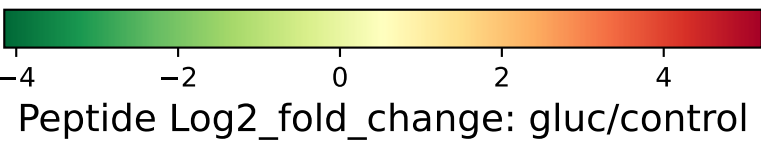
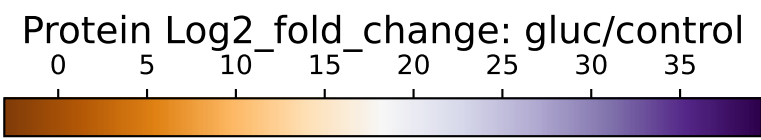
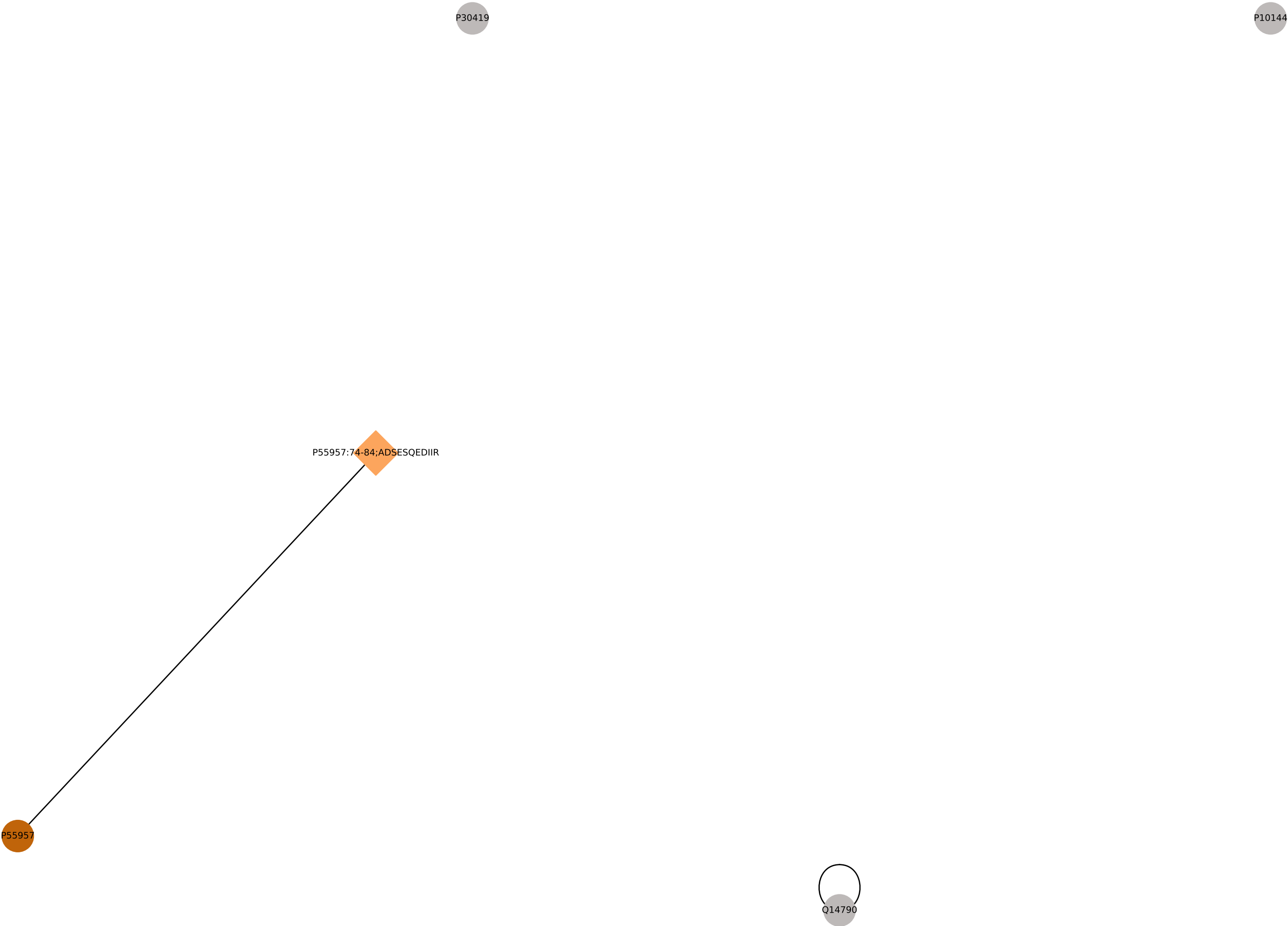
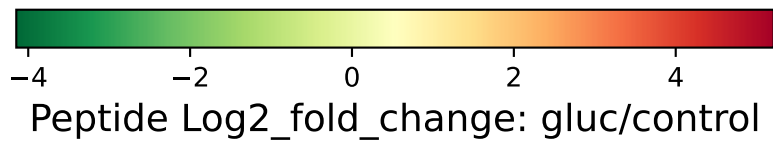
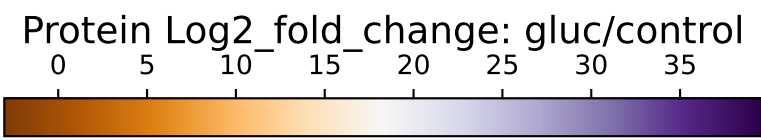
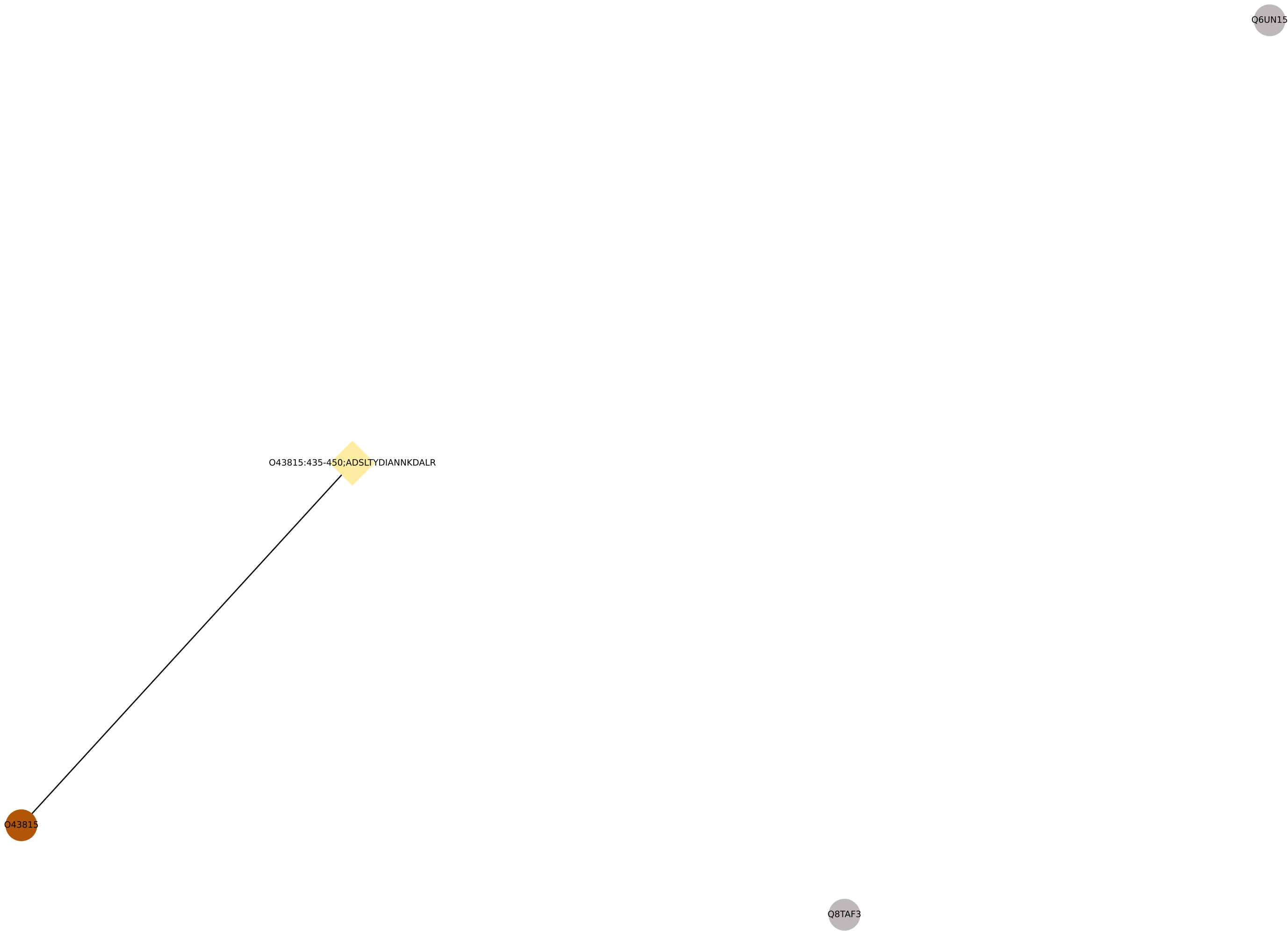


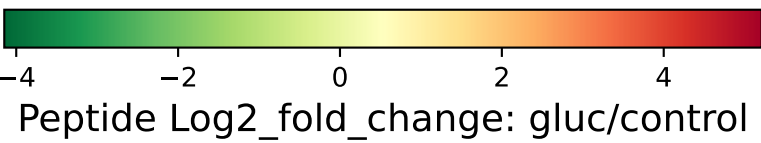
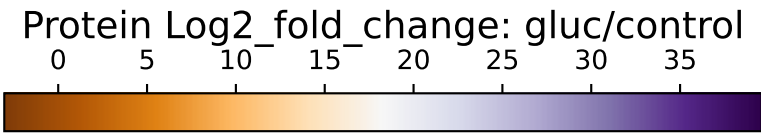
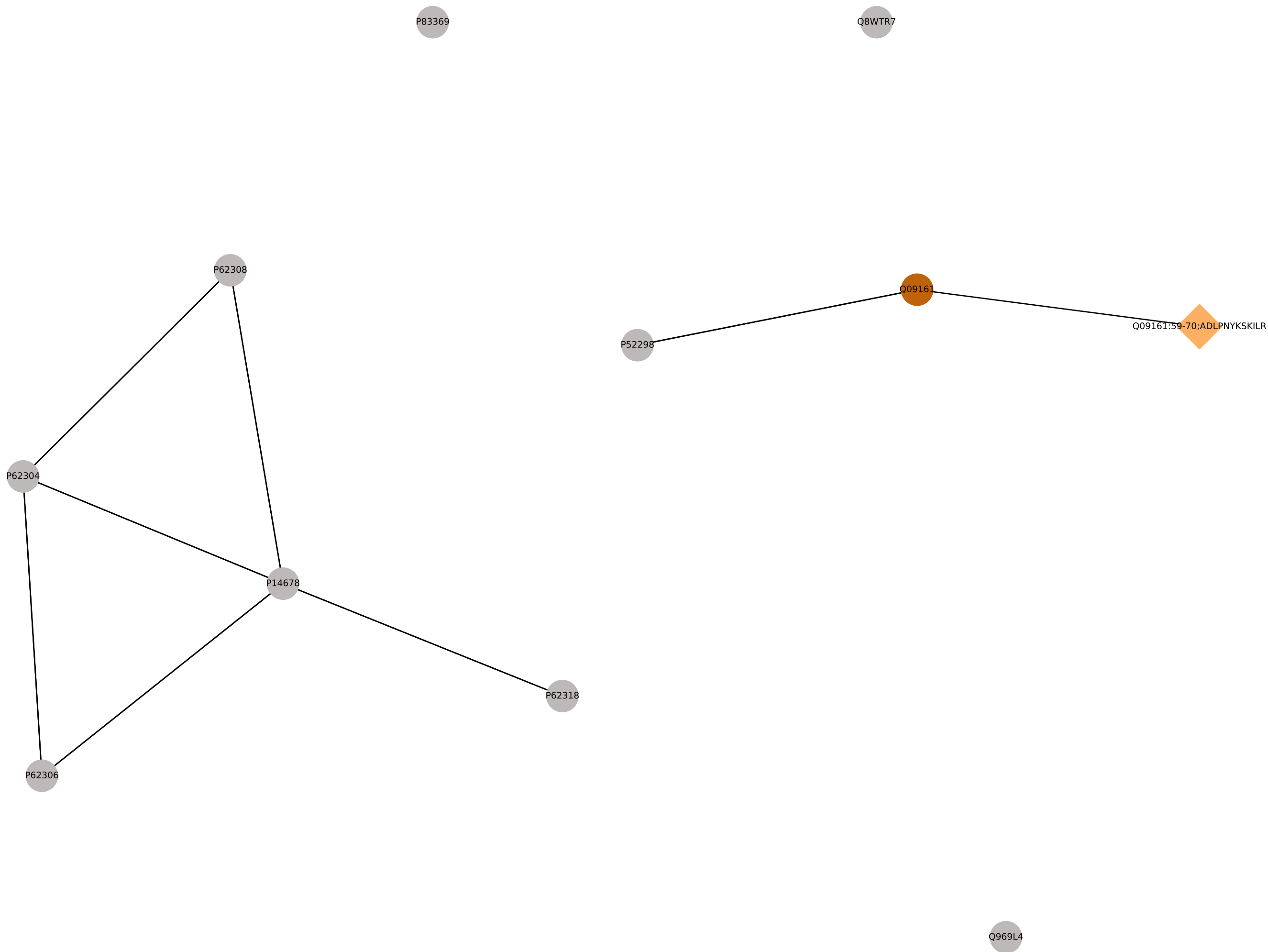
Log2_fold_change: gluc/control
R-HSA-75108: Activation, myristoylation of BID and translocation to mitochondria
p-value: 0.015117656007649471



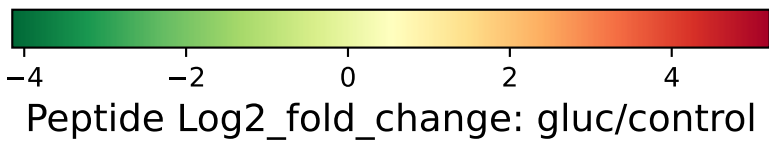
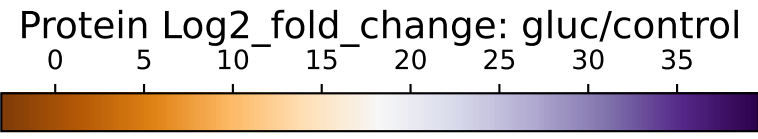
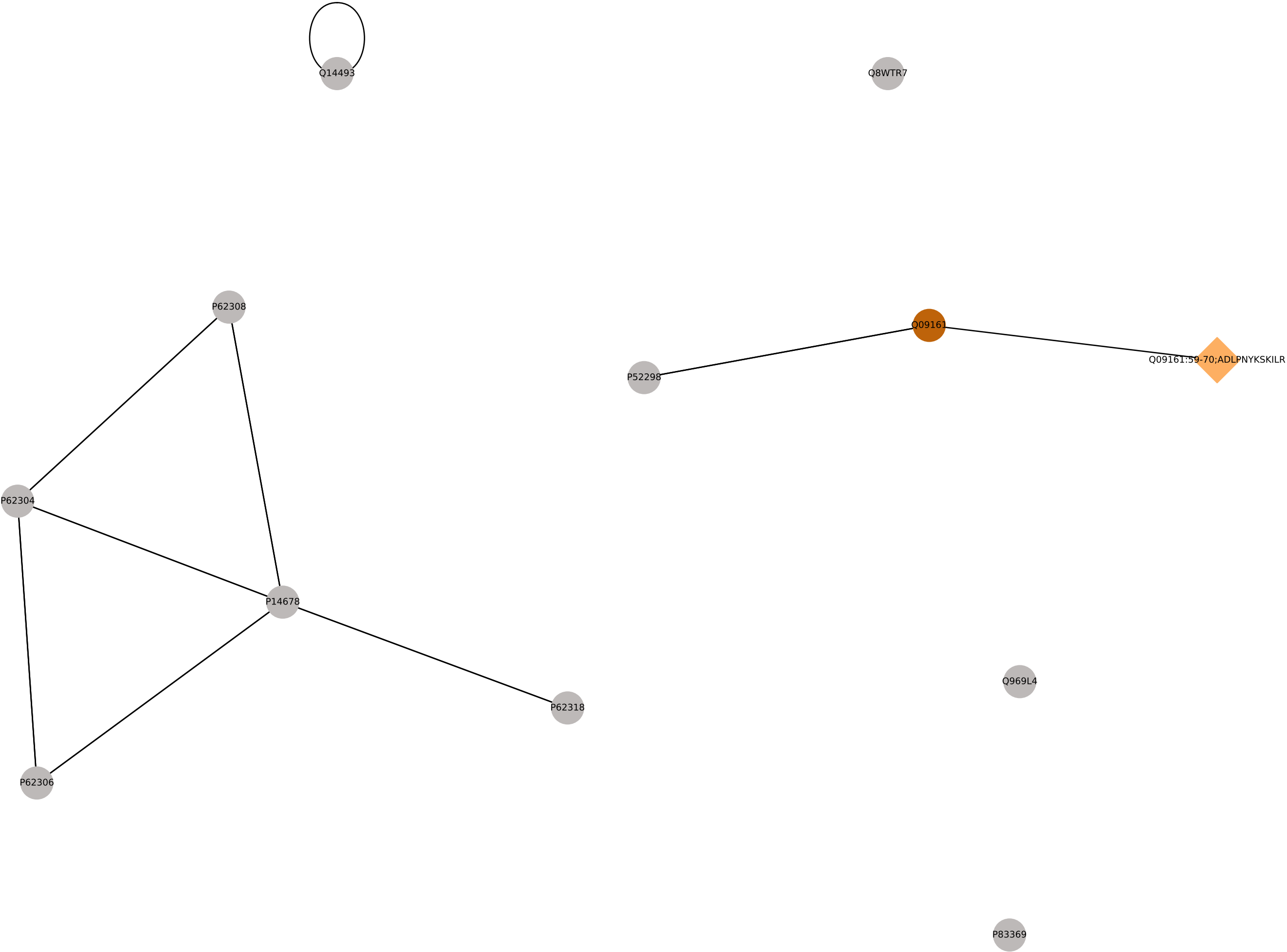
Log2_fold_change: gluc/control
R-HSA-9673766: Signaling by cytosolic PDGFRA and PDGFRB fusion proteins
p-value: 0.018861837637962453



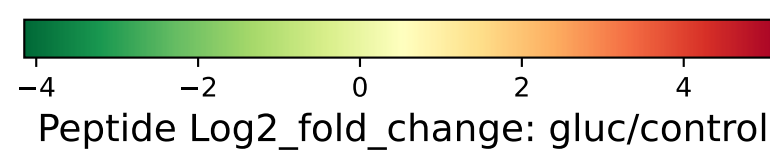
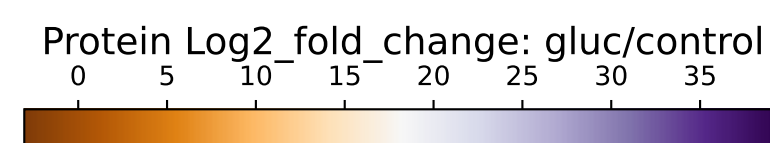
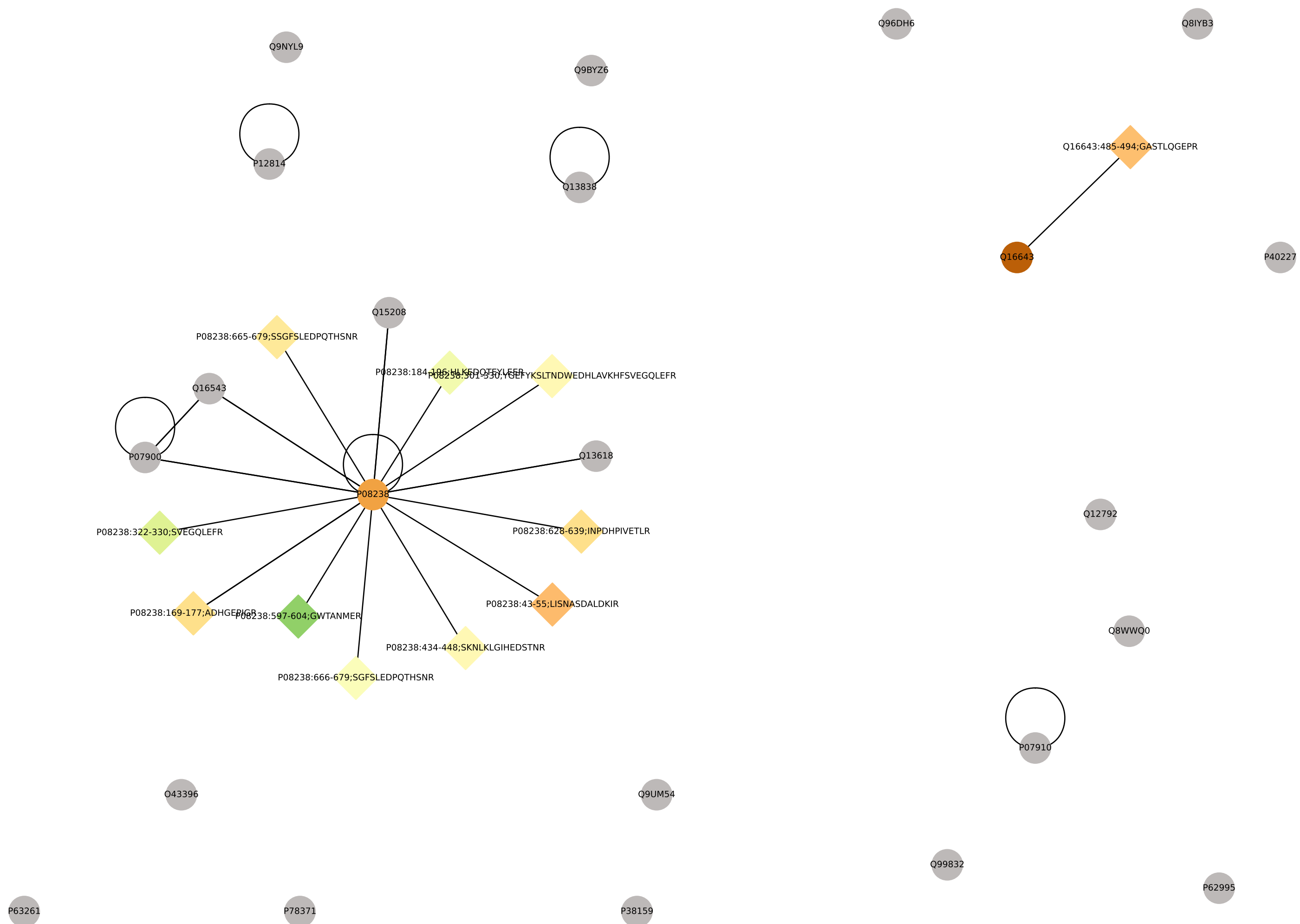
Log2_fold_change: gluc/control
R-HSA-111367: SLBP independent Processing of Histone Pre-mRNAs
p-value: 0.03737392638204595



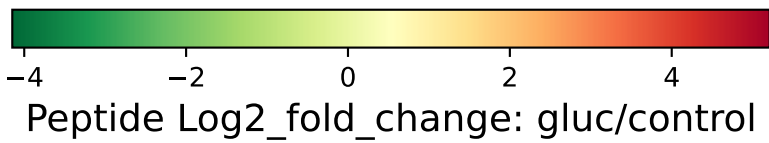
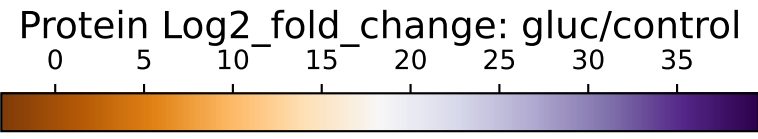
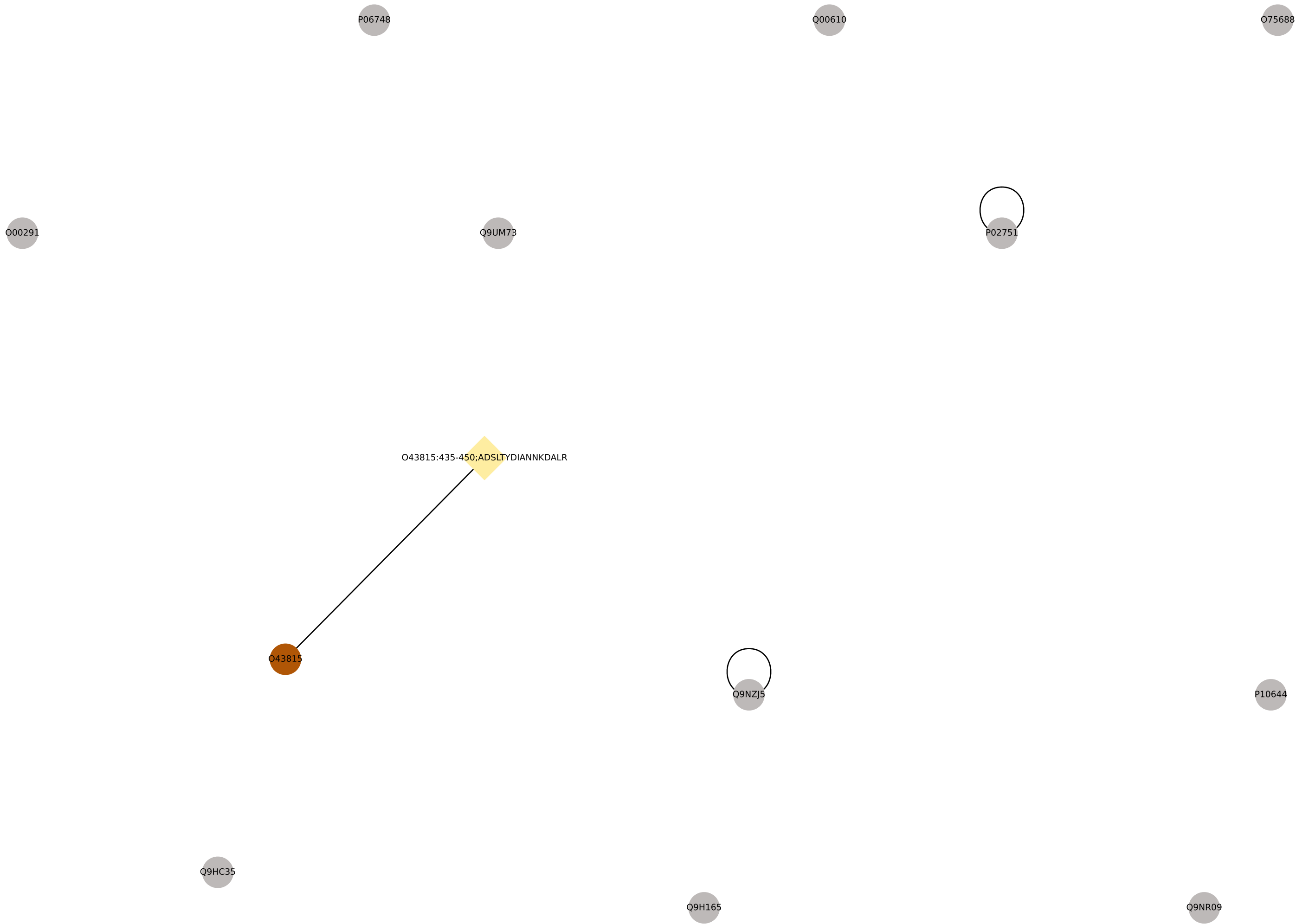
Log2_fold_change: gluc/control
R-HSA-77588: SLBP Dependent Processing of Replication-Dependent Histone Pre-mRNAs
p-value: 0.04103493715974438



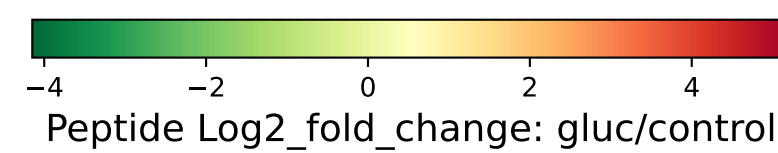
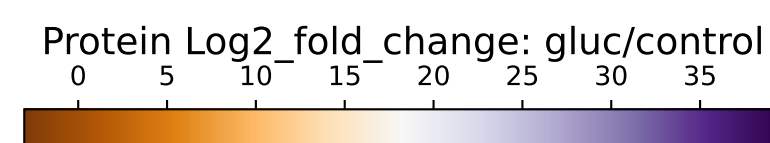
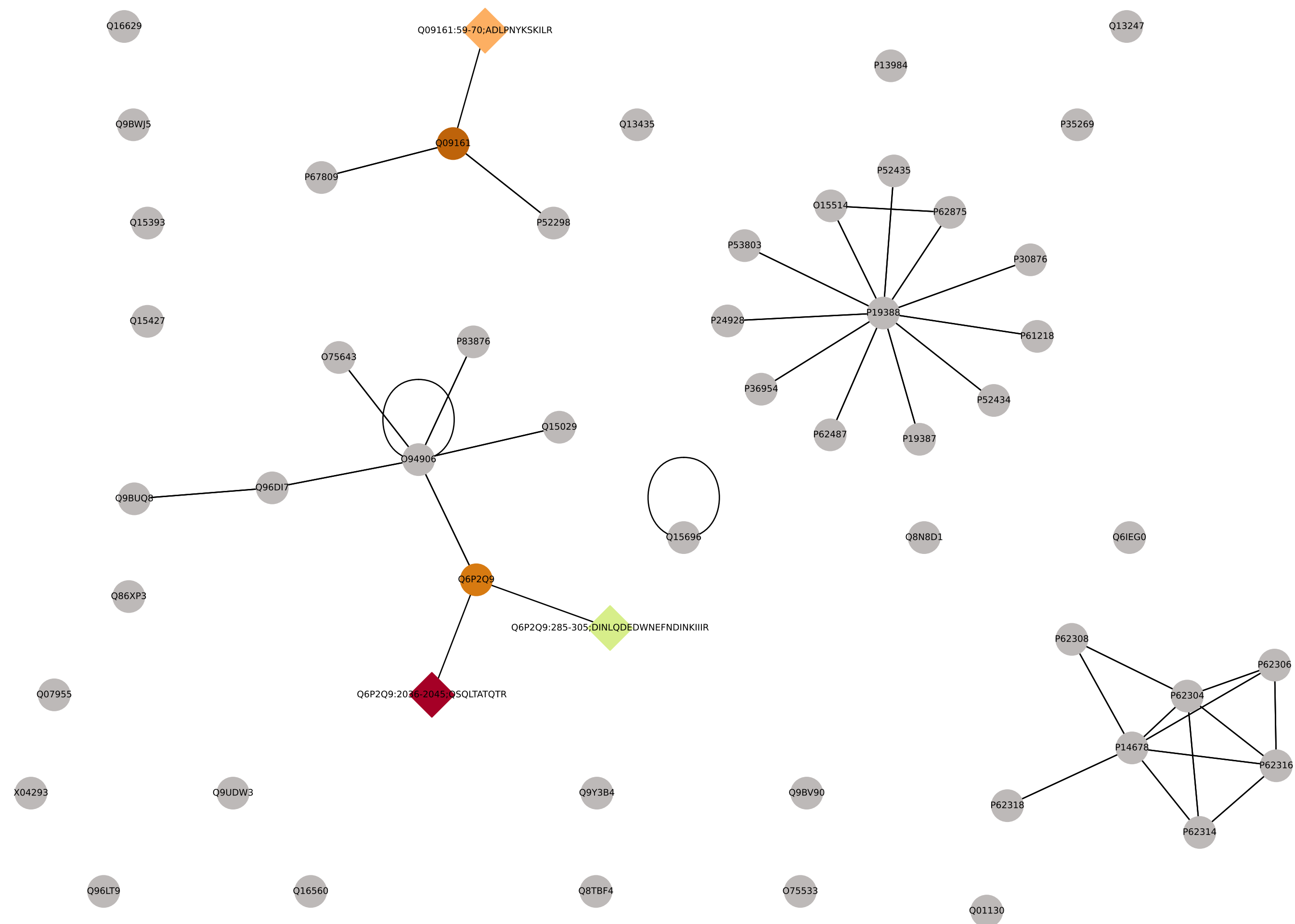
Log2_fold_change: gluc/control
R-HSA-9013418: RHOBTB2 GTPase cycle
p-value: 0.003870027935771292



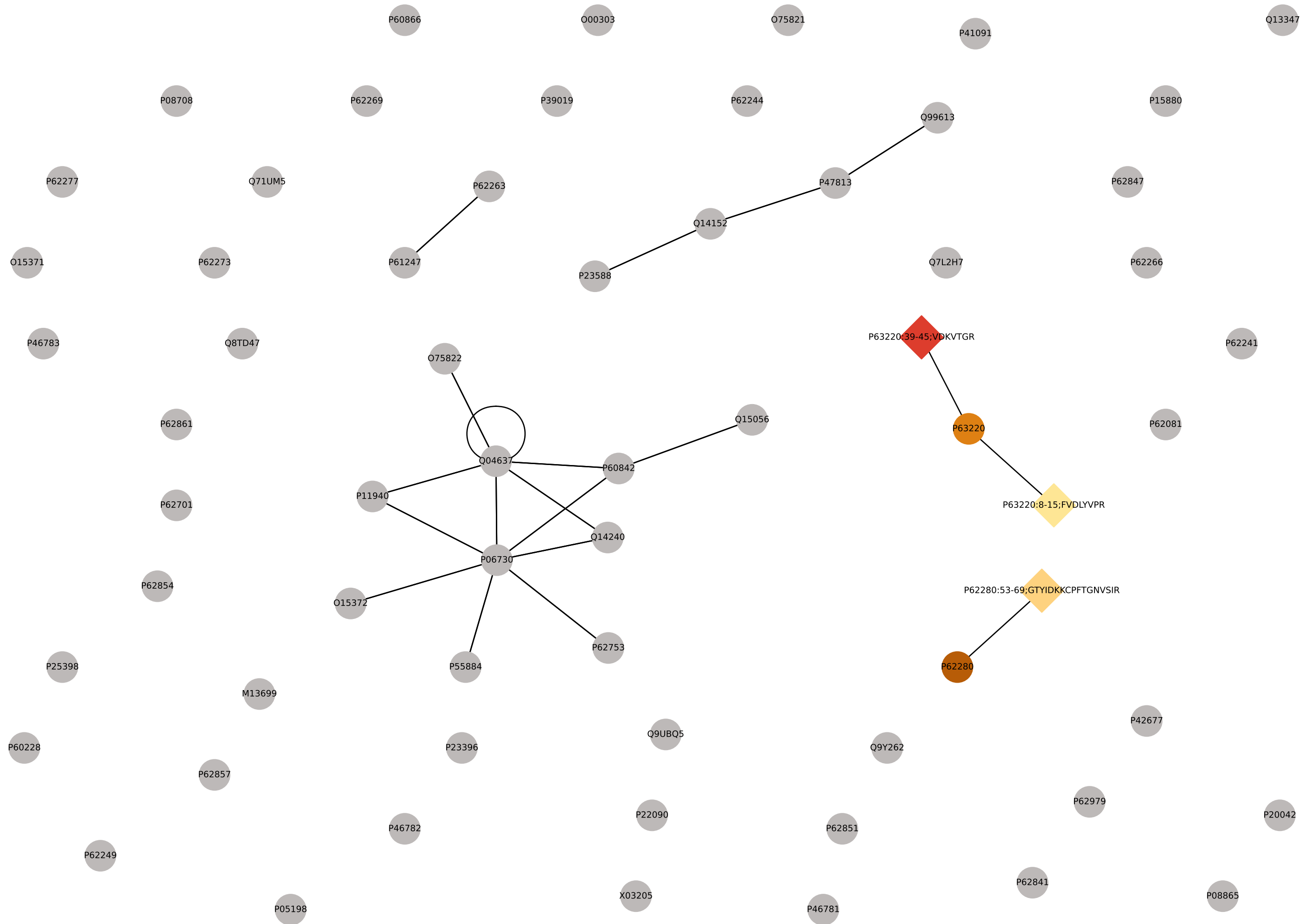
Log2_fold_change: gluc/control
R-HSA-9700645: ALK mutants bind TKIs
p-value: 0.04468226372702311



Log2_fold_change: gluc/control
R-HSA-72165: mRNA Splicing - Minor Pathway
p-value: 0.018216773752471993



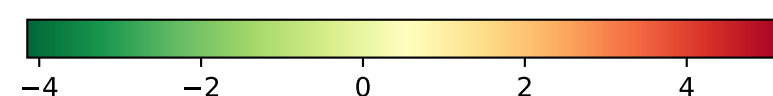
Log2_fold_change: gluc/control
R-HSA-72649: Translation initiation complex formation
p-value: 0.023554931232115828



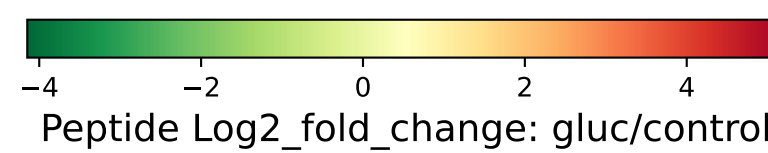
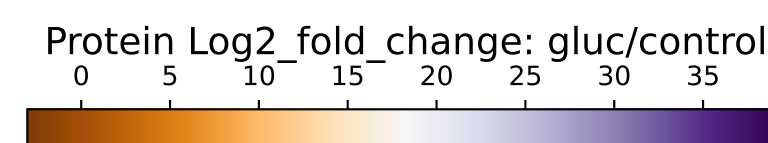
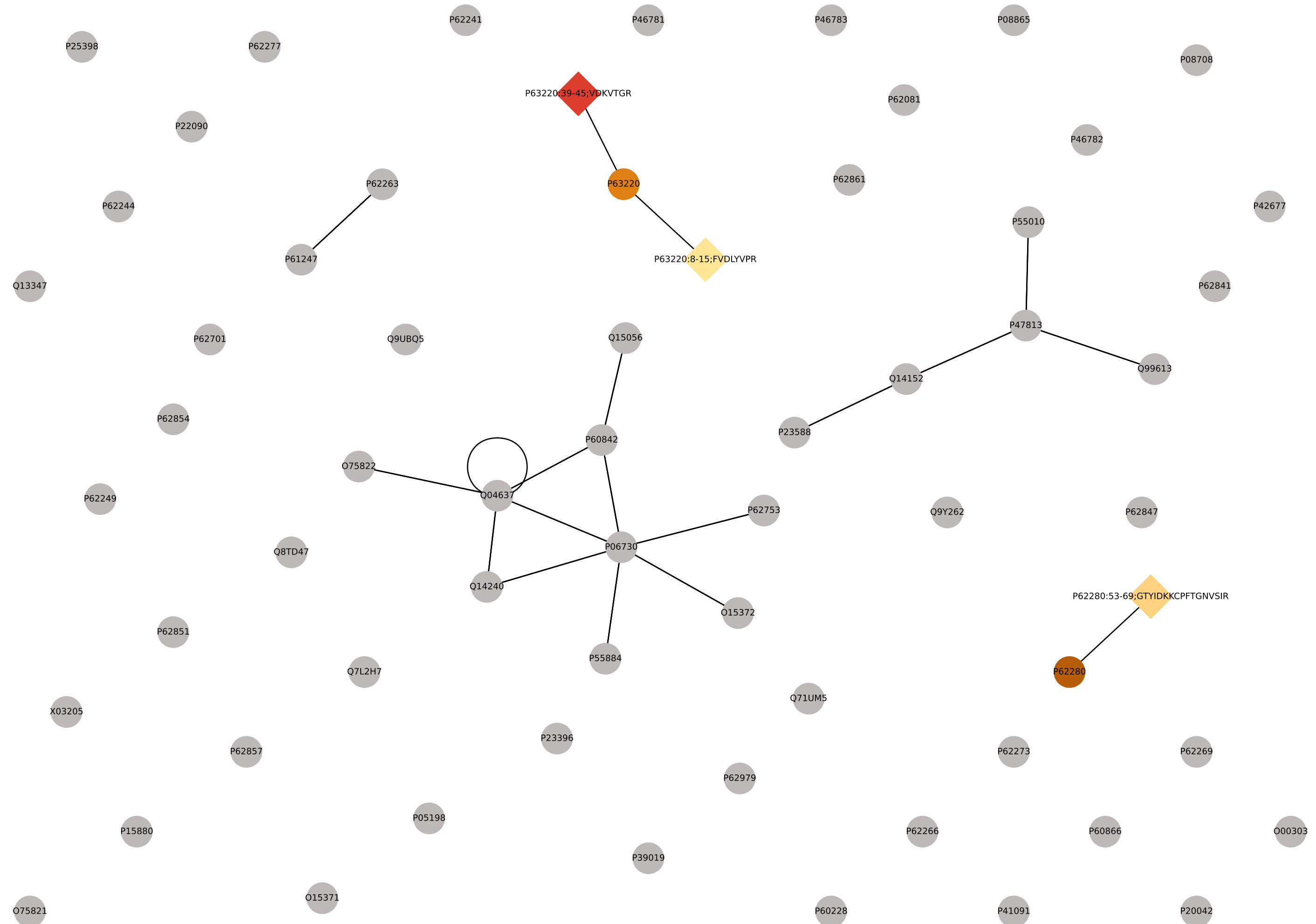
Protein Log2_fold_change: gluc/control



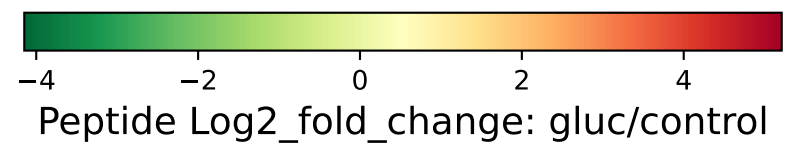
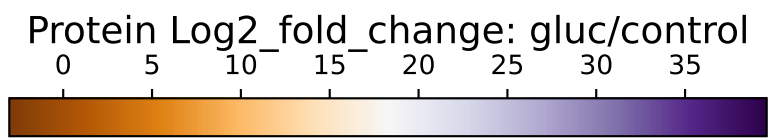
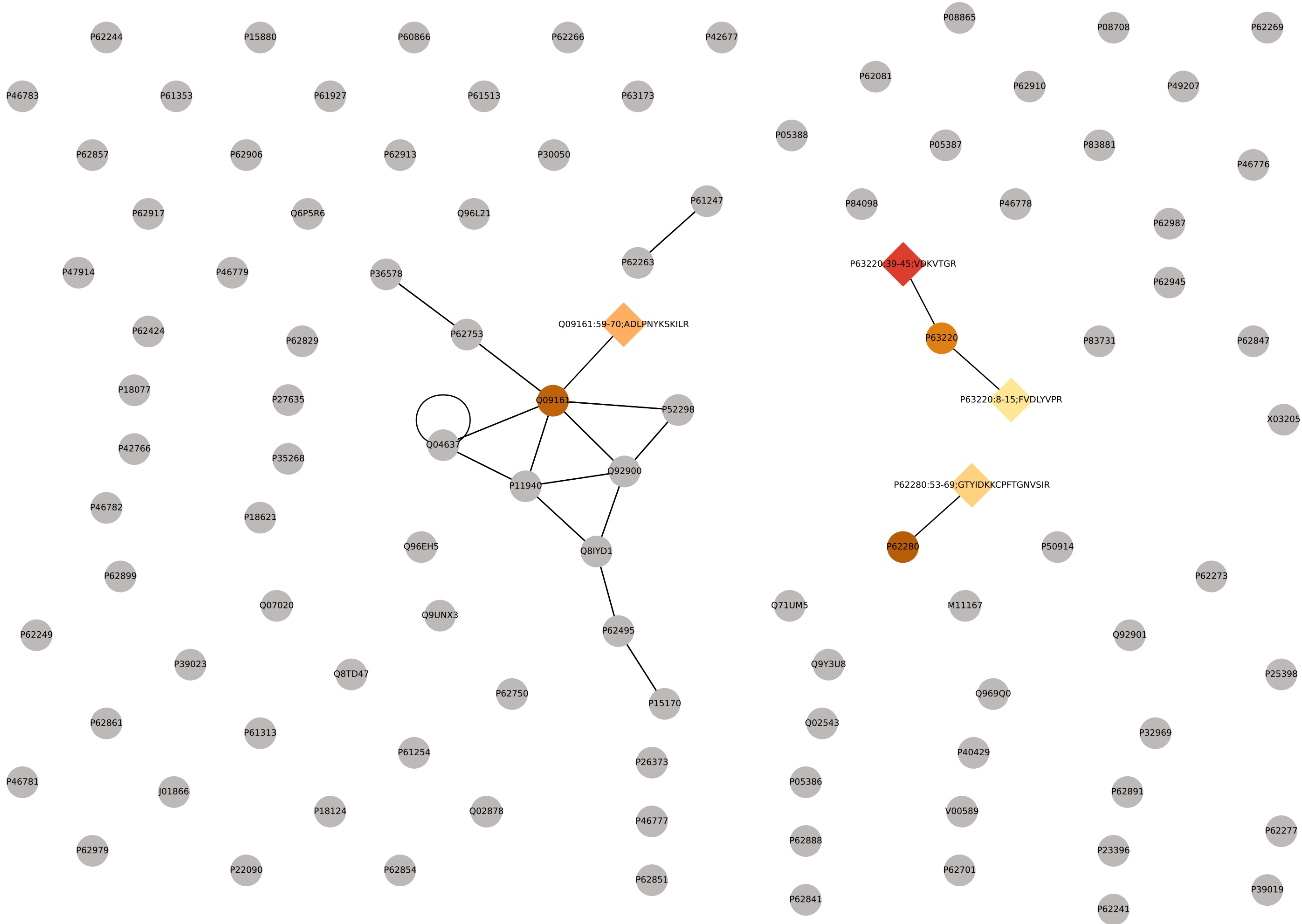
Peptide Log2_fold_change: gluc/control



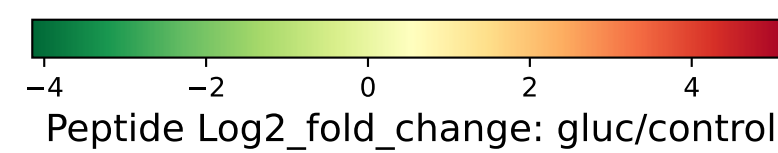
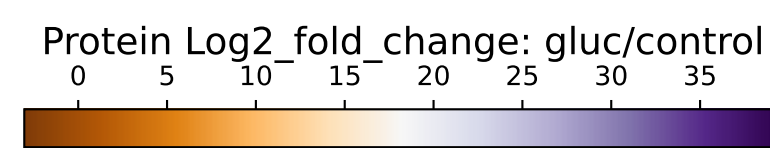
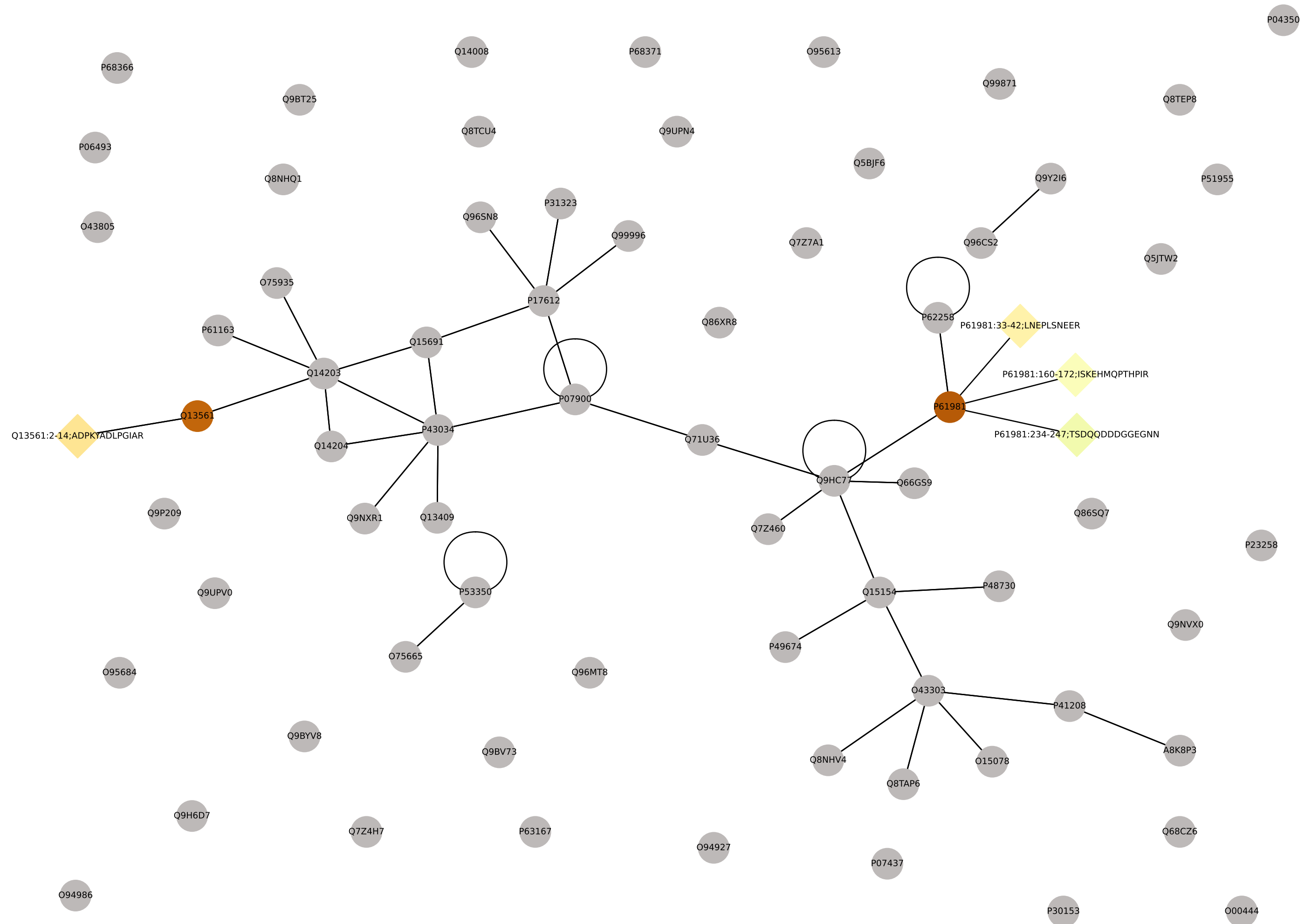
Log2_fold_change: gluc/control
R-HSA-72702: Ribosomal scanning and start codon recognition
p-value: 0.024978417082091475



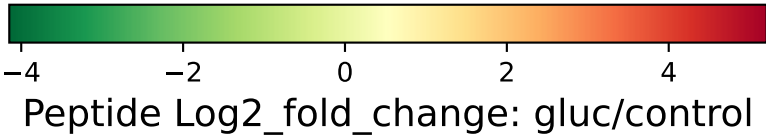
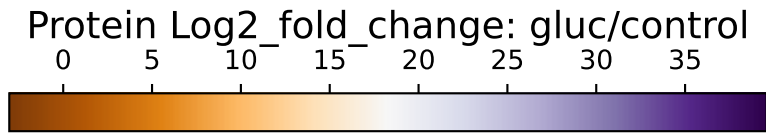
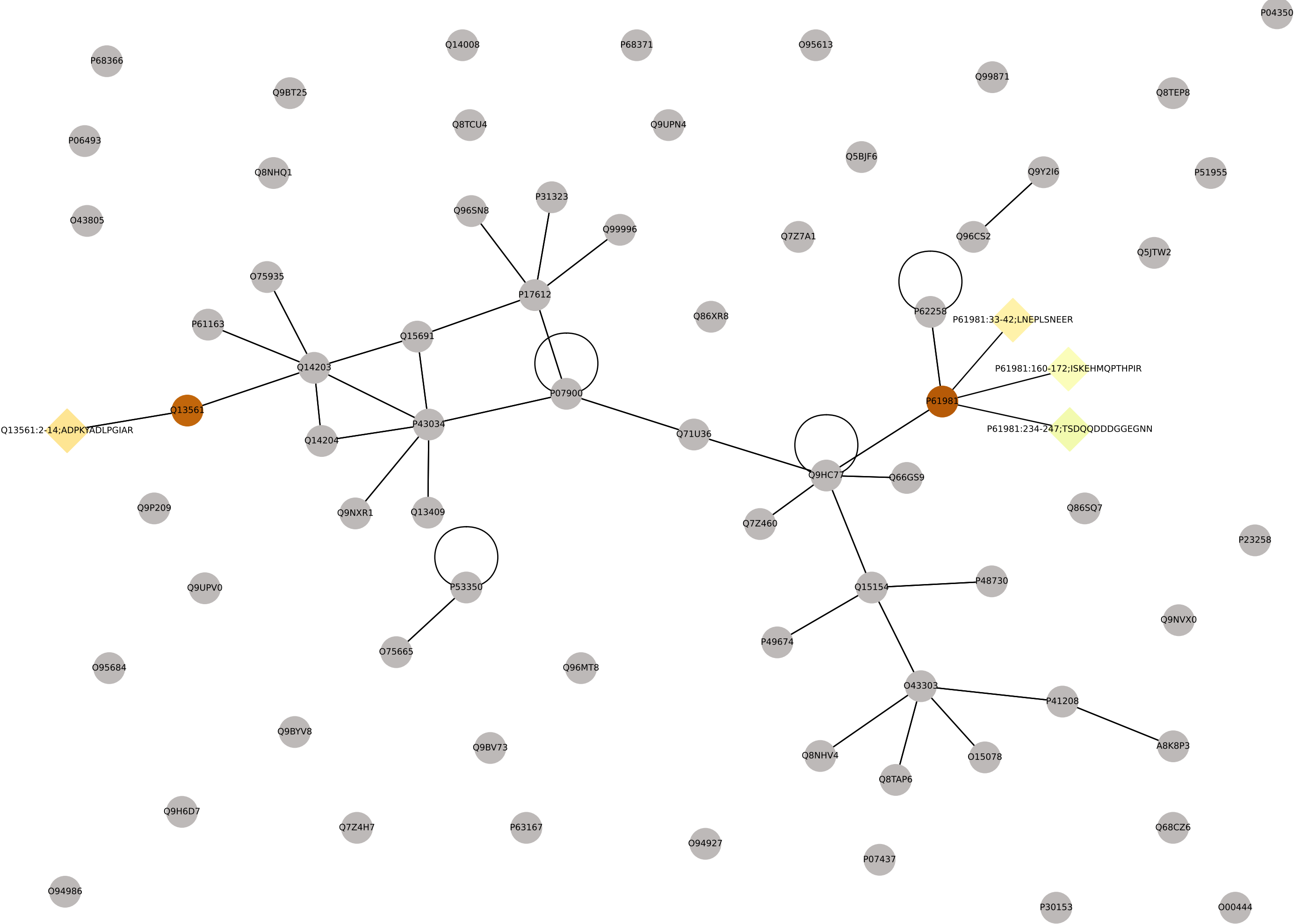
Log2_fold_change: gluc/control
R-HSA-975956: Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC)
p-value: 0.006855569728165922



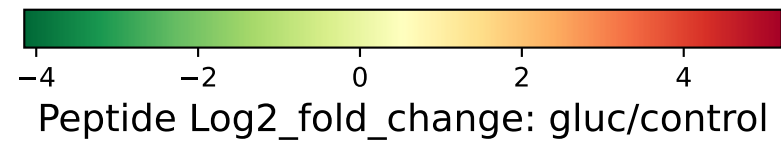
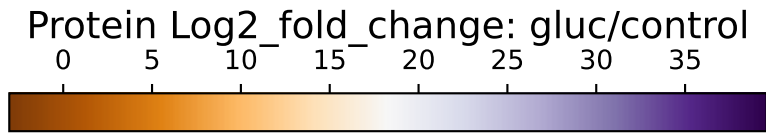
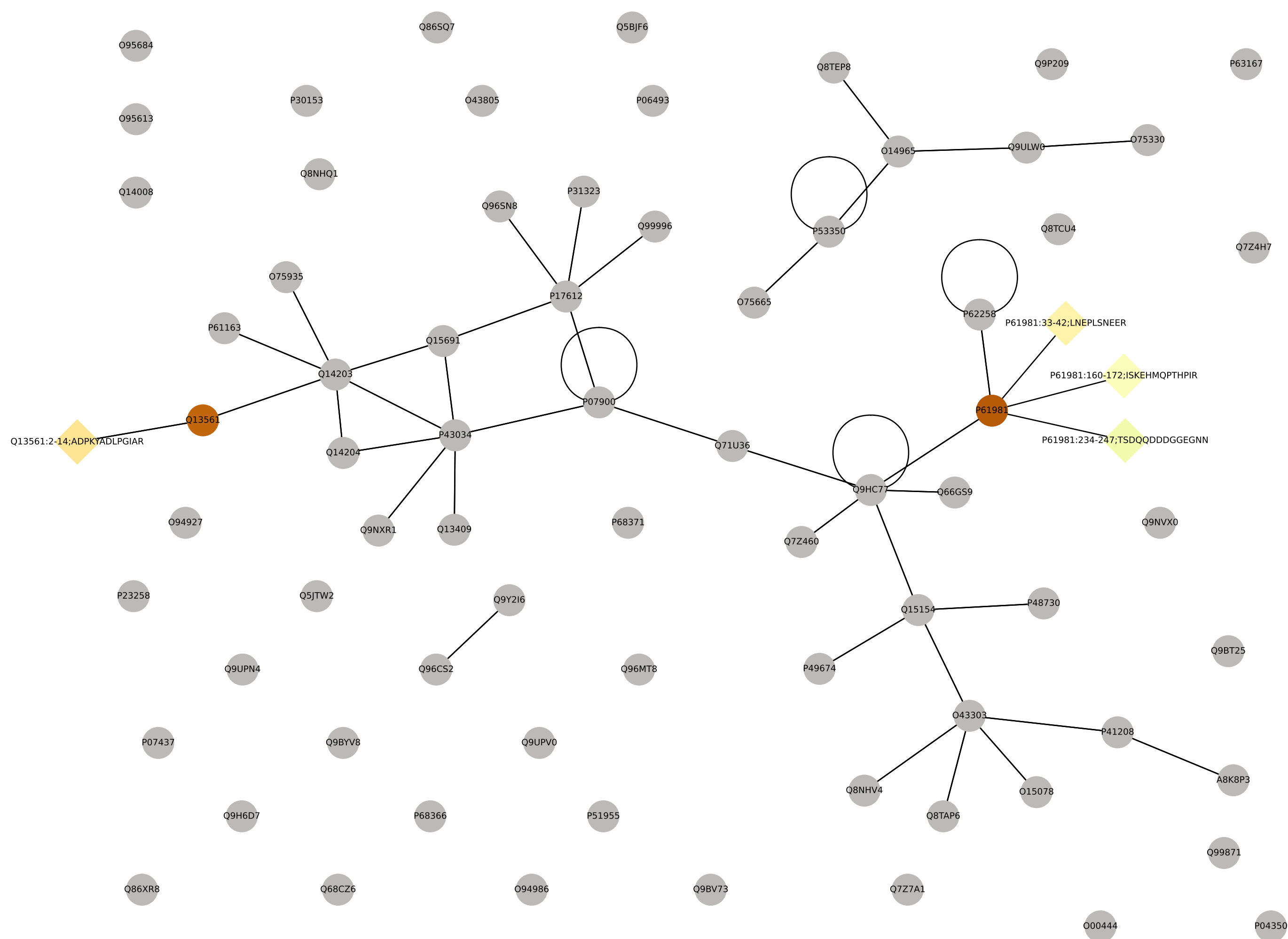
Log2_fold_change: gluc/control
R-HSA-380284: Loss of proteins required for interphase microtubule organization from the centrosome
p-value: 0.030227589686308676



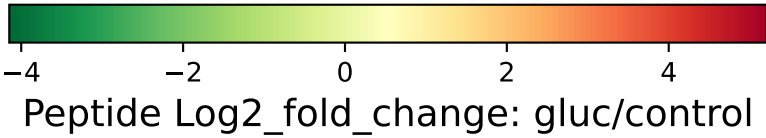
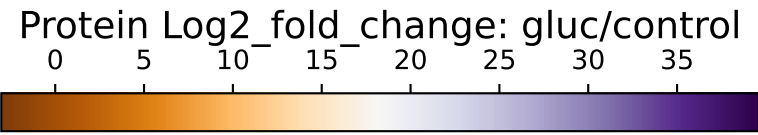
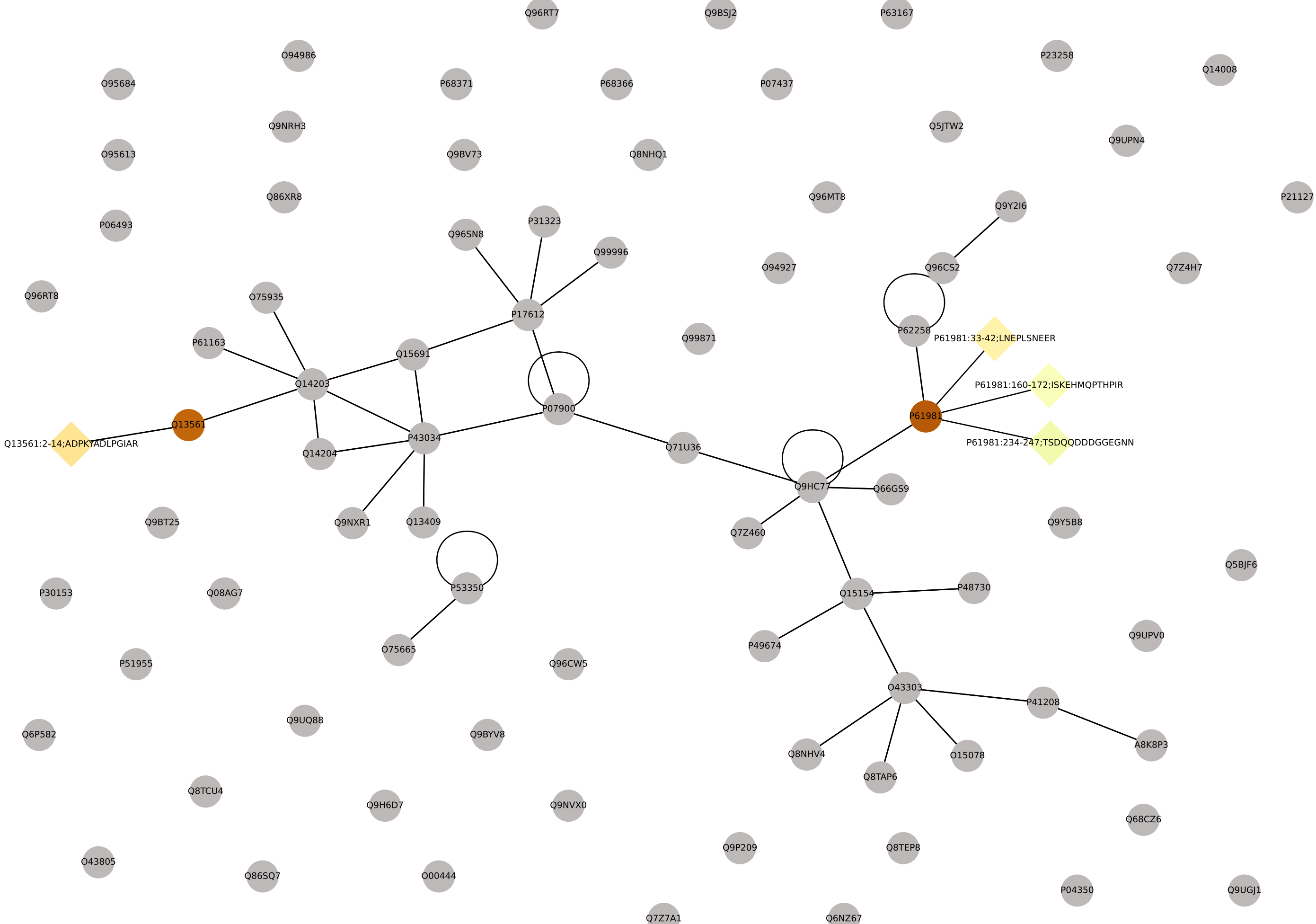
Log2_fold_change: gluc/control
R-HSA-380259: Loss of Nlp from mitotic centrosomes
p-value: 0.030227589686308676



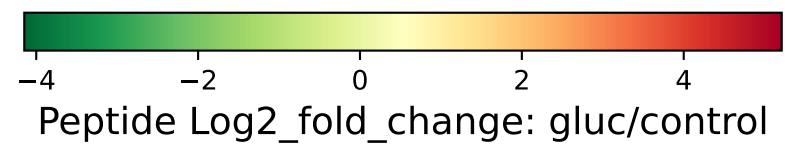
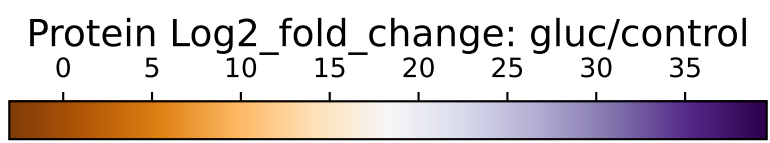
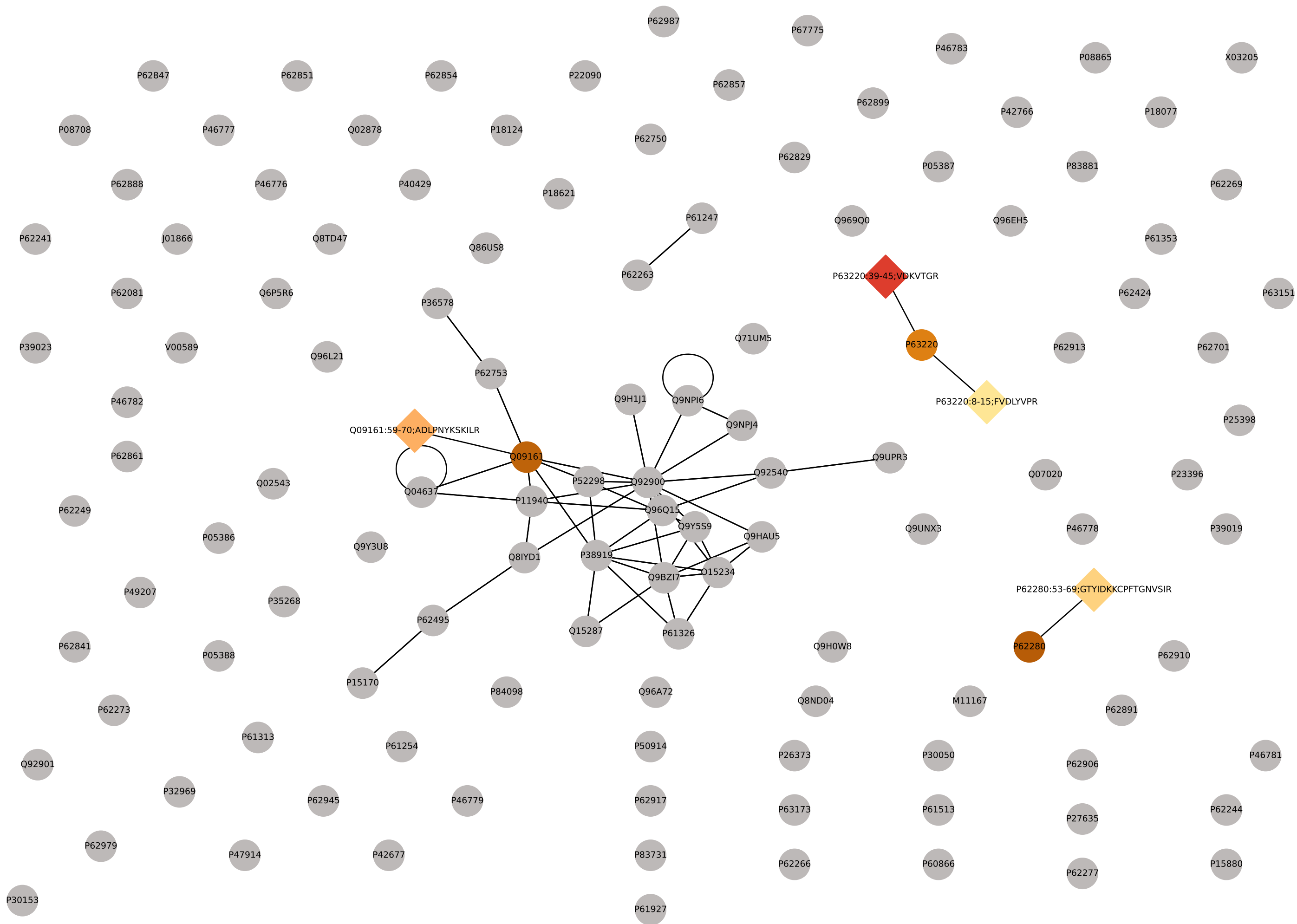
Log2_fold_change: gluc/control
R-HSA-8854518: AURKA Activation by TPX2
p-value: 0.032600049302680456



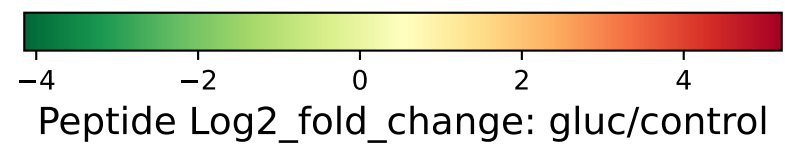
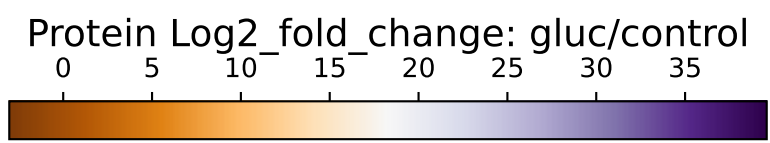
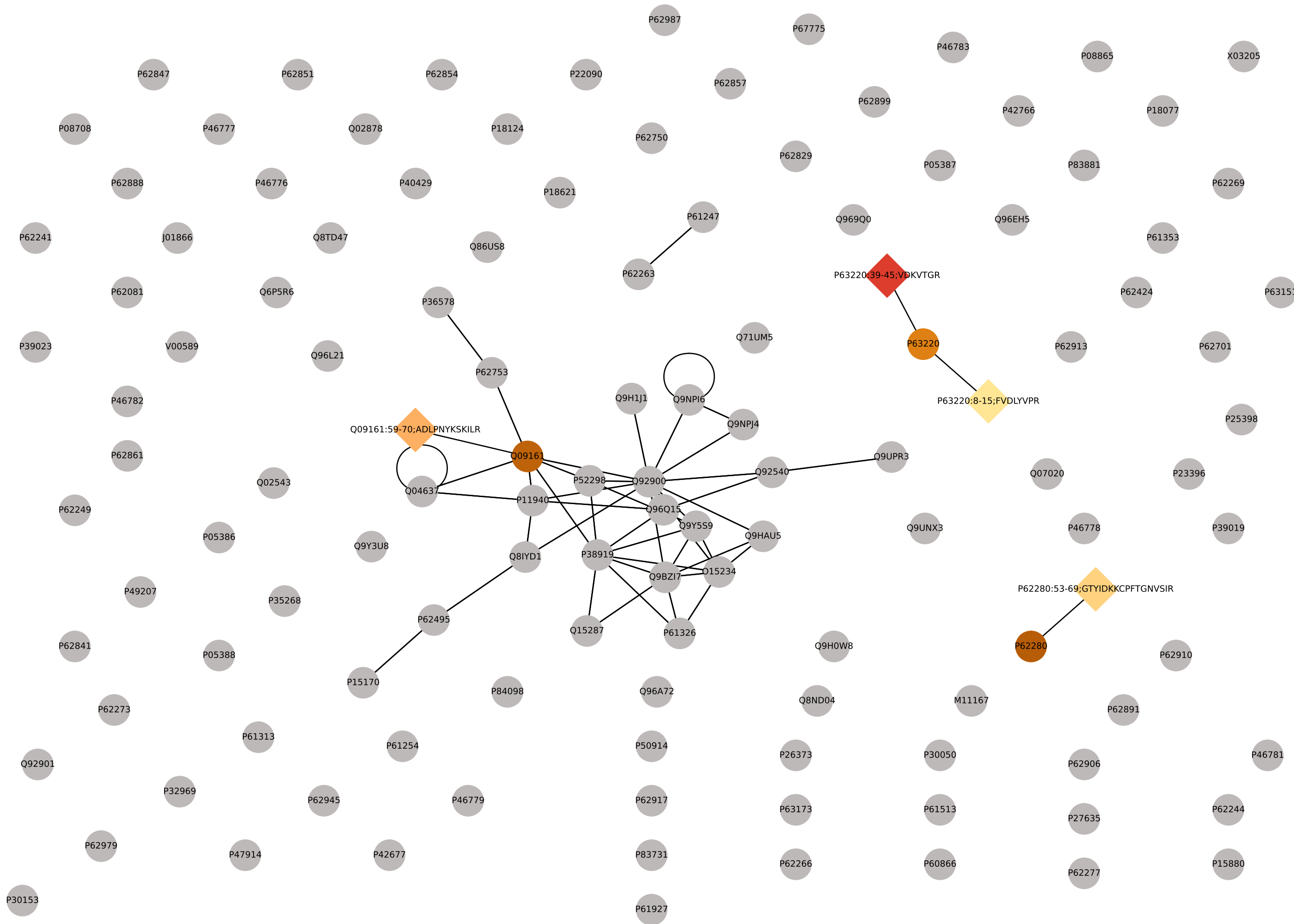
Log2_fold_change: gluc/control
R-HSA-380270: Recruitment of mitotic centrosome proteins and complexes
p-value: 0.0384084717376354



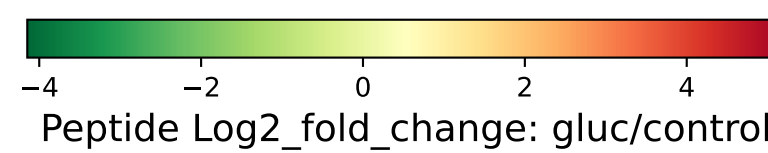
Log2_fold_change: gluc/control
R-HSA-927802: Nonsense-Mediated Decay (NMD)
p-value: 0.011931898374331729



Log2_fold_change: gluc/control
R-HSA-975957: Nonsense Mediated Decay (NMD) enhanced by the Exon Junction Complex (EJC)
p-value: 0.011931898374331729



The diagram illustrates a network of protein interactions. The nodes are UniProt IDs, and the edges represent interactions. Two nodes are highlighted in orange: Q13561 and P61981. Three regions are highlighted with yellow diamonds: Q13561:2-14;ADPKTADLPGIAR, P61981:33-42;LNEPLSNEER, and P61981:160-172;ISKEHMQPTHPPIR. The network shows a complex web of connections between various proteins, with some nodes having self-loops.



Log2_fold_change: gluc/control
R-HSA-72163: mRNA Splicing - Major Pathway
p-value: 0.008907459881584257

