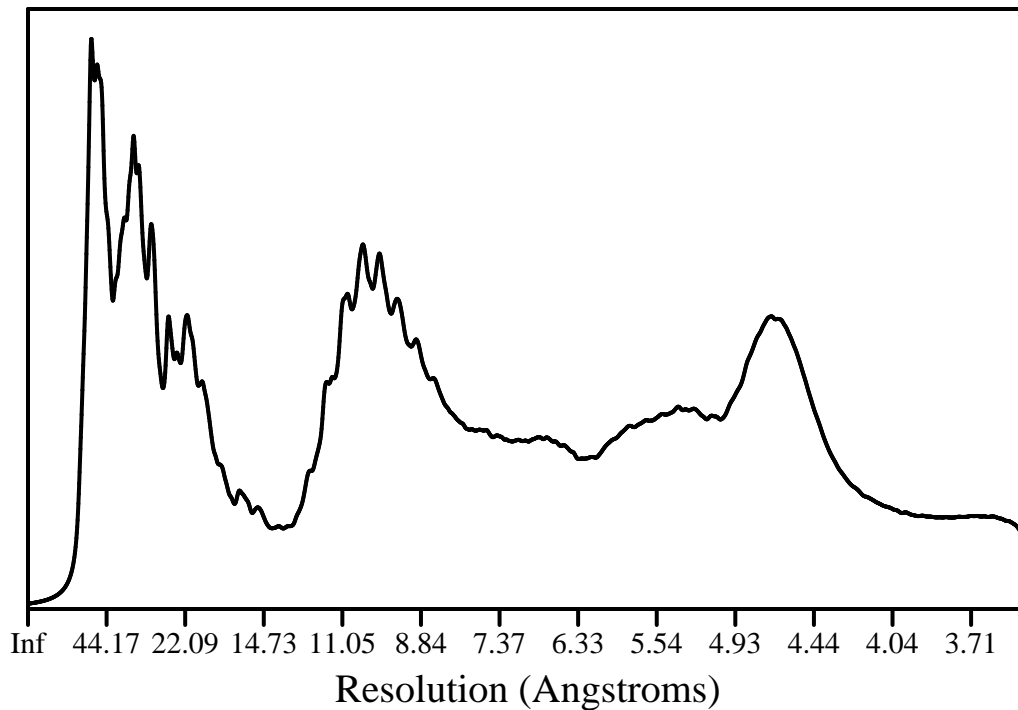


# Simulated powder diffraction: stg06-phi06.4-wc-03.8-rc1.0-m4-12



stg06-phi06.4-wc-03.8-rc1.0-m4-12.pdb

=====

stg6: phi 6.4, wc -3.8, rc 1.0, mono 4, lyrs 1:2, ht 14.1

=====

model generated by super-helix  
 super-helix is (C) James C Stroud, 2009  
 name: stg06-phi06.4-wc-03.8-rc1.0-m4-12  
 date and time: Wed Mar 20 11:58:53 2013  
 protomer pdb file: grab42-6.pdb  
 protomer pdb file md5: f07eccf5a055d8043b79ffb36158725a  
 protomer height: 14.10 Ang  
 protomer width correction: -3.8 Ang  
 protomer transformations: { center\_com }  
 adjust vector: None  
 helix axis: [0 1 0]  
 thickening vector: None, transform it: False  
 vsym: (0, 0), hsym: (0, 0)  
 fiber pitch, direction: 280.64 Ang, [ 0.0 1.0 0.0]  
 phi of primary helical line: 6.4 deg  
 prime radius: 5.01 Ang  
 prime length: 282.40 Ang  
 form: wrap, radial correction: 1.0  
 stretch to exact pitch: False  
 first - last layers: 1 - 2  
 protofibrils kept: all  
 segment length: 56.40 Ang  
 monomers per protofibril: 4  
 super helix: pitch None, radius None, ang 0.0 deg  
 super tilt: True  
 protofibril shift: 0.00  
 final transforms: { None }  
 chain jitter: None  
 reset b to: 20.000, occupancy to: 1.00000

