

Supplementary Data -A STUDY ON SOME STRUCTURAL FEATURES RESPONSIBLE FOR SARS-COV-2 INFECTION FATALITY

Data Availability - [10 ,1.5] [20,2] [50,2.5] [100,3.5] [200,4.5] [500,6] , [1000,8.5]

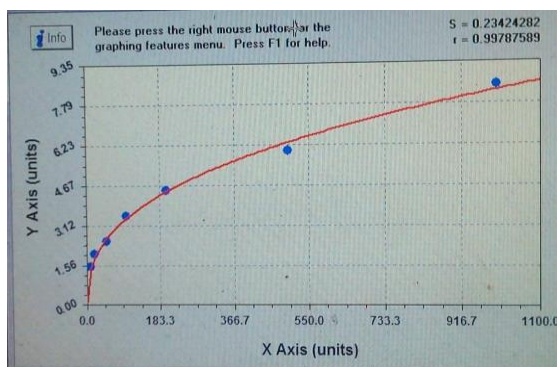
REF : *Molecular weight–gyration radius relation of globular proteins: a comparison of light scattering, small-angle X-ray scattering and structure-based data* , P. 1604

<http://dx.doi.org/10.1107/S1600576715015551> J. Appl. Cryst. (2015). 48, 1604–1606

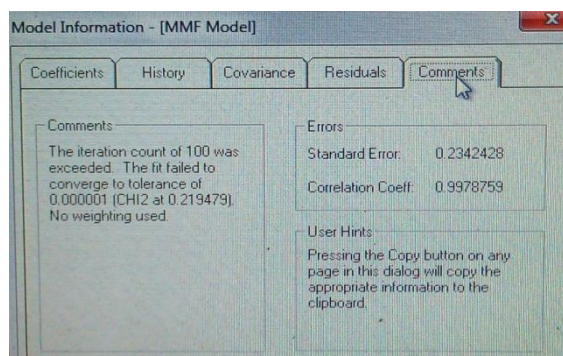
<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4603275/#> ,

(<https://dx.doi.org/10.1107%2FS1600576715015551>)

1. Standard Curve (**Figure –III**) – Software used : Curve Expert 1.4



2. Software Output –



$r = 0.9978$, $s = 0.2342$, $p < 0.0001$, @ 0.01 interval

Radius of Gyration (R_g) – SARS-COV-2 (Computed) - $3.9 \pm 2.95 \pm 0.7$ nm for

Molecular Weight of spike protein 180KDa ,110KDa ,35 KDa respectively .

REF : Characterization of the SARS-CoV-2 Spike in an Early Prefusion Conformation-

<https://doi.org/10.1101/2020.03.16.994152> , (line No .116-118) .