Supplementary data to article **PTI-1: novel way to oncogenicity**

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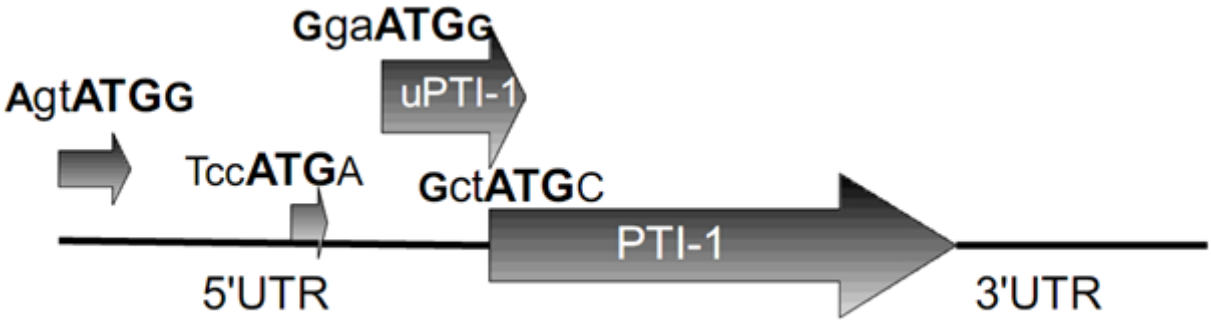
Suppl. Table 1 – Comparison of mRNA translation efficiency and protein half-life of the PTI-1 and uPTI-1 proteins based on N-end rule.
Prediction was performed using TermiNator [33, 34].

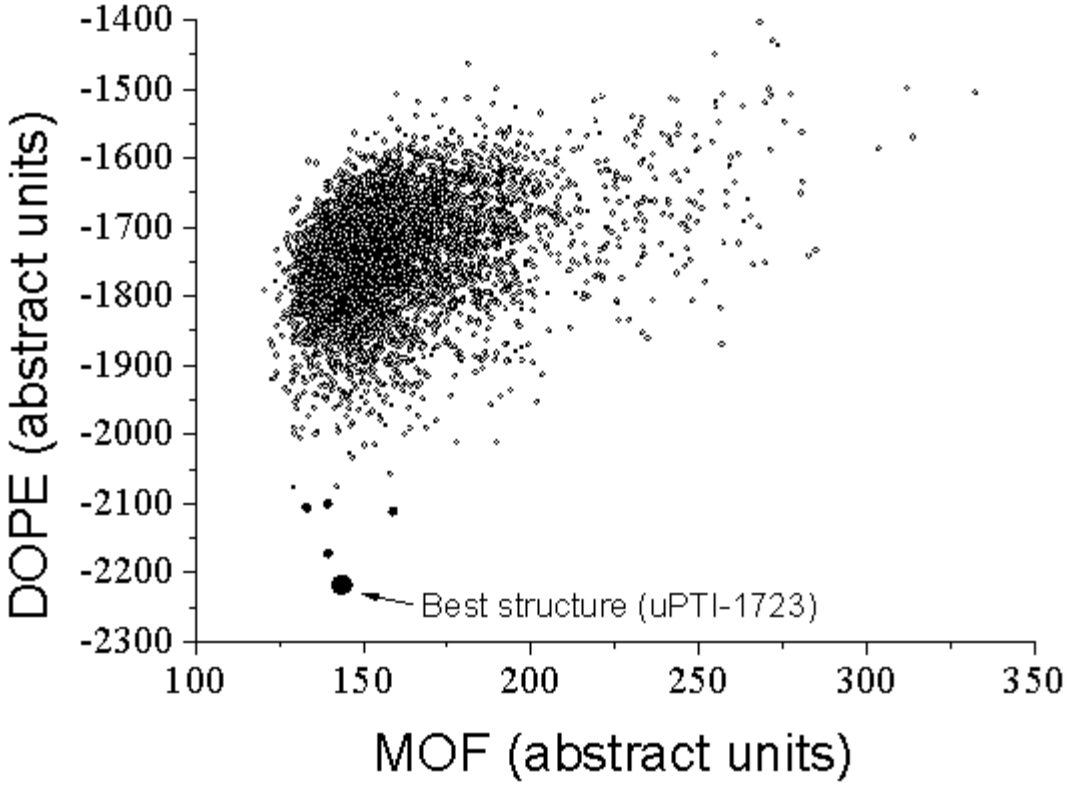
Protein	*N-terminal sequence or entry code (first20 characters)*	*Predicted N-terminus of the mature protein*	*Likelihood (%)*	*Translation efficiency*	*Predicted Half-life (hours)*
PTI-1	MQSERGITIDISLWKFETSK	M(1)	89	1	5-31
uPTI-1	MAASSCTDYNQTPNTIKIKL	Ac-A(2)	83	5	220

Suppl. Table 2 – Prediction of cellular localization of uPTI-1 peptide.

Program used to predict subcellular localization	*Predicted localization*
Euk-mPLoc 2.0	extracellular
MultiLoc2	secretory
WoLF PSORT	extracellular



Suppl. Fig. 1- Schematic representation of upstream ORFs in the PTI-1 mRNA. Kozak context elements marked with bold type.



Suppl. Fig. 2- Ensemble of 5000 structures (uPTI-1) was generated in Modeller 9.8. Five structures were selected using the Modeller Objective Function (MOF) and the Discrete Optimized Protein Energy (DOPE) score. The structure of uPTI-1 1723 was selected as the best from the ensemble.