Table S3. Salient features of protein sequences listed in Table S1 and Table S2 containing potential O-GlcNAc and phospho tyrosine binary switch.

Selection criteria #1 (No. of sequence listed - 17)	Selection criteria #2 (No. of sequence listed - 30)
1. Number of proteins with a proline residue at -/+1 and/or -/+3 position from known *O*-GlcNAc site: 10 (59%). respectively. 2. Proline residue within -/+ 5 residue from known *O*-GlcNAc site: 14 (82.%) 3. Number of proteins containing potential tyrosine phosphorylation site within -/+ 5 residue of known OGN site: 12 (71%).	1. Number of proteins with a proline residue at -/+1 and/or -/+3 position from potential *O*-GlcNAc site: 28 (93%). 2. Proline residue within -/+ 5 residue from a known phospho tyrosine site: 26 (87%). 3. Number of potential *O*-GlcNAc sites within -/+ 5 residues of known tyrosine phosphorylation site: 26 (87%).