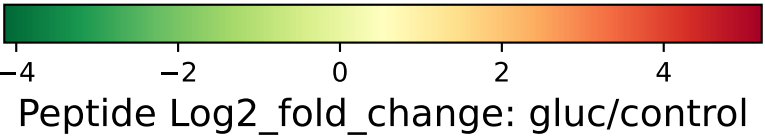
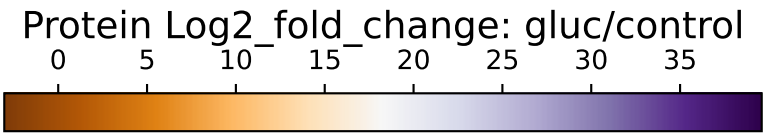
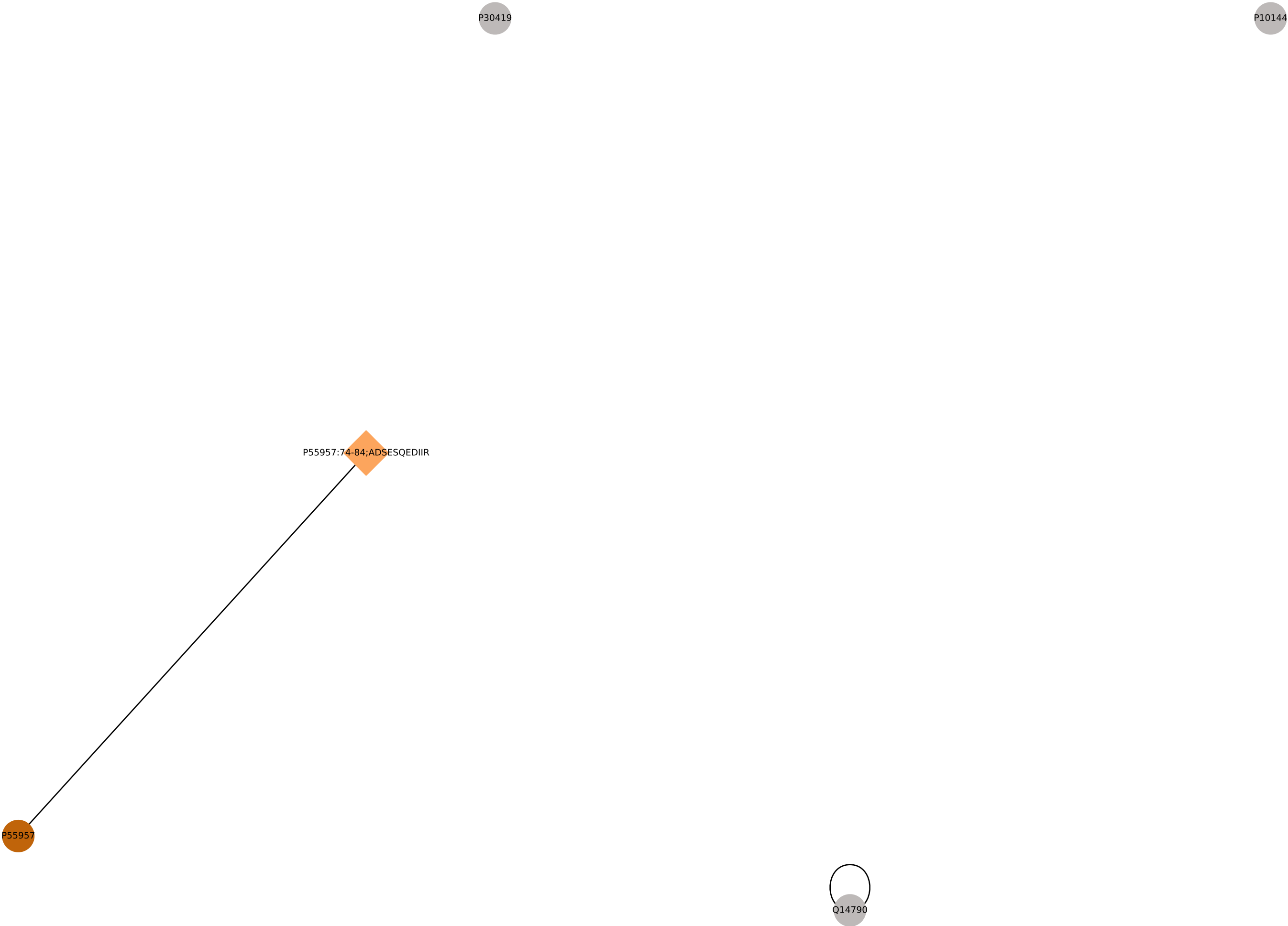
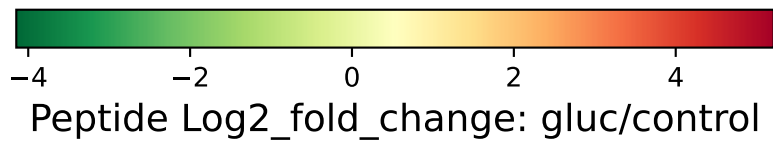
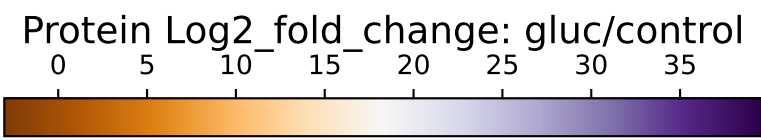
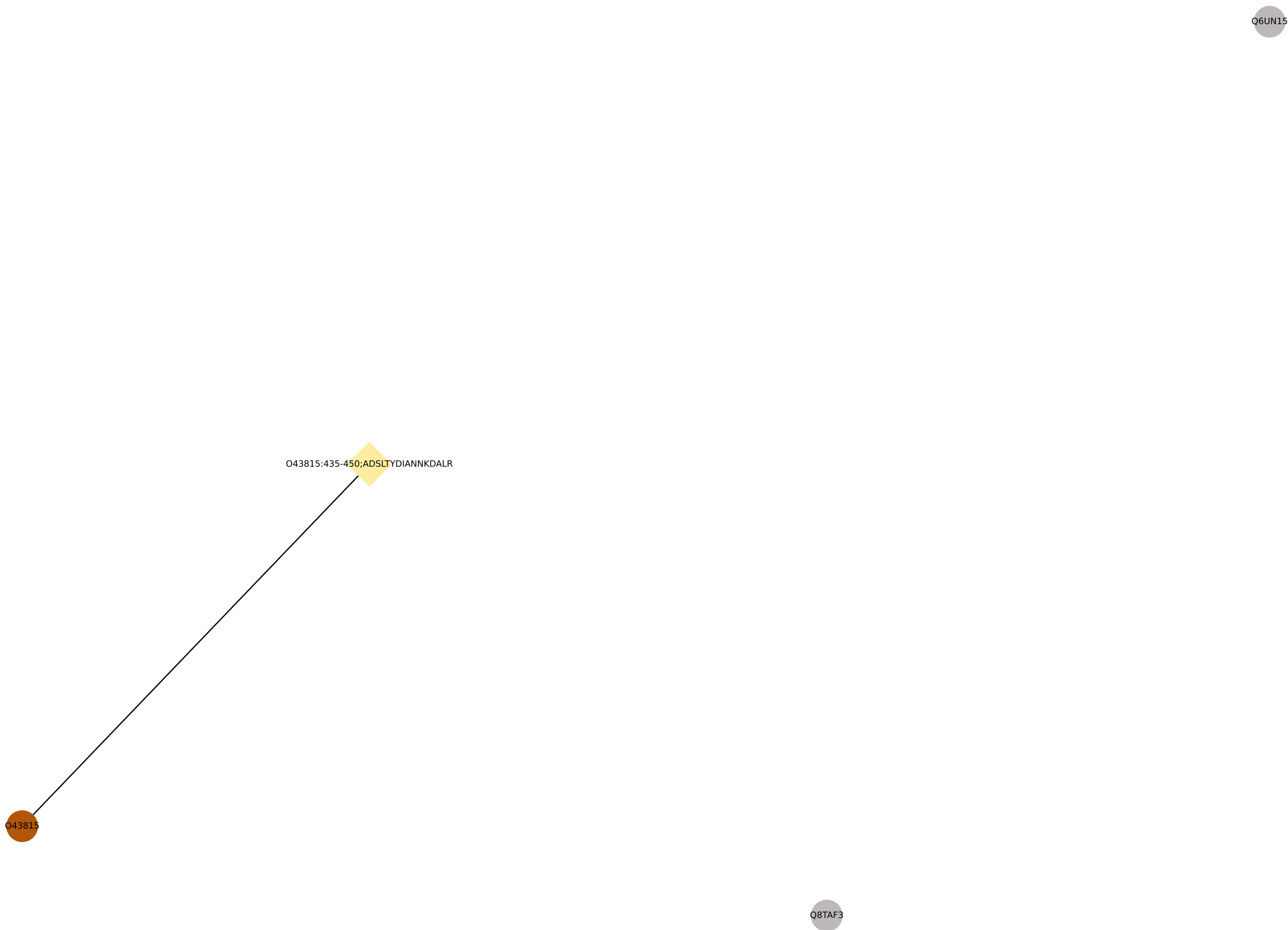


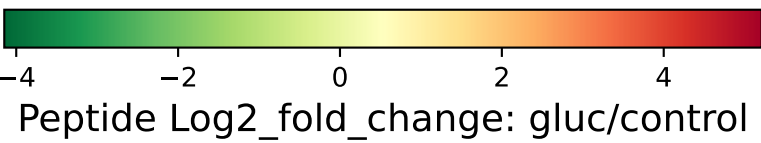
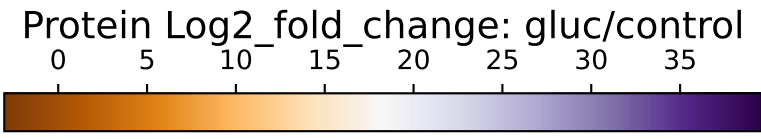
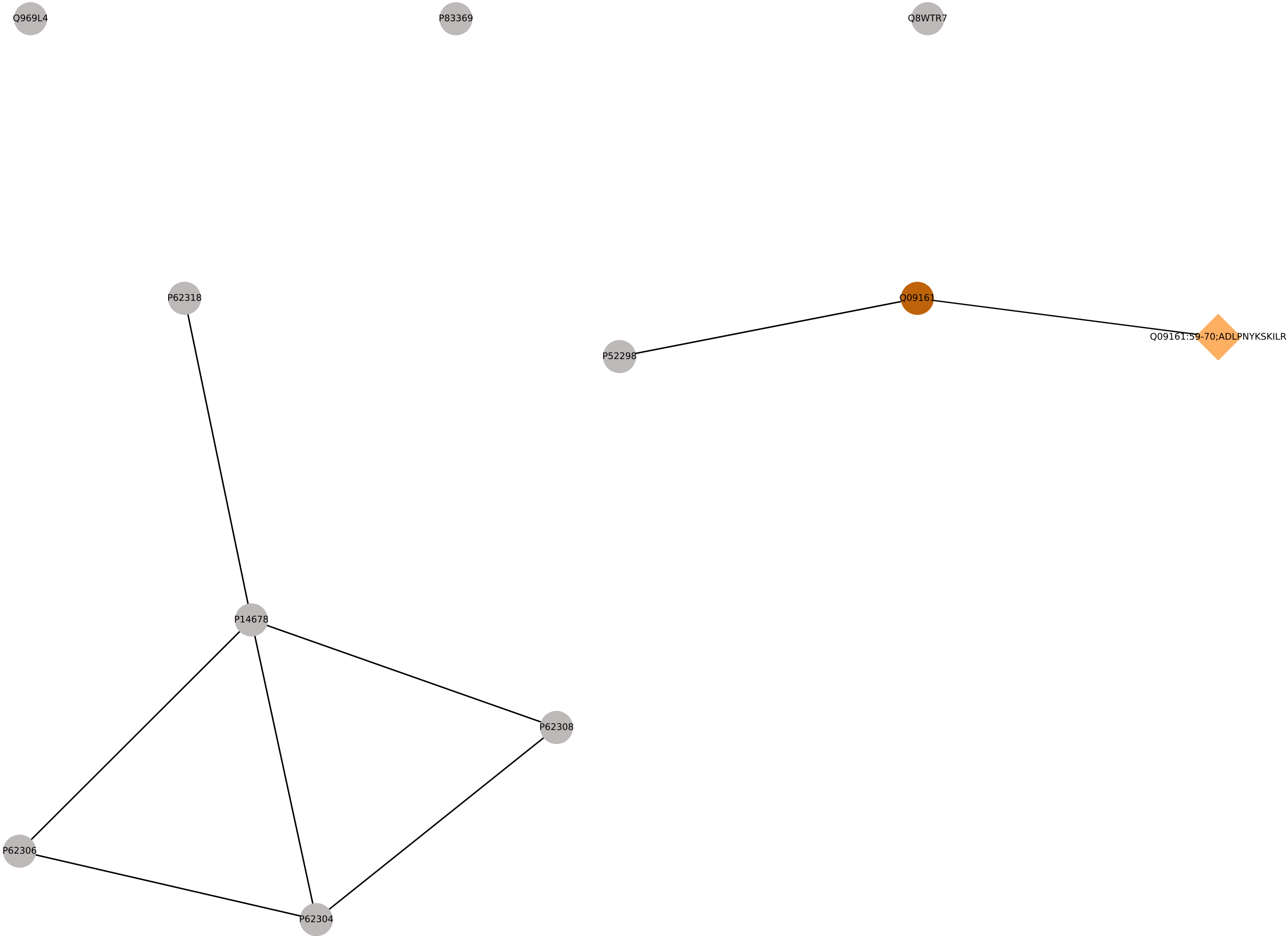
Log2_fold_change: gluc/control
R-HSA-75108: Activation, myristoylation of BID and translocation to mitochondria
p-value: 0.0151760001661293



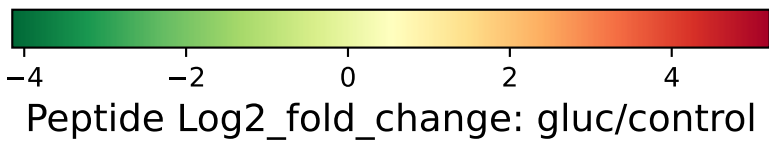
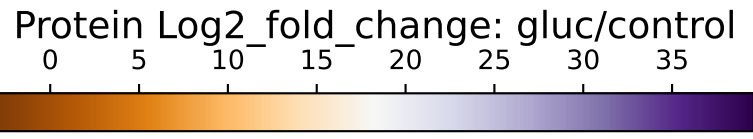
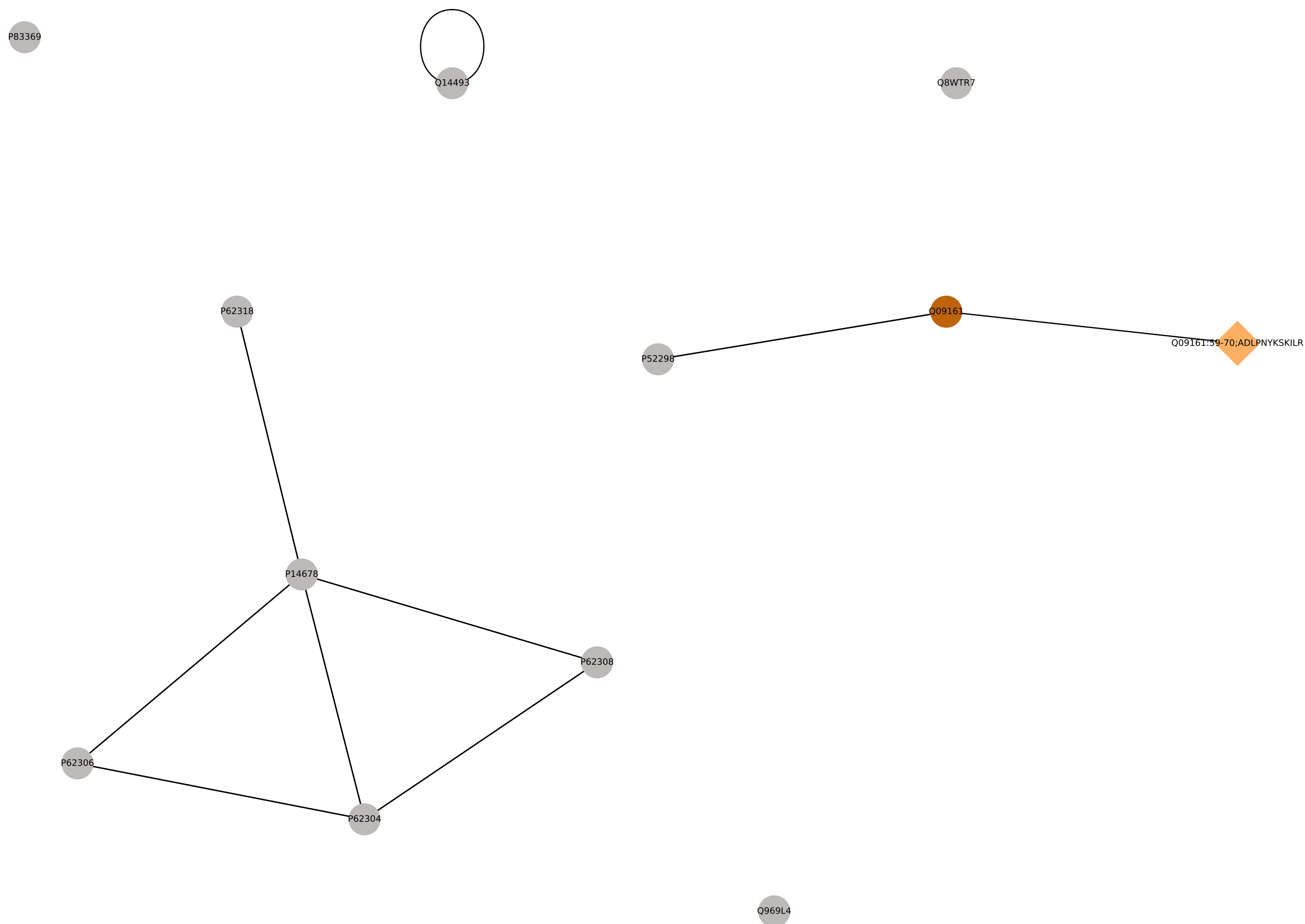
Log2_fold_change: gluc/control
R-HSA-9673766: Signaling by cytosolic PDGFRA and PDGFRB fusion proteins
p-value: 0.01893449482309495



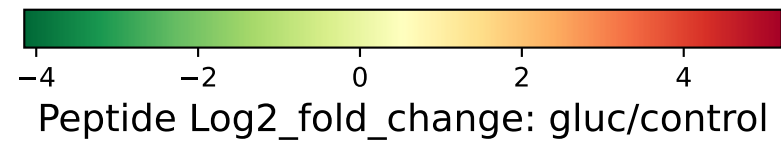
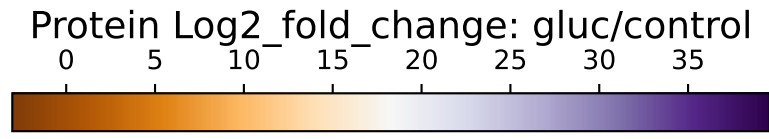
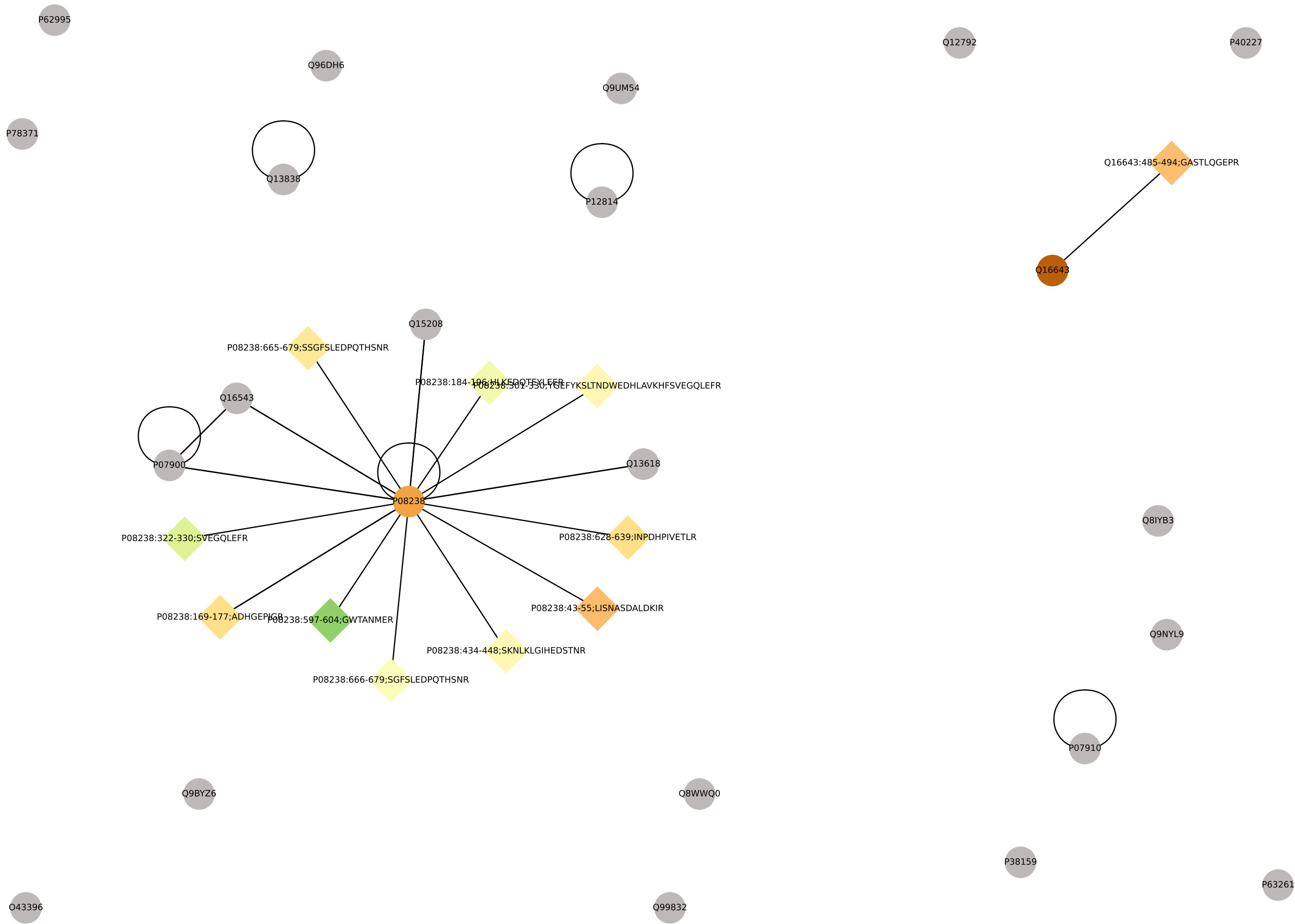
Log2_fold_change: gluc/control
R-HSA-111367: SLBP independent Processing of Histone Pre-mRNAs
p-value: 0.03751654060258469



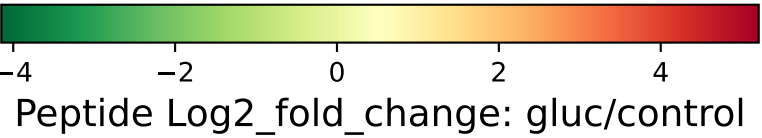
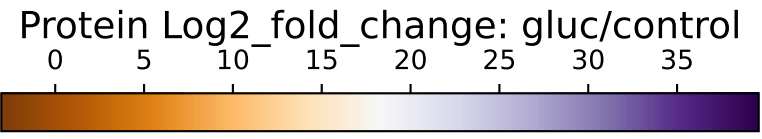
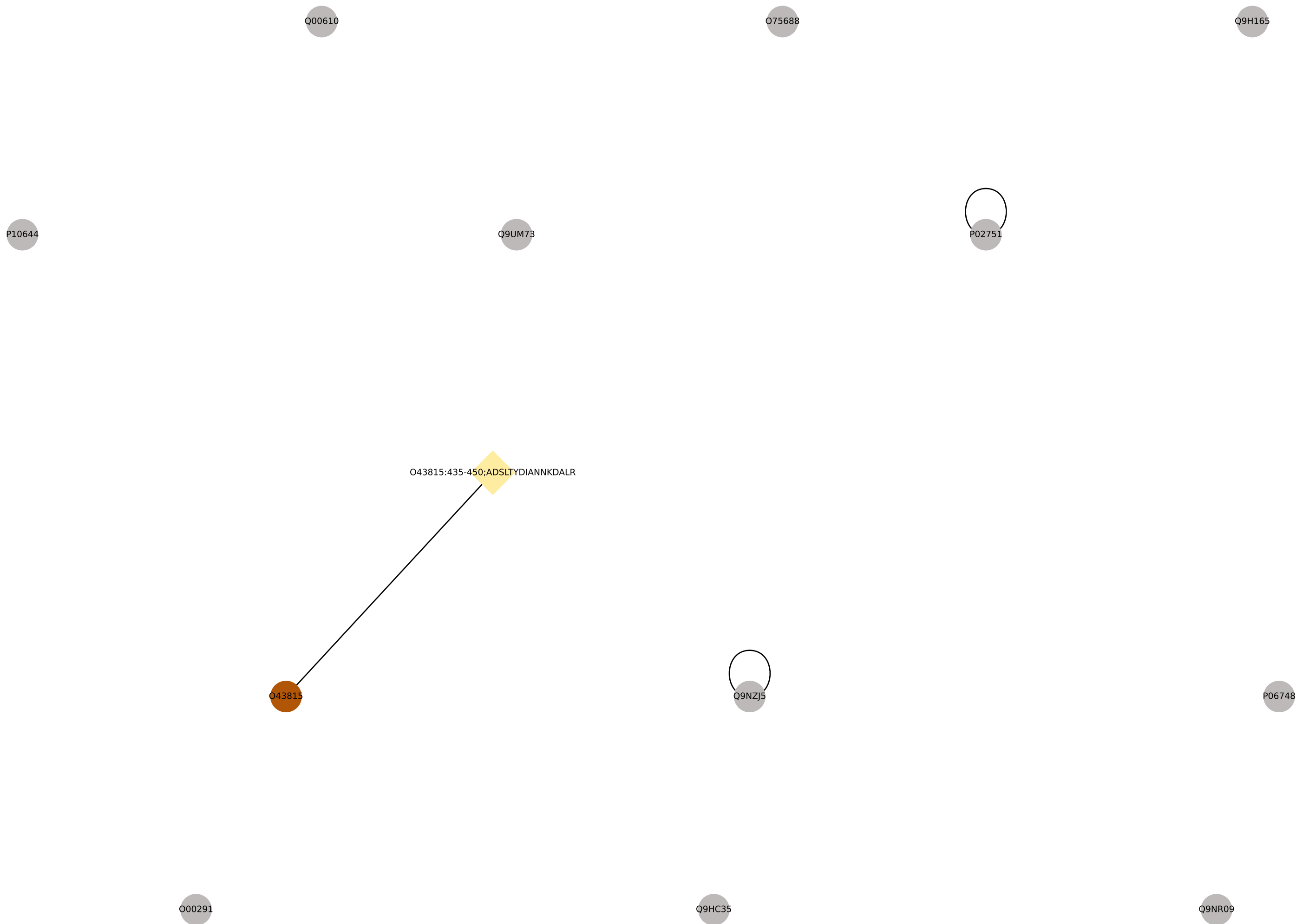
Log2_fold_change: gluc/control
R-HSA-77588: SLBP Dependent Processing of Replication-Dependent Histone Pre-mRNAs
p-value: 0.04119122530952668



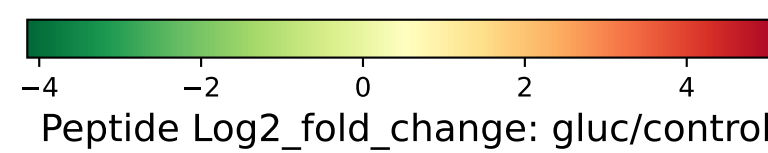
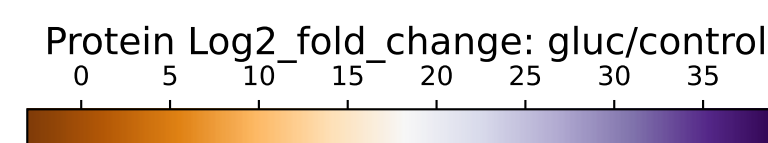
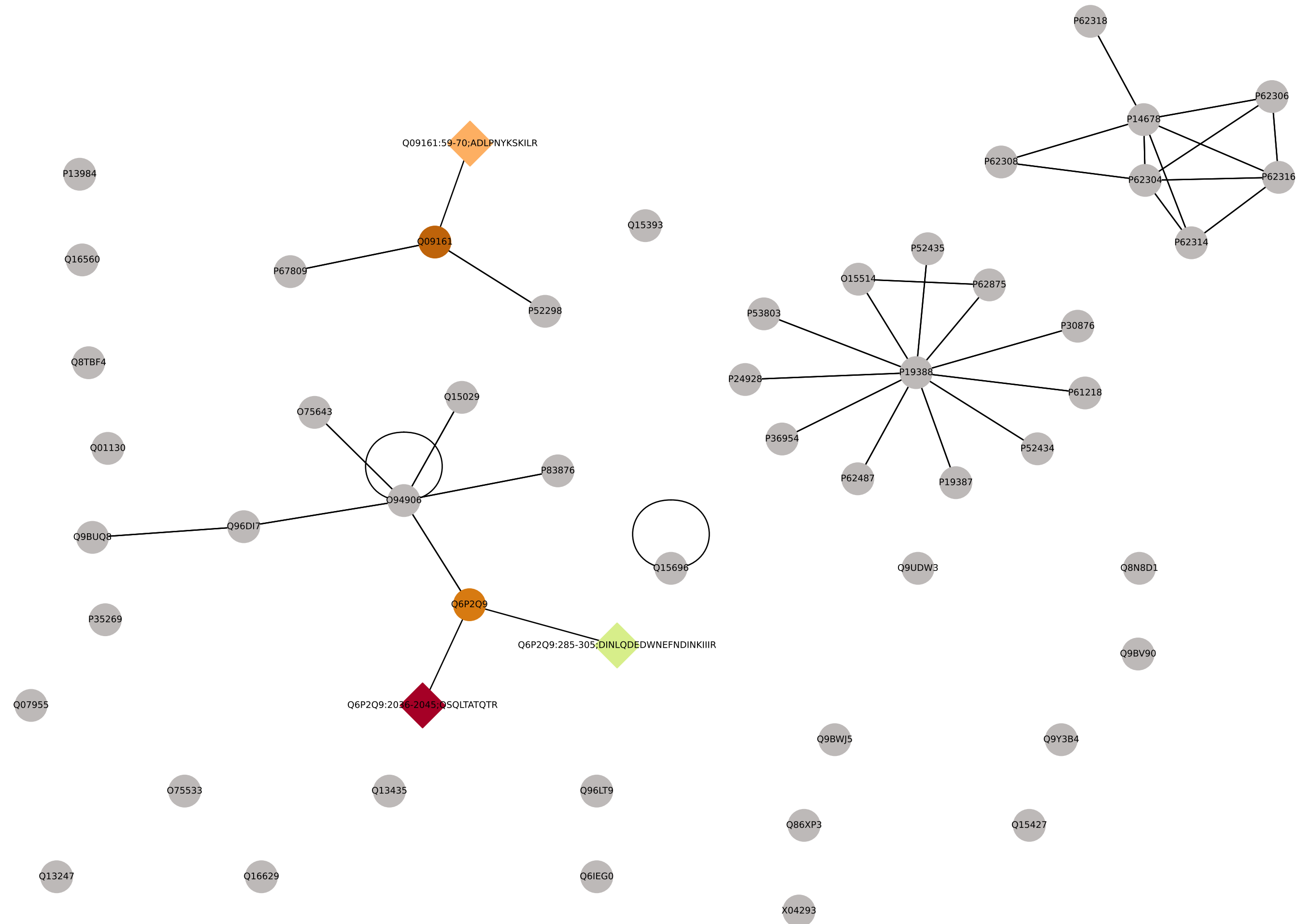
Log2_fold_change: gluc/control
R-HSA-9013418: RHOBTB2 GTPase cycle
p-value: 0.0038992971180269453



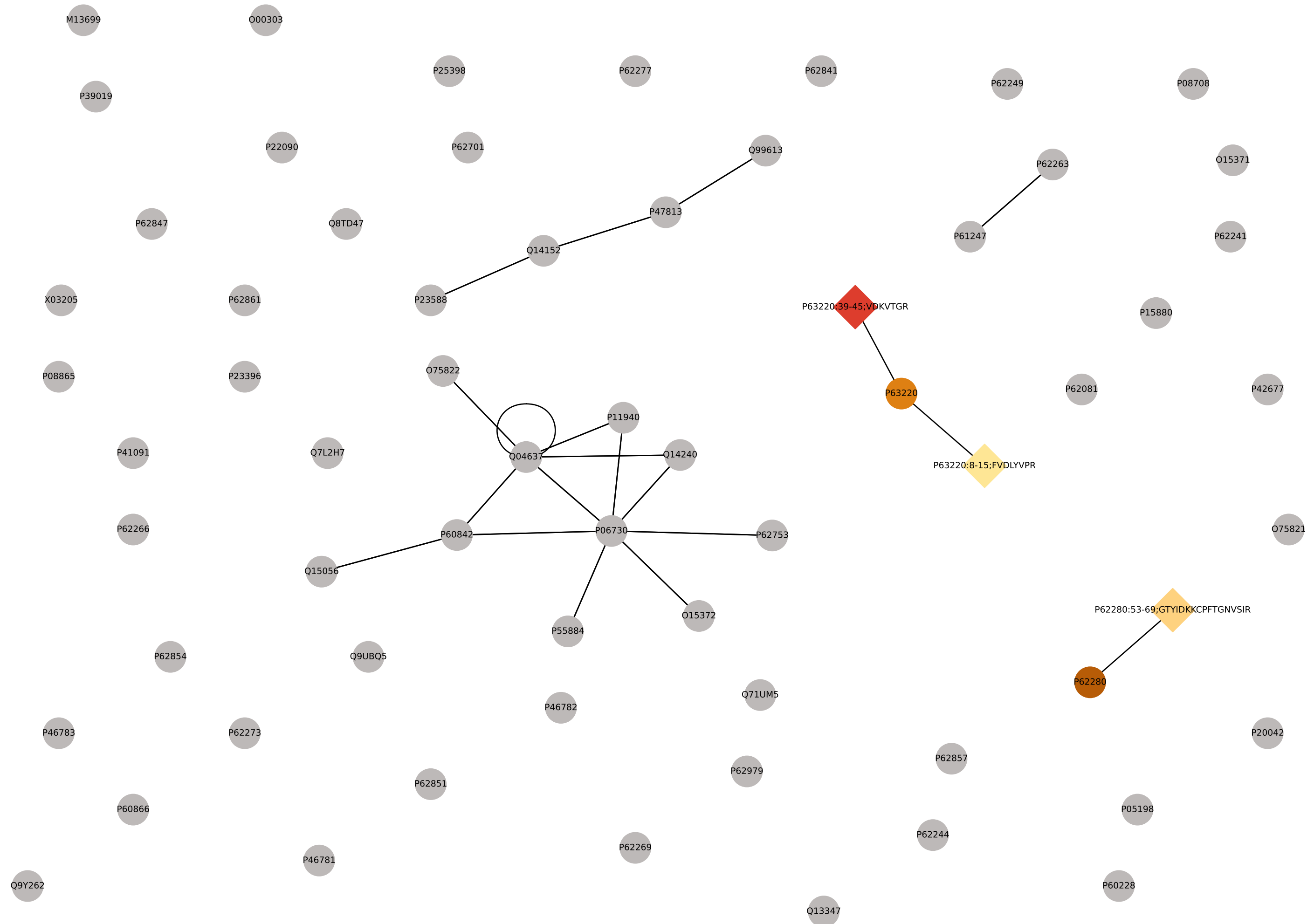
Log2_fold_change: gluc/control
R-HSA-9700645: ALK mutants bind TKIs
p-value: 0.04485212134737271



Log2_fold_change: gluc/control
R-HSA-72165: mRNA Splicing - Minor Pathway
p-value: 0.01834940897301718



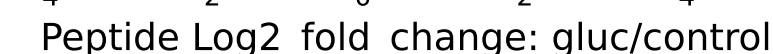
Log2_fold_change: gluc/control
R-HSA-72649: Translation initiation complex formation
p-value: 0.02372468033749031



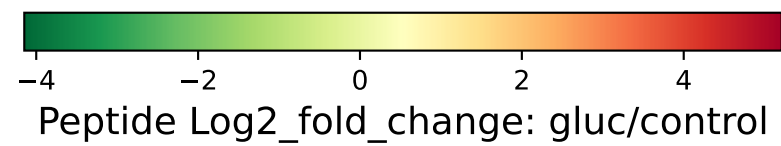
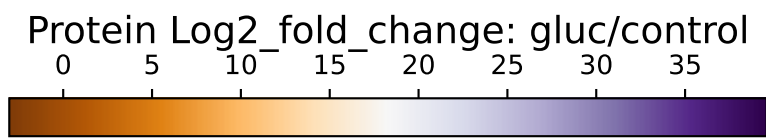
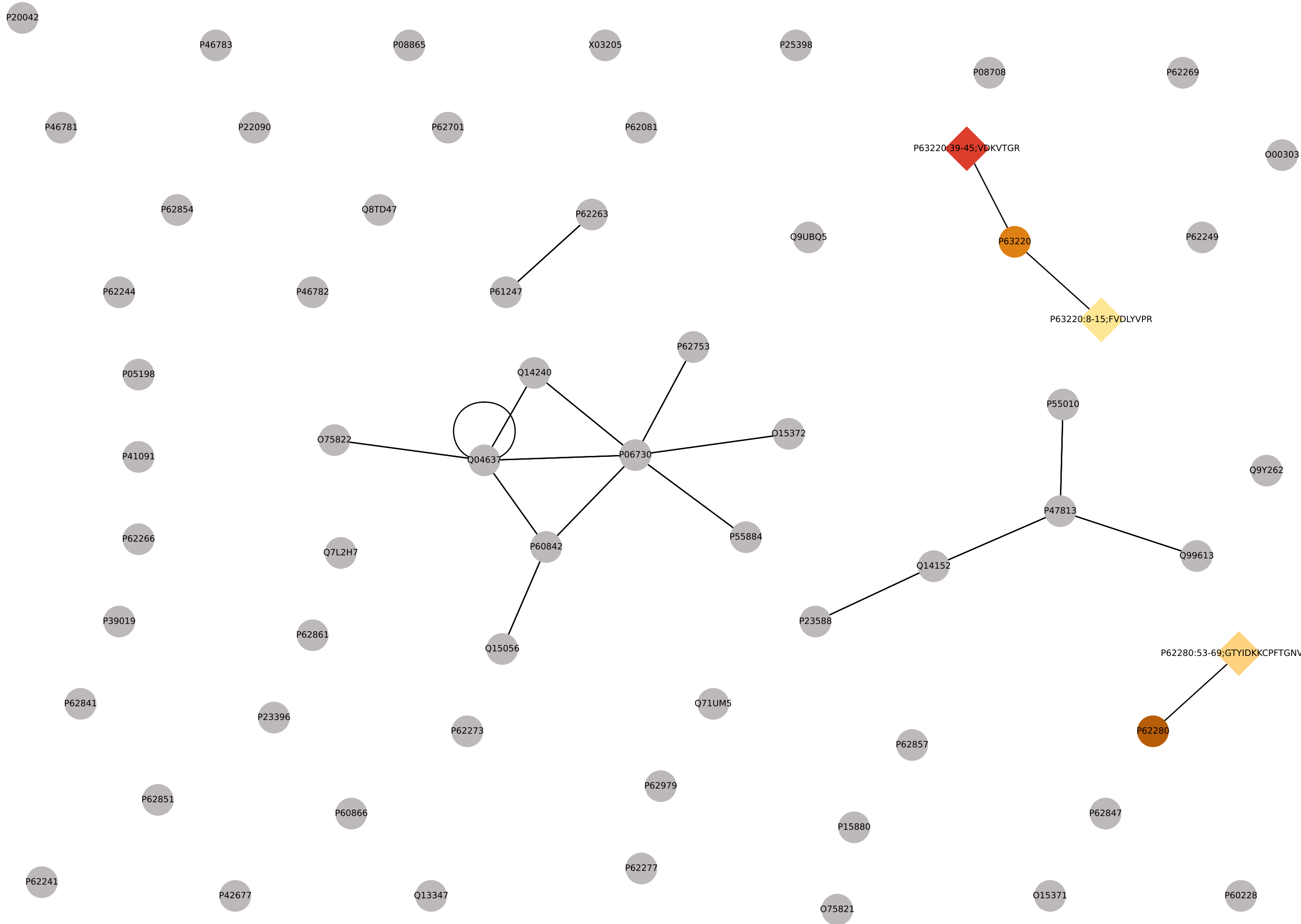
Protein Log2_fold_change: gluc/control



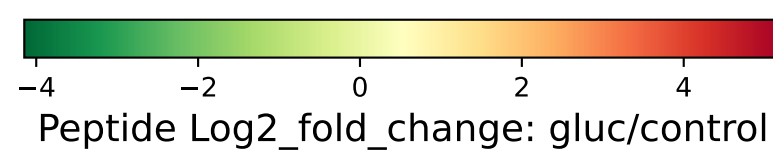
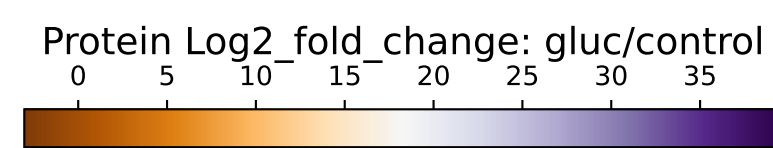
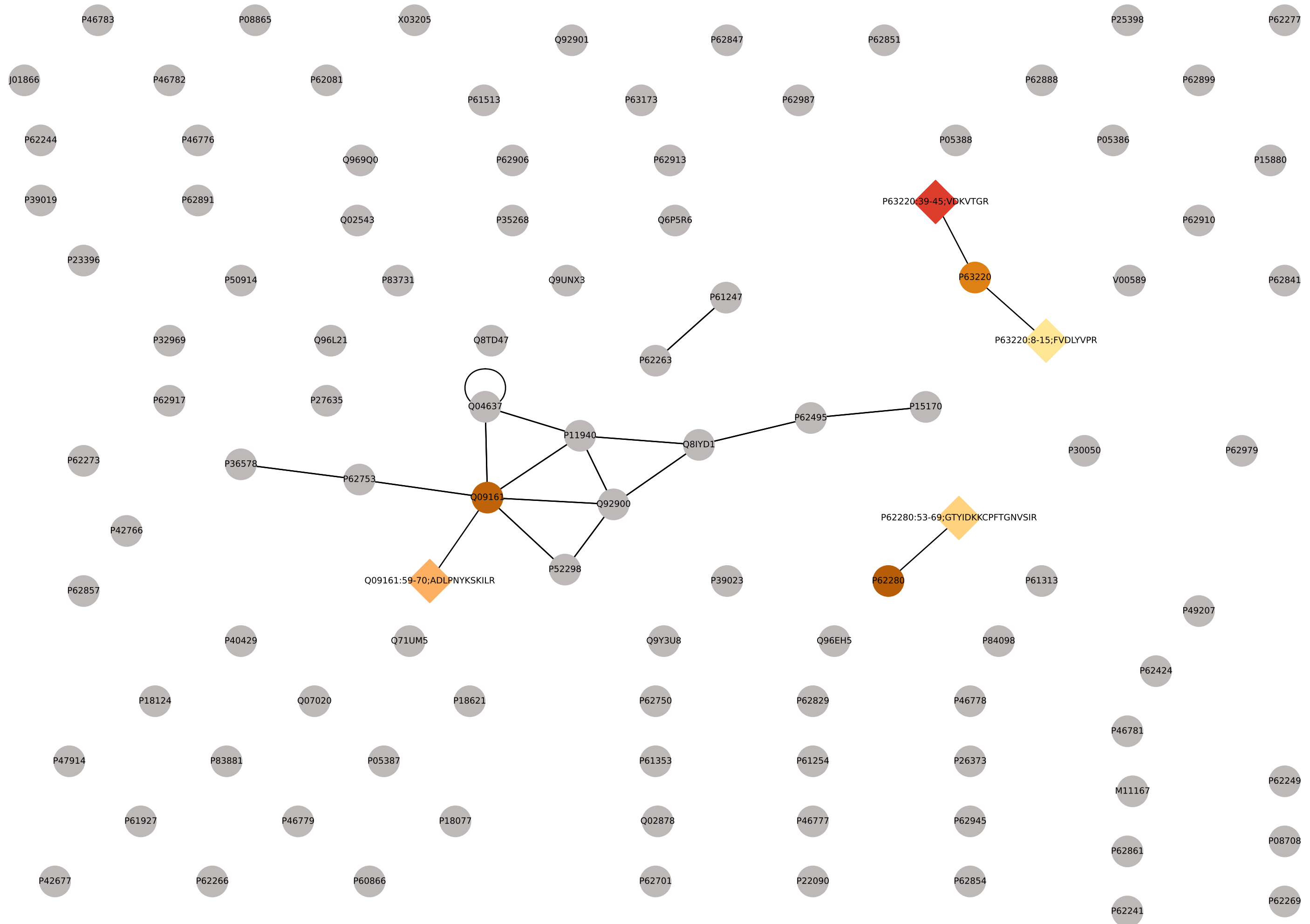
Peptide Log2_fold_change: gluc/control



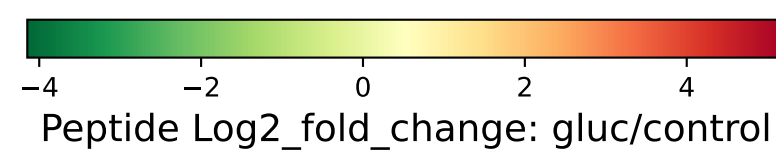
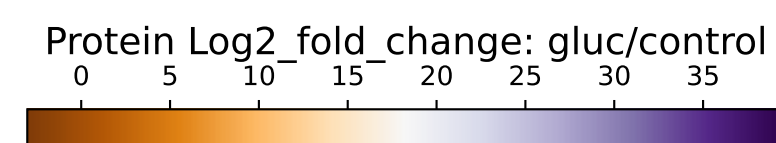
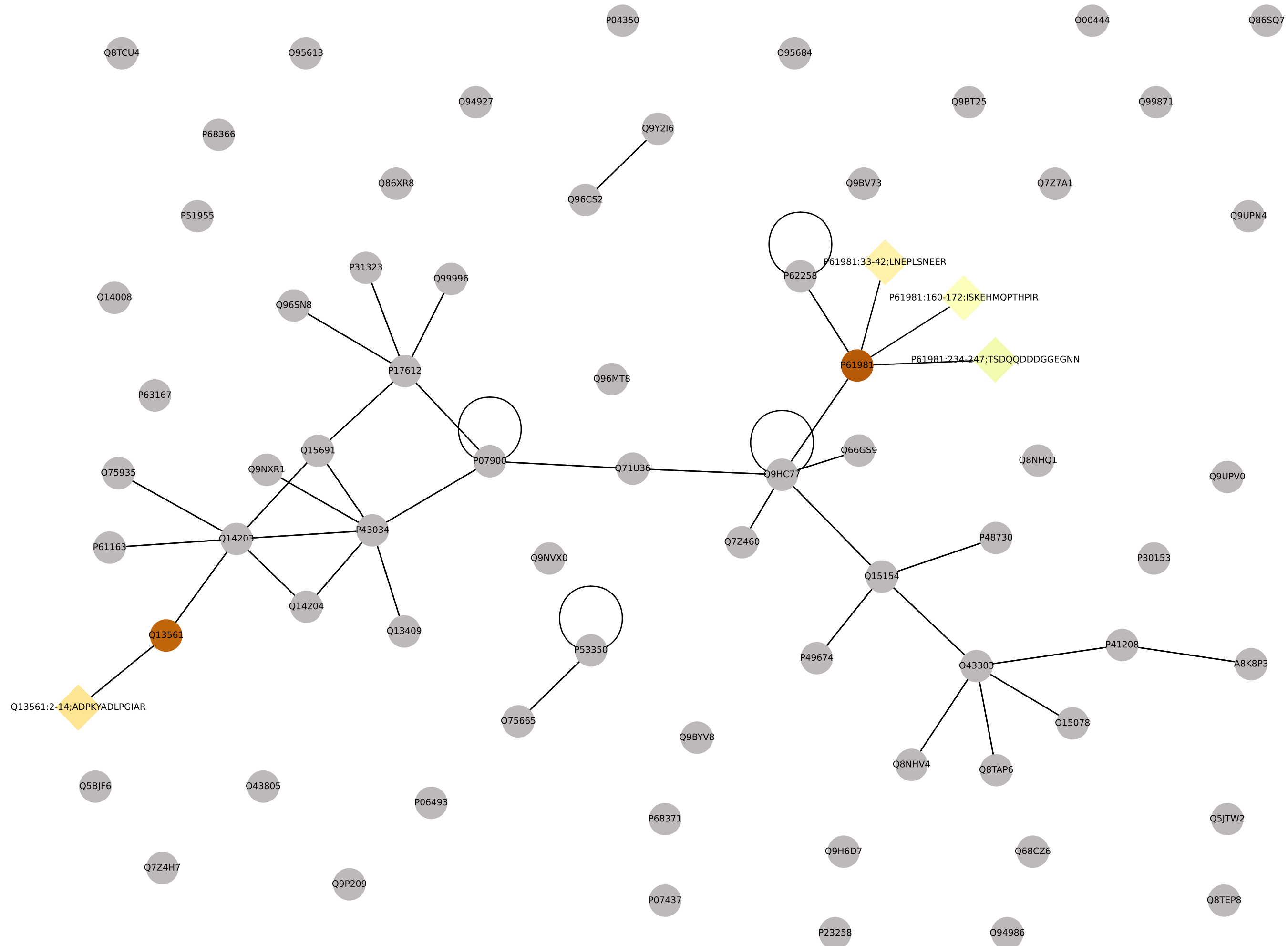
Log2_fold_change: gluc/control
R-HSA-72702: Ribosomal scanning and start codon recognition
p-value: 0.025157961205597323



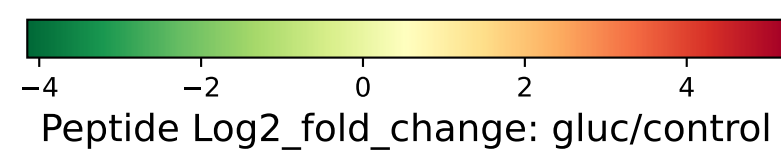
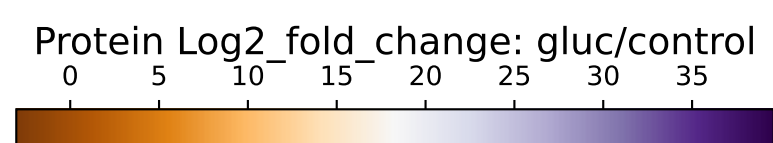
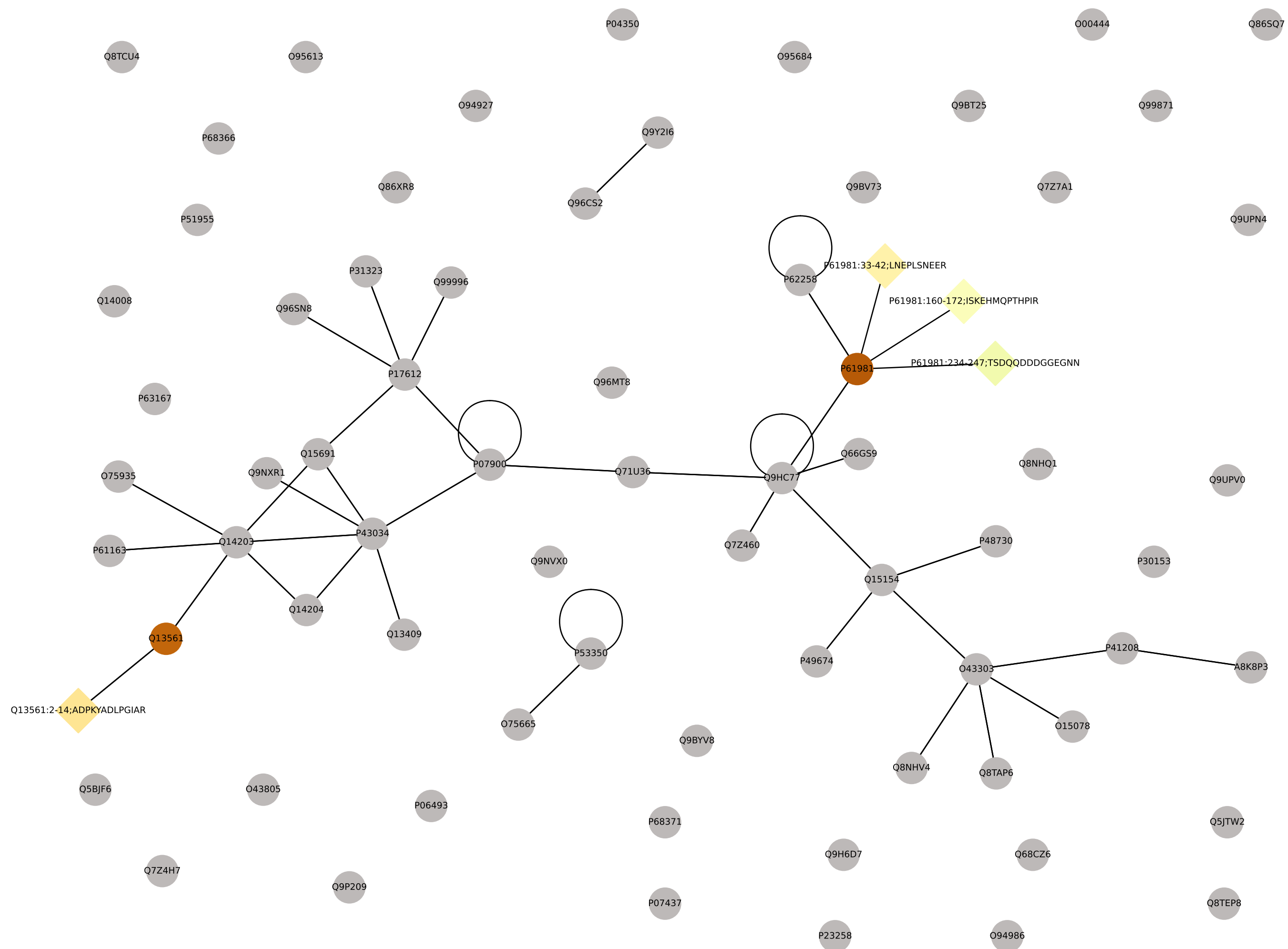
Log2_fold_change: gluc/control
R-HSA-975956: Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC)
p-value: 0.0069285827914021825



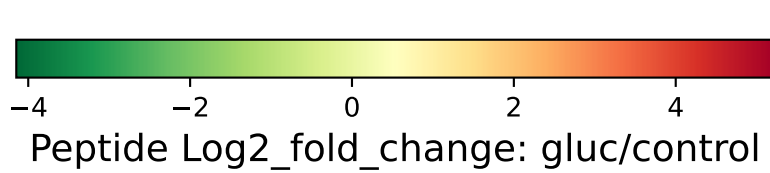
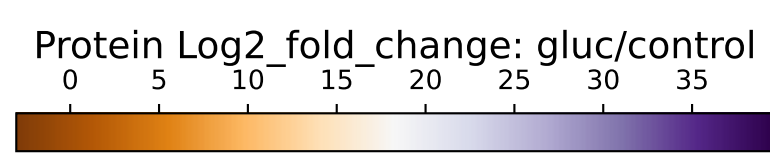
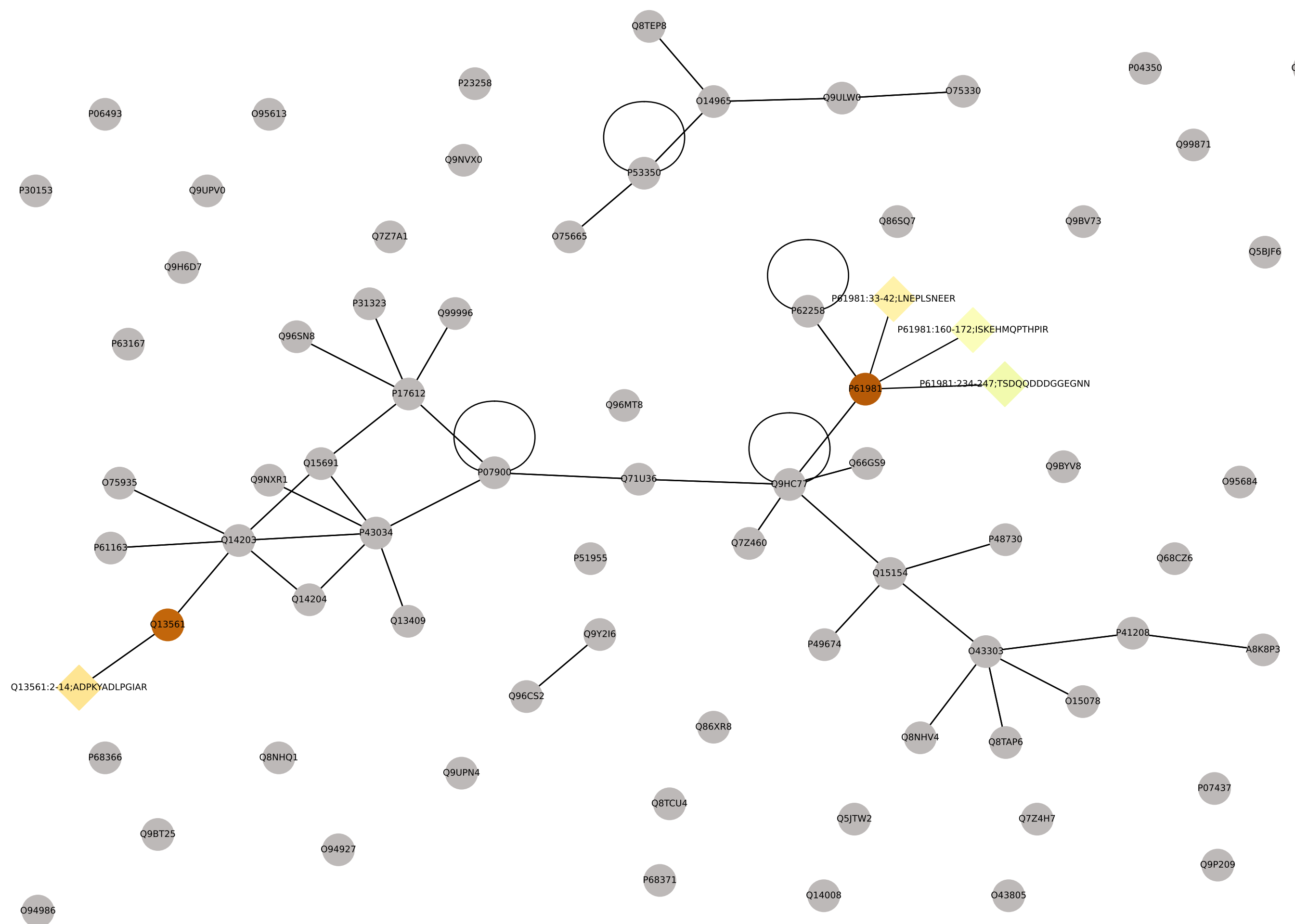
Log2_fold_change: gluc/control
R-HSA-380284: Loss of proteins required for interphase microtubule organization from the centrosome
p-value: 0.030442907302830946



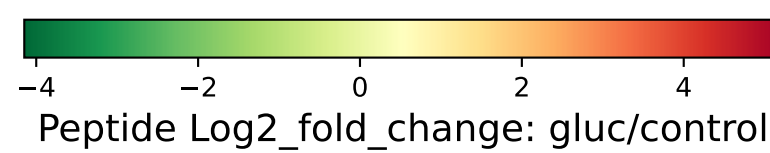
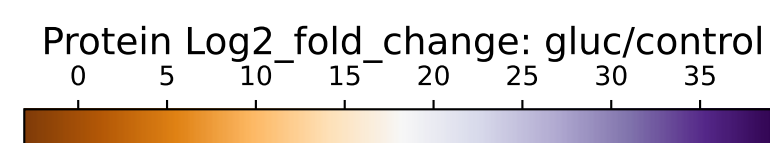
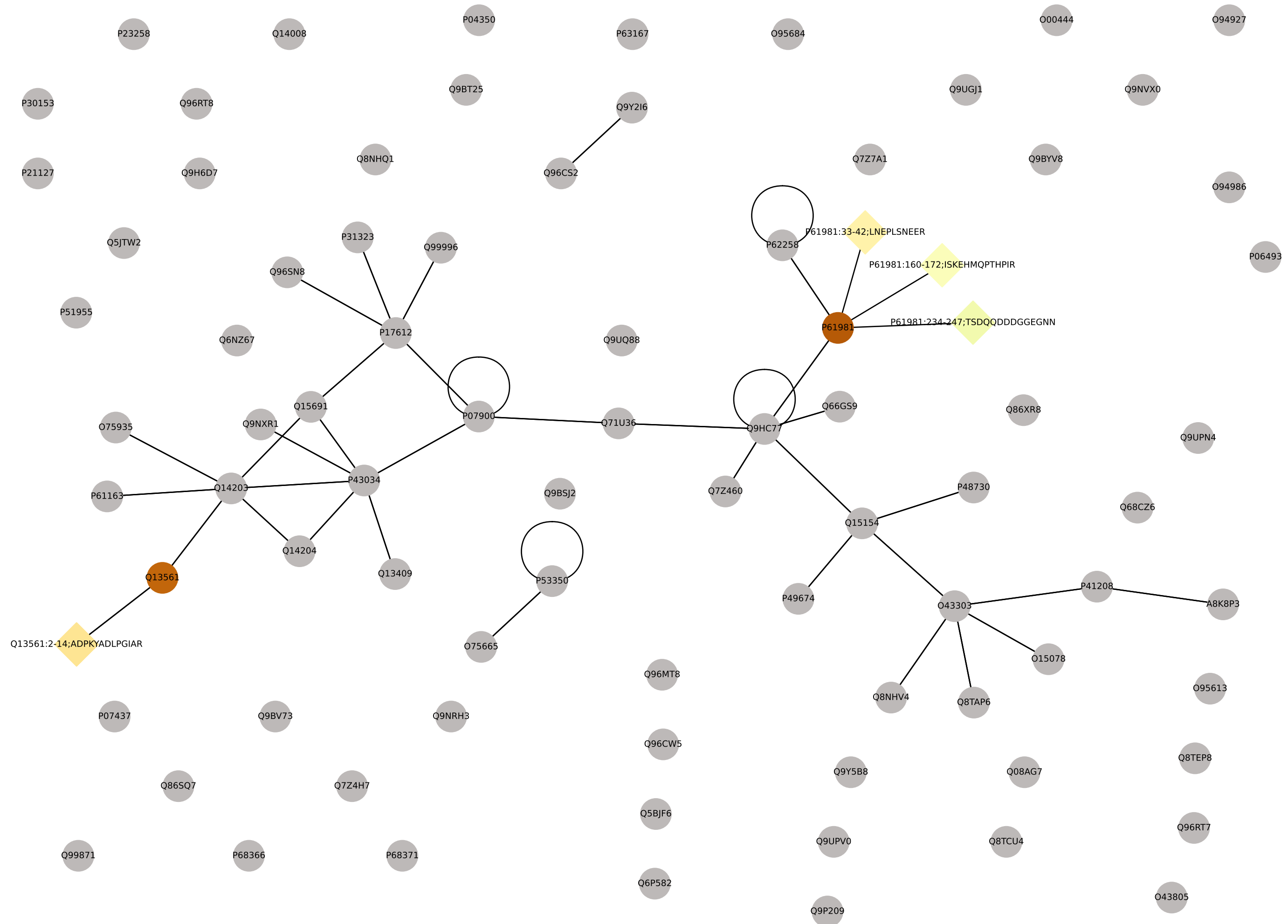
Log2_fold_change: gluc/control
R-HSA-380259: Loss of Nlp from mitotic centrosomes
p-value: 0.030442907302830946



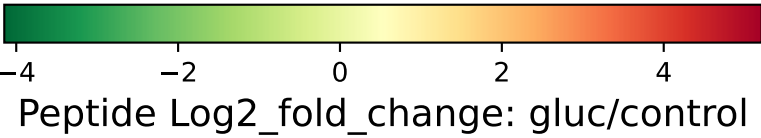
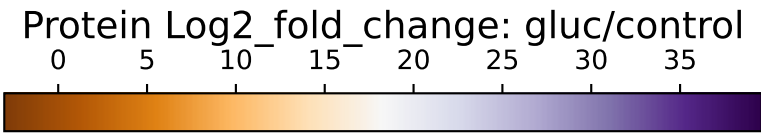
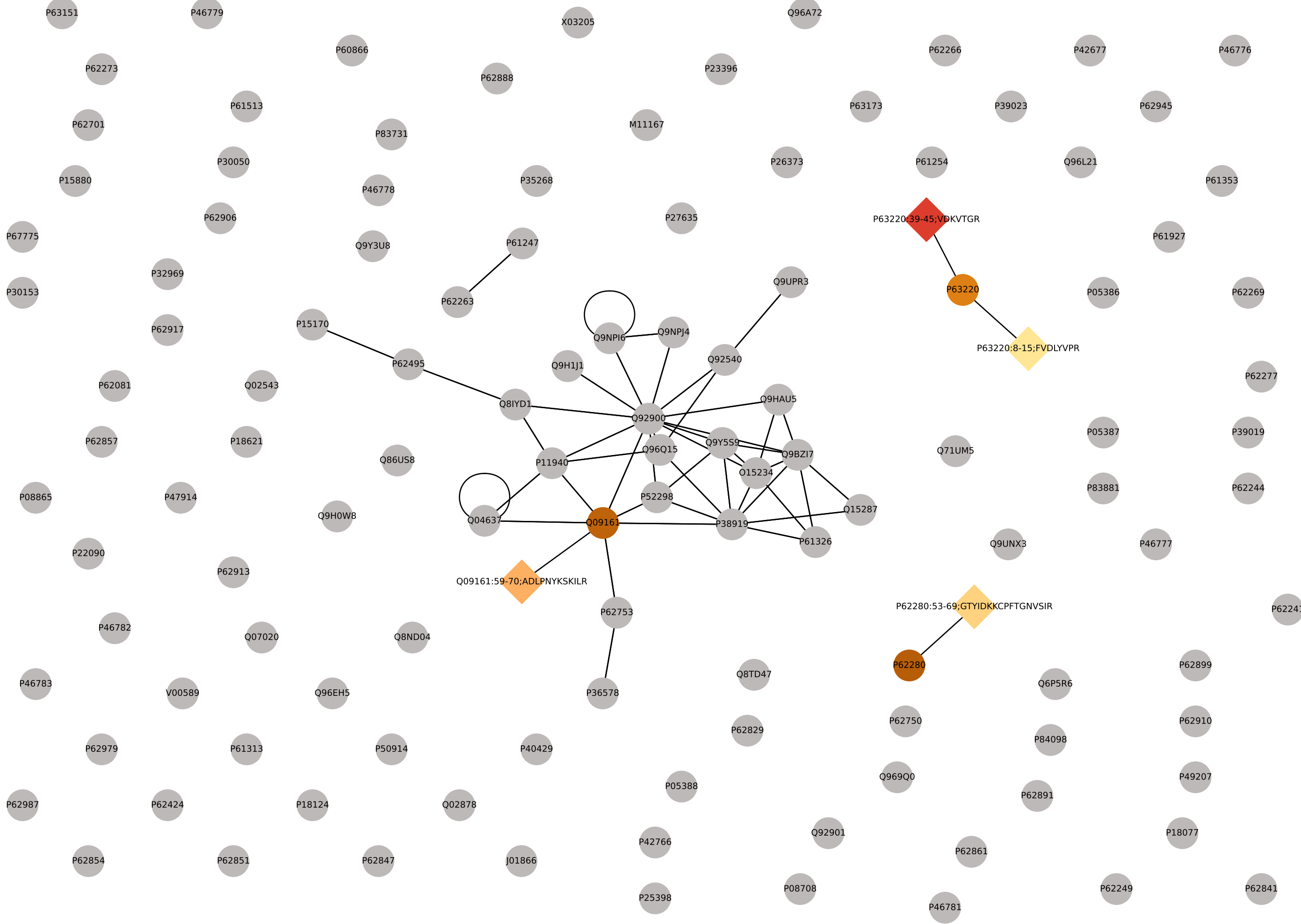
Log2_fold_change: gluc/control
R-HSA-8854518: AURKA Activation by TPX2
p-value: 0.032831364399555585



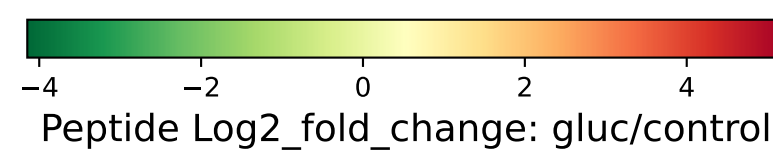
Log2_fold_change: gluc/control
R-HSA-380270: Recruitment of mitotic centrosome proteins and complexes
p-value: 0.038678528314858074



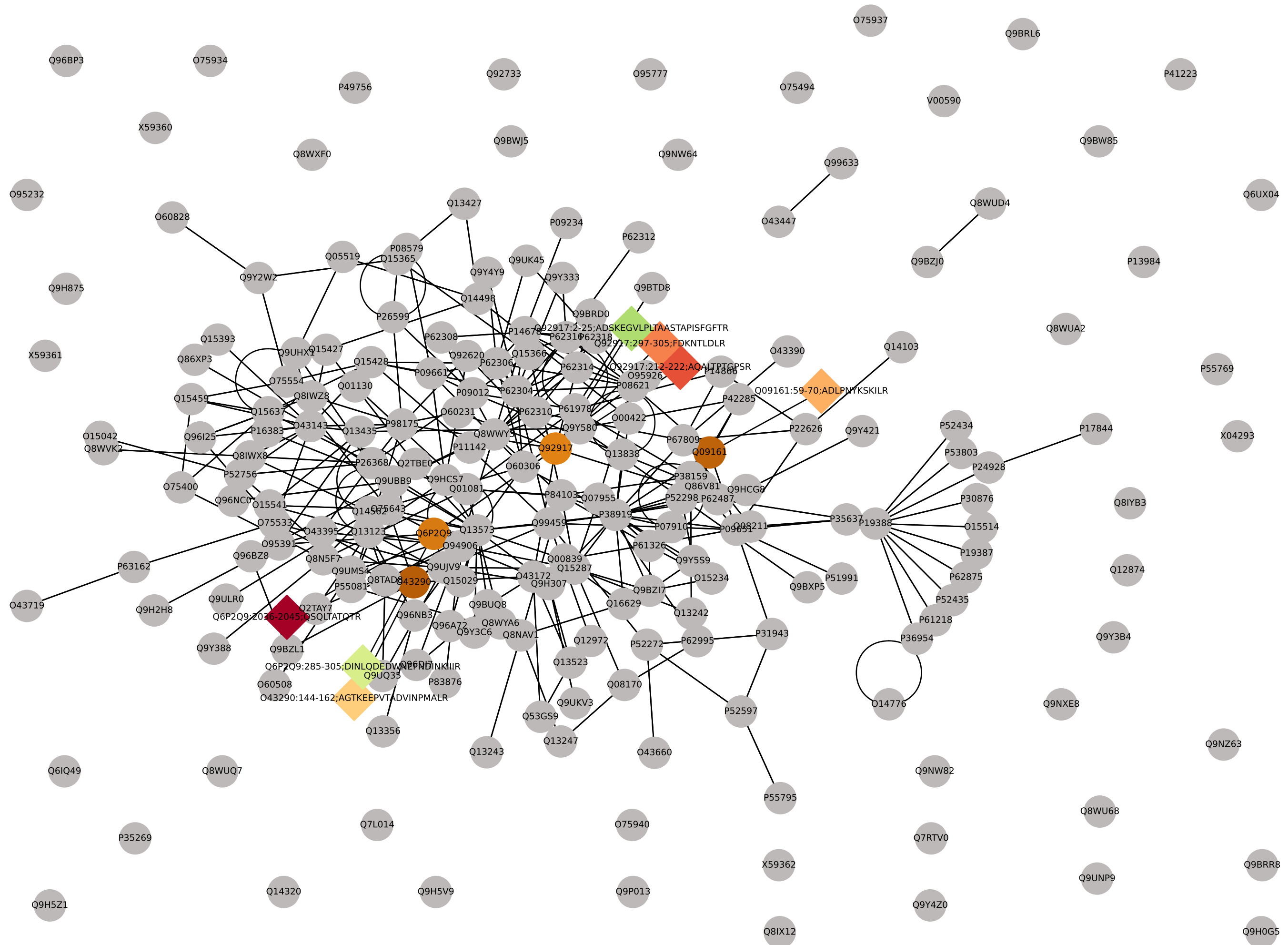
Log2_fold_change: gluc/control
R-HSA-927802: Nonsense-Mediated Decay (NMD)
p-value: 0.012056147753095936



The diagram illustrates a network of protein interactions. The nodes are represented by grey circles, each labeled with a UniProt ID. Two nodes are highlighted in orange: Q13561 and P61981. Three regions are highlighted in yellow: Q13561:2-14;ADPKYADLPGIAR, P61981:33-42;LNEPLSNEER, and P61981:160-172;ISKHEMQPHTPIR. The diagram shows a complex web of connections between various proteins, with some nodes having multiple connections and others being isolated.



Log2_fold_change: gluc/control
R-HSA-72163: mRNA Splicing - Major Pathway
p-value: 0.009025927255451371



Log2_fold_change: gluc/control
R-HSA-72172: mRNA Splicing
p-value: 0.010705014590971396

