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Synthesis and characterization of graphene oxide coated silica nanoparticles

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Graphene oxide (GO) is capable of absorbing many common pollutants of water such as heavy metals and organic contaminants. However, graphene oxide membranes easily disintegrate in water and aggregates. This decreases its adsorption capacity and diminishes its practical applications. Therefore, to prevent the above problems graphene oxide is combined with silica nanoparticles.

GO coated silica nanoparticles were characterized using Fourier Transform Infrared Attenuated Total Reflection Spectroscopy (FT-IR ATR), Scanning Electron Microscopy (SEM) and Energy Dispersive X-ray Spectrometry (EDXAS). FT-IR ATR of graphene oxide coated silica nanoparticles showed the presence of the following absorptions; peaks for silica at 1059 cm^{-1} for the asymmetric stretching of Si-O-Si bond and at 791 cm^{-1} for symmetric stretching of Si-O-Si bonds and peaks for graphene oxide at 3444 cm^{-1} for the stretching vibration of hydroxyl (–OH) groups, at 1739 cm^{-1} for the stretching vibration of carbonyl (C=O) functional groups and at 1391 cm^{-1} for the epoxy (C-OH) groups. EDXAS data showed the presence of corresponding elements in each sample. EDXAS data of graphene oxide coated silica nanoparticles showed the presence C (carbon), O (oxygen), Si (silicon) as the main elements. According to SEM data, graphene oxide membranes on silica nanoparticles and the interphase between silica and graphene oxide could be clearly observed. Therefore, the successful synthesis of graphene oxide coated silica nanoparticles can be confirmed using SEM data, FT-IR ATR data and EDXAS data.

Keywords
Graphene oxide, silica nanoparticles, coatings, water treatment, characterization

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Binding interactions of coumarin derivatives with Hodgkin's disease related protein ADAM-10; an *in-silico* approach

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Hodgkin's disease is a malignant tumor which is one of the most common cancers among the elderly and children. It is characterized by the overexpression of ADAM-10 protein with increased release of NKG2D ligand which causes impaired immune response against tumor cells.[1] The selective inhibition of ADAM10 is one of the major approaches that is used to treat Hodgkin's disease.[1] However, there is still no synthetic selective inhibitor for ADAM10. This study focuses on the selective inhibitory activity of the 4,5- disubstituted-7-hydroxy coumarins on ADAM10 over ADAM17 and MMP9 in the sub site *S*1′ –*S*3′ of the MMP like catalytic site, using molecular docking approach.

Docking software used were AutoDock Vina and Gold. The following crystal structures were obtained from PDB (Protein Data Base); extracellular domain of ADAM10 (PDB ID: 6BDZ), cysteine rich domain of ADAM10 (PDB ID: 5LOQ), extracellular domain of ADAM17 (PDB ID: 1BKC) and human matrix metalloproteinase MMP9 (PDB ID: 1L6J). All nonstandard residues were deleted. The hydrogens and charges were added using UCSF chimera 1.9. The ligands and references were prepared using Spartan '14 and the equilibrium geometry at the ground level was calculated with density functional (DFT) B3LYP and basis set 6-311+G** in vacuum. The hydrogen bonding, pi-pi stacked interactions and pi-alkyl interactions were considered as favorable interactions. Abbreviations of ligands are provided in Table 1.

Table 1: Ligands and their abbreviations

Abbreviation	IUPAC name of ligand
LIG1	7-hydroxy-5-methyl-4-phenoxymethyl-chromen-2-one
LIG2	4-(4-chloro-phenoxymethyl)-7-hydroxy-5-methyl-4-methyl-chromen-2-one
LIG3	4-(2, 4-dichloro-phenoxymethyl)-7-hydroxy-5-methyl-4-methyl-chromen-2-one
LIG4	4-(3-chloro-phenoxymethyl) -7-hydroxy-5-methyl-4-methyl-chromen-2-one
LIG5	7-hydroxy-4-(4-nitro-phenoxymethyl)-chromen-2-one
LIG6	7-hydroxy-4-(4-methoxy-phenoxymethyl)-chromen-2-one
LIG7	7-hydroxy-4-(2, 4-dinitro-phenoxymethyl)-chromen-2-one
REF1	Methyl (5S, 6S)-5-(hydroxycarbamoyl)-6-(4-phenyl3,6-dihydro-2H-pyridine-1-carbonyl)-7-azaspiro[2.5]octane-7-carboxylate
REF2	(2R)-N-[(1S)-2, 2-Dimethyl-1-[(methylamino) carbonyl]-propyl]-2-[(1S)-1-[formyl (hydroxyl) amino] ethyl]-5-phenylpentanamide

Table 2: CHEMPLP scores of the highest scored docking complex poses

Ligand	CHEMPLP score of best docking complex poses			
	extracellular domain of ADAM10	cysteine rich domain of ADAM10	extracellular domain of ADAM17	human matrix metalloproteinase MMP9
LIG1	57.50	39.23	77.31	65.35
LIG2	57.68	43.89	75.31	66.71
LIG3	55.40	43.89	66.47	63.31
LIG4	60.73	42.97	79.83	59.30
LIG5	57.72	51.33	78.80	64.94
LIG6	56.45	43.03	88.64	67.55
LIG7	57.59	40.14	78.75	60.19
REF1	58.04	52.15	84.50	80.23
REF2	65.35	51.49	79.26	51.96

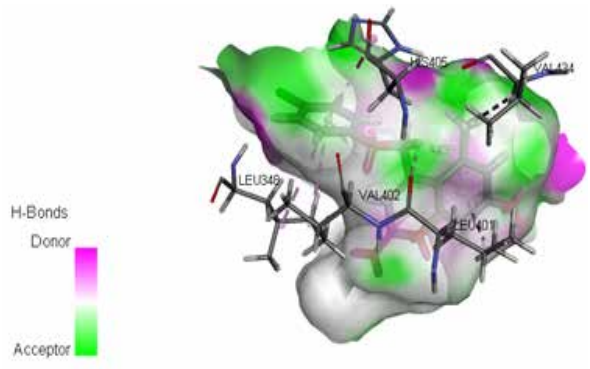

Figure 1. Interaction diagram for top scored docked pose for LIG2 with 1BKC

The scores given in Table 2 were derived using 'Gold' software. The results revealed that LIG1, LIG2, LIG3, LIG5 and LIG7 showed high possibility of inhibiting ADAM10 protein and that LIG1, LIG2, LIG5 and LIG7 showed selective inhibition of ADAM10 over ADAM17. It was also revealed that LIG4 showed selective inhibition of ADAM10 over MMP9. Xxneed to cite Figure 1, authors please indicate placexx

We can conclude that all coumarin derivatives showed higher possibility of binding to sub site *S*1′ –*S*3′ of the MMP like catalytic site of ADAM proteins than to the substrate binding cysteine rich domain to form a stable complex. All seven coumarin derivatives showed the possibility of being dual inhibitors of ADAM10 and ADAM17. LIG 1, LIG2, LIG3, LIG4 and LIG7 showed higher affinity to ADAM10 over ADAM17 and MMP9.

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