**An iridovirus from the Antarctic Seaspider *Pentanymphon antarcticum* (Pycnogonida)**

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Supplementary Table 1: Layout of the coding genes for each annotated gene on the new iridovirus genome. A comparison of the draft iridovirus genome annotations including the predicted function and BlastP results.

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| Iridovirus genomic segment | Gene ID | Predicted function | Blastp result | Similarity | Coverage | e-value |
| Segment 1 (OQ791181) | 1 | Hypothetical protein | - | - | - | - |
| 2 | Hypothetical protein | - | - | - | - |
| 3 | Hypothetical protein | - | - | - | - |
| 4 | Major capsid protein | UUT40469; carnivorous sponge associated iridovirus | 74% | 99% | 0.0 |
| 5 | Hypothetical protein | - | - | - | - |
| 6 | Hypothetical protein | - | - | - | - |
| 7 | Thioredoxin | UUT40463; carnivorous sponge associated iridovirus | 51% | 97% | 2e-40 |
| 8 | Hypothetical protein | - | - | - | - |
| 9 | Hypothetical protein | - | - | - | - |
| 10 | DNA repair exonuclease D subunit | UUT40542; carnivorous sponge associated iridovirus | 57% | 87% | 2e-117 |
| 11 | SAP domain protein  | QBK85302; Iridovirus LCIVAC01 | 25% | 98% | 7e-07 |
| 12 | Hypothetical protein | UUT40451; carnivorous sponge associated iridovirus | 32% | 97% | 7e-96 |
| 13 | Hypothetical protein | - | - | - | - |
| 14 | Tyrosine kinase/LPS-modifying enzyme  | UUT40405; carnivorous sponge associated iridovirus | 47% | 99% | 0.0 |
| 15 | Papain-like proteinase  | UUT40459; carnivorous sponge associated iridovirus | 41% | 85% | 3e-76 |
| 16 | Hypothetical protein | UUT40565; carnivorous sponge associated iridovirus | 37% | 100% | 0.0 |
| 17 | Hypothetical protein | - | - | - | - |
| 18 | Hypothetical protein | - | - | - | - |
| 19 | Hypothetical protein | UUT40446; carnivorous sponge associated iridovirus | 55% | 46% | 4e-14 |
| 20 | Hypothetical protein | UUT40518; carnivorous sponge associated iridovirus | 36% | 90% | 2e-24 |
| 21 | Hypothetical protein | UUT40519; carnivorous sponge associated iridovirus | 27% | 96% | 1e-06 |
| 22 | Hypothetical protein | UUT40522; carnivorous sponge associated iridovirus | 47% | 97% | 2e-87 |
| 23 | RAD2 | UUT40506; carnivorous sponge associated iridovirus | 40% | 96% | 9e-77 |
| 24 | Hypothetical protein | - | - | - | - |
| 25 | Hypothetical protein | - | - | - | - |
| 26 | Hypothetical protein | - | - | - | - |
| 27 | Hypothetical protein | - | - | - | - |
| 28 | Zinc-Finger protein | UUT40505; carnivorous sponge associated iridovirus | 26% | 66% | 2e-16 |
| 29 | 5'-3' exoribonuclease 1 | UUT40402; carnivorous sponge associated iridovirus | 45% | 100% | 2e-115 |
| 30 | Hypothetical protein | - | - | - | - |
| 31\* | Hypothetical protein | UPA43425; Iridovirus CN01 | 46% | 91% | 3e-49 |
| 32 | TFIID | YP\_009552440; ‘Cherax quadricarinatus iridovirus’ | 43% | 97% | 9e-54 |
| 33 | Hypothetical protein | UUT40428; carnivorous sponge associated iridovirus | 43% | 99% | 3e-63 |
| 34 | NIF/NLI interacting factor | UUT40404; carnivorous sponge associated iridovirus | 66% | 80% | 5e-72 |
| 35 | Hypothetical protein | - | - | - | - |
| 36 | Helicase NTPase | UUT40399; carnivorous sponge-associated iridovirus | 55% | 99% | 0.0 |
| 37 | BRO-like protein | YP\_009021212; ‘Anopheles minimus iridovirus’ | 29% | 98% | 3e-22 |
| Segment 2 (OQ791182) | 38 | Hypothetical | UUT40475; carnivorous sponge associated iridovirus | 40% | 96 | 0.038 |
| 39 | Ribonucleotide reductase beta subunit  | UUT40489; carnivorous sponge associated iridovirus | 65% | 100% | 5e-148 |
| 40 | ATP-dependent DNA helicase PIF1  | UUT40412; carnivorous sponge-associated iridovirus | 48% | 98% | 4e-120 |
| 41 | Hypothetical protein | - | - | - | - |
| 42 | Ser/Thr kinase | YP\_009552338; ‘Cherax quadricarinatus iridovirus’ | 36% | 97% | 6e-68 |
| 43 | Hypothetical protein | - | - | - | - |
| 44 | D5 family NTPase ATPase | UUT40434; carnivorous sponge associated iridovirus | 60% | 98% | 0.0 |
| 45 | Hypothetical protein | - | - | - | - |
| 46 | DNA polymerase elongation (B family) | YP\_009552323; ‘Cherax quadricarinatus iridovirus’ | 53% | 60% | 5e-151 |
| 47 | Delta DNA polymerase (B family)  | YP\_009010295; Invertebrate iridescent virus 30 | 46% | 98% | 6e-127 |
| 48 | Hypothetical protein | - | - | - | - |
| 49 | Hypothetical protein | - | - | - | - |
| 50 | Hypothetical protein | - | - | - | - |
| 51 | Papain-like proteinase  | UUT40459; carnivorous sponge associated iridovirus | 47% | 86% | 3e-24 |
| 52 | Hypothetical protein | - | - | - | - |
| 53 | Hypothetical protein | - | - | - | - |
| 54 | Hypothetical protein | - | - | - | - |
| 55 | Hypothetical protein | - | - | - | - |
| 56 | Hypothetical protein | - | - | - | - |
| Segment 3 (OQ791183) | 57 | Hypothetical protein | - | - | - | - |
| 58 | Hypothetical protein | - | - | - | - |
| 59 | Hypothetical protein | - | - | - | - |
| 60 | Hypothetical protein | UUT40440; carnivorous sponge associated iridovirus | 52% | 99% | 4e-171 |
| 61 | Hypothetical protein | UUT40441; carnivorous sponge-associated iridovirus 4 | 44% | 80% | 3e-27 |
| 62 | Hypothetical protein | - | - | - | - |
| 63 | Hypothetical protein | UUT40528; carnivorous sponge-associated iridovirus 4 | 42% | 92% | 4e-83 |
| 64 | Hypothetical protein | Invertebrate iridescent virus 3 | 29% | 60% | 9e-22 |
| 65 | DNA-directed RNA polymerase II largest subunit | UUT40526; carnivorous sponge associated iridovirus | 65% | 97% | 0.0 |
| 66 | Hypothetical protein | - | - | - | - |
| 67 | DNA-directed RNA polymerase II largest subunit | UUT40526; carnivorous sponge associated iridovirus | 61% | 98% | 0.0 |
| 68 | Hypothetical protein | UUT40535; carnivorous sponge associated iridovirus | 57% | 81% | 1e-36 |
| 69 | Hypothetical protein | UUT40534; carnivorous sponge-associated iridovirus 4 | 38% | 88% | 5e-26 |
| 70 | Hypothetical protein | - | - | - | - |
| 71 | Hypothetical protein | - | - | - | - |
| Segment 4 (OQ791184) | 72 | DNA double-strand break repair rad50 ATPase-like protein | UUT40398; carnivorous sponge-associated iridovirus 4 | 46% | 71% | 2e-56 |
| 73 | Hypothetical protein | - | - | - | - |
| 74 | Hypothetical protein | QBK85229; Iridovirus LCIVAC01 | 27% | 84% | 2e-18 |
| 75 | Immediate early ICP-46  | YP\_010084825; Shrimp haemocyte iridescent virus | 35% | 97% | 5e-61 |
| 76 | MutT/NUDIX hydrolase | YP\_009552361; ‘Cherax quadricarinatus iridovirus’ | 38% | 93% | 7e-28 |
| 77 | Hypothetical protein | UUT40495; carnivorous sponge-associated iridovirus 4 | 49% | 98% | 2e-84 |
| 78 | Hypothetical protein | UUT40418; carnivorous sponge associated iridovirus | 52% | 57% | 5e-27 |
| 79 | Helicase | UUT40419; carnivorous sponge associated iridovirus | 46% | 99% | 4e-127 |
| 80 | Hypothetical protein | UUT40547; carnivorous sponge-associated iridovirus 4 | 42% | 94% | 4e-32 |
| 81 | 023L | YP\_009552304; ‘Cherax quadricarinatus iridovirus’ | 37% | 93% | 1e-29 |
| 82 | Hypothetical protein | UUT40422; carnivorous sponge-associated iridovirus 4 | 40% | 100% | 6e-54 |
| 83 | Hypothetical protein | UUT40414; carnivorous sponge-associated iridovirus 4 | 65% | 45% | 1e-33 |
| Segment 5 (OQ791185) | 84 | BRO-like protein | YP\_009021212; ‘Anopheles minimus iridovirus’ | 26% | 87% | 1e-16 |
| 85 | Hypothetical protein | - | - | - | - |
| 86 | 092L | YP\_009552373; ‘Cherax quadricarinatus iridovirus’ | 34% | 98% | 3e-48 |
| 87 | Replicating factor | UUT40563; carnivorous sponge associated iridovirus | 59% | 89% | 4e-140 |
| 88 | Neurofilament triplet H1-like protein | UUT40458; carnivorous sponge associated iridovirus | 37% | 35% | 1e-15 |
| 89 | Hypothetical protein | UUT40579; carnivorous sponge associated iridovirus | 33% | 98% | 7e-52 |
| 90 | 169R | UUT40579; carnivorous sponge associated iridovirus | 35% | 55% | 1e-26 |
| 91 | RuVC-like Holliday junction resolvase | YP\_009552433; ‘Cherax quadricarinatus iridovirus’ | 47% | 98% | 1e-46 |
| 92 | dUTPase | YP\_009552293; ‘Cherax quadricarinatus iridovirus’ | 57% | 86% | 2e-49 |
| 93 | Hypothetical protein | UUT40536; carnivorous sponge-associated iridovirus 4 | 31% | 35% | 3e-11 |
| 94 | Hypothetical protein | - | - | - | - |
| Segment 6 (OQ791186) | 95 | Hypothetical protein | - | - | - | - |
| 96 | Hypothetical protein | UUT40467; carnivorous sponge associated iridovirus | 33% | 85% | 7e-78 |
| 97 | Hypothetical protein | UUT40479; carnivorous sponge associated iridovirus | 41% | 97% | 9e-74 |
| 98 | 147R | YP\_009552428; ‘Cherax quadricarinatus iridovirus’ | 39% | 97% | 2e-18 |
| 99 | Hypothetical protein | - | - | - | - |
| 100 | Hypothetical protein | - | - | - | - |
| 101 | BRO-like protein | YP\_009021212; ‘Anopheles minimus iridovirus’ | 59% | 80% | 2e-07 |
| 102 | RAD2 | UUT40506; ‘carnivorous sponge associated iridovirus’ | 40% | 96% | 9e-77 |
| 103 | Hypothetical protein | UUT40522; ‘carnivorous sponge associated iridovirus’ | 47% | 97% | 2e-87 |
| 104 | Hypothetical protein | UUT40519; ‘carnivorous sponge associated iridovirus’ | 27% | 96% | 2e-11 |
| 105 | Hypothetical protein | UUT40518; carnivorous sponge associated iridovirus | 36% | 90% | 2e-24 |
| 106 | Hypothetical protein | UUT40446; carnivorous sponge associated iridovirus | 55% | 46% | 4e-14 |
| Segment 7 (OQ791187) | 107 | Putative 2-cysteine adaptor domain protein  | AYV88192; Mandarin fish ranavirus | 35% | 37% | 1e-12 |
| 108 | Ser/Thr-like protein kinase lyk4  | YP\_009046747; ‘Armadillidium vulgare iridescent virus’ | 30% | 50% | 1e-14 |
| 109 | NTPase/helicase-like protein  | YP\_009046681; ‘Armadillidium vulgare iridescent virus’ | 37% | 88% | 8e-91 |
| 110 | Hypothetical protein | UUT40486; ‘carnivorous sponge associated iridovirus’ | 29% | 79% | 7e-30 |
| 111 | Hypothetical protein | UUT40568; ‘carnivorous sponge associated iridovirus’ | 54% | 99% | 5e-89 |
| 112 | BRO-like protein | UUT40471; ‘carnivorous sponge associated iridovirus’ | 61% | 46% | 0.004 |
| Segment 8 (OQ791188) | 113 | Hypothetical protein | UUT40539; ‘carnivorous sponge associated iridovirus’ | 42% | 85% | 2e-04 |
| 114 | Hypothetical protein | - | - | - | - |
| 115 | Hypothetical protein | - | - | - | - |
| 116 | Hypothetical protein | - | - | - | - |
| 117 | Hypothetical protein | - | - | - | - |
| 118 | Hypothetical protein | - | - | - | - |
| 119 | Hypothetical protein | UUT40497; ‘carnivorous sponge-associated iridovirus’ | 49% | 44% | 9e-05 |
| 120 | DNA-directed RNA polymerase II second largest subunit | UUT40578; ‘carnivorous sponge-associated iridovirus’ | 63% | 99% | 0.0 |
| 121 | BRO-like protein | UUT40471; ‘carnivorous sponge-associated iridovirus’ | 53% | 50% | 0.003 |
| Segment 9 (OQ791189) | 122 | Hypothetical protein | UUT40435; ‘carnivorous sponge-associated iridovirus’ | 29% | 87% | 1e-11 |
| 123 | T5orf172 domain protein | YP\_009010354; Invertebrate iridescent virus 30 | 33% | 61% | 2e-22 |
| 124 | Transcription elongation factor SII | YP\_009552344; ‘Cherax quadricarinatus iridovirus’ | 50% | 99% | 5e-39 |
| 125 | Ribonuclease-like protein  | AAL77809; Tiger frog virus | 45% | 81% | 1e-56 |
| 126 | Hypothetical protein | - | - | - | - |
| 127 | Hypothetical protein | - | - | - | - |
| 128 | Hypothetical protein | - | - | - | - |
| 129 | Hypothetical protein | - | - | - | - |
| 130 | Hypothetical protein | - | - | - | - |
| 131 | RING-finger-containing protein  | UUT40426; ‘carnivorous sponge associated iridovirus’ | 29% | 95% | 1e-10 |
| 132 | Patatin-like phospholipase | UUT40417; carnivorous sponge associated iridovirus | 59% | 99% | 3e-116 |
| Segment 10 (OQ791190) | 133 | Hypothetical protein | - | - | - | - |
| 134 | Hypothetical protein | - | - | - | - |
| 135 | Hypothetical protein | - | - | - | - |
| 136 | Hypothetical protein | - | - | - | - |
| 137 | IIV25\_153R  | YP\_009010686; ‘Invertebrate iridovirus 25’ | 36% | 72% | 0.025 |
| 138 | BRO-like protein  | UUT40471; ‘carnivorous sponge associated iridovirus’ | 49% | 78% | 9e-14 |
| 139 | Hypothetical protein | - | - | - | - |
| 140 | Papain-like proteinase  | UUT40459; ‘carnivorous sponge associated iridovirus’ | 58% | 90% | 4e-138 |
| 141 | Hypothetical protein | - | - | - | - |
| 142 | Hypothetical protein | UUT40430; ‘carnivorous sponge associated iridovirus’ | 53% | 81% | 7e-27 |
| 143 | Hypothetical protein | UUT40431; ‘carnivorous sponge associated iridovirus’ | 52% | 95% | 6e-24 |
| 144 | Hypothetical protein | UUT40445; carnivorous sponge associated iridovirus | 40% | 98% | 3e-43 |
| Segment 11 (OQ791191) | 145 | Hypothetical protein | - | - | - | - |
| 146 | Hypothetical protein | - | - | - | - |
| 147 | Hypothetical protein | YP\_004732860; Wiseana iridescent virus | 39% | 95% | 4e-85 |
| 148 | p31k protein  | QXT57840; ‘Rhinella marina erythrocytic-like virus’ | 31% | 92% | 5e-31 |
| 149 | AAA-ATPase | UUT40433; ‘carnivorous sponge associated iridovirus’ | 73% | 95% | 3e-136 |
| 150 | Hypothetical protein | UUT40453; ‘carnivorous sponge associated iridovirus’ | 56% | 91% | 8e-24 |
| 151 | Hypothetical protein | UUT40481; ‘carnivorous sponge associated iridovirus’ | 42% | 88% | 3e-92 |
| 152 | Hypothetical protein | - | - | - | - |
| Segment 12 (OQ791192) | 153 | Hypothetical protein | UUT40484; carnivorous sponge associated iridovirus | 51% | 75% | 5e-19 |
| 154 | DNA topoisomerase II | UUT40530; carnivorous sponge associated iridovirus | 58% | 98% | 0.0 |
| 155 | Tyrosine phosphatase | UUT40500; carnivorous sponge associated iridovirus | 51% | 93% | 6e-71 |
| Segment 13 (OQ791193) | 156 | Myristylated membrane protein | UUT40472; carnivorous sponge associated iridovirus | 52% | 98% | 0.0 |
| 157 | Myristylated membrane protein | UUT40460; carnivorous sponge associated iridovirus | 53% | 95% | 1e-118 |
| 158 | Hypothetical protein | UUT40416; carnivorous sponge associated iridovirus | 38% | 86% | 6e-21 |
| 159 | Proliferating cell nuclear antigen | UUT40397; carnivorous sponge associated iridovirus | 52% | 90% | 9e-79 |
| Segment 14 (OQ791194) | 160 | Hypothetical protein | UPA43425; Iridovirus CN01 | 57% | 82% | 3e-31 |
| 161 | Hypothetical protein | UUT40564; ‘carnivorous sponge associated iridovirus’ | 48% | 86% | 1e-36 |
| 162 | 078R | YP\_009552359; ‘Cherax quadricarinatus iridovirus’ | 84% | 98% | 9e-42 |
| 163 | Hypothetical protein | - | - | - | - |
| 164 | Metallopeptidase | UUT40420; ‘carnivorous sponge associated iridovirus’  | 60% | 100% | 7e-58 |
| 165 | 150R | YP\_009552431; ‘Cherax quadricarinatus iridovirus’ | 30% | 81% | 7e-25 |
| Segment 15 (OQ791195) | 166 | BRO-like protein | UUT40471; ‘carnivorous sponge associated iridovirus’ | 56% | 52% | 0.007 |
| 167 | NAD-dependent DNA ligase | YP\_009552368; ‘Cherax quadricarinatus iridovirus’ | 43% | 98% | 5e-142 |
| 168 | Putative high mobility group protein | UUT40420; carnivorous sponge-associated iridovirus 4 | 41% | 99% | 5e-29 |
| 169 | Hypothetical protein | - | - | - | - |
| 170 | Hypothetical protein | - | - | - | - |
| Segment 16 (OQ791196) | 171 | Hypothetical protein | - | - | - | - |
| 172 | Hypothetical protein | - | - | - | - |
| 173 | Hypothetical protein | - | - | - | - |
| 174 | 395R | NP\_149858; ‘Invertebrate iridescent virus 6’ | 30% | 90% | 0.001 |
| 175 | Ervl/Alr family protein  | UUT40423; ‘carnivorous sponge-associated iridovirus’ | 66% | 99% | 2e-61 |
| 176 | Hypothetical protein | - | - | - | - |
| 177 | Thioredoxin 2 | UUT40443; ‘carnivorous sponge associated iridovirus’ | 41% | 78% | 1e-27 |
| 178 | Hypothetical protein | - | - | - | - |
| Segment 17 (OQ791197) | 179 | Hypothetical protein  | UUT40513; ‘carnivorous sponge associated iridovirus’ | 59% | 85% | 8e-36 |
| 180 | Hypothetical protein | UUT40515; ‘carnivorous sponge associated iridovirus’ | 56% | 98% | 3e-24 |
| 181 | Uvr/REP helicase  | UUT40488; ‘carnivorous sponge-associated iridovirus’ | 63% | 81% | 6e-67 |
| 182 | Hypothetical protein | - | - | - | - |
| Segment 18 (OQ791198) | 183 | Hypothetical protein | UUT40438; ‘carnivorous sponge associated iridovirus’ | 40% | 67% | 3e-09 |
| 184 | 039R | YP\_009552320; ‘Cherax quadricarinatus iridovirus’ | 46% | 75% | 3e-12 |
| 185 | Ribonucleoside-diphosphate reductase large subunit  | UUT40499; ‘carnivorous sponge associated iridovirus’ | 70% | 99% | 0.0 |
| 186 | Hypothetical protein | - | - | - | - |
| 187 | Hypothetical protein | - | - | - | - |
| 188 | NTPase/helicase-like protein | YP\_009046681; Armadillidium vulgare iridescent virus | 31% | 56% | 3e-22 |

\*This gene was used to develop the diagnostic PCR.