

Rule	Effect in TP	Process with role in CSML	HFPNe diagram
1-1	binding phosphorylation cleavage ubiquitination processing sumoylation dephosphorylation acetylation degradation exchange oligomerization hydrolysis translocation automodification; phosphorylation	ME_Binding ME_Phosphorylation ME_Cleavage ME_Ubiquitination ME_Processing ME_Sumoylation ME_Dephosphorylation ME_Acetylation ME_Degradation ME_Exchange ME_Dimerization ME_Hydrolysis ME_Translocation ME_AutoPhosphorylation	
1-2	binding; regulation of localization binding; regulation of protein activity binding; phosphorylation binding; oligomerization	ME_Binding with role MR_Regulation_of_Localization MR_Regulation_of_Protein_Activity MR_Phosphorylation MR_Dimerization	
1-3	dissociation; phosphorylation	ME_Dissociation with role MR_Phosphorylation	
2-1	increase of abundance increase of secretion increase of phosphorylation decrease of phosphorylation increase of processing activation increase of binding decrease of binding transactivation	ME_UnknownProcess ME_UnknownProcess ME_Phosphorylation ME_Phosphorylation ME_Processing ME_UnknownActivation ME_Binding ME_Binding ME_Transcription	
2-2	activation; increase of phosphorylation activation; increase of abundance	ME_Phosphorylation with role MR_Activation ME_UnknownProcess with role MR_Activation	
2-3	transrepression	ME_Transcription	
2-4	regulation of localization regulation of phosphorylation	ME_Translocation ME_Phosphorylation	
3-1	decrease of abundance decrease of secretion activation; binding decrease of protein stability degradation; destabilization	ME_UnknownProcess ME_UnknownProcess ME_Binding ME_ProteasomeDegradation ME_ProteasomeDegradation	
3-2	inhibition	ME_UnknownProcess	
4-1	DNA binding DNA binding; transactivation	ME_DnaBinding (p1) and ME_Transcription (p2)	
4-2	DNA binding; transrepression		
4-3	DNA binding; transregulation		
5-1	expression	ME_Transcription (p1) and ME_Translation (p2)	
5-2	activation; expression	ME_Transcription (p1) and ME_Translation (p2)	
6-1	regulation of activity regulation of protein activity	ME_UnknownInactivation (p1) and ME_UnknownActivation (p2)	
6-2	regulation of abundance regulation of secretion	ME_UnknownProcess (p1) and ME_UnknownProcess (p2)	
7	predicted	ME_Translation	