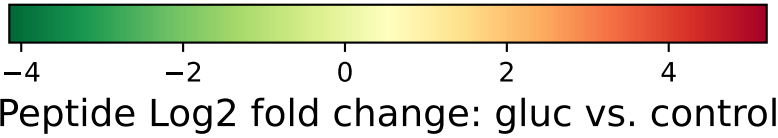
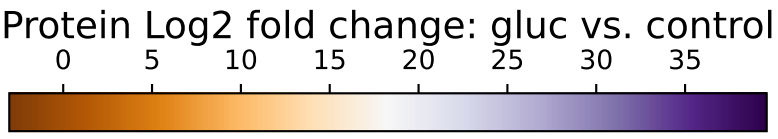
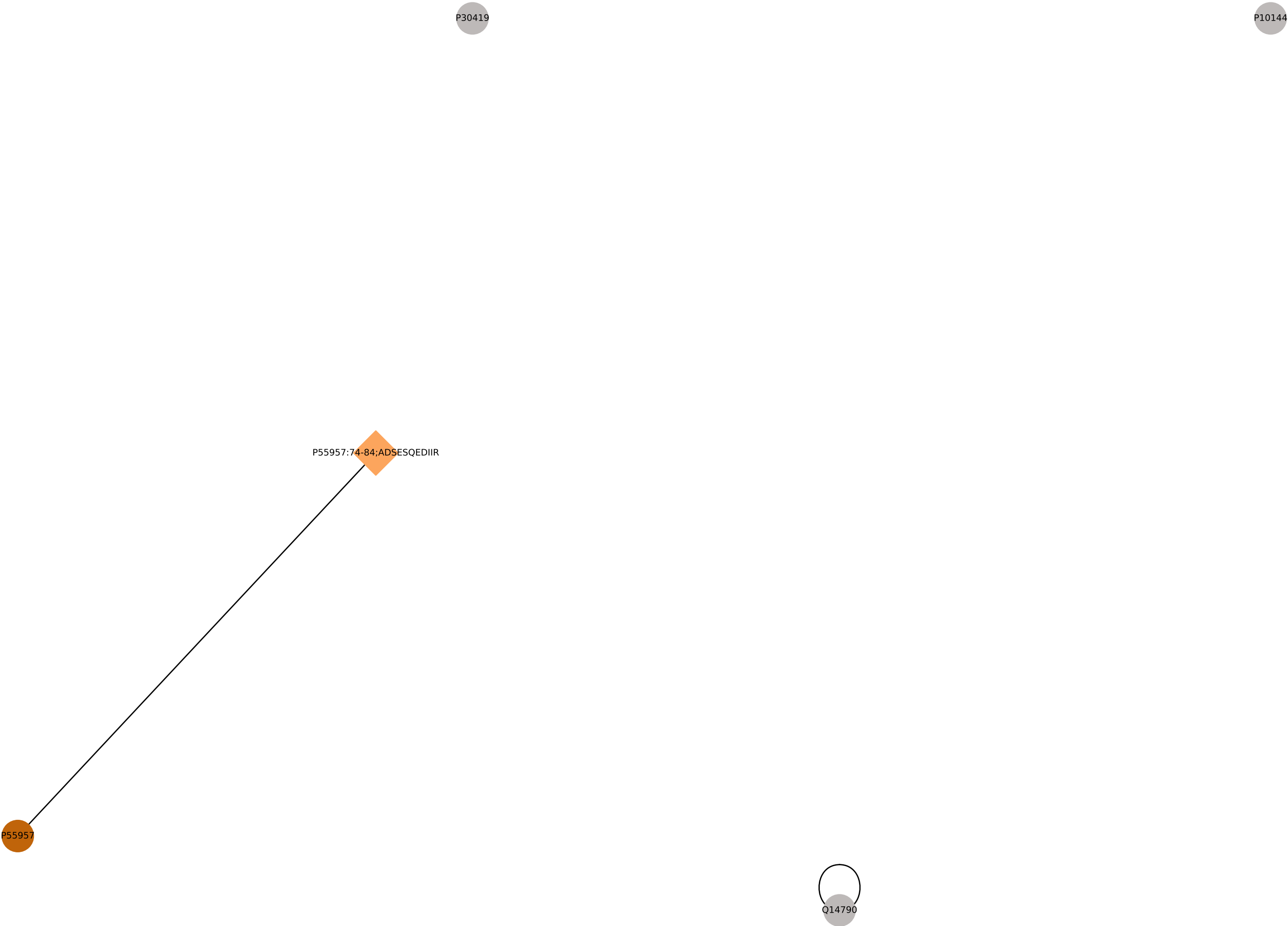
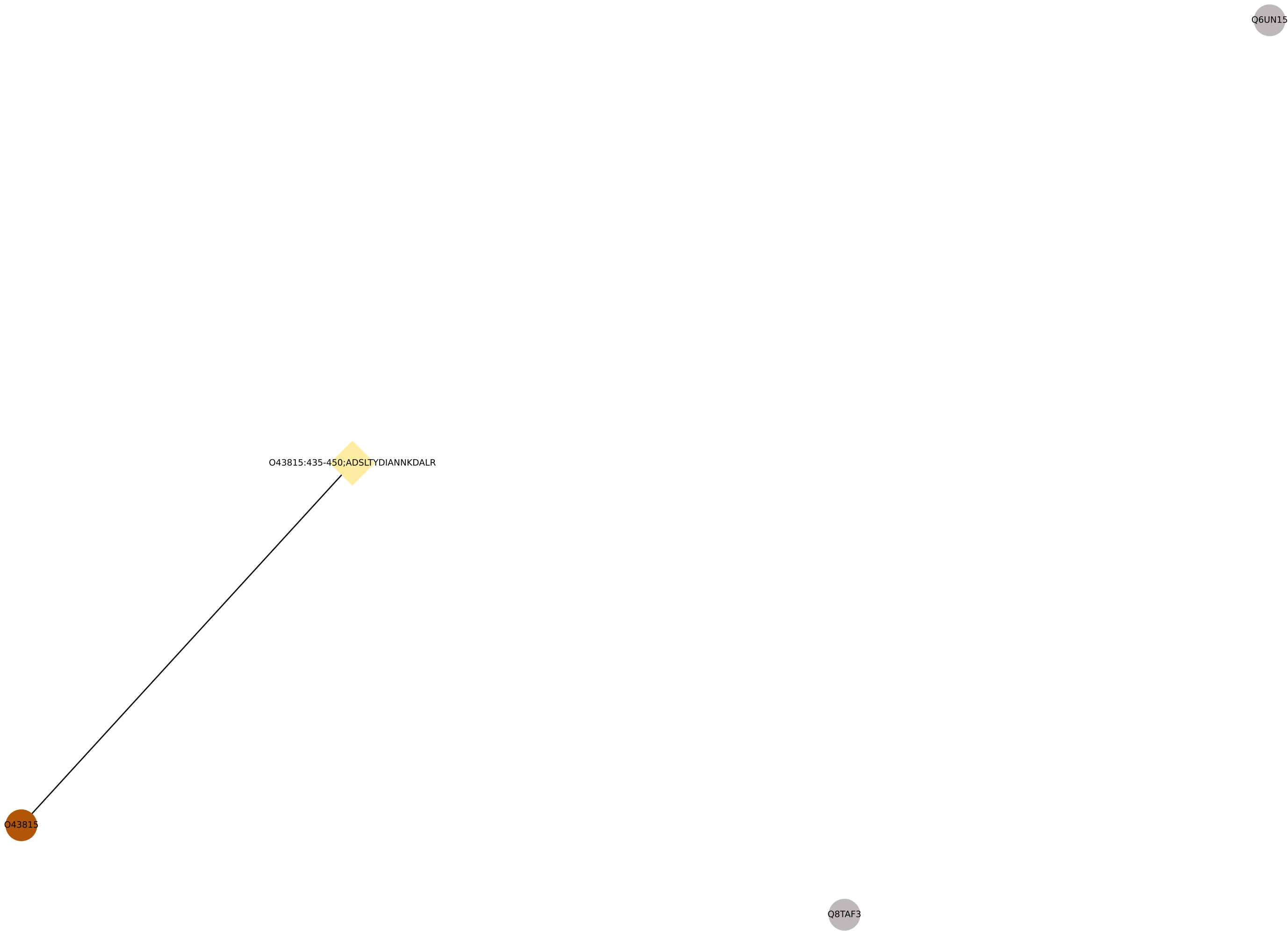


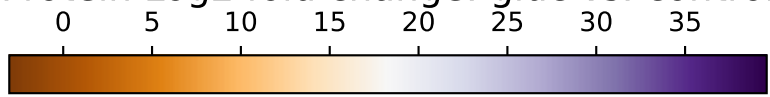
Log2 fold change: gluc vs. control
R-HSA-75108: Activation, myristoylation of BID and translocation to mitochondria
p-value: 0.015117656007649471



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

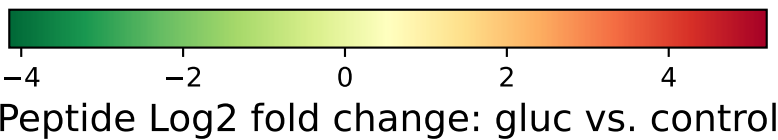
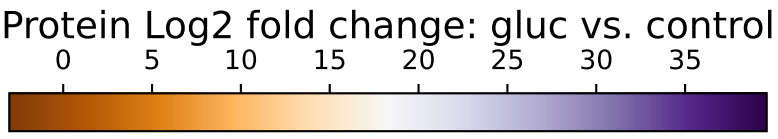
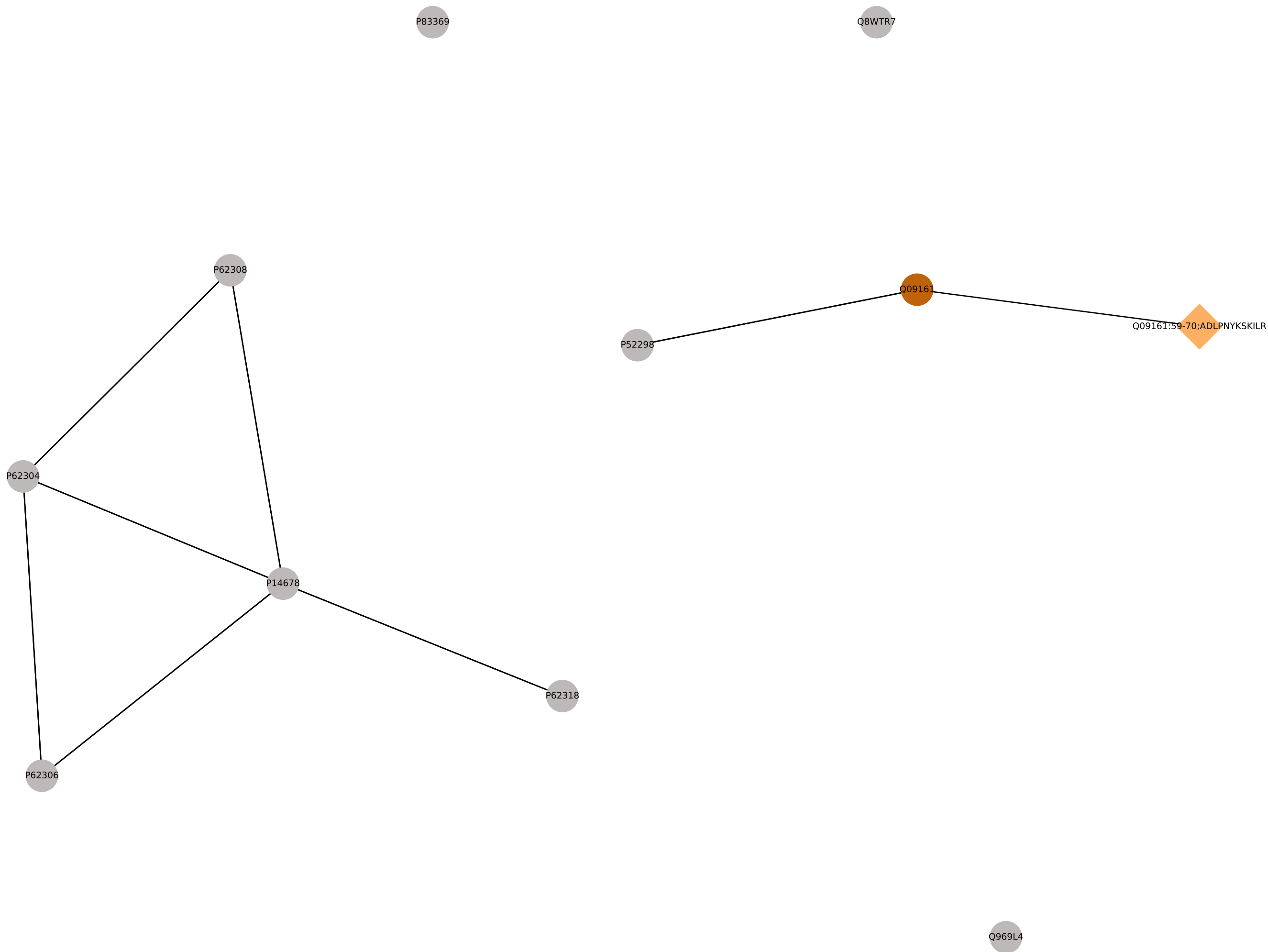


Protein Log2 fold change: gluc vs. control

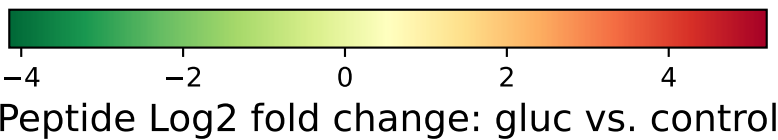
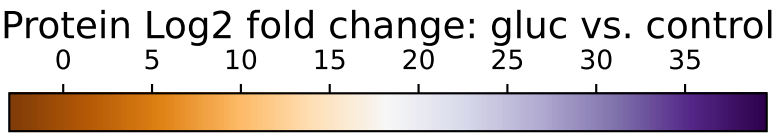
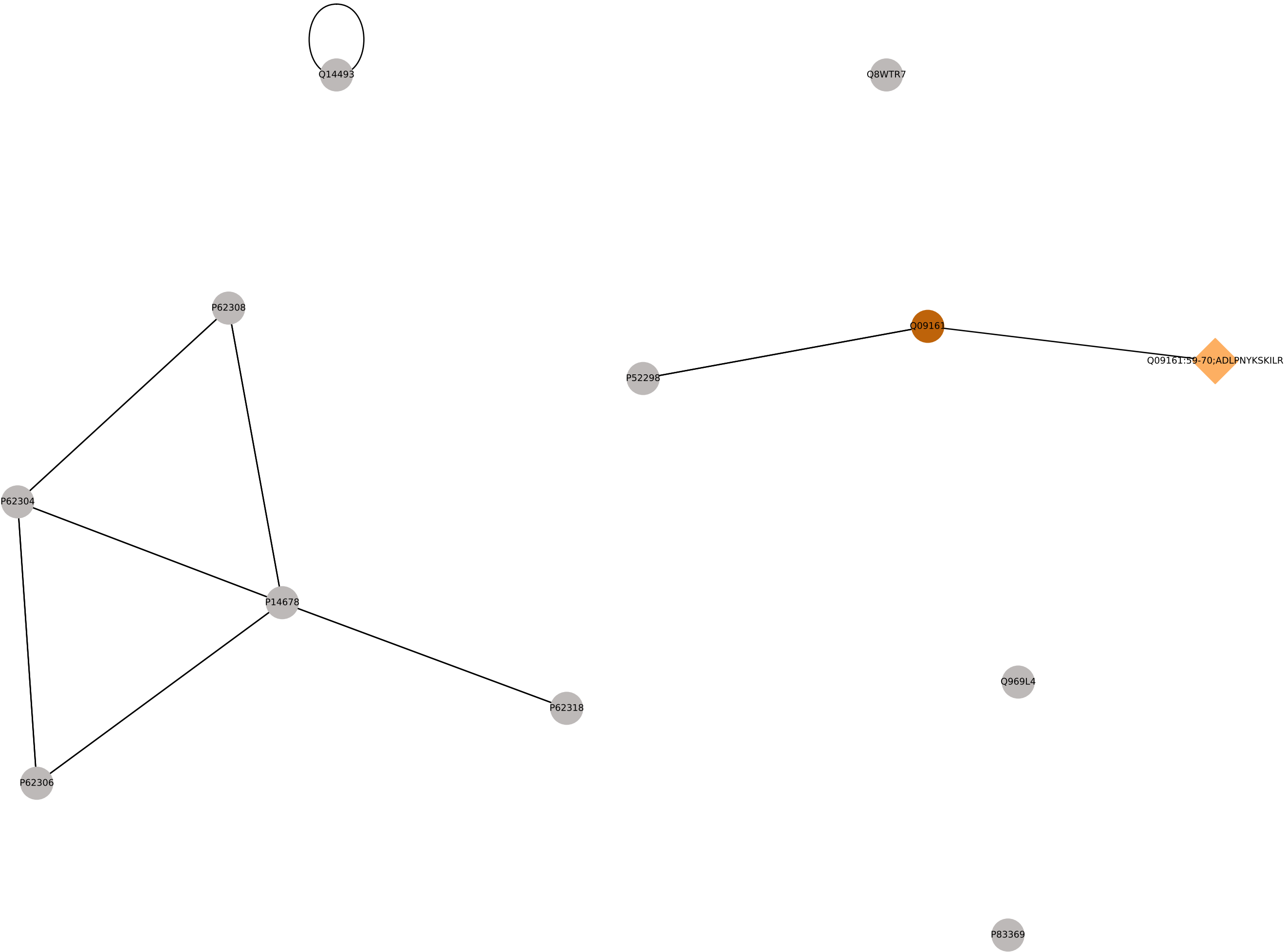


Peptide Log2 fold change: gluc vs. control

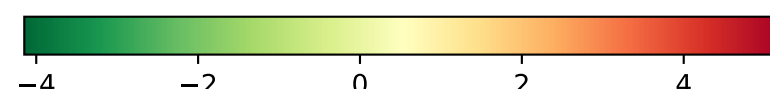
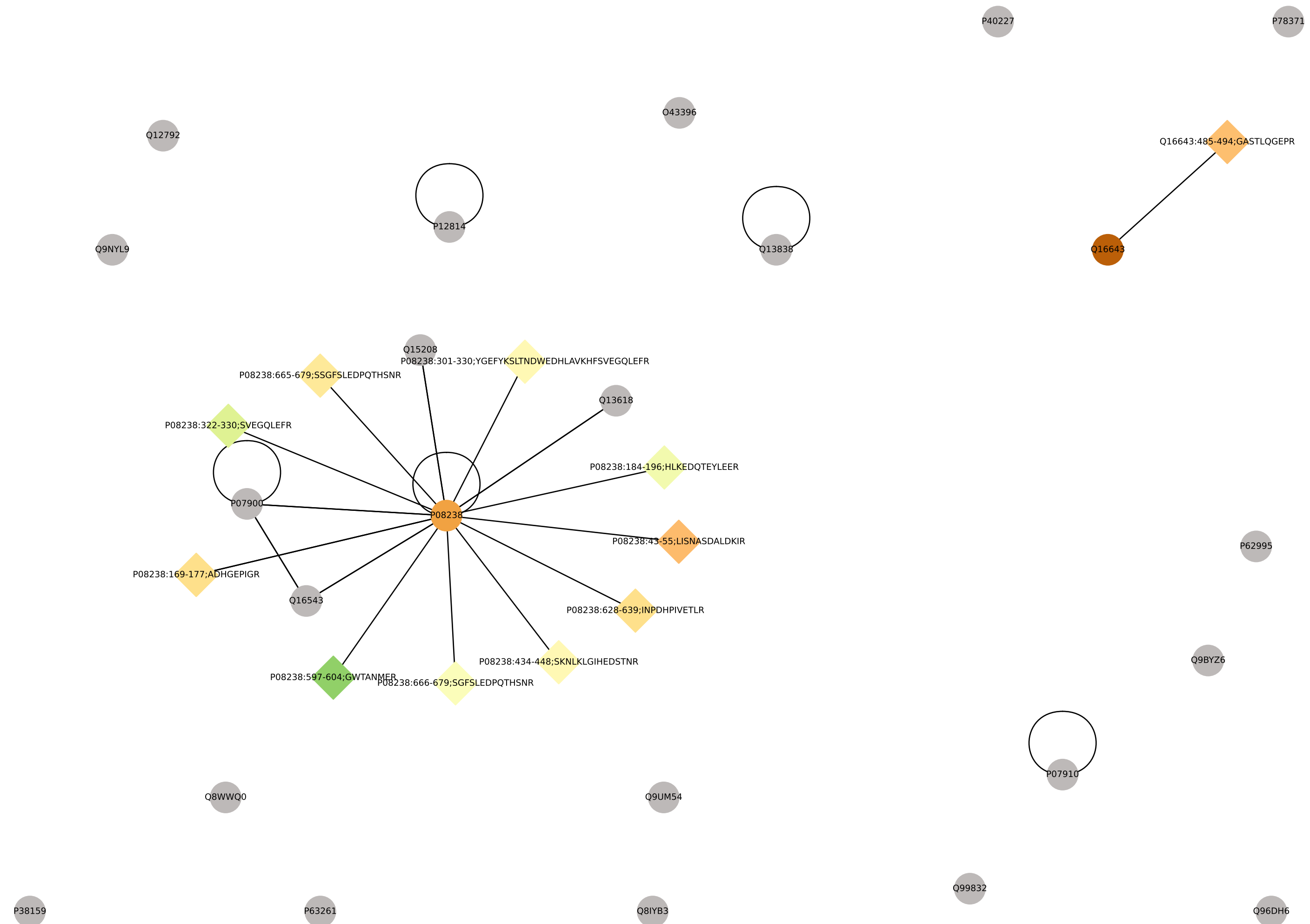
Log2 fold change: gluc vs. control
R-HSA-111367: SLBP independent Processing of Histone Pre-mRNAs
p-value: 0.03737392638204595



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

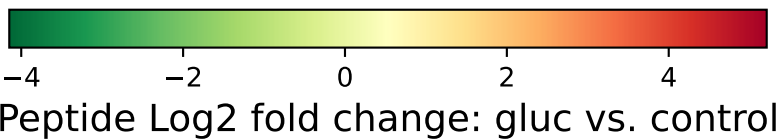
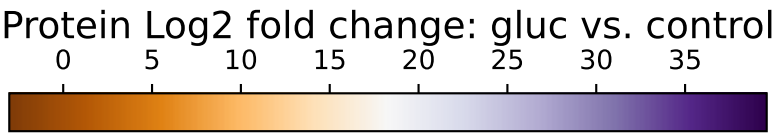
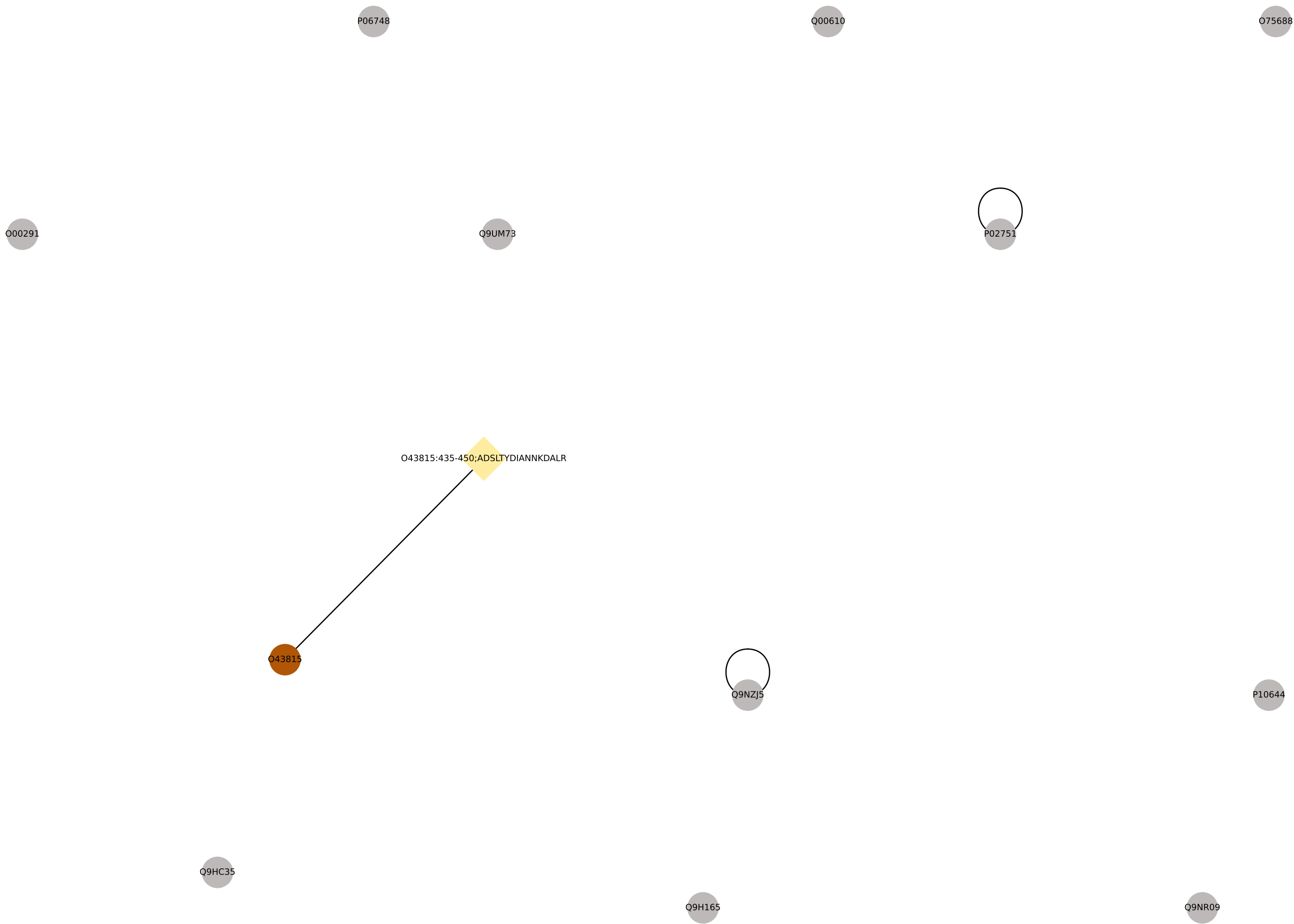


Log2 fold change: gluc vs. control
R-HSA-9013418: RHOBTB2 GTPase cycle
p-value: 0.003870027935771292

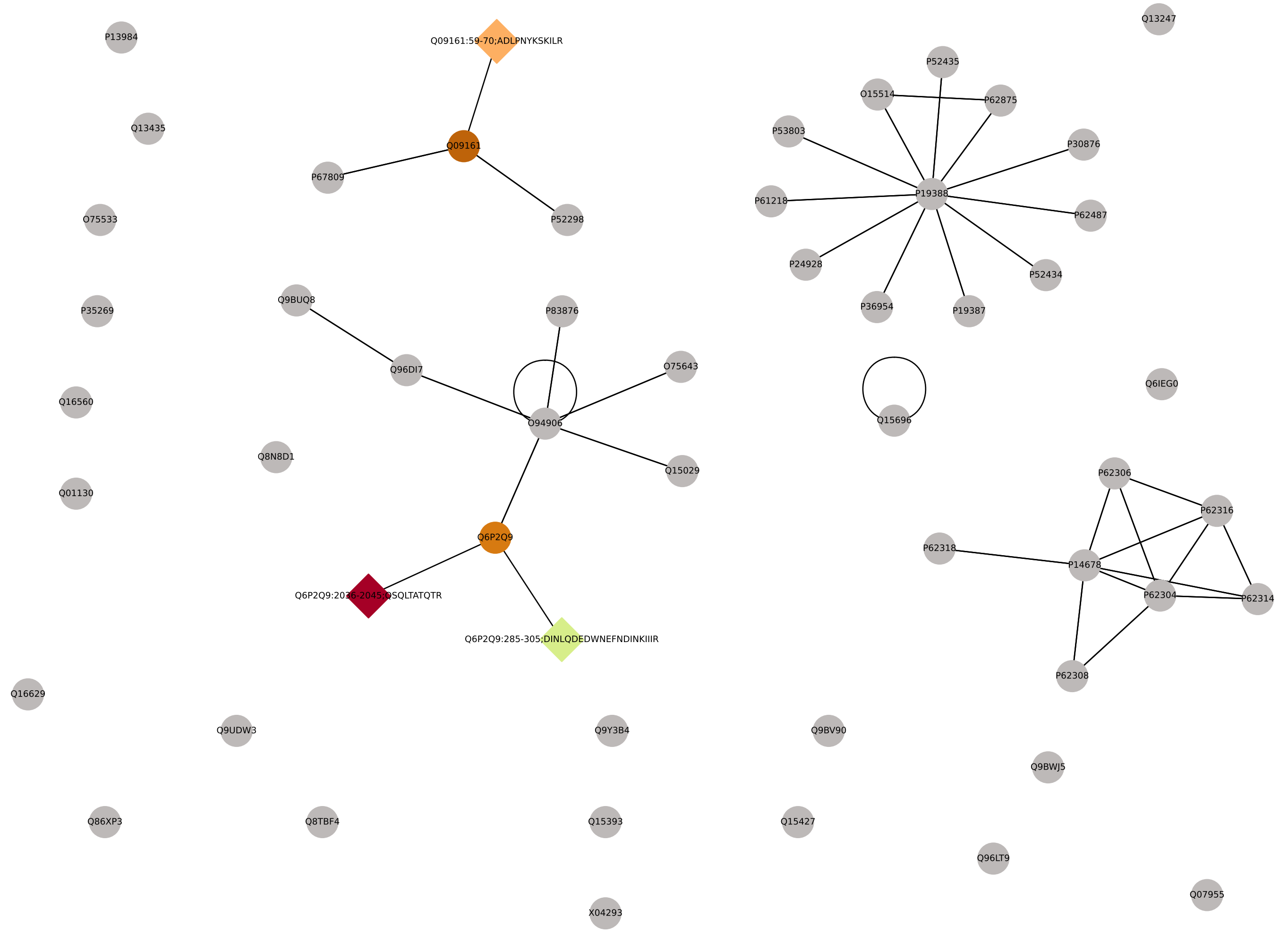


Peptide Log2 fold change: gluc vs. control

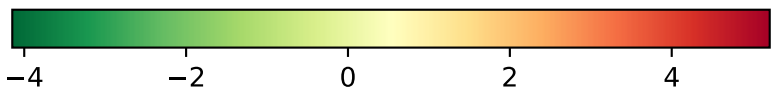
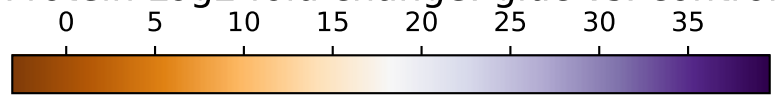
Log2 fold change: gluc vs. control
R-HSA-9700645: ALK mutants bind TKIs
p-value: 0.04468226372702311



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

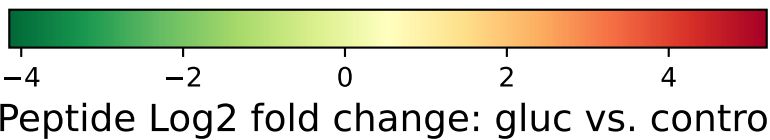
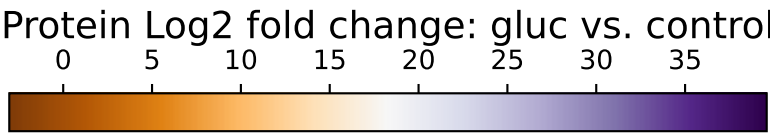
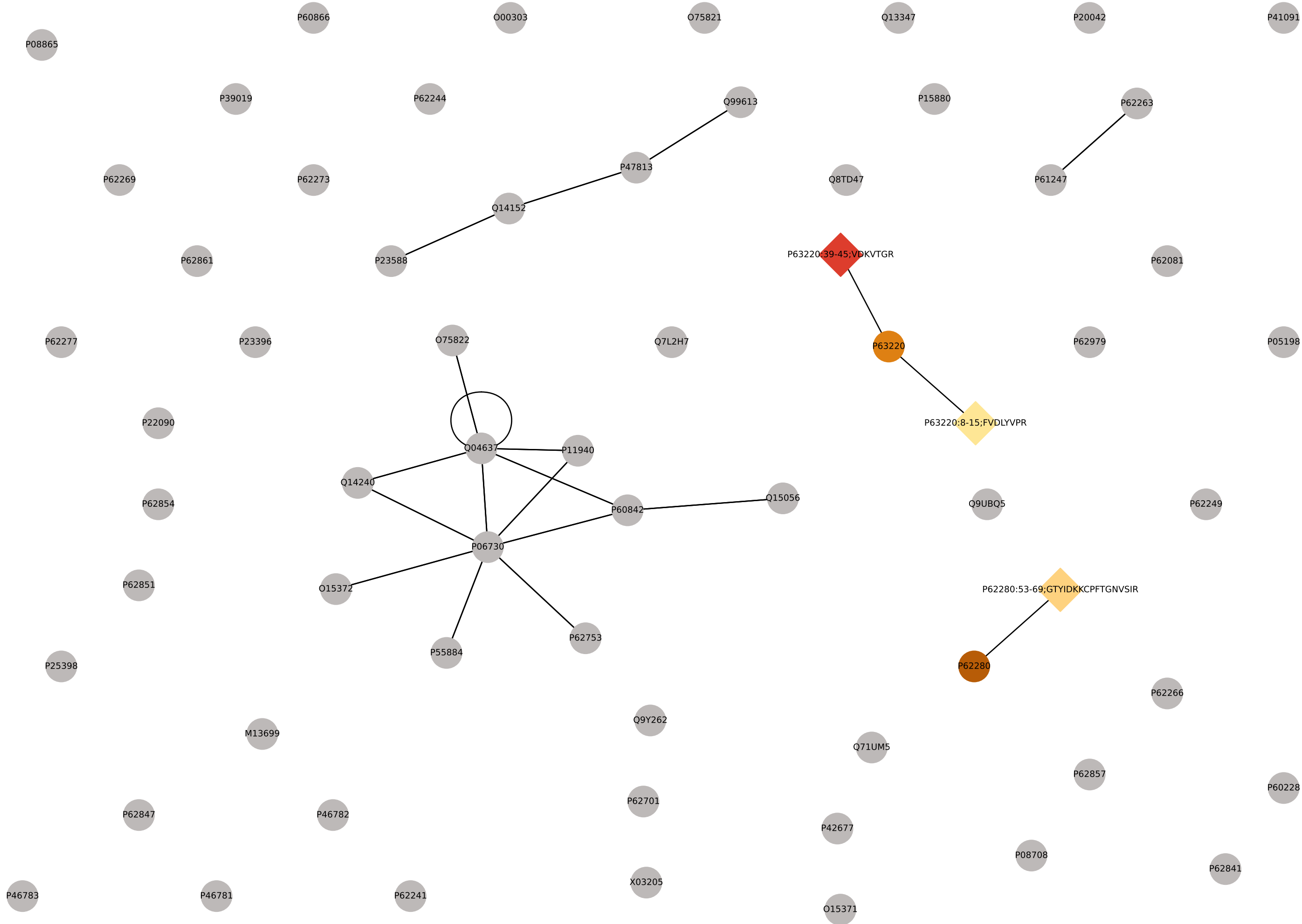


Protein Log2 fold change: gluc vs. control

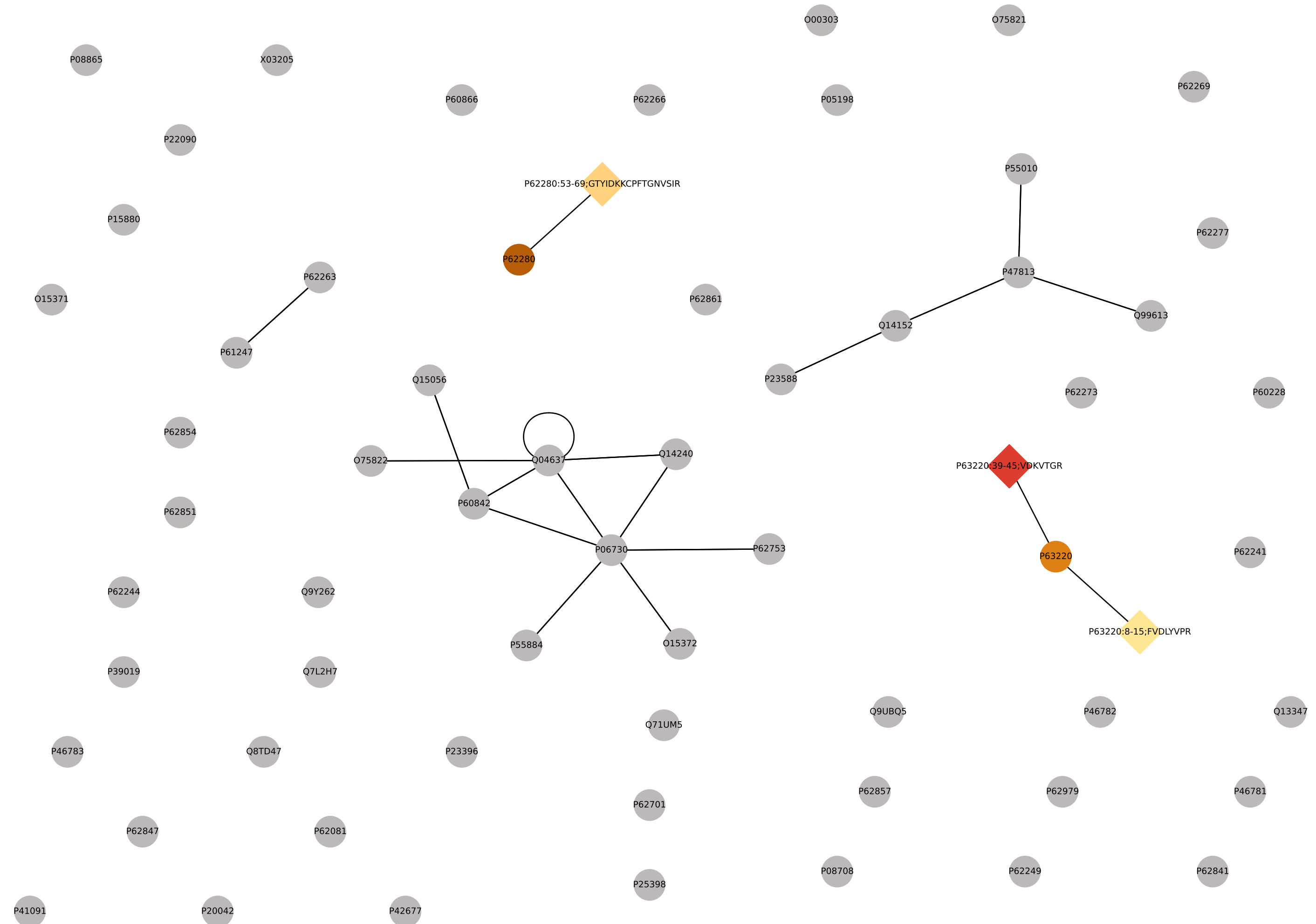


Peptide Log2 fold change: gluc vs. control

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

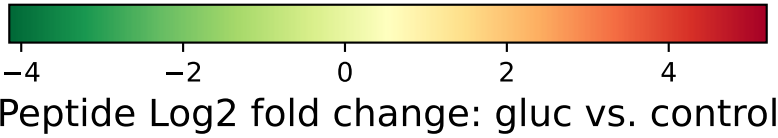
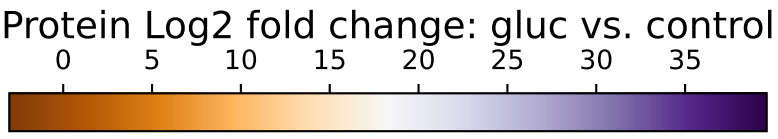
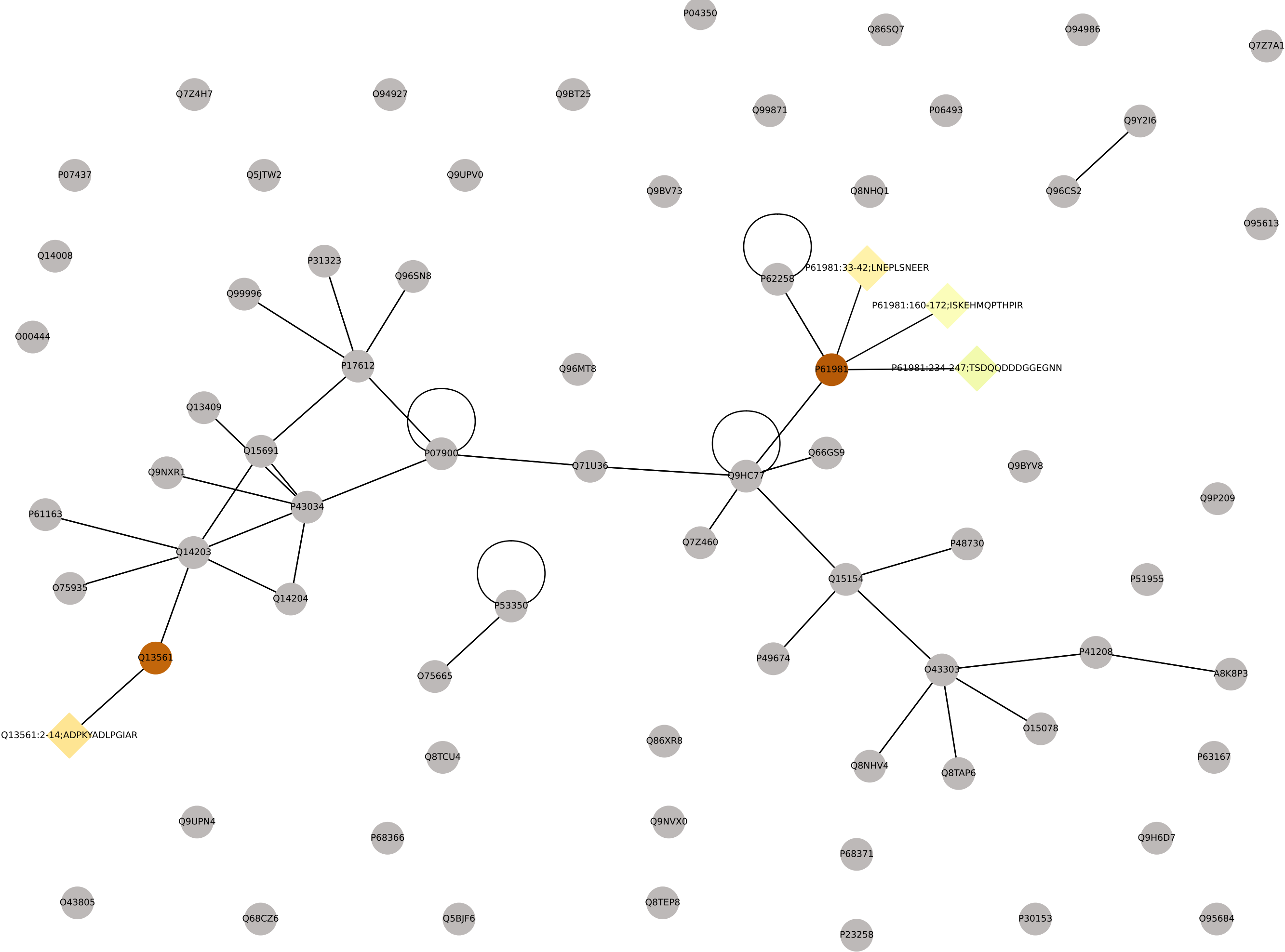


Log2 fold change: gluc vs. control
R-HSA-72702: Ribosomal scanning and start codon recognition
p-value: 0.024978417082091475

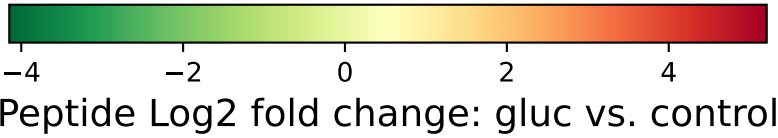
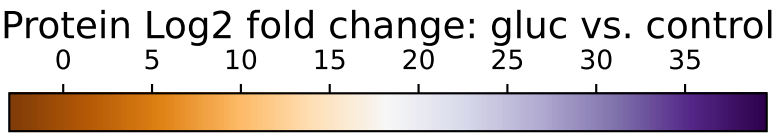
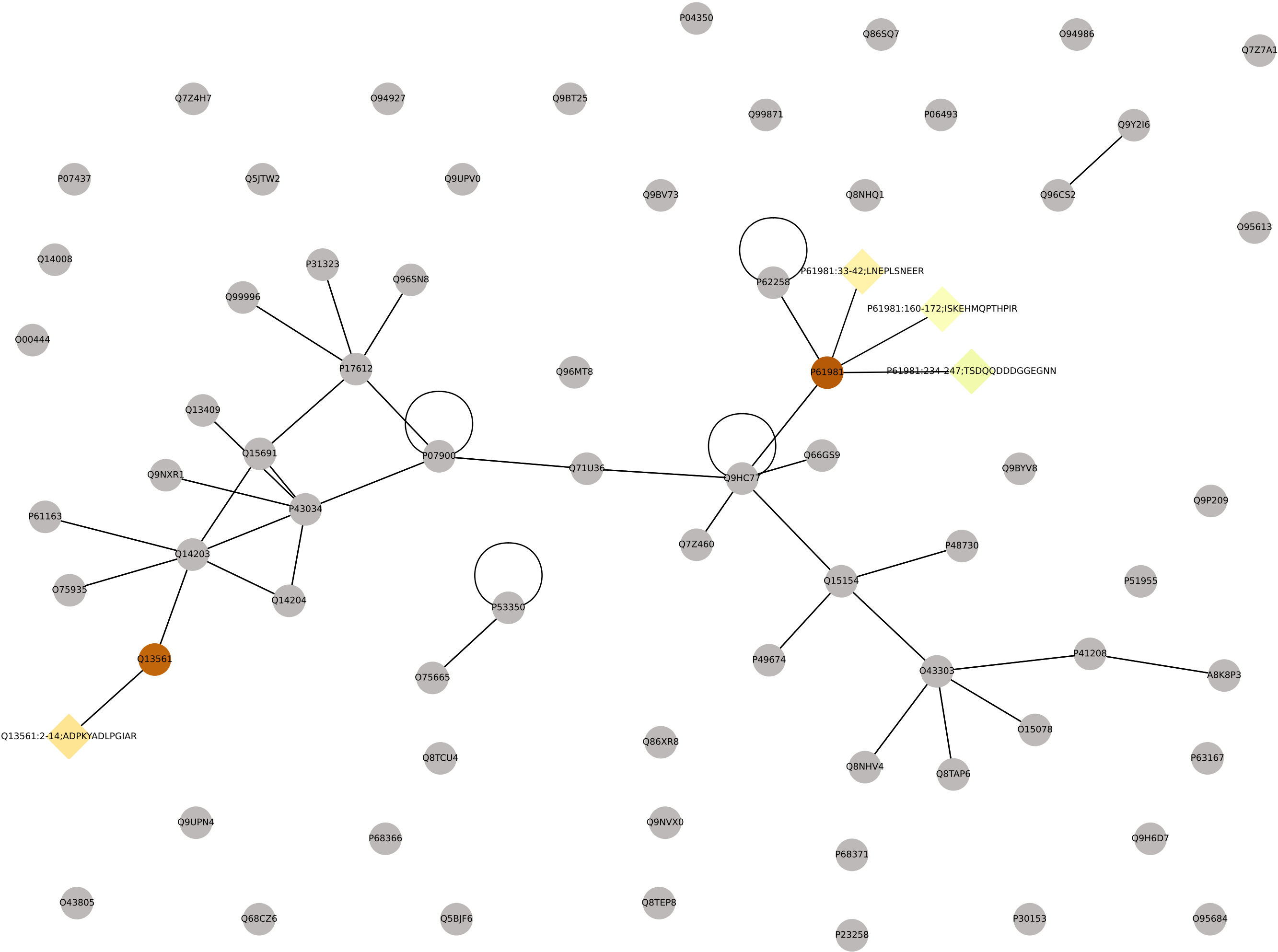


Peptide Log2 fold change: gluc vs. control

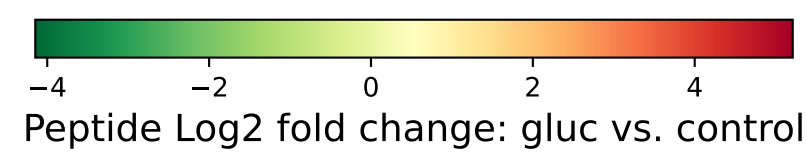
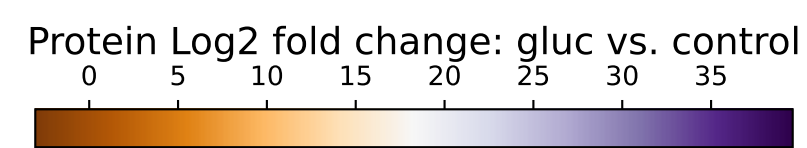
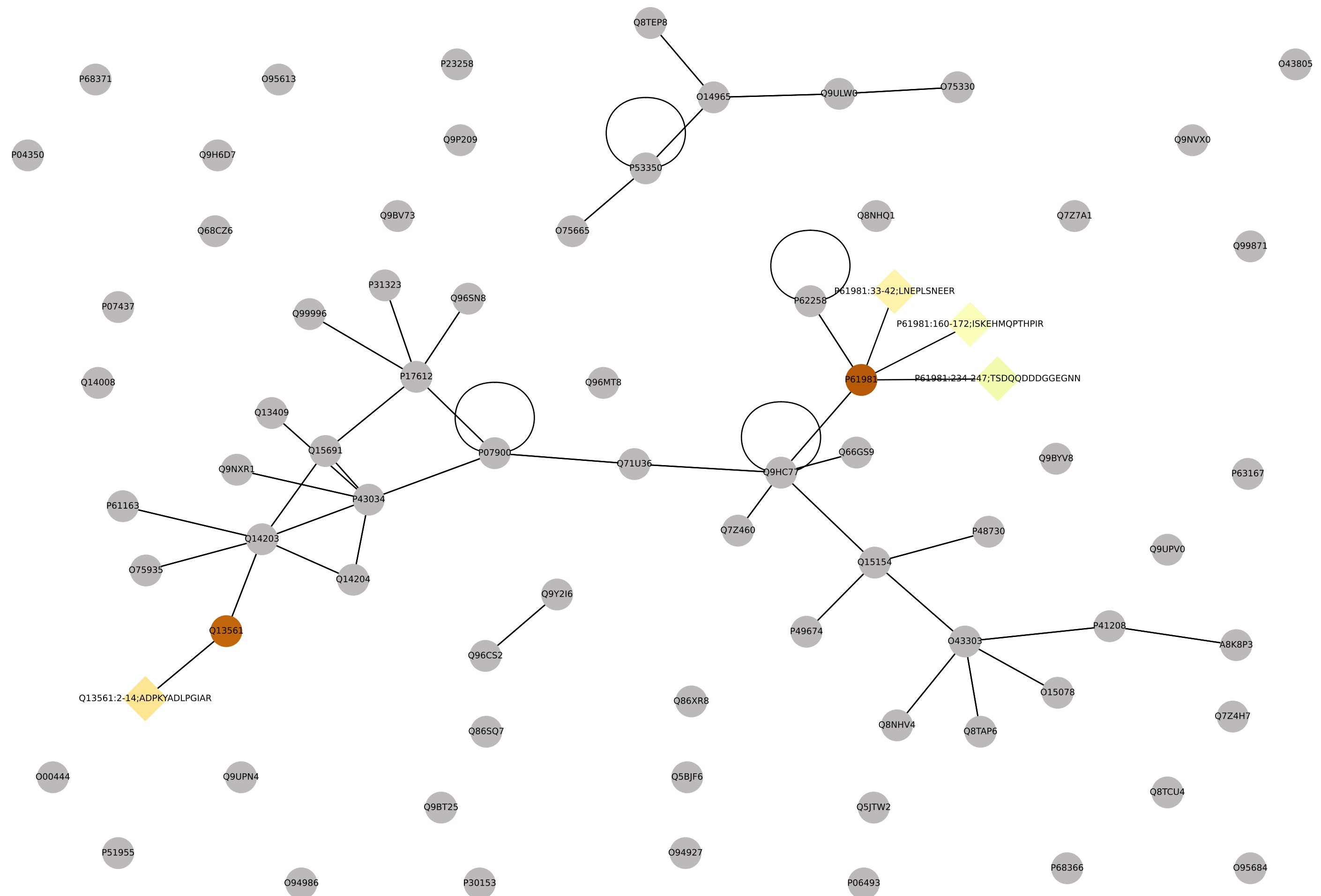
Log2 fold change: gluc vs. control
R-HSA-380284: Loss of proteins required for interphase microtubule organization from the centrosome
p-value: 0.030227589686308676



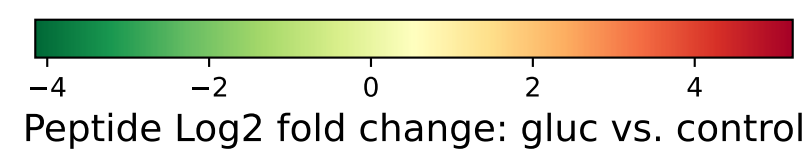
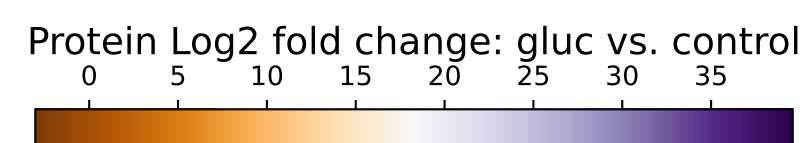
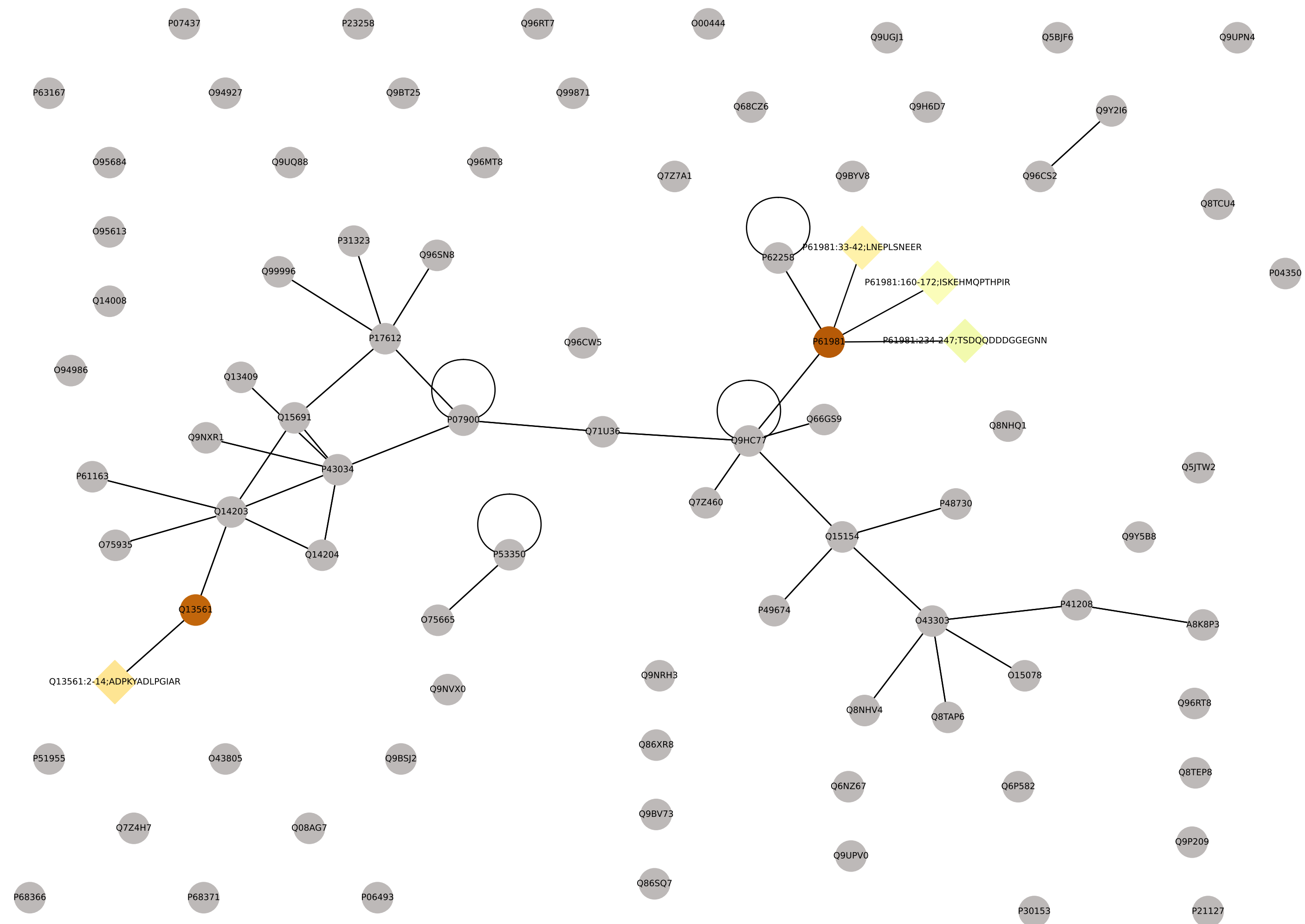
Log2 fold change: gluc vs. control
R-HSA-380259: Loss of Nlp from mitotic centrosomes
p-value: 0.030227589686308676



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



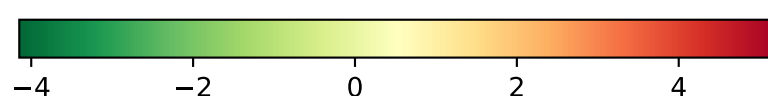
Log2 fold change: gluc vs. control
R-HSA-380270: Recruitment of mitotic centrosome proteins and complexes
p-value: 0.0384084717376354



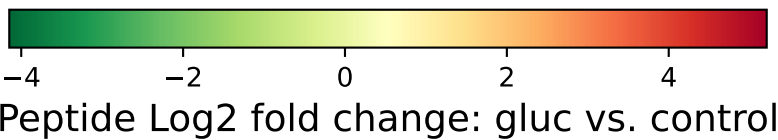
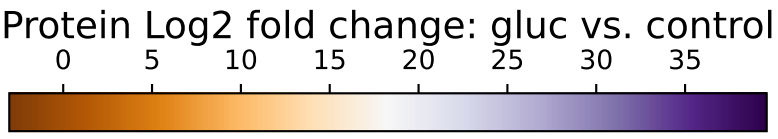
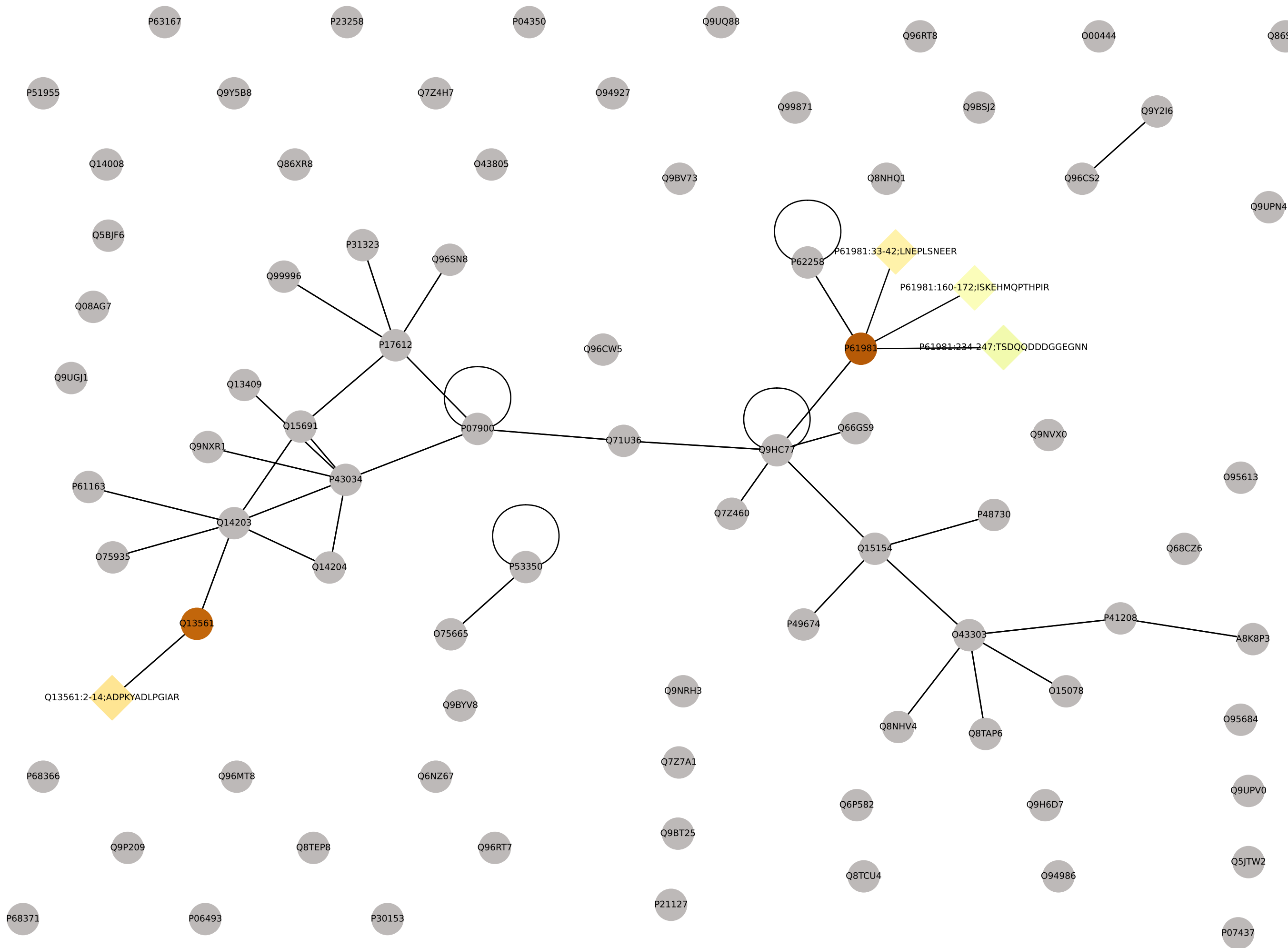
The image displays a network graph with nodes and edges. The nodes are represented by circles, many of which are labeled with protein IDs. A central cluster of nodes is highlighted with orange and red colors, indicating a core network. Several nodes are connected to this central cluster by lines, representing interactions. The graph is set against a white background with a light gray grid.

Key nodes and their connections include:

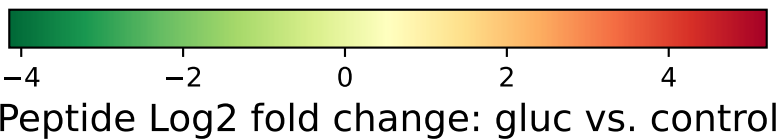
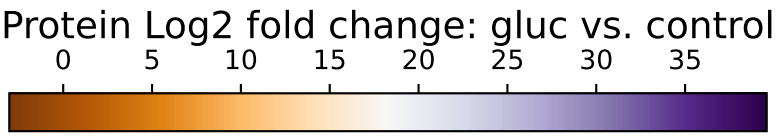
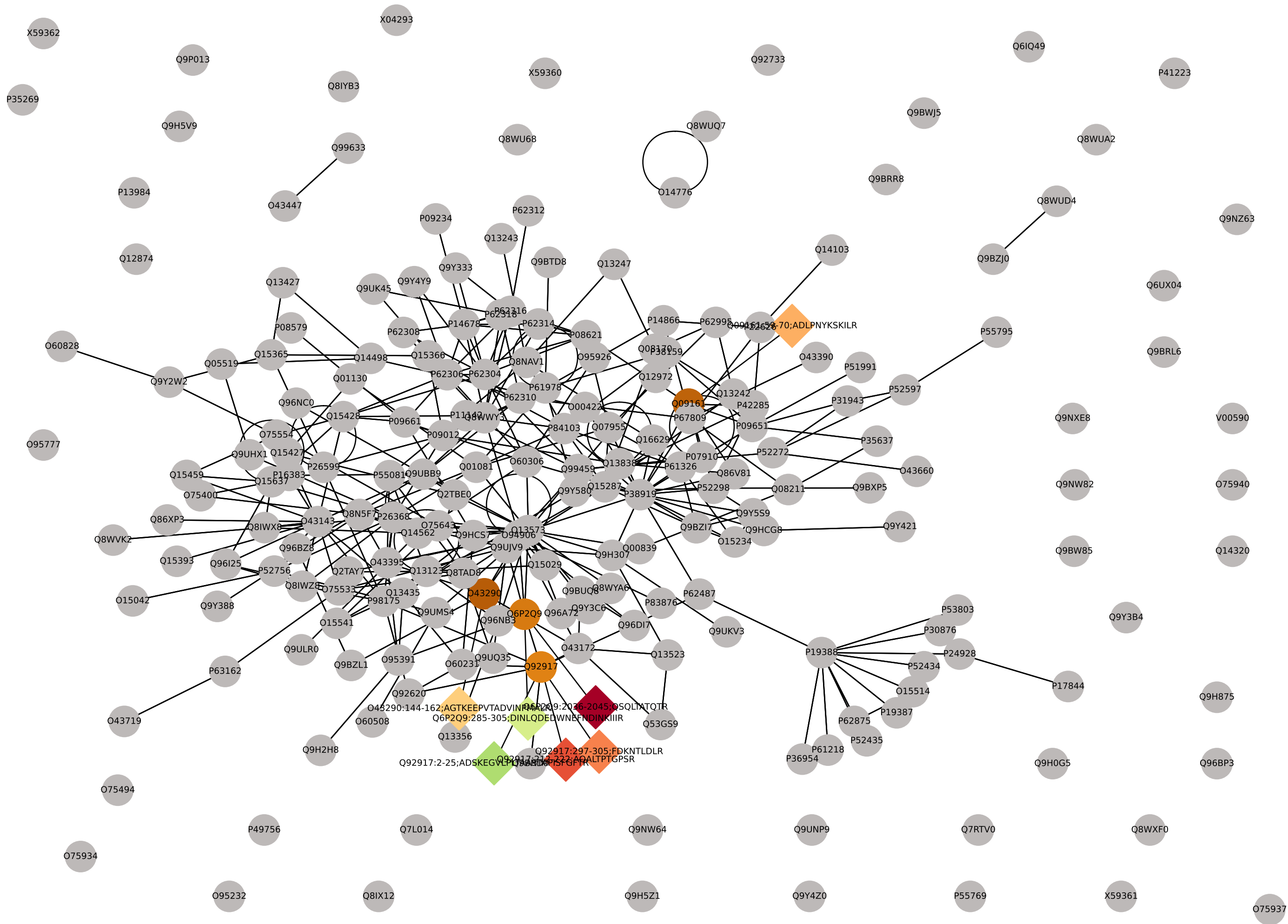
- Central Cluster (Orange/Red Nodes):**
 - P63220:39-45:YDKVTGR** (Red diamond)
 - P63220** (Orange circle)
 - P63220:8-15:FVDLYVPR** (Yellow diamond)
 - P62280:53-69:GTIIDKKCPFTGNVSIR** (Yellow diamond)
 - P62280** (Orange circle)
 - Q09161:59-70:ADLPNYKSKILR** (Orange diamond)
 - Q09161** (Orange circle)
- Other Nodes:**
 - P30153, P67775, P63151, P15880, P60866, P62266, P23396, P62861, P46782, P62249, P62244, J01866, P05386, M11167, Q86US8, P26373, P83731, P62945, P61254, Q07020, Q96L21, P02543, P62891, P27635, P35268, P42766, P18124, P62906, P62851, P46781, P42677, P46779, Q02878, P46778, P62979, P40429, P62829, P92901, P39019, P62987, P46777, P05388, Q8TD47, Q969Q0, P62750, P49207, P62277, P62269, P08708, P39023, P62495, P15170, P62913, P61927, P08708, P50914, P62424, P62854, P25398, P62910, P83881, P62263, P61247, Q6P5R6, V00589, P62701, X03205, P05387, P62899, P22090, P61353, P08865, P62081, P18077, Q9UNX3, P2280:53-69:GTIIDKKCPFTGNVSIR, P62280, P63220:8-15:FVDLYVPR, P63220:39-45:YDKVTGR, Q09161:59-70:ADLPNYKSKILR, Q09161, Q04637, P11940, Q9H1J1, Q8IYD1, Q9NPJ4, Q9NP16, Q92540, Q9UPR3, Q9HAU5, Q15234, Q9BZ17, P61326, Q15287, P38919, P52298, Q9Y559, Q96Q15, Q92900, P84098, Q9Y3U8, P50914, P62424, P62854, P25398, P62910, P83881, P62263, P61247, Q6P5R6, V00589, P62701, X03205, P05387, P62899, P22090, P61353, P08865, P62081, P18077, Q9UNX3, P2280:53-69:GTIIDKKCPFTGNVSIR, P62280, P63220:8-15:FVDLYVPR, P63220:39-45:YDKVTGR, Q09161:59-70:ADLPNYKSKILR, Q09161, Q04637, P11940, Q9H1J1, Q8IYD1, Q9NPJ4, Q9NP16, Q92540, Q9UPR3, Q9HAU5, Q15234, Q9BZ17, P61326, Q15287, P38919, P52298, Q9Y559, Q96Q15, Q92900, P84098, Q9Y3U8, P50914, P62424, P62854, P25398, P62910, P83881, P62263, P61247, Q6P5R6, V00589, P62701, X03205, P05387, P62899, P22090, P61353, P08865, P62081, P18077, Q9UNX3, P2280:53-69:GTIIDKKCPFTGNVSIR, P62280, P63220:8-15:FVDLYVPR, P63220:39-45:YDKVTGR, Q09161:59-70:ADLPNYKSKILR, Q09161, Q04637, P11940, Q9H1J1, Q8IYD1, Q9NPJ4, Q9NP16, Q92540, Q9UPR3, Q9HAU5, Q15234, Q9BZ17, P61326, Q15287, P38919, P52298, Q9Y559, Q96Q15, Q92900, P84098, Q9Y3U8, P50914, P62424, P62854, P25398, P62910, P83881, P62263, P61247, Q6P5R6, V00589, P62701, X03205, P05387, P62899, P22090, P61353, P08865, P62081, P18077, Q9UNX3, P2280:53-69:GTIIDKKCPFTGNVSIR, P62280, P63220:8-15:FVDLYVPR, P63220:39-45:YDKVTGR, Q09161:59-70:ADLPNYKSKILR, Q09161, Q04637, P11940, Q9H1J1, Q8IYD1, Q9NPJ4, Q9NP16, Q92540, Q9UPR3, Q9HAU5, Q15234, Q9BZ17, P61326, Q15287, P38919, P52298, Q9Y559, Q96Q15, Q92900, P84098, Q9Y3U8, P50914, P62424, P62854, P25398, P62910, P83881, P62263, P61247, Q6P5R6, V00589, P62701, X03205, P05387, P62899, P22090, P61353, P08865, P62081, P18077, Q9UNX3, P2280:53-69:GTIIDKKCPFTGNVSIR, P62280, P63220:8-15:FVDLYVPR, P63220:39-45:YDKVTGR, Q09161:59-70:ADLPNYKSKILR, Q09161, Q04637, P11940, Q9H1J1, Q8IYD1, Q9NPJ4, Q9NP16, Q92540, Q9UPR3, Q9HAU5, Q15234, Q9BZ17, P61326, Q15287, P38919, P52298, Q9Y559, Q96Q15, Q92900, P84098, Q9Y3U8, P50914, P62424, P62854, P25398, P62910, P83881, P62263, P61247, Q6P5R6, V00589, P62701, X03205, P05387, P62899, P22090, P61353, P08865, P62081, P18077, Q9UNX3, P2280:53-69:GTIIDKKCPFTGNVSIR, P62280, P63220:8-15:FVDLYVPR, P63220:39-45:YDKVTGR, Q09161:59-70:ADLPNYKSKILR, Q09161, Q04637, P11940, Q9H1J1, Q8IYD1, Q9NPJ4, Q9NP16, Q92540, Q9UPR3, Q9HAU5, Q15234, Q9BZ17, P61326, Q15287, P38919, P52298, Q9Y559, Q96Q15, Q92900, P84098, Q9Y3U8, P50914, P62424, P62854, P25398, P62910, P83881, P62263, P61247, Q6P5R6, V00589, P62701, X03205, P05387, P62899, P22090, P61353, P08865, P62081, P18077, Q9UNX3, P2280:53-69:GTIIDKKCPFTGNVSIR, P62280, P63220:8-15:FVDLYVPR, P63220:39-45:YDKVTGR, Q09161:59-70:ADLPNYKSKILR, Q09161, Q04637, P11940, Q9H1J1, Q8IYD1, Q9NPJ4, Q9NP16, Q92540, Q9UPR3, Q9HAU5, Q15234, Q9BZ17, P61326, Q15287, P38919, P52298, Q9Y559, Q96Q15, Q92900, P84098, Q9Y3U8, P50914, P62424, P62854, P25398, P62910, P83881, P62263, P61247, Q6P5R6, V00589, P62701, X03205, P05387, P62899, P22090, P61353, P08865, P62081, P18077, Q9UNX3, P2280:53-69:GTIIDKKCPFTGNVSIR, P62280, P63220:8-15:FVDLYVPR, P63220:39-45:YDKVTGR, Q09161:59-70:ADLPNYKSKILR, Q09161, Q04637, P11940, Q9H1J1, Q8IYD1, Q9NPJ4, Q9NP16, Q92540, Q9UPR3, Q9HAU5, Q15234, Q9BZ17, P61326, Q15287, P38919, P52298, Q9Y559, Q96Q15, Q92900, P84098, Q9Y3U8, P50914, P62424, P62854, P25398, P62910, P83881, P62263, P61247, Q6P5R6, V00589, P62701, X03205, P05387, P62899, P22090, P61353, P08865, P62081, P18077, Q9UNX3, P2280:53-69:GTIIDKKCPFTGNVSIR, P62280, P63220:8-15:FVDLYVPR, P63220:39-45:YDKVTGR, Q09161:59-70:ADLPNYKSKILR, Q09161, Q04637, P11940, Q9H1J1, Q8IYD1, Q9NPJ4, Q9NP16, Q92540, Q9UPR3, Q9HAU5, Q15234, Q9BZ17, P61326, Q15287, P38919, P52298, Q9Y559, Q96Q15, Q92900, P84098, Q9Y3U8**



Log2 fold change: gluc vs. control
R-HSA-380287: Centrosome maturation
p-value: 0.04013568745556928



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

