Protein engineering

Protein engineering describes the intentional alteration of a protein's amino acid sequence, usually with the aim of achieving either:

- a better understanding of the relationship between a protein's primary and higher-level structure, or its structure and function; or
- the development of a protein variant which, relative to the wild-type protein, displays some enhanced property in the context of its commercial use.

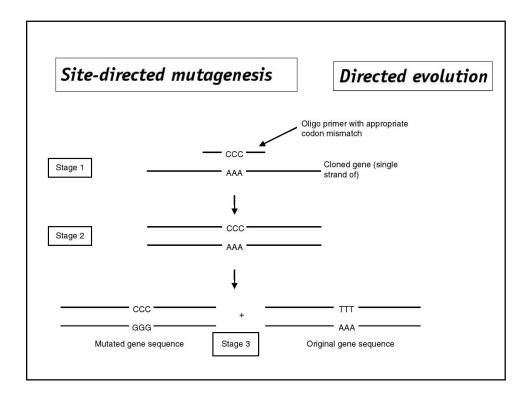
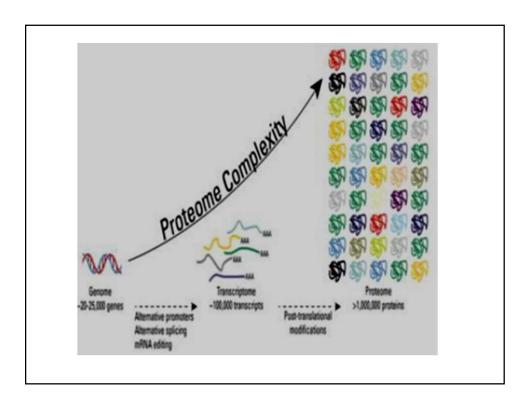
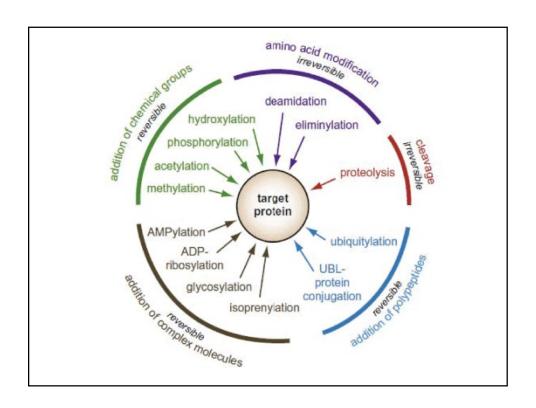


Table 2.6 Representative engineered proteins which are now used commercially. These and other examples are considered in later chapters of this book.

Protein	Use	Engineering detail	Chapte
Tissue plasminogen activator (tPA)	Thrombolytic agent	Various engineered products developed with altered amino acid sequences or with whole domains deleted in order to make clot degradation more efficient or lengthen serum half-life	
Antibodies	Various, including cancer treatment	Various engineered products developed, including mouse- derived antibodies in which large segments have been replaced by human antibody domains (in order to reduce immunogenicity in humans), or the development of antigen- binding antibody fragments (which could for example penetrate tumours more effectively)	
Fusion proteins	Various, including treating rheumatoid arthritis and cancer	Generation of novel hybrid proteins by combining one or more domains from two different proteins together. The fusion product 'Enbrel' for example consists of the extracellular domain of the tumour necrosis factor (TNF) receptor (allowing it bind TNF), fused to antibody constant (Fc) domains (which increases its serum half-life)	
Engineered insulins	Diabetes	The replacement/alteration of amino acids in the insulin backbone in order to make the engineered product either faster-acting or slower-acting than un-engineered insulin	
Various detergent proteases and amylases	Added to detergents to enhance cleaning	Removal/replacement of oxidation-sensitive amino acid residues, allowing the enzymes to retain activity in the presence of oxidants usually also present in detergents	
DNA polymerase	PCR reactions	Enhances enzyme's affinity for DNA	13



Post-translational modifications (PTMs)



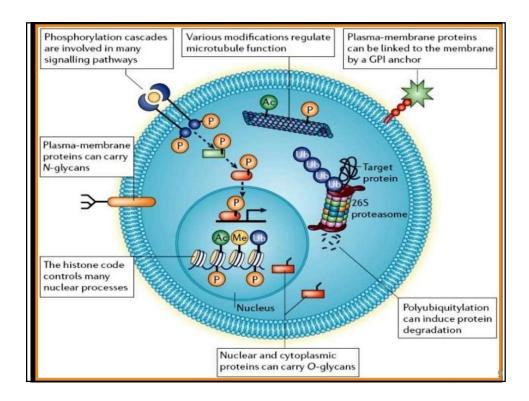
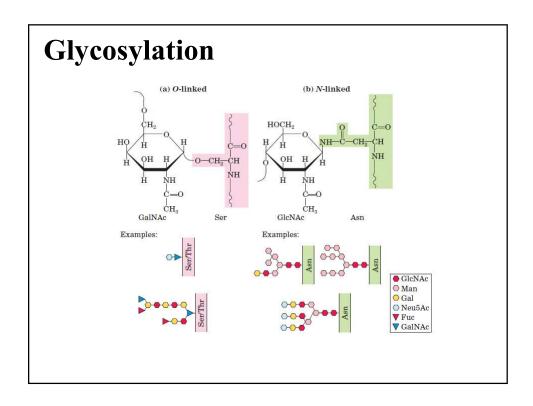
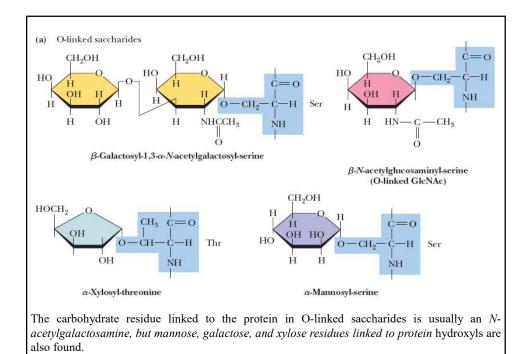
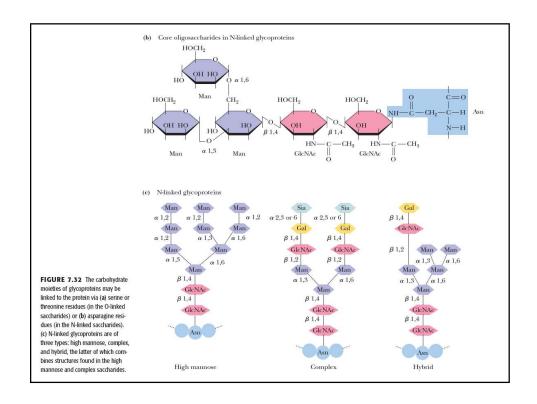


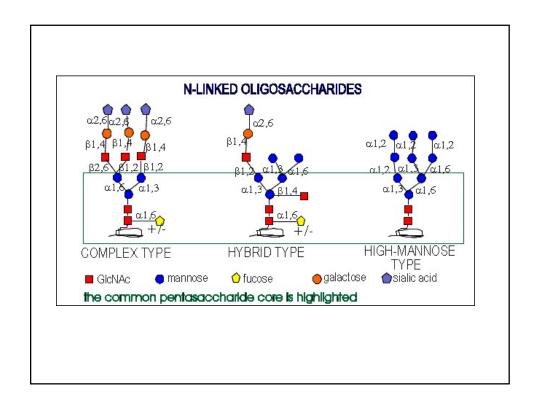
Table 2.7 The more common forms of post-translational modifications that polypeptides may undergo. Refer to text for additional details.

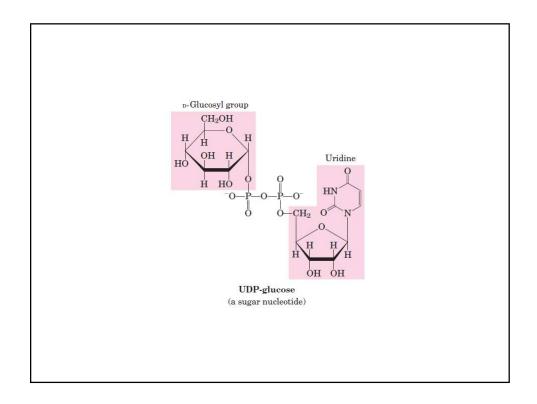
Modification	Comment	
Glycosylation	For some proteins glycosylation can increase solubility, influence biological half-life and/or biological activity	
Proteolytic processing	Various proteins become biologically active only on their proteolytic cleavage (e.g. some blood factors)	
Phosphorylation	Influences/regulates biological activity of various regulatory proteins including polypeptide hormones	
Acetylation	Modulation of target protein activity	
Acylation	May help some polypeptides interact with/anchor in biological membranes	
Amidation	Influences biological activity/stability of some polypeptides	
Sulfation	Influences biological activity of some neuropeptides and the proteolytic processing of some polypeptides	
Hydroxylation	Important to the structural assembly of certain proteins	
γ-Carboxyglutamate formation	Important in allowing some blood proteins to bind calcium	
ADP-ribosylation	Regulates biological activity of various proteins	
Disulfide bond formation	Helps stabilize conformation of some proteins	

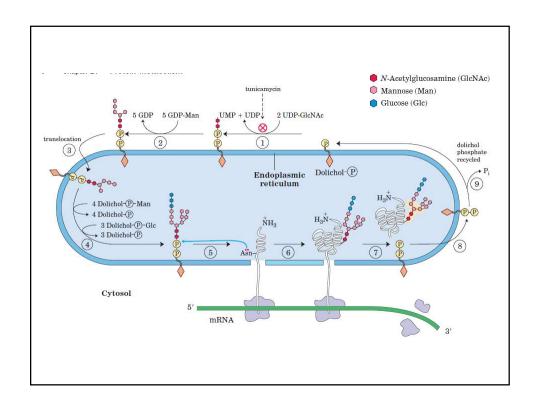




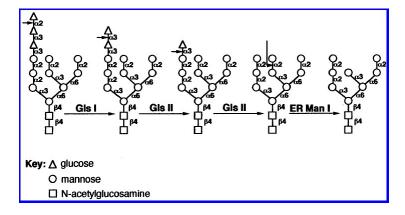


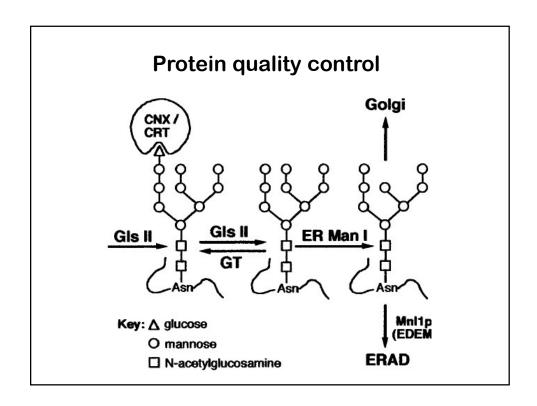


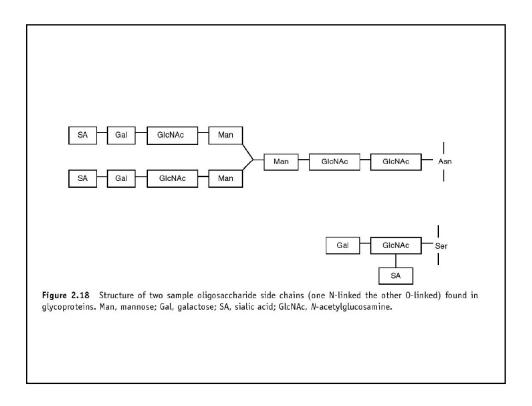


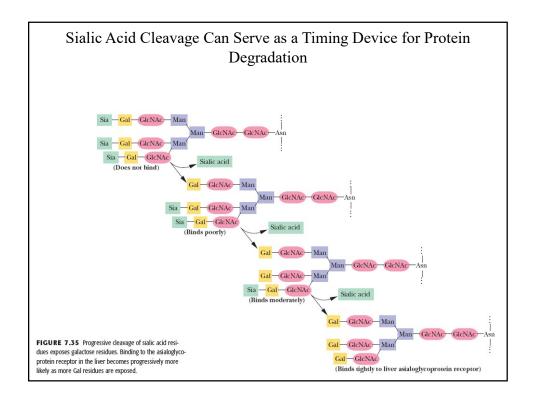


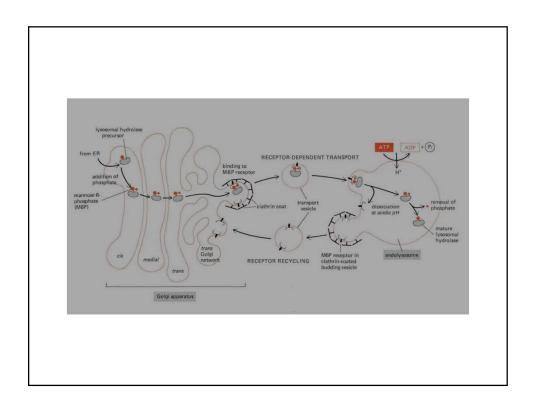
Protein N-glycosylation in ER

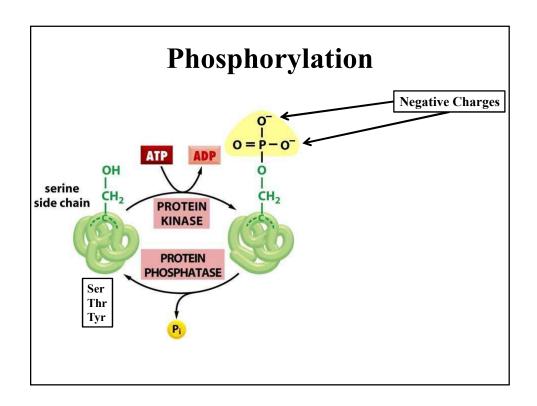


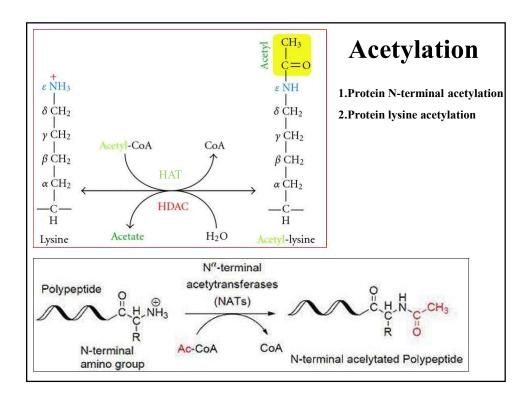


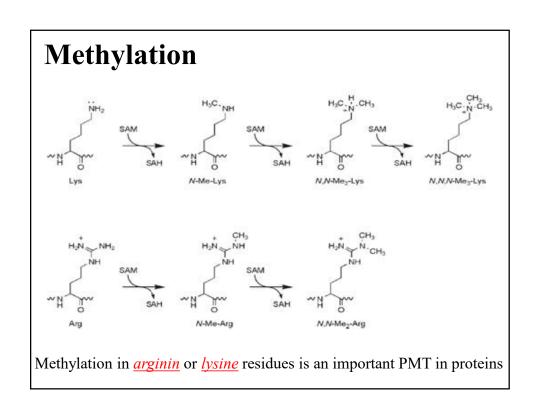


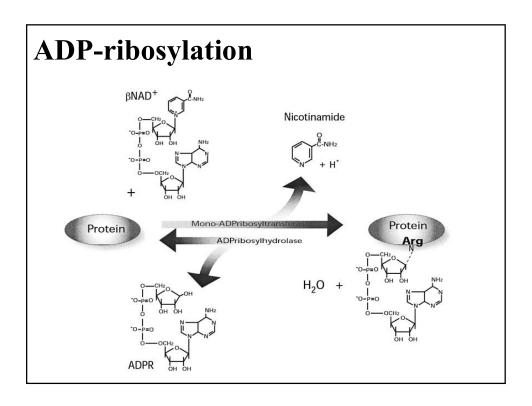


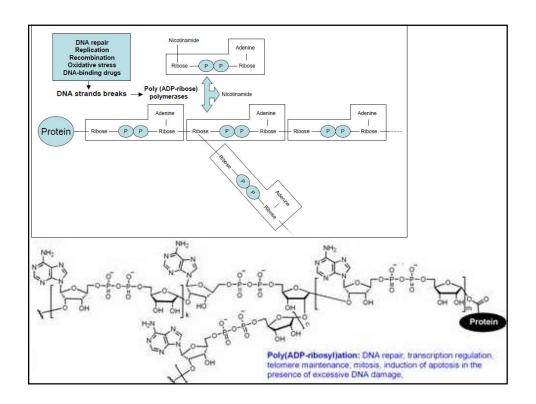


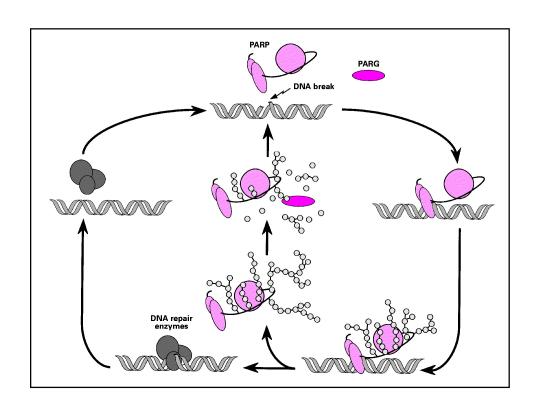


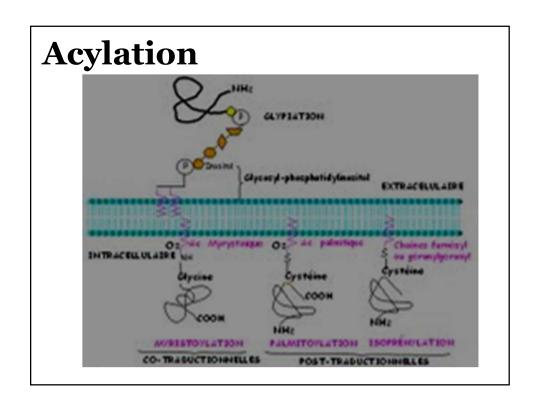












Acylation

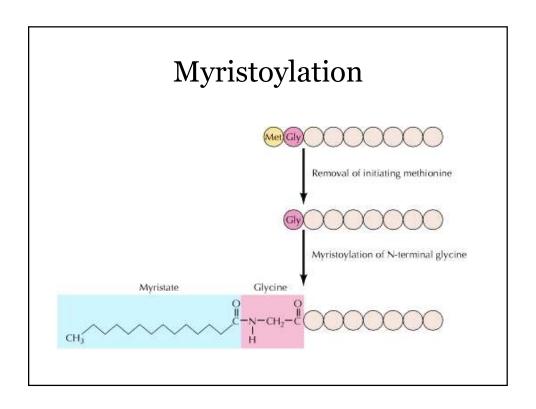
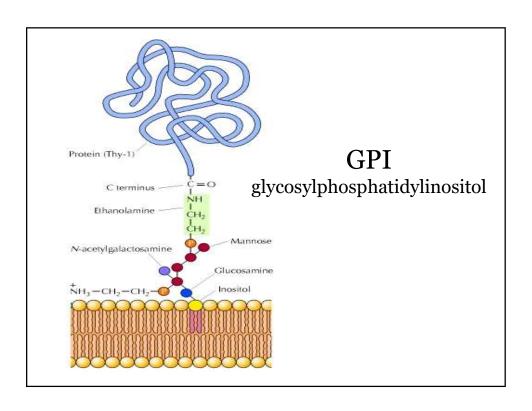
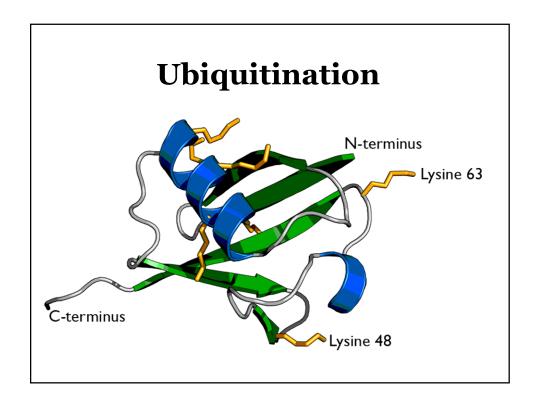
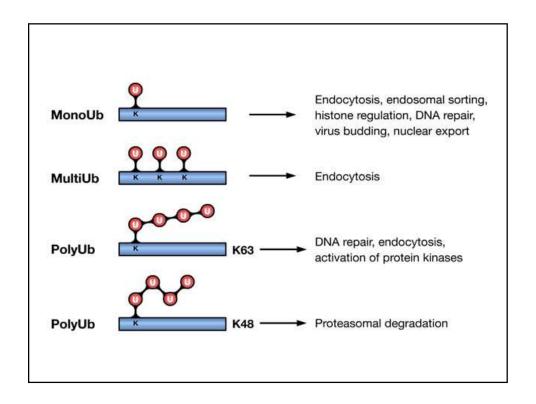


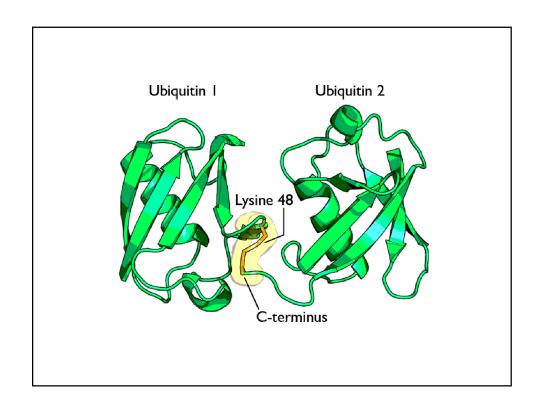
Table 2.8 Representative examples of some acylated proteins. The fatty acid moiety attached and the location of eukaryotic-derived acylated proteins are also listed.

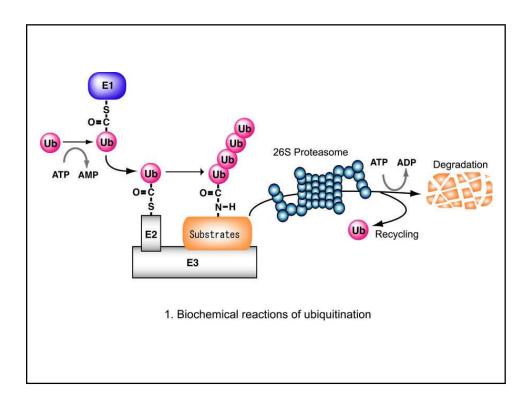
Protein	Cellular location	Fatty acid Myristic acid	
cAMP-dependent protein kinase	Cytoplasm		
Cytochrome b _s reductase	ER and mitochondria	Myristic acid	
$G_{_{\! 1}}$ and $G_{_{\! 0}}$ $\!$	Plasma membrane	Myristic acid	
Insulin receptor	Plasma membrane	Palmitic acid	
Interleukin 1 receptor	Plasma membrane	Palmitic acid	
Transferrin receptor	Plasma membrane	Palmitic acid	
Rhodopsin	Disc membranes in retina	Palmitic acid	
P55 and P28	HIV	Myristic acid	
VP4	Picornaviruses	Myristic acid	
P19 (gag)	HTLV I	Myristic acid	
на	Influenza virus	Palmitic acid	
gE	Herpes simplex virus	Palmitic acid	

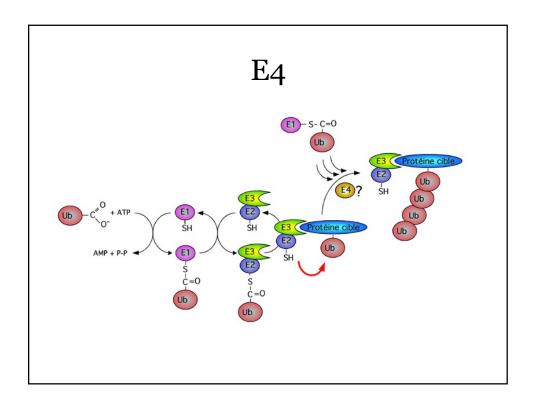












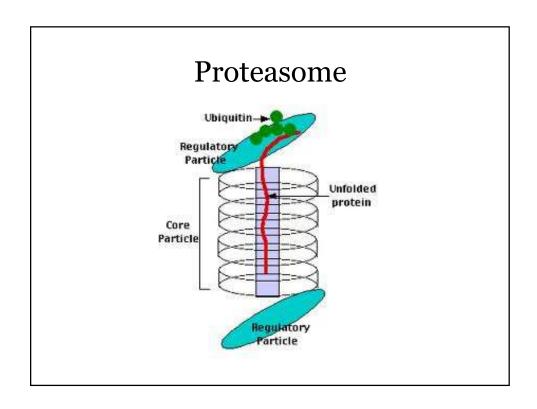


Table 2.9 Some post-translational modifications (PTMs) associated with proteins for therapeutic use. The vast majority of such proteins are (recombinant forms of) native human extracellular proteins, and as such their PTM profile is biased towards PTMs characteristic of extracellular proteins derived from higher eukaryotes. The list is representative only, with specific examples being found throughout Chapters 6–9.

Protein	Therapeutic application	PTM detail
Blood factor VIII	Haemophilia A (Chapter 6)	Glycosylation, disulfide bond formation, sulfation
Hirudin	Anticoagulant (Chapter 6)	Disulfide bond formation, sulfation
Tissue plasminogen activator (tPA)	Thrombolytic (Chapter 6)	Glycosylation, disulfide bond formation, proteolytic processing
α -Galactosidase	Fabry disease (Chapter 6)	Glycosylation, disulfide bond formation
Antibodies	Various (Chapter 7)	Glycosylation, disulfide bond formation
Insulin	Diabetes (Chapter 8)	Disulfide bond formation, proteolytic processing
Human growth hormone (hGH)	Dwarfism (Chapter 8)	Disulfide bond formation, phosphorylation
Erythropoietin (EPO)	Anaemia (Chapter 8)	Disulfide bond formation, glycosylation
Interferon β	Multiple sclerosis	Disulfide bond formation, glycosylation, phosphorylation

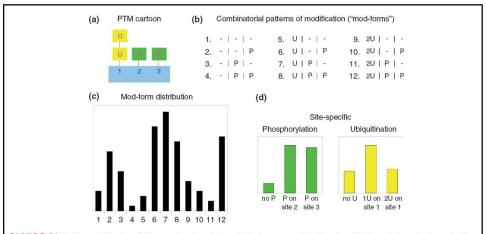


FIGURE 6 | Mod-form distributions. (a) Cartoon depiction of a hypothetical substrate with 3 sites of modification; site 1 is ubiquitinated with a chain of up to two monomers; sites 2 and 3 are phosphorylated. (b) There are $12 = 3 \times 2 \times 2$ global patterns of modification, enumerated as shown (c) A hypothetical mod-form distribution, showing the proportions in the population of each of the 12 mod-forms, following the numbering used in (b). The mod-form distribution can be viewed as a probability distribution, which gives, for each mod-form, the probability of finding a substrate molecule in that mod-form. The vertical scale has been omitted to focus on qualitative aspects. (d) In current practice, only limited information may be available. The separate phosphoryl- and ubiquityl-modifications calculated from (c) are shown, with the phosphoryl-modifications given as site-specific stoichiometries (the proportion of unphosphorylated substrate and of substrate phosphorylated on each site). Such summaries lose considerable information compared to the underlying mod-form distribution, making it harder to infer correlations between modification states and downstream responses.

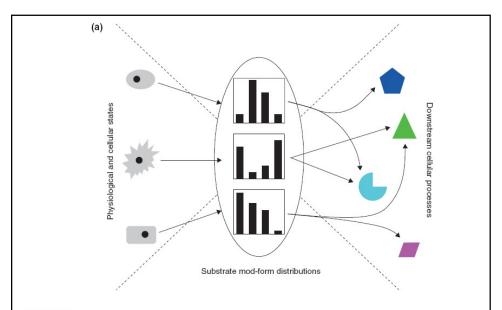


FIGURE 7 | Encoding of information by mod-form distributions. (a) A bow-tie architecture describes the behavior of many of the examples discussed here. Distinct physiological and cellular states on the left can be represented ('encoded') by distinct mod-form distributions of a single substrate at the center of the bow-tie ('fan-in'). Each mod-form distribution can then orchestrate its own mix of downstream cellular processes, as on the right ('fan-out'), Figure 1 of Ref 45 reflects a similar architecture for the particular case of SRC-3. The mod-form distribution plays a central role here as the quantitative representation of the encoded information.