Scientists discover why some proteins are speedier than others

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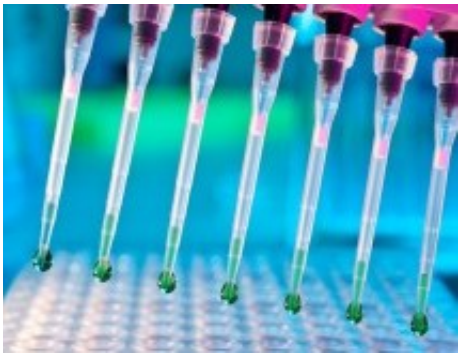

(Phys.org) —Scientists from our Department of Biology & Biochemistry have solved a problem that has frustrated biologists for years – why different parts of proteins are made at different rates.

Their discovery, published in the online journal *PLOS Biology*, should help scientists make proteins that would be otherwise tricky to produce in the lab.

Proteins are made in the cell by machines called ribosomes, which read gene transcripts (called mRNA) and 'translate' the genetic code into strands of protein.

The researchers looked at yeast proteins that were made at different

rates. They found that the parts of proteins that took the longest to make were composed of mostly positively charged amino acids.

Co-author Laurence Hurst, Professor of Evolutionary Genetics at the University, explained: "If you imagine the ribosome as a doughnut with a hole in it, the mRNA strand is fed through the hole in the centre, translating the genetic code to give the corresponding amino acid chain, which comes out of a tunnel in the side of the doughnut.

"If the protein being created is positively charged, it gums up the negatively charged tunnel and slows down the protein production."

Lead author Katie Charneski, added: "This was a real surprise as most people before had assumed that it was something about the mRNA that caused slowing or speeding of the ribosome."

"Many organisms, including humans, have 'tails' on the ends of their mRNAs that normally the ribosome does not translate. But if mistakes occur in protein production, the tail may be erroneously translated, always producing a string of positively charged amino acids.

"These charges might act as a tagging signal for the cell to destroy the potentially toxic protein."

The speed at which proteins are made has consequences for the cell and has been puzzled over by biologists for years. Changes in this speed can affect how well proteins fold and where they end up in the cell, and hence their eventual function.

Professor Hurst added: "This knowledge could help us identify which novel engineered proteins would be difficult to make in the lab."

Provided by University of Bath