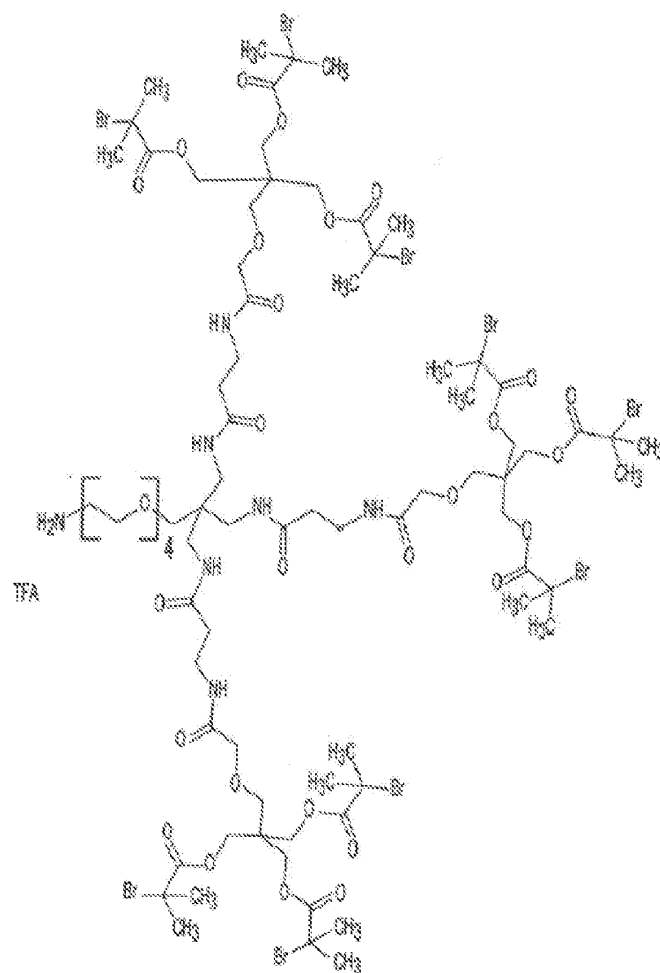
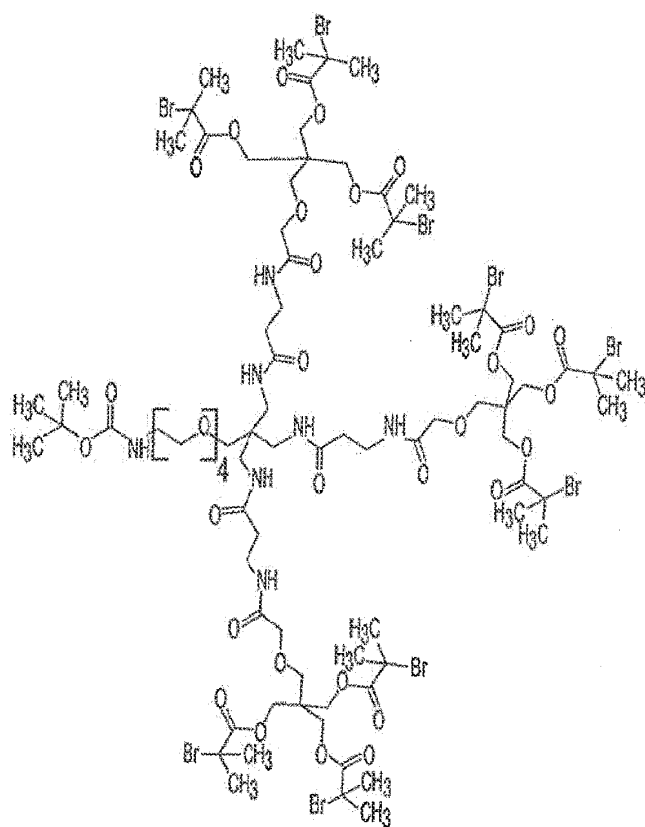




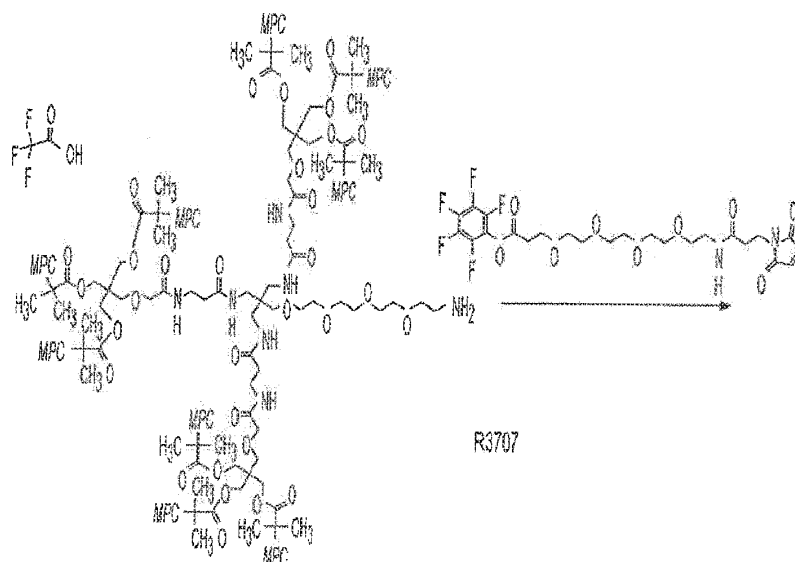
COMPOUND 1

FIG. 1

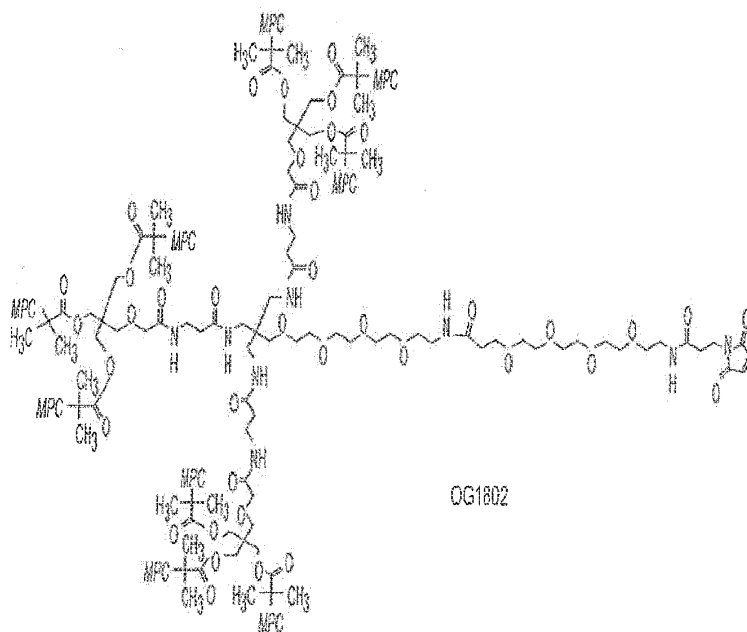


COMPOUND K

FIG. 2

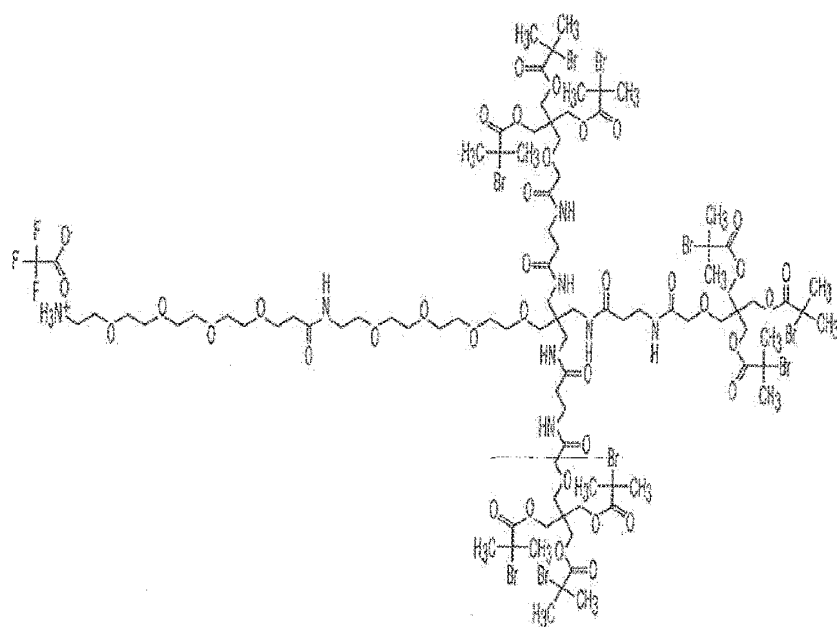


R3707



OG1802

FIG. 3



CG1786

FIG. 4

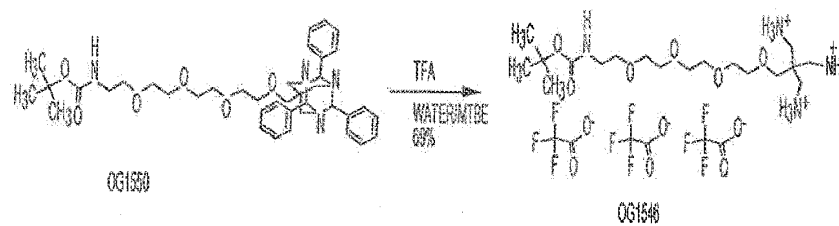


FIG. 5

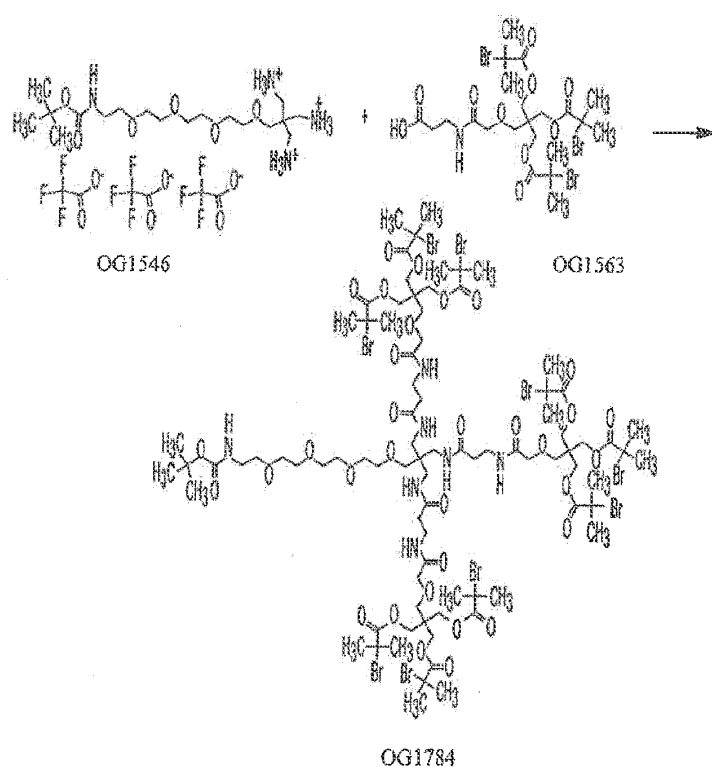


FIG. 6

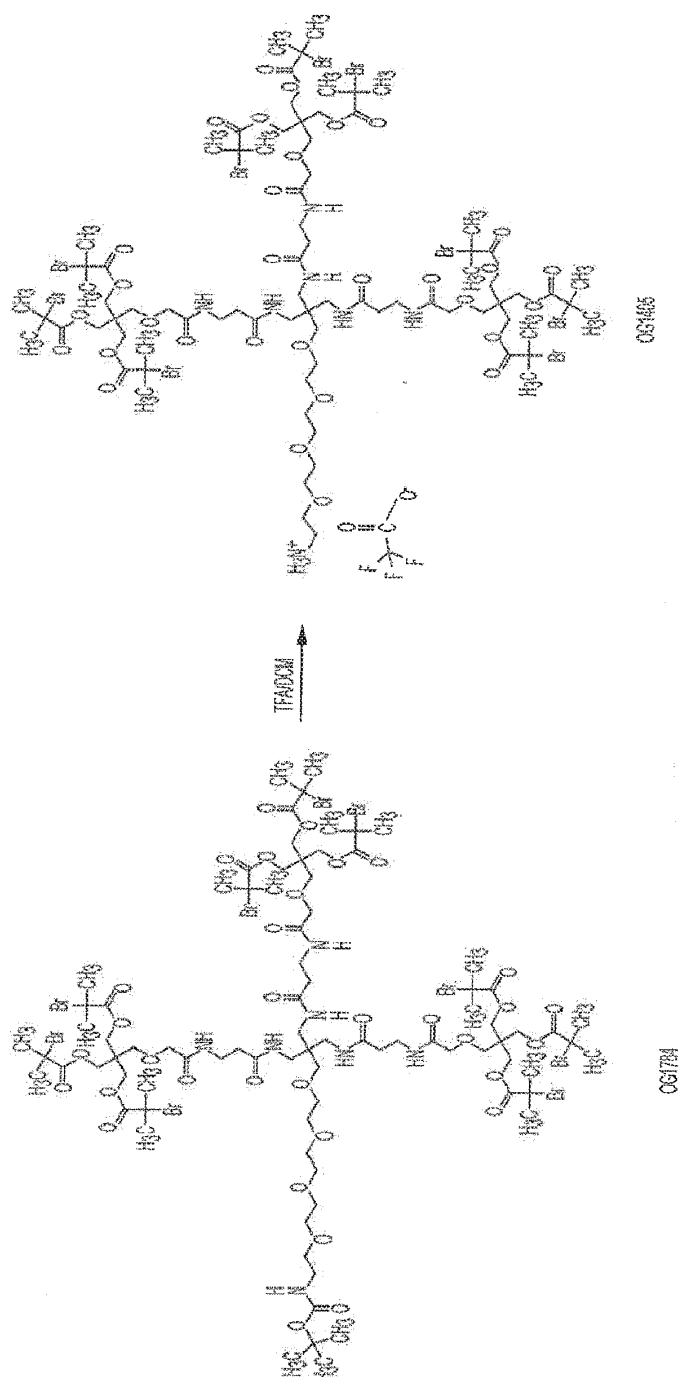


FIG. 7

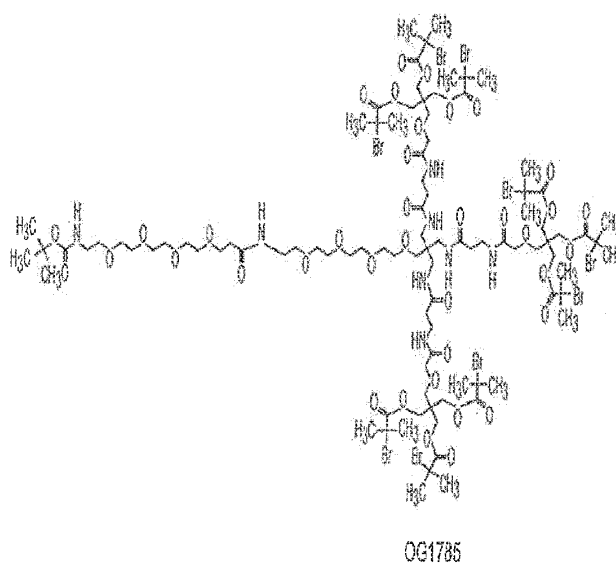
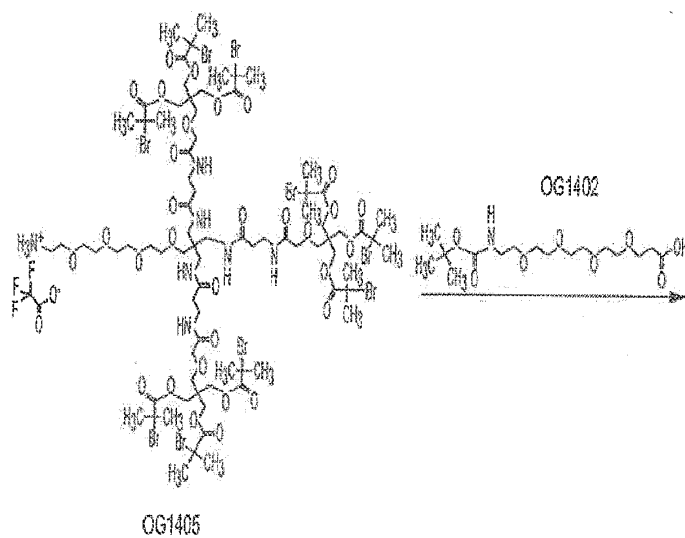


FIG. 8

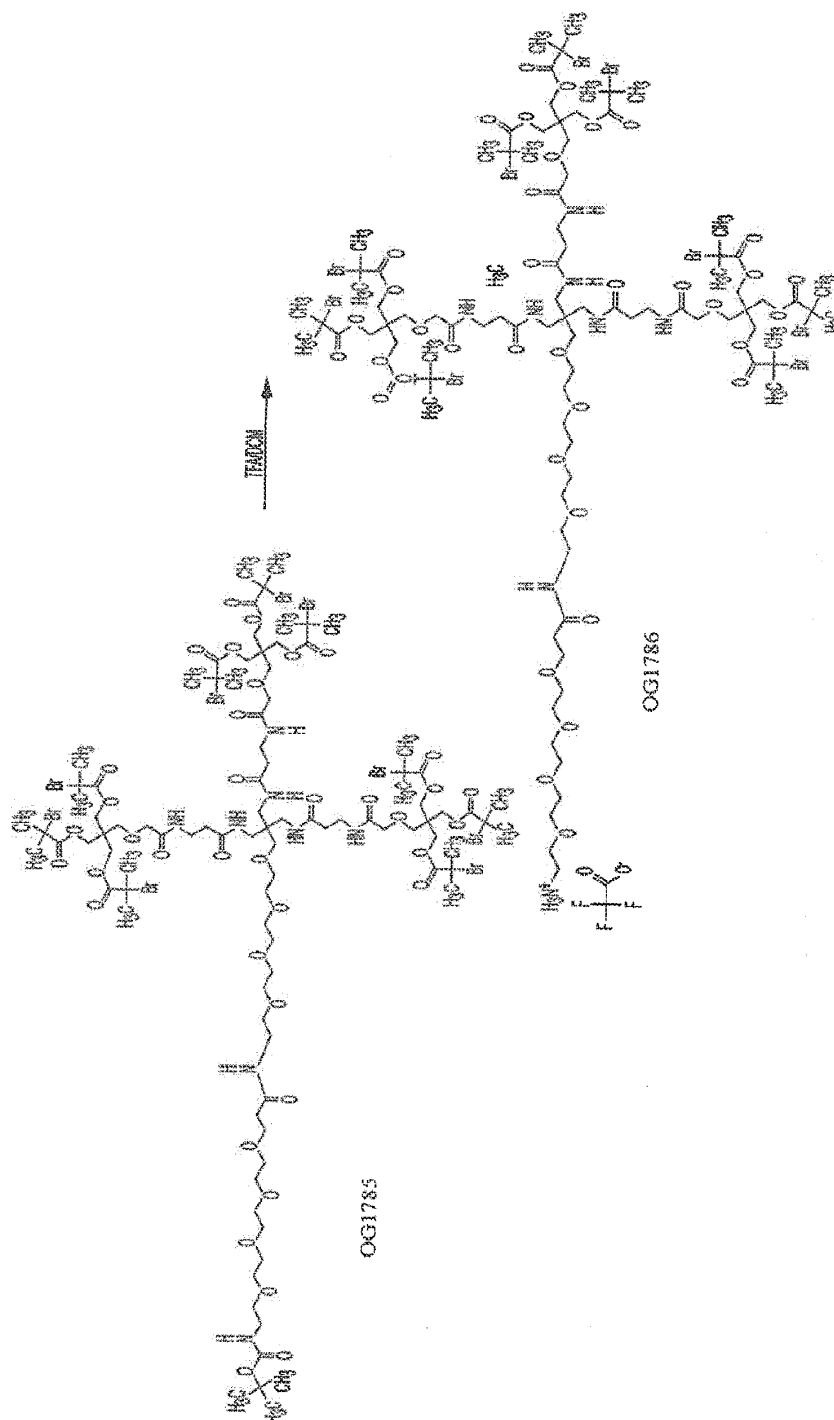


FIG. 9

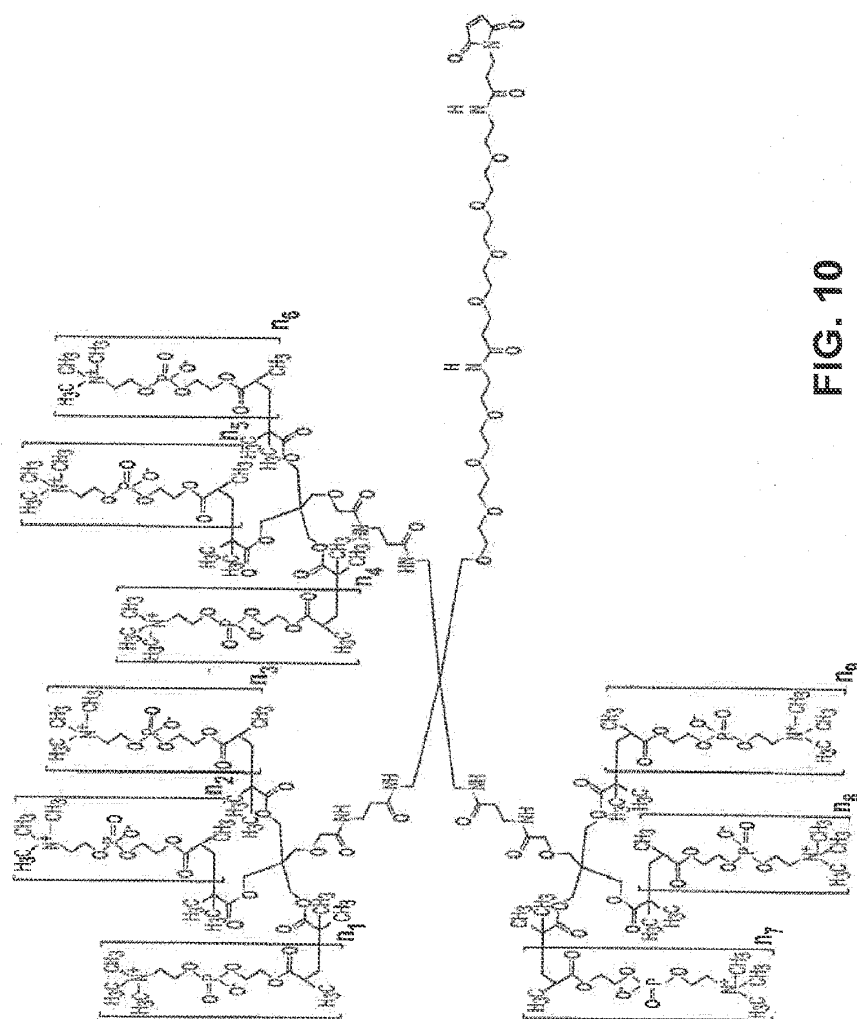


FIG. 10

SEQ ID NO. 1

1 EVQLVESGGG LVQPGGSLRL SCAASGYDFT HYGMNWVRQA PGKGLEWVGW INTYTGEPTY
AADEKRRRTF SLDTSKSTAY
81 LQMNSLRAED TAVYYCAKYP YYYGTSHWYF DVWGQGT LVT VSSASTKGPS VFPLAPSSKS
TSGGTAALGC LVKDYFPEPV
161 TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG TQTYICNVNH KPSNTKVDKK
VEPKSCDKTH TCPPCPAPEA
241 AGAPSVFLEP PKPKDTLMIS RTPEVTCVVV DVSHEDPEVK FNWYVDGVEV HNAKTKPREE
QYNSTYRVVS VLTVLHQDWL
321 NCKEYKCKVS NKALPAPIEK TISKAKQQR EPQVYTLPPS REEMTKNQVS LTCLVKGFPY
SDIAVEWESN GQFENNYKTT
401 PPVLESDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTKSLSCS PGK

FIG.12

SEQ ID NO. 2

1 DIQLTQSPSS LSASVGDRVT ITCASQDIS NYLNWYQQKP GKAPKVLIIYF TSSLHSGVPS
RFGSGSGSGTD FTLTISSLQP
81 EDFATYYCQQ YSTVPWTFGQ GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNIFY
PREAKVQWKV DNALQSGNSQ
161 ESVTEQDSKD STYLSSTLT LSKADYEKHK VYACEVTHQG LSSPVTKSPN EGEC

FIG. 13

SEQ ID NO. 3

1 EVQLVESGGG LVQPGGSLRL SCAASGYTFT NYGMNWVRQA PGKGLEWVGW INTYTGEPTY
AADEKRRRTF SLDTSKSTAY
81 LQMNSLRAED TAVYYCAKYP HYYGSSHWYF DWGQGTLLVT VSSASTKGPS VFPLAPSSKS
TSGGTAALGC LVKDYFPEPV
161 TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG TQTYICNVNH KPSNTKVDKK
VEPKSCDKTH TCPPCPAPEL
241 LGGPSVFLFP PKPKDTLMIS RTPEVTCVVV DVSHEDPEVK FNWYVDGVEV HNAKTKPREE
QYNSTYRVVS VLTVLHQDWL
321 NGKEYKCKVS NKALPAPIEK TISKAKGQPR EPQVYTLPPS REEMTKNQVS LTCLVKGFYP
SDIAVEWESN GQPENNYKTT
401 PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTKSLSLSS PGK

FIG. 14

SEQ ID NO. 4

1 DIQMTQSPSS LSASVGDRVT ITCASQDIS NYLNWYQQKP GKAPKVLIVF TSSLHSGVPS
RFGSGSGSTD FTLTISLQP
81 EDFATYYCQQ YSTVPWTFGQ GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY
PREAKVQWKV DNALQSGNSQ
161 ESVTEQDSKD STYLSSTLT LSKADYEKKH VYACEVTHQG LSSPVTKSFN RGEC

FIG. 15

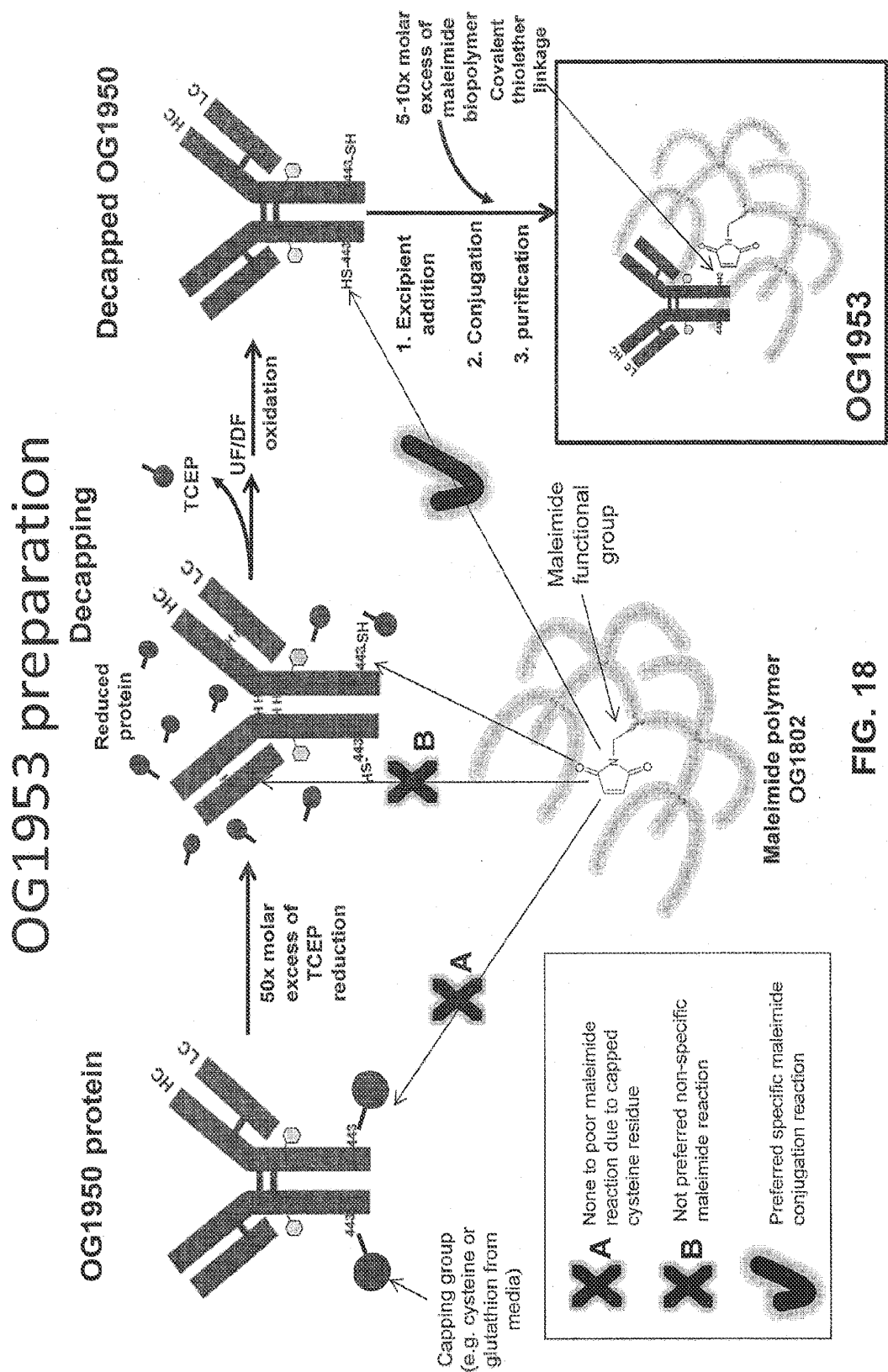
SEQ ID NO. 5

1 EVQLVESGGG LVQPGGSLRL SCAASGYDET HYGMNWRQA PGKGLEWVGW INTYTGEPTY
AADFKRRFTF SLDTSKSTAY
81 LQMNSLRAED TAVYYCAKYP YYYGTSHWYF DWVGQGTILVT VSSASTKGPS VFPLAPSSKS
TSGGTAALGC LVKDYFPEFV
161 TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG TQTYICNVNH KPSNTKVDKK
VEPKSCDKTH L

FIG. 16

SEQ ID NO. 6
1 DIQLTQSPSS LSASVGDRVT ITCSASQDIS NYLNWYQQKP GKAPKVLIIYF TSSLHSGVPS
RFGSGSGSGTD FTLTISSLQP
81 EDFATYYCQQ YSTVPWTFGQ GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY
PREAKVQWKV DNALQSGNSQ
161 ESVTEQDSKD STYLSSTLT LSKADYEKHK VYACEVTHQG LSSPVTKSFN RREC

FIG. 17



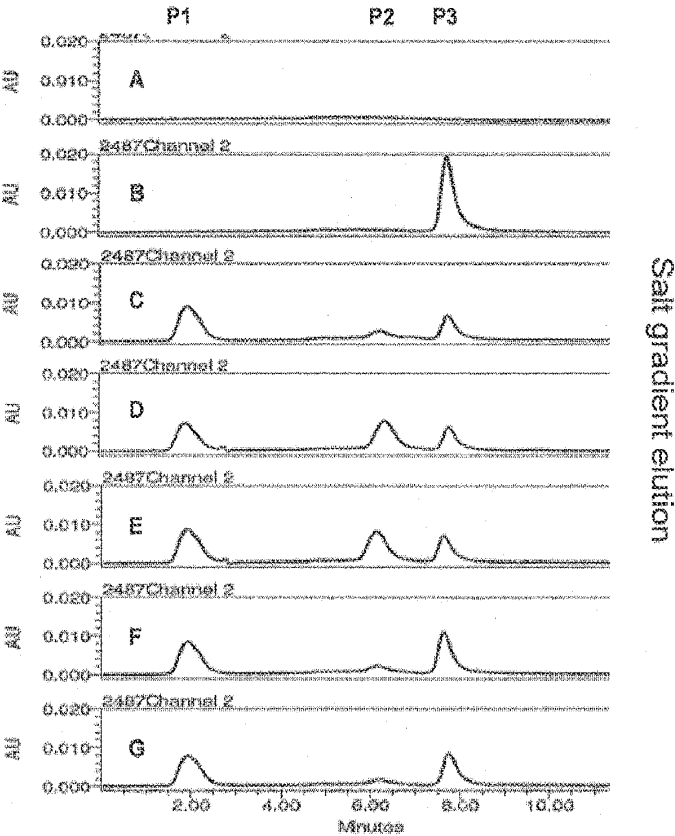
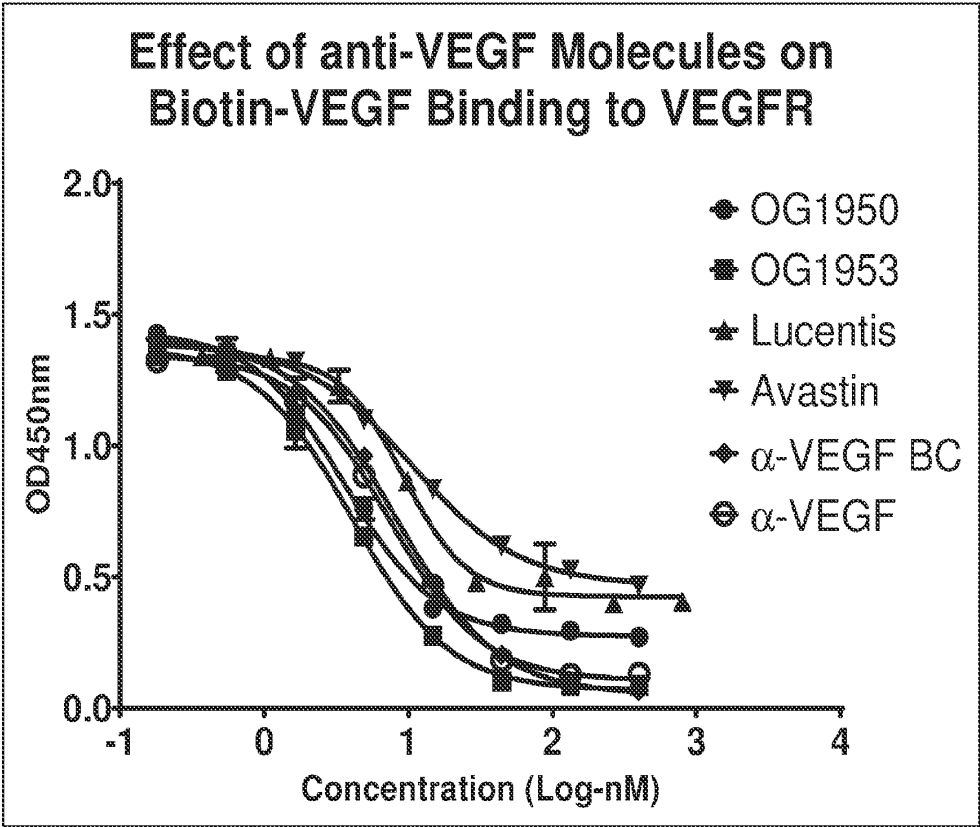


FIG. 19

Effect of Various anti-VEGF Molecules on Binding of biotin-VEGF to Plate bound VEGFR EDC-Fc Protein



Agent	IC50 (nM)
OG1950	3.612
OG1953	4.085
Lucentis	9.262
Avastin	10.420
α -VEGF BC	8.129
α -VEGF	7.236

FIG. 20

OG1950 binding affinity to VEGF measured by BIAcore single cycle kinetics

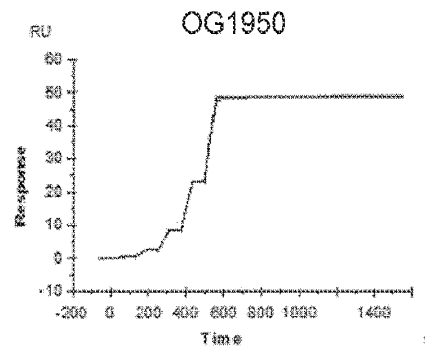


FIG. 21

Binding of OG1950 to Fc gamma receptor I

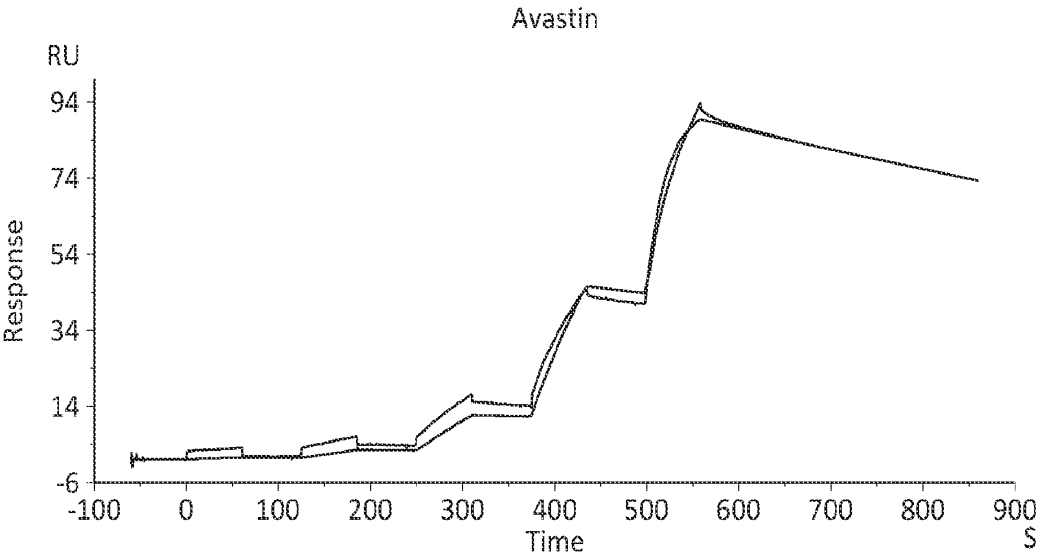
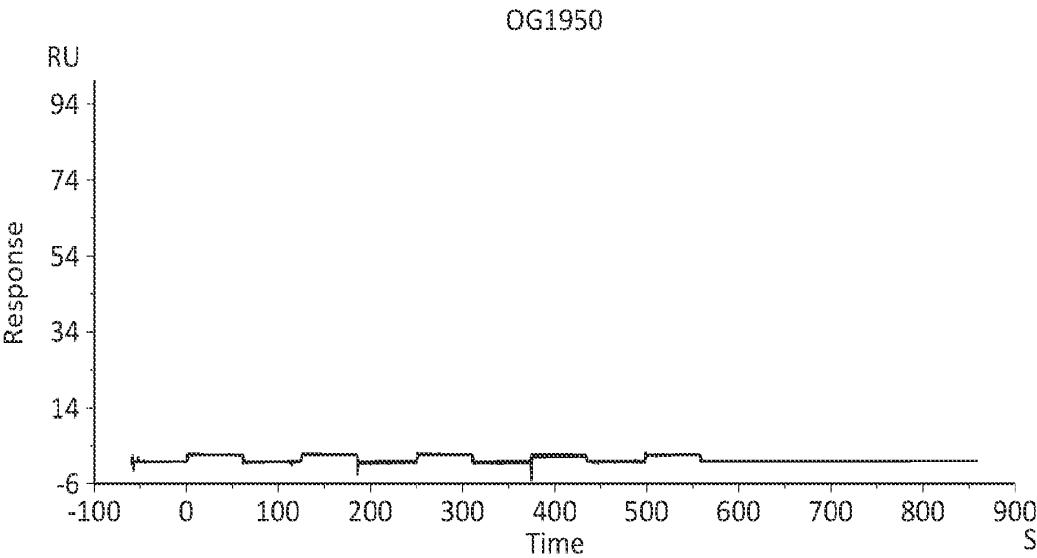


FIG. 22

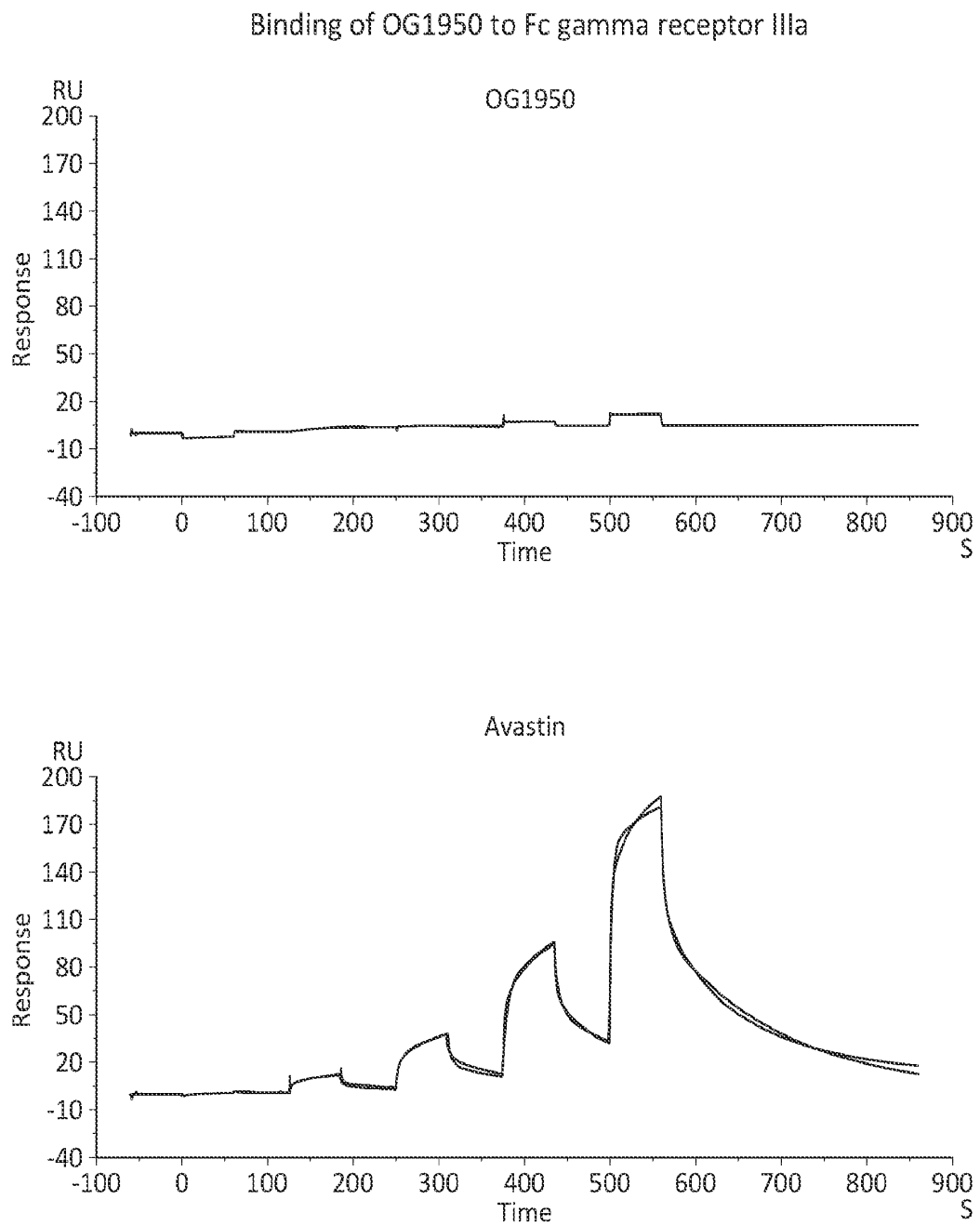


FIG. 23

Binding of OG1950 to human complement protein C1q

Binding of C1q to Plate-bound Antibodies

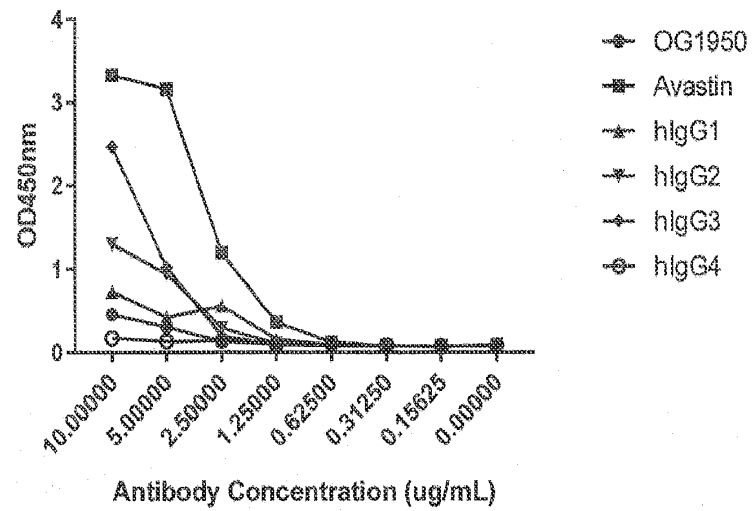


FIG. 24

Proliferation assay

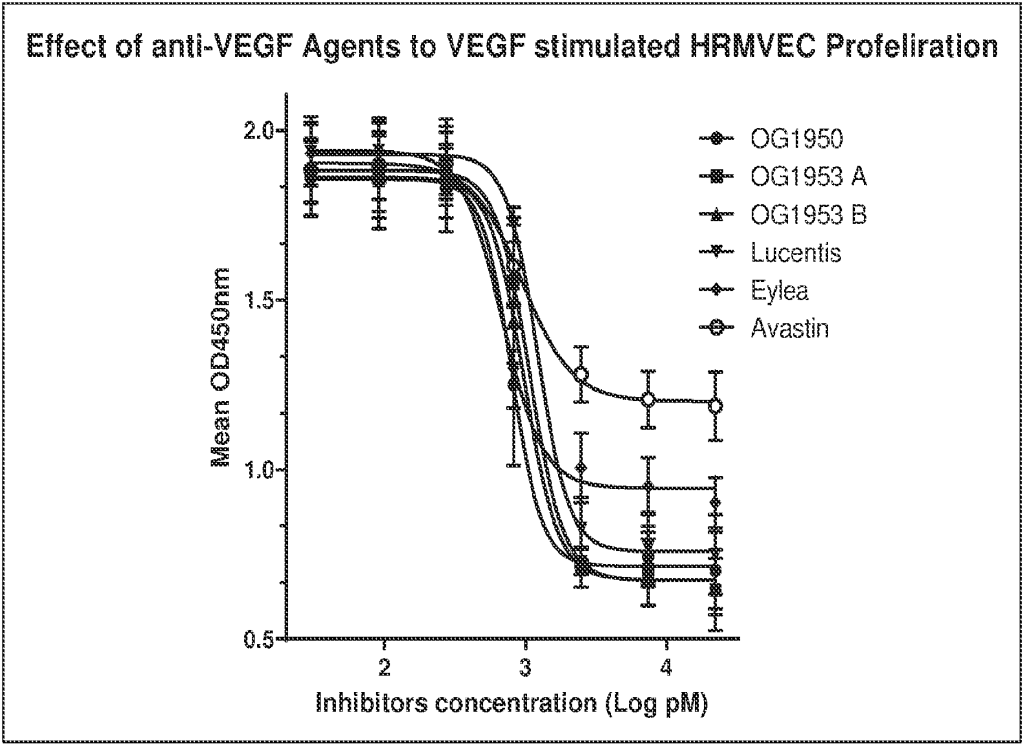
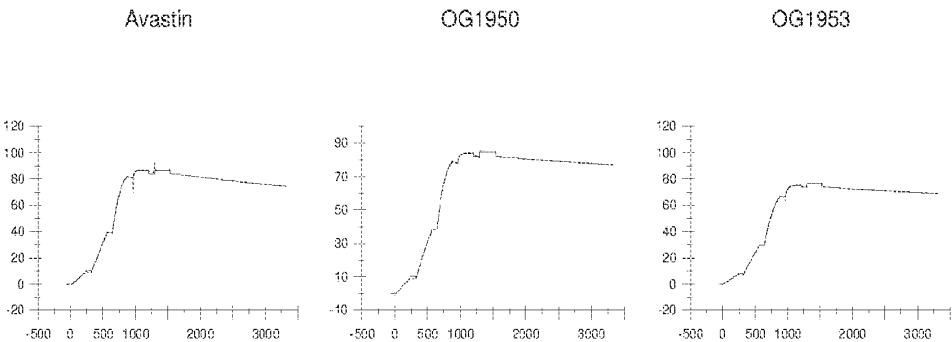
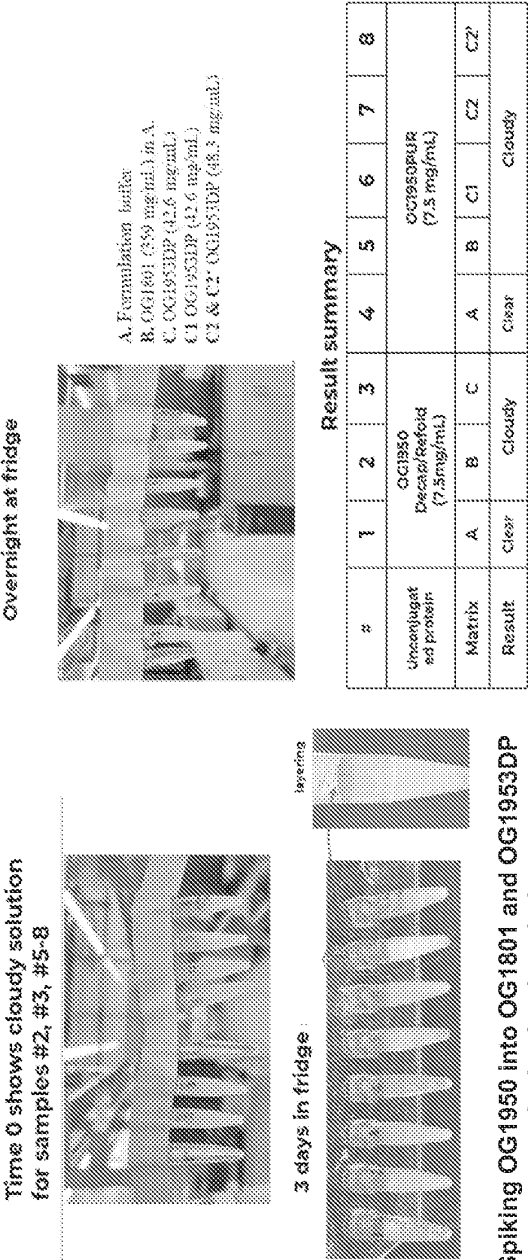


FIG. 25



Ligand	ka (1/Ms)	kd (1/s)	KD (M)	Rmax (RU)	Chi² (RU²)
Avastin	3.49E+06	8.23E-05	2.36E-11	84.6	0.419
OG1950	2.95E+06	3.86E-05	1.31E-11	82	0.171
OG1953	2.11E+06	4.09E-05	1.94E-11	73.9	0.343

FIG. 26



Spiking OG1950 into OG1801 and OG1953DP results in cloudy solutions.

FIG. 28

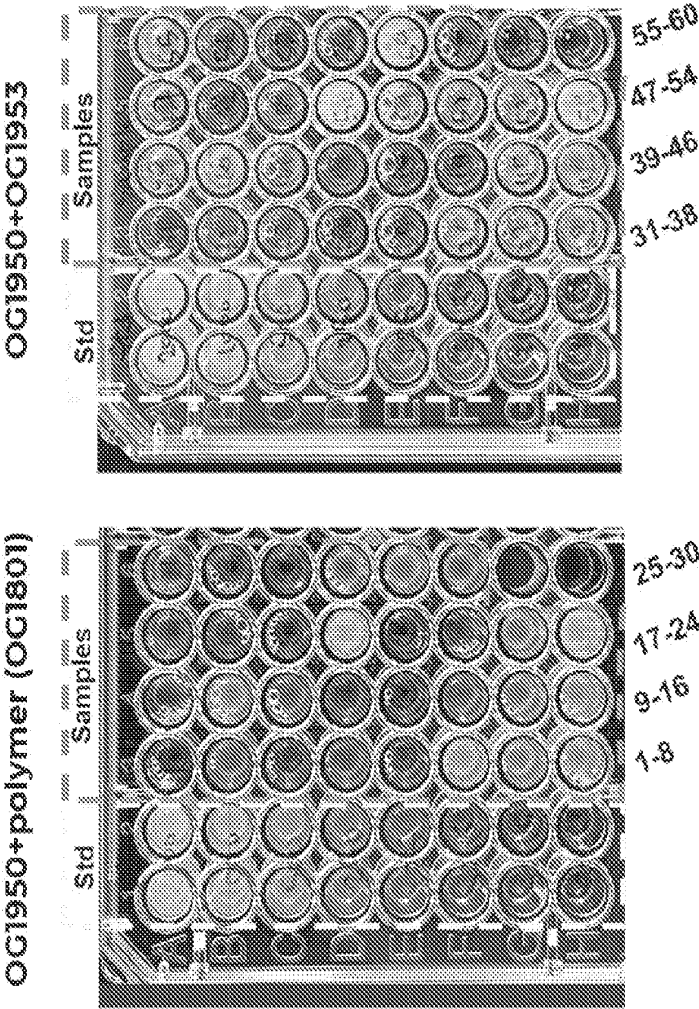


FIG. 29

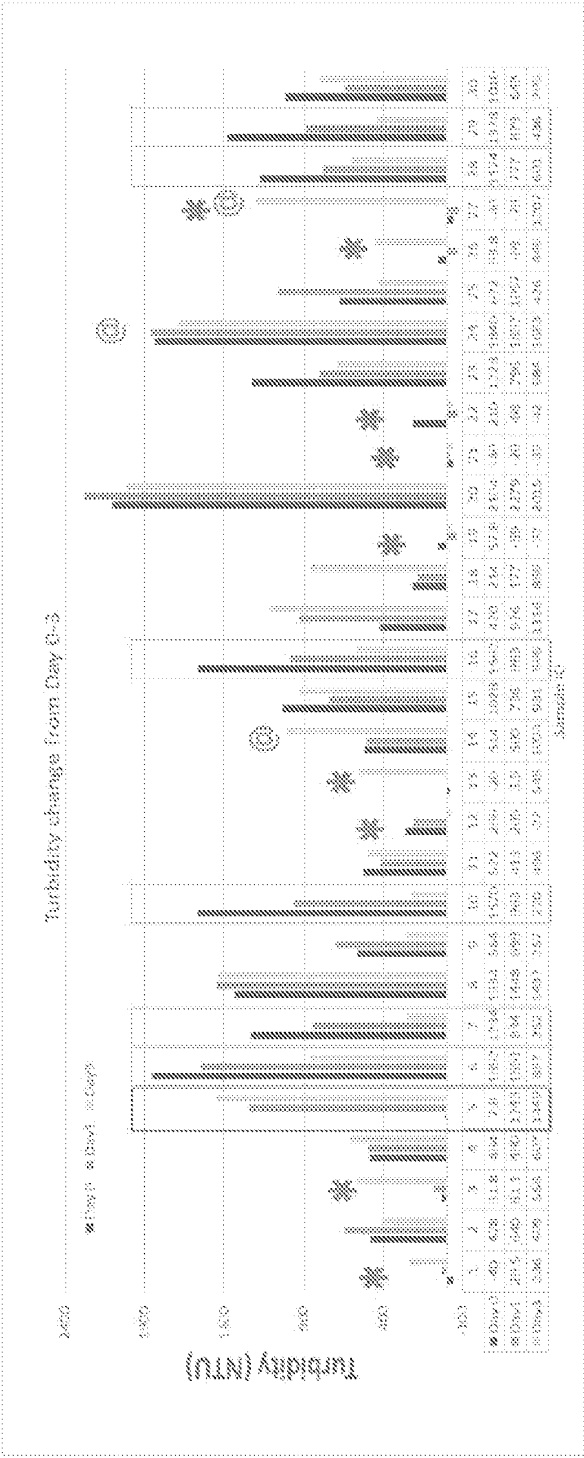
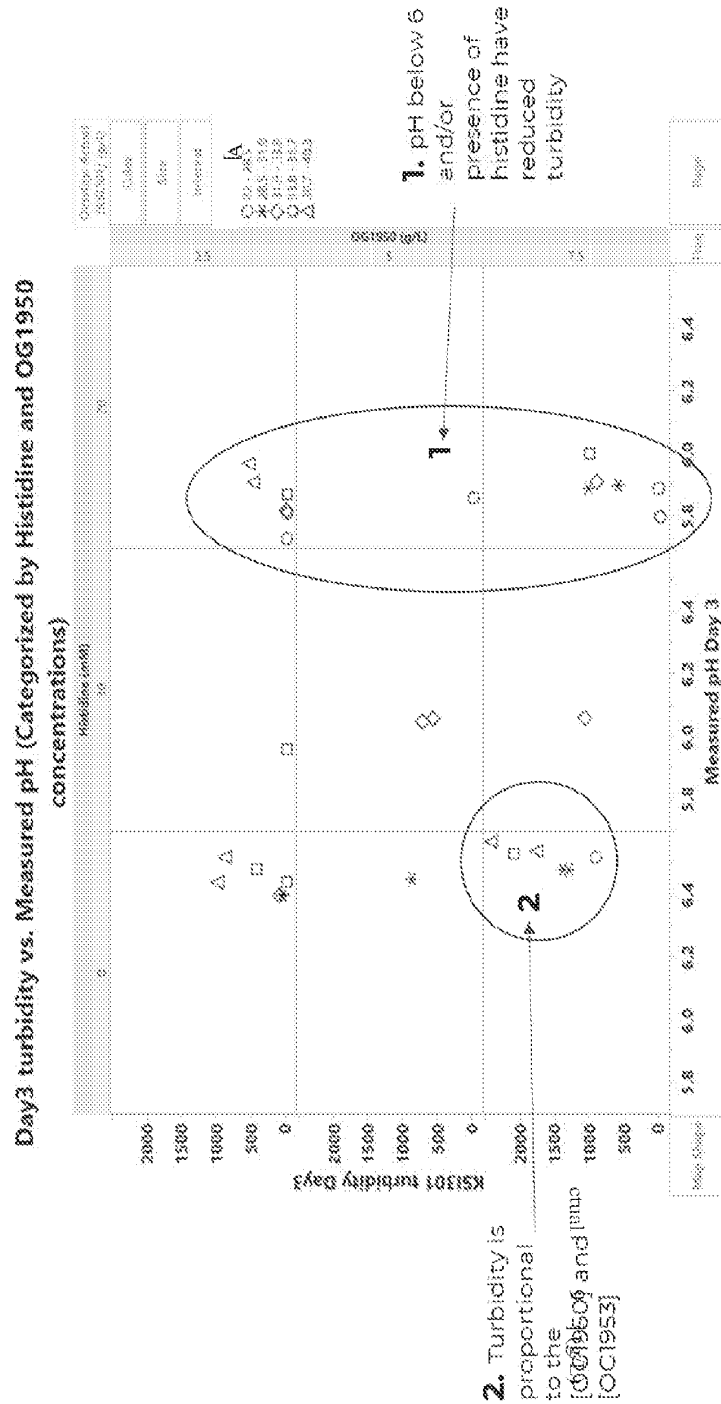


FIG. 30



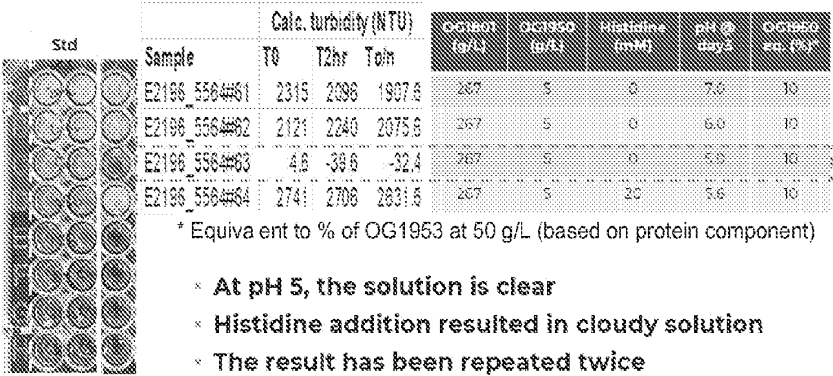
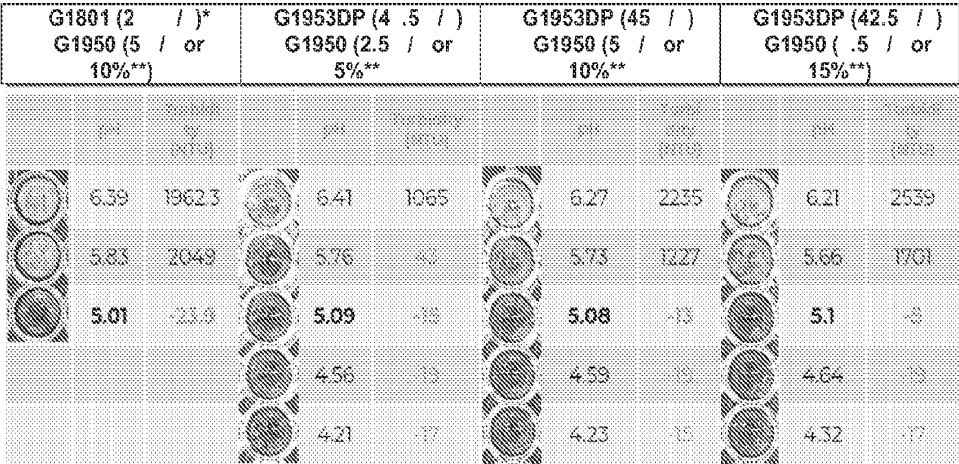


FIG. 32



^{*} Equivalent to polymer concentration of 45 g/L OG1953 (based on protein component)
^{**} Percent relative to total OG1950 in the formulation with 45 g/L as conjugated form or OG1953

FIG. 33

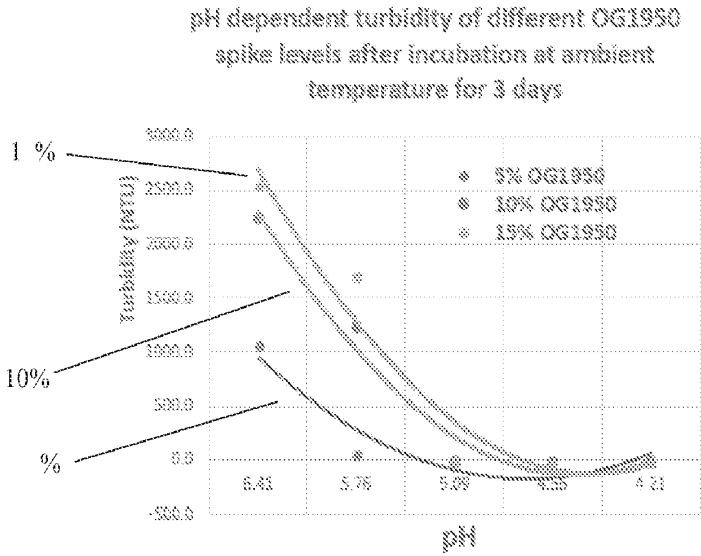


FIG. 34

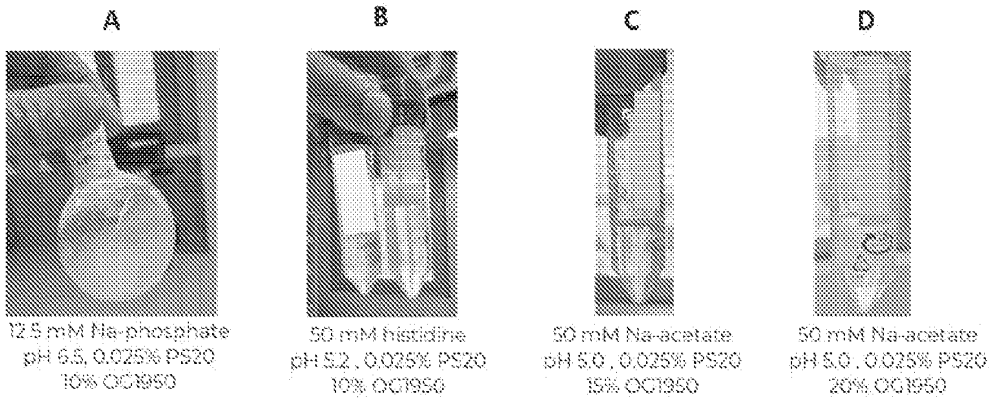
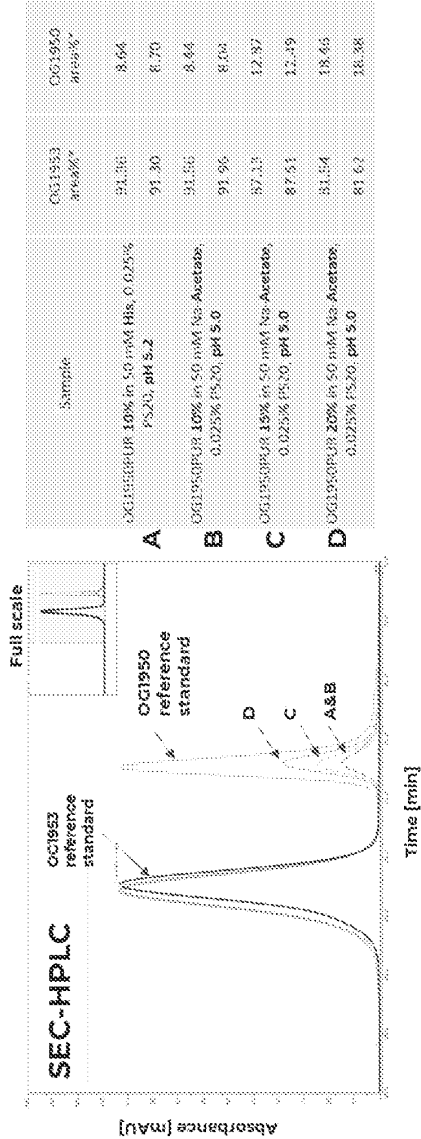
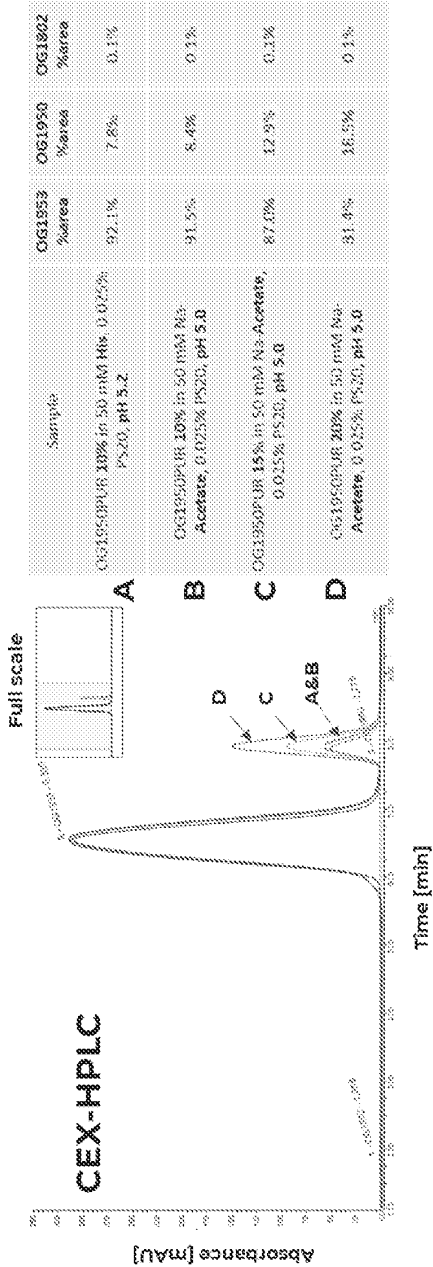


FIG. 35A



OG2072 polymer (220 g/L) OG2072 free protein(5.25 g/L or 10%*)					OG2074 conjugate (47.5 g/L) OG2072 free protein(5.25 g/L or 10%*)					* Equivalent to polymer concentration of 45 g/L OG2074 conjugate ** Percent relative to total OG2072 in the formulation with 45 g/L as conjugated form or OG2074
Sample ID	pH		Turbidity (NTU)		Sample ID	pH		Turbidity (NTU)		
	Day0	Day3	Day0	Day3		Day0	Day3	Day0	Day3	
89	6.1	6.1	1774	223	91	5.4	5.3	286	663	
90	4.4	4.4	342	-12	92	5.2	5.2	234	201	

FIG. 36

Matrix #1	Protein	M (kD)	pI	Final pH (Day 6)	Formulation buffer	Turbidity Day 1 [NT]
1	BSA	66	5.7	6.0	1xPBS pH 7.5	432
2	BSA	66	5.7	5.8	5 mM NaOAc pH 6.5, 0.01% PS20	510
3	BSA	66	5.7	5.5	20 mM NaOAc pH 5.0, 50 mM NaCl	1515
4	Lysozyme	16	9.4	3.9	1xPBS pH 7.5	-25
5	Lysozyme	16	9.4	3.8	5 mM NaOAc pH 6.5, 0.01% PS20	-23
6	Lysozyme	16	9.4	4.0	20 mM NaOAc pH 5.0, 50 mM NaCl	-25
7	Protein X	22	5.0	6.5	10mM Hepes pH 7.0	842
8	Protein Y	27	9.1	3.7	20 mM glycine pH 3	-23
9	Fab	50	8.6	5.1	10mM sodium acetate pH 5	-25
10	Protein Z	19	5.3	6.4	20 mM Hepes pH 7.5, 100 mM NaCl	1627
11	IgG1 monoclonal	147	7.4	5.5	PBS pH 7.2	752
12	IgG1 monoclonal	147	7.4	4.9	12.5mM Na-Phosphate pH6.5	199
13	IgG1 monoclonal	147	7.4	4.1	12.5mM NaOAc pH 5.0, 100 mM NaCl	-18
14	IgG1 monoclonal	145	7.4	5.6	20 mM Tris pH 7.5, 100 mM NaCl	1127
15	IgG1 fusion	211	5.4	5.5	10mM Sodium Phosphate pH 6.5, 100mM NaCl, 5% sucrose	387

FIG. 37A

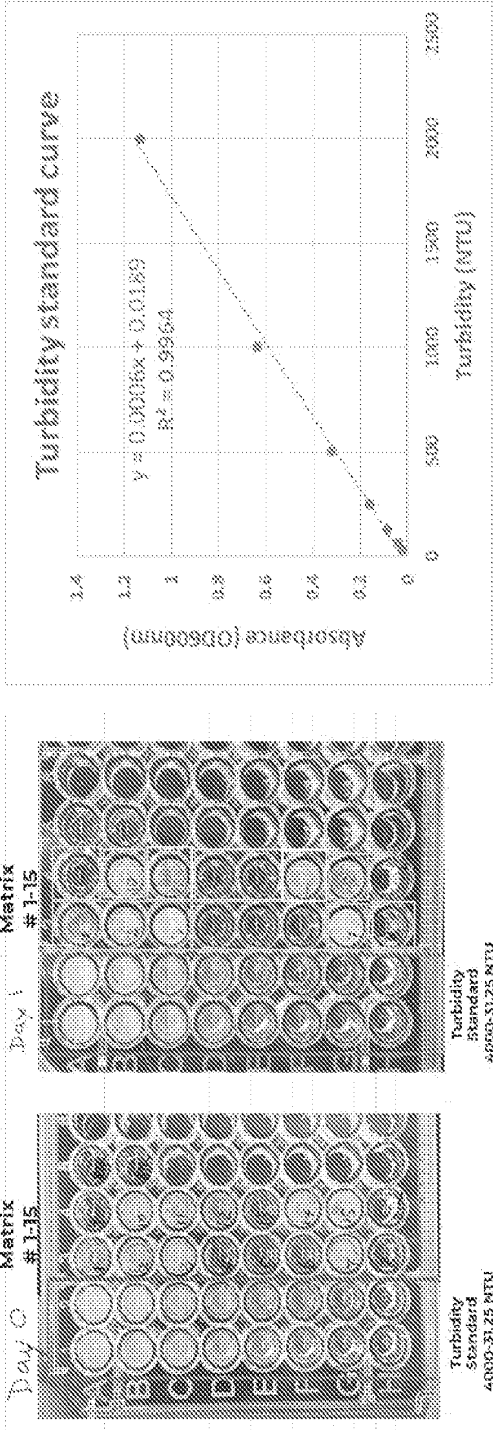


FIG. 37B

SampleID	Protein name	MW (kDa)	pI	Final actual pH (Day 6)	Turbidity @ Day 1 [NTU]	Post pH adjustment @ day 6	Turbidity @Day 6 post pH adjustment [NTU]
1	BSA	66	5.7	6.0	452	9.0	-24
2	BSA	66	5.7	5.8	510	7.2	-24
3	BSA	66	5.7	5.5	1515	NA	2401
4	Lysozyme	15	9.4	3.9	-25	5.7	-28
5	Lysozyme	15	9.4	3.8	-23	7.6	-23
6	Lysozyme	15	9.4	4.0	-25	12.0	2142
7	protein X	22	5.0	6.5	842	3.1	-3
8	Protein Y	27	9.1	9.7	-23	9.0	1331
9	Fab	50	8.6	5.1	-25	7.7	546
10	protein Z	18	5.3	6.4	1627	10.9	131
11	IgG1 monoclonal#1	147	7.4	5.5	752	NA	426
12	IgG1 monoclonal#1	147	7.4	4.9	199	NA	-26
13	IgG1 monoclonal#1	147	7.4	4.1	-18	NA	-26
14	IgG1 monoclonal#2	145	7.4	5.6	1127	3.9	-26
15	IgG1 monoclonal-fusion	211	5.4	5.5	587	3.7	67
Blank							

NA- No pH adjustment

FIG. 38A

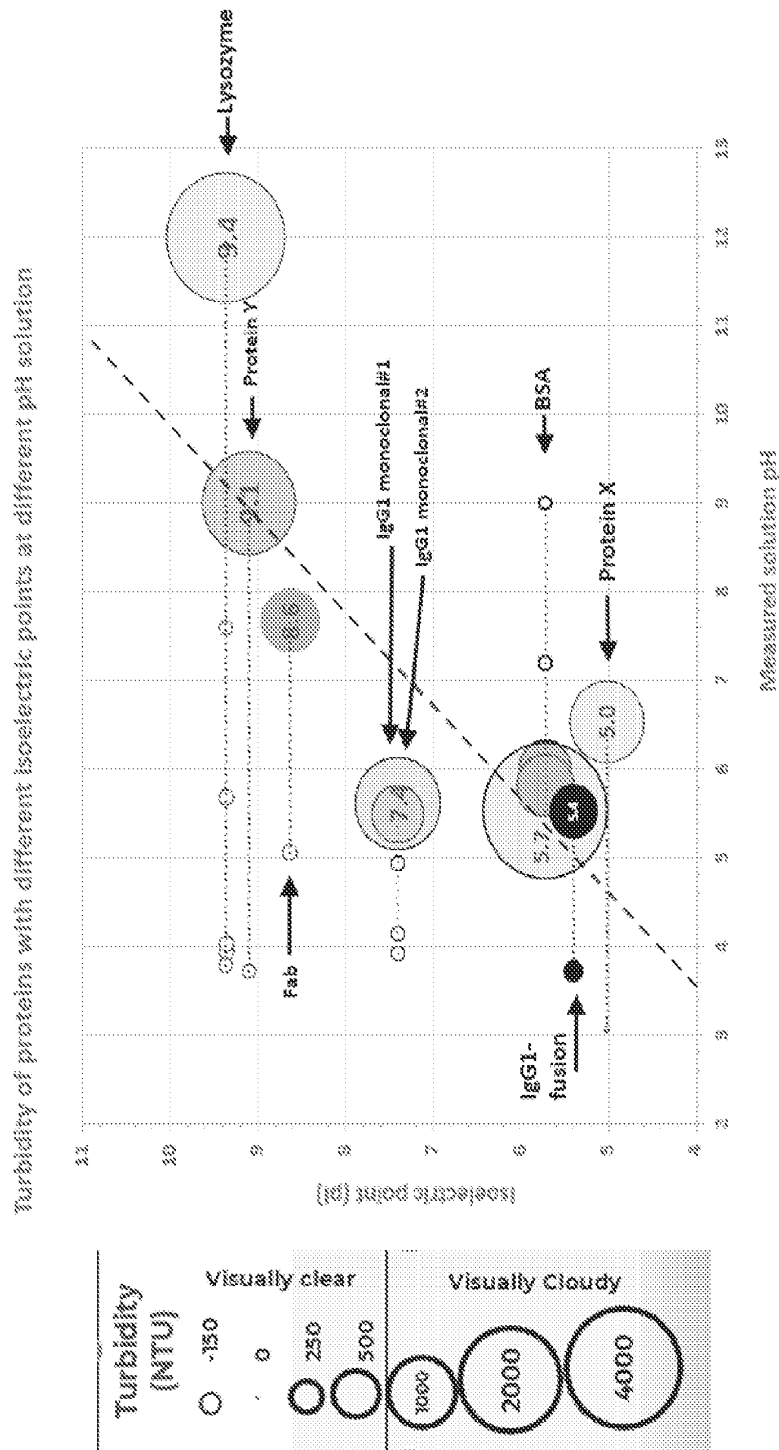


FIG. 38B

E2196_5688	#1	#2	#3	#4	#5
Free protein	A			B	
[Conjugate, C] mg/ml*	21.2	5.1	11.3	2.9	47.9
[Free protein] mg/ml	20.7	44.6	32.2	38.4	2.3
[Total protein] mg/ml	41.8**	49.7	43.5	41.3	50.2
[Free protein] / [Total protein] (w/w)	49.4%	89.9%	74.1%	93.0%	4.6%
Molar ratio Free protein/conjugated form	0.98	8.80	0.98	4.53	0.02

*Only the protein moiety is included in the concentration. Polymer is not included in the concentration, which is an 850 kDa polymer.

**The final concentration is at 41.8mg/ml after addition of 20ul buffer to the original 100ul total mixture.

FIG. 39

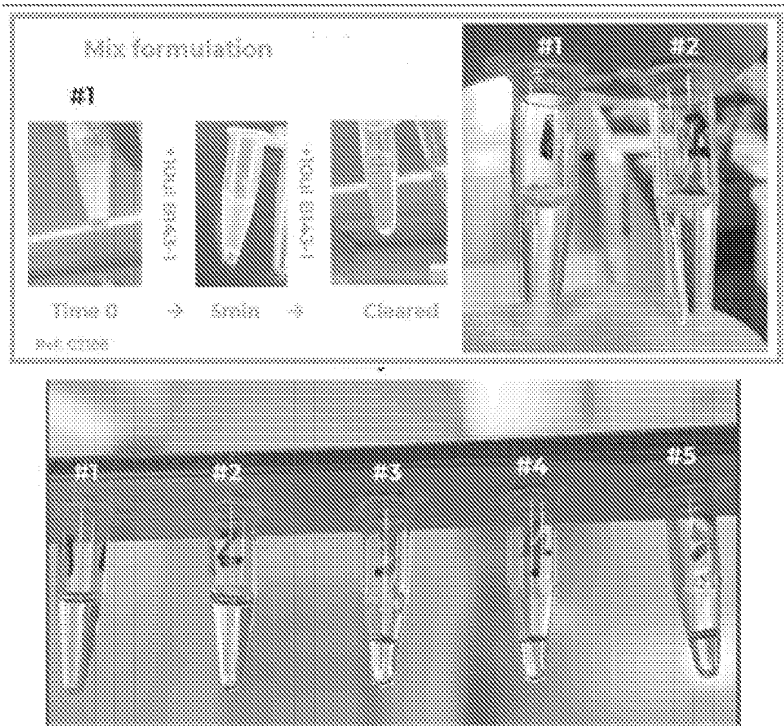


FIG. 40A

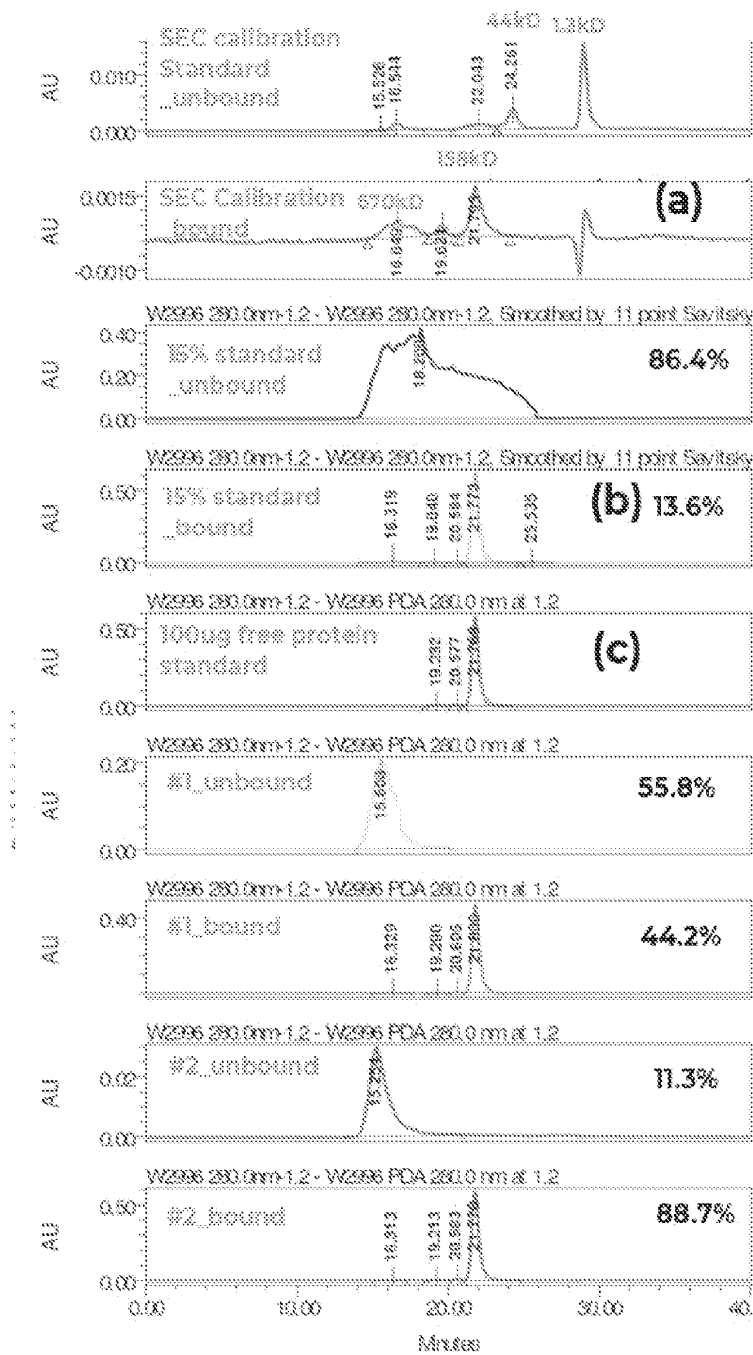


FIG. 40B

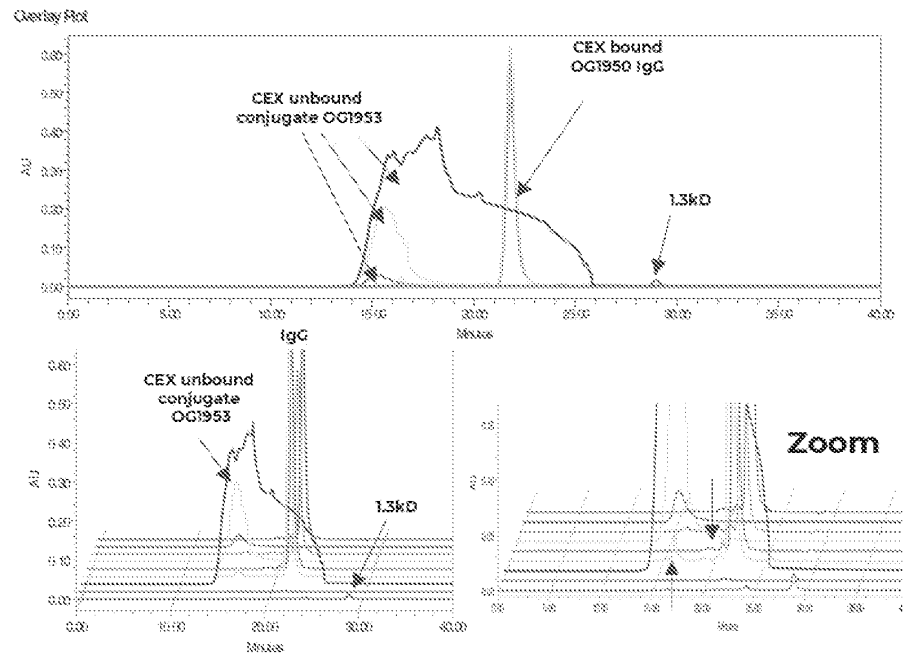


FIG. 40C

Sample name	Peak retention Time (min)	Peak protein mass (ug)	Fraction purity based on protein mass	CEX-unbound and CEX-bound fraction partitioning to the total protein mass loaded (X)	Expected % (Y)
OG1950 protein Std	19.2	0.6	0.5%	NA	NA
	20.6	0.9	0.9%		
	21.8	99.0	98.5%		
R50031(15% standard)_CEX-unbound	18.2	758.2	100.0%	86.4%	85.0%
R50031(15% standard)_CEX-bound	16.3	4.4	3.7%	13.6%	15.0%
	19.0	0.9	0.7%		
	20.6	1.3	1.1%		
	21.8	112.1	93.8%		
#1_CEX-unbound	15.6	108.2	100.0%	55.8%	52.3%
#1_CEX-bound	16.3	0.8	0.9%	44.2%	47.7%
	19.3	0.5	0.6%		
	20.6	0.7	0.7%		
	21.8	83.5	85.9%		
#2_CEX-unbound	15.3	19.5	100.0%	11.3%	10.9%
#2_CEX-bound	16.3	0.2	0.2%	88.7%	89.1%
	19.2	0.7	0.6%		
	20.6	1.0	0.9%		
	21.8	104.4	98.2%		

FIG. 40D

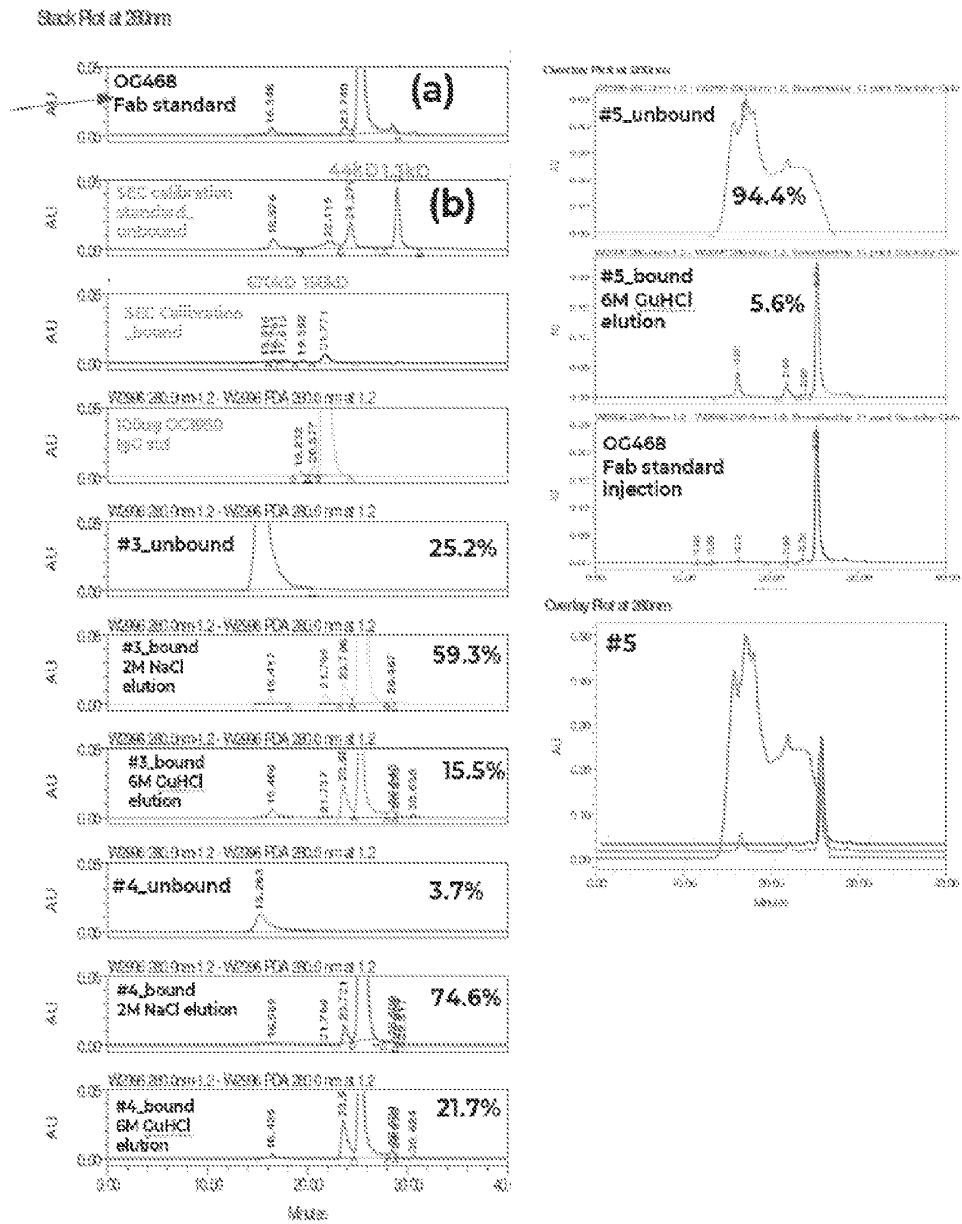


FIG. 40E

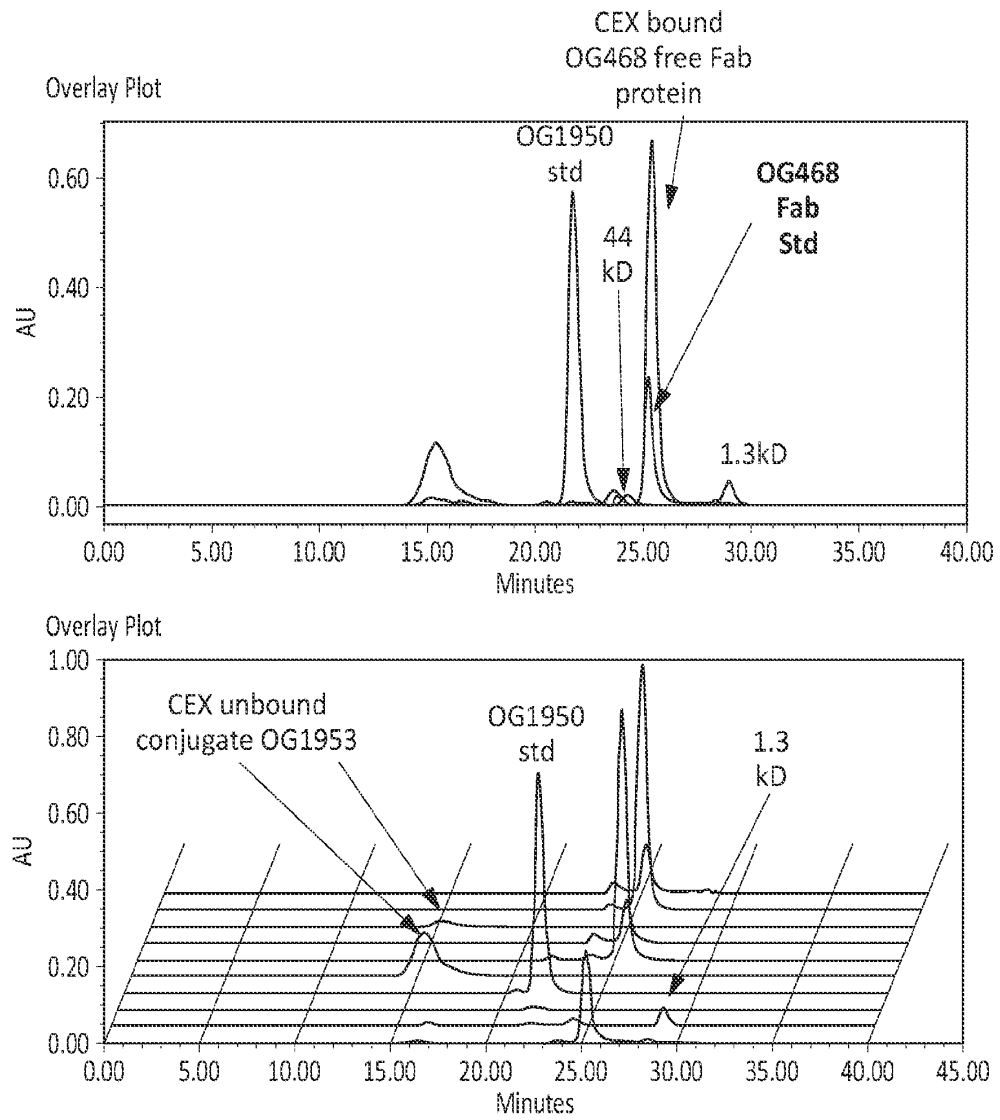


FIG. 40F

Sample Name	Peak retention Time (min)	Peak protein mass (ug)**	Peak percent based on ug	CEX-unbound and CEX-bound fraction partitioning to the total protein mass loaded [X]	Expected % [Y]
OG486_Fab_standard_6M GuHCl stripping*	16.3	1.70	3.7%	100.0%	NA
	23.7	0.00	0.0%		
	25.2	43.83	96.3%		
OG1950_IgG_standard	19.2	0.62	0.6%	100.0%	NA
	20.6	0.93	0.9%		
	21.8	99.00	99.5%		
#3_CEX-unbound	15.4	52.05	100.0%	25.2%	25.7%
#3_CEX-bound	16.4	1.19	1.0%	59.3%	74.3%
	21.8	1.53	1.2%		
	23.7	2.67	2.2%		
	25.4	116.52	95.2%		
	26.5	0.46	0.4%		
#3_CEX-bound_6M GuHCl stripping	16.4	1.57	4.9%	15.5%	74.3%
	21.7	0.09	0.3%		
	23.6	5.69	17.5%		
	25.3	23.31	72.8%		
	28.5	1.02	3.2%		
	28.9	0.26	0.8%		
#4_CEX-unbound	30.6	0.23	0.7%	3.7%	6.9%
	15.3	6.14	100.0%		
#4_CEX-bound	16.5	0.28	0.2%	74.6%	93.1%
	21.8	0.08	0.1%		
	23.7	2.47	2.0%		
	25.4	119.52	97.4%		
	28.5	0.28	0.2%		
	29.0	0.07	0.1%		
#4_CEX-bound_6M GuHCl stripping	29.5	0.07	0.1%	21.7%	93.1%
	16.4	0.82	2.3%		
	23.6	6.77	18.9%		
	25.3	26.75	74.8%		
	26.5	0.94	2.6%		
	28.9	0.27	0.8%		
#5_unbound	30.6	0.23	0.6%	94.4%	95.4%
#5_bound_6M GuHCl stripping	17.1	960.49	100.0%	5.6%	4.6%
	16.3	8.88	15.9%		
	21.8	4.07	7.1%		
	23.9	1.31	2.3%		
	25.3	43.13	75.1%		

* OG486_Fab has been found to have solubility issue and stringent elution conditions of using 6M Guanidine hydrochloride (6M GuHCl) is used to strip the tightly bound residual protein.

** Calculated based on protein extinction coefficient

FIG. 40G

Sample ID	Formulation buffer	Intended free antibody OG1950	Protein conc. (mg/ml)
#1	OG1950PUR_10%, OG1953_90% + 50mM histidine, 0.025% Tween20, pH 5.2	10.0%	53.4
#2	OG1950PUR_10%, OG1953_90% + 50mM sodium acetate, 0.025% Tween20, pH 5.0	10.0%	50.9
#3	OG1950PUR_15%, OG1953_85% + 50mM sodium acetate, 0.025% Tween20, pH 5.0	15.0%	50.5*
#4	OG1950PUR_20%, OG1953_80% + 50mM sodium acetate, 0.025% Tween20, pH 5.0	20.0%	49.8
#5	OG1950PUR_7.5%, OG1953_92.5% + 50mM histidine, 0.025% Tween20, pH 5.2	7.5%	51.9
#6	OG1950IAM_10%, OG1953_90% + 50mM histidine, 0.025% Tween20, pH 5.2	10.0%	52.6
#7	OG1950IAM_10%, OG1953_90% + 50mM sodium acetate, 0.025% Tween20, pH 5.0	10.0%	61.9
#8	OG1950IAM_15%, OG1953_85% + 50mM sodium acetate, 0.025% Tween20, pH 5.0	15.0%	53.5
#9	OG1950IAM_20%, OG1953_80% + 50mM sodium acetate, 0.025% Tween20, pH 5.0	20.0%	52.6
#10	7.5mg/ml OG1950PUR + 230mg/ml OG1801 polymer pH 5.2	100%	7.5

* Sample #3 contains 7.5mg/ml OG1950PUR as unconjugated form, 42.5mg/ml OG1950 in conjugated form with 225mg/ml polymer.
Sample #10 is setup to evaluate the impact of polymer on 7.5mg/ml unconjugated protein.

FIG. 41

Sample ID	Formulation buffer	IC50 (µM)	Percent relative potency (%RP)
Plate 1	OG1953 reference standard		
	5mM sodium phosphate, 0.01% Tween 20, pH 6.5	1507	100%
	OG1950PUR_10%, OG1953_90% + 50mM histidine, 0.025% Tween20, pH 5.2	1598	94%
	OG1950PUR_10%, OG1953_90% + 50mM sodium acetate, 0.025% Tween20, pH 5.0	1632	92%
	OG1950PUR_15%, OG1953_85% + 50mM sodium acetate, 0.025% Tween20, pH 5.0	1669	90%
Plate 2	OG1953 reference standard		
	5mM sodium phosphate, 0.01% Tween 20, pH 6.5	1652	91%
	OG1950PUR_7.5%, OG1953_92.5% + 50mM histidine, 0.015% Tween20, pH 5.2	1505	100%
	OG1950IAM_10%, OG1953_90% + 50mM histidine, 0.025% Tween20, pH 5.2	1561	96%
	OG1950IAM_10%, OG1953_90% + 50mM sodium acetate, 0.025% Tween20, pH 5.0	1622	93%
	OG1950IAM_15%, OG1953_85% + 50mM sodium acetate, 0.025% Tween20, pH 5.0	1585	95%
	OG1950IAM_20%, OG1953_80% + 50mM sodium acetate, 0.025% Tween20, pH 5.0	1565	96%
		1526	99%

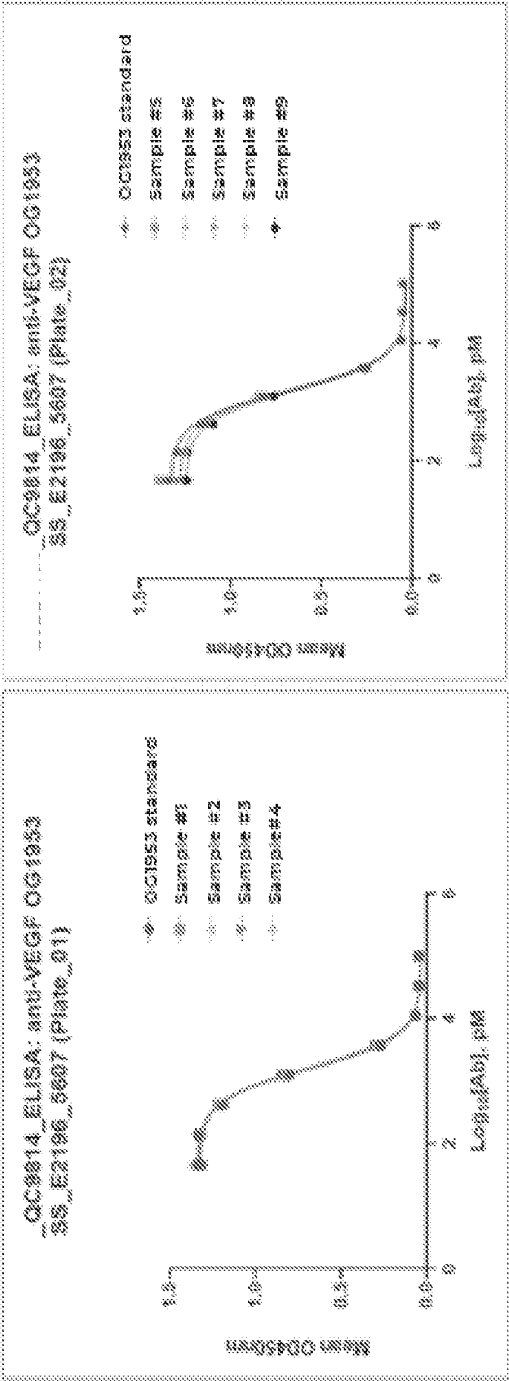


FIG. 42

Sample/Sample ID	Sample Description	Time (Month)	Temp (C°)	Plate 1	%RP
				Plate 2	
R9407A INT Scale DS (RS 1)	5mM Sodium phosphate pH 6.5, 0.01% Tw20			1768	100%
R9407A INT Scale DS (RS 2)	5mM Sodium phosphate pH 6.5, 0.01% Tw20			1993	100%
Sample #4	OG1950PUR 20%, OG1953 80% - 50mM Na-acetate, 0.025% Tween, pH 5.0	2	37	1882	94%
Sample #4		2	25	1828	97%
Sample #4		2	5	1776	100%
Sample #9		2	37	2024	98%
Sample #9	OG1950iAM 20%, OG1953 80% - 50mM Na-acetate, 0.025% Tween, pH 5.0	2	25	2058	97%
Sample #9		2	5	2051	97%

FIG. 43

Legends	Time	Temp	Sample#	10.0%		10.0%		15.0%		20.0%		7.5%	
				#1	#2	#3	#4	#5	#6	#7	#8	#9	#10 (control)
	0		T0_QC9772	53.45	50.94	50.48	49.81	51.86					
	1	5	T1M_5°C	53.59	50.20	50.02	49.31	51.02					
	1	25	T1M_25°C	53.49	50.13	49.74	49.19	51.14					
	1	37	T1M_37°C	52.42	49.89	49.49	48.93	50.74					
	2	5	T2M_5°C	53.17	49.82	49.06	49.29	50.85					
	2	25	T2M_25°C	52.48	49.98	49.61	49.27	51.08					
	2	37	T2M_37°C	52.23	49.67	49.59	48.96	51.17					
	6	5	T6M_5°C	53.30	50.35	49.70	48.74	50.89					
	6	25	T6M_25°C	52.83	50.29	49.77	49.39	51.92					
	6	37	T6M_37°C	51.17	51.18	50.05	49.93	52.10					
			Mean=	53.49	50.82	50.40	49.85	51.94					
			%SD/mean=	3.5%	2.7%	2.6%	2.8%	3.1%					

Legends	Time	Temp	Sample#	10.0%		10.0%		15.0%		20.0%		100.0%	
				#6	#7	#8	#9	#10 (control)					
	0		T0_QC9772	52.59	61.92	53.46	52.60						
	1	5	T1M_5°C	53.29	61.37	52.72	52.20						
	1	25	T1M_25°C	51.73	61.20	52.40	52.28						
	1	37	T1M_37°C	51.61	60.66	51.85	52.07						
	2	5	T2M_5°C	51.71	61.09	52.24	52.30						
	2	25	T2M_25°C	51.57	60.63	52.37	51.77						
	2	37	T2M_37°C	54.63	60.60	52.39	51.91						
	6	5	T6M_5°C	52.13	62.37	52.67	51.76						
	6	25	T6M_25°C	51.39	63.14	52.94	51.66						
	6	37	T6M_37°C	48.70	62.37	54.42	51.78						
			Mean=	52.46	62.40	53.32	52.65						
			%SD/mean=	3.4%	3.2%	2.7%	2.7%						

FIG. 44

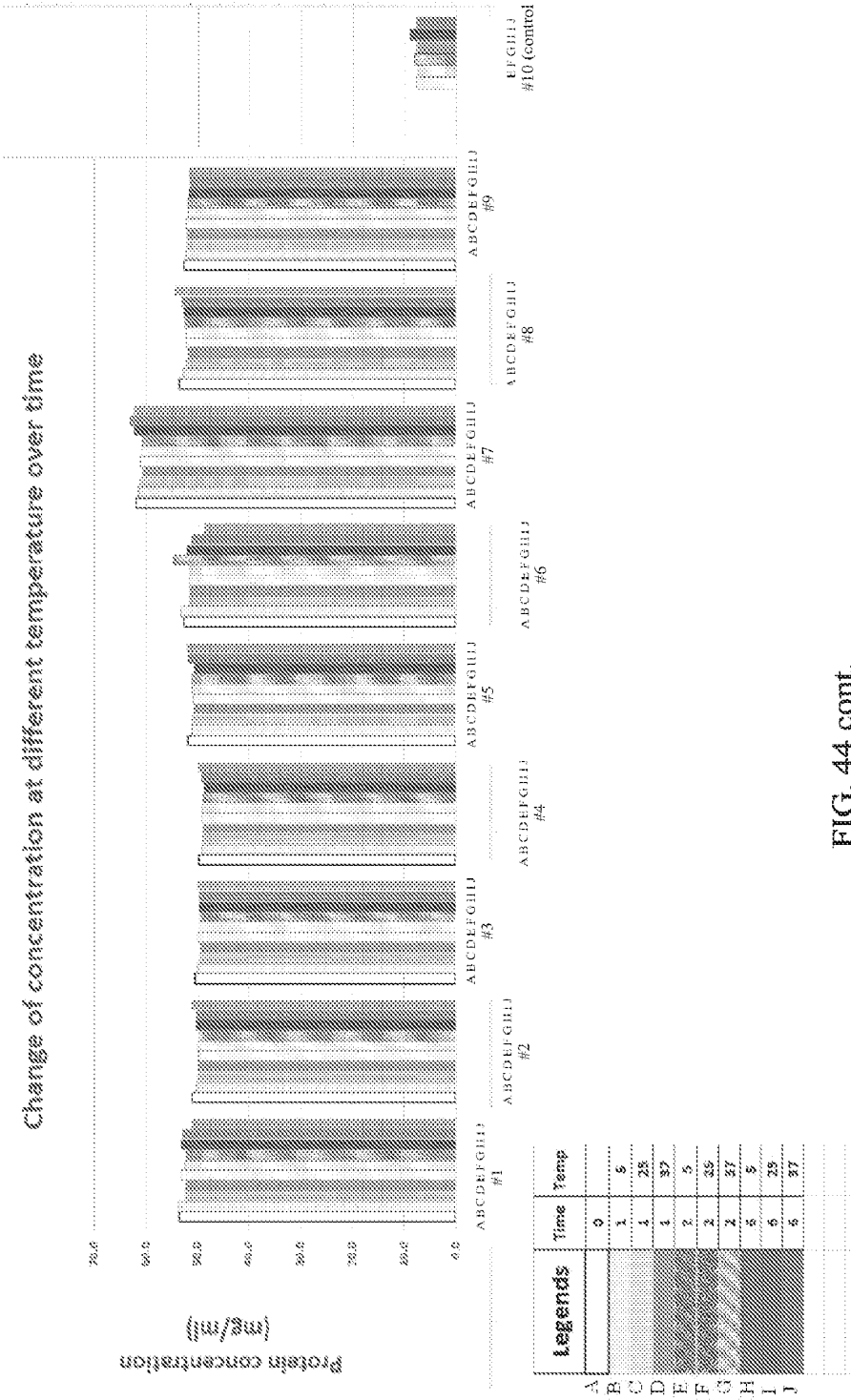


FIG. 44 cont.

		Time (Month)	5°C								
	Formulations		#1	#2	#3	#4	#5	#6	#7	#8	#9
Appearance	Color and clarity (Visual)	0	CCS ¹	CCS	CCS	CCS	CCS	CCS	CCS	CCS	CCS
		1	CCS	CCS	CCS	CCS	CCS	CCS	CCS	CCS	CCS
		2	CCS	CCS	CCS	CCS	CCS	CCS	CCS	CCS	CCS
		3	Cloudy white	CCS	CCS	CCS	CCS	Cloudy white	CCS	CCS	CCS
		6	Cloudy white	CCS	CCS	CCS	CCS	Cloudy white	CCS	CCS	CCS
SolovPE (Strength)	Protein concentration (mg/ml)	0	51.45	50.94	50.46	49.83	51.86	51.58	61.92	53.46	52.60
		1	55.59	50.20	50.02	49.33	51.02	59.29	61.37	52.72	51.20
		2	53.17	49.62	49.96	49.29	50.25	51.71	61.09	52.24	52.30
		3	56.57	55.45	55.86	52.60	55.59	55.48	66.26	56.13	55.49
		6	53.30	50.35	49.70	46.74	50.69	52.19	62.37	52.67	51.78
Tandem method analysis (Purity)	Bioconjugate main peak percent (IP1)		90.3%	90.0%	85.0%	80.0%	92.5%	90.0%	90.0%	85.0%	80.0%
		0			86.5%	81.3%					80.9%
		1			86.5%	81.4%					81.3%
		2			87.1%	82.0%					81.8%
		3			86.4%	81.1%					84.3%
	Free unconjugated protein monomer peak percent (monomer)				86.9%	80.3%					84.5%
		0		10.0%	10.0%	15.0%	20.0%	7.5%	10.0%	10.0%	20.0%
		1			12.6%	17.8%					18.1%
		2			12.5%	17.6%					17.6%
		3			12.2%	17.1%					17.2%
	All other peak percent	0			12.4%	17.4%					17.9%
		1			12.2%	17.6%					18.9%
		2			0.2%	0.9%					1.0%
		3			0.9%	1.0%					1.1%
		6			0.7%	0.9%					0.9%
SEC-HPLC (Purity)	Bioconjugate specific aggregate	0									
		1									
		2									
		3									
		6									
SEC/MALS (Purity and Identity)	weighted averaged molecular weight (M _w) kDa	0	1007.0	997.8	998.0	976.2	986.1	974.0	982.3	976.3	981.1
		6	1011.0	987.2	977.3	973.4	983.8	972.5	977.2	989.4	968.1
	Polydispersity index (PDI)	0	1.063	1.058	1.054	1.056	1.054	1.047	1.051	1.052	1.047
		1	1.084	1.078	1.076	1.072	1.082	1.073	1.073	1.076	1.072
		2	1.065	1.057	1.051	1.051	1.056	1.051	1.047	1.057	1.048
		3	1.067	1.059	1.054	1.053	1.061	1.051	1.058	1.059	1.057
		6	1.080	1.056	1.053	1.049	1.058	1.049	1.054	1.051	1.050
	Percent activity relative to Reference standard	0	91	92	90	91	96	93	95	96	95
		1									
		2				106					97
		3				102					
Competitive ELISA (Potency)	Percent activity relative to Reference standard	6				93					

¹There is assay measurement issue that result in arbitrarily higher values.
²CCS is a clear and colorless solution; Cloudy white is the solution appears visually cloudy and/or no longer colorless.

FIG. 45

		Time (Month)	25°C									
	Formulations		#1	#2	#3	#4	#5	#6	#7	#8	#9	
Appearance	Color and clarity (Visual)	0	CCS ^a	CCS	CCS	CCS	CCS	CCS	CCS	CCS	CCS	
		1	CCS	CCS	CCS	CCS	CCS	CCS	CCS	CCS	CCS	
		2	Cloudy white	CCS	CCS	CCS	CCS	Cloudy white	CCS	CCS	CCS	
		3	Cloudy white	CCS	CCS	CCS	CCS	Cloudy white	CCS	CCS	CCS	
		6	Cloudy white	CCS	CCS	CCS	CCS	Cloudy white	CCS	CCS	CCS	
SoloVPE (Strength)	Protein concentration (mg/ml)	0	53.45	50.94	50.48	49.81	51.86	52.59	61.92	59.46	52.60	
		1	52.49	50.12	49.74	49.19	51.14	51.73	61.20	52.40	52.28	
		2	52.48	49.98	49.61	49.27	51.08	51.57	60.83	52.37	51.77	
		3	58.18	53.95	52.48	52.80	55.19	54.85	66.73	56.25	55.94	
		6	52.83	50.29	49.77	49.39	51.92	51.13	63.14	52.94	51.66	
Tandem method analysis (Purity)	Bioconjugate main peak percent (LP1)	0	90.0%	90.0%	85.0%	80.0%	92.5%	90.0%	90.0%	85.0%	80.0%	
		1			85.5%	81.3%					80.9%	
		2			85.8%	80.6%					80.3%	
		3			85.1%	81.1%					80.8%	
		6			84.6%	79.3%					81.0%	
	Free unconjugated protein monomer peak percent (monomer)	0	10.0%	10.0%	15.0%	20.0%	7.5%	10.0%	10.0%	15.0%	20.0%	
		1			12.6%	17.8%					18.1%	
		2			12.7%	18.0%					18.1%	
		3			12.2%	17.4%					17.5%	
		6			13.2%	18.2%					17.9%	
	All other peak percent	0			11.1%	18.9%					17.8%	
		1			0.9%	0.9%					1.0%	
		2			1.4%	1.4%					1.6%	
		3			1.7%	1.6%					1.7%	
		6			2.2%	2.4%					1.4%	
SEC-MPLC (Purity)	Bioconjugate specific aggregate	0			3.2%	3.6%					3.8%	
		1										
		2										
		3										
		6										
SEC/MALS (Purity and Identity)	weighted averaged molecular weight (M _w) kDa	0	1007.0	997.2	968.0	976.2	968.1	974.0	962.1	972.9	981.1	
		6	997.2	998.1	973.5	970.9	993.0	975.3	993.5	971.1	968.3	
	Polydispersity Index (PDI)	0	1.053	1.059	1.054	1.056	1.054	1.047	1.061	1.052	1.047	
		1	1.082	1.080	1.075	1.089	1.079	1.068	1.075	1.076	1.078	
		2	1.054	1.055	1.054	1.049	1.059	1.054	1.064	1.053	1.052	
		3	1.058	1.061	1.047	1.061	1.059	1.051	1.060	1.053	1.049	
		6	1.062	1.095	1.053	1.052	1.060	1.053	1.059	1.054	1.049	
Competitive ELISA (Potency)	Percent activity relative to Reference standard	0	94	92	90	91	96	93	90	96	93	
		1										
		2				97					97	
		3				97						
		6				96						

FIG. 45 cont.

		Time (Month)	37°C								
	Formulations		#1	#2	#3	#4	#5	#6	#7	#8	#9
Appearance	Color and clarity (Visual)	0	CCS ²	CCS	CCS	CCS	CCS	CCS	CCS	CCS	CCS
		1	CCS	CCS	CCS	CCS	CCS	CCS	CCS	CCS	CCS
		2	Cloudy white	CCS	CCS	CCS	CCS	Cloudy white	CCS	CCS	CCS
		3									
		6	Cloudy white	CCS	CCS	CCS	CCS	Cloudy white	CCS	CCS	CCS
SoloVPE (Strength)	Protein concentration (mg/ml)	0	53.45	50.94	50.43	49.81	51.86	52.59	61.92	53.46	52.60
		1	52.42	49.89	49.43	48.93	50.74	51.61	60.66	51.85	52.07
		2	52.23	49.67	49.59	48.96	51.17	54.63	60.80	52.39	51.91
		3									
		6	51.17	51.18	50.65	49.93	52.10	46.70	62.37	54.43	52.76
Tandem method analysis (Purity)	Bioconjugate main peak percent (LP1)	0	90.0%	90.0%	85.0%	80.0%	92.5%	90.0%	90.0%	85.0%	90.0%
		1			86.5%	81.3%					80.9%
		2			83.7%	78.9%					78.6%
		3			81.8%	77.5%					77.6%
		6			77.1%	71.7%					71.8%
	Free unconjugated protein monomer peak percent (monomer)	0	10.0%	10.0%	15.0%	20.0%	7.5%	10.0%	10.0%	15.0%	20.0%
		1			12.6%	17.8%					18.1%
		2			13.7%	18.6%					18.9%
		3			14.7%	18.8%					19.1%
		6			15.2%	20.1%					20.1%
	All other peak percent	0			0.9%	0.9%					1.0%
		1			2.6%	2.5%					2.5%
		2			4.0%	3.7%					3.3%
		3									
		6			7.7%	8.3%					8.1%
SEC-MPLC (Purity)	Bioconjugate specific aggregate	0									
		1									
		2									
		3									
		6									
SEC/MALS (Purity and Identity)	weighted averaged molecular weight (M_w) kDa	0	1007.0	997.9	968.0	976.2	966.1	974.6	982.3	978.9	981.1
		6	1143.6	1084.2	987.5	970.7	1024.2	1077.2	1807.4	976.9	966.1
	Polydispersity Index (PDI)	0	1.063	1.059	1.054	1.056	1.094	1.087	1.061	1.052	1.047
		1	1.084	1.083	1.075	1.072	1.052	1.070	1.061	1.071	1.074
		2	1.056	1.062	1.052	1.050	1.063	1.052	1.055	1.051	1.046
		3									
		6	1.087	1.062	1.063	1.030	1.063	1.072	1.065	1.057	1.054
Competitive ELISA (Potency)	Percent activity relative to Reference standard	0	94	92	90	91	96	93	96	96	93
		1									
		2				94					98
		3									
		6				87					

FIG. 45 cont.

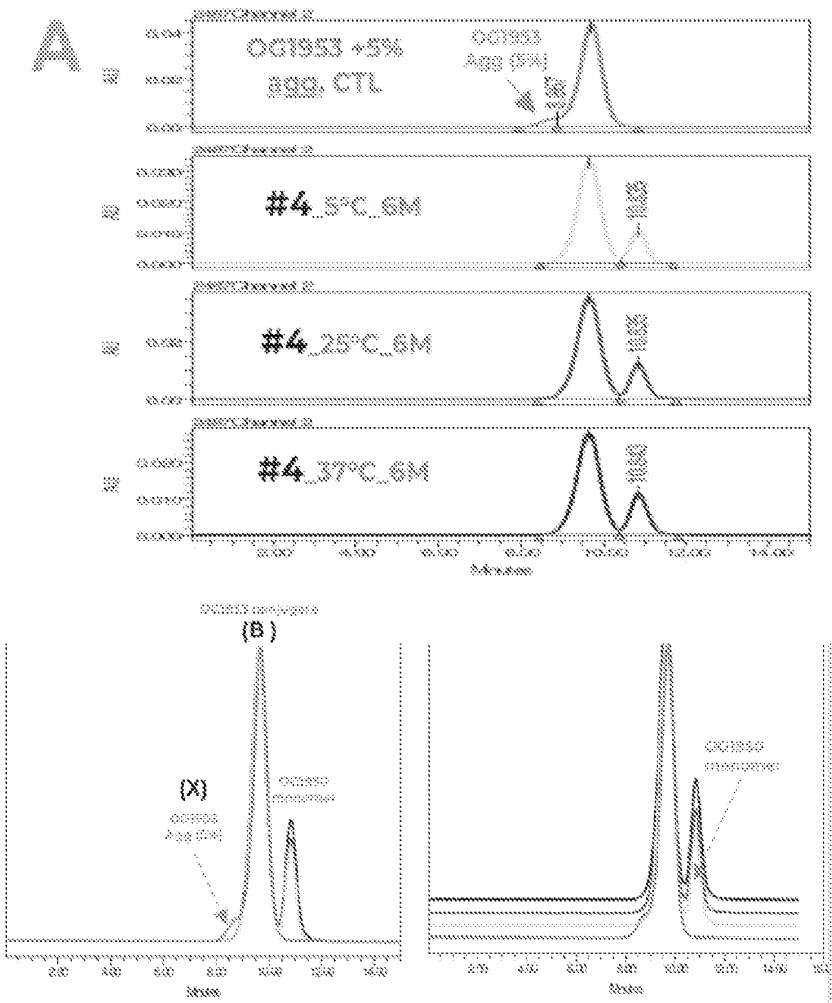


FIG. 46A

	#1	#2	#3	#4	#5	#6	#7	#8	#9
T0									
T1M_5°C	92.6%	93.8%	92.1%	92.8%	94.2%	91.5%	92.1%	87.5%	92.6%
T1M_25°C	92.3%	92.6%	87.5%	92.4%	93.7%	91.1%	91.6%	87.0%	92.6%
T1M_37°C	89.4%	90.7%	86.5%	81.4%	93.5%	88.5%	90.6%	85.8%	81.4%
T2M_5°C	93.2%	93.3%	90.8%	84.0%	94.9%	92.6%	93.0%	88.9%	84.0%
T2M_25°C	92.3%	92.4%	88.3%	83.4%	94.6%	92.4%	92.6%	87.8%	83.8%
T2M_37°C	89.7%	91.1%	86.4%	81.6%	93.4%	89.5%	90.7%	87.1%	84.8%
T3M_5°C	93.5%	93.7%	89.5%	85.0%	94.9%	92.4%	93.1%	89.2%	84.8%
T3M_25°C	87.6%	92.5%	88.6%	83.5%	94.4%	92.0%	92.2%	88.0%	83.5%
T6M_5°C	92.2%	92.4%	87.7%	82.3%	94.0%	91.9%	92.1%	88.1%	82.0%
T6M_25°C	91.9%	90.6%	86.5%	80.6%	93.8%	92.5%	91.2%	86.8%	80.7%
T6M_37°C	91.5%	87.0%	82.4%	77.4%	91.3%	91.9%	88.1%	81.9%	78.9%
Change vs Time: ΔM_5°C	-0.7%	-4.1%	4.2%	-3.5%	-1.3%	0.7%	-1.8%	-2.1%	-2.8%

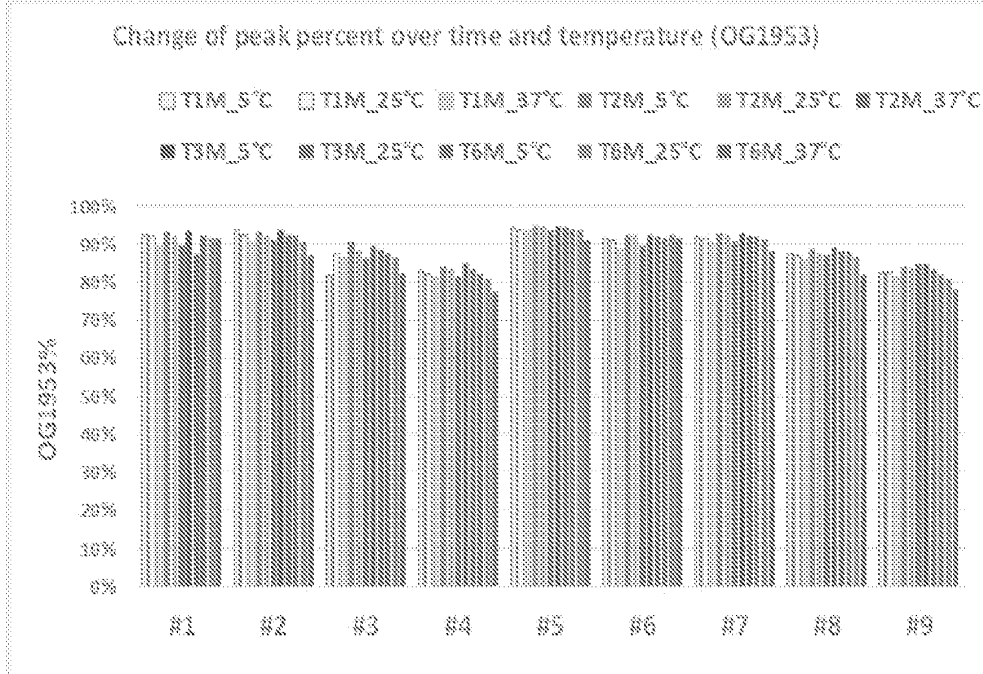


FIG. 46B

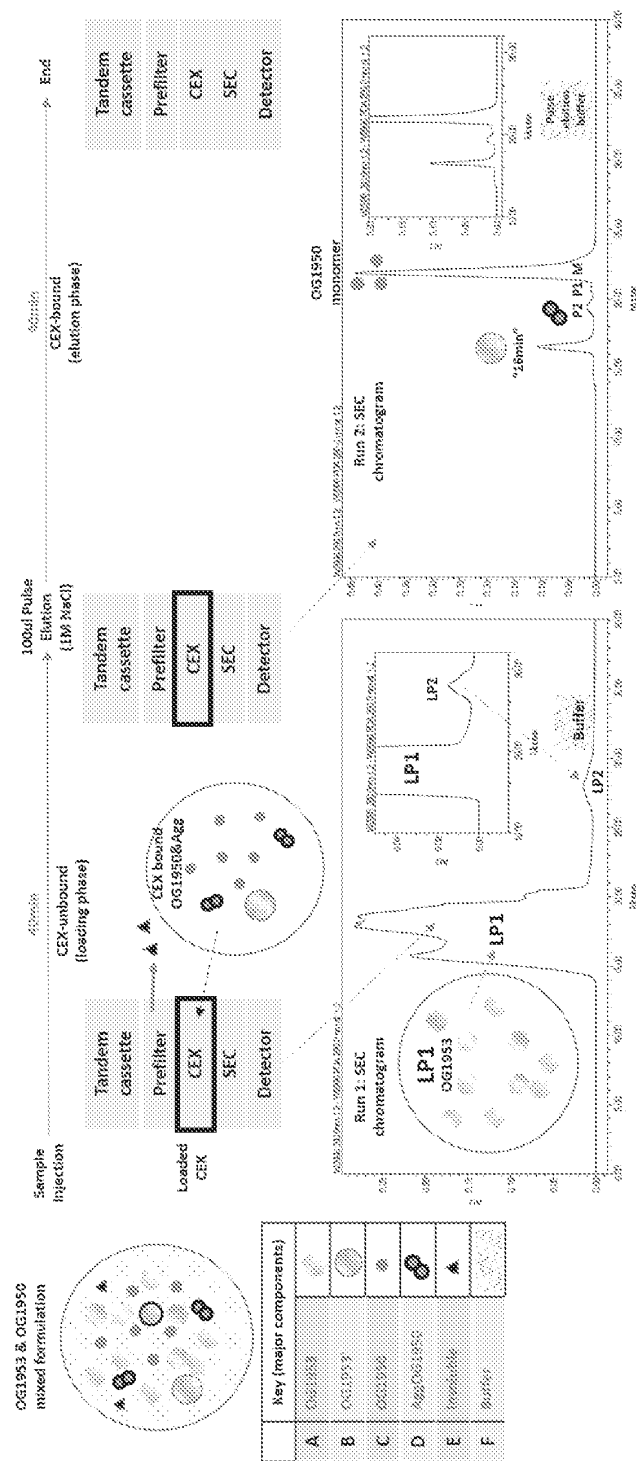


FIG. 47A

Total OG1950 free protein (monomer + P1+P2)/Total protein percent change over time and temperature												
	#1	#2	#3	#4	#5	#6	#7	#8	#9	#10	#11	#12
Target%	10.0%	21.0%	15.0%	22.0%	7.5%	10.0%	10.0%	10.0%	22.0%	22.0%	100.0%	
T0	7.55%	8.21%	11.55%	12.12%	6.55%	8.69%	8.85%	11.69%	18.35%	18.35%	31.0%	
T1M_5°C	7.55%	7.95%	12.78%	17.97%	6.72%	8.41%	8.55%	11.25%	18.00%	18.00%	80.18%	
T1M_15°C	7.73%	8.34%	13.06%	18.45%	6.59%	8.56%	8.55%	13.56%	18.56%	18.56%	80.98%	
T1M_37°C	8.45%	9.46%	14.08%	19.24%	7.02%	9.84%	9.48%	14.89%	19.56%	19.56%	80.39%	
T2M_5°C	6.91%	7.43%	12.37%	17.32%	6.17%	8.02%	8.06%	12.91%	17.41%	17.41%	79.61%	
T2M_15°C	7.48%	7.92%	12.37%	17.69%	5.83%	7.75%	8.31%	11.30%	17.66%	17.66%	78.93%	
T2M_37°C	9.88%	9.84%	14.55%	19.53%	7.65%	10.19%	9.72%	14.86%	19.77%	19.77%	79.25%	
T3M_5°C	7.43%	7.83%	12.69%	17.84%	6.70%	8.39%	8.74%	11.34%	18.47%	18.47%	81.62%	
T3M_15°C	8.13%	8.76%	13.58%	18.78%	6.42%	8.10%	8.85%	11.84%	17.88%	17.88%	81.84%	
T3M_37°C					Not sampled							
T6M_5°C			12.46%	18.08%							17.30%	
T6M_15°C			13.43%	19.47%							18.41%	
T6M_37°C			16.21%	21.54%							21.71%	

FIG. 47B

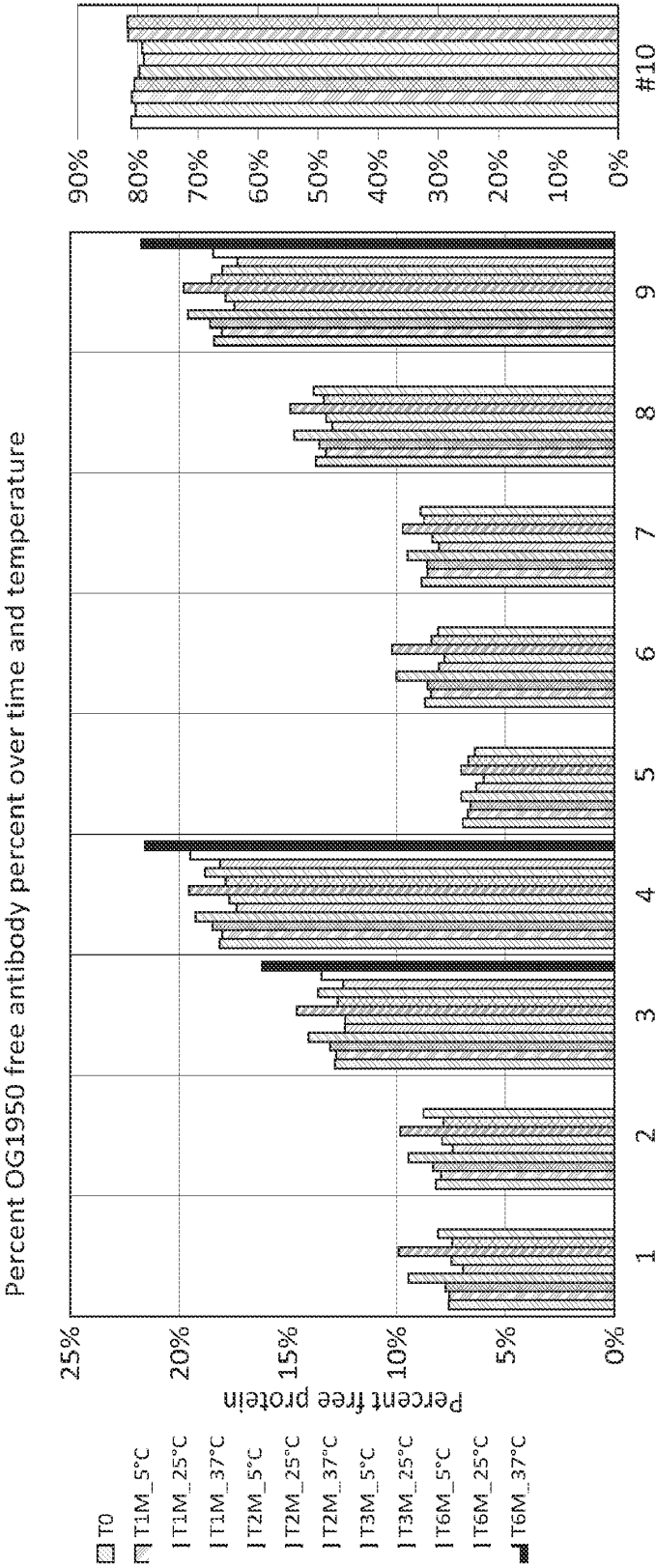
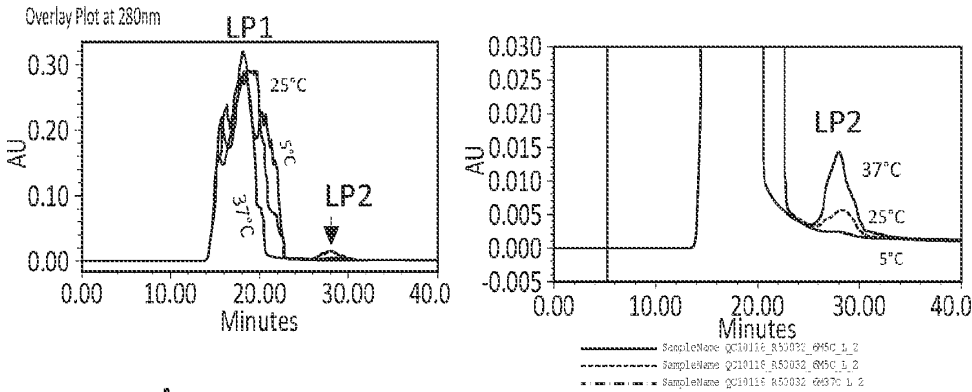


FIG. 47B cont.

B. Sample #4 280nm chromatograms

a. CEX-unbound fraction with load peak 1&2 (LP1 & 2)



b. CEX-bound fraction elution run profile

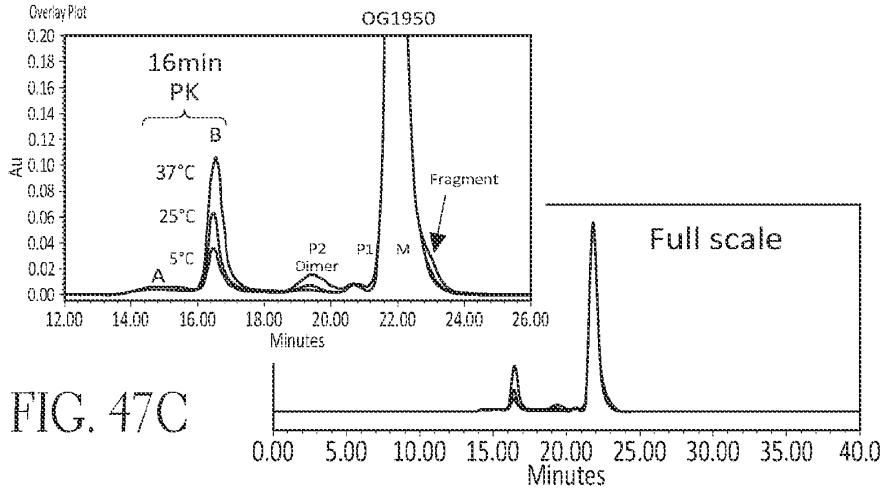


FIG. 47C

Temp	Time	OG1953	Impurities					Monomer	All impurities ¹	Recovery
°C	Month	LP1 (main)	LP2 (side)	16min	P2	P1	M	LP2+16min+P2+P1	Mean actual	
5°C	0	81.3%	0.00%	0.61%	0.12%	0.17%	17.8%	0.9%	97.6%	
	1	81.4%	0.00%	0.62%	0.16%	0.21%	17.6%	1.0%	100.3%	
	2	82.0%	0.00%	0.66%	0.07%	0.16%	17.1%	0.9%	105.2%	
	3	81.1%	0.00%	1.05%	0.18%	0.22%	17.4%	1.4%	99.5%	
	6	80.3%	0.00%	1.64%	0.22%	0.22%	17.6%	2.1%	108.3%	
25°C	0	81.3%	0.00%	0.61%	0.12%	0.17%	17.8%	0.9%	97.6%	
	1	80.6%	0.08%	0.88%	0.20%	0.22%	18.0%	1.4%	98.8%	
	2	81.1%	0.18%	1.10%	0.12%	0.16%	17.4%	1.6%	107.0%	
	3	79.3%	0.25%	1.69%	0.29%	0.23%	18.2%	2.4%	98.8%	
37°C	0	81.3%	0.00%	0.61%	0.12%	0.17%	17.8%	0.9%	97.6%	
	1	78.9%	0.37%	1.52%	0.36%	0.23%	18.6%	2.5%	97.5%	
	2	77.5%	0.74%	2.35%	0.36%	0.21%	18.8%	3.7%	97.3%	
	6	71.7%	2.14%	4.65%	1.08%	0.40%	20.1%	8.3%	97.5%	

¹Sum of all degradants percent includes only LP2, 16min, P2, and P1. The retro reaction derived monomeric form OG1950 is excluded from this calculation.

FIG. 47D

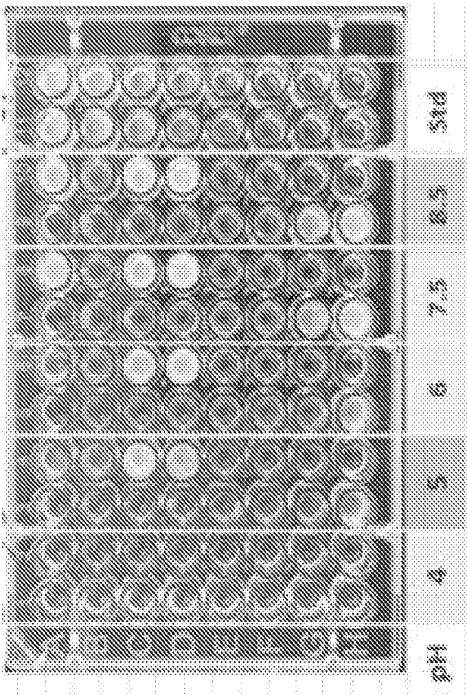


FIG. 48B

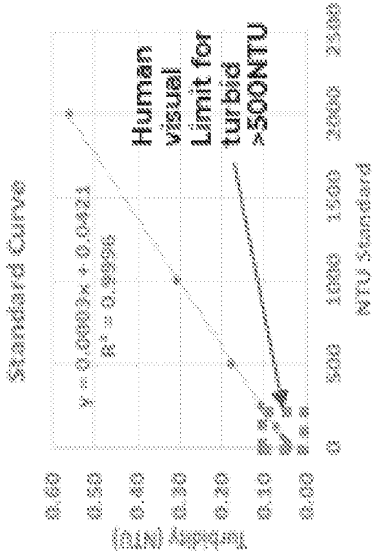
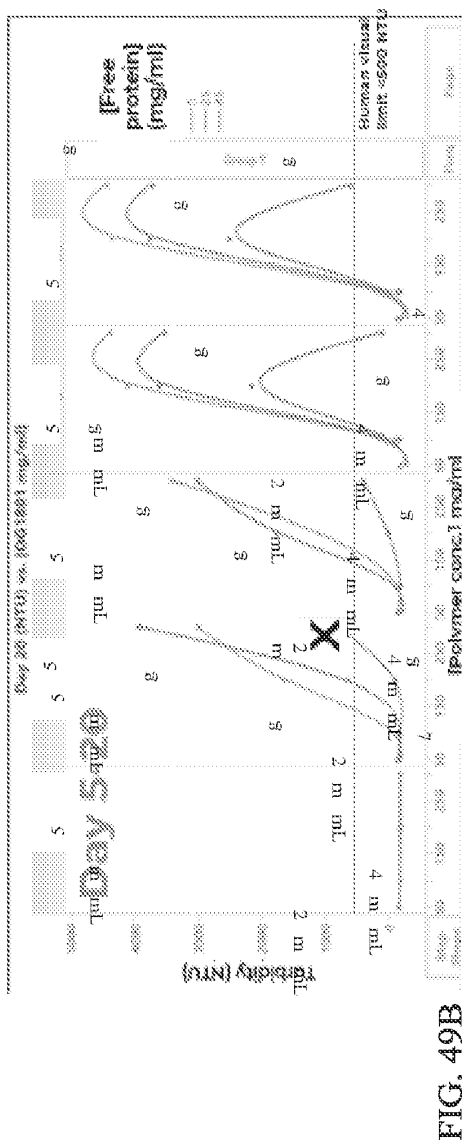
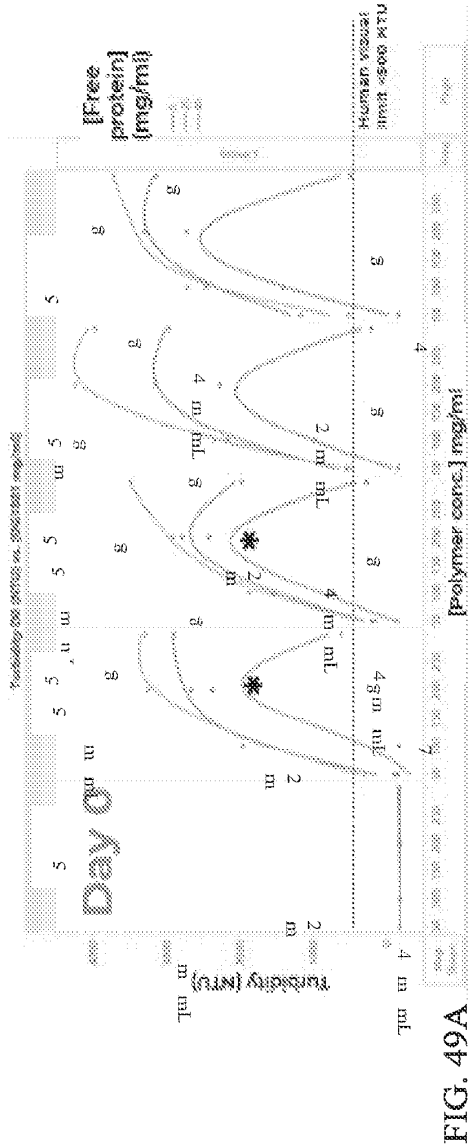
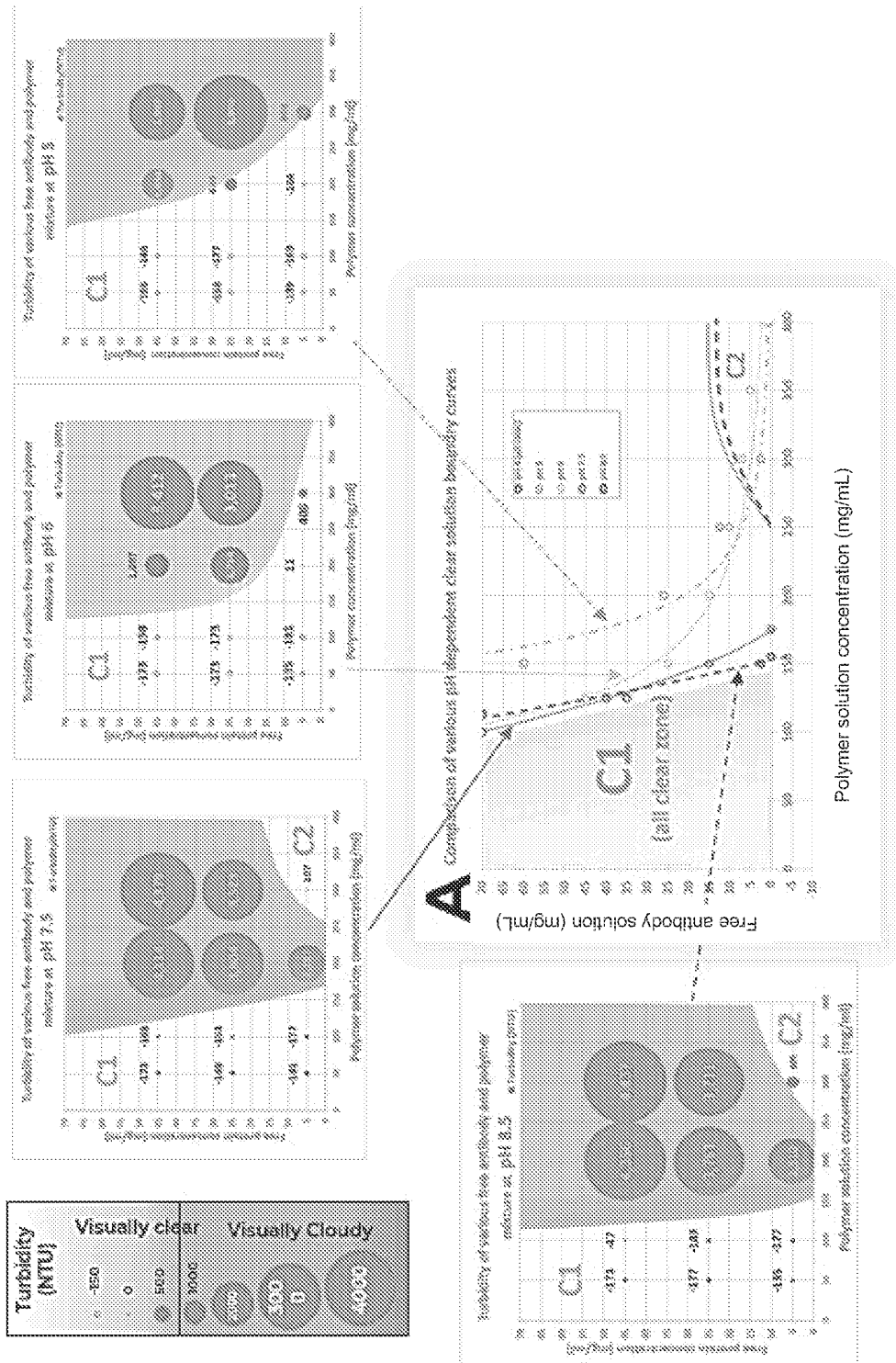


FIG. 48C

pH	[0.0003] mg/ml	[0.0550] mg/ml	well ID
4	50	5, 25 & 45	A01, B01, C01
	100	5, 25 & 45	D01, E01, F01
	200	5, 25 & 45	G01, H01, A02
	300	5, 25 & 45	B02, C02, D02
5	50	5, 25 & 45	A03, B03, C03
	100	5, 25 & 45	D03, E03, F03
	200	5, 25 & 45	G03, H03, A04
	300	5, 25 & 45	B04, C04, D04
6	50	5, 25 & 45	A05, B05, C05
	100	5, 25 & 45	D05, E05, F05
	200	5, 25 & 45	G05, H05, A06
	300	5, 25 & 45	B06, C06, D06
7.5	50	5, 25 & 45	A07, B07, C07
	100	5, 25 & 45	D07, E07, F07
	200	5, 25 & 45	G07, H07, A08
	300	5, 25 & 45	B08, C08, D08
8.5	50	5, 25 & 45	A09, B09, C09
	100	5, 25 & 45	D09, E09, F09
	200	5, 25 & 45	G09, H09, A10
	300	5, 25 & 45	B10, C10, D10

FIG. 48A





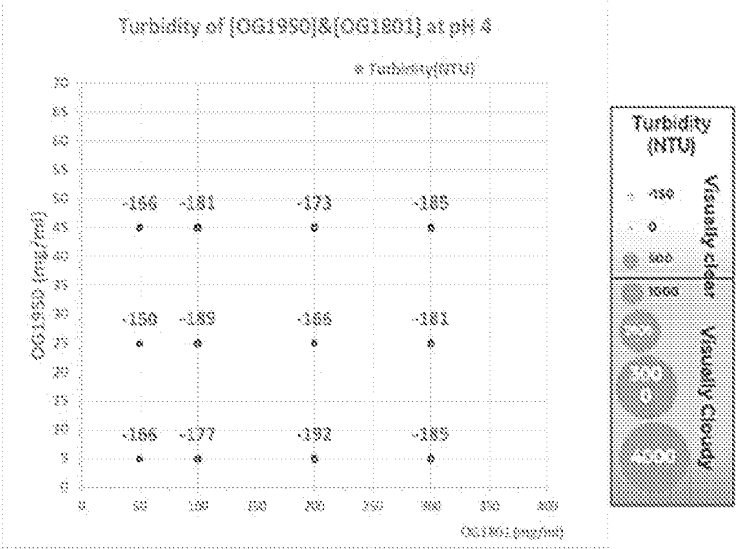


FIG. 49D

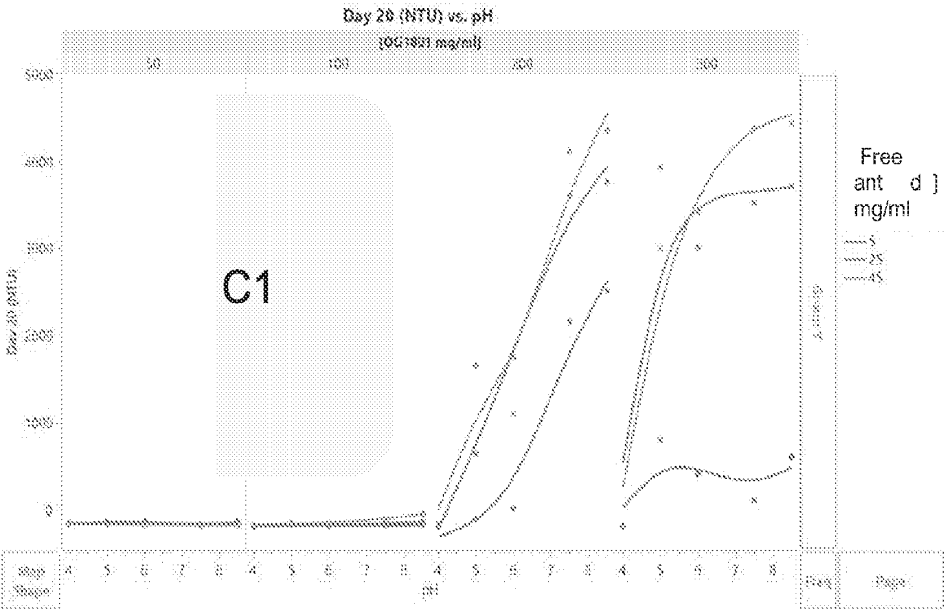


FIG. 49E

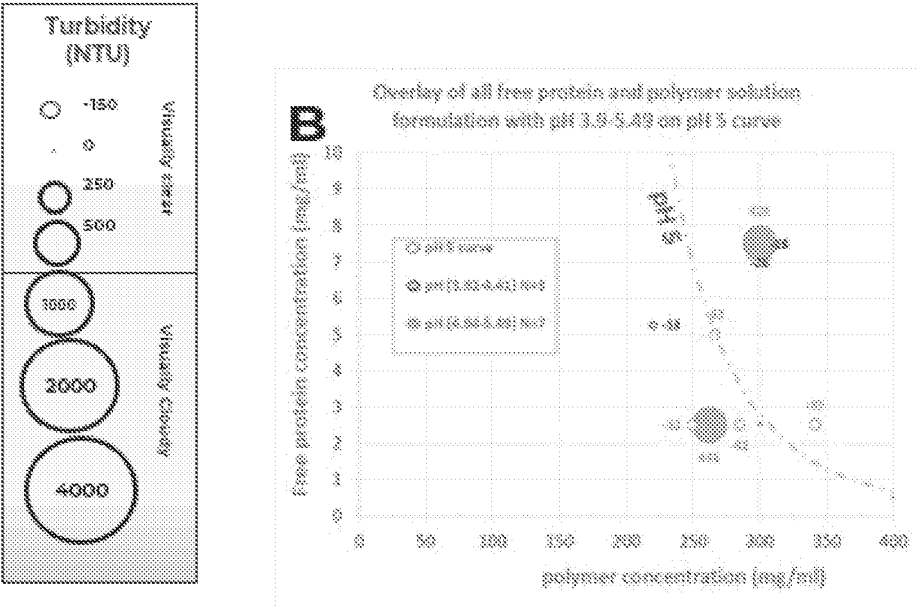


FIG. 49F

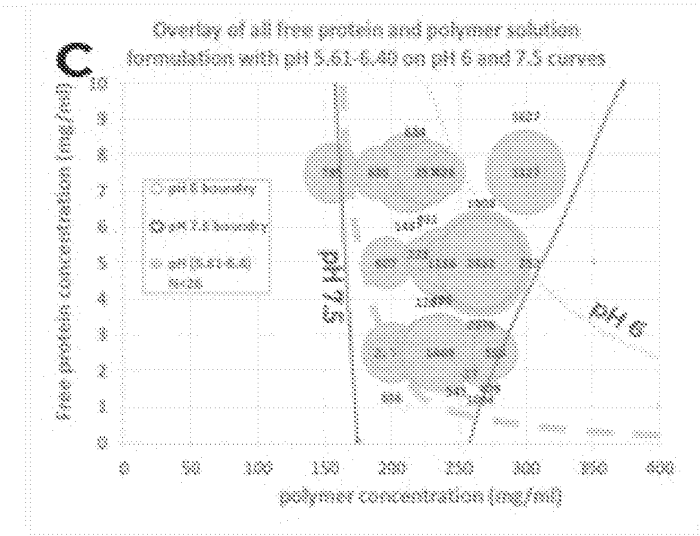


FIG. 49G

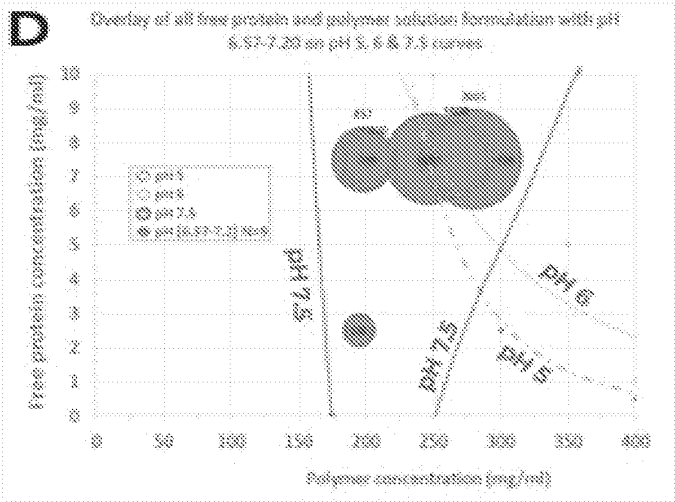


FIG. 49H

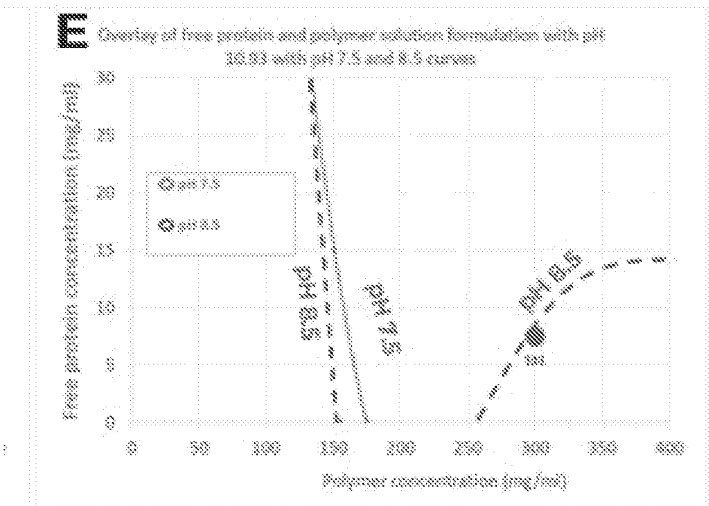


FIG. 49I

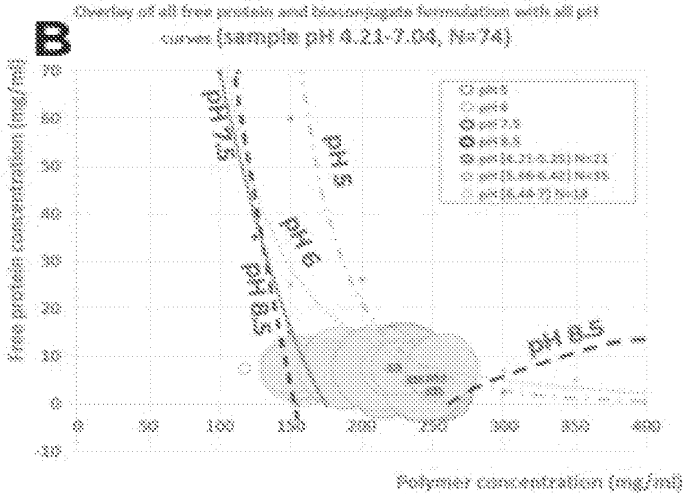
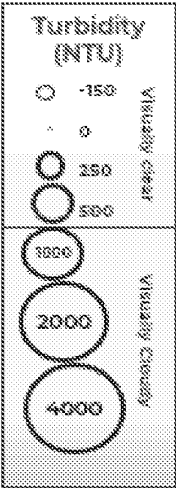


FIG. 49J

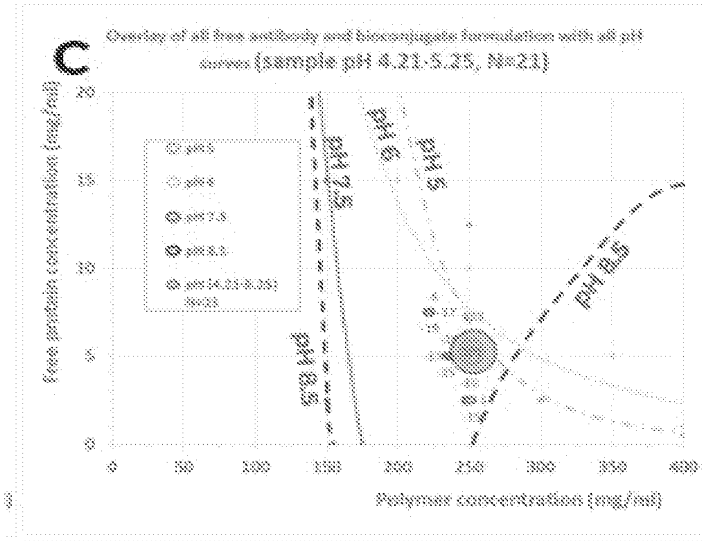


FIG. 49K

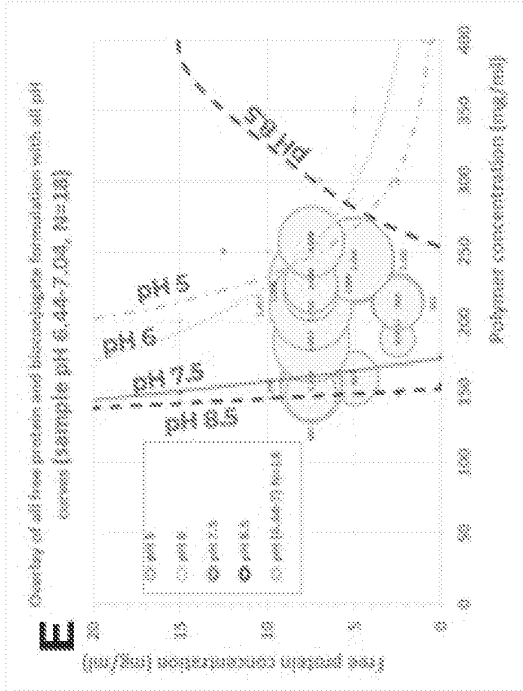


FIG. 49M

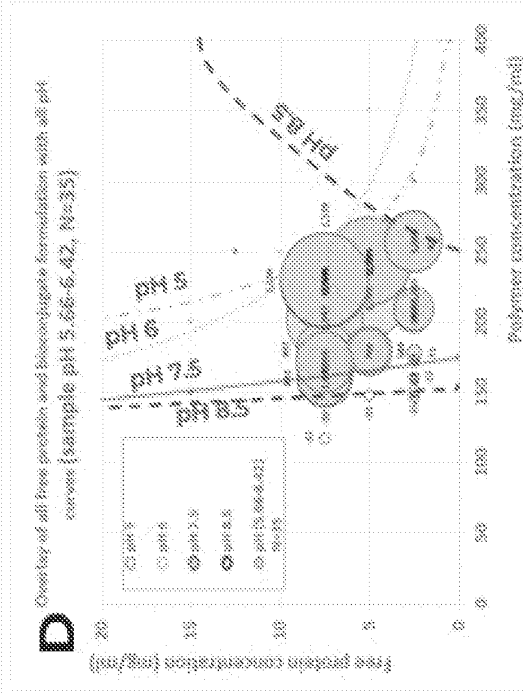


FIG. 49L

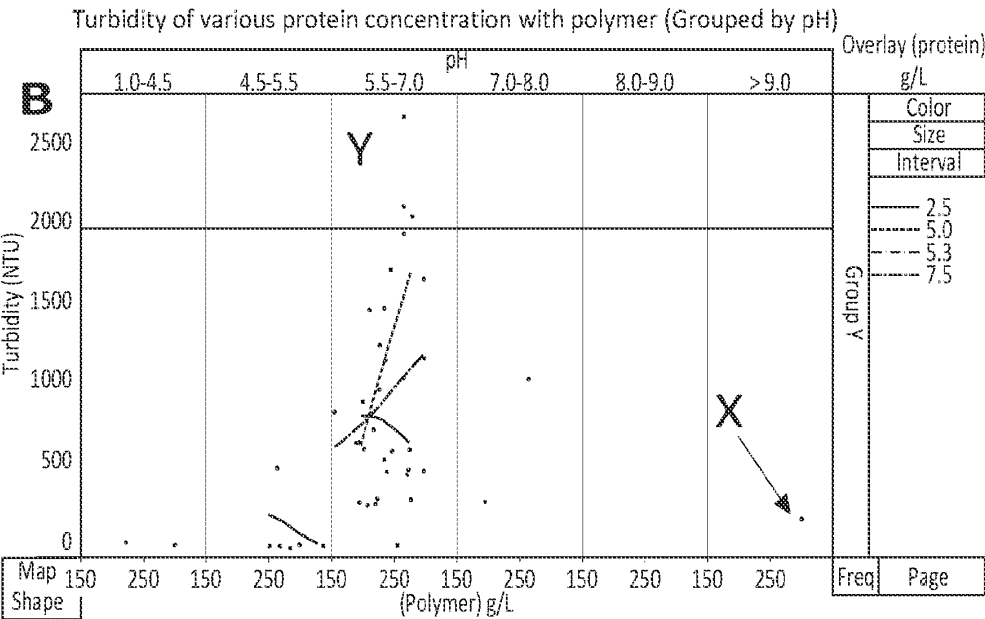


FIG. 49N

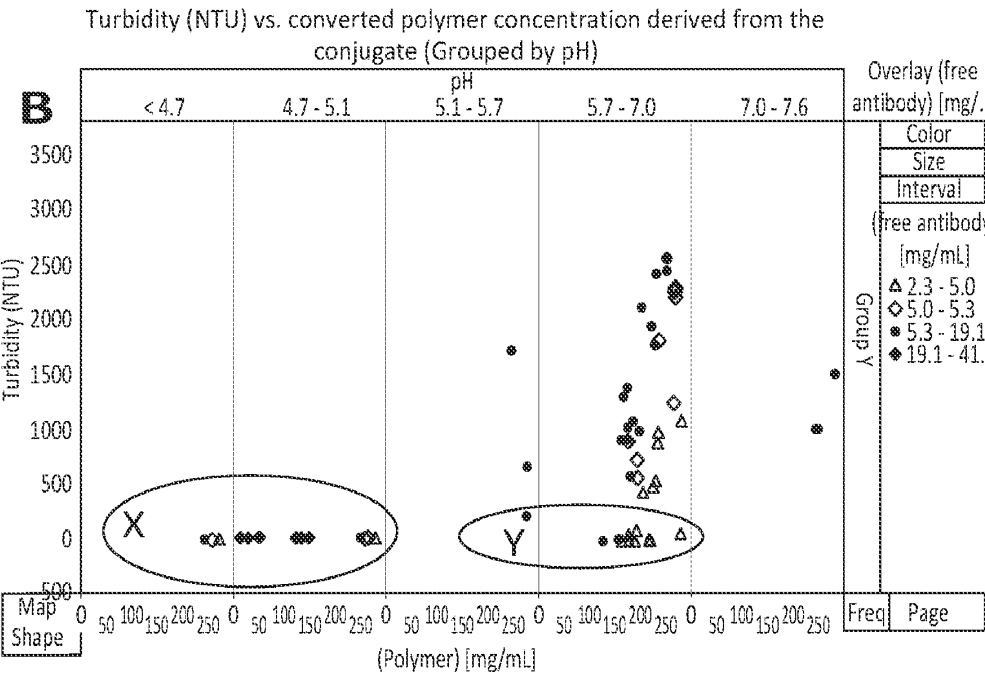


FIG. 49O

Impact of Increasing % Unconjugated Ab on Viscosity of OG1953 at 25°C

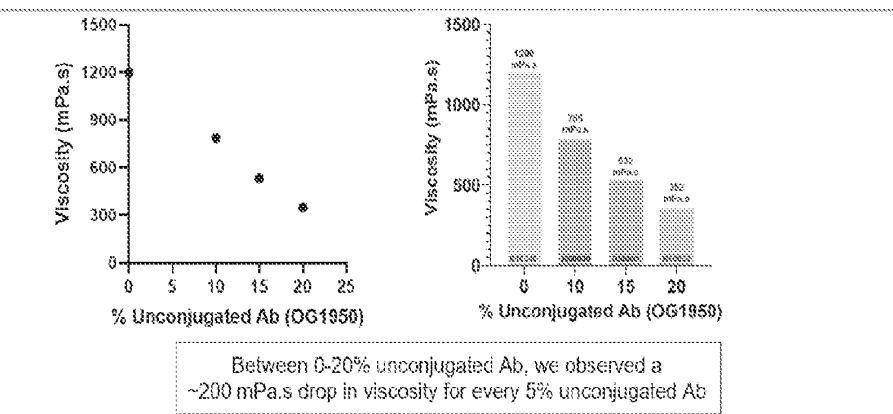


FIG. 50B

Sample Description	Batch	Formulation	Concentration (mg/mL)	Viscosity (mPa.s)	Replicates
0% Unconjugated Ab	R15546	12.5 mM NaOH pH 8.5, 0.025% PEG20	51.2	1200 ± 34	4
10% Unconjugated Ab	650030		51.4	795	1
15% Unconjugated Ab	650031	50 mM NaAc pH 5.0, 0.025% PEG20	52.7	630	1
20% Unconjugated Ab	650032		52.1	352	1

FIG. 50C

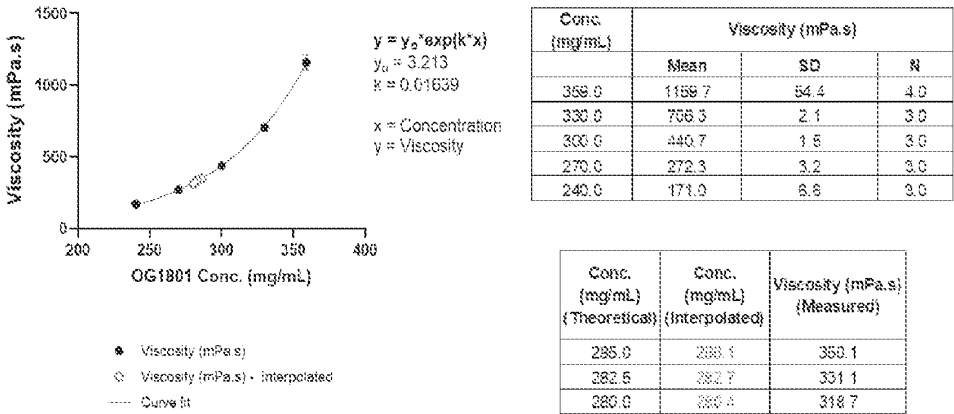


FIG. 50D

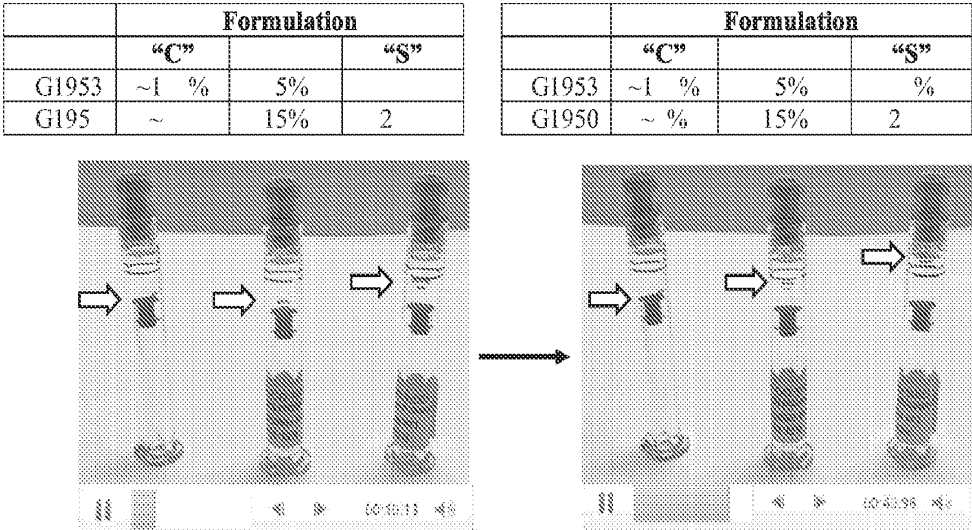


FIG. 51

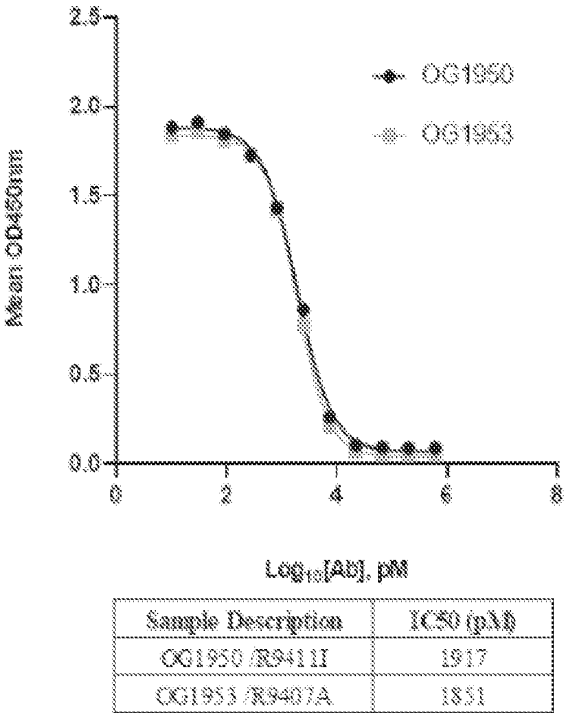


FIG. 52A

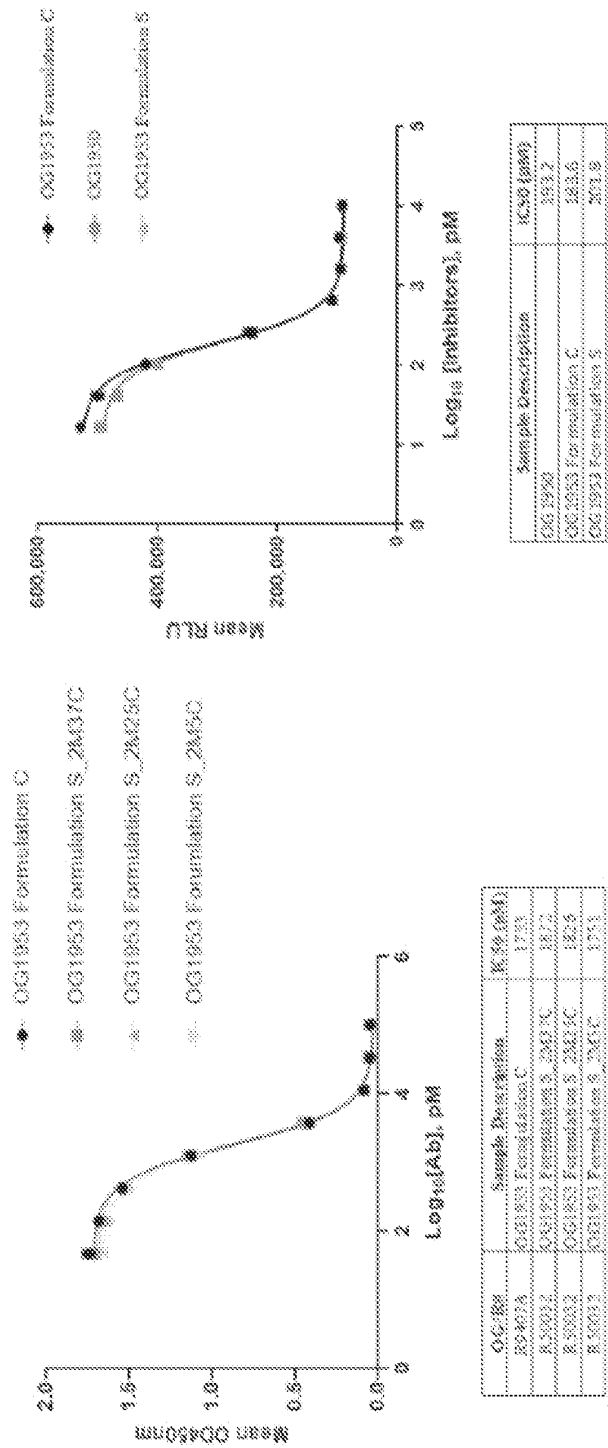


FIG. 52C

FIG. 52B

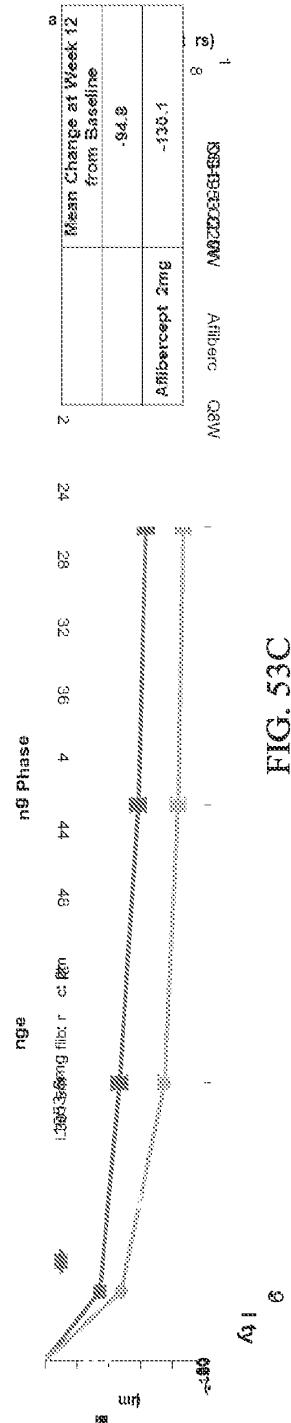
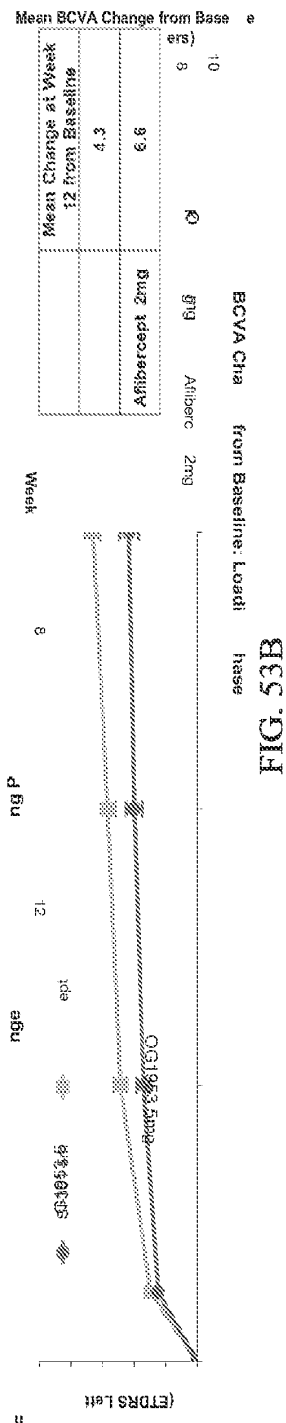
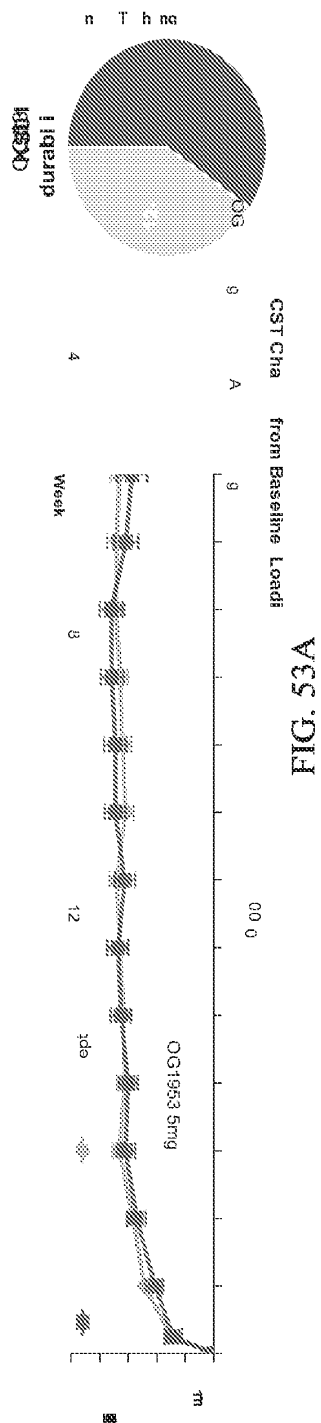


Figure. CST Change at Week 36 From (A) Baseline in Anti-VEGF Treatment-Naive Participants (Group 1) and (B) Week 12 Baseline in Anti-VEGF Incomplete Responders (Group 2)

A. Least squares means from linear model analysis of study eye central subfield thickness (CST) change from baseline in treatment-naive participants (group 1). B. Least squares means from linear model analysis of study eye CST change from week 12 baseline in anti-vascular endothelial growth factor (VEGF) incomplete responders (group 2). A. B. Error bars represent 80% CI. Arm A: ranibizumab 0.5 mg every 4 weeks (Q4W); arm B: faricimab 1.5 mg Q4W; arm C: faricimab 6.0 mg Q4W up to week 12, followed by faricimab 6.0 mg every 8 weeks (Q8W); arm D: ranibizumab 0.5 mg Q4W up to week 8, followed by faricimab 6.0 mg Q4W.

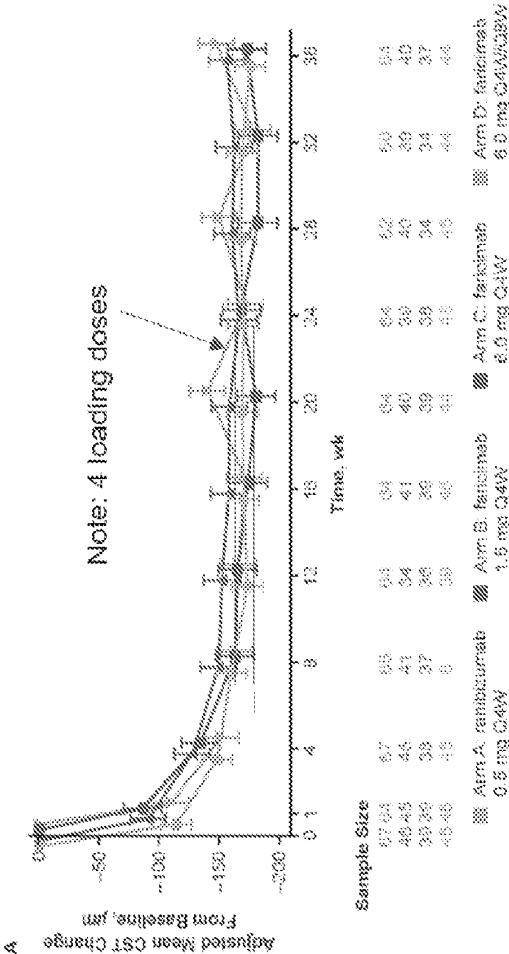


FIG. 53D

Light chain sequence

IQLTQSPSSLS S R TIT S SIS S L W QQKP K PKLLI SSL S PSRFS S S
T FTLTISSLQPE F T QQWS P TF Q TKVEIKRTVAAPSVFIFPPSDEQLKSGTA
SVV LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLSKADYEK
HKVYA EVTHQGLSSPVTKSFNRGE (SEQ ID NO: 106)

L
R (Kabat numbering)

Heavy chain sequence with notations

SDTGRPFVEMYSEIPEIHMTEGRELVIP RVTSPNITVTLKKEPLDTLIPDGKRIIWDSSRKG
FIISNATYKEIGLLT EATVNGHLYKTNLYTHRQTNTIHDVVLSPSHGIELSVGEKLVN
TARTELVNGIDFNWEYPSSKHQHKLVNRDLKTQSGSEMKKFLSTLTIDGVTRSDQGLY
T AASSGLMTKKNSTFVRVHEKGGGSGGGGSE QL ES L QP SLRLS S F
TFSPF MHW RQ P K LEW KISP SWT S T T RFTFSL TSKST LQMNSLR E
T RQ W L IW Q TL T SSASTKGPSVFPLAPSSKSTSGGTAALG LVKD
YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYI NVNHKPSN
TKVDKKVEPKS DKTHT PP PAPEAAAGAPSVFLFPPKPKDTLMISRTPEVT VVVDVSH
EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK KVS
NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT LVKGFYPSDIAVEWESN
GQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS SVMHEALHNHYTQKSLS
SPGK
(SEQ ID NO:105)

VEGF Trap

Linker

H
R (Kabat numbering)

FIG. 54

1 LVVTPPGPEL VLVNSSTFVL TCSGSAPVVW ERMSQEPPOE MAKAQDGTFS SVLTLTNLTG
LDTGEYFCTH NDSRGLETDE
81 RKRLYIFVPD PTVGFLPND A EELFIFLTEI TEITIPCRVT DFQLVVTLHE KKGDVALPVP
YDHQRGFSGI FEDRSYICKT
161 TIGDREVDS AYYVYRLQVS SINVSVNAVQ TVVRQGENIT LMCIVICNEV VNFEWTYPRK
ESGRLVEPVT DFLLDMPYHI
241 RSLIHPSAE LEDSGTYTCN VTESVNDHQD EKAINITVVE SGGGGGSGGG GSEVQLVESG
GGLVQPGGSL RLSCAASGYD
321 FTHYGMNVWR QAPGKGLEWV GWINTYTGEF TYAADFKRRF TFSLDTSKST AYIQMNSLRA
EDTAVYYCAK YPYYYGTSHW
401 YFDVWGQGT L VTVSSASTKG PSVFFLAPSS KSTSGGTAAL GCLVKDYFPE PVTVSWNSGA
LTSCGVHTFPA VLQSSGLYSL
481 SSVVTVFSSS LGTQTYICNV NHKPSNTKVD KKVEPKSCDK THTCPPCPAP EAAGAPSVFL
FPPKEKDTLM ISRTPEVTCV
561 VVDVSHEDPE VKENWYVDGV EVHNAKTKPR EEQYNSTYRV VSVLTVLHQD WLNKEYKCK
VSNKALPAPI EKTISKAKGQ
641 PREPQVYTLF PSREEMTKNQ VSLTCLVKGF YPSDIAVEWE SNGQPENNYK TTPPVLDSDG
SFFLYSKLTV DKSRWQQGNV
721 FSCSVMHEAL HNHYTQKSLS CSPGK

(SEQ ID NO:131)

FIG. 55A

1 DIQLTQSPSS LSASVGDRTV ITCSASQDIS NYLNNYQQKF GKAPKVLIIYF TSSLHSGVPS
RFSGSGSGTD FTLTISLQF
81 EDFATYYCQQ YSTVPWTFGQ GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY
BREAKVQNKV DNALQSGNSQ
161 ESVTEQDSKD STYSLSSLT LSKADYEKHK VYACEVTHQG LSSPVTKSFN RGEC

(SEQ ID NO:132)

FIG. 55B

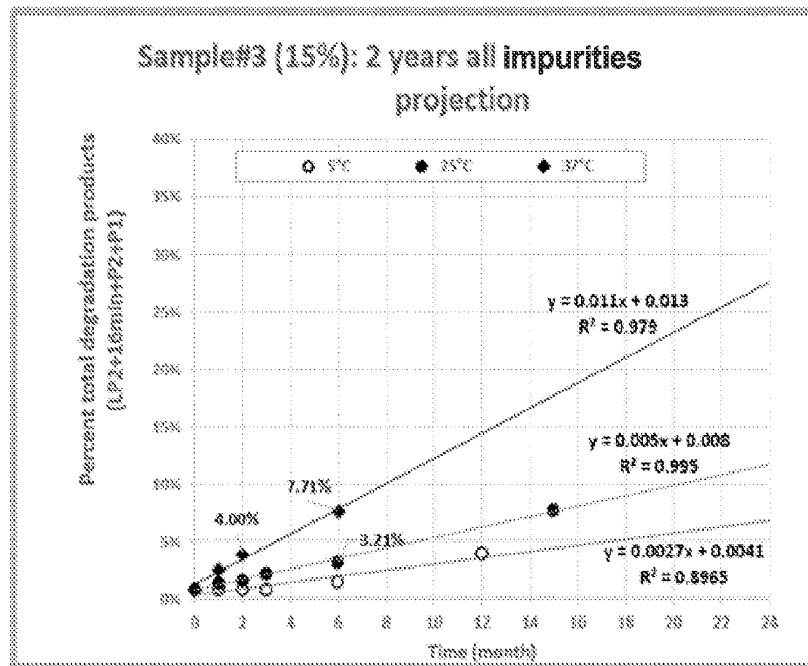


FIG. 56A

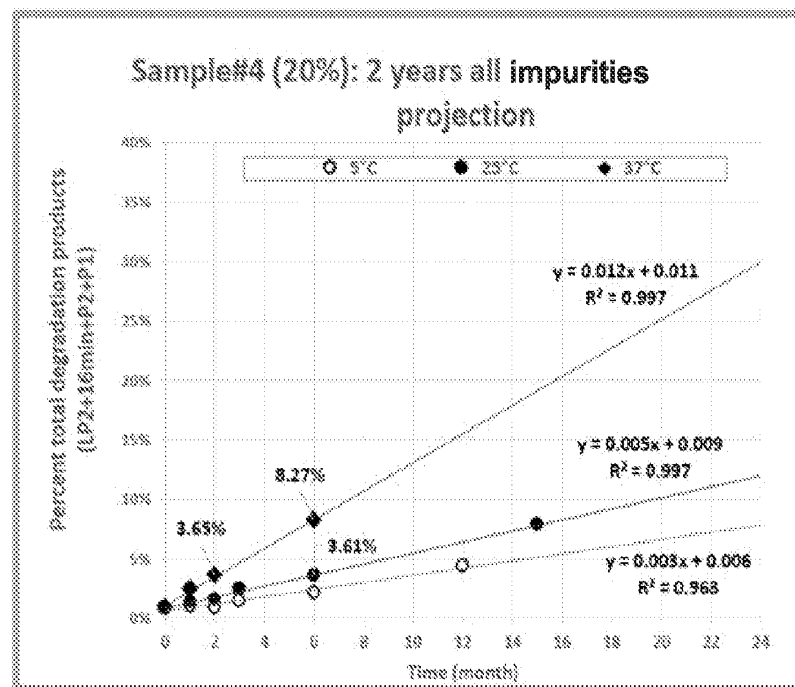


FIG. 56B

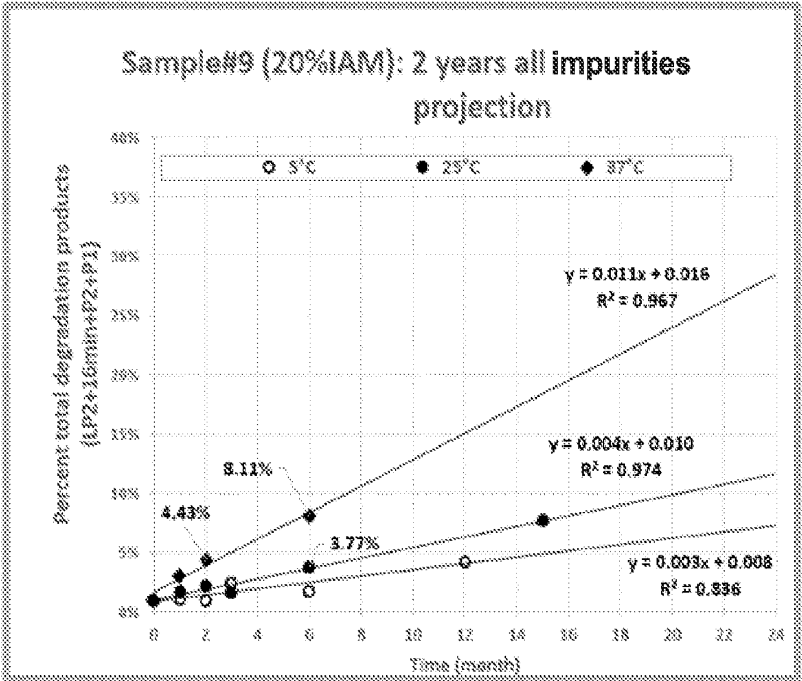


FIG. 56C

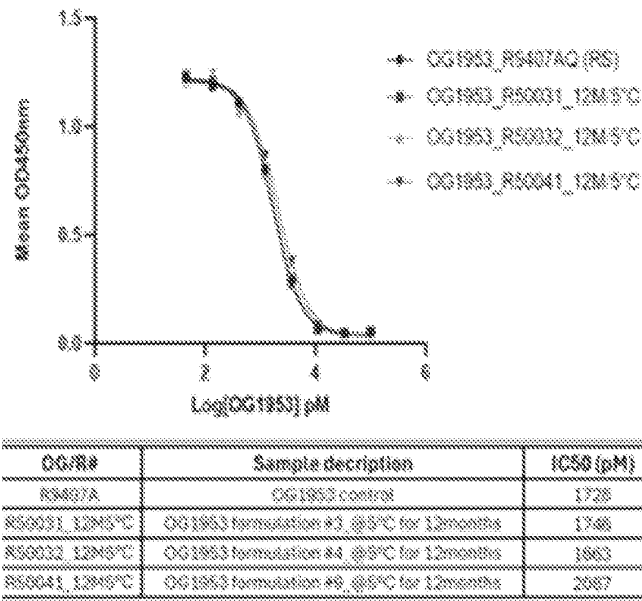


FIG. 57A

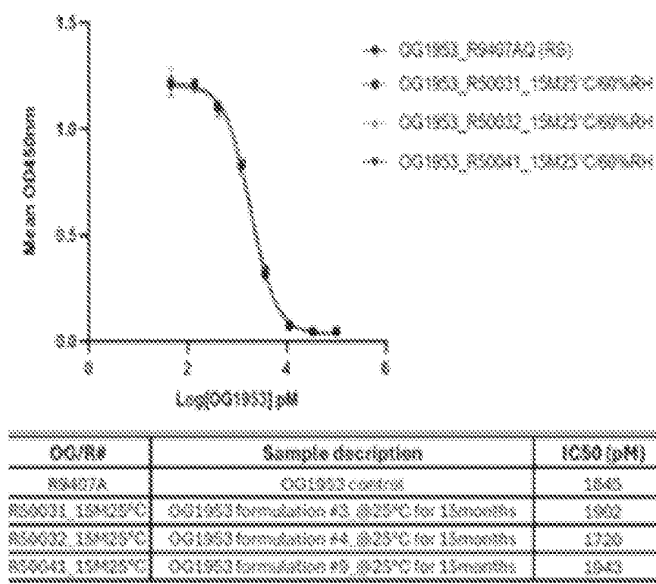


FIG. 57B

Anti-VEGF antibody (e.g., OG1950)
Anti-VEGF antibody conjugate (e.g., OG1953)
Sodium Acetate
Polysorbate 20
~pH4.5-5.5 (e.g., ~pH5)

FIG. 58A

Anti-IL-6 antibody fused to VEGF trap (e.g., OG2072)
Anti-IL-6 antibody fused to VEGF trap conjugate (e.g., OG2074)
Sodium Acetate
Polysorbate 20
Sucrose (optional)
~pH4.5-5.5 (e.g., ~pH5)

FIG. 58B

Anti-IL-6 antibody fused to VEGF trap (e.g., OG2072)
Anti-IL-6 antibody fused to VEGF trap conjugate (e.g., OG2074)
Histidine Acetate
Polysorbate 20
Sucrose (optional)
~pH5.2-6.2 (e.g., ~pH5.7)

FIG. 58C

Tandem method run with PDA
(200-800nm but showing only 200-350nm)

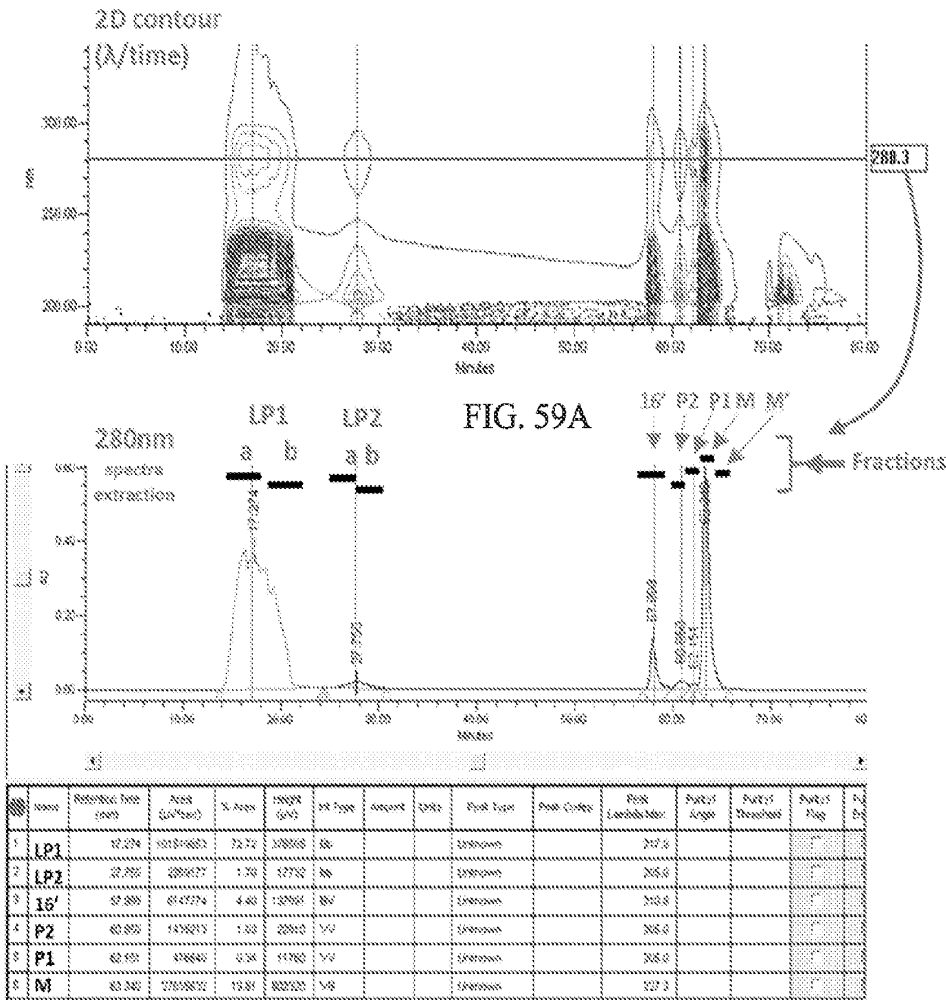


FIG. 59B

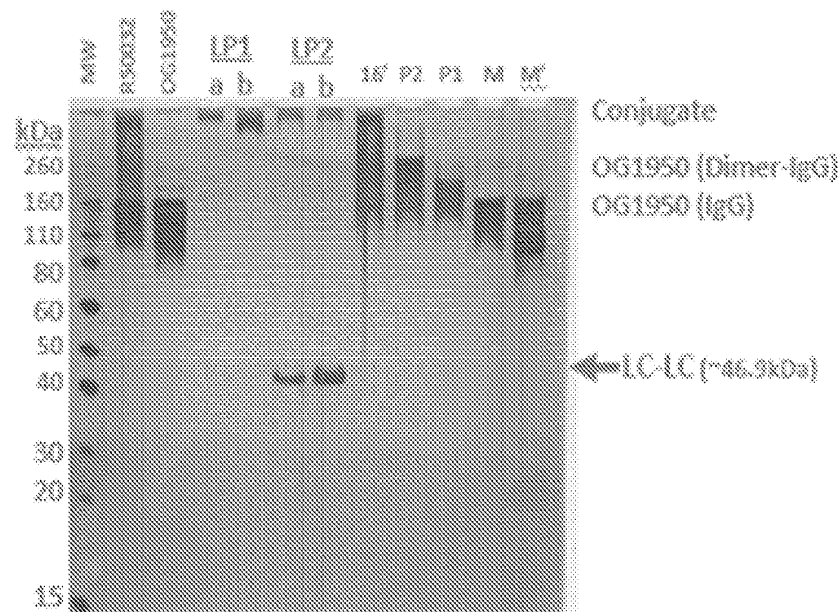


FIG. 59C

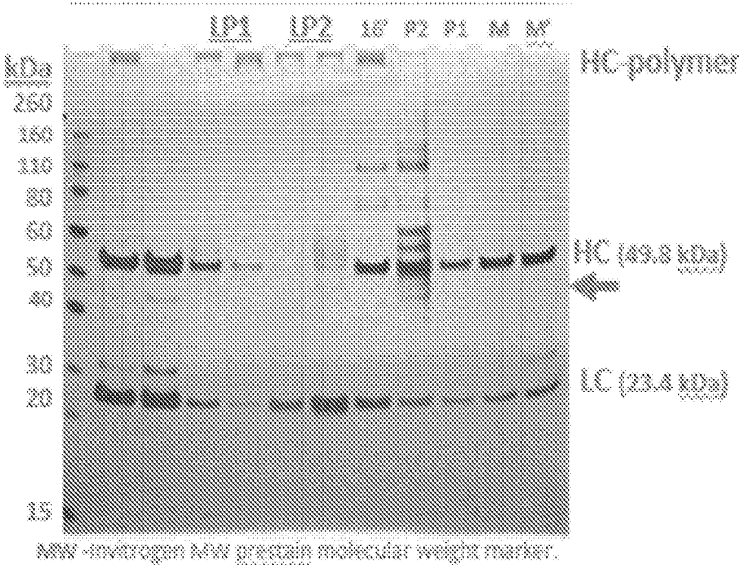


FIG. 59D

Test	Method	Stability Test Interval (Months)			
		Storage Condition: -20 ± 5°C			
		0	3	6	9
Color	Visual	< Y6	< Y6	< Y6	≤ Y6
Clarity	Visual	Conforms	Conforms	Conforms	Conforms
pH	Potentiometry	4.8	4.8	4.8	4.7
Protein Concentration (mg/mL)	UV A _{280nm} SoloVPE	51.5	51.7	52.0	50.4
OG1953 Molecular Weight (kDa)	SEC-MALS	959	948	961	936
OG1953 Polydispersity		1.064	1.066	1.069	1.063
OG1953: Bioconjugate (% area)	CEX-HPLC	78.3	78.7	78.8	78.9
OG1950: Unconjugated Antibody (% area)		21.7	21.3	21.2	21.1
OG1802: Unreacted Polymer (mg/mL)		≤ 5	≤ 5	≤ 10	≤ 5
Sum of LC + HC (% area)	CE-SDS, reduced	98.8	98.5	98.5	98.7
OG1953 HMW Forms (% area)	SEC-HPLC	0	0	0	0
OG1953 Bioconjugate (% area)	Tandem-HPLC	75.5	76.7	76.8	TBD
OG1950 Antibody (% area)		20.7	21.1	21.0	TBD
Impurities (% area)		3.8	2.3	2.3	TBD
Inhibition of huVEGF Binding to huVEGFR (Potency) (% relative to reference standard)	ELISA	103	102	109	97

FIG. 60A

Test	Method	Stability Test Interval (Months)			
		Storage Condition: 5 ± 3°C			
		0	3	6	9
Color	Visual	< Y6	< Y6	< Y6	≤ Y6
Clarity	Visual	Conforms	Conforms	Conforms	Conforms
pH	Potentiometry	4.8	4.8	4.8	4.8
Protein Concentration (mg/mL)	UV A _{280nm} SoloVPE	51.5	51.6	51.3	52.4
OG1953 Molecular Weight (kDa)	SEC-MALS	959	950	961	936
OG1953 Polydispersity		1.064	1.067	1.073	1.060
OG1953: Bioconjugate (% area)	CEX-HPLC	78.3	78.7	78.7	78.9
OG1950: Unconjugated Antibody (% area)		21.7	21.3	21.3	21.1
OG1802: Unreacted Polymer (mg/mL)		≤ 5	≤ 5	≤ 10	≤ 5
Sum of LC + HC (% area)	CE-SDS, reduced	98.8	98.1	98.3	98.6
OG1953 HMW Forms (% area)	SEC-HPLC	0	0	0	0
OG1953 Bioconjugate (% area)	Tandem-HPLC	75.5	76.5	76.5	TBD
OG1950 Antibody (% area)		20.7	21.1	21.0	TBD
Impurities (% area)		3.8	2.6	2.6	TBD
Inhibition of huVEGF Binding to huVEGFR (Potency) (% relative to reference standard)	ELISA	103	113	106	94

FIG 60B

Test	Method	Stability Test Interval (Months)				
		Storage Condition: 25 ± 2°C/60 ± 5%RH				
		0	1	2	3	6
Color	Visual	< Y6	< Y6	Y6	< Y6	< Y6
Clarity	Visual	Conforms	Conforms	Conforms	Conforms	Conforms
pH	Potentiometry	4.8	4.8	4.8	4.8	4.8
Protein Concentration (mg/mL)	UV A _{280nm} SoloVPE	51.5	51.6	52.4	52.1	53.1
OG1953 Molecular Weight (kDa)	SEC-MALS	959	969	957	951	963
OG1953 Polydispersity		1.064	1.066	1.062	1.067	1.077
OG1953: Bioconjugate (% area)	CEX-HPLC	78.3	79.2	78.8	78.1	77.6
OG1950: Unconjugated Antibody (% area)		21.7	20.8	21.2	21.9	22.4
OG1802: Unreacted Polymer (mg/mL)		≤ 5	≤ 10	≤ 10	≤ 10	≤ 10
Sum of LC + HC (% area)	CE-SDS, reduced	98.8	98.6	98.2	97.6	97.2
OG1953 HMW Forms (% area)	SEC-HPLC	0	0	0	0	0
OG1953 Bioconjugate (% area)	Tandem-HPLC	75.5	74.9	75.3	75.1	74.1
OG1950 Antibody (% area)		20.7	20.5	21.0	21.2	21.7
Impurities (% area)		3.8	4.6	3.7	3.7	4.2
Inhibition of huVEGF Binding to huVEGFR (Potency) (% relative to reference standard)	ELISA	103	94	102	94	99

FIG. 60C

KSI-501 Drug Substance Batch Number		KSI-501DS_102	KSI-501DS_103	KSI-501DS_104
Test	Method	Results		
Colour	Visual	=Y5 Slightly yellow	=Y5 Slightly yellow	≤Y5 Slightly yellow
Clarity	Instrumental	2.70 NTU =Ref. 1 clear	2.63 NTU =Ref. 1 clear	2.40 NTU <Ref. 1 clear
pH	Potentiometry	4.8	4.7	4.8
Protein Concentration (mg/mL)	UA A _{250nm} Solo VPE	51.5	50.4	50.4
OG2074 Molecular Weight (kDa)	SEC-MALS	1118	1075	1126
OG2074 Polydispersity		1.074	1.074	1.070
OG2074 Bioconjugate (% area)	CEX-HPLC	69.1	65.2	70.1
OG2072 Unconjugated Antibody (% area)		30.9	34.8	29.9
OG1802 Unreacted Polymer (mg/mL)		≤5	≤5	≤5
OG2074 Bioconjugate Main Peak (% area)	SEC-HPLC	72.0	68.9	72.5
OG2074 HMW Forms (% area)		0.0	0.0	0.0
OG2074 LMW Forms (including OG2072 Antibody) (% area)		28.0	31.1	27.5
OG2074 Bioconjugate (% area)	Tandem-HPLC	65.4	61.5	66.1
OG2072 Antibody (% area)		29.4	32.2	29.3
Impurities (% area)		5.2	6.3	4.6
Potency (αVECF) (% relative to reference standard)	Cell Based Assay (HEK293)	100	105	91
Potency (αIL-6) (% relative to reference standard)	ELISA	87	76	80

FIG. 61

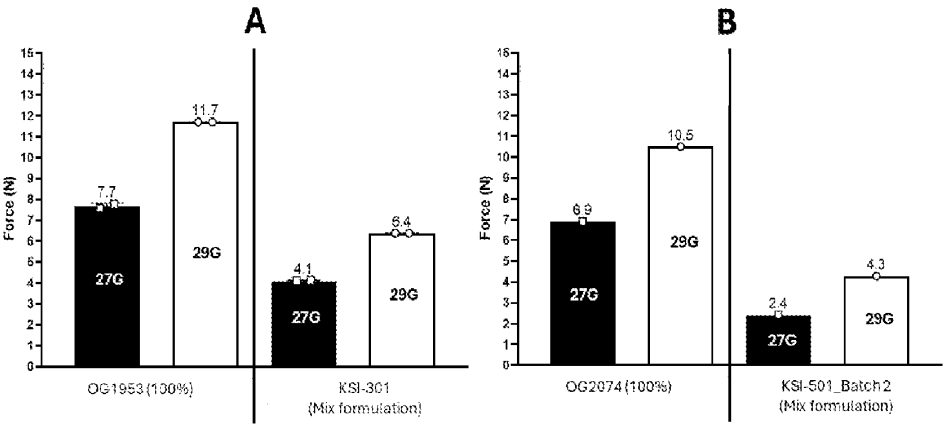


FIG. 62

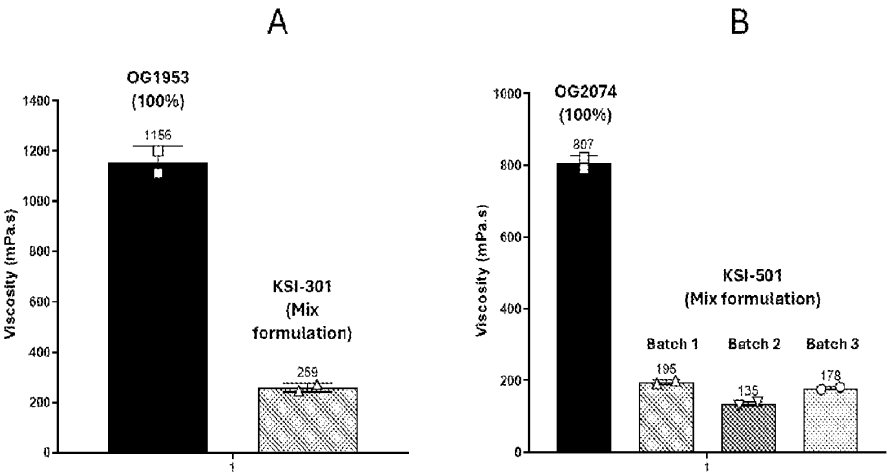


FIG. 63