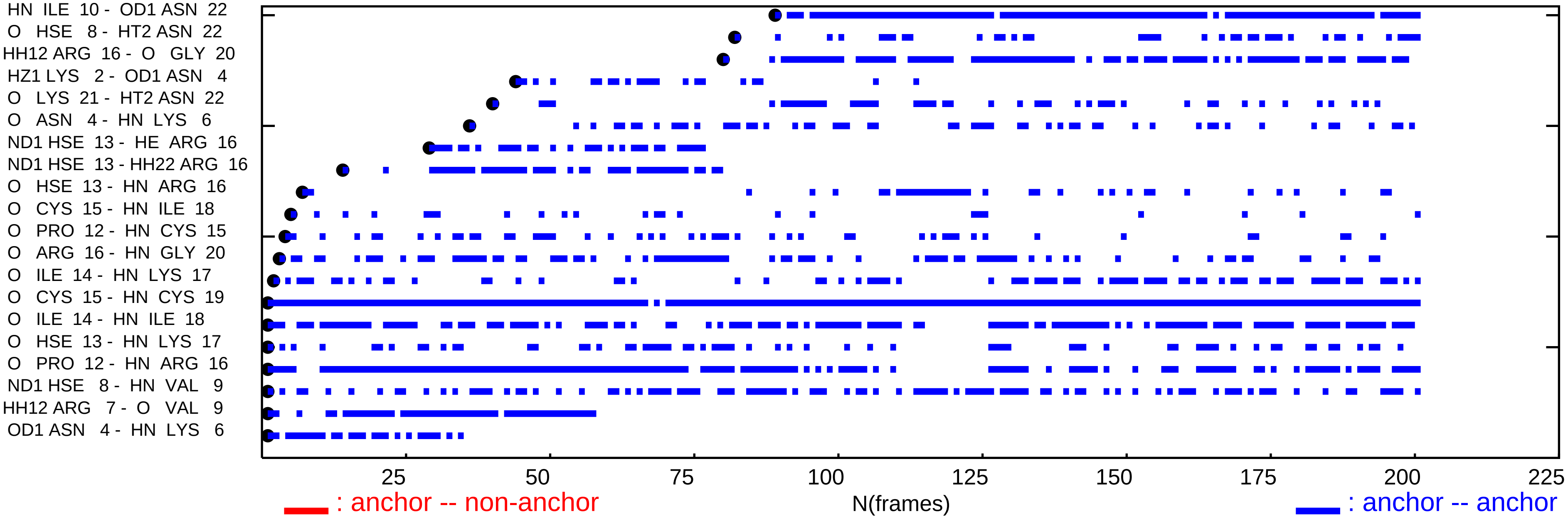
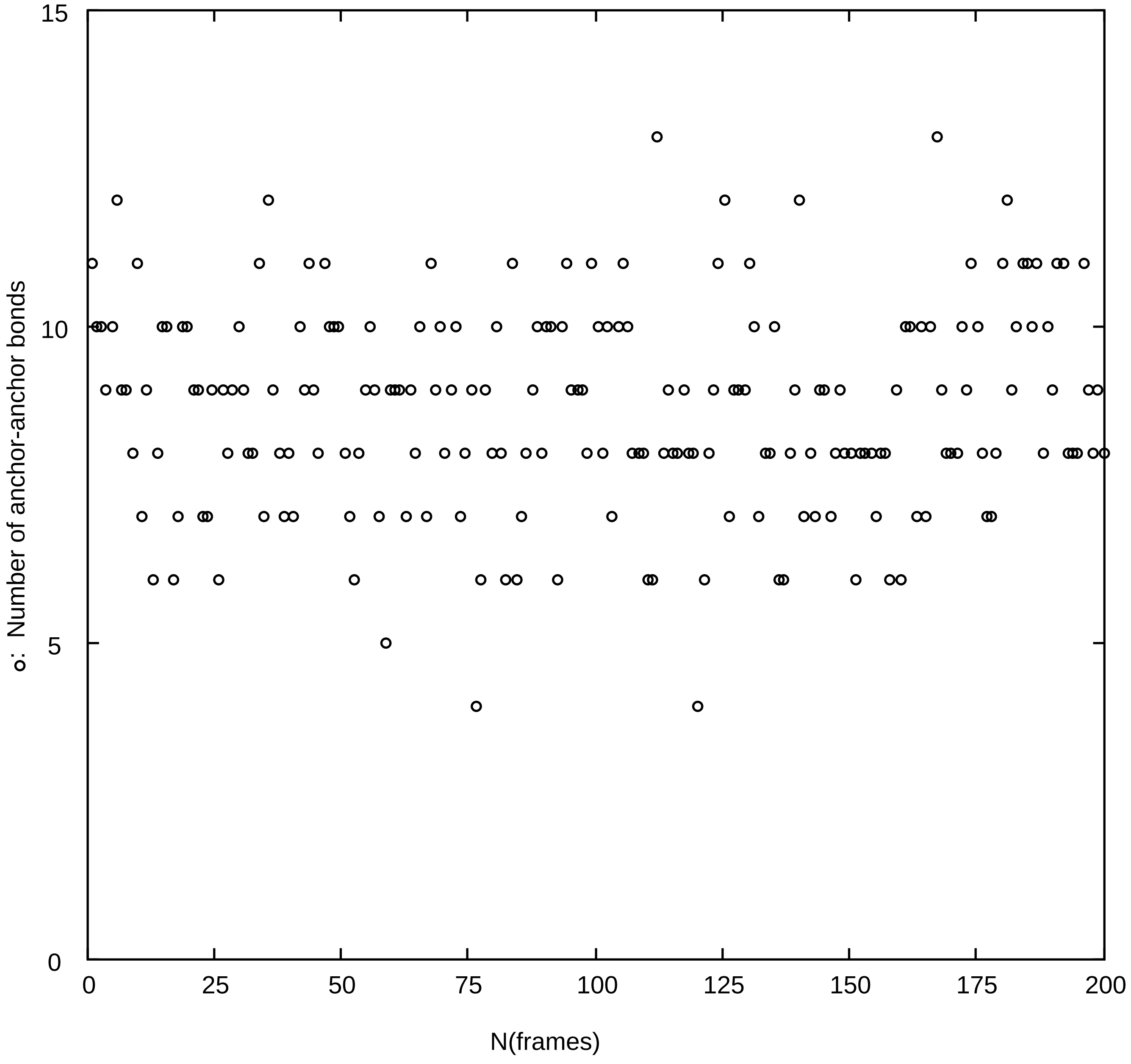
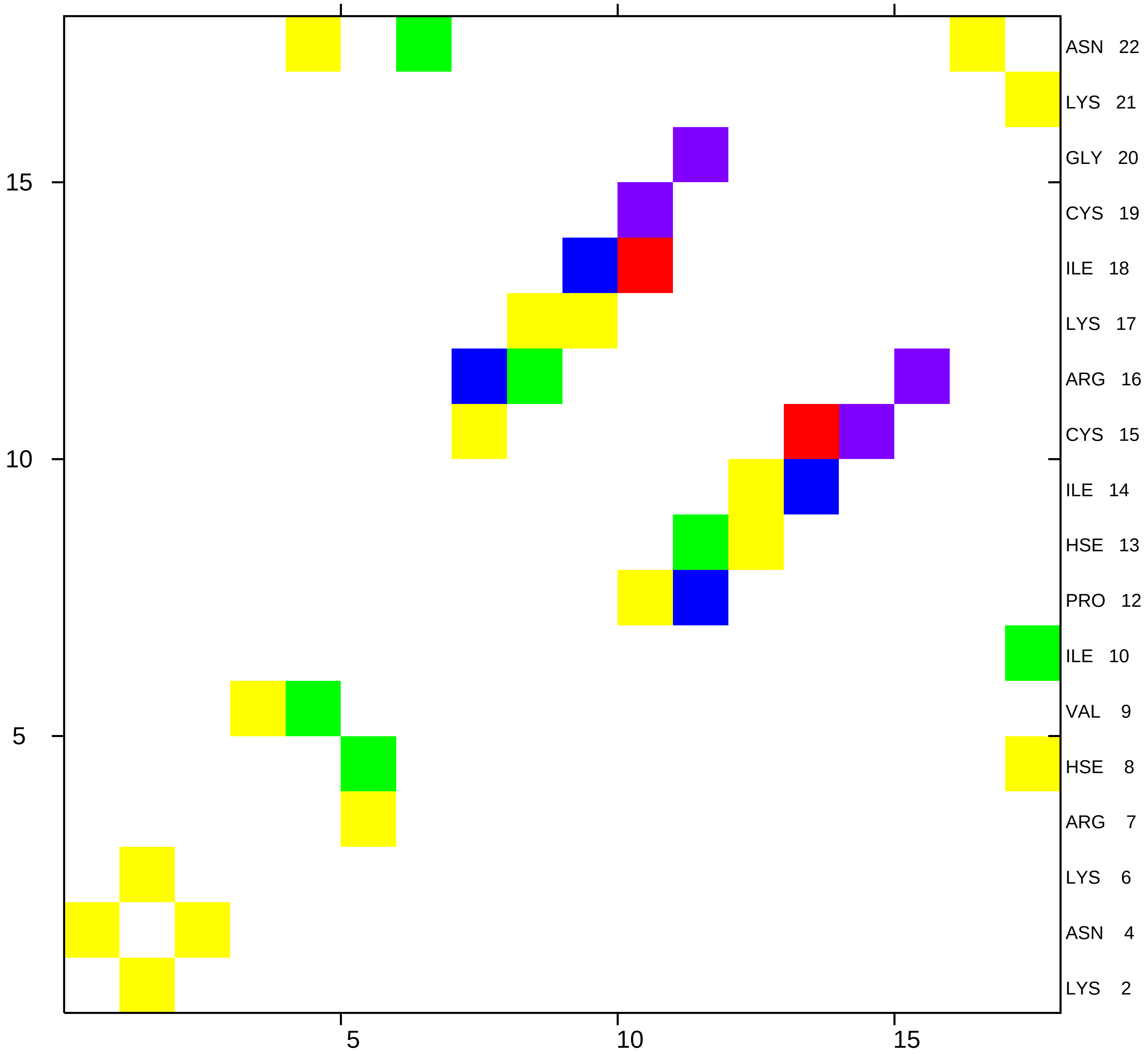
Analysis type: Hydrogen-bond list
System: MCD - Mast Cell Degranulating Peptide
Configuration file analyzed: mcd.pdb
Trajectory analyzed: mcd.dcd Frames 1 - 201 Increment: 1
Unclustered plot, original hydrogen-bond order
Minimum and maximum interresidue distances to show= 1 and 21 residues
Minimum and maximum % occurrences to show=10.0 100.0
Hydrogen-bond parameters: hblimfac= 1.500 angmin= 120.00 deg



Analysis type: Hydrogen-bond list
System: MCD - Mast Cell Degranulating Peptide
Configuration file analyzed: mcd.pdb
Trajectory analyzed: mcd.dcd Frames 1 - 201 Increment: 1
<NB>= 8.7 S.D.= 1.6 CI(1sig)= 0.2
Number of data points averaged= 1



Analysis type: Hydrogen-bond list
System: MCD - Mast Cell Degranulating Peptide
Configuration file analyzed: mcd.pdb
Trajectory analyzed: mcd.dcd Frames 1 - 201 Increment: 1
Residue-residue hydrogen bond strength (fraction)



<=0/5: <=1/5: <=2/5: <=3/5: <=4/5: <=5/5: >5/5:
<= 0.000 <= 0.198 <= 0.396 <= 0.594 <= 0.792 <= 0.990 > 0.990

Range of the hydrogen-bond fraction scale: 0.000 - 0.990
Multiple contacts are accumulated

Analysis type: Hydrogen-bond list
System: MCD - Mast Cell Degranulating Peptide
Configuration file analyzed: mcd.pdb
Trajectory analyzed: mcd.dcd Frames 1 - 201 Increment: 1
Unclustered plot, original hydrogen-bond order
Residue aggregated time course of hydrogen bonds
Minimum and maximum interresidue distances to show= 1 and 21 residues
Minimum and maximum % occurrences to show=10.0 100.0
Hydrogen-bond parameters: hblimfac= 1.500 angmin= 120.00 deg