

**Table 1.2 Mass Changes on Some Common Posttranslational Modifications of Protein Residues**

Type of Modification	Mass Changes	Example
Acetylation	42	Histone Lys N-acetylation
Amidation	-1	C-Terminal amide
Biotinylation	226	Pyruvate carboxylase
Carbamoylation	43	$\beta$ -Lactamase (D type)
$\gamma$ -Carboxylation	44	Glu residues in prothrombin
C-Mannosylation	162	Erythropoietin receptor
Cys sulfenic acid	16	NADH peroxidase
Deamidation	1	Rho (Gln <sub>63</sub> )
N-Terminal acyl diacylglyceride (tripalmitate)	789	Bacterial lipoproteins
Dimethylation	28	Histone Arg dimethylation
Farnesylation	204	Ras GTPase
Formylglycine	-17	Maturation of sulfatases
Geranylgeranylation	272	Rab GTPases
O-GlcNAc	203	Sp1 transcription factor
O-Glucosylation	162	Notch
N-Glycoproteins	>2000	Variable: Initial tetradecasaccharyl Glc <sub>3</sub> Man <sub>9</sub> GlcNAc <sub>2</sub> chain trimmed to many variants
GPI lipid anchors	>1000	Variable, depending on lipid and ethanolamine chains
Hydroxylation	16	HIF-1 $\alpha$
Lipoylation	188	Lipoyl transacetylase component of pyruvate dehydrogenase
Methylation	14	Histone Lys monomethylation
Myristoylation	210	Src kinase
Nitrosylation	29	Tubulin
Palmitoylation	238	Ras GTPase
Phosphorylation	80	Protein kinase A
Phosphopantetheinylation	339	Fatty acid synthase
Sulfation	80	CCR5 receptor
Transamidation	-17	Transglutaminase products
Trimethylation	42	Histone Lys N-trimethylation