468 [protein=hypothetical protein] [protein\_id=AHH02034.1] | 55.1 | 55% | 7,00E-12 | 30.71% |   |
| 253 | pv\_468 [protein=hypothetical protein] [protein\_id=AHH02034.1] | 53.9 | 39% | 2,00E-11 | 35.53% | 5 more hits |
| 255 | pv\_222 [protein=hypothetical protein] [protein\_id=AHH01789.1] | 107 | 91% | 9,00E-28 | 27.79% | 17 more hits |
| 264 | pv\_75 [protein=RNAse III] [protein\_id=AHH01642.1] | 28.9 | 38% | 20 | 21.37% |   |
| 267 | No significant similarity found | - | - | - | - | Exclusive |
| 271 | pv\_121 [protein=hypothetical protein] [protein\_id=AHH01688.1] | 37.4 | 14% | 5,00E-05 | 45.10% |   |
| 272 | pv\_120 [protein=EGF-like domain protein] [protein\_id=AHH01687.1]pv\_398 [protein=hypothetical protein] [protein\_id=AHH01964.1]pv\_121 [protein=hypothetical protein] [protein\_id=AHH01688.1] | 17658.945.1 | 83%86%54% | 1,00E-536,00E-122,00E-07 | 39.07%29.03%28.64% |   |
| 273 | pv\_73 [protein=hypothetical protein] [protein\_id=AHH01640.1] | 52.4 | 47% | 5,00E-13 | 40.38% |   |
| 274 | No significant similarity found | - | - | - | - | Exclusive |
| 275 | No significant similarity found | - | - | - | - | Exclusive |
| 276 | pv\_70 [protein=hypothetical protein] [protein\_id=AHH01637.1]pv\_195 [protein=hypothetical protein] [protein\_id=AHH01762.1] | 13142.4 | 82%33% | 5,00E-405,00E-07 | 39.44%32.10% |   |
| 278 | No significant similarity found | - | - | - | - | Exclusive |
| 280 | pv\_73 [protein=hypothetical protein] [protein\_id=AHH01640.1] | 50.1 | 47% | 6,00E-12 | 38.46% |   |
| 282 | No significant similarity found | - | - | - | - | Exclusive |
| 284 | pv\_92 [protein=hypothetical protein] [protein\_id=AHH01659.1] | 145 | 96% | 3,00E-42 | 28.71% |   |
| 285 | No significant similarity found | - | - | - | - | Exclusive |
| 286 | pv\_94 [protein=hypothetical protein] [protein\_id=AHH01661.1] | 276 | 100% | 6,00E-92 | 39.66% | 6 more hits |
| 293 | pv\_393 [protein=DEAD/SNF2 DNA/RNA helicase] [protein\_id=AHH01959.1] | 296 | 100% | 3,00E-100 | 47.27% |   |
| 294 | pv\_393 [protein=DEAD/SNF2 DNA/RNA helicase] [protein\_id=AHH01959.1] | 156 | 97% | 8,00E-49 | 54.55% |   |
| 295 | pv\_411 [protein=hypothetical protein] [protein\_id=AHH01977.1] | 65.5 | 85% | 6,00E-16 | 29.01% |   |
| 296 | pv\_408 [protein=hypothetical protein] [protein\_id=AHH01974.1] | 310 | 87% | 2,00E-108 | 60.00% |   |
| 297 | pv\_222 [protein=hypothetical protein] [protein\_id=AHH01789.1] | 74.7 | 37% | 5,00E-17 | 31.65% | 17 more hits |
| 302 | No significant similarity found | - | - | - | - | Exclusive |
| 304 | No significant similarity found | - | - | - | - | Exclusive |
| 305 | pv\_393 [protein=DEAD/SNF2 DNA/RNA helicase] [protein\_id=AHH01959.1] | 210 | 95% | 2,00E-68 | 53.44% |   |
| 306 | pv\_411 [protein=hypothetical protein] [protein\_id=AHH01977.1] | 63.2 | 85% | 5,00E-15 | 29.77% |   |
| 307 | pv\_408 [protein=hypothetical protein] [protein\_id=AHH01974.1] | 310 | 87% | 5,00E-108 | 59.61% |   |
| 310 | pv\_222 [protein=hypothetical protein] [protein\_id=AHH01789.1] | 108 | 54% | 3,00E-15 | 31.43% | 21 more hits |
| 311 | pv\_222 [protein=hypothetical protein] [protein\_id=AHH01789.1] | 75.9 | 36% | 2,00E-17 | 34.06% | 23 more hits |
| 312 | pv\_292 [protein=hypothetical protein] [protein\_id=AHH01859.1] | 72.8 | 48% | 2,00E-16 | 34.10% | 19 more hits |
| 313 | No significant similarity found | - | - | - | - | Exclusive |
| 317 | pv\_222 [protein=hypothetical protein] [protein\_id=AHH01789.1] | 76.6 | 35% | 1,00E-17 | 32.45% | 19 more hits |
| 318 | No significant similarity found | - | - | - | - | Exclusive |
| 319 | pv\_418 [protein=protein kinase] [protein\_id=AHH01984.1] | 302 | 81% | 3,00E-97 | 36.85% |   |
| 323 | pv\_423 [protein=hypothetical protein] [protein\_id=AHH01989.1] | 105 | 88% | 3,00E-30 | 36.08% |   |
| 325 | No significant similarity found | - | - | - | - | Exclusive |
| 326 | pv\_398 [protein=hypothetical protein] [protein\_id=AHH01964.1]pv\_121 [protein=hypothetical protein] [protein\_id=AHH01688.1]pv\_120 [protein=EGF-like domain protein] [protein\_id=AHH01687.1] | 17093.649.7 | 97%51%96% | 3,00E-524,00E-105,00E-09 | 40.35%35.03%26.17% |   |
| 327 | pv\_397 [protein=hypothetical protein] [protein\_id=AHH01963.1] | 89 | 100% | 2,00E-25 | 78.85% |   |
| 328 | pv\_395 [protein=hypothetical protein] [protein\_id=AHH01961.1]pv\_293 [protein=AP-endonuclease] [protein\_id=AHH01860.1] | 73.234.3 | 93%44% | 8,00E-174,00E-04 | 23.80%25.34% |   |
| 331 | pv\_395 [protein=hypothetical protein] [protein\_id=AHH01961.1]pv\_293 [protein=AP-endonuclease] [protein\_id=AHH01860.1] | 73.228.1 | 90%43% | 1,00E-160.043 | 25.27%23.97% |   |
| 333 | pv\_436 [protein=DNA-directed RNA Pol II C-term-like phosphatase] [protein\_id=AHH02002.1] | 263 | 98% | 5,00E-92 | 56.74% |   |
| 338 | No significant similarity found | - | - | - | - | Exclusive |
| 340 | pv\_436 [protein=DNA-directed RNA Pol II C-term-like phosphatase] [protein\_id=AHH02002.1] | 259 | 98% | 2,00E-90 | 56.28% |   |
| 345 | pv\_448 [protein=hypothetical protein] [protein\_id=AHH02014.1] | 37.7 | 79% | 1,00E-06 | 27.43% |   |
| 353 | pv\_450 [protein=helicase nuclease] [protein\_id=AHH02016.1] | 201 | 97% | 2,00E-68 | 53.43% |   |
| 355 | pv\_141 [protein=hypothetical protein] [protein\_id=AHH01708.1] | 156 | 97% | 1,00E-49 | 38.06% |   |
| 356 | pv\_141 [protein=hypothetical protein] [protein\_id=AHH01708.1]pv\_144 [protein=hypothetical protein] [protein\_id=AHH01711.1] | 147131 | 98%99% | 5,00E-465,00E-40 | 35.98%31.69% |   |
| 357 | pv\_141 [protein=hypothetical protein] [protein\_id=AHH01708.1]pv\_144 [protein=hypothetical protein] [protein\_id=AHH01711.1] | 170142 | 93%92% | 5,00E-554,00E-44 | 40.17%34.35% |   |
| 358 | pv\_141 [protein=hypothetical protein] [protein\_id=AHH01708.1]pv\_144 [protein=hypothetical protein] [protein\_id=AHH01711.1] | 10795.9 | 89%99% | 1,00E-303,00E-26 | 33.76%29.89% |   |
| 359 | pv\_141 [protein=hypothetical protein] [protein\_id=AHH01708.1]pv\_144 [protein=hypothetical protein] [protein\_id=AHH01711.1] | 137120 | 93%98% | 3,00E-429,00E-36 | 35.62%33.33% |   |
| 360 | pv\_141 [protein=hypothetical protein] [protein\_id=AHH01708.1]pv\_144 [protein=hypothetical protein] [protein\_id=AHH01711.1] | 146130 | 98%99% | 8,00E-469,00E-40 | 35.15%31.69% |   |
| 361 | pv\_141 [protein=hypothetical protein] [protein\_id=AHH01708.1] | 83.6 | 99% | 6,00E-22 | 31.76% |   |
| 362 | No significant similarity found | - | - | - | - | Exclusive |
| 363 | pv\_456 [protein=hypothetical protein] [protein\_id=AHH02022.1] | 150 | 85% | 1,00E-46 | 38.08% |   |
| 364 | pv\_458 [protein=hypothetical protein] [protein\_id=AHH02024.1] | 91.7 | 87% | 2,00E-28 | 56.58% |   |
| 365 | No significant similarity found | - | - | - | - | Exclusive |
| 368 | pv\_463 [protein=hypothetical protein] [protein\_id=AHH02029.1] | 133 | 84% | 3,00E-44 | 63.37% |   |
| 371 | pv\_466 [protein=hypothetical protein] [protein\_id=AHH02032.1] | 104 | 100% | 8,00E-33 | 54.43% |   |
| 372 | pv\_456 [protein=hypothetical protein] [protein\_id=AHH02022.1] | 124 | 97% | 1,00E-37 | 40.24% |   |
| 373 | pv\_458 [protein=hypothetical protein] [protein\_id=AHH02024.1] | 73.6 | 80% | 1,00E-21 | 66.00% |   |
| 375 | No significant similarity found | - | - | - | - | Exclusive |
| 377 | pv\_463 [protein=hypothetical protein] [protein\_id=AHH02029.1] | 130 | 84% | 4,00E-43 | 61.39% |   |
| 380 | pv\_466 [protein=hypothetical protein] [protein\_id=AHH02032.1] | 100 | 95% | 9,00E-31 | 53.49% |   |
| 381 | pv\_2 [protein=hypothetical protein] [protein\_id=AHH01569.1] | 226 | 82% | 2,00E-73 | 49.39% |   |
| 382 | pv\_2 [protein=hypothetical protein] [protein\_id=AHH01569.1] | 138 | 97% | 3,00E-41 | 42.51% |   |
| 383 | pv\_4 [protein=hypothetical protein] [protein\_id=AHH01571.1] | 273 | 99% | 4,00E-94 | 48.44% |   |
| 385 | No significant similarity found | - | - | - | - | Exclusive |
| 386 | No significant similarity found | - | - | - | - | Exclusive |
| 387 | No significant similarity found | - | - | - | - | Exclusive |
| 388 | pv\_11 [protein=hypothetical protein] [protein\_id=AHH01578.1] | 57.8 | 100% | 1,00E-13 | 33.99% |   |
| 389 | No significant similarity found | - | - | - | - | Exclusive |
| 390 | No significant similarity found | - | - | - | - | Exclusive |
| 393 | pv\_13 [protein=hypothetical protein] [protein\_id=AHH01580.1] | 181 | 97% | 2,00E-57 | 34.20% |   |
| 394 | No significant similarity found | - | - | - | - | Exclusive |
| 398 | No significant similarity found | - | - | - | - | Exclusive |
| 404 | No significant similarity found | - | - | - | - | Exclusive |
| 405 | No significant similarity found | - | - | - | - | Exclusive |
| 406 | pv\_27 [protein=VV D6-like helicase] [protein\_id=AHH01594.1] | 1065 | 100% | 0 | 48.38% |   |
| 407 | pv\_224 [protein=hypothetical protein] [protein\_id=AHH01791.1] | 75.5 | 89% | 3,00E-17 | 24.09% | 19 more hits |
| 412 | pv\_222 [protein=hypothetical protein] [protein\_id=AHH01789.1] | 72.4 | 41% | 5,00E-17 | 37.25% | 24 more hits |
| 414 | pv\_29 [protein=transcription elongation factor TFIIS] [protein\_id=AHH01596.1] | 172 | 99% | 5,00E-58 | 50.30% |   |
| 415 | No significant similarity found | - | - | - | - | Exclusive |
| 416 | pv\_123 [protein=hypothetical protein] [protein\_id=AHH01690.1]pv\_124 [protein=hypothetical protein] [protein\_id=AHH01691.1] | 59.758.5 | 26%33% | 2,00E-135,00E-13 | 48.94%45.90% |   |
| 417 | pv\_468 [protein=hypothetical protein] [protein\_id=AHH02034.1]pv\_18 [protein=hypothetical protein] [protein\_id=AHH01585.1] pv\_123 [protein=hypothetical protein] [protein\_id=AHH01690.1]pv\_124 [protein=hypothetical protein] [protein\_id=AHH01691.1] | 44.343.141.241.2 | 31%78%42%34% | 5,00E-081,00E-07 6,00E-076,00E-07 | 33.90%25.49%34.88%34.38% |   |
| 418 | No significant similarity found | - | - | - | - | Exclusive |
| 429 | No significant similarity found | - | - | - | - | Exclusive |
| 430 | No significant similarity found | - | - | - | - | Exclusive |
| 434 | pv\_18 [protein=hypothetical protein] [protein\_id=AHH01585.1]pv\_468 [protein=hypothetical protein] [protein\_id=AHH02034.1]pv\_354 [protein=hypothetical protein] [protein\_id=AHH01921.1] | 43.143.133.9 | 41%30%22% | 1,00E-072,00E-072,00E-04 | 29.89%34.38%39.58% |   |
| 439 | pv\_468 [protein=hypothetical protein] [protein\_id=AHH02034.1] | 60.8 | 72% | 1,00E-14 | 37.04% | 5 more hits |
| 440 | pv\_31 [protein=RNA polymerase II RPB5 subunit] [protein\_id=AHH01598.1] | 170 | 98% | 2,00E-55 | 40.00% |   |
| 442 | pv\_45 [protein=hypothetical protein] [protein\_id=AHH01612.1] | 142 | 48% | 7,00E-39 | 36.13% |   |
| 447 | pv\_468 [protein=hypothetical protein] [protein\_id=AHH02034.1] | 60.8 | 73% | 1,00E-14 | 36.78% | 6 more hits |
| 448 | pv\_31 [protein=RNA polymerase II RPB5 subunit] [protein\_id=AHH01598.1] | 169 | 98% | 5,00E-55 | 40.00% |   |
| 450 | pv\_45 [protein=hypothetical protein] [protein\_id=AHH01612.1] | 140 | 65% | 3,00E-39 | 36.97% |   |
| 451 | No significant similarity found | - | - | - | - | Exclusive |
| 454 | No significant similarity found | - | - | - | - | Exclusive |
| 463 | pv\_60 [protein=hypothetical protein] [protein\_id=AHH01627.1] | 78.6 | 85% | 2,00E-21 | 39.47% |   |
| 464 | No significant similarity found | - | - | - | - | Exclusive |
| 468 | pv\_60 [protein=hypothetical protein] [protein\_id=AHH01627.1]pv\_195 [protein=hypothetical protein] [protein\_id=AHH01762.1] | 17294.7 | 98%100% | 4,00E-563,00E-25 | 45.23%32.11% |   |
| 469 | No significant similarity found | - | - | - | - | Exclusive |
| 472 | No significant similarity found | - | - | - | - | Exclusive |
| 476 | pv\_146 [protein=hypothetical protein] [protein\_id=AHH01713.1] | 403 | 99% | 1,00E-141 | 51.75% |   |
| 479 | No significant similarity found | - | - | - | - | Exclusive |
| 482 | pv\_145 [protein=hypothetical protein] [protein\_id=AHH01712.1] | 175 | 97% | 1,00E-54 | 34.97% |   |
| 483 | pv\_146 [protein=hypothetical protein] [protein\_id=AHH01713.1] | 397 | 98% | 3,00E-139 | 50.25% |   |
| 493 | pv\_150 [protein=DNA-directed RNA polymerase RPB1 [protein\_id=AHH01717.1] | 607 | 99% | 0 | 44.20% |   |
| 497 | pv\_403 [protein=hypothetical protein] [protein\_id=AHH01969.1] | 185 | 84% | 4,00E-62 | 54.27% |   |
| 507 | pv\_404 [protein=hypothetical protein] [protein\_id=AHH01970.1] | 40.4 | 52% | 1,00E-06 | 27.37% |   |
| 514 | pv\_413 [protein=hypothetical protein] [protein\_id=AHH01979.1] | 236 | 75% | 2,00E-79 | 51.68% |   |
| 515 | pv\_405 [protein=Ser/Thr protein kinase] [protein\_id=AHH01971.1] | 322 | 63% | 7,00E-106 | 43.53% | 6 more hits |
| 516 | pv\_292 [protein=hypothetical protein] [protein\_id=AHH01859.1] | 62.4 | 83% | 9,00E-13 | 24.87% | 6 more hits |
| 518 | No significant similarity found | - | - | - | - | Exclusive |
| 519 | No significant similarity found | - | - | - | - | Exclusive |
| 523 | pv\_413 [protein=hypothetical protein] [protein\_id=AHH01979.1] | 229 | 77% | 9,00E-77 | 49.58% |   |
| 527 | No significant similarity found | - | - | - | - | Exclusive |
| 528 | pv\_408 [protein=hypothetical protein] [protein\_id=AHH01974.1] | 226 | 91% | 4,00E-75 | 44.64% |   |
| 537 | pv\_418 [protein=protein kinase] [protein\_id=AHH01984.1] | 209 | 75% | 9,00E-65 | 40.42% |   |
| 539 | pv\_422 [protein=transcription initiation factor TFIIB] [protein\_id=AHH01988.1] | 214 | 97% | 5,00E-74 | 57.14% |   |
| 541 | pv\_423 [protein=hypothetical protein] [protein\_id=AHH01989.1] | 103 | 93% | 2,00E-29 | 36.32% |   |
| 542 | pv\_424 [protein=hypothetical protein] [protein\_id=AHH01990.1]pv\_145 [protein=hypothetical protein] [protein\_id=AHH01712.1] | 34039.3 | 99%73% | 6,00E-1161,00E-05 | 40.65%23.15% |   |
| 550 | pv\_423 [protein=hypothetical protein] [protein\_id=AHH01989.1] | 99.8 | 94% | 6,00E-28 | 34.43% |   |
| 552 | pv\_424 [protein=hypothetical protein] [protein\_id=AHH01990.1]pv\_145 [protein=hypothetical protein] [protein\_id=AHH01712.1] | 34143.1 | 99%65% | 3,00E-1161,00E-06 | 40.31%23.51% |   |
| 556 | pv\_73 [protein=hypothetical protein] [protein\_id=AHH01640.1] | 56.2 | 51% | 1,00E-14 | 50.00% |   |
| 557 | pv\_75 [protein=RNAse III] [protein\_id=AHH01642.1] | 310 | 98% | 1,00E-106 | 46.45% |   |
| 558 | No significant similarity found | - | - | - | - | Exclusive |
| 563 | pv\_79 [protein=hypothetical protein] [protein\_id=AHH01646.1] | 253 | 100% | 2,00E-84 | 62.44% |   |
| 572 | pv\_115 [protein=hypothetical protein] [protein\_id=AHH01682.1] | 246 | 97% | 7,00E-78 | 30.58% |   |
| 573 | pv\_114 [protein=DNA-directed RNA polymerase RPB10 [protein\_id=AHH01681.1] | 46.6 | 82% | 2,00E-10 | 35.90% |   |
| 574 | pv\_109 [protein=hypothetical protein] [protein\_id=AHH01676.1] | 324 | 99% | 4,00E-115 | 60.63% |   |
| 582 | pv\_115 [protein=hypothetical protein] [protein\_id=AHH01682.1] | 237 | 97% | 2,00E-74 | 30.52% |   |
| 584 | pv\_109 [protein=hypothetical protein] [protein\_id=AHH01676.1] | 324 | 99% | 3,00E-115 | 60.63% |   |
| 594 | pv\_9 [protein=hypothetical protein] [protein\_id=AHH01576.1] | 80.9 | 94% | 4,00E-22 | 31.71% |   |
| 597 | No significant similarity found | - | - | - | - | Exclusive |
| 598 | pv\_9 [protein=hypothetical protein] [protein\_id=AHH01576.1] | 76.3 | 94% | 2,00E-20 | 31.33% |   |
| 601 | No significant similarity found | - | - | - | - | Exclusive |
| 602 | pv\_6 [protein=hypothetical protein] [protein\_id=AHH01573.1] | 64.3 | 36% | 6,00E-14 | 40.59% |   |
| 603 | No significant similarity found | - | - | - | - | Exclusive |
| 608 | pv\_6 [protein=hypothetical protein] [protein\_id=AHH01573.1] | 111 | 56% | 4,00E-29 | 35.21% |   |
| 610 | pv\_3 [protein=hypothetical protein] [protein\_id=AHH01570.1] | 50.1 | 85% | 3,00E-10 | 22.92% |   |
| 615 | pv\_464 [protein=ATP-dependent DNA ligase] [protein\_id=AHH02030.1] | 462 | 97% | 3,00E-164 | 55.11% |   |
| 621 | pv\_461 [protein=hypothetical protein] [protein\_id=AHH02027.1] | 126 | 97% | 2,00E-36 | 30.70% |   |
| 624 | pv\_456 [protein=hypothetical protein] [protein\_id=AHH02022.1] | 159 | 83% | 8,00E-50 | 39.56% |   |
| 625 | No significant similarity found | - | - | - | - | Exclusive |
| 626 | No significant similarity found | - | - | - | - | Exclusive |
| 636 | pv\_454 [protein=mRNA-capping enzyme] [protein\_id=AHH02020.1] | 745 | 97% | 0 | 42.13% |   |
| 646 | No significant similarity found | - | - | - | - | Exclusive |
| 651 | pv\_449 [protein=hypothetical protein] [protein\_id=AHH02015.1] | 158 | 88% | 2,00E-50 | 46.51% |   |
| 652 | pv\_446 [protein=VETF-like early transcription factor large subunit] [protein\_id=AHH02012.1] | 1030 | 98% | 0 | 44.39% |   |
| 654 | pv\_444 [protein=polyA polymerase reg subunit] [protein\_id=AHH02010.1] | 89 | 92% | 2,00E-23 | 30.92% |   |
| 657 | pv\_437 [protein=5'-3' exoribonuclease] [protein\_id=AHH02003.1] | 355 | 97% | 5,00E-121 | 50.57% |   |
| 660 | No significant similarity found | - | - | - | - | Exclusive |
| 665 | pv\_449 [protein=hypothetical protein] [protein\_id=AHH02015.1] | 142 | 95% | 3,00E-44 | 43.78% |   |
| 666 | pv\_446 [protein=VETF-like early transcription factor large subunit] [protein\_id=AHH02012.1] | 1030 | 99% | 0 | 44.32% |   |
| 670 | pv\_438 [protein=cyclin-dependent kinase] [protein\_id=AHH02004.1]pv\_405 [protein=Ser/Thr protein kinase] [protein\_id=AHH01971.1] | 19765.9 | 100%63% | 4,00E-625,00E-14 | 35.01%25.34% |   |
| 671 | pv\_437 [protein=5'-3' exoribonuclease] [protein\_id=AHH02003.1] | 349 | 100% | 5,00E-119 | 50.29% |   |
| 672 | pv\_437 [protein=5'-3' exoribonuclease] [protein\_id=AHH02003.1] | 168 | 83% | 3,00E-51 | 49.49% |   |
| 674 | No significant similarity found | - | - | - | - | Exclusive |
| 675 | No significant similarity found | - | - | - | - | Exclusive |
| 677 | pv\_216 [protein=hypothetical protein] [protein\_id=AHH01783.1] | 138 | 96% | 5,00E-40 | 33.54% | 16 more hits |
| 678 | No significant similarity found | - | - | - | - | Exclusive |
| 679 | pv\_222 [protein=hypothetical protein] [protein\_id=AHH01789.1] | 75.9 | 44% | 9,00E-18 | 36.76% | 16 more hits |
| 684 | pv\_216 [protein=hypothetical protein] [protein\_id=AHH01783.1] | 124 | 97% | 5,00E-33 | 26.69% | 20 more hits |
| 690 | No significant similarity found | - | - | - | - | Exclusive |
| 692 | No significant similarity found | - | - | - | - | Exclusive |
| 693 | No significant similarity found | - | - | - | - | Exclusive |
| 695 | pv\_63 [protein=mannosyl phosphorylinositol ceramide synthase] [protein\_id=AHH01630.1] | 151 | 96% | 3,00E-49 | 63.64% |   |
| 700 | No significant similarity found | - | - | - | - | Exclusive |
| 704 | pv\_405 [protein=Ser/Thr protein kinase] [protein\_id=AHH01971.1]pv\_438 [protein=cyclin-dependent kinase] [protein\_id=AHH02004.1] | 58.556.6 | 54%42% | 2,00E-115,00E-11 | 24.23%24.24% |   |
| 706 | pv\_438 [protein=cyclin-dependent kinase] [protein\_id=AHH02004.1]pv\_405 [protein=Ser/Thr protein kinase] [protein\_id=AHH01971.1] | 53.553.5 | 45%47% | 5,00E-107,00E-10 | 23.89%25.33% |   |
| 708 | No significant similarity found | - | - | - | - | Exclusive |
| 714 | pv\_231 [protein=hypothetical protein] [protein\_id=AHH01798.1] | 139 | 80% | 3,00E-42 | 34.68% |   |
| 720 | No significant similarity found | - | - | - | - | Exclusive |
| 723 | pv\_202 [protein=hypothetical protein] [protein\_id=AHH01769.1] | 90.9 | 45% | 2,00E-21 | 27.88% | 16 more hits |
| 724 | No significant similarity found | - | - | - | - | Exclusive |
| 725 | No significant similarity found | - | - | - | - | Exclusive |
| 745 | No significant similarity found | - | - | - | - | Exclusive |
| 747 | pv\_16 [protein=hypothetical protein] [protein\_id=AHH01583.1] | 93.6 | 94% | 1,00E-27 | 42.11% |   |
| 756 | pv\_19 [protein=alpha/beta hydrolase] [protein\_id=AHH01586.1] | 206 | 93% | 2,00E-68 | 42.41% |   |
| 762 | pv\_19 [protein=alpha/beta hydrolase] [protein\_id=AHH01586.1] | 197 | 100% | 5,00E-65 | 43.03% |   |
| 766 | pv\_382 [protein=hypothetical protein] [protein\_id=AHH01948.1] | 42.7 | 27% | 6,00E-08 | 54.29% |   |
| 778 | pv\_352 [protein=hypothetical protein] [protein\_id=AHH01919.1] | 172 | 95% | 2,00E-51 | 33.66% |   |
| 779 | pv\_350 [protein=hypothetical protein] [protein\_id=AHH01917.1] | 59.3 | 50% | 4,00E-13 | 37.50% |   |
| 780 | pv\_18 [protein=hypothetical protein] [protein\_id=AHH01585.1] | 87.4 | 94% | 6,00E-24 | 27.04% |   |
| 781 | No significant similarity found | - | - | - | - | Exclusive |
| 782 | pv\_38 [protein=hypothetical protein] [protein\_id=AHH01605.1] | 399 | 96% | 1,00E-133 | 40.00% |   |
| 784 | No significant similarity found | - | - | - | - | Exclusive |
| 786 | No significant similarity found | - | - | - | - | Exclusive |
| 787 | No significant similarity found | - | - | - | - | Exclusive |
| 788 | No significant similarity found | - | - | - | - | Exclusive |
| 789 | pv\_216 [protein=hypothetical protein] [protein\_id=AHH01783.1] | 62.4 | 29% | 6,00E-13 | 37.39% | 17 more hits |
| 792 | No significant similarity found | - | - | - | - | Exclusive |
| 798 | pv\_284 [protein=hypothetical protein] [protein\_id=AHH01851.1] | 26.6 | 47% | 12 | 26.53% |   |
| 799 | No significant similarity found | - | - | - | - | Exclusive |
| 800 | No significant similarity found | - | - | - | - | Exclusive |
| 801 | pv\_150 [protein=DNA-directed RNA polymerase RPB1 [protein\_id=AHH01717.1] | 27.3 | 31% | 16 | 31.82% |   |
| 802 | pv\_101 [protein=hypothetical protein] [protein\_id=AHH01668.1] | 172 | 91% | 2,00E-53 | 34.42% |   |
| 803 | pv\_222 [protein=hypothetical protein] [protein\_id=AHH01789.1] | 113 | 77% | 2,00E-18 | 44.33% | 22 more hits |
| 804 | No significant similarity found | - | - | - | - | Exclusive |
| 806 | pv\_135 [protein=hypothetical protein] [protein\_id=AHH01702.1] | 166 | 99% | 5,00E-54 | 42.67% |   |
| 807 | pv\_18 [protein=hypothetical protein] [protein\_id=AHH01585.1]pv\_468 [protein=hypothetical protein] [protein\_id=AHH02034.1]pv\_123 [protein=hypothetical protein] [protein\_id=AHH01690.1] | 74.358.536.2 | 83%46%20% | 5,00E-197,00E-133,00E-05 | 30.22%31.18%42.50% |   |
| 810 | pv\_114 [protein=DNA-directed RNA polymerase RPB10 [protein\_id=AHH01681.1] | 25.4 | 20% | 30 | 43.48% |   |
| 817 | pv\_18 [protein=hypothetical protein] [protein\_id=AHH01585.1]pv\_468 [protein=hypothetical protein] [protein\_id=AHH02034.1]pv\_123 [protein=hypothetical protein] [protein\_id=AHH01690.1]pv\_286 [protein=hypothetical protein] [protein\_id=AHH01853.1] | 73.255.8 32.330.4 | 83%46%20%44% | 1,00E-186,00E-126,00E-040.003 | 30.22%30.11%40.00% 31.87% |   |
| 824 | No significant similarity found | - | - | - | - | Exclusive |
| 828 | pv\_138 [protein=topoisomerase IIA] [protein\_id=AHH01705.1] | 528 | 97% | 4,00E-180 | 54.99% |   |
| 838 | No significant similarity found | - | - | - | - | Exclusive |
| 840 | No significant similarity found | - | - | - | - | Exclusive |
| 841 | No significant similarity found | - | - | - | - | Exclusive |

****

**Supplementary Figure 1** Quality control of purified Cedratvirus particles.  The virion proteins from 107 and 108 viral particles were analyzed by SDS-PAGE. (a) Proteins resolved by SDS-PAGE for protein distribution analysis or (b) MS analysis were stained with Coomassie Brilliant Blue (Biorad).

****

**Supplementary Figure 2** VENN diagram of identified proteins from LC-MS.