

```

"Contig_213_101.679:1.6825_3" : {
  "Contig" : "Contig_213_101.679:1.6825",
  "Protein_id" : "Contig_213_101.679:1.6825_3",
  "Start" : 1576,
  "Stop" : 2980,
  "Strand" : 1,
  "Length_aa" : 467,
  "Orflength" : 1401,
  "pI" : 6.09124755859,
  "Molecular_weight" : 53.5625,
  "Instability_index" : 36.6983083512,
  "SRR" : "SRR6659510",
  "Organism" : "Edwardsiella phage PEi21",
  "Hitscore" : 0.736478082660833,
  "Virus_quotient" : 0.832707055,
  "Description" : "phage terminase, large subunit",
  "Sources" : {
    "VOG4544" : {
      "Evaluate" : 7.4e-28,
      "Coverage" : 70.1754385965,
      "Similarity" : 56
    },
    "DIAMOND" : {
      "Coverage" : 98.07,
      "Similarity" : 51.1,
      "Evaluate" : 1.5e-119
    }
  }
}

```

// Entry ID or primary key
 // Prediction template
 // Protein | ORF ID
 // Predicted start position [nt]
 // Predicted stop position [nt]
 // Direction: 1=fwd, -1=rev
 // Length of predicted protein [aa]
 // Length of predicted protein [nt]
 // Estimated Isoelectric point
 // Estimated molecular weight [kDa]
 // Estimated Instability Index
 // SRR accession of contig
 // Source organism of prediction source
 // Score of prediction
 // Viral quotient
 // Sources used in VIGA
 // HMM hit (pVOG or RVDBs)
 // Evaluate/Significance of hit
 // Coverage to closest reference [%]
 // Similarity to closest reference [%]
 // Prediction source
 // Coverage to closest reference [%]
 // Similarity to closest reference [%]
 // Evaluate/Significance of hit