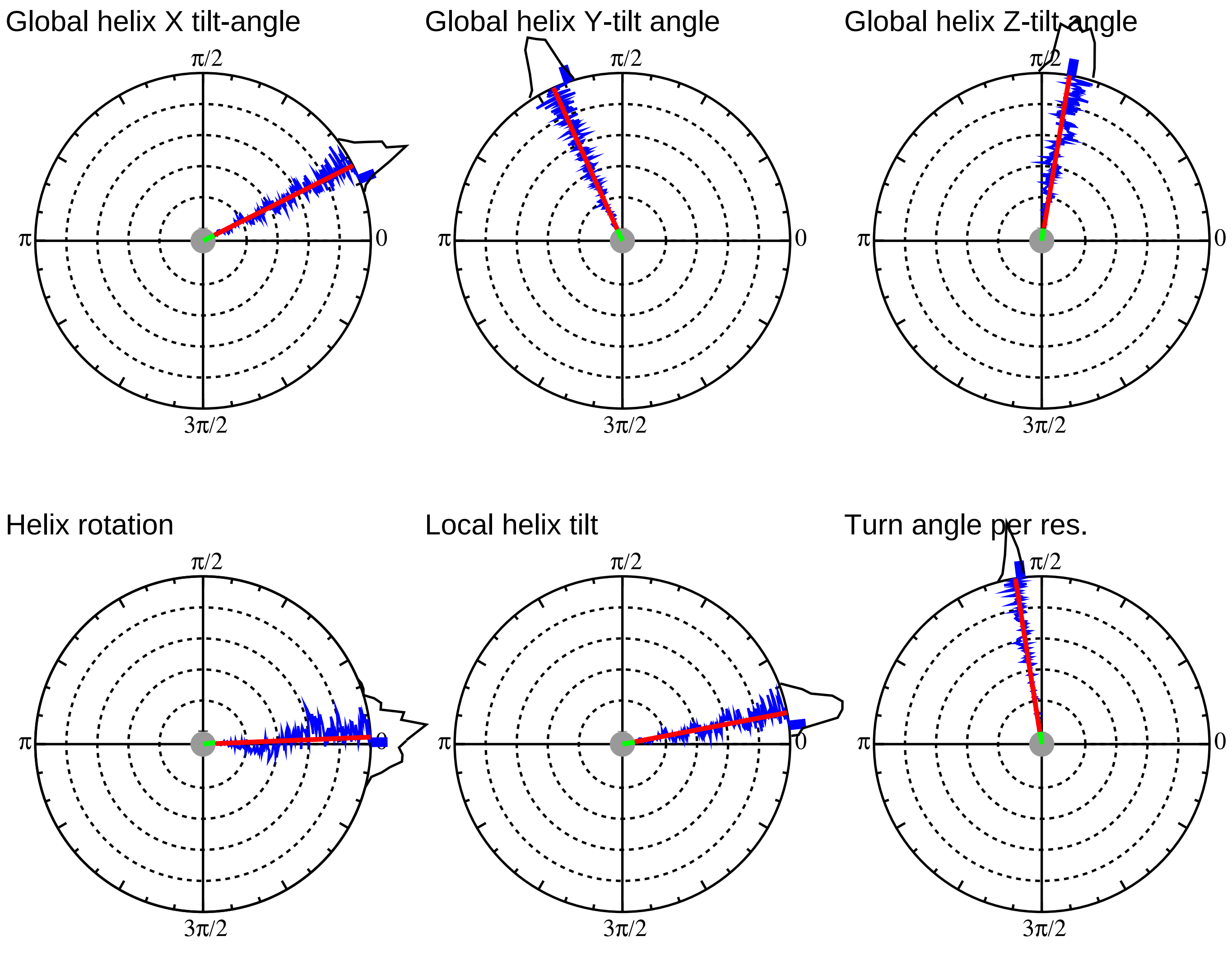
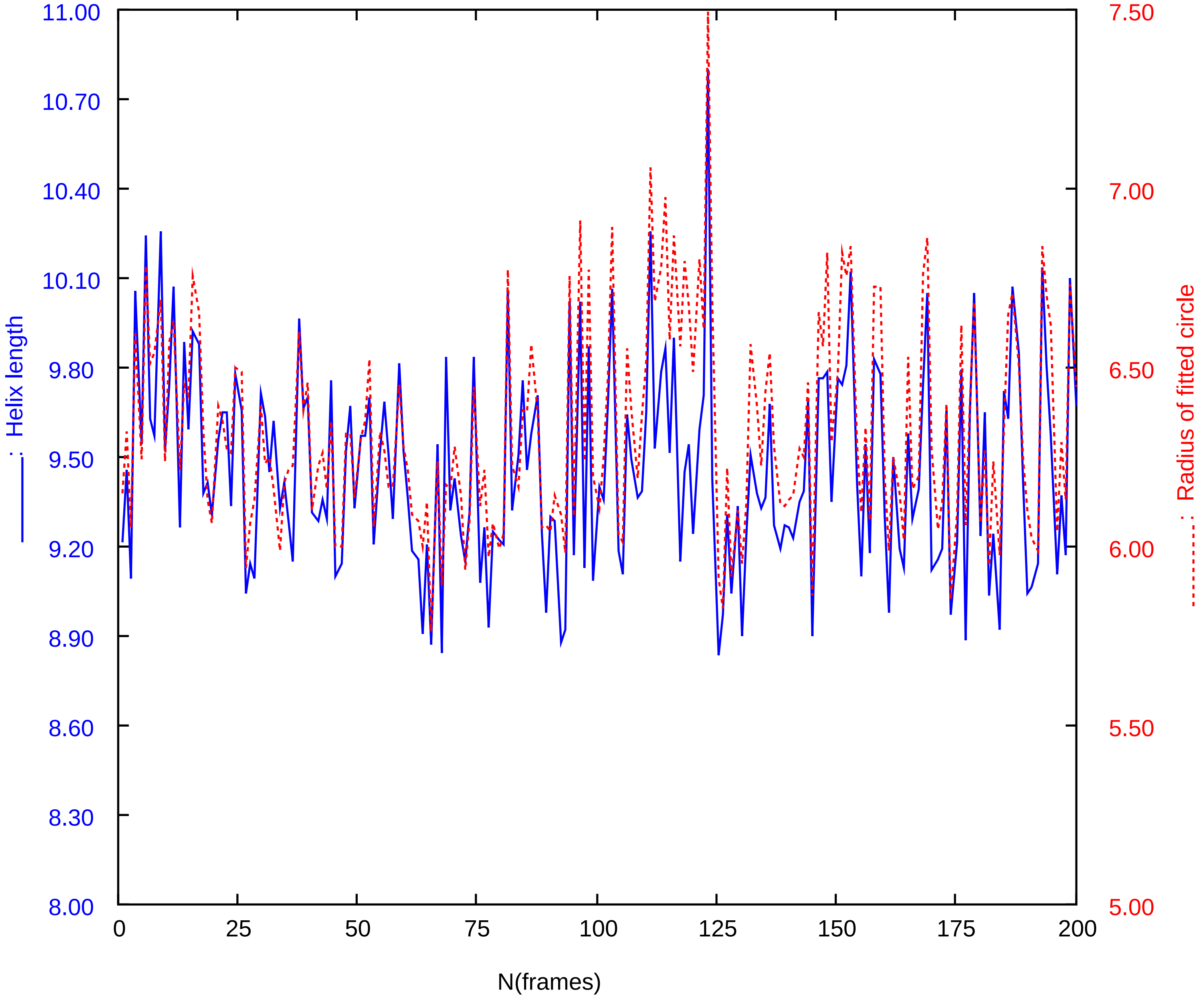
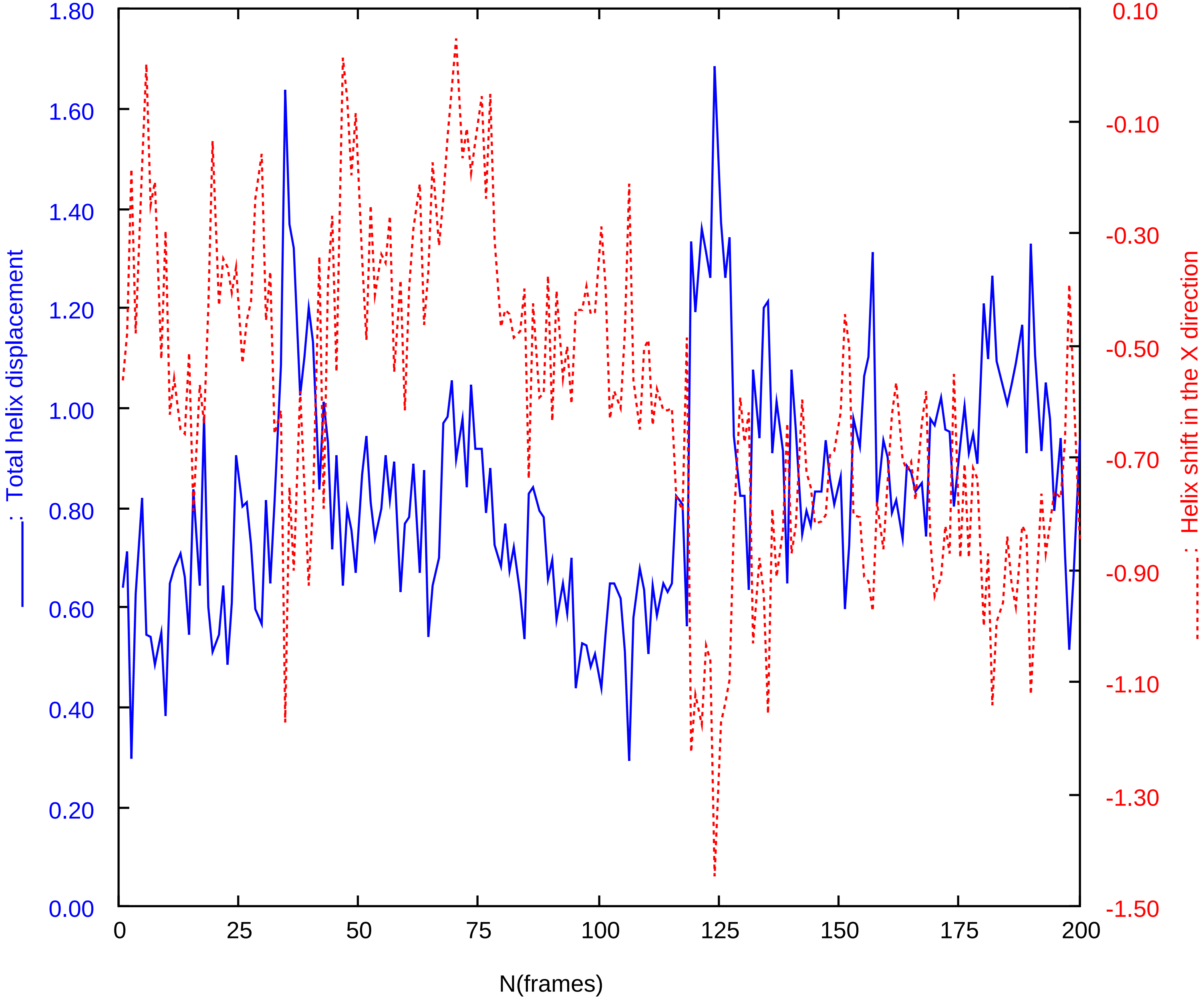
Analysis type: Helix axis directions
System: MCD - Mast Cell Degranulating Peptide
Configuration file analyzed: mcd.pdb
Trajectory analyzed: mcd.dcd Frames 1 - 201 Increment: 1



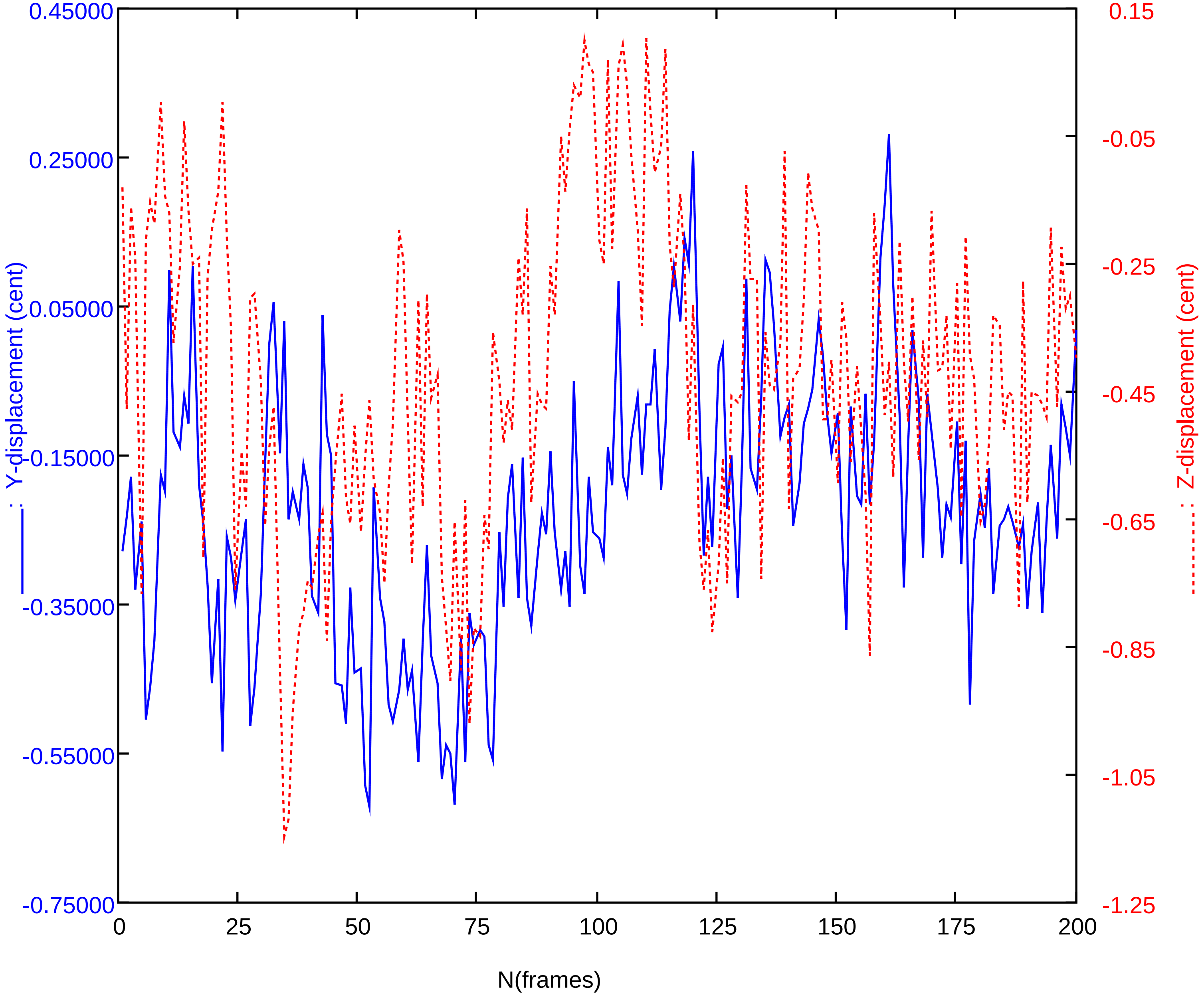
Analysis type: Helix axis directions
System: MCD - Mast Cell Degranulating Peptide
Configuration file analyzed: mcd.pdb
Trajectory analyzed: mcd.dcd Frames 1 - 201 Increment: 1
Residues 13 - 19
Number of data points averaged= 1



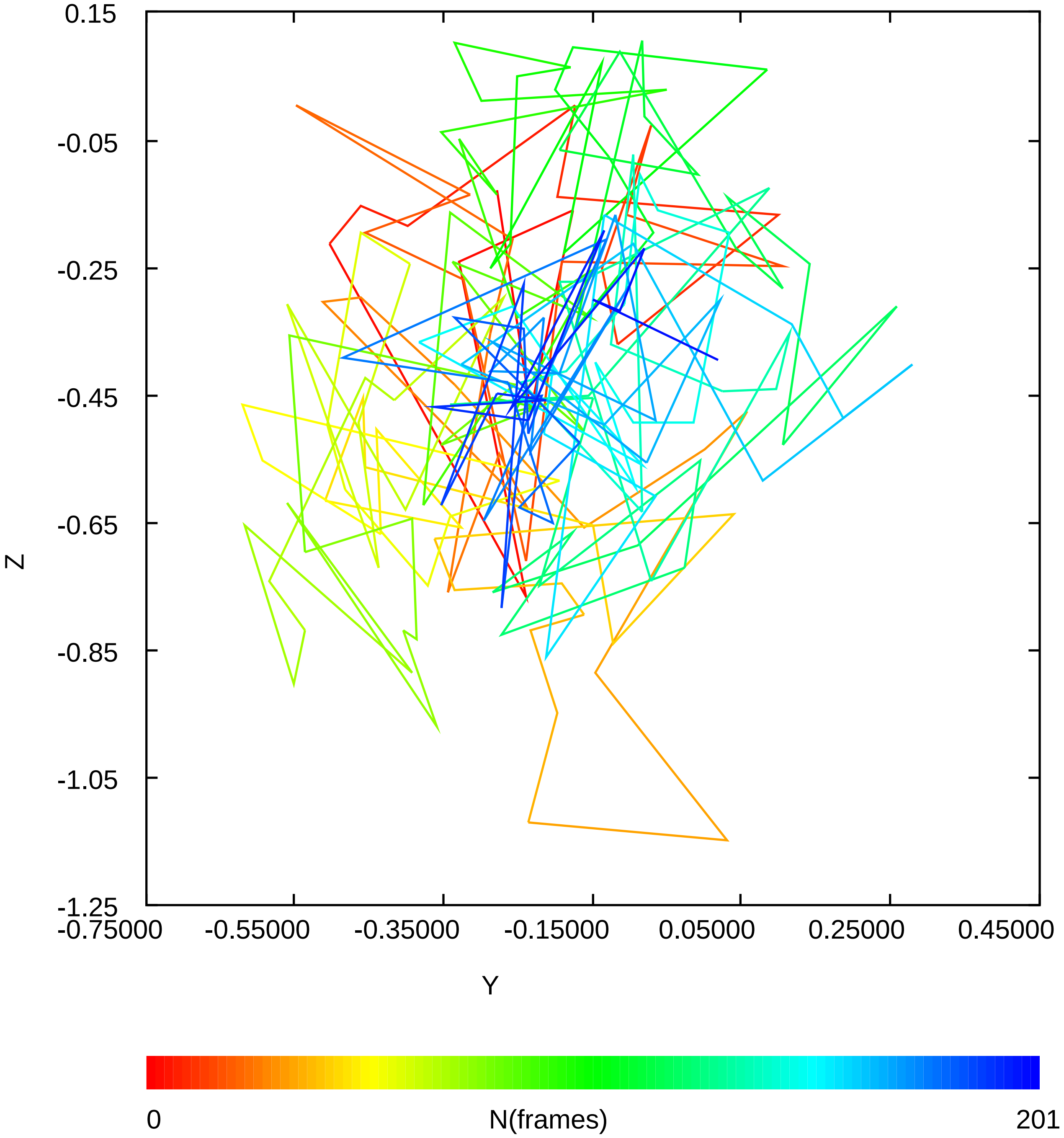
Analysis type: Helix axis directions
System: MCD - Mast Cell Degranulating Peptide
Configuration file analyzed: mcd.pdb
Trajectory analyzed: mcd.dcd Frames 1 - 201 Increment: 1
Residues 13 - 19
Number of data points averaged= 1



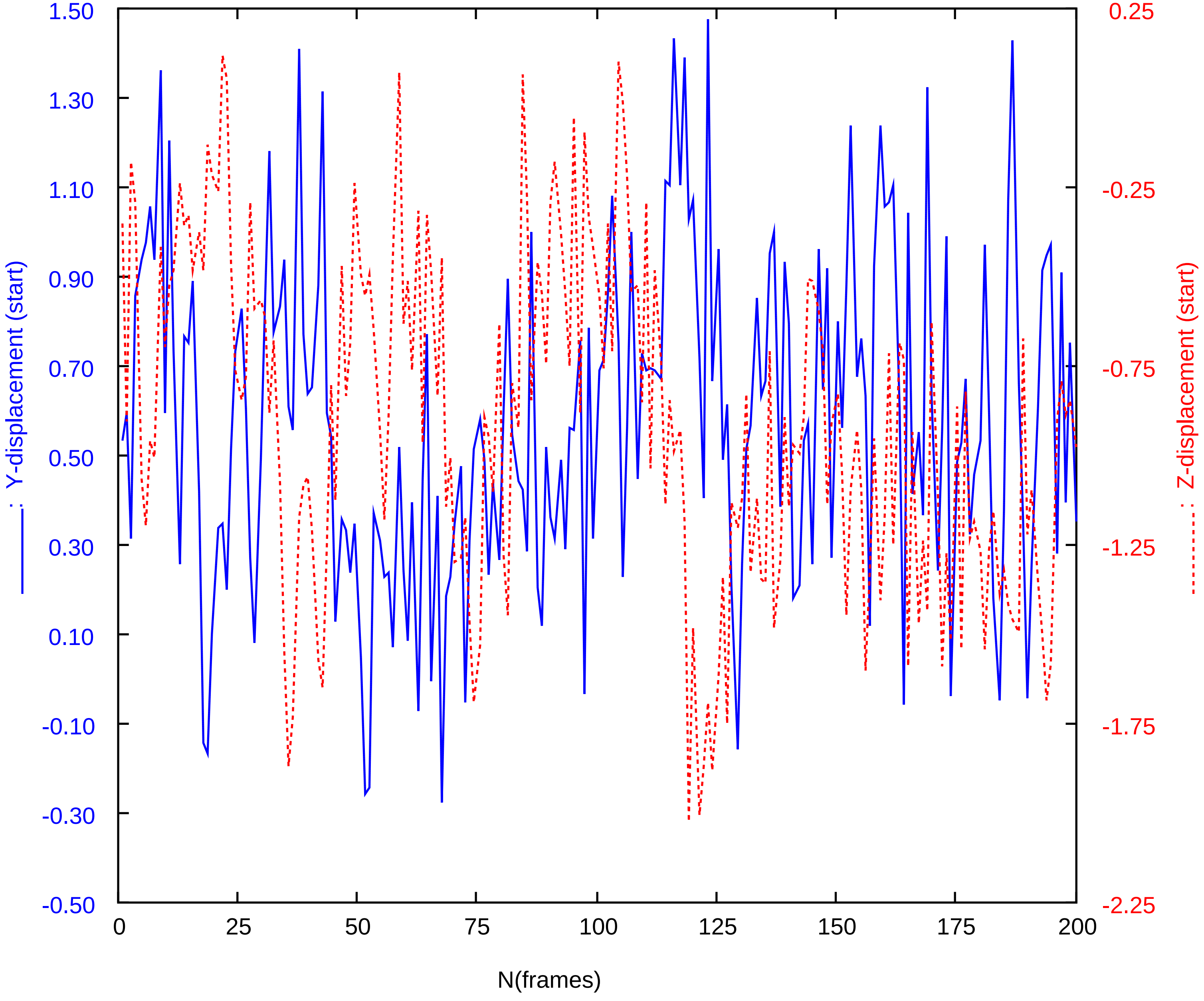
Analysis type: Helix axis directions
System: MCD - Mast Cell Degranulating Peptide
Configuration file analyzed: mcd.pdb
Trajectory analyzed: mcd.dcd Frames 1 - 201 Increment: 1
Residues 13 - 19
Number of data points averaged= 1



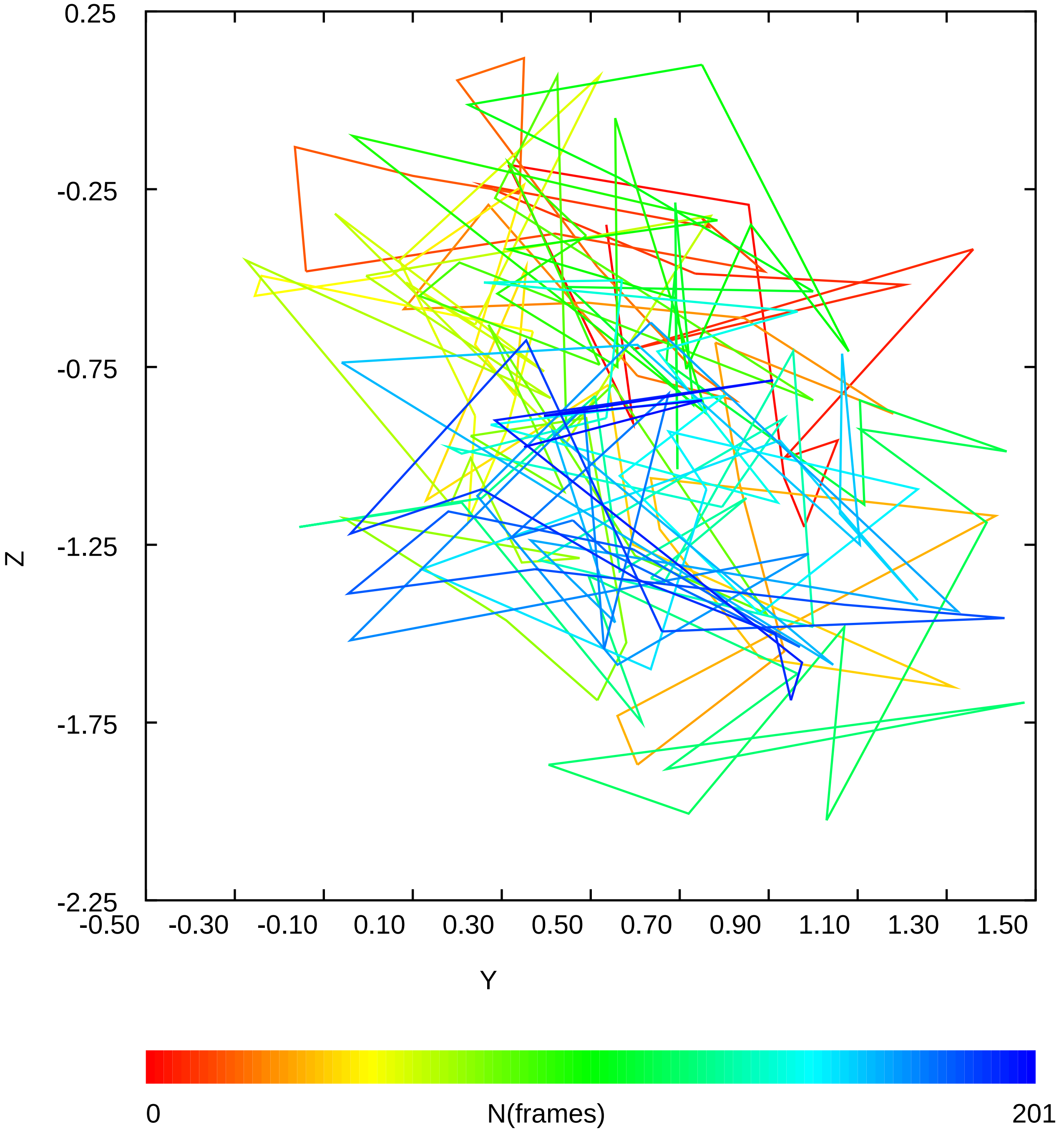
Analysis type: Helix axis directions
System: MCD - Mast Cell Degranulating Peptide
Configuration file analyzed: mcd.pdb
Trajectory analyzed: mcd.dcd Frames 1 - 201 Increment: 1
Residues 13 - 19

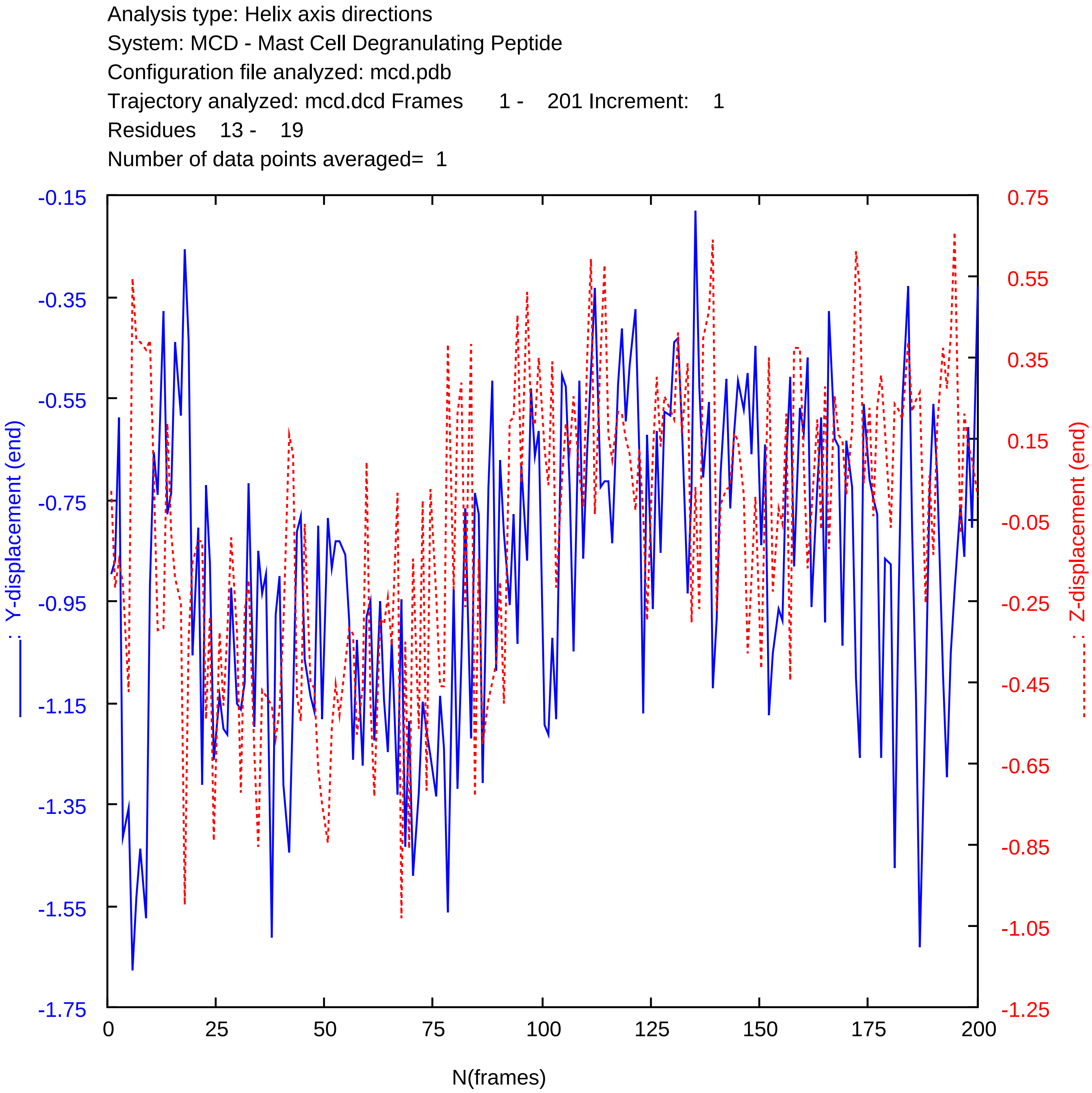


Analysis type: Helix axis directions
System: MCD - Mast Cell Degranulating Peptide
Configuration file analyzed: mcd.pdb
Trajectory analyzed: mcd.dcd Frames 1 - 201 Increment: 1
Residues 13 - 19
Number of data points averaged= 1

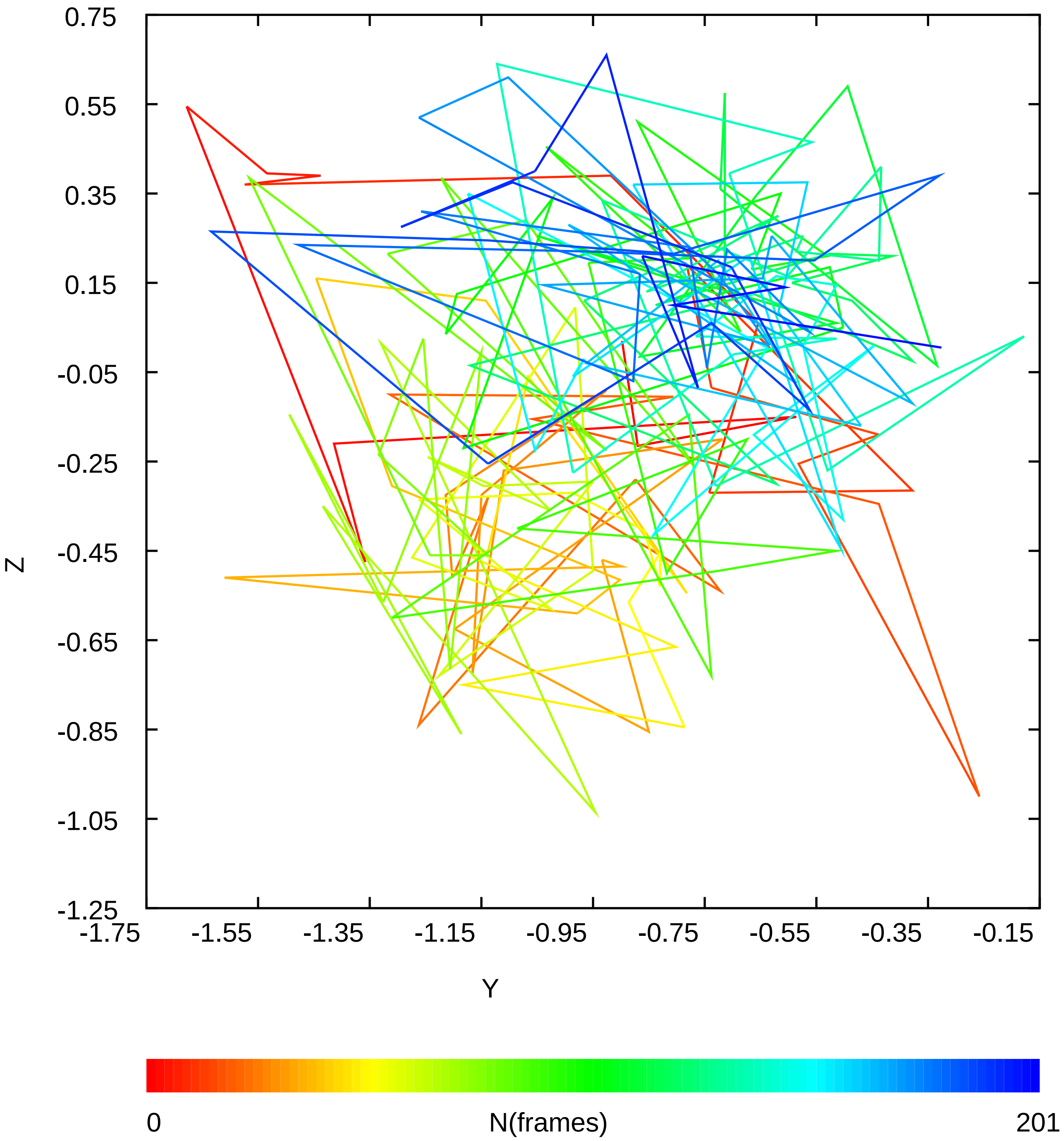


Analysis type: Helix axis directions
System: MCD - Mast Cell Degranulating Peptide
Configuration file analyzed: mcd.pdb
Trajectory analyzed: mcd.dcd Frames 1 - 201 Increment: 1
Residues 13 - 19

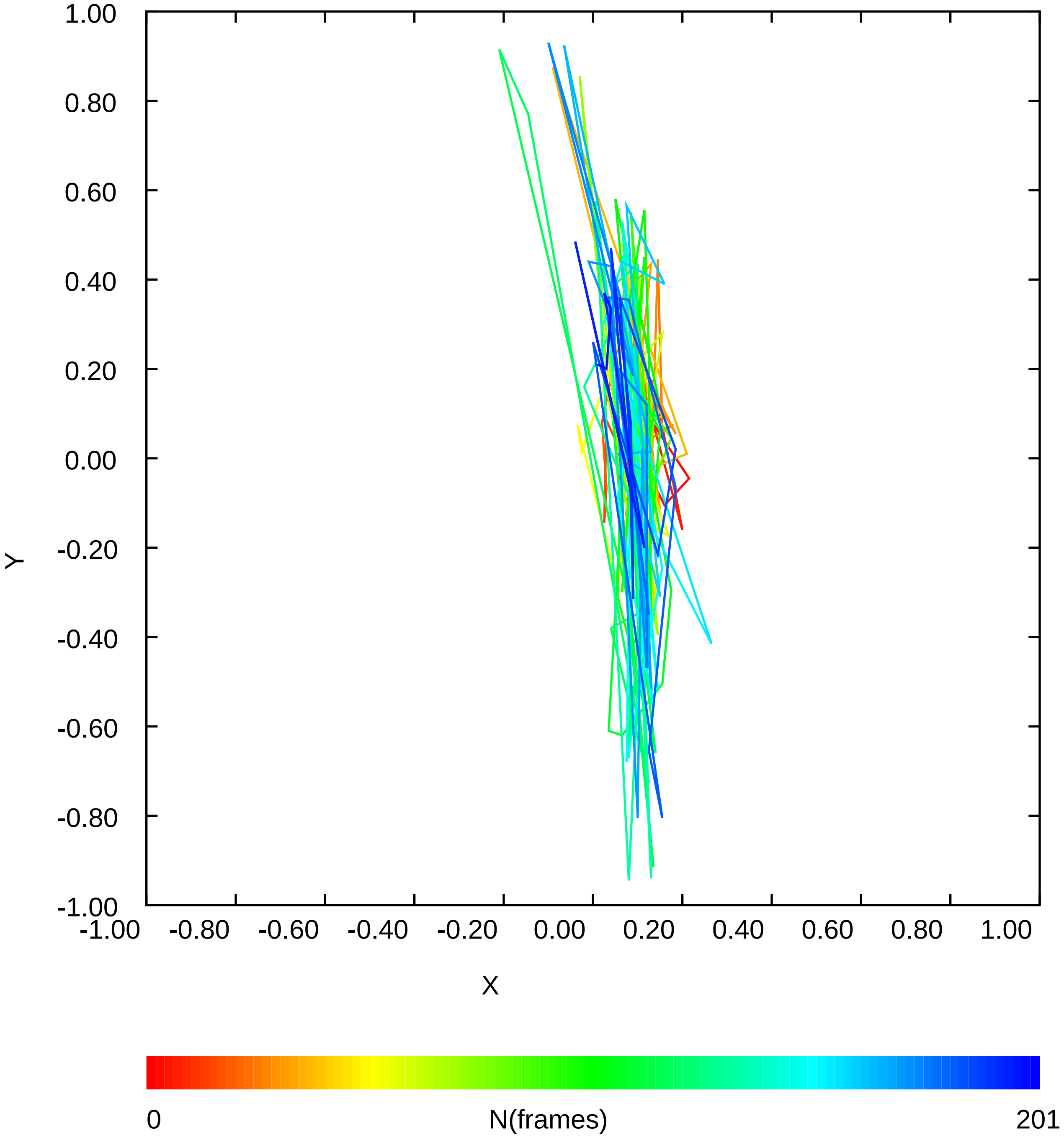


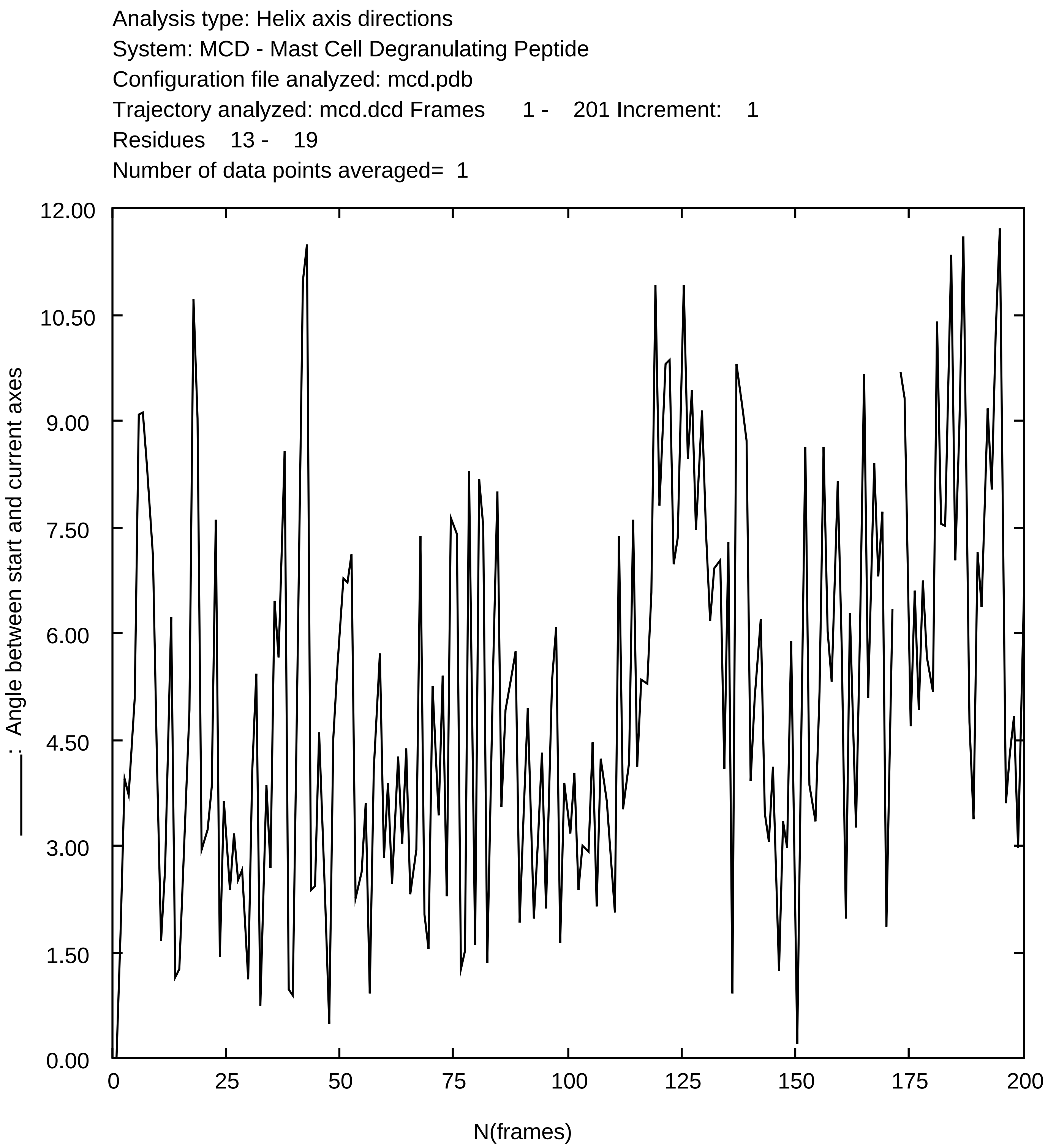

Analysis type: Helix axis directions
System: MCD - Mast Cell Degranulating Peptide
Configuration file analyzed: mcd.pdb
Trajectory analyzed: mcd.dcd Frames 1 - 201 Increment: 1
Residues 13 - 19
Number of data points averaged= 1
-0.15
-0.35
-0.55
-0.75
-0.95
-1.15
-1.35
-1.55
-1.75
0.75
0.55
0.35
0.15
-0.05
-0.25
-0.45
-0.65
-0.85
-1.05
-1.25
0
25
50
75
100
125
150
175
200
N(frames)
Y-displacement (end)
Z-displacement (end)

Analysis type: Helix axis directions
System: MCD - Mast Cell Degranulating Peptide
Configuration file analyzed: mcd.pdb
Trajectory analyzed: mcd.dcd Frames 1 - 201 Increment: 1
Residues 13 - 19



Analysis type: Helix axis directions
System: MCD - Mast Cell Degranulating Peptide
Configuration file analyzed: mcd.pdb
Trajectory analyzed: mcd.dcd Frames 1 - 201 Increment: 1
Residues 13 - 19 Helix axis is in the X direction




Analysis type: Helix axis directions
System: MCD - Mast Cell Degranulating Peptide
Configuration file analyzed: mcd.pdb
Trajectory analyzed: mcd.dcd Frames 1 - 201 Increment: 1
Residues 13 - 19
Number of data points averaged= 1
12.00
10.50
9.00
7.50
6.00
4.50
3.00
1.50
0.00
0
25
50
75
100
125
150
175
200
Angle between start and current axes
N(frames)