**Lesson: Golgi Apparatus**
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## Chapter: Golgi apparatus

# Introduction

One of the important components of the endomembrane system is the organelle- Golgi apparatus (also called Golgi complex) that is principally involved in modifications and exocytic (the outside of the cell) protein trafficking. The Golgi apparatus is organized into stacks of usually four to six (as may as 60 in unicellular flagellates) flattened membrane bound compartments called **cisternae** that are stacked one over the other.

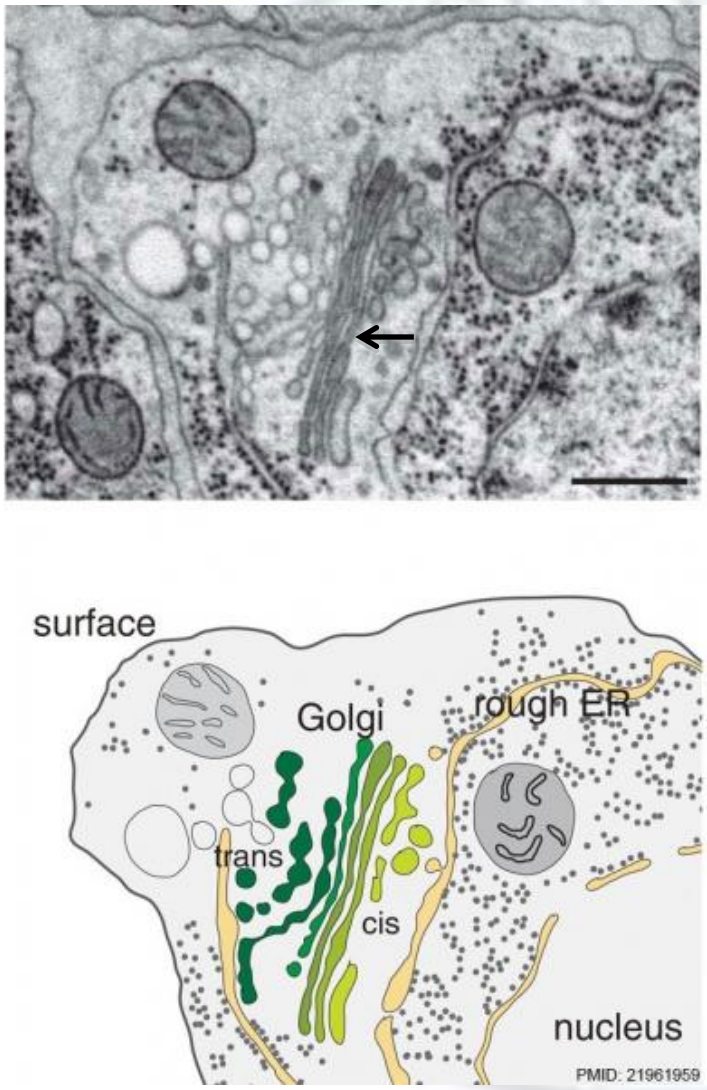



**Figure :** Electron micrograph and a diagrammatic representation of Golgi apparatus

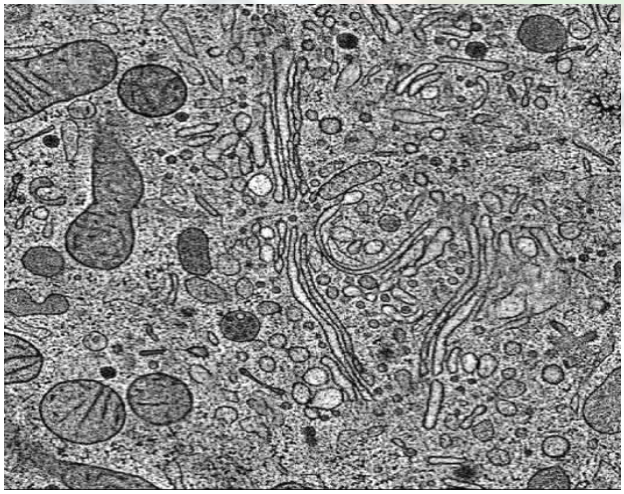
Source:
http://php.med.unsw.edu.au/cellbiology/images/thumb/4/41/Golgi_apparatus_EM_and_cartoon.jpg/391px-Golgi_apparatus_EM_and_cartoon.jpg

The Golgi apparatus (also called Golgi complex) was named after its discoverer, Camillio Golgi (an Italian biologist), who for the first time described the structure in 1898 (http://www.nobelprize.org/nobel_prizes/medicine/laureates/1906/golgi-bio.html).

**Figure**: Camilio Golgi

Source: http://upload.wikimedia.org/wikipedia/commons/6/69/Camillo_Golgi,_1889.JPG

Golgi complex generally functions as the "**Director**" of the cell since it has very little role in synthesis, rather it is involved primarily in the **biochemical modification and sorting** of the materials already synthesized within the ER, to their specific destinations within the cell, to maintain cellular integrity of an active cell. The three major destinations of the processed proteins and lipids from the Golgi, already synthesized in the lumen of the ER are the lysosomes, plasma membrane and extra cellular secretion. The close interrelationship among the three cellular organelles namely ER, Golgi and Lysosome is referred to as **GERL Complex**.



**Embed Animation** :Inside of the cell

Source: http://publications.nigms.nih.gov/insidethecell/extras/tomogram.mov

**Embed Animation:** The transport of proteins through the endomembrane system.

Source: http://bcs.whfreeman.com/thelifewire/content/chp04/0402002.html

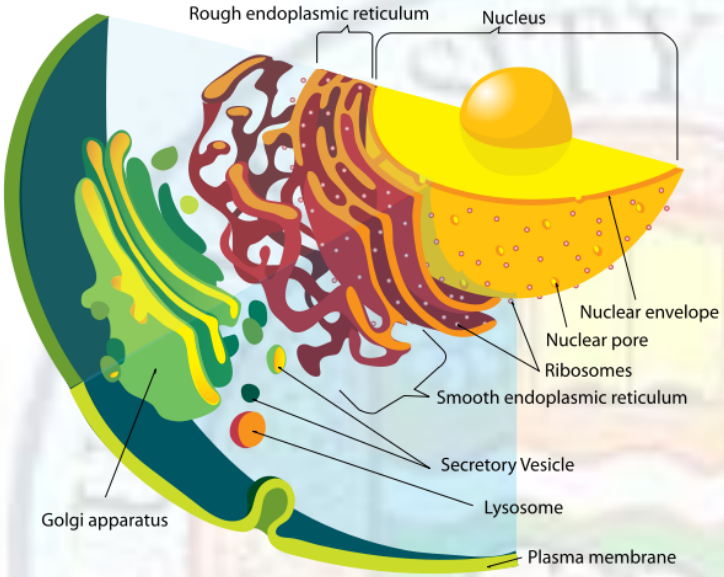



**Figure :** Endomembrane system

Source: http://commons.wikimedia.org/wiki/File:Endomembrane_system_diagram_en.svg

## Structural organization of the Golgi Complex

(a) The structure of the Golgi differ in different types of tissues, also varies with the metabolic status of the cell.

(b) Golgi complex is characterised by a series of oval, flattened membrane bound discs with enlarged ends called the cisternae, arranged in stacks.

(c) The series of **cisternae**, each having a diameter of 500-1000 nm, is called a **Golgi Stack** in animal cells and **dictyosome**s (means stack like) in plant cells.

(d) The number of cisternae per Golgi stack varies from 4-8, though in secretory cells there may be 100-1000 Golgi stacks.

(e) The cisternae margins of each Golgi stacks, are slightly curved to give the Golgi complex a bow-like appearance.

(f) The **convex** end of the complex that is closer to ER is referred to as the **cis-face** or **forming face** and the **concave** end comprise the **trans face** or the **maturing face**.

(g) Depending on the cisternae position within the stacks, they are referred to as cis, medial and trans cisternae.

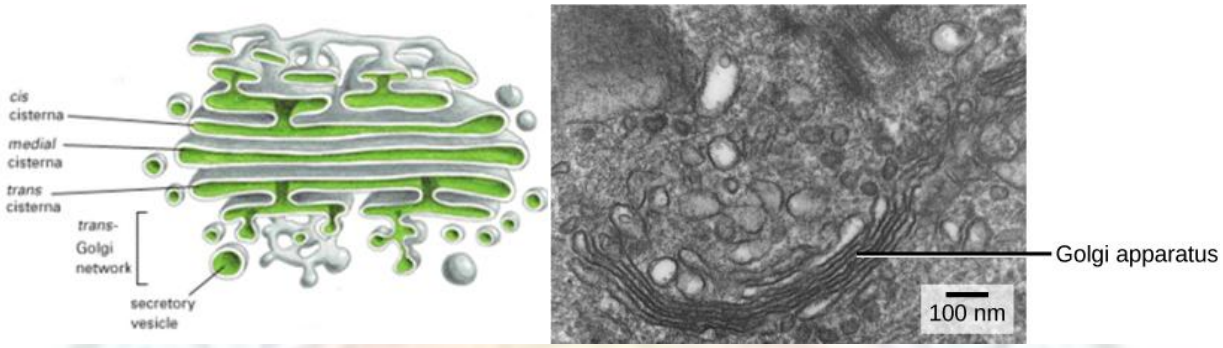



**Figure: A.**Three dimensional reconstruction and **B.** Electron micrograph of Golgi apparatus.

Source: Author, http://cnx.org/content/m44435/latest/Figure_04_04_03.jpg

(h) Small vesicles containing packaged proteins (that are already synthesised by the bound ribosomes), from the RER lumen fuse with the cis Golgi cisternae and through the formation of **shuttle vesicles** (vesicles bud off from one cisternae and fuse with the next and so on), enter the successive cisternae for various modifications. The biochemically modified proteins, finally packaged in bigger **secretory vesicles, get pinched /bud** from the trans face of the Golgi, for their final destinations.

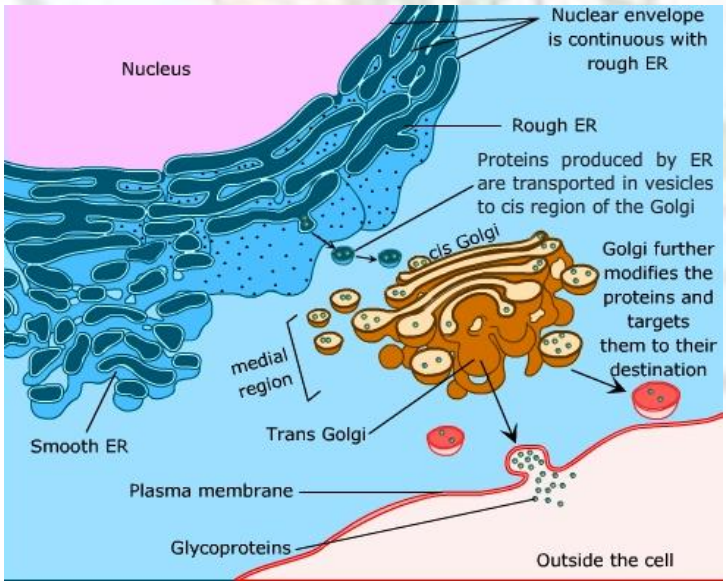


**Figure:** Proteins targeted from endoplasmic reticulum are transported for sorting and modification to Golgi Apparatus
Source: Author

(i) Hence, the Golgi complex is always associated with lots of secretory vesicles.
(j) Unlike the rER, the Golgi cisternae membranes are devoid of ribosomes. The smooth margins of the cisternae may be perforated or form tubular extensions that branch and anastomose. The interconnected network of tubules in the cis face of Golgi is referred as cis Golgi network (CGN) and in the trans face, it is called the trans Golgi network (TGN).

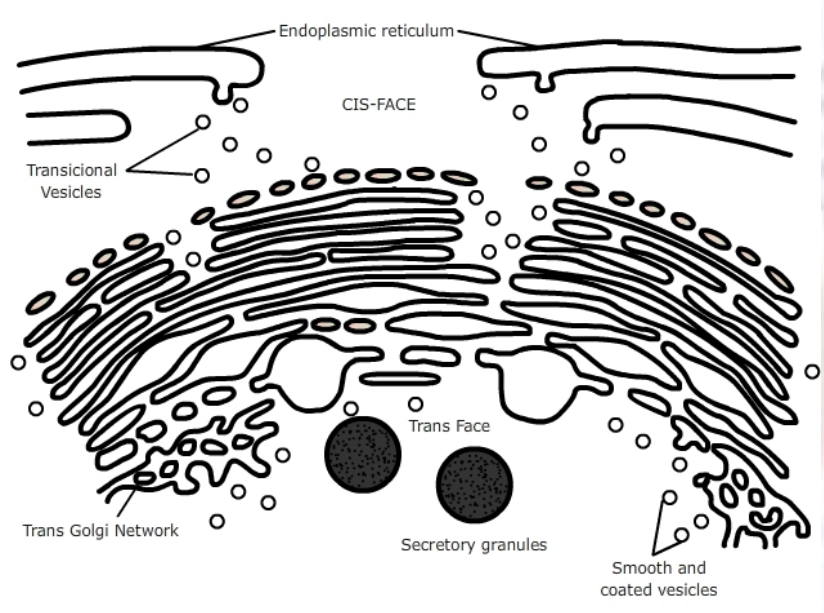



**Figure :** The connect between ER and Golgi
Source: Author

## Functions performed by the Golgi Complex

(a) One of the major functions of Golgi is in cellular secretion.The packaging of different processed materials take place within the Golgi cisternae, which get pinched off as secretory vesicles from the trans-face of the Golgi. The secretory materials are released into the extracellular space by exocytosis.
(b) Golgi plays an important role in the post- translational processing of the proteins.
(c) Glycosylation of protein and lipids take place within the Golgi cisternae.
(d) Golgi helps in the metabolism of membrane lipids and polysaccharides.

(e) Proliferation of the plasma membrane takes place by adding new plasma membrane proteins, processed by the Golgi complex.

(f) Reprocessing of the plasma membrane components that are returned to the cytosol by the process of endocytosis.

(g) Different types of protein modification takes place within the Golgi, which are then despatch to their specified destinations.

(h) The Golgi apparatus is actively involved in the development of acrosome in sperm cells.

(i) Vesicles from the Golgi are actively involved in cell plate and cell wall formation in plants.

(j) Golgi help in the acrosome formation in animal cells.

**Embed Animation:**Functions of Golgi apparatus

Source: http://www.sinauer.com/cooper5e/animation1002.html

Source: http://users.uma.maine.edu/SBaker/nucleus_endo.html

Following are some of the important details of Golgi complex functions.

## Role in Secretion

L.Caro and G.Palade , using radioactive amino acids and by applying "Pulse Chase" technique (Short term use of label amino acid "pulse" followed by prolong use of un-label amino acids and trace the path way of the label amino acids containing proteins), showed that acinar cells of pancreas tissues are involved in packaging of precursors into zymogen granules prior to secretion. The experiment clearly indicated that the protein containing the label amino acids appeared first in the rER lumen, following which the label get shifted to the Golgi complex. By continuing with the "pulse-chase", the label was seen to be completely transferred to the zymogen granules and then to the extra cellular space. It was also noticed that, "label" proteins gradually travel from the cis face to the trans face, which clearly indicated that each **cisternae of the Golgi stack is biochemically different** that is different enzymes are localized in different cisternae. Hence, for the complete processing, the protein has to travel the entire Golgi cisternae before being secreted out. Similar experiment as described for acinar cells, was also employed by Caro, Palade et al. (1966) for the secretion of mucus by the Goblet cells of intestinal epithelium.

**Embed Animation:** Pulse chase experiment

http://www.sumanasinc.com/webcontent/animations/content/pulsechase/pulsechase.html

## Protein processing

Golgi plays an important role in the post- translational changes of proteins, in the form of **glycosylation** (addition of sugar residues). The proteins that are already synthesised in the rER, through vesicular transport enter the cis-cisternae of the Golgi stack via the ERGIC (Endoplasmic Golgi Intermediate Compartment). The protein glycosylation occur in a gradual progressive manner, starting in the cis face following the medial and trans cisternae and after crossing the TGN finally the modified proteins packaged within the vesicles bud off for their final target.

The three important destinations for the modified proteins are (a) Plasma membrane (b) Lysosome and (c) Extra cellular secretion.

In eukaryotic cells there are two different modes of exocytotic secretion, namely

a) **Constitutive secretion,** which involves the continuous discharge of vesicles at the membrane surface for example the continuous release of mucus by the inner lining of the intestine and the secretion of the glycoproteins of the extracellular matrix
b) **Regulated secretion,** which involves the release of the secretory products at intervals, usually in response to an external signal for example the release of insulin from the acinar cells of pancreas and the release of digestive enzymes at specific times.

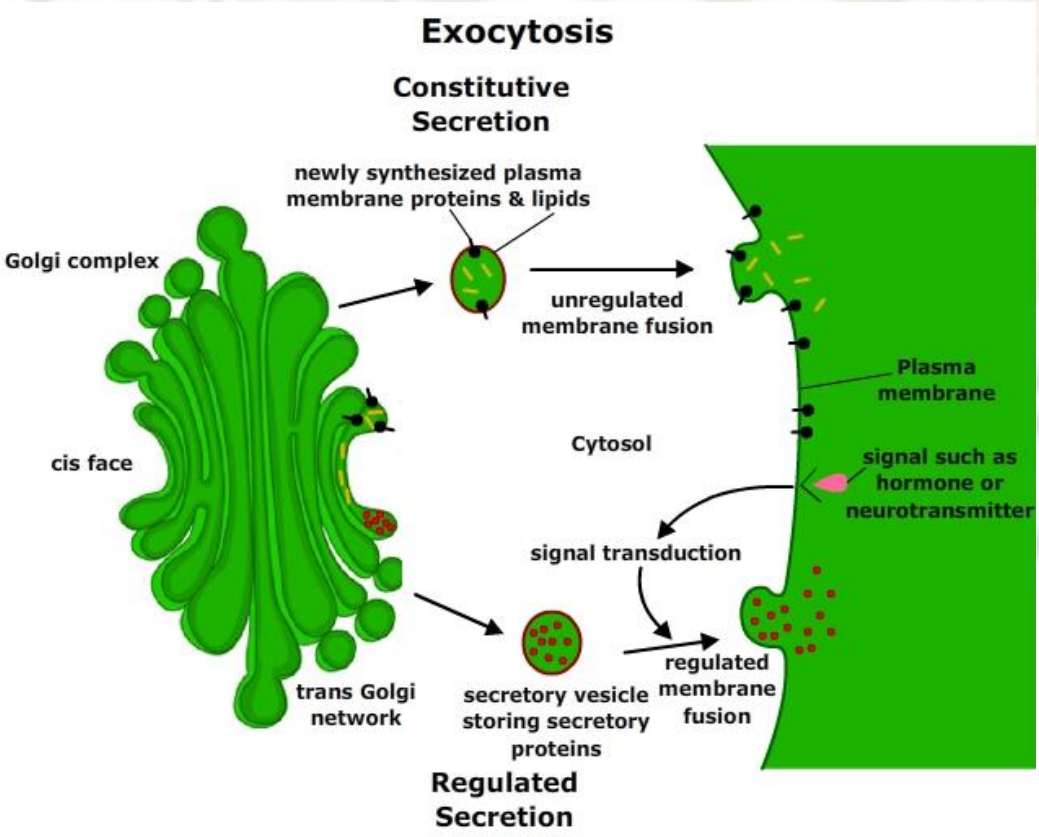



**Figure:** The pathways followed by proteins modified in Golgi

Source: Author

The major steps in the glycosylation process are as follows:

(1) Protein glycosylation begins within the rER lumen are further modified in the Golgi stacks .

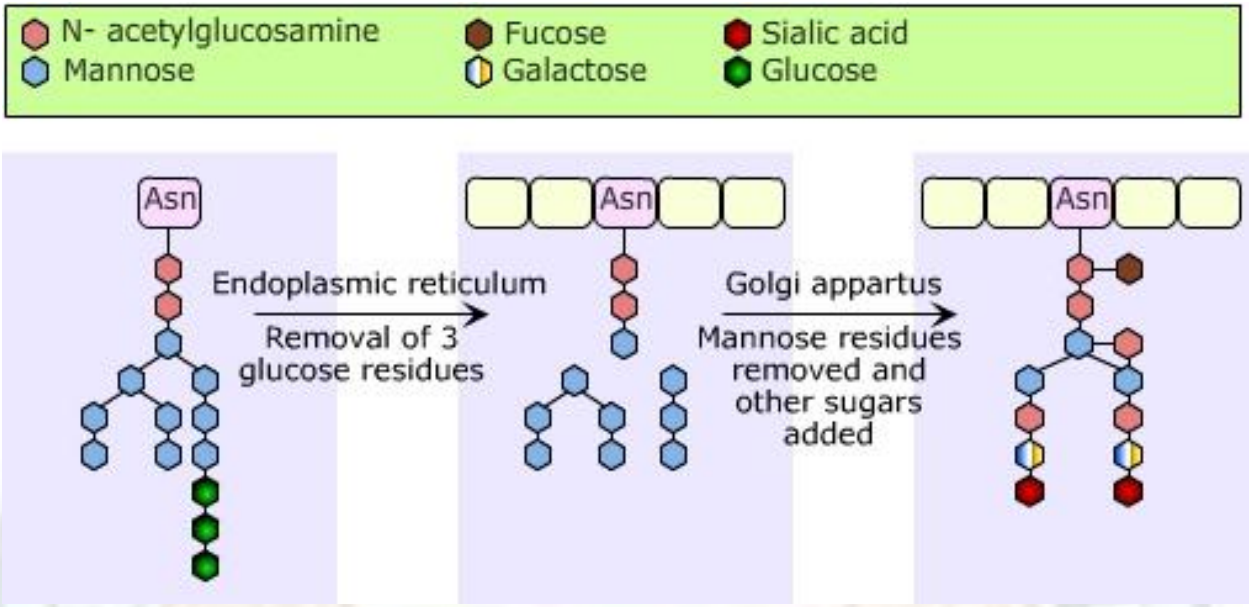



**Figure**: Glycosylation of proteins in ER and Golgi.

Source: Author

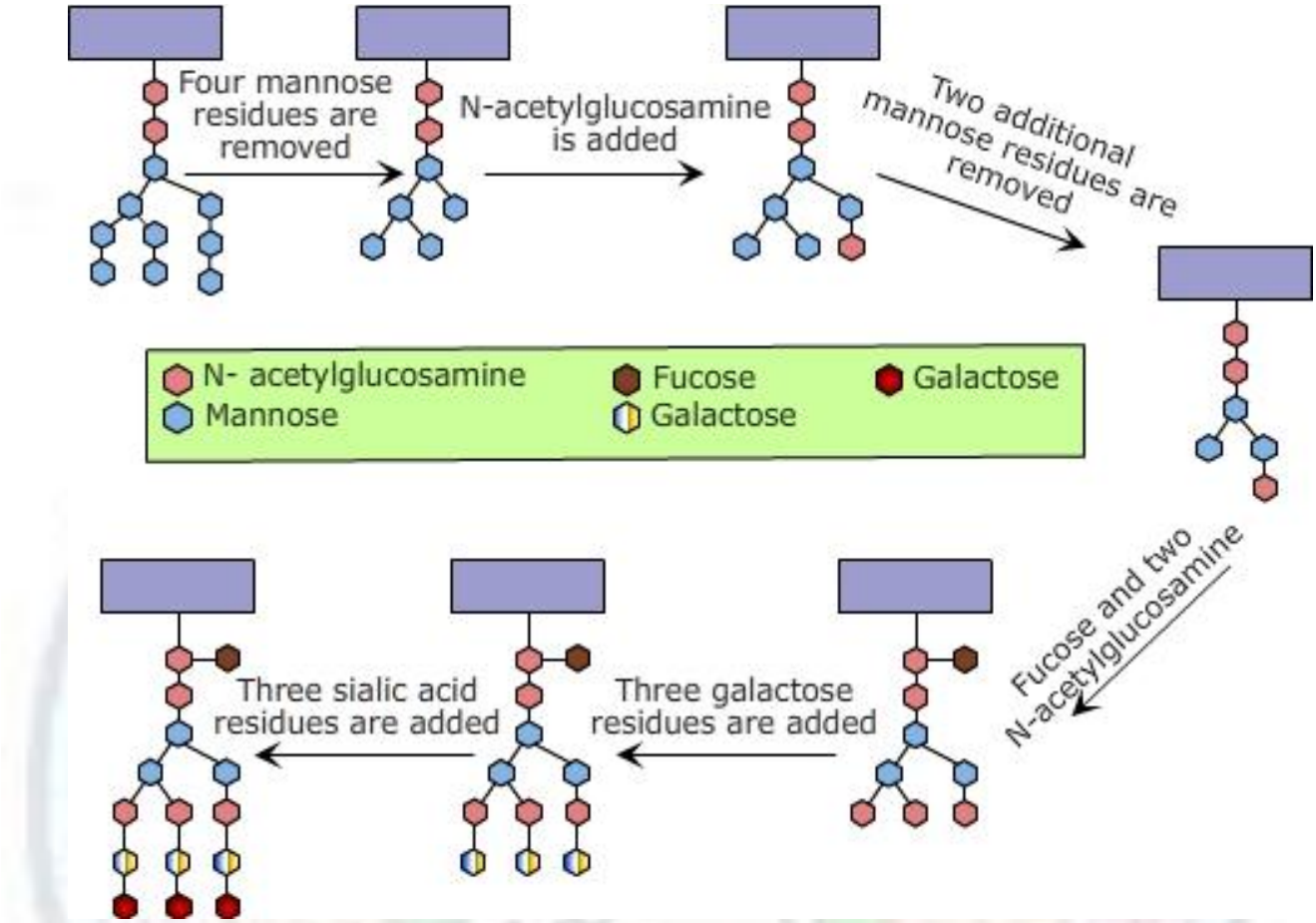



**Figure:** N-linked Glycosylation in Golgi

Source: Author

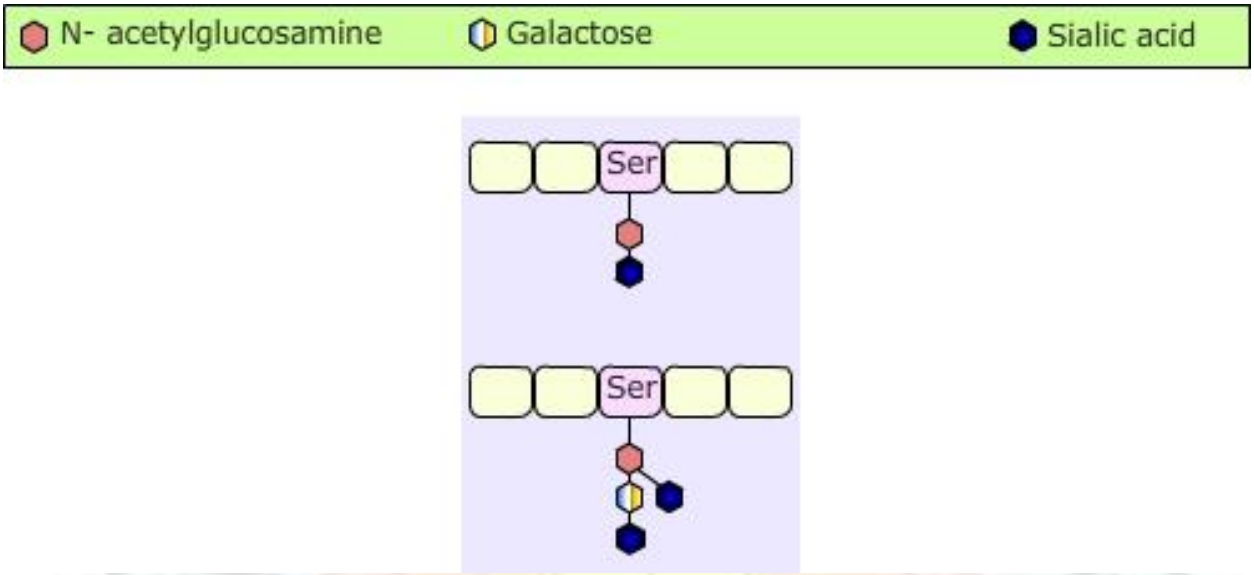



**Figure :** Examples of O-linked oligosaccharides

Source**:** Author

N- linked glycosylation continues in Golgi with sugars being added and removed in different patterns by glycosyltransferases present in Golgi

(2) The preliminary glycosylation, that takes place in the rER is called **core glycosylation**

(3) Most glycosylated proteins are classified either as N-linked or O-linked, depending on the site of attachment of carbohydrate to the side chains of the amino acids . In N-linked, the carbohydrate residues are attached to the nitrogen (N) atom in the side chain (R) of asparagine, whereas in O-linked, the carbohydrate residues are attached to oxygen(O) atom in the side chains (R-group) of serine or threonine.

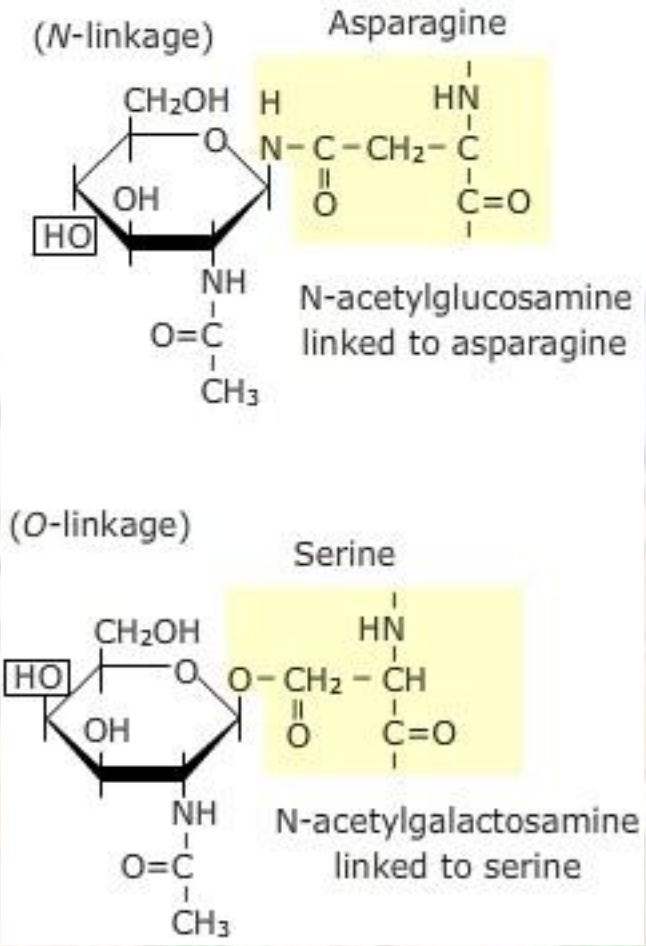



**Figure**: Comparing the N-linked and O- linked glycosylation
Source: Author

(4) N-linked glycosylation takes place within the rER lumen and in the Golgi stack, O-linked glycosylation along with further modifications of the N-linked glycosylation occur.

(5) During core glycosylation, specific branched oligosaccharide consisting of 14 sugar units including : 2 molecules of N-acetyl glucose amine(NAG) + 9 molecules of mannose + 3 molecules of glucose get covalently linked to the R-group of asparagine residues (N-linked).

(6) Within the r-ER lumen, shortly after the oligosaccharide attachment, one mannose and all the three glucose units get removed, before the glycoproteins are transported to the Golgi. Hence, the Golgi receives the glycoproteins only with ten sugars (14-4).

(7) As the glycoproteins enter the cis cisternae of the Golgi stack, phosphate groups get attached to mannose units situated in the terminal ends of the oligosaccharide chain, resulting in the formation of **mannose phosphate**. The mannose phosphorylation alters the 3-D conformation of the glycoprotein, which target such proteins to the lysosomes.

Such determinants, which is used by the cells for specific protein identification is called **signal patches** in contrast to the **signal sequence**, which are liner sequence of specific amino acids.

(8) Proteins that are destined for the plasma membrane and extra cellular secretion, undergo extensive changes.

(9) In the cis compartments of Golgi stack, five mannose molecules are removed, which get replaced by two molecules of N-acetylglucose amine (NAG) in the medial compartment (-5man + 2 NAG).

(10) In the trans cisternae, disaccharides consisting of galctose and N-acetylneumaric acd (NANA; also called sialic acid) get attached to the ends of each glycosylation.

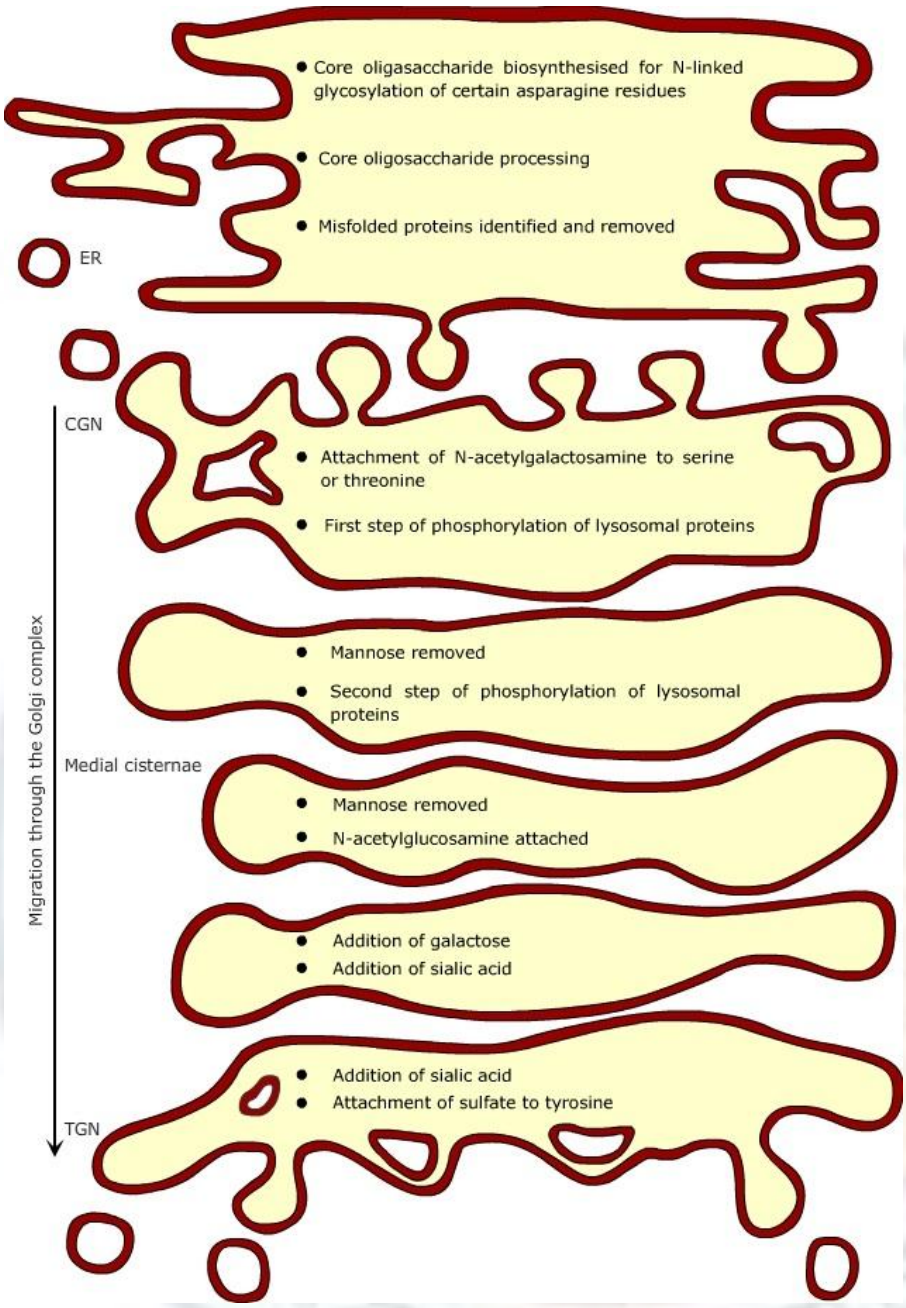



**Figure**: Significant events in glycosylation of proteins that occur in ER and cis, medial and trans Golgi .

Source: Author

(11) In addition to the modifications of the N-linked glycosylation, discussed above, some proteins also are modified by the addition of carbohydrate residues to the R-groups of threonine and serine residues. The oligosaccharides linked covalently to the oxygen atom of the R-group, hence called O-linked glycosylation.

(12) During the O-linked glycosyltion, the oligosaccharides are not randomly attached, but only the serine and threonine present in a specific sequence ( ser-X- thre; where X is any other amino acid) get glycosylated.

**Use of Glycosylation:** The two principal use of protein glycosylation are (a) oligosaccharide attachment prevent protein aggregation within the lumen of both rER and Golgi cisternae. (b) Different types of glycosylation provide signals for further transport and sorting of the proteins for their specific destination. (c) Glycosylation acts as an error checking system for incorrectly folded proteins by the calnexin-calreticulin system.

## Proliferation of plasma membrane

As discussed, proteins discharged within the rER lumen, enter the Golgi stacks after core glycosylation through vesicular transport, where further glycosylation occurs. The proteins that are destined for the plasma membrane and lysosomal membrane remain anchored within the ER membrane and not released within the lumen even after the process of translation. These anchored proteins constitute the wall of the vesicles, which fuse with the membrane of the Golgi cisternae.

The plasma membrane proteins can either be trans- membrane proteins or remain attached to glycolipids. Most of the membrane anchor glycolipids contain glycosylphophatidylinositol (GPI), hence these are referred as GPI anchors.

The transport of the glycosylated proteins from one Golgi compartment to the successive compartments, mediated through vesicle budding and fusion (shuttle vesicles). These anchored proteins help in the proliferation of the plasma membrane or organelle (lysosome) membrane. Not all membrane proteins are glycosylated, the proteins, which are glycosylated are synthesized by the **bound ribosomes** and the rest are synthesized by the **free ribosomes**.

The secretory products processed in the Golgi, finally released in the extracellular space, through the process of exocytosis (see detail in Chapter on Membrane Properties). During the process of exocytosis, the vesicle membrane fuse with the plasma membrane resulting in its increase surface area, which is compensated by the process of endocytosis, where a small portion of the plasma membrane get pinched off . This process is called membrane retrieval.

## Metabolism of lipids and polysaccharide

Along with the processing and sorting of glycolipids the Golgi complex also help in the synthesis of glycolipids and sphingomyelin. Smooth ER is the site of synthesis for the major plasma membrane lipids like glycerol phospholipid, cholesterol and ceramide. Sphingomyelin and glycolipids are synthesized from the ceramide in the Golgi complex. Sphingomyelin (the only non-glycerol phospholipid in cell membrane) is synthesized by the transfer of a phosphotidylcholin (lecithin) to ceramide. Different types of glycolipids formed by the addition of carbohydrates to ceramide residues. The glucose molecules are added to the ceramide on the cytosolic side of the membrane, which then apparently flips and additional carbohydrates are then added on the luminal side of the membrane. The glycolipid, like sphingomyelin are located only on the luminal side of the membrane since the translocation of glycolipids across the Golgi membrane is not possible due to the presence of hydrophilic oligosaccharide. These glycolipid, however get localized to the exterior half (cytosolic side) of the plasma membrane, with their polar groups extend to the cell surface, following vesicular transport. Oligosaccharide portion of the glycolipids always face the outer surface of the membrane, which help in cell-cell recognition, and adds to membrane asymmetry.

## Sorting and Export of protein

Justifying the role of Golgi complex as the "director" of the cell, the various components like lipids and protein, which are processed (biochemically modified) within the Golgi are transported to their specific destinations through secretory pathway or vesicular transport. The proteins, which enter from the cis face has to travel through the entire Golgi stack before being released from the TGN to target the correct destination. This is because each Golgi cisternae though are physically alike, have distinct biochemical differences as proved by cytochemical and immunological staining. Specific enzymes are present in the cis, medial and trans cisternae sequentially process the proteins and the proteins if released in between remain functionally inactive. Different levels of post-translation sorting and segregation of the proteins are listed below:

a) The three major destinations for the processed materials from the Golgi complex are I plasma membrane II lysosome III exracellular secretion. Besides the transport proteins, some proteins are retained within the Golgi cisternae for various biochemical reactions known as **resident proteins.**

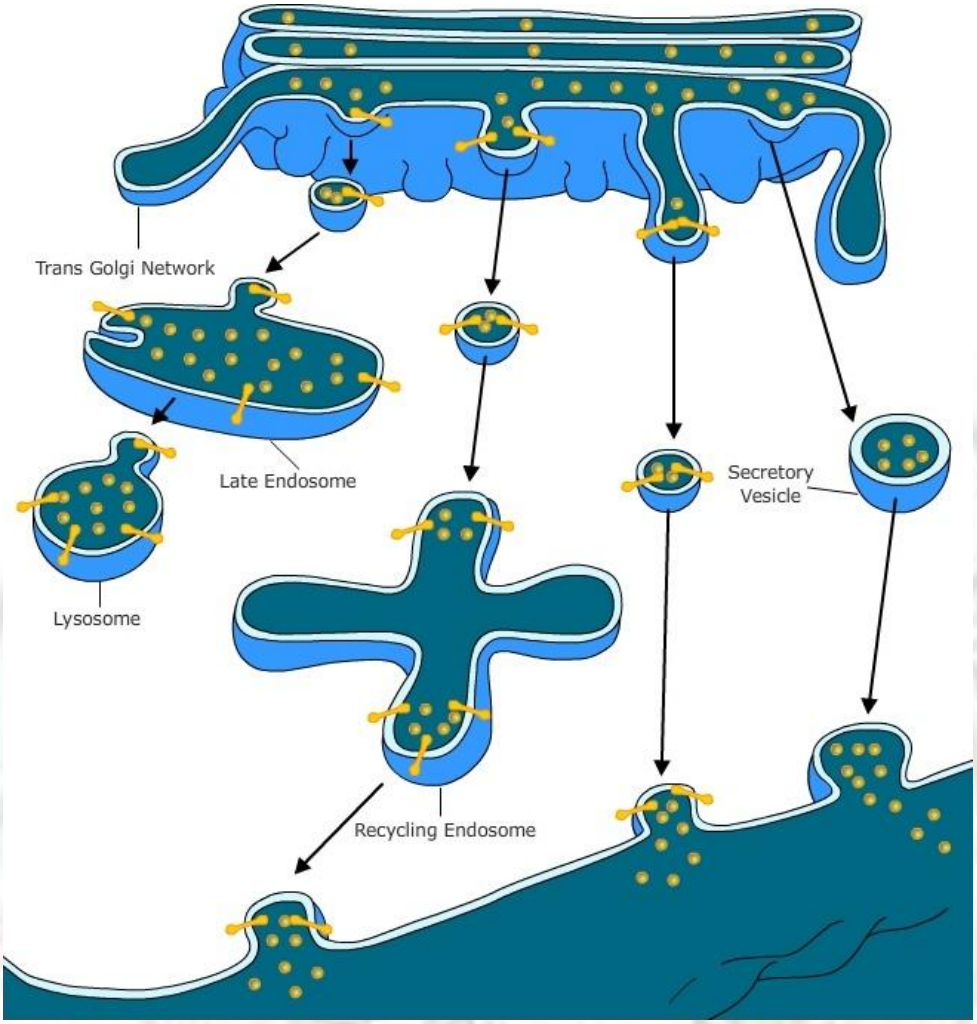



**Figure:** Sorting of proteins from the Golgi apparatus to various destinations

Source: ILLL Inhouse

**Embed Animation :** Protein transported from Golgi to various destinations

Source: http://publications.nigms.nih.gov/insidethecell/extras/golgi/ITC_VesicularShuttle.html

(a) The proteins, which function as enzymes for various post-translational modifications within the Golgi cisternae must always reside within the cisternae and are known as **resident proteins or retention proteins.** The resident proteins are prevented from further transport by two mechanisms such as (a) **retention** of the proteins through certain biochemical signals (prevent the proteins from vesicular transport) and (b) **retrieval of the** molecules, which leave the lumen by default, comes back to the compartment where they belong. The resident proteins of the Golgi are associated with the **cisternae membranes** unlike being soluble within the lumen as in ER. Glycosyl transferases (catalyse the attachment of sugar residues to the protein during glycosylation) and Glucan synthetases (catalyse the formation of polysaccharide from

sugar nucleotides) are the two examples of resident proteins. Presence of specific signal sequence like KKXX (K-Gly; X- any other amino acid) prevent further transport of the retention proteins. In addition, signal sequence in the cytoplasmic tails of some Golgi proteins mediate the retrieval of these proteins from subsequent secretory pathway.

(b) The proteins and lipids destined for plasma membrane always remain anchored to the cisternae membrane and unlike the secretory proteins, not discharged within the lumen of the cisternae. These proteins remain anchored to the membrane even after glycosylation and form the wall of the transport vesicles, which fuse with the plasma membrane to proliferate the membrane.

(c) The transport of lysosomal proteins from the Golgi is a well- known pathway. Shortly after the proteins enter the cis cisternae, the selected lysosomal proteins are marked by the attached of mannose-6-phosphate residues with the modified N-linked oligosaccharide at their terminal position. The **mannose-6-Phosphate tags act as signal patches**, which are recognised at the TGN by **mannose phosphate receptors (MPRs),** which are integral proteins present in TGN and where the proteins are packaged into the transport vesicles destined for the late endosomes that subsequently mature into lysosome. Lysosomal membranes also contain signal patches attached to the cytoplasmic tails of the membrane- anchored proteins that form the transport vesicles, hence both the lysosomal enzymes as well as lysosomal membranes are characterised by specific recognition sites.

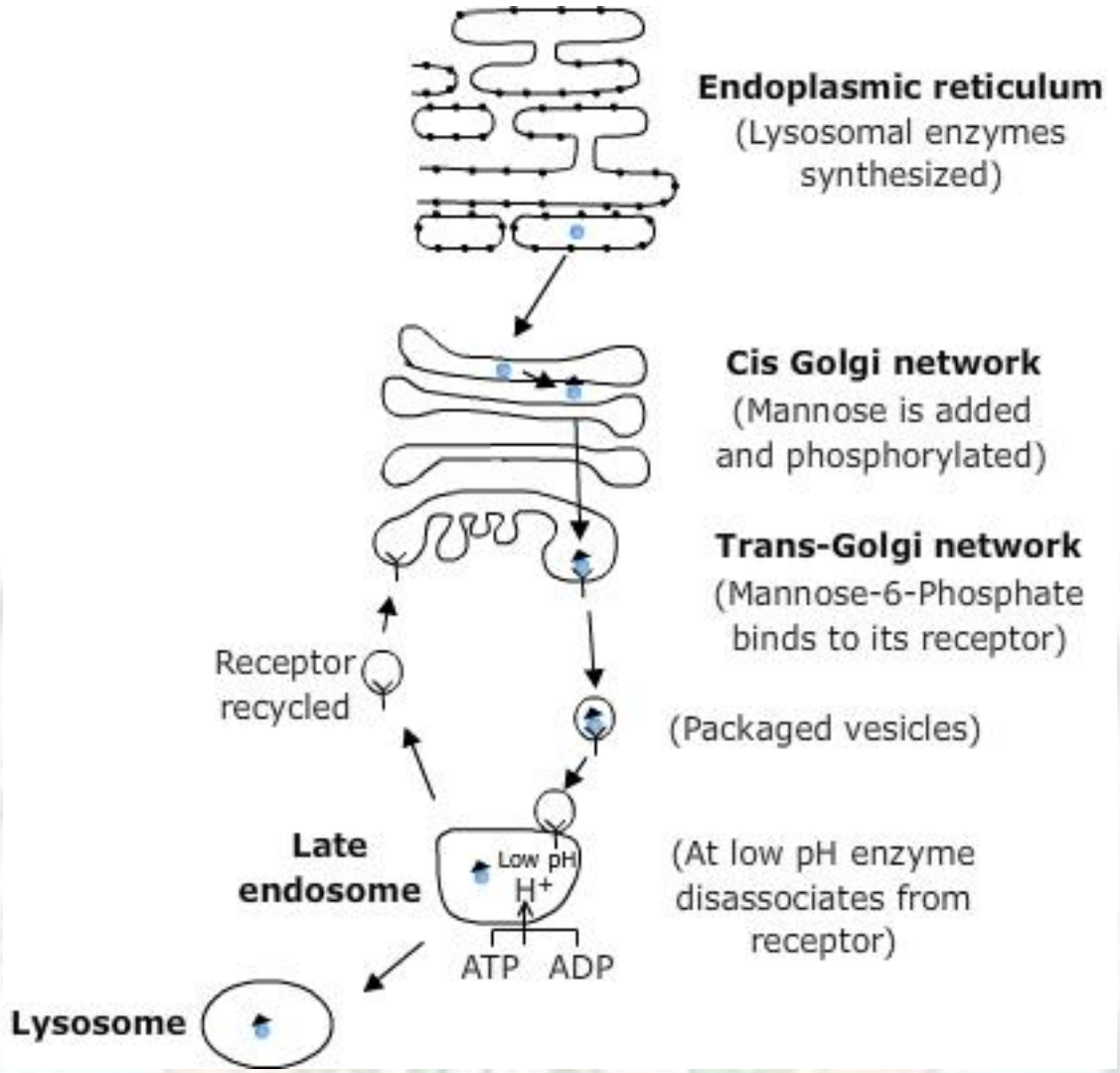



**Figure :** Targeting of lysosomal proteins

Source: ILLL Inhouse

Plant cells including unicellular yeast lack lysosomes, the transport proteins from the Golgi complex are targeted to an additional destination namely the **vacuoles**. Plant vacuoles, which help in storing nutrients, maintaining osmotic balance and turgor pressure of the cell also perform the function of the lysosomes. The proteins destined for the vacuoles are attached to short "**signal peptide sequences**" unlike the carbohydrate signal patches described for the lysosomes.

(d) Proteins meant for extracellular secretion are segregated within the Golgi. In certain cellular systems, there exist a distinct and well- regulated secretory pathway, where the secretion is controlled by specific environmental signals. Release of neurotransmitters from the neuron cells, the secretion of digestive enzymes from the pancreatic acinar cells are good examples of regulated secretion. The proteins are packaged into specialized secretory vesicles

in the TGN. These vesicles with their stored contents wait for specific signal to direct the fusion and release of their contents (secrete) by the process of exocytosis. The release of digestive enzymes produced by the pancreatic acinar cells are stored in mature specialised secretory vesicles, until the presence of food (environmental signal) in the stomach and small intestine, which act as signal for the secretion of the digestive enzymes. A further complicated type of protein segregation has been noted in some polarized cells, where the cell has two functionally different domains. For example, the intestinal epithelial cell has an apical domain that faces the lumen, which is specialized for active adsorption of nutrients and a basolateral domain. For such polarized cells, the transport vesicles selectively packaged the proteins for distinct domains of the plasma membrane even within the same cell, which selectively fuse with either the apical or the basolateral domain.

**Transport of materials through Golgi Complex**: Lipids and proteins move through Golgi Complex. This complex can be of two types, i) Anterogrde and ii) Retrograde transport. Movement of materials from Golgi Complex to plasmamembrane is called anterograde transport (in latin antero means front, while grade means 'step'. In anterograde movement vesicles which originate from Golgi complex fuse with plasma membrane, membrane of golgi complex become part of the plasma membrane. Recycling of lipid and proteins of the membrane is balanced by retrograde transport (in Latin retro means 'back'), where vesicles move bakwards from Golgi Complex to ER.

There are two contrasting views for the movement of various materials through the Golgi cisternae. During mid-1980s, it was believed that Golgi cisternae were transient structures; it was supposed that they formed at the cis face of the stack by fusion of vesicles from the ER and that each cisternae physically move from the cis to trans end of the stack, changing in composition as it progressed. This is known as **cisternae maturation model** (for watching an animation on the cisternae mauration model visit:

**Embed Animation:** Cisternae maturation model
http://publications.nigms.nih.gov/insidethecell/extras/golgi/ITC_Cisternae Maturation.html)**.**

Recent researches favours an alternative model which contends that the cisternae of a Golgi stack remains in place as stable entities held together by a protein scaffold and the material from cis to trans cisternae move in the form of vesicles that bud from one cisternae and fuse with the neighbouring cisternae known as **vesicular transport model**

**Embed Animation :** Protein transported from Golgi to various destinations

Source: http://publications.nigms.nih.gov/insidethecell/extras/golgi/ITC_VesicularShuttle.html

**Role of Coat Proteins in cargo selection and vesicle budding**

**Embed Animation:**

Source:http://www.garlandscience.com/garlandscience_resources/resource_detail.jsf?landing=student&resource_id=9780815341055_CH13_QTM03

Coat proteins as the name suggest, enclose the transport vesicles and help them not only recognize the correct destination but also rectify any default pathway. Vesicles coated with cytosolic coat proteins are called **coated vesicles.** The vesicles meant for different transport pathways are coated with different types of coat proteins.

Three families of coat proteins has been characterised namely (a) Clathrin-coated (b) COPI (c) COPII.

(a) Clathrin-coated vesicles carry **cargo onward** from mature cisternae and also any **cargo back** from the plasma membrane to endosomes and other organelles such as TGN and lysosome. Hence Clathrin–coated vesicles are responsible for **transport in both directions**.

(b) COPI-coated vesicles act as retrieval vesicles that bring back proteins, which enter the default pathway. For example, the ER resident proteins (disulphide isomerase, Bip etc) enter back from the ERGIC and cis Golgi cisternae into the ER lumen, similarly the Golgi resident proteins are retrieved back from TGN to earlier cisternae.

(c) COPII-coated vesicles carry out the transport from the ER lumen to successive cisternae of the Golgi complex.

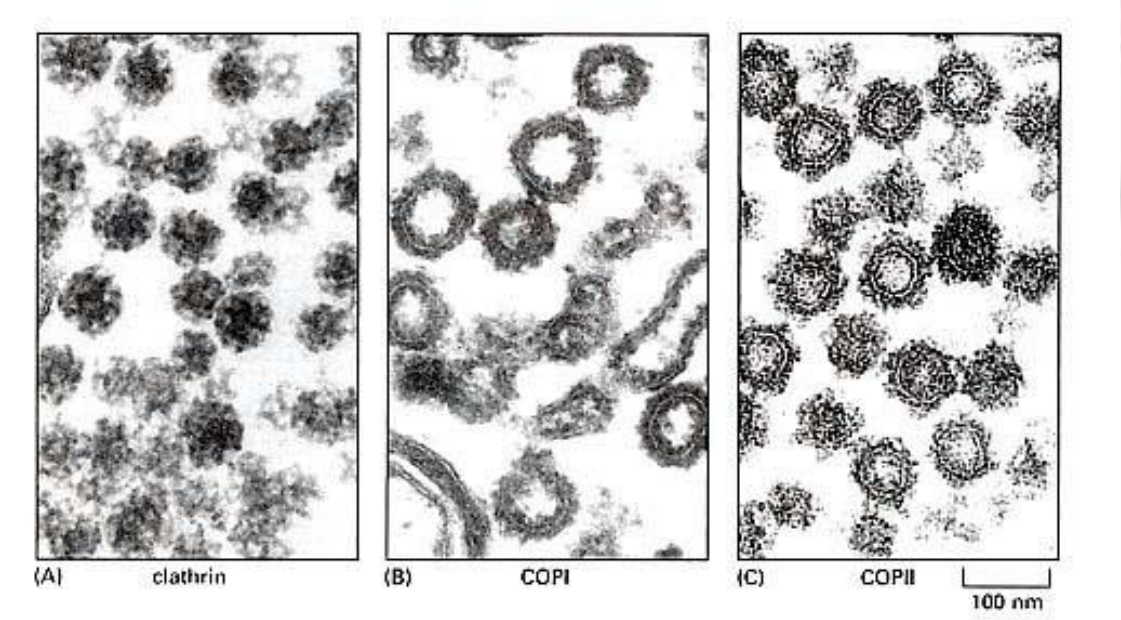



**Figure :** Coated Vesicles

Source: http://jpkc.scu.edu.cn/ywwy/zbsw(E)/pic/ech7-42.jpg

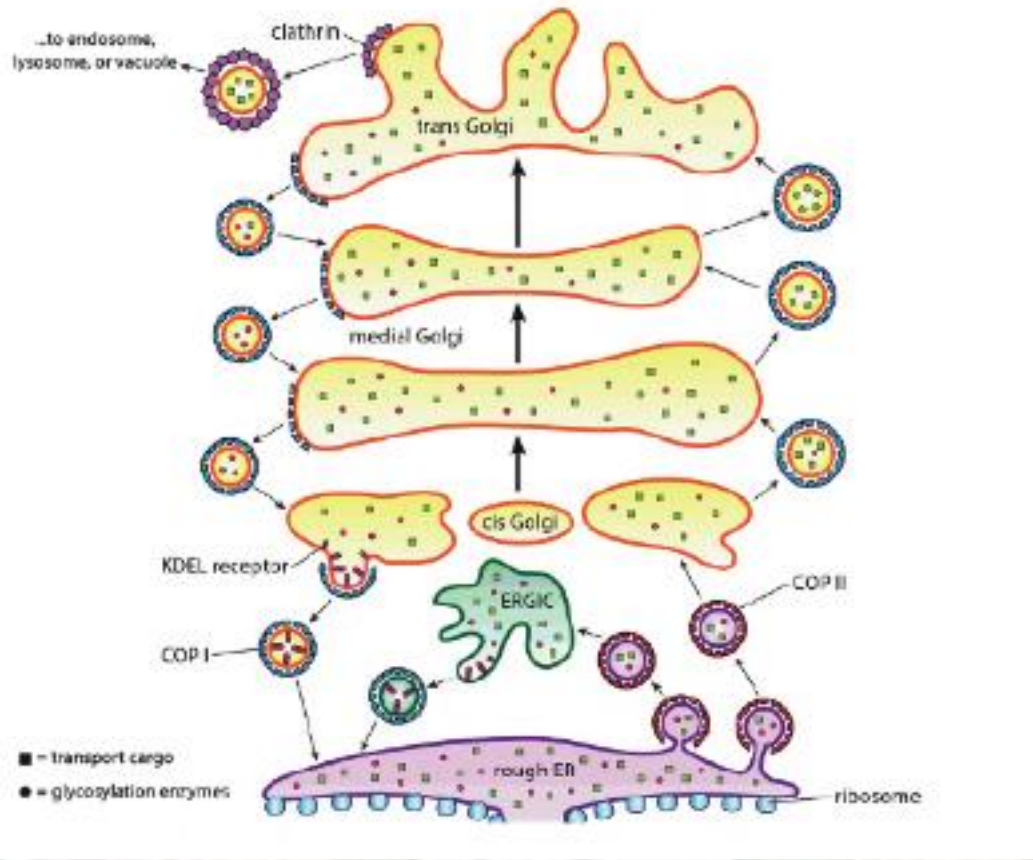



**Figure :** Different types of coated vesicles and their targeting

Source: E.V. Wong Ph.D. 2009. Cells: Molecules and Mechanisms. Axolotl Academic Publishing Company, Louisville, KY.( CC-BY-SA)

The coat proteins generally assemble as the secretory proteins containing vesicles bud off from the donor membrane (ER cisternae or Golgi cisternae) and generally removed in the cytosol before reaching its target. The formation of the coated vesicle is regulated by small GTP-bound proteins, which are related to Ras and Ran. The budding, of the transport vesicles is controlled by two families of ADP-ribosyl factor (ARF 1-3 and sar) along with a large family of Rab proteins.

**Vesicle fusion**

Two steps are involved in the fusion of a transport vesicle its target.

- First, the vesicles must recognise the correct target membrane and
- in the second step the fusion of the vesicles with the target membrane takes place.

The interactions between specific pairs of **transmembrane proteins** called, **SNARE** on the vesicle and the target membrane (v-SNARE and t-SNARE respectively) mediate the fusion of the vesicles.

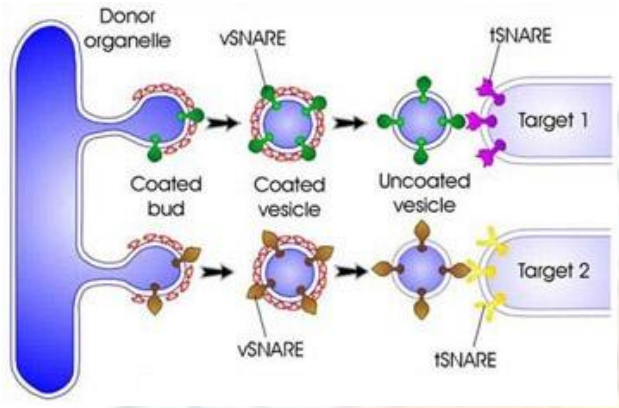



**Figure:** Vesicle fusion is mediated by interactions between complementary proteins- SNAREs. Vesicles with specific v-SNARE bud from donor compartments and are targeted to receptor compartments having complementary t-SNAREs.

Source: Picture courtsey Professor Danton H. O'Day, University of Toronto, Mississauga

Subsequent research has confirmed that complex formation between v-SNARE and t-SNARE requires energy to bring the two bilayers (vesicle+target) close enough to destabilize and fuse. The rab family of small GTP binding proteins help in docking of the vesicles to its target membrane.

## Plant cell wall formation

In plant cells, after karyokinesis (nuclear division) during the late anaphase and telophase of mitosis and meiosis II, the cell plate and cell wall is formed in between the two newly divided nuclei. Golgi complex is found outside the spindle prior to anaphse. Small vesicles containing non-cellulose cell wall materials like pectin and hemicellulose, are released from the Golgi cisternae, which invade the equatorial region of the spindle and aggregate to form a plate like structure in between the two newly divided nuclei. As much as 80% of the metabolic activities of the dictyosomes in plant cells may be devoted to polysaccharide synthesis. The vesicles derived from the dictyosomes (the plant cell's Golgi stack) appear to be guided to the midplane by **microtubules** that are derived from the polar microtubules and that are oriented at right angles to the developing cell plate. The parallel array of microtubules forms the phragmoplast (see details in lesson on Cell Wall). Fusion of these vesicles forms a large, flattened sac called the early cell plate, which eventually form the cell wall. Plasma membrane in plant cells is formed on both sides of the developing cell plate and grows inwards to fuse with the mother

cell membrane, unlike in animal cells , where the cytokinesis (division of the cytoplasm) takes place by the inward pinching of the cell membrane.

### Acrosome development in animals

The sperm cells in most animals contain a membrane–bound structure called the **acrosome** at its anterior region. Acrosome help in the recognition and binding of the sperms to the egg surface and contain hydrolytic enzymes (most abundant being hyaluronidase), which help in hydrolysing the protective surface of the egg. The hydrolysing enzymes enter the acrosomes through the vesicular transport from the Golgi. Acrosome is considered to be a giant lysosome since it contain only hydrolysing enzymes. There is a reduction in the growth of the Golgi complex along with the acrosomal growth, leading to complete disappearance of Golgi complex in mature sperm cells. The presence of glycosylated proteins in the acrosome also confirmed their origin in the Golgi apparatus.

## Summary

Golgi complex or dictyosome consists of stacks of slightly curved cisternae, to give a bow like appearance. Each Golgi has a cis face or forming side (convex portion) and the trans-face or maturing side (concave region). The major function of the Golgi complex is to biochemically modify the secretory proteins and some membrane lipids, that are synthesized by the r- ER and after sorting and segregating the proteins are packaged into transport vesicles to different destinations. The major destinations of these secretory proteins are plasma membrane, lysosome and extracellular secretion. Golgi cisternae though are physically alike are biochemically very different. Different types of processing like glycosylation of proteins and lipids, phosphorylation, sulphation etc take place in different Golgi cisternae. Different types of cytosolic coat proteins such as clathrin, COPI and COPII, which are responsible for the coated vesicle formation, finally segregate the transport vesicles for their correct destinations including the retrieval of the resident proteins which escape by default pathway. Specific pair of transmembrane protein called SNARE, mediates the fusion of the transport vesicles with the target membrane. Golgi also plays important role in plant cell wall formation and acrosome formation in animal sperm cells. The close interrelationship among the three cellular organelles like ER, Golgi and lysosome is referred as GERL complex.

## Glossary

**Cis-face:** It is the forming side of the Golgi complex from where the material containing vesicles enter the complex

**Coated vesicles:** the vesicles which are coated with cytosolic coat proteins like COPI, COPII or Clathrin

**Fenestrae:** The perforated margins of the Golgi cisternae

**Glycosylation:** Addition of sugar residues to other biopolymers

**Retention protein:** proteins, which are prevented from further transport either from the ER or Golgi cisternae lumen

**Shuttle vesicles:** vesicles that bud off from one cisternae and fuse with the next and so on

**Signal patches:** recognition determinant formed by the 3-D conformation of the protein

**Signal sequence:** recognition determinant formed by the specific amino acid sequence of the protein

**SNARE:** a transmembrane protein that help in the fusion of the transport vesicles with the target

**Trans-face:** It is the maturing face of the Golgi complex from where the secretory vesicles are released for their final destination

## Exercises

1. Described the structure of Golgi apparatus and draw a labelled diagram. Why it is called Golgi complex or Dictyosome?
2. Briefly mention the important functions of Golgi complex.
3. Explain the significance of GERL .
4. How Golgi help in despatching the packaged proteins to their correct destinations?
5. Describe the role of Golgi in vesicular transport of proteins.
6. Write short notes on

   (a) Role played by Golgi in cell wall synthesis and acrosome formation.
   (b) Glycosylation within Golgi compartments

(c) Use of glycosylation

(d) Vesicular transport and fusion

(e) Protein sorting

7. Explain the following:

a) TGN

b) Cis and trans face of Golgi

c) Signal sequence

d) Retention protein

e) Signal patch

f) Retrieval pathway

g) GERL complex

h) SNARE

i) KKXX sequence

j) Post-translational modification Mannose phosphate tag

k) O-linked glycosylation

l) N-linked glycosylation

8. Justify the following statements:

a) Golgi cisternae are biochemically different

b) Golgi complex has an important role in cellular secretion

c) Lysosomal proteins are glycosylated

d) GERL complex plays an important role in cellular synthesis

e) Dictyosomes plays an important role in cell plate formation

f) Coat proteins are important for protein sorting

g) Protein glycosylation within Golgi cisternae has importance

h) Movement of materials within the Golgi cisternae is directional