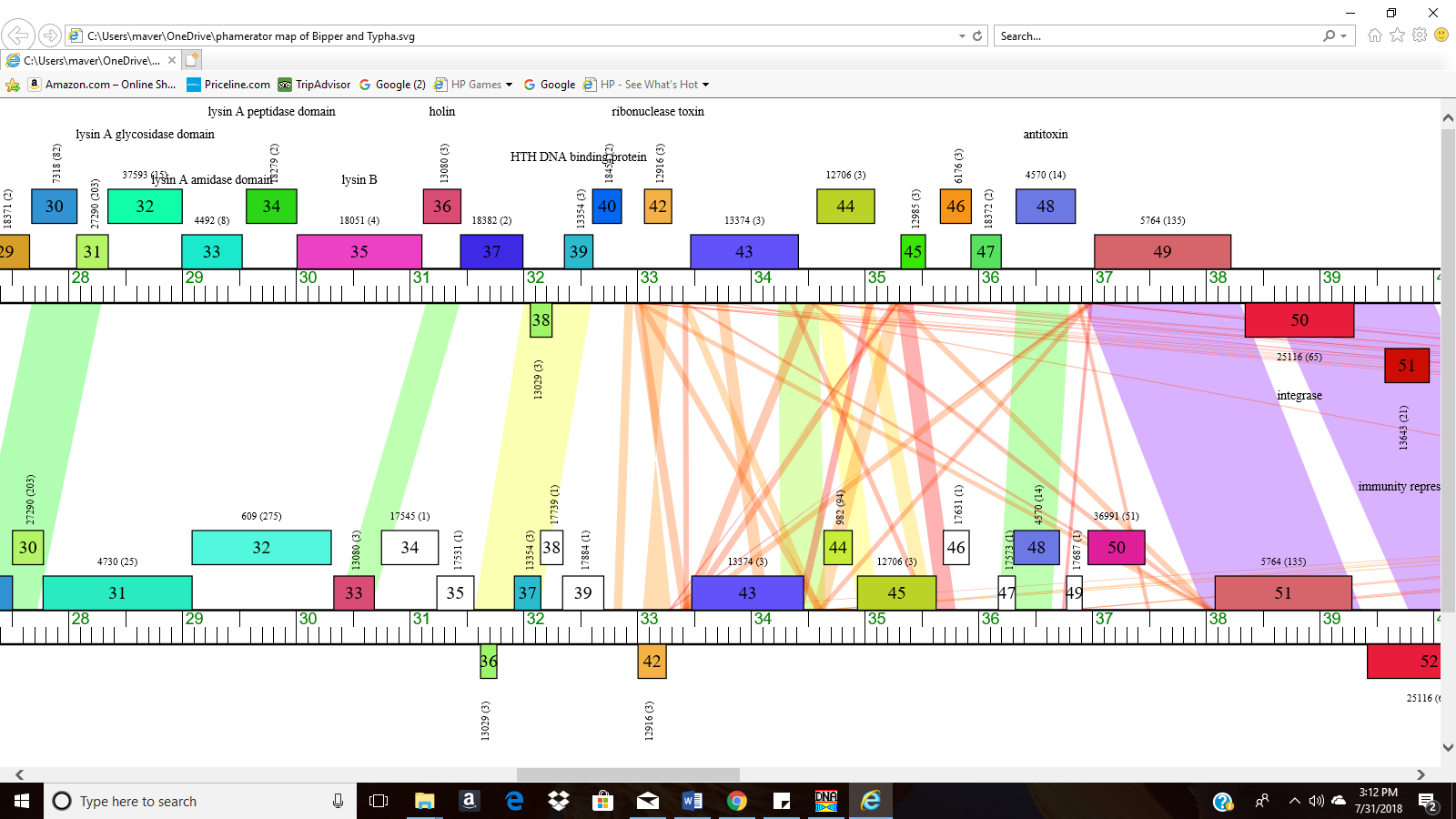
Gene 42 (first after tRNA)

Product:

MSQFVKITRSARKHGVSKGRIRTAMRHANPTVVEAKGQVVFIGRDNRGTWLEVIARDGNRSPNELVVFHAMPLRWRPASHQRZ

Issues:

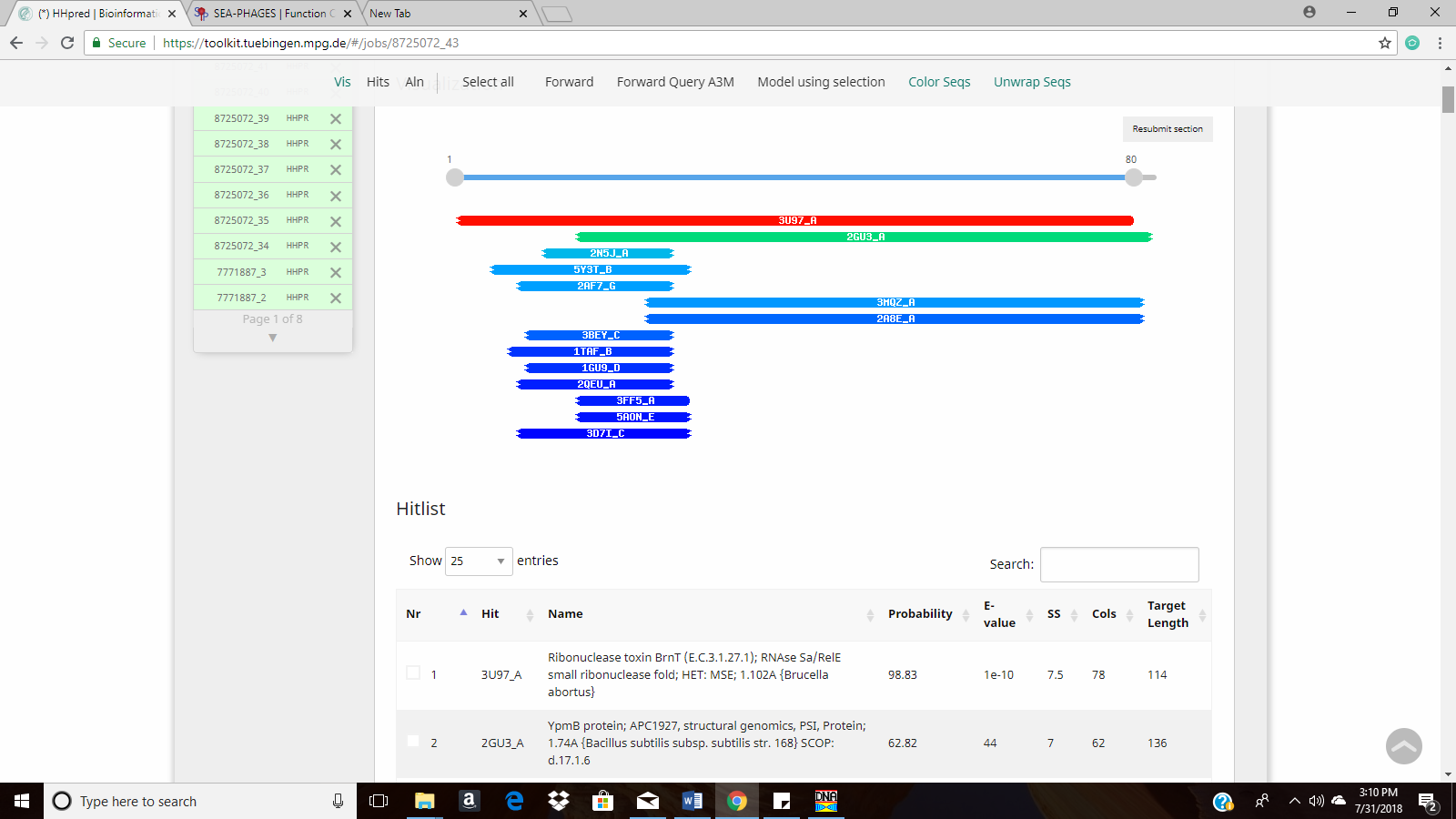
Typha has it coding in reverse, but Bipper has it forward; coding potential has Bipper's in forward; Can't check Cracklewink, 3rd member of pham because no GeneMark data with no GPS info on phage page. As Ribonuclease toxin BrnT is not an accepted function, what can we do for function? According to HHpred, it is under the classification of a hydrolase. Could that be used? Listing it as NKF for now.

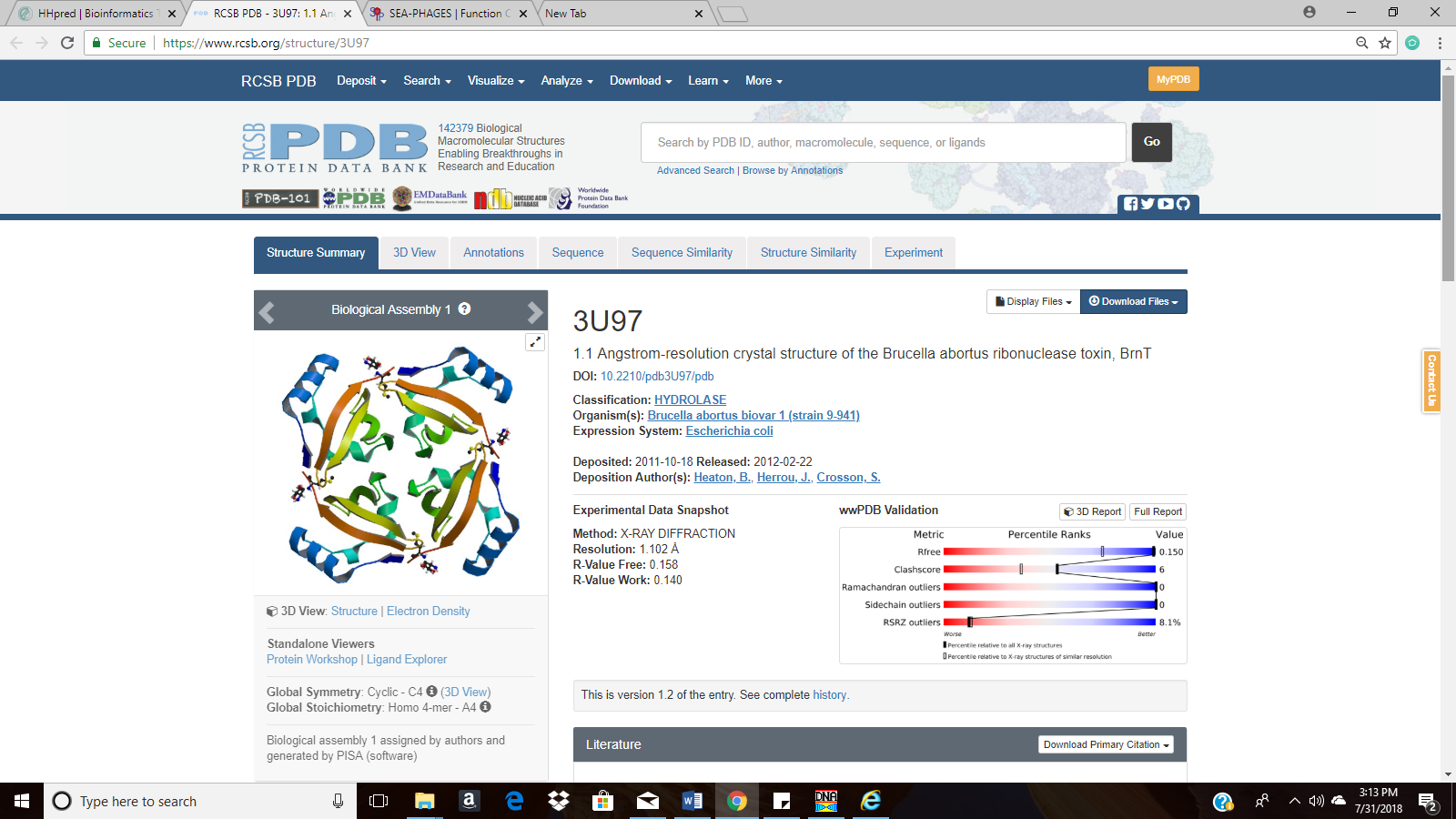


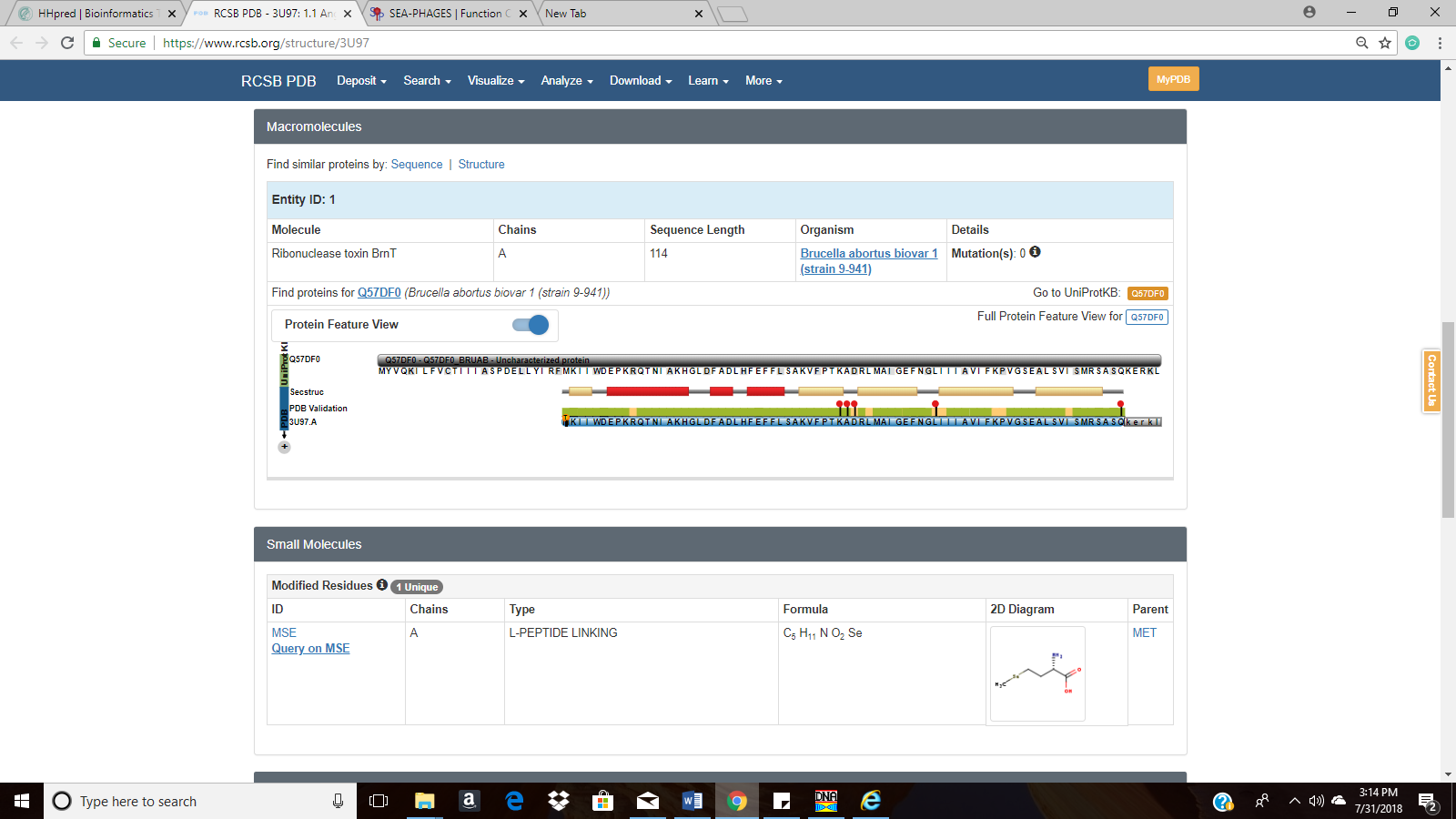
My notes:

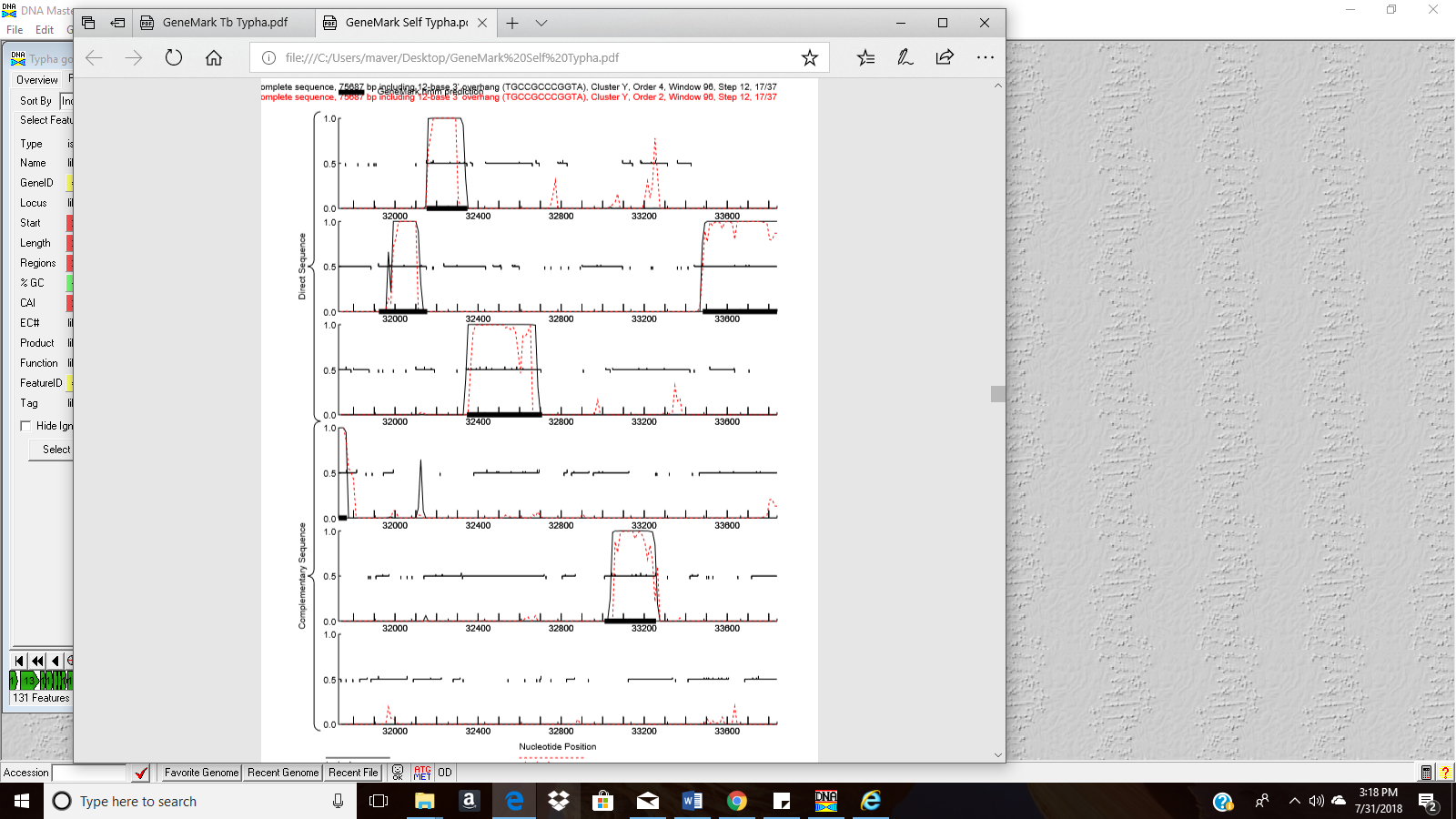
Original Glimmer call @bp 33257 has strength 12.83

**SSC: Start: 33257bp, Stop: 33009bp;** CP: Some, Coverage over most of area, Smeg and Tb end (5') around 33050/later; SCS: Both, Original Glimmer call @bp 33257; ST: Suggested Start 33257; BLAST-Start: Matches Bipper gp42, Phagesdb, Query 1: Subject 1, 50%, 6e-12; Matches Bipper gp42, NCBI, Query 1: Subject 1, 49%, 90% query cover, 1e-13; Gap: 139bp to previous tRNA, 225bp gap to next forward; LO: Yes; RBS: Z score: 2.098, Final score: -4.516, not best scores; F: NKF; SIF-BLAST: Matches ribonuclease toxin, Bipper gp42, Phagesdb, Query 1: Subject 1, 50%, 6e-12; Matches ribonuclease toxin, Bipper gp42, NCBI, Accession number YP\_009303189.1, Query 1: Subject 1, 49% positives, 90% query cover, 1e-13; SIF-HHPred: Matches Brucella abortus, hit number 3U97\_A, Ribonuclease toxin BrnT, RNAse Sa/RelE small ribonuclease fold, 97% alignment, 98.83% probability; SIF-Syn: Not applicable

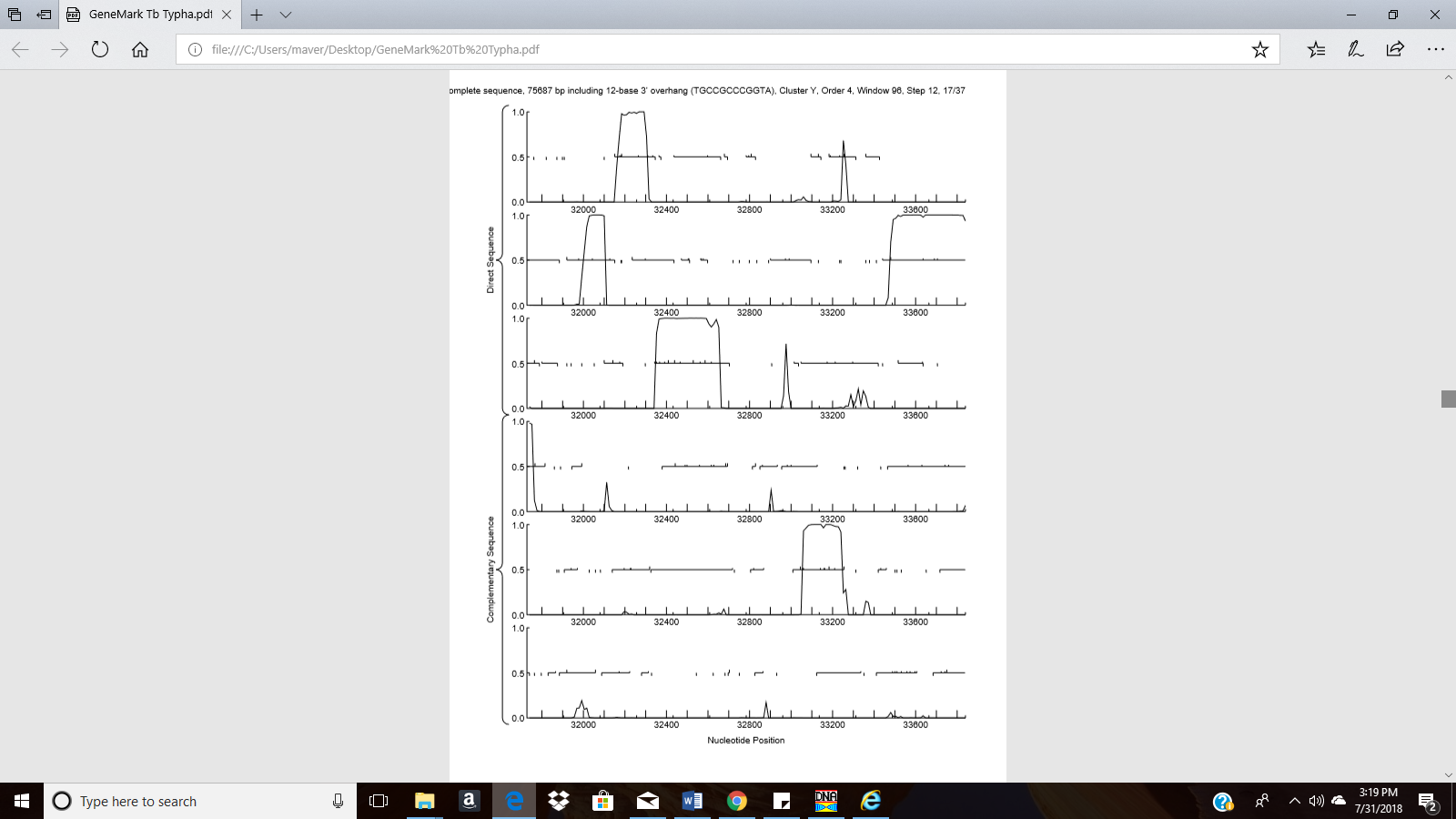


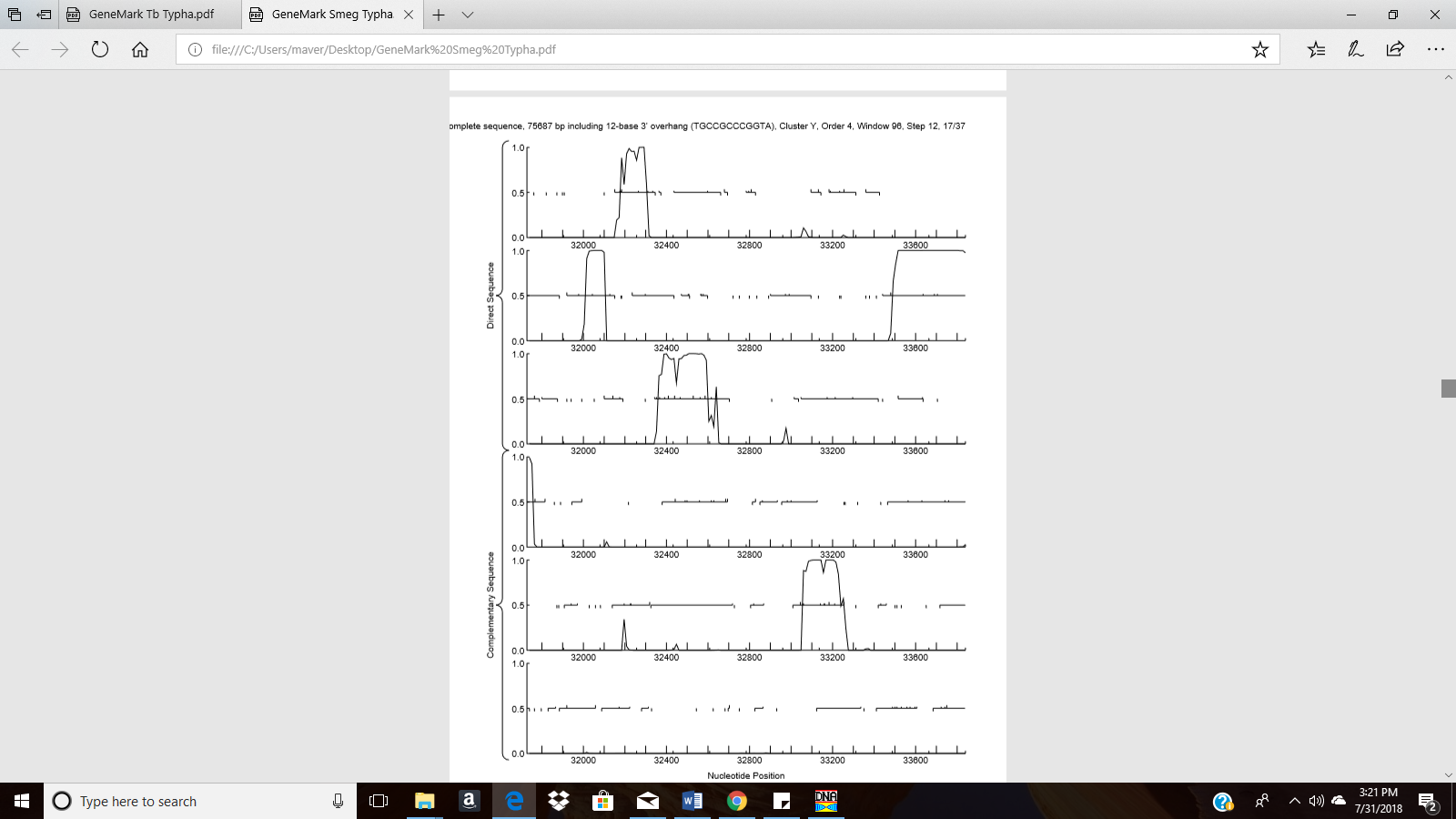






GeneMark Self for Typha

GeneMark Tb for Typha



GeneMark Smeg