**Supplementary data legend.**

**Supplementary data1.** – FastQC (multiqc) reports of the quality of the original *Conus virgo* Illumina HiSeq Sequencing data.

**Supplementary data2.** – Trinity assemblies of *Conus virgo*, *C. geographus*, *C. rolani*, *C. striatus*, *C. episcopatus* and *C. quercinus*.

**Supplementary data3.** – In-house toxin database, and BLASTx output files constituting the basis of reference based transcript annotation of *Conus virgo*, *C. geographus*, and *C. rolani.*

**Supplementary data4.** – HMMER annotation and BLASTp against the Uniprot database annotation of the predicted secreted transcripts of *Conus virgo*.

**Supplementary data5**. – Scripts used run analyses, and parse data files. All files are run through Spyder environment for Python.

**Supplementary data6**. – Confidence of alpha-fold conformation predictions, and resulting pbd files.