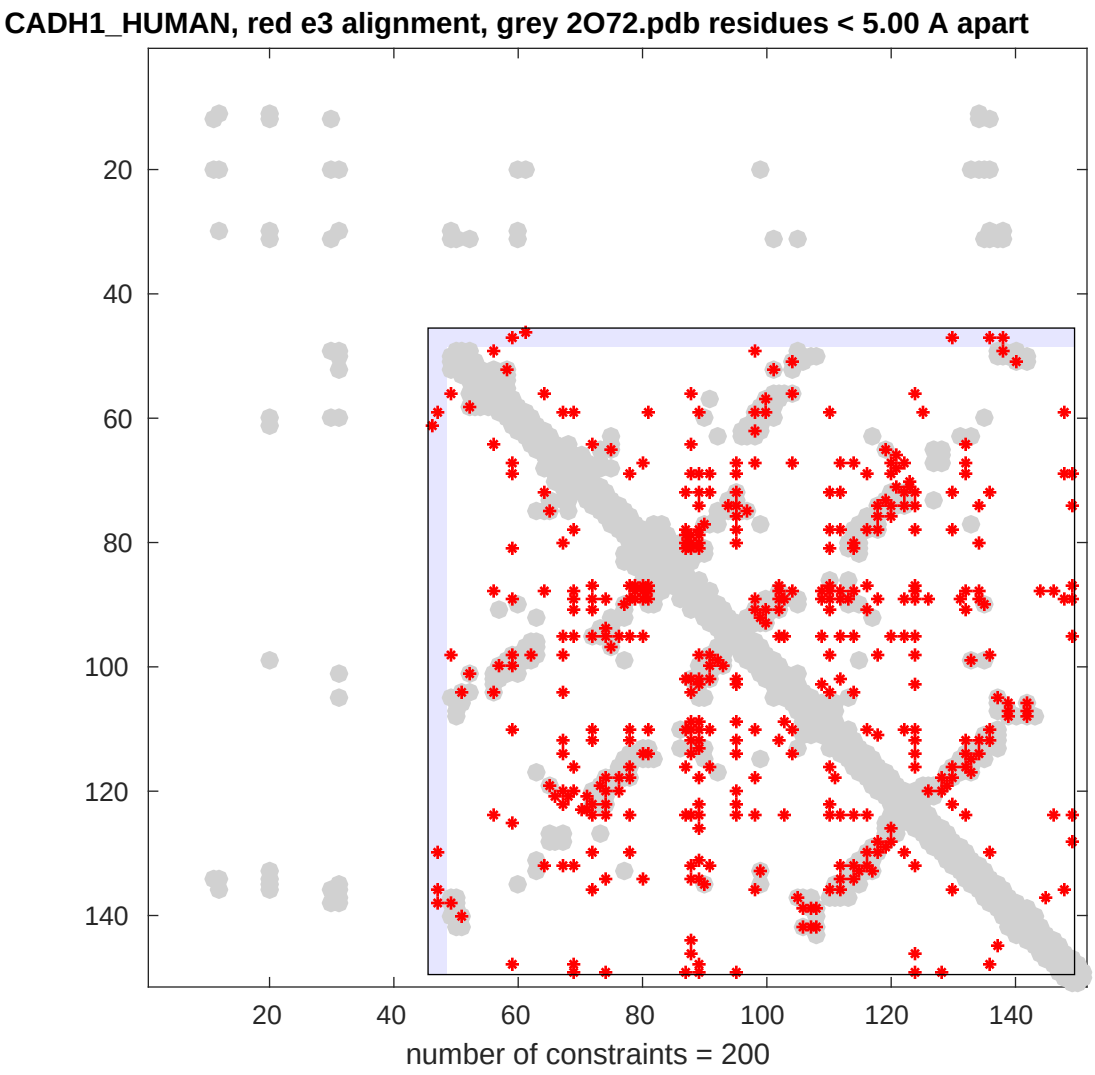
CADH1_HUMAN, red e3 alignment, grey 2O72.pdb residues < 5.00 A apart
20
40
60
80
100
120
140
20
40
60
80
100
120
140
number of constraints = 200