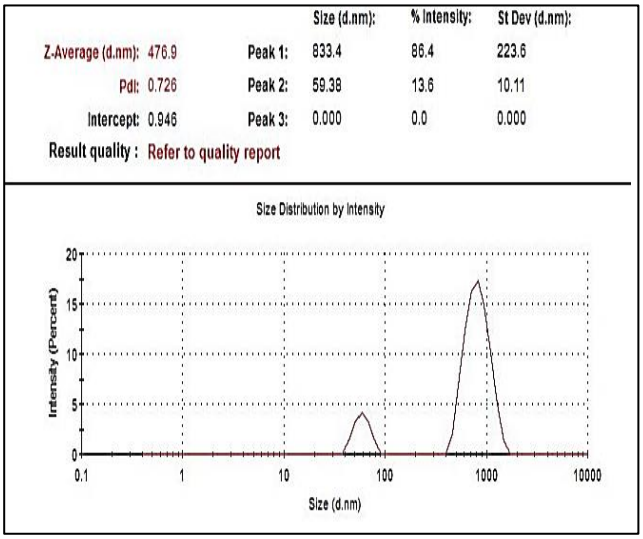
nanomaterials

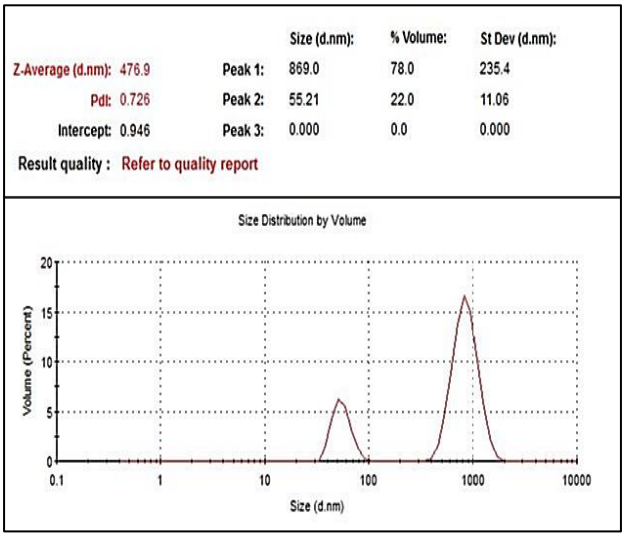
# Fe/Mg-Modified Carbonate Apatite with Uniform Particle Size and Unique Transport Protein-Related Protein Corona Efficiently Delivers Doxorubicin into Breast Cancer Cells

**Sheikh Tanzina Haque [1], Md. Emranul Karim [1], Syafiq Asnawi Zainal Abidin [1], Iekhsan Othman [1], Mark M. Banaszak Holl [2] and Ezharul Hoque Chowdhury [1,2,3,*]**

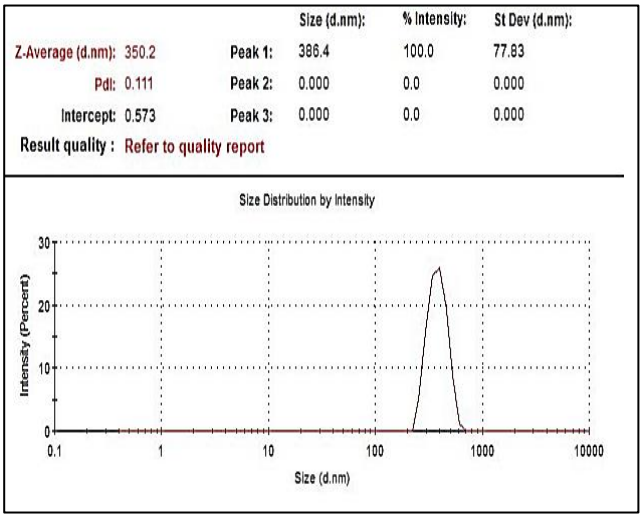
*Supplemental Materials:*

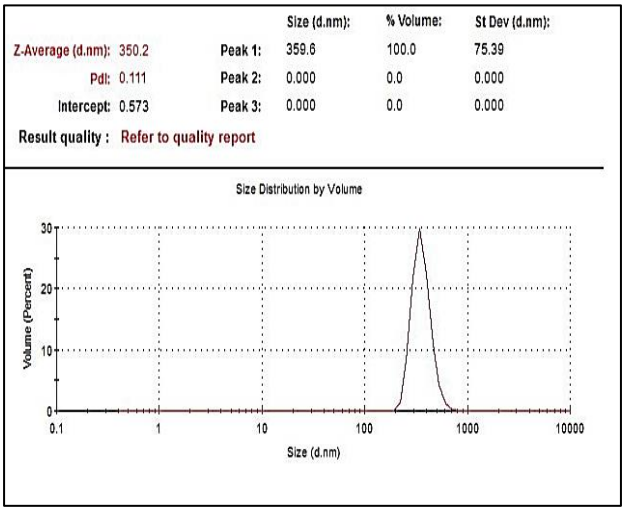
A. **CA**




B. **Low Fe/Mg-CA**



C. **High Fe/Mg-CA**

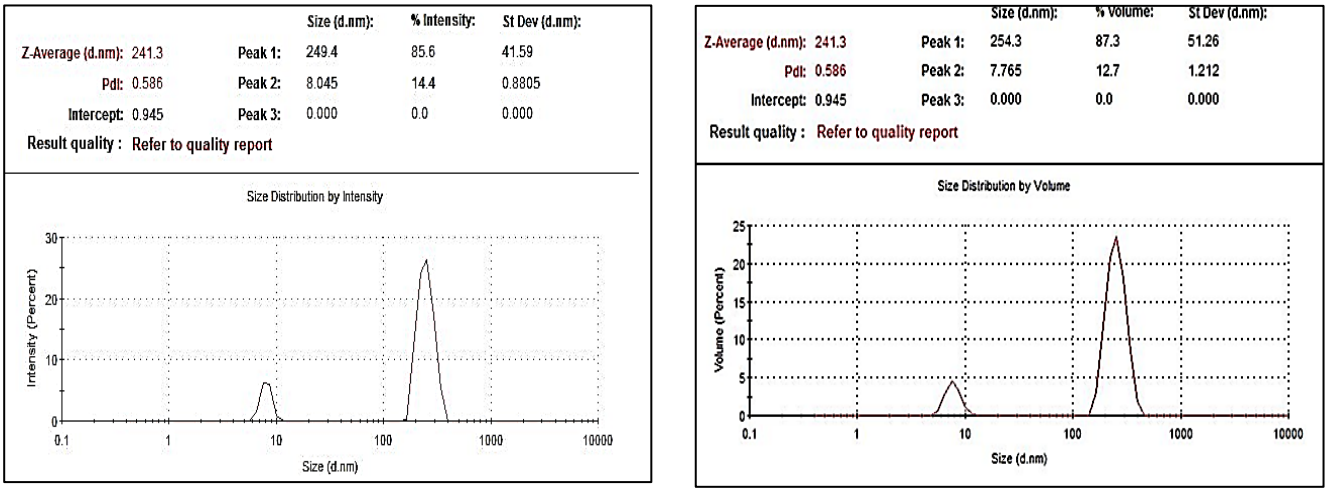



**Figure S1:** Representative data for dynamic light scattering technique used to demonstrate the particle size distribution by intensity and volume for CA and Fe/Mg-CA NPs. (A) Size distribution by intensity and volume for CA NPs. (B) Size distribution by intensity and volume for low Fe/Mg-CA NPs. (C) Size distribution by intensity and volume for high Fe/Mg-CA NPs.

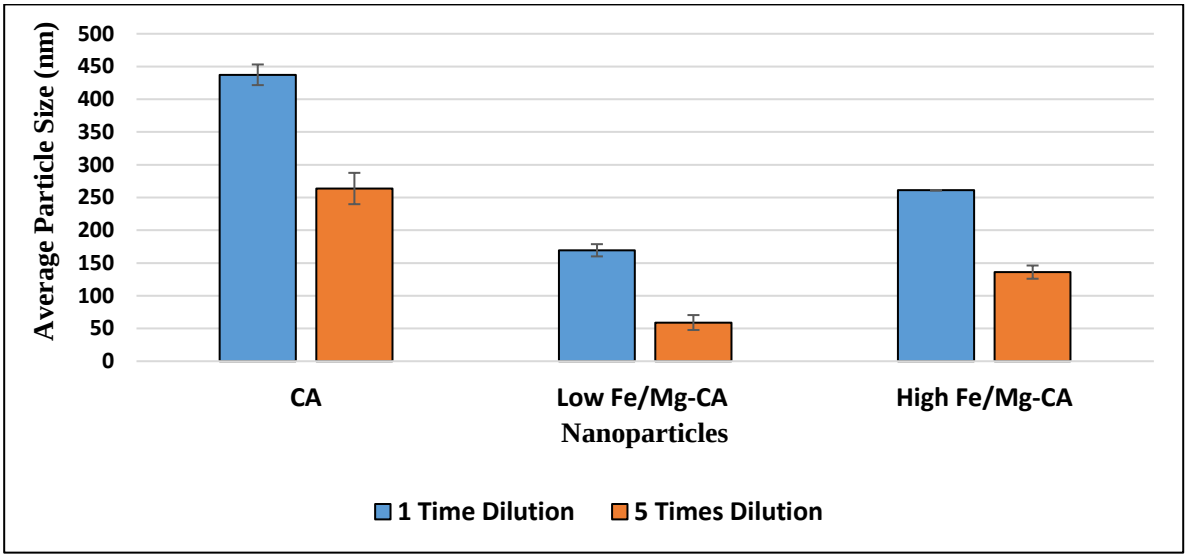
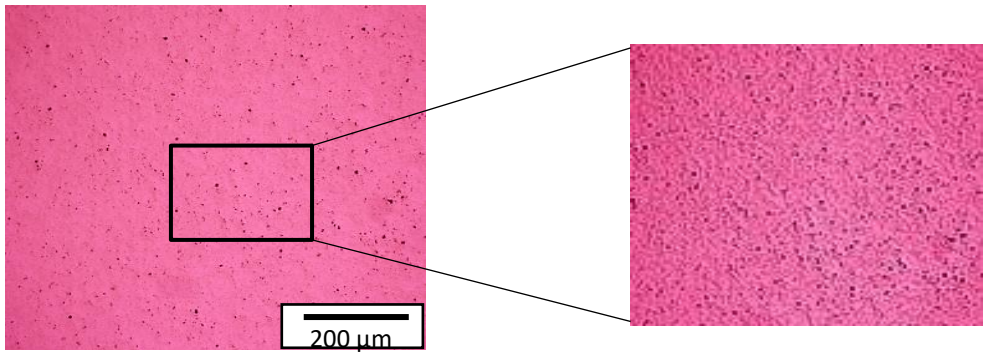
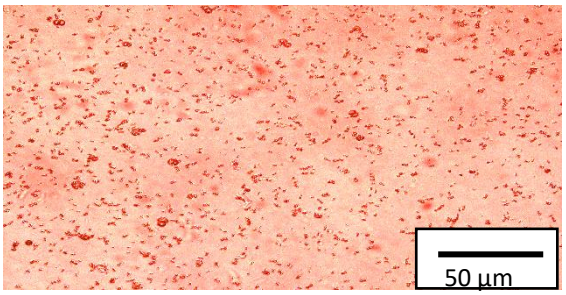


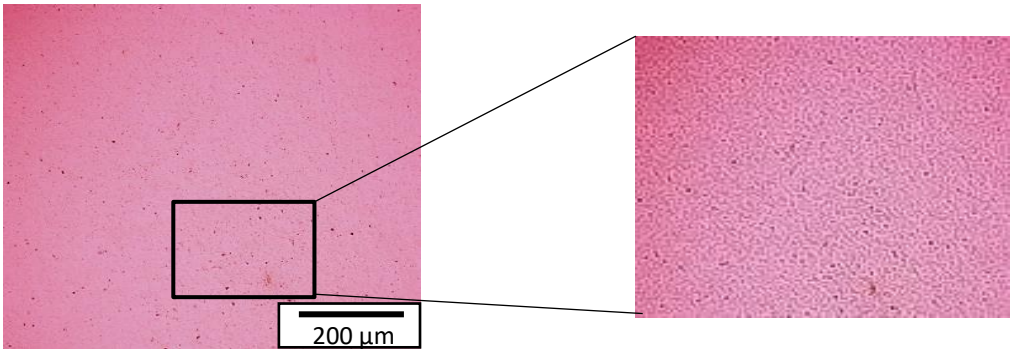

**Figure S2:** Comparison of z-average diameter of 1× and 5× diluted samples of CA, low Fe/Mg-CA and high Fe/Mg-CA NPs.

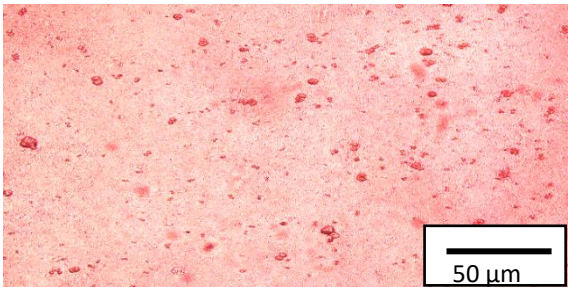
**A. CA**




**B. Low Fe/Mg-CA**



**C. High Fe/Mg-CA**

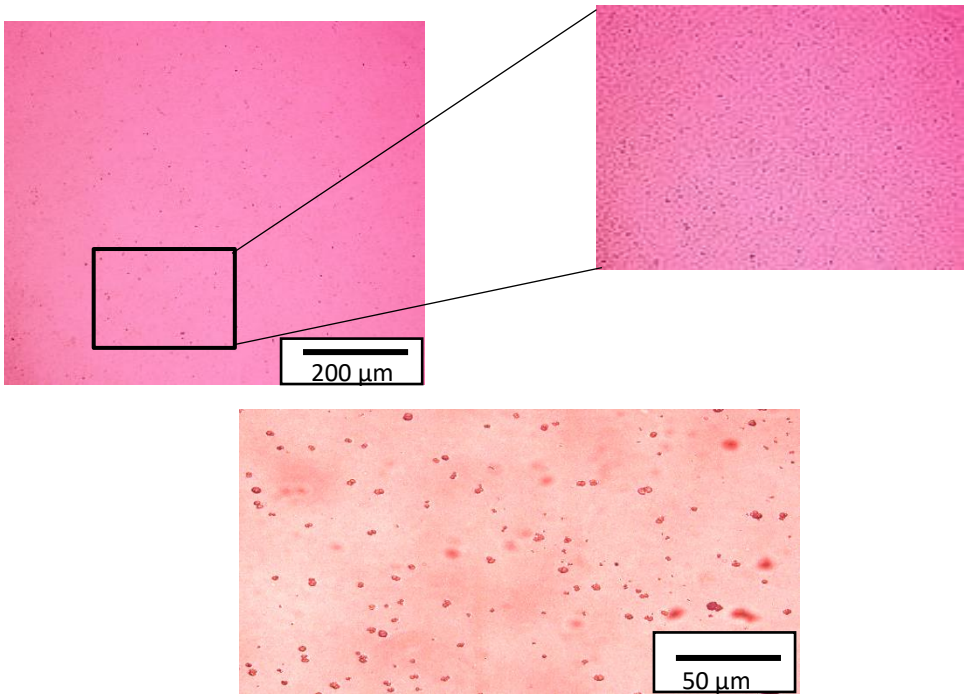



**Figure S3:** Observation of particle aggregates by optical microscopy with different magnifications, i.e. 40× (scale bar of 200 µm), 10× (scale bar of 50 µm) in presence of 10% FBS after 1 hour incubation. (A) CA, (B) Low Fe/Mg-CA and (C) High Fe/Mg-CA.

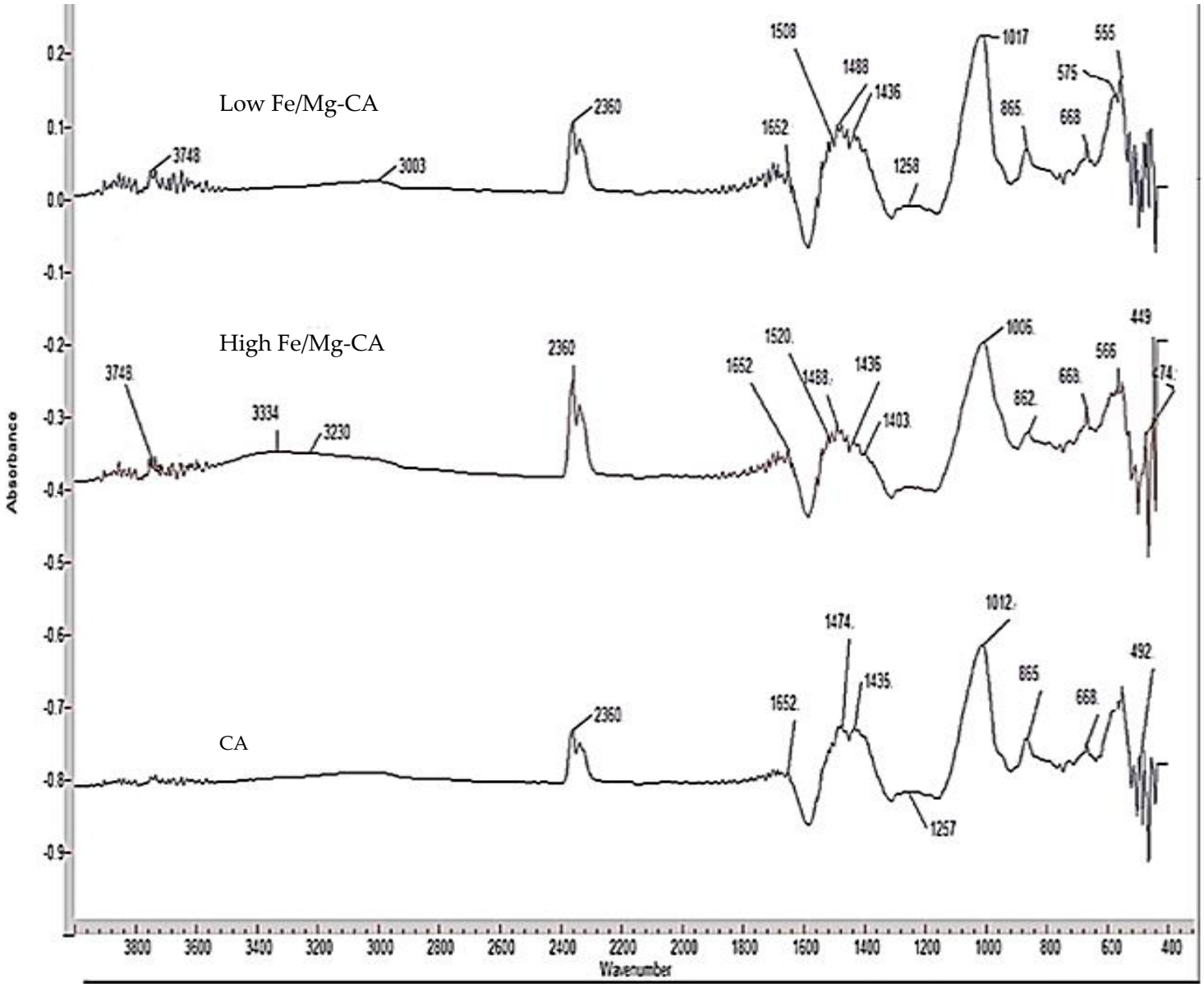



**Figure S4:** FTIR spectra for CA formulated with 40 mM $Ca^{2+}$, low Fe/Mg-CA generated with 40 mM $Ca^{2+}$, 10 μM $Fe^{3+}$ and 40 mM $Mg^{2+}$, and high Fe/Mg-CA synthesized with 40 mM $Ca^{2+}$, 50 μM $Fe^{3+}$ and 120 mM $Mg^{2+}$. The change in formulation was done in order to obtain significant amount of lyophilized powder for the analysis.

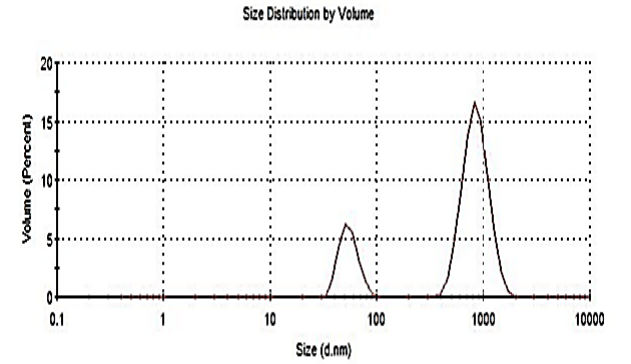
**CA**

0 H

A.

| | | Size (d.nm): | % Volume: | St Dev (d.nm): |
|---|---|---|---|---|
| Z-Average (d.nm): 476.9 | Peak 1: | 869.0 | 78.0 | 235.4 |
| Pdi: 0.726 | Peak 2: | 55.21 | 22.0 | 11.06 |
| Intercept: 0.946 | Peak 3: | 0.000 | 0.0 | 0.000 |

Result quality : Refer to quality report

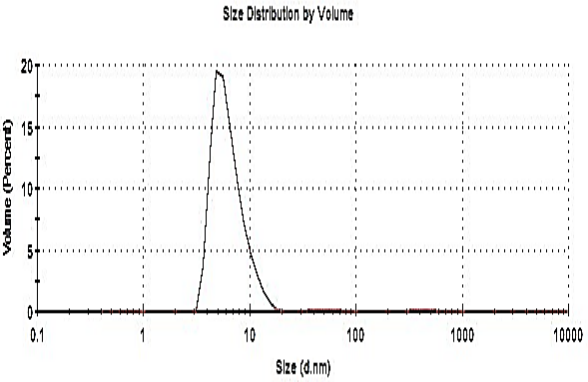



4 H

B.

| | | Size (d.nm): | % Volume: | St Dev (d.nm): |
|---|---|---|---|---|
| Z-Average (d.nm): 275.1 | Peak 1: | 451.4 | 0.5 | 127.0 |
| Pdi: 0.459 | Peak 2: | 54.35 | 0.9 | 16.72 |
| Intercept: 0.975 | Peak 3: | 6.403 | 98.6 | 2.279 |

Result quality : Refer to quality report

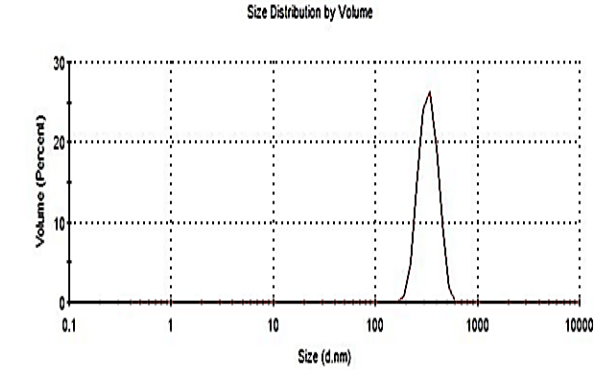



24 H

C.

| | | Size (d.nm): | % Volume: | St Dev (d.nm): |
|---|---|---|---|---|
| Z-Average (d.nm): 334.8 | Peak 1: | 334.7 | 100.0 | 59.19 |
| Pdi: 0.343 | Peak 2: | 0.000 | 0.0 | 0.000 |
| Intercept: 0.939 | Peak 3: | 0.000 | 0.0 | 0.000 |

Result quality : Refer to quality report

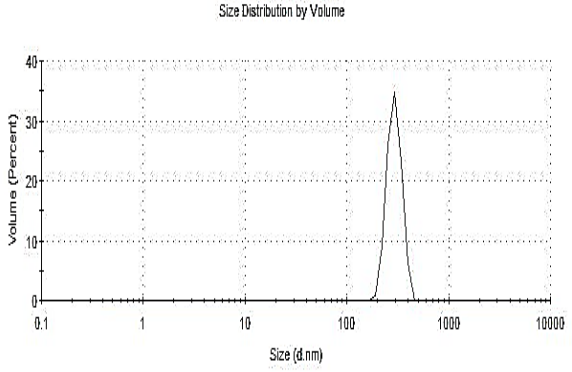



72 H

D.

| | | Size (d.nm): | % Volume: | St Dev (d.nm): |
|---|---|---|---|---|
| Z-Average (d.nm): 361.9 | Peak 1: | 294.1 | 100.0 | 46.41 |
| Pdi: 0.652 | Peak 2: | 0.000 | 0.0 | 0.000 |
| Intercept: 0.949 | Peak 3: | 0.000 | 0.0 | 0.000 |

Result quality : Refer to quality report



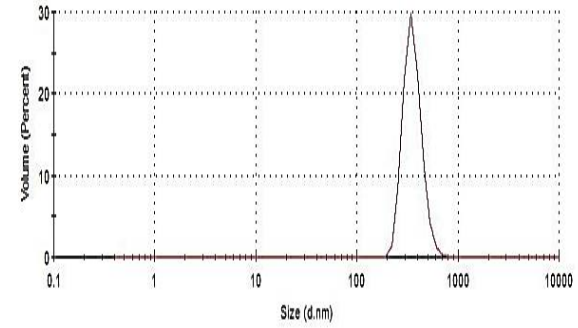
## Low Fe/Mg-CA

0 H

E.

| | | Size (d.nm): | % Volume: | St Dev (d.nm): |
|---|---|---|---|---|
| Z-Average (d.nm): 350.2 | Peak 1: | 359.6 | 100.0 | 75.39 |
| PdI: 0.111 | Peak 2: | 0.000 | 0.0 | 0.000 |
| Intercept: 0.573 | Peak 3: | 0.000 | 0.0 | 0.000 |

Result quality : Refer to quality report

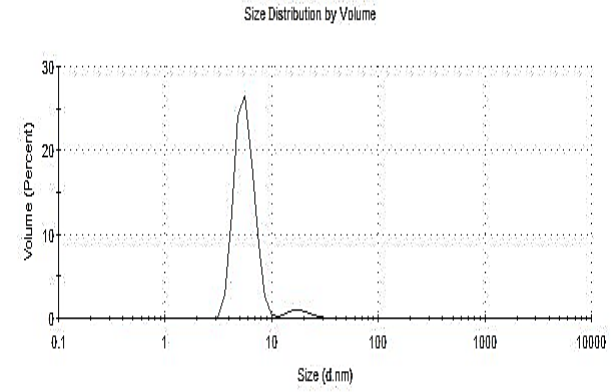



4 H

F.

| | | Size (d.nm): | % Volume: | St Dev (d.nm): |
|---|---|---|---|---|
| Z-Average (d.nm): 223.5 | Peak 1: | 273.0 | 0.1 | 88.54 |
| PdI: 0.412 | Peak 2: | 17.98 | 3.9 | 3.904 |
| Intercept: 0.979 | Peak 3: | 5.639 | 96.0 | 1.188 |

Result quality : Refer to quality report

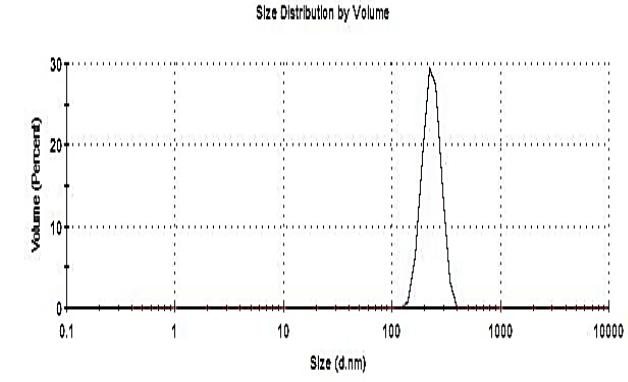



24 H

G.

| | | Size (d.nm): | % Volume: | St Dev (d.nm): |
|---|---|---|---|---|
| Z-Average (d.nm): 296.4 | Peak 1: | 234.9 | 100.0 | 42.79 |
| PdI: 0.031 | Peak 2: | 0.000 | 0.0 | 0.000 |
| Intercept: 0.971 | Peak 3: | 0.000 | 0.0 | 0.000 |

Result quality : Refer to quality report

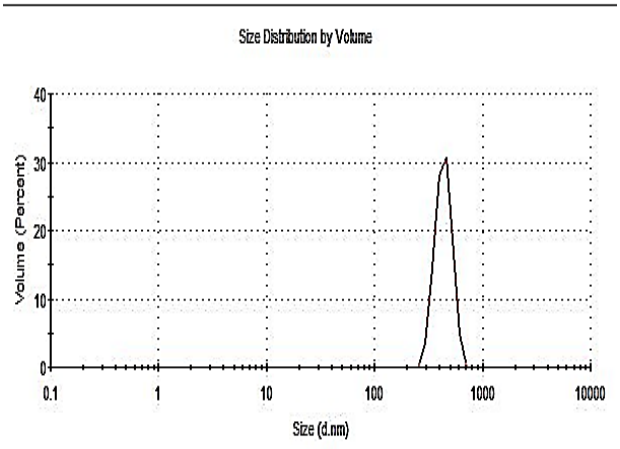



72 H

H.

| | | Size (d.nm): | % Volume: | St Dev (d.nm): |
|---|---|---|---|---|
| Z-Average (d.nm): 374.9 | Peak 1: | 440.0 | 100.0 | 76.14 |
| PdI: 0.264 | Peak 2: | 0.000 | 0.0 | 0.000 |
| Intercept: 0.947 | Peak 3: | 0.000 | 0.0 | 0.000 |

Result quality : Refer to quality report



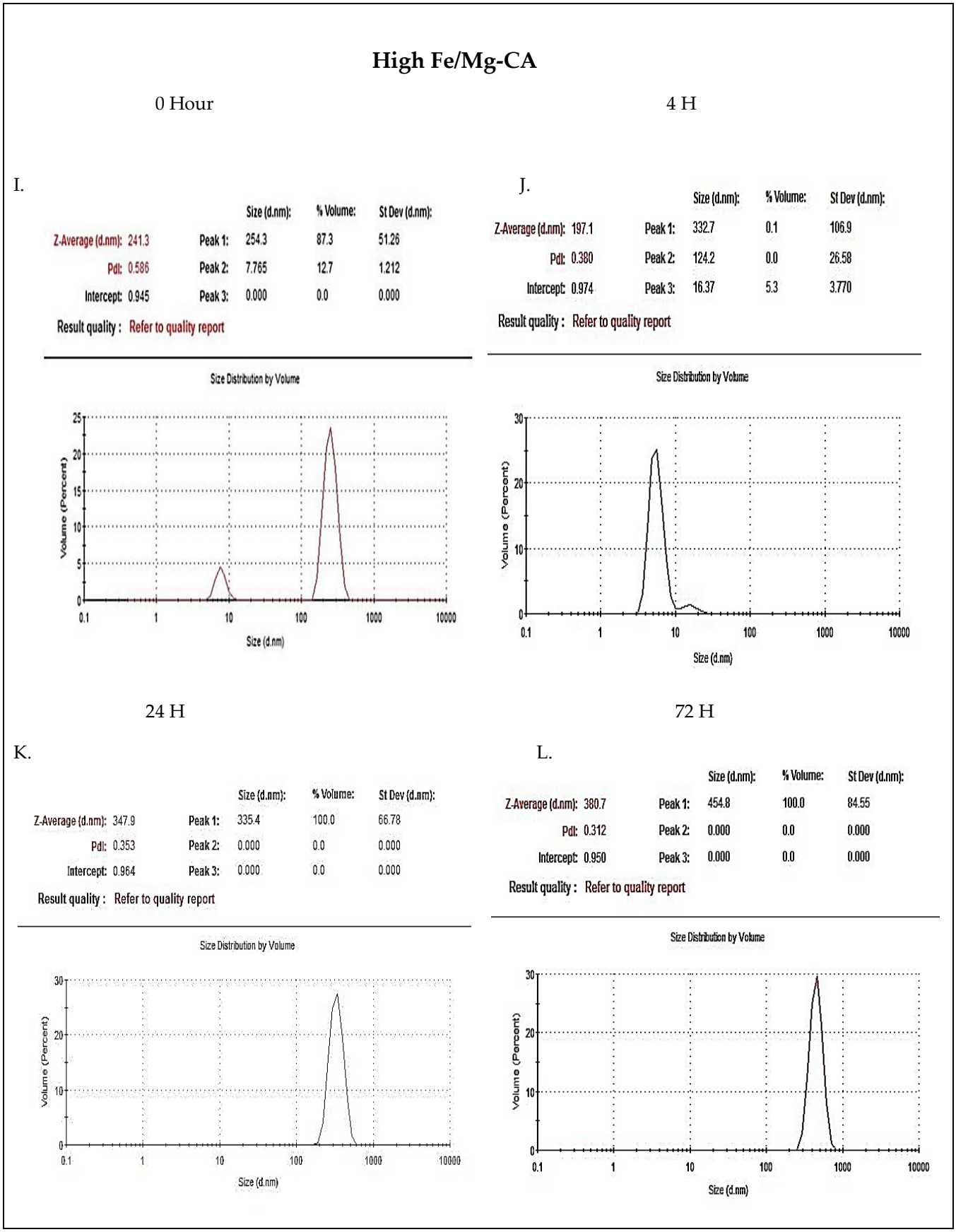
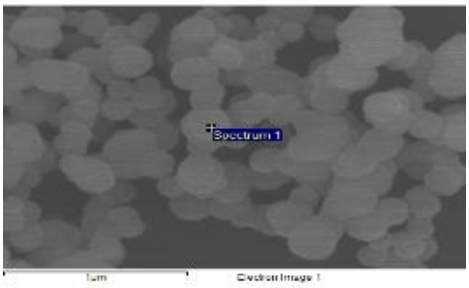



**Figure S5:** Representative data for dynamic light scattering technique used to demonstrate the PDI value and particle size distribution by volume for CA and Fe/Mg-CA NPs. (A) CA at 0 h. (B) CA at 4 h. (C) CA at 24 h. (D) CA at 72 h. (E) Low Fe/Mg-CA at 0 h. (F) Low Fe/Mg-CA 4 h. (G) Low Fe/Mg-CA at 24 h. (H) Low Fe/Mg-CA at 72 h. (I) High Fe/Mg-CA at 0 h. (J) High Fe/Mg-CA at 4 h. (K) High Fe/Mg-CA at 24 h. (L) High Fe/Mg-CA at 72 h.

The representative data for the elemental analysis of CA, low Fe/Mg-CA and high Fe/Mg-CA were presented below-

A. CA



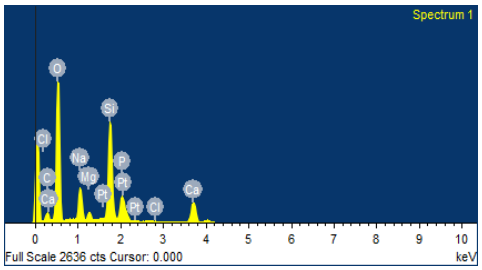
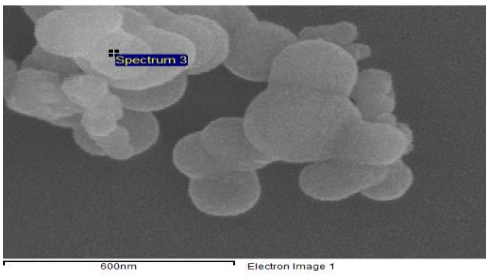




**Table S1:** Elemental analysis for CA.

| Element | Weight % | Atomic % |
|---|---|---|
| Ca | 11.67 | 12.76 |
| Mg | 1.09 | 0.94 |
| C | 5.04 | 8.86 |
| P | 4.24 | 2.89 |
| O | 47.38 | 62.55 |
| Si | 16.97 | 12.76 |
| Pt | 8.08 | 0.87 |
| Na | 5.16 | 4.74 |
| Cl | 0.34 | 0.22 |
| Total | 100 | |

B. Low Fe/Mg-CA



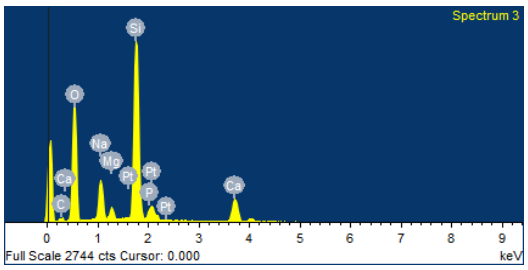



**Table S2:** Elemental analysis for low Fe/Mg-CA.

| Element | Weight % | Atomic % |
|---|---|---|
| Ca | 6.71 | 3.39 |
| Mg | 1.55 | 1.29 |
| C | 4.57 | 7.70 |
| P | 1.46 | 0.95 |
| O | 49.49 | 62.58 |
| Si | 24.48 | 17.63 |
| Pt | 4.98 | 0.52 |
| Na | 6.75 | 5.94 |
| Total | 100 | |

**C.** High Fe/Mg-CA

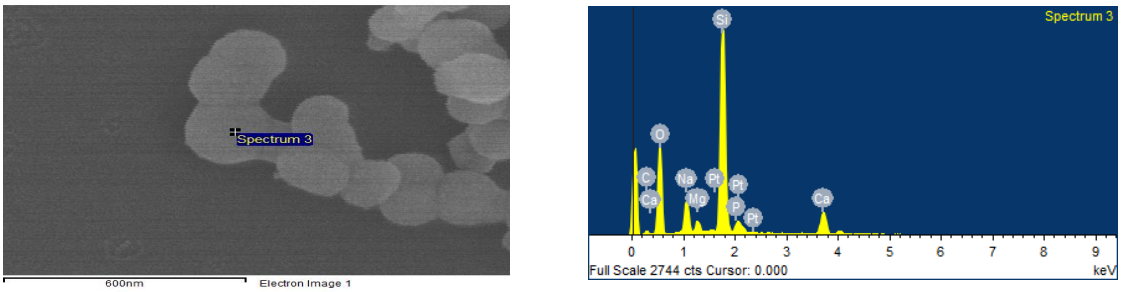



**Table S3:** Elemental analysis for high Fe/Mg-CA.

| Element | Weight % | Atomic % |
|---|---|---|
| Ca | 7.1 | 3.69 |
| Mg | 1.74 | 1.49 |
| C | 4.44 | 7.69 |
| P | 1.24 | 0.83 |
| O | 44.6 | 58.03 |
| Si | 30.47 | 22.58 |
| Pt | 4.69 | 0.5 |
| Na | 5.73 | 5.19 |
| Total | 100 | |

**Figure S6:** Representative data for the elemental analysis for (A) CA (B) Low Fe/Mg-CA (C) High Fe/Mg-CA.

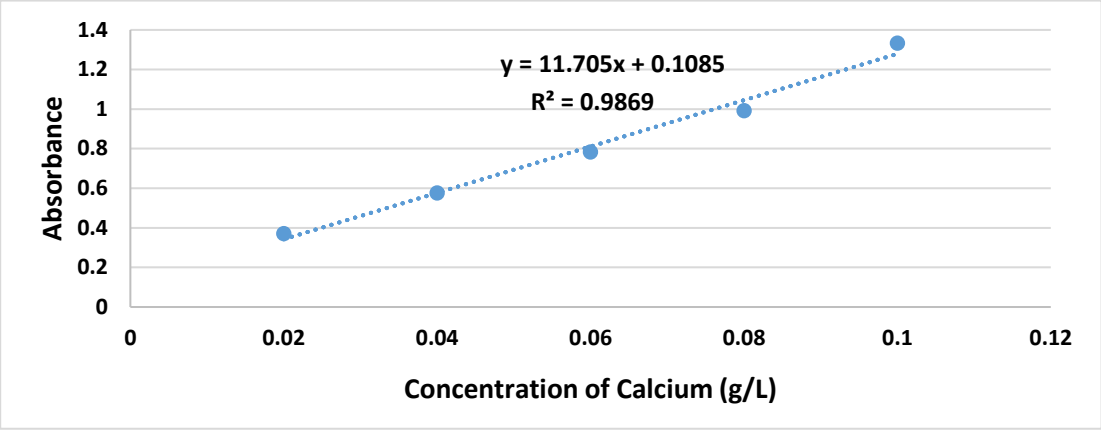



**Figure S7:** Standard curve for Calcium.

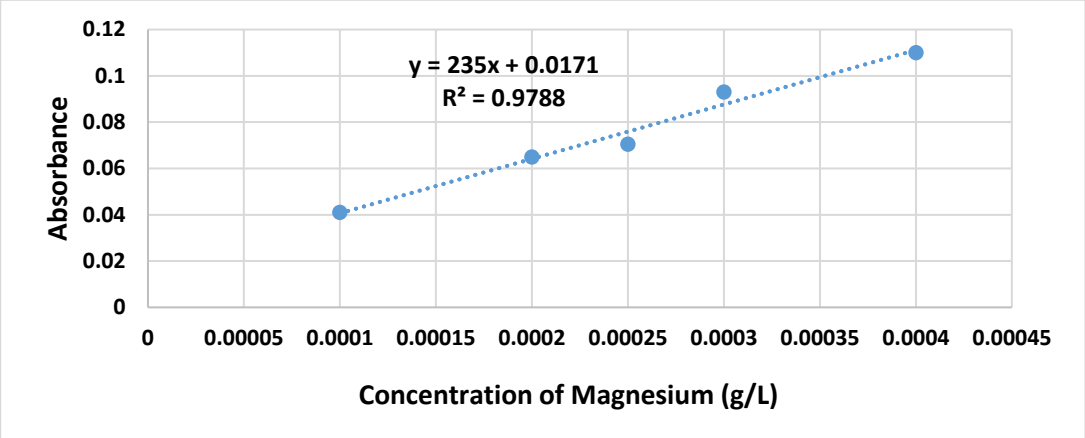



**Figure S8:** Standard curve for Magnesium.

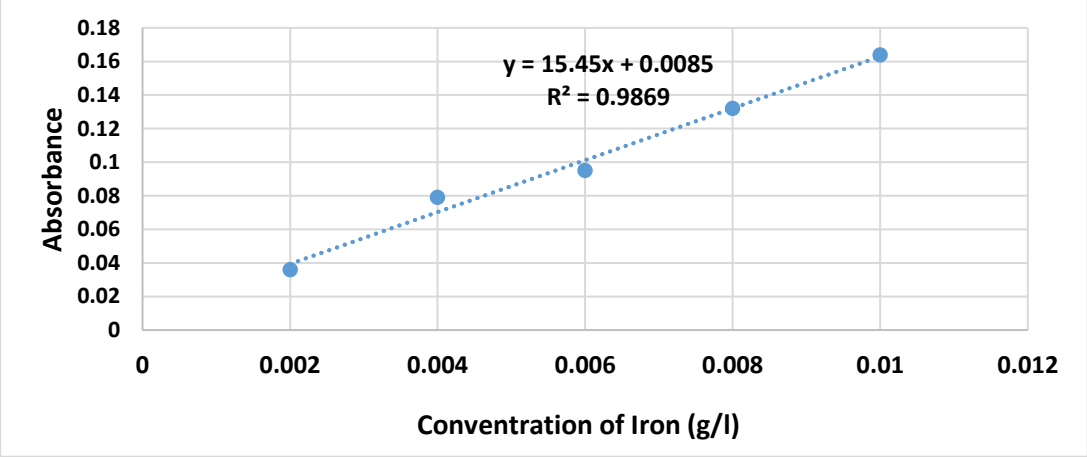



**Figure S9:** Standard curve for Iron.

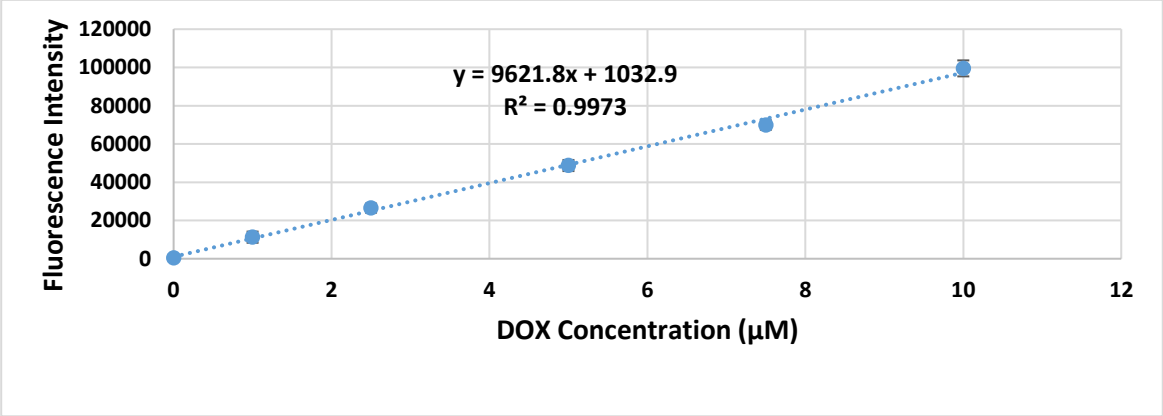



**Figure S10:** Standard Curve for free DOX at different concentrations.

**Table S4:** Cytotoxicity enhancement (%) of DOX-CA and DOX-Fe/Mg-CA NPs by thiazolyl blue tetrazolium bromide (MTT) assay in Michigan Cancer Foundation-7 (MCF-7) cells after 48 h of treatment.

| NPs with different concentrations of DOX | Cytotoxicity enhancement (%) in MCF-7 cells |
|---|---|
| CA+DOX 1 nM | 1± 0.45 |
| CA+DOX 10 nM | 3 ± 0.38 |
| CA+DOX 100 nM | 2 ± 0.29 |
| CA+DOX 1µM | 11± 0.81 |
| Low Fe/Mg-CA+DOX 1 nM | 3± 0.48 |
| Low Fe/Mg-CA+DOX 10 nM | 5± 0.79 |
| Low Fe/Mg-CA+DOX 100 nM | 15± 0.29 |
| Low Fe/Mg-CA+DOX 1µM | 11± 0.82 |
| High Fe/Mg-CA+DOX 1 nM | 2± 0.48 |
| High Fe/Mg-CA+DOX 10 nM | 6± 0.38 |
| High Fe/Mg-CA+DOX 100 nM | 12± 0.28 |
| High Fe/Mg-CA+DOX 1µM | 13± 0.44 |

**Table S5.** List of identified proteins with CA in 10% FBS along with their isoelectric point (pI) and major biological functions.

| Functional classification of protein | Identified Protein | pI | Detailed Function |
|---|---|---|---|
| **Transport Protein** | ALB protein | 5.7 | 1. $Zn^{2+}$ binding |
| | Serum Albumin | 5.53 | 1. Transport<br>2. Lipid binding<br>3. Metal binding<br>4. Bilirubin binding<br>5. Helps maintain osmolarity of blood<br>6. Dysopsonin |
| | Alpha-2-HS glycoprotein | 5.94 | 1. Enhance endocytosis<br>2. $Ca^{2+}$ binding<br>3. Post-translational protein modification<br>4. Protein metabolism |
| | cDNA FLJ51509 | 7.42 | 1. Behaves similar to Alpha-fetoprotein, i.e- it takes part in metal, fatty acids and bilirubin binding, involved in cellular protein and progesterone metabolism |
| | Transthyretin | 5.6 | 1. Thyroid hormone binding<br>2. Identical protein binding<br>3. Transport iron<br>4. Transport thyroxine to the brain<br>5. Cellular protein metabolism<br>6. Neutrophil degranulation<br>7. Retinol metabolism |
| | Serotransferrin | 6.81 | 1. $Fe^{3+}$ binding<br>2. Bicarbonate binding<br>3. Transport iron |
| | Transferrin variant | 6.68 | 1. $Fe^{3+}$ binding<br>2. Transport $Fe^{3+}$ within transmembrane<br>3. Involved in iron ion homeostasis in cells |
| | Transferrin | 6.97 | 1. $Fe^{3+}$ binding<br>2. Transport $Fe^{3+}$ within transmembrane<br>3. Involved in iron ion homeostasis in cells |
| | LMAN1 protein | 6.3 | 1. Mannose (monosaccharide hexose) binding.<br>2. Endoplasmic reticulum (ER) to golgi body facilitated transport |
| | Globin C1 | 9.79 | 1. Metal binding (binding with $Ca^{2+}$, $Mg^{2+}$ and $Fe^{3+}$)<br>2. Heme-binding<br>3. Transport oxygen |
| | Globin B1 | 6.75 | 1. $Fe^{2+}$, $Fe^{3+}$ binding<br>2. Heme binding<br>3. Organic acid binding<br>4. Oxygen binding<br>5. Hemoglobin alpha binding<br>6. Transports oxygen |
| | Globin A1 | 7.02 | 1. $Fe^{2+}$, $Fe^{3+}$ binding<br>2. Heme binding<br>3. Oxygen binding<br>4. Transports oxygen |
| | Alpha-1-acid glycoprotein (positive acute phase protein) | 4.93 | 1. Behave as transport protein in blood stream.<br>2. Involved in regulation of immune system.<br>3. Inhibits aggregation of platelets and neutrophils. |

| | | | |
|---|---|---|---|
| | Mutant hemoglobin alpha 1 globin chain | 8.08 | 1. $Fe^{2+}$, $Fe^{3+}$ binding<br>2. Heme binding<br>3. Oxygen binding<br>4. Transport oxygen<br>5. Transport bicarbonate |
| | Hemoglobin alpha-1 globin chain | 8.08 | 1. $Fe^{2+}$, $Fe^{3+}$ binding<br>2. Heme binding<br>3. Oxygen binding<br>4. Transport oxygen<br>5. Transport bicarbonate |
| | Hemoglobin subunit alpha | 8.72 | 1. $Fe^{2+}$, $Fe^{3+}$ binding<br>2. Heme binding<br>3. Oxygen binding<br>4. Transport oxygen |
| | Alpha-2 globin chain | 8.72 | 1. $Fe^{2+}$, $Fe^{3+}$ binding<br>2. Heme binding<br>3. Oxygen binding<br>4. Transport oxygen<br>5. Transport bicarbonate |
| | Mutant hemoglobin alpha 2 globin chain | 8.72 | 1. $Fe^{2+}$, $Fe^{3+}$ binding<br>2. Heme binding<br>3. Oxygen binding<br>4. Transport oxygen |
| | Lactoferrin | 8.70 | 1. $Fe^{2+}$, $Fe^{3+}$ binding<br>2. Involved in serine-type endopeptidase activity<br>3. Engender antimicrobial humoral response<br>4. Regulates the production of cytokine |
| | Beta-globin protein | 6.64 | 1. Heme binding<br>2. Metal ion binding<br>3. Oxygen binding<br>4. Transports oxygen<br>5. Makes haemoglobin (HbA) along with alpha-globin in adults |
| | Hemoglobin fetal subunit beta | 6.75 | 1. $Fe^{2+}$, $Fe^{3+}$ binding<br>2. Heme binding<br>3. Organic acid binding<br>4. Oxygen binding<br>5. Hemoglobin alpha binding<br>6. Transports oxygen |
| | Truncated beta-globin | 7.96 | 1. Heme binding<br>2. Oxygen binding |
| | Mutant beta-globin | 7.92 | 1. Heme binding<br>2. Oxygen binding<br>3. Transports oxygen |
| | Beta-globin chain | 5.57 | 1. $Fe^{2+}$, $Fe^{3+}$ binding<br>2. Heme binding<br>3. Oxygen binding<br>4. Transport oxygen |
| | Hemoglobin subunit beta | 6.25 | 1. Heme binding<br>2. Oxygen binding<br>3. Transports oxygen |
| | Hemoglobin beta chain | 6.74 | 1. $Fe^{2+}$, $Fe^{3+}$ binding<br>2. Heme binding<br>3. Oxygen binding<br>4. Transport oxygen |
| | Hemoglobin beta chain variant Hb.Sinai-Bel Air | 5.41 | 1. $Fe^{2+}$, $Fe^{3+}$ binding<br>2. Heme binding<br>3. Oxygen binding |

| | | | |
|---|---|---|---|
| | | | 4. Transport oxygen |
| | Hemoglobin beta chain variant Hb-I_Toulouse | 5.41 | 1. $Fe^{2+}$, $Fe^{3+}$ binding<br>2. Heme binding<br>3. Oxygen binding<br>4. Transport oxygen |
| | Vitamin D-binding protein | 5.2 | 1. Vitamin D binding<br>2. Transport vitamin within transmembrane |
| **Cell adhesive protein** | cDNA FLJ54111 | 6.95 | 1. $Ca^{2+}$ binding<br>2. Collagen binding |
| **Coagulation protein** | Prothrombin | 5.64 | 1. Non-covalently calcium ions ($Ca^{2+}$) binding.<br>2. Blood coagulation<br>3. Involved in serine-type endopeptidase activity |
| **Metabolic Protein** | Adiponectin | 5.42 | 1. Involved in fat metabolism and hormonal activity<br>2. Identical protein binding<br>3. Sialic acid binding<br>4. Signaling receptor binding<br>5. Involved in glucose metabolism<br>6. Involved in the negative regulation of macrophage differentiation and phagocytosis |
| **Protease inhibitor** | Kininogen-1 | 6.02 | 1. Inhibits thiol proteases<br>2. Inhibits the thrombin- and plasmin-induced aggregation of thrombocytes in blood coagulation<br>3. Heparin binding<br>4. Zinc ion binding<br>5. Regulates cell adhesion |
| | KNG1 protein | 6.4 | 1. Inhibits cysteine-type endopeptidase |
| | Fetuin-B | 8.7 | 1. Inhibits metalloenzyme, metalloprotease and protease, i.e- inhibits cysteine-type endopeptidase and metallo-endopeptidase.<br>2. Involved in fertilization. |
| | Alpha-1-antiproteinase | 6.05 | 1. Inhibits protease and serine protease.<br>2. Inhibits trypsin, chymotrypsin and plasminogen activator.<br>3. Identical protein and protease binding. |
| **Structural Protein** | Keratin, type I cytoskeletal 10 | 5.13 | 1. Cross linking of peptides<br>2. Protein heterodimerization and heterotetramerization activity<br>3. Keratinization |
| | Keratin 1 | 8.15 | 1. Involved in structural molecular activity |
| | KRT6A protein | 8.09 | 1. Involved in the structural molecular activity |
| | Keratin, type I cytoskeletal 14 | 5.09 | 1. Responsing to $Zn^{2+}$<br>2. Keratin filament binding<br>3. Structural constituent of cytoskeleton<br>4. Keratinization |
| | Histone H2B | 10.32 | 1. DNA binding<br>2. Involved in protein heterodimerization and nucleosome assembly |
| **Regulatory Protein** | Junction mediating and regulatory protein p53 cofactor | 5.95 | 1. Actin binding.<br>2. Arp2/3 complex binding<br>3. Involved in transcription coactivator activity.<br>4. Involved in cell cycle arrest.<br>5. Involved in positive regulation of apoptosis. |
| **Others** | Uncharacterized protein | 6.28 | 1. $Fe^{2+}$, $Fe^{3+}$ binding<br>2. Heme binding<br>3. Oxygen binding<br>4. Transport oxygen |

| | | | |
|---|---|---|---|
| | Epididymis secretory protein Li 51 | 5.4 | 1. Vitamin D binding<br>2. Transports vitamin transmembrane |
| | Alpha-fetoprotein | 4.57 | 1. Metal (copper, nickel) binding<br>2. Fatty acids binding<br>3. Bilirubin binding<br>4. Cellular protein metabolism<br>5. Progesterone metabolism |
| | cDNA FLJ95666 | 5.92 | 1. Involved in aspirin acetylated lysine<br>2. Bilirubin binding |
| | cDNA FLJ57154 | 6.29 | 1. Helps in heterologous expression |
| | cDNA FLJ55606 | 5.84 | 1. Cysteine-type endopeptidase inhibitor |

**Table S6.** List of identified proteins with low Fe/Mg-CA in 10% FBS along with their isoelectric point (pI) and major biological functions.

| Functional classification of protein | Identified Protein | pI | Detailed Function |
|---|---|---|---|
| **Transport protein** | Albumin | 5.53 | 1.Transport<br>2. Systemic calcification inhibitor<br>3. Lipid binding<br>4. Metal binding<br>*5.* Maintaining intravascular colloid osmotic pressure (COP)<br>*6.* Dysopsonin |
| | Mutant hemoglobin alpha 1 globin chain | 8.72 | 1. $Fe^{2+}$, $Fe^{3+}$ binding<br>2. Heme binding<br>3. Oxygen binding<br>4. Transport oxygen<br>5. Transport bicarbonate |
| | Hemoglobin alpha-1 globin chain | 8.72 | 1. $Fe^{2+}$, $Fe^{3+}$ binding<br>2. Heme binding<br>3. Oxygen binding<br>4. Transport oxygen<br>5. Transport bicarbonate |
| | Alpha-2 globin chain | 8.72 | 1. $Fe^{2+}$, $Fe^{3+}$ binding<br>2. Heme binding<br>3. Oxygen binding<br>4. Transport oxygen<br>5. Transport bicarbonate |
| | Hemoglobin subunit alpha piens | 8.72 | 1. $Fe^{2+}$, $Fe^{3+}$ binding<br>2. Heme binding<br>3. Oxygen binding<br>4. Transport oxygen<br>5. Transport bicarbonate<br>6. Receptor mediated endocytosis<br>7. Regulation of cell death<br>8. Protein heterooligomerization |
| | Mutant hemoglobin alpha 2 globin chain | 8.72 | 1. $Fe^{2+}$, $Fe^{3+}$ binding<br>2. Heme binding<br>3. Oxygen binding<br>4. Transport oxygen |
| | Hemoglobin subunit alpha | 8.72 | 1. $Fe^{2+}$, $Fe^{3+}$ binding<br>2. Heme binding<br>3. Oxygen binding |

| | | | |
|---|---|---|---|
| | | | 4. Transport oxygen |
| | Globin C1 | 9.79 | 1. Metal binding (binding with $Ca^{2+}$, $Mg^{2+}$ and $Fe^{3+}$)<br>2. Heme-binding<br>3. Transport oxygen |
| | Beta-globin protein | 6.64 | 1. Heme binding<br>2. $Fe^{2+}$, $Fe^{3+}$ binding<br>3. Oxygen binding<br>4. Transports oxygen<br>5. Makes haemoglobin (HbA) along with alpha-globin in adults |
| | Beta-globin chain | 5.57 | 1. $Fe^{2+}$, $Fe^{3+}$ binding<br>2. Heme binding<br>3. Oxygen binding<br>4. Transport oxygen |
| | Truncated beta-globin | 7.96 | 1. Heme binding<br>2. Oxygen binding |
| | Mutant beta-globin | 7.92 | 1. Heme binding<br>2. Oxygen binding<br>3. Transports oxygen |
| | Hemoglobin subunit beta | 6.25 | 1. Heme binding<br>2. Oxygen binding<br>3. Transports oxygen |
| | Hemoglobin beta | 5.45 | 1. $Fe^{2+}$, $Fe^{3+}$ binding<br>2. Heme binding<br>3. Oxygen binding<br>4. Transport oxygen |
| | Hemoglobin beta chain variant Hb-I_Toulouse | 5.41 | 1. $Fe^{2+}$, $Fe^{3+}$ binding<br>2. Heme binding<br>3. Oxygen binding<br>4. Transport oxygen |
| | Mutant hemoglobin beta chain (Fragment) | 6.5 | 1. $Fe^{2+}$, $Fe^{3+}$ binding<br>2. Heme binding<br>3. Oxygen binding<br>4. Transport oxygen |
| | Hemoglobin beta globin chain | 6.74 | 1. $Fe^{2+}$, $Fe^{3+}$ binding<br>2. Heme binding<br>3. Oxygen binding<br>4. Transport oxygen |
| | Hemoglobin beta | 6.74 | 1. $Fe^{2+}$, $Fe^{3+}$ binding<br>2. Heme binding<br>3. Oxygen binding<br>4. Transport oxygen |
| | Hemoglobin beta chain variant Hb.Sinai-Bel Air | 5.41 | 1. $Fe^{2+,}$ $Fe^{3+}$ binding<br>2. Heme binding<br>3. Oxygen binding<br>4. Transport oxygen |
| | Alpha-2-HS glycoprotein | 5.94 | 1. Enhance endocytosis<br>2. $Ca^{2+}$ binding<br>3. Post-translational protein modification<br>4. Protein metabolism |
| | Transthyretin | 5.6 | 1. Thyroid hormone binding<br>2. Identical protein binding<br>3. Transport iron<br>4. Transport thyroxine to the brain<br>5. Cellular protein metabolism<br>6. Neutrophil degranulation<br>7. Retinol metabolism |

| | | | |
|---|---|---|---|
| | Serotransferrin | 6.81 | 1. $Fe^{3+}$ binding<br>2. Bicarbonate binding<br>3. Transport iron |
| | Transferrin variant | 6.68 | 1. $Fe^{3+}$ binding<br>2. Transport $Fe^{3+}$ within transmembrane<br>3. Involved in iron ion homeostasis in cells |
| | Transferrin | 6.97 | 1. $Fe^{3+}$ binding<br>2. Transport $Fe^{3+}$ within transmembrane<br>3. Involved in iron ion homeostasis in cells |
| | Lactotransferrin | 8.7 | 1. $Fe^{3+}$ binding<br>2. $Cu^{2+}$ binding<br>3. Bicarbonate binding<br>4. Involved in serine-type endopeptidase activity<br>5. Engender antimicrobial humoral response<br>6. Regulates the production of cytokine |
| | Lactoferrin | 8.7 | 1. $Fe^{2+}$, $Fe^{3+}$ binding<br>2. Involved in serine-type endopeptidase activity<br>3. Engender antimicrobial humoral response<br>4. Regulates the production of cytokine |
| | Delta globin | 7.85 | 1. $Fe^{2+}$, $Fe^{3+}$ binding<br>2. Heme binding<br>3. Oxygen binding<br>4. Transport oxygen<br>5. Blood coagulation |
| | Hbbm fused globin protein | 6.17 | 1. $Fe^{2+}$, $Fe^{3+}$ binding<br>2. Heme binding<br>3. Oxygen binding<br>4. Transport oxygen |
| **Coagulation protein** | Prothrombin | 5.64 | 1. Non-covalently calcium ions ($Ca^{2+}$) binding.<br>2. Blood coagulation<br>3. Involved in serine-type endopeptidase activity |
| **Cell adhesive protein** | cDNA FLJ54111 | 6.95 | 1. $Ca^{2+}$ binding<br>2. Collagen binding |
| | Proliferation-inducing protein 33 | 4.71 | 1. $Ca^{2+}$ binding<br>2. Collagen binding |
| | C-type lectin domain family 3 member B isoform CRA_a | 5.21 | 1. Carbohydrate binding<br>2. Ossification |
| **Enzymes** | N-acetyltransferase 5 | 5.84 | 1. Involved in transferase activity<br>2. Catalyzes the transfer of acetyl groups from acetyl CoA to arylamines |
| **Structural protein** | cDNA FLJ56708 | 8.44 | 1. Involved in structural molecular activity |
| | Keratin, type I cytoskeletal 10 | 5.13 | 1. Cross linking of peptides<br>2. Protein heterodimerization and heterotetramerization activity<br>3. Keratinization |
| | Keratin, type I cytoskeletal 28 | 5.33 | 1. Involved in structural molecular activity<br>2. Cornification<br>3. keratinization |
| | Keratin 1 | 8.15 | 1. Involved in structural molecular activity |
| | Keratin, type II cytoskeletal 2 | 8.07 | 1.Cytoskeletal protein binding<br>2. Cross linking of peptides<br>3. Structural constituent of cytoskeleton<br>4. Keratinization |

| | | | |
|---|---|---|---|
| **Others** | Protein unc-13 homolog B | 5.67 | 1. $Ca^{2+}$binding<br>2. Calmodulin binding<br>3. Phospholipid binding<br>4. Diacylglycerol binding<br>5. Intracellular signal transduction<br>6. Presynaptic and synaptic vesicle Exocytosis |
| | MHC class I antigen | 6.64 | 1. Peptide binding engendered by cytosolic protein degradation via the proteasome<br>2. Exhibit intracellular proteins to cytotoxic T cells<br>3. Function as an inhibitory ligand for natural killer cells |
| | Alpha-fetoprotein | 4.57 | 1. Metal (copper, nickel) binding<br>2. Fatty acids binding<br>3. Bilirubin binding<br>4. Cellular protein metabolism<br>5. Progesterone metabolism |
| | cDNA FLJ57154 | 6.29 | 1. Helps in heterologous expression |
| | cDNA FLJ79229 | 8.10 | 1. $Fe^{2+}$, $Fe^{3+}$ binding<br>2. Controls cytokine production<br>3. Involved in antimicrobial humoral response |
| | Uncharacterized protein | 6.28 | 1. $Fe^{2+}$, $Fe^{3+}$ binding<br>2. Heme binding<br>3. Oxygen binding<br>4. Transport oxygen |
| | A-kinase anchor protein | 8.84 | 1. Protein kinase A (PKA) binding<br>2. Specific substrate targeting by means of phosphorylation (through PKA) and dephosphorylation (through phosphatases) |
| | Zinc finger SWIM domain-containing protein 4 | 6.47 | 1. $Zn^{2+}$ binding<br>2. DNA binding |
| | Capsid scaffolding protein | 8.10 | 1.Identical protein binding<br>2. Involved in nuclear capsid macromolecular assembly<br>3. Involved in serine-type endopeptidase activity |
| | cDNA FLJ51509 | 7.42 | 1.Behaves similar to Alpha-fetoprotein, i.e- takes part in metal, fatty acids and bilirubin binding, involved in cellular protein and progesterone metabolism |
| | cDNA FLJ55606 | 5.84 | 1. Cysteine-type endopeptidase inhibitor |

**Table S7.** List of identified proteins with high Fe/Mg-CA in 10% FBS along with their isoelectric point (pI) and major biological functions.

| Functional classification of protein | Identified Protein | pI | Detailed Function |
|---|---|---|---|
| **Transport protein** | Albumin | 5.53 | 1.Transport<br>2. Systemic calcification inhibitor<br>3. Lipid binding<br>4. Metal binding<br>5. Maintaining intravascular colloid osmotic pressure (COP) |

| | | | |
|---|---|---|---|
| | Globin C1 | 9.79 | 1. Metal binding (binding with $Ca^{2+}$, $Mg^{2+}$ and $Fe^{3+}$).<br>2. Heme-binding<br>3. Transport oxygen. |
| | Alpha-2 globin chain | 8.72 | 1. $Fe^{2+}$, $Fe^{3+}$ binding<br>2. Heme binding<br>3. Oxygen binding<br>4. Transport oxygen<br>5. Transport bicarbonate |
| | Hemoglobin subunit alpha | 8.72 | 1. $Fe^{2+}$, $Fe^{3+}$ binding<br>2. Heme binding<br>3. Oxygen binding<br>4. Transport oxygen |
| | Mutant hemoglobin alpha 1 globin chain | 8.72 | 1. $Fe^{2+}$, $Fe^{3+}$ binding<br>2. Heme binding<br>3. Oxygen binding<br>4. Transport oxygen<br>5. Transport bicarbonate |
| | Hemoglobin alpha-1 globin chain | 8.72 | 1. $Fe^{2+}$, $Fe^{3+}$ binding<br>2. Heme binding<br>3. Oxygen binding<br>4. Transport oxygen<br>5. Transport bicarbonate |
| | Mutant hemoglobin alpha 2 globin chain | 8.72 | 1. $Fe^{2+}$, $Fe^{3+}$ binding<br>2. Heme binding<br>3. Oxygen binding<br>4. Transport oxygen |
| | Beta-globin protein | 6.64 | 1. Heme binding<br>2. Makes haemoglobin (HbA) along with alpha-globin in adults |
| | Alpha-2-HS glycoprotein | 5.94 | 1. Enhance endocytosis<br>2. $Ca^{2+}$ binding<br>3. Post-translational protein modification<br>4. Protein metabolism |
| | Transthyretin | 5.6 | 1. Thyroid hormone binding<br>2. Identical protein binding<br>3. Transport iron<br>4. Transports thyroxine to the brain<br>5. Cellular protein metabolism<br>6. Neutrophil degranulation<br>7. Retinol metabolism |
| | Serotransferrin | 6.81 | 1. $Fe^{3+}$ binding<br>2. Bicarbonate binding<br>3. Transport iron |
| | Transferrin variant | 6.68 | 1. $Fe^{3+}$ binding<br>2. Transport $Fe^{3+}$ within transmembrane<br>3. Involved in iron ion homeostasis in cells |
| | Transferrin | 6.97 | 1. $Fe^{3+}$ binding<br>2. Transport $Fe^{3+}$ within transmembrane<br>3. Involved in iron ion homeostasis in cells |
| | Tetranectin | 5.8 | 1. $Ca^{2+}$ binding<br>2. Heparin binding<br>3. Carbohydrate binding<br>4. Cellular metabolism<br>5. Bone mineralization<br>6. Ossification<br>7. Platelet degranulation |
| | cDNA FLJ54839 | 7.42 | 1. Behaves similar to Lactotransferrin precursor |
| | cDNA FLJ53691 | 6.81 | 1. $Fe^{3+}$ binding |

| | | | |
|---|---|---|---|
| | | | 2. Transport $Fe^{3+}$ within transmembrane |
| | Lactotransferrin | 8.7 | 1. $Fe^{3+}$ binding<br>2. $Cu^{2+}$ binding<br>3. Bicarbonate binding<br>4. Involved in serine type endopeptidase activity<br>5. Engender antimicrobial humoral response<br>6. Regulates the production of cytokine |
| | Lactoferrin | 8.7 | 1. $Fe^{2+}$, $Fe^{3+}$ binding<br>2. Involved in serine type endopeptidase activity<br>3. Engender antimicrobial humoral response<br>4. Regulates the production of cytokine |
| | Delta globin | 7.85 | 1. $Fe^{2+}$, $Fe^{3+}$ binding<br>2. Heme binding<br>3. Oxygen binding<br>4. Transport oxygen<br>5. Blood coagulation |
| | Hemoglobin subunit gamma-2 | 6.64 | 1. $Fe^{2+}$, $Fe^{3+}$ binding<br>2. Heme binding<br>3. Oxygen binding<br>4. Transport oxygen<br>5. Blood coagulation |
| | Globin B3 | 8.67 | 1. $Fe^{2+}$, $Fe^{3+}$ binding<br>2. Heme binding<br>3. Hemoglobin alpha binding<br>4. Oxygen binding<br>5. Transport oxygen |
| | Gamma-G globin | 7.2 | 1. $Fe^{2+}$, $Fe^{3+}$ binding<br>2. Heme binding<br>3. Oxygen binding<br>4. Transport oxygen |
| | Hbbm fused globin protein | 6.17 | 1. $Fe^{2+}$, $Fe^{3+}$ binding<br>2. Heme binding<br>3. Oxygen binding<br>4. Transport oxygen |
| **Cell adhesive protein** | SPARC-like protein 1 | 4.73 | 1. $Ca^{2+}$ binding<br>2.Collagen binding<br>3. Extracellular matrix binding<br>4. Adhession of synaptic membrane<br>5.Cellular protein metabolism |
| | Proliferation-inducing protein 33 | 4.71 | 1. $Ca^{2+}$ binding<br>2. Collagen binding |
| | C-type lectin domain family 3 member B isoform CRA_a | 5.21 | 1. Carbohydrate binding<br>2. Ossification |
| | cDNA FLJ54111 | 6.95 | 1. $Ca^{2+}$ binding<br>2. Collagen binding |
| | cDNA FLJ54278 | 4.83 | 1. $Ca^{2+}$ binding<br>2. Collagen binding |
| | cDNA FLJ54387 | 4.71 | 1. $Ca^{2+}$ binding<br>2. Collagen binding |
| | cDNA FLJ55140 | 4.73 | 1. $Ca^{2+}$ binding<br>2. Collagen binding |

| | | | |
|---|---|---|---|
| **Coagulation protein** | Prothrombin | 5.64 | 1. Non-covalently calcium ions ($Ca^{2+}$) binding.<br>2. Blood coagulation<br>3. Involved in serine-type endopeptidase activity |
| **Structural protein** | Keratin, type II cytoskeletal 2 epidermal | 8.07 | 1.Cytoskeletal protein binding<br>2. Cross linking of peptides<br>3. Structural constituent of cytoskeleton<br>4. Keratinization |
| | Keratin, type II cytoskeletal 5 | 7.58 | 1. Scaffold protein binding<br>2. Structural constituent of cytoskeleton<br>3. Keratinization |
| | Keratin, type I cytoskeletal 14 | 5.09 | 1. Responsing to $Zn^{2+}$<br>2. Keratin filament binding<br>3. Structural constituent of cytoskeleton<br>4. Keratinization |
| | Keratin 77 | 5.8 | 1. Involved in structural integrity of epithelial cells<br>2. Involved in structural molecular activity |
| | Keratin 1 | 8.15 | 1. Significant for structural integrity of a complex or its assembly within or outside a cell. |
| | Keratin, type I cytoskeletal 9 | 5.14 | 1. Keratin filament binding<br>2. Structural constituent of cytoskeleton<br>3. Keratinization<br>4. Epidermis development<br>5. Intermediate filament organization |
| | Keratin, type I cytoskeletal 10 | 5.13 | 1. Cross linking of peptides<br>2. Protein heterodimerization and heterotetramerization activity<br>3. Structural constituent of epidermis<br>4. Keratinization |
| **Others** | cDNA FLJ57154 | 6.29 | 1. Helps in heterologous expression |
| | cDNA FLJ58606 | 7.82 | 1. Helps in heterologous expression |
| | Protein S100-A7A | 6.89 | 1. $Ca^{2+}$ binding<br>2. Transition metal binding<br>3. Involved in protein self-association |
| | A-kinase anchor protein | 8.84 | 1. Protein kinase A (PKA) binding<br>2. Specific substrate targeting by means of phosphorylation (through PKA) and dephosphorylation (through phosphatases) |
| | Epididymis luminal protein 110 | 7.8 | 1. $Fe^{2+}$, $Fe^{3+}$ binding<br>2. Involved in serine type endopeptidase action<br>3. Engender antimicrobial humoral response<br>4. Regulates the production of cytokine |
| | Zinc finger SWIM domain-containing protein 4 | 6.47 | 1. $Zn^{2+}$ binding<br>2. DNA binding |
| | Alpha-fetoprotein | 4.57 | 1. Metal (copper, nickel) binding<br>2. Fatty acids binding<br>3. Bilirubin binding<br>4. Cellular protein metabolism<br>5. Progesterone metabolism |
| | Protein unc-13 homolog B | 5.67 | 1. $Ca^{2+}$ binding<br>2. Calmodulin binding<br>3. Phospholipid binding<br>4. Diacylglycerol binding<br>5. Intracellular signal transduction<br>6. Presynaptic and synaptic vesicle exocytosis |

**Table S8:** Protein corona profile of CA in 10% FBS in terms of their molecular weight (Da), -10lgP and coverage (%).

| Functional classification of protein | Identified Protein | Molecular Weight (Da) | -10lgP | Coverage (%) |
|---|---|---|---|---|
| **Transport Protein** | ALB protein | 69294 | 260.46 | 80 |
| | Serum Albumin | 69227 | 207.46 | 40 |
| | Alpha-2-HS glycoprotein | 39325 | 121.73 | 11 |
| | cDNA FLJ51509 | 54207 | 107.1 | 15 |
| | Transthyretin | 15872 | 80.92 | 28 |
| | Serotransferrin | 77064 | 92.84 | 7 |
| | Transferrin variant | 77080 | 92.84 | 7 |
| | Transferrin | 76960 | 92.84 | 7 |
| | LMAN1 protein | 57549 | 21.54 | 1 |
| | Globin C1 | 19232 | 78.40 | 23 |
| | Globin B1 | 16071 | 33.31 | 7 |
| | Globin A1 | 15954 | 33.31 | 7 |
| | Alpha-1-acid glycoprotein (positive acute phase protein) | 23512 | 37.40 | 6 |
| | Mutant hemoglobin alpha 1 globin chain | 10753 | 78.40 | 40 |
| | Hemoglobin alpha-1 globin chain | 10783 | 78.40 | 40 |
| | Hemoglobin subunit alpha | 20146 | 78.40 | 28 |
| | Alpha-2 globin chain | 15258 | 78.40 | 28 |
| | Mutant hemoglobin alpha 2 globin chain | 15258 | 78.40 | 28 |
| | Lactoferrin | 78357 | 69.91 | 4 |
| | Beta-globin protein | 4550 | 59.21 | 56 |
| | Hemoglobin fetal subunit beta | 15859 | 33.31 | 7 |
| | Truncated beta-globin | 6998 | 59.21 | 37 |
| | Mutant beta-globin | 9689 | 59.21 | 26 |
| | Beta-globin chain | 11476 | 59.21 | 26 |
| | Hemoglobin subunit beta | 9670 | 59.21 | 26 |
| | Hemoglobin beta chain | 11023 | 59.21 | 23 |

| | | | | |
|---|---|---|---|---|
| | Hemoglobin beta chain variant Hb.Sinai-Bel Air | 11548 | 59.21 | 22 |
| | Hemoglobin beta chain variant Hb-I_Toulouse | 11505 | 59.21 | 22 |
| | Vitamin D-binding protein | 53021 | 47.50 | 1 |
| **Cell adhesive protein** | cDNA FLJ54111 | 63437 | 92.84 | 8 |
| **Coagulation protein** | Prothrombin | 35932 | 39.89 | 3 |
| **Metabolic Protein** | Adiponectin | 26133 | 39.64 | 4 |
| **Protease inhibitor** | Kininogen-1 | 71957 | 43.16 | 2 |
| | KNG1 protein | 33055 | 43.16 | 3 |
| | Fetuin-B | 42663 | 49.43 | 11 |
| | Alpha-1-antiproteinase | 46104 | 118.31 | 18 |
| **Structural Protein** | Keratin, type I cytoskeletal 10 | 54848 | 86.65 | 14 |
| | Keratin 1 | 66126 | 101.91 | 11 |
| | KRT6A protein | 60045 | 62.63 | 4 |
| | Keratin, type I cytoskeletal 14 | 51561 | 72.04 | 8 |
| | Histone H2B | 13926 | 20.26 | 7 |
| **Regulatory Protein** | Junction mediating and regulatory protein p53 cofactor | 109383 | 21.54 | 1 |
| **Others** | Uncharacterized protein | 18931 | 59.21 | 13 |
| | Epididymis secretory protein Li 51 | 52964 | 47.50 | 1 |
| | Alpha-fetoprotein | 68678 | 107.1 | 12 |
| | cDNA FLJ95666 | 69393 | 206.8 | 39 |
| | cDNA FLJ57154 | 50756 | 107.10 | 16 |
| | cDNA FLJ55606 | 46627 | 121.73 | 9 |

**Table S9:** Protein corona profile of low Fe/Mg-CA in 10% FBS in terms of their molecular weight (Da), -10lgP and coverage (%).

| Functional classification of protein | Identified Protein | Molecular Weight (Da) | -10lgP | Coverage (%) |
|---|---|---|---|---|
| **Transport protein** | Albumin | 66531 | 180.69 | 36 |
| | Mutant hemoglobin alpha 1 globin chain | 10753 | 95.34 | 47 |
| | Hemoglobin alpha-1 globin chain | 10783 | 95.34 | 47 |
| | Alpha-2 globin chain | 15258 | 95.34 | 33 |
| | Hemoglobin subunit alpha piens | 15258 | 95.34 | 33 |
| | Mutant hemoglobin alpha 2 globin chain | 15258 | 95.34 | 33 |
| | Hemoglobin subunit alpha | 20146 | 95.34 | 33 |
| | Globin C1 | 19232 | 95.34 | 27 |
| | Beta-globin protein | 4550 | 57.88 | 56 |
| | Beta-globin chain | 11476 | 62.94 | 22 |
| | Truncated beta-globin | 6998 | 57.88 | 37 |
| | Mutant beta-globin | 9689 | 62.94 | 26 |
| | Hemoglobin subunit beta | 9670 | 57.88 | 26 |
| | Hemoglobin beta chain | 11023 | 57.88 | 23 |
| | Hemoglobin beta chain variant Hb-I_Toulouse | 11505 | 62.94 | 22 |
| | Mutant hemoglobin beta chain (Fragment) | 11501 | 57.88 | 22 |
| | Hemoglobin beta globin chain | 11494 | 57.88 | 22 |
| | Hemoglobin beta | 11482 | 62.94 | 22 |
| | Hemoglobin beta chain variant Hb.Sinai-Bel Air | 11548 | 57.88 | 22 |
| | Alpha-2-HS glycoprotein | 39325 | 62.15 | 13 |
| | Transthyretin | 15872 | 88.27 | 44 |
| | Serotransferrin | 77064 | 77.82 | 5 |
| | Transferrin variant | 77080 | 77.82 | 5 |
| | Transferrin | 76960 | 77.82 | 5 |
| | Lactotransferrin | 76626 | 55.45 | 3 |
| | Lactoferrin | 77981 | 55.45 | 3 |
| | Delta globin | 16055 | 48.92 | 7 |
| | Hbbm fused globin protein | 10928 | 40.72 | 10 |
| **Coagulation protein** | Prothrombin | 35932 | 37.17 | 3 |
| **Cell adhesive protein** | cDNA FLJ54111 | 63437 | 71.87 | 6 |
| | Proliferation-inducing protein 33 | 75230 | 72.24 | 5 |
| | C-type lectin domain family 3 member B isoform CRA_a | 22537 | 48.09 | 10 |
| **Enzymes** | N-acetyltransferase 5 | 18857 | 24.33 | 4 |
| **Structural protein** | cDNA FLJ56708 | 18049 | 62.03 | 15 |
| | Keratin, type I cytoskeletal 10 | 58827 | 154.11 | 34 |
| | Keratin, type I cytoskeletal 28 | 50567 | 59.40 | 5 |

| | | | | |
|---|---|---|---|---|
| | Keratin 1 | 66126 | 145.46 | 22 |
| | Keratin, type II cytoskeletal 2 | 65433 | 103.32 | 13 |
| **Others** | Protein unc-13 homolog B | 180679 | 21.64 | 1 |
| | MHC class I antigen | 12392 | 23.42 | 4 |
| | Alpha-fetoprotein | 68678 | 70.56 | 6 |
| | cDNA FLJ57154 | 50756 | 54.72 | 7 |
| | cDNA FLJ79229 | 73170 | 68.49 | 3 |
| | Uncharacterized protein | 18931 | 57.88 | 13 |
| | A-kinase anchor protein | 161184 | 21.18 | 1 |
| | Zinc finger SWIM domain-containing protein 4 | 99649 | 29.84 | 1 |
| | Capsid scaffolding protein | 66941 | 21.94 | 1 |
| | cDNA FLJ51509 | 54207 | 70.56 | 8 |
| | cDNA FLJ55606 | 46627 | 62.15 | 11 |

**Table S10:** Protein corona profile of high Fe/Mg-CA in 10% FBS in terms of their molecular weight (Da), -10lgP and coverage (%).

| Functional classification of protein | Identified Protein | Molecular Weight (Da) | -10lgP | Coverage (%) |
|---|---|---|---|---|
| **Transport protein** | Albumin | 66531 | 158.89 | 27 |
| | Globin C1 | 19232 | 90.79 | 23 |
| | Alpha-2 globin chain | 15258 | 86.99 | 28 |
| | Hemoglobin subunit alpha | 20146 | 86.99 | 28 |
| | Mutant hemoglobin alpha 1 globin chain | 10753 | 86.99 | 40 |
| | Hemoglobin alpha-1 globin chain | 10783 | 86.99 | 40 |
| | Mutant hemoglobin alpha 2 globin chain | 15258 | 86.99 | 28 |
| | Beta-globin protein | 2104 | 40.72 | 59 |
| | Alpha-2-HS glycoprotein | 39325 | 55.71 | 9 |
| | Transthyretin | 15872 | 47.21 | 24 |
| | Serotransferrin | 77064 | 71.87 | 5 |
| | Transferrin variant | 77080 | 71.87 | 5 |
| | Transferrin | 76960 | 71.87 | 5 |
| | Tetranectin | 17794 | 48.09 | 13 |
| | cDNA FLJ54839 | 54207 | 55.45 | 7 |
| | cDNA FLJ53691 | 74832 | 71.87 | 5 |
| | Lactotransferrin | 76626 | 55.45 | 3 |
| | Lactoferrin | 77981 | 55.45 | 3 |
| | Delta globin | 16055 | 48.92 | 7 |
| | Hemoglobin subunit gamma-2 | 15319 | 40.72 | 7 |
| | Globin B3 | 16203 | 40.72 | 7 |

| | | | | |
|---|---|---|---|---|
| | Gamma-G globin | 16969 | 40.72 | 6 |
| | Hbbm fused globin protein | 10928 | 40.72 | 10 |
| **Cell adhesive protein** | SPARC-like protein 1 | 75208 | 72.24 | 5 |
| | Proliferation-inducing protein 33 | 75230 | 72.24 | 5 |
| | C-type lectin domain family 3 member B isoform CRA_a | 22537 | 48.09 | 10 |
| | cDNA FLJ54111 | 63437 | 71.87 | 6 |
| | cDNA FLJ54278 | 58507 | 72.24 | 7 |
| | cDNA FLJ54387 | 64141 | 72.24 | 6 |
| | cDNA FLJ55140 | 55519 | 72.24 | 7 |
| **Coagulation protein** | Prothrombin | 35932 | 35.09 | 3 |
| **Structural protein** | Keratin, type II cytoskeletal 2 epidermal | 65433 | 131.06 | 13 |
| | Keratin, type II cytoskeletal 5 | 62378 | 97.24 | 11 |
| | Keratin, type I cytoskeletal 14 | 51562 | 95.71 | 13 |
| | Keratin 77 | 61802 | 81.98 | 5 |
| | Keratin 1 | 66126 | 232.15 | 40 |
| | Keratin, type I cytoskeletal 9 | 62064 | 183.04 | 33 |
| | Keratin, type I cytoskeletal 10 | 58827 | 172.78 | 37 |
| **Others** | cDNA FLJ57154 | 50756 | 54.72 | 7 |
| | cDNA FLJ58606 | 91670 | 29.84 | 1 |
| | Protein S100-A7A | 11305 | 36.53 | 11 |
| | A-kinase anchor protein | 161184 | 21.18 | 1 |
| | Epididymis luminal protein 110 | 78182 | 55.45 | 3 |
| | Zinc finger SWIM domain-containing protein 4 | 99649 | 29.84 | 1 |
| | Alpha-fetoprotein | 68678 | 54.72 | 5 |
| | Protein unc-13 homolog B | 180679 | 21.64 | 1 |