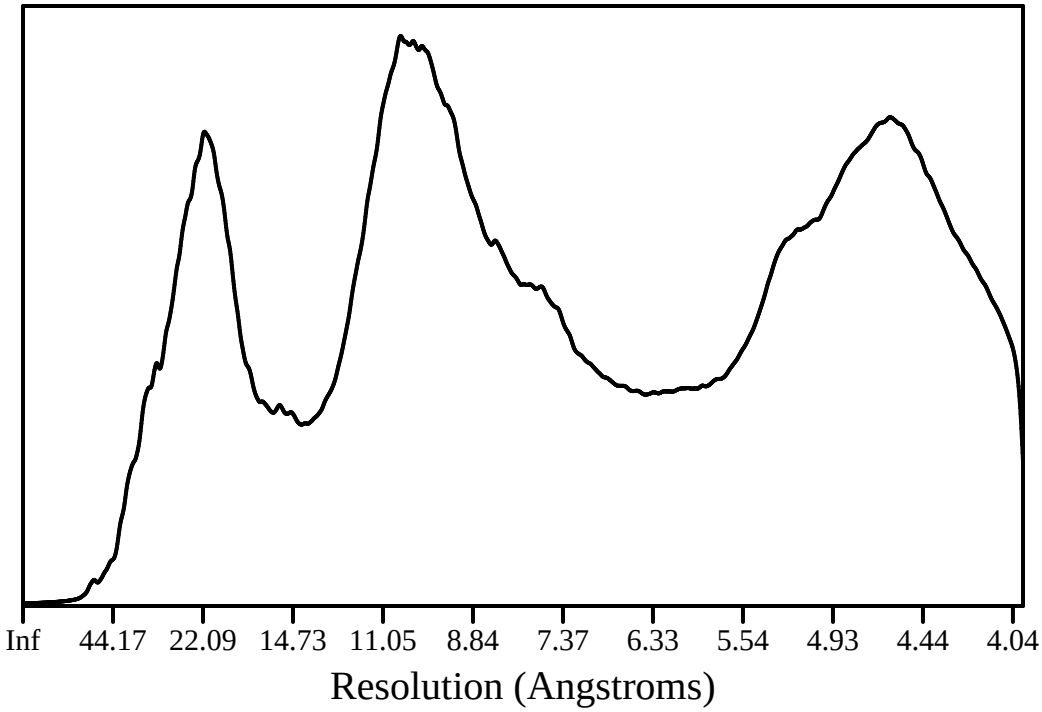
Simulated powder diffraction: rn2b−lddr60o120−bend200−40



rn2b-lddr60o120-bend200-40.pdb

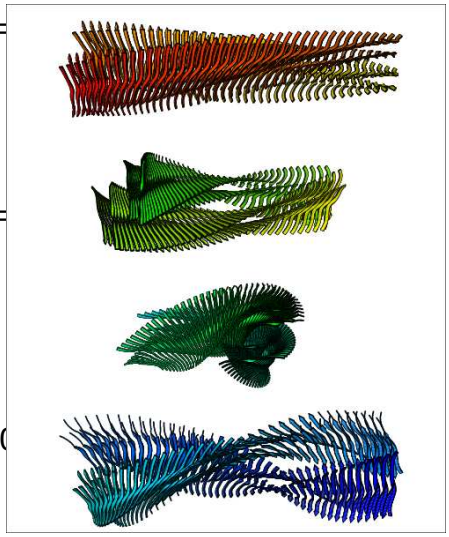
==========

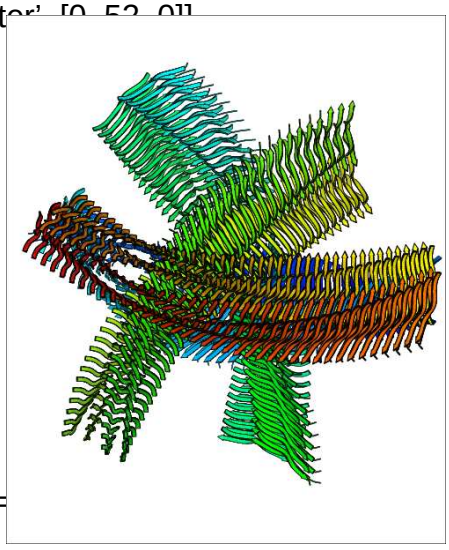
GNNQQN(Y)GNNQQNY Paired Protomer Ladder Super
Doubled 1yjp matched with the closest sister molecule
ladder of 60, 80, 100, 120 protomers ; bend r = 200
40 protomers - 1-1 layers ; ladder helicity

==========

model generated by super-helix
super-helix is (C) James C Stroud, 2009
name: rn2b-lddr60o120-bend200-40
date and time: Mon Aug 9 12:52:21 2010
protomer pdb file: rn2b-fixed.pdb
protomer pdb file md5: 36bf613c8863af21c1ad4bb5bf03cce0
protomer height: 4.87 A
protomer width correction: -2.0 A
protomer transformations: [[[0, 0, 1], 25], [[1, 0, 0], -20], 'center', [0, 52, 0]]
phi of primary helical line: None deg
form: ladder
stretch to exact pitch: False
fiber direction, pitch: [' 0.0', ' 1.0', ' 0.0'], 291.96 A A
first, last layers: 1, 1
protofibrils kept: all
segment length: 190.26 A
monomers per protfibril: 40
super helix: pitch 0.00, radius 200.00, ang 0.0
super tilt: True
final transforms: ['center']
chain jitter: None

==========





GNNQQN(Y)GNNQQNY Paired Protomer Ladder Super