



S2 Fig. Blr0566_ISGA gene and protein. **A)** The blr0566_ISGA gene is weakly expressed at the mRNA level and is probably co-transcribed with upstream genes. Shown are cDNA reads and relevant annotated features (annotated genes, TSSs, promoter and terminators) at the blr0566_ISGA locus [15]. Only the plus strand is shown. The differential RNA-seq (dRNA-seq) was described previously [15]. The analyzed RNA was isolated from exponentially growing, free-living cells (F) in liquid cultures and from nodules (N). RNA samples were treated (+) or not treated (–) with terminal exonuclease (TEX), which degrades 5′-monophosphorylated (processed) transcripts. The scale of each library is indicated (Reads). **B)** Gene sequence with upstream region. The genomic coordinates are indicated, the start and stop codons are in red and the putative Shine-Dalgarno sequence is underlined. **C)** Protein sequence with proposed secondary structure. Blue, peptides detected by proteomics [15]. The peptides were detected only in nodules. **D)** Proposed three-dimensional structure of indicated protein parts. Pyre² was used for secondary and tertiary structure modeling [43].