

H. PYLORI PROJECT

The Helicobacter Pylori Protein Interaction Map

261 H. pylori bait proteins have been screened against a highly complex library using Hybrigenics' high-throughput proprietary yeast two-hybrid-based technology. Over 1,200 interactions connecting 46.6% of the proteome were then identified. This work has been published in Nature (Rain et al., January 2001).

Curation Process and Annotation Rules

H. pylori protein interaction map has been carefully annotated by Hybrigenics' H. pylori expert Ivo Gomperts Boneca in collaboration with the team of A. Labigne at the Institut Pasteur in Paris, France.

The curation process has been designed to ensure the delivery of high-quality data to scientists and to avoid the propagation of erroneous or unjustified functional annotations. The curation process is based on the manual and exhaustive analysis of publicly available scientific literature. There is no automatic or indiscriminate retrieval of papers based only on keywords. Emphasis has been put on selecting publications which add real value on what is known about H. pylori genes and proteins.

The numerous annotations provided for each proteins allows for the rapid identification of relevant information, whatever the user's field of interest. The data format can also be easily adapted for XML-based data exchange and reformatting, which is especially useful for further genome-wide studies such as the ones performed in comparative genomics. If you have any question regarding the curation process and the annotation rules in PIMRider Hp please contact iboneca.pimhp@hybrigenics.fr.

Rules for PIMRider naming fields

Several rules have been set up and strictly enforced throughout the curation process, especially about naming of genes/proteins and annotation of protein product and function: we provide in the PIMRider® field 'Original name' the standard name found in the TIGR (HPxxxx) or Astra (JHPxxxx) databases and usually found in post-sequencing studies.

The PIMRider® field 'Biological name' is attributed only if this alternative naming is supported by explicit and direct experimental evidences, and the corresponding papers are linked (e.g. 'glmM' for 'HP0075'). In this case, the fields 'Function' and 'Product' are filled. In other words, the Function field is not understood here as a 'putative function' but as a 'proven enough function'.

If an H. pylori gene has not been directly studied, but has a strong homology (blastp) with a protein from another organism, and if this homologous protein possesses direct evidence supporting its function-related naming and annotation, then we propagate this name as an 'Alias' (ex: 'yxjE' for 'HP0692' / 'scoB'), the functional annotation is summed up in the PIMRider® fields 'Comments' and 'Product', and the corresponding papers are linked.

The 'Biological Name' remains identical to the 'Original Name', and 'Function' remains empty. In all other cases, the 'Biological Name' remains the 'Original Name', and 'Product' and 'Function' are empty. If a biological name had been attributed by homology by TIGR or ASTRA, without experimental evidence, this name is kept only as an 'Alias'. Any H. pylori gene/protein not yet processed by our team is tagged with the explicit mention "not yet curated by Hybrigenics".