**SUPPLEMENTARY INFORMATION**

**TABLES**

**Table S1**: All the curated infectious diseases-associated human genes from DisGeNET.

**Table S2**: All the mapped gene name to uniprot id using mapping table of DisGeNET.

**Table S3**: Positive dataset for 10-fold cross-validation.

**Table S4**: Positive blind dataset (not used in training or testing of 10-fold cross-validation techniques for developing the prediction model).

**Table S5**: All the disease-associated human reviewed proteins in DisGeNET.

**Table S6**: All the reviewed human proteins collected from UniProtKB dated 12/01/2018.

**Table S7**: All the reviewed human proteins not associated with any diseases.

**Table S8:** Negative dataset for 10-fold cross-validation.

**Table S9:** Negative blind dataset (not used in training or testing of 10-fold cross-validation techniques for developing the prediction model).

**Table S10:** Independent dataset (Befree text mining genes from DisGeNET associated with infectious diseases).

**Table S11:** All human protein-protein interactions (PPIs) from Human Protein Reference Database (HPRD) (Release 9).

**Table S12:** All unique human in HPRD (Release 9).

**Table S13:** All the mapped human protein-protein interactions (PPIs) in uniprot id format.

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**Table S15:** 9 topological properties of protein-protein interaction networks using HPRD PPIs dataset.

**Table S16:** Features wise performance measures on disease and non-disease associated proteins dataset using deep neural network classifier.

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**Table S22:** Top 100 proteins (genes) are predicted by our proposed DNN based method.

**Table S23:** Significantly enriched disease-ontology terms for top 100 proteins (genes) based on Genetic Association Database (GAD).

**Table S24:**  Significantly enriched gene-ontology biological process terms for top 100 proteins (genes).

**FIGURES**

**Fig. SF1:** Venn diagram of All reviewed and DisGeNET human proteins.

**Fig. SF2:** Venn diagram of positive curated and Befree text mining disease-associated proteins (DisGeNET confident score > greater than 0.002738764 ).

**Fig. SF3:** Venn diagram of highly predicted infectious disease-associated proteins and virus and bacteria targeted interaction of human proteins by PHISTO.