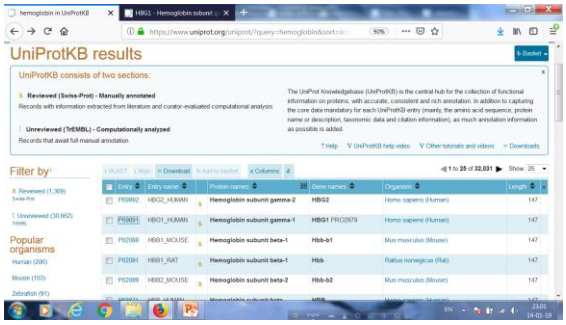
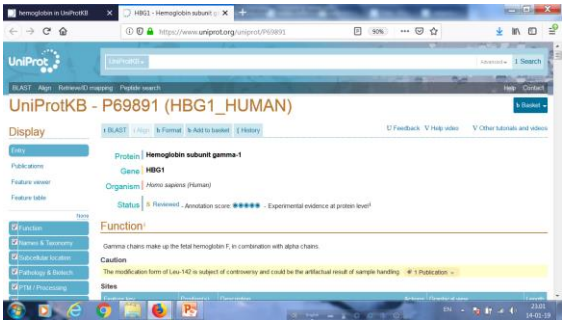
Dept. of Computer Science and Engineering
University of Rajshahi
www.ru.ac.bd

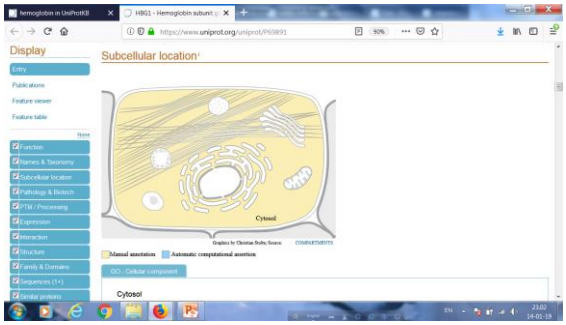
Dr. Shamim Ahmad

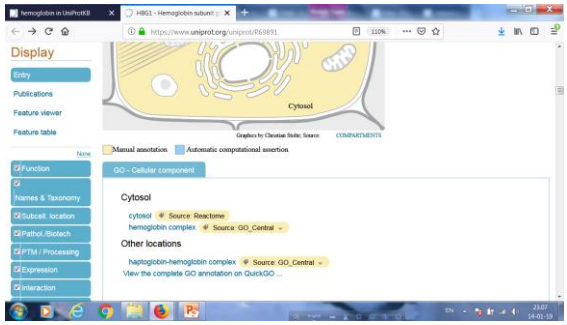
PTM Database

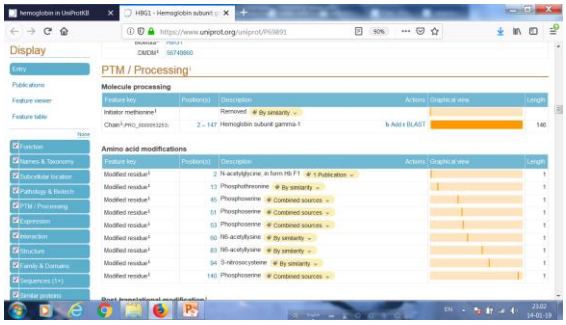
Example: Hemoglobin

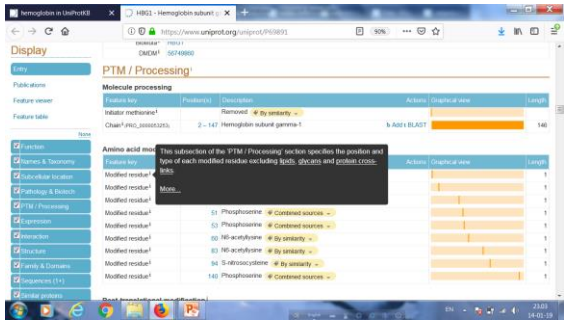


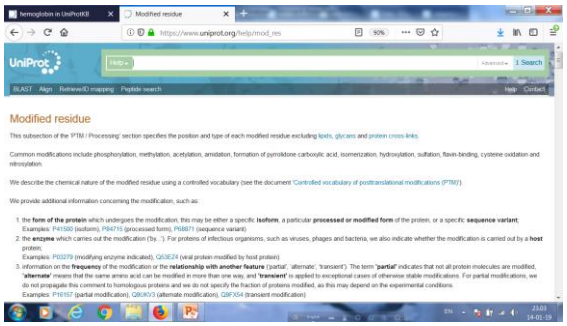


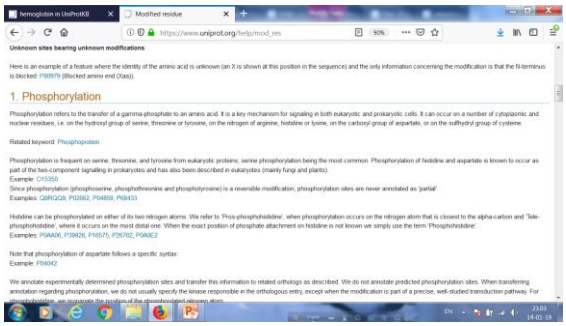

Display
Subcellular location
Cytosol
Manual annotation
Automatic computational assertion
GO - Cellular component
Cytosol

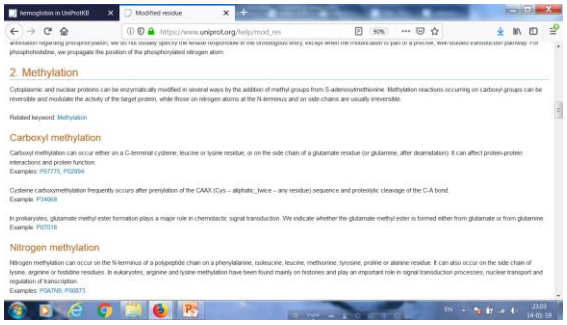

Display
Cytosol
Manual annotation
Automatic computational assertion
GO - Cellular component
Cytosol
cytosol
Source: Reactome
hemoglobin complex
Source: GO_Central
Other locations
haptoglobin-hemoglobin complex
Source: GO_Central
View the complete GO annotation on QuickGO

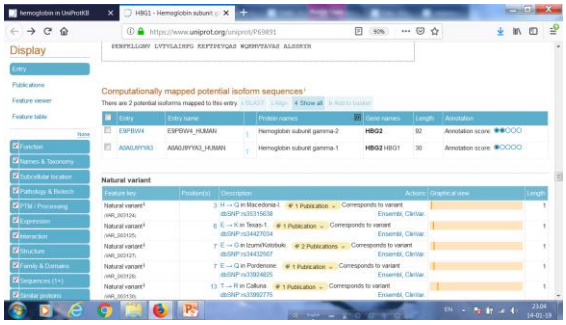

Display
PTM / Processing
Molecule processing
Amino acid modifications

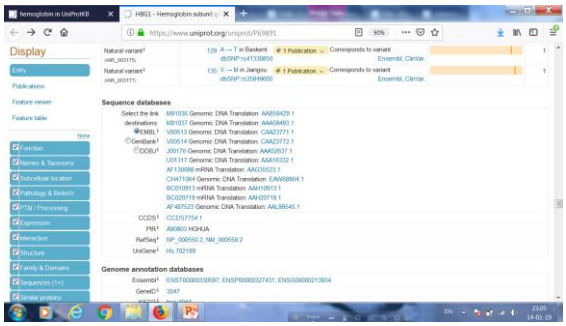

Display
PTM / Processing
Molecule processing
Amino acid modifications
This subsection of the 'PTM / Processing' section specifies the position and type of each modified residue excluding lipids, glycans and protein cross-links.
More...

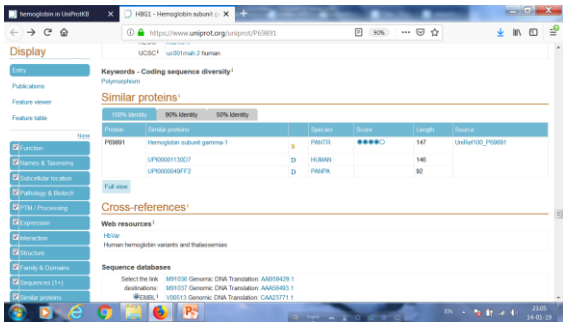

Modified residue
This subsection of the 'PTM / Processing' section specifies the position and type of each modified residue excluding lipids, glycans and protein cross-links.
Common modifications include phosphorylation, methylation, acetylation, amidation, formation of pyrrolidone carboxylic acid, isomerization, hydroxylation, sulfation, flavin-binding, cysteine oxidation and nitrosylation.
We describe the chemical nature of the modified residue using a controlled vocabulary (see the document 'Controlled vocabulary of posttranslational modifications (PTM)').
We provide additional information concerning the modification, such as:
1. the form of the protein which undergoes the modification; this may be either a specific isoform, a particular processed or modified form of the protein, or a specific sequence variant;
2. the enzyme which carries out the modification (by...). For proteins of infectious organisms, such as viruses, phages and bacteria, we also indicate whether the modification is carried out by a host protein;
3. information on the frequency of the modification or the relationship with another feature ('partial', 'alternate', 'transient'). The term "partial" indicates that not all protein molecules are modified, "alternate" means that the same amino acid can be modified in more than one way, and "transient" is applied to exceptional cases of otherwise stable modifications. For partial modifications, we do not propagate this comment to homologous proteins and we do not specify the fraction of proteins modified, as this may depend on the experimental conditions.


Unknown sites bearing unknown modifications
Here is an example of a feature where the identity of the amino acid is unknown (an X is shown at this position in the sequence) and the only information concerning the modification is that the N-terminus is blocked.
1. Phosphorylation
Phosphorylation refers to the transfer of a gamma-phosphate to an amino acid. It is a key mechanism for signaling in both eukaryotic and prokaryotic cells. It can occur on a number of cytoplasmic and nuclear residues, i.e. on the hydroxyl group of serine, threonine or tyrosine, on the nitrogen of arginine, histidine or lysine, on the carboxyl group of aspartate, or on the sulfhydryl group of cysteine.
Related keyword: Phosphoprotein
Phosphorylation is frequent on serine, threonine, and tyrosine from eukaryotic proteins, serine phosphorylation being the most common. Phosphorylation of histidine and aspartate is known to occur as part of the two-component signalling in prokaryotes and has also been described in eukaryotes (mainly fungi and plants).
Example: O15350
Since phosphorylation (phosphoserine, phosphothreonine and phosphotyrosine) is a reversible modification, phosphorylation sites are never annotated as 'partial'.
Examples: Q8R1Q8, P32662, P04859, P68433
Histidine can be phosphorylated on either of its two nitrogen atoms. We refer to 'Pros-phosphohistidine', when phosphorylation occurs on the nitrogen atom that is closest to the alpha-carbon and 'Tele-phosphohistidine', where it occurs on the most distal one. When the exact position of phosphate attachment on histidine is not known we simply use the term 'Phosphohistidine'.
Examples: P0A9X9, P39929, P16575, P26702, P0A9E2
Note that phosphorylation of aspartate follows a specific syntax.
Example: P84942
We annotate experimentally determined phosphorylation sites and transfer this information to related orthologs as described. We do not annotate predicted phosphorylation sites. When transferring annotation regarding phosphorylation, we do not usually specify the kinase responsible in the orthologous entry, except when the modification is part of a precise, well-studied transduction pathway. For


2. Methylation
Cytoplasmic and nuclear proteins can be enzymatically modified in several ways by the addition of methyl groups from S-adenosylmethionine. Methylation reactions occurring on carboxyl groups can be reversible and modulate the activity of the target protein, while those on nitrogen atoms at the N-terminus and on side-chains are usually irreversible.
Related keyword: Methylation
Carboxyl methylation
Carboxyl-methylation can occur either on a C-terminal cysteine, leucine or lysine residue, or on the side chain of a glutamate residue (or glutamine, after deamidation). It can affect protein-protein interactions and protein function.
Examples: P07775, P02994
Cysteine carboxymethylation frequently occurs after prenylation of the CAAX (Cys – aliphatic_twice – any residue) sequence and proteolytic cleavage of the C-A bond.
Example: P34068
In prokaryotes, glutamate methyl ester formation plays a major role in chemotactic signal transduction. We indicate whether the glutamate methyl ester is formed either from glutamate or from glutamine.
Example: P07018
Nitrogen methylation
Nitrogen methylation can occur on the N-terminus of a polypeptide chain on a phenylalanine, isoleucine, leucine, methionine, tyrosine, proline or alanine residue. It can also occur on the side chain of lysine, arginine or histidine residues. In eukaryotes, arginine and lysine methylation have been found mainly on histones and play an important role in signal transduction processes, nuclear transport and regulation of transcription.
Examples: P0A7N9, P00873


Display
Computationally mapped potential isoform sequences
There are 2 potential isoforms mapped to this entry
Natural variant


Display
Entry
Publications
Feature viewer
Feature table
Function
Names & Taxonomy
Subcellular location
Pathology & Biotech
PTM / Processing
Expression
Interaction
Structure
Family & Domains
Sequences (1+)
Similar proteins
Sequence databases
Genome annotation databases


Display
Keywords - Coding sequence diversity
Polymorphism
Similar proteins
Cross-references
Web resources
Sequence databases