Supporting Information

Colorimetric sensor assay for discrimination of proteins based on exonuclease I-triggered aggregation of DNA-functionalized gold nanoparticles

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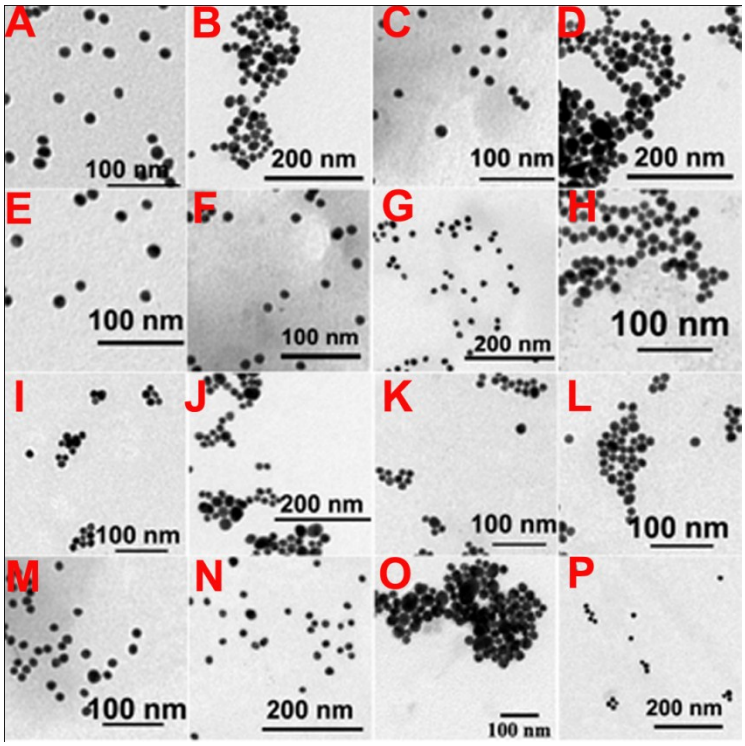

Fig. S1 TEM images of DNA-AuNPs (A) in the absence of Exo I, (B) Hem-DNA-AuNPs, (C) Try-DNA-AuNPs, (D) BSA-DNA-AuNPs, (E) UAO-DNA-AuNPs, (F) Pep-DNA-AuNPs, (G) Lys-DNA-AuNPs, (H) EA-DNA-AuNPs, (I) Myo-DNA-AuNPs, (J) HRP-DNA-AuNPs, (K) TRF-DNA-AuNPs, (L) Cyt-C-DNA-AuNPs, (M) Thr-DNA-AuNPs, (N) Lip-DNA-AuNPs, (O) Con-DNA-AuNPs, and (P) Fib-DNA-AuNPs in presence of Exo I in salt media.

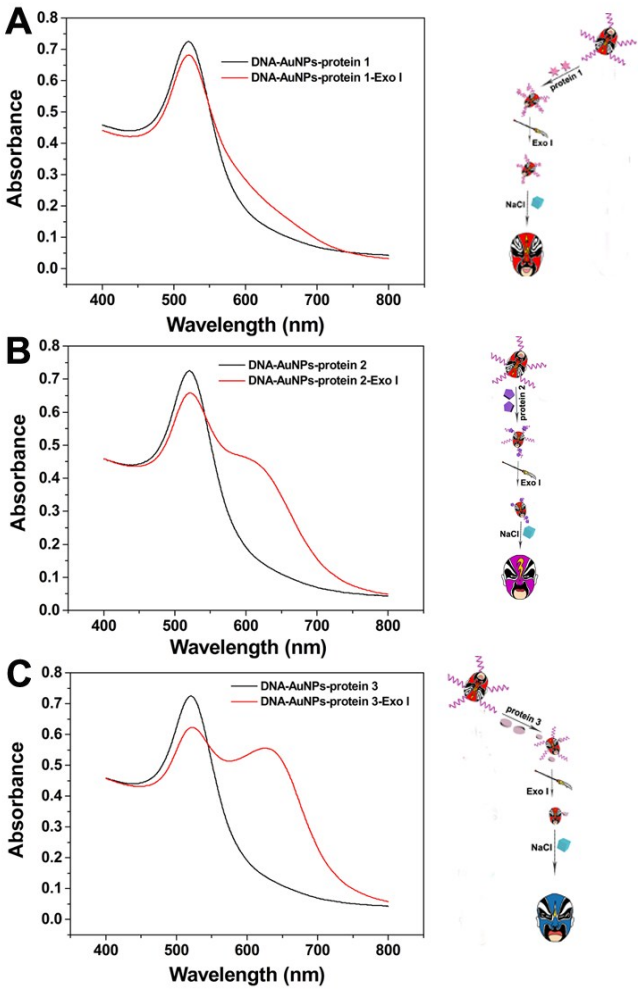

Fig. S2 UV-vis spectra of AuNPs corresponding to (A) DNA-AuNPs-protein 1, (B) DNA-AuNPs-protein 1,, and (C) DNA-AuNPs-protein 3 in the absence and presence of Exo I. AuNP concentration: 5 nM, Exo I concentration: 40 U/mL, NaCl concentration: 0.3 M, and protein concentration: 20 nM.

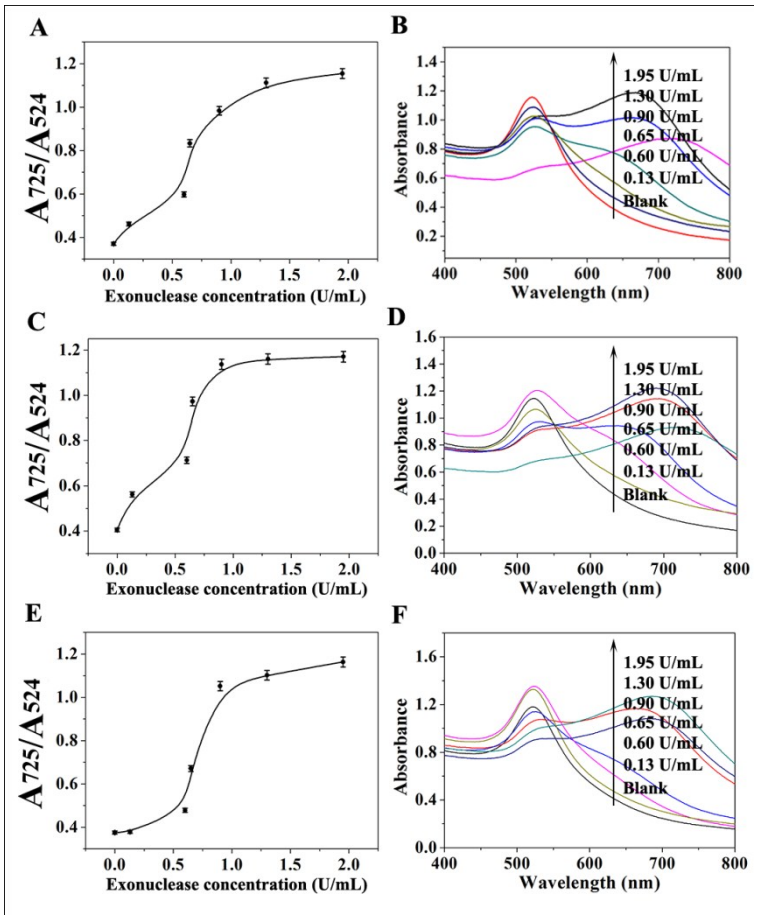

Fig. S3 Plots of AuNP absorbance ratio (A_{725}/A_{524}) vs Exo I concentration for (A) A15, (C) C15, and (E) T15, respectively. Corresponding UV-vis spectra of (B), (D), and (F) corresponding to (A), (C), and (E), respectively. Error bars indicate the standard deviation of three independent experiments. The solution does contain proteins. Incubation time of NaCl and DNA is 5 min and 3 h, respectively.

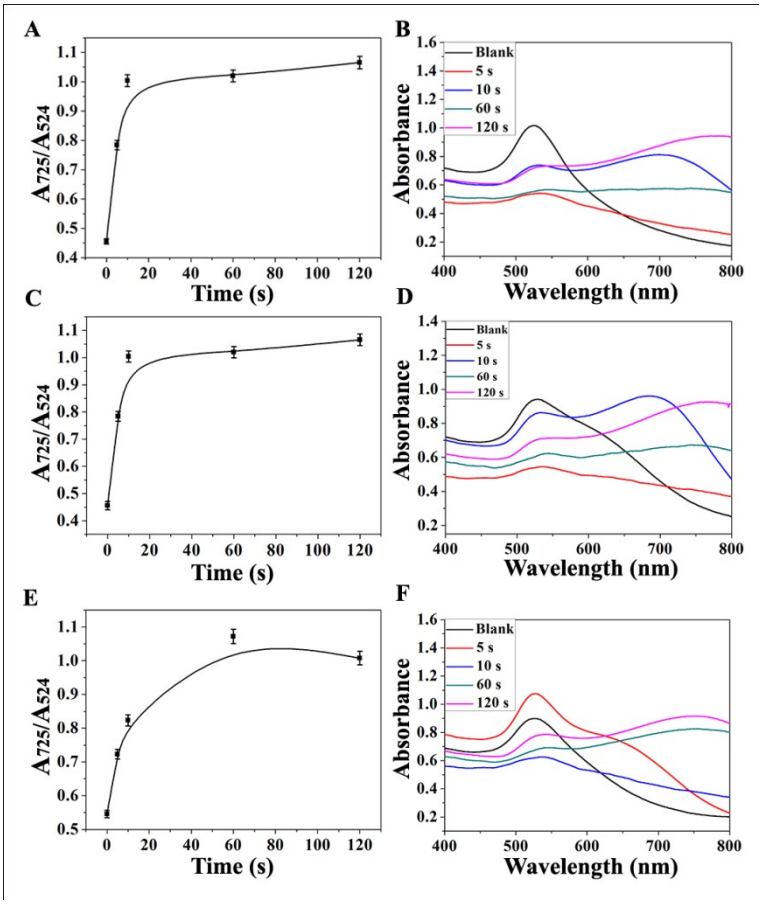

Fig. S4 Plots of AuNP absorbance ratio (A_{725}/A_{524}) vs the incubation time of Exo I for (A) A15, (C) C15, and (E) T15, respectively. Corresponding UV-vis spectra of (B), (D), and (F) corresponding to (A), (C), and (E), respectively. Error bars indicate the standard deviation of three independent experiments. The solution does contain proteins. Incubation time of NaCl and DNA is 5 min and 3 h, respectively.

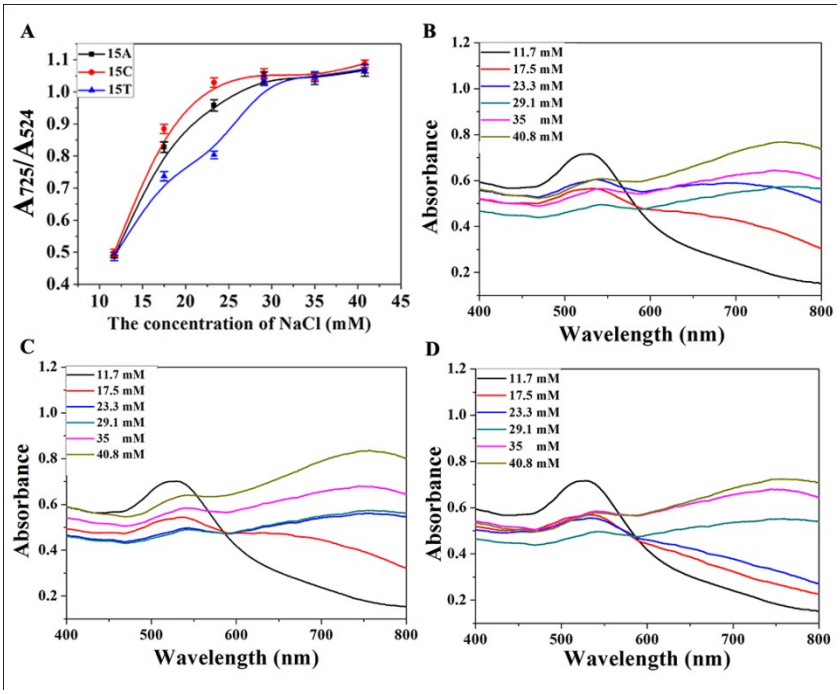

Fig. S5 (A) The colorimetric responses (A_{725}/A_{524}) of the sensor array plotted vs different concentrations of NaCl for A15, C15, and T15, respectively. UV-vis spectra of AuNPs followed with Exo I digestion in the presence of different concentrations of NaCl for (B) A15, (C) C15, and (D) T15, respectively. Error bars indicate the standard deviation of three independent experiments.

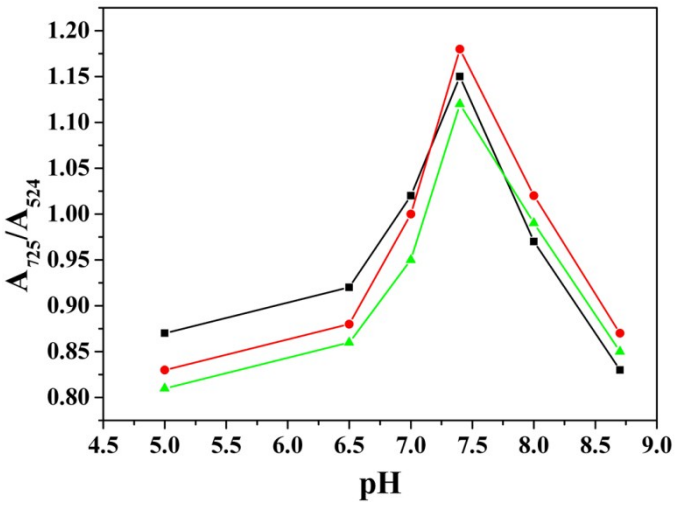

Fig. S6 The colorimetric responses (A_{725}/A_{524}) of the sensor array plotted vs different pH value of the solution for A15 (black line), C15 (red line), and T15 (green line), respectively.

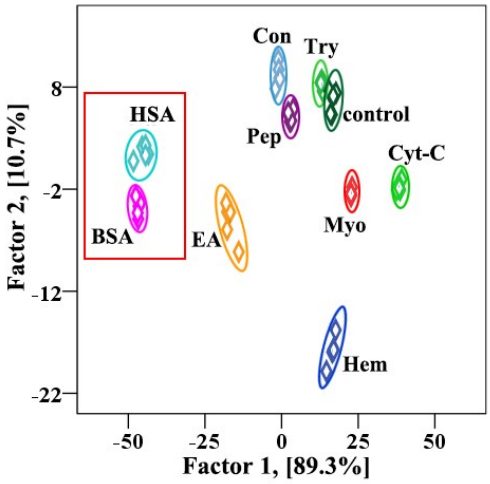

Fig. S7. Canonical score plot for the sensor array against the 9 proteins (HSA, BSA, EA, Hem, Myo, Pep, Con, Try, and Cyt-C) at 20 nM.

Table S1. Jackknifed classification matrix obtained using LDA based on 15A, 15C, 15T, 15A+15C, 15A+15T, 15C+15T, and 15A+15C+15T as receptors for the 15 proteins of 20 nM, respectively.

Proteins	UV-15A	UV-15C	UV-15T	UV-15A+15C	UV-15A+15T	UV-15C+15T	UV-15A+15C+15T
Hem	100%	100%	0%	100%	100%	100%	100%
Try	100%	100%	40%	100%	100%	100%	100%
BSA	80%	20%	80%	80%	100%	80%	100%
UAO	100%	80%	100%	100%	100%	100%	100%
Pep	100%	100%	100%	100%	100%	100%	100%
Lys	100%	60%	100%	100%	100%	100%	100%
EA	60%	100%	20%	100%	100%	100%	100%
Myo	100%	100%	0%	100%	80%	80%	100%
HRP	100%	100%	40%	100%	100%	100%	100%
TRF	100%	100%	100%	100%	100%	100%	100%
Cyt-C	40%	100%	100%	100%	100%	100%	100%
Thr	80%	60%	100%	100%	100%	100%	100%
Lip	80%	80%	60%	100%	100%	80%	100%
Con	60%	40%	80%	100%	100%	80%	100%
Fib	80%	40%	60%	100%	100%	40%	100%

Table S2. The training matrix of the colorimetric response patterns against 15 proteins using this sensor assay. The concentrations of 15A, 15C, and 15T are all 1 μM; AuNPs, 5 nM; Exo-I, 40 U/ml; NaCl, 300 mM.

Proteins	15A	15C	15T
Hem	0.960557	0.991905	0.992123
Hem	0.960925	0.991148	0.99458
Hem	0.95961	0.990428	0.992734
Hem	0.959452	0.990439	0.99491
Hem	0.960912	0.991186	0.993783
Try	0.981959	0.994573	0.98327
Try	0.981264	0.994429	0.985256
Try	0.981319	0.994625	0.983251
Try	0.981453	0.994627	0.985726
Try	0.982081	0.994175	0.988478
BSA	0.948779	0.983972	0.973623
BSA	0.948085	0.987786	0.973758
BSA	0.94242	0.987659	0.972164
BSA	0.947477	0.988519	0.972279
BSA	0.949336	0.986047	0.97338
UAO	0.969946	0.985336	0.974162
UAO	0.969834	0.984517	0.974348
UAO	0.969998	0.984794	0.974323
UAO	0.968736	0.985622	0.974287
UAO	0.968996	0.985991	0.973944
Pep	0.956399	0.979543	1.001765
Pep	0.955918	0.980717	1.000295
Pep	0.956186	0.979689	1.001487
Pep	0.956148	0.980924	1.00004
Pep	0.95637	0.979498	1.001749
Lys	0.951748	0.989742	1.010698
Lys	0.952369	0.989141	1.016524
Lys	0.953274	0.989881	1.013689
Lys	0.951809	0.989654	1.0164
Lys	0.953168	0.990701	1.012389
EA	0.964425	0.983013	0.982276
EA	0.962667	0.983048	0.984865
EA	0.96457	0.983392	0.984751
EA	0.962866	0.983408	0.984749
EA	0.963594	0.982875	0.98392
Myo	0.936413	0.988315	0.98409
Myo	0.935464	0.988288	1.002535
Myo	0.935746	0.988847	1.000591
Myo	0.93594	0.989142	1.003126
Myo	0.936849	0.988012	1.001673

HRP	0.958242	0.976293	0.994677
HRP	0.957884	0.977278	0.993121
HRP	0.958324	0.976281	0.993304
HRP	0.957828	0.976324	0.993184
HRP	0.958407	0.977296	0.994621
TRF	0.857358	0.905013	0.952427
TRF	0.855123	0.899865	0.952718
TRF	0.850787	0.903234	0.948797
TRF	0.850272	0.905056	0.952628
TRF	0.851294	0.899648	0.950468
Cyt-C	0.931694	0.943749	0.980472
Cyt-C	0.928439	0.932902	0.9807
Cyt-C	0.936953	0.936643	0.981154
Cyt-C	0.932504	0.938912	0.980859
Cyt-C	0.934954	0.934562	0.982113
Thr	0.943969	0.984472	1.00635
Thr	0.940071	0.98276	1.007194
Thr	0.939932	0.984342	1.006688
Thr	0.94012	0.98435	1.006921
Thr	0.940642	0.98322	1.006038
Lip	0.94527	0.995996	0.989125
Lip	0.944063	0.997831	0.987682
Lip	0.944017	0.998264	0.985254
Lip	0.946795	0.997942	0.987685
Lip	0.944673	0.994856	0.986895
Con	0.964455	0.975397	0.990009
Con	0.962779	0.973545	0.98988
Con	0.963094	0.977545	0.992326
Con	0.963861	0.974436	0.990246
Con	0.962289	0.973121	0.98999
Fib	0.931221	0.975505	0.992612
Fib	0.929608	0.968013	0.997053
Fib	0.926855	0.976112	0.990673
Fib	0.928355	0.972022	0.992739
Fib	0.92526	0.977087	0.992424

Table S3. The training matrix of the colorimetric response patterns against Try with different concentrations (2.5-30 nM) using this sensor assay.

Ptoteins	UV-15A	UV-15C	UV-15T	EDs
2.5 nM	1.024171	1.032481	0.995454	1.762349
2.5 nM	1.024059	1.03236	0.995329	1.762142
2.5 nM	1.024296	1.032604	0.995571	1.76256
2.5 nM	1.024327	1.032632	0.995619	1.762621
2.5 nM	1.024183	1.032481	0.995458	1.762358
5 nM	1.022822	1.02606	0.994902	1.757496
5 nM	1.022947	1.026188	0.995028	1.757715
5 nM	1.022956	1.026191	0.995039	1.757728
5 nM	1.022621	1.025858	0.994687	1.757139
5 nM	1.022732	1.025973	0.99479	1.757329
10 nM	1.022378	1.014711	0.973618	1.738627
10 nM	1.022489	1.014816	0.973726	1.738814
10 nM	1.022492	1.01482	0.973739	1.738826
10 nM	1.022483	1.014826	0.973719	1.738813
10 nM	1.022268	1.014551	0.97351	1.738409
15 nM	1.020301	1.008467	0.935284	1.712535
15 nM	1.021511	1.009637	0.936474	1.714595
15 nM	1.020411	1.008582	0.935474	1.712772
15 nM	1.020415	1.008595	0.935419	1.712752
15 nM	1.02018	1.008326	0.93514	1.712301
20 nM	1.017317	1.003541	0.908506	1.693343
20 nM	1.018557	1.004961	0.909956	1.695708
20 nM	1.017408	1.003584	0.908604	1.693476
20 nM	1.017431	1.00365	0.908612	1.693533
20 nM	1.017207	1.003394	0.908347	1.693105
30 nM	0.997447	0.994814	0.864288	1.65274
30 nM	0.997568	0.994955	0.864421	1.652968
30 nM	0.997581	0.994953	0.864426	1.652977
30 nM	0.997592	0.994956	0.864435	1.65299
30 nM	0.997336	0.994699	0.864171	1.652543

Table S4. Training matrix of the response patterns against BSA and Hem at the same concentration (20 nM), respectively, as well as the mixtures of these two proteins samples with various molar ratios (total concentration: 20 nM) using the sensor array.

Proteins	UV-15A	UV-15C	UV-15T
100% Hem	1.039	0.970	0.986
100% Hem	1.035	0.970	0.988
100% Hem	1.049	0.971	0.986
100% Hem	1.032	0.971	0.996
100% Hem	1.047	0.970	0.989
100% BSA	0.660	0.931	0.549
100% BSA	0.674	0.927	0.557
100% BSA	0.664	0.925	0.553
100% BSA	0.663	0.931	0.558
100% BSA	0.658	0.921	0.553
10% Hem+90% BSA	0.455	0.474	0.476
10% Hem+90% BSA	0.456	0.473	0.476
10% Hem+90% BSA	0.454	0.473	0.477
10% Hem+90% BSA	0.455	0.473	0.477
10% Hem+90% BSA	0.456	0.473	0.477
30% Hem+70% BSA	0.499	0.626	0.683
30% Hem+70% BSA	0.499	0.626	0.682
30% Hem+70% BSA	0.498	0.631	0.684
30% Hem+70% BSA	0.499	0.625	0.684
30% Hem+70% BSA	0.491	0.625	0.680
50% Hem+50% BSA	0.660	0.718	0.749
50% Hem+50% BSA	0.659	0.718	0.753
50% Hem+50% BSA	0.663	0.720	0.750
50% Hem+50% BSA	0.663	0.712	0.752
50% Hem+50% BSA	0.662	0.715	0.750
70% Hem+30% BSA	0.703	0.874	0.781
70% Hem+30% BSA	0.713	0.876	0.781
70% Hem+30% BSA	0.706	0.874	0.781
70% Hem+30% BSA	0.708	0.869	0.781
70% Hem+30% BSA	0.706	0.870	0.781
90% Hem+10% BSA	1.027	1.162	1.116
90% Hem+10% BSA	1.022	1.161	1.115
90% Hem+10% BSA	1.026	1.166	1.121
90% Hem+10% BSA	1.026	1.164	1.118
90% Hem+10% BSA	1.027	1.162	1.124

Table S5. Training matrix of the response patterns against Try and HRP at the same concentration (20 nM), respectively, as well as the mixtures of these two proteins samples with various molar ratios (total concentration: 20 nM) using the sensor array.

Proteins	UV-15A	UV-15C	UV-15T
100% Try	0.994	0.948	0.976
100% Try	1.107	0.940	0.969
100% Try	1.049	0.953	0.967
100% Try	1.059	0.949	0.972
100% Try	1.049	0.947	0.972
100% HRP	0.690	0.755	0.803
100% HRP	0.689	0.756	0.801
100% HRP	0.690	0.755	0.801
100% HRP	0.690	0.755	0.805
100% HRP	0.690	0.757	0.801
10% Try+90% HRP	0.981	1.237	0.793
10% Try+90% HRP	0.987	1.242	0.794
10% Try+90% HRP	0.992	1.244	0.799
10% Try+90% HRP	0.979	1.246	0.792
10% Try+90% HRP	0.981	1.243	0.795
30% Try+70% HRP	1.081	1.232	1.042
30% Try+70% HRP	1.088	1.282	1.041
30% Try+70% HRP	1.091	1.255	1.042
30% Try+70% HRP	1.092	1.243	1.043
30% Try+70% HRP	1.082	1.220	1.041
50% Try+50% HRP	1.149	1.203	1.047
50% Try+50% HRP	1.150	1.202	1.031
50% Try+50% HRP	1.149	1.203	1.049
50% Try+50% HRP	1.148	1.205	1.048
50% Try+50% HRP	1.149	1.201	1.051
70% Try+30% HRP	1.120	1.126	1.111
70% Try+30% HRP	1.101	1.127	1.112
70% Try+30% HRP	1.129	1.126	1.110
70% Try+30% HRP	1.128	1.126	1.113
70% Try+30% HRP	1.122	1.127	1.111
90% Try+10% HRP	1.041	1.166	1.104
90% Try+10% HRP	1.043	1.174	1.109
90% Try+10% HRP	1.043	1.169	1.108
90% Try+10% HRP	1.043	1.165	1.108
90% Try+10% HRP	1.043	1.166	1.104

Table S6. Training matrix of the response patterns against the mixtures of proteins (total concentration 20 nM) using this sensor array.

Protiens	UV-15A	UV-15C	UV-15T
Hem+Try	0.898314	1.014467	1.012944
Hem+Try	0.897097	1.014486	1.012965
Hem+Try	0.899115	1.014859	1.014084
Hem+Try	0.899217	1.015899	1.016609
Hem+Try	0.899026	1.016956	1.015444
BSA+UAO	0.957476	0.980979	0.972611
BSA+UAO	0.959259	0.980948	0.97564
BSA+UAO	0.956383	0.982292	0.973567
BSA+UAO	0.956477	0.981146	0.977869
BSA+UAO	0.9553	0.98325	0.975723
Pep+Lys	0.900804	1.00279	1.006606
Pep+Lys	0.897658	1.002792	1.005157
Pep+Lys	0.899683	1.003144	1.00656
Pep+Lys	0.899784	1.004185	1.006326
Pep+Lys	0.897717	1.005247	1.006346
EA+Myo	0.971702	0.974304	1.017217
EA+Myo	0.969462	0.974266	1.017254
EA+Myo	0.969565	0.975628	1.016978
EA+Myo	0.973733	0.974455	1.018437
EA+Myo	0.970528	0.975526	1.018266
HRP+TRF	0.974221	1.027735	1.026747
HRP+TRF	0.968802	1.02748	1.026555
HRP+TRF	0.973127	1.027584	1.026611
HRP+TRF	0.970068	1.028724	1.030794
HRP+TRF	0.971896	1.027818	1.027559
Cyt-C+Thr	1.03387	1.013209	1.029843
Cyt-C+Thr	1.027083	1.013232	1.027324
Cyt-C+Thr	1.032886	1.013186	1.02736
Cyt-C+Thr	1.030542	1.013491	1.03108
Cyt-C+Thr	1.031666	1.014543	1.027279
Lip+Con	0.967237	0.98905	1.02116
Lip+Con	0.971585	0.988827	1.024391
Lip+Con	0.967275	0.989272	1.019709
Lip+Con	0.968436	0.987567	1.022186
Lip+Con	0.967067	0.988835	1.025613
Fib+Hem+BSA	0.98648	0.952705	1.017742
Fib+Hem+BSA	0.986164	0.951381	1.01536
Fib+Hem+BSA	0.988563	0.951649	1.016488
Fib+Hem+BSA	0.985459	0.952753	1.01894
Fib+Hem+BSA	0.639517	0.953972	1.018791
Con+Try+Myo	1.003749	1.008063	1.029513

Con+Try+Myo	0.999264	1.008081	1.02551
Con+Try+Myo	1.002654	1.009553	1.032463
Con+Try+Myo	1.000514	1.008335	1.030891
Con+Try+Myo	1.003533	1.009385	1.025049
Lip+UAO+EA	0.991604	1.008322	1.046692
Con+Try+Myo	0.993211	1.008344	1.04209
Con+Try+Myo	0.991514	1.007177	1.046714
Con+Try+Myo	0.988619	1.0086	1.041692
Con+Try+Myo	0.989545	1.011192	1.047772
Thr+HRP+Fib	0.97311	0.998089	1.038948
Thr+HRP+Fib	0.970708	0.997834	1.040362
Thr+HRP+Fib	0.969852	0.999645	1.041397
Thr+HRP+Fib	0.969964	0.999813	1.042421
Thr+HRP+Fib	0.971817	0.99768	1.042738
Cyt-C+Pep+TRF	1.0138	1.024319	1.021632
Cyt-C+Pep+TRF	1.012568	1.024014	1.021672
Cyt-C+Pep+TRF	1.015148	1.027629	1.022785
Cyt-C+Pep+TRF	1.01512	1.025914	1.021568
Cyt-C+Pep+TRF	1.014947	1.023744	1.022901
Lys+Hem+Pep+HRP	1.030093	0.982339	1.007024
Lys+Hem+Pep+HRP	1.028635	0.978694	1.008414
Lys+Hem+Pep+HRP	1.028997	0.980862	1.008258
Lys+Hem+Pep+HRP	1.026892	0.976992	1.006847
Lys+Hem+Pep+HRP	1.031124	0.983496	1.008062
Try+BSA+EA+Cyt-C	1.008975	1.014743	1.037215
Try+BSA+EA+Cyt-C	1.007737	1.014777	1.037416
Try+BSA+EA+Cyt-C	1.007972	1.01328	1.036131
Try+BSA+EA+Cyt-C	1.009053	1.015048	1.037271
Try+BSA+EA+Cyt-C	1.006569	1.01609	1.037071
UAO+Lys+TRF+Lip	1.03242	1.020269	1.024846
UAO+Lys+TRF+Lip	1.030937	1.023051	1.026049
UAO+Lys+TRF+Lip	1.03096	1.022071	1.023541
UAO+Lys+TRF+Lip	1.030908	1.020423	1.027242
UAO+Lys+TRF+Lip	1.032326	1.022999	1.025903
Pep+Myo+Thr+Fib	1.007541	0.909416	0.977928
Pep+Myo+Thr+Fib	1.006139	0.910318	0.977997
Pep+Myo+Thr+Fib	1.005275	0.907553	0.979093
Pep+Myo+Thr+Fib	1.005426	0.909433	0.979
Pep+Myo+Thr+Fib	1.007403	0.909494	0.979071

Table S7. Identification of unknown protein samples at 20 nM using the sensor array.

Samples	UV-15A	UV-15C	UV-15T	Identification	Verification
1	0.960557	0.991905	0.992123	Hem	Hem
2	0.960925	0.991148	0.99458	Hem	Hem
3	0.95961	0.990428	0.992734	Hem	Hem
4	0.959452	0.990439	0.99491	Hem	Hem
5	0.960912	0.991186	0.993783	Hem	Hem
6	0.981959	0.994573	0.98327	Try	Try
7	0.981264	0.994429	0.985256	Try	Try
8	0.981319	0.994625	0.983251	Try	Try
9	0.981453	0.994627	0.985726	Try	Try
10	0.982081	0.994175	0.988478	Try	Try
11	0.948779	0.983972	0.973623	BSA	BSA
12	0.948085	0.987786	0.973758	BSA	BSA
13	0.94242	0.987659	0.972164	BSA	Thr
14	0.947477	0.988519	0.972279	BSA	BSA
15	0.949336	0.986047	0.97338	BSA	BSA
16	0.969946	0.985336	0.974162	UAO	UAO
17	0.969834	0.984517	0.974348	UAO	UAO
18	0.969998	0.984794	0.974323	UAO	UAO
19	0.968736	0.985622	0.974287	UAO	UAO
20	0.968996	0.985991	0.973944	UAO	UAO
21	0.956399	0.979543	1.001765	Pep	Pep
22	0.955918	0.980717	1.000295	Pep	Pep
23	0.956186	0.979689	1.001487	Pep	Pep
24	0.956148	0.980924	1.00004	Pep	Pep
25	0.95637	0.979498	1.001749	Pep	Pep
26	0.951748	0.989742	1.010698	Lys	Lys
27	0.952369	0.989141	1.016524	Lys	Lys
28	0.953274	0.989881	1.013689	Lys	Lys
29	0.951809	0.989654	1.0164	Lys	Lys
30	0.936413	0.932902	0.98409	Lys	Cyt-C
31	0.964425	0.983013	0.982276	EA	EA
32	0.962667	0.983048	0.984865	EA	EA
33	0.96457	0.983392	0.984751	EA	EA
34	0.962866	0.983408	0.984749	EA	EA
35	0.963594	0.982875	0.98392	EA	EA

Table S8. Training matrix of the response patterns against proteins (each at 20nM) in the presence of serum using the sensor array.

Proteins	UV-15A	UV-15C	UV-15T
Hem	1.096903	1.063452	0.989415
Hem	1.092568	1.060907	0.990389
Hem	1.085584	1.065793	0.992585
Hem	1.086013	1.066516	0.988414
Hem	1.092498	1.064474	0.991526
Try	1.157922	1.057323	0.969762
Try	1.156124	1.050643	0.973823
Try	1.148546	1.056873	0.969964
Try	1.153101	1.055873	0.970799
Try	1.150557	1.057344	0.973827
BSA	0.652544	1.091286	0.937824
BSA	0.653416	1.089584	0.939686
BSA	0.650039	1.089827	0.942784
BSA	0.648065	1.093207	0.93876
BSA	0.6528	1.09126	0.941724
UAO	1.105319	1.076541	0.989951
UAO	1.10993	1.069672	0.98883
UAO	1.106179	1.077653	0.993077
UAO	1.104433	1.079581	0.98577
UAO	1.104517	1.077705	0.990952
Pep	1.18152	1.059253	1.039247
Pep	1.18241	1.061303	1.04373
Pep	1.174771	1.057363	1.0414
Pep	1.176733	1.060913	1.036904
Pep	1.179294	1.062223	1.040264
Lys	1.191316	1.093958	0.974527
Lys	1.194937	1.089305	0.976197
Lys	1.187152	1.093001	0.977271
Lys	1.183727	1.092445	0.97196
Lys	1.186459	1.093559	0.974991
EA	1.165969	1.065377	0.970531
EA	1.165488	1.054164	0.972369
EA	1.161859	1.062014	0.976794
EA	1.165103	1.059646	0.968224
EA	1.163814	1.060837	0.972367
Myo	1.13543	1.072677	1.014456
Myo	1.139901	1.070208	1.015946
Myo	1.131263	1.072411	1.014478
Myo	1.136806	1.074229	1.015401
Myo	1.131977	1.074166	1.01466

HRP	1.175168	1.005667	0.969518
HRP	1.174707	1.00399	0.97359
HRP	1.171002	1.006071	0.976947
HRP	1.170351	1.004464	0.971712
HRP	1.17427	1.006519	0.974743
TRF	1.285588	1.116561	1.056362
TRF	1.282354	1.109952	1.064436
TRF	1.271685	1.110662	1.063127
TRF	1.278093	1.118673	1.057376
TRF	1.273502	1.116696	1.06079
Cyt-C	1.148569	1.093716	1.002061
Cyt-C	1.147978	1.087891	1.006222
Cyt-C	1.147174	1.090016	1.005196
Cyt-C	1.146466	1.089421	1.001009
Cyt-C	1.149124	1.090514	1.006301
Thr	1.183345	1.077796	0.993375
Thr	1.186901	1.065197	0.996383
Thr	1.185893	1.07027	0.996405
Thr	1.18794	1.076645	0.992246
Thr	1.185231	1.075132	0.995375
Lip	1.122927	1.038606	0.956021
Lip	1.121311	1.032995	0.958866
Lip	1.122599	1.032471	0.961053
Lip	1.121948	1.034571	0.955906
Lip	1.122041	1.036982	0.95774
Con	1.16077	1.057407	0.96862
Con	1.162933	1.045826	0.968862
Con	1.16057	1.050843	0.973746
Con	1.159913	1.052934	0.965843
Con	1.161248	1.051137	0.968859
Fib	0.957718	1.068271	0.979204
Fib	0.956157	1.062435	0.982081
Fib	0.959	1.064689	0.980774
Fib	0.957109	1.066727	0.980262
Fib	0.953797	1.065104	0.982096

Table S9 The relative standard deviations (RSDs) for results from the sensor array for each protein at 20 nM.

protein	Hem	Try	BSA	UAO	Pep	Lys	EA	Myo	HRP	TRF	Cyt-C	Thr	Lip	Con	Fib
RSD (%)	3.19	4.54	2.15	3.88	3.51	5.74	3.09	4.79	3.06	3.38	5.11	4.05	2.07	3.92	1.80