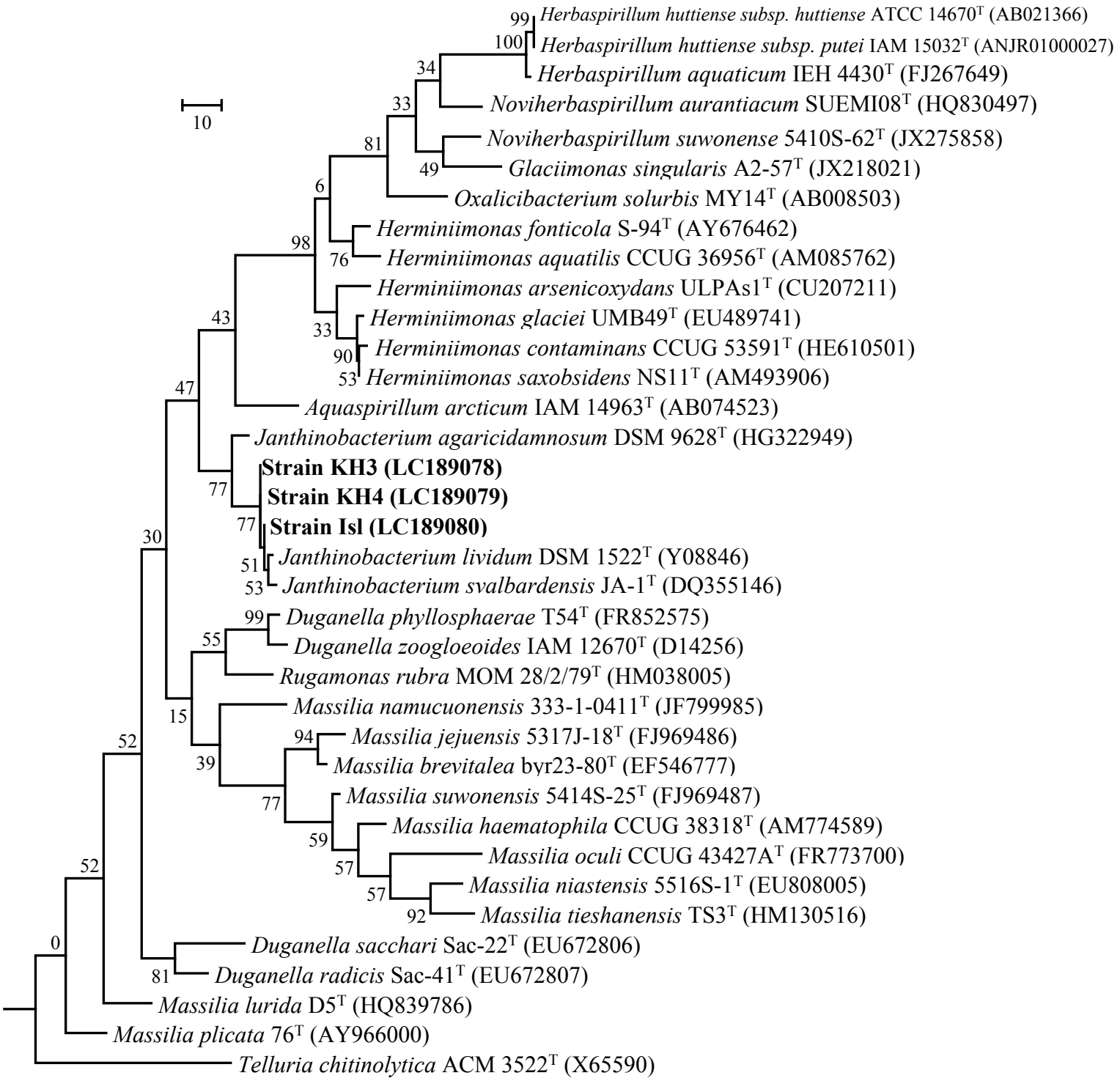

Figure S1: Maximum parsimony phylogenetic tree constructed based on 16S rRNA gene sequence of isolated strains with the closely related validly published species. The tree was rooted by using Telluria chitinolytica ACM 3522T (X65590) as an out-group. Bootstrap values (only > 60 % are shown) are given at the branching points. Bar indicates 1.0 % sequence divergence.

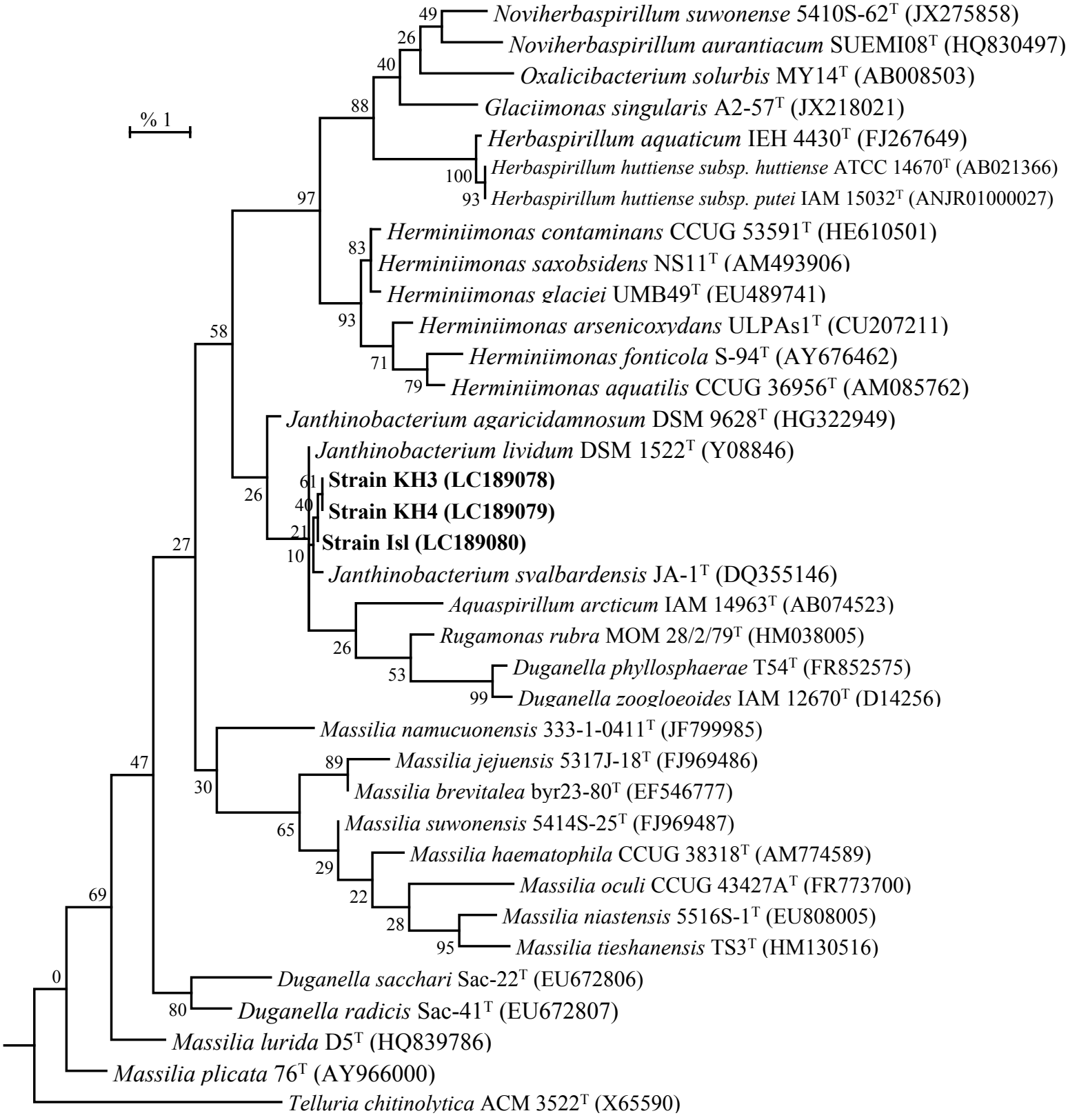

Figure S2: Maximum likelihood phylogenetic tree constructed based on 16S rRNA gene sequence of isolated strains with the closely related validly published species. The tree was rooted by using *Telluria chitinolytica* ACM 3522^T (X65590) as

an out-group. Bootstrap values (only > 60 % are shown) are given at the branching points. Bar indicates 1.0 % sequence divergence.

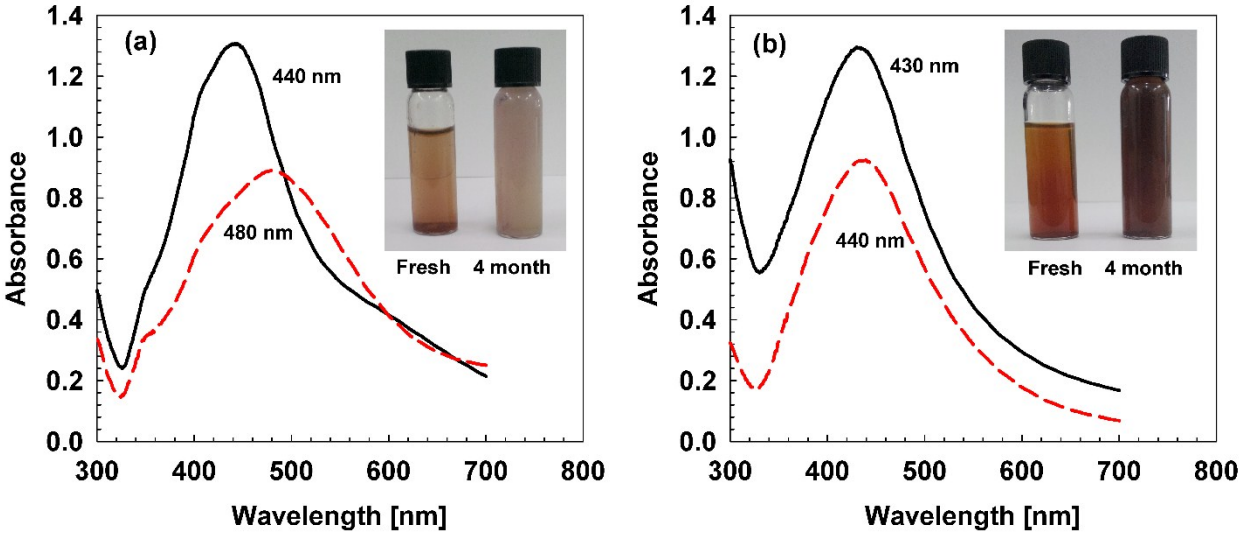

Figure S3: UV-Vis spectra indicating aging of AgNPs. **(a)** cAgNPs and (b) vAgNPs. **(——)** denote freshly prepared samples and **(– – –)** denote storage time of 4 months.

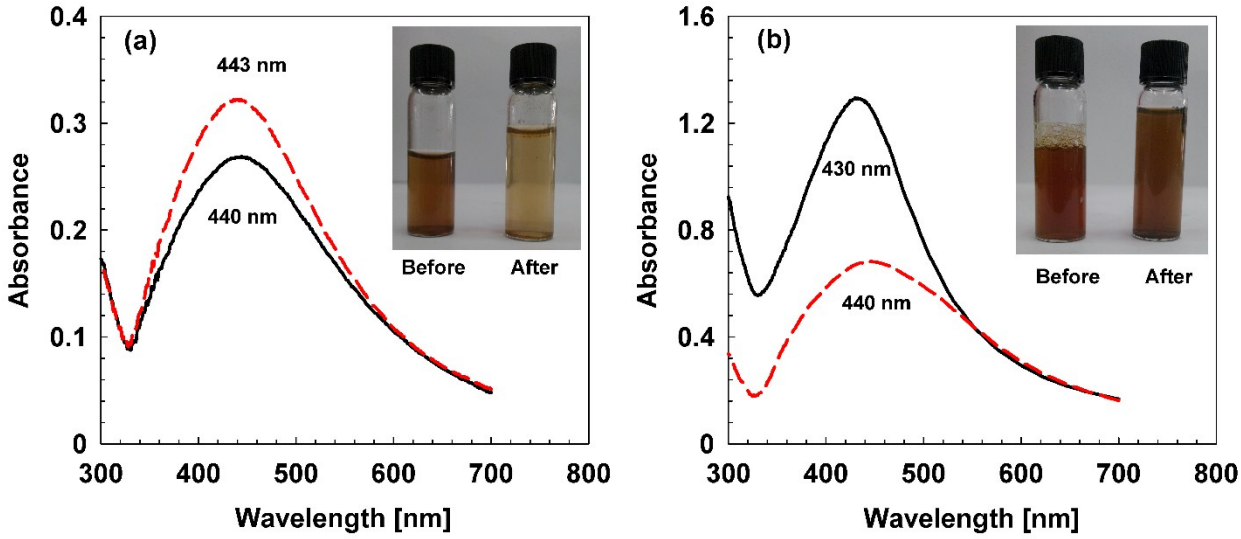

Figure S4: UV-Vis Spectra indicating effect of temperature on AgNPs**.** (a) cAgNPs (b) vAgNPs. **(——)** denote absorbance before heating and **(– – –)** denote absorbance after heating at 60°C.

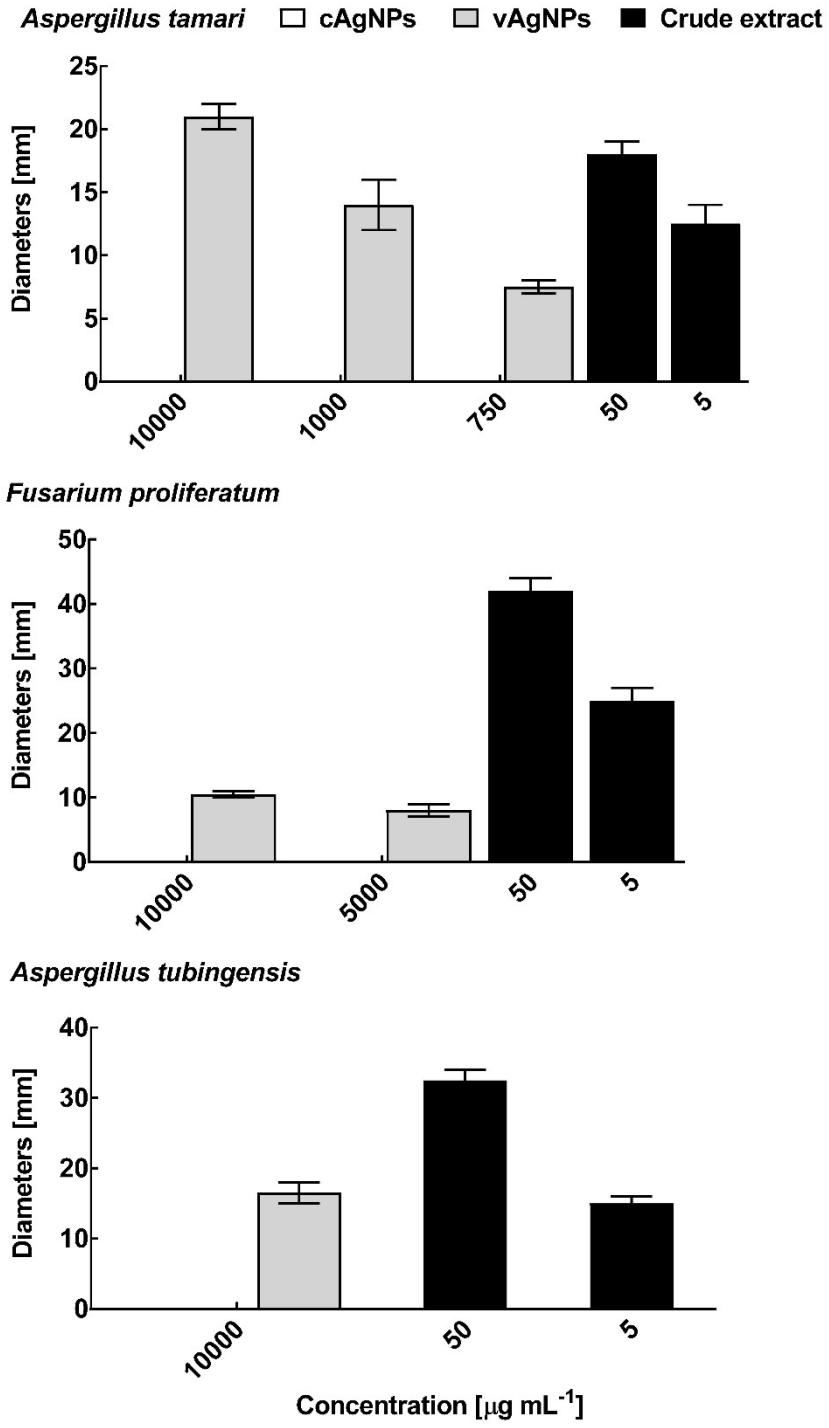

Figure S5: Antifungal activity of AgNPs and crude violacein**.** The error bars represent the standard error of mean. Greater the error bars, greater is the deviation between repetitive values.

Table S1: Crystalline Size Measurement for the AgNPs. (a) cAgNPs and (b) vAgNPs

(a)

Phases cAgNPs	Peak position (°2θ)	β Observed	β Standard	β Structural	Size (Å)	Size (nm)
111	32.24	0.197	0.008	0.19	**437.55**	**43.75**
200	43.91	0.134	0.008	0.13	**679.82**	**67.98**
220	64.33	0.472	0.008	0.46	**202.26**	**20.23**

Average=44.01

(b)

Phases vAgNPs	Peak position (°2θ)	β Observed	β Standard	β Structural	Size (Å)	Size (nm)
111	32.2	0.276	0.008	0.19	**309.01**	**30.90**
200	44.04	0.203	0.008	0.13	**439.47**	**43.95**
220	64.40	0.63	0.008	0.46	**150.94**	**15.09**

Average=29.98