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Supplemental information

An inventory of crosstalk between ubiquitination

and other post-translational modifications

in orchestrating cellular processes

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Data S1. Glossary and Inventory of the Resources Tables

1. **Acetyltransferase**: Group of enzymes that acetylate specific lysine amino acids on histones or non-histone proteins.

2. **Arginylation**: Post-translational modification mediated by arginyltransferase (ATE1), which catalyzes tRNA-dependent addition of arginine to proteins substrate.

3. **Autophagy**: Catabolic mechanism involved in protein degradation by the lysosome in the cytoplasm.

4. **Chromatin remodeling**: Process that consists of structural chromatin reorganization by displacing or removing proteins such as nucleosomes from the chromatin. These changes regulate chromatin condensation and opening states during transcription and DNA repair.

5. **Chromodomain**: Structural domain of proteins containing about 40–50 amino acid residues that recognize and bind methylated proteins.

6. **Cryptochrome genes**: Genes that encode for CRY (Cryptochrome Circadian Regulator) proteins, which were originally identified in plants as photoreceptor sensing blue light. It also controls the circadian rhythm and the circadian clock in plants.

7. **Deacetylases**: Enzymes that catalyse the removal of acetyl groups from proteins and reverse the acetylation process.

8. Demethylase: Class of enzymes that remove methyl group from substrates.

9. **Deubiquitinase**: Enzyme that reverses the reaction of ubiquitination by catalyzing the removal of ubiquitin from substrates.

10. **E3 ligases**: Components of the ubiquitin proteasome system that recognize protein substrates and catalyze their ubiquitination.

11. **ERAD system**: The Endoplasmic Reticulum-Associated Degradation (ERAD) is a multi-protein system that ensures protein quality control in the ER and induces protein degradation through the ubiquitin-proteasome system.

12. **FANCI/FANCD2 complex**: Heterodimeric complex that plays a crucial role in the interstrand crosslinks repair mechanism by the Fanconi anemia pathway.

13. **F-box domain**: Structural domain of F-box proteins that mediates proteinprotein interaction with the core ubiquitin ligase complex important for the ubiquitination process.

14. **FIST domain**: Intracellular signal transduction domain present in signal transduction proteins and might be involved in binding amino acid residues.

15. **H2AX**: Histone variant of H2A, which replaces conventional H2A in a subset of nucleosomes.

16. **HECT domain**: E3 ligase domain which receives first the ubiquitin from E2 enzyme and then promotes the attachment of ubiquitin to the substrate.

17. **Hox genes**: Development-associated genes which encode for transcription factors involved in the specification of the anterior-posterior body axis during embryonic development.

18. **Homologous recombination (HR)**: Double strand break repair pathway that uses the homologous sequence of the sister chromatid as a template to copy the genetic information for the DNA repair.

19. **IRX gene**: The Iroquois (Irx) gene encodes a homeoprotein transcription factor involved in embryonic development.

20. **Methyltransferases**: Class of enzymes that catalyse the transfer of a methyl group from S-adenosylmethionine onto the lysine or arginine residues of substrates.

21. **N and C-degrons**: Sequences within a protein, which act as destruction signals and target the protein for UPS-mediated degradation.

22. **NHEJ**: Double strand break repair pathway that consists in the direct ligation of broken DNA strands.

23. **OGT**: O-linked N-acetylglucosamine transferase, is an enzyme that catalyzes OGlcNAcylation, which consists of the addition of the N-acetyl glucosamine (OGlcNAc) monosaccharide molecule on the hydroxyl groups of threonine and serine residues.

24. **PARP**: The poly (ADP ribose) polymerase is a glycosyltransferase that synthetizes a polymer of ADP-ribose from NAD.

25. **PCNA**: Proliferating cell nuclear antigen is a multifunctional protein that plays a central role in stimulating DNA polymerases, promoting processive DNA synthesis and is also involved in DNA repair.

26. **PEPCK1**: Phosphoenolpyruvate Carboxykinase is a gluconeogenic enzyme which converts oxaloacetate into CO2 and phosphoenolpyruvate.

27. **Period genes**: Genes that encode for the proteins PER (Period Circadian Regulator) which control circadian rhythms.

28. **PHD domain:** Plant homeodomain is a type of zinc finger domain which promotes protein-protein interactions and acts as a PTM reader of histone.

29. **Polycomb group complex**: Transcriptional repressors which modify several histones and proteins and play a crucial role in gene silencing during development.

30. **Reader protein**: Protein containing a reader domain used to recognize a specific PTM on substrates.

31. **Ribonuclease**: Enzyme that interacts with RNA and catalyzes its degradation.

32. **RING domain**: E3 ligase domain involved in the ligation of ubiquitin to the substrate through interaction with the E2-conjugating enzyme.

33. **SBD domain**: Sugar-binding domain of Fbs1 protein that recognizes sugar chains such as Man(3)GlcNAc(2) and allows the ubiquitination of glycoproteins.

34. **SENP proteases**: Enzymes that mediate removal of SUMO from protein substrates.

35. **STUbL**: E3 ligase that recognizes SUMOylated proteins to promote their ubiquitination.

36. **Tankyrases**: Poly(ADP-ribosyl) transferase enzymes that contain an ankyrin repeat protein-interaction domain and are involved in various cellular functions.

37. **Translesion DNA synthesis**: DNA damage tolerance mechanism where TLS polymerase bypasses a DNA lesion during replication.

38. **TUDOR domain**: Structural domain that acts as a reader and binds methylated arginine or methylated lysine residues.

39. **WW domain**: Small protein domain which has two conserved tryptophan residues. WW domain interacts with short proline-rich peptide, protein containing

proline motifs ([AP]-P-P-[AP]-Y) or phosphoserine and phosphothreonine-containing motifs.

40. **WWE domain**: Protein-protein interaction domain containing two conserved tryptophan residues. This domain can mediate protein-ADP-ribose interaction.

41. **ZZ domain**: The ZZ-type zinc finger domain is an unusual zing finger, which bind two zinc ions and is involved in protein-protein interactions.