

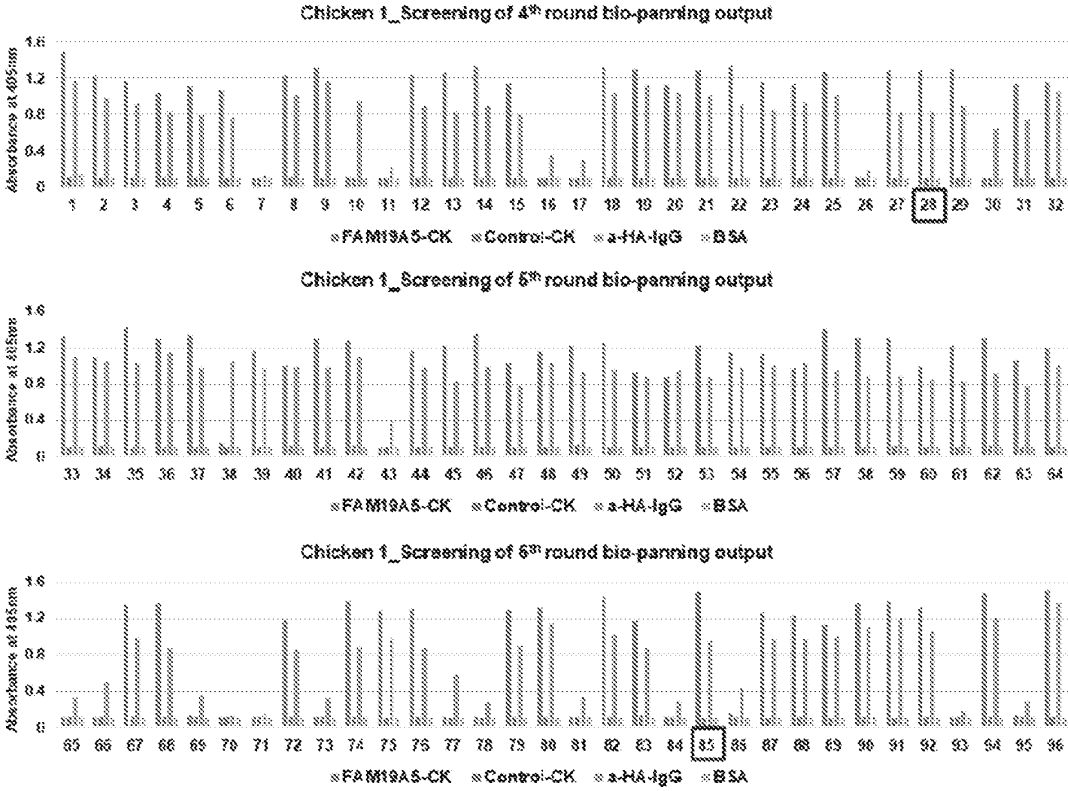


FIG. 1A

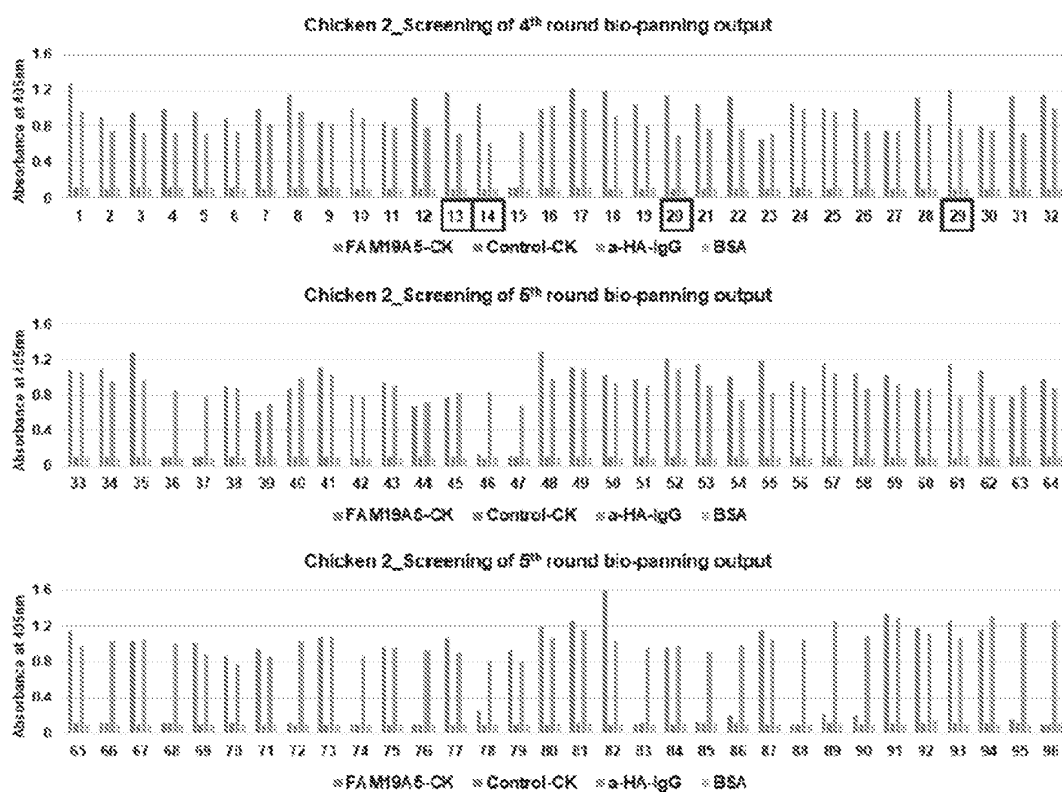


FIG. 1B

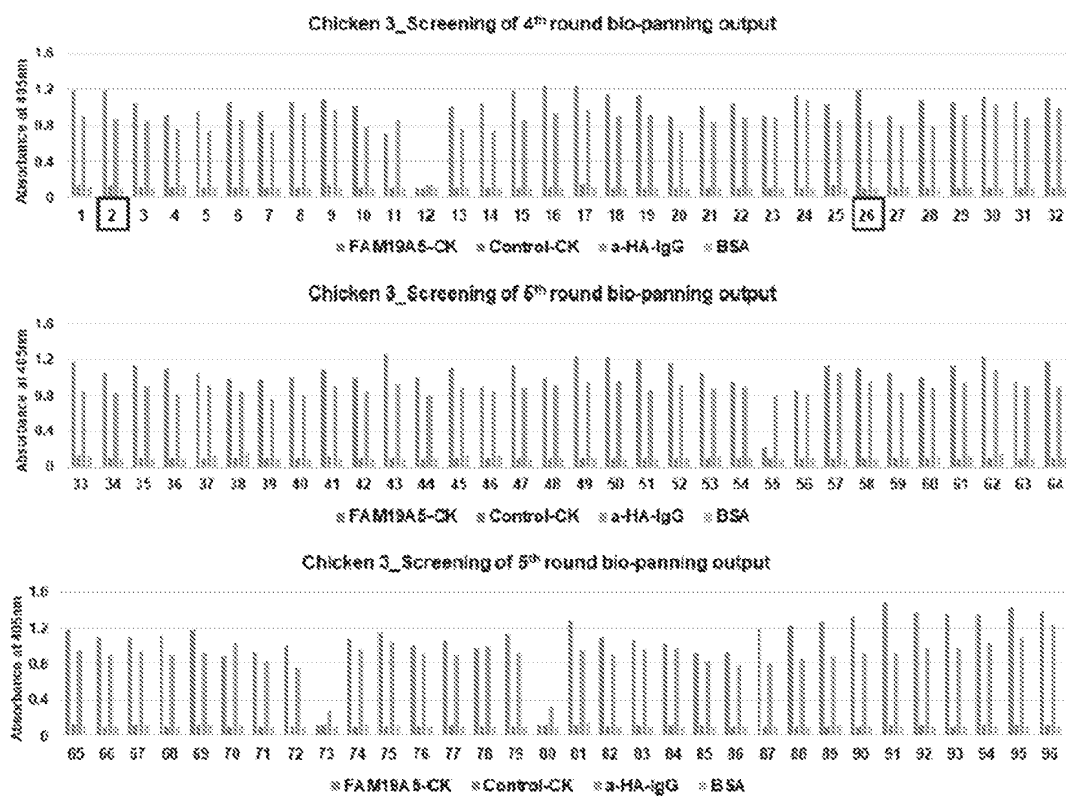


FIG. 1C

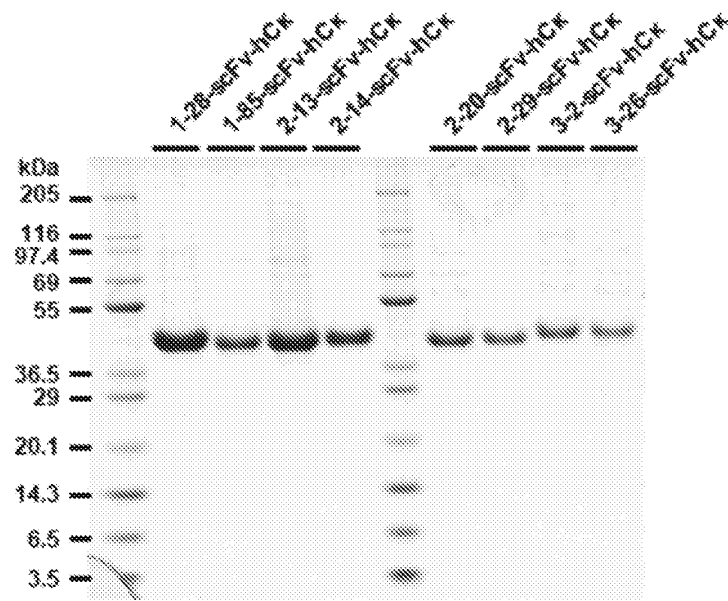


FIG. 2A

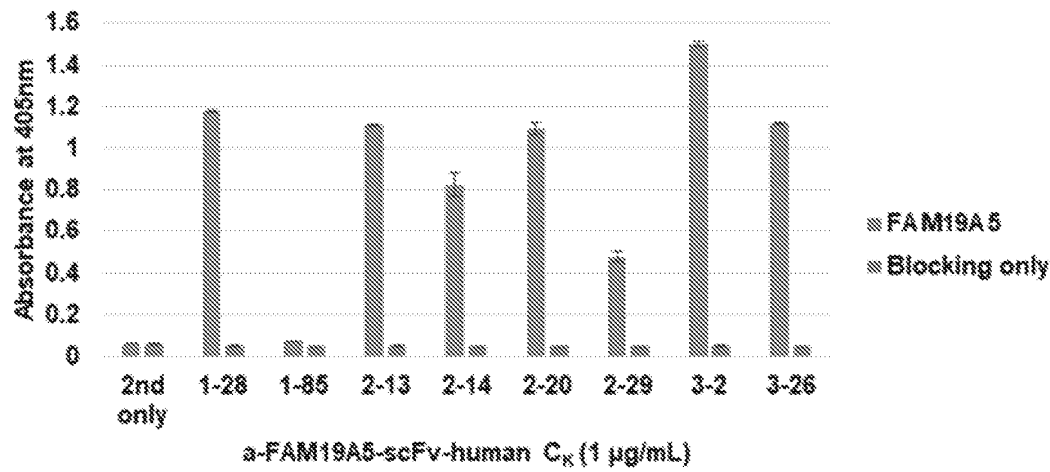


FIG. 2B

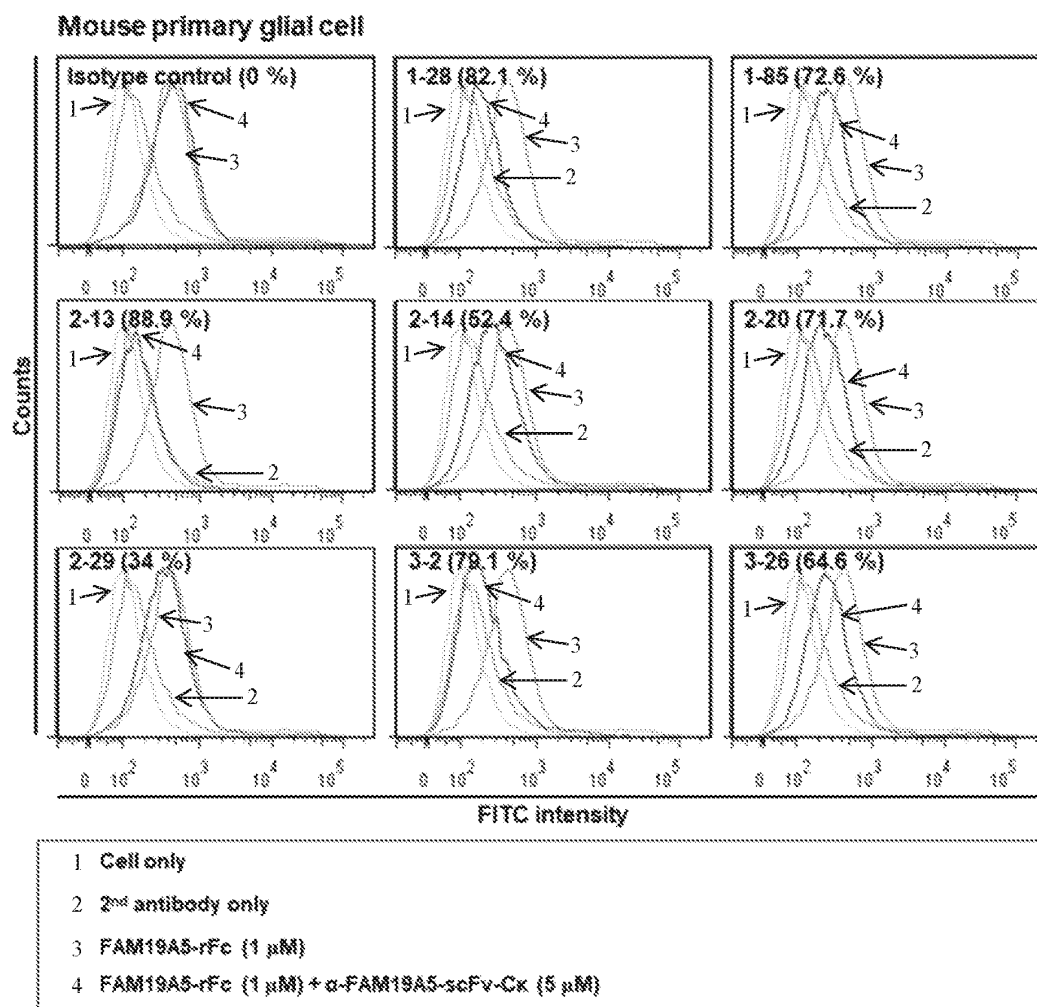


FIG. 3A

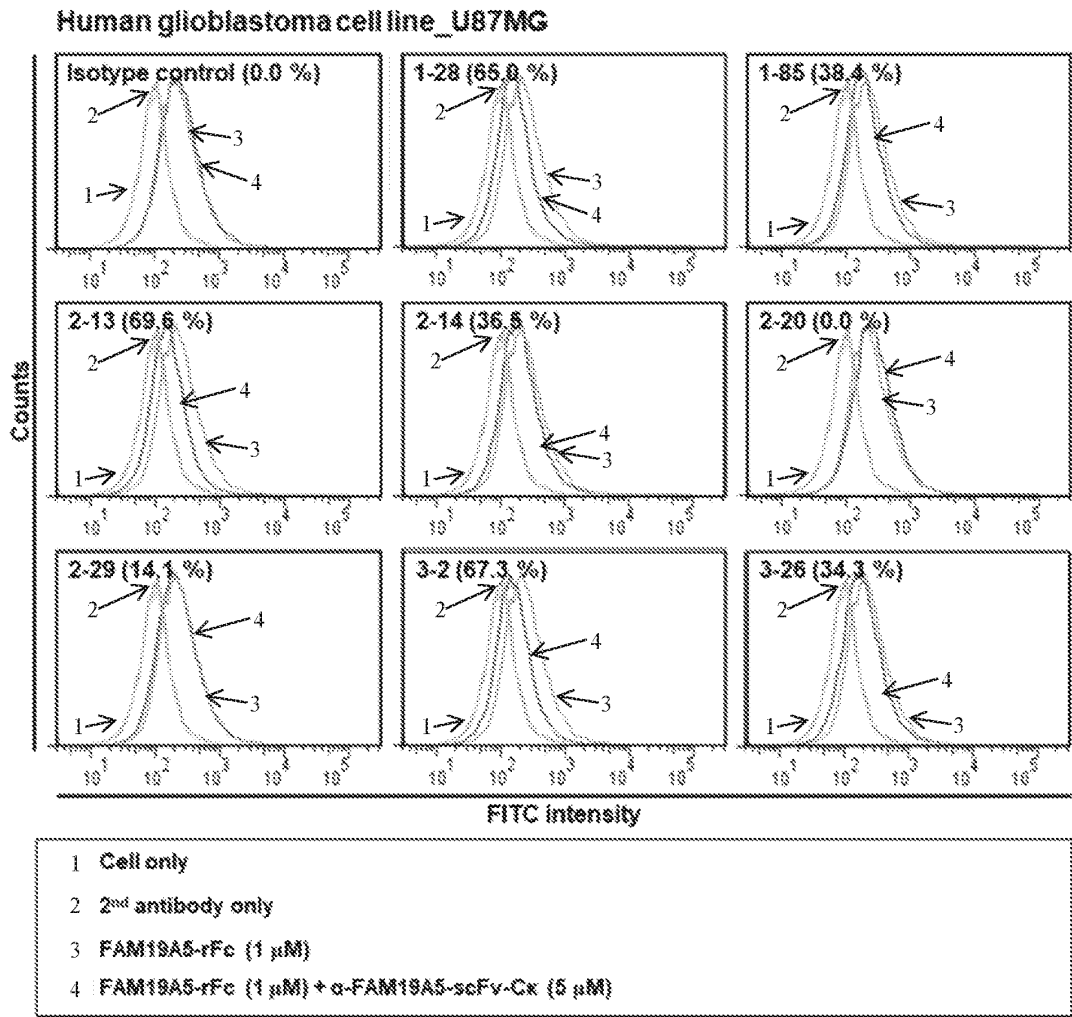


FIG. 3B

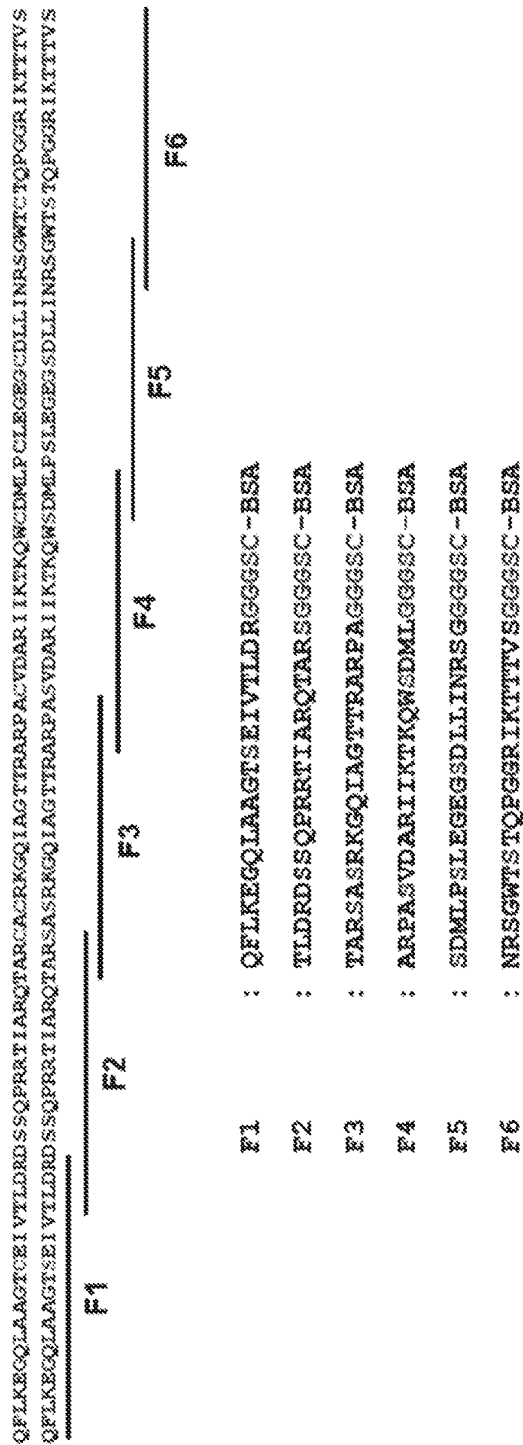


FIG. 4

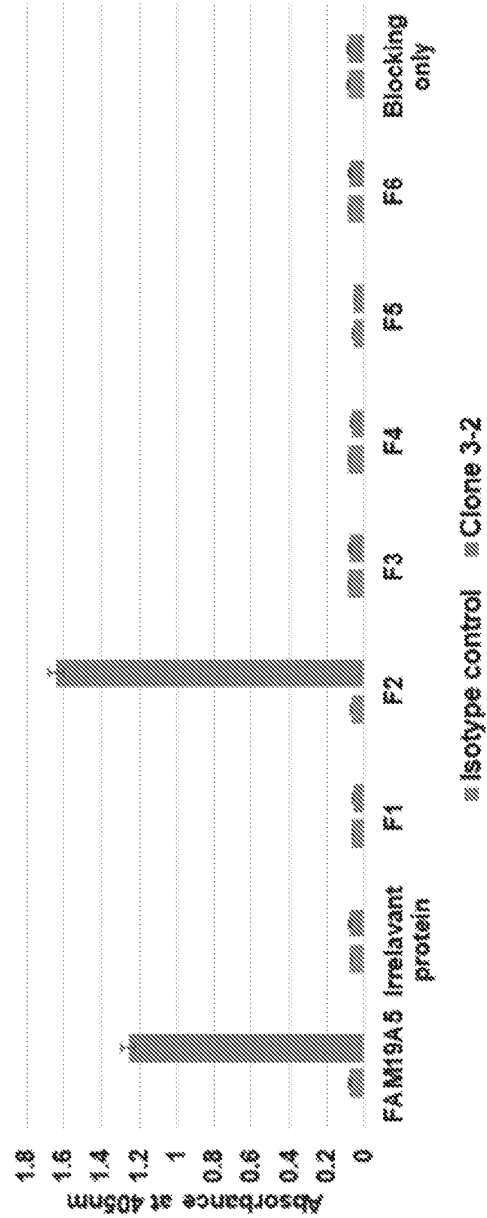


FIG. 5

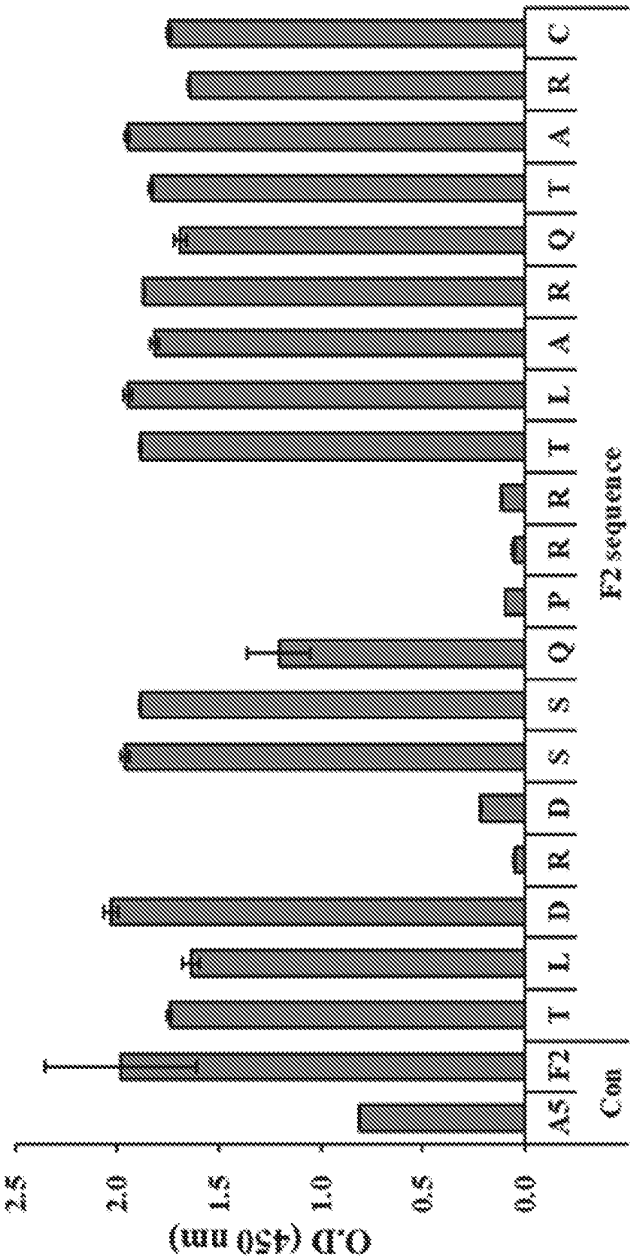


FIG. 6A

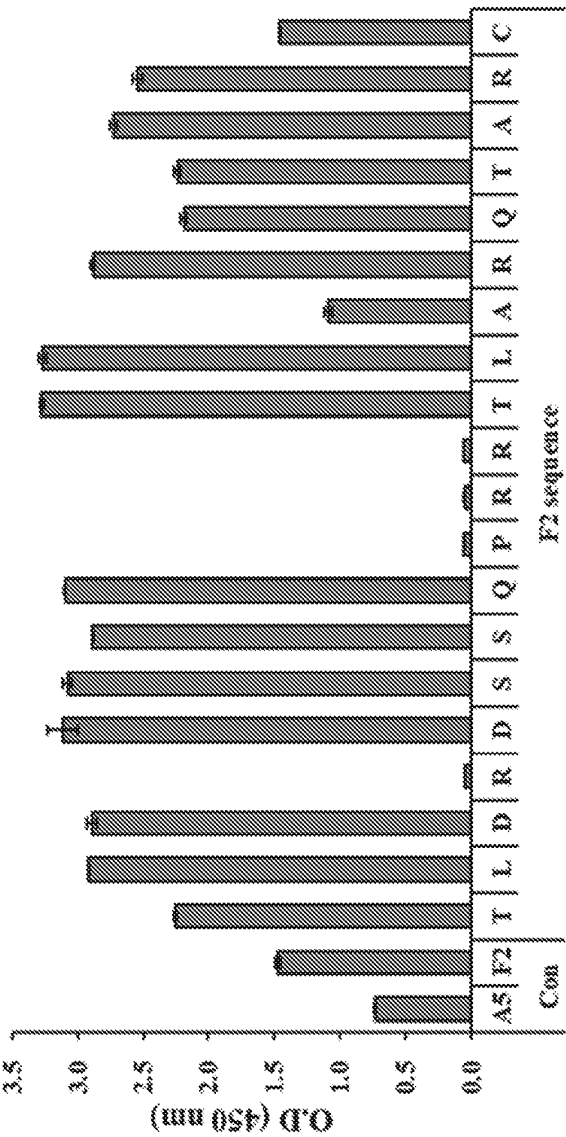


FIG. 6B

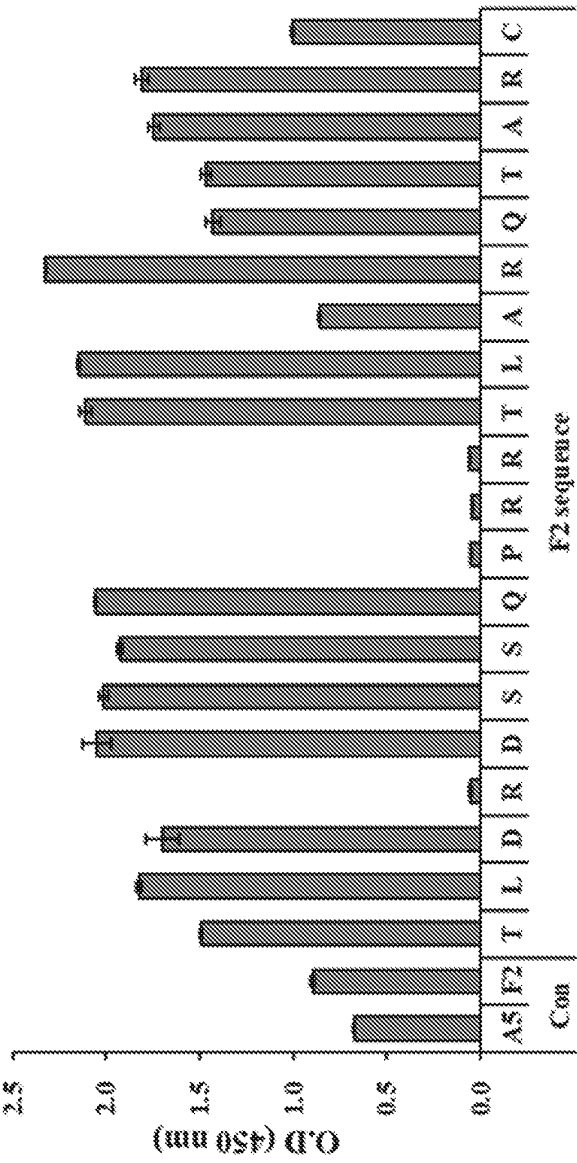


FIG. 6C

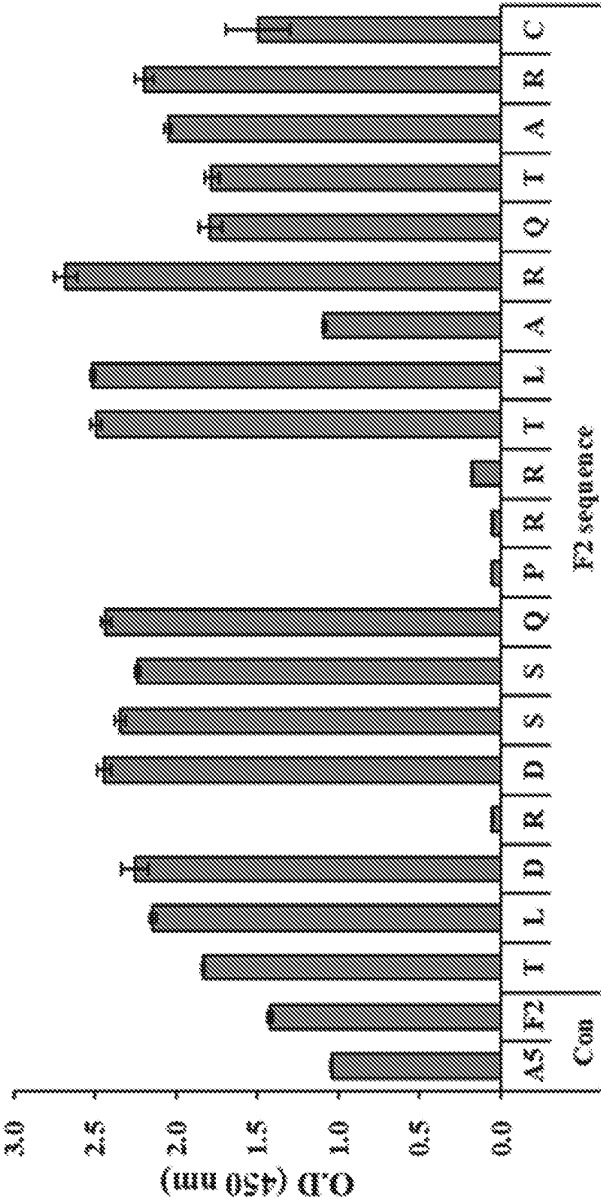


FIG. 6D

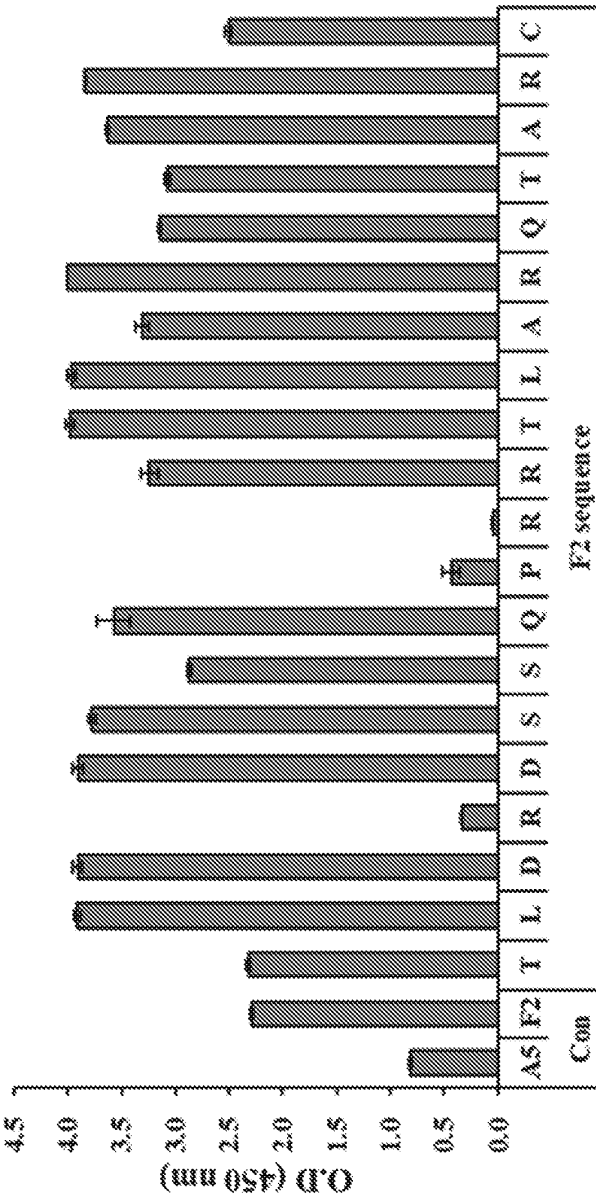


FIG. 6E

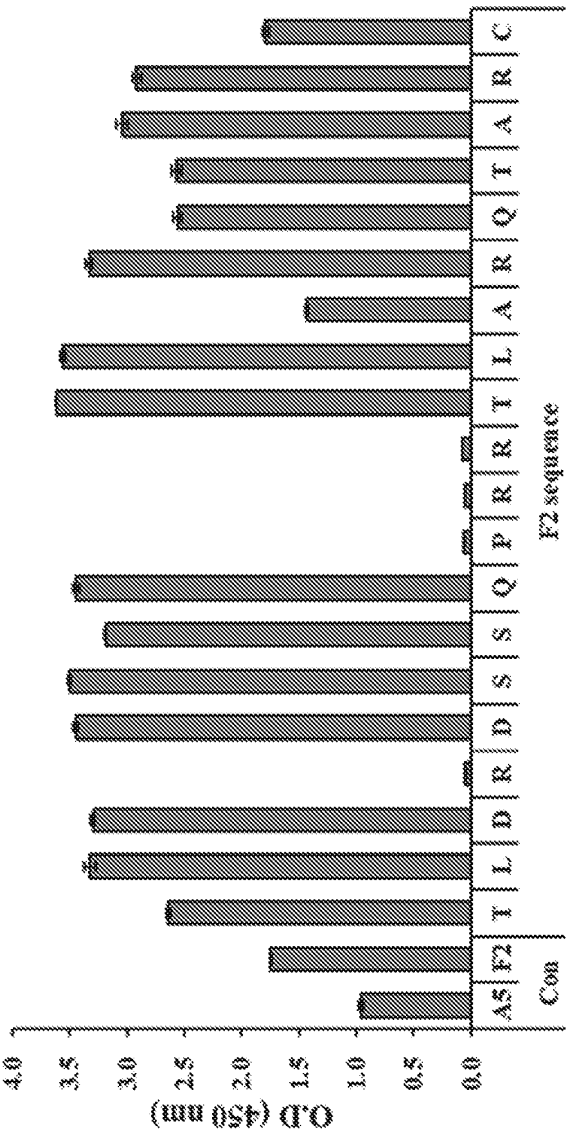


FIG. 6F

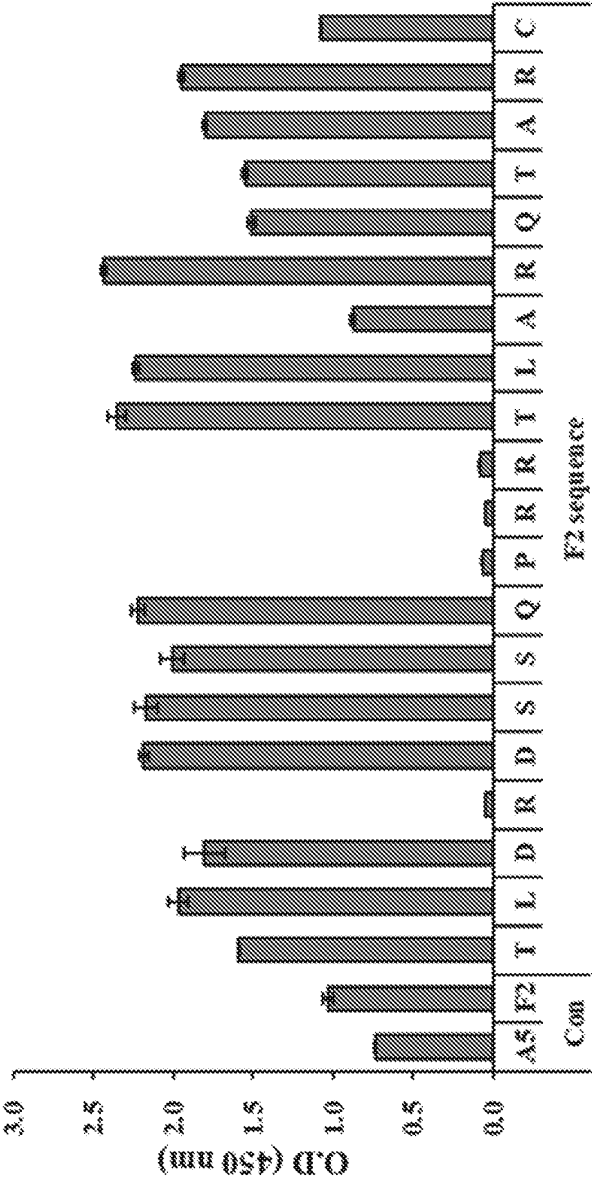


FIG. 6G

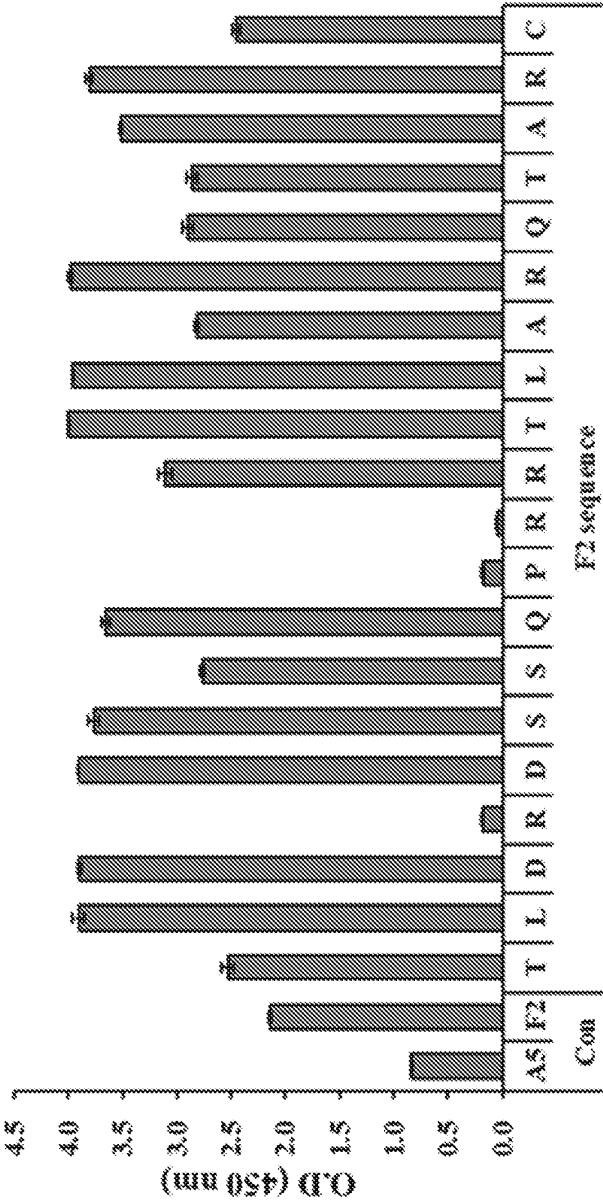


FIG. 6H

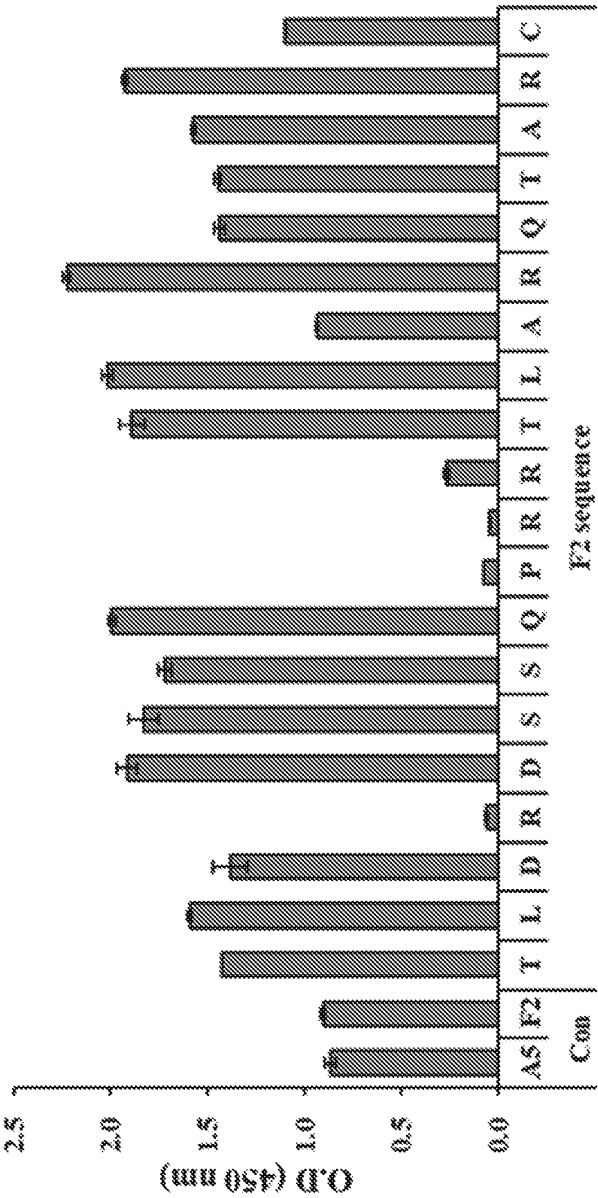


FIG. 6I

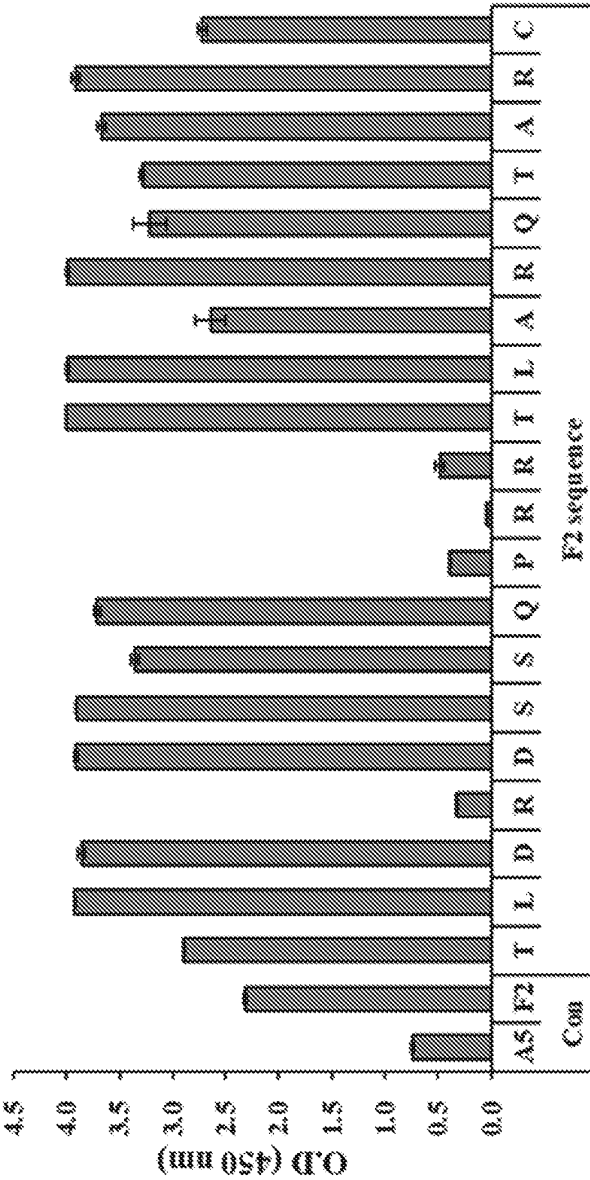


FIG. 6J

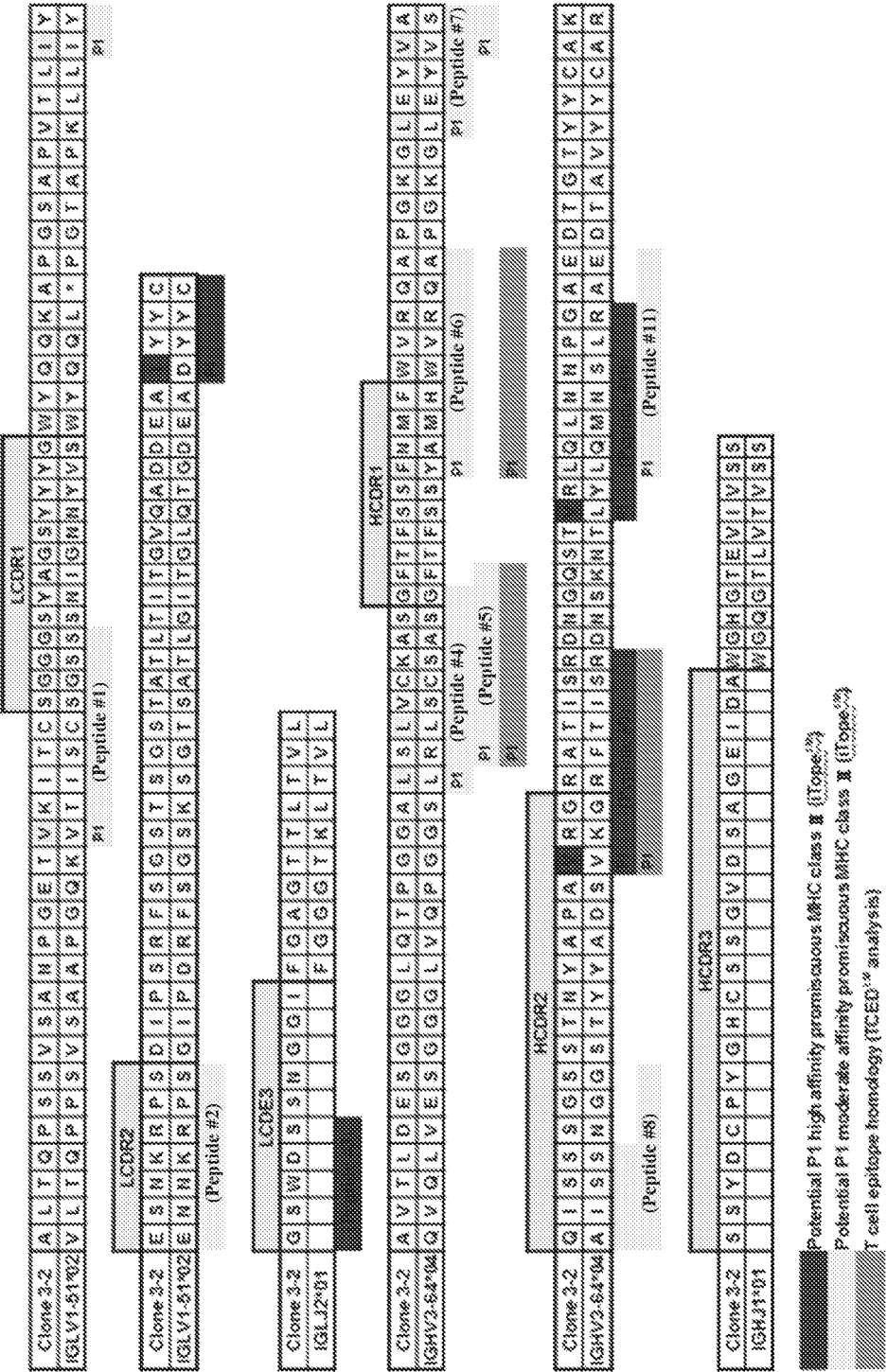


FIG. 7

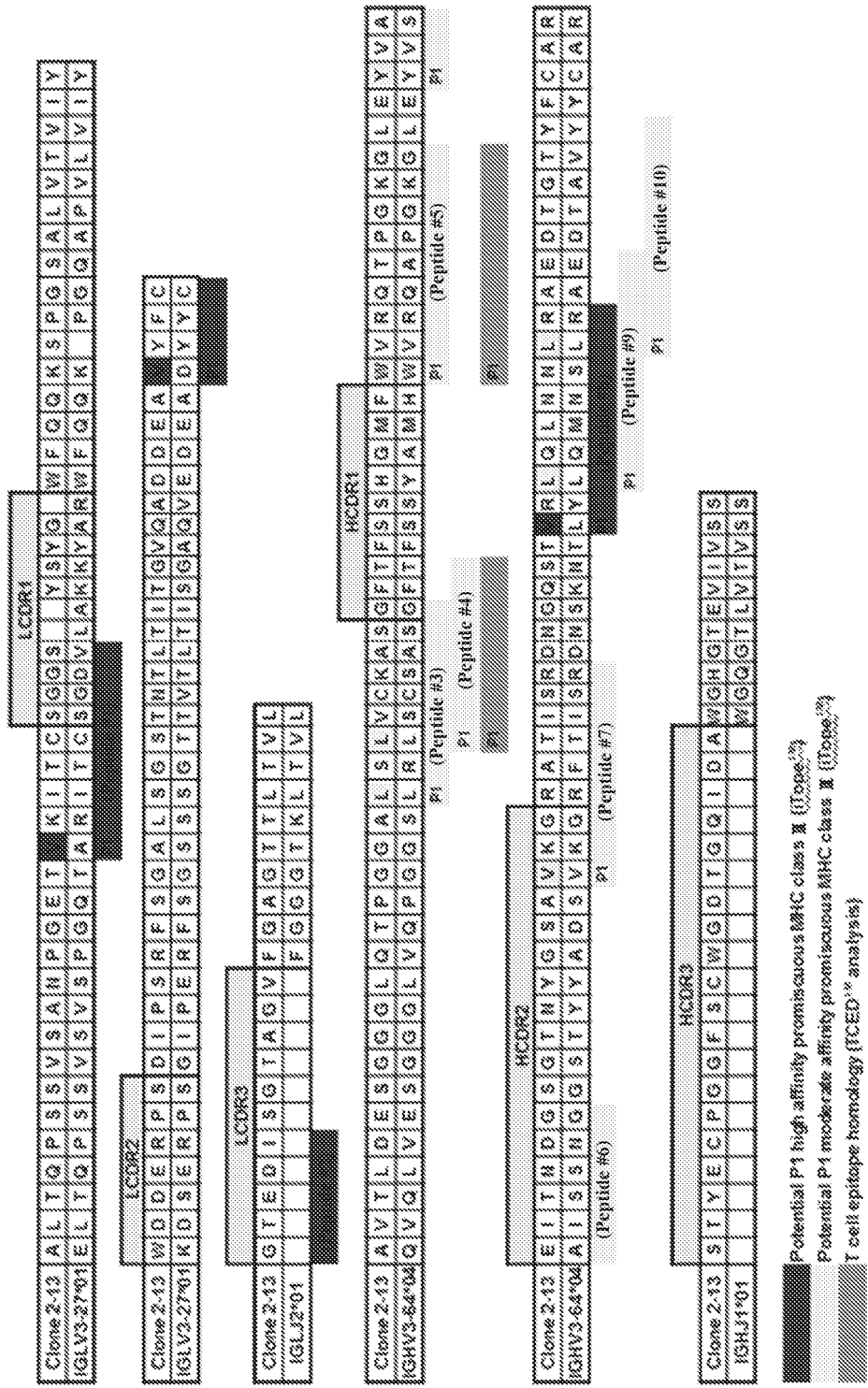


FIG. 8

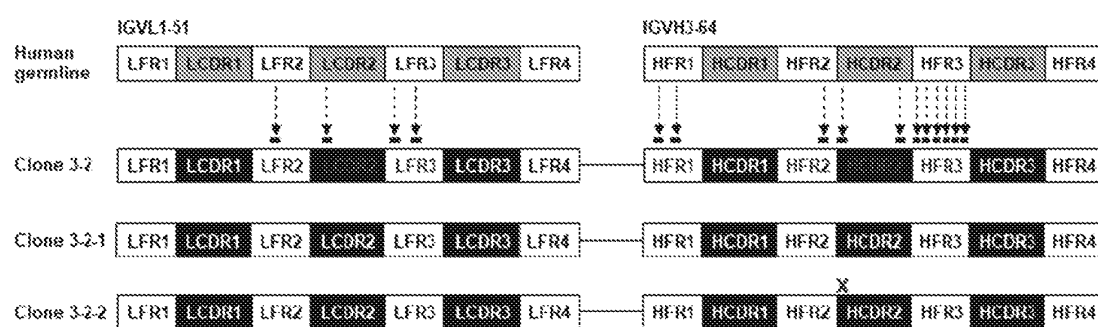


FIG. 9A

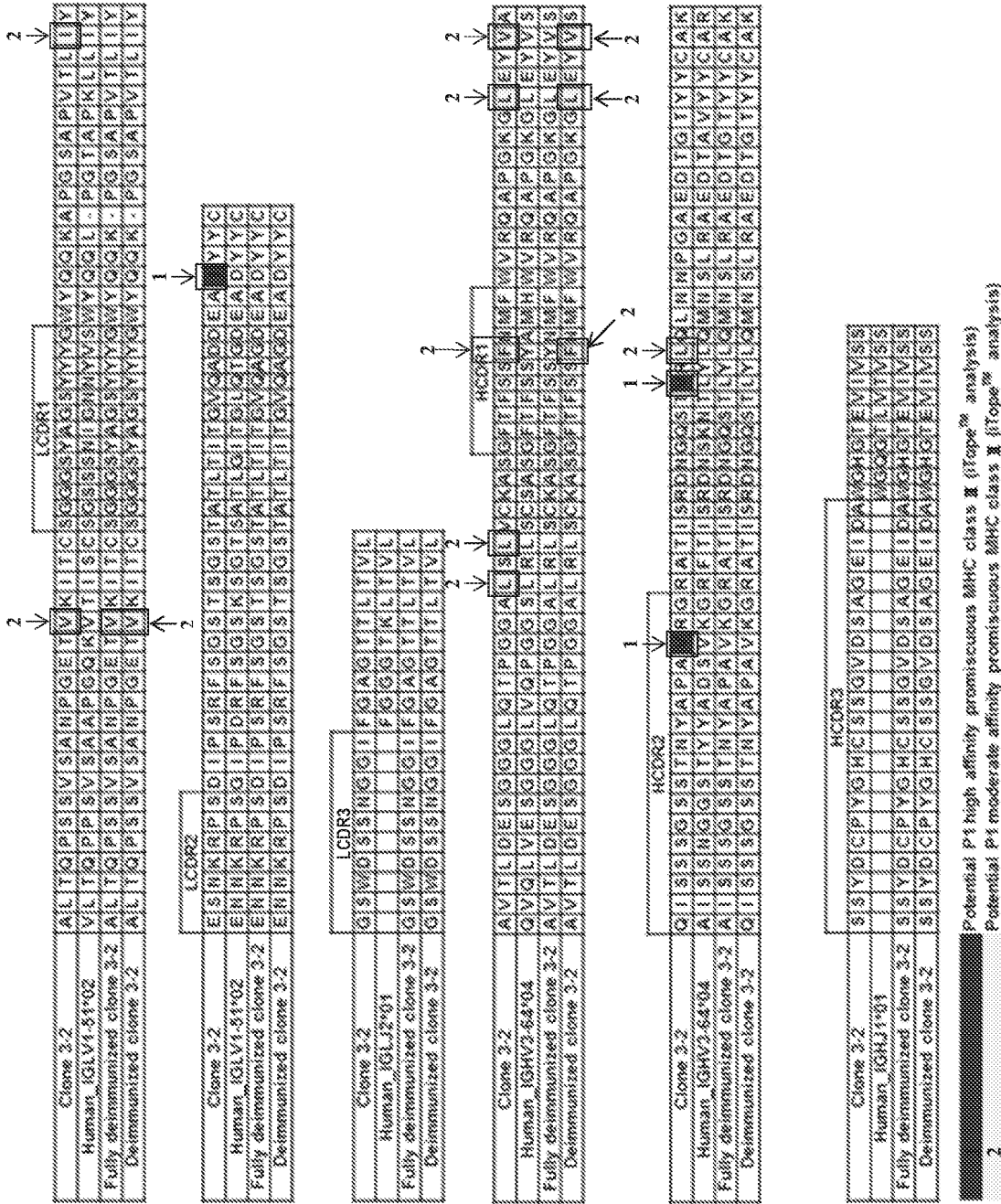


FIG. 9B

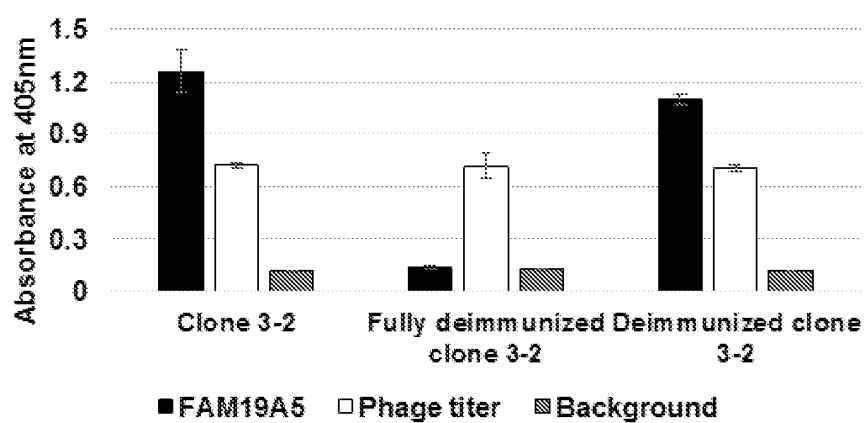


FIG. 9C



FIG. 10A

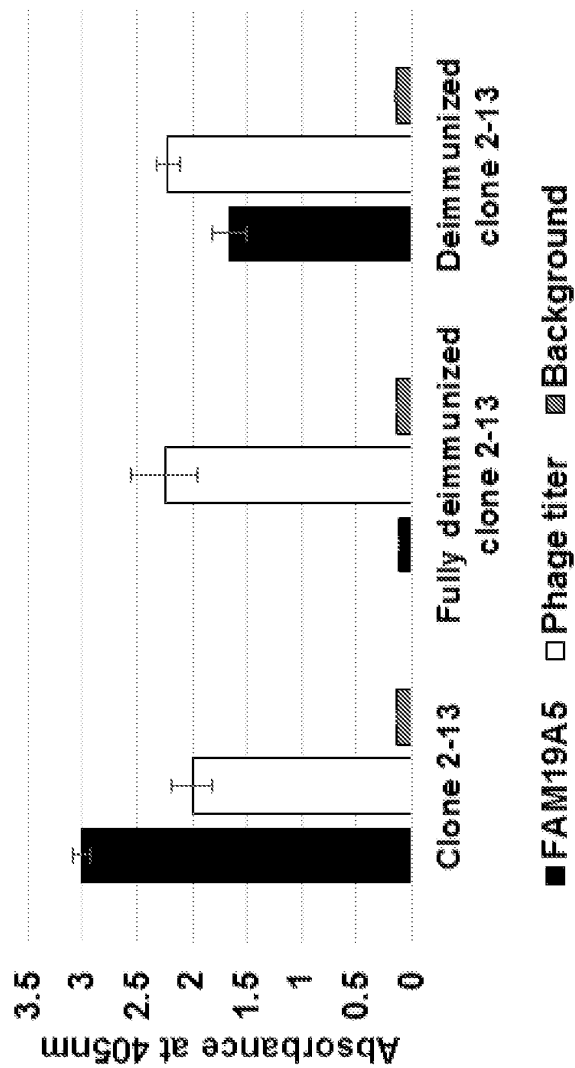


FIG. 10B

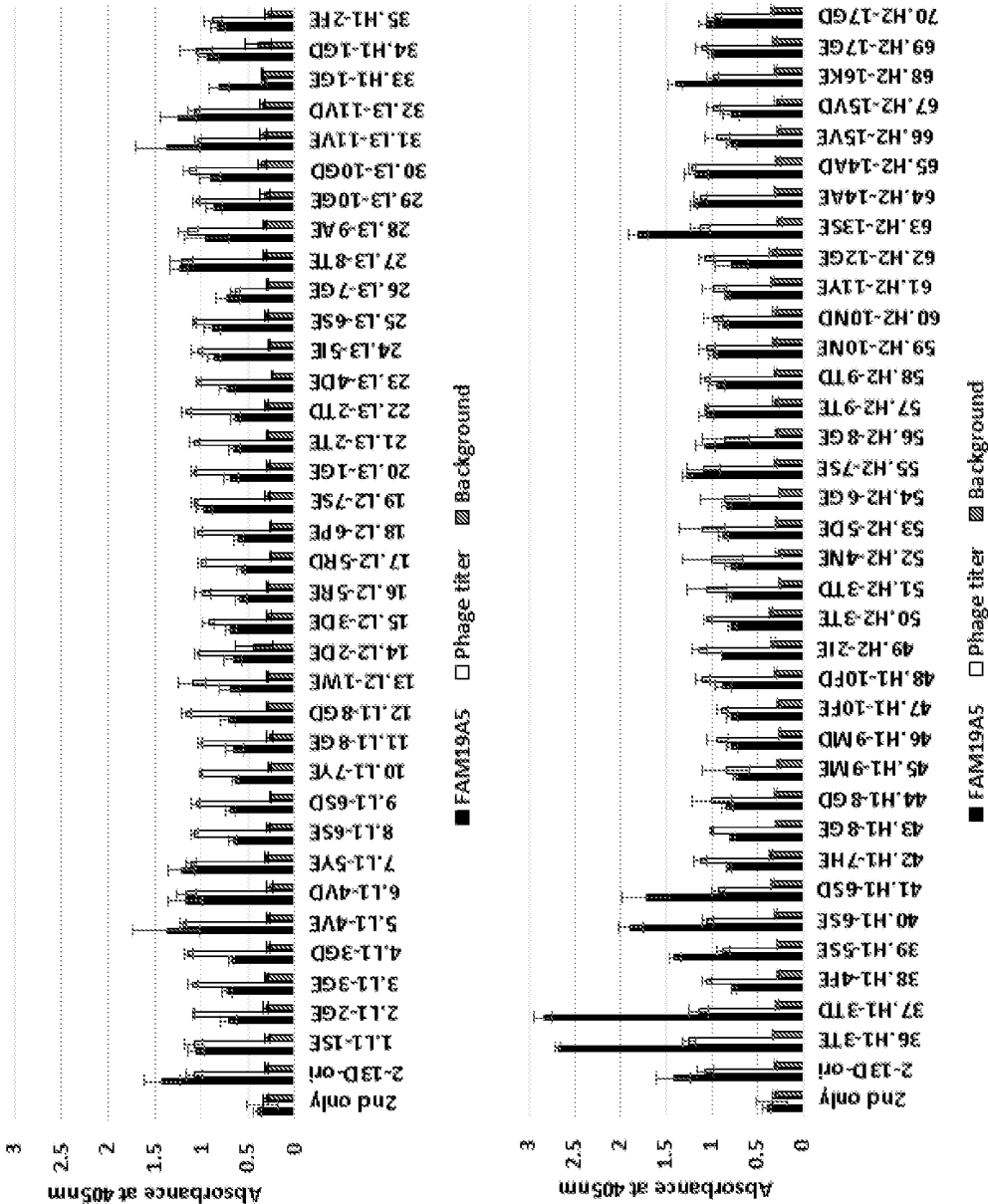


FIG. 11

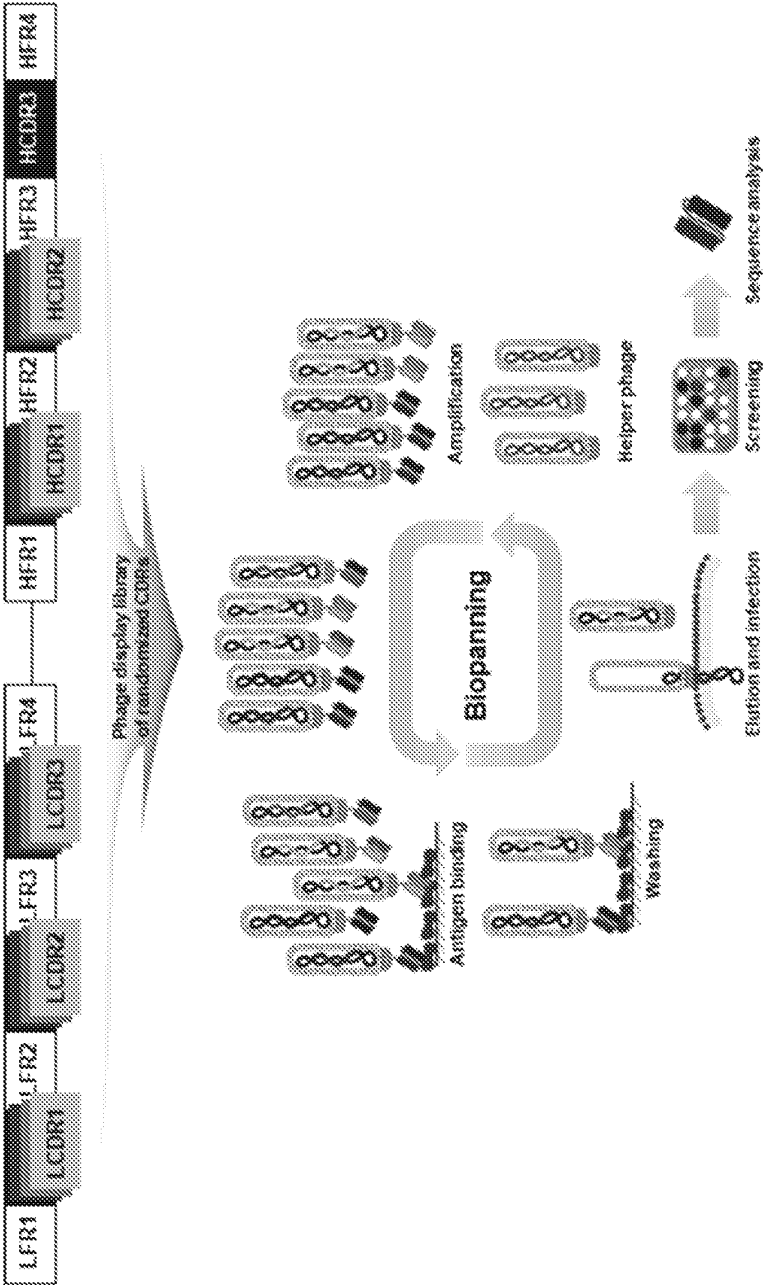


FIG. 12

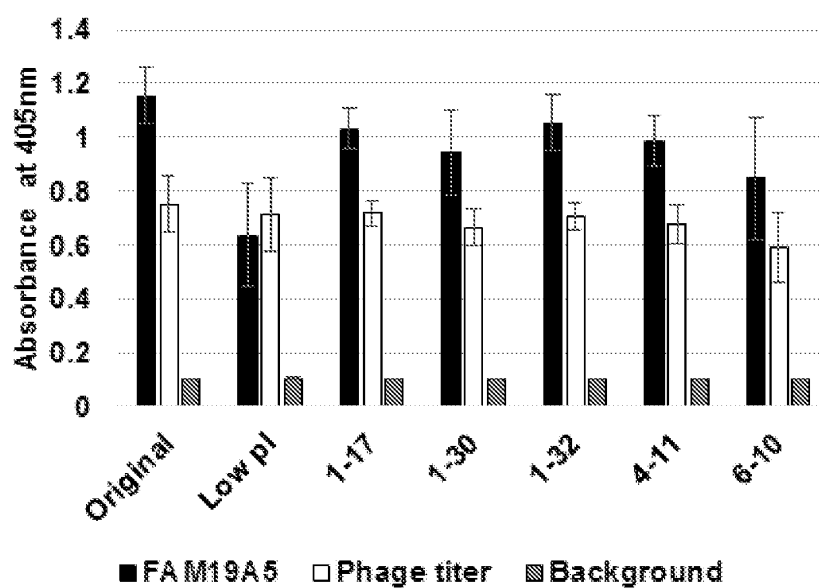
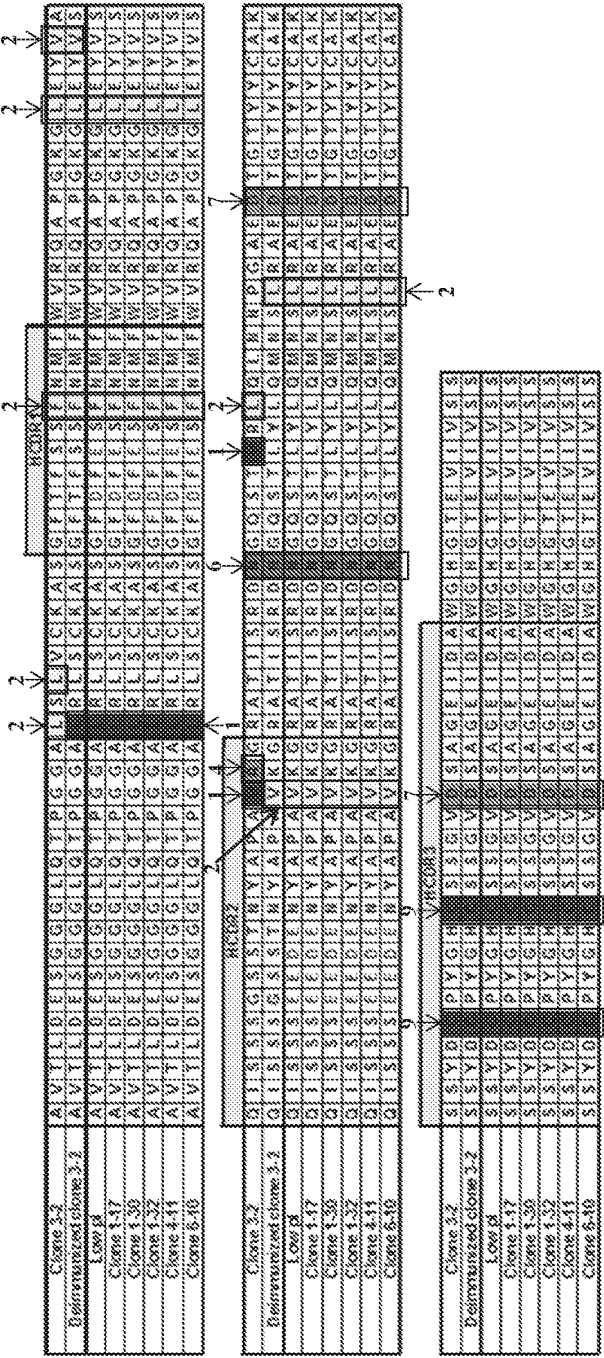


FIG. 13A

Clone	CamSol score	GRAVY score
Original	0.177	-0.384
Low pl	0.991	-0.465
1-17	0.734	-0.445
1-30	0.906	-0.465
1-32	0.717	-0.445
4-11	0.681	-0.441
6-10	0.378	-0.401

FIG. 13B



- Potential P4 high affinity promiscuous MHC class II
- Potential P4 moderate affinity promiscuous MHC class II
- Differences in closest human germline sequence
- Potential arginine or lysine methylation
- Potential tryptophan or methionine oxidation
- Potential asparagine deamidation
- Potential asparagine isomerization
- Rare amino acid insertion
- Free cysteine or non-canonical cysteine pair

FIG. 14A

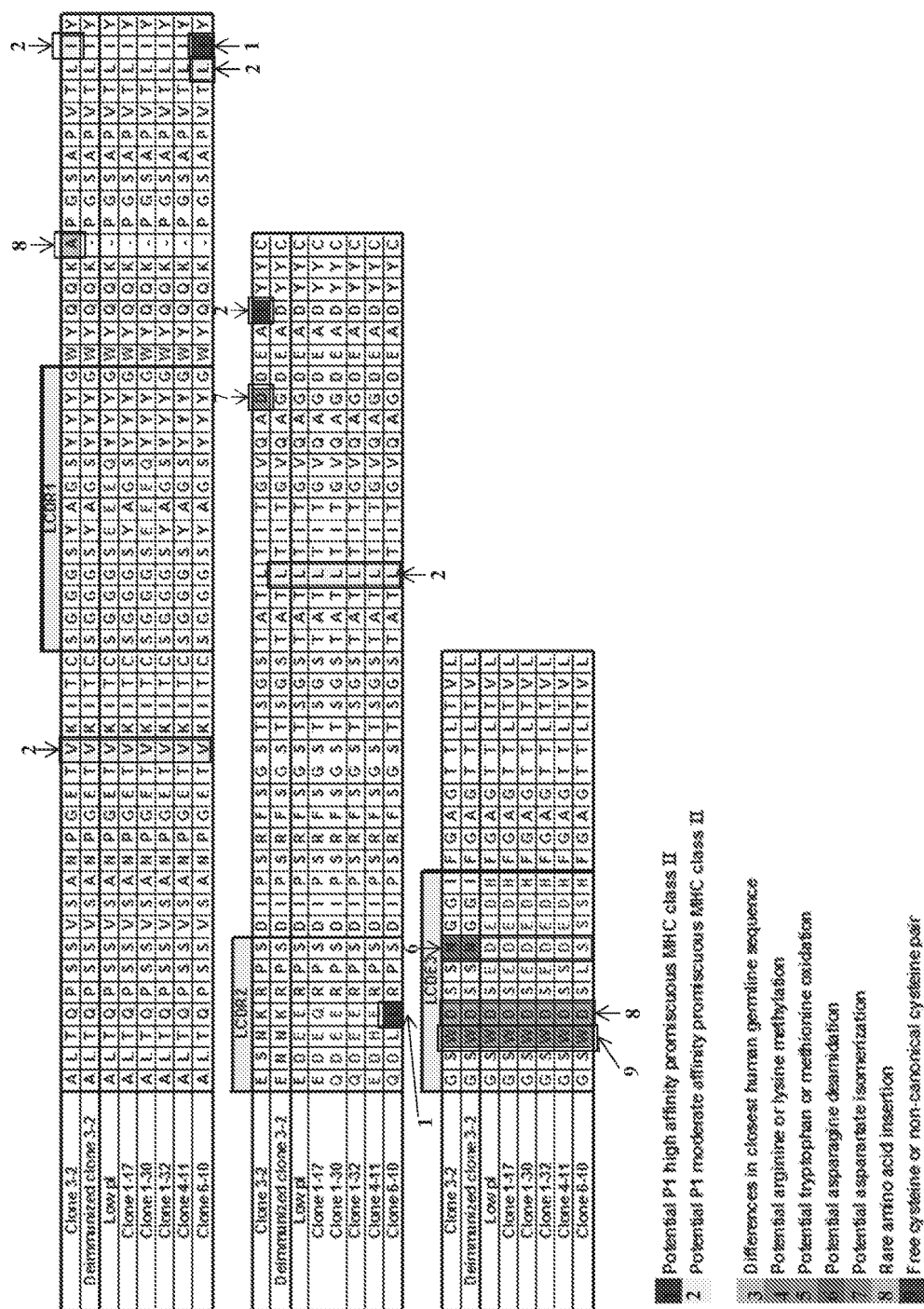
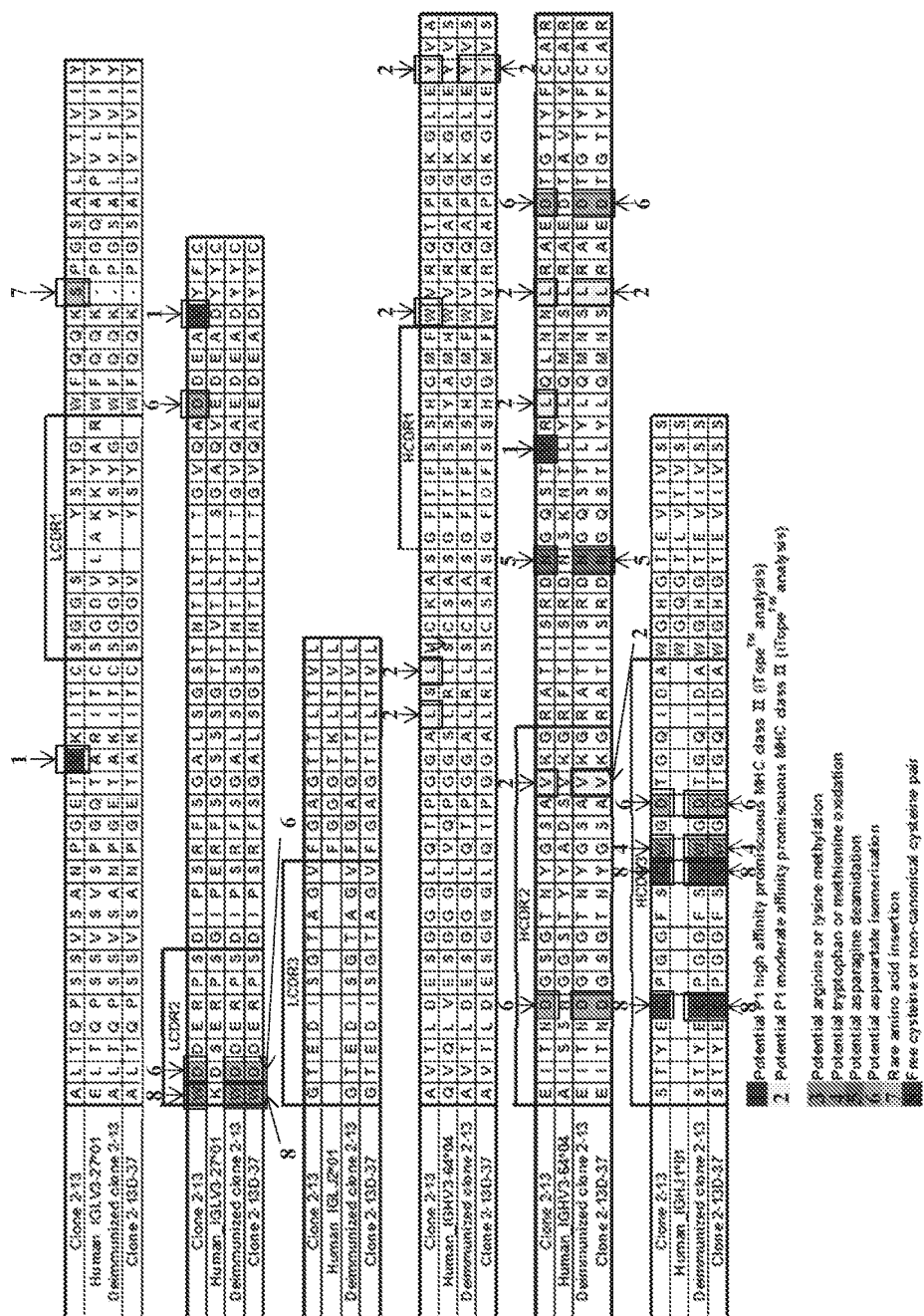


FIG. 14B



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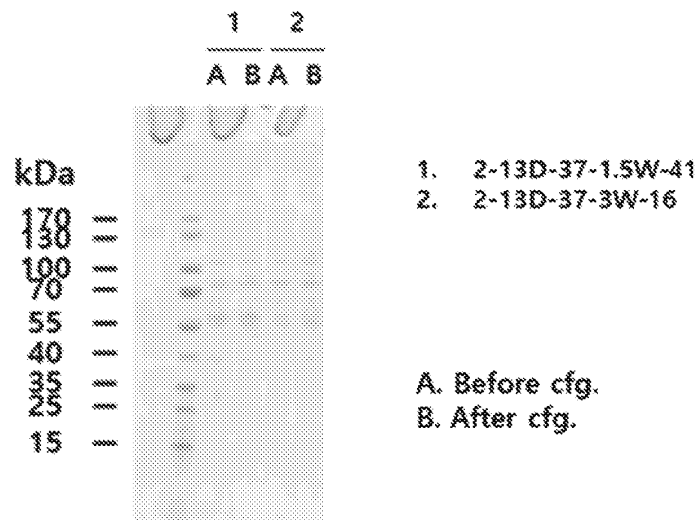


FIG. 16A

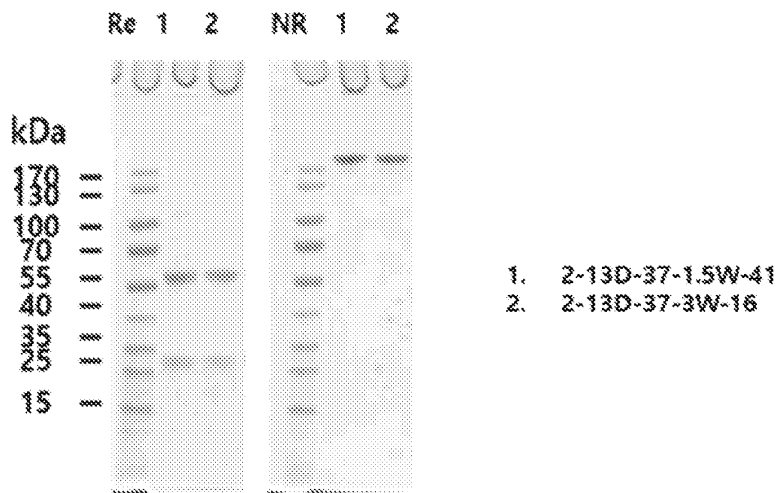


FIG. 16B

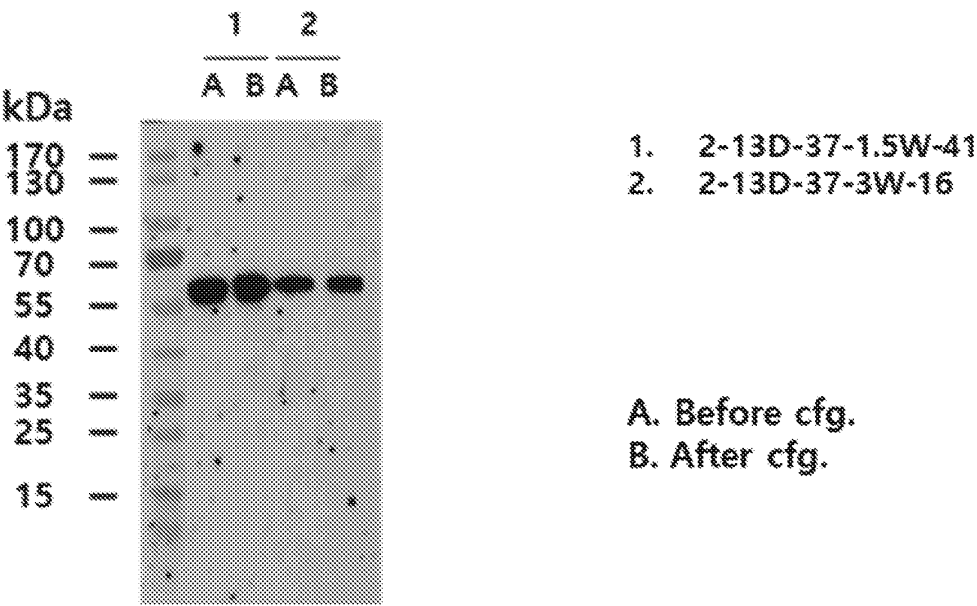


FIG. 16C

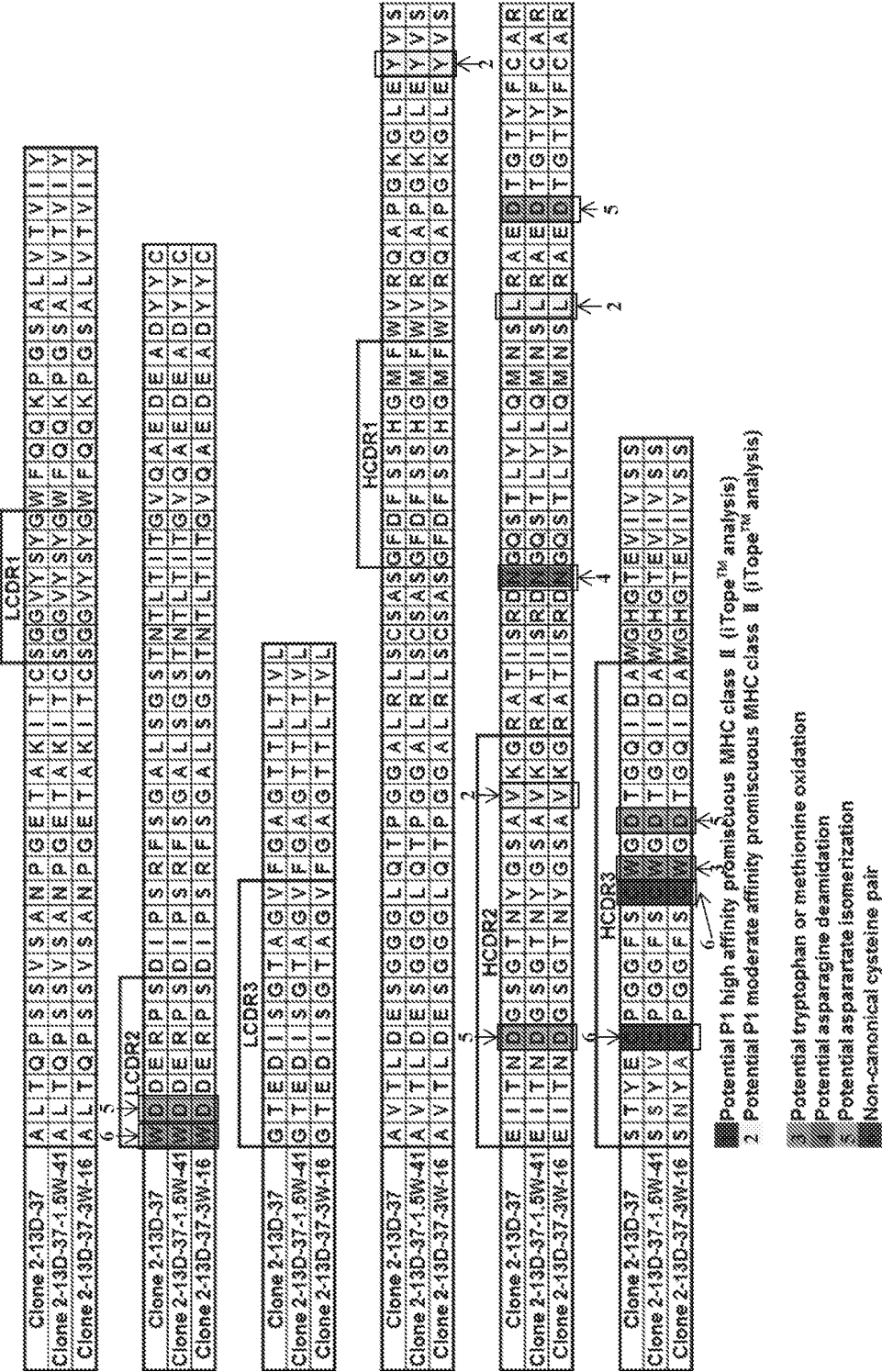


FIG. 17A

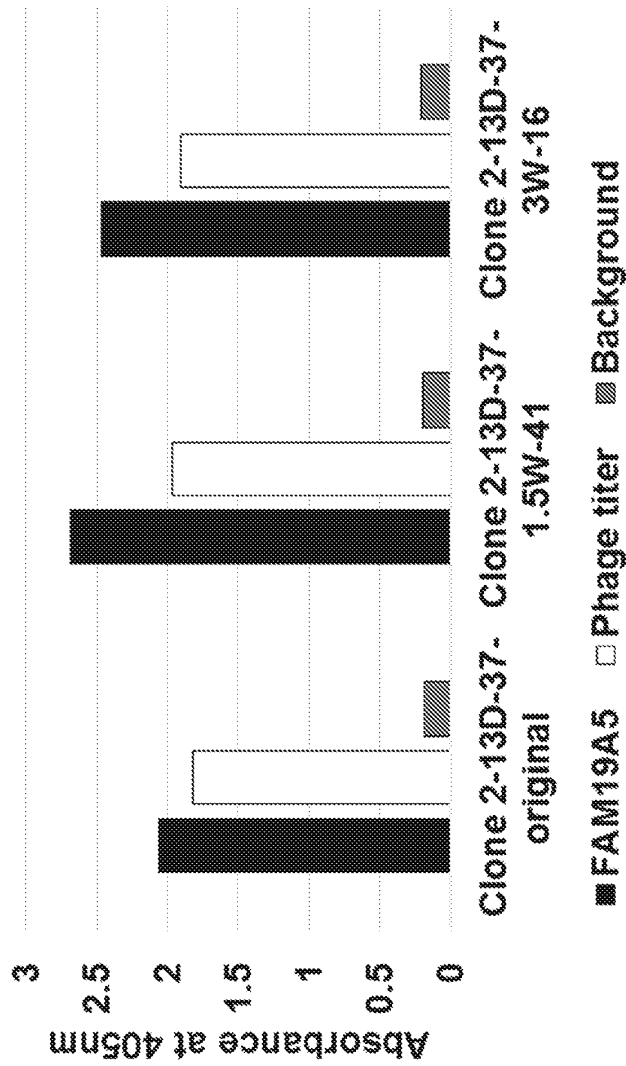


FIG. 17B

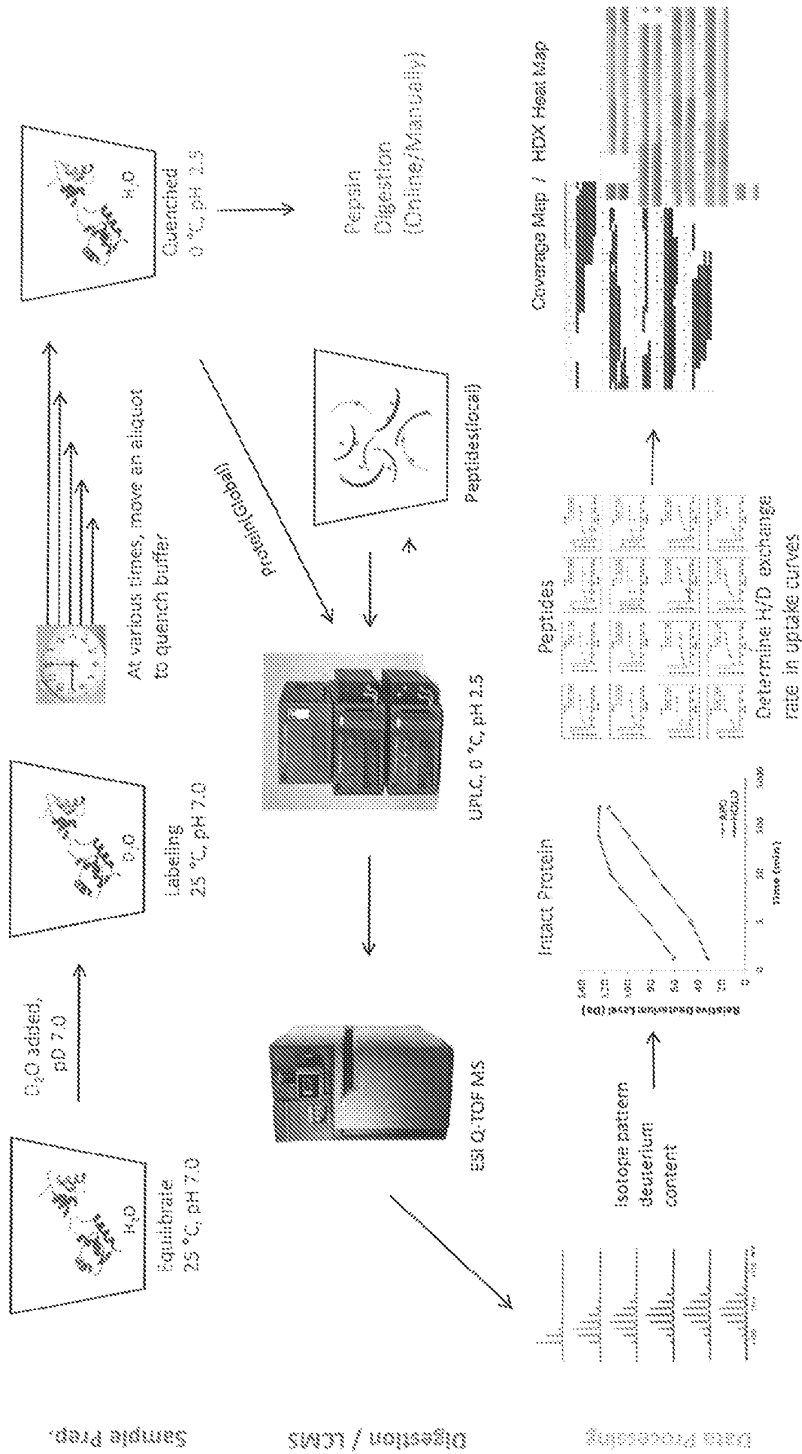


FIG. 18

Sample Conc.	Quench condition	Roxy system or Gradient type	Pepsin (on ice 5min)	Quench holding time (min)	Coverage (%)
Pepsin column(on), C18					
30pmol	100mM K.phosphate pH 2.66	FG			19.1
30pmol	100mM K.phosphate, 500mM TCEP, 2M guanidine-HCl pH 2.66	FG			65.0
30pmol	100mM K.phosphate, 500mM TCEP, 4M guanidine-HCl pH 2.66	FG			19.6
30pmol	100mM K.phosphate, 500mM TCEP pH 2.66	FG			65.0
40pmol	100mM K.phosphate, 250mM TCEP, 2M guanidine-HCl pH 2.66	FG			43.9
40pmol	200mM Na.phosphate, 500mM TCEP, 2M guanidine-HCl pH 2.66	FG			26.5
40pmol	His-tag 100mM K.phosphate, 500mM TCEP, 2M guanidine-HCl pH 2.66	FG			37.6
40pmol	100mM K.phosphate, 500mM TCEP, 2M guanidine-HCl pH 2.66	FG	5		72.0
40pmol	100mM K.phosphate, 500mM TCEP, 2M guanidine-HCl pH 2.66	FG	5		72.0
40pmol	100mM K.phosphate, 500mM TCEP, 2M guanidine-HCl pH 2.66	FG	5		89.0
40pmol	100mM K.phosphate, 500mM TCEP, 2M guanidine-HCl pH 2.66	FG	5		93.0
40pmol	100mM K.phosphate, 500mM TCEP, 2M guanidine-HCl pH 2.66	FG	5		80.0
40pmol	100mM K.phosphate, 500mM TCEP, 2M guanidine-HCl pH 2.66	FG	5		72.0
40pmol	100mM K.phosphate, 500mM TCEP, 2M guanidine-HCl pH 2.66	FG	5		72.0
Pepsin column(on), C18, Concentration sample					
40pmol	100mM K.phosphate, 500mM TCEP, 2M guanidine-HCl pH 2.66	FG	5		90.0
40pmol	100mM K.phosphate, 500mM TCEP, 2M guanidine-HCl pH 2.66	FG	5		92.0
40pmol	100mM K.phosphate, 500mM TCEP, 2M guanidine-HCl pH 2.66	FG	5		72.0
40pmol	100mM K.phosphate, 500mM TCEP, 2M guanidine-HCl pH 2.66	FG	5		76.0
40pmol	100mM K.phosphate, 500mM TCEP, 2M guanidine-HCl pH 2.66	FG	5		77.6
40pmol	100mM K.phosphate, 500mM TCEP, 2M guanidine-HCl pH 2.66	FG	5		92.0
40pmol	100mM K.phosphate, 150mM TCEP pH 2.66	FG			43.9
40pmol	200mM Na.phosphate, 750mM TCEP, 4M guanidine-HCl pH 2.66	FG			19.0
40pmol	100mM K.phosphate, 750mM TCEP, 2M guanidine-HCl pH 2.66	FG			38.8
40pmol	100mM TCEP, 400mM guanidine-HCl pH 2.66	FG			38.8
40pmol	500mM K.phosphate, 375mM TCEP, 1M guanidine-HCl pH 2.66	FG			43.9
40pmol	100mM K.phosphate, 500mM TCEP, 1M guanidine-HCl pH 2.66	FG			84.1
40pmol	1M TCEP, 2M U pH 2.66	FG			68.4
40pmol	500mM TCEP, 1M U pH 2.66	FG			48.0
40pmol	1M TCEP, 2M U pH 1.7	FG	5		95.0
45pmol	1M TCEP, 2M U pH 2.66	FG			96.0
45pmol	1M TCEP, 2M U pH 2.66	FG	5		98.0
45pmol	1M TCEP, 2M U pH 2.66	FG		5	79.0

FIG. 19

Sample Conc.	Quench condition	Revs system or Gradient type	Pepsin (on ice 5min)	Quench holding time (min)	Coverage (%)
Pepsin column(on), C18, Concentration sample					
45pmol	1M TCEP, 2M U pH 2.66	FG	1:2(5)		92.0
45pmol	1M TCEP, 2M U pH 2.66	FG	1:2(5)		93.9
45pmol	1M TCEP, 2M U pH 2.66	FG	1:2(5)		94.0
45pmol	1M TCEP, 2M U pH 2.66	FG	1:2(5)		76.0
45pmol	1M TCEP, 2M U pH 2.66	FG	1:2(5)		94.0
45pmol	1M TCEP, 2M U pH 2.66	FG	1:2(5)		80.0
45pmol	1M TCEP, 2M U pH 2.66	FG	1:3(5)		85.0
Waters Pepsin column(on), C18					
45pmol	1M TCEP, 2M U pH 2.66	FG	1:2(5)		99.0
45pmol	1M TCEP, 2M U pH 2.66	FG	1:2(5)		97.0
45pmol	1M TCEP, 2M U pH 2.66	FG	1:2(5)		97.0
45pmol	1M TCEP, 2M U pH 2.66	FG	1:2(5)		92.0
45pmol	1M TCEP, 2M U pH 2.66	FG	1:2(5)		97.0
45pmol	1M TCEP, 2M U pH 2.66	FG	1:2(5)		92.0
Pepsin column(on), C8					
40pmol	His-tag; 100mM K.phosphate, 500mM TCEP, 2M guanidine-HCl pH 2.66	FG			29.5
40pmol	His-tag; 100mM K.phosphate, 500mM TCEP, 2M guanidine-HCl pH 2.66	FG	5		52.0
40pmol	100mM K.phosphate, 500mM TCEP, 2M guanidine-HCl pH 2.66	FG			57.0
40pmol	100mM K.phosphate, 500mM TCEP, 2M guanidine-HCl pH 2.66	FG	5		79.8
Pepsin column(off), C8					
40pmol	100mM K.phosphate, 500mM TCEP, 2M guanidine-HCl pH 2.66	FG	5		20.8

FIG. 19
(cont'd)

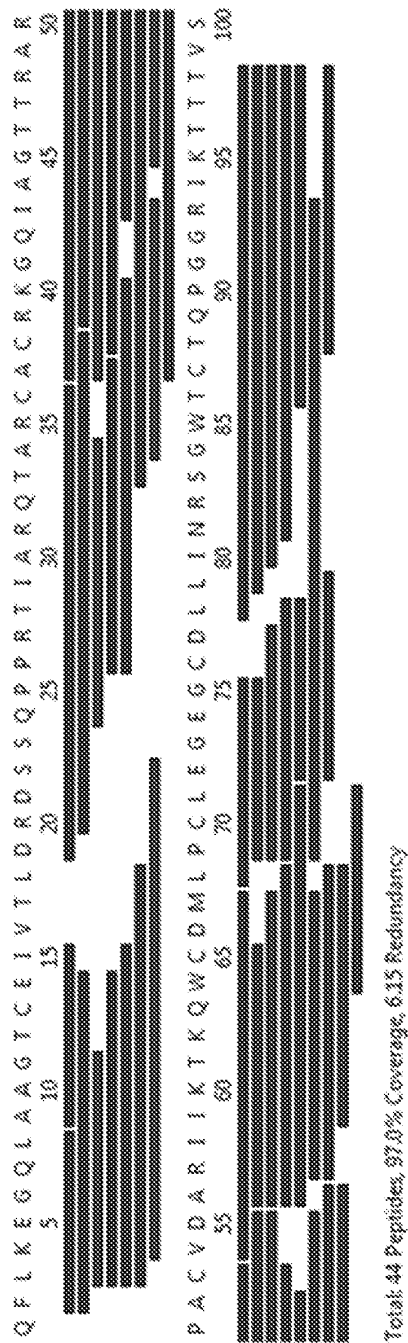


FIG. 20A

Sequence	Start	End	MHP	RT
FAM19A5_HUMAN				
FLKEGQL	2	8	834.4720	6.56
FLKEGQLAAGTCE	2	14	1366.6571	6.34
LKEGQLAAG	3	11	886.4993	5.30
LKEGQLAAGTCE	3	14	1219.5987	5.69
LKEGQLAAGTCEI	3	15	1332.6828	6.83
LKEGQLAAGTCEVTL	3	18	1645.8829	7.71
KEGQLAAGTCEVTLDRDS	4	22	2005.9859	5.04
AAGTCEI	9	15	664.2971	6.41
DRDSSQPPRTIARQTARC	19	36	2058.0257	4.56
RDSSQPPRTIARQTARCAC	20	38	2117.0451	4.65
QPPRTIARQTA	24	34	1238.6964	6.41
PRTIARQTARCA	26	37	1343.7325	6.38
PRTIARQTARCACRK	26	40	1730.9377	4.56
TARCACRKGQIAGTTRARPACVI	33	55	2405.2071	5.89
ARCACRKGQI	34	43	1105.5717	5.45
ACRKGQIAGTTRARPAC	37	53	1759.9167	4.32
ACRKGQIAGTTRARPACVD	37	55	1974.0120	4.63
ACRKGQIAGTTRARPACVDA	37	56	2045.0491	4.77
CRKGQIAGTTRARPAC	38	53	1688.8795	4.96
RKGQIAGTTRARPACVD	39	55	1799.9657	5.77
IAGTTRARPA	43	52	1013.5851	6.21
GTTRARPACVDA	45	56	1217.6055	6.29
VDARIKTKQWCDM	54	67	1706.8717	6.78
ARIKTKQWC	56	65	1246.7089	5.65
ARIKTKQWCDM	56	67	1492.7763	6.38
ARIKTKQWCDML	56	68	1605.8604	7.27
ARIKTKQWCDMLPCL	56	71	1919.0064	8.15
RIKTKQWCDM	57	67	1421.7392	6.37
RIKTKQWCDML	57	68	1534.8233	7.28
IKTKQWCDML	59	68	1265.6381	7.60
WCDMLPCL	64	71	980.4038	9.97
LPCEGEG	68	75	817.3760	6.85
PCLEGE	69	75	704.2920	5.73
PCLEGECD	69	77	922.3281	6.05
PCLEGECDL	69	78	1035.4122	7.42
PCLEGECDLLINRSOWTCTQPC	69	93	2662.2170	8.79
EGEGCDL	72	78	722.2661	6.48
EGEGCDLL	72	79	835.3502	7.72
LLINRSOWTCTQPGGRIKTTT	78	98	2303.2289	6.42
LINRSOWTCTQPGGRIKTTT	79	98	2190.1448	5.90
INRSOWTCTQPGGRIKTTT	80	98	2077.0607	5.79
NRSGWTCTQPGGRIKTTT	81	98	1963.9767	5.71
TCTQPGGRIKTTT	86	98	1363.6998	5.67
TQPGGRIKTTT	88	98	1159.6430	5.40

FIG. 20B

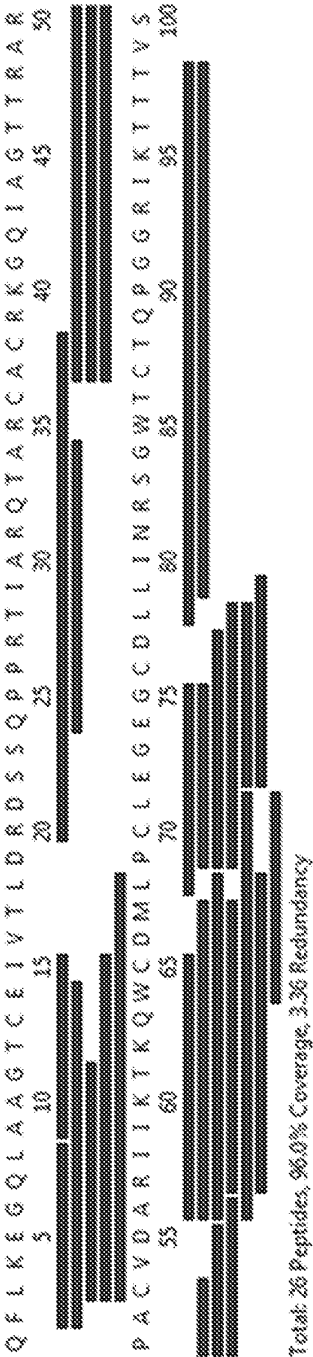


FIG. 21

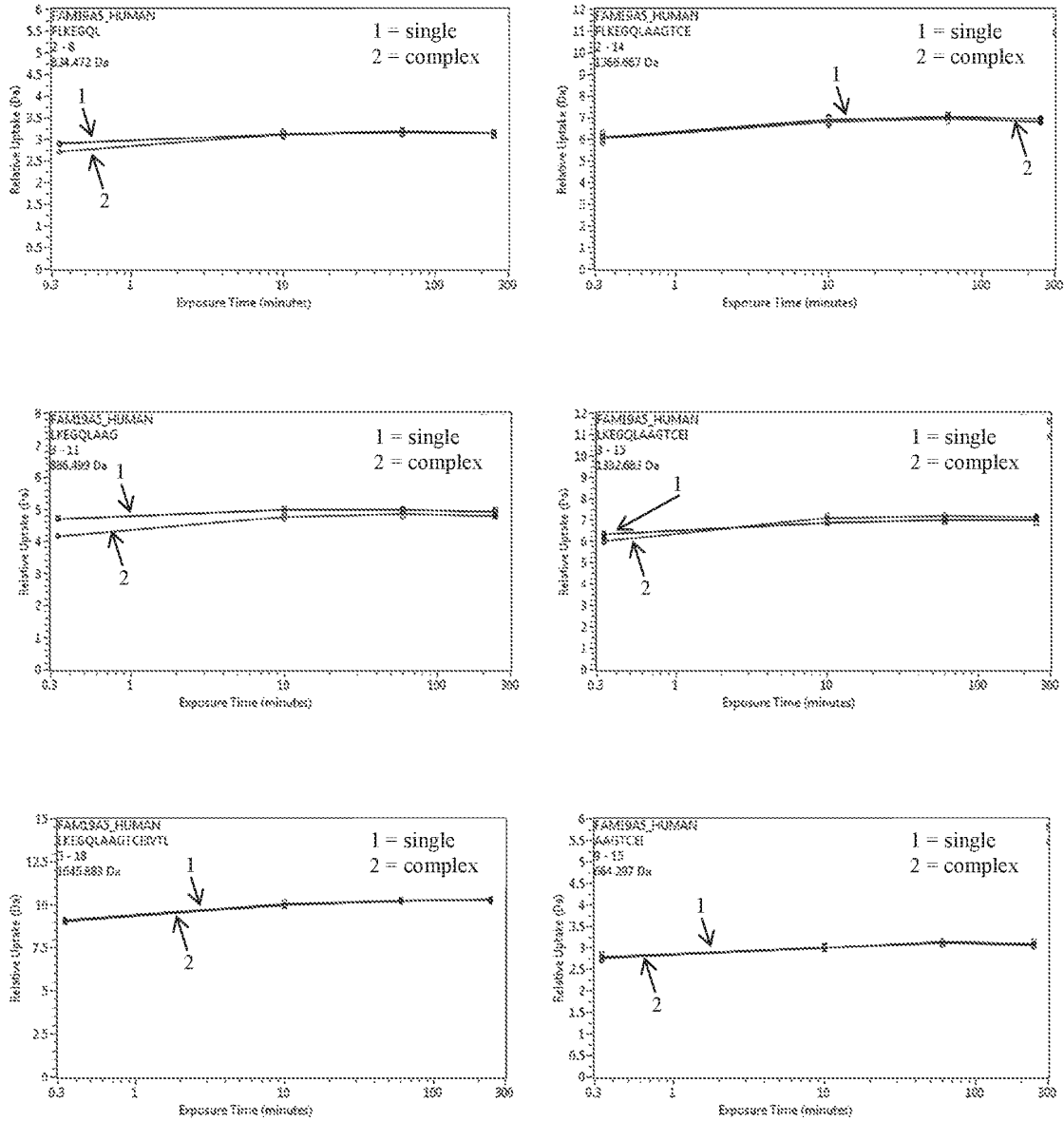


FIG. 22A

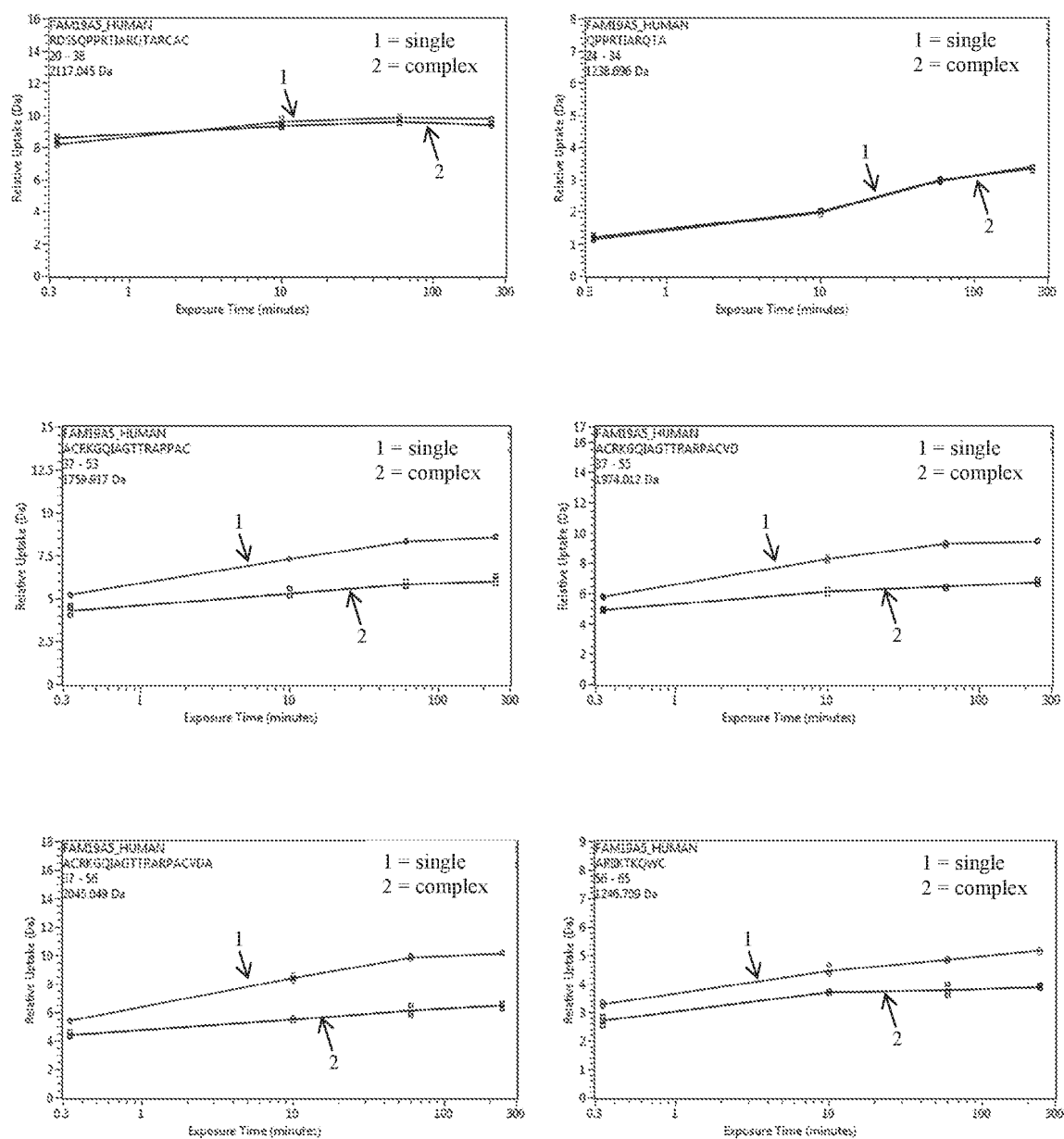


FIG. 22B

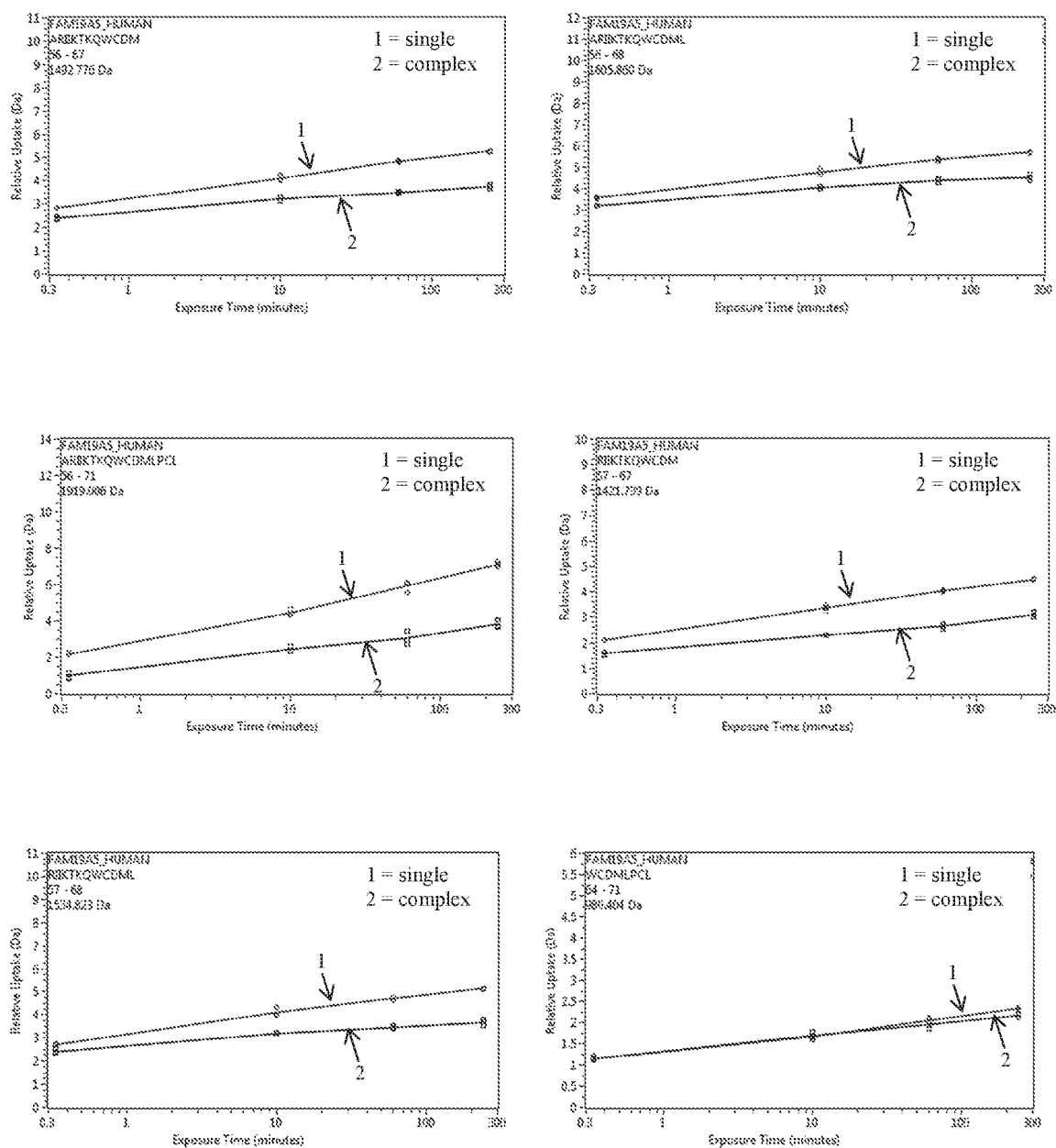


FIG. 22C

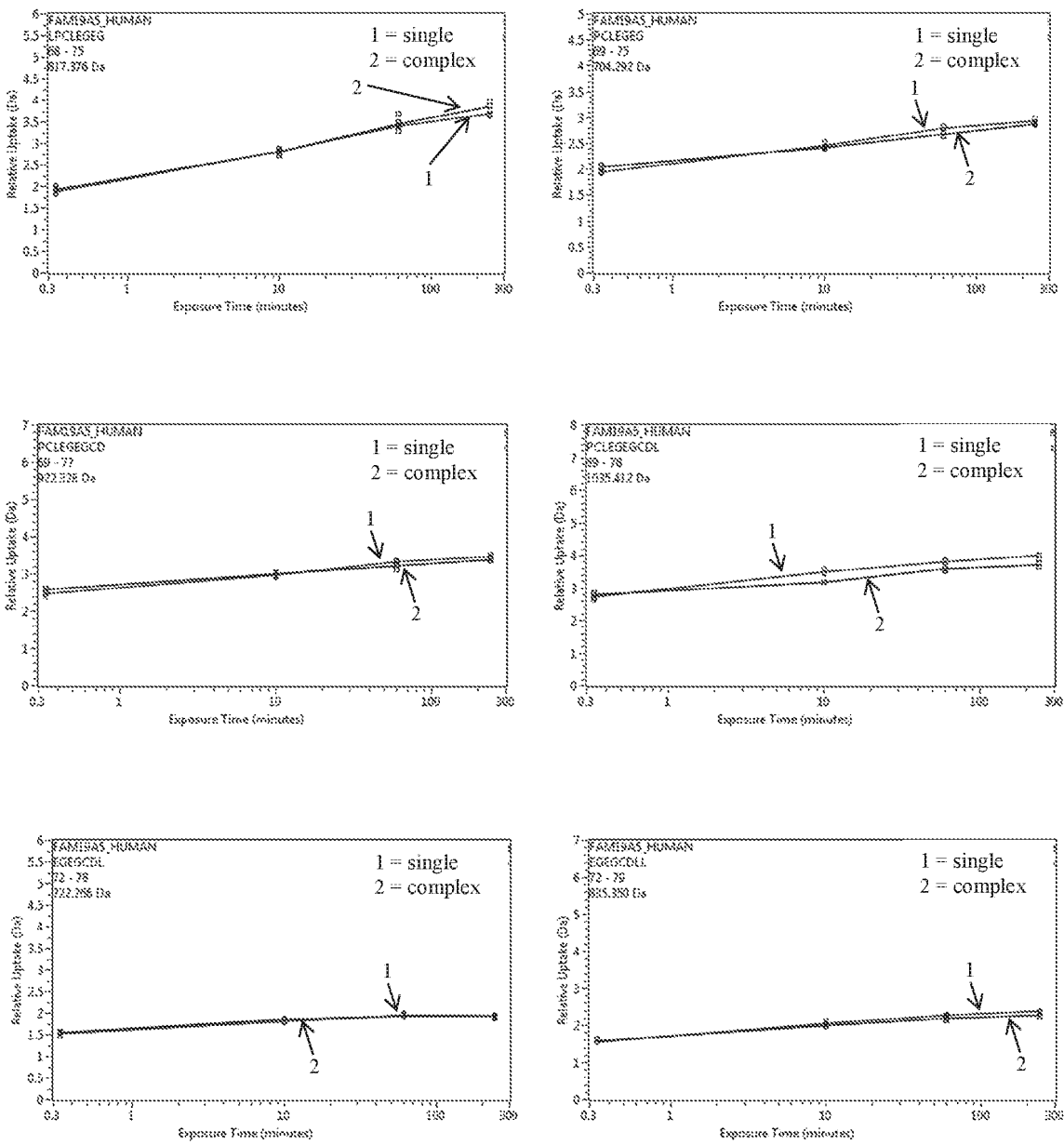


FIG. 22D

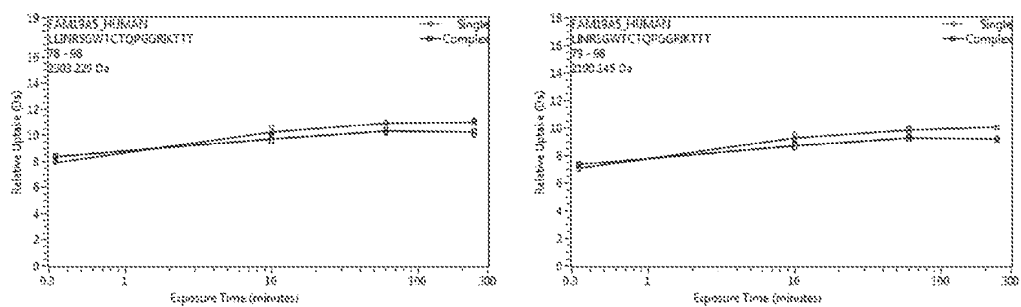


FIG. 22E

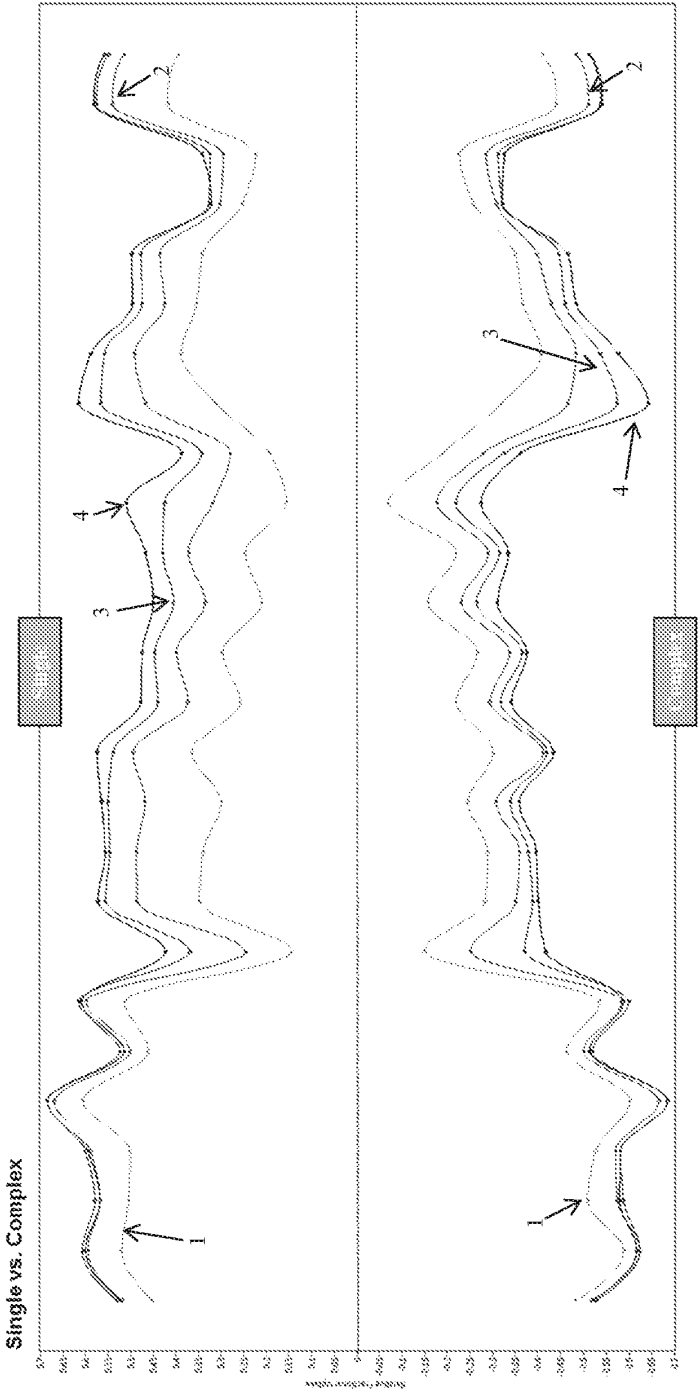


FIG. 23A

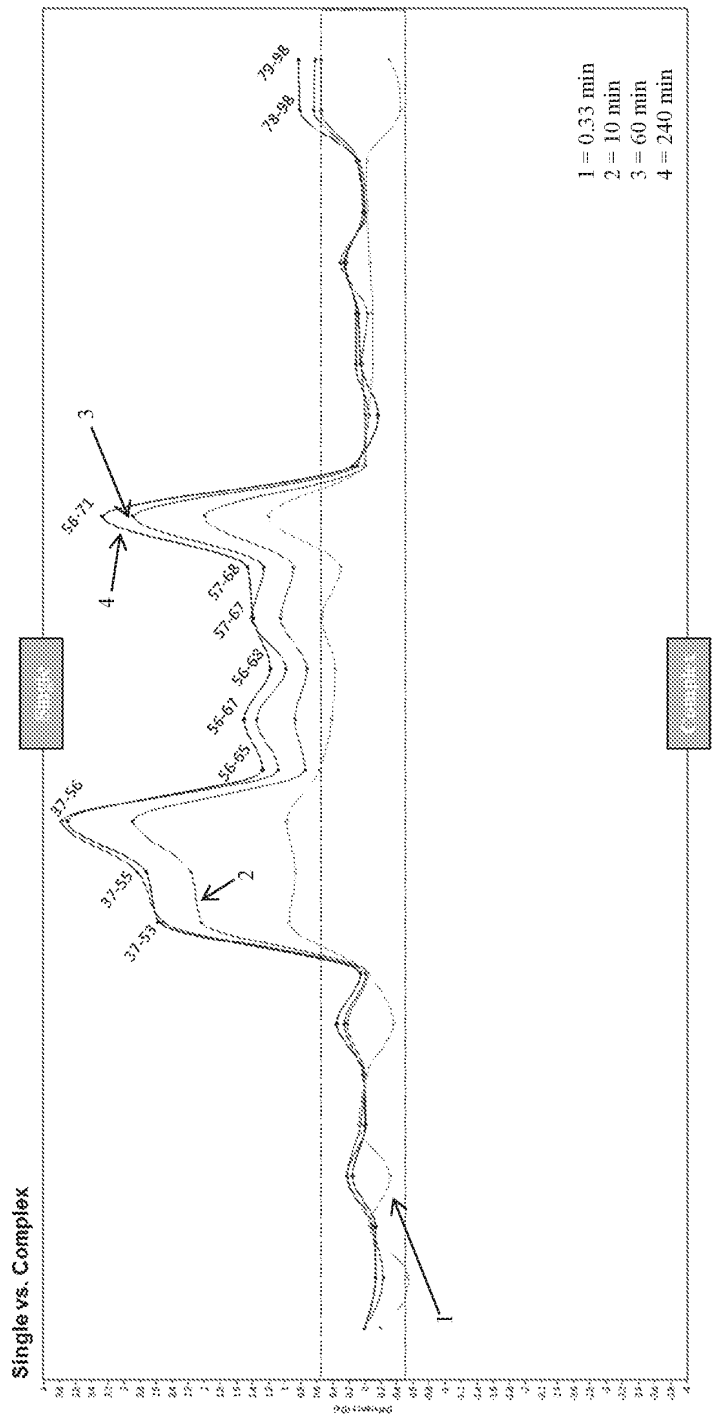


FIG. 23B

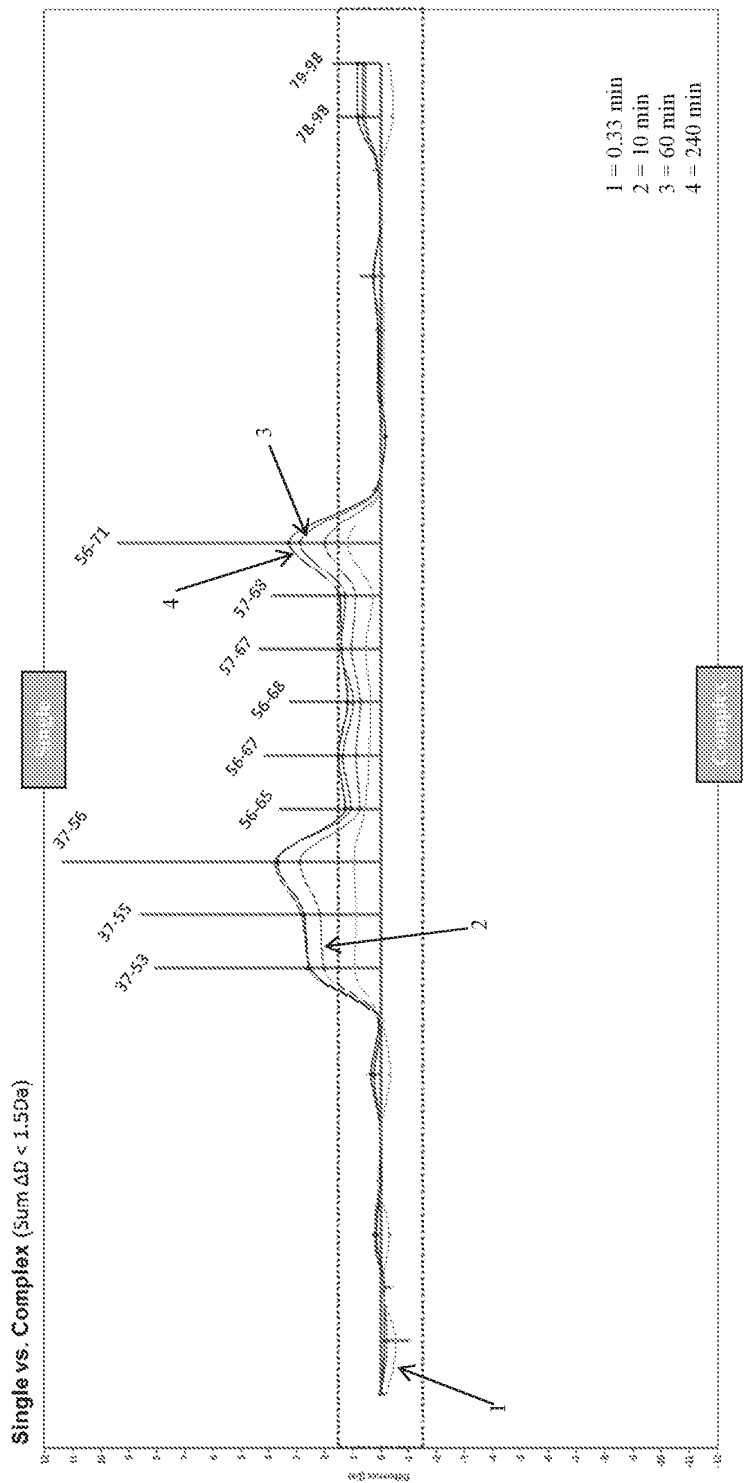


FIG. 23C

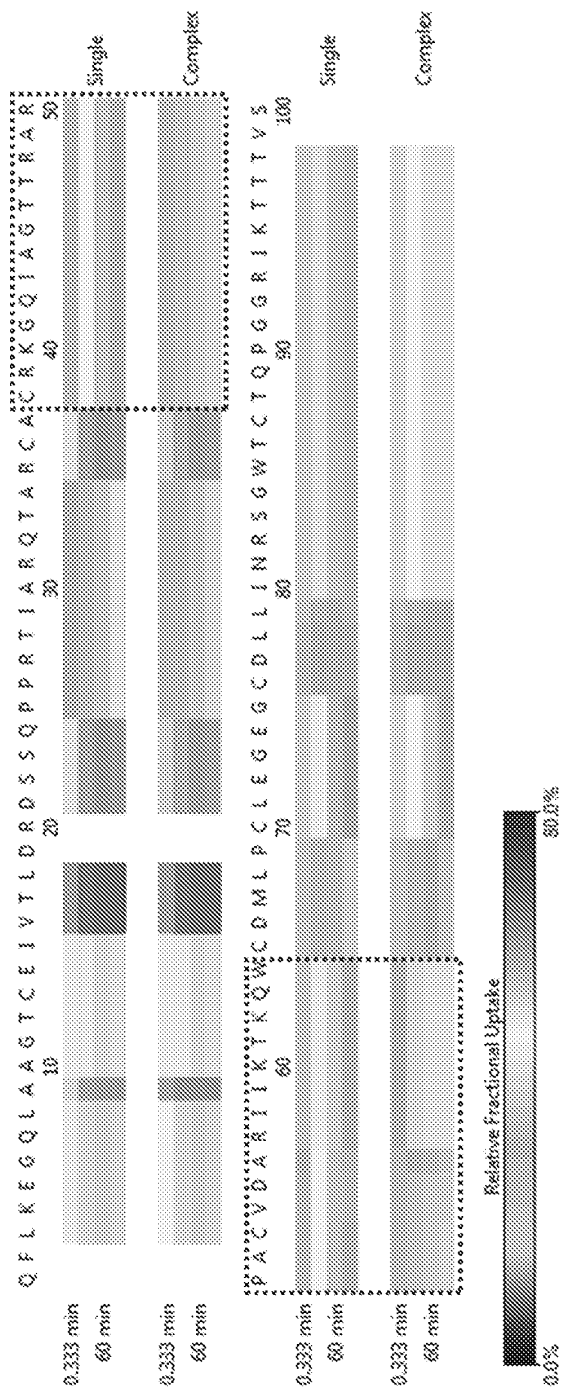


FIG. 24

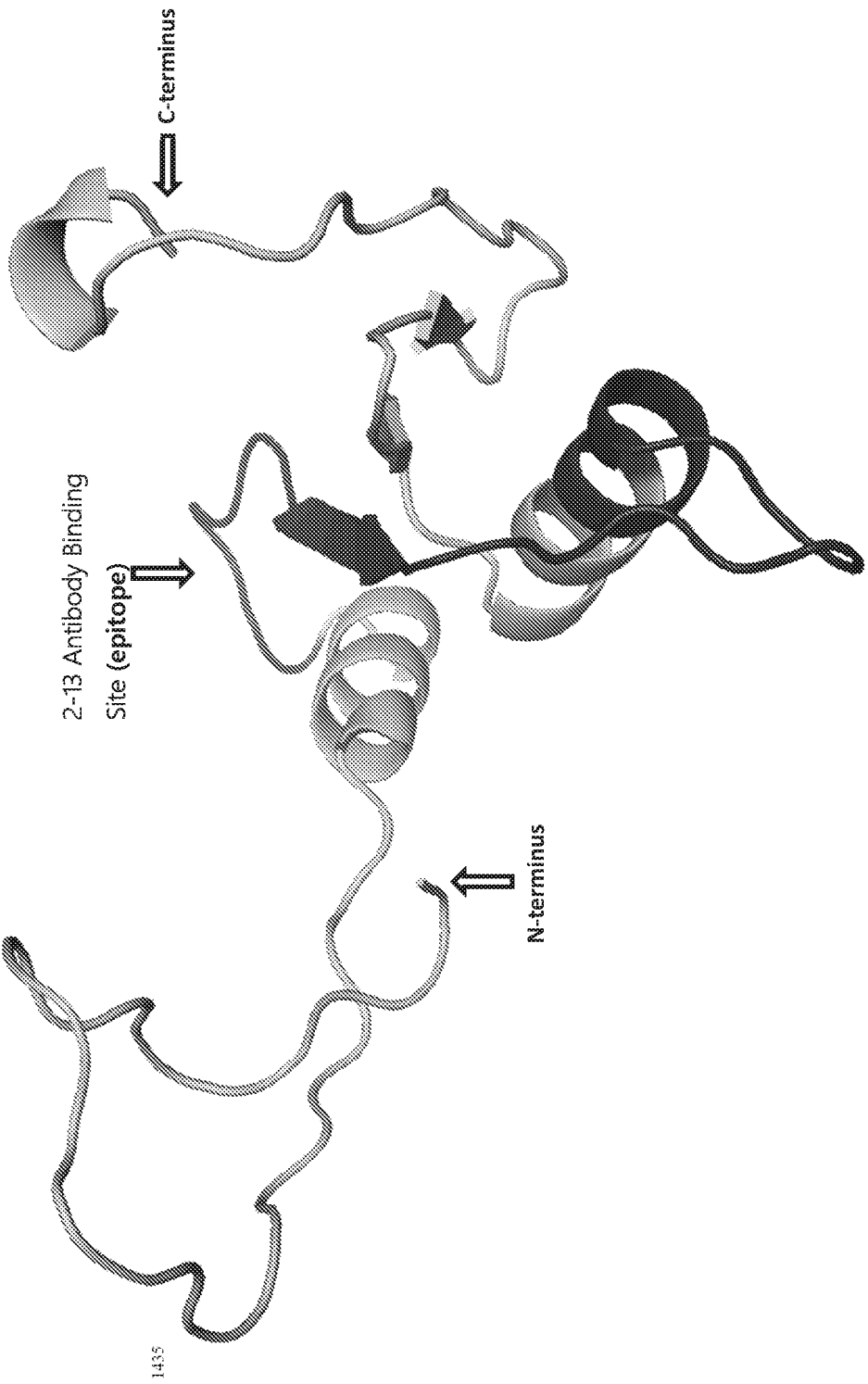


FIG. 25