Figure 1

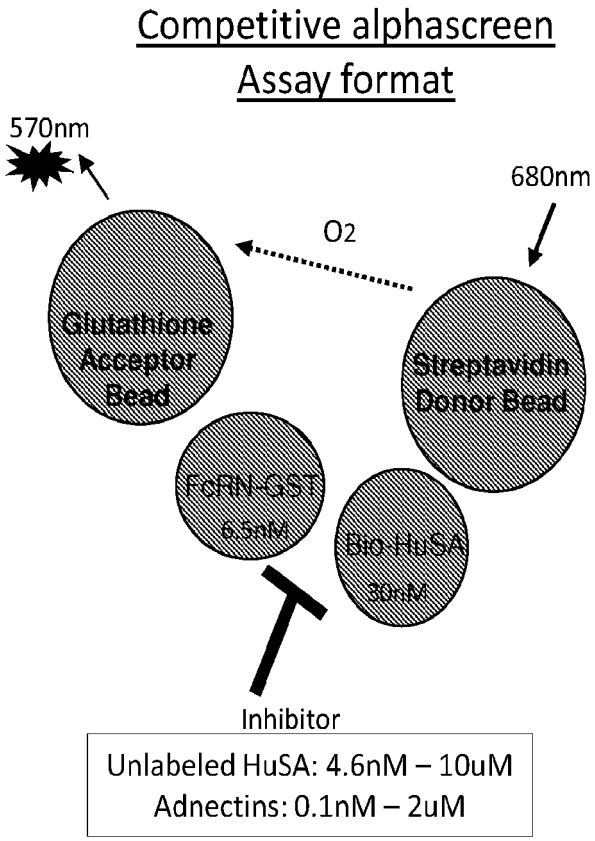

Competitive alphascreen
Assay format
570nm
680nm
O2
Glutathione Acceptor Bead
Streptavidin Donor Bead
FcRN-GST 6.5nM
Bio-HuSA 30nM
Inhibitor
Unlabeled HuSA: 4.6nM – 10uM
Adnectins: 0.1nM – 2uM

Figure 2

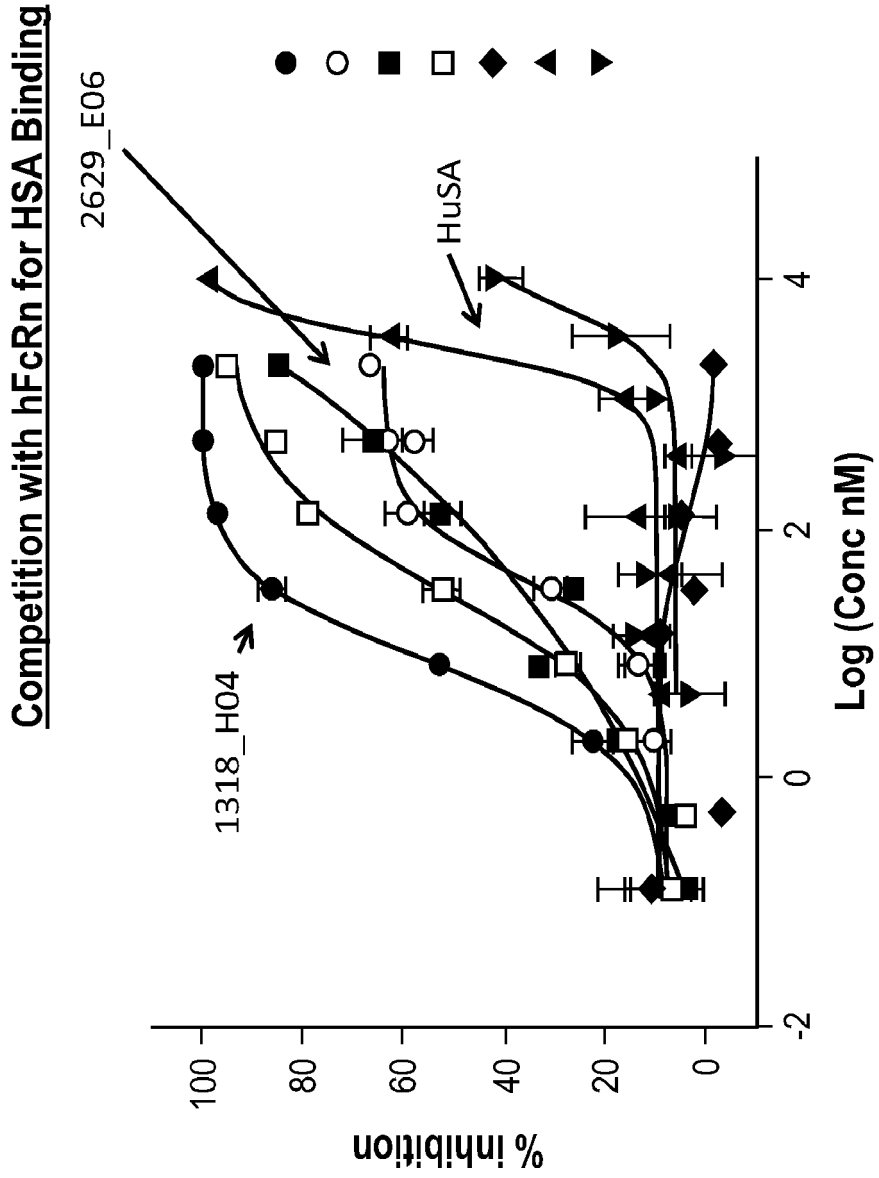

Competition with hFcRn for HSA Binding
ATI-836-136 (ADX_1318_H04)
ATI-1131-145 (ADX_2270_C01)
ATI-1490-102 (ADX_2629_E06)
ATI-1491-102 (ADX_2630_D02)
SGE
HuSA
HuSA domIII
2629_E06
HuSA
1318_H04
% inhibition
100
80
60
40
20
0
-2
0
2
4
Log (Conc nM)

Figure 3

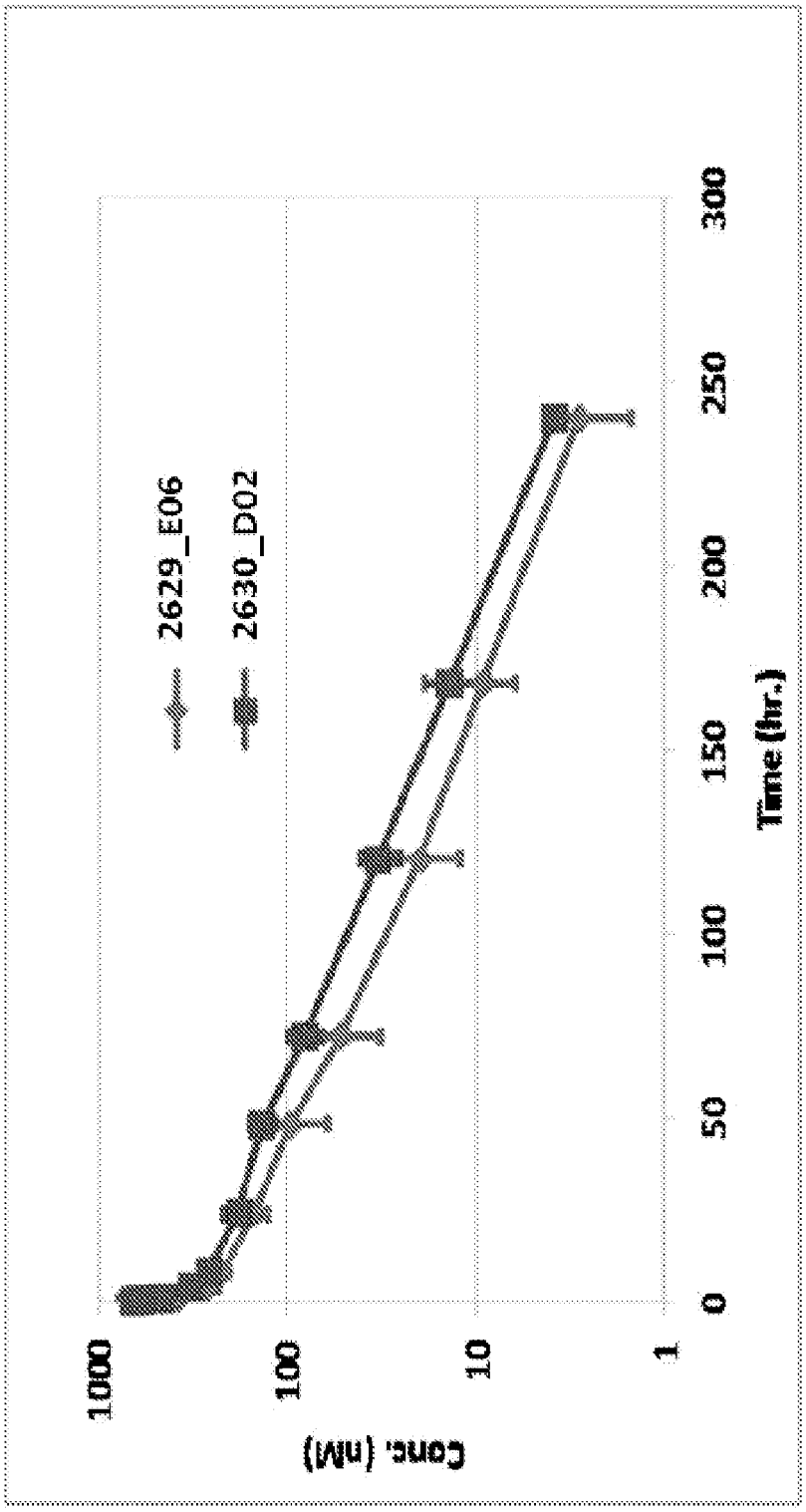

2629_E06
2630_D02
Conc. (nM)
1000
100
10
1
0
50
100
150
200
250
300
Time (hr.)

Figure 4

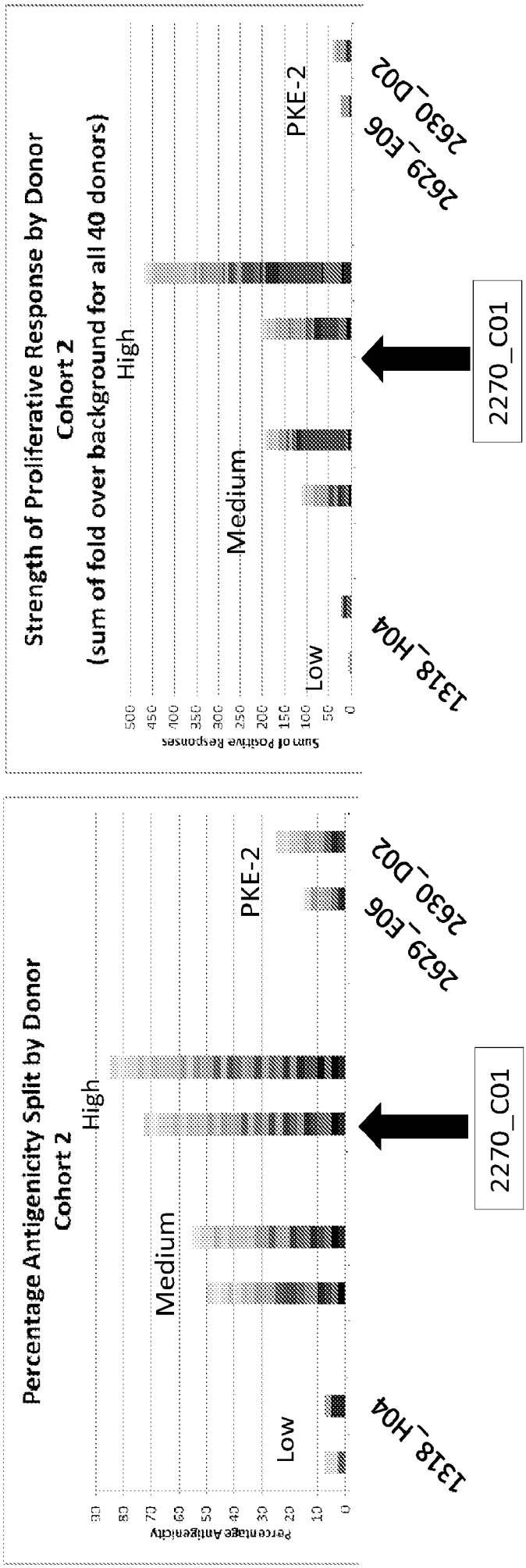

Strength of Proliferative Response by Donor
Cohort 2
(sum of fold over background for all 40 donors)
Sum of Positive Responses
High
Medium
Low
PKE-2
2270_C01
1318_H04
2629_E06
2630_D02
Percentage Antigenicity Split by Donor
Cohort 2
Percentage Antigenicity
High
Medium
Low
PKE-2
2270_C01
1318_H04
2629_E06
2630_D02

Figure 5

Adnectin		2987_H07 (myo)		2013_E01 (PCSK9)	
PKE	HSA EC_{50} (nM)	X-PKE	PKE-X	X-PKE	PKE-X
1318_H04	5	31% (8/26)	0% (0/26)	31% (8/26)	X
2629_E06	20	30% (3/10)	80% (8/10)	90% (9/10)	80% (8/10)
2630_D02	9	20% (2/10)	60% (6/10)	50% (5/10)	80% (8/10)

HSA $EC_{50_tandem}/EC_{50_mono}$

≤ 2
2—5
5—10
10

X = tandems not made

Figure 6

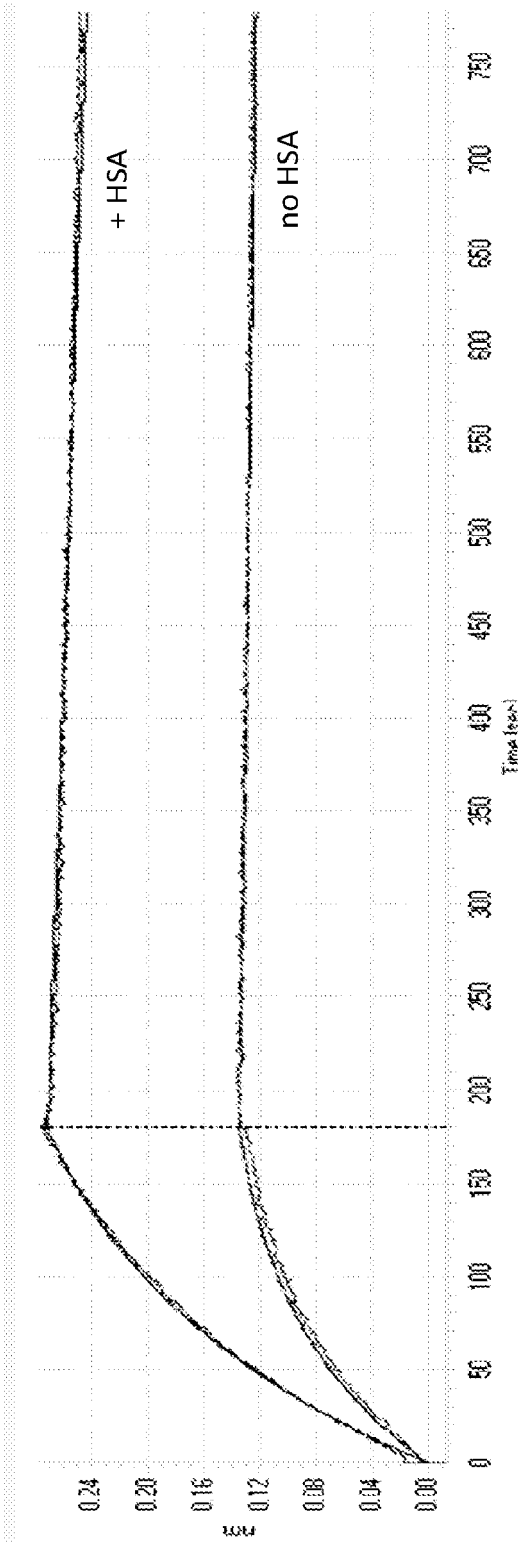

+ HSA
no HSA
0.24
0.20
0.16
0.12
0.08
0.04
0.00
0
50
100
150
200
250
300
350
400
450
500
550
600
650
700
750

Figure 7

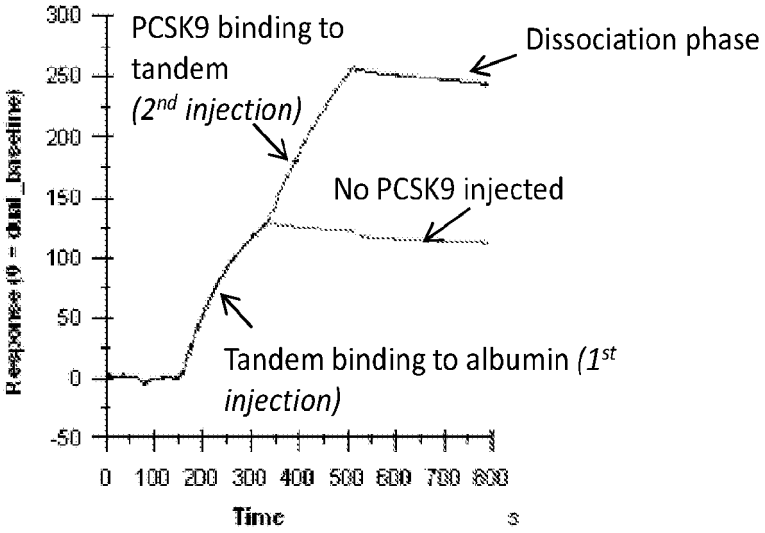

PCSK9 binding to tandem (2nd injection)
Dissociation phase
No PCSK9 injected
Tandem binding to albumin (1st injection)
Response (0 = dual_baseline)
Time
s
300
250
200
150
100
50
0
-50
0 100 200 300 400 500 600 700 800

Figure 8

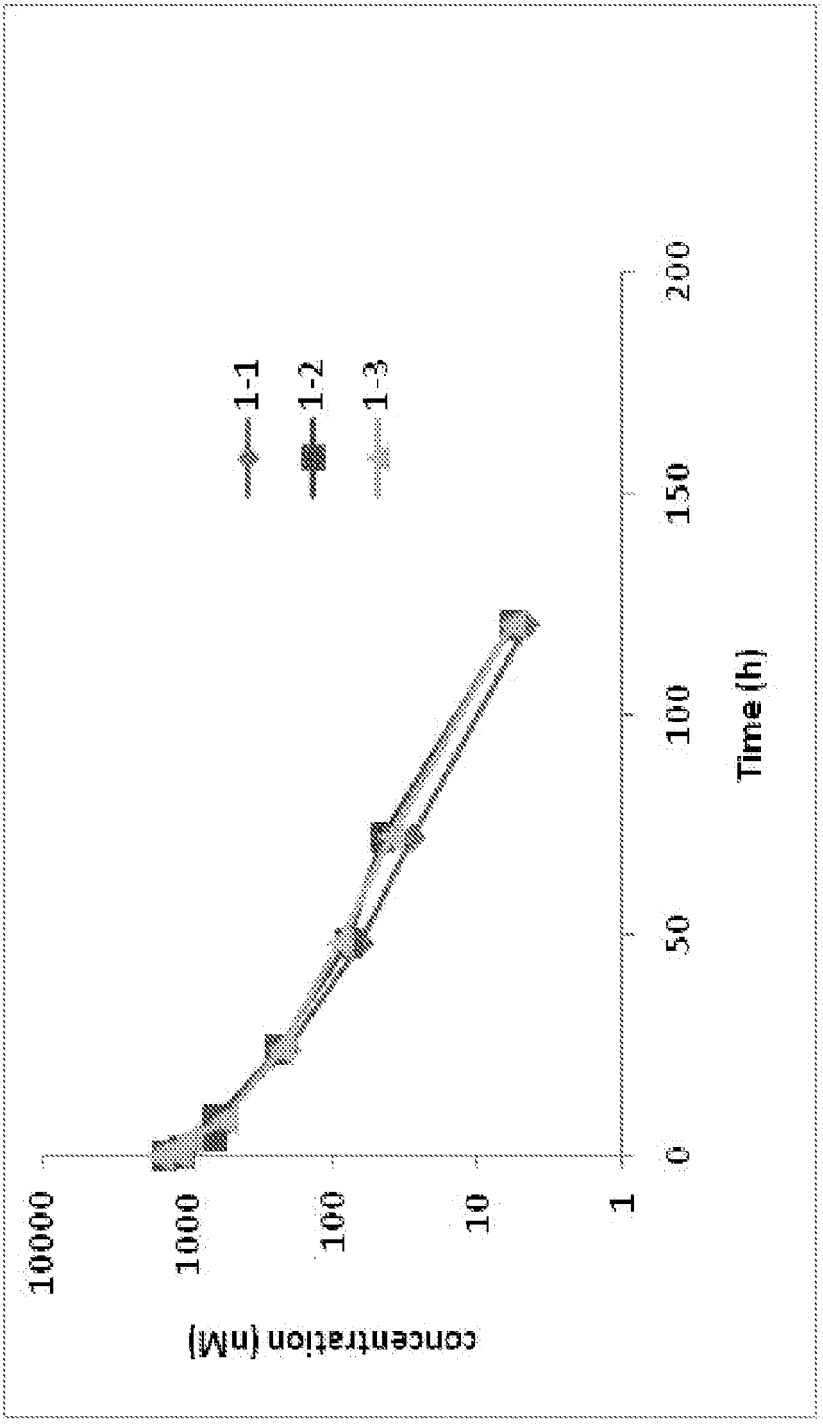

concentration (nM)
10000
1000
100
10
1
0
50
100
150
200
Time (h)
1-1
1-2
1-3

Figure 9

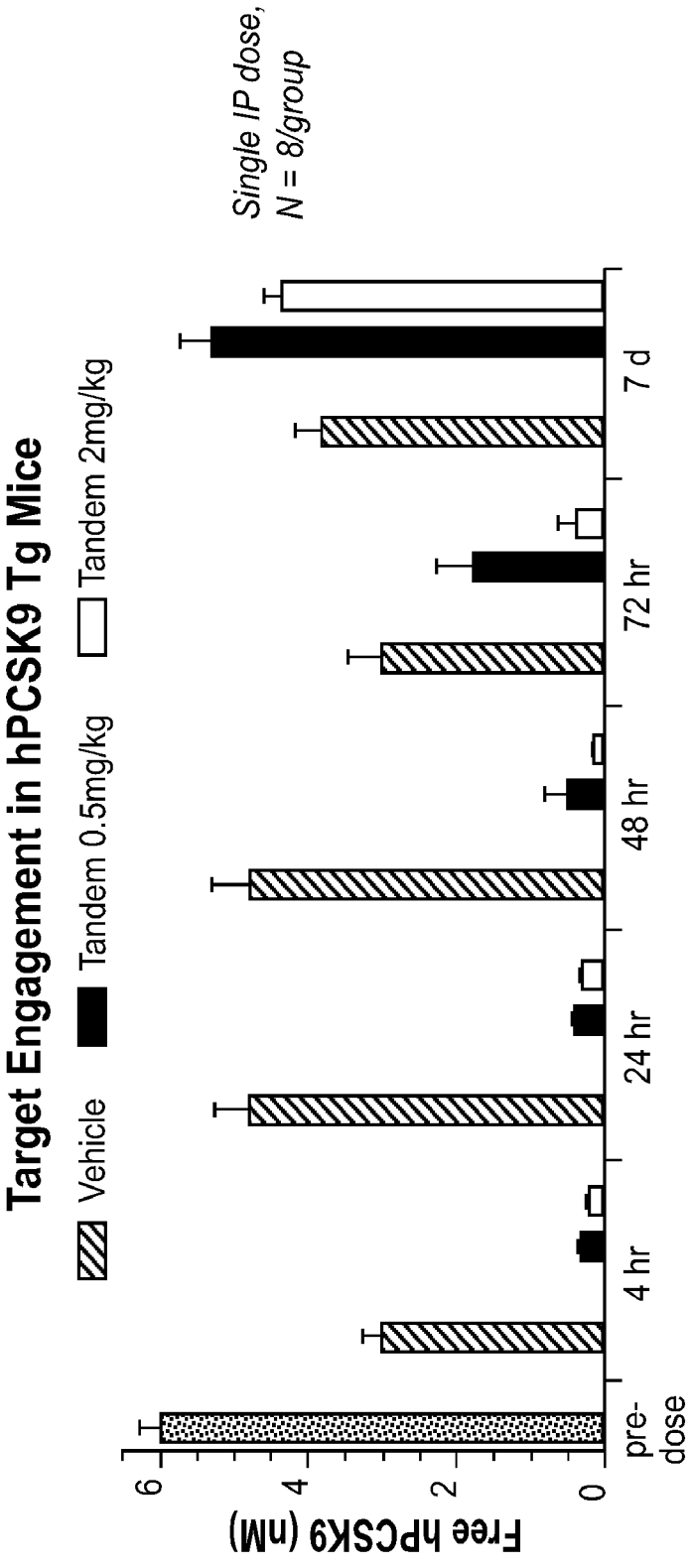

Target Engagement in hPCSK9 Tg Mice
Vehicle
Tandem 0.5mg/kg
Tandem 2mg/kg
Single IP dose,
N = 8/group
Free hPCSK9 (nM)
0
2
4
6
pre-dose
4 hr
24 hr
48 hr
72 hr
7 d

Figure 10

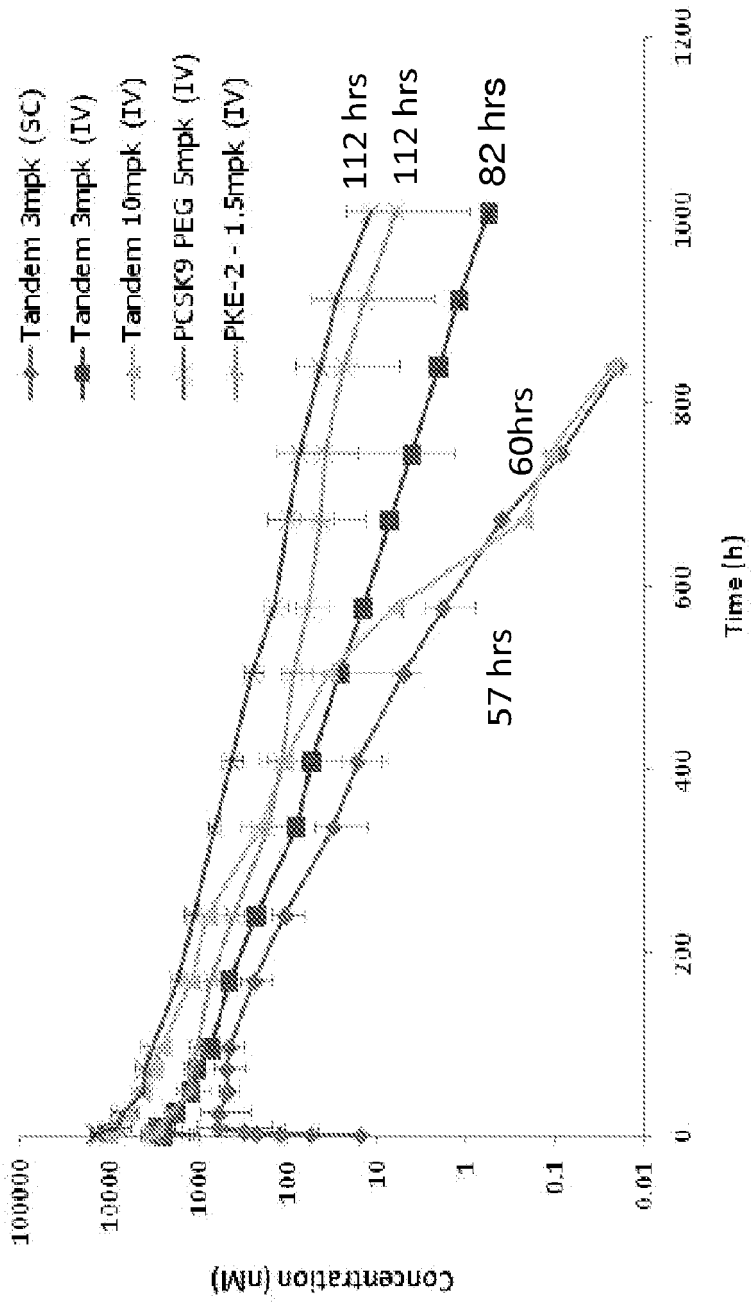

Tandem 3mpk (SC)
Tandem 3mpk (IV)
Tandem 10mpk (IV)
PCSK9 PEG 5mpk (IV)
PKE-2 - 1.5mpk (IV)
112 hrs
112 hrs
82 hrs
60hrs
57 hrs
Concentration (nM)
100000
10000
1000
100
10
1
0.1
0.01
0
200
400
600
800
1000
1200
Time (h)

Figure 11

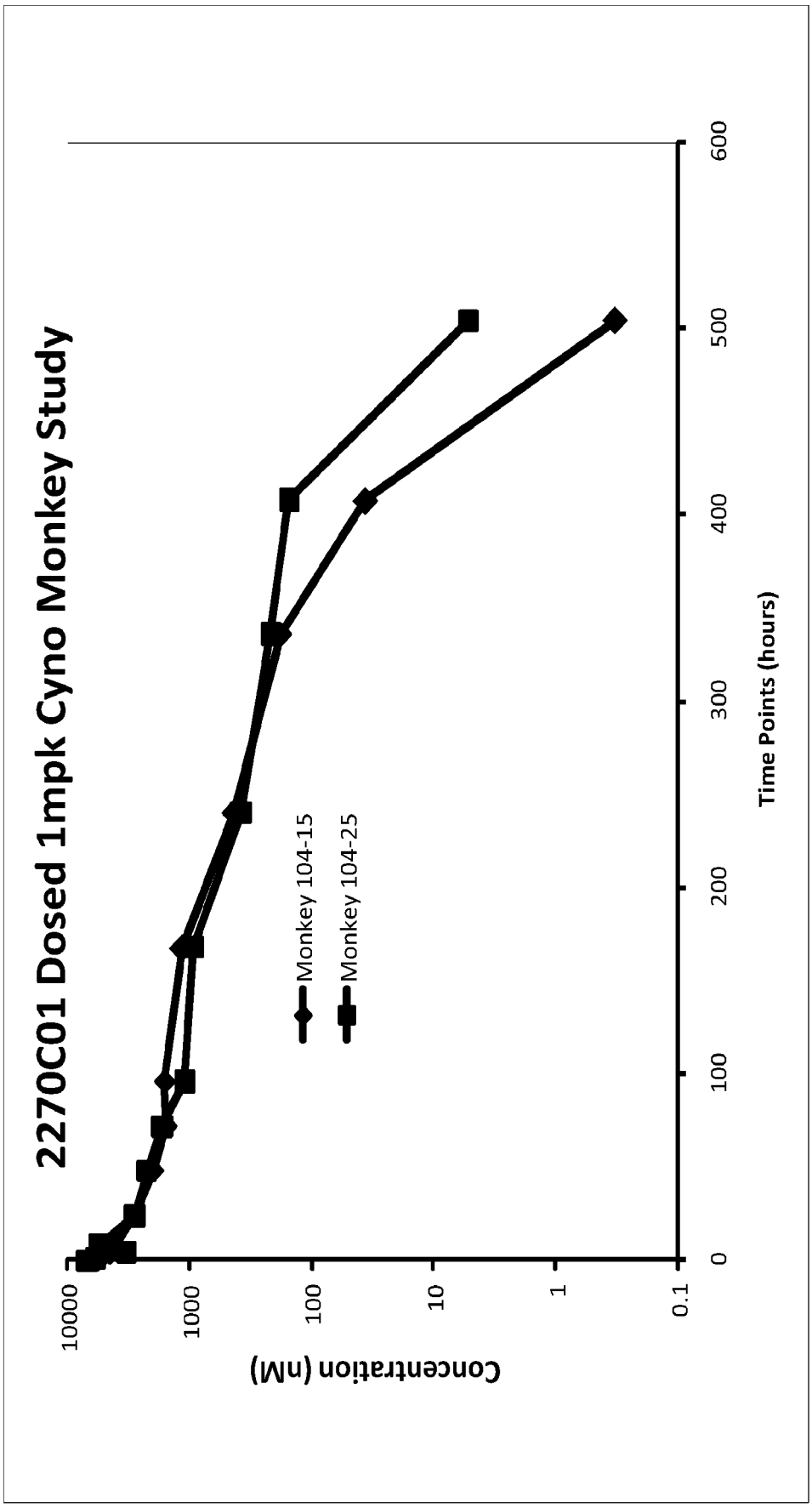

2270C01 Dosed 1mpk Cyno Monkey Study
Concentration (nM)
10000
1000
100
10
1
0.1
0
100
200
300
400
500
600
Time Points (hours)
Monkey 104-15
Monkey 104-25

Figure 12

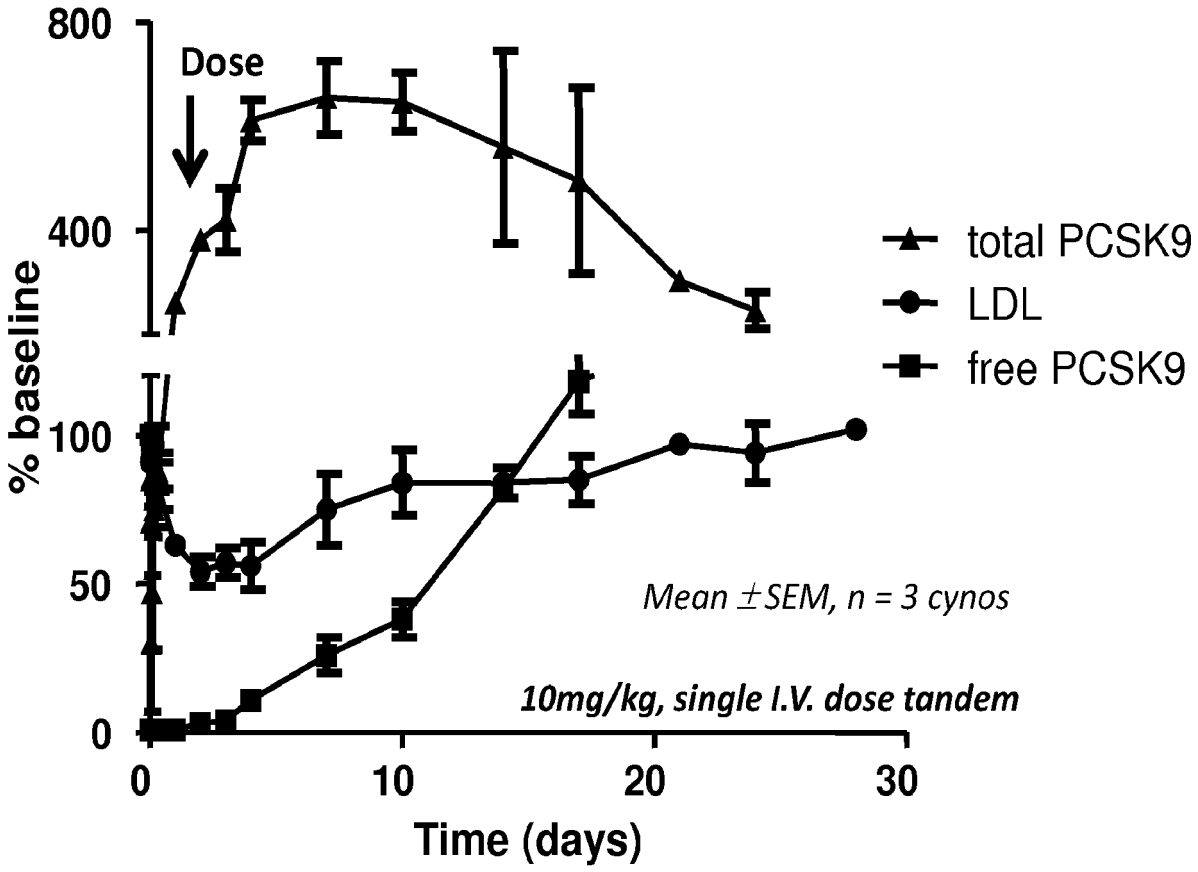

800
400
100
50
0
% baseline
Dose
total PCSK9
LDL
free PCSK9
Mean ±SEM, n = 3 cynos
10mg/kg, single I.V. dose tandem
0
10
20
30
Time (days)

Figure 13

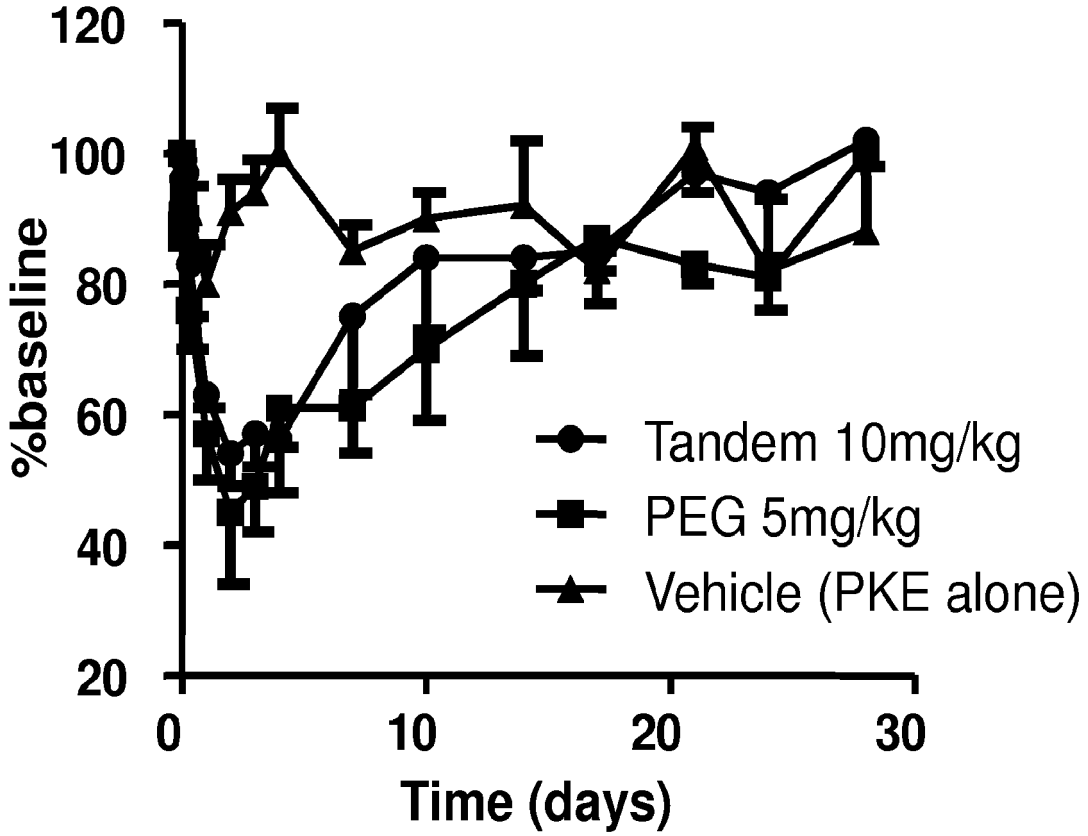

120
100
80
60
40
20
%baseline
0
10
20
30
Time (days)
Tandem 10mg/kg
PEG 5mg/kg
Vehicle (PKE alone)

Figure 14

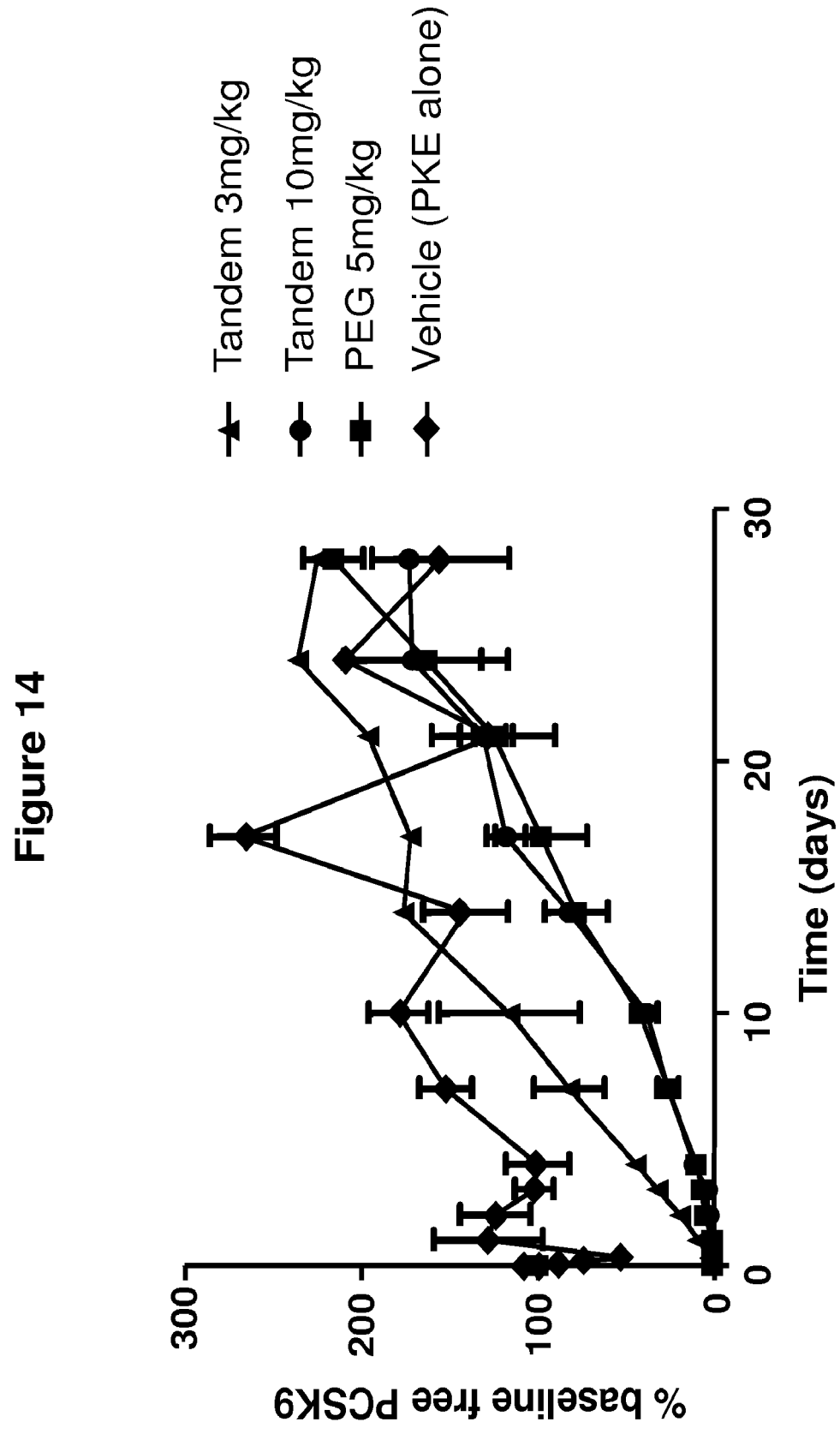

Tandem 3mg/kg
Tandem 10mg/kg
PEG 5mg/kg
Vehicle (PKE alone)
% baseline free PCSK9
300
200
100
0
0
10
20
30
Time (days)

Figure 15

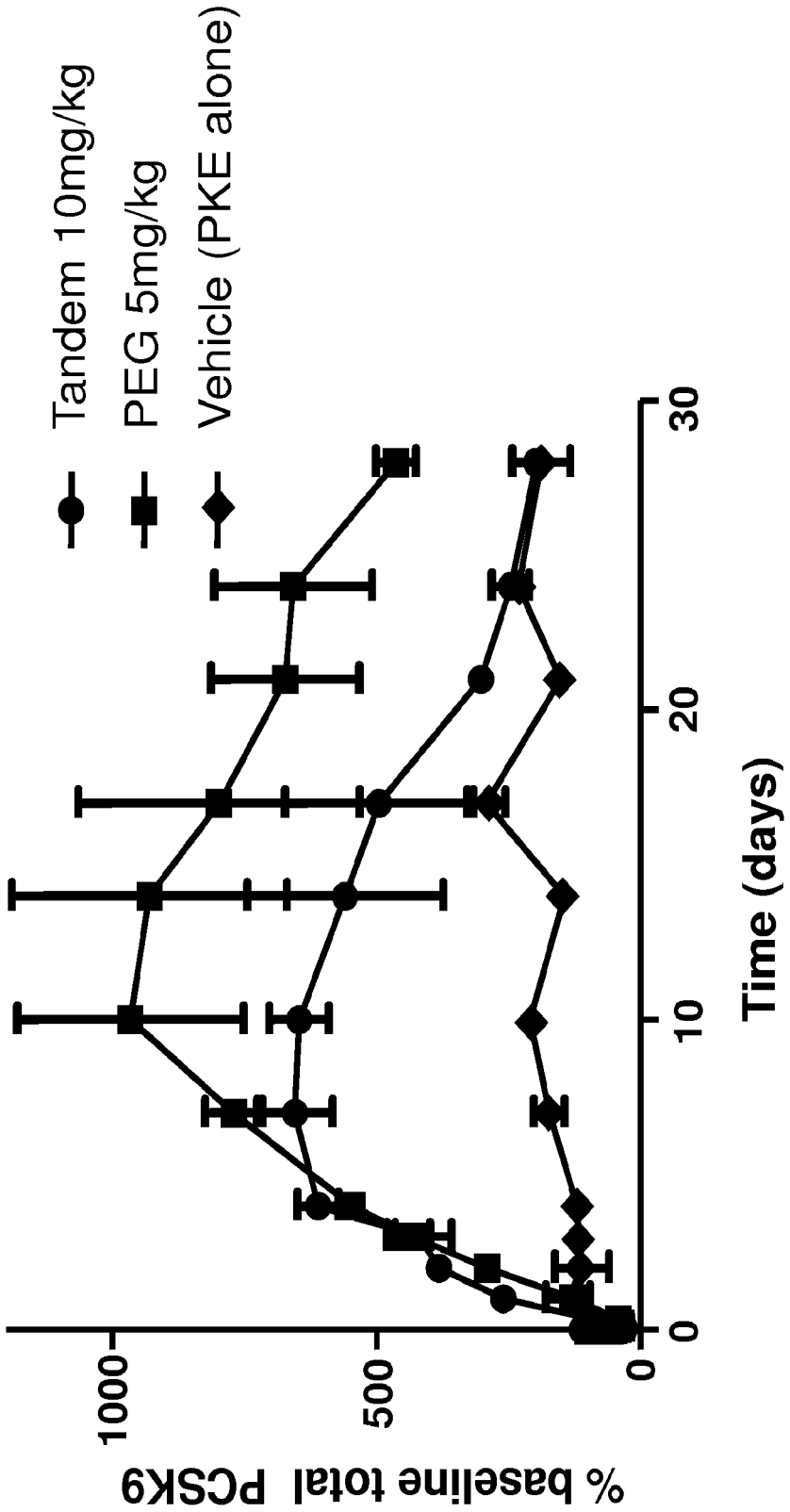

Tandem 10mg/kg
PEG 5mg/kg
Vehicle (PKE alone)
% baseline total PCSK9
1000
500
0
0
10
20
30
Time (days)

Figure 16

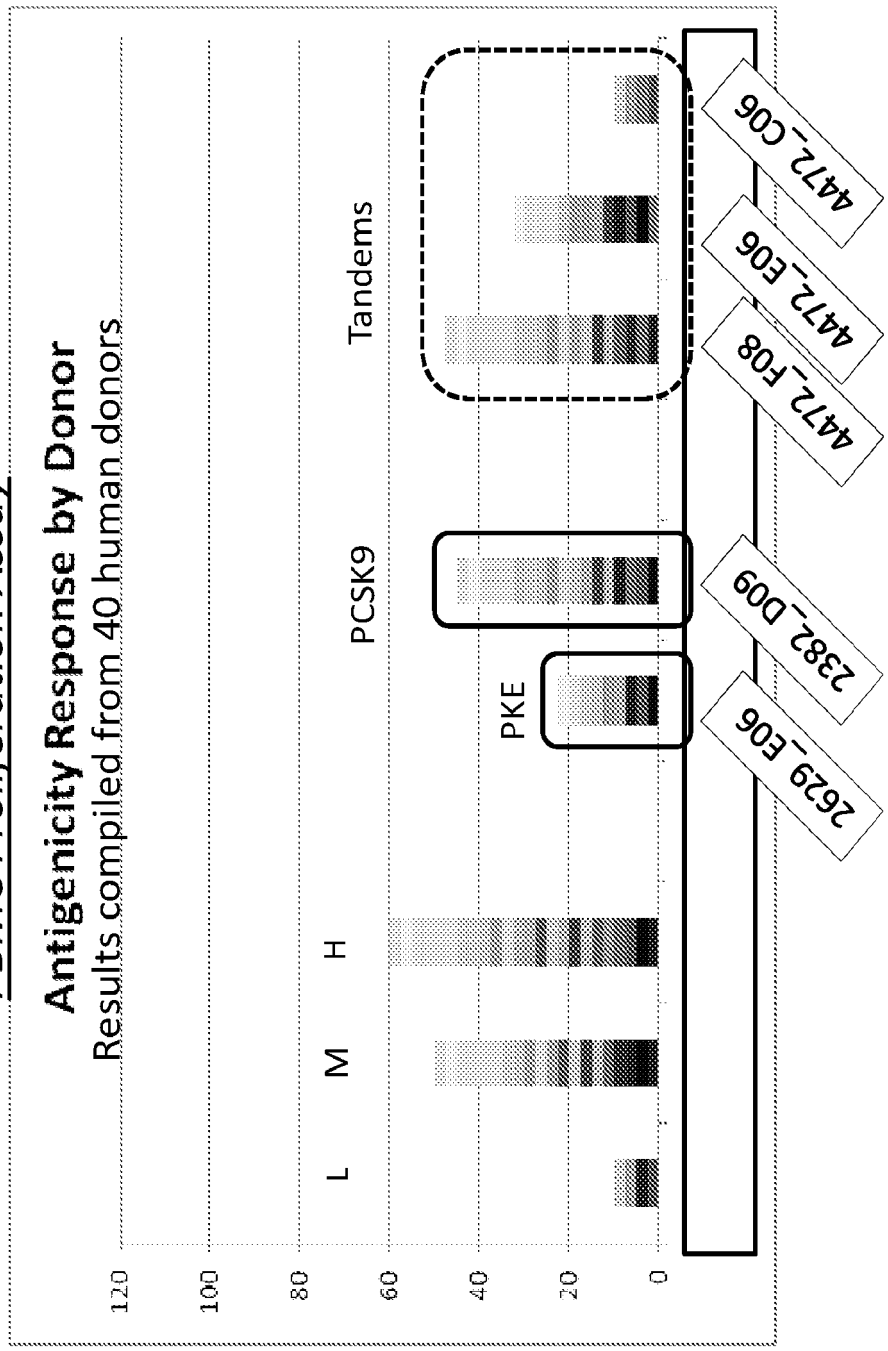

PBMC Proliferation Assay
Antigenicity Response by Donor
Results compiled from 40 human donors
120
100
80
60
40
20
0
L
M
H
PCSK9
PKE
Tandems
2629_E06
2382_D09
4472_F08
4472_E06
4472_C06

Figure 17

Adnectin	Full Protein Sequence
2270_C01	MASTSGVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGWQVQMYSDWGPLYIYKEFTVPGSKSTATISGLKPGVDYTITVYAVTGSGESPASSKPISINYRTEGDKPSQHHHHHH*
2629_A09	MGVSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGRHVQIYSDLGPLYIYTEFTVPGSKSTATISGLKPGVDYTITVYAVTGSGESPASSKPISINYRTEIDKPSQHHHHHH*
2629_A11	MGVSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGRHVHIYSDWGPMYIYTEFTVPGSKSTATISGLKPGVDYTITVYAVTGSGESPASSKPISINYRTEIDKPSQHHHHHH*
2629_C10	MGVSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGREVQKYSVLGPLYIYTEFTVPGSKSTATISGLKPGVDYTITVYAVTGSGESPASSKPISINYRTEIDKPSQHHHHHH*
2629_D09	MGVSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGREVQMYSDLGPLYVYSEFTVPGSKSTATISGLKPGVDYTITVYAVTGSGESPASSKPISINYRTEIDKPSQHHHHHH*
2629_E05	MGVSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGREVQKFSDWGPLYIYTEFTVPGSKSTATISGLKPGVDYTITVYAVTGSGESPASSKPISINYRTEIDKPSQHHHHHH*
2629_E06	MGVSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGREVQKYSDLGPLYIYQEFTVPGSKSTATISGLKPGVDYTITVYAVTGSGESPASSKPISINYRTEIDKPSQHHHHHH*
2629_F04	MGVSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGREVHQYSDWGPMYIYNEFTVPGSKSTATISGLKPGVDYTITVYAVTGSGESPASSKPISINYRTEIDKPSQHHHHHH*
2629_H01	MGVSDVPRDLEVVAATPTSLLISWDAPAVTVXYYRITYGREVHKNSDWGTLYIYTEFTVPGSKSTATISGLKPGVDYTITVXAVTGSGEXPASSKPISINYRTEIDKXSQHHHHHH*
2629_H06	MGVSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGREVQKYSDLGPLYIYAEFTVPGSKSTATISGLKPGVDYTITVYAVTGSGESPASSKPISINYRTEIDKPSQHHHHHH*
2629_H07	MGVSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGREVHLYSDWGPMYIYTEFTVPGSKSTATISGLKPGVDYTITVYAVTGSGESPASSKPISINYRTEIDKPSQHHHHHH*
2630_A02	MGVSDVPRDLEVVATTPTSLLISWDAPAVTVRYYRITYGRHVQMYSDLGPLYIFSEFTVPGSKSTATISGLKPGVDYTITVYAVTGSGESPASSKPISINYRTEIDKPSQHHHHHH*
2630_A11	MGVSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGREVHMYSDFGPMYIYTEFTVPGSKSTATISGLKPGVDYTITVYAVTGSGESPASSKPISINYRTEIDKPSQHHHHHH*
2630_D02	MGVSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGREVQKYSDWGPLYIYNEFTVPGSKSTATISGLKPGVDYTITVYAVTGSGESPASSKPISINYRTEIDKPSQHHHHHH*
2630_D10	MGVSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGREVQMYSDLGPLYIYNEFTVPGSKSTATISGLKPGVDYTITVYAVTGSGESPASSKPISINYRTEIDKPSQHHHHHH*
2630_F04	MGVSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGREVQMYSDLGPLYIYTEFTVPGSKSTATISGLKPGVGYTITVYAVTGSGESPASSKPISINYRTEIDKPSQHHHHHH*
2630_G03	MGVSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGRHVQIYSDLGPLYIYNEFTVPGSKSTATISGLKPGVDYTITVYAVTGSGESPASSKPISINYRTEIDKPSQHHHHHH*
2630_G10	MGVSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGREVQIYSDWGPLYIYNEFTVPGSKSTATISGLKPGVDYTITVYAVTGSGESPASSKPISINYRTEIDKPSQHHHHHH*
2630_H03	MGVSDVPRDLEVVAATXTSLLISWDAPAVTVXYYRITYGREVQKYSDWGPLYIYQEFTVPGSXSTATISGLKPGVDYTITVYAVTGSGESPASSKPISINYRTEIDKXSQHHHHHH*
2631_B04	MGVSDVPRDLEVVAATPTSLLISWDVPAVTVRYYRITYGRHVHLYSEFGPMYIYNEFTVPGSKSTATISGLKPGVDYTITVYAVTGSGESPASSKPISINYRTEIDKPSQHHHHHH*
2631_E03	MGVSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGRDVHMYSDWGPMYIYQEFTVPGSKSTATISGLKPGVDYTITVYAVTGSGESPASSKPISINYRTEIDKPSQHHHHHH*
2631_G01	MGVSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGRHVQIYSDWGPLYIYNEFTVPGSKSTATISGLKPGVDYTITVYAVTGSGESPASSKPISINYRTEIDKPSQHHHHHH*
2631_G03	MGVSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGRYVQLYSDWGPMYIYTEFTVPGSKSTATISGLKPGVDYTITVYAVTGSGESPASSKPISINYRTEIDKPSQHHHHHH*
2631_H09	MGVSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGRQVQVFSDLGPLYIYNEFTVPGSKSTATISGLKPGVDYTITVYAVTGSGESPASSKPISINYRTEIDKPSQHHHHHH*
2632_G01	MGVSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGRQVQIYSDWGPLYIYNEFTVPGSKSTATISGLKPGVDYTITVYAVTGSGESPASSKPISINYRTEIDKPSQHHHHHH*
4079_A04	MGVSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGRQVQMYSDWGPLYIYAEFTVPGSKSTATISGLKPGVDYTITVYAVTGSGESPASSKPISINYRTEIDKPSQHHHHHH*

SUBSTITUTE SHEET (RULE 26)

Figure 18A

2270_C01	ATGGCTAGCACTAGTGGCGTGCCGCGCGACTTGGAAGTGGTTGCCGCGACCCCGACGTCTCTGCTTATTAGCTGGGATGCACCTGCCGTCACAGTGAGATATTATCG CATTACATATGGTTGGCAGGTTCAGATGTACTCTGACTGGGGTCCGCTGTACATCTACAAAGAGTTCACGGTACCTGGGAGCAAGTCCACAGCTACCATCAGCGGTC TCAAACCTGGAGTTGATTACACCATTACGGTATACGCAGTCACCGGCTCTGGAGAGAGCCCCGCAAGCAGCAAGCCAATTTCCATTAATTATCGGACCGAAGGCGAC AAACCATCCCAGCACCATCACCACCACCACTGA
2629_A09	ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGATGCACCTGCCGTCACAGTGCGATATTACCGCAT CACTTACGGACGGCATGTTCAGATCTATTCTGACTTAGGCCCGCTGTACATCTACACAGAGTTCACTGTGCCTGGGAGCAAGTCCACAGCTACCATCAGCGGCCTTAA ACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGGCTCTGGAGAGAGCCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGCACAGAAATTGACAAACC ATCCCAGCACCATCACCACCACCACTGA
2629_A11	ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGATGCACCTGCCGTCACAGTGCGATATTACCGCAT CACTTACGGTAGACACGTTCATATCTACTCAGACTGGGGTCCGATGTACATCTACACAGAGTTCACTGTGCCTGGGAGCAAGTCCACAGCTACCATCAGCGGCCTTAA ACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGGCTCTGGAGAGAGCCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGCACAGAAATTGACAAACC ATCCCAGCACCATCACCACCACCACTGA
2629_C10	ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGATGCACCTGCCGTCACAGTGCGATATTACCGCAT CACTTACGGGAGAGAGGTTCAGAAATACTCTGTCTTGGGTCCACTGTACATATACACGGAGTTCACTGTGCCTGGGAGCAAGTCCACAGCTACCATCAGCGGCCTTA AACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGGCTCTGGAGAGAGCCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGCACAGAAATTGACAAAC CATCCCAGCACCATCACCACCACCACTGA
2629_D09	ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGATGCACCTGCCGTCACAGTGCGATATTACCGCAT CACTTACGGGAGAGGAGGTTCAGATGTACTCTGACTTGGGTCCATTGTACGTATACAGCGAGTTCACTGTGCCTGGGAGCAAGTCCACAGCTACCATCAGCGGCCTTA AACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGGCTCTGGAGAGAGCCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGCACAGAAATTGACAAAC CATCCCAGCACCATCACCACCACCACTGA
2629_E05	ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGATGCACCTGCCGTCACAGTGCGATATTACCGCAT CACTTACGGTCGGGAGGTACAGAAGTTCTCGGACTGGGGTCCGCTGTACATCTACACAGAGTTCACTGTGCCTGGGAGCAAGTCCACAGCTACCATCAGCGGCCTTA AACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGGCTCTGGAGAGAGCCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGCACAGAAATTGACAAAC CATCCCAGCACCATCACCACCACCACTGA
2629_E06	ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGATGCACCTGCCGTCACAGTGCGATATTACCGCAT CACTTACGGCAGGGAGGTTCAGAAGTACTCGGACTTGGGTCCGTTGTACATCTACCAAGAGTTCACTGTGCCTGGGAGCAAGTCCACAGCTACCATCAGCGGCCTTA AACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGGCTCTGGAGAGAGCCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGCACAGAAATTGACAAAC CATCCCAGCACCATCACCACCACCACTGA
2629_F04	ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGATGCACCTGCCGTCACAGTGCGATATTACCGCAT CACTTACGGTAGGGAGGTTCATCAATACTCTGACTGGGGTCCGATGTACATCTACAACGAGTTCACTGTGCCTGGGAGCAAGTCCACAGCTACCATCAGCGGCCTTA AACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGGCTCTGGAGAGAGCCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGCACAGAAATTGACAAAC CATCCCAGCACCATCACCACCACCACTGA
2629_H01	ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGATGCACCTGCCGTCACAGTGCRATATTACCGCAT CACTTACGGTCGGGAGGTTCATAAGAACTCAGACTGGGGTACGCTGTACATCTACACAGAGTTCACTGTGCCTGGGAGCAAGTCCACAGCTACCATCAGCGGCCTTA AACCTGGCGTTGATTATACCATCACTGTGTRTGCTGTCACTGGCTCTGGAGAGARCCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGCACAGAAATTGACAAA MCATCCCAGCACCATCACCACCACCACTGA
2629_H06	ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGATGCACCTGCCGTCACAGTGCGATATTACCGCAT CACTTACGGACGGGAGGTTCAGAAGTATTCAGACTTGGGTCCACTGTACATCTACGCAGAGTTCACTGTGCCTGGGAGCAAGTCCACAGCTACCATCAGCGGCCTTA AACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGGCTCTGGAGAGAGCCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGCACAGAAATTGACAAAC CATCCCAGCACCATCACCACCACCACTGA

Figure 18B

2629_H07	ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGATGCACCTGCCGTCACAGTG CGATATTACCGCATCACTTACGGGCGGGAGGTCCACCTGTACTCCGACTGGGGGCCGATGTACATCTACACAGAGTTCACTGTGCCTGGGAGC AAGTCCACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGGCTCTGGAGAGGCCCCGCAAGCA GCAAGCCAATTTCCATTAATTACCGCACACAGAAATTGACAAACCATCCCAGCACCATCACCACTGA
2630_A02	ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTACCACCCCCACCAGCCTGCTGATCAGCTGGGATGCACCTGCCGTCACAGTG CGATATTACCGCATCACTTACGGTAGGCACGTTCAAATGTACTCTGACCTTGGTCCGTTGTACATCTTCAGTGAGTTCACTGTGCCTGGGAGCA AGTCCACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGGCTCTGGAGAGGCCCCGCAAGCAG CAAGCCAATTTCCATTAATTACCGCACACAGAAATTGACAAACCATCCCAGCACCATCACCACCACTGA
2630_A11	ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGATGCACCTGCCGTCACAGTG CGATATTACCGCATCACTTACGGACGGGAGGTTCATATGTACTCTGACTTCGGTCCGATGTACATATACACAGAGTTCACTGTGCCTGGGAGCA AGTCCACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGGCTCTGGAGAGGCCCCGCAAGCAG CAAGCCAATTTCCATTAATTACCGCACACAGAAATTGACAAACCATCCCAGCACCATCACCACCACTGA
2630_D02	ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGATGCACCTGCCGTCACAGTG CGATATTACCGCATCACTTACGGTAGAGAAGTTCAGAAATACTCTGACTGGGGCCCCGCTCTACATCTACAATGAGTTCACTGTGCCTGGGAGCA AGTCCACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGGCTCTGGAGAGGCCCCGCAAGCAG CAAGCCAATTTCCATTAATTACCGCACACAGAAATTGACAAACCATCCCAGCACCATCACCACCACTGA
2630_D10	ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGATGCACCTGCCGTCACAGTG CGATATTACCGCATCACTTACGGTCGGGAGGTTCAGATGTACTCGGACTTGGGTCCGCTCTACATCTACAACGAGTTCACTGTGCCTGGGAGCA AGTCCACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGGCTCTGGAGAGGCCCCGCAAGCAG CAAGCCAATTTCCATTAATTACCGCACACAGAAATTGACAAACCATCCCAGCACCATCACCACCACTGA
2630_F04	ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGATGCACCTGCCGTCACAGTG CGATATTACCGCATCACTTACGGTAGAGAGGTCCAGATGTACTCAGACTTGGGGCCGCTGTACATCTATACAGAGTTCACTGTGCCTGGGAGC AAGTCCACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGGTTATACCATCACTGTGTATGCTGTCACTGGCTCTGGAGAGAGCCCCGCAAGCA GCAAGCCAATTTCCATTAATTACCGCACACAGAAATTGACAAACCATCCCAGCACCATCACCACCACTGA
2630_G03	ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGATGCACCTGCCGTCACAGTG CGATATTACCGCATCACTTACGGACGGCATGTTCAGATCTACTCCGACTTGGGTCCTCTGTATATCTACAATGAGTTCACTGTGCCTGGGAGCA AGTCCACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGGCTCTGGAGAGAGCCCCGCAAGCAG CAAGCCAATTTCCATTAATTACCGCACACAGAAATTGACAAACCATCCCAGCACCATCACCACCACTGA
2630_G10	ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGATGCACCTGCCGTCACAGTG CGATATTACCGCATCACTTACGGTCGGGAGGTTCAAATATACTCTGACTGGGGTCCGCTGTATATATACAACGAGTTCACTGTGCCTGGGAGCA AGTCCACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGGCTCTGGAGAGAGCCCCGCAAGCAG CAAGCCAATTTCCATTAATTACCGCACACAGAAATTGACAAACCATCCCAGCACCATCACCACCACTGA
2630_H03	ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCSCCACCAGCCTGCTGATCAGCTGGGATGCACCTGCCGTCACAGTG CSATATTACCGCATCACTTACGGACGTGAAGTRCAGAAATACTCTGACTGGGGCCCGCTGTACATCTACCAAGAGTTCACTGTGCCTGGGAGCR AGTCCACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGGCTCTGGAGAGAGCCCCGCAAGCAG CAAGCCAATTTCCATTAATTACCGCACACAGAAATTGACAAAMCATCCCAGCACCATCACCACCACTGA
2631_B04	ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGATGTACCTGCCGTTACAGTG CGATATTACCGCATCACTTACGGCAGGCACGTACATTTGTACTCGGAGTTCGGTCCGATGTATATCTACAACGAGTTCACTGTGCCTGGGAGCA AGTCCACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGGCTCTGGAGAGAGCCCCGCAAGCAG CAAGCCAATTTCCATTAATTACCGCACACAGAAATTGACAAACCATCCCAGCACCATCACCACCACCACTGA

Figure 18C

2631_E03	ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGATGCACCTGCCGTCACAGTGCGAT ATTACCGCATCACTTACGGTAGGGATGTCCACATGTACTCTGACTGGGGTCCGATGTACATATACCAAGAGTTCACTGTGCCTGGGAGCAAGTCCAC AGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGGCTCTGGAGAGAGCCCCGCAAGCAGCAAGCCAATTT CCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACTGA
2631_G01	ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGATGCACCTGCCGTCACAGTGCGAT ATTACCGCATCACTTACGGTAGGCATGTTCAGATATACTCGGACTGGGGTCCGCTGTACATCTACAATGAGTTCACTGTGCCTGGGAGCAAGTCCACA GCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGGCTCTGGAGAGAGCCCCGCAAGCAGCAAGCCAATTTC CATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACTGA
2631_G03	ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTACTGATCAGCTGGGATGCACCTGCCGTCACAGTGCGAT ATTACCGCATCACTTACGGAAGGTATGTTCAGCTATACTCTGACTGGGGTCCGATGTACATCTACACGGAGTTCACTGTGCCTGGGAGCAAGTCCACA GCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGGCTCTGGAGAGAGCCCCGCAAGCAGCAAGCCAATTTC CATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACTGA
2631_H09	ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGATGCACCTGCCGTCACAGTGCGAT ATTACCGCATCACTTACGGACGGCAAGTGTTCTCAGACTTGGGTCCGCTGTACATATACAACGAGTTCACTGTGCCTGGGAGCAAGTCCAC AGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGGCTCTGGAGAGAGCCCCGCAAGCAGCAAGCCAATTT CCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACTGA
2632_G01	ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGATGCACCTGCCGTCACAGTGCGAT ATTACCGCATCACTTACGGTAGACAGGTGCAGATCTACTCTGACTGGGGACCGCTGTACATCTACAATGAGTTCACTGTGCCTGGGAGCAAGTCCAC AGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGGCTCTGGAGAGAGCCCCGCAAGCAGCAAGCCAATTT CCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACTGA
3852_F10	ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGACGCTCCGGCTGTTGACGGTCGAT ATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTTCTAAATCTACAGCTACCATCAGCGGCCTTAAA CCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTCCGTACGAATTCCATTTCCCGTACACTCATTACTCTTCTAAACCAATTTCCATTAATTACC GCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACCACTGA
4079_A04	ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGATGCACCTGCCGTCACAGTGCGAT ATTACCGCATCACTTACGGTAGGCAGGTACAGATGTACTCTGACTGGGGTCCACTTTACATCTACGCCGAGTTCACTGTGCCTGGGAGCAAGTCCACA GCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGGCTCTGGAGAGAGCCCCGCAAGCAGCAAGCCAATTTC CATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACCACTGA
5190_E01	ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGACGCTCCGGCTGAAGGGTACGGT TATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGTTTCTAAAGGTACAGCTACCATCAGCGGCCTTAA ACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCGAATTCGACTTCCCCGGCGCCGGTTACTACCATCGTCCAATTTCCATTAATTACCGGACCGA ACCGAGCACACCTCCGACCCCGAGTCCGTCAACACCACCGACACCGTCACCGAGCGGAGTTTCTGACGTCCCGCGCGACCTGGAAGTGGTTGCTGCC ACCCCCACCAGCCTGCTGATCAGCTGGGATGCACCTGCCGTCACAGTGCGATATTACCGCATCACTTACGGCAGGGAGGTTCAGAAGTACTCGGACT TGGGTCCGTTGTACATCTACCAAGAGTTCACTGTGCCTGGGAGCAAGTCCACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACT GTGTATGCTGTCACTGGCTCTGGAGAGAGCCCCGCAAGCAGCAAGCCAATTTCCATTAATTACCGCACACCGTGA