

In silico characterization unveils *Helicobacter pylori* protein HP0973 as a novel EGFR-interacting virulence factor

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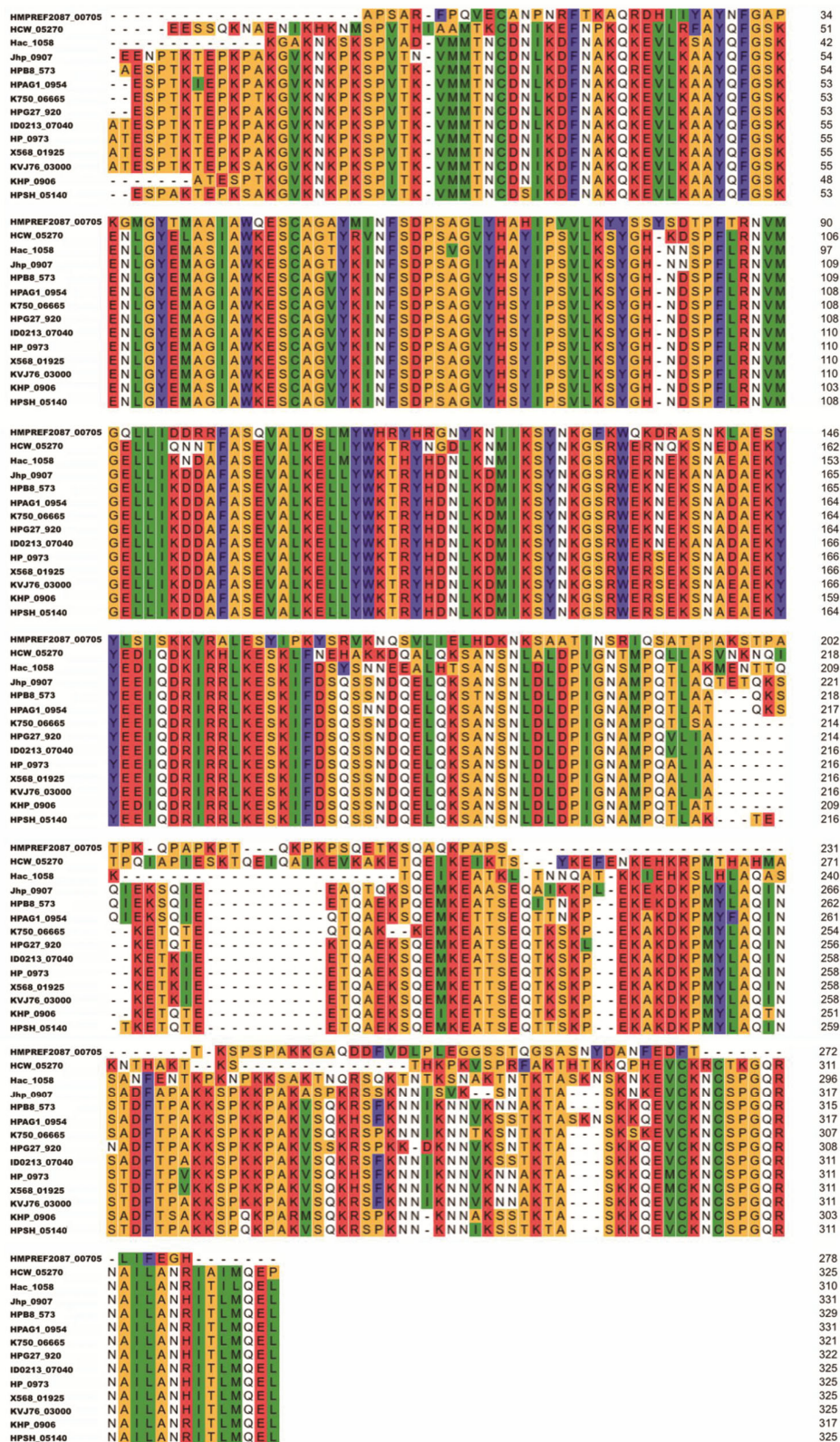
Supplementary data

Suppl. Table S1 — The properties of HP0973 protein retrieved from NCBI protein database

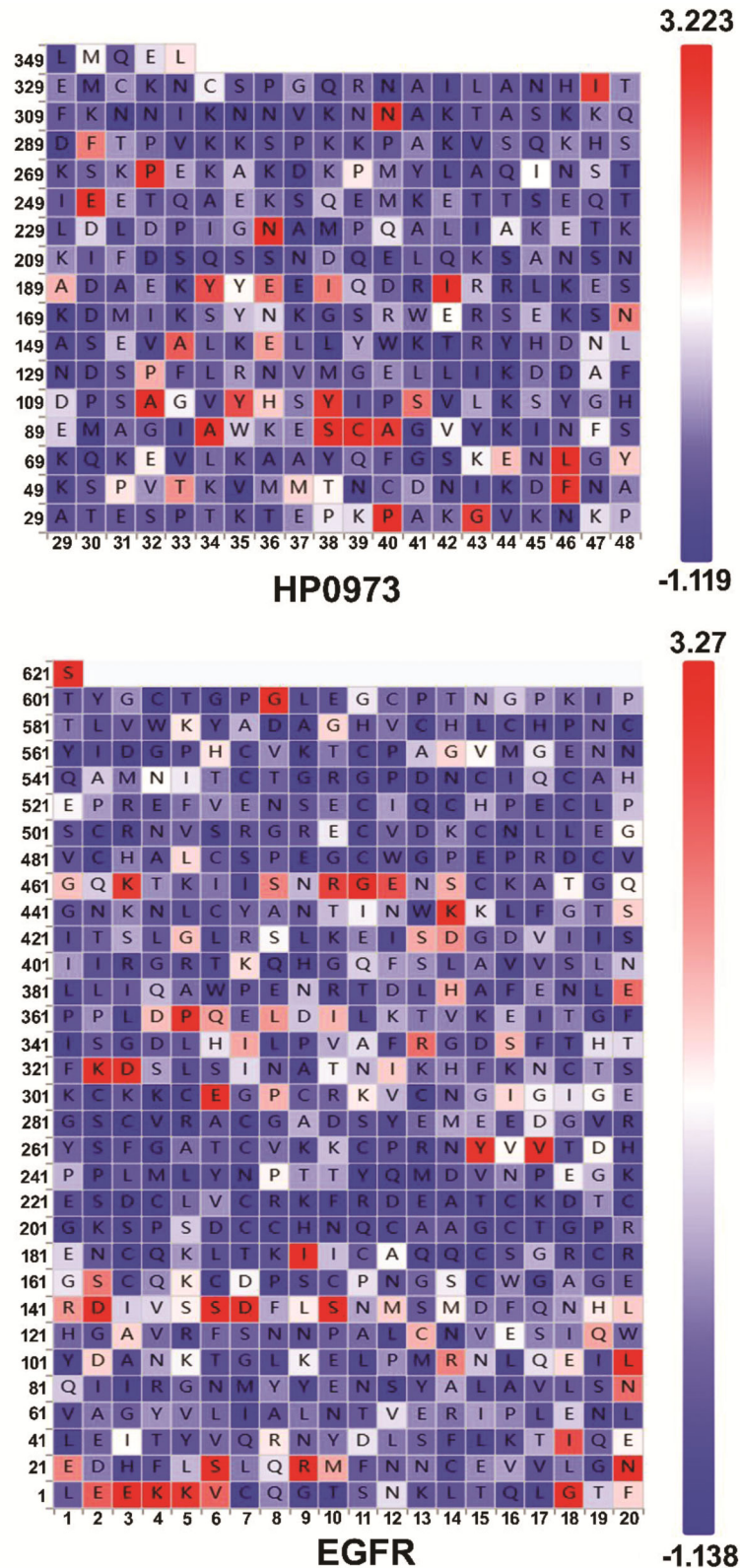
Properties	HP0973
Locus	AAD08028
Defination	Predicted coding region HP0973 [<i>H. pylori</i> 26695].
Accession	AAD08028
Version	AAD08028.1
Amino acid	353
Organism	<i>H. pylori</i> 26695
FASTA sequence	>AAD08028.1 predicted coding region HP0973 [<i>Helicobacter pylori</i> 26695] MKHLTPLTHTIFKALWLGTAALSASLSLAATESPTKTEPKPAKGVKNKPKSPVTKVMMTNCDNIKDFNAKQK EVLKAAYQFGSKENLGEMAGIAWKESCAGVYKINFSDPSAGVYHSYIPSVLKSYPGHNDSPFLRNVMGELLI KDDAFASEVALKELLYWKTRYHDNLKDKMIKSYNKGSRWERSEKSNADAKEYEYEEIQDRIRRLKESKIFDSQS SNDQELQKSANSNLDLDPIGNAMPQALIAKETKIEETQAEKSQEMKETTSEQTKSKPEKAKDKPMYLAQINS TDFTPVKKSPKKPAKVSQKHSFKNNIKNNVKNNAKTASKKQEMCKNCSPGQRNAILANHITLMQEL

Suppl. Table S2 — Antigenic peptide predicted on HP0973 protein sequence (353 aa) by Kolaskar and Tongaonkar method 1990. Start and end positions indicating the residue number within the complete protein sequence.

S. No.	Start Position	Sequence	End Position	Length (aa)
1	48	PKSPVTK	54	6
2	70	QKEVLKAAYQ	79	9
3	95	WKESCAGVYKI	105	10
4	109	DPSAGVYHSYIPSVLK S	125	16
5	138	MGELLIKD	145	7
6	148	FASEVALKELLYWK	161	13
7	238	MPQALIAK	245	7
8	278	KPMYLAQ	284	6
9	289	DFTPVKK	295	6
10	297	PKKPAKVSQK	306	9
11	330	MCKNCSP	336	6
12	342	ILANHITL	349	7



Suppl. Fig. S1 — Multiple sequence alignment of HP0973 protein sequence with homologous protein sequences from different strains of *Helicobacter pylori* strains. Different colour shading represents conserved and semiconserved residues, while variable regions may suggest strain-specific divergence



Suppl. Fig. S2 — Heatmap of important residues predicted by HPInet for HP0973 and the ectodomain of the protein sequence of EGFR interaction