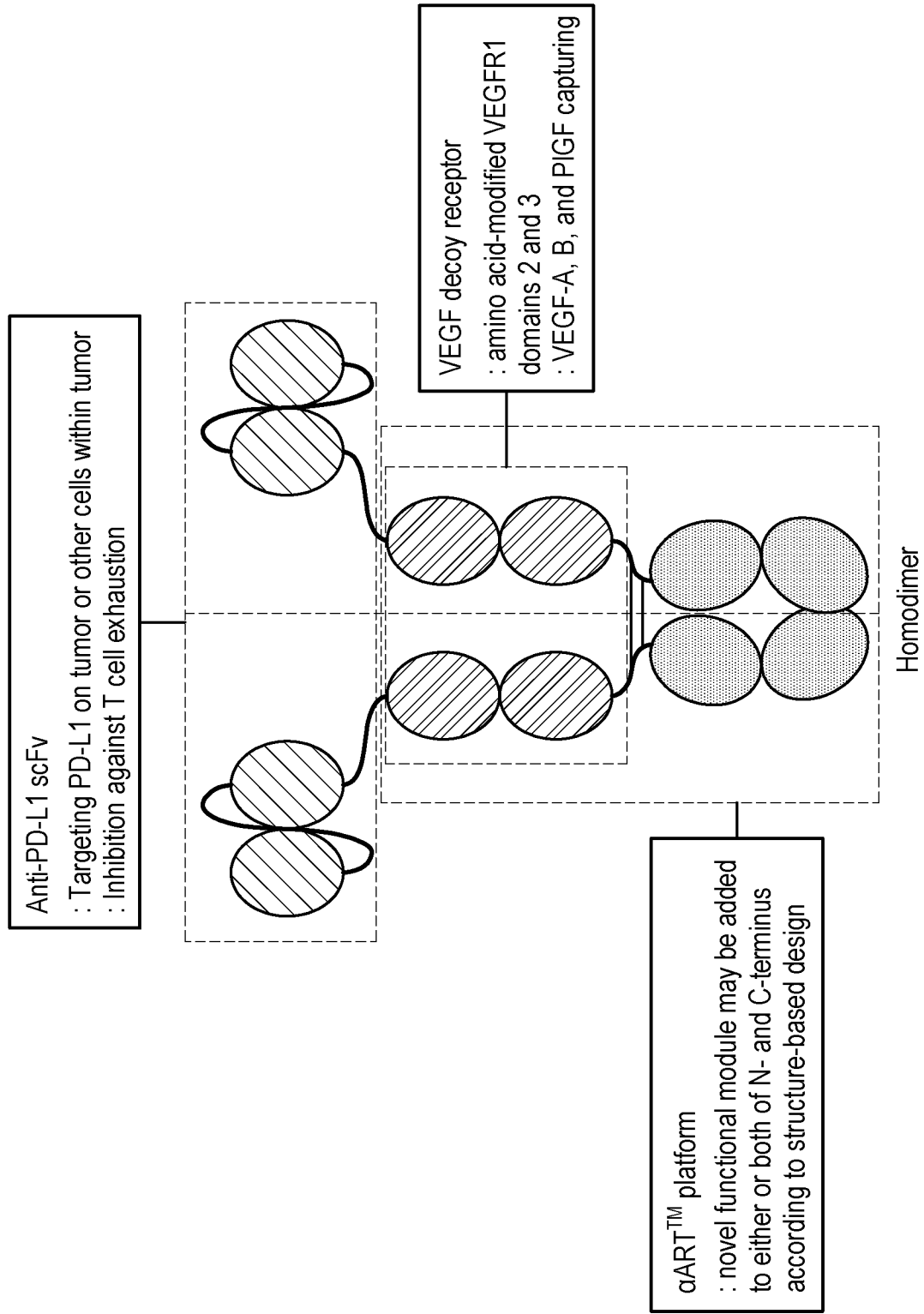


FIG. 1



PB203 prototype

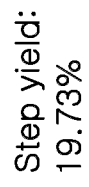


FIG. 2B
PB203 lead candidate substance

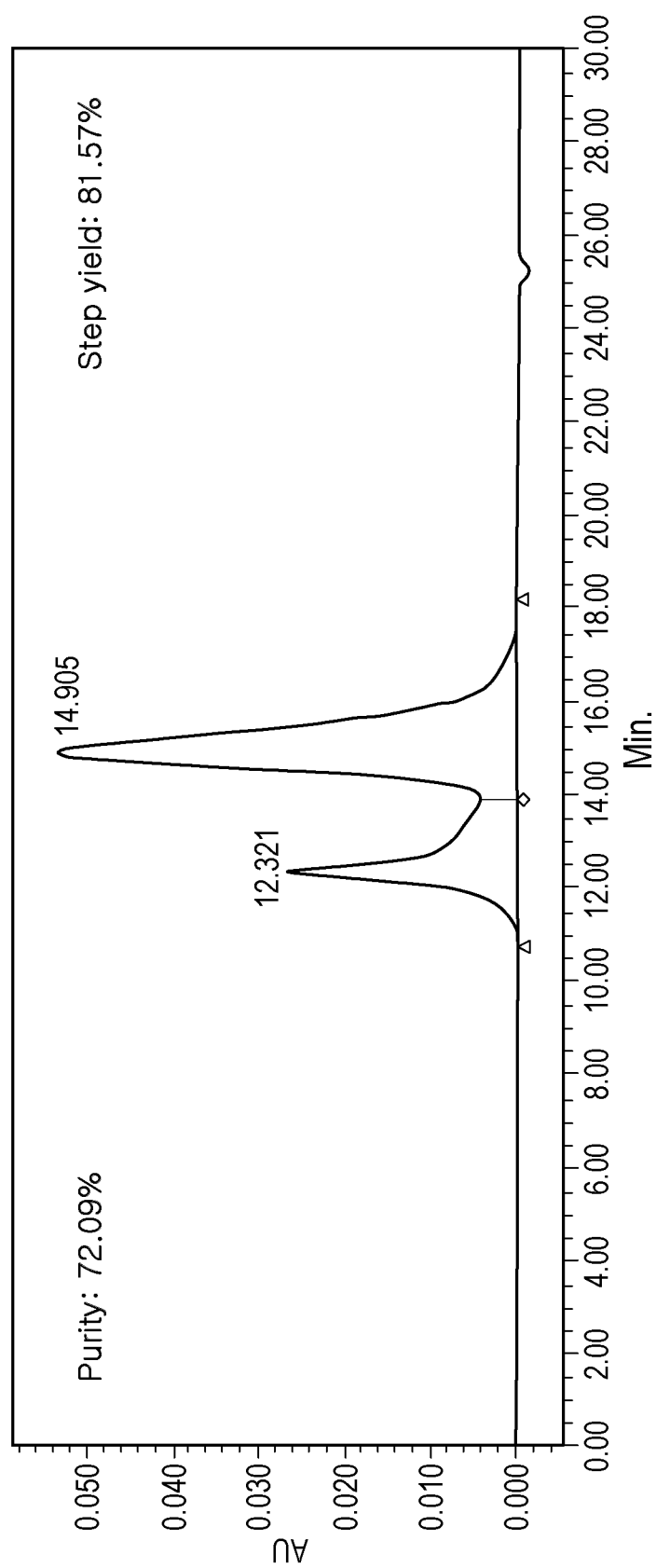


FIG. 2C

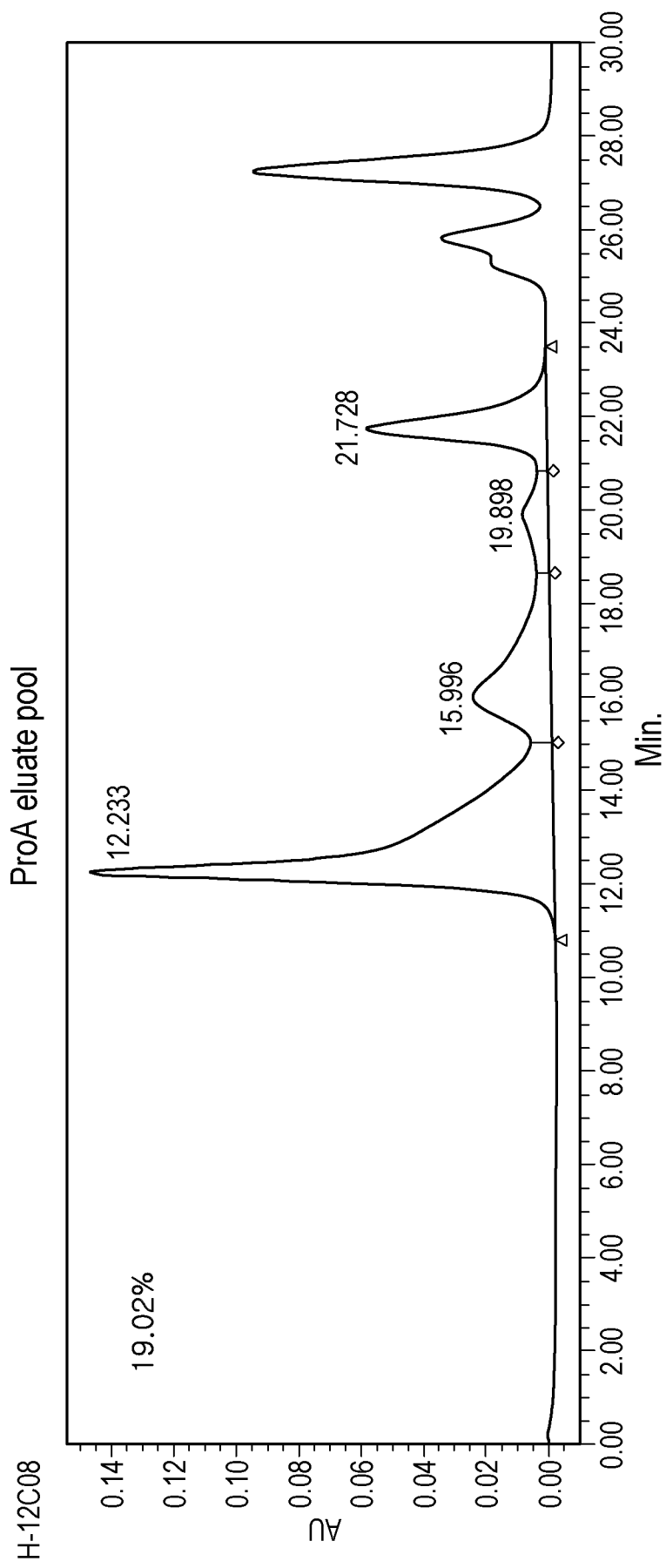


FIG. 2D
After Neutralization

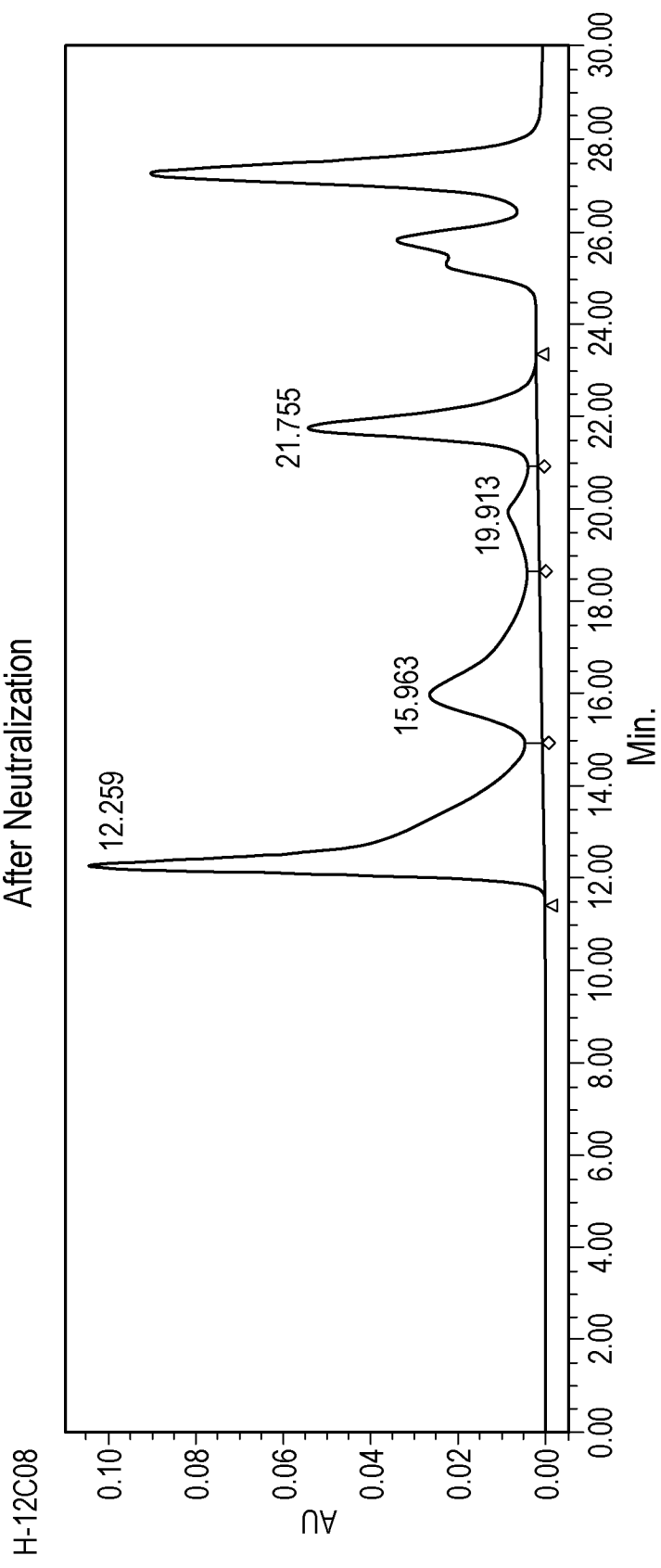


FIG. 2E

ProA eluate pool

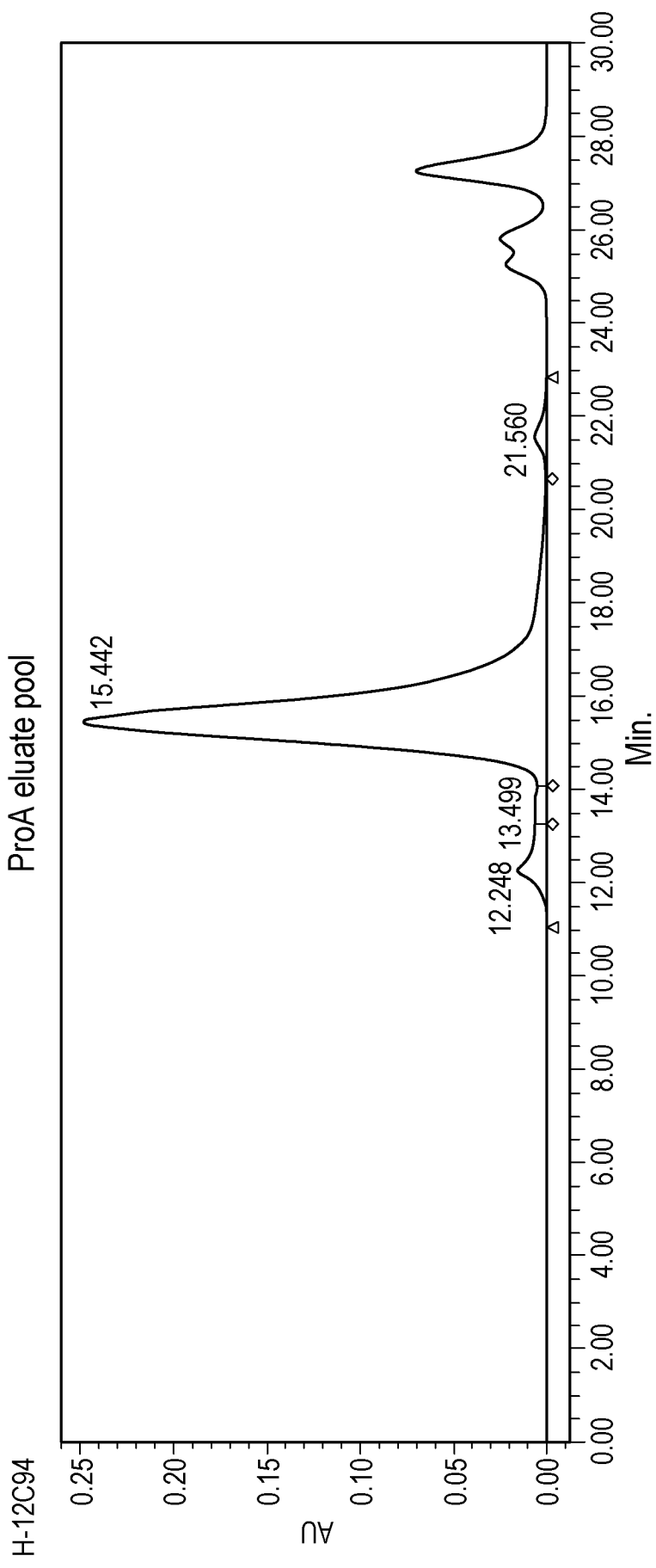


FIG. 2F

After Neutralization

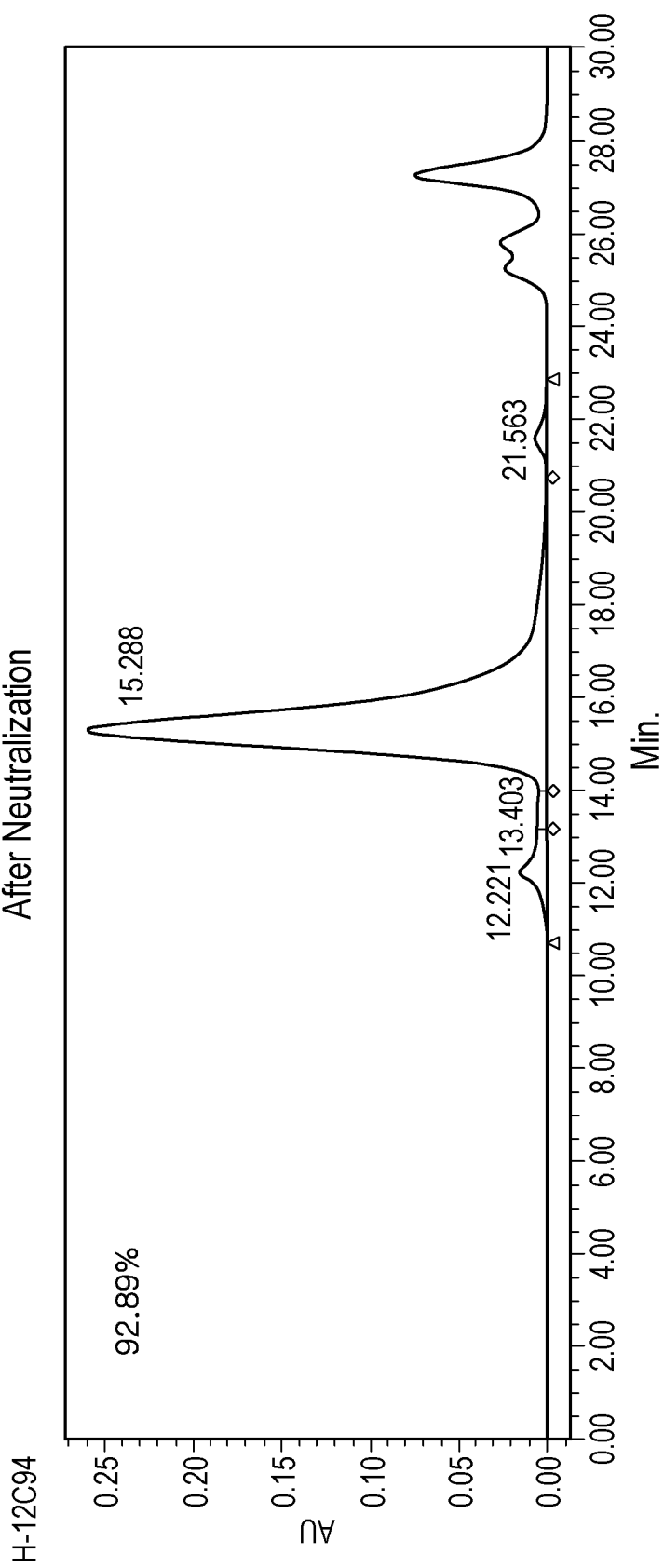


FIG. 2G

ProA eluate pool

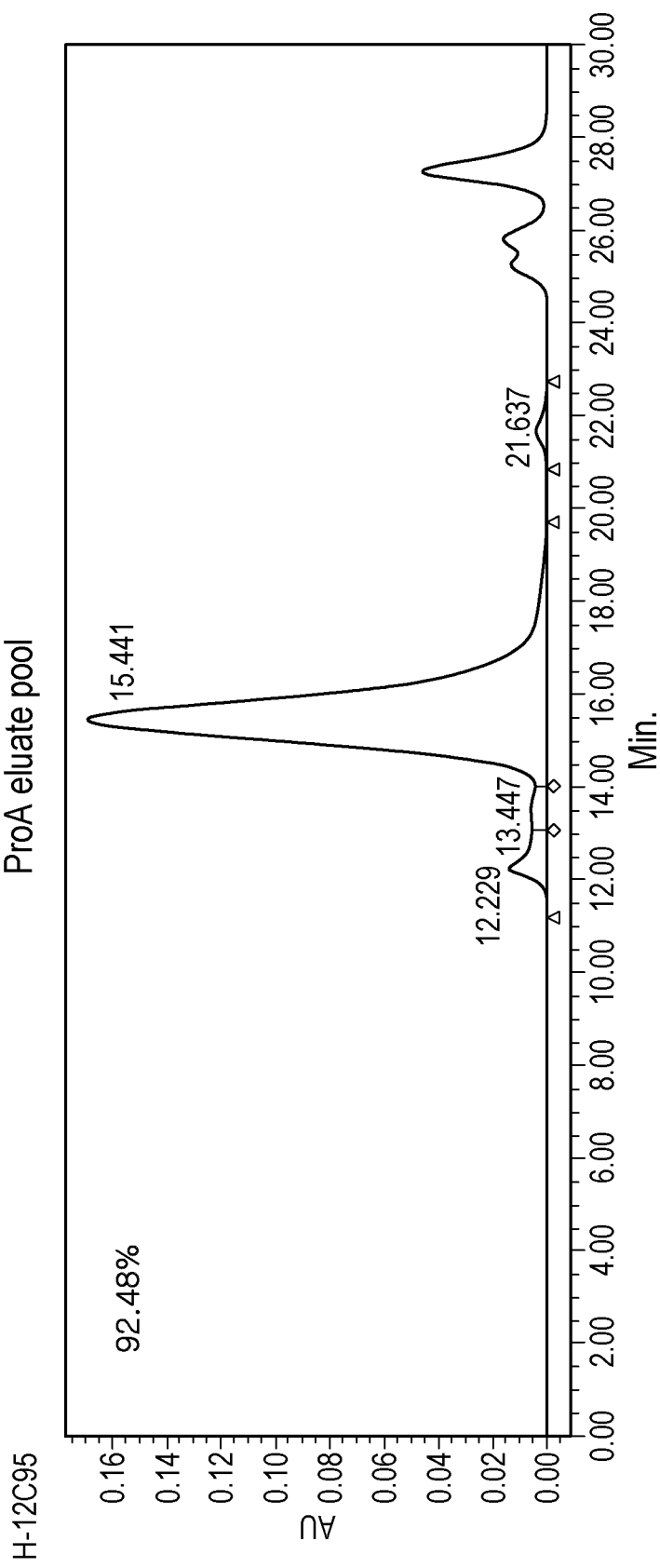


FIG. 2H

After Neutralization

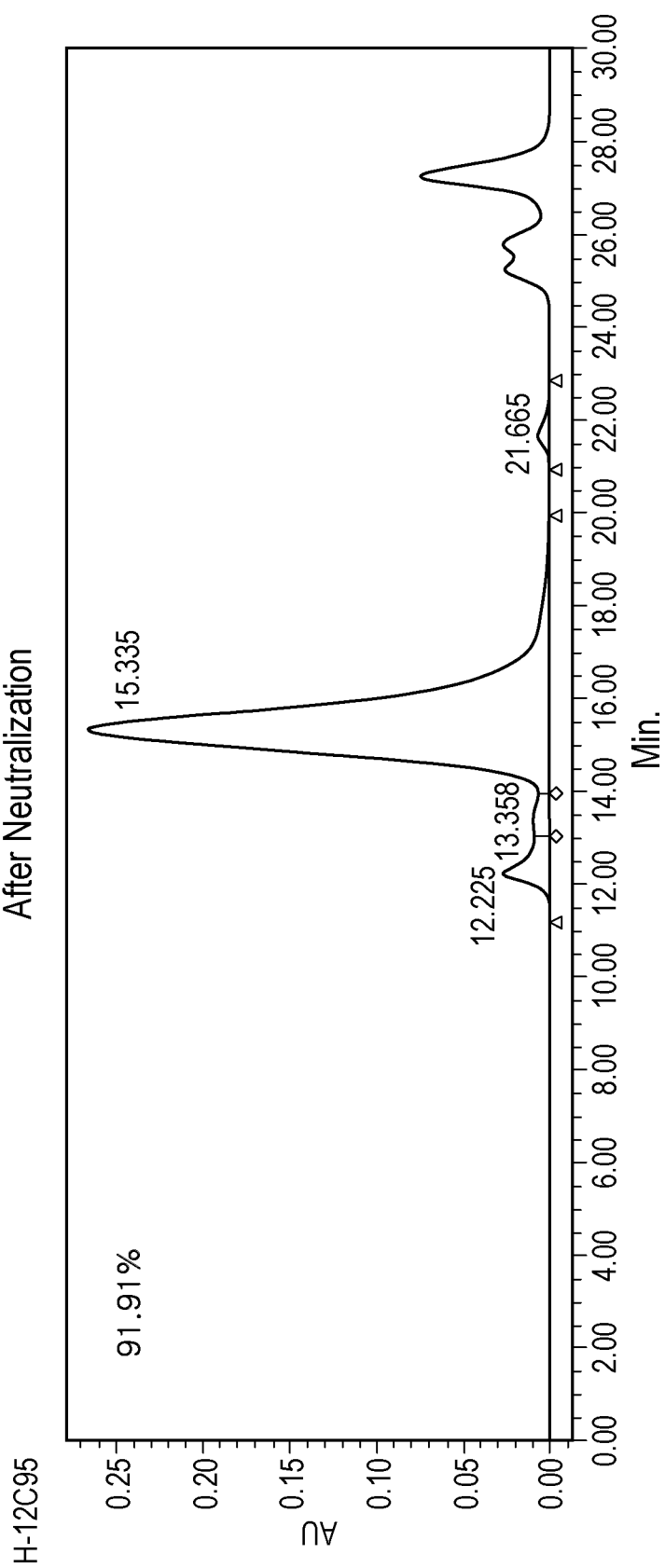


FIG. 2I

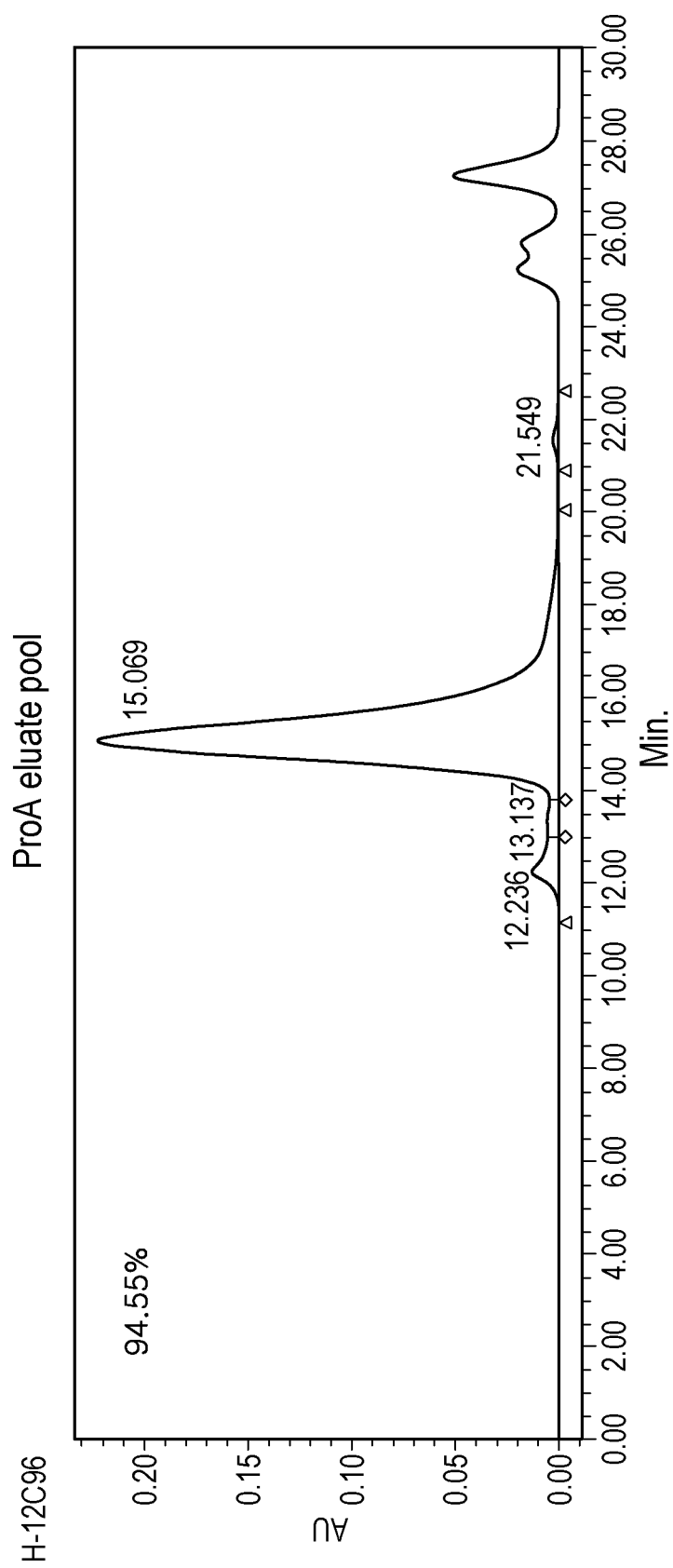


FIG. 2J

After Neutralization

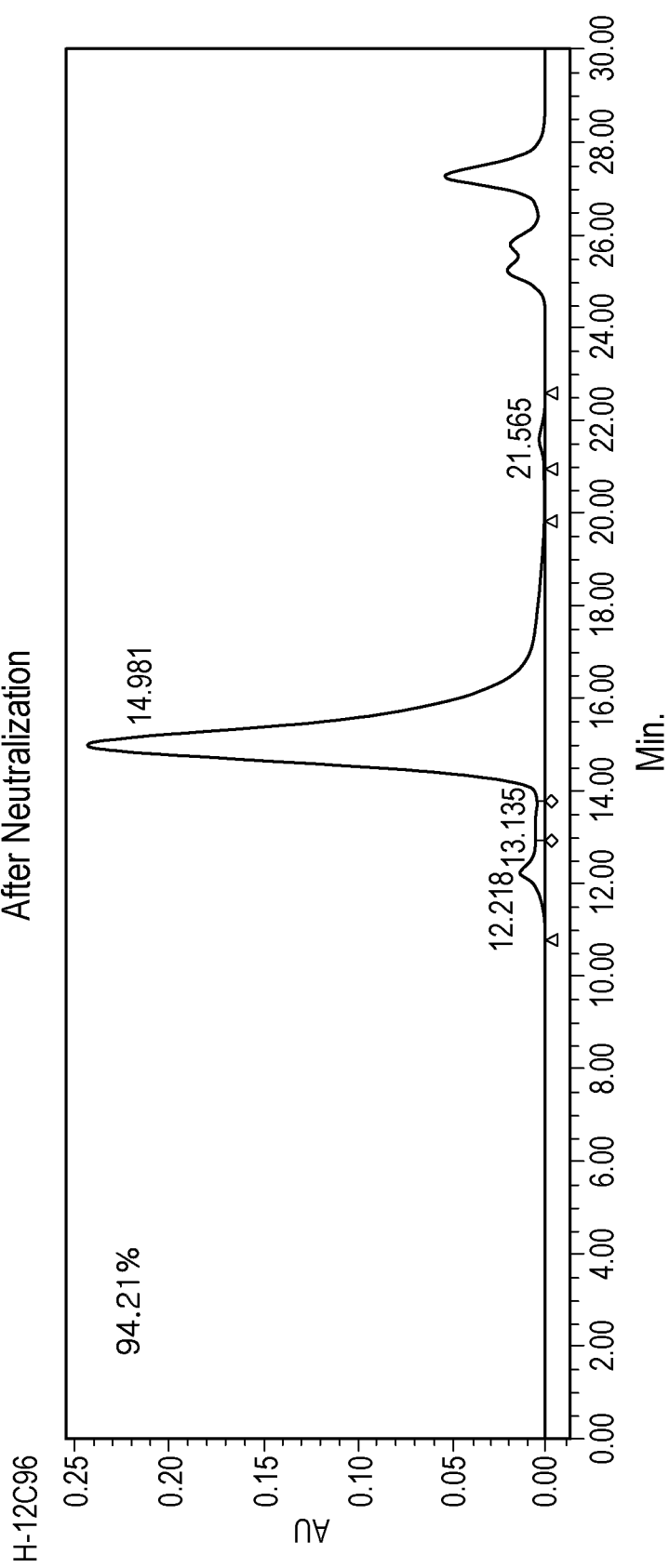


FIG. 2K

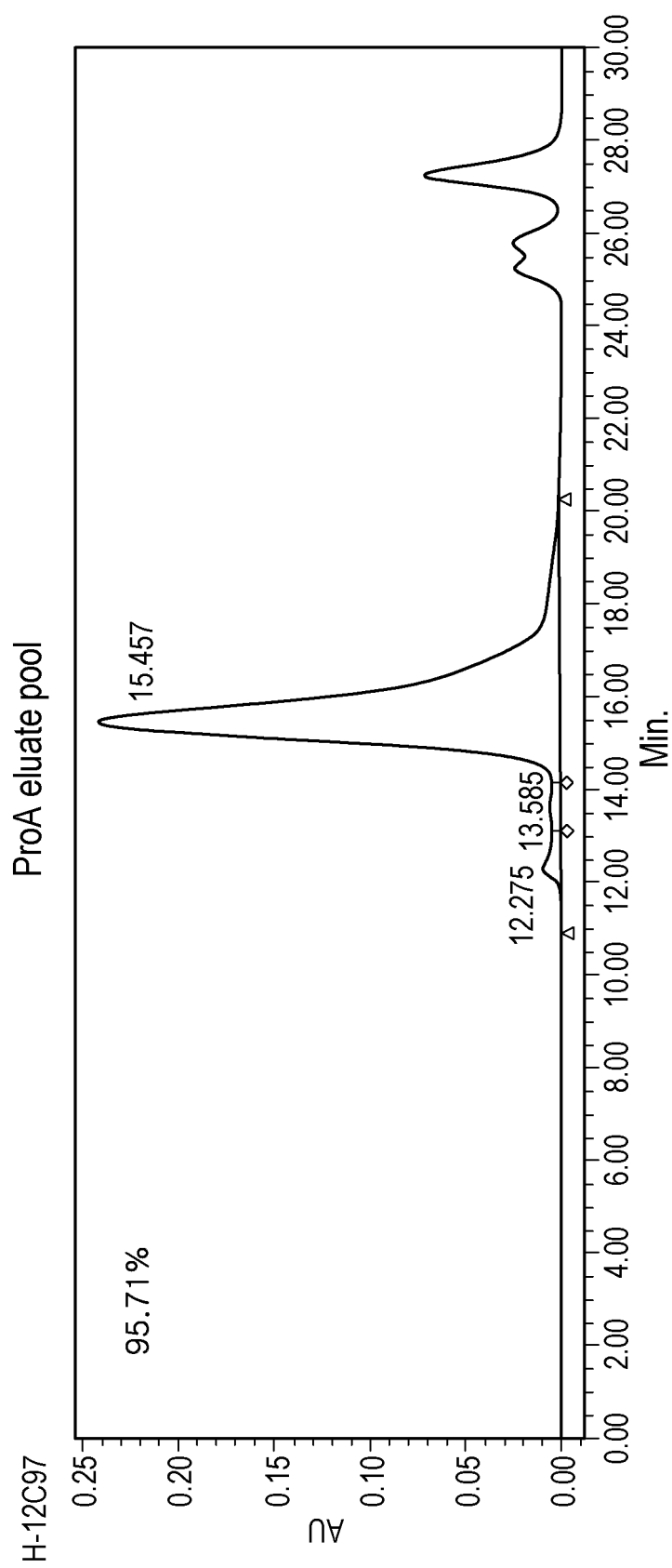


FIG. 2L

After Neutralization

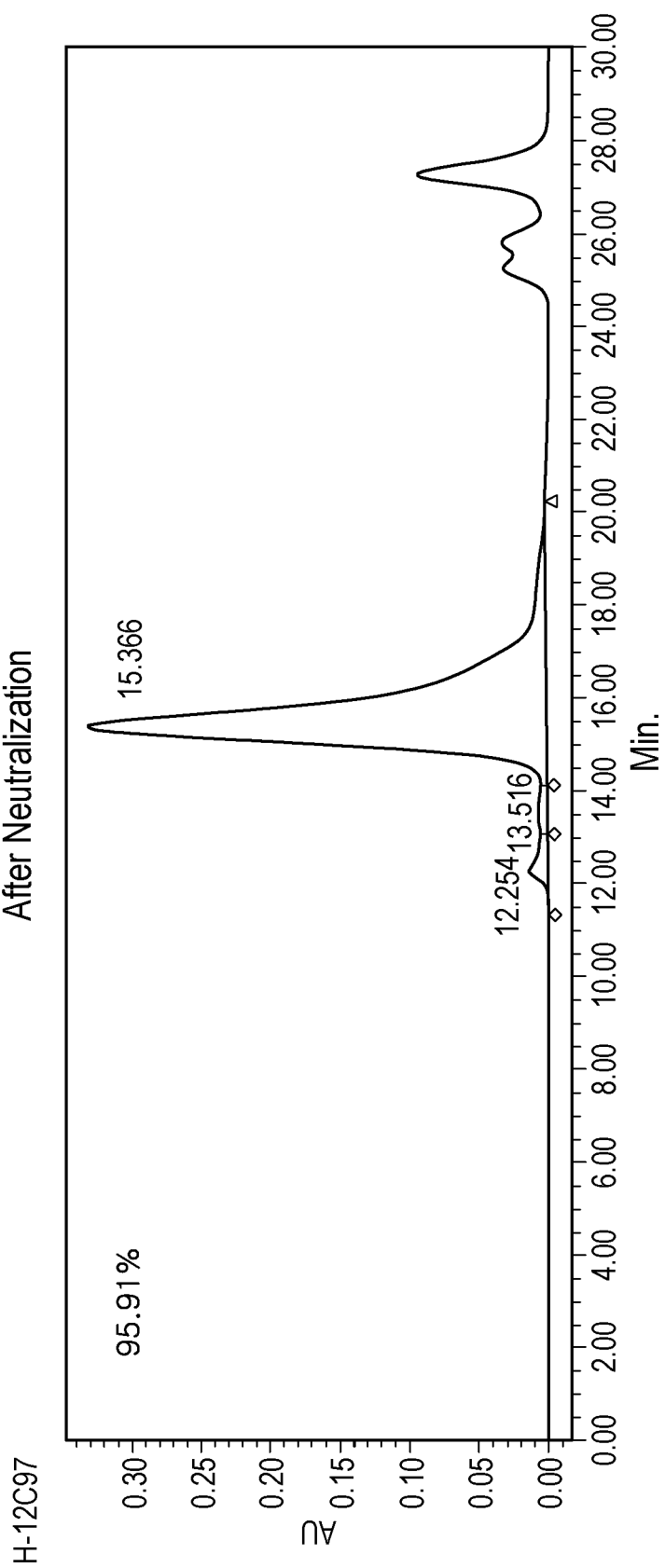


FIG. 2M

ProA eluate pool

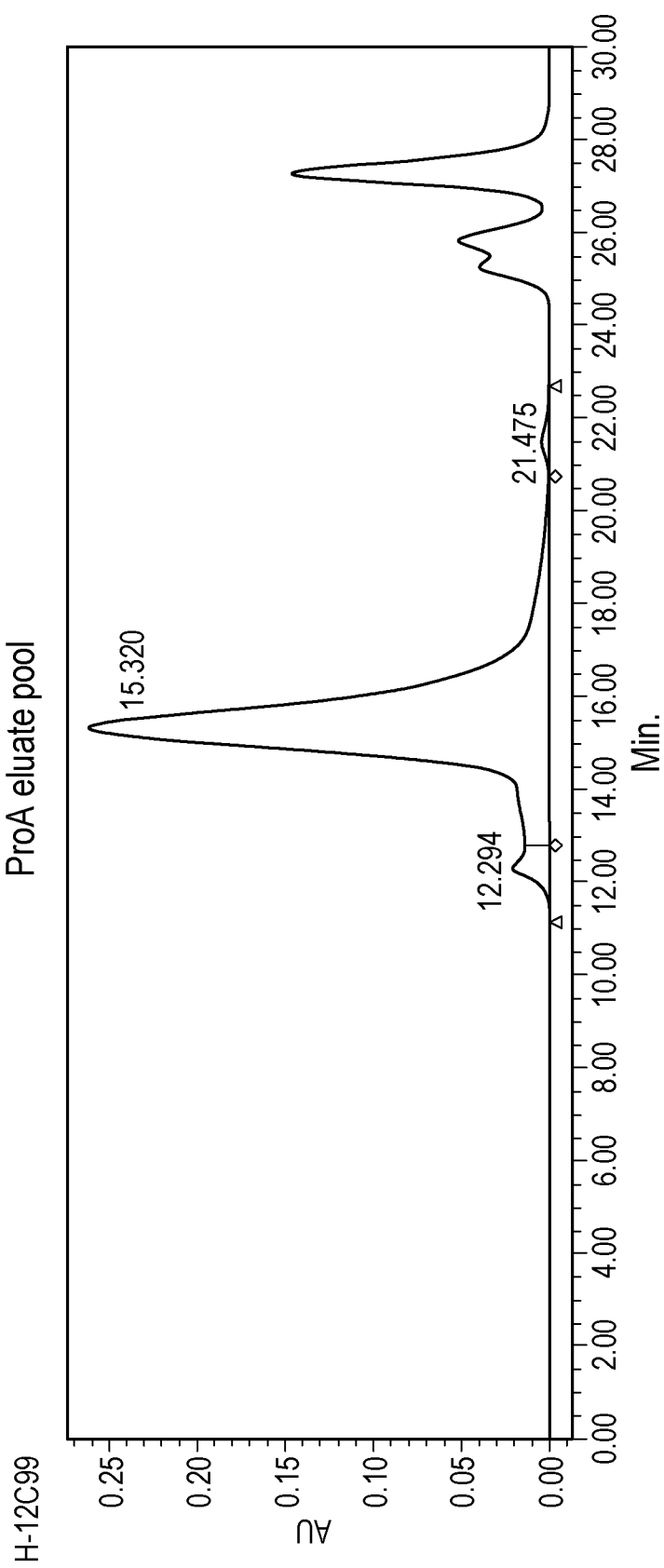


FIG. 2N

After Neutralization

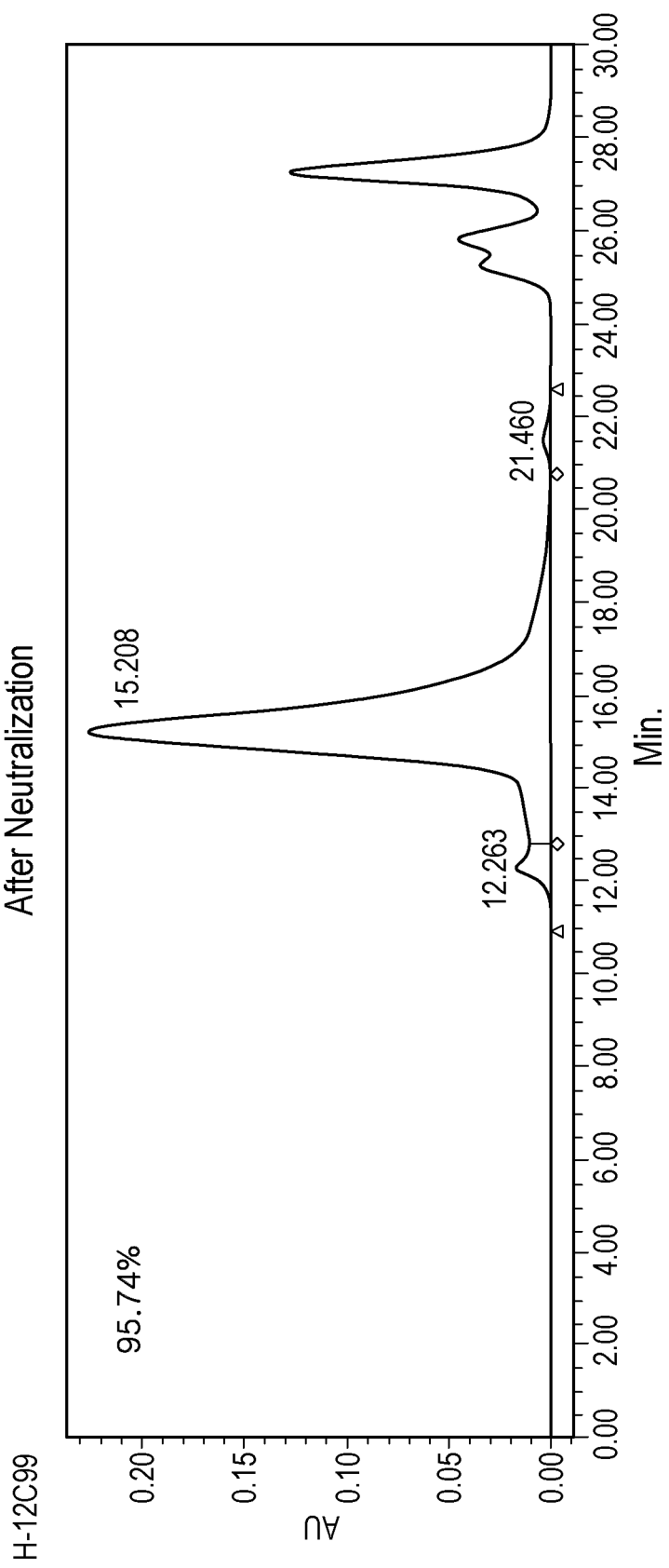


FIG. 3A

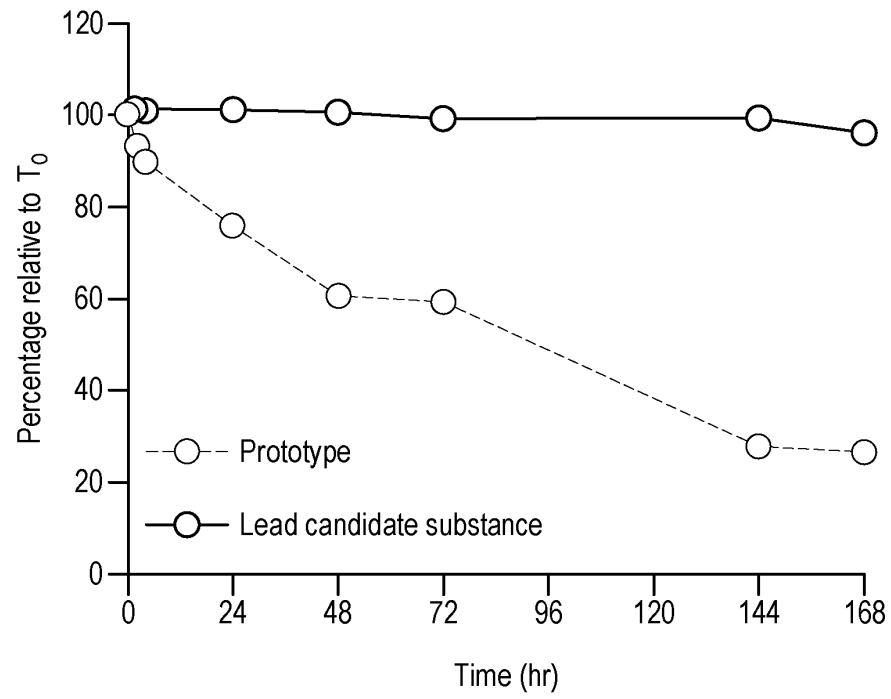


FIG. 3B

VEGF-A

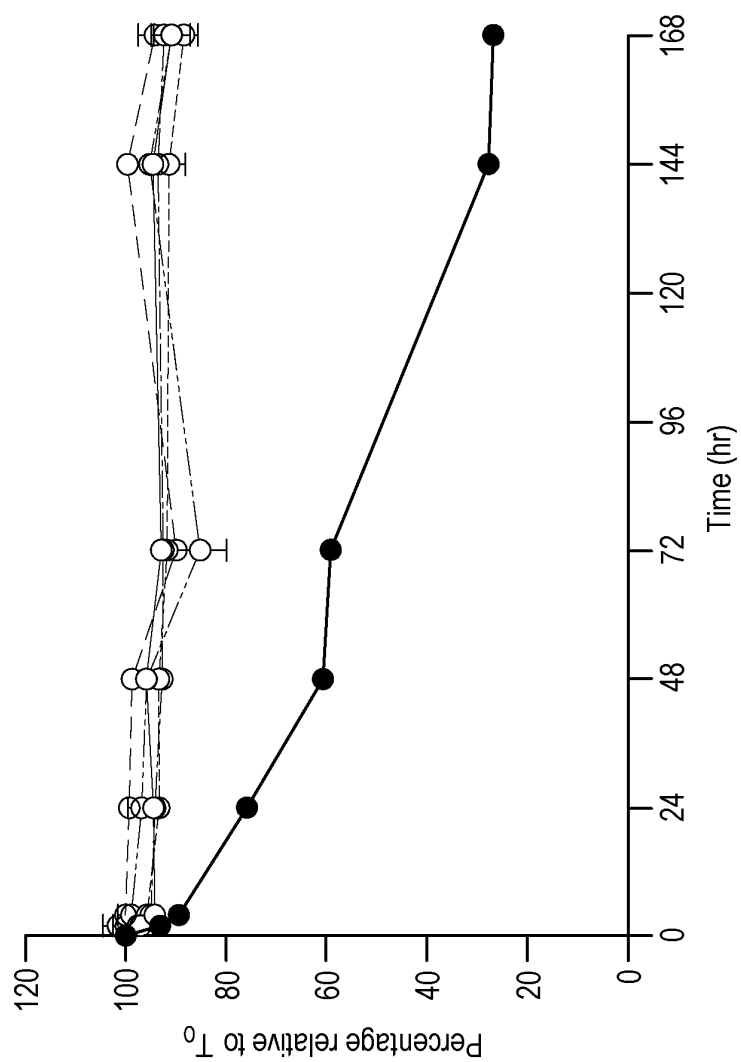


FIG. 3C

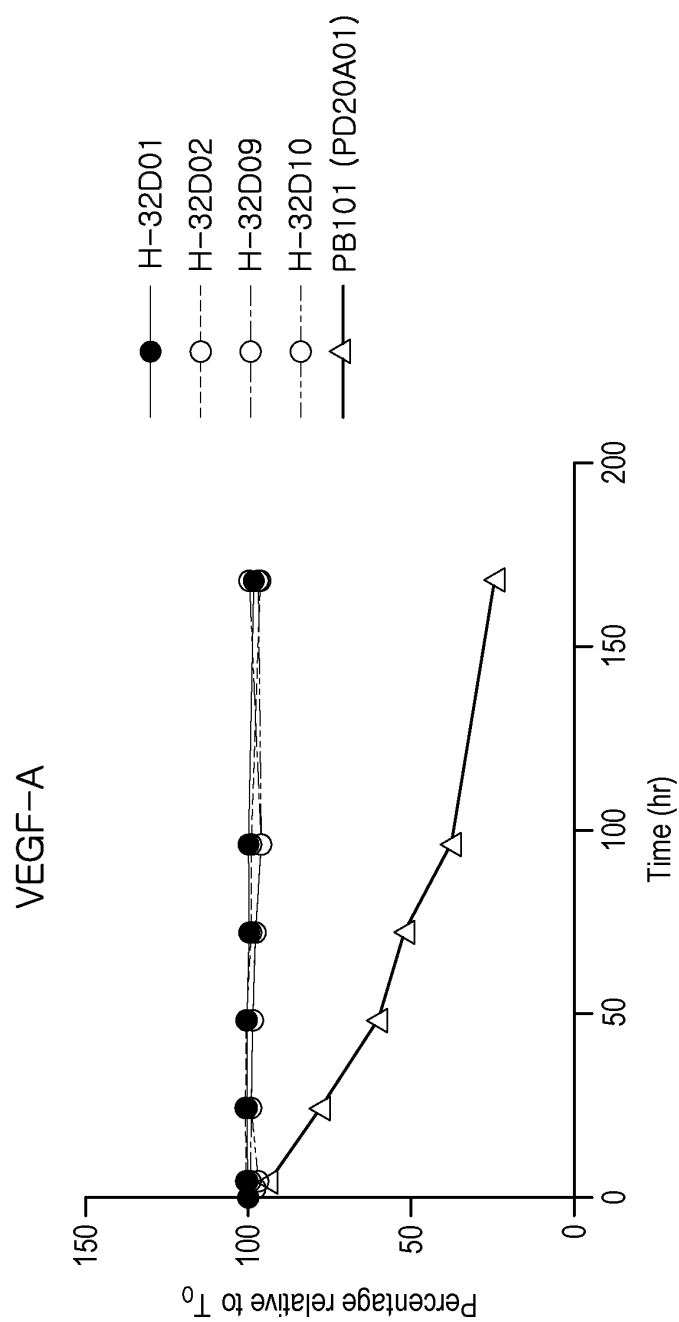
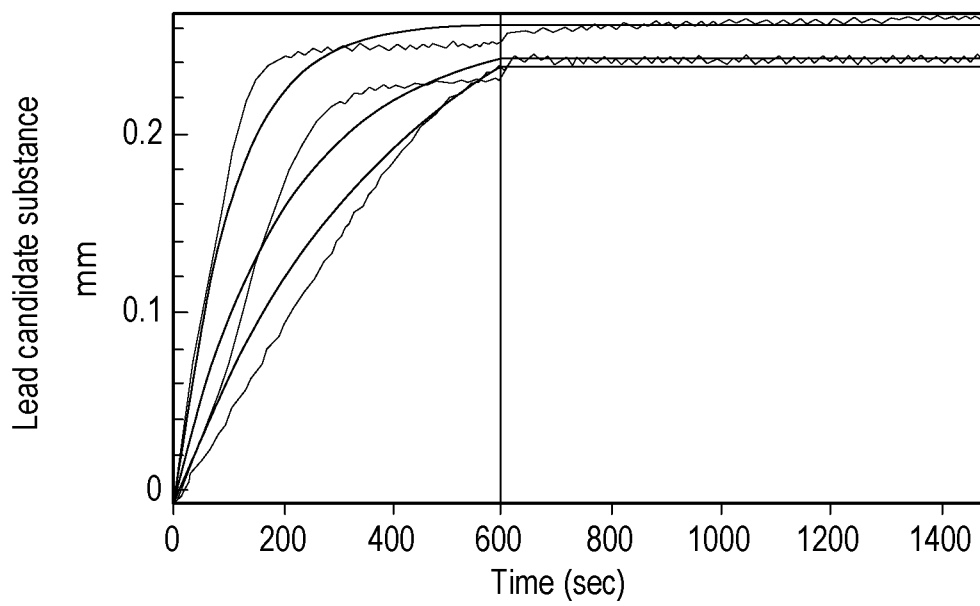
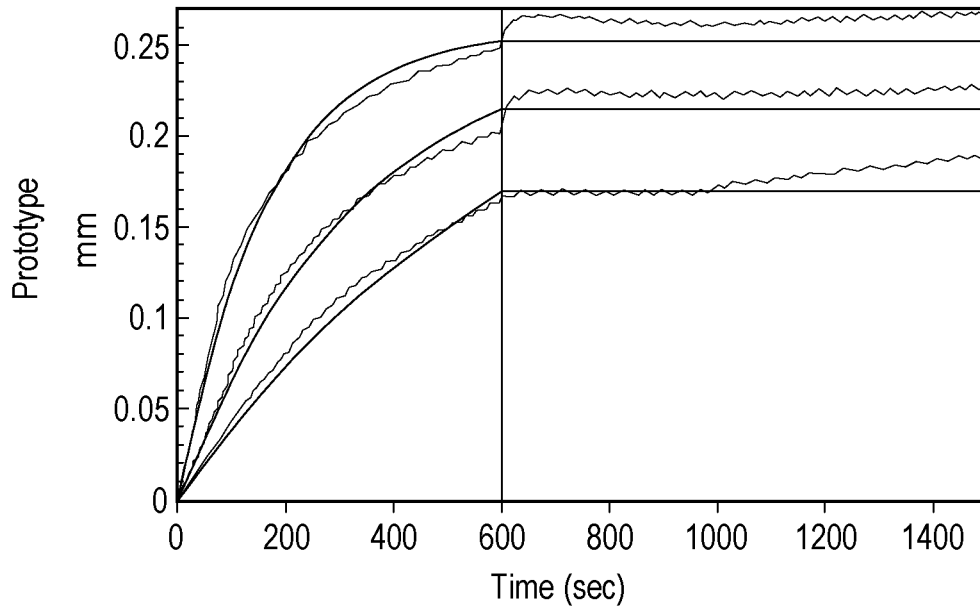


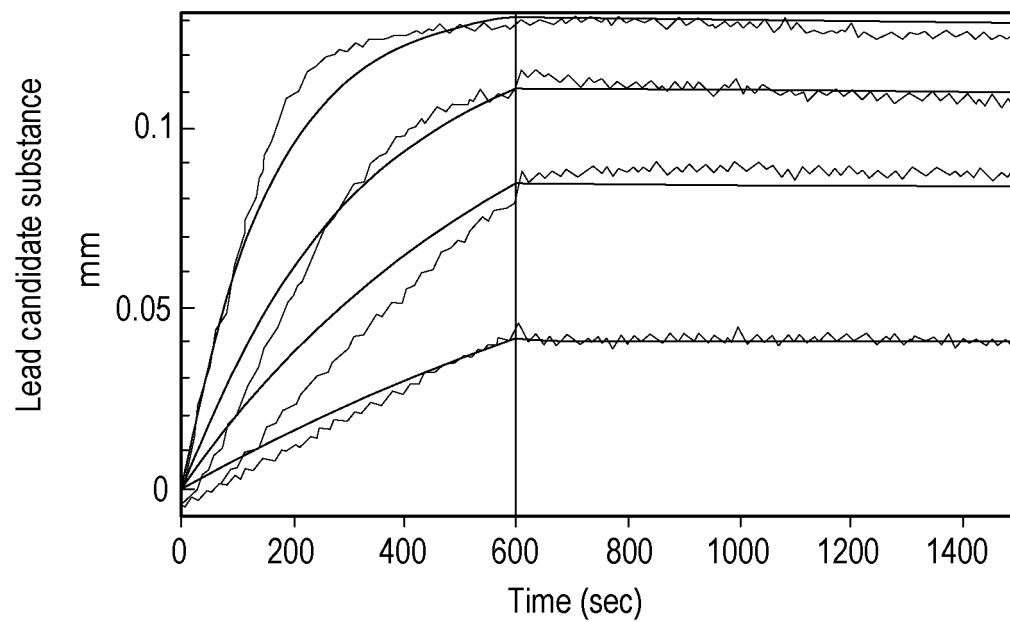
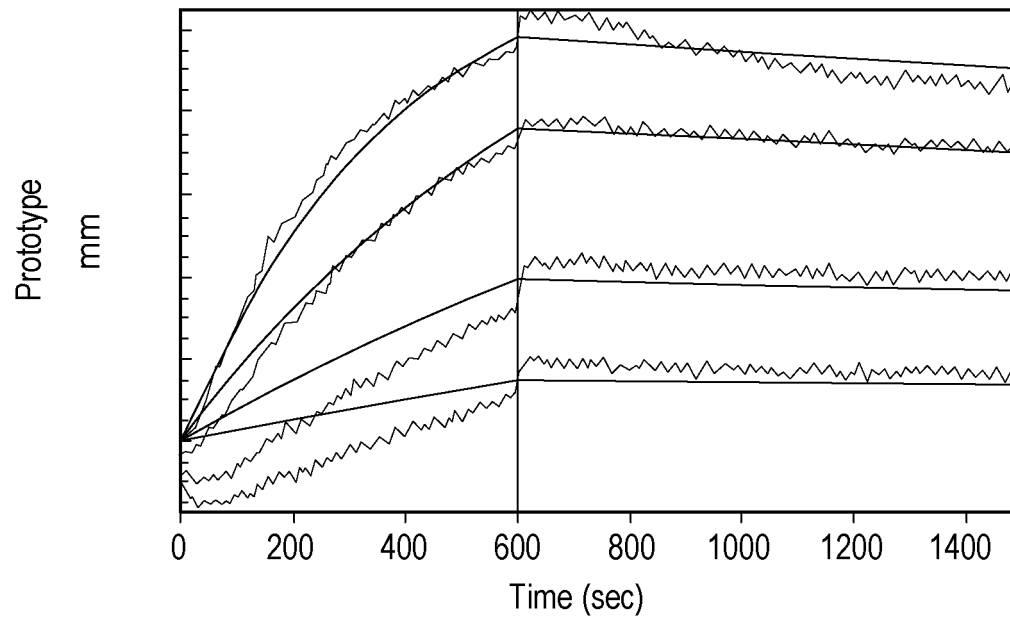
FIG. 4A
VEGF-A



kon and kD increase

FIG. 4B

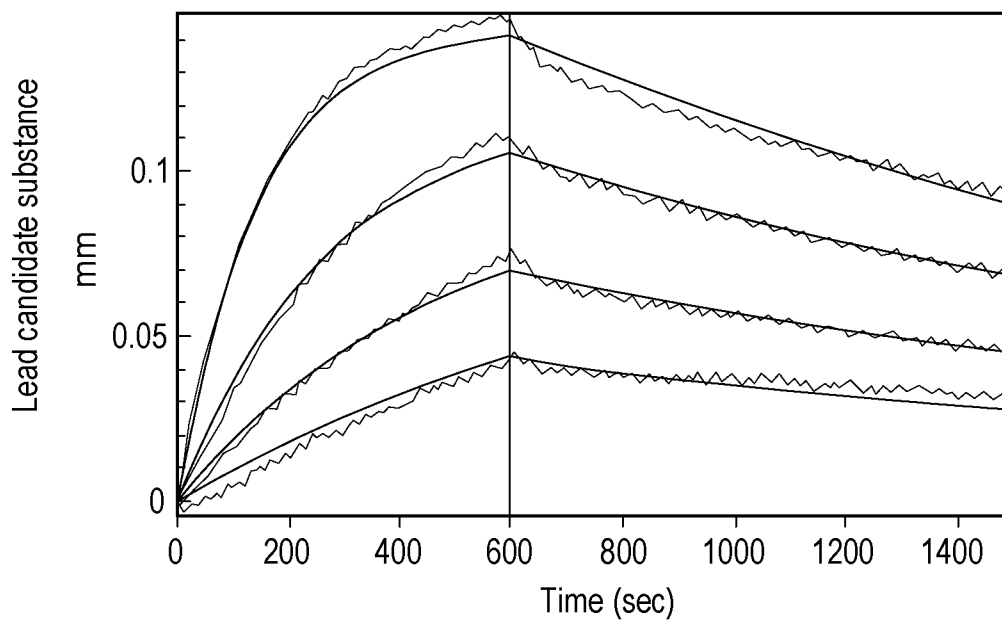
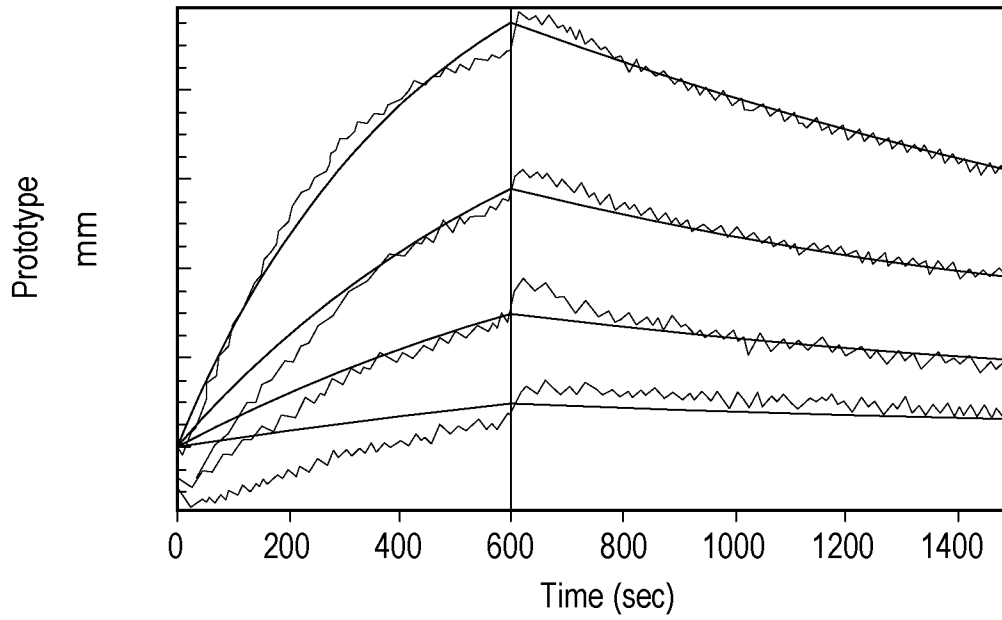
PIGF



kon and kD increase

FIG. 4C

PD-L1



kD maintenance

FIG. 4D

VEGF-A

	KD (M)	kon(1/Ms)	kdis(1/s)	Full X ²	Full R ²
H-12C08	1.00E-12	6.72E+05	1.00E-07	0.0843	0.9798
H-12C95	7.14E-12	9.19E+05	5.69E-06	0.0669	0.9798
H-12C94	2.16E-11	6.99E+05	1.75E-05	0.1182	0.9861
H-12C96	2.40E-11	7.67E+05	1.19E-05	0.0895	0.9751
H-12C99	2.61E-11	1.18E+06	2.90E-05	0.0282	0.9915
H-12C97	3.79E-11	1.22E+06	4.39E-05	0.0171	0.9940

FIG. 4E

PIGF

	KD (M)	kon(1/Ms)	kdis(1/s)	Full X ²	Full R ²
H-12C08	8.78E-11	1.05E+06	9.73E-05	2.55E-02	9.89E-01
H-12C95	9.30E-11	1.61E+06	1.57E-04	2.55E-02	9.73E-01
H-12C96	1.53E-10	1.78E+06	2.64E-04	3.00E-02	9.58E-01
H-12C97	1.79E-10	1.87E+06	3.26E-04	1.96E-02	9.76E-01
H-12C99	1.82E-10	2.00E+06	3.55E-04	5.75E-02	9.25E-01
H-12C94	2.21E-10	1.23E+06	2.45E-04	7.75E-02	9.65E-01

FIG. 4F

PD-L1

	KD (M)	kon(1/Ms)	kdis(1/s)	Full X ²	Full R ²
H-12C08	6.58E-10	1.08E+06	7.14E-04	0.0212	0.9910
H-12C95	8.39E-10	9.06E+05	7.66E-04	0.0251	0.9886
H-12C96	8.51E-10	9.90E+05	8.43E-04	0.0251	0.9854
H-12C99	8.79E-10	9.69E+05	8.52E-04	0.0128	0.9930
H-12C94	9.51E-10	8.99E+05	8.55E-04	0.0187	0.9960
H-12C97	1.00E-09	1.06E+06	1.06E-03	0.0148	0.9938

FIG. 4G

Loading sample ID	KD (M)	kon(1/Ms)	kdis(1/s)	Full X ²	Full R ²
H-32D01	<1.0E-12	1.01E+06	<1.0E-07	0.335	0.9802
H-32D02	<1.0E-12	9.70E+05	<1.0E-07	0.4793	0.9728
H-32D09	<1.0E-12	9.07E+05	<1.0E-07	0.2889	0.9834
H-32D10	<1.0E-12	9.02E+05	<1.0E-07	0.3736	0.9799
PB101 (DP)	<1.0E-12	6.50E+05	<1.0E-07	0.9929	0.9671

FIG. 4H

Code name	KD (M)	kon(1/Ms)	kdis(1/s)	Full X ²	Full R ²
H-32D01	1.18E-10	2.06E+06	2.43E-04	0.1426	0.9837
H-32D02	8.08E-11	9.07E+05	7.32E-05	0.5452	0.9563
H-32D09	6.47E-11	1.41E+06	9.09E-05	0.2435	0.9776
H-32D10	<1.0E-12	4.00E+06	<1.0E-07	2.384	0.8278
PB101 DP	1.69E-10	1.12E+06	1.89E-04	0.2627	0.9818

FIG. 4I

Code	KD (M)	kon(1/Ms)	kdis(1/s)	Full X ²	Full R ²
H-32D01	8.73E-10	6.07E+05	5.30E-04	0.0866	0.9959
H-32D02	1.39E-09	5.51E+05	7.64E-04	0.2048	0.9875
A167 scFv	1.04E-09	5.65E+05	2.27E-06	0.2297	0.9922
H-32D09	6.29E-10	5.10E+05	3.21E-04	0.0783	0.9959
H-32D10	7.54E-10	4.65E+05	3.51E-04	0.122	0.9928
Atezolizumab scFv	4.70E-10	4.92E+05	2.31E-04	0.0692	0.9981

FIG. 4J

Sample ID	Loading sample ID	KD (M)	kon(1/Ms)	kdis(1/s)	Full X ²	Full R ²
hVEGF-A	H-01C65	<1.0E-12	9.39E+05	<1.0E-07	0.2154	0.9887
	PD20A01	<1.0E-12	1.18E+06	<1.0E-07	0.0461	0.9961
	H-32D02	<1.0E-12	5.95E+05	<1.0E-07	0.467	0.9844
	H-32D04	<1.0E-12	9.43E+05	<1.0E-07	0.4766	0.9724
	H-32D06	2.52E-11	8.55E+05	2.15E-05	0.2382	0.9851
	H-32D08	1.26E-11	1.00E+06	1.26E-05	0.2177	0.9841

FIG. 4K

Sample ID	Loading sample ID	KD (M)	kon(1/Ms)	kdis(1/s)	Full X^2	Full R^2
PIGF	H-01C65	<1.0E-12	1.76E+06	<1.0E-07	0.2048	0.9807
	PB101	2.07E-10	1.08E+06	2.23E-04	0.1203	0.9877
	H-32D02	1.21E-11	1.24E+06	1.50E-05	0.1819	0.982
	H-32D04	5.62E-11	1.40E+06	7.87E-05	0.103	0.985
	H-32D06	6.42E-12	1.68E+06	1.08E-05	0.1448	0.9755
	H-32D08	8.05E-11	1.91E+06	1.54E-04	0.2179	0.9563

FIG. 5A

Sample	1st	2nd	KD (M)	Kon (1/Ms)	Kdis (1/s)	Full X^2	Full R^2	Ranking
H-32D02	VEGF-A	PD-L1	1.93E-09	4.87E+05	9.41E-04	0.0789	0.9897	H-32D02
H-32D04			3.40E-09	4.72E+05	1.60E-03	0.1196	0.9684	H-32D04
H-32D06			7.79E-09	3.12E+05	2.43E-03	0.0626	0.9705	H-32D08
H-32D08			4.79E-09	4.69E+05	2.25E-03	0.0621	0.9727	H-32D06

FIG. 5B

Sample	1st	2nd	KD (M)	Kon (1/Ms)	Kdis (1/s)	Full X^2	Full R^2	Ranking
H-32D02	PIGF	PD-L1	2.67E-09	6.51E+05	1.74E-03	0.1626	0.9498	H-32D02
H-32D04			7.18E-09	3.19E+05	2.29E-03	0.055	0.9784	H-32D08
H-32D06			8.80E-09	3.89E+05	3.42E-03	0.1133	0.9584	H-32D04
H-32D08			4.26E-09	5.04E+05	2.15E-03	0.1042	0.945	H-32D06

FIG. 5C

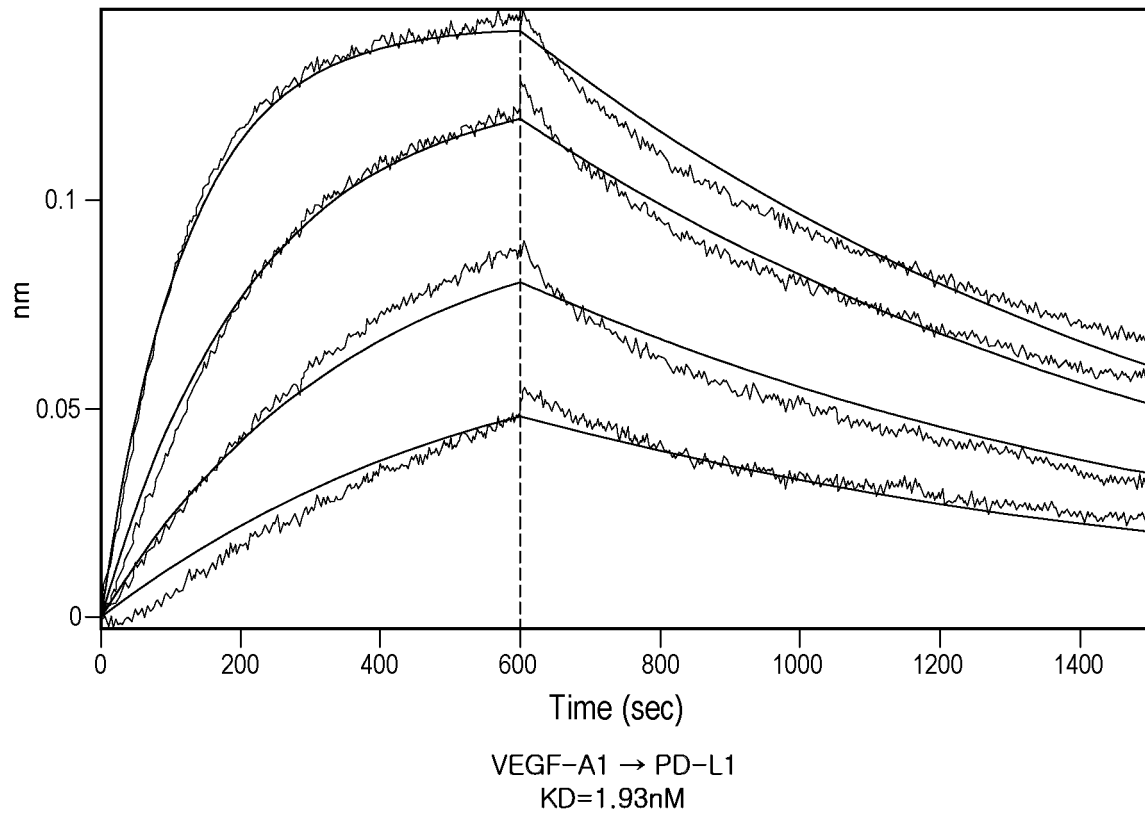


FIG. 5D

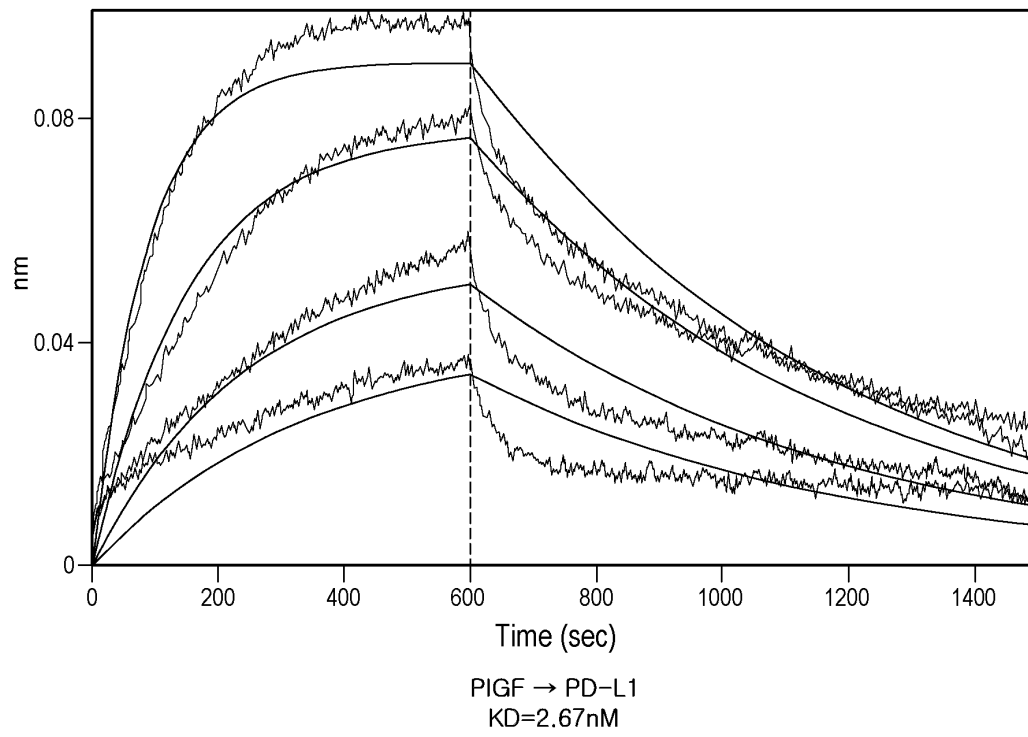


FIG. 5E

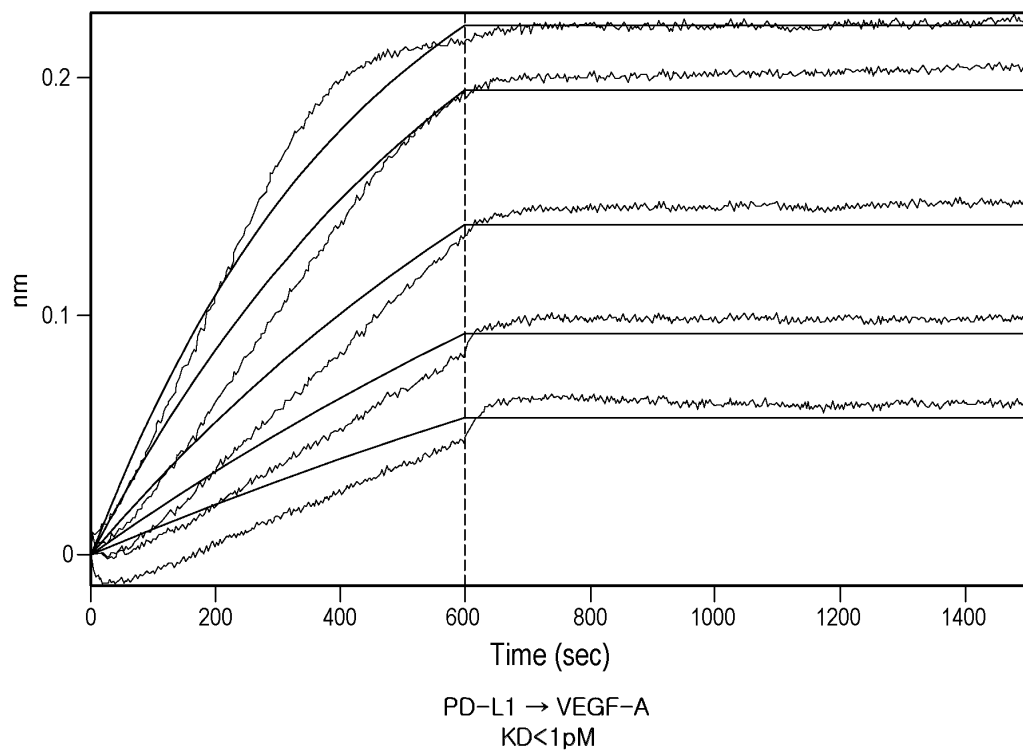


FIG. 5F

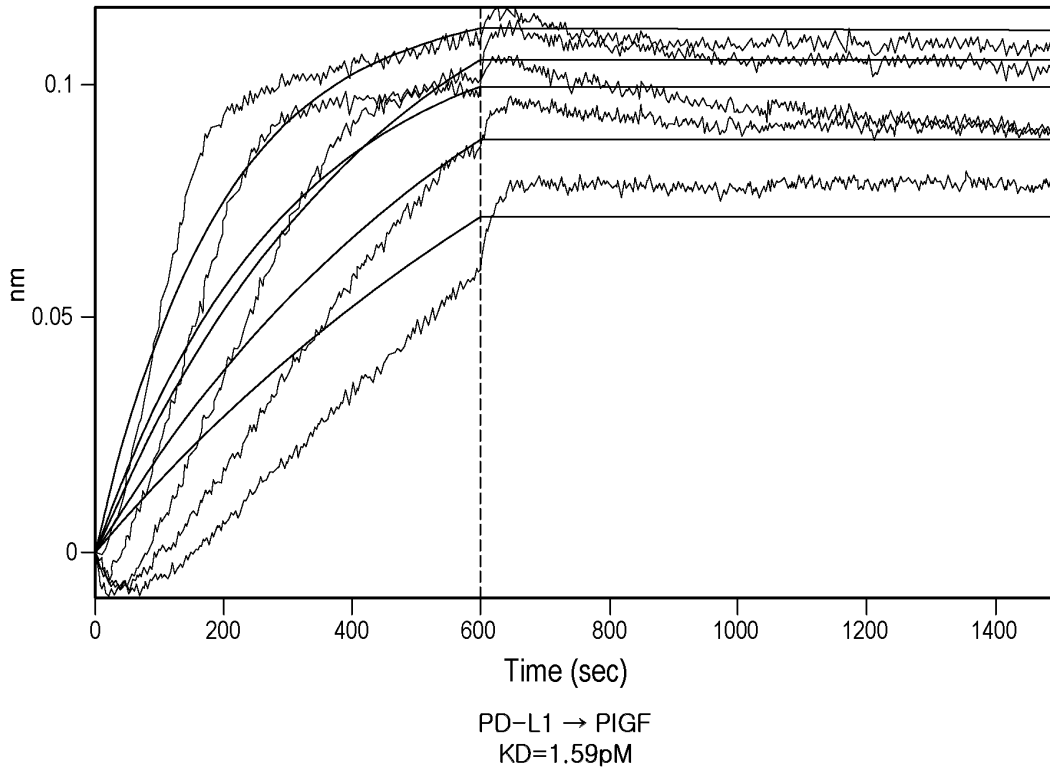


FIG. 6A

Cell-based VEGF-A inhibition experiment

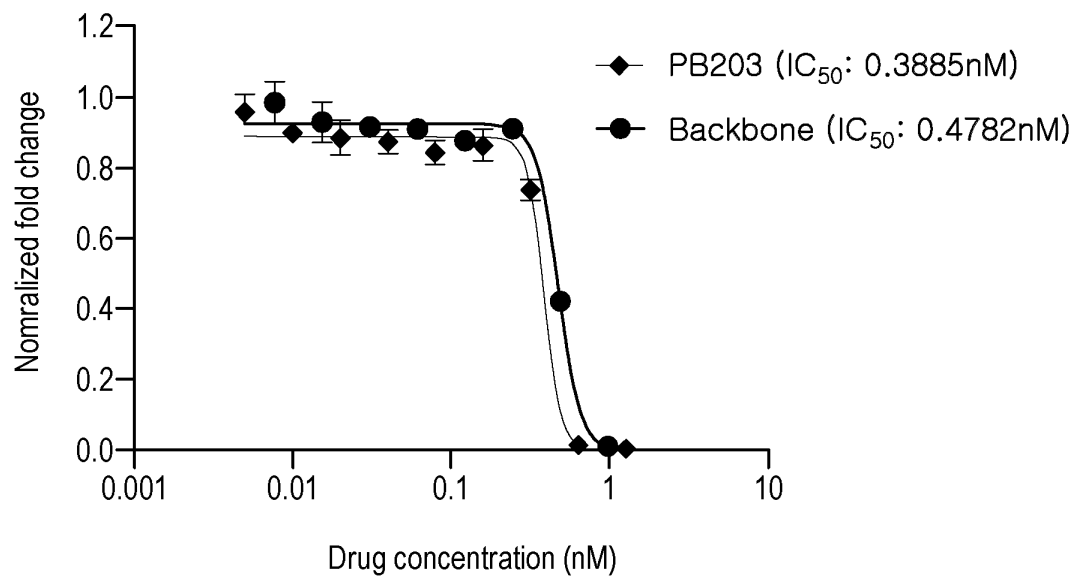


FIG. 6B

Cell-based PD-L1 inhibition experiment

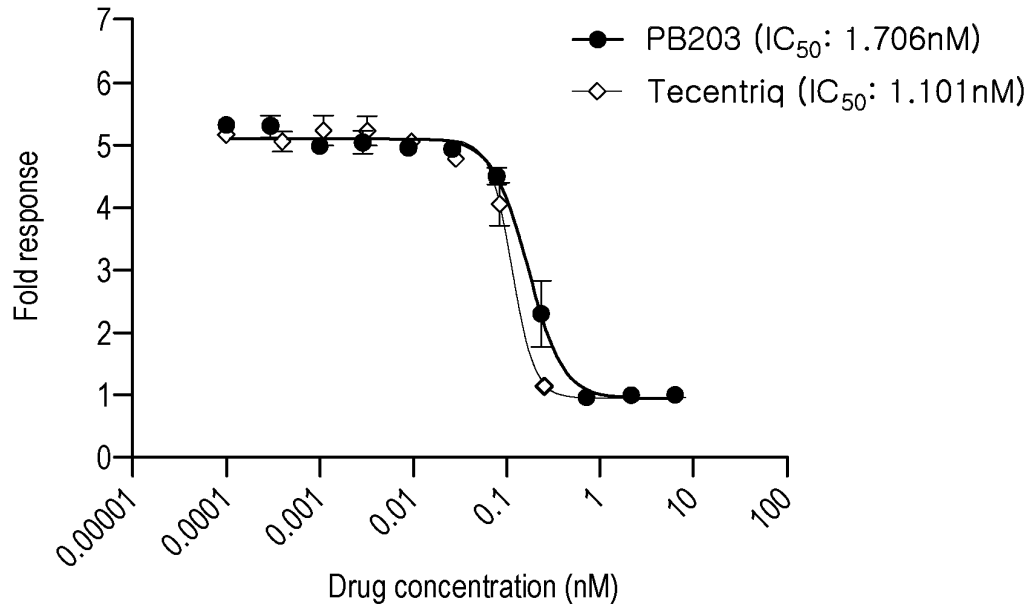


FIG. 6C

Inhibitor vs. response-variable slopes (4 parameters)					
Best-fit value	PB101	H-32D01	H-32D02	H-32D09	H-32D10
IC ₅₀	0.6243	0.1732	0.3848	0.3656	0.3821

FIG. 6D

VEGF-A stimulus

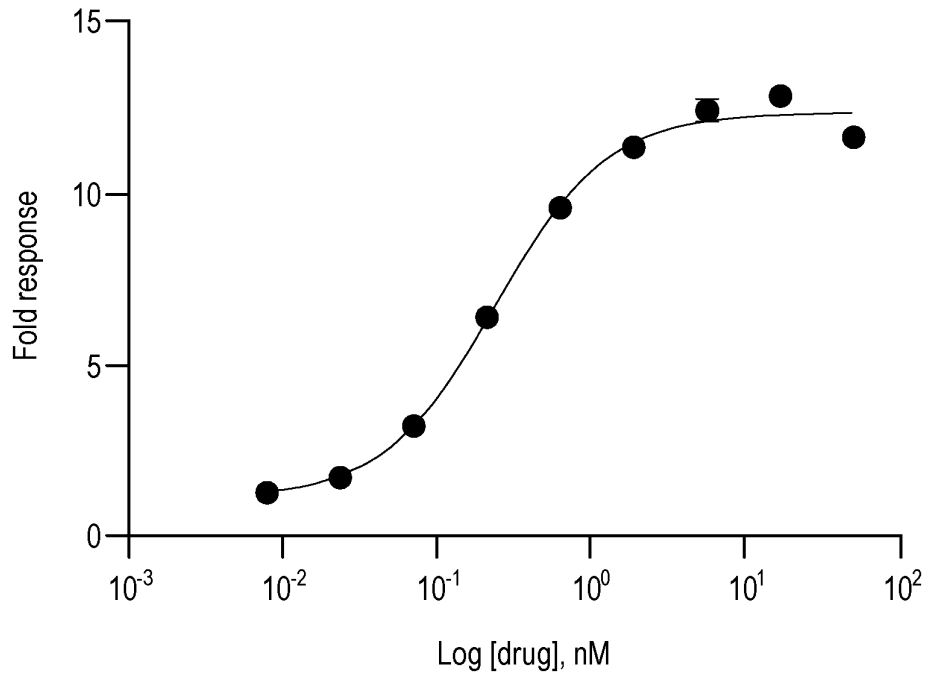


FIG. 6E

H-32D09

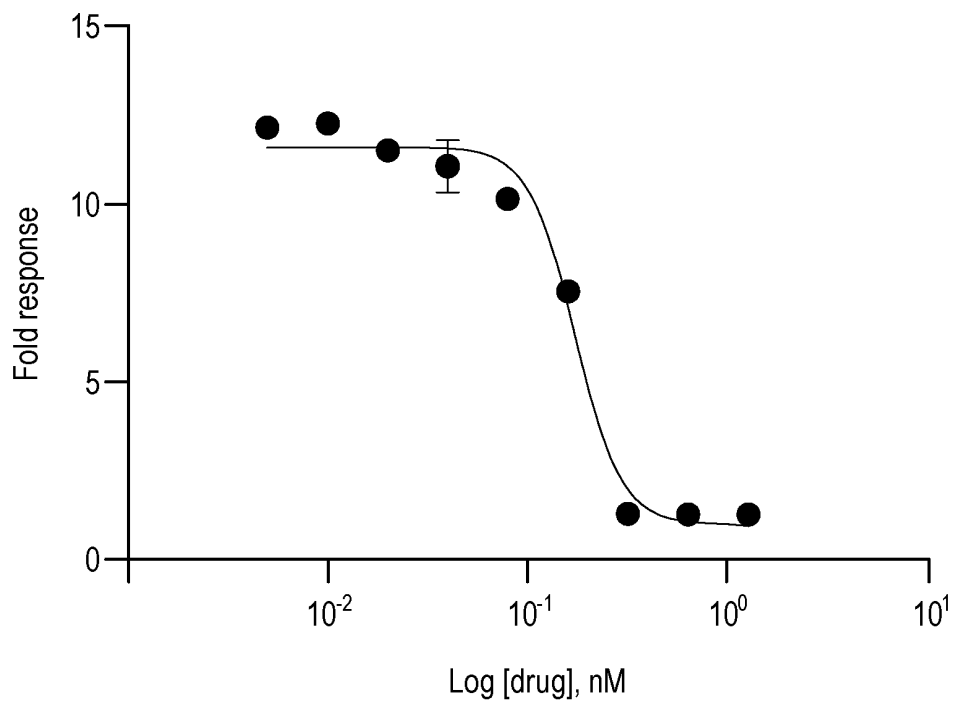


FIG. 6F

PB101 (DP)

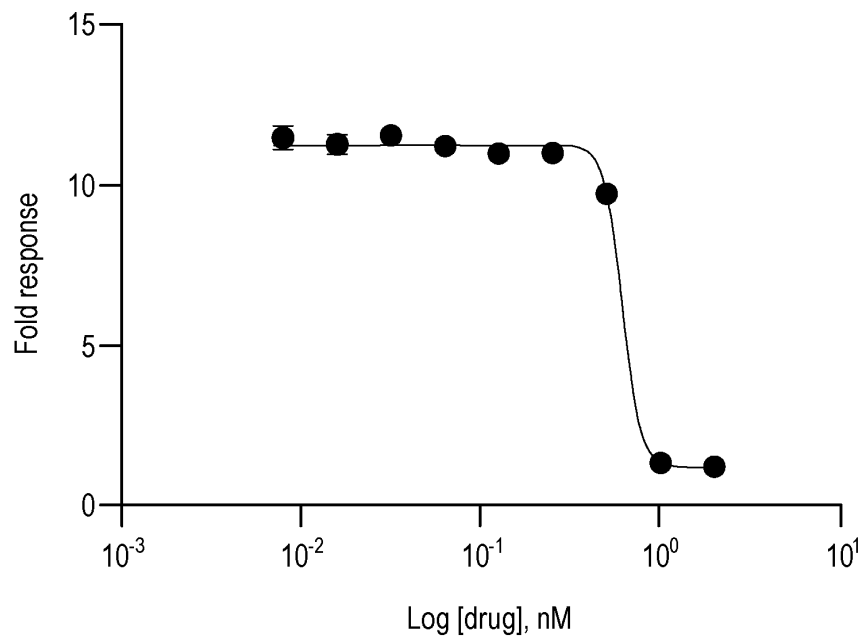


FIG. 6G

H-32D09

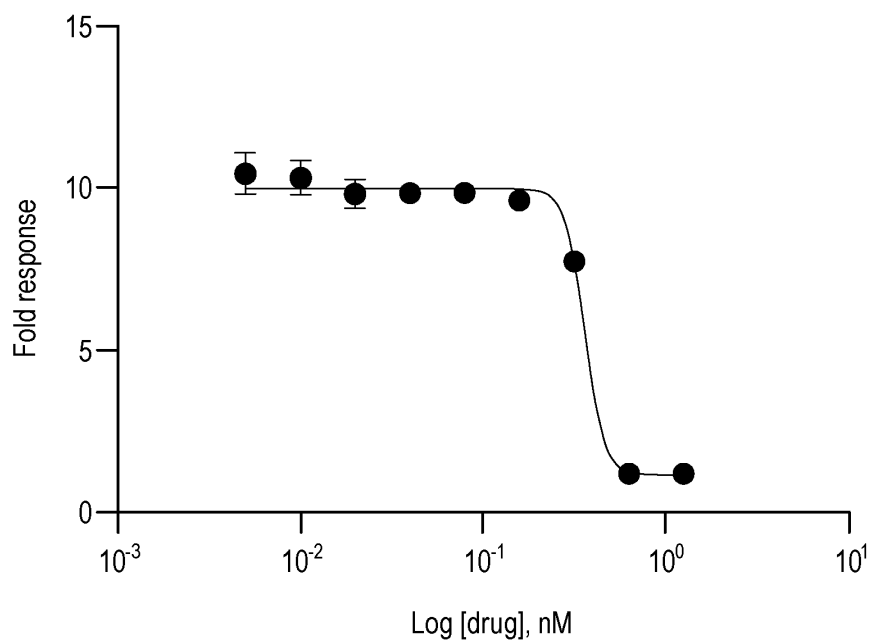


FIG. 6H

H-32D10

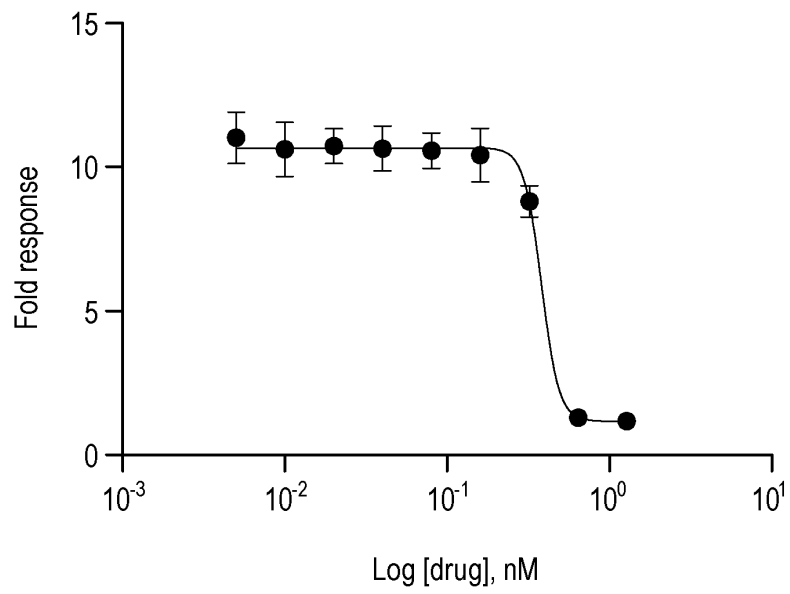


FIG. 6I

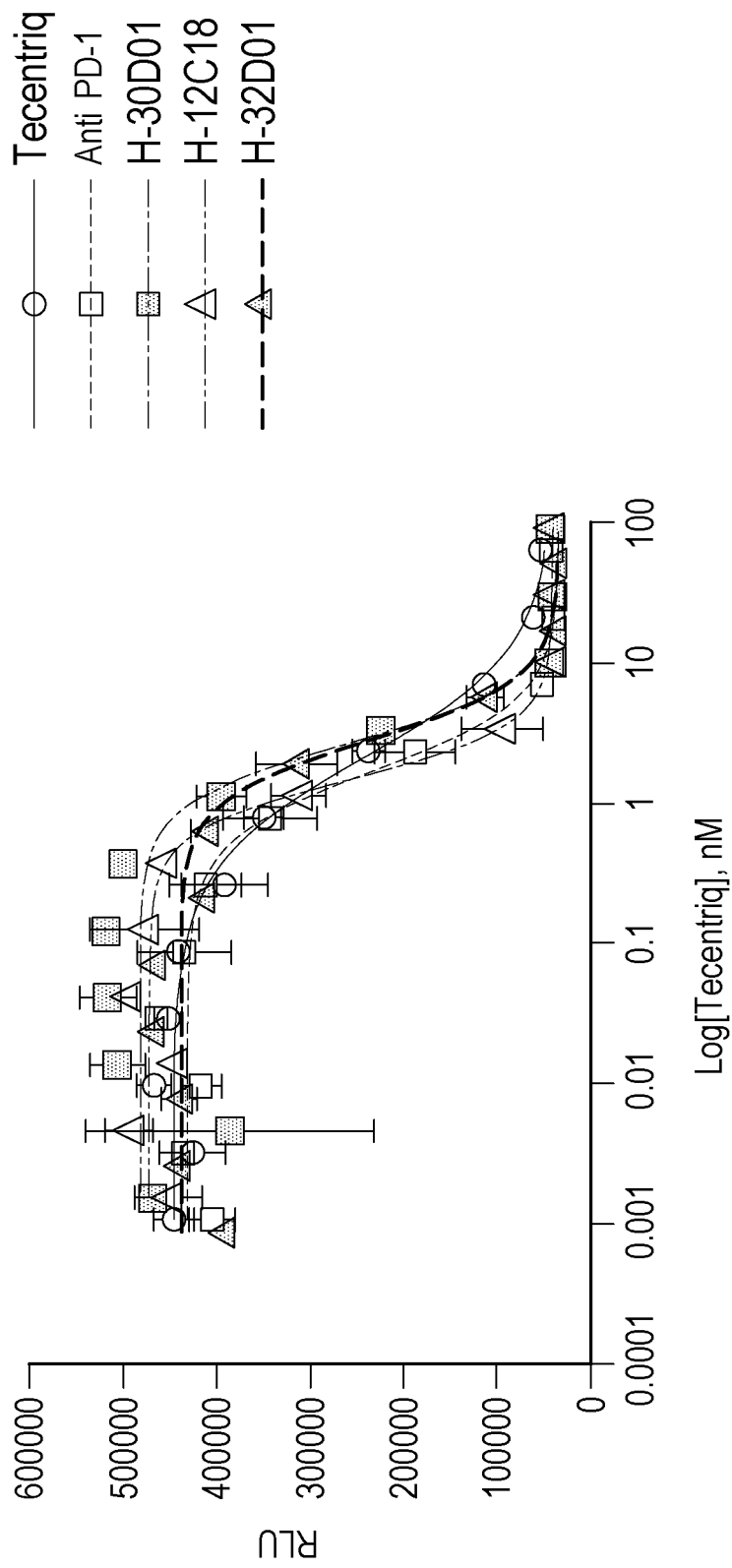


FIG. 6J

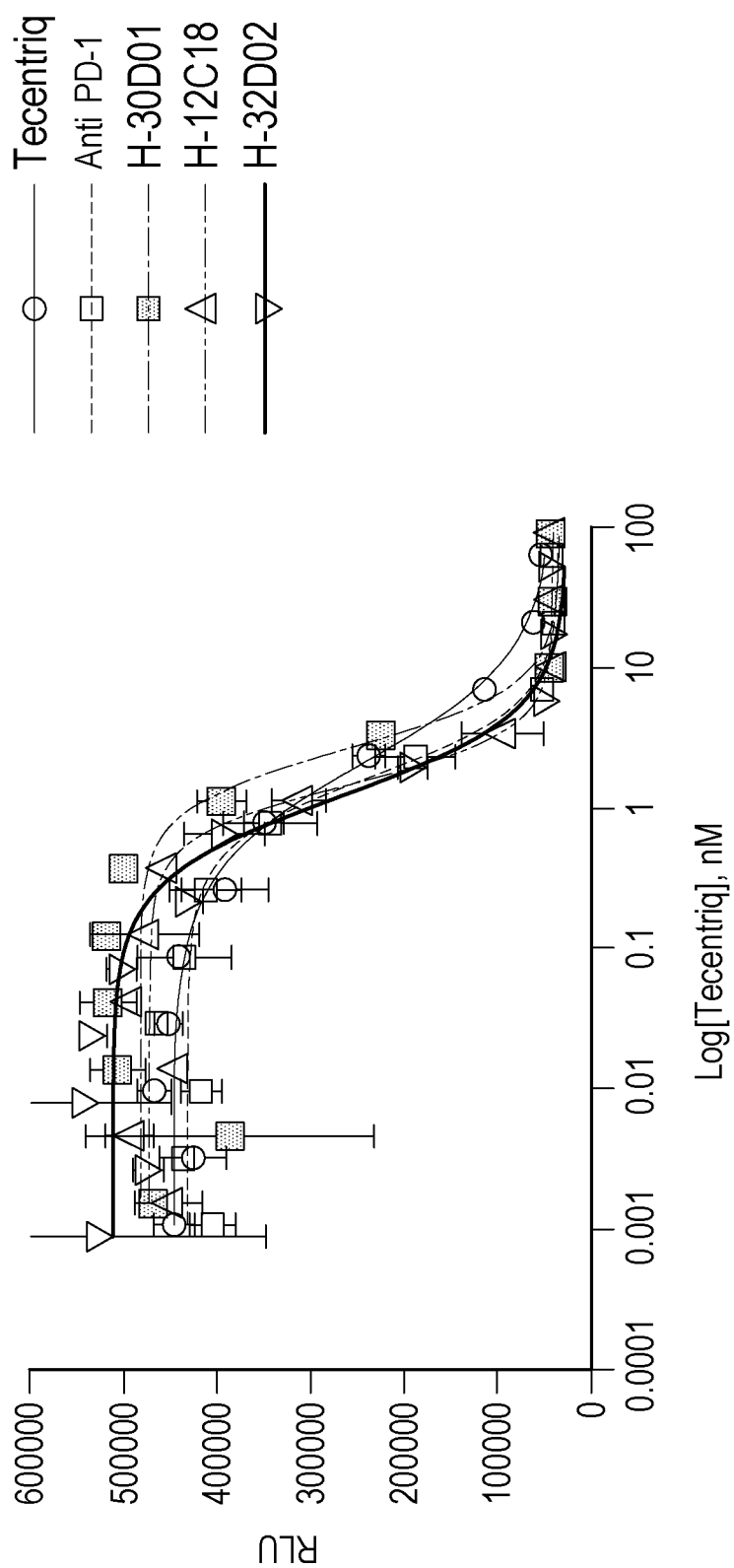


FIG. 6K

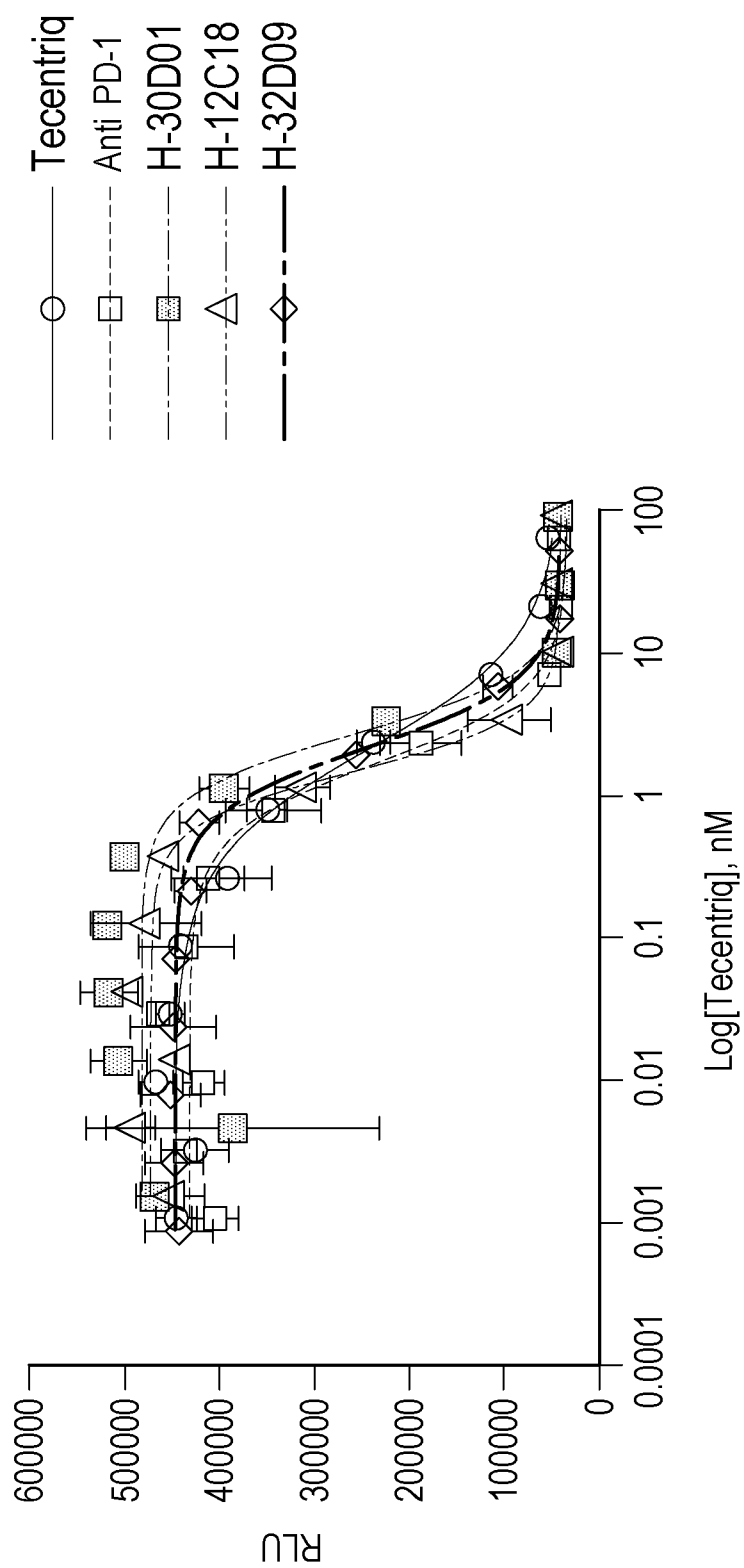


FIG. 6L

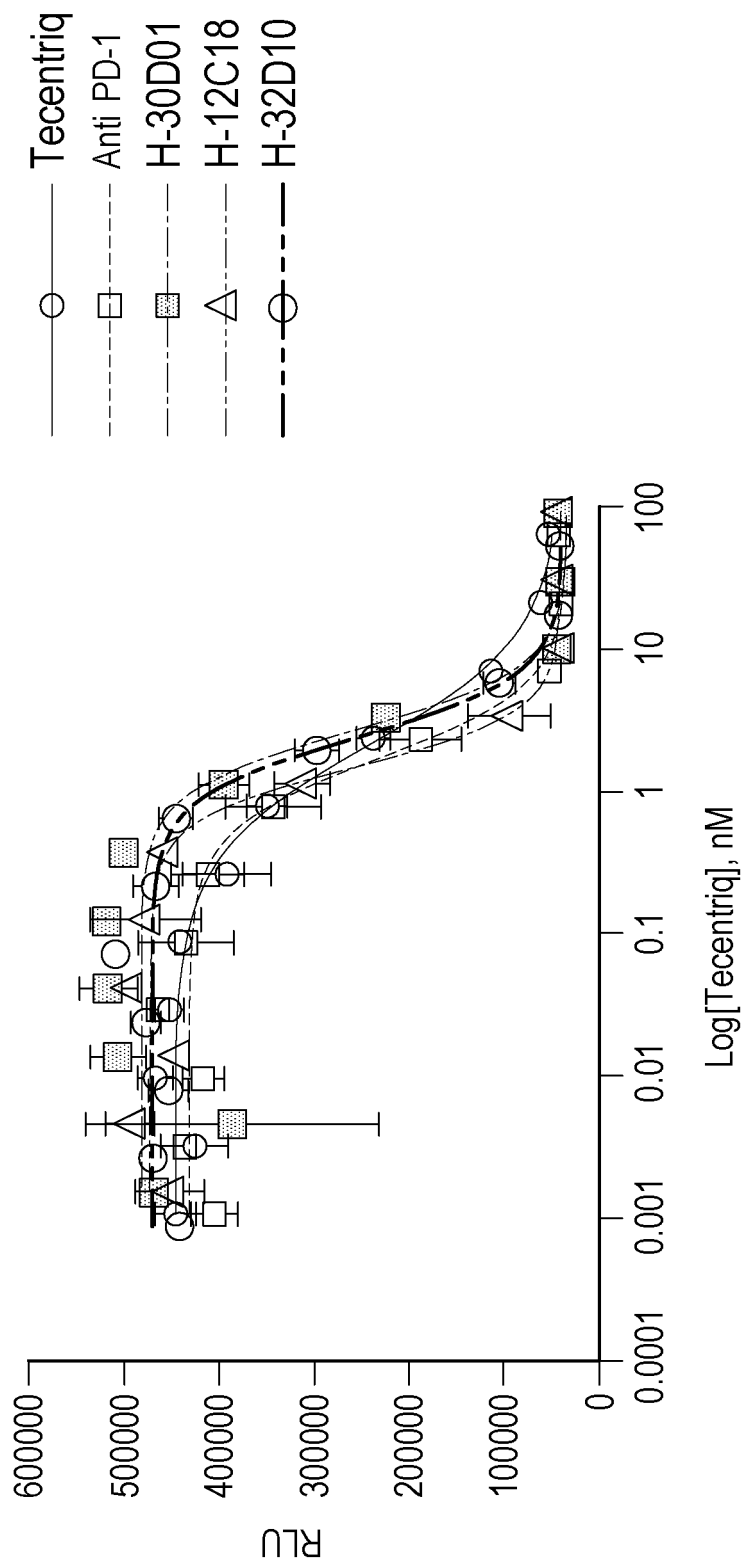


FIG. 6M

Inhibitor vs. response- variable slopes (4 parameters)	Tecentriq	Anti-PD-1 antibody	H-32D01	H-32D02	H-32D09	H-32D10	H-30D01	H-12C18
IC50	10.62	9.117	14.51	8.554	12.17	12.89	9.976	6.666

FIG. 6N

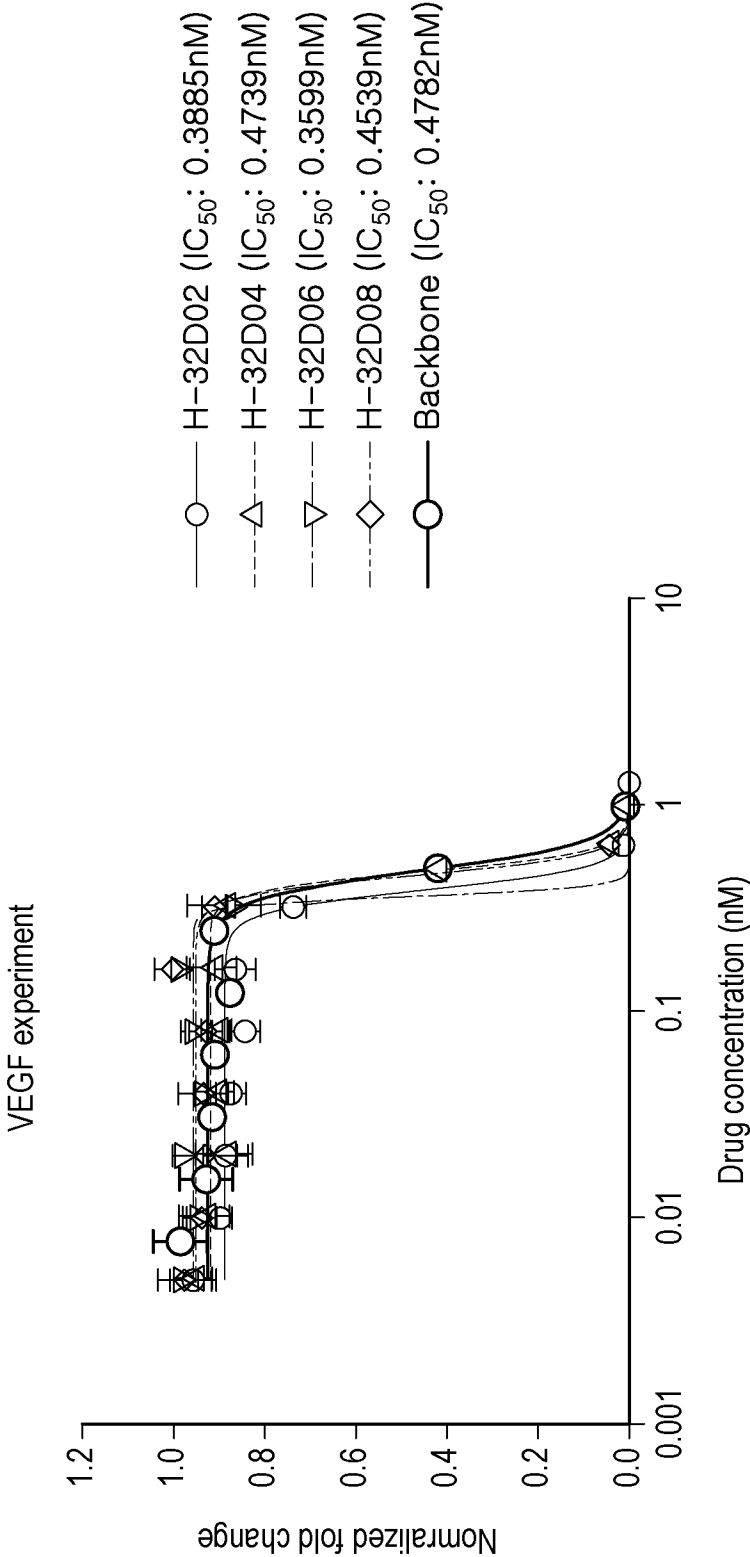


FIG. 60

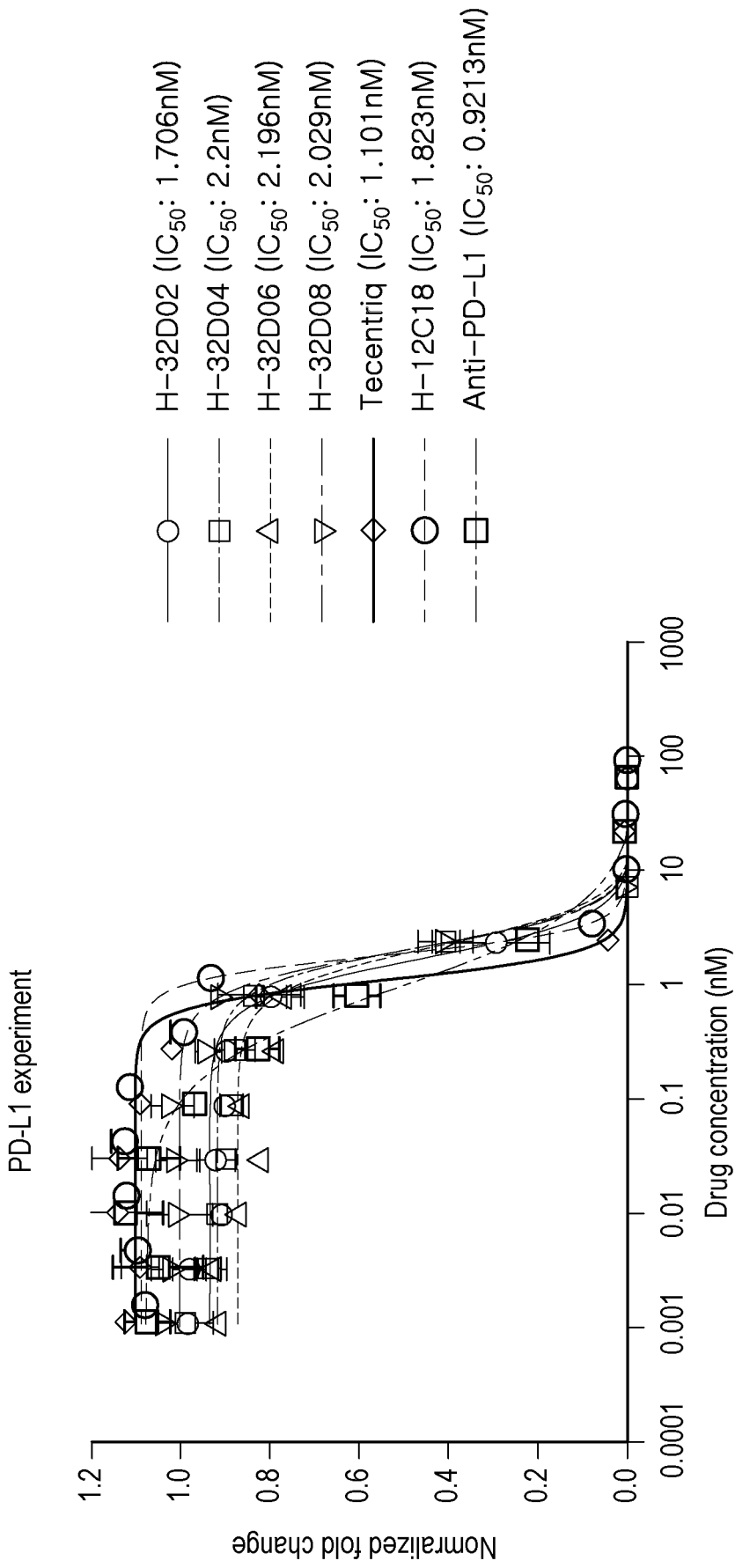


FIG. 7A

H-12C08

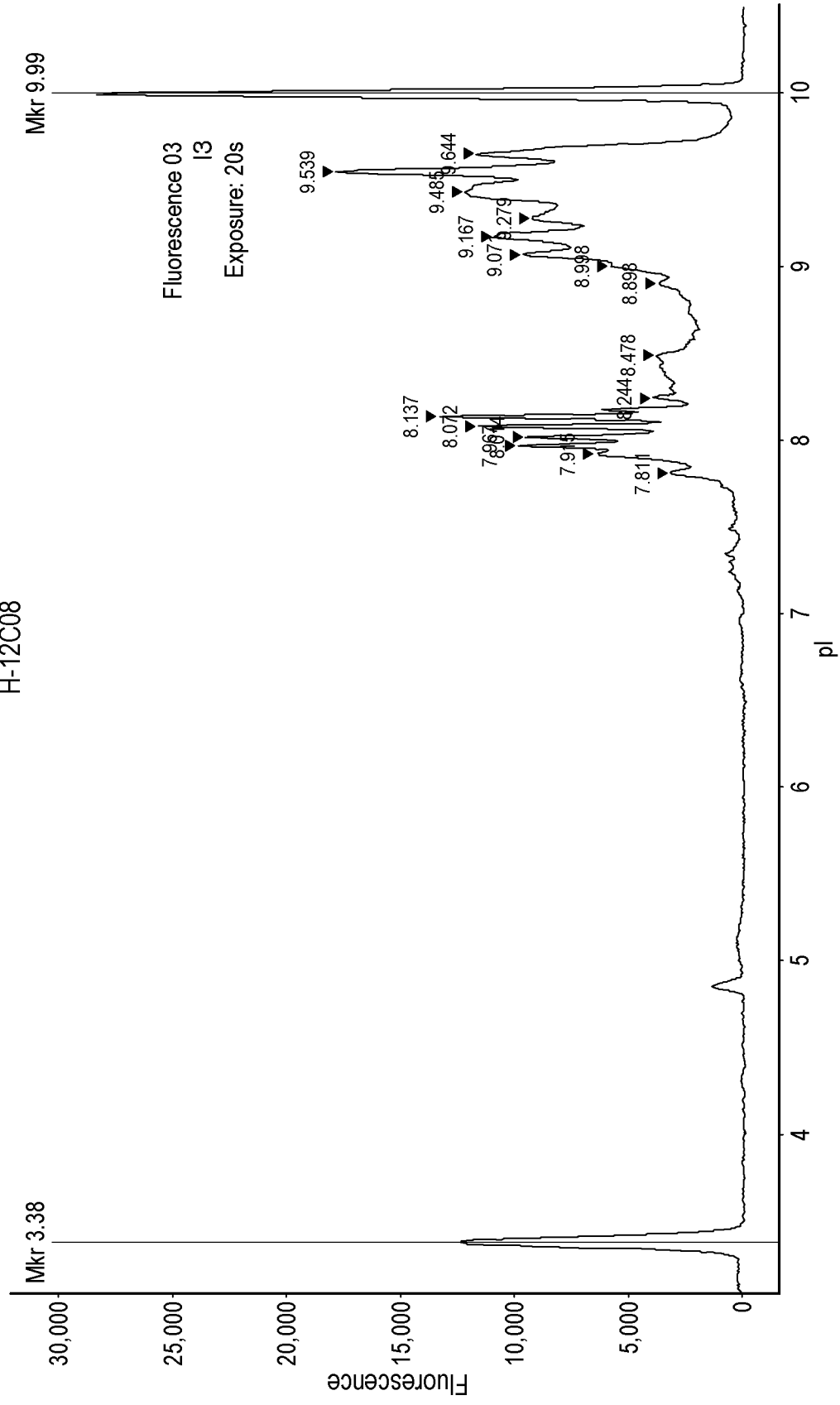


FIG. 7B

H-12C94

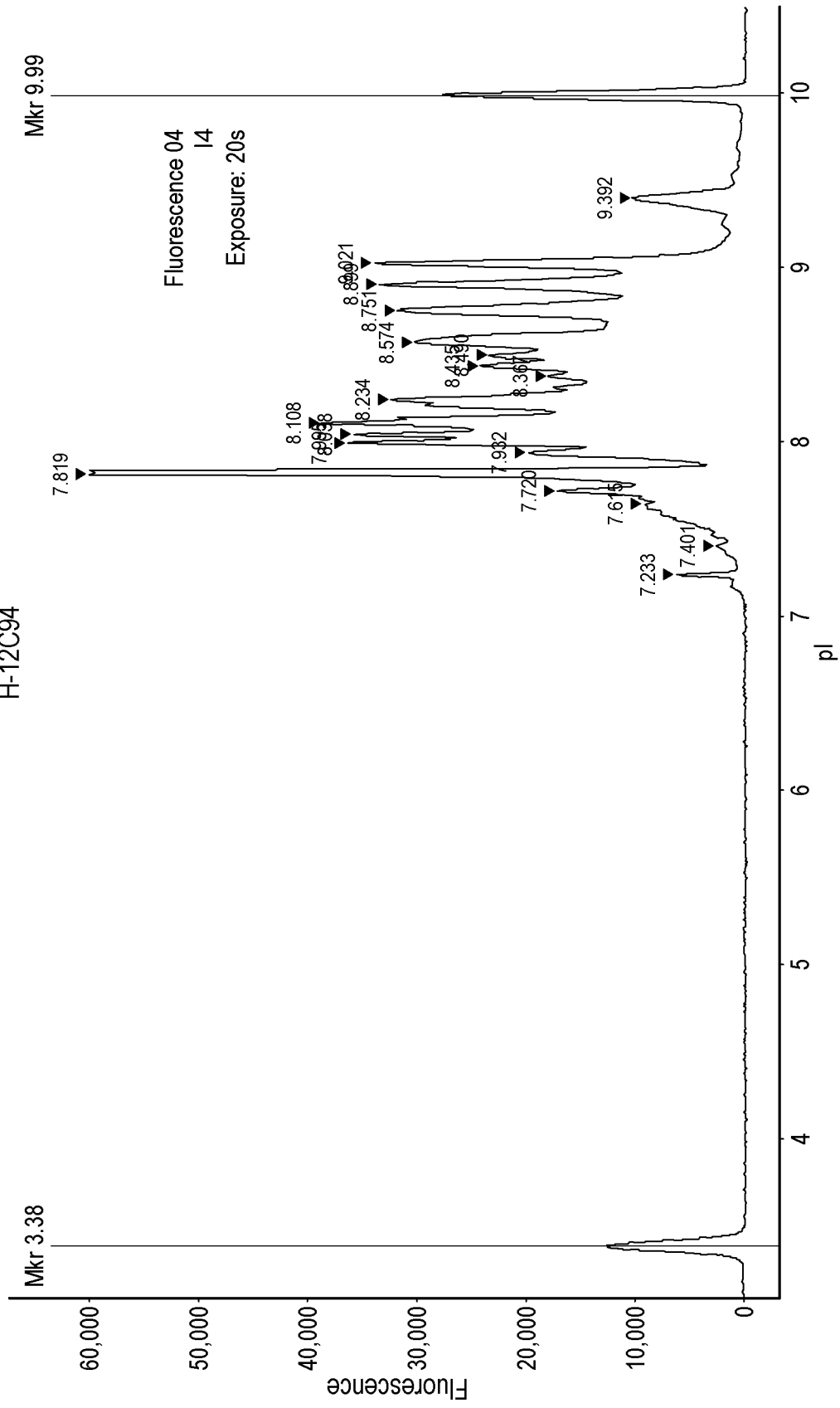


FIG. 7C

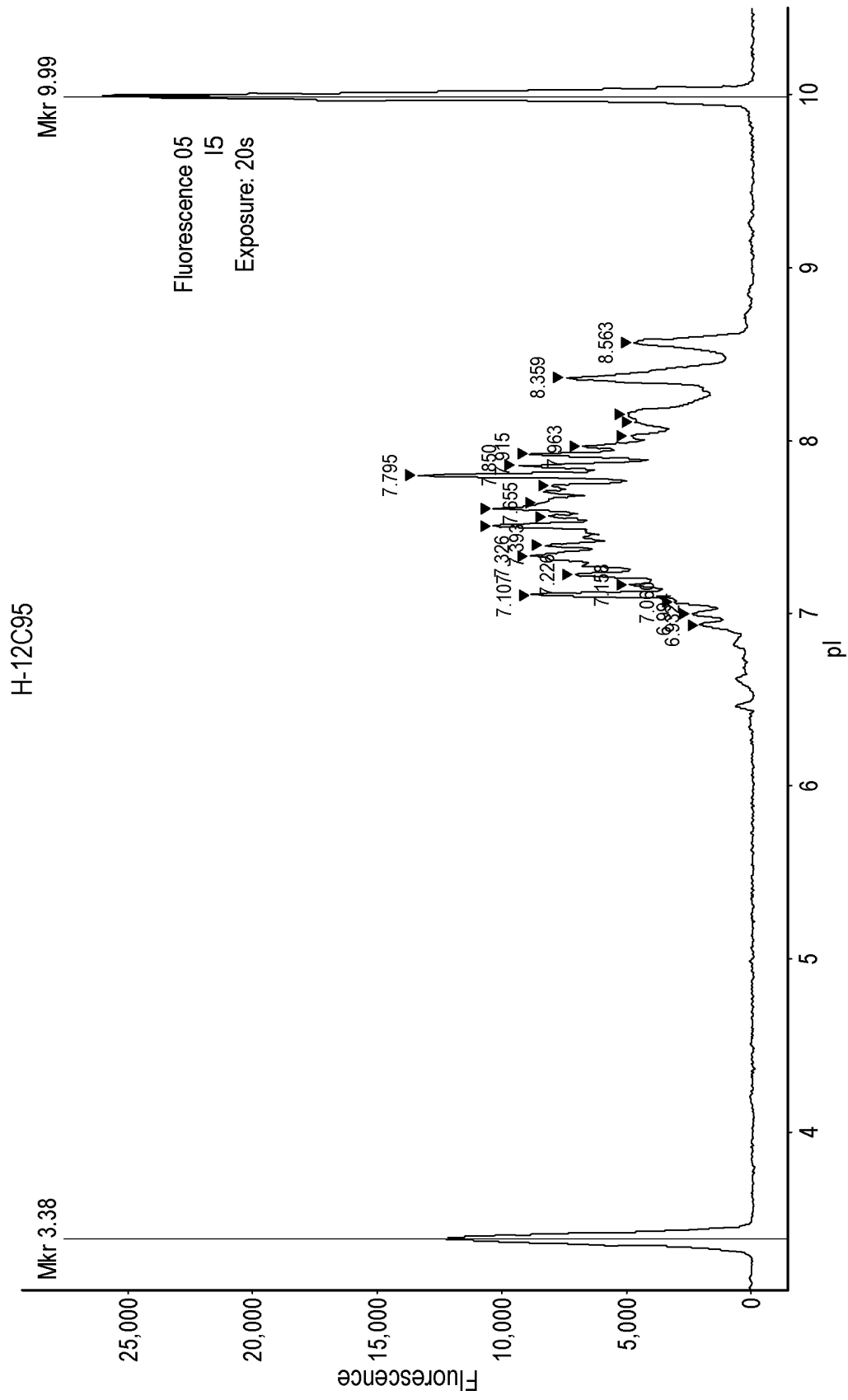


FIG. 7D

H-12C96

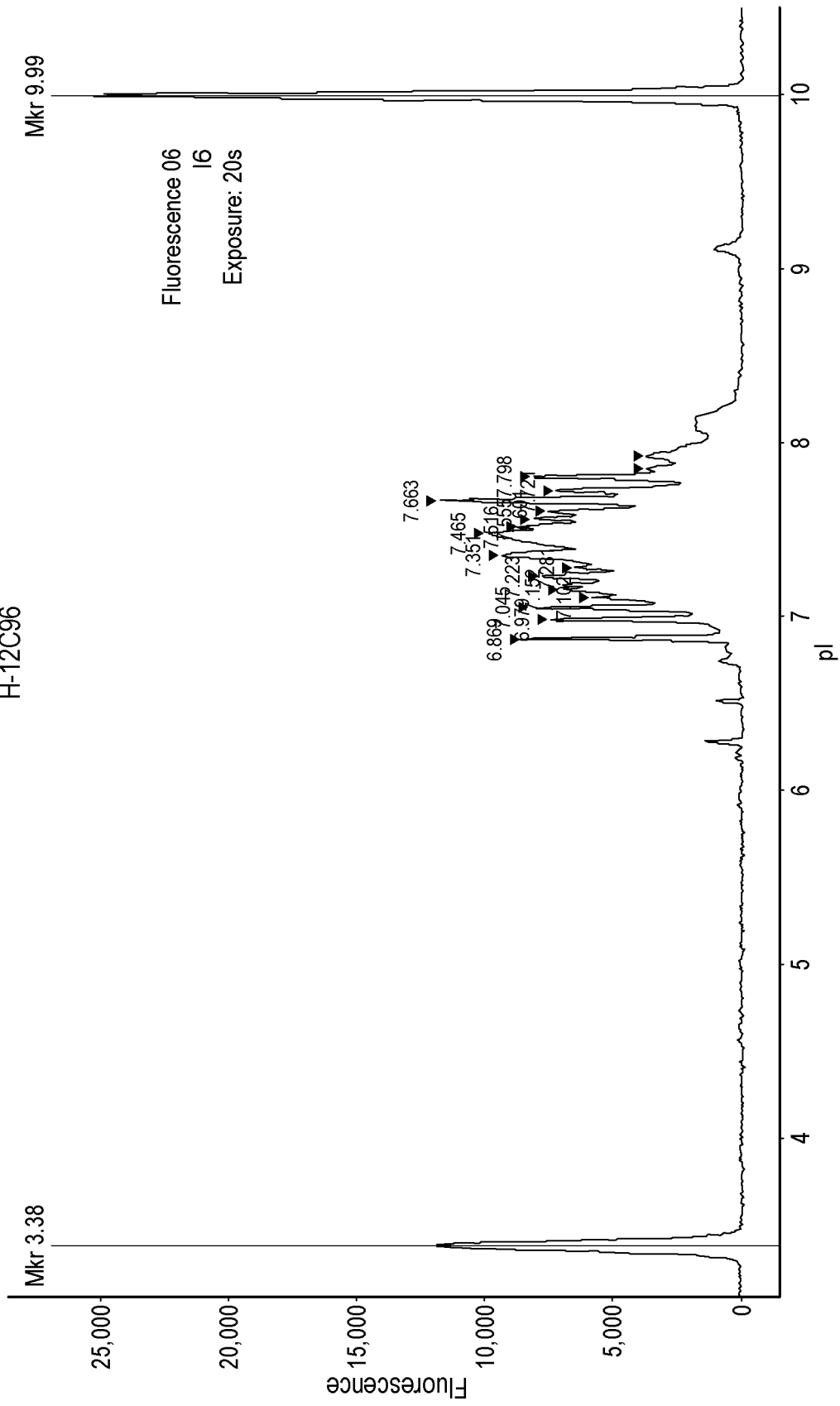


FIG. 7E

H-32D08

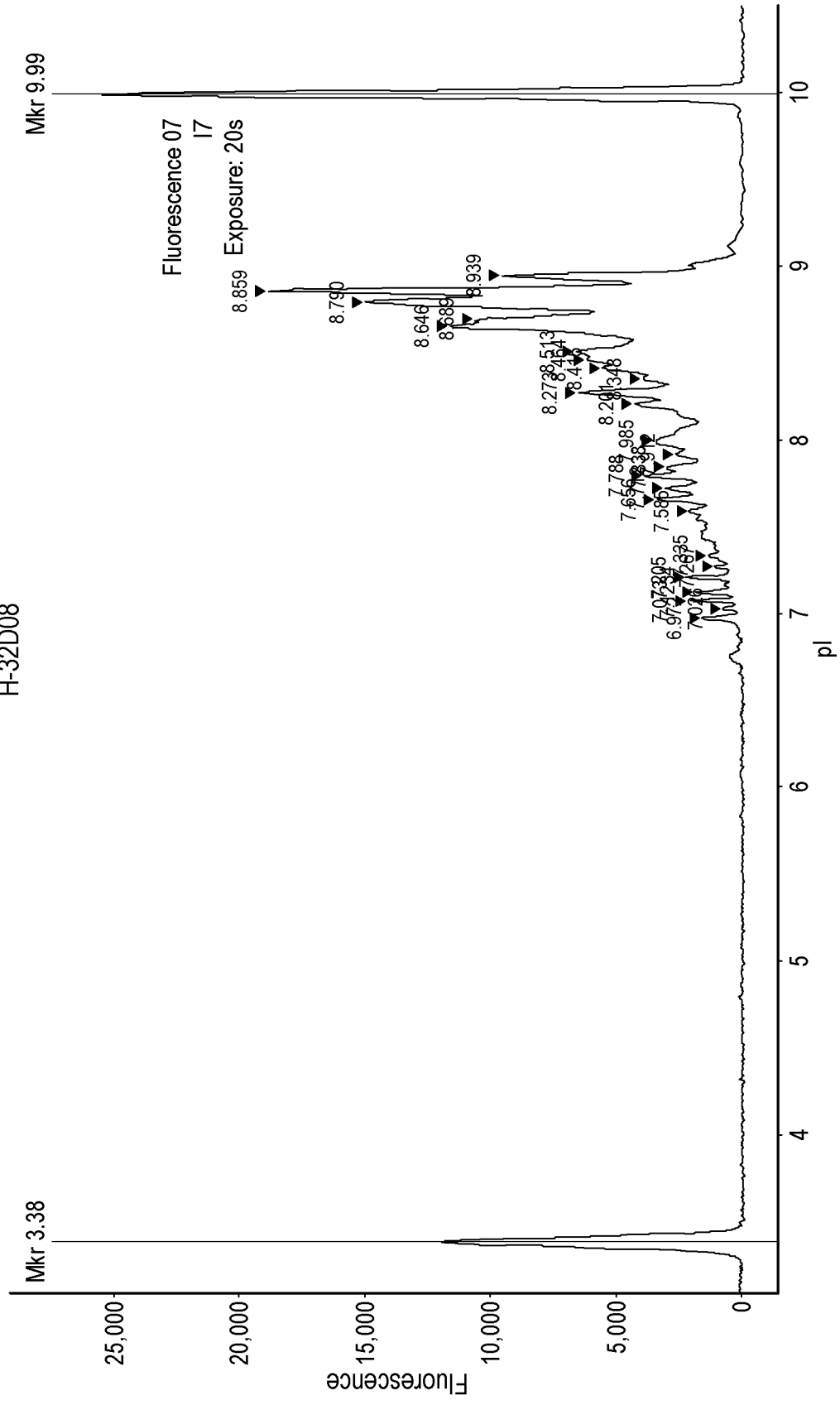


FIG. 7F

H-12C99

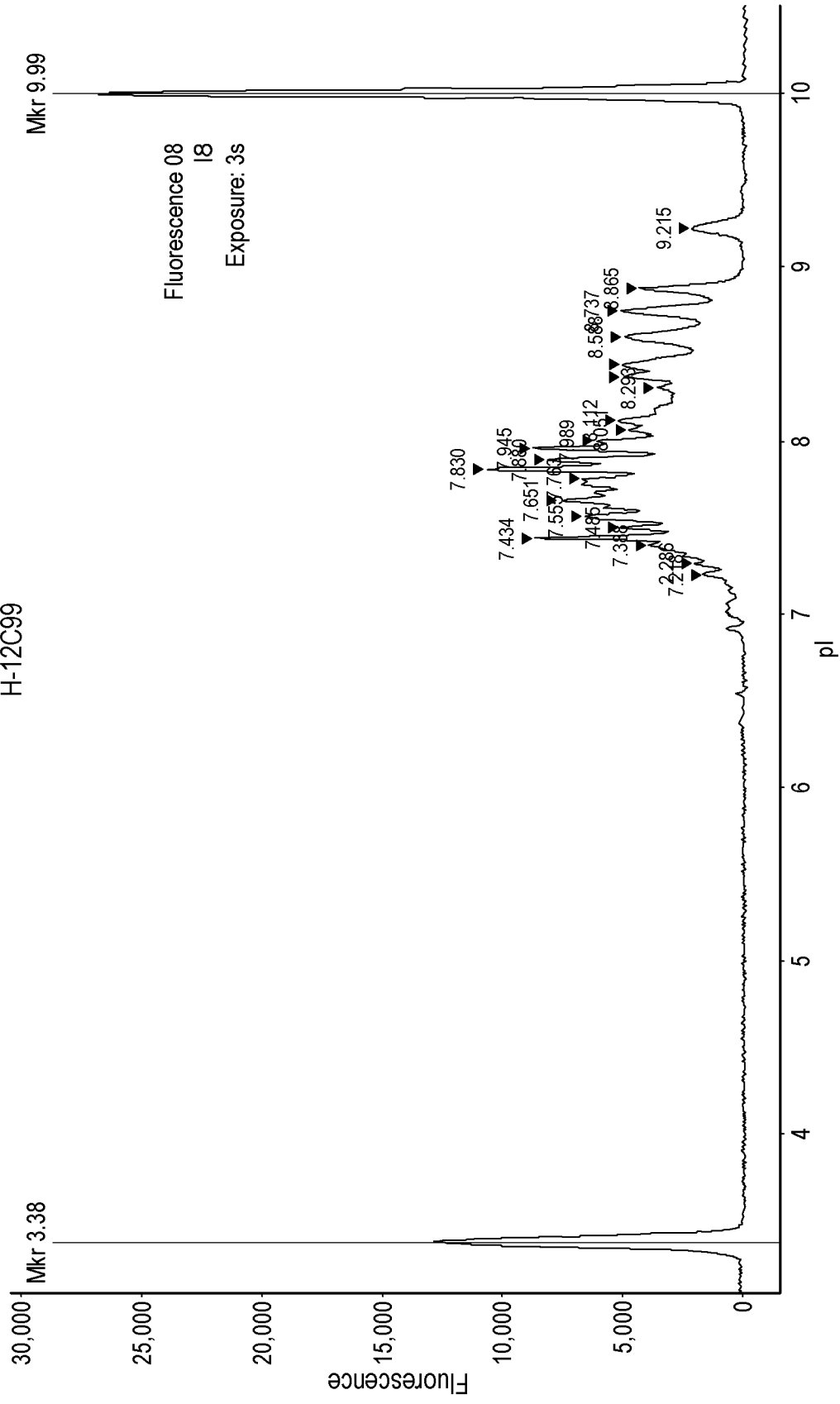


FIG. 7G

	% Total (area)			
Sample name	Acidic (pI <7)	Neutral (pI 7~8)	Basic (pI 8<)	Sum
PB101 (PD20A01)		49.4	50.6	100
H-12C08		9.6	90.5	100.1
H-12C94		26.8	73	99.8
H-12C95	2.7	75.8	21.4	99.9
H-12C96	7.1	93		100.1
H-12C97	0.8	21.7	77.6	100.1
H-12C99		58.5	41.5	100

FIG. 7H

H-12C08

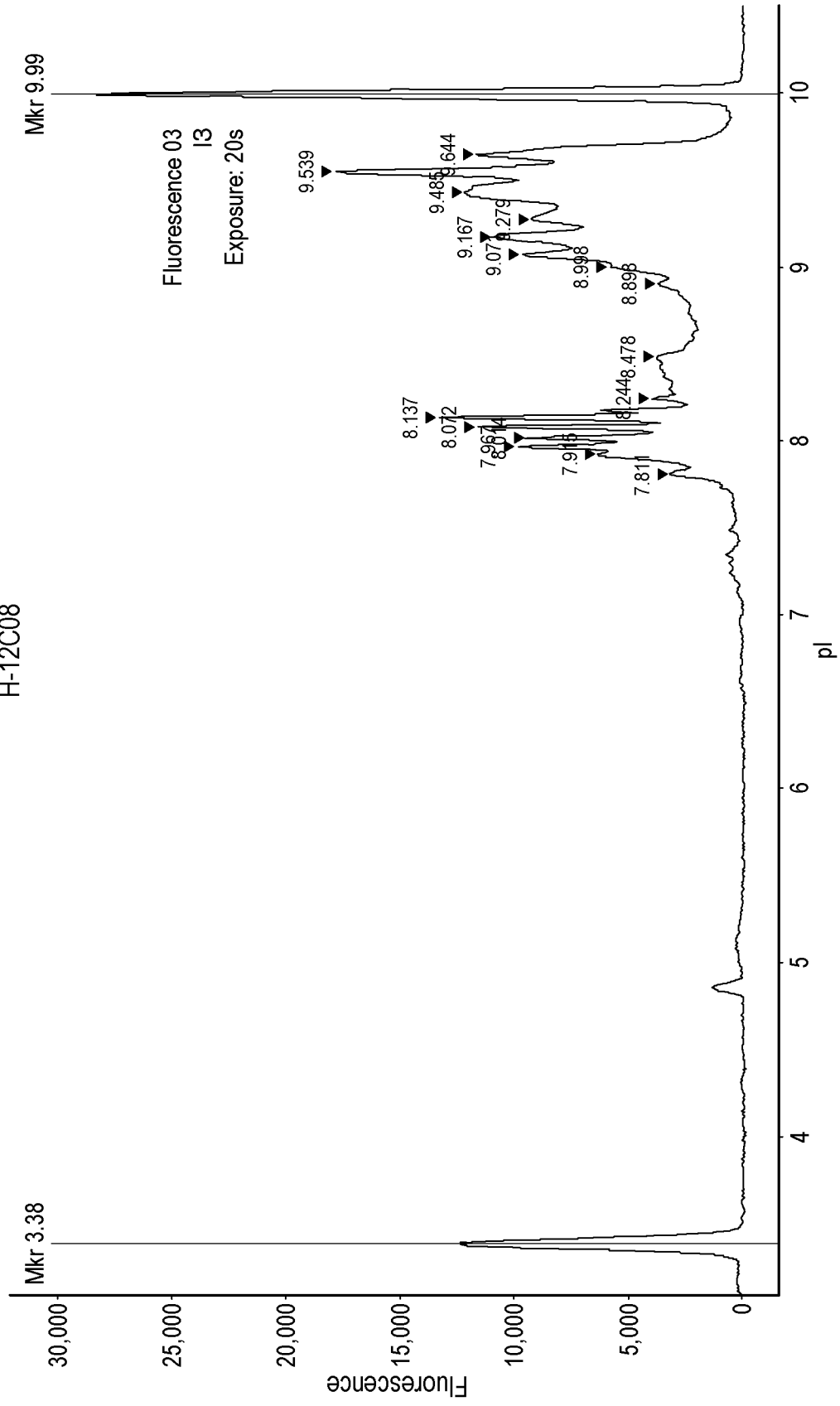


FIG. 71

H-32D01

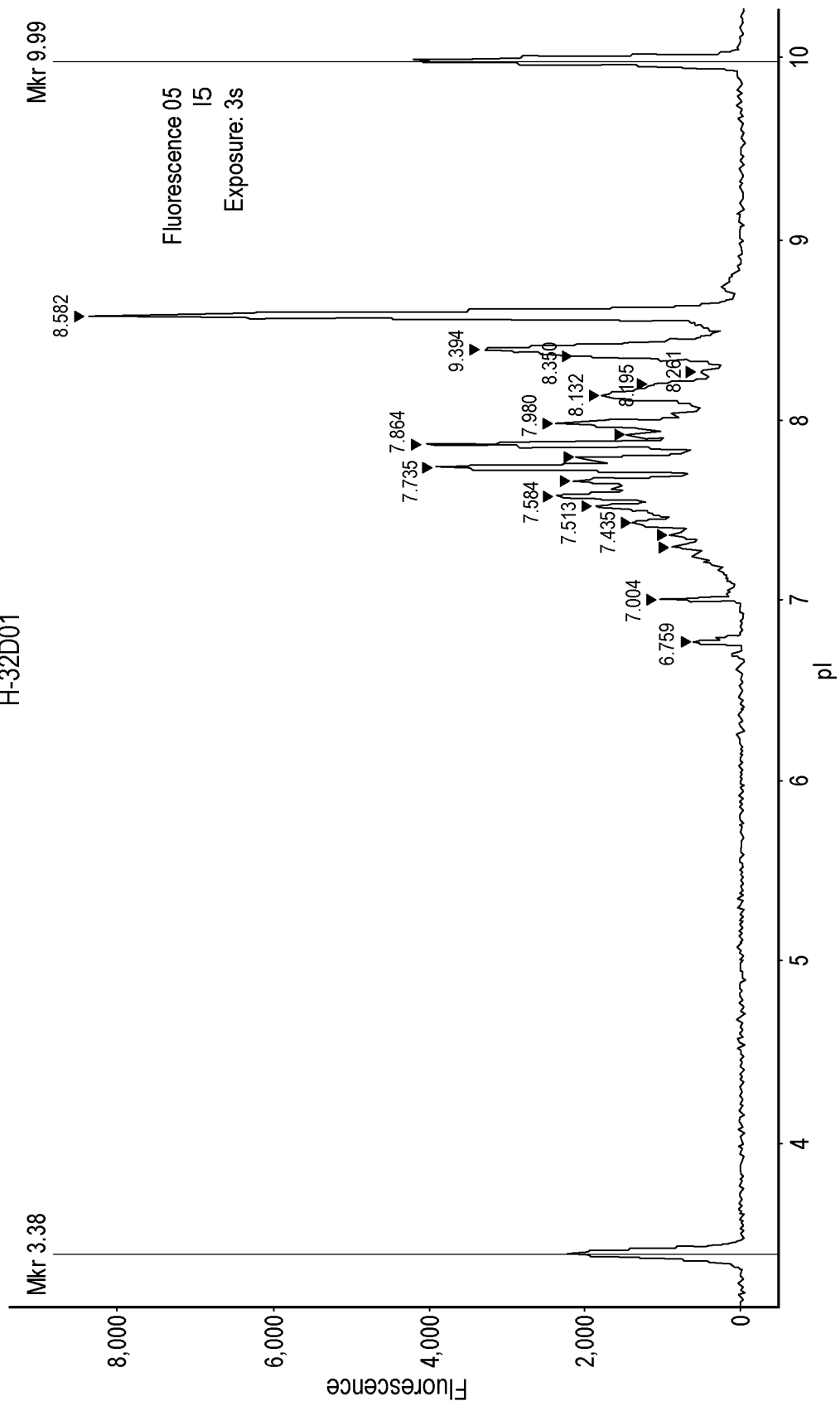


FIG. 7J

H-32D02

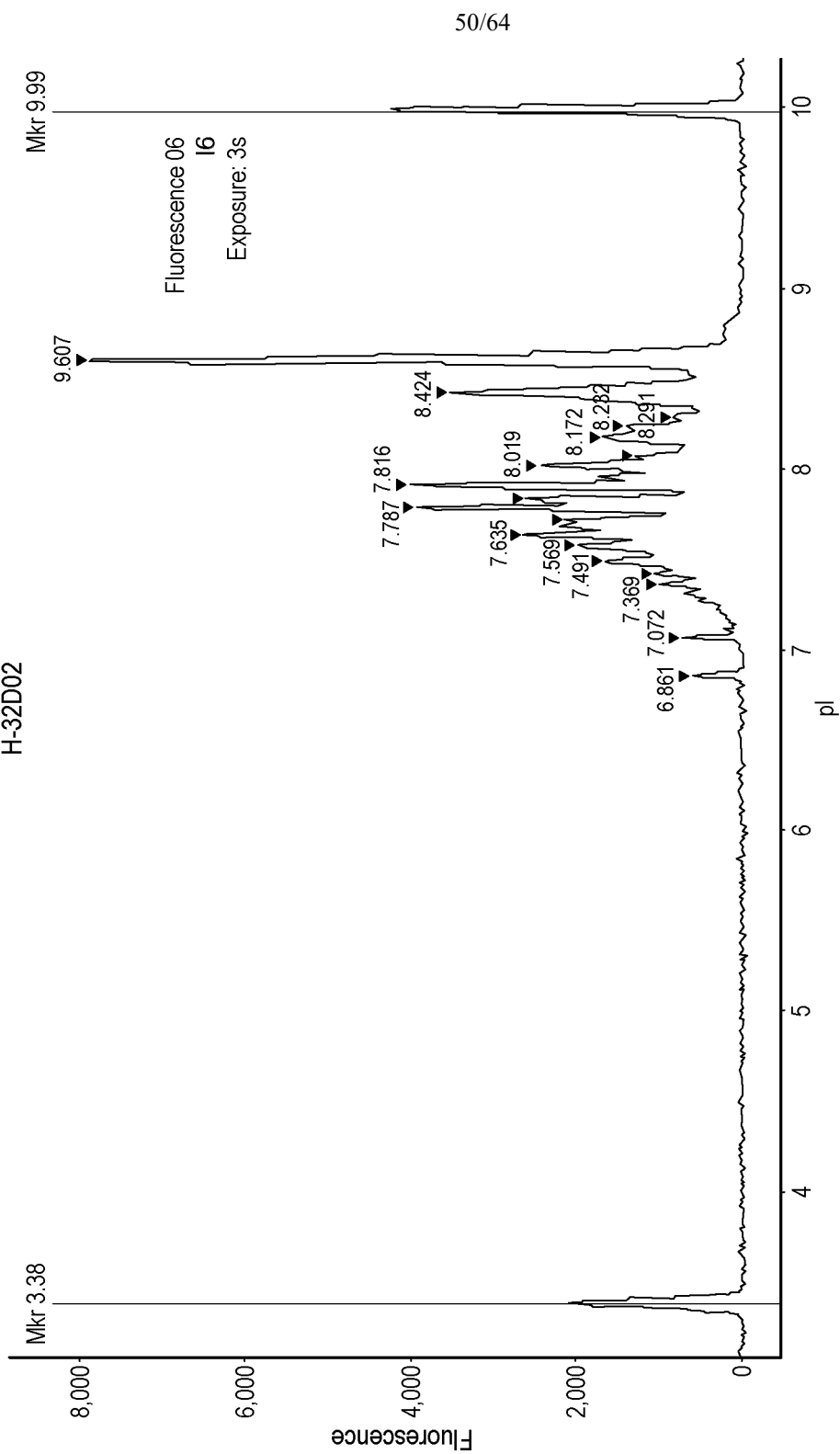


FIG. 7K

H-32D09

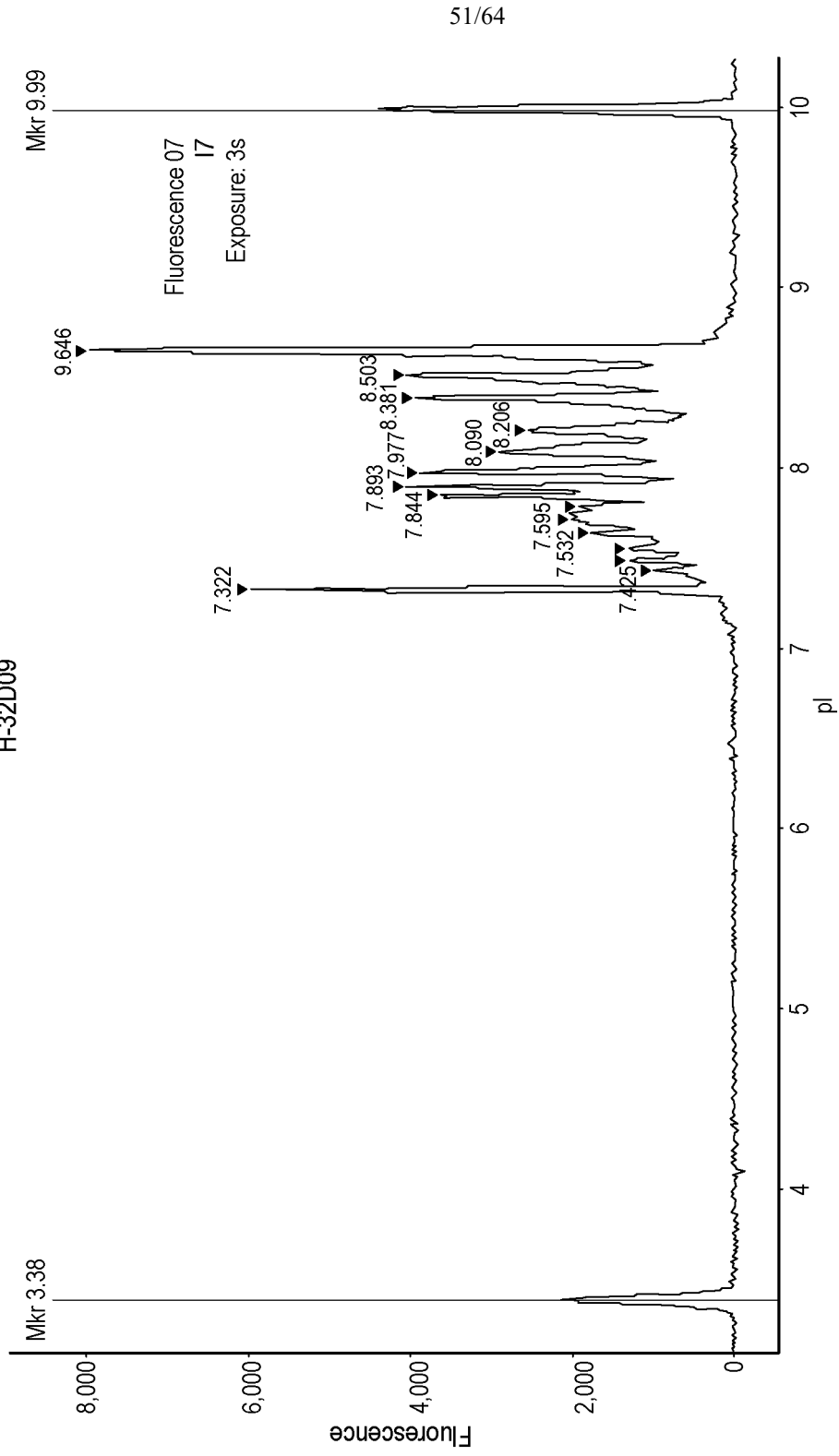


FIG. 7L

H-32D10

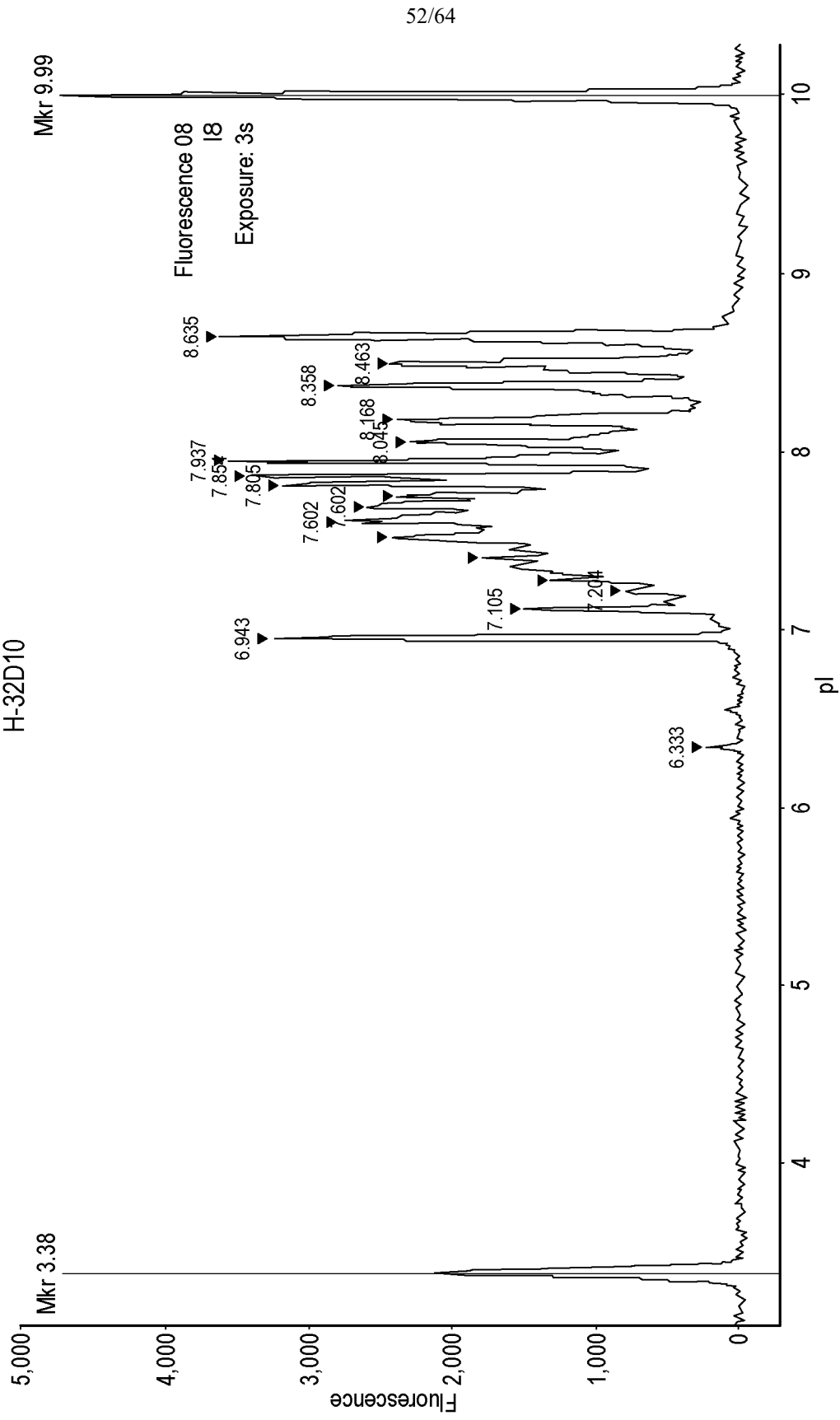


FIG. 7M

Sample name	% Total (area)			
	Acidic (pI <7)	Neutral (pI 7~8)	Basic (pI 8<)	Sum
H-12C08		9.6	90.5	100.1
H-32D01	0.9	56.7	42.5	100.1
H-32D02	0.7	47.5	51.7	99.9
H-32D09		46.6	53.4	100
H-32D10	3.6	62.5	34.2	100.3

FIG. 7N

H-32D02

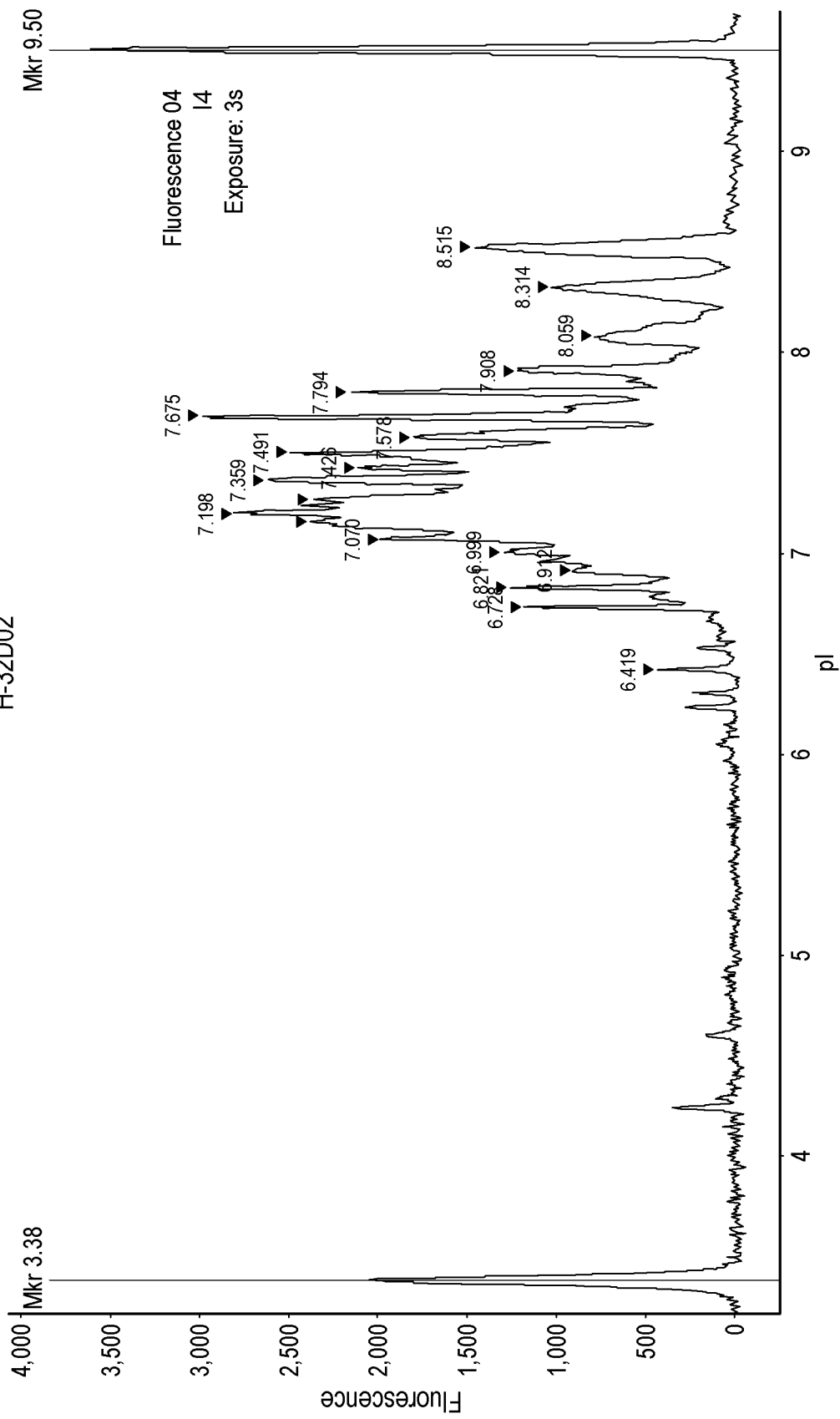


FIG. 70

H-32D04

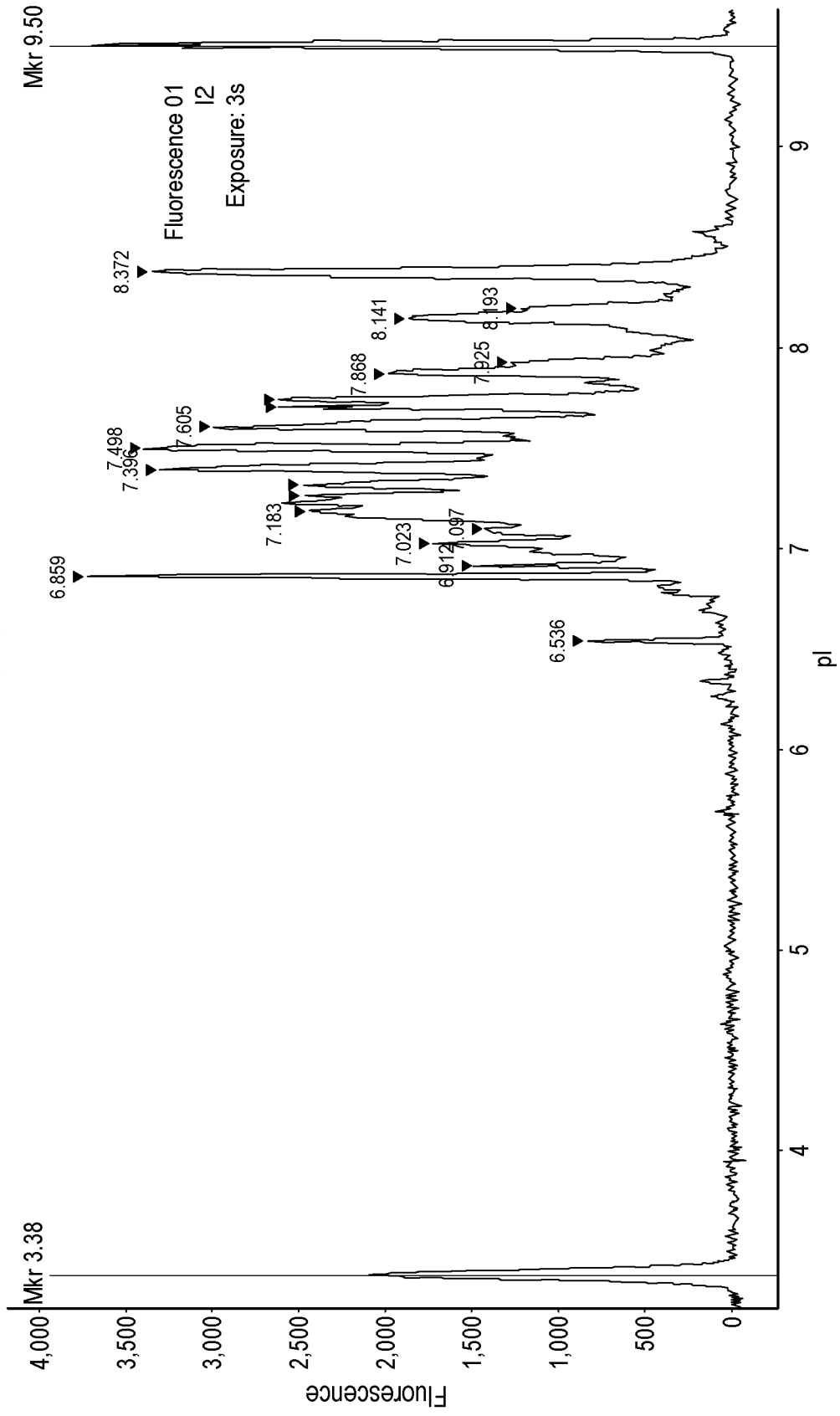


FIG. 7P

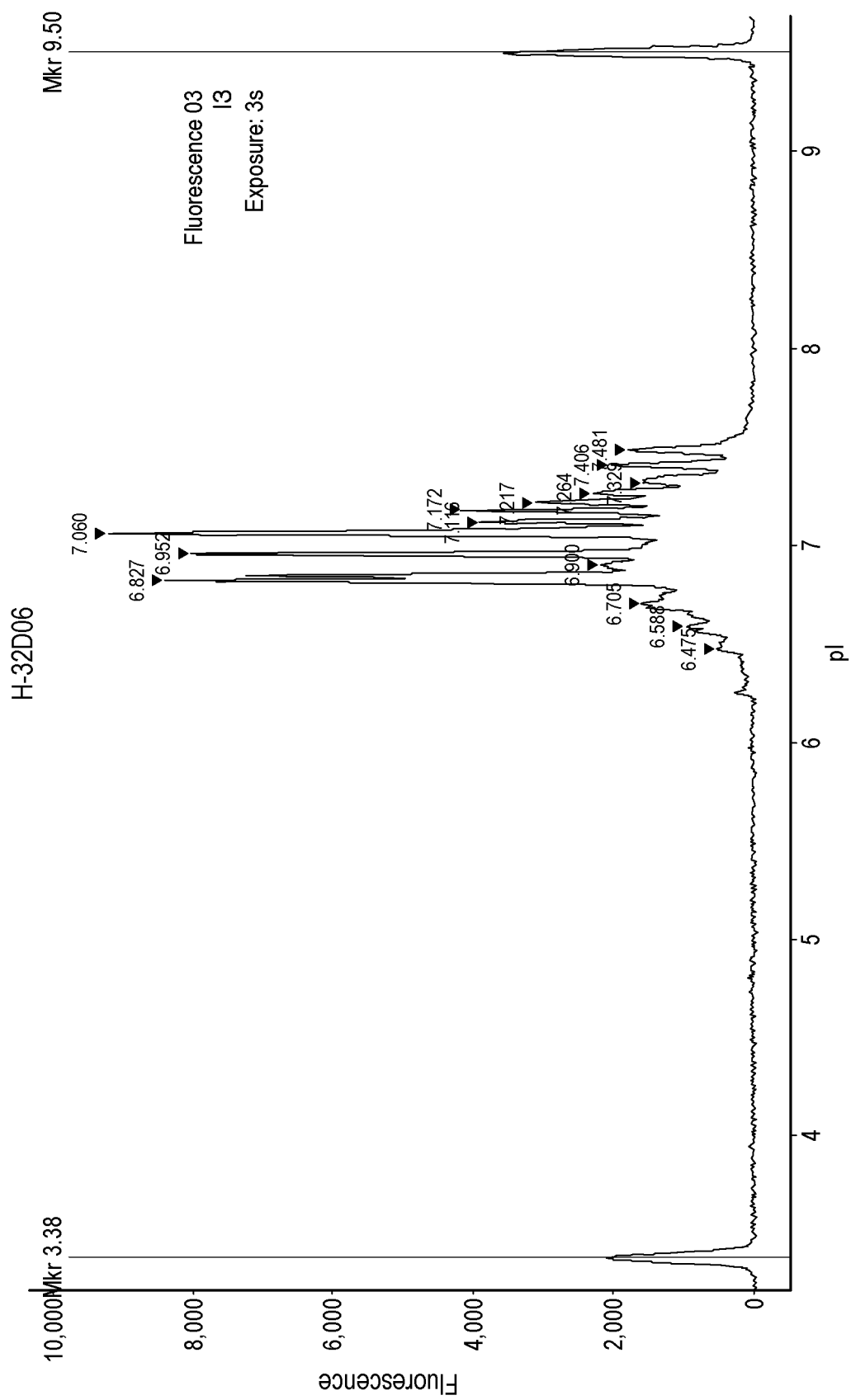


FIG. 7Q

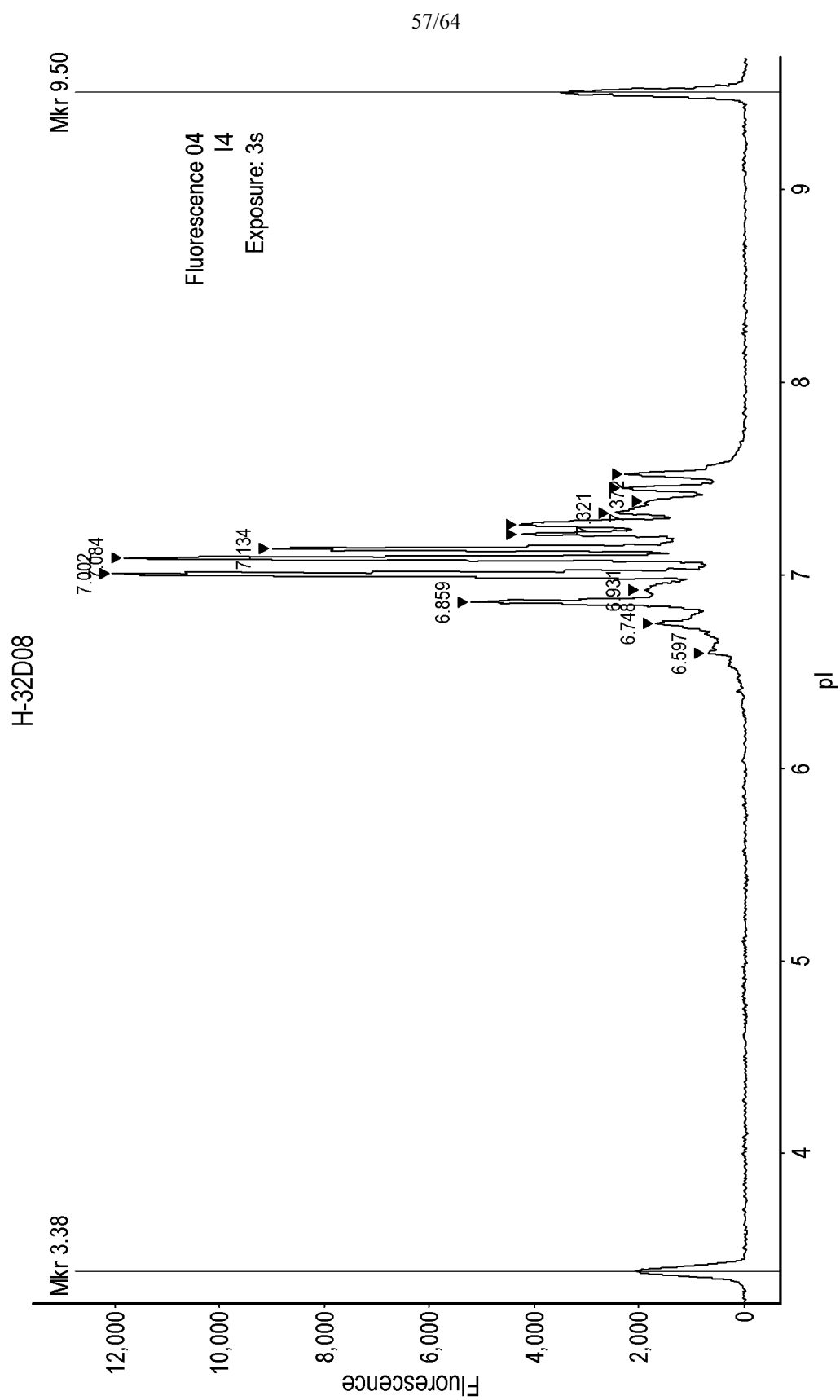
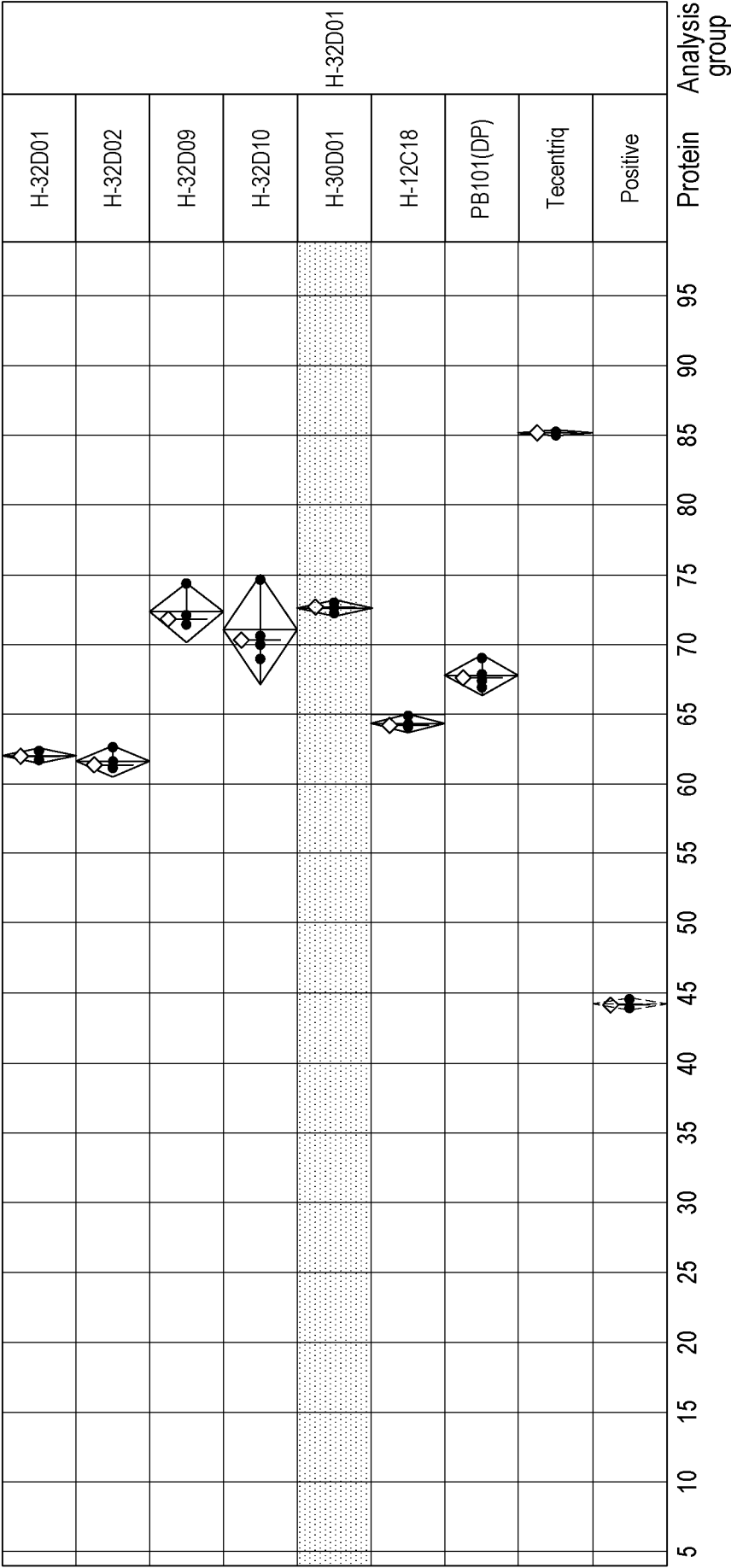


FIG. 7R

Sample name	% Total (area)			
	Acidic (pI <7)	Neutral (pI 7~8)	Basic (pI 8<)	Sum
H-32D02	13.83	73.21	12.98	100.02
H-32D04	11.27	71.29	17.43	99.99
H-32D06	58.6	41.4		100
H-32D08	43.42	56.58		100
H-01C65	48.15	51.84		99.99
PD20A01		46.28	53.71	99.99
Tecentriq			99.99	99.99

FIG. 8A



◆ Reference replication group (1) ◆ Sample replication group (8) × Omission
● Round 2 of protein thermal stability experiment (36)

FIG. 8B

Protein	Tm D - mean	Tm D lower 95%	Tm D upper 95%	Tm D - median value	Tm D - standard error	Tm D - minimum	Tm D - maximum
H-32D02	61.62978	60.51751	62.74204	61.37045	0.3495	61.14817	62.63004
H-32D01	62.01505	61.5289	62.5012	61.978	0.152759	61.7557	62.3485
H-32D09	72.33633	70.15385	74.5188	71.81767	0.685785	71.37311	74.33686
H-32D10	71.04514	67.12593	74.96436	70.30475	1.231512	68.97205	74.59901
Positive	44.23773	67.12593	44.6405	44.20068	0.126559	43.97836	44.57121

FIG. 8C

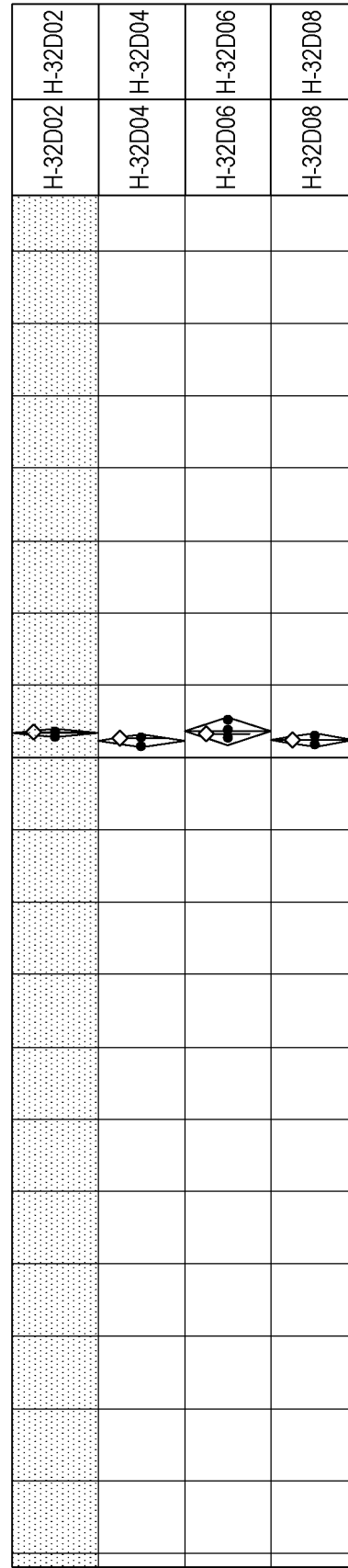


FIG. 8D

Protein	Tm D - mean	Tm D lower 95%	Tm D upper 95%	Tm D - median value	Tm D - standard error	Tm D - minimum	Tm D - maximum
H-32D02	61.684063	61.448215	61.91991	61.75817	0.07410908	61.461735	61.75817
H-32D04	61.1653	60.693604	61.636993	61.313515	0.14821815	60.720642	61.313515
H-32D06	61.83365	60.88089	62.786407	61.685493	0.2993802	61.315105	62.6485
H-32D08	61.203987	60.850365	61.55761	61.16695	0.11111641	61.018795	61.46326
Positive	46.3065	46.009777	46.60322	46.343548	0.09323691	46.04716	46.491745

FIG. 9A

Summary

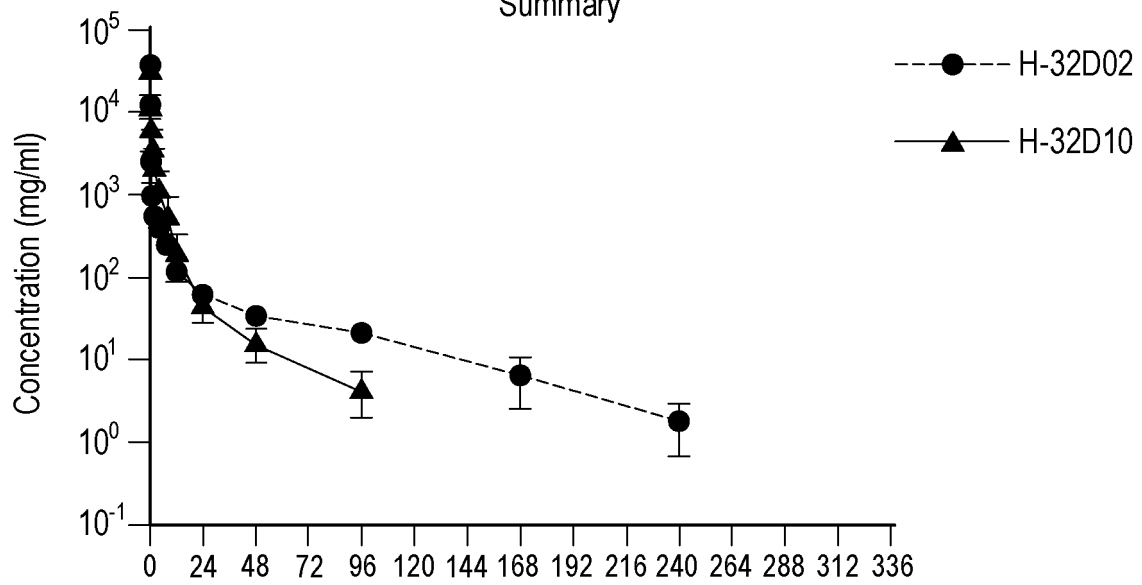


FIG. 9B

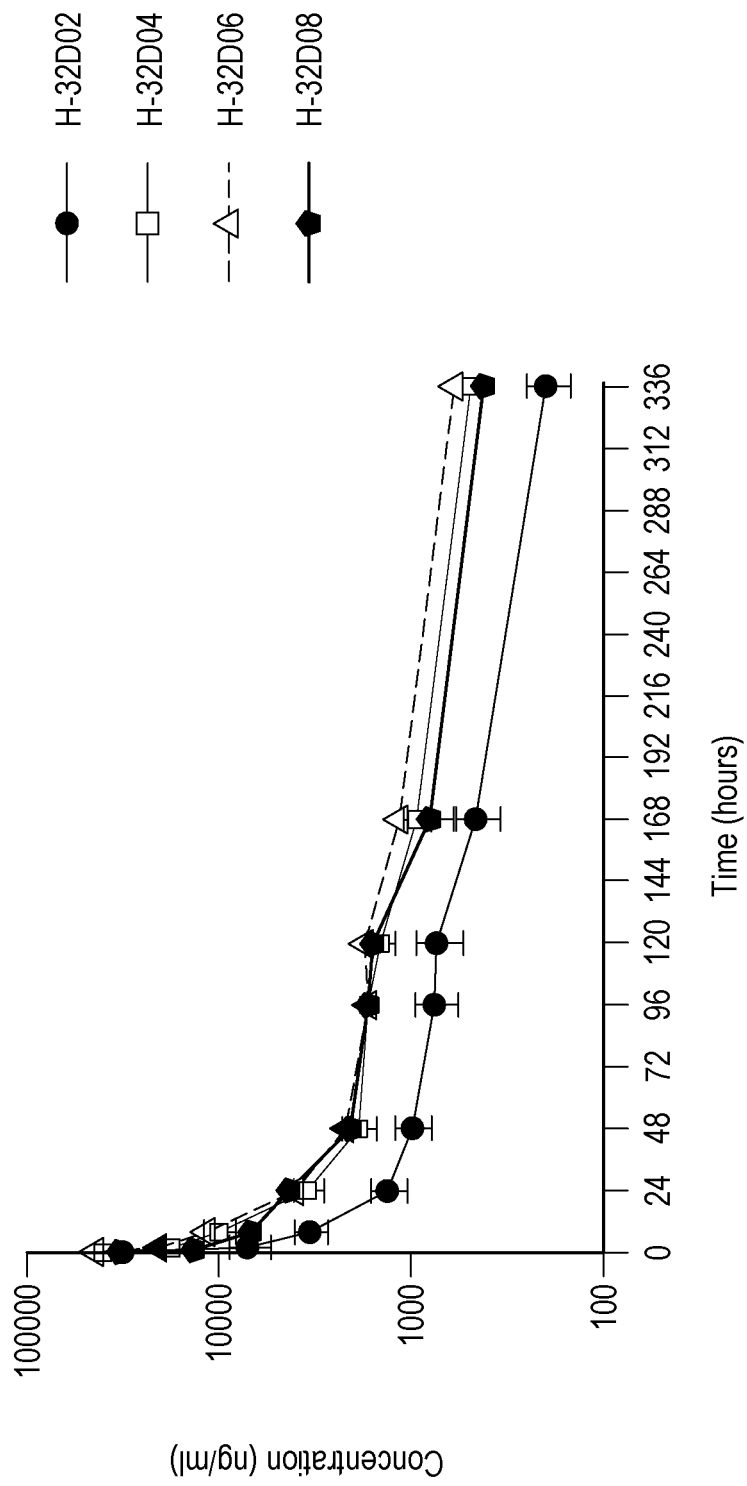


FIG. 10

