

# Cellular Response of Polyvalent Oligonucleotide Gold Nanoparticle Conjugates

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## Supplemental Table S1

Nanoparticle Type	Size (nm)	Zeta Potential (mV)
Citrate	17.19 +/- 1.05	-32.33 +/- 1.59
BSA	74.25 +/- 1.61	-34.30 +/- 0.85
ssDNA	25.81 +/- 0.97	-30.73 +/- 1.22
dsDNA	26.63 +/- 0.76	-28.33 +/- 1.55
dsRNA	27.00 +/- 1.05	-28.83 +/- 2.57

### Table S1.

Average size and zeta potential measurements for the nanoparticle types tested in this study. These measurements were taken using a Zetasizer Nano ZS (Malvern).

## Supplemental Table S2

Gene ID	Gene Name	Fold Change	P-value
10572	SIVA1, apoptosis-inducing factor	-2.13	2.01E-10
25824	peroxiredoxin 5	-2.01	4.09E-09
517	ATP synthase, H <sup>+</sup> transporting, mitochondrial F0 complex, subunit C2 (subunit 9)	-2.00	2.31E-09
23016	exosome component 7	-1.99	8.14E-10
126328	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 11, 14.7kDa	-1.98	5.33E-07
3692	eukaryotic translation initiation factor 6	-1.97	1.76E-08
10519	calcium and integrin binding 1 (calmyrin)	-1.96	6.30E-05

8673	vesicle-associated membrane protein 8 (endobrevin)	-1.96	1.68E-04
92856	IMP4, U3 small nucleolar ribonucleoprotein, homolog (yeast)	-1.96	8.67E-04
389541	chromosome 7 open reading frame 59	-1.93	2.56E-08
51264	mitochondrial ribosomal protein L27	-1.93	2.04E-09
5693	proteasome (prosome, macropain) subunit, beta type, 5	-1.91	3.45E-08
64951	mitochondrial ribosomal protein S24	-1.90	1.56E-07
389	ras homolog gene family, member C	-1.86	6.28E-07
113246	chromosome 12 open reading frame 57	-1.86	1.21E-07
5694	proteasome (prosome, macropain) subunit, beta type, 6	-1.86	1.56E-07
2109	electron-transfer-flavoprotein, beta polypeptide	-1.85	7.84E-08
79019	centromere protein M	-1.85	2.77E-07
51596	cutA divalent cation tolerance homolog (E. coli)	-1.85	2.21E-09
26519	translocase of inner mitochondrial membrane 10 homolog (yeast)	-1.85	7.74E-09
10567	Rab acceptor 1 (prenylated)	-1.84	3.46E-07
10430	transmembrane protein 147	-1.84	2.74E-06
28989	methyltransferase like 11A	-1.84	4.91E-06
51693	trafficking protein particle complex 2-like	-1.83	9.58E-05
516	ATP synthase, H <sup>+</sup> transporting, mitochondrial F0 complex, subunit C1 (subunit 9)	-1.81	4.80E-06
29074	mitochondrial ribosomal protein L18	-1.78	3.06E-06
201254	stimulated by retinoic acid 13 homolog (mouse)	-1.78	1.32E-05
6415	selenoprotein W, 1	-1.77	2.39E-10
6274	S100 calcium binding protein A3	-1.76	2.80E-05
140465	myosin, light chain 6B, alkali, smooth muscle and non-muscle	-1.74	6.59E-05
4815	ninjurin 2	-1.74	1.22E-04
29100	transmembrane protein 208	-1.74	1.20E-08
51399	trafficking protein particle complex 4	-1.74	2.55E-05
9636	ISG15 ubiquitin-like modifier	-1.73	5.50E-07
10084	polyglutamine binding protein 1	-1.73	1.60E-06
5435	polymerase (RNA) II (DNA directed) polypeptide F	-1.73	4.21E-07
118472	zinc finger protein 511	-1.73	3.39E-05
10998	solute carrier family 27 (fatty acid transporter), member 5	-1.72	6.85E-08
725	complement component 4 binding protein, beta	-1.72	1.54E-07
90637	zinc finger, AN1-type domain 2A	-1.71	9.08E-04
3028	hydroxysteroid (17-beta) dehydrogenase 10 NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa (NADH-coenzyme Q reductase)	-1.71	4.52E-08 9.62E-08
4722			
114915	chromosome 5 open reading frame 26	-1.70	9.23E-08
9533	polymerase (RNA) I polypeptide C, 30kDa	-1.70	2.62E-06
51024	fission 1 (mitochondrial outer membrane) homolog (S. cerevisiae)	-1.70	2.68E-08
83443	splicing factor 3b, subunit 5, 10kDa	-1.70	7.33E-06
533	ATPase, H <sup>+</sup> transporting, lysosomal 21kDa, V0 subunit b	-1.69	1.34E-05
2987	guanylate kinase 1	-1.69	2.55E-08
151903	coiled-coil domain containing 12	-1.68	1.54E-04
27243	chromatin modifying protein 2A	-1.68	1.73E-06
55272	IMP3, U3 small nucleolar ribonucleoprotein, homolog (yeast)	-1.68	1.02E-05
25915	chromosome 3 open reading frame 60	-1.66	8.31E-05
60673	chromosome 12 open reading frame 44	-1.66	4.87E-07
51728	polymerase (RNA) III (DNA directed) polypeptide K, 12.3 kDa	-1.66	8.55E-08
644	biliverdin reductase A	-1.65	1.38E-07
54512	exosome component 4	-1.65	5.10E-08
10591	chromosome 6 open reading frame 108	-1.64	1.30E-05

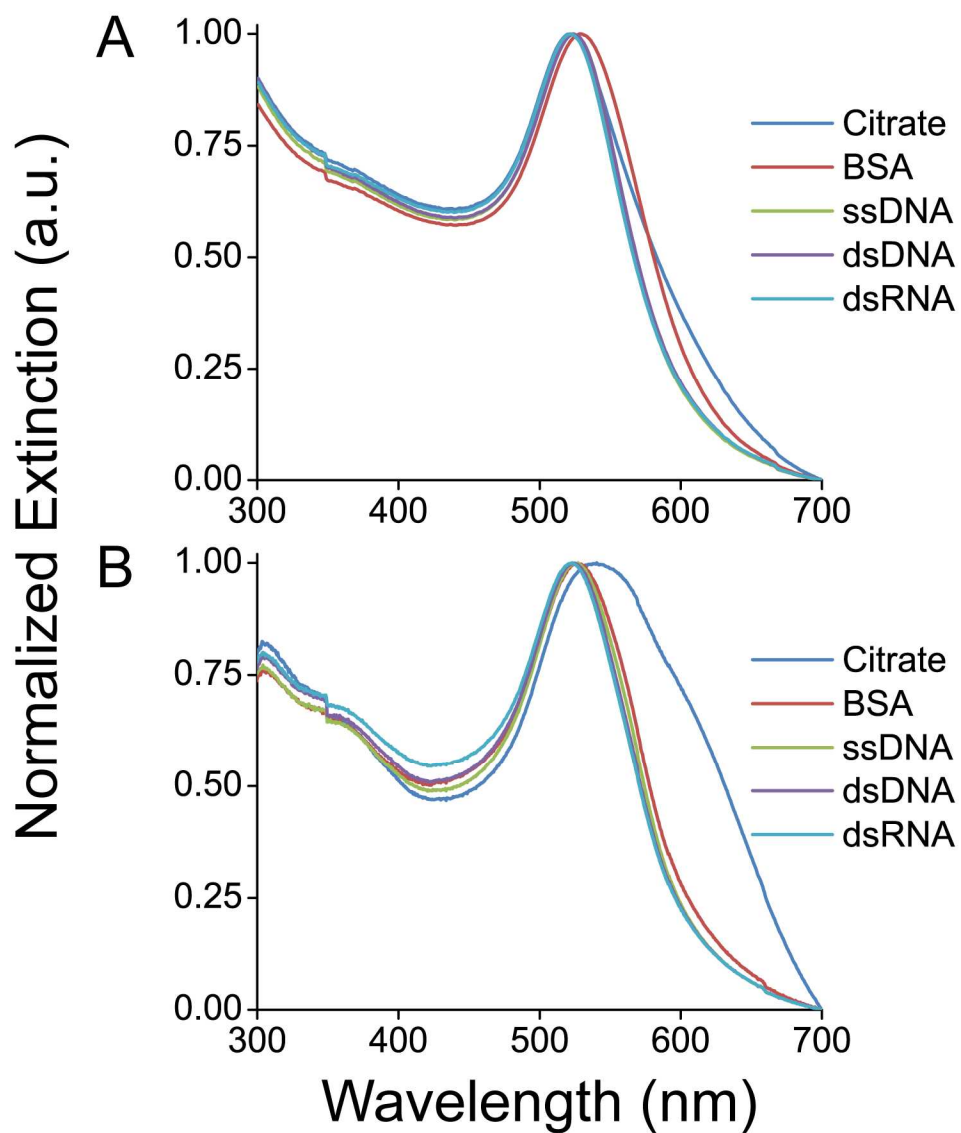
1351	cytochrome c oxidase subunit 8A (ubiquitous)	-1.64	2.39E-05
5692	proteasome (prosome, macropain) subunit, beta type, 4	-1.64	1.41E-05
2644	GTP cyclohydrolase I feedback regulator	-1.64	3.95E-04
4637	myosin, light chain 6, alkali, smooth muscle and non-muscle	-1.64	6.66E-05
10436	EMG1 nucleolar protein homolog ( <i>S. cerevisiae</i> )	-1.64	9.64E-07
4713	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7, 18kDa	-1.63	7.40E-06
4521	nudix (nucleoside diphosphate linked moiety X)-type motif 1	-1.63	7.83E-06
126003	trafficking protein particle complex 5	-1.63	9.88E-05
51070	nitric oxide synthase interacting protein	-1.62	3.65E-06
84058	WD repeat domain 54	-1.62	1.07E-03
2950	glutathione S-transferase pi 1	-1.62	6.83E-06
51398	chromosome 19 open reading frame 56	-1.62	1.51E-05
1174	adaptor-related protein complex 1, sigma 1 subunit	-1.62	3.70E-04
64949	mitochondrial ribosomal protein S26	-1.62	2.00E-04
51042	zinc finger protein 593	-1.61	5.34E-07
5691	proteasome (prosome, macropain) subunit, beta type, 3	-1.61	1.88E-06
64963	mitochondrial ribosomal protein S11	-1.61	2.40E-03
28971	chromosome 11 open reading frame 67	-1.60	2.84E-06
63905	mannosidase, beta A, lysosomal-like	-1.60	6.86E-05
128308	mitochondrial ribosomal protein L55	-1.60	6.58E-04
5441	polymerase (RNA) II (DNA directed) polypeptide L, 7.6kDa	-1.59	4.07E-07
6132	ribosomal protein L8	-1.59	1.41E-08
28958	coiled-coil domain containing 56	-1.58	7.54E-04
22921	methionine sulfoxide reductase B2	-1.58	1.20E-03
10535	ribonuclease H2, subunit A	-1.58	1.28E-07
9718	endothelin converting enzyme 2	-1.57	4.11E-07
30834	zinc ribbon domain containing 1	-1.57	1.25E-06
11258	dynactin 3 (p22)	-1.57	1.36E-06
11018	transmembrane emp24 protein transport domain containing 1	-1.57	1.47E-03
4830	non-metastatic cells 1, protein (NM23A) expressed in	-1.57	9.31E-06
54849	differentially expressed in FDCP 8 homolog (mouse)	-1.56	2.19E-04
374395	transmembrane protein 179B	-1.56	6.24E-07
10467	zinc finger, HIT type 1	-1.56	7.63E-04
10134	B-cell receptor-associated protein 31	-1.56	9.79E-07
79159	nucleolar protein 12	-1.56	1.00E-04
3420	isocitrate dehydrogenase 3 (NAD+) beta	-1.55	7.88E-09
79622	chromosome 16 open reading frame 33	-1.55	4.40E-04
4809	NHP2 non-histone chromosome protein 2-like 1 ( <i>S. cerevisiae</i> )	-1.55	7.09E-05
5245	prohibitin	-1.54	1.95E-03
6590	secretory leukocyte peptidase inhibitor	-1.54	1.42E-05
55011	PIH1 domain containing 1	-1.54	3.71E-05
2091	fibrillarin	-1.54	1.29E-04
22949	prostaglandin reductase 1	-1.54	2.00E-07
59	actin, alpha 2, smooth muscle, aorta	-1.54	1.60E-03
51013	exosome component 1	-1.54	2.06E-03
58477	signal recognition particle receptor, B subunit	-1.53	2.44E-03
11145	HRAS-like suppressor 3	-1.53	8.82E-07
84967	LSM10, U7 small nuclear RNA associated	-1.53	1.95E-06
643997	similar to peptidylprolyl isomerase A-like	-1.53	1.24E-05
56915	exosome component 5	-1.53	5.87E-06

51647	family with sequence similarity 96, member B	-1.53	2.81E-04
6648	superoxide dismutase 2, mitochondrial	-1.53	2.16E-04
125144	chromosome 17 open reading frame 45	-1.52	1.25E-03
1327	cytochrome c oxidase subunit IV isoform 1	-1.52	7.31E-04
2879	glutathione peroxidase 4 (phospholipid hydroperoxidase)	-1.52	4.26E-06
56655	polymerase (DNA-directed), epsilon 4 (p12 subunit)	-1.52	1.86E-06
7389	uroporphyrinogen decarboxylase	-1.51	1.48E-05
4792	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	-1.51	2.33E-03
79001	vitamin K epoxide reductase complex, subunit 1	-1.51	3.30E-05
6175	ribosomal protein, large, P0	-1.51	3.51E-07
147184	transmembrane protein 99	-1.51	5.65E-05
6183	mitochondrial ribosomal protein S12	-1.51	3.01E-04
51335	neugrin, neurite outgrowth associated	-1.50	8.84E-04
8878	sequestosome 1	1.50	3.18E-04
6448	N-sulfoglucosamine sulfohydrolase	1.51	5.01E-04
64764	cAMP responsive element binding protein 3-like 2	1.53	1.76E-03
9612	nuclear receptor co-repressor 2	1.53	1.83E-04
1717	7-dehydrocholesterol reductase	1.54	3.45E-06
4627	myosin, heavy chain 9, non-muscle	1.55	9.29E-04
4047	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)	1.58	5.14E-05
3157	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	1.67	3.31E-06

### Table S2.

Names of genes with significant changes in expression levels as compared to untreated control cells following 24 hour treatment with 10 nM citrate stabilized gold nanoparticles. A threshold of 1.5 fold change in gene expression and p-values < 0.05 was applied.

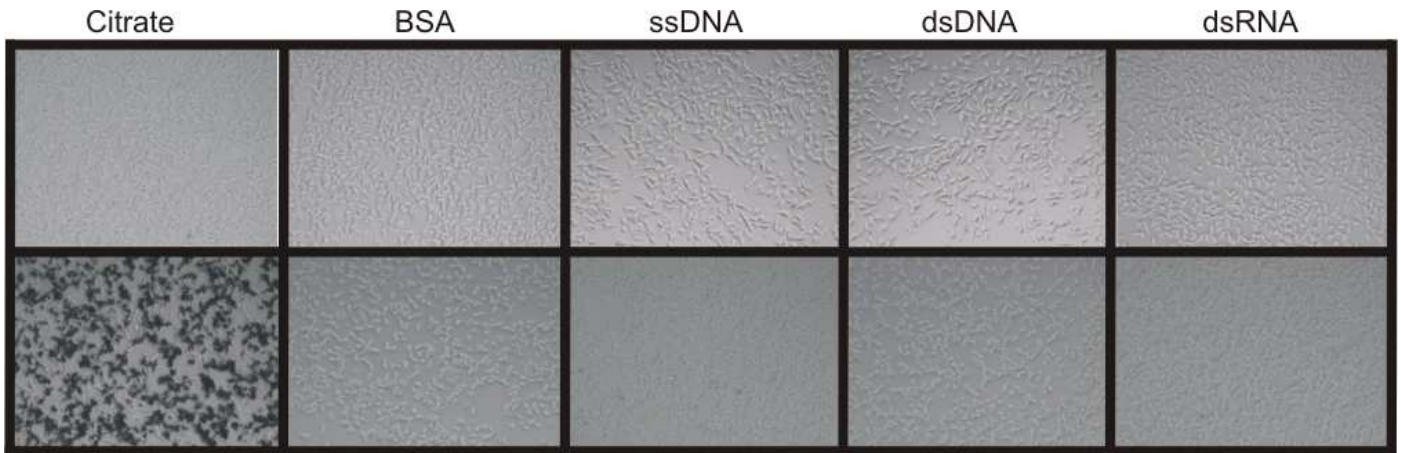
## Supplemental Figure S1



### Figure S1.

(A) UV-Vis spectra of each of the nanoparticle types following synthesis and functionalization. (B) UV-Vis spectra of each of the nanoparticle types following 24 hours of incubation with cell culture medium. A distinct red-shift in the plasmon resonance of the citrate stabilized nanoparticles is observed following incubation with the cell culture medium.

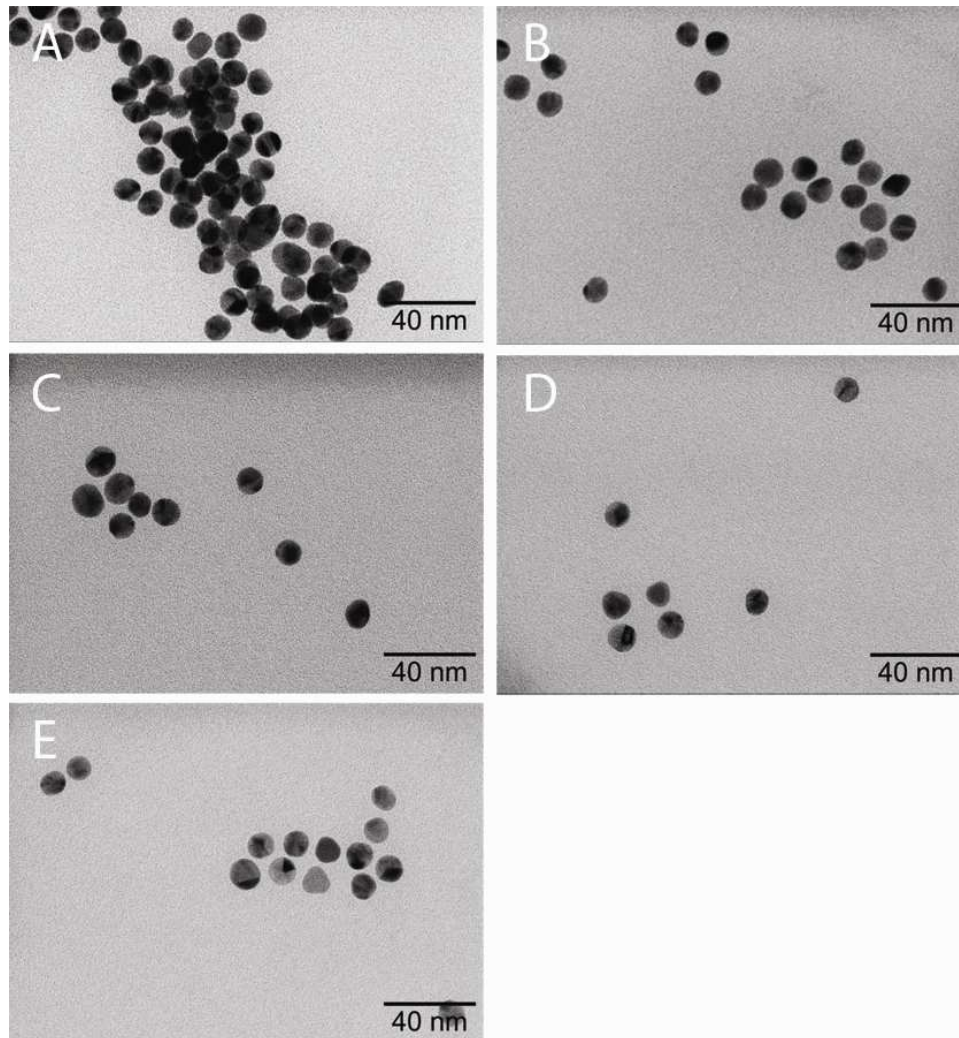
## Supplemental Figure S2



### Figure S2.

Immediately following transfection (top row), the citrate stabilized nanoparticles shifted in color from red to purple indicating particle aggregation, but no signs of particles settling out of solution were observed. However, by 24 hours (bottom row) the citrate stabilized gold nanoparticles have clearly aggregated and settled to the bottom of the culture dish. All other nanoparticle treatment conditions maintained their red color and remained stable under cell culture conditions over the 24 hour time period.

### Supplemental Figure S3



#### Figure S3.

TEM images of citrate stabilized nanoparticles (A), BSA coated nanoparticles (B), ssDNA functionalized nanoparticles (C), dsDNA functionalized nanoparticles (D), and dsRNA functionalized nanoparticles (E) following 24 hours of incubation in cell culture medium. Although still distinct particles, the citrate stabilized particles were found to be more often localized in tighter clusters of nanoparticles than the other particle types.