

## Supporting Information

**Inhibitory effects of iron-based carbonaceous nanocomposites on mushroom tyrosinase activity: molecular aspects and mechanistic insights.**

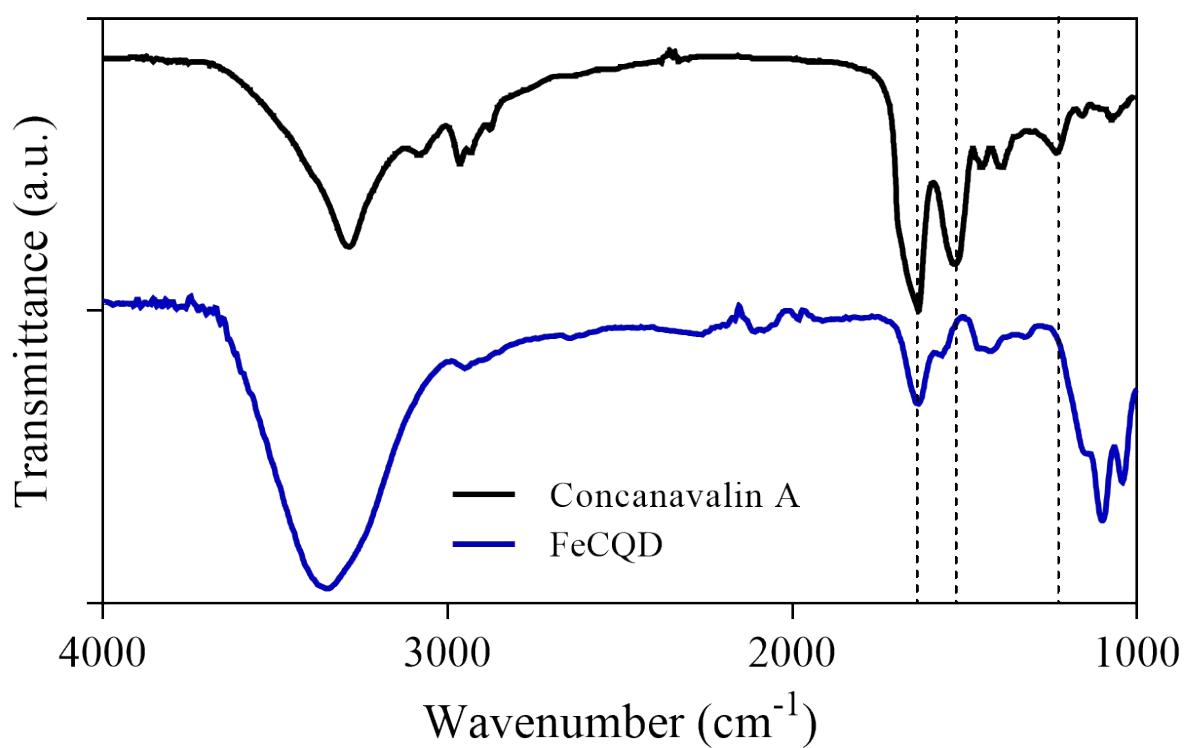
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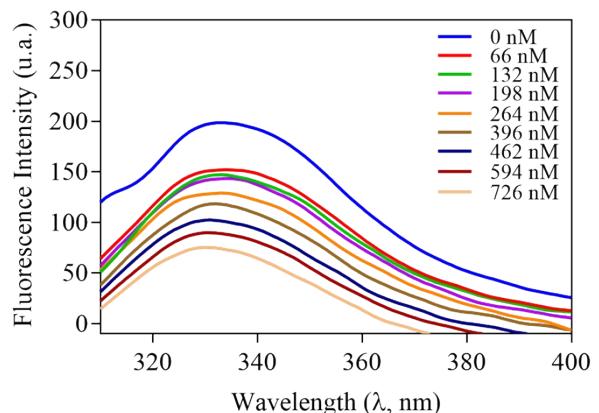
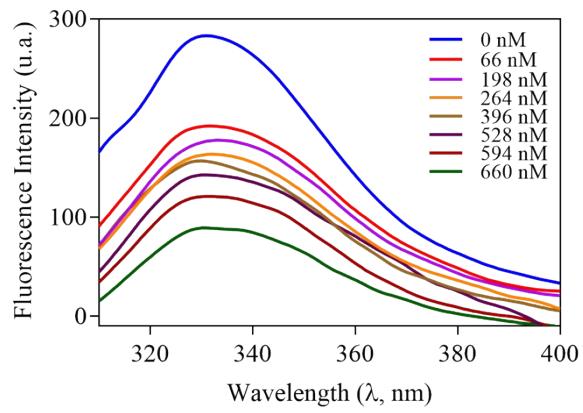
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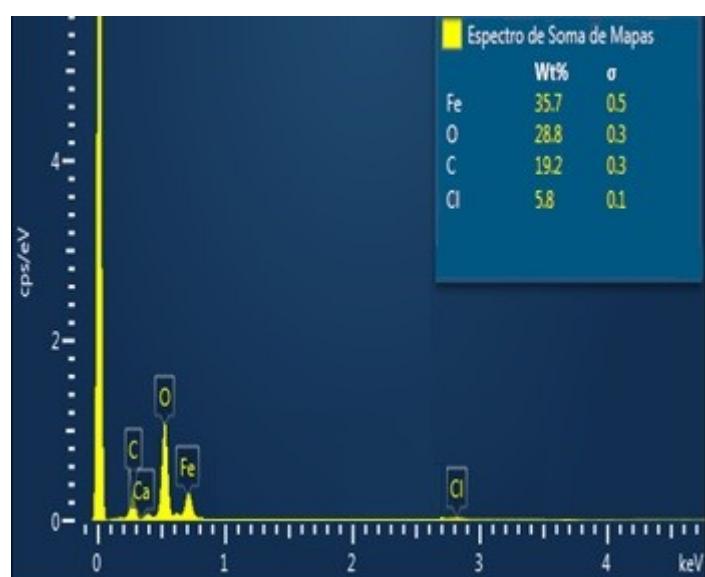
<sup>d</sup> Centro de Estudios Avanzados de Cuba (CEAC), CITMA, La Lisa, 17100 La Habana, Cuba.



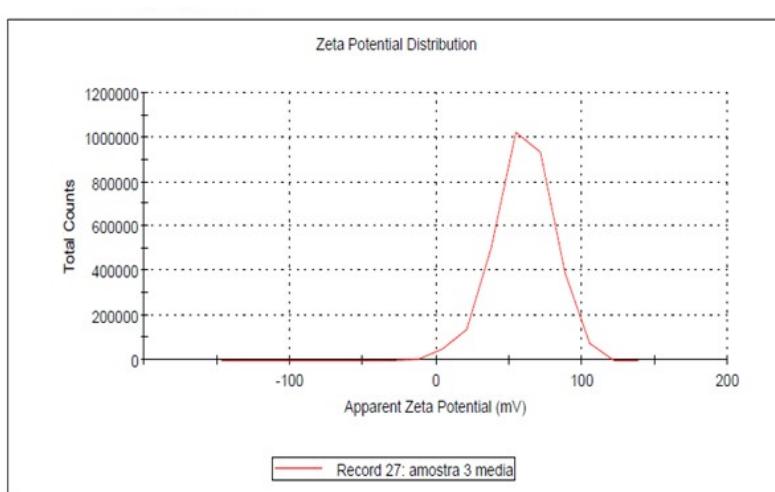
**Figure S1.** FTIR spectra of the protein Concanavalin A (red) and the synthesized CDs (blue), showing similarities and differences between the spectra.



**Figure S2.** Fluorescence quenching of Tyrosinase by CDs in two temperatures: 303K(a), and 313K(b); showing the fluorescence intensity decrease due to the CDs titration.



**Figure S3:** EDS spectrum of FeCQD.



**Figure S4:** Zeta potential of FeCQD in PBS.

## Supplementary Script: *Color\_h*.

This code can be found at <[https://pymolwiki.org/index.php/Color\\_h](https://pymolwiki.org/index.php/Color_h)>

```
# color_h
#
# -----
#
# PyMOL command to color protein molecules according to the Eisenberg
# hydrophobicity scale
#
# Source: http://us.expasy.org/tools/pscale/Hphob.Eisenberg.html
# Amino acid scale: Normalized consensus hydrophobicity scale
# Author(s): Eisenberg D., Schwarz E., Komaromy M., Wall R.
# Reference: J. Mol. Biol. 179:125-142 (1984)
#
# Amino acid scale values:
#
# Ala:  0.620
# Arg: -2.530
# Asn: -0.780
# Asp: -0.900
# Cys:  0.290
# Gln: -0.850
# Glu: -0.740
# Gly:  0.480
# His: -0.400
# Ile:  1.380
# Leu:  1.060
# Lys: -1.500
# Met:  0.640
# Phe:  1.190
```

```

# Pro:  0.120
# Ser: -0.180
# Thr: -0.050
# Trp:  0.810
# Tyr:  0.260
# Val:  1.080
#
# Usage:
# color_h (selection)
#
from pymol import cmd

def color_h(selection='all'):
    s = str(selection)

    print(s)

    cmd.set_color('color_ile',[0.996,0.062,0.062])
    cmd.set_color('color_phe',[0.996,0.109,0.109])
    cmd.set_color('color_val',[0.992,0.156,0.156])
    cmd.set_color('color_leu',[0.992,0.207,0.207])
    cmd.set_color('color_trp',[0.992,0.254,0.254])
    cmd.set_color('color_met',[0.988,0.301,0.301])
    cmd.set_color('color_ala',[0.988,0.348,0.348])
    cmd.set_color('color_gly',[0.984,0.394,0.394])
    cmd.set_color('color_cys',[0.984,0.445,0.445])
    cmd.set_color('color_tyr',[0.984,0.492,0.492])
    cmd.set_color('color_pro',[0.980,0.539,0.539])
    cmd.set_color('color_thr',[0.980,0.586,0.586])
    cmd.set_color('color_ser',[0.980,0.637,0.637])

```

```
cmd.set_color('color_his',[0.977,0.684,0.684])
cmd.set_color('color_glu',[0.977,0.730,0.730])
cmd.set_color('color_asn',[0.973,0.777,0.777])
cmd.set_color('color_gln',[0.973,0.824,0.824])
cmd.set_color('color_asp',[0.973,0.875,0.875])
cmd.set_color('color_lys',[0.899,0.922,0.922])
cmd.set_color('color_arg',[0.899,0.969,0.969])
cmd.color("color_ile","("+s+" and resn ile)")
cmd.color("color_phe","("+s+" and resn phe)")
cmd.color("color_val","("+s+" and resn val)")
cmd.color("color_leu","("+s+" and resn leu)")
cmd.color("color_trp","("+s+" and resn trp)")
cmd.color("color_met","("+s+" and resn met)")
cmd.color("color_ala","("+s+" and resn ala)")
cmd.color("color_gly","("+s+" and resn gly)")
cmd.color("color_cys","("+s+" and resn cys)")
cmd.color("color_tyr","("+s+" and resn tyr)")
cmd.color("color_pro","("+s+" and resn pro)")
cmd.color("color_thr","("+s+" and resn thr)")
cmd.color("color_ser","("+s+" and resn ser)")
cmd.color("color_his","("+s+" and resn his)")
cmd.color("color_glu","("+s+" and resn glu)")
cmd.color("color_asn","("+s+" and resn asn)")
cmd.color("color_gln","("+s+" and resn gln)")
cmd.color("color_asp","("+s+" and resn asp)")
cmd.color("color_lys","("+s+" and resn lys)")
cmd.color("color_arg","("+s+" and resn arg)")

cmd.extend('color_h',color_h)
```

```
def color_h2(selection='all'):  
    s = str(selection)  
  
    print(s)  
  
    cmd.set_color("color_ile2", [0.938,1,0.938])  
    cmd.set_color("color_phe2", [0.891,1,0.891])  
    cmd.set_color("color_val2", [0.844,1,0.844])  
    cmd.set_color("color_leu2", [0.793,1,0.793])  
    cmd.set_color("color_trp2", [0.746,1,0.746])  
    cmd.set_color("color_met2", [0.699,1,0.699])  
    cmd.set_color("color_ala2", [0.652,1,0.652])  
    cmd.set_color("color_gly2", [0.606,1,0.606])  
    cmd.set_color("color_cys2", [0.555,1,0.555])  
    cmd.set_color("color_tyr2", [0.508,1,0.508])  
    cmd.set_color("color_pro2", [0.461,1,0.461])  
    cmd.set_color("color_thr2", [0.414,1,0.414])  
    cmd.set_color("color_ser2", [0.363,1,0.363])  
    cmd.set_color("color_his2", [0.316,1,0.316])  
    cmd.set_color("color_glu2", [0.27,1,0.27])  
    cmd.set_color("color_asn2", [0.223,1,0.223])  
    cmd.set_color("color_gln2", [0.176,1,0.176])  
    cmd.set_color("color_asp2", [0.125,1,0.125])  
    cmd.set_color("color_lys2", [0.078,1,0.078])  
    cmd.set_color("color_arg2", [0.031,1,0.031])  
  
    cmd.color("color_ile2", "(+s+" and resn ile)")  
    cmd.color("color_phe2", "(+s+" and resn phe)")  
    cmd.color("color_val2", "(+s+" and resn val)")  
    cmd.color("color_leu2", "(+s+" and resn leu)")
```

```
cmd.color("color_trp2","("+s+" and resn trp)")  
cmd.color("color_met2","("+s+" and resn met)")  
cmd.color("color_ala2","("+s+" and resn ala)")  
cmd.color("color_gly2","("+s+" and resn gly)")  
cmd.color("color_cys2","("+s+" and resn cys)")  
cmd.color("color_tyr2","("+s+" and resn tyr)")  
cmd.color("color_pro2","("+s+" and resn pro)")  
cmd.color("color_thr2","("+s+" and resn thr)")  
cmd.color("color_ser2","("+s+" and resn ser)")  
cmd.color("color_his2","("+s+" and resn his)")  
cmd.color("color_glu2","("+s+" and resn glu)")  
cmd.color("color_asn2","("+s+" and resn asn)")  
cmd.color("color_gln2","("+s+" and resn gln)")  
cmd.color("color_asp2","("+s+" and resn asp)")  
cmd.color("color_lys2","("+s+" and resn lys)")  
cmd.color("color_arg2","("+s+" and resn arg)")  
  
cmd.extend('color_h2',color_h2)
```