

Peptide	SEQ ID	pH	Sequence
T-001	01	0.574	DWFKAFYDKVAEKFKEAF (Positive Control)
T-002	02	0.317	LRKLRKRLLRDWLKAFYDKVAEKLKEAF (Positive Control)
T-003	03	0.537	EVRSKLEEWFAAFREFAEFLARLKS (Positive Control)
T-004	04	0.298	DWLKAFYDKVAEKLKEAFPDWAKAAYDKAAEKAKEAA (Positive Control)
T-033	33	0.344	DWLKAFYDKVAEKLKEAFPDWLKAFYDKVAEKLKEAF (Positive Control)
T-034	34	0.698	GIKKFLGSIWKFIKAFVG (Positive Control)
T-031	31	0.1	MKIEHKWFFEETKIEMGK (Negative Control)
T-032	32	0.1	NMDENNKLKAAYVHGEKWEADT (Negative Control)
T-081	81	0.598	KWFKAFYKDVAEDFKEAF (Positive control)
T-082	82	0.636	DKFKAFYDKVAEWFKEAF (Positive control)
T-083	83	0.810	AKAWEKVFKEFAKYFDDF (Positive control)

FIG. 1A

Peptide	SEQ ID	pH	Sequence
T-005	05	0.279	PLRAELQEGARQKLHELQEKLS
T-006	06	0.235	QDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLN
T-007	07	0.389	EELRVRLASHLRKLRKRLLRDADDLQKRLAVYQA
T-008	08	0.655	HLRKLKRLLR
T-009	09	0.360	EELRVRLASHLRKLRKRLLRDADDLQKRLAVYQAGAREGAERGLSAIRER
T-010	10	0.309	RDADDLQKRLAVYQAGAREGAE
T-011	11	0.290	DADDLQKRLAVYQAGAREGAER
T-012	12	0.397	QSTEELRVRLASHLRKLRKRL
T-013	13	N/A	TRARLSKELQAAQARLGADMEDVRGRLVQYRGEVQAMLGQSTEELRVRLASHLRKLRKRLLRDADDLQKRLAVYQA
T-014	14	0.370	EQAQQIRLQAEAFQARLKSWFE
T-015	15	0.597	LVGRQLEEF
T-016	16	0.489	SLVSQYFQTVTDYGKDLM
T-017	17	0.079	PLRAELQEGARQKLHELQEKLSPLRAELQEGARQKLHELQEKLS
T-018	18	0.319	HLRKLKRLLRPPEQAQQIRLQAEAFQARLKSWFE
T-019	19	0.450	NMDEINKRLHAYEEGVKKADE
T-020	20	0.550	DGDKLCDRLAEYCARAKEAFDR
T-021	21	0.304	HLRKLKRLLRDWFKAFYDKVAEKFKEAF
T-022	22	0.406	DWFKAFYDKVAEKFKEAFPEQAQQIRLQAEAFQARLKSWFE
T-023	23	0.582	DWFKAFYDKVAENFKEAF
T-024	24	0.581	FEHWISGIYSECKHLIQE
T-025	25	0.512	HLRKLKRLLRFEHWISGIYSECKHLIQE
T-026	26	0.602	GFGDWIDSIEAFSRLHS
T-027	27	0.314	HLRKLKRLLRSLVSQYFQTVTDYGKDLM
T-028	28	0.582	HLRKLKRLLRLVGRQLEEF
T-029	29	0.572	HLRKLKRLLRDGDKLCDRLAEYCARAKEAFDR

FIG. 1B

Peptide	SEQ ID	pH	Sequence
T-030	30	0.500	EHLCELIERACRKLVELQEKLKWLIAELGEGWRQWLHSLKEFLS
	35	N/A	XAWERFRXLXKELADYFX
	36	N/A	AWERFRXLXKELADYF
	37	N/A	ADALEXALKELKXFIXEWT
	38	N/A	ADALEXALKELKXFI
	39	N/A	RXXADALEXALKELKXFIXEWT
T-040	40	0.505	HLRKLRKRLLRDGDQLQDRLAEYQARAKEAFDR
T-041	41	0.507	HLRRLRRRLLRDGDQLQDRLAEYQARAKEAFDR
T-042	42	0.05	ALRLDRLDLKRKGLALQDRKYEQAQARDKEHRRF
T-043	43	0.411	HLRKLRKRLLRDADDLQKRLAVYQAGAREGAER
T-044	44	0.462	LASHLRKLRKRLLRDADDLQKRLAVYQA
T-045	45	0.451	HLRKLRKRLLRDADDLQKRLAVYQA
T-046	46	0.423	LASHLRKLRKRLLRDADDLQKRLAVYQAGAREGAER
T-047	47	0.456	LARHLRKLRKRLARDADDLQKRLAVYQAGAREGAER
T-048	48	0.507	LASHLRKLRKRLLRDGDQLQDRLAEYQARAKEAFDR
T-049	49	0.534	LARHLRKLRKRLARDGDQLQDRLAEYQARAKEAFDR
T-050	50	0.514	HLRKLRKRLLRDADKLQDRLAEYQARAKEAFDR
T-051	51	0.501	HLRKLRKRLLRDGDQLQDRLAEYQARAKEAFDR
T-052	52	0.512	HLRKLRKRLLRDGDQLQKRLAEYQARAKEAFDR
T-053	53	0.455	HLRKLRKRLLRDGDQLQDRLAVYQARAKEAFDR
T-054	54	0.494	HLRKLRKRLLRDGDQLQDRLAEYQAGAKEAFDR
T-055	55	0.505	HLRKLRKRLLRDGDQLQDRLAEYQARAREAFDR
T-056	56	0.503	HLRKLRKRLLRDGDQLQDRLAEYQARAKEGFDR
T-057	57	0.465	HLRKLRKRLLRDGDQLQDRLAEYQARAKEAADR

FIG. 1C

Peptide	SEQ ID	pH	Sequence
T-058	58	0.503	HLRKLKRLLRDGDGLQDRLAEYQARAKEAFER
T-059	59	0.555	HLRKLVKRLFRDGDGLQDRLAEYQARAKEAFDR
T-060	60	0.506	HLRKLKRLFRDGDGLQDRLAEYQARAKEAFDR
T-061	61	0.538	HLRKLKRLLRDGDGLQDR
T-062	62	0.549	HLRKLKRLLRDGDGLYDRLAEYYARAKEAFDR
T-063	63	0.509	HLRKLKRLLRDADDLQDRLAEYQARAKEAFDR
T-064	64	0.516	HLRKLKRLLRDADDLQKRLAEYQARAKEAFDR
T-065	65	0.298	LASHLRKLRKRLRSLVSQYFQTVTDYGKDLM
T-066	66	0.284	LARHLRKLKRLARSLVSQYFQTVTDYGKDLM
T-067	67	0.050	HYKRLRKRLMDSVLQYFSTDLLGVRLK
T-068	68	N/A	MEDVRGRLVQYRGEVQAMLGQSTEELRVRLASHLRKLRKRLLRDADDLQKRLAVYQA
T-069	69	0.288	VRGRLVQYRGEVQAMLGQSTEELRVRLASHLRKLRKRLLRDADDLQKRLAVYQA
T-070	70	0.311	LVQYRGEVQAMLGQSTEELRVRLASHLRKLRKRLLRDADDLQKRLAVYQA
T-071	71	0.335	LVQYRGEVQAMLGQSTEELRVRLASHLRKLRKRLLRDADDLQ
T-072	72	0.633	LASHLRKLRKRLLR
T-073	73	0.545	LASHLRKLRKRLLRDADD
T-074	74	0.460	EELRVRLASHLRKLRKRLLR
T-075	75	0.419	EELRVRLASHLRKLRKRLLRDADD
T-076	76	0.604	HLRKLKRLLRDADDL
T-077	77	0.559	HLRKLKRLLRDGDGLVDRLAEYVARAKEAFDR
T-078	78	0.512	HLRKLKRLLRDGDGLSDRLAEYSARAKEAFDR
T-079	79	0.529	HLRKLKRLLRDGDGLVDRLAEYSARAKEAFDR
T-080	80	0.540	HLRKLKRLLRDGDGLSDRLAEYVARAKEAFDR

FIG. 1D

Peptide	SEQ ID	pH	Sequence
T-084	84	0.709	REFRALFKELADYFRDAW
T-085	85	0.709	WREFRALFKELADYFRDA
T-086	86	0.693	WERFRALFKELADYFRDA
T-087	87	0.693	DAWERFRALFKELADYFR
T-088	88	0.632	FDDYLSRFYSQLRRAFHE
T-089	89	0.548	FRDYASRFYSQLRDAFHE
T-090	90	0.625	HEFDDSLSRFYSQLRRAF
T-091	91	0.590	FEHWISGIYSELKHLIQE
T-092	92	0.517	FEHWISGIYSEAKHLIQE
T-093	93	0.417	LPVLESFKVSFLSALEEYTKKL
T-094	94	0.619	EKEIRSVLSGATKHFEKILDKL
T-095	95	0.613	EREIRSVLSGATRHFEDILDKL
T-096	96	0.627	AKSLSRVLSGATKHFRTILDEL
T-097	97	0.381	ARMEEMGSRTDRDLDEVKEQVA
T-098	98	0.616	KRMERMLDETRDTLTRFSEQWT
T-099	99	0.700	RRMKDYLLKKFQETLKREFRDWE
T-100	100	0.597	RRGDKALSDTKDELKRFIEEWT
T-101	101	0.641	RSGADALESAKELKRFIREWT
T-102	102	0.289	TVGSLAGQPLQERAQAWGERLR

FIG. 1E

Peptide	SEQ ID	pH	Sequence
T-103	103	0.550	TVGRLAKDHLHELTRGWGKFER
T-104	104	0.540	TVRGSADALLEHLTRAWDGFNR
T-105	105	0.620	DALSRGVEGLARAWDTFNRHLT
T-106	106	0.608	EALSKGVEGLAKAWETFNKHLT
T-107	107	0.666	NHINDVQRDVKKTIERLF
T-108	108	0.621	DHINKVQRKVTHEIERLF
T-109	109	0.355	HLRKLKRLLRSLVSQYFQTVTDYGKDL
T-110	110	0.406	HLRKLKRLLRSLVSQYRQTVTDYGKDL
T-111	111	0.431	HLRKLVKLLRSLVSQYRQTVTDYGEDL
T-112	112	N/A	YKDFGERVERALGRQLEMLGQSTEELRVRLASHLRKLKRLLRDADDLQKRLAVYQA
T-113	113	N/A	WKDFGERVERALREQFEDLGQSTEELRVRLASHLRKLKRLLRDADDLQKRLAVYQA
T-114	114	N/A	LKDFGERVARALREQFEDLGQSTEELRVRLASHLRKLKRLLRDADDLQKRLAVYQA
T-115	115	N/A	DHINKVQRKVTHEIERLFLGQSTEELRVRLASHLRKLKRLLRDADDLQKRLAVYQA
T-116	116	N/A	DAWERFRALFKELADYFRLGQSTEELRVRLASHLRKLKRLLRDADDLQKRLAVYQA
T-117	117	N/A	RSGADALESALKELKRFIREWTLGQSTEELRVRLASHLRKLKRLLRDADDLQKRLAVYQA
T-118	118	N/A	LVARLLKELTAAMARLGRDAEDIRGNLFQYFDEVWAMLGQSTEELRVRLASHLRKLKRLLRDADDLQKRLAVYQA
T-119	119	N/A	DVKRLFKEFTAAMARFARKAEDIRGNFDQYFDEVFAMLGQSTEELRVRLASHLRKLKRLLRDADDLQKRLAVYQA
T-120	120	N/A	DVKRLLKELTEAMAELARKAEDIRGNLDQYFRKVFAMLGQSTEELRVRLASHLRKLKRLLRDADDLQKRLAVYQA
T-121	121	0.595	ASGADALESALKELKRFIREWT
T-122	122	0.634	RAGADALESALKELKRFIREWT
T-123	123	0.655	RSAADALESALKELKRFIREWT

FIG. 1F

Peptide	SEQ ID	pH	Sequence
T-124	124	0.644	RSGPDALESALKELKRFIREWT
T-125	125	0.592	RSGAAALESALKELKRFIREWT
T-126	126	0.646	RSGADPLESALKELKRFIREWT
T-127	127	0.560	RSGADAAESA AKELKRFIREWT
T-128	128	0.619	RSGADALASALKELKRFIREWT
T-129	129	0.630	RSGADALEAALKELKRFIREWT
T-130	130	0.656	RSGADALESPLKELKRFIREWT
T-131	131	0.615	RSGADALESAAKELKRFIREWT
T-132	132	0.585	RSGADALESALAELKRFIREWT
T-133	133	0.637	RSGADALESALKALKRFIREWT
T-134	134	0.578	RSGADALESALKEAKRFIREWT
T-135	135	0.631	RSGADALESALKELARFIREWT
T-136	136	0.586	RSGADALESALKELKAFIREWT
T-137	137	0.608	RSGADALESALKELKRAIREWT
T-138	138	0.593	RSGADALESALKELKRFAREWT
T-139	139	0.595	RSGADALESALKELKRFIAEWT
T-140	140	0.623	RSGADALESALKELKRFIRAWT
T-141	141	0.558	RSGADALESALKELKRFIREAT
T-142	142	0.642	RSGADALESALKELKRFIREWA
T-143	143	0.640	RSGGDALESALKELKRFIREWT
T-144	144	0.638	RSGADGLESALKELKRFIREWT

FIG. 1G

Peptide	SEQ ID	pH	Sequence
T-145	145	0.630	RSGADALESGLKELKRFIREWT
T-146	146	0.600	AAAADALESALKELKRFIREWT
T-147	147	0.548	RSGADAAAAALKELKRFIREWT
T-148	148	0.556	RSGADALESAAAALKRFIREWT
T-149	149	0.511	RSGADALESALKEAAAFIREWT
T-150	150	0.510	RSGADALESALKELKRAAAEWT
T-151	151	0.538	RSGADALESALKELKRFIRAAA
T-152	152	0.648	AAWERFRALFKELADYFR
T-153	153	0.711	DPWERFRALFKELADYFR
T-154	154	0.680	DGWERFRALFKELADYFR
T-155	155	0.646	DAAERFRALFKELADYFR
T-156	156	0.644	DAWARFRALFKELADYFR
T-157	157	0.684	DAWEAFRALFKELADYFR
T-158	158	0.611	DAWERARALFKELADYFR
T-159	159	0.684	DAWERFAALFKELADYFR
T-160	160	0.672	DAWERFRPLFKELADYFR
T-161	161	0.709	DAWERFRGLFKELADYFR
T-162	162	0.658	DAWERFRAAFKELADYFR
T-163	163	0.632	DAWERFRALAKELADYFR
T-164	164	0.640	DAWERFRALFAELADYFR
T-165	165	0.668	DAWERFRALFKALADYFR

FIG. 1H

Peptide	SEQ ID	pH	Sequence
T-166	166	0.621	DAWERFRALFKEAADYFR
T-167	167	0.698	DAWERFRALFKELPDYFR
T-168	168	0.690	DAWERFRALFKELGDYFR
T-169	169	0.633	DAWERFRALFKELAAYFR
T-170	170	0.688	DAWERFRALFKELADAFR
T-171	171	0.617	DAWERFRALFKELADYAR
T-172	172	0.660	DAWERFRALFKELADYFA
T-173	173	0.607	AAAERFRALFKELADYFR
T-174	174	0.551	DAWAAARALFKELADYFR
T-175	175	0.657	DAWERFAAAFKEADYFR
T-176	176	0.551	DAWERFRALAAALADYFR
T-177	177	0.561	DAWERFRALFKEAAAYFR
T-178	178	0.578	DAWERFRALFKELADAAA

FIG. 1I

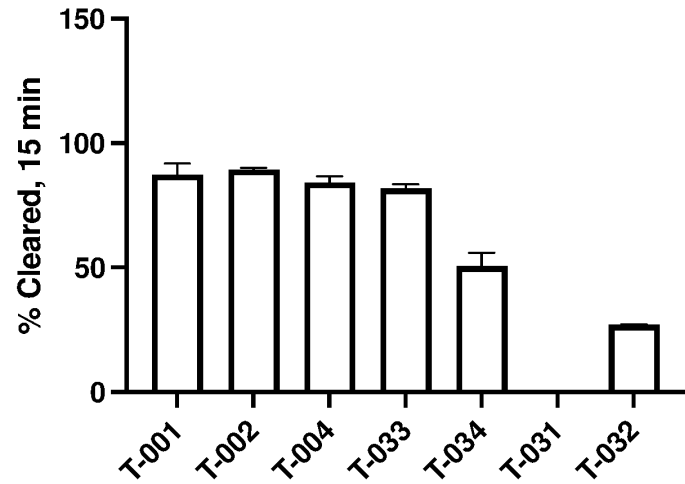


FIG. 2A

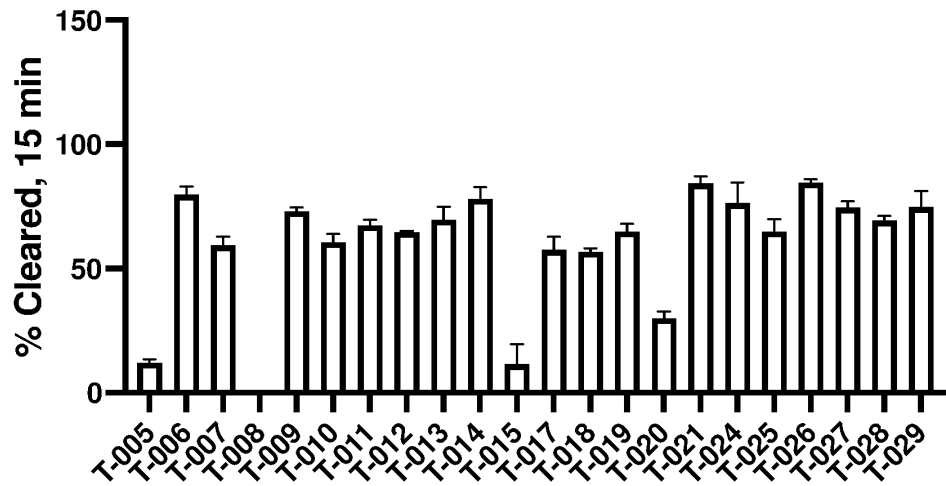


FIG. 2B

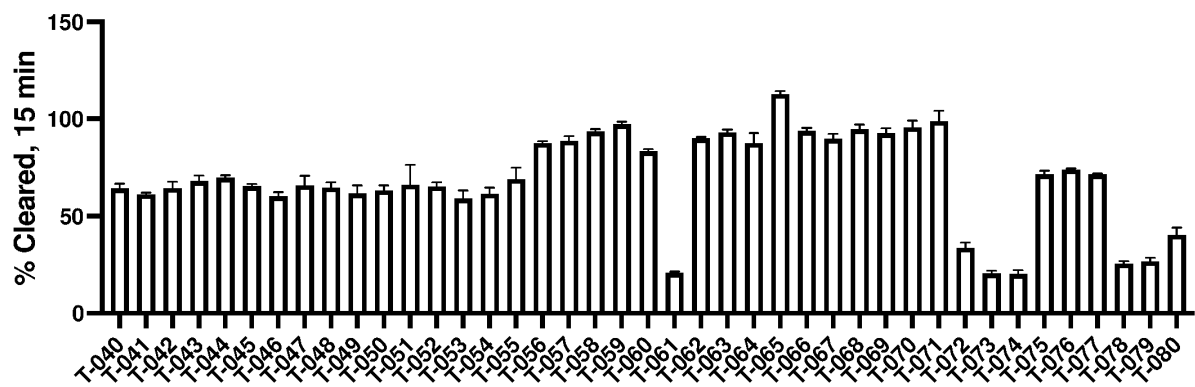


FIG. 2C

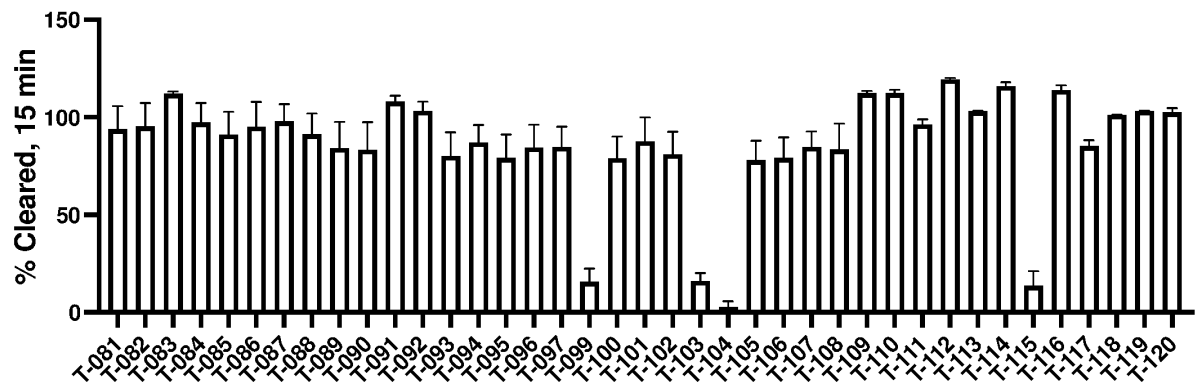


FIG. 2D

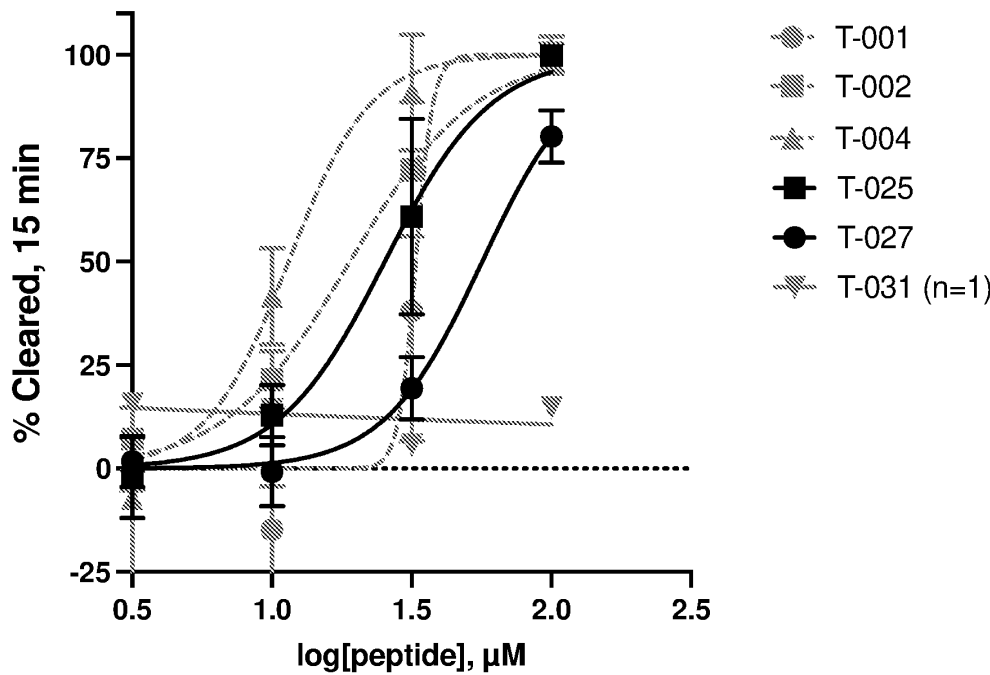


FIG. 3A

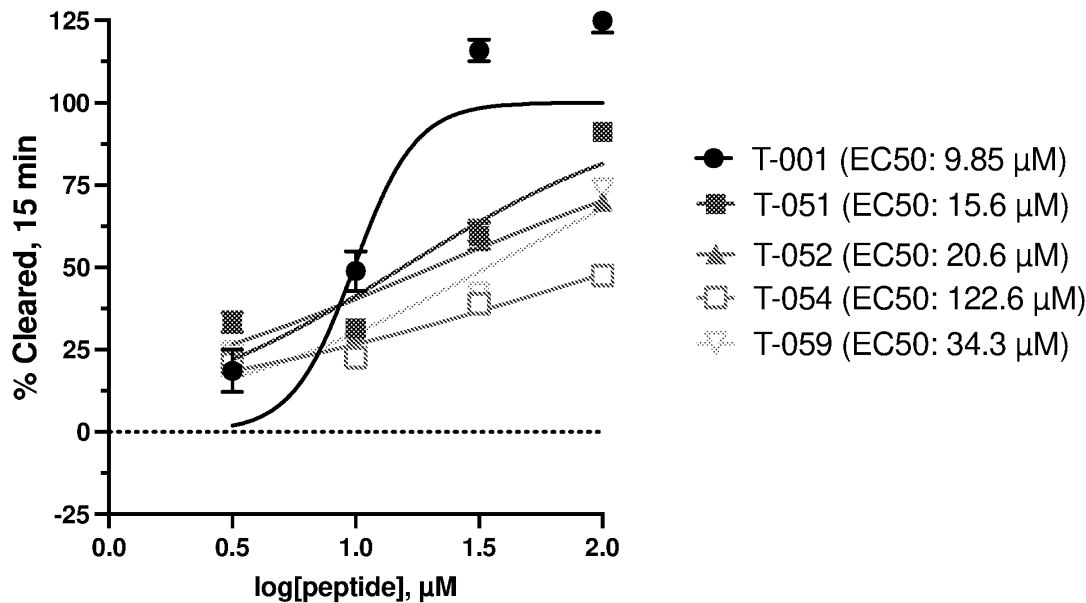


FIG. 3B

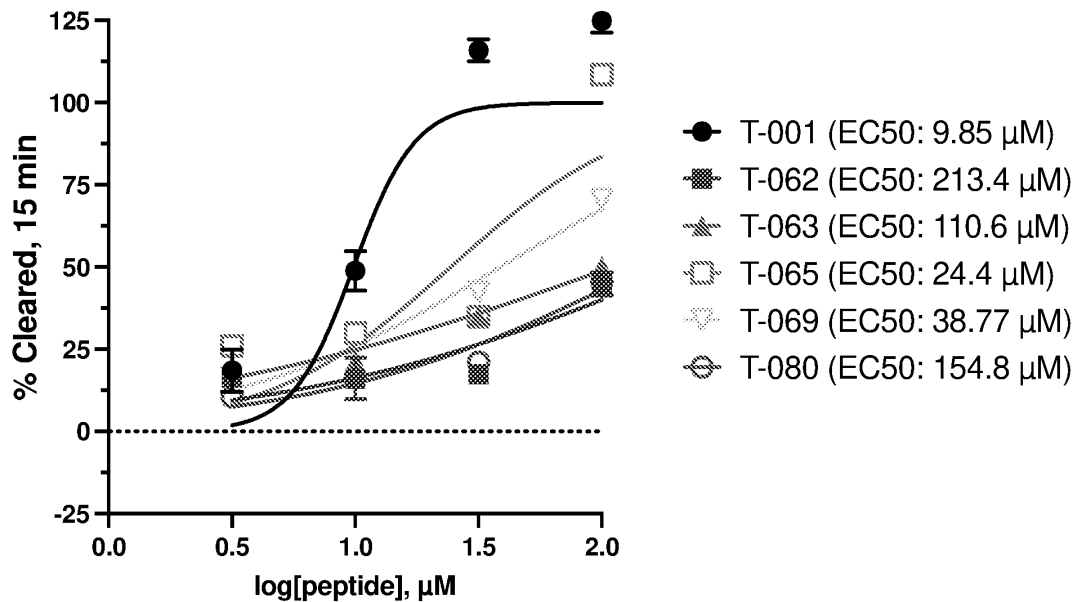


FIG. 3C

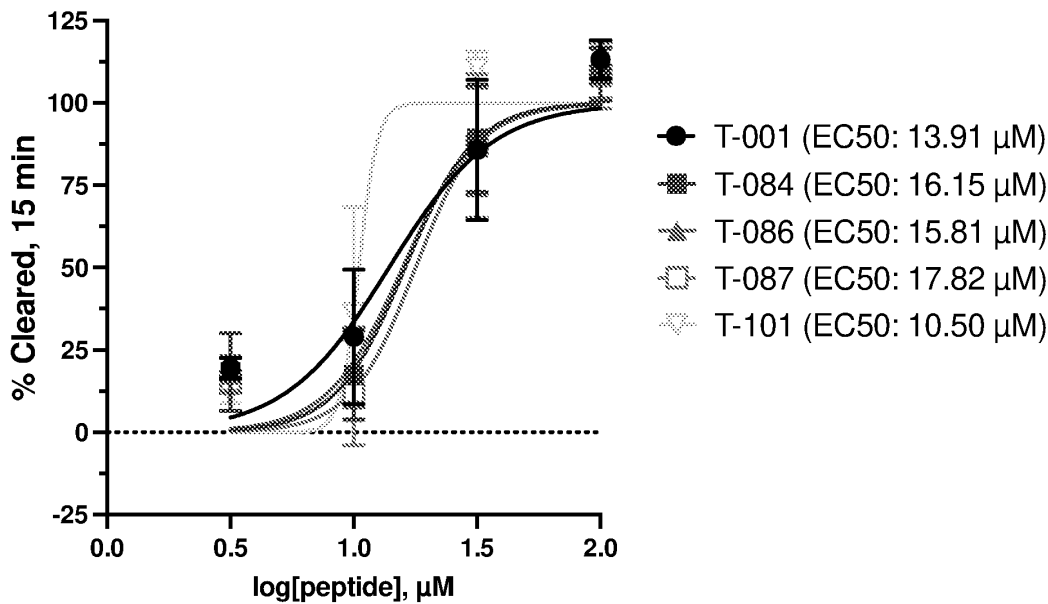


FIG. 4A

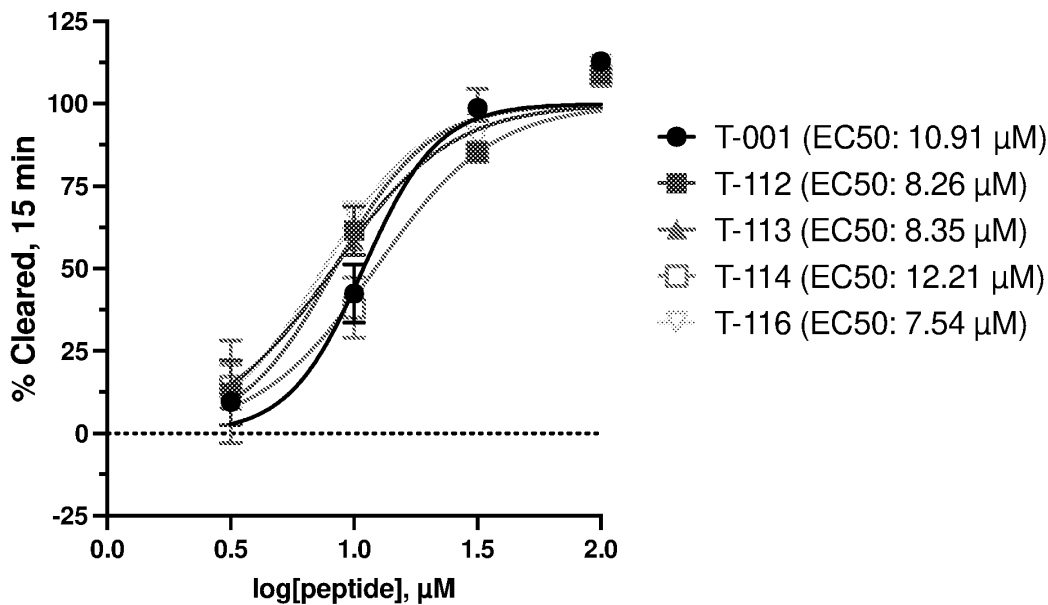


FIG. 4B

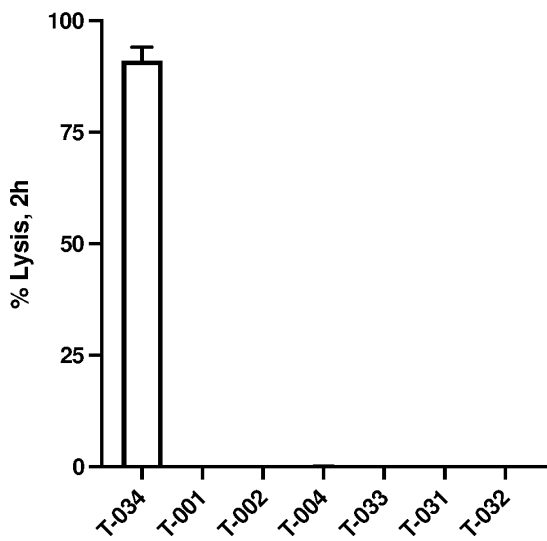


FIG. 5A

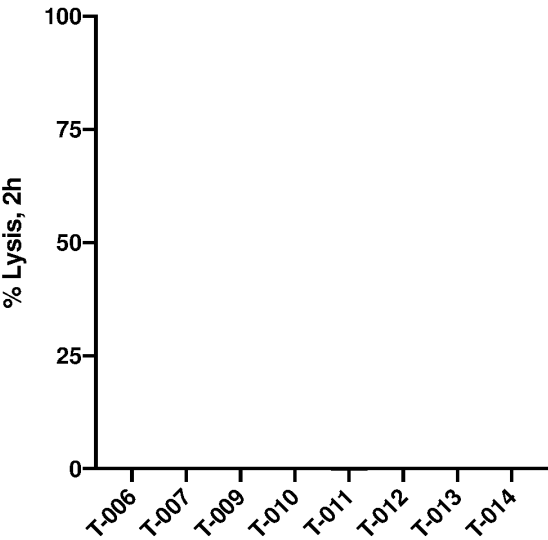


FIG. 5B

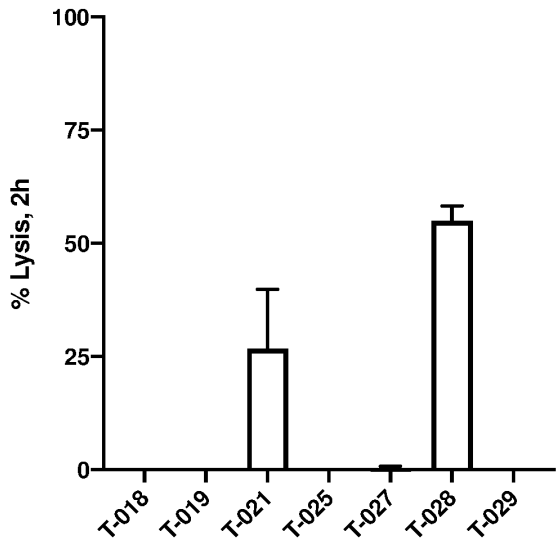


FIG. 5C

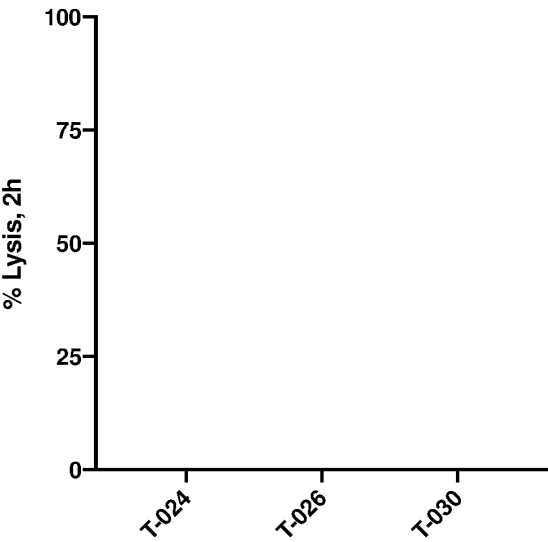


FIG. 5D

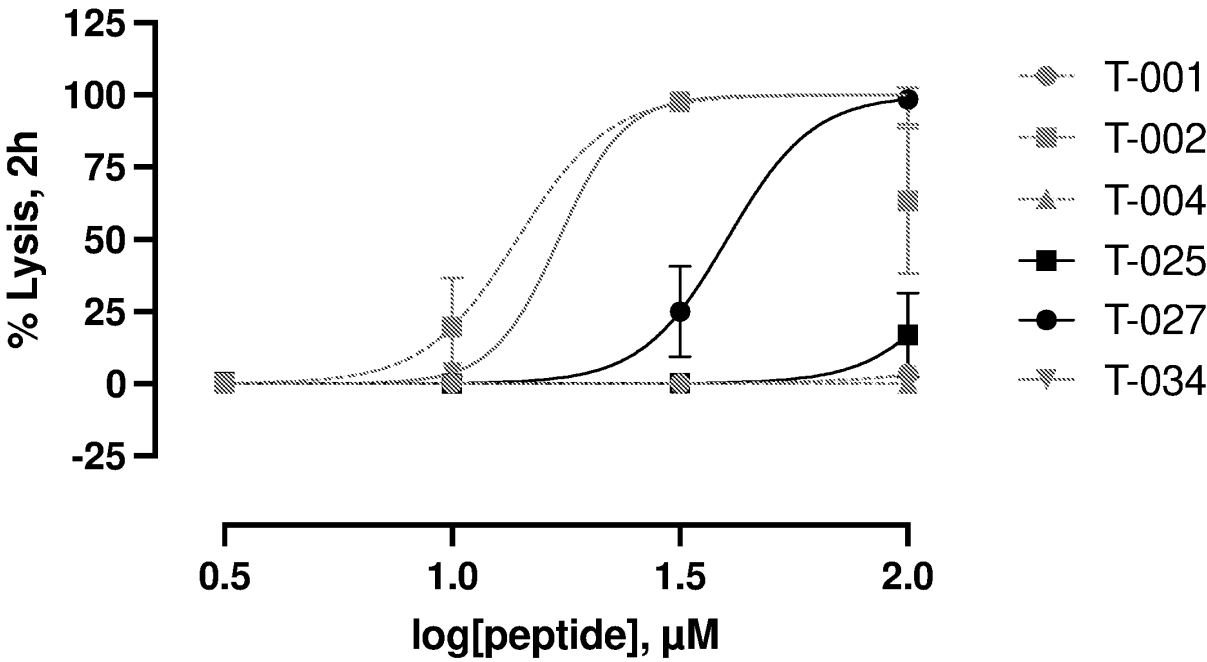


FIG. 6

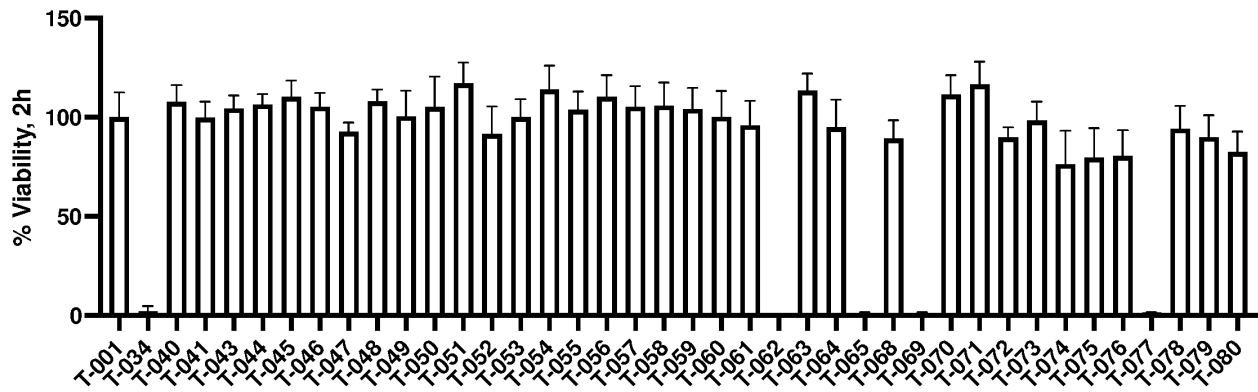


FIG. 7A

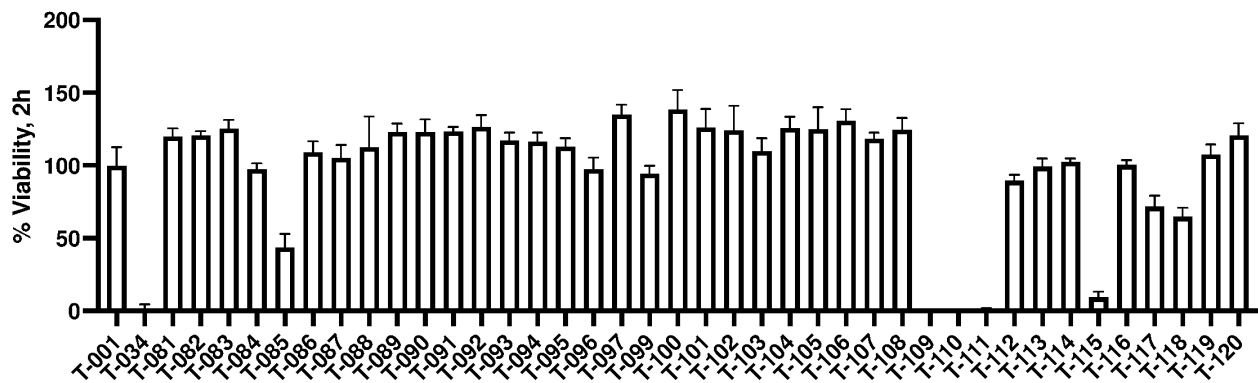


FIG. 7B

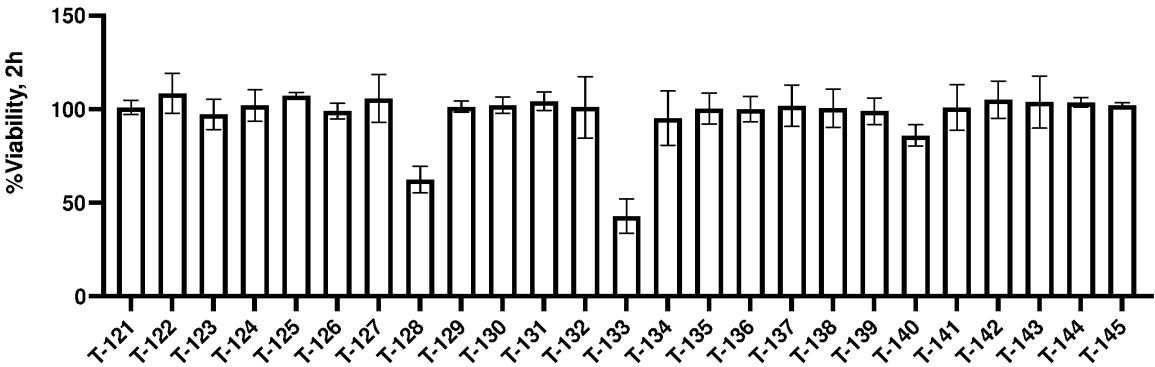


FIG. 7C

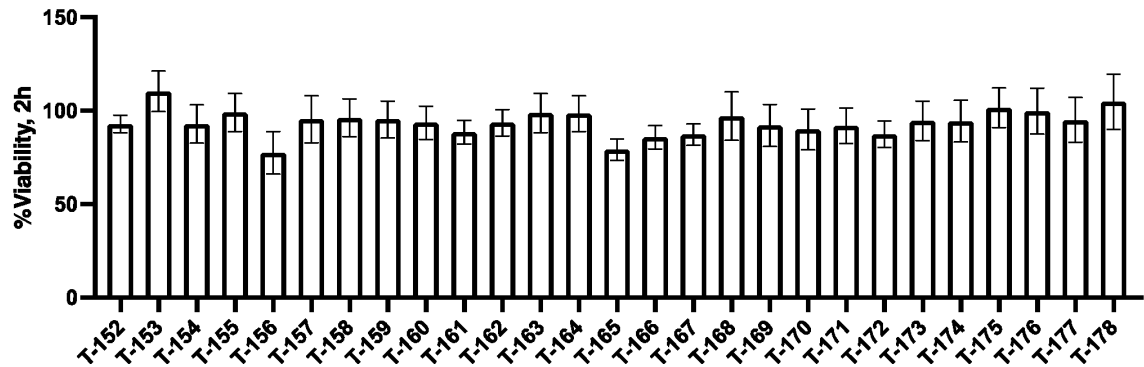


FIG. 7D

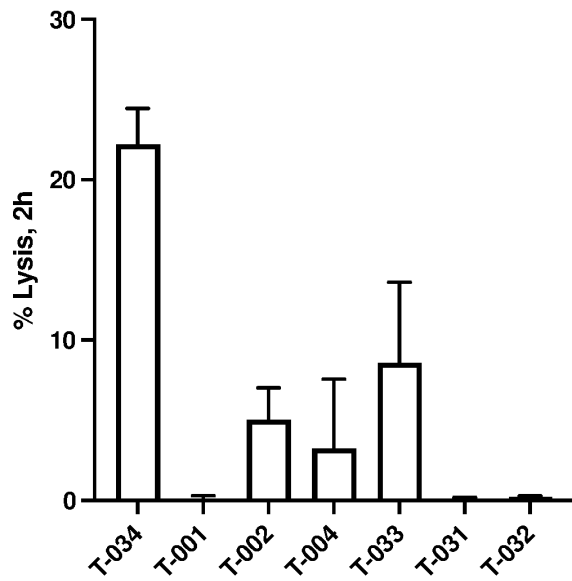


FIG. 8A

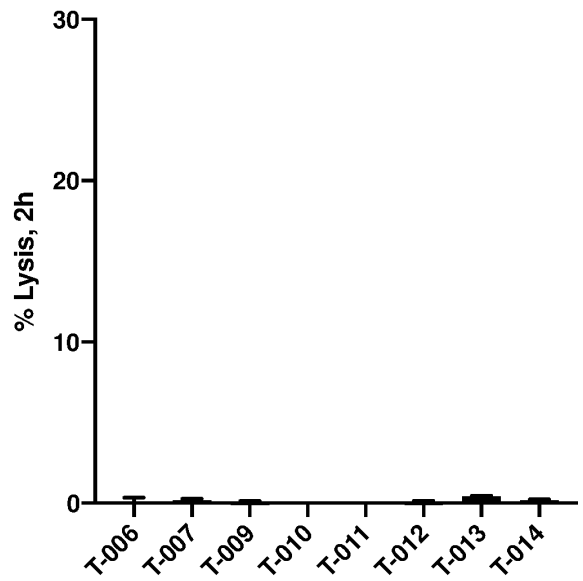


FIG. 8B

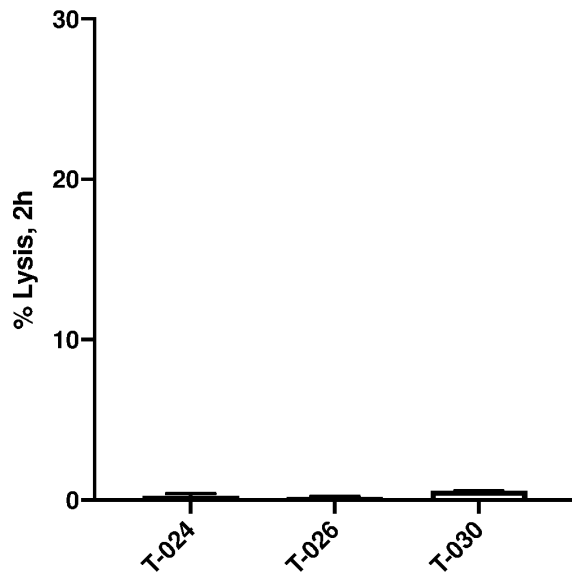


FIG. 8C

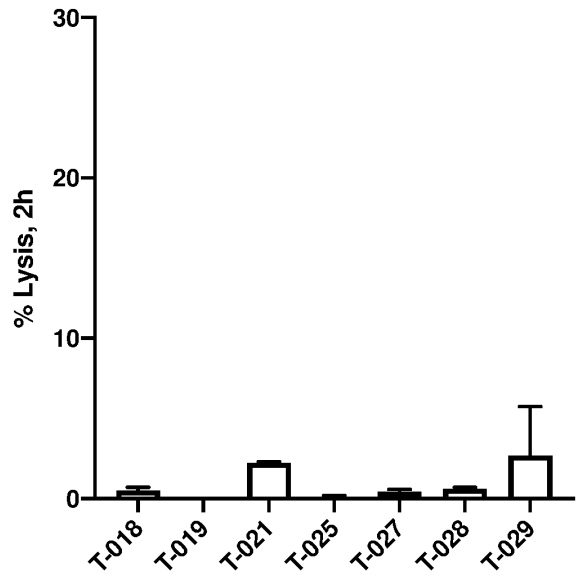


FIG. 8D

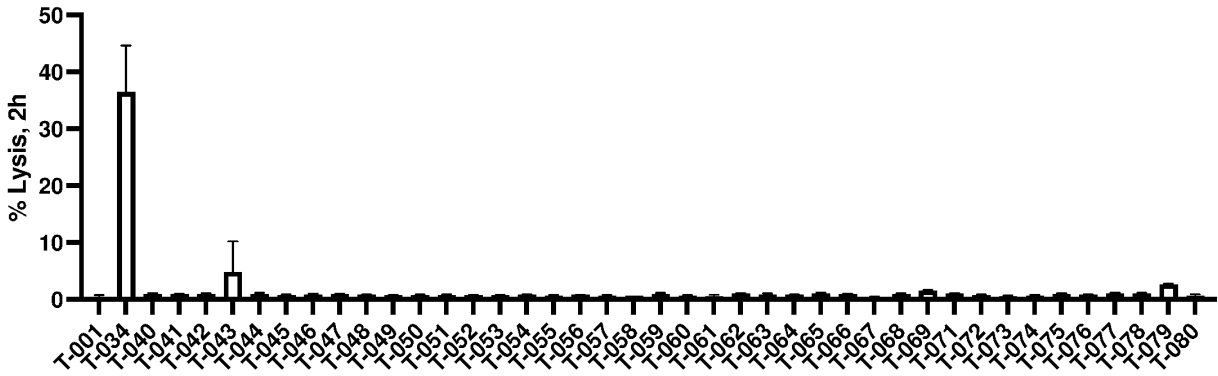


FIG. 9A

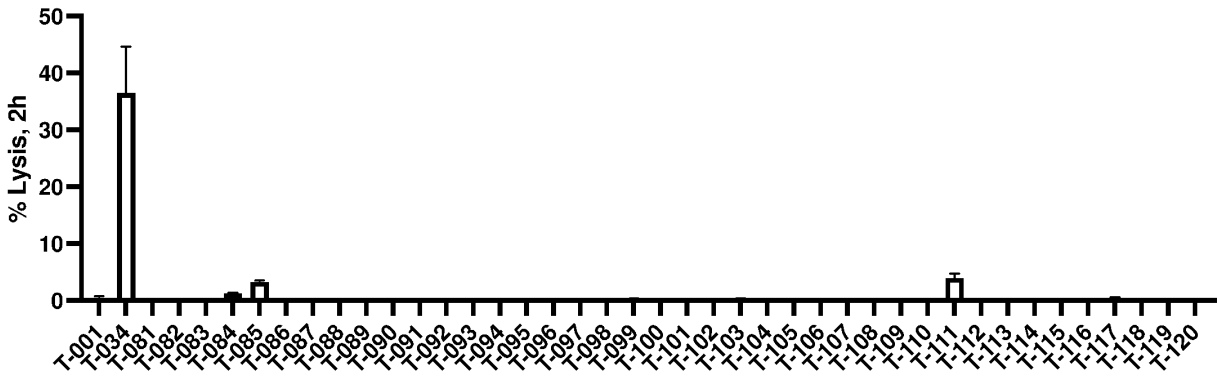


FIG. 9B

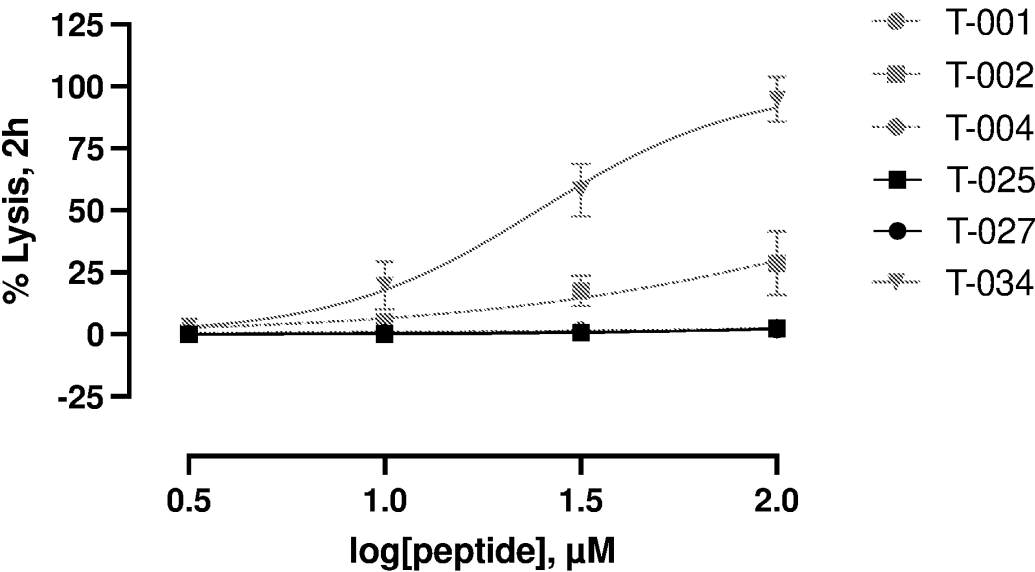


FIG. 10

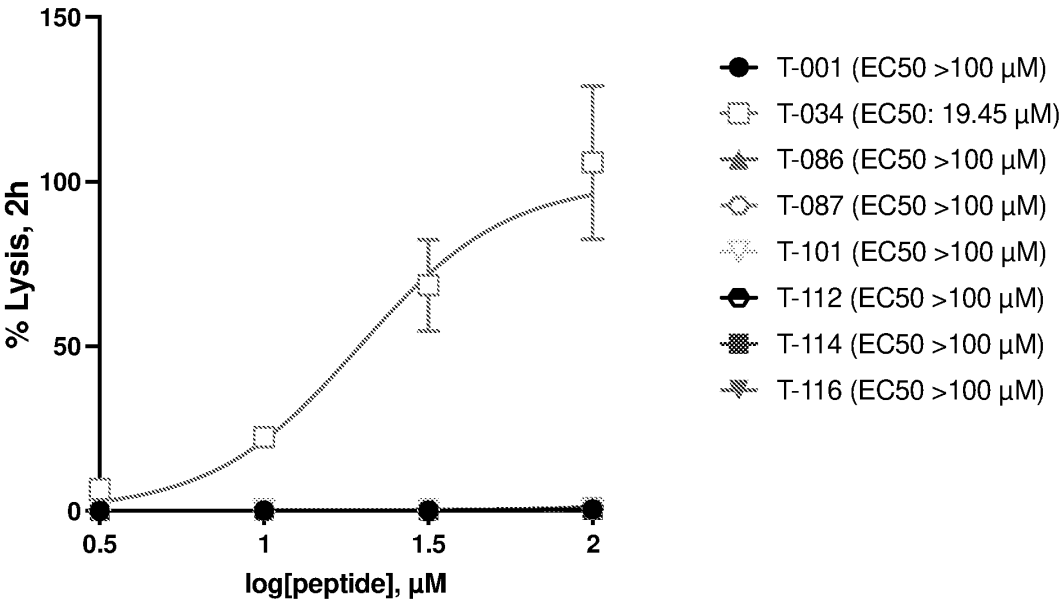


FIG. 11

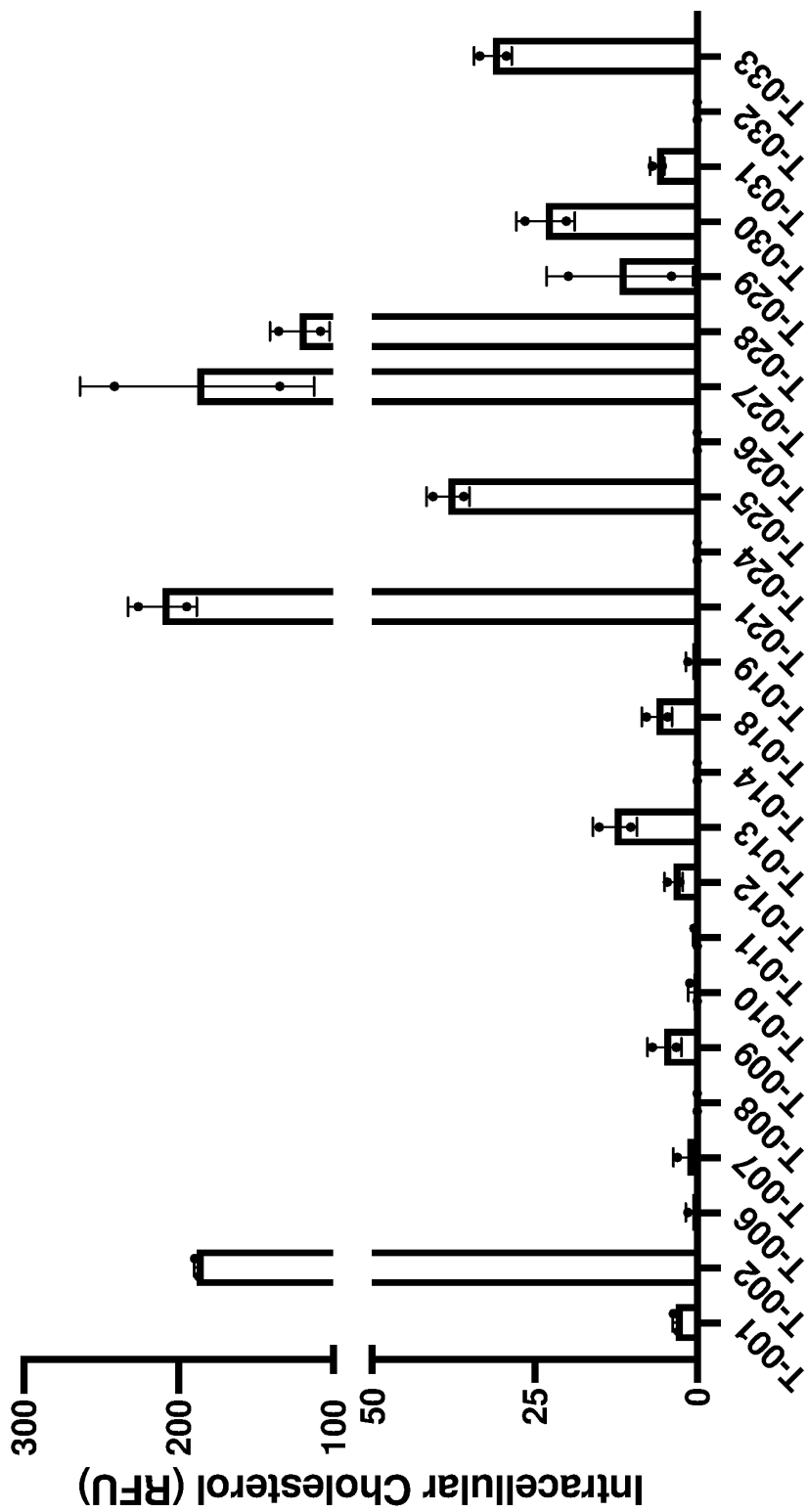


FIG. 12

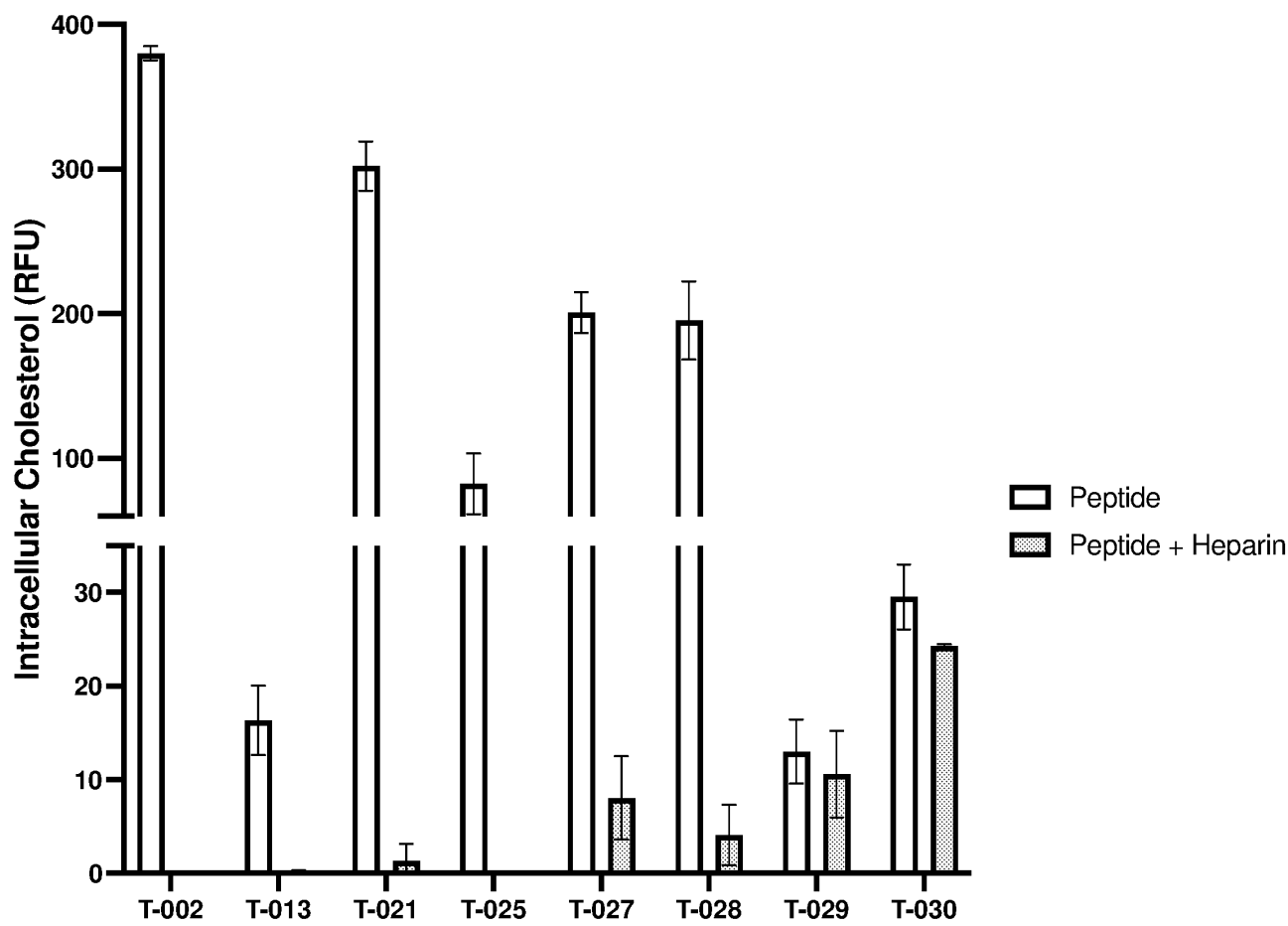


FIG. 13

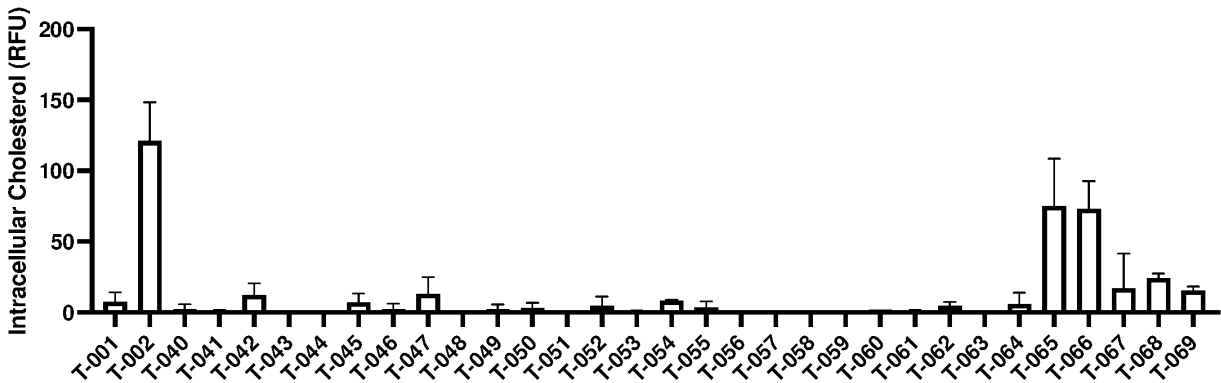


FIG. 14A

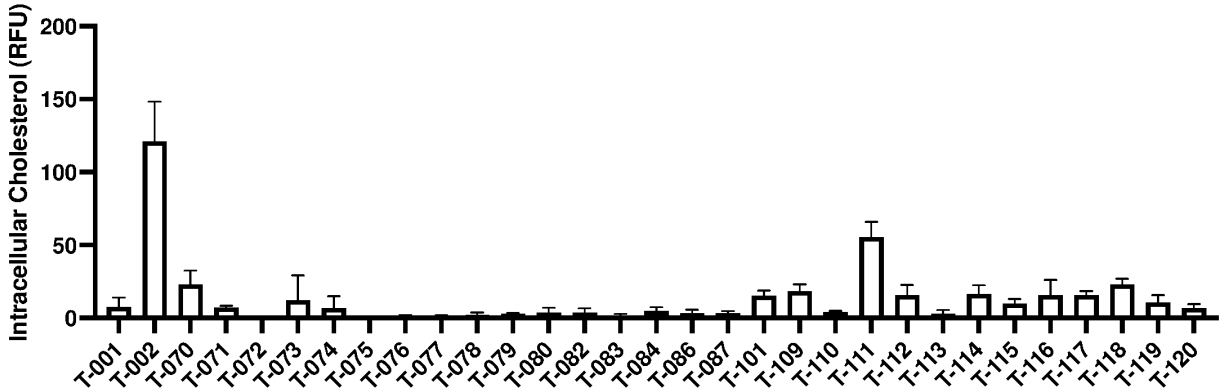


FIG. 14B

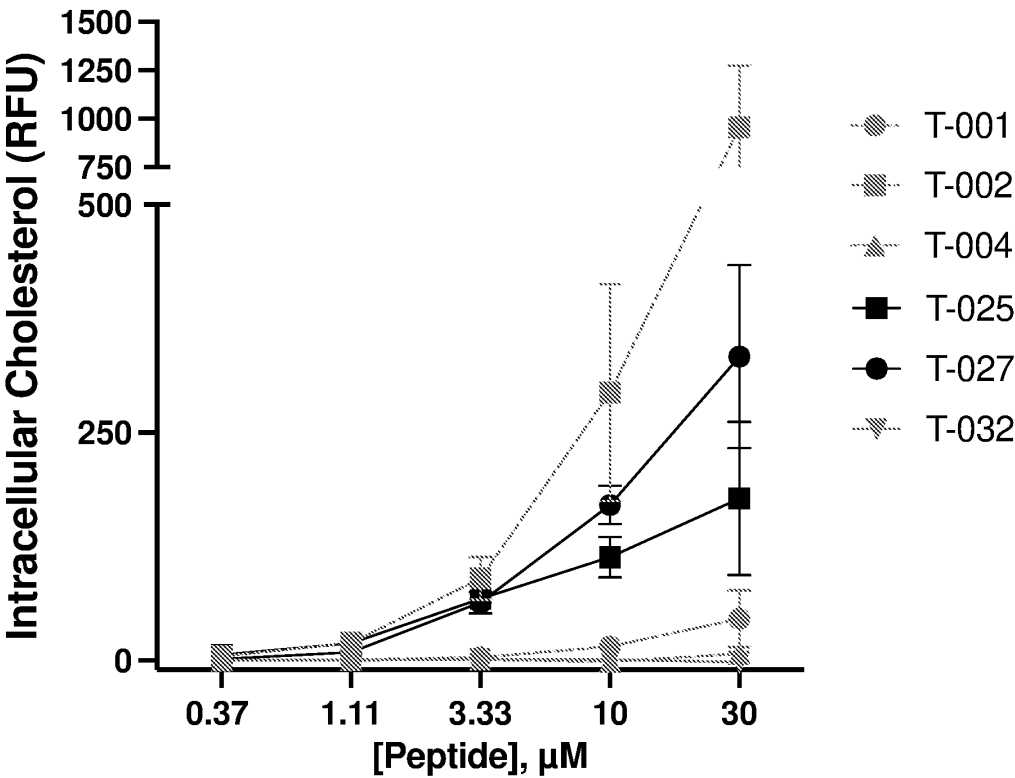


FIG. 15

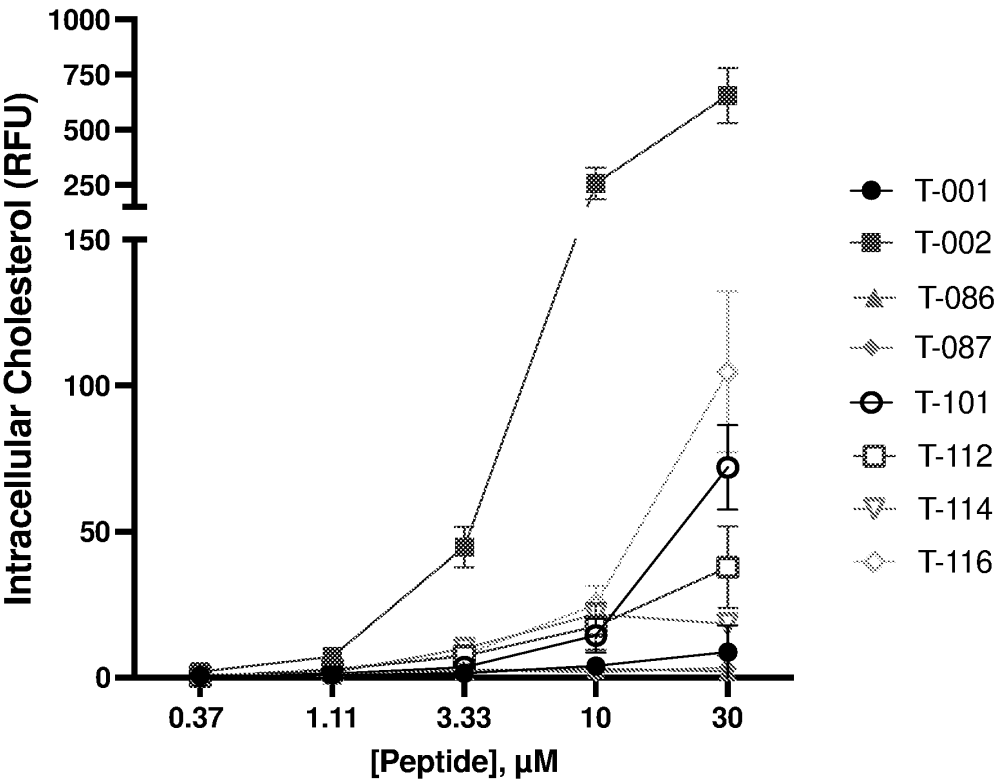


FIG. 16

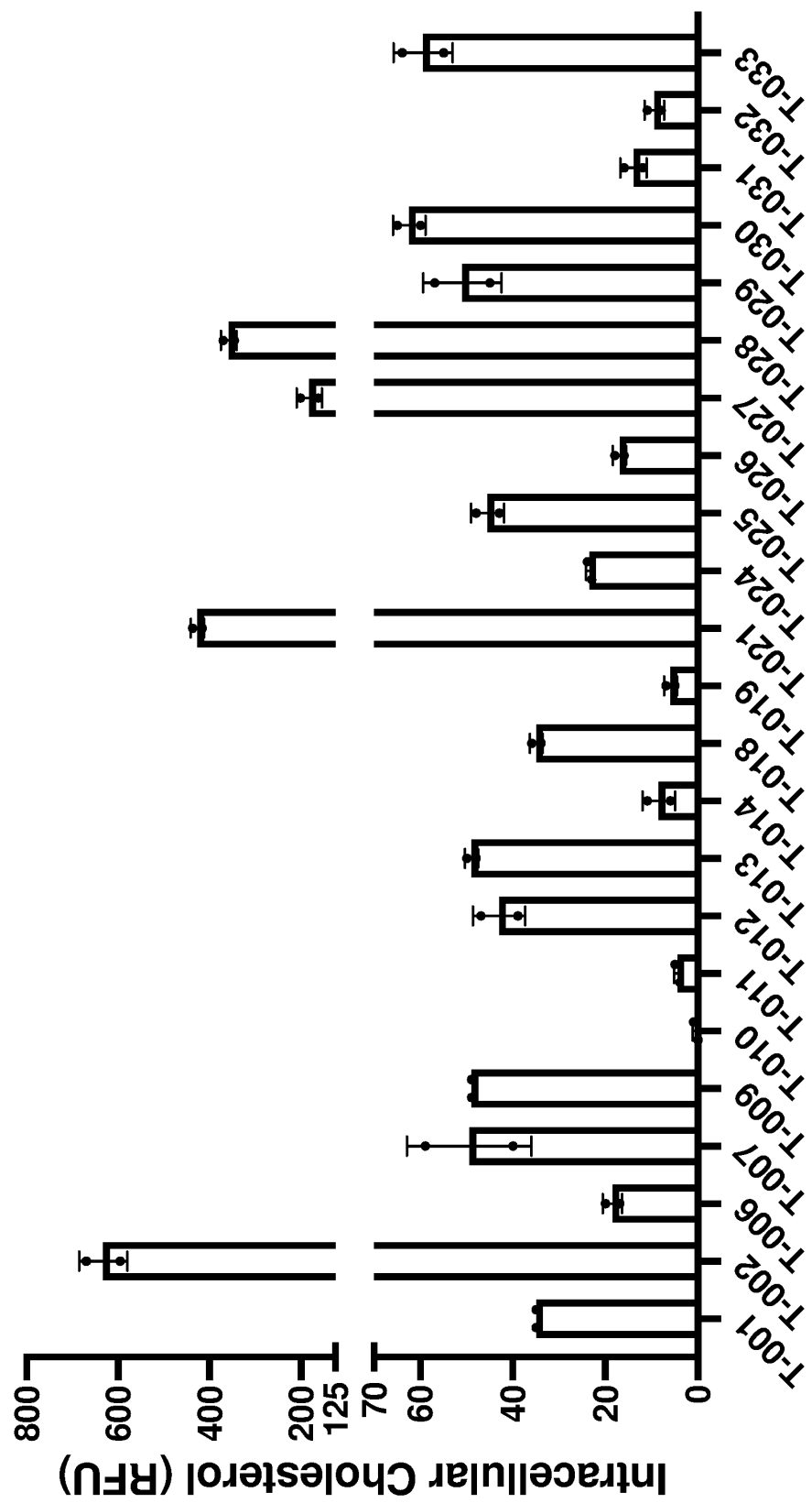


FIG. 17

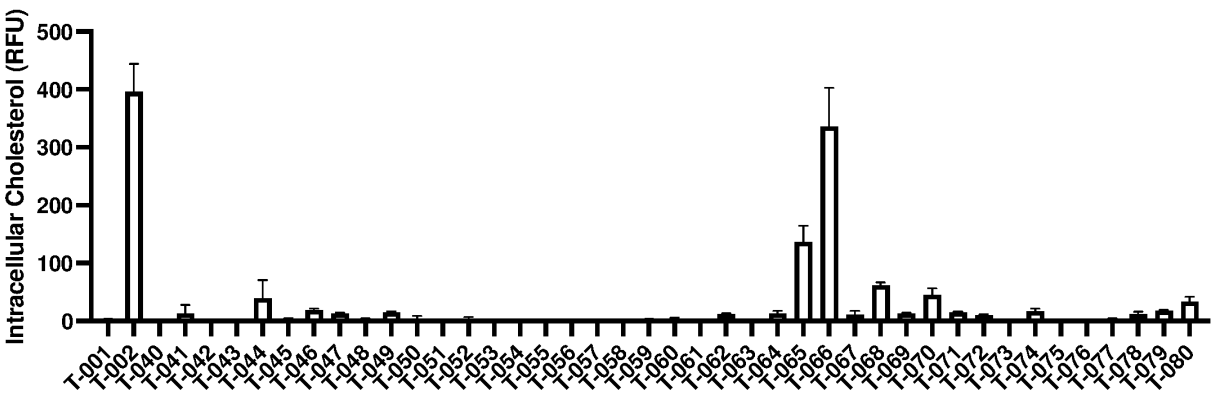


FIG. 18

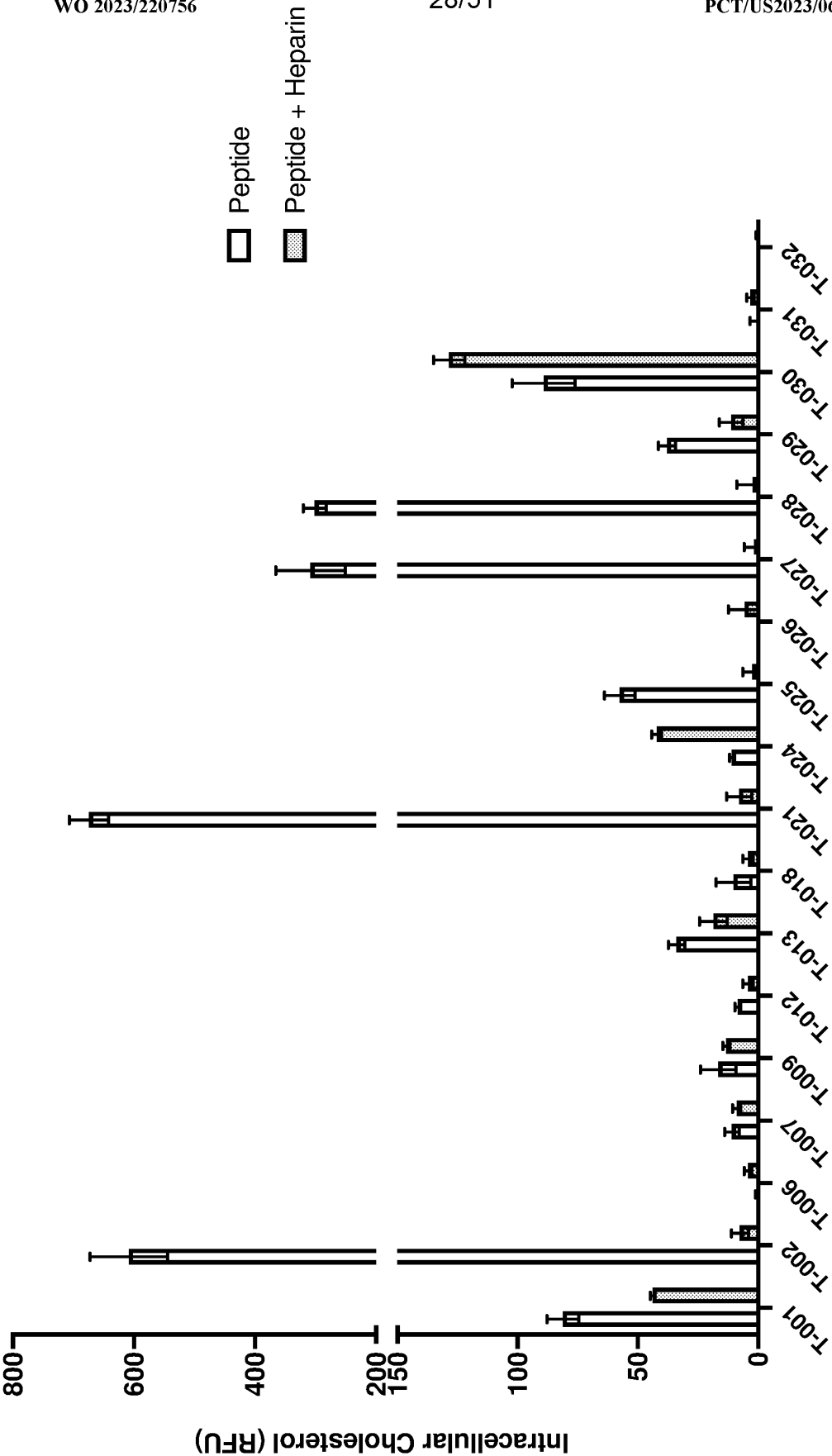


FIG. 19

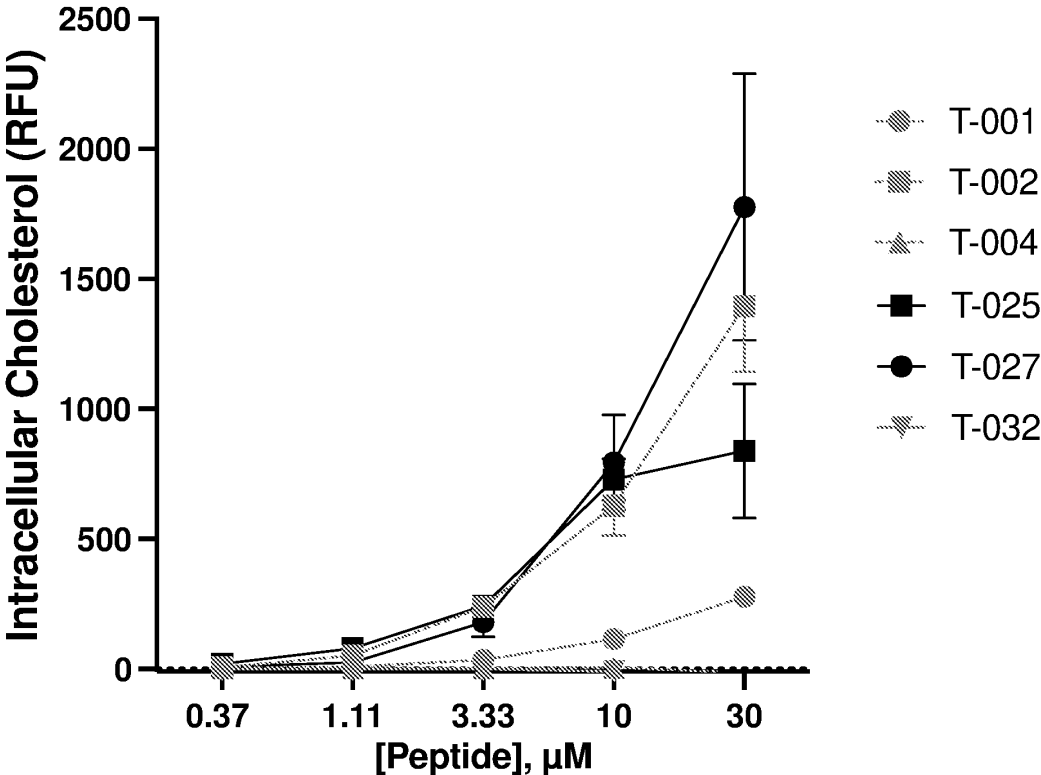


FIG. 20

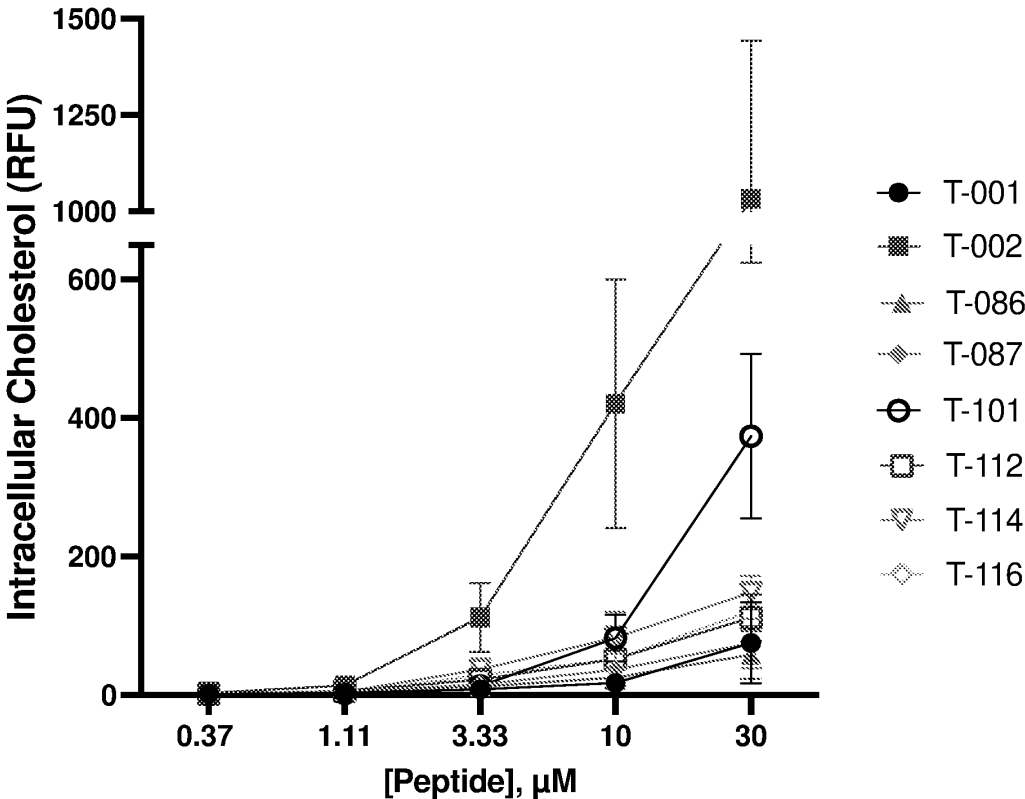


FIG. 21

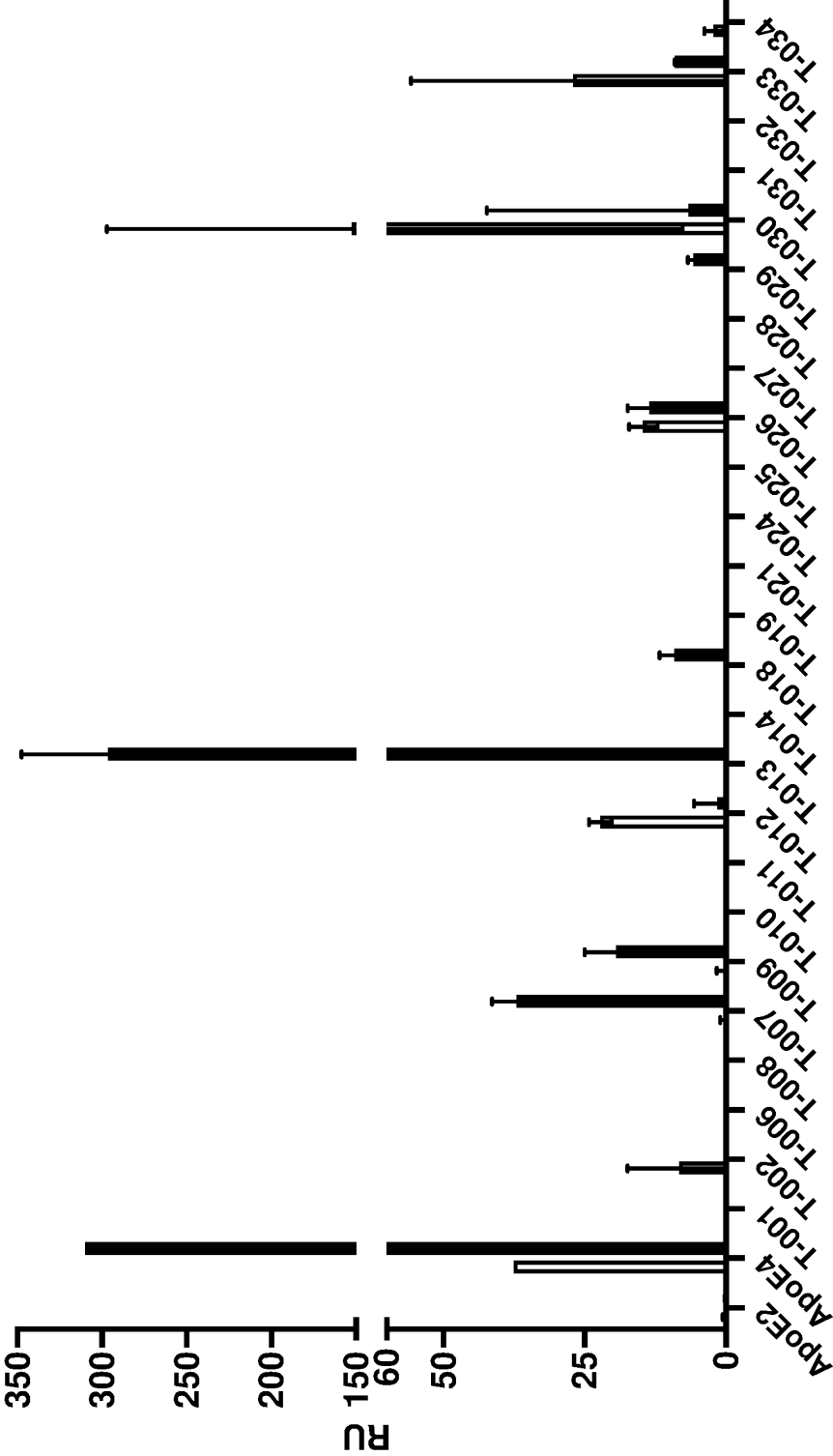


FIG. 22

Buffer: HBS + 0.05% P20

Peptide	KD (μ M)	Peptide	KD (μ M)	Peptide	KD (μ M)
T-040	5.54 ± 0.23	T-057	No Binding	T-076	No Binding
T-041	7.49 ± 0.67	T-058	No Binding	T-086	No Binding
T-043	48.6 ± 0	T-059	7.27 ± 1.40	T-087	No Binding
T-044	7.97 ± 0.47	T-060	149.5 ± 41.7	T-101	No Binding
T-045	71.2 ± 31.8	T-061	No Binding	T-109	1.20 ± 0.09
T-046	3.56 ± 0.37	T-062	2.23 ± 0.01	T-110	1.15 ± 0.04
T-047	3.26 ± 0.23	T-063	No Binding	T-111	1.06 ± 0
T-048	5.24 ± 0.46	T-064	6.81 ± 1.24	T-112	0.72 ± 0.46
T-049	3.26 ± 0.20	T-065	0.75 ± 0.35	T-113	1.82 ± 1.13
T-050	528.5 ± 0.71	T-066	2.42 ± 0.19	T-114	1.27 ± 0.02
T-051	No binding	T-068	1.98 ± 0.93	T-115	2.81 ± 2.78
T-052	1.75 ± 0.08	T-069	2.39 ± 0.42	T-116	1.21 ± 0.19
T-053	121.5 ± 14.9	T-072	4.85 ± 0.05	T-117	4.49 ± 3.18
T-054	No Binding	T-073	No Binding	T-118	2.72 ± 1.51
T-055	5.09 ± 0.04	T-074	2.43 ± 0.52	T-119	No Binding
T-056	No Binding	T-075	No Binding	T-120	11.8 ± 0.56

FIG. 23

Buffer: HBS + 0.005% P20

Peptide	KD, Peptide (μM)	KD, DMPC Complex (μM)	Rel. Change, Lipid vs. Peptide
T-040	882 $\pm$ 1030	No Binding	N/A
T-041	701 $\pm$ 974	No Binding	N/A
T-043	840 $\pm$ 1150	No Binding	N/A
T-044	11.4 $\pm$ 6.58	1160 $\pm$ 709	0.01
T-045	11800 $\pm$ 1250	No Binding	N/A
T-046	6.72 $\pm$ 1.36	56.3 $\pm$ 56.1	0.12
T-048	11.4 $\pm$ 5.29	666 $\pm$ 369	0.02
T-050	No Binding	No Binding	N/A
T-051	No Binding	No Binding	N/A
T-052	1.18 $\pm$ 0.19	202 $\pm$ 109	0.01
T-053	43000 $\pm$ 34000	No Binding	N/A
T-054	No Binding	No Binding	N/A
T-059	7.72 $\pm$ 9.39	No Binding	N/A
T-062	9.36 $\pm$ 4.61	52.9 $\pm$ 84.1	0.18
T-065	1.07 $\pm$ 0.69	0.18 $\pm$ 0.09	5.88
T-066	2.06 $\pm$ 1.92	0.11 $\pm$ 0.07	18.33
T-068	1.48 $\pm$ 0.09	0.66 $\pm$ 0.03	2.25
T-069	1.12 $\pm$ 0.48	0.56 $\pm$ 0.36	1.99
T-070	1.38 $\pm$ 0.35	0.68 $\pm$ 0.19	2.02
T-071	18.5 $\pm$ 2.69	348 $\pm$ 157	0.05

FIG. 24A

Buffer: HBS + 0.005% P20

Peptide	KD, Peptide (μM)	KD, DMPC Complex (μM)	Rel. Change, Lipid vs. Peptide
T-072	8.27 ± 0.55	No Binding	N/A
T-073	4.27 ± 0.19	No Binding	N/A
T-074	2.37 ± 0.98	77.0 ± 118	0.03
T-075	No Binding	No Binding	N/A
T-076	No Binding	No Binding	N/A
T-077	33.2 ± 37.7	189 ± 67.8	0.18
T-086	No Binding	No Binding	N/A
T-087	2.27 ± 0.06	No Binding	N/A
T-101	11.7 ± 7.54	No Binding	N/A
T-109	3.15 ± 0.09	1.05 ± 0.01	3
T-110	2.97 ± 0.23	1.20 ± 0.13	2.48
T-111	2.98 ± 0.01	0.46 ± 0.04	6.51
T-112	1.14 ± 0.33	0.17 ± 0.003	15.5
T-113	1.44 ± 0.39	0.29 ± 0.01	4.84
T-114	2.70 ± 0.85	0.17 ± 0.004	16.12
T-115	0.42 ± 0.11	0.21 ± 0.15	2
T-116	4.53 ± 2.31	0.28 ± 0.12	16.24
T-117	0.40 ± 0.03	0.01 ± 0.000	36.41
T-118	0.32 ± 0.39	94.3 ± 1330	0
T-119	2.31 ± 2.26	No Binding	N/A
T-120	0.80 ± 0.23	No Binding	N/A

FIG. 24B

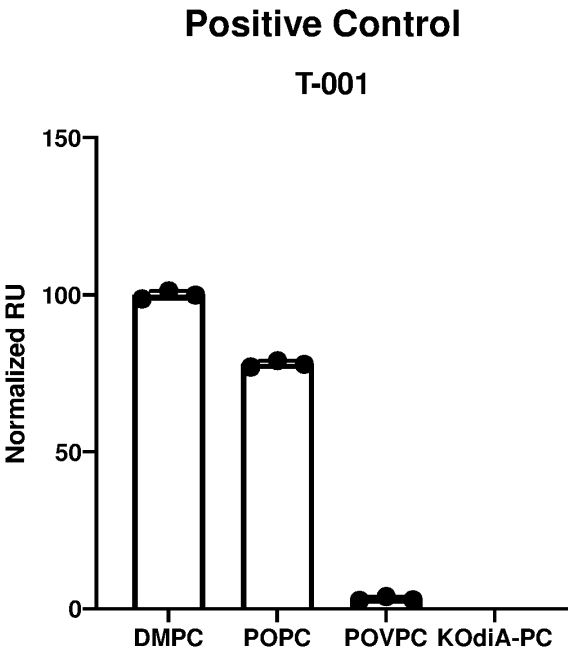


FIG. 25A

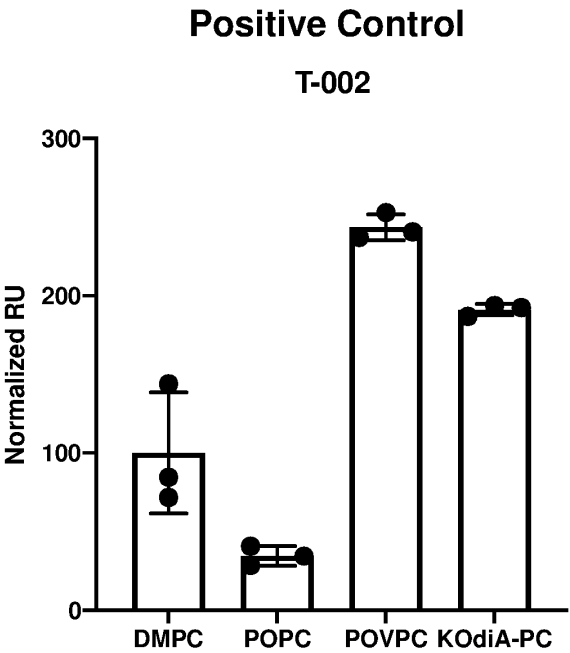


FIG. 25B

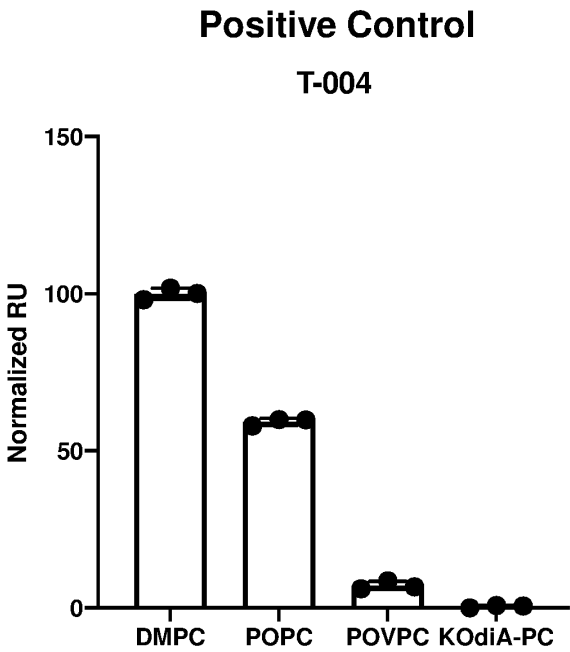


FIG. 25C

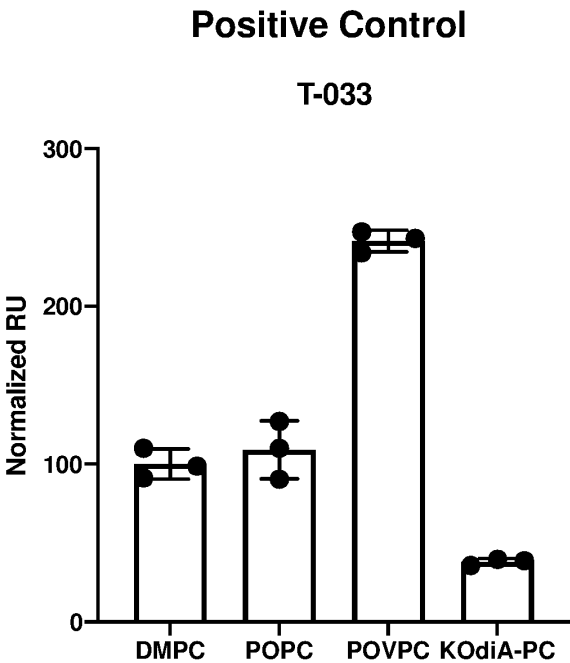


FIG. 25D

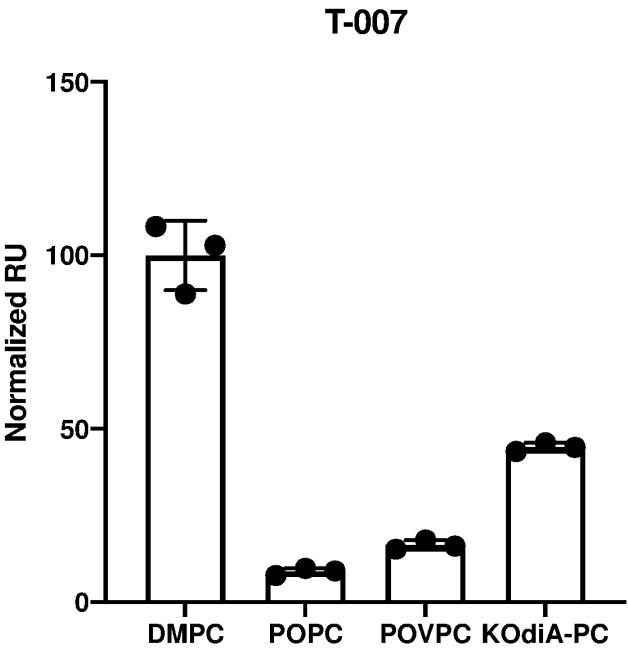


FIG. 25E

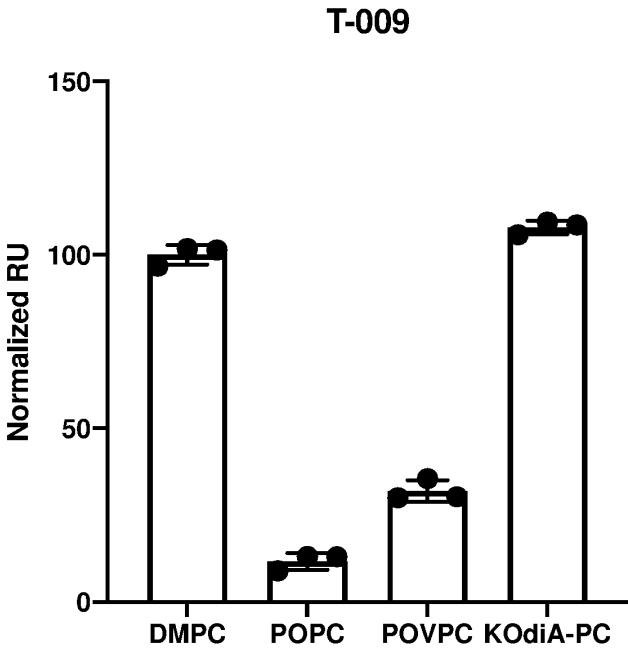


FIG. 25F

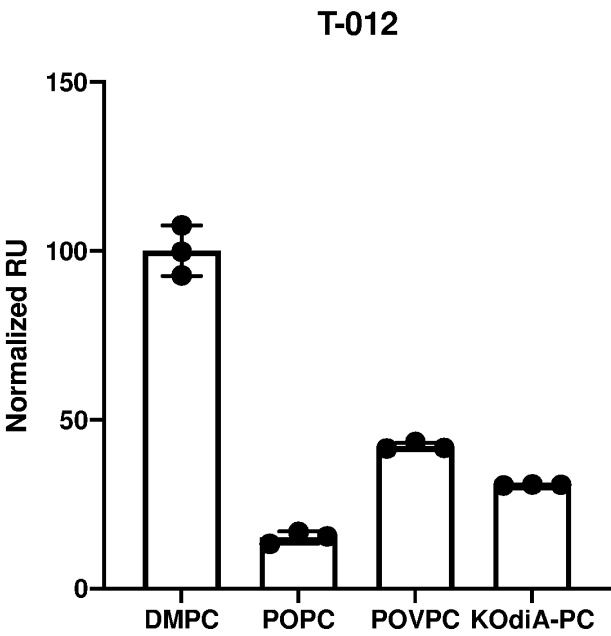


FIG. 25G

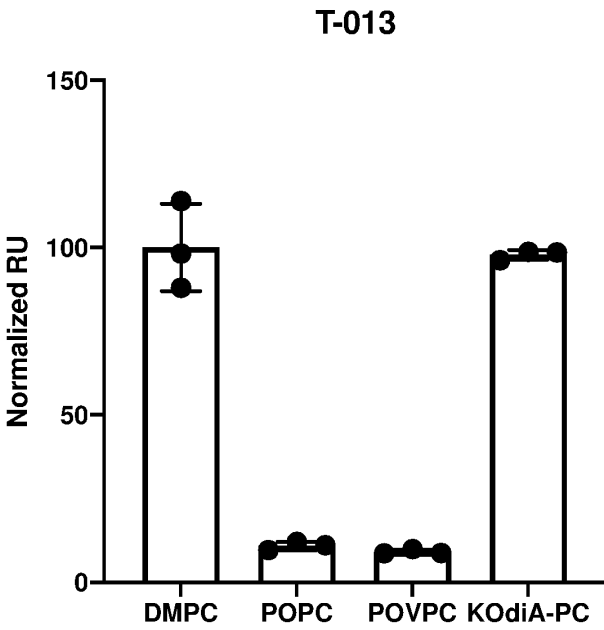


FIG. 25H

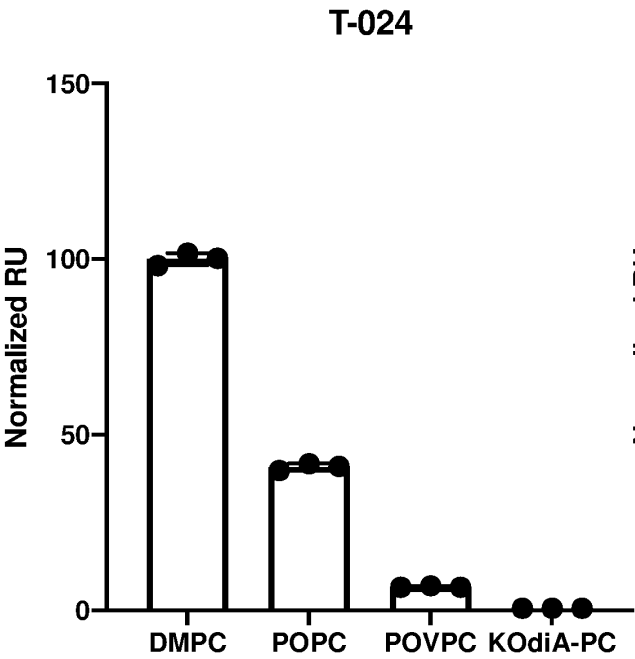


FIG. 25I

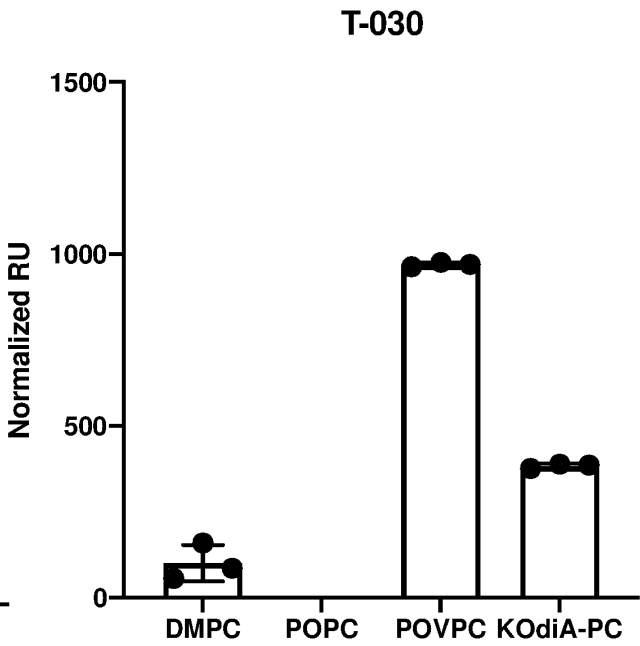


FIG. 25J

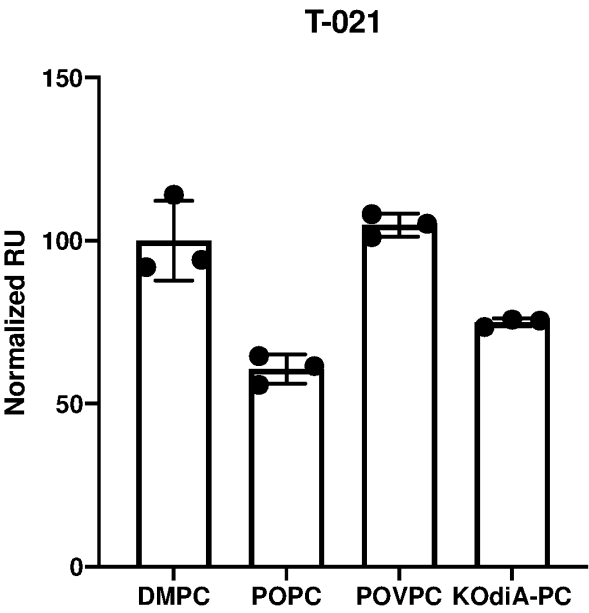


FIG. 25K

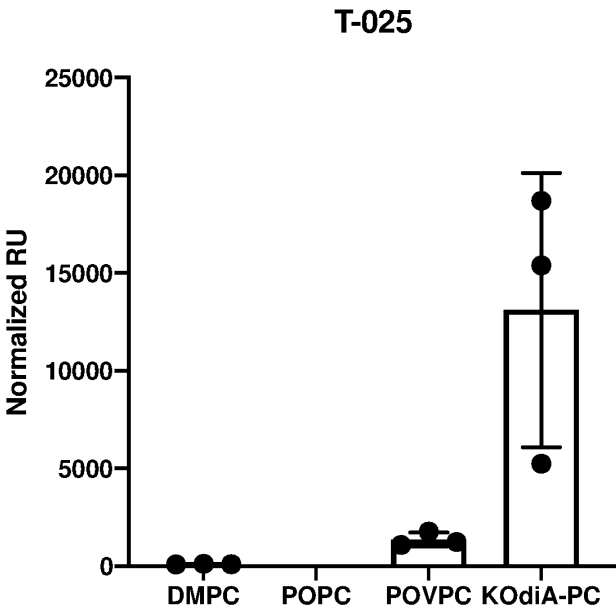


FIG. 25L

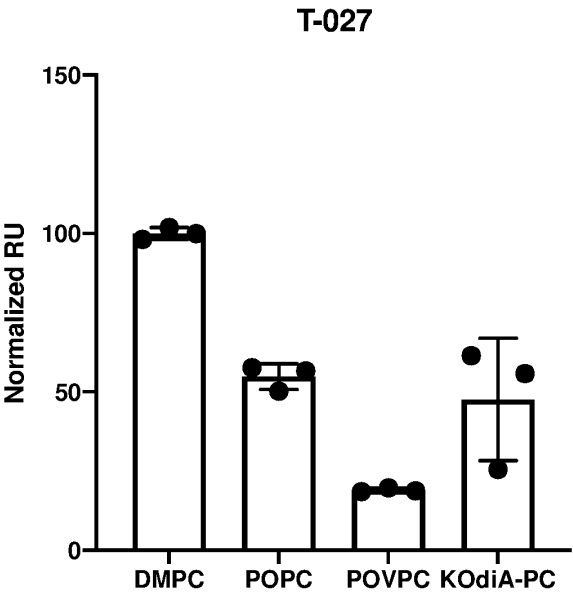


FIG. 25M

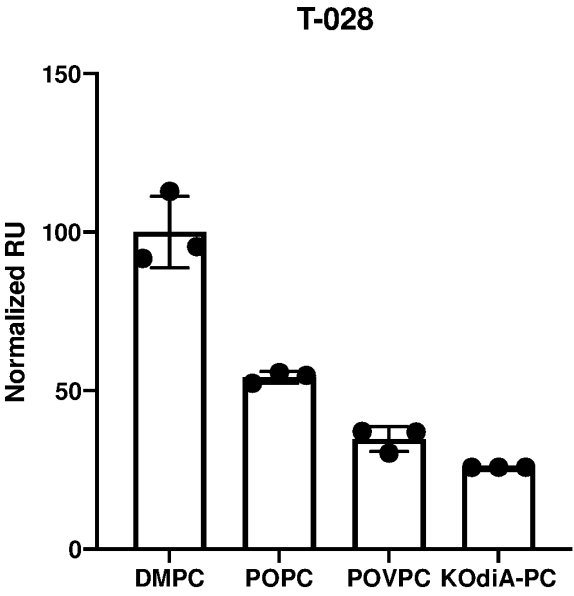


FIG. 25N

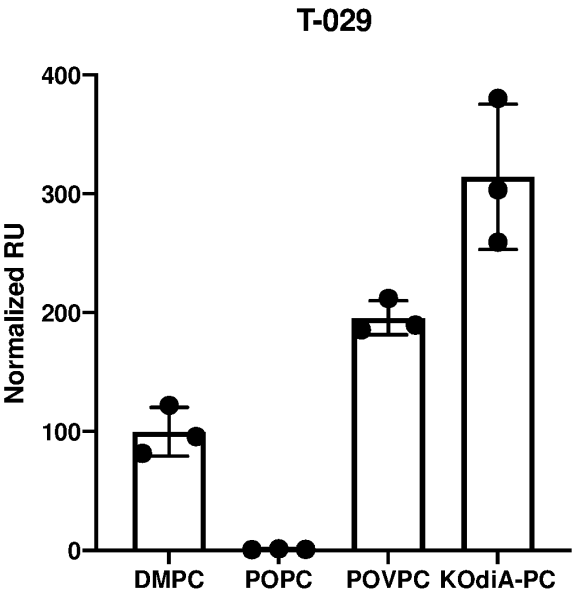


FIG. 25o

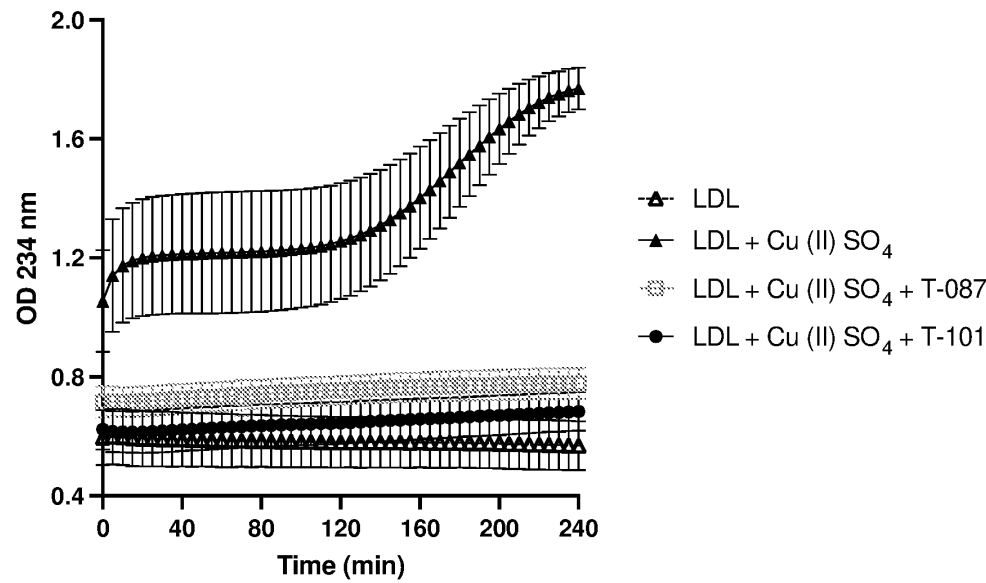


FIG. 26A

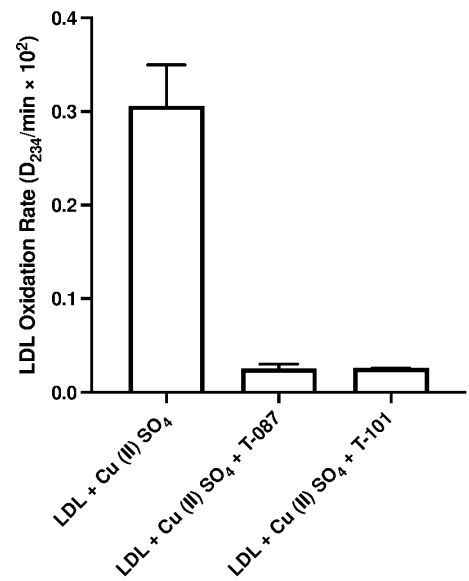


FIG. 26B

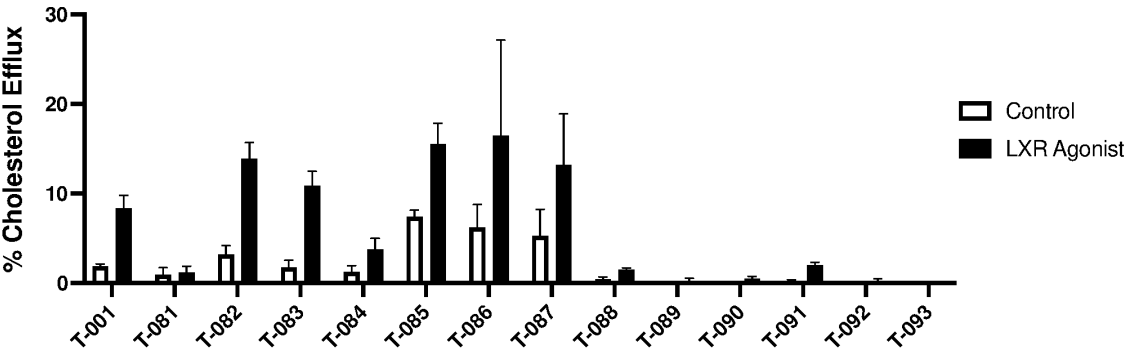


FIG. 27A

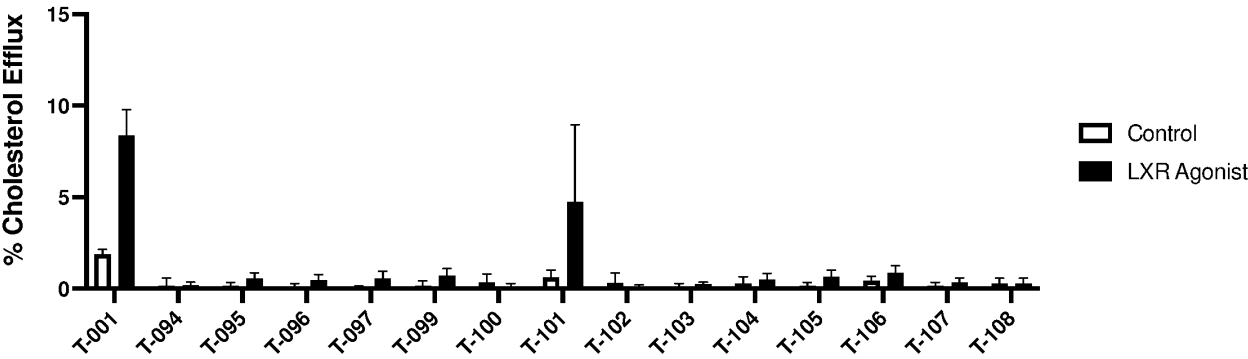


FIG. 27B

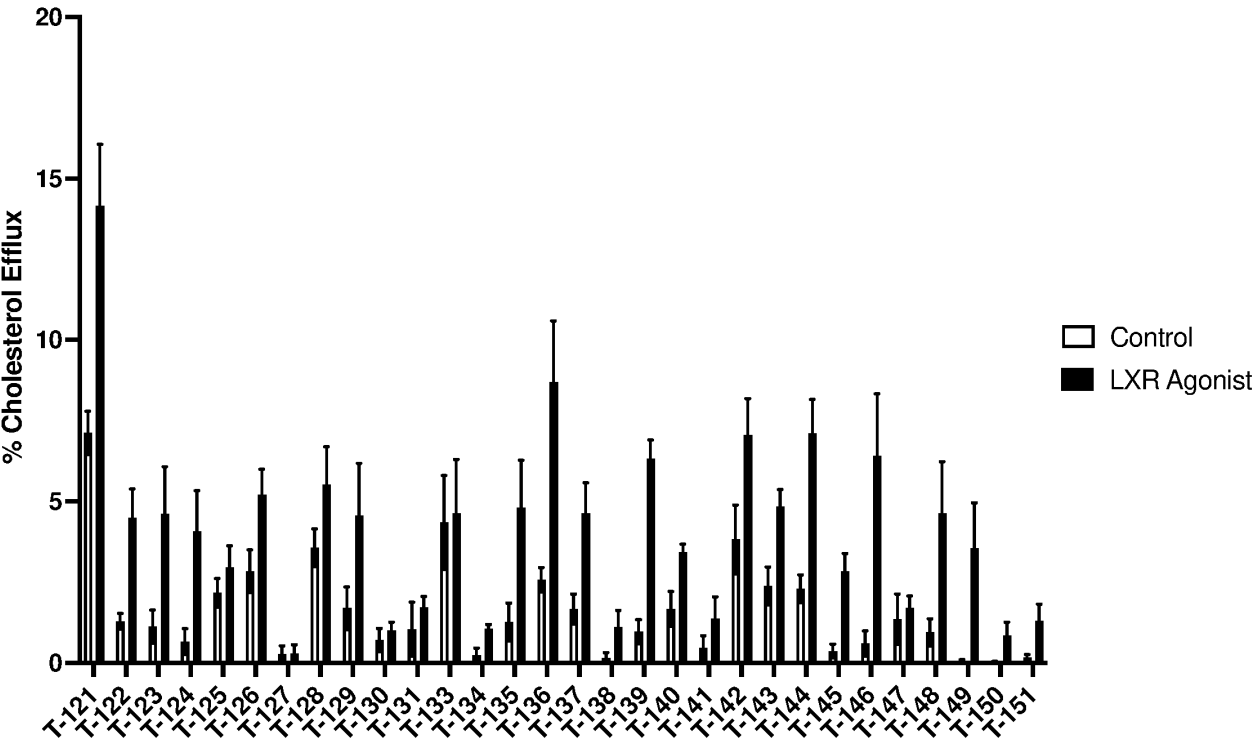


FIG. 28

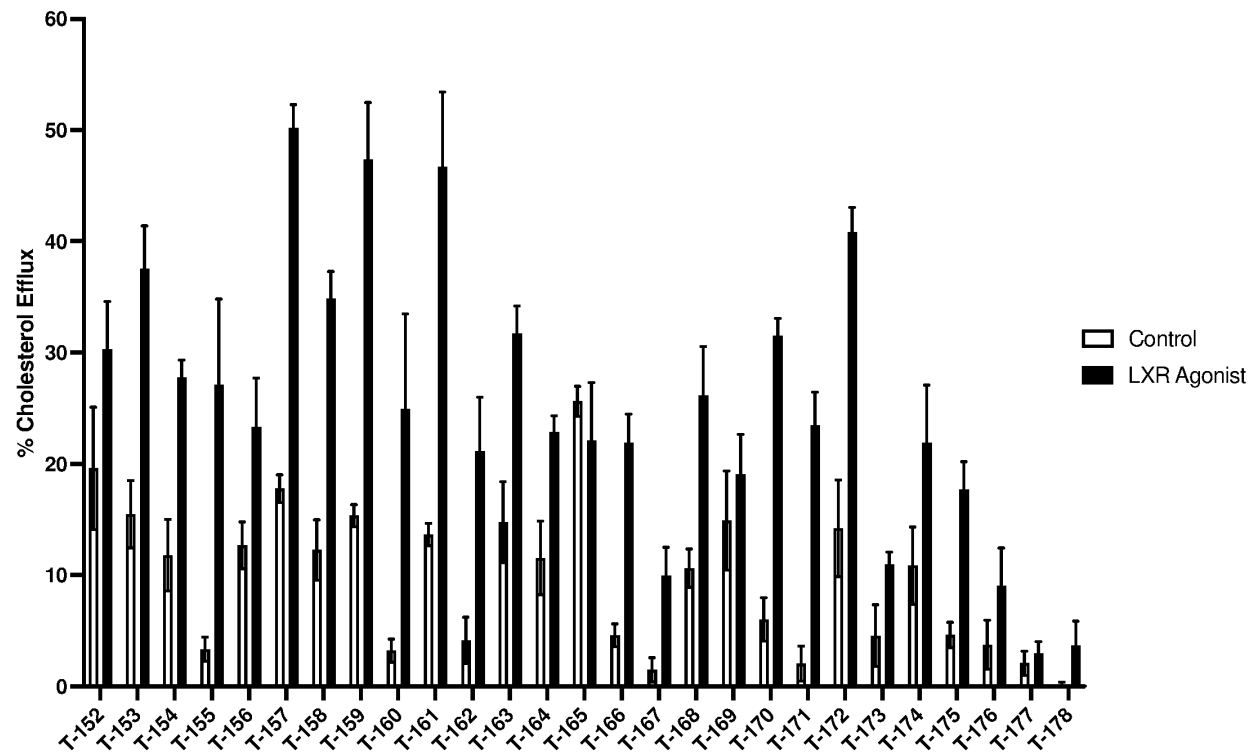


FIG. 29

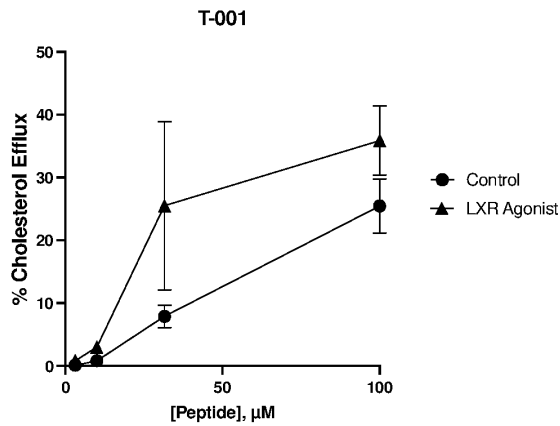


FIG. 30A

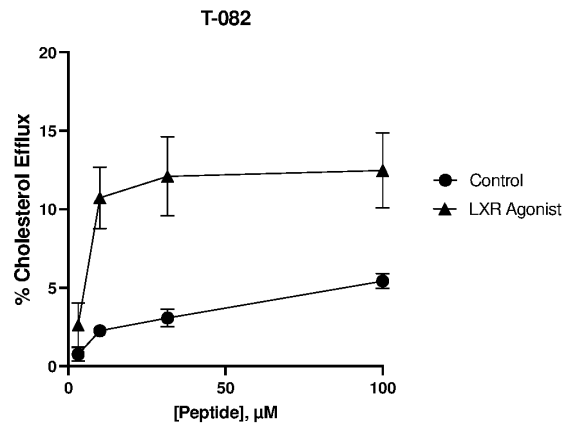


FIG. 30B

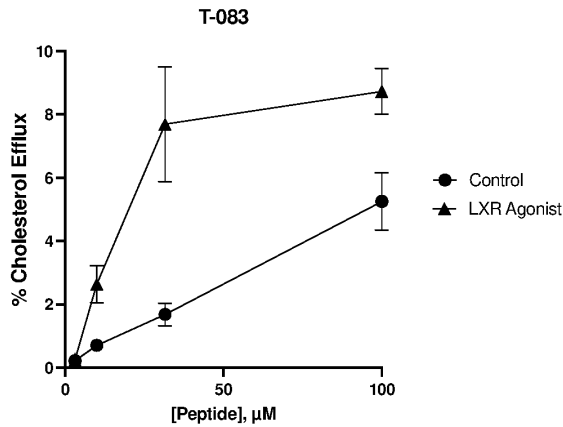


FIG. 30C

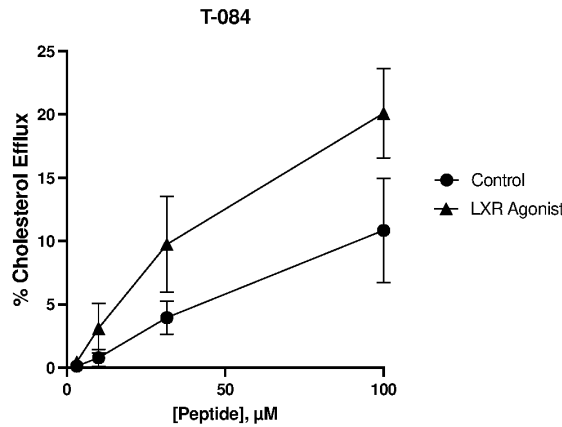


FIG. 30D

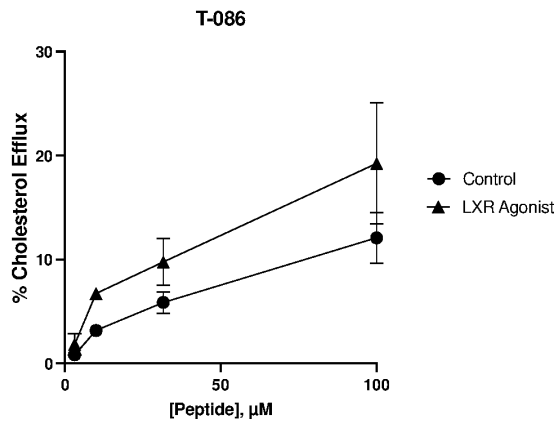


FIG. 30E

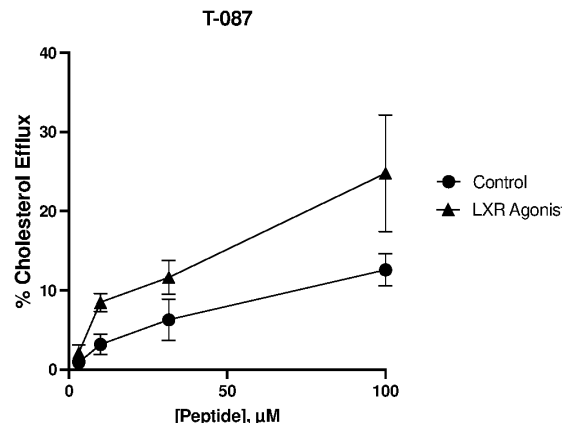


FIG. 30F

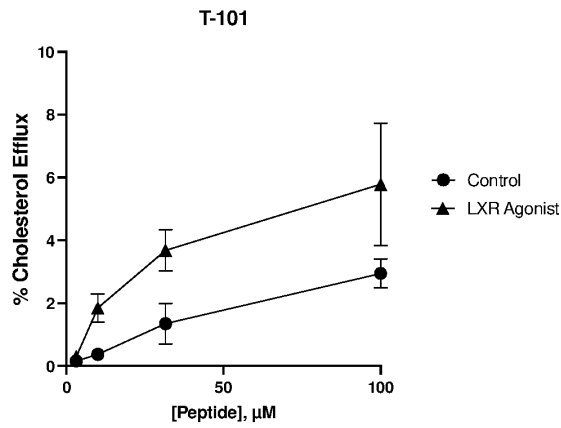


FIG. 30G

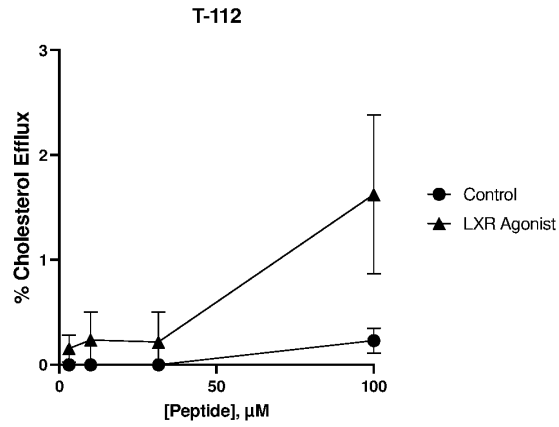


FIG. 30H

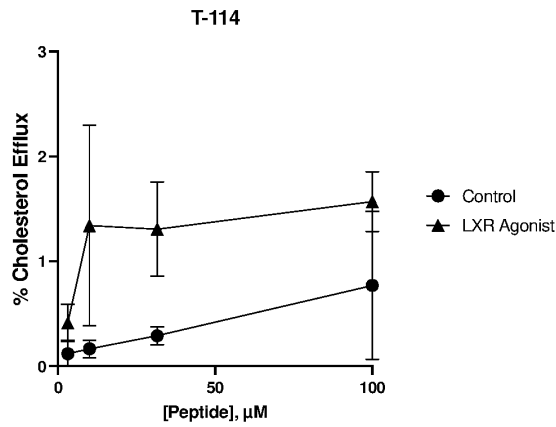


FIG. 30I

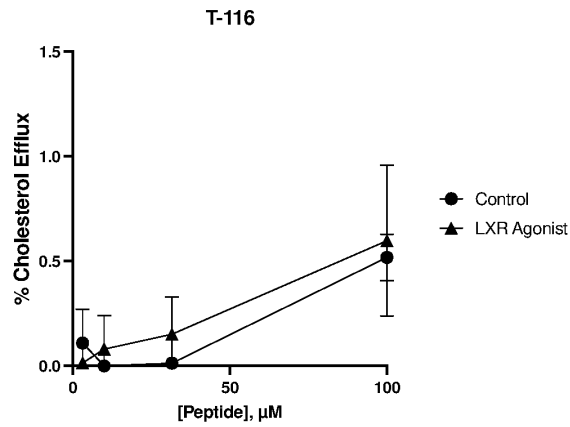


FIG. 30J

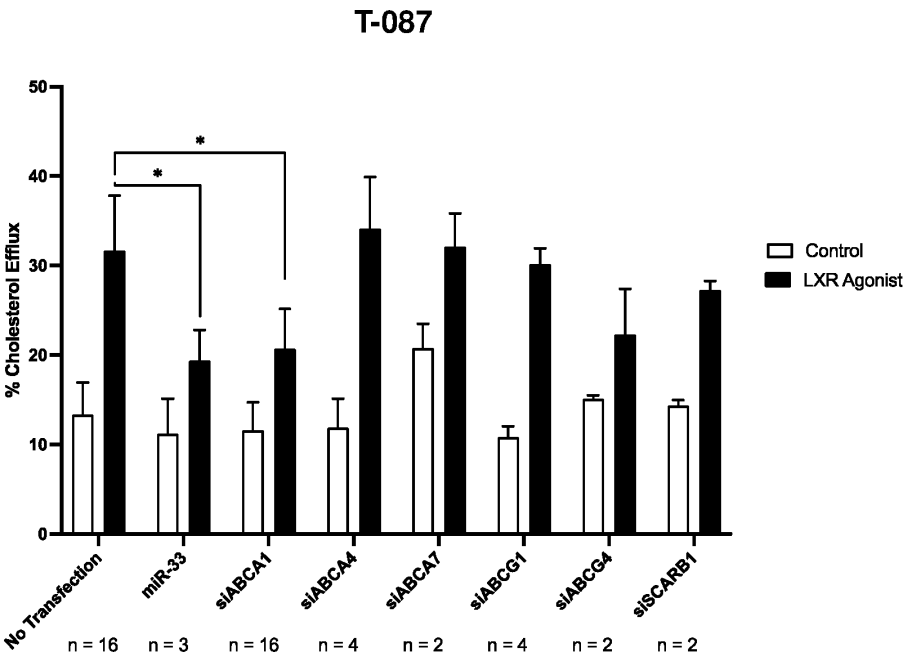


FIG. 31A

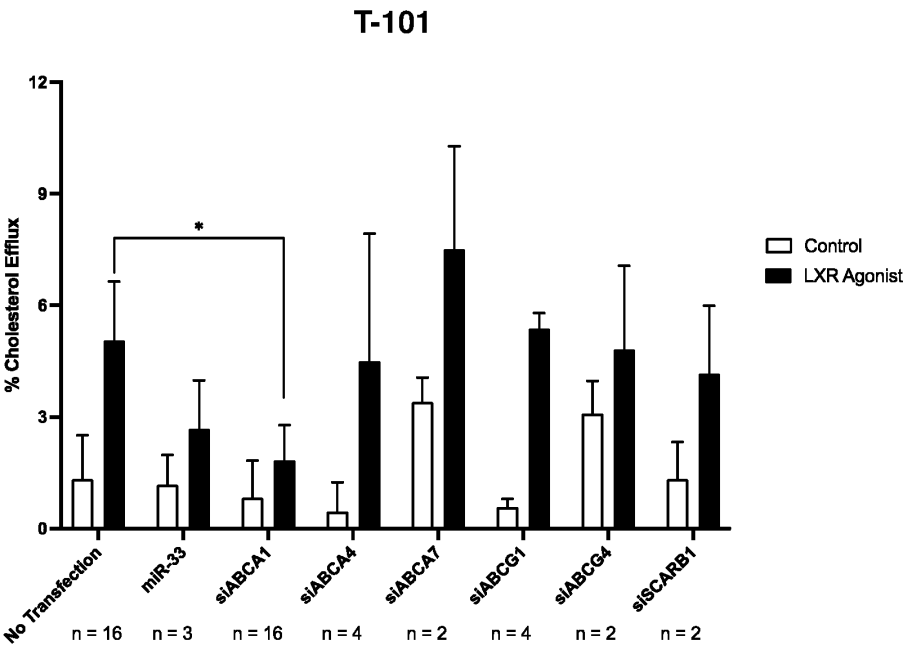


FIG. 31B

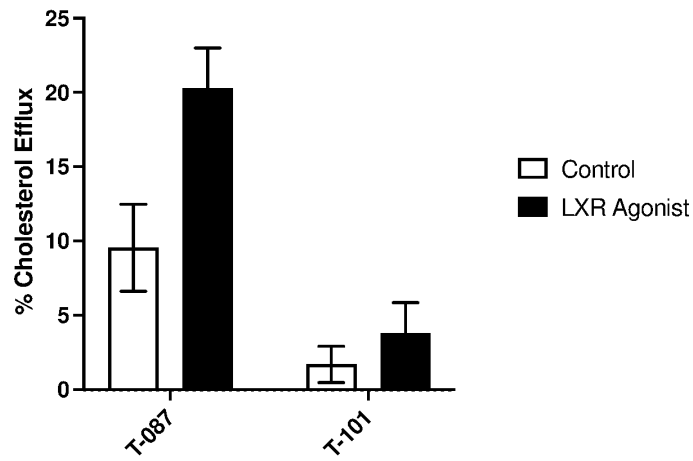


FIG. 32

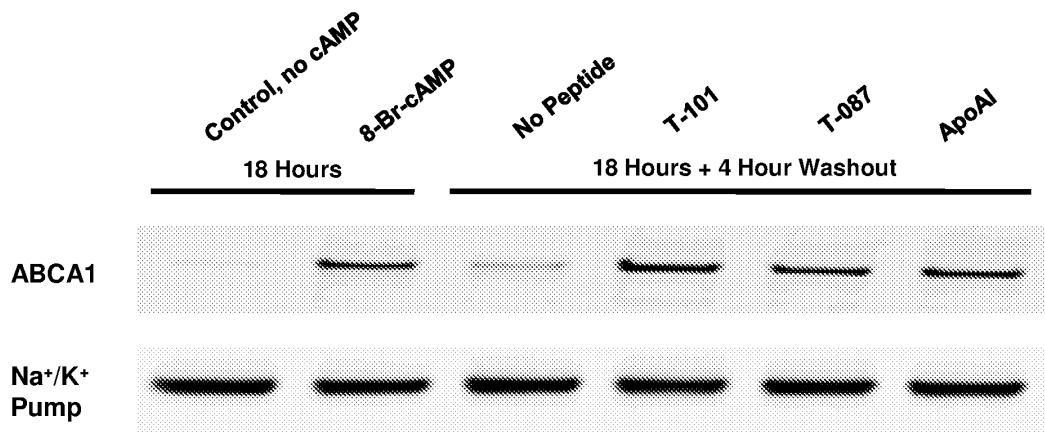


FIG. 33A

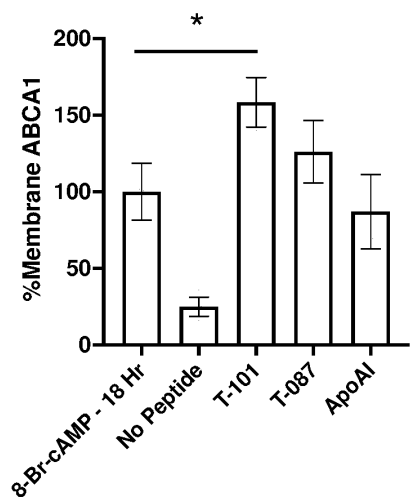


FIG. 33B

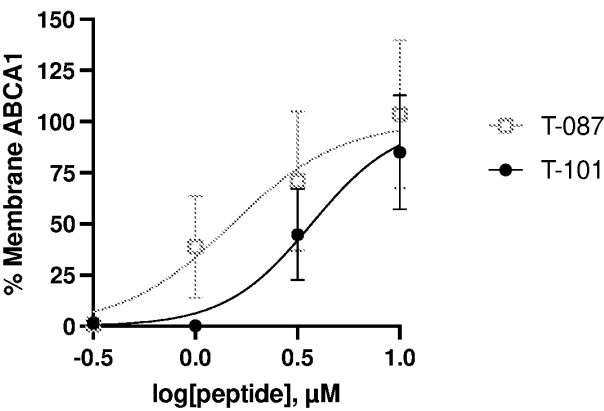


FIG. 33C

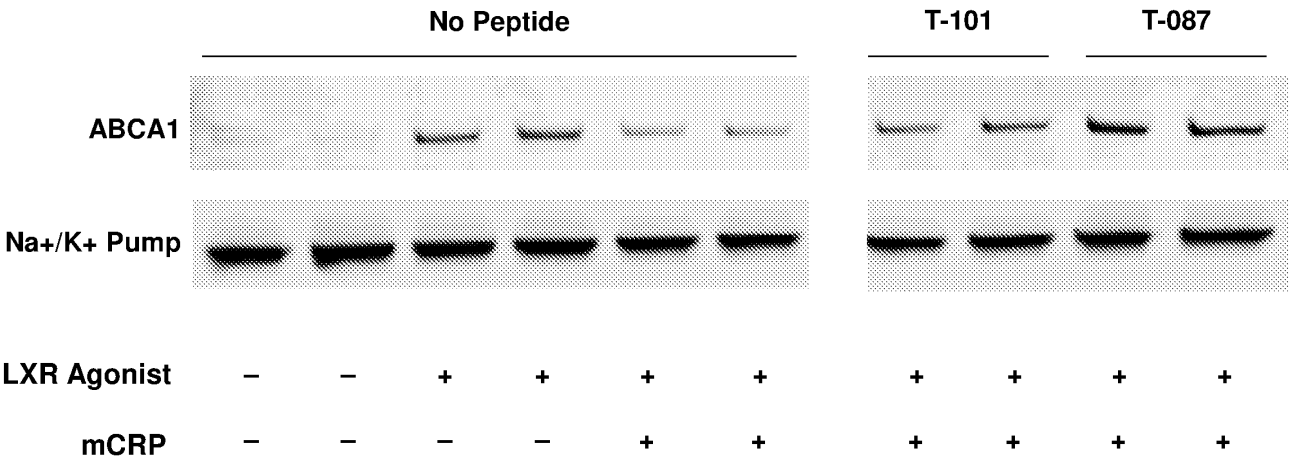


FIG. 34A

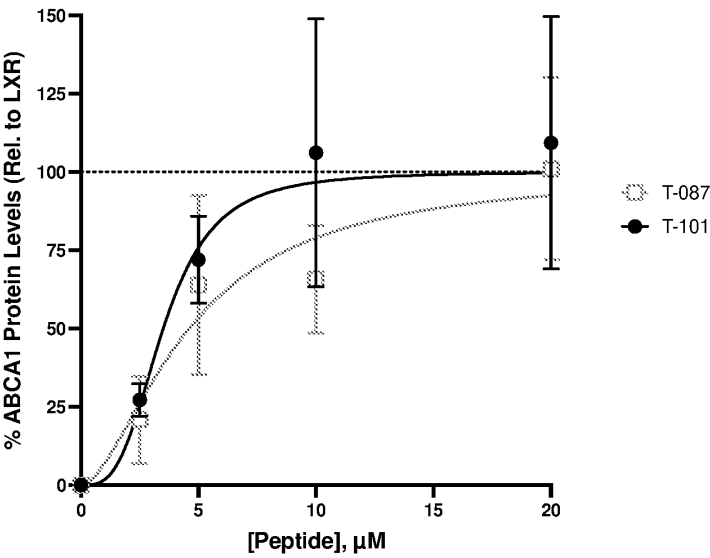


FIG. 34B

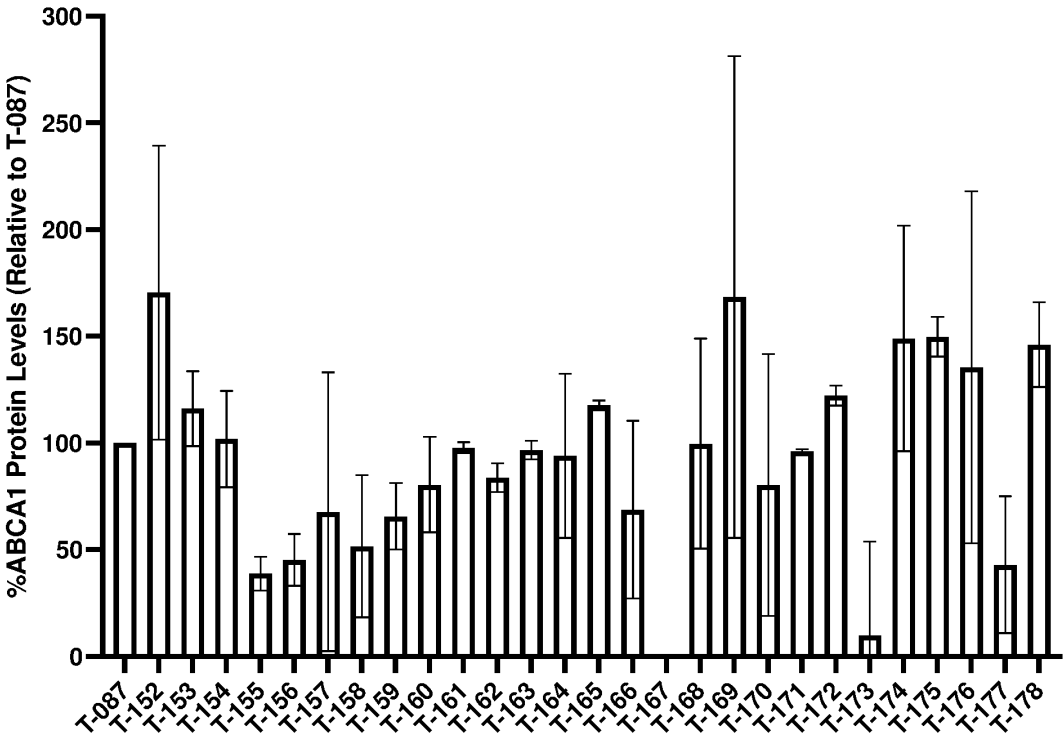


FIG. 35

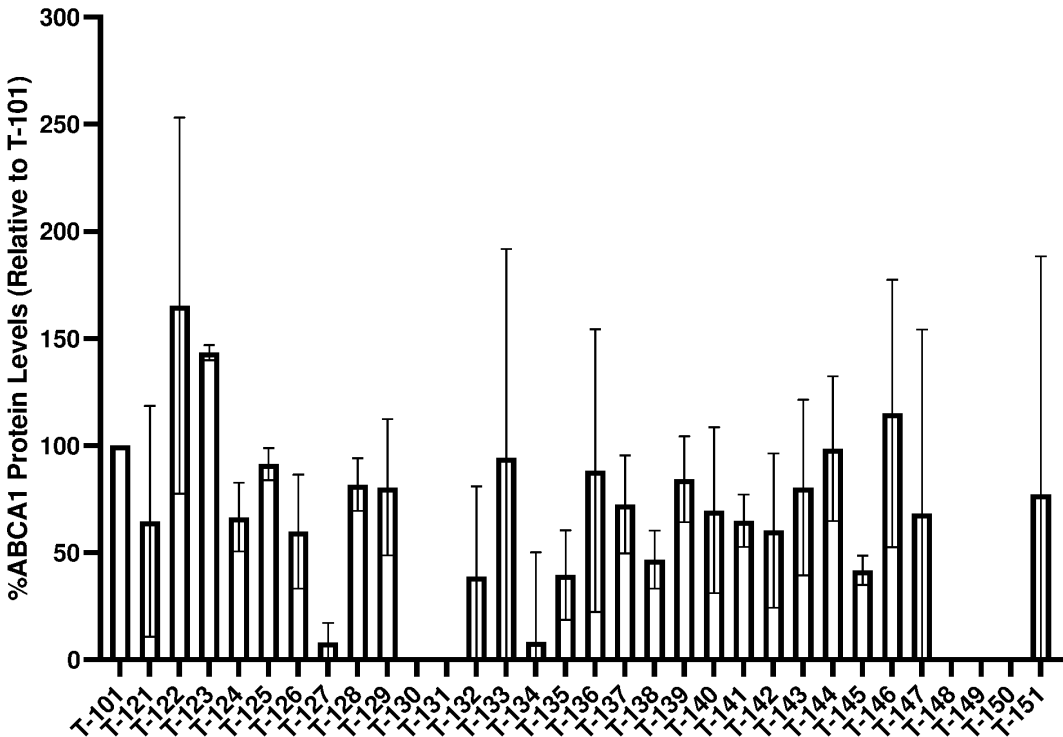


FIG. 36

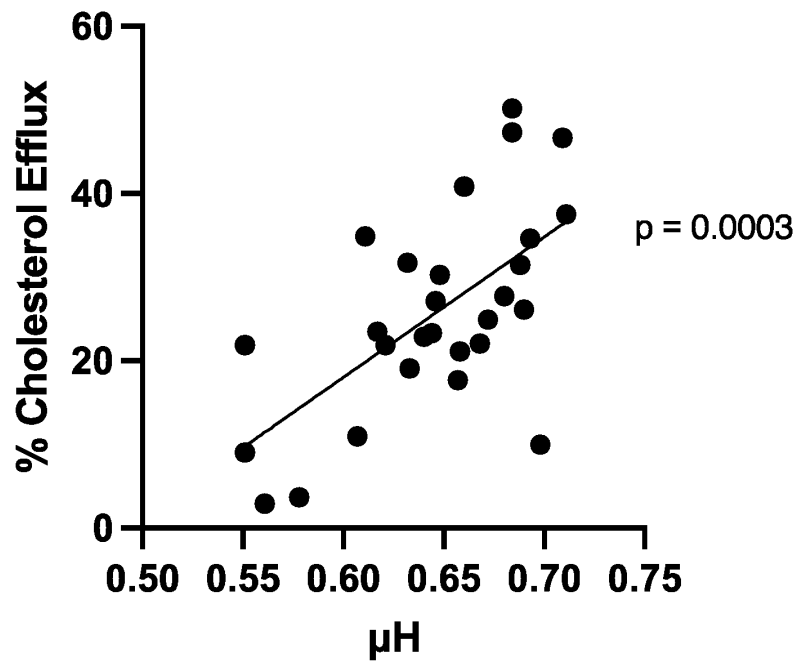


FIG. 37

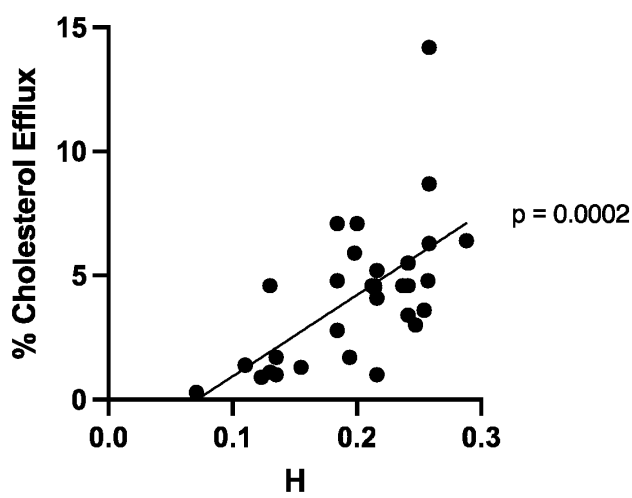


FIG. 38A

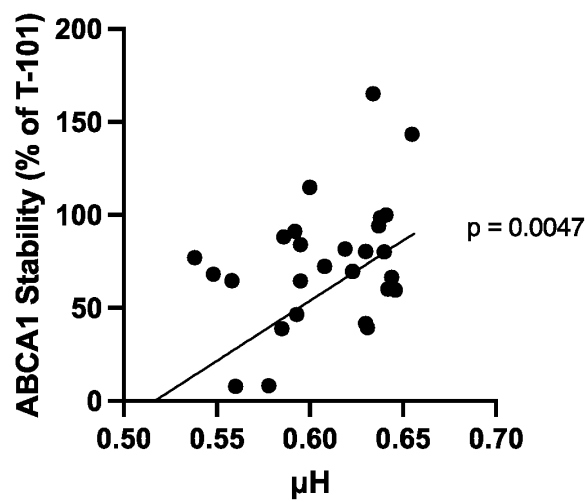


FIG. 38B

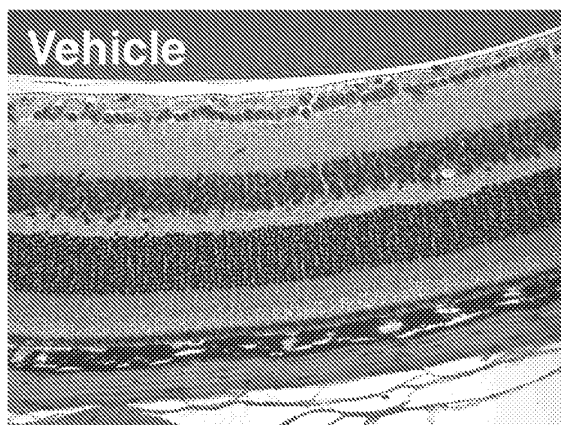


FIG. 39A

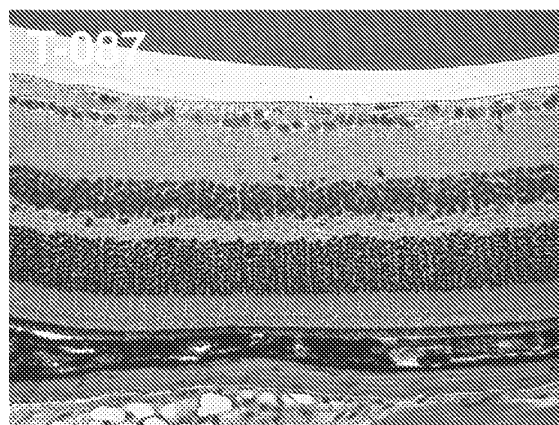


FIG. 39B

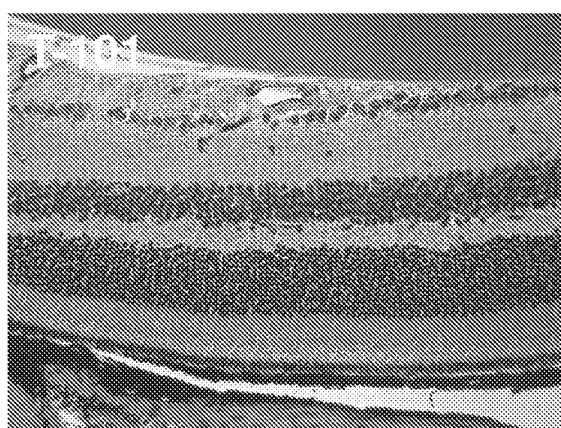


FIG. 39C

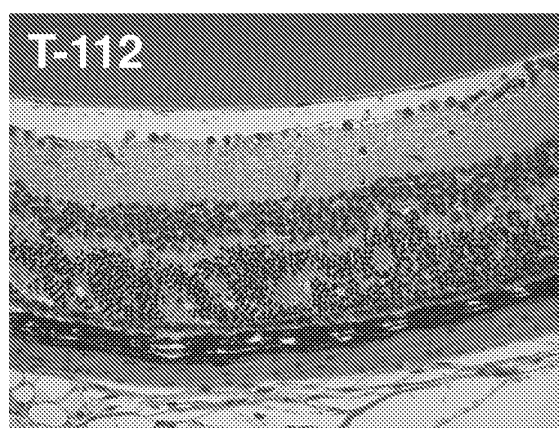


FIG. 39D

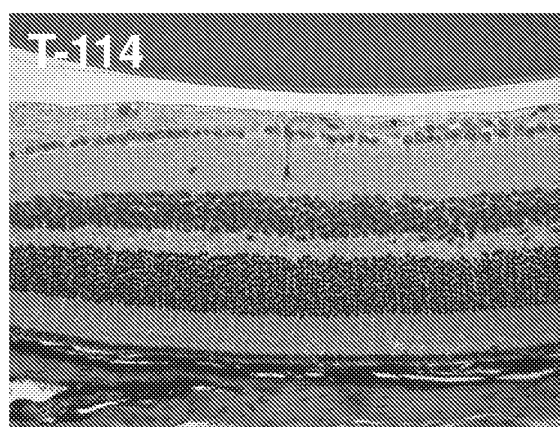


FIG. 39E

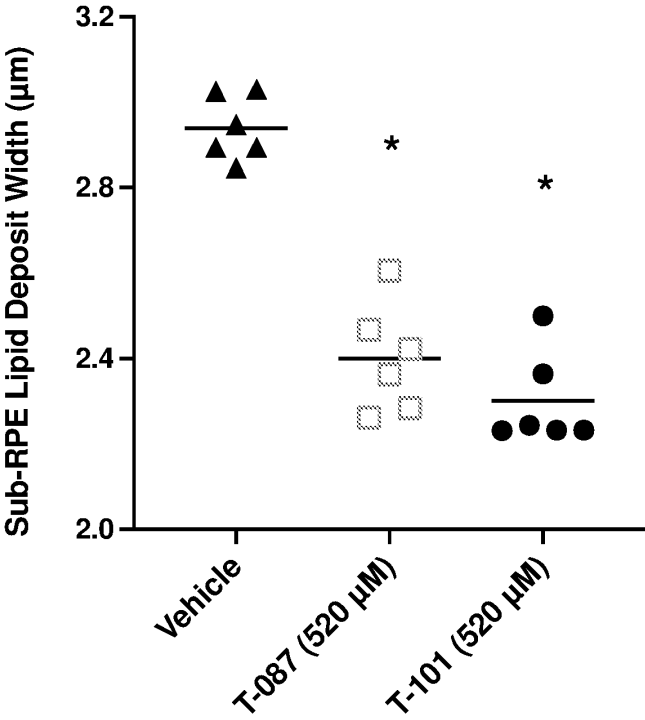


FIG. 40A

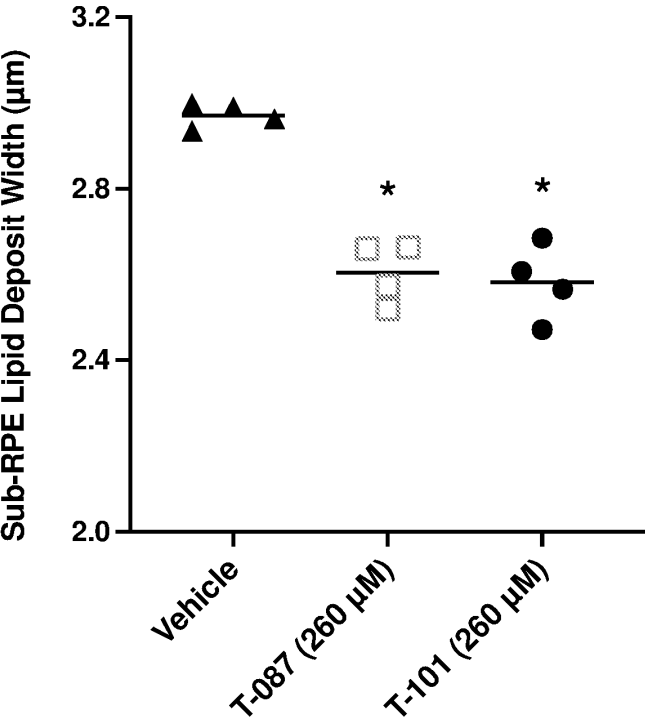


FIG. 40B

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18

D	A	W	E	R	F	R	A	L	F	K	E	L	A	D	Y	F	R
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FIG. 41A

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22

R	S	G	A	D	A	L	E	S	A	L	K	E	L	K	R	F	I	R	E	W	T
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FIG. 41B