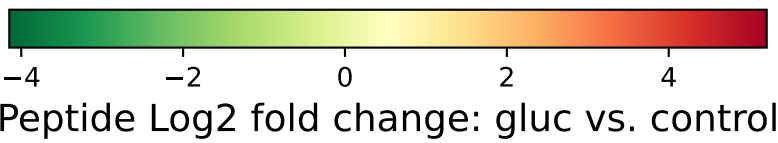
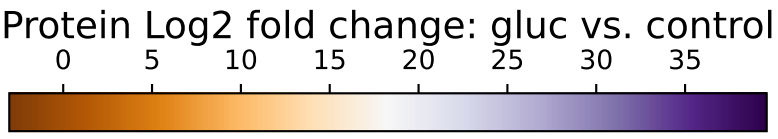
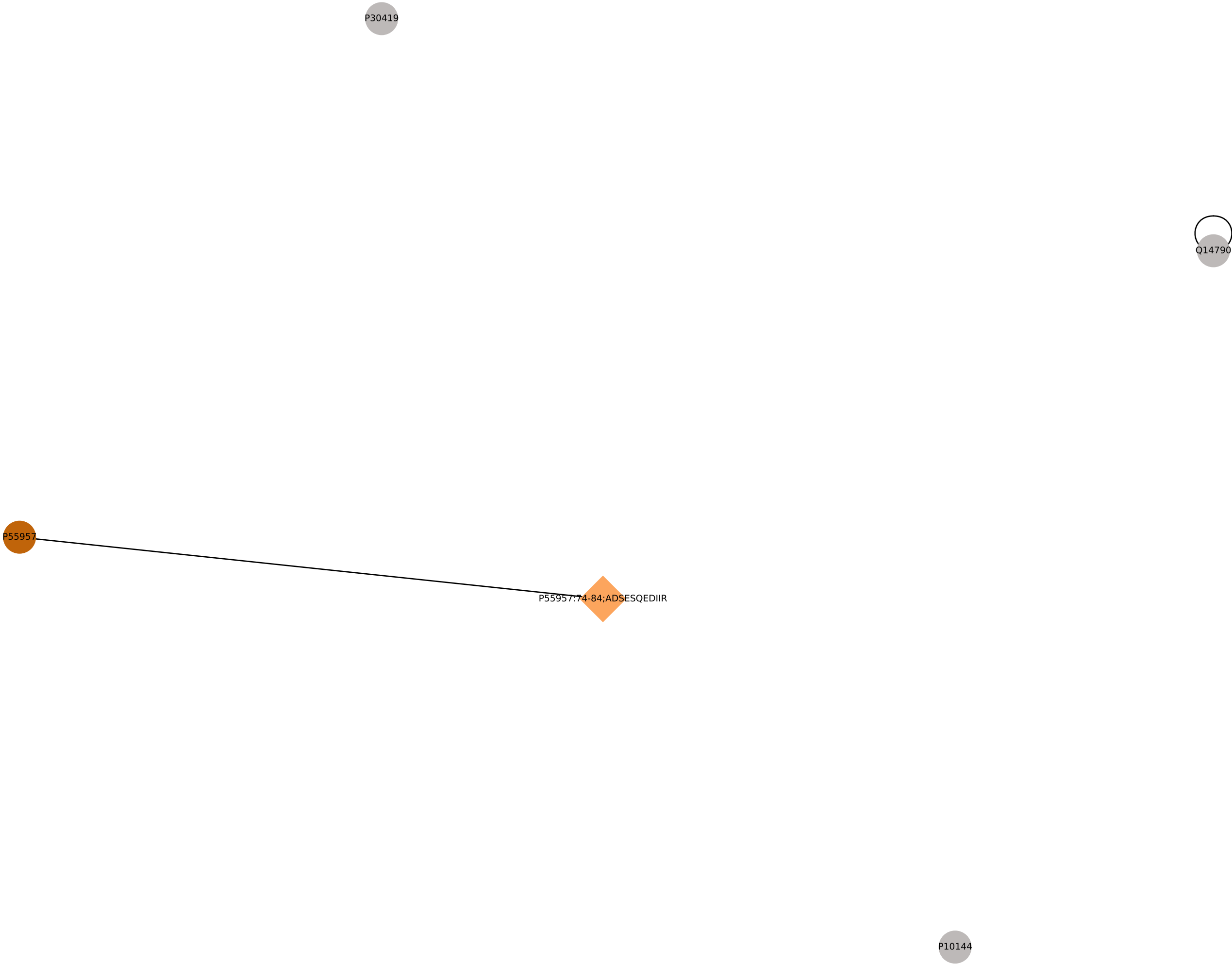
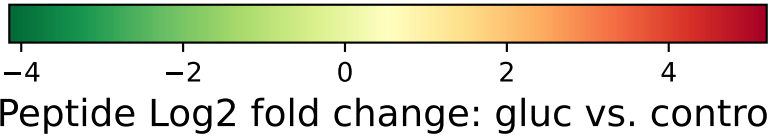
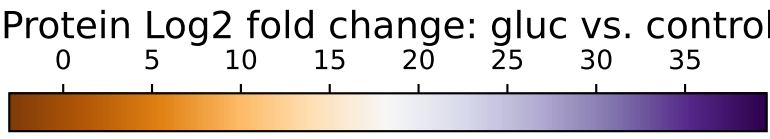
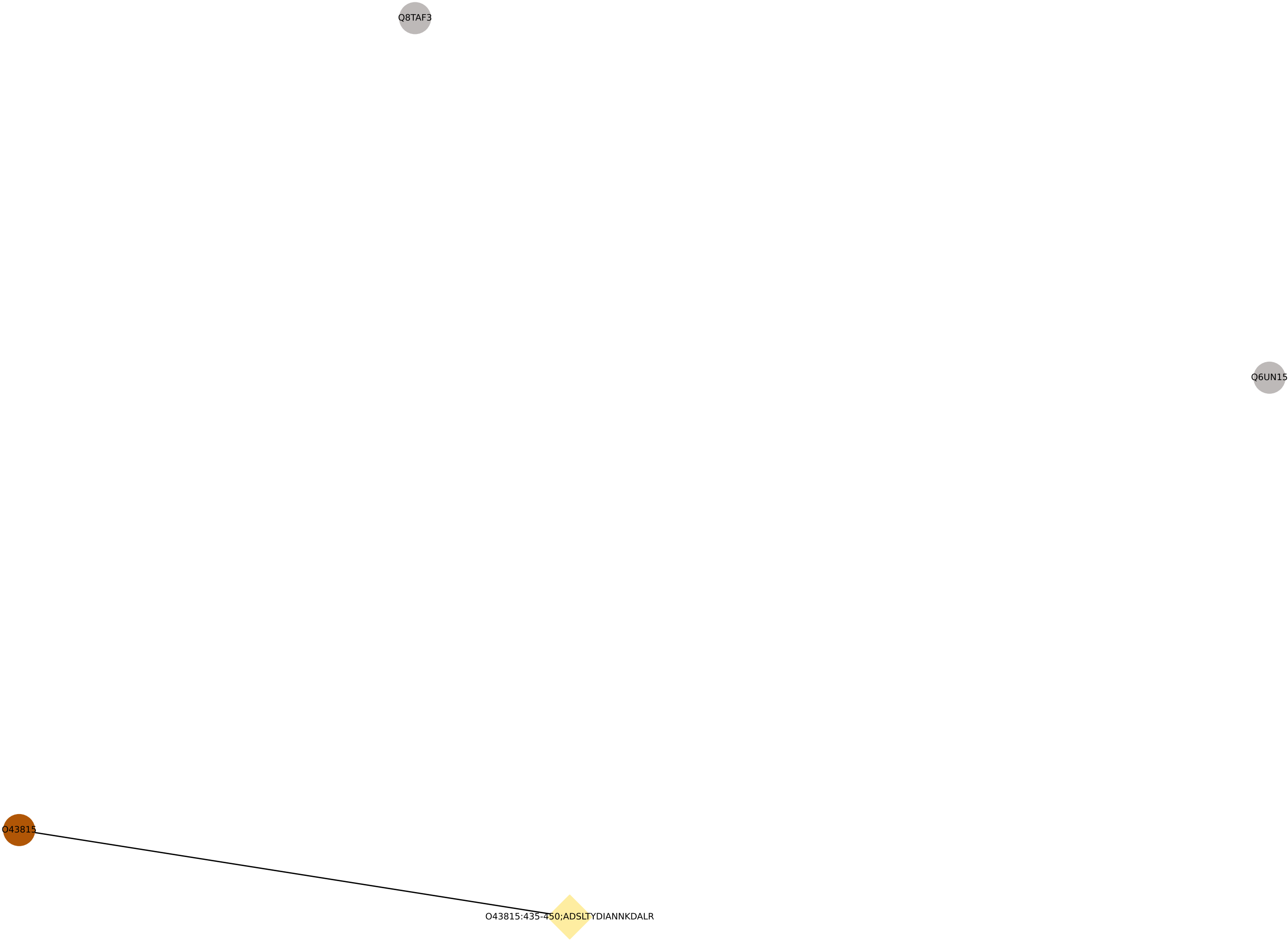


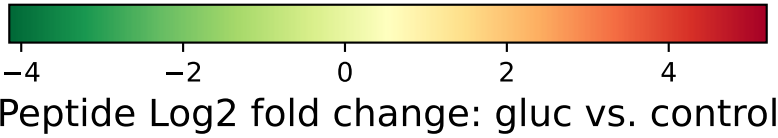
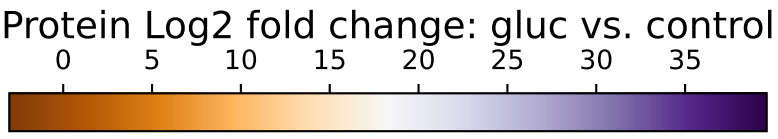
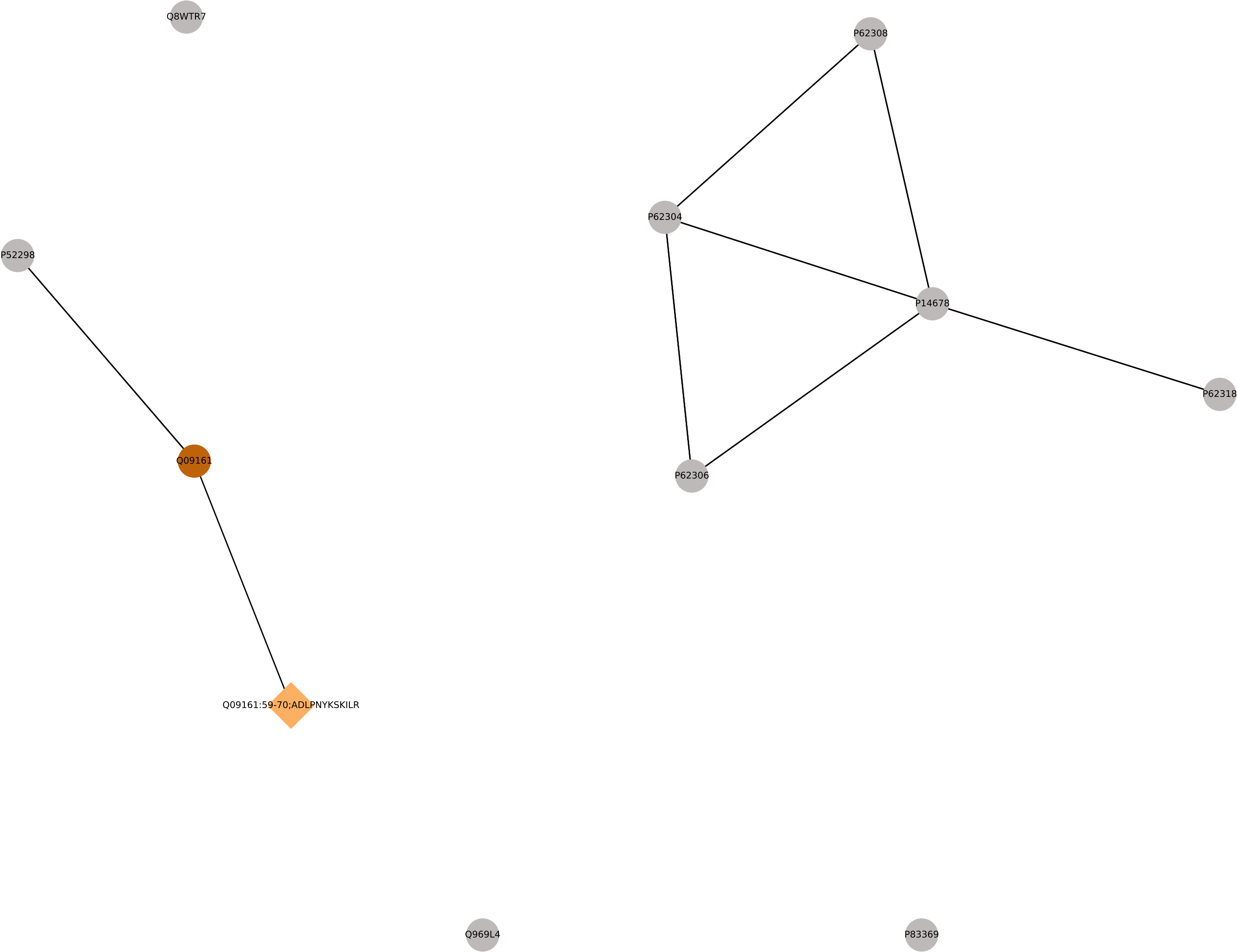
Log2 fold change: gluc vs. control  
R-HSA-75108: Activation, myristoylation of BID and translocation to mitochondria  
p-value: 0.015117656007649471



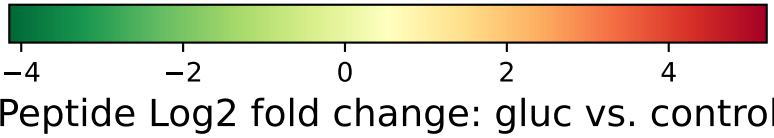
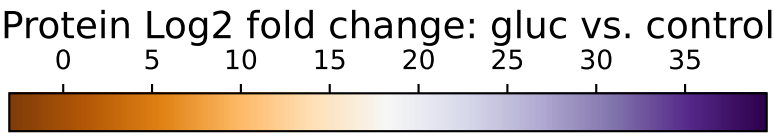
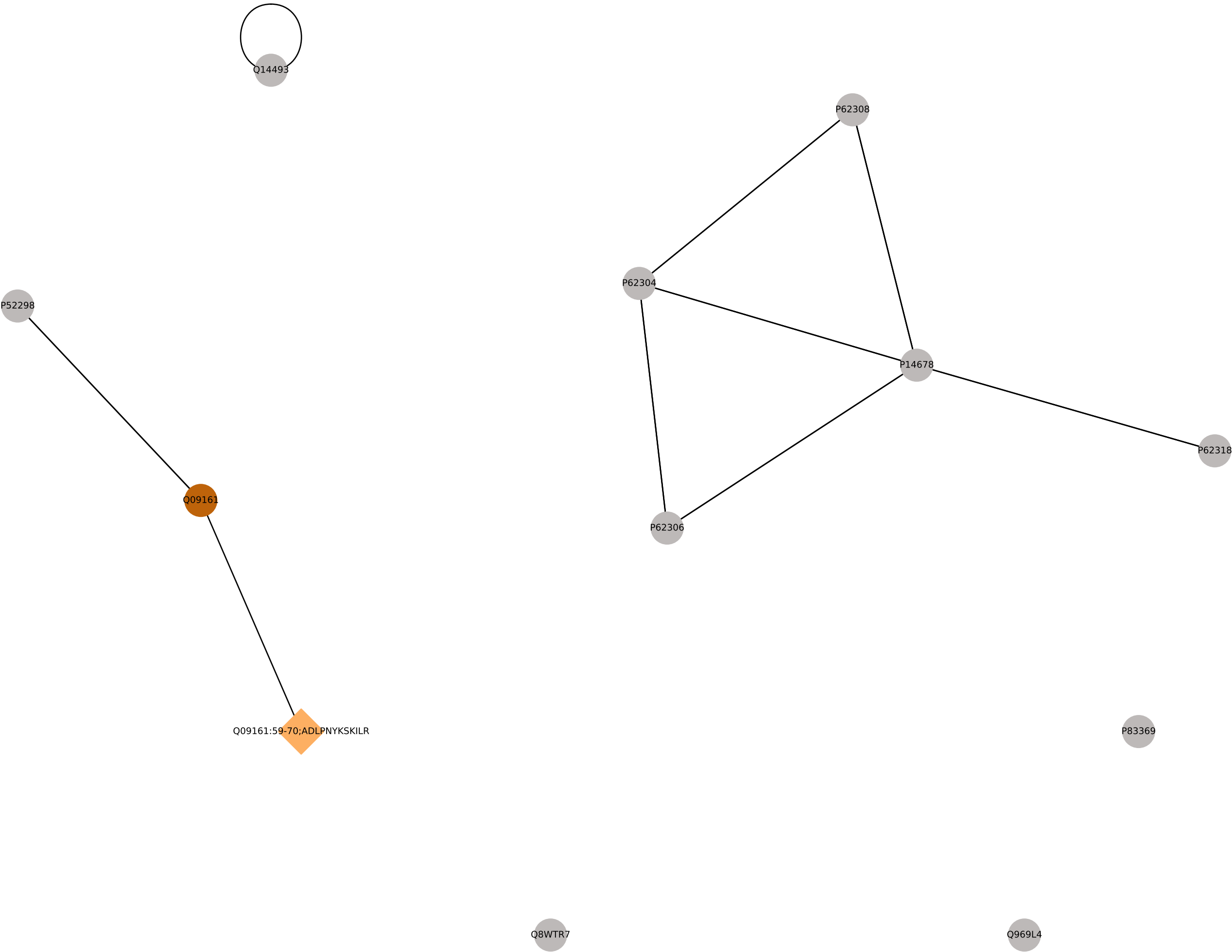
Log2 fold change: gluc vs. control  
R-HSA-9673766: Signaling by cytosolic PDGFRA and PDGFRB fusion proteins  
p-value: 0.018861837637962453



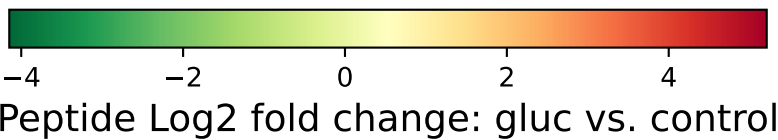
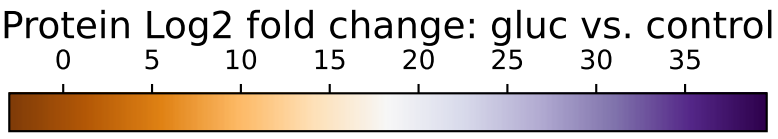
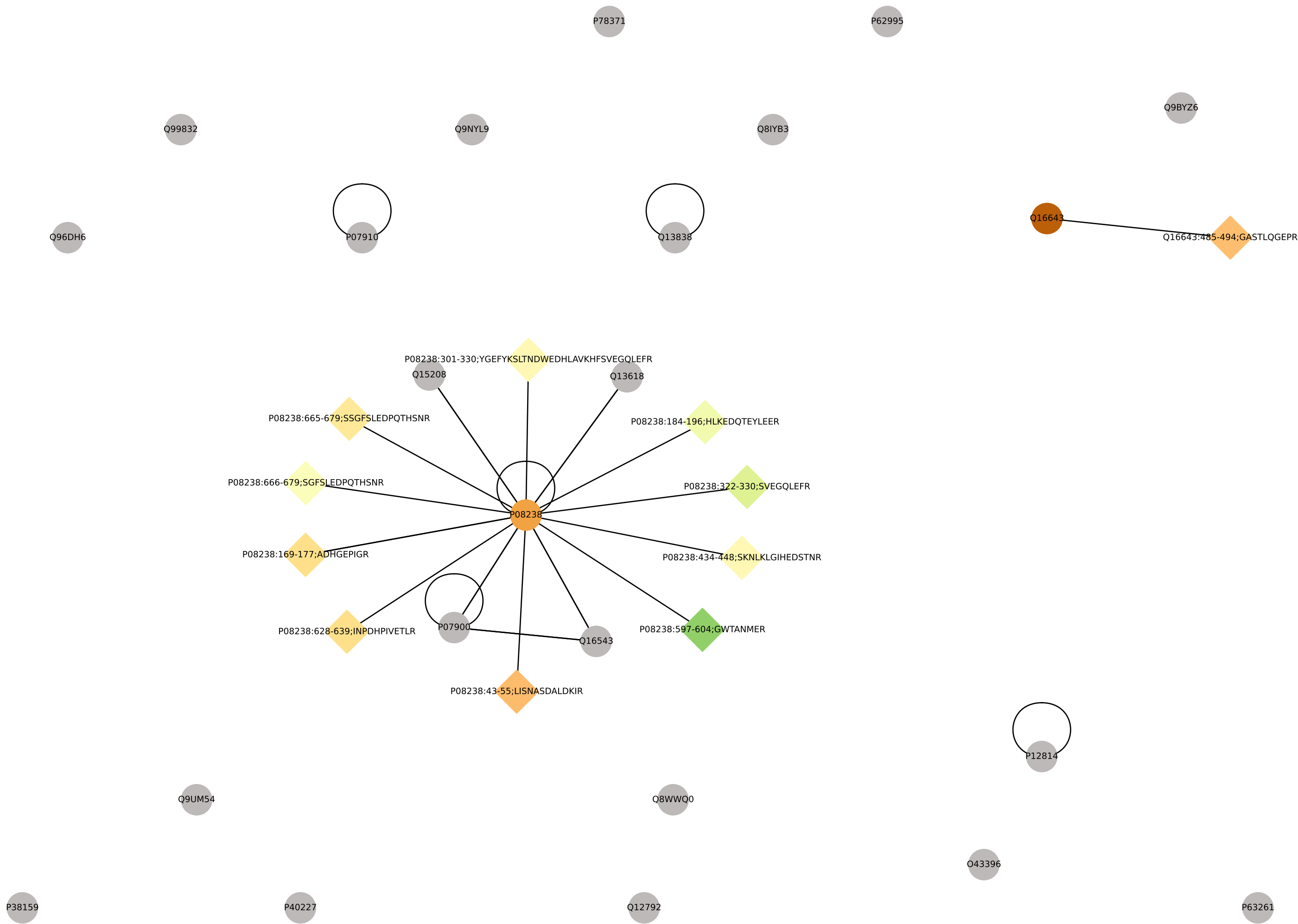
Log2 fold change: gluc vs. control  
R-HSA-111367: SLBP independent Processing of Histone Pre-mRNAs  
p-value: 0.03737392638204595



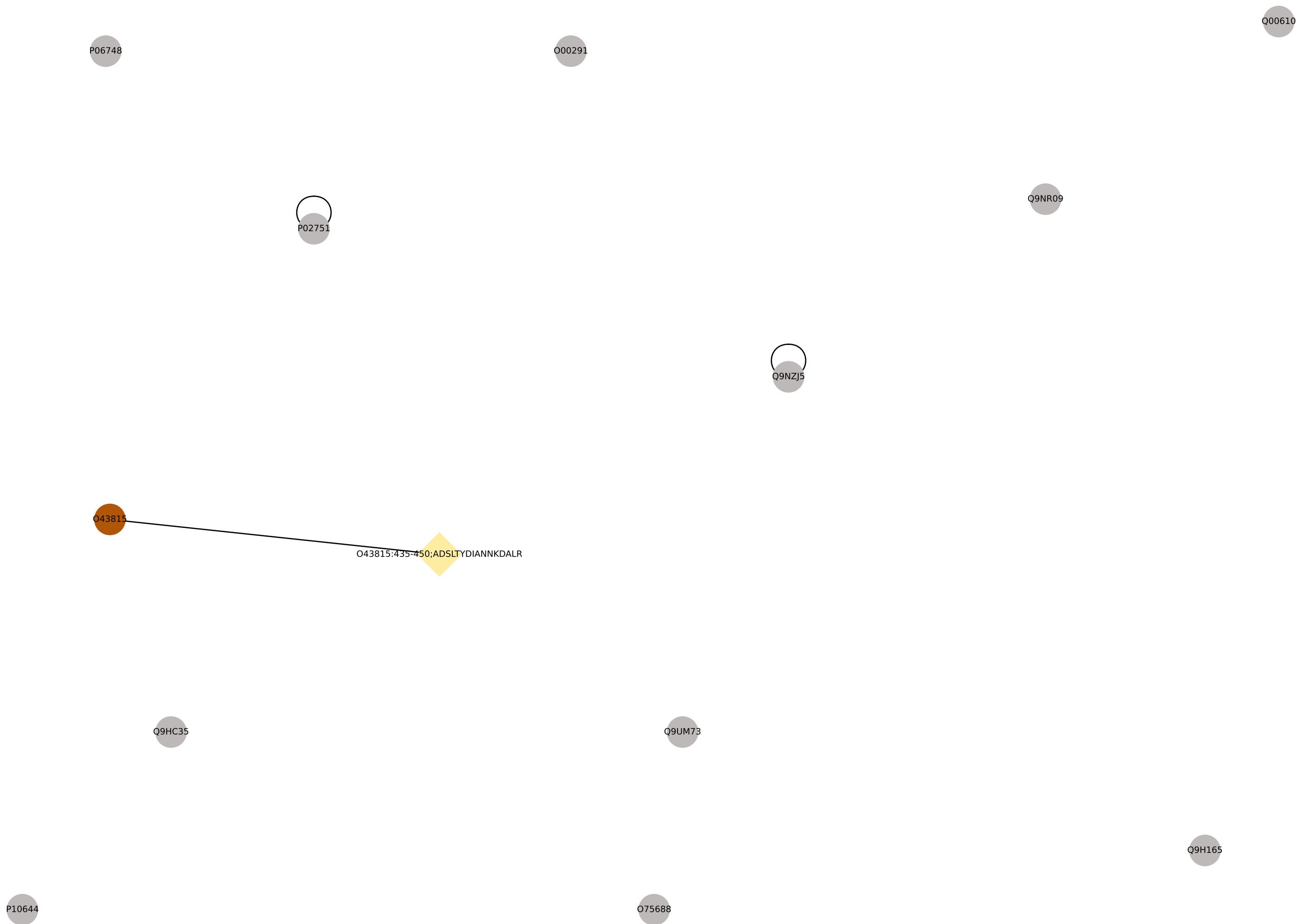
Log2 fold change: gluc vs. control  
R-HSA-77588: SLBP Dependent Processing of Replication-Dependent Histone Pre-mRNAs  
p-value: 0.04103493715974438



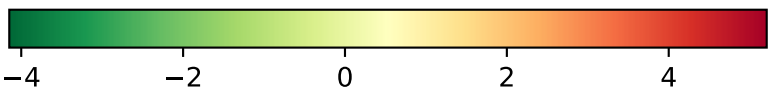
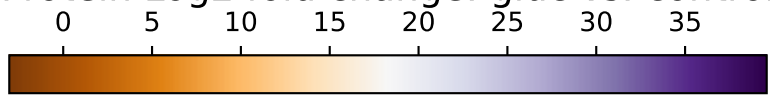
Log2 fold change: gluc vs. control  
R-HSA-9013418: RHOBTB2 GTPase cycle  
p-value: 0.003870027935771292



Log2 fold change: gluc vs. control  
R-HSA-9700645: ALK mutants bind TKIs  
p-value: 0.04468226372702311

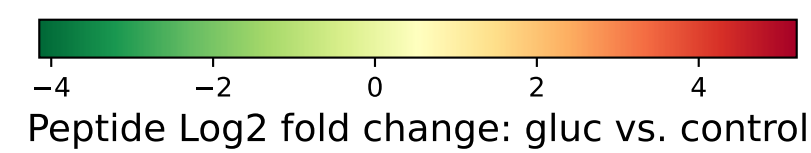
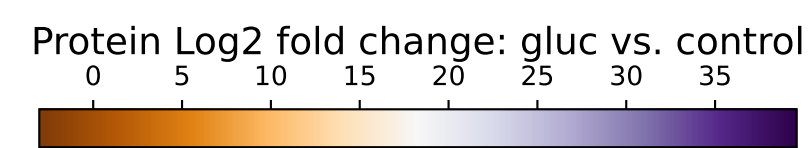
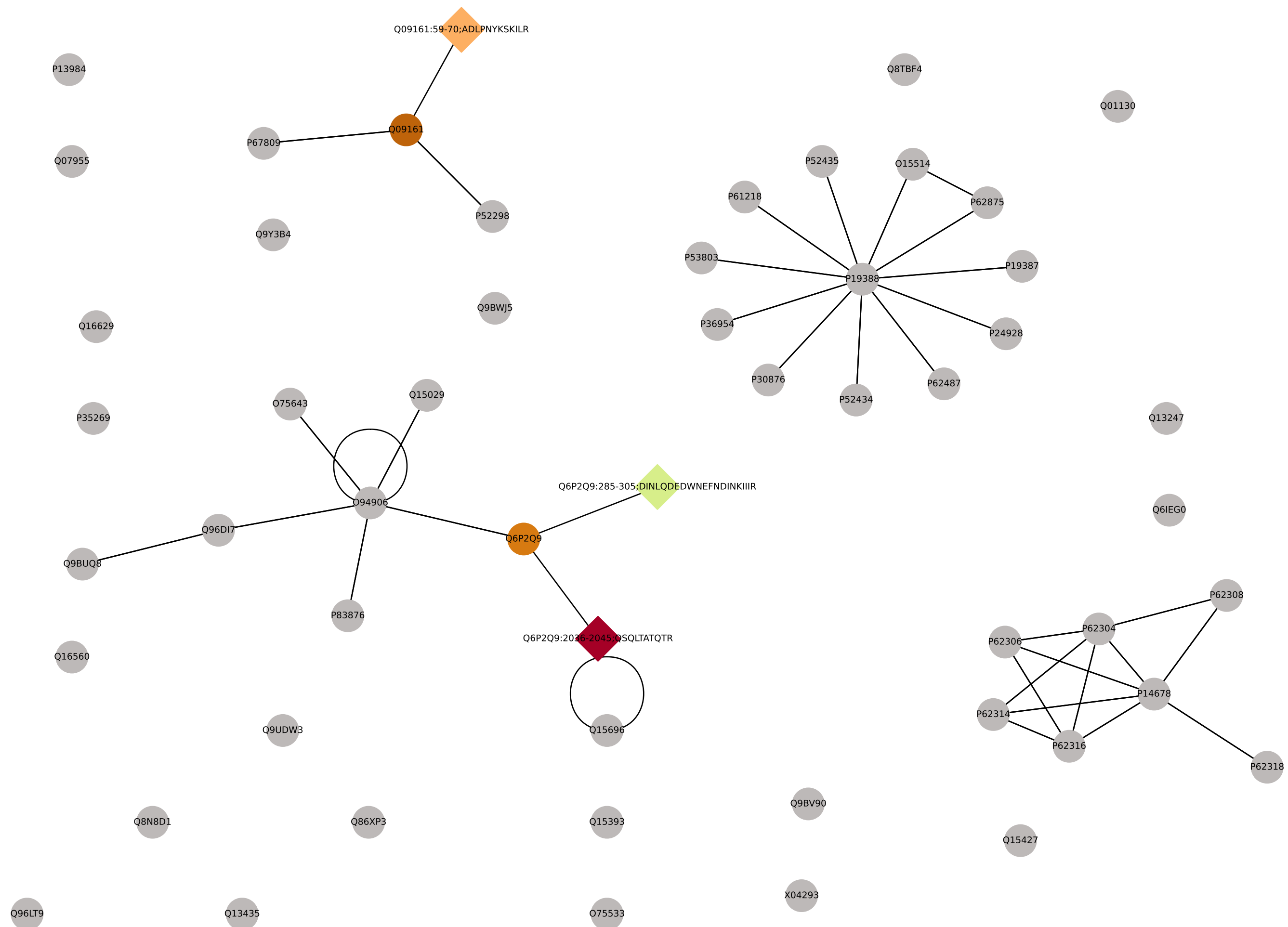


Protein Log2 fold change: gluc vs. control

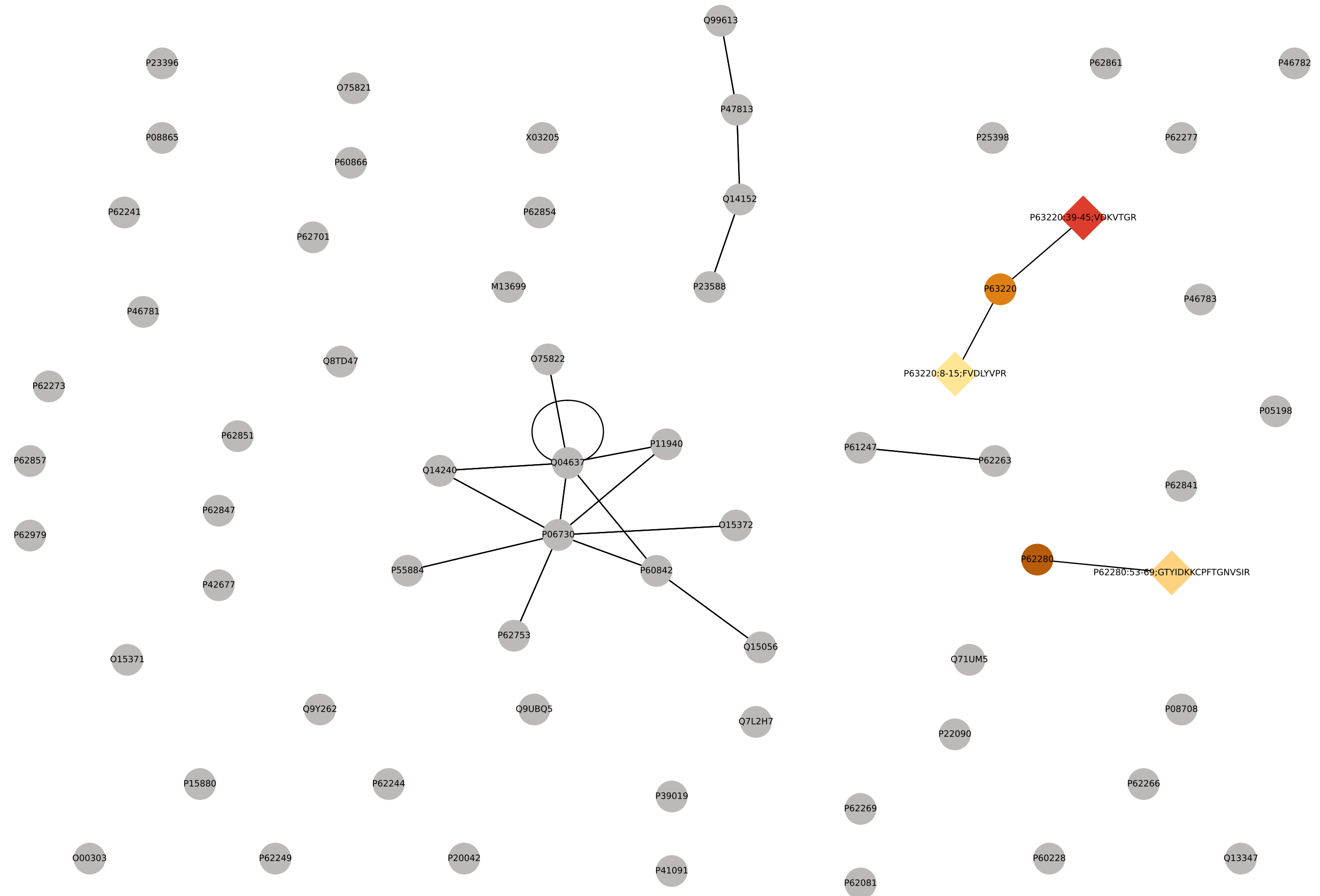


Peptide Log2 fold change: gluc vs. control

Log2 fold change: gluc vs. control  
R-HSA-72165: mRNA Splicing - Minor Pathway  
p-value: 0.018216773752471993

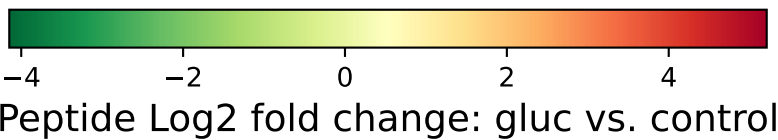
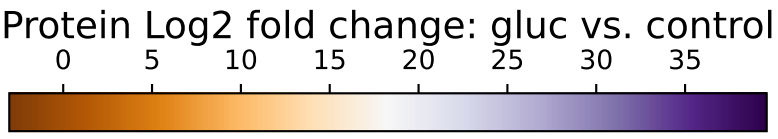
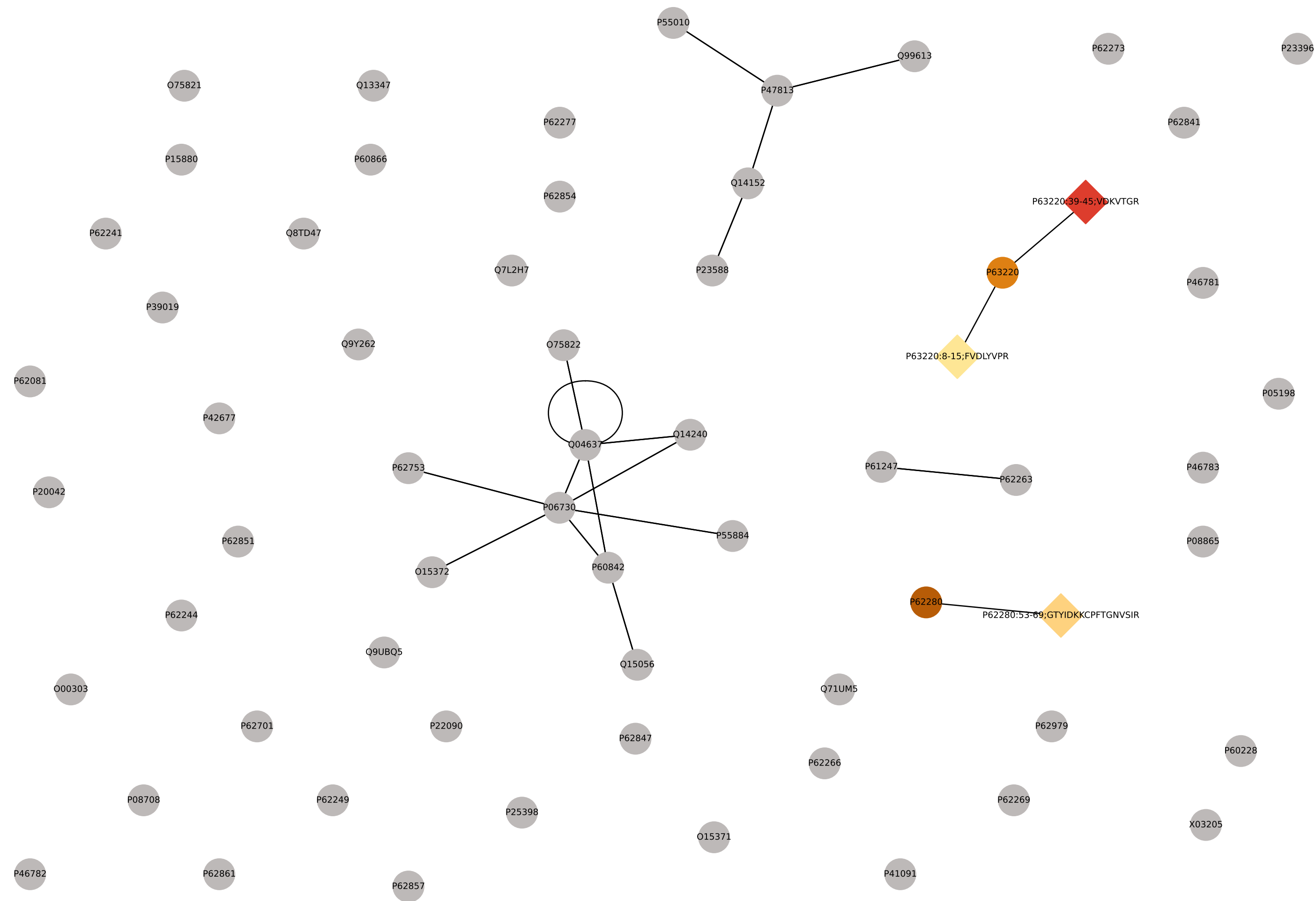


Log2 fold change: gluc vs. control  
R-HSA-72649: Translation initiation complex formation  
p-value: 0.023554931232115828

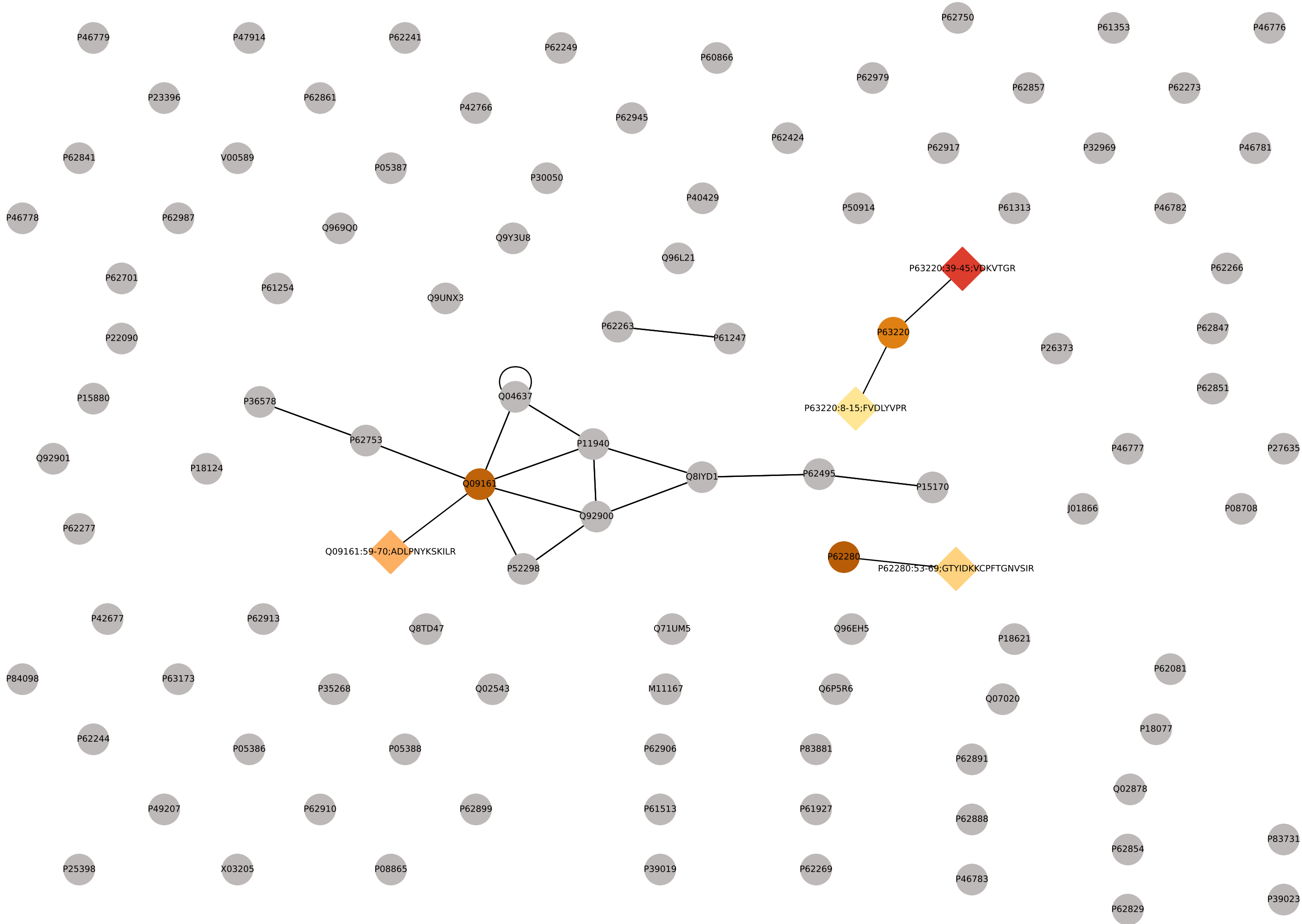




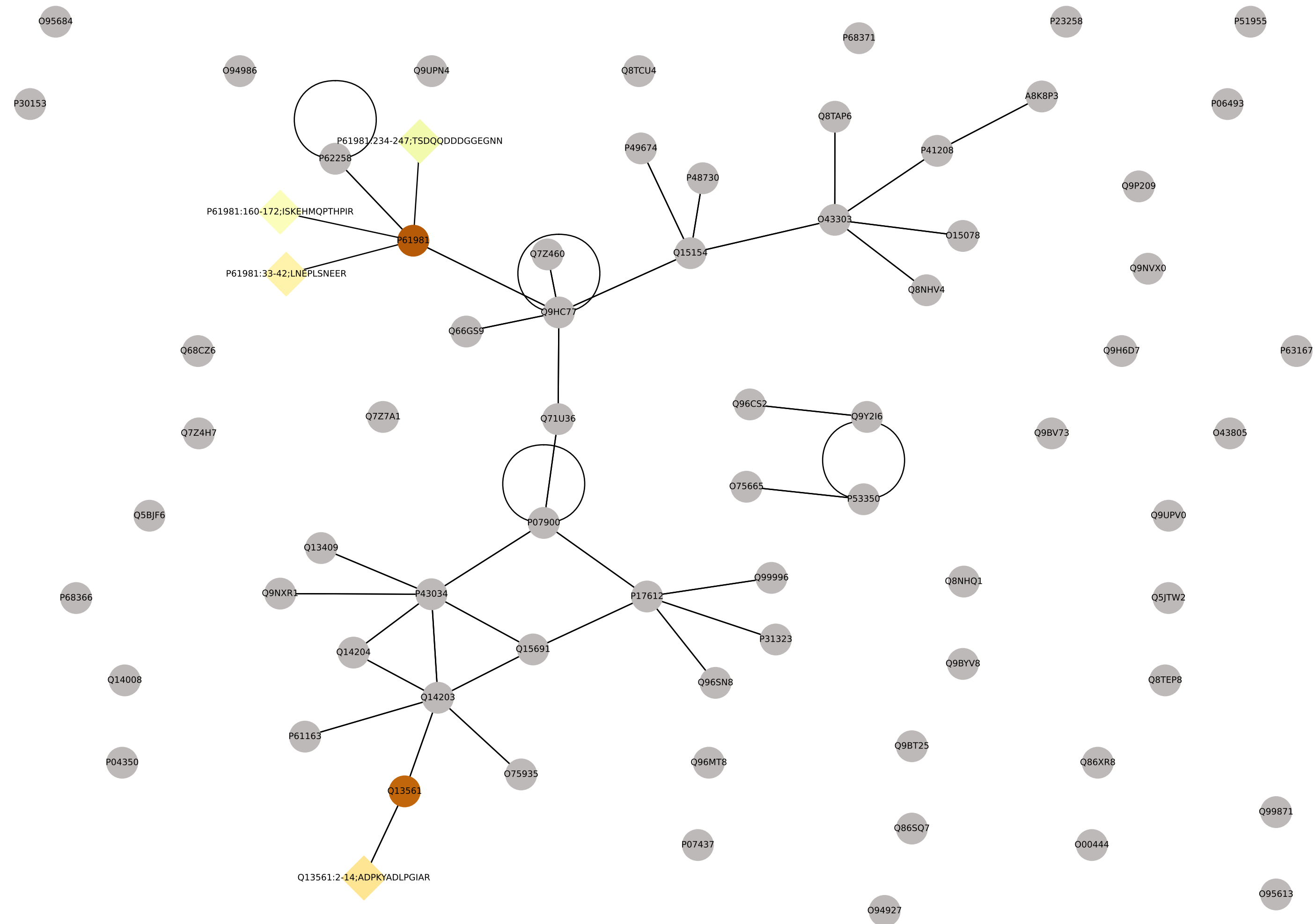
Log2 fold change: gluc vs. control  
R-HSA-72702: Ribosomal scanning and start codon recognition  
p-value: 0.024978417082091475



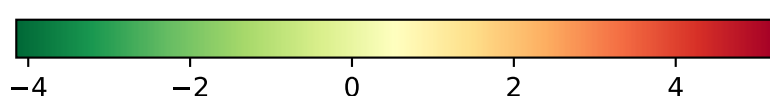
Log2 fold change: gluc vs. control  
R-HSA-975956: Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC)  
p-value: 0.006855569728165922



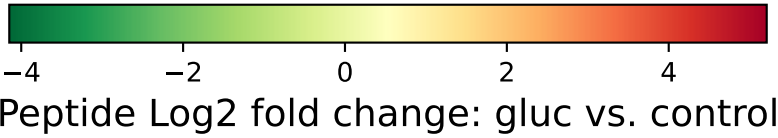
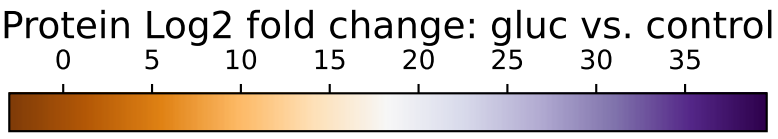
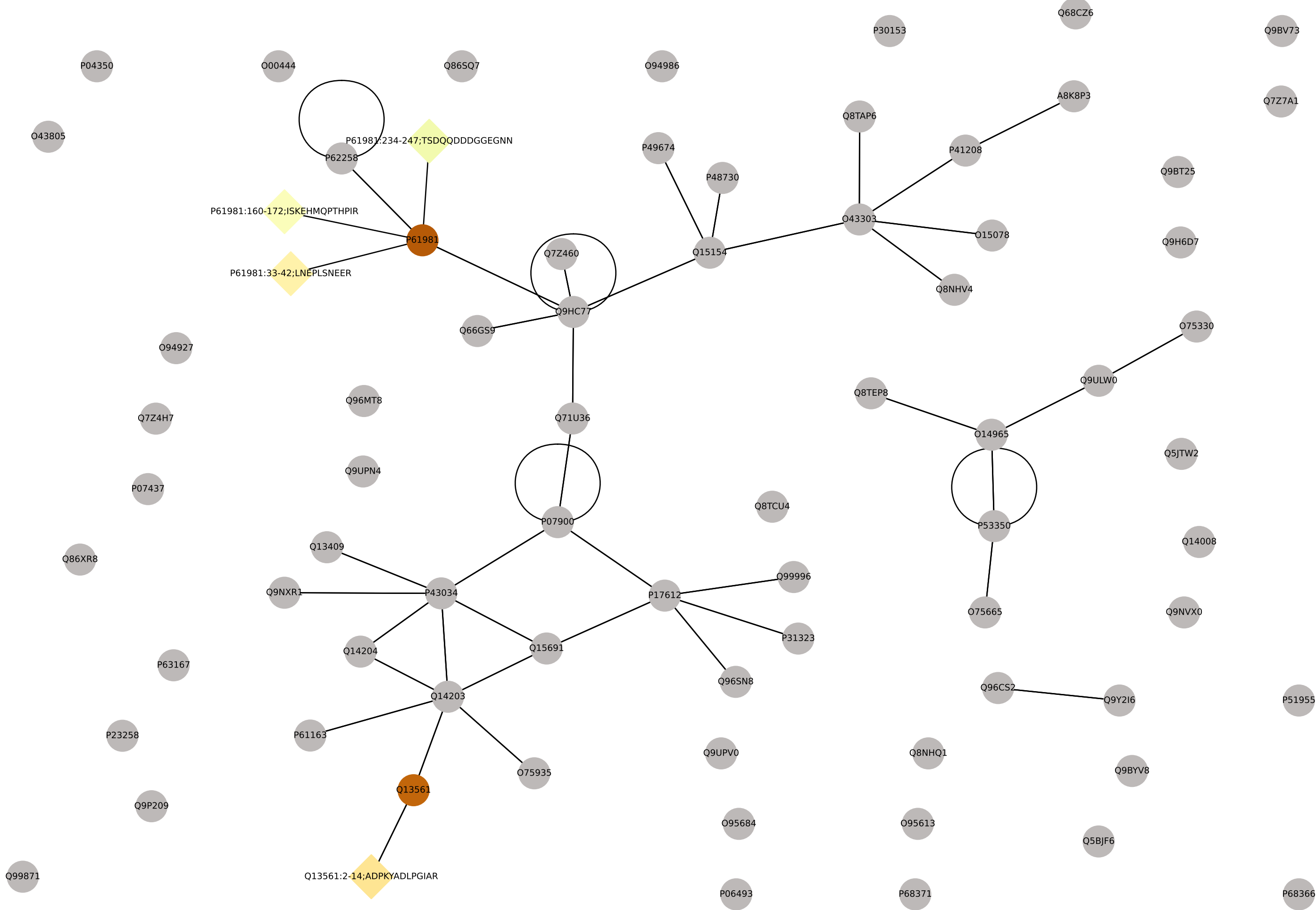
Log2 fold change: gluc vs. control  
R-HSA-380284: Loss of proteins required for interphase microtubule organization from the centrosome  
p-value: 0.030227589686308676



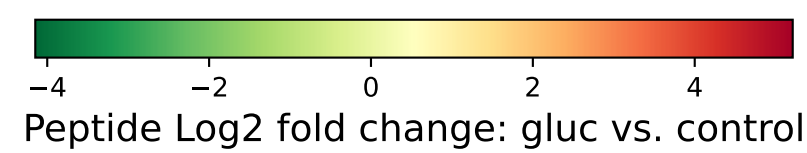
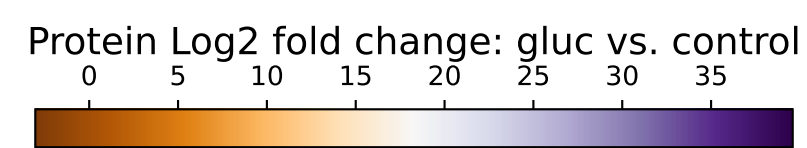
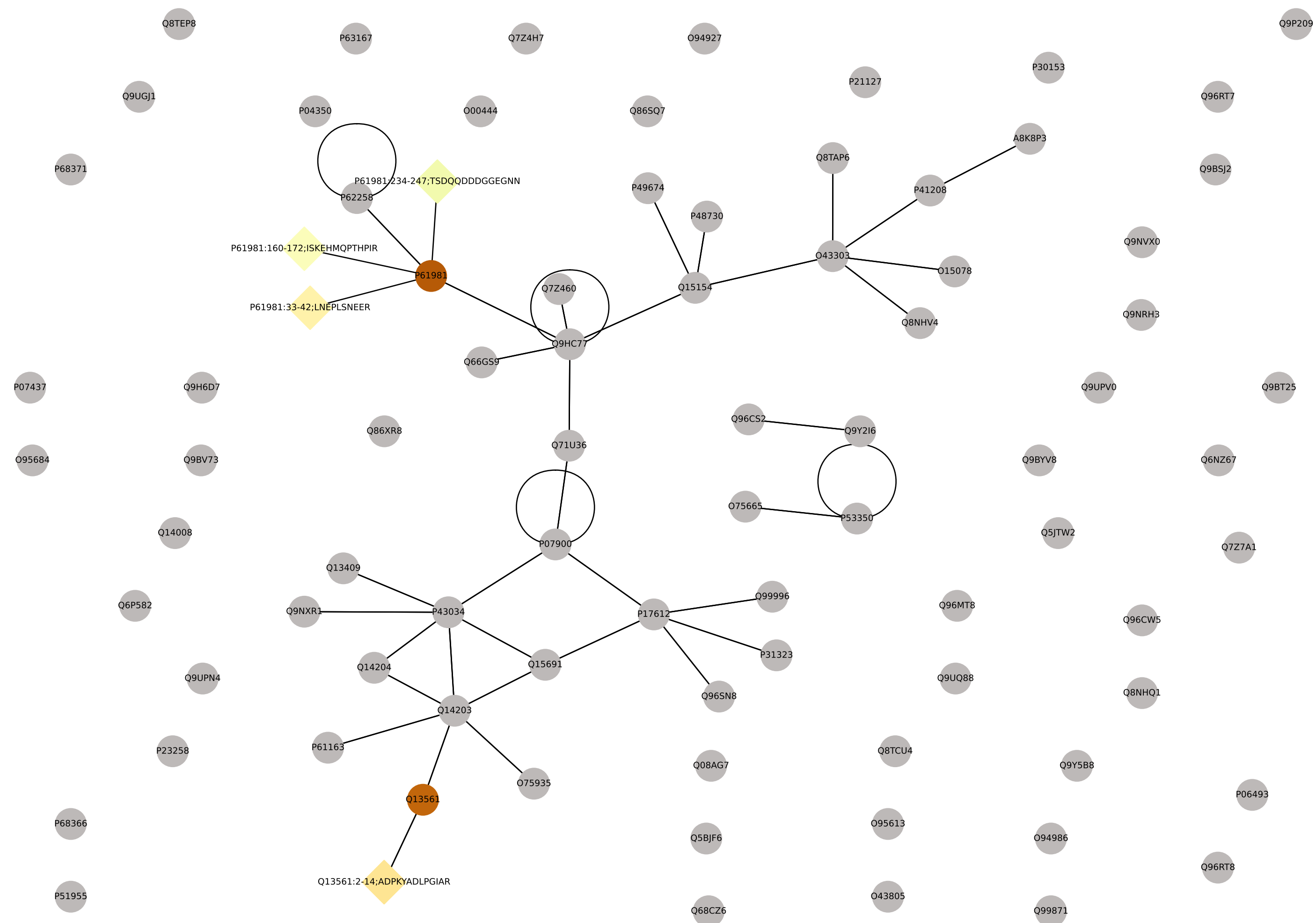
The diagram illustrates a complex network of protein-protein interactions. Nodes are represented by circles, some labeled with protein IDs (e.g., P61981, Q13561) and others with gene names (e.g., P61981:234-247;TSDQDDDDGGEGNN). Nodes are connected by lines representing interactions. Some nodes are highlighted in yellow (e.g., P61981:160-172;ISKHEMQPTHPIR, Q13561:2-14;ADPKYADLPGIAR) and others in orange (e.g., P61981, Q13561). The diagram illustrates a dense network of protein-protein interactions, with several clusters and a central hub-and-spoke structure.



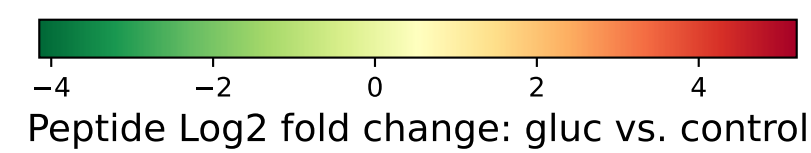
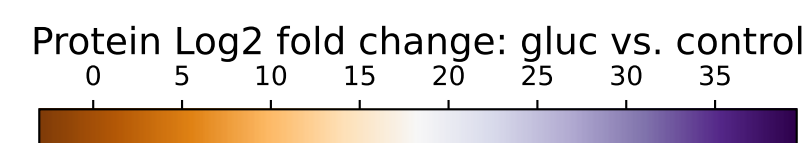
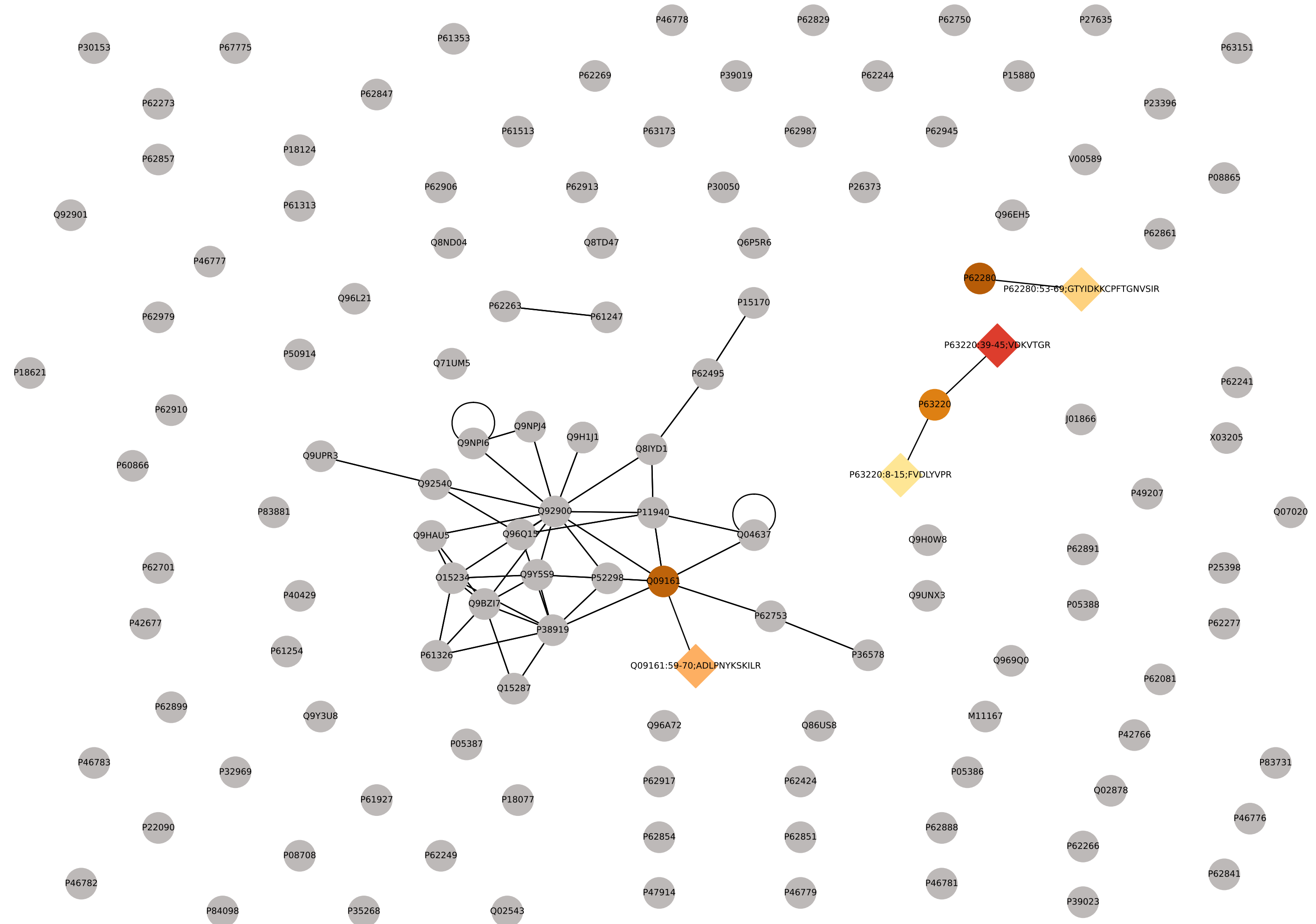
Log2 fold change: gluc vs. control  
R-HSA-8854518: AURKA Activation by TPX2  
p-value: 0.032600049302680456



Log2 fold change: gluc vs. control  
R-HSA-380270: Recruitment of mitotic centrosome proteins and complexes  
p-value: 0.0384084717376354



Log2 fold change: gluc vs. control  
R-HSA-927802: Nonsense-Mediated Decay (NMD)  
p-value: 0.011931898374331729





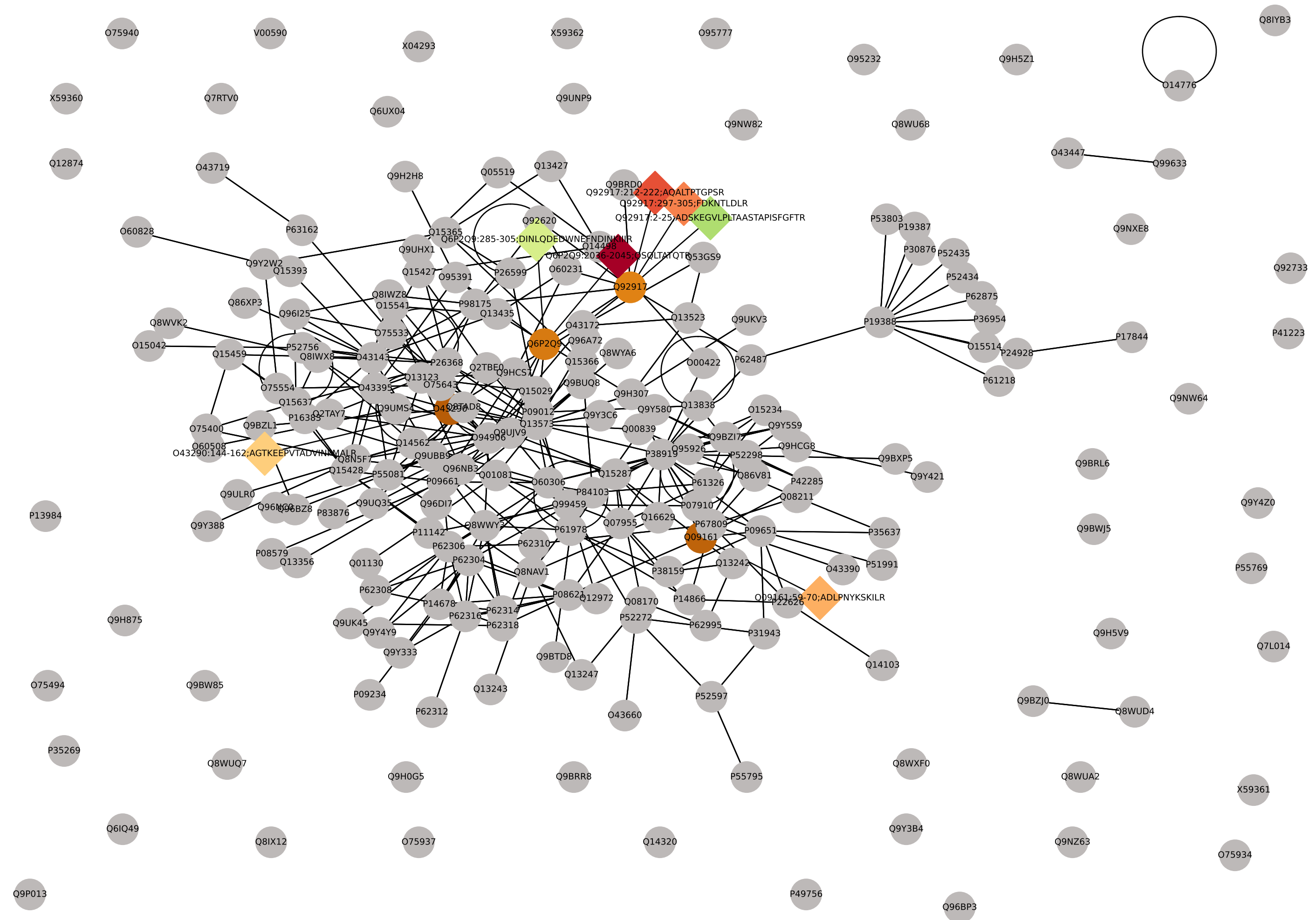




The diagram illustrates a protein-protein interaction network. The nodes are labeled with UniProt IDs, and the edges represent interactions. The network is highly interconnected, with many nodes having multiple connections. The layout is circular, with nodes arranged in concentric rings around a central cluster. The nodes are color-coded: grey for standard nodes, orange for nodes of interest (P61981 and Q13561), and yellow for specific protein regions (P61981:234-247:TSDQDDDDGGEGNN, P61981:160-172:ISKHEMQPTHPIR, and Q13561:2-14:ADPKYADLPGIAR).



Log2 fold change: gluc vs. control  
R-HSA-72163: mRNA Splicing - Major Pathway  
p-value: 0.008907459881584257



Log2 fold change: gluc vs. control  
R-HSA-72172: mRNA Splicing  
p-value: 0.01056574513476305

