First, the peptides connected to multiple proteins are eliminated and then the averaged values of the remaining peptides will be assigned to connected proteins

Peptide-2(v2)

Peptide-3(v3)

Peptide-5(v5)

Peptide-1(v1)

Peptide-4(v4)

Protein-2(P2)

Protein-3(P3)

Protein-4(P4)

Protein-1(P1)

P1; P2 = (v2 + v3)/3;

P3 = v4; P4 = v5;