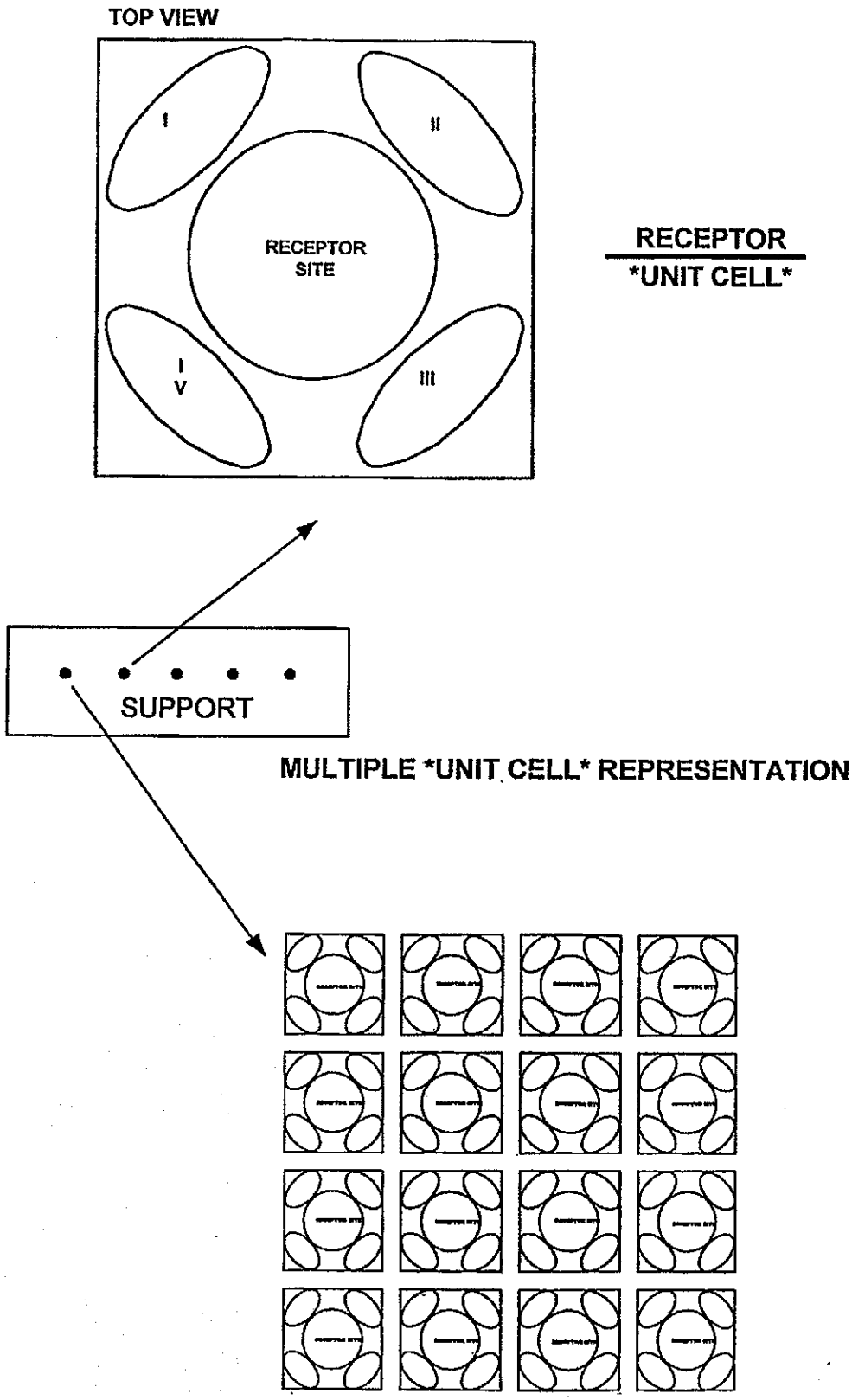
FIG.1


TOP VIEW
I
II
RECEPTOR SITE
IV
III
RECEPTOR
UNIT CELL
SUPPORT
MULTIPLE *UNIT CELL* REPRESENTATION

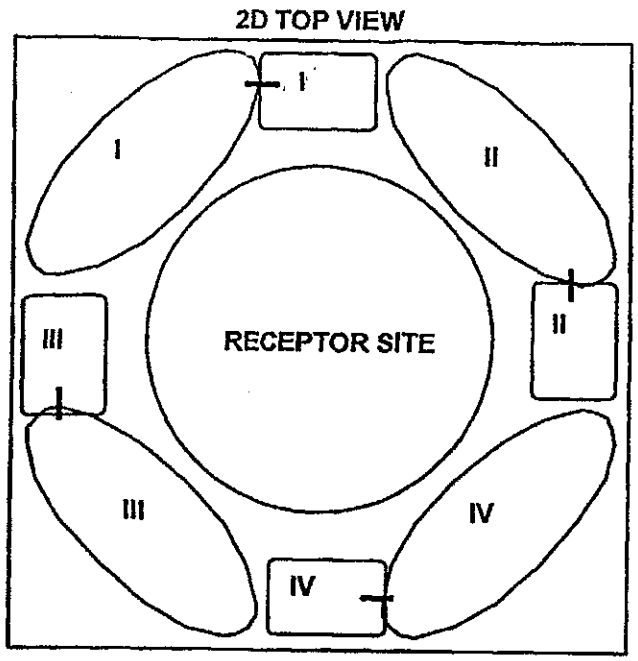
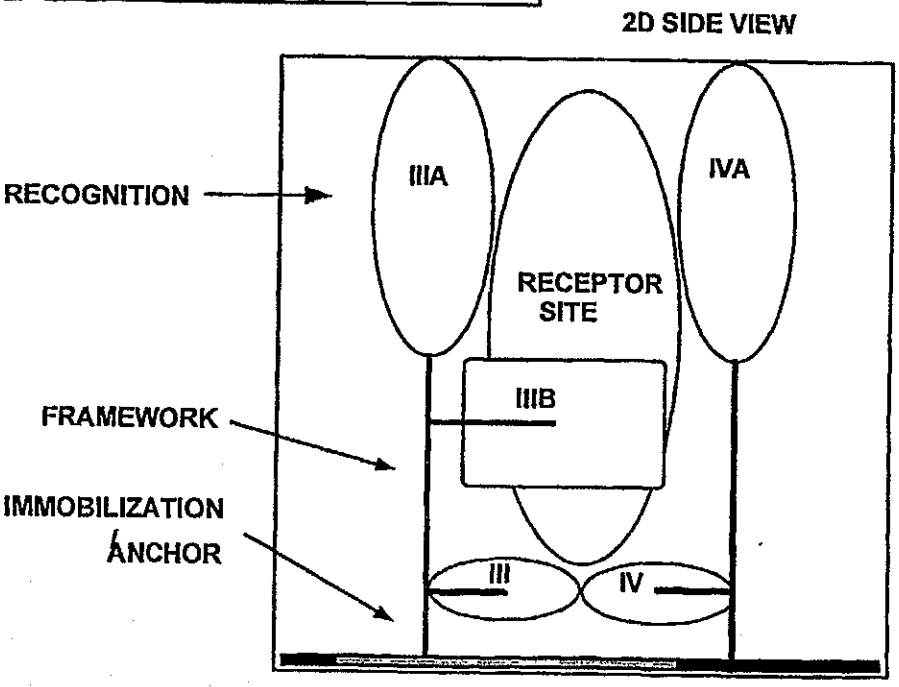

2D TOP VIEW
I
I
II
II
III
RECEPTOR SITE
III
IV
IV

FIG.2


2D SIDE VIEW
RECOGNITION
IIIA
IVA
RECEPTOR SITE
FRAMEWORK
IIIB
IMMOBILIZATION ANCHOR
III
IV

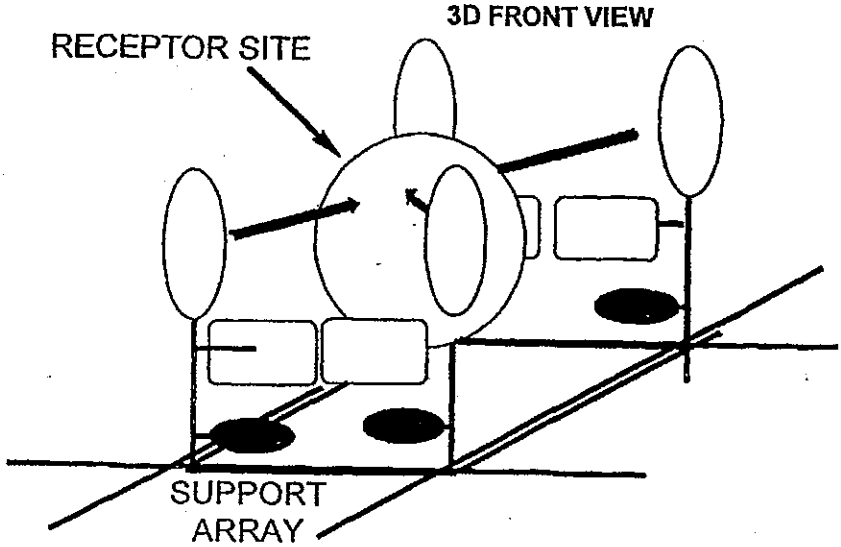
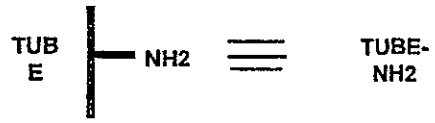
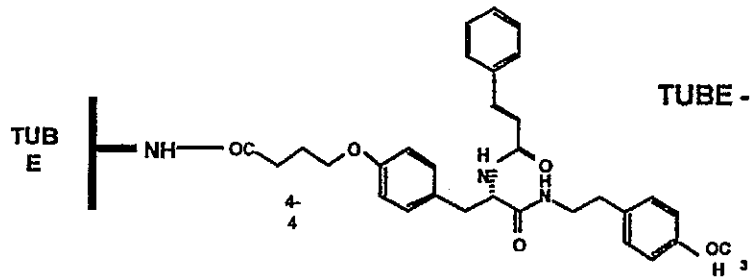
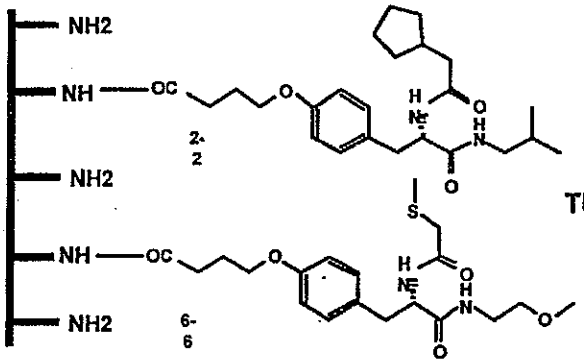

3D FRONT VIEW
RECEPTOR SITE
SUPPORT ARRAY

FIG.3A





TUBE - TyrA4B4



TUBE - TyrA2B2 plus TyrA6B6

FIG.3B

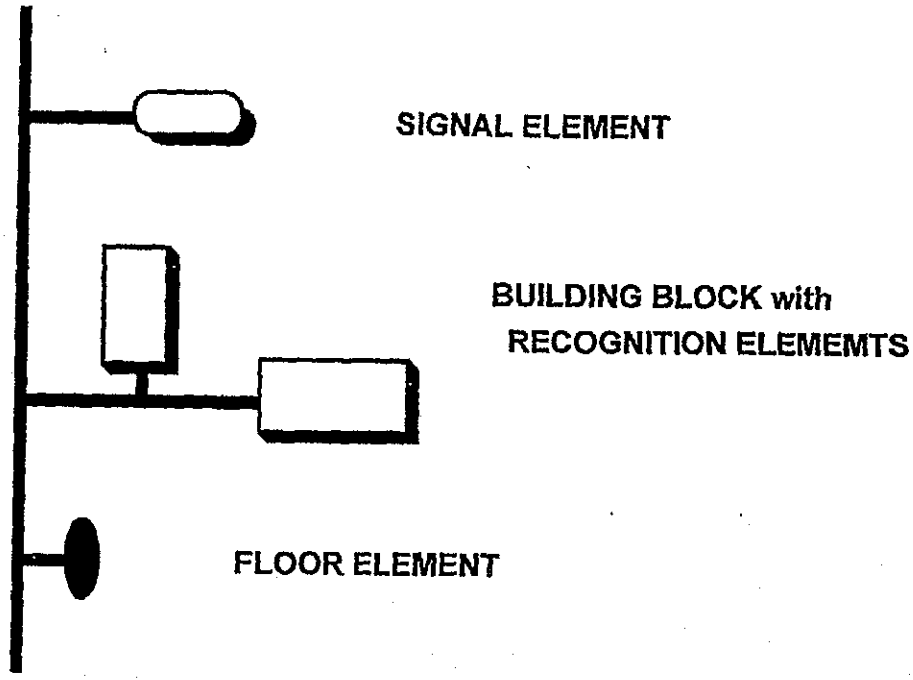

SIGNAL ELEMENT
BUILDING BLOCK with
RECOGNITION ELEMEMTS
FLOOR ELEMENT

FIG.4

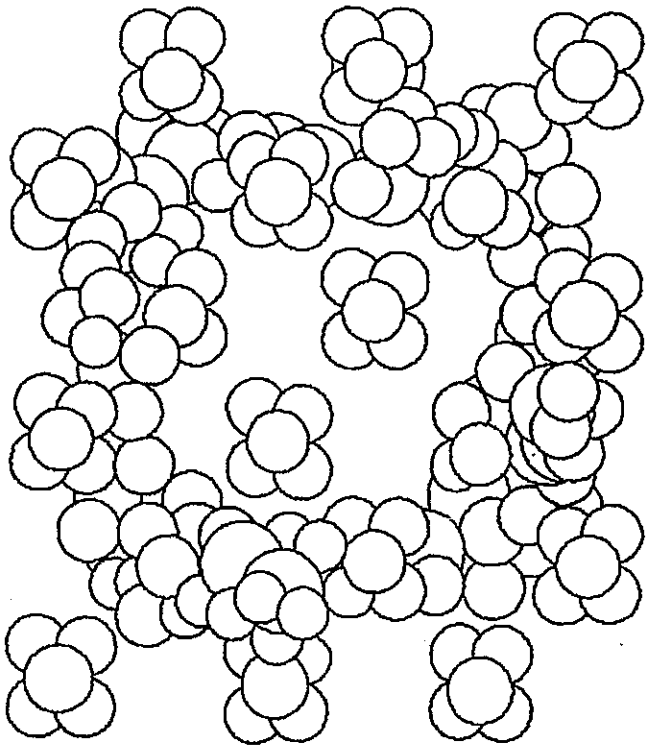


FIG.5

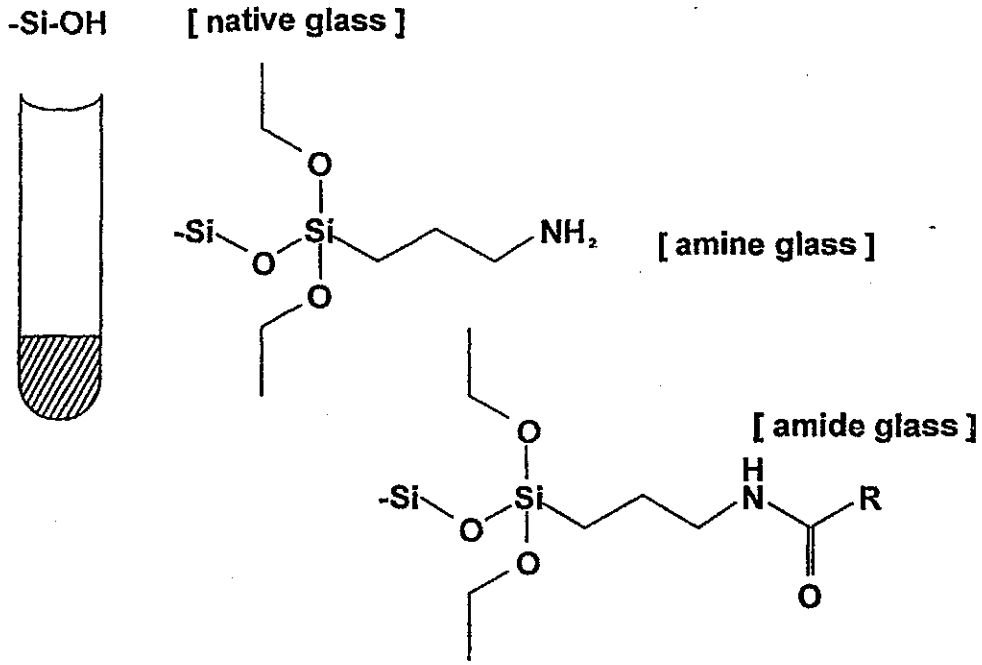

-Si-OH
[native glass]
-Si
O
Si
O
O
NH2
[amine glass]
[amide glass]
-Si
O
Si
O
O
H
N
R
O

FIG.6

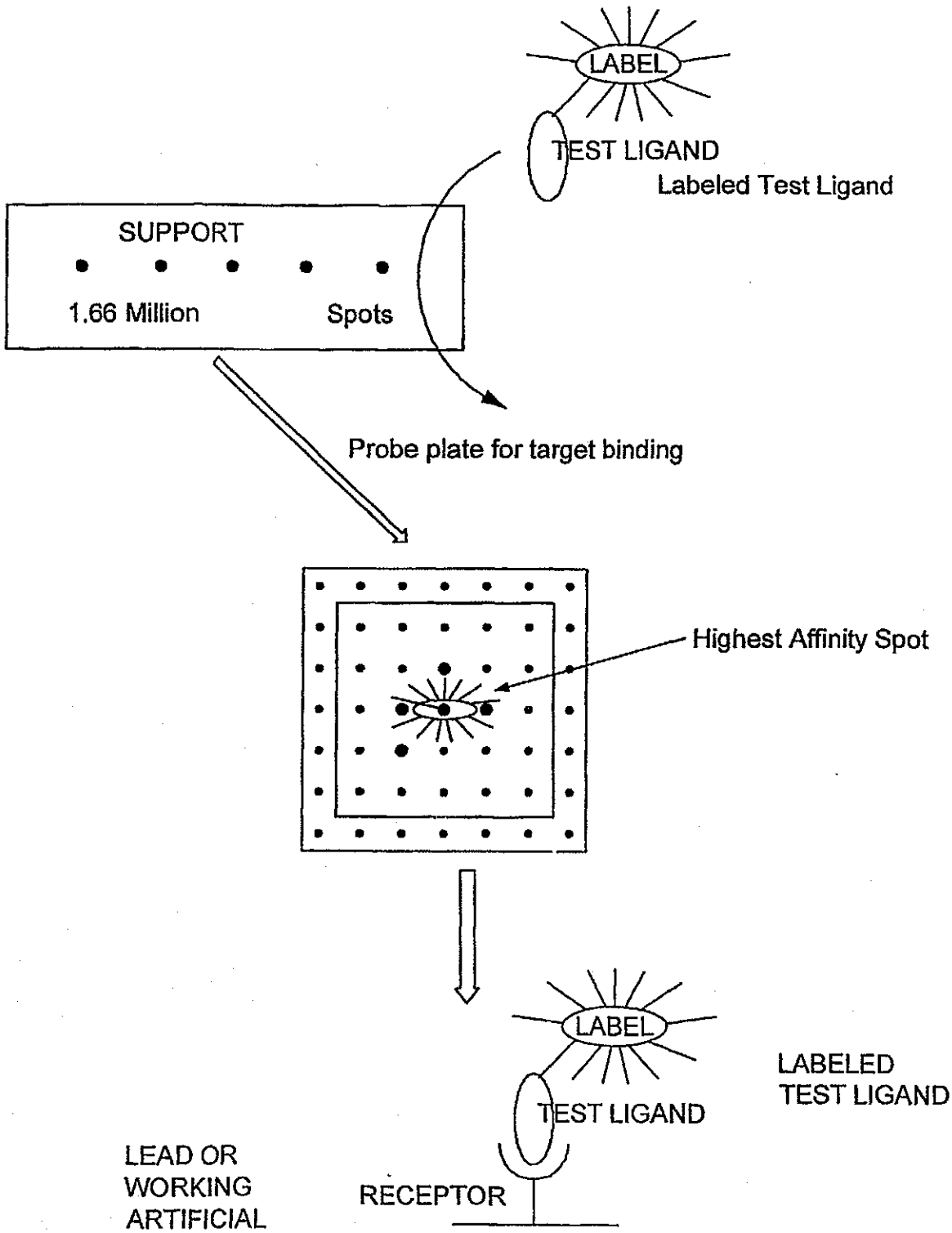

LABEL
TEST LIGAND
Labeled Test Ligand
SUPPORT
1.66 Million
Spots
Probe plate for target binding
Highest Affinity Spot
LABEL
TEST LIGAND
LABELED
TEST LIGAND
LEAD OR
WORKING
ARTIFICIAL
RECEPTOR

FIG.7

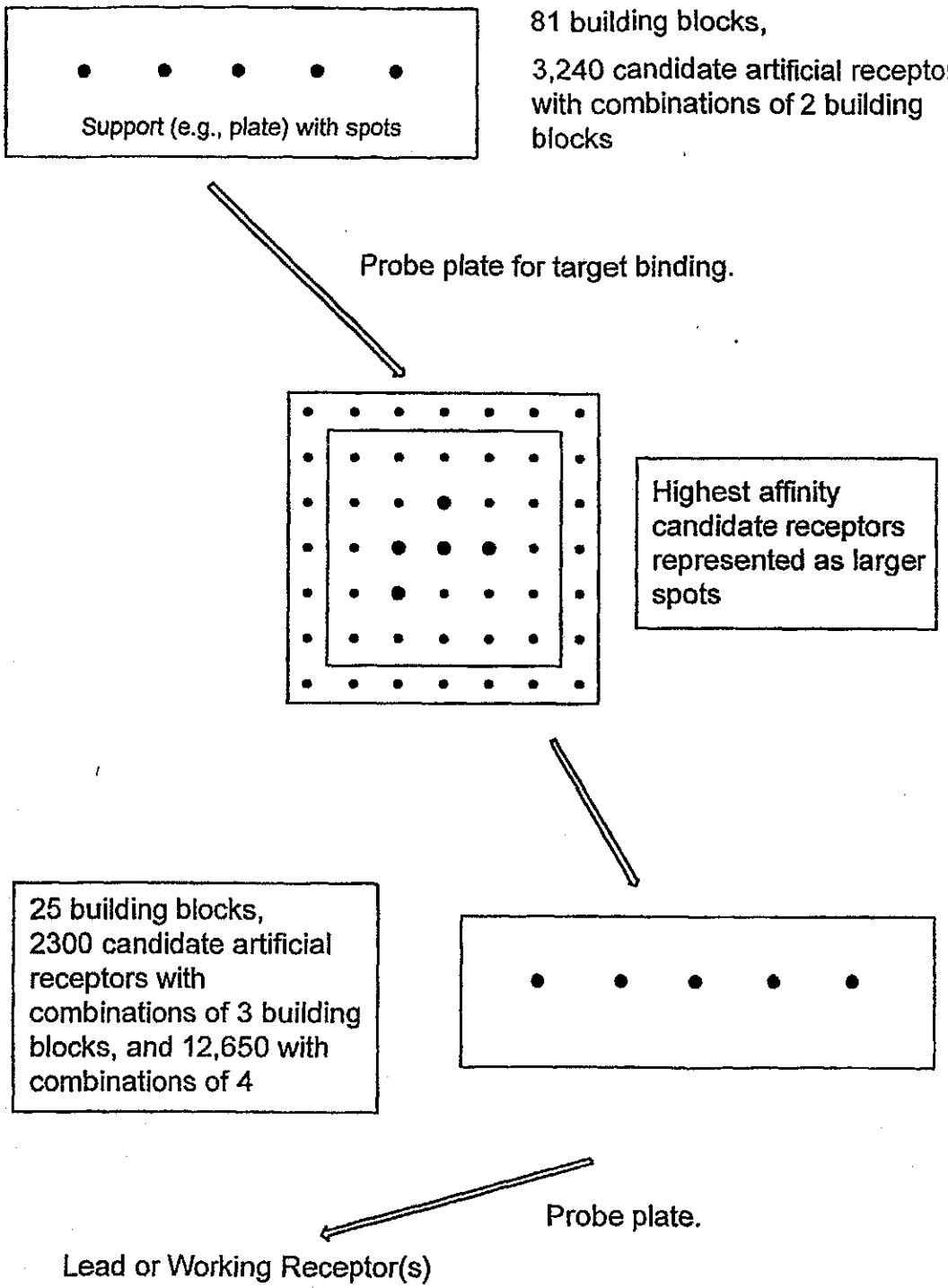
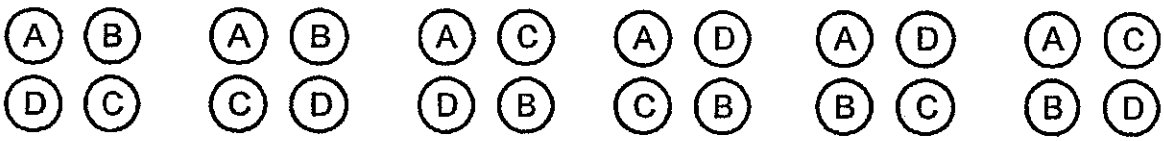
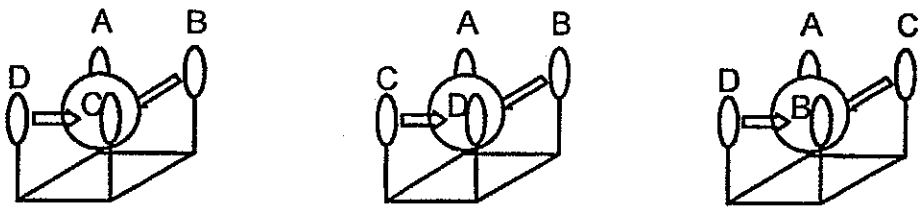

Support (e.g., plate) with spots
81 building blocks,
3,240 candidate artificial receptors with combinations of 2 building blocks
Probe plate for target binding.
Highest affinity candidate receptors represented as larger spots
25 building blocks, 2300 candidate artificial receptors with combinations of 3 building blocks, and 12,650 with combinations of 4
Probe plate.
Lead or Working Receptor(s)

FIG.8

6 POSITIONAL ISOMERS OF 4 BUILDING BLOCKS AT VERTICES OF A QUADRILATERAL



POSITIONAL ISOMERS ON A SCAFFOLD



ISOMER "1" ISOMER "2" ISOMER "3"

FIG.9

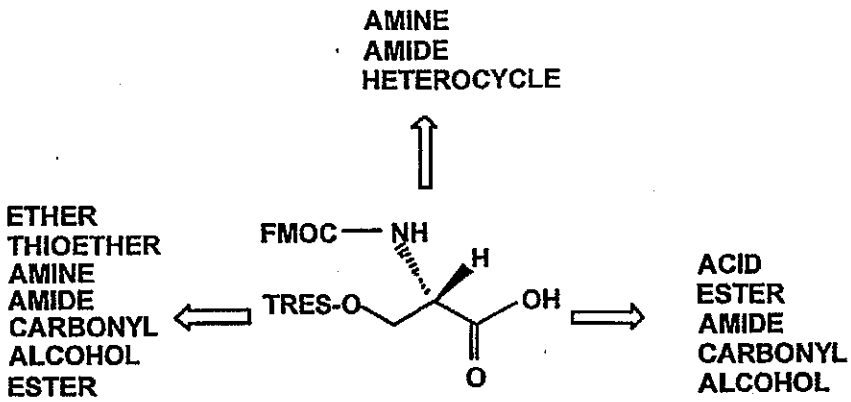

AMINE
AMIDE
HETEROCYCLE
ETHER
THIOETHER
AMINE
AMIDE
CARBONYL
ALCOHOL
ESTER
FMOC
NH
H
TRES-O
OH
O
ACID
ESTER
AMIDE
CARBONYL
ALCOHOL

FIG.10

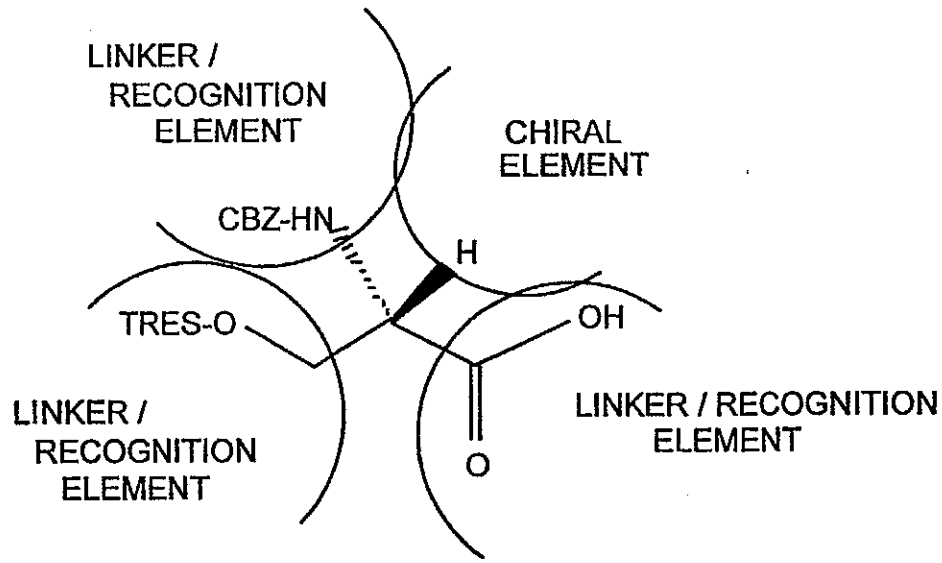
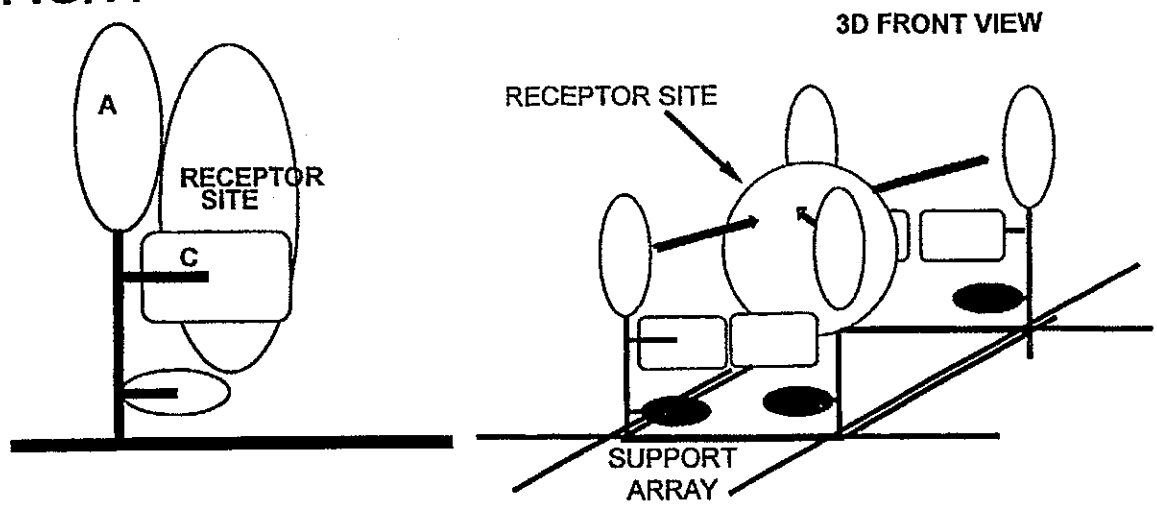
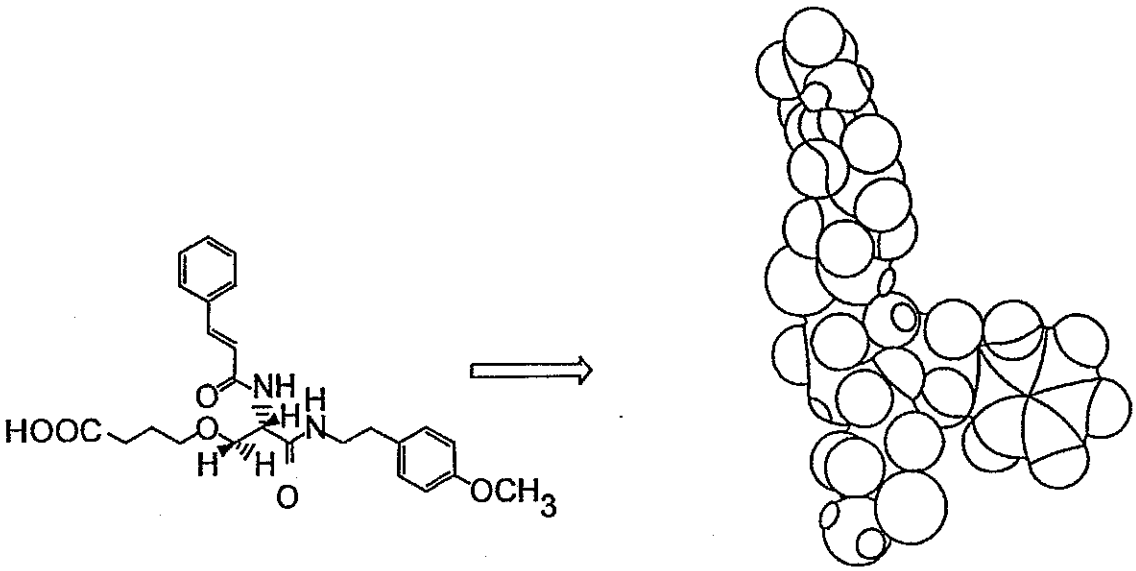

LINKER / RECOGNITION ELEMENT
CHIRAL ELEMENT
CBZ-HN
H
TRES-O
OH
LINKER / RECOGNITION ELEMENT
LINKER / RECOGNITION ELEMENT
O

FIG.11


A
RECEPTOR SITE
C
3D FRONT VIEW
RECEPTOR SITE
SUPPORT ARRAY


HOOC
NH
H
N
O
OCH3

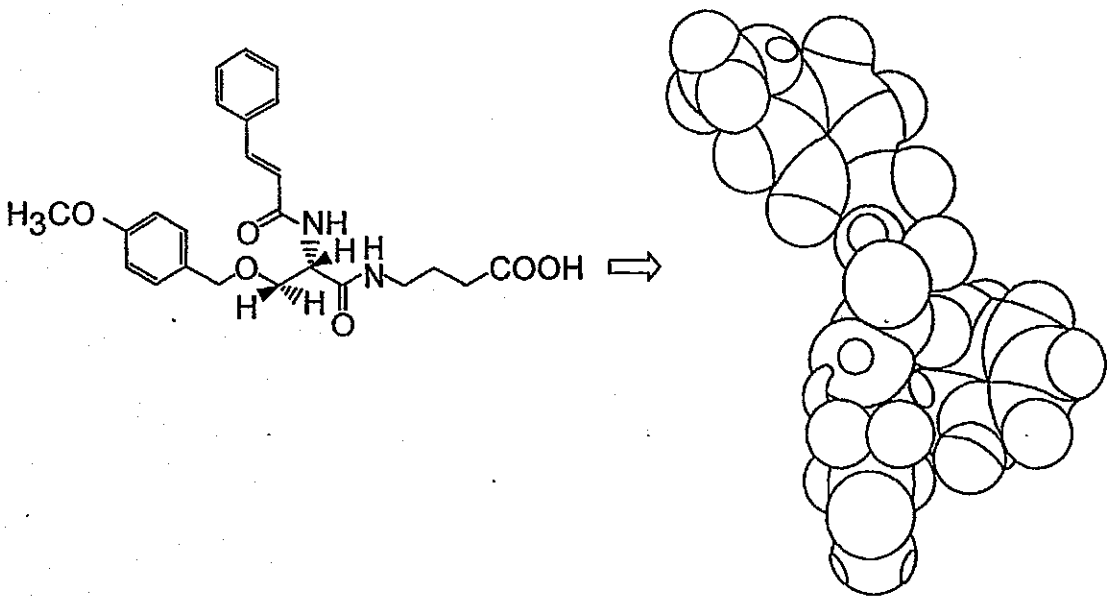

H3CO
NH
H
N
COOH
O

FIG.12

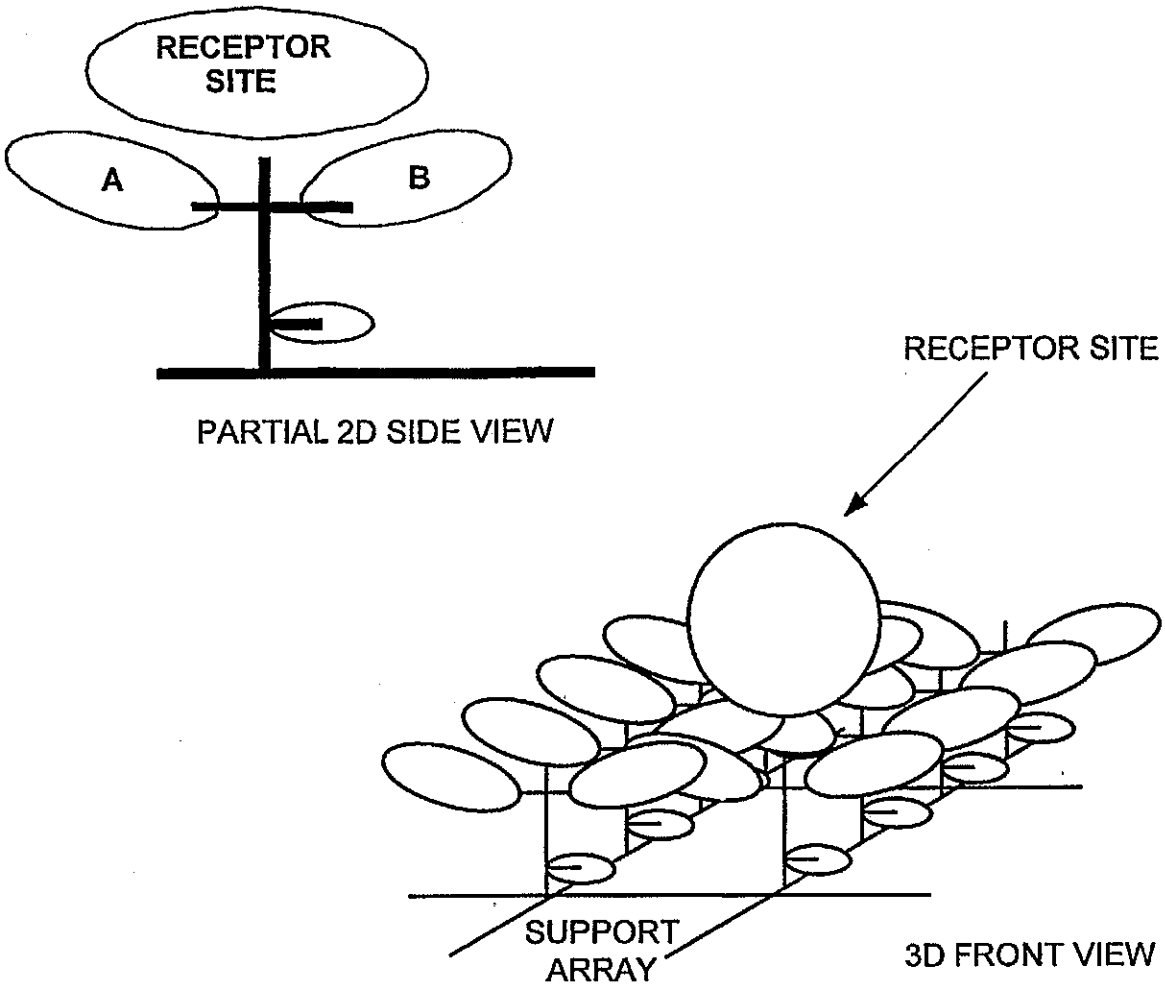
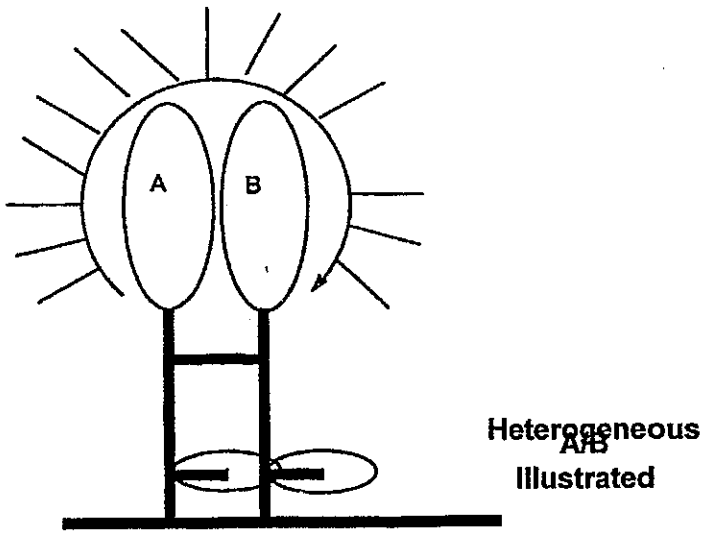

RECEPTOR SITE
A
B
PARTIAL 2D SIDE VIEW
RECEPTOR SITE
SUPPORT ARRAY
3D FRONT VIEW
H3CO
O
H
H
N
H
O
HN
O
COOH

FIG.13


A
B
Heterogeneous
A/B
Illustrated

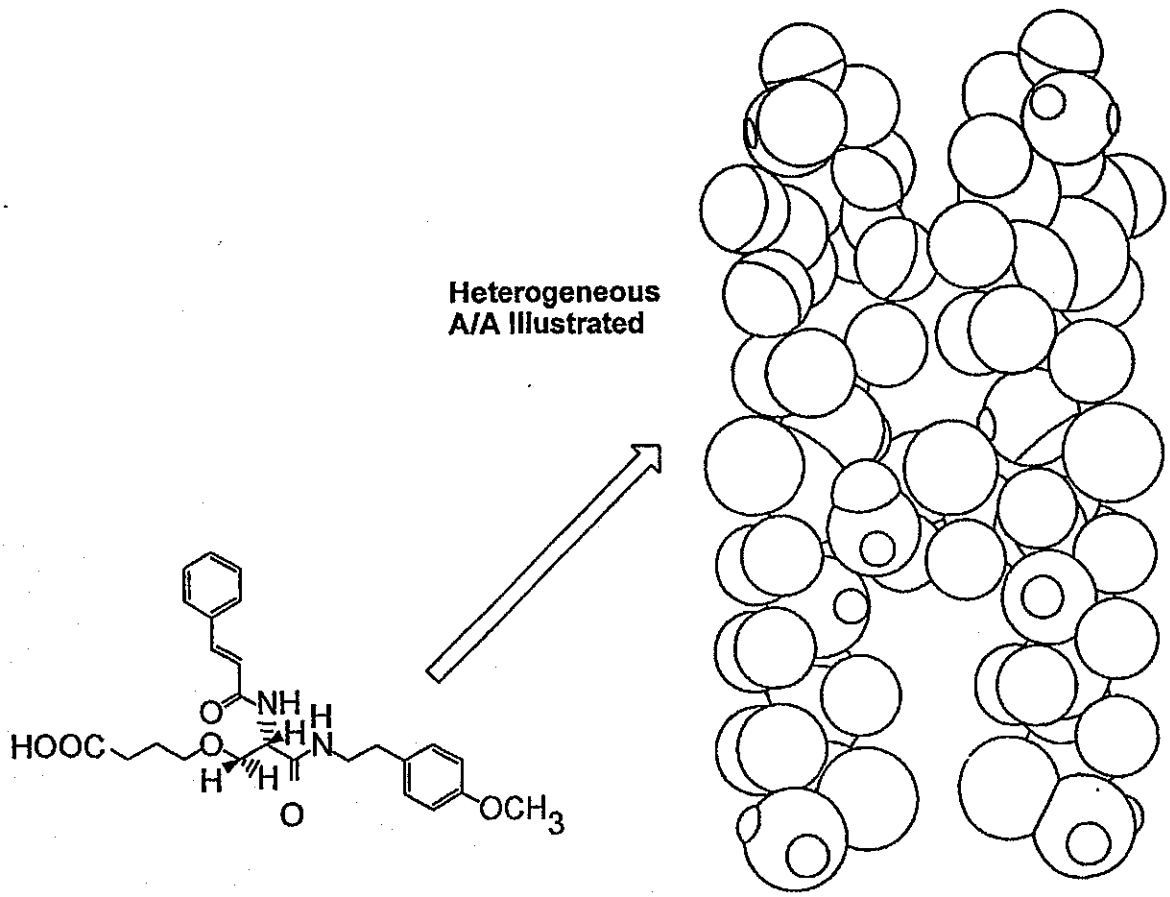

Heterogeneous
A/A Illustrated
HOOC
O
NH
H
H
N
O
H
H
O
OCH3

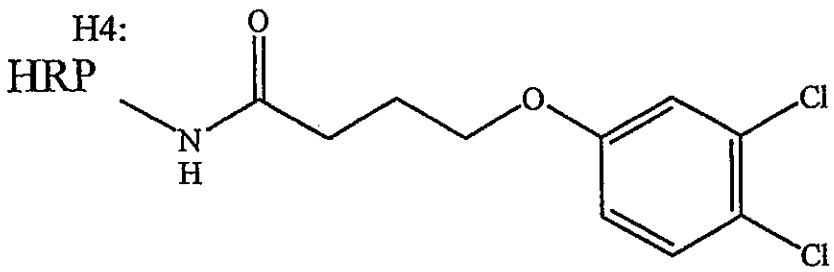
FIG.14

Formula H1: HRP-$(NH_2)_2$

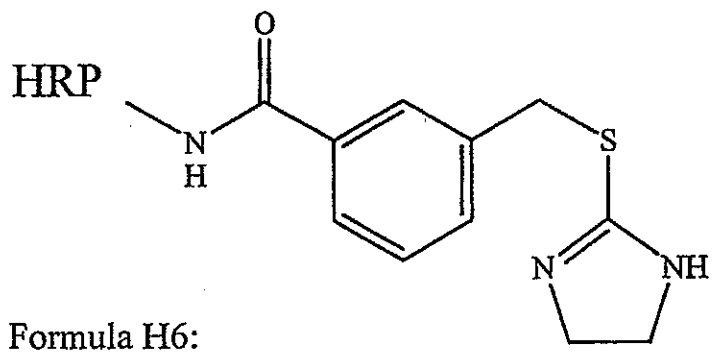
Formula H2: HRP-$(NH_2)_{20}$

Formula H3: HRP-$(NHCOCH_3)_{20}$

Formula H4:



Formula H5:



Formula H6:

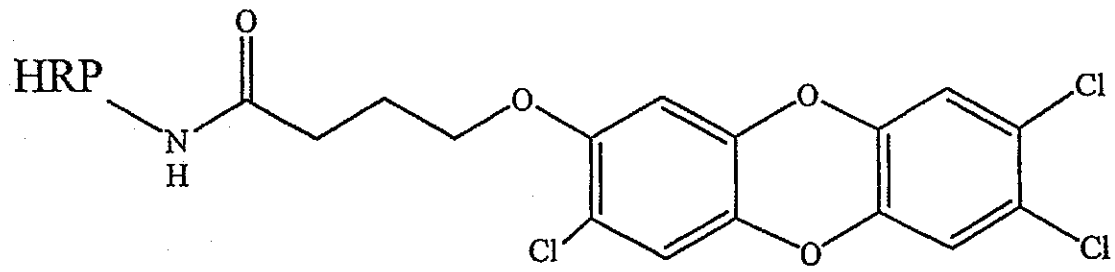


FIG.15A

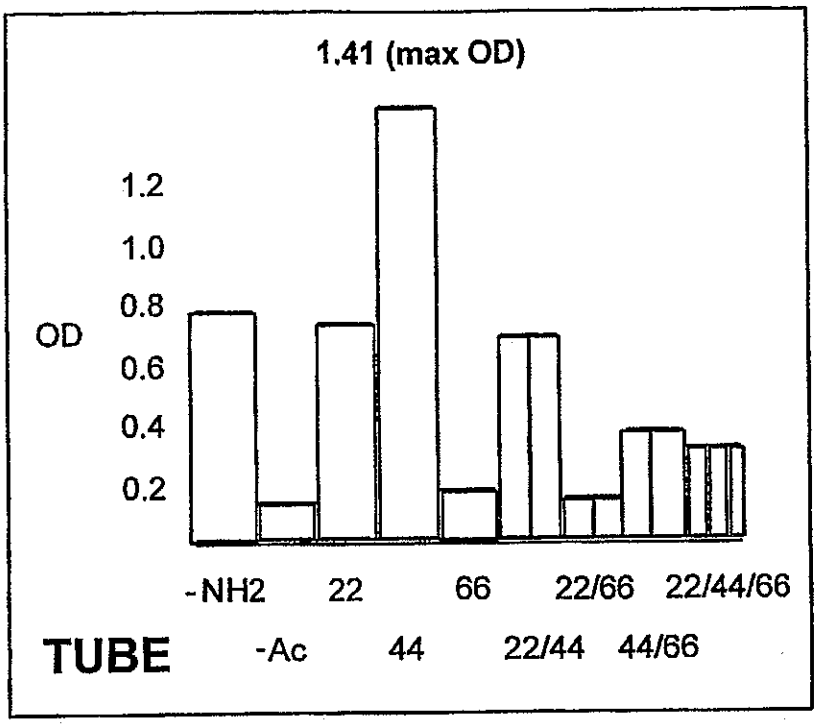

1.41 (max OD)
OD
1.2
1.0
0.8
0.6
0.4
0.2
-NH2
22
66
22/66
22/44/66
TUBE
-Ac
44
22/44
44/66

FIG.15B

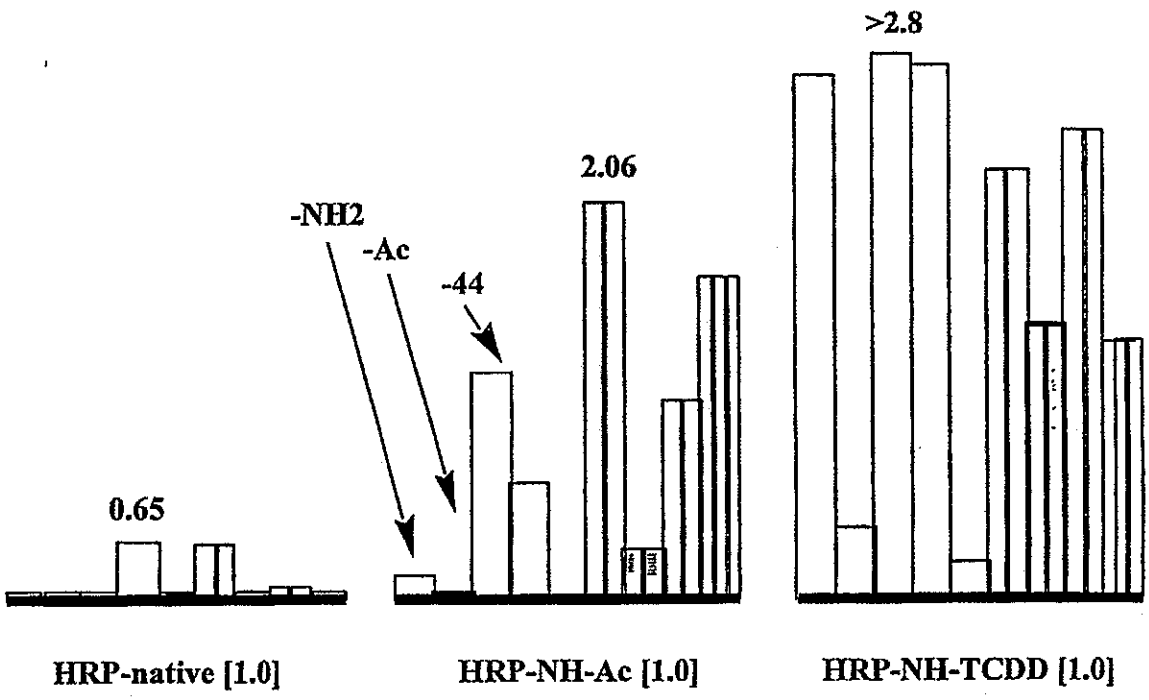
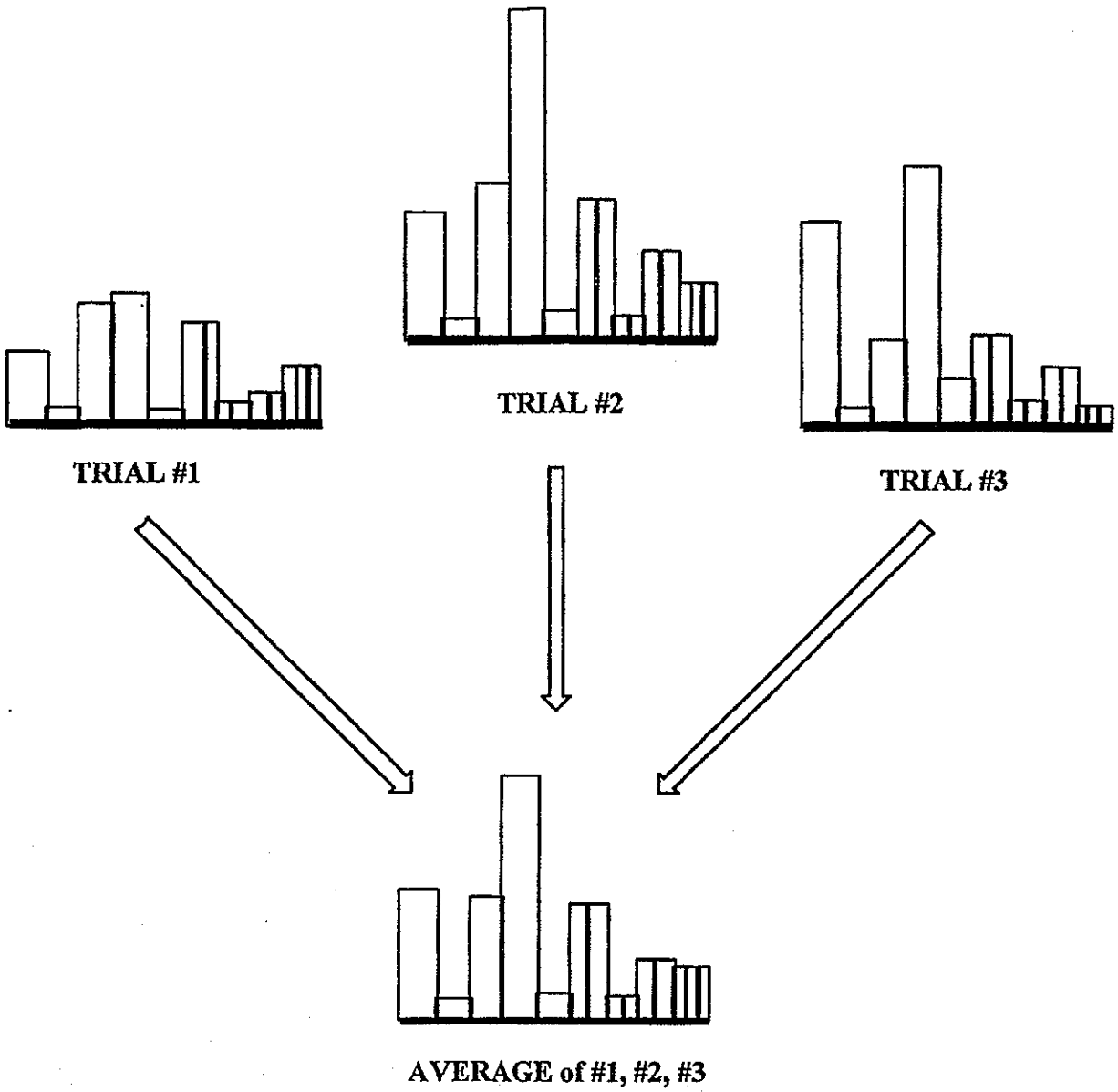


FIG.16



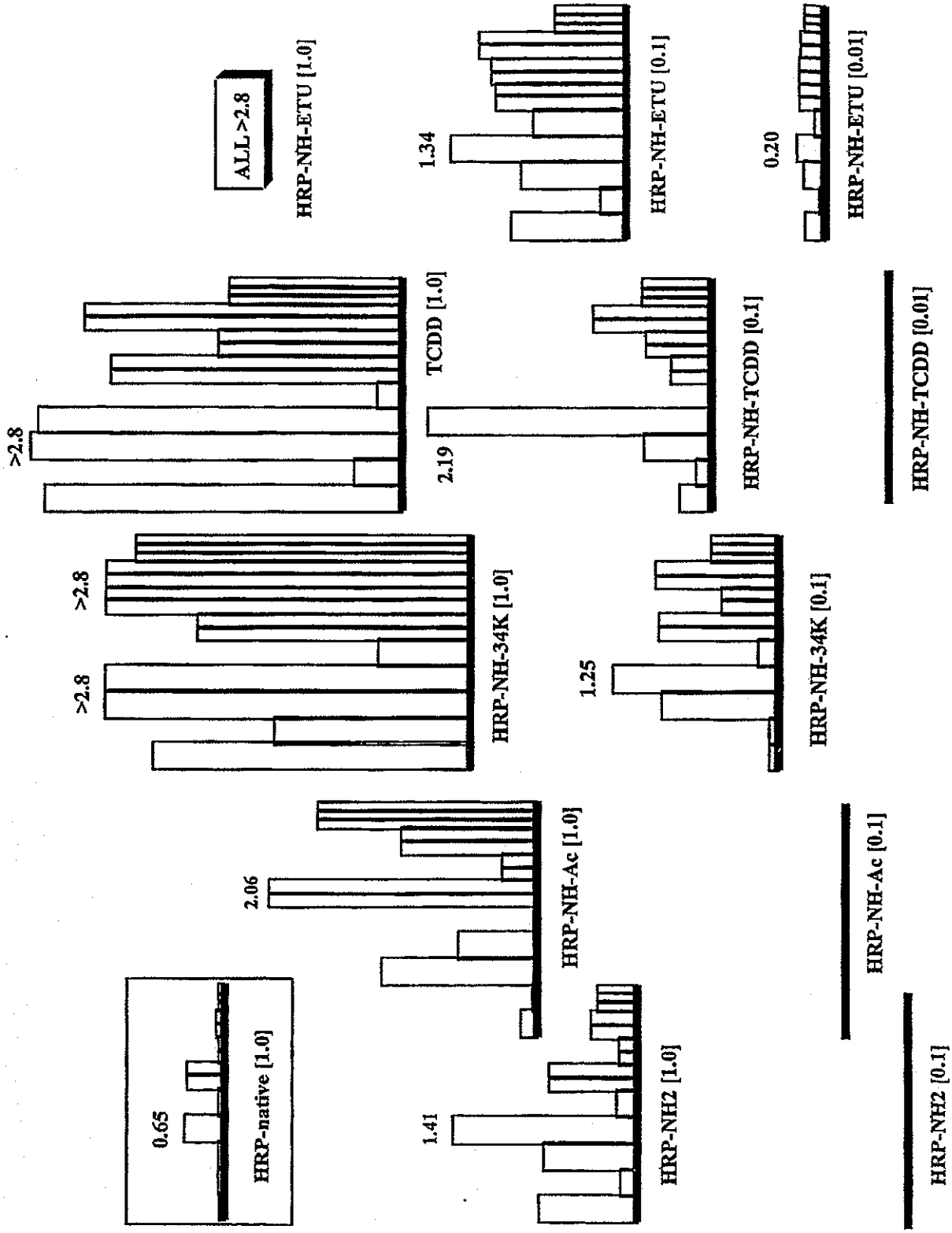

ALL >2.8
HRP-NH-ETU [1.0]
1.34
HRP-NH-ETU [0.1]
0.20
HRP-NH-ETU [0.01]
>2.8
TCDD [1.0]
2.19
HRP-NH-TCDD [0.1]
HRP-NH-TCDD [0.01]
>2.8
>2.8
HRP-NH-34K [1.0]
1.25
HRP-NH-34K [0.1]
2.06
HRP-NH-Ac [1.0]
HRP-NH-Ac [0.1]
0.65
HRP-native [1.0]
1.41
HRP-NH2 [1.0]
HRP-NH2 [0.1]

FIG.17

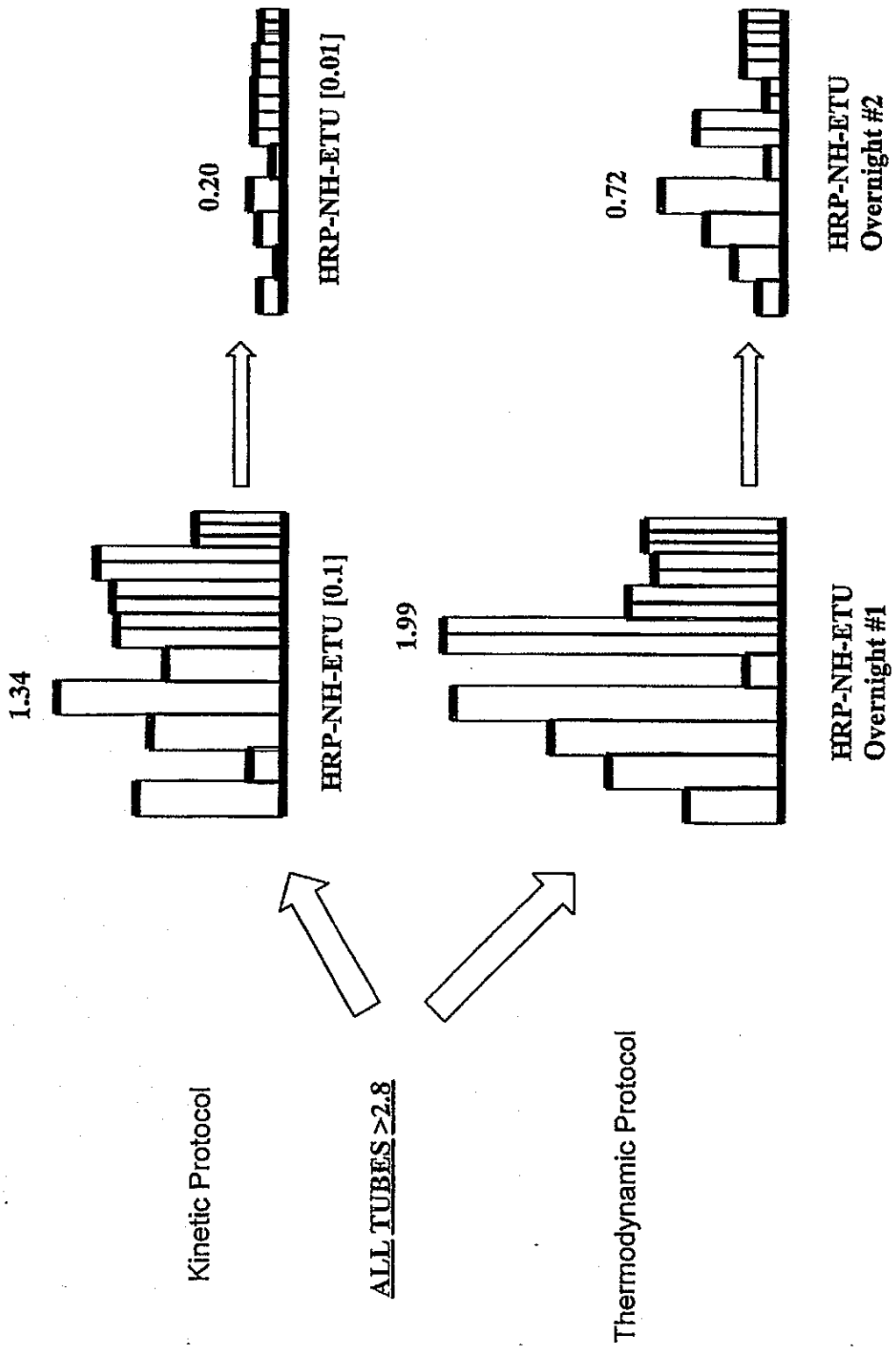
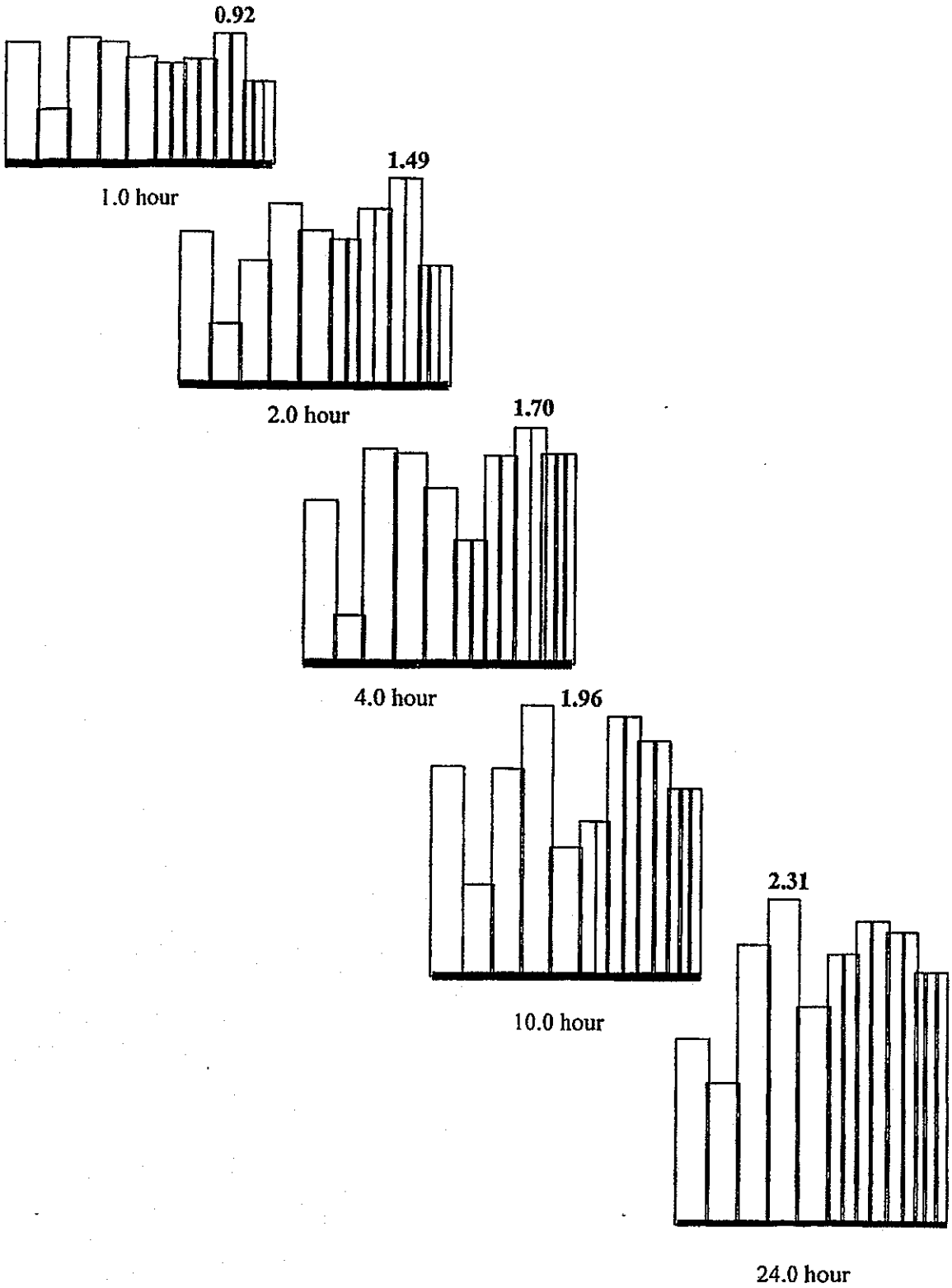

0.20
HRP-NH-ETU [0.01]
1.34
HRP-NH-ETU [0.1]
0.72
HRP-NH-ETU Overnight #2
1.99
HRP-NH-ETU Overnight #1
Kinetic Protocol
ALL TUBES ≥2.8
Thermodynamic Protocol

FIG.18

FIG.19



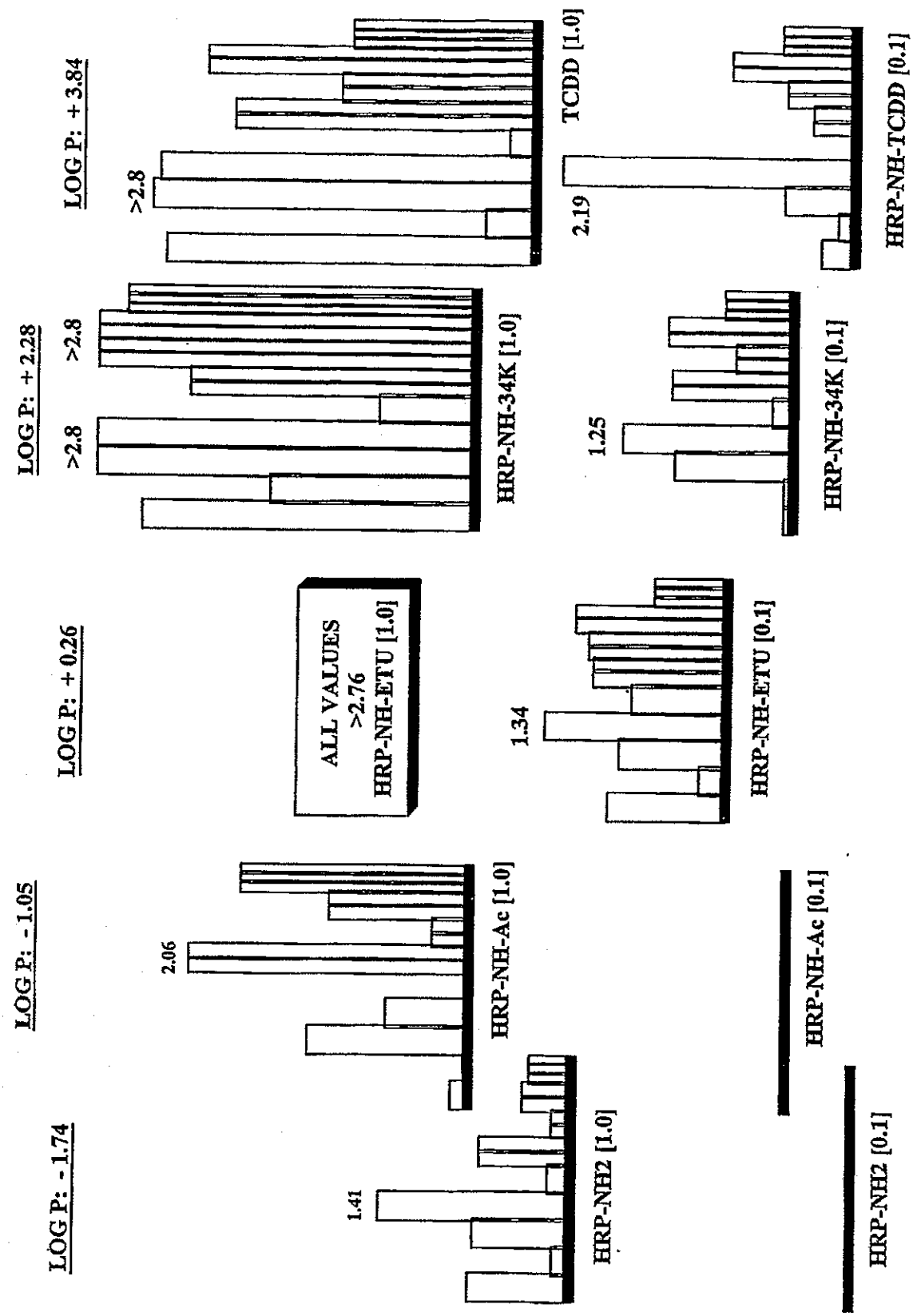
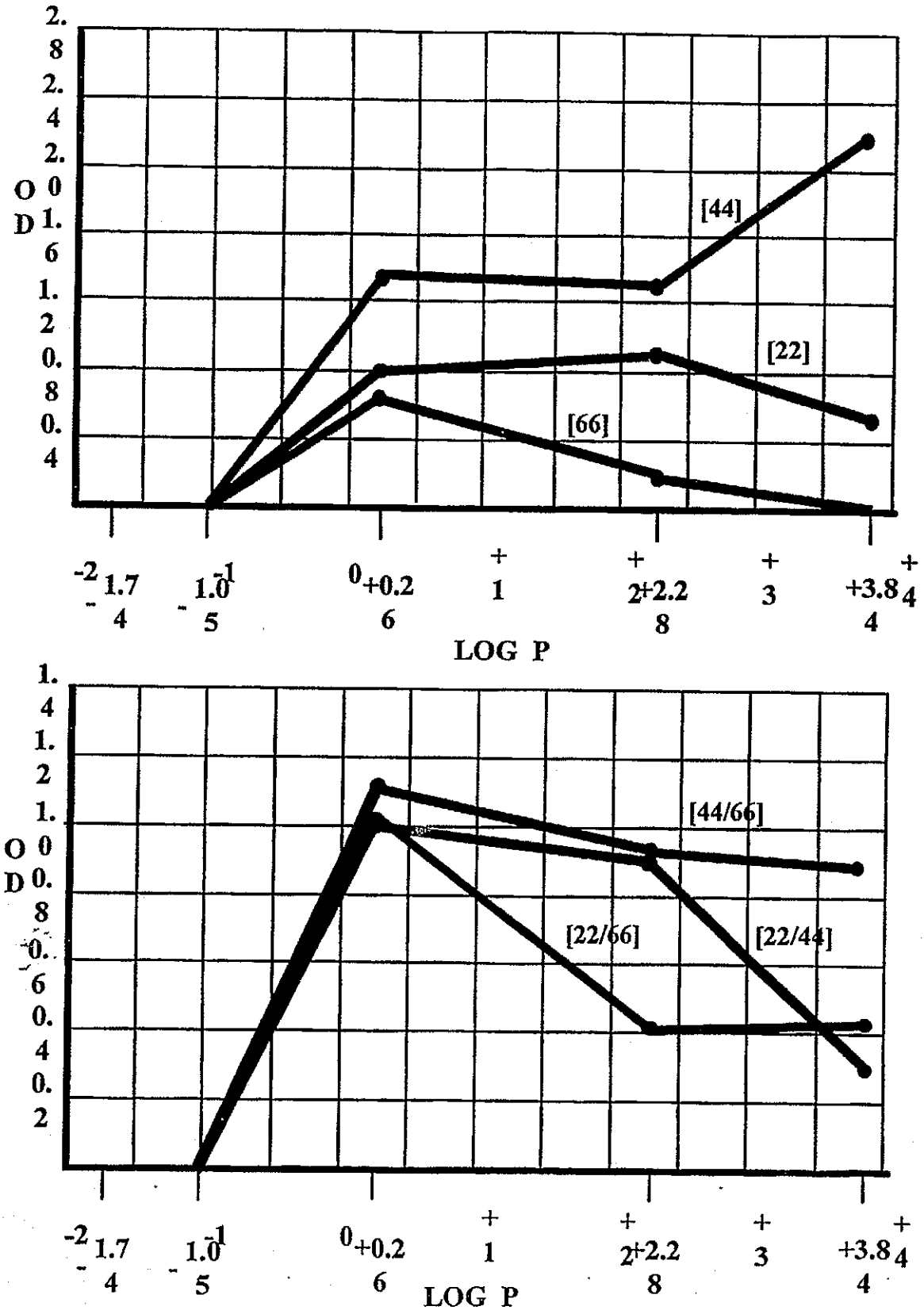

LOG P: - 1.74
LOG P: - 1.05
LOG P: + 0.26
LOG P: + 2.28
LOG P: + 3.84
1.41
HRP-NH2 [1.0]
2.06
HRP-NH-Ac [1.0]
ALL VALUES
>2.76
HRP-NH-ETU [1.0]
>2.8
>2.8
HRP-NH-34K [1.0]
>2.8
TCDD [1.0]
HRP-NH2 [0.1]
HRP-NH-Ac [0.1]
1.34
HRP-NH-ETU [0.1]
1.25
HRP-NH-34K [0.1]
2.19
HRP-NH-TCDD [0.1]

FIG.20

FIG.21


OD
2.8
2.4
2.0
1.6
1.2
0.8
0.4
[44]
[22]
[66]
-2
-1.74
-1.05
0
+0.26
+1
+2.28
+3
+3.84
LOG P
OD
1.4
1.2
1.0
0.8
0.6
0.4
0.2
[44/66]
[22/66]
[22/44]
-2
-1.74
-1.05
0
+0.26
+1
+2.28
+3
+3.84
LOG P

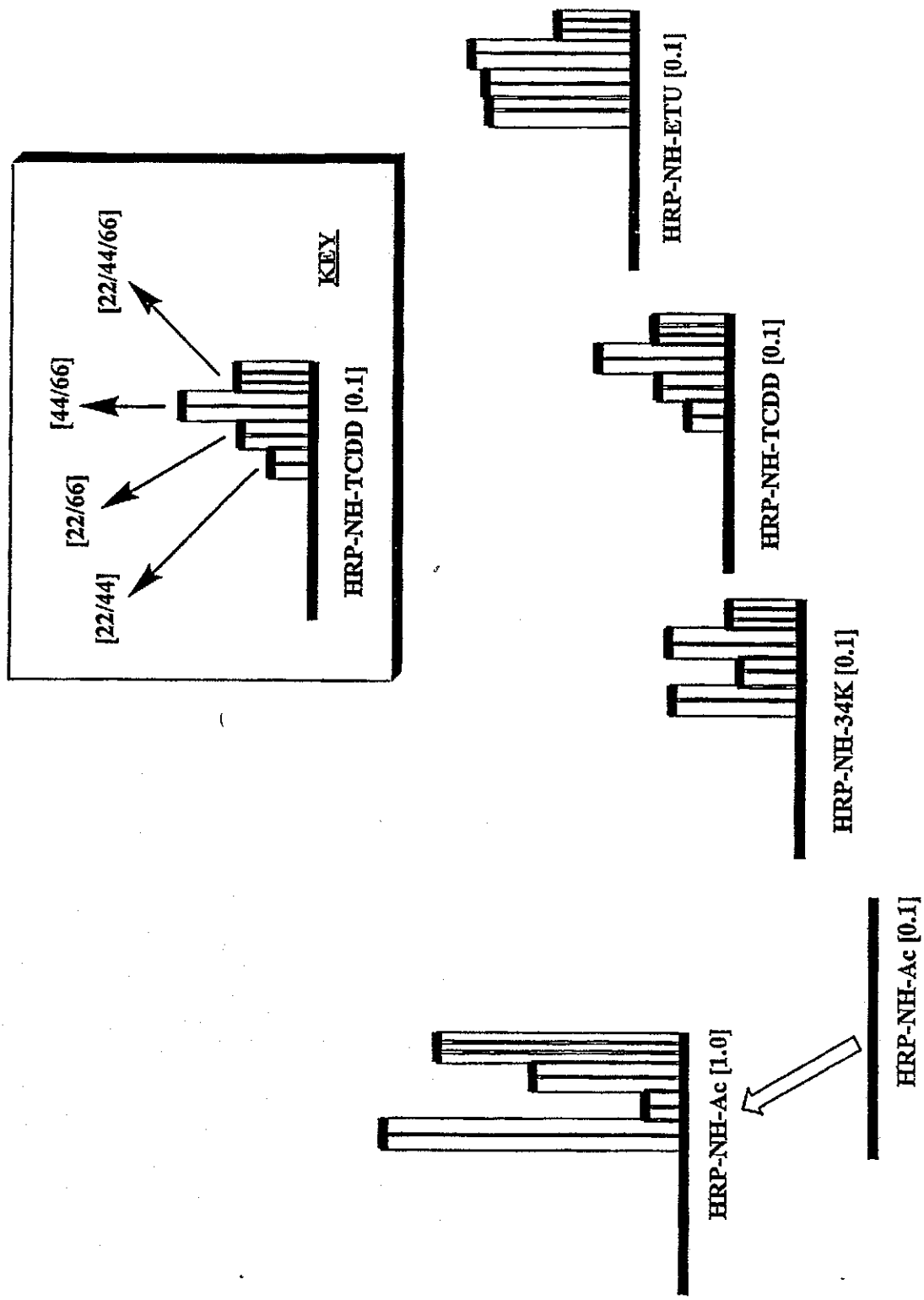

KEY
[22/44/66]
[44/66]
[22/66]
[22/44]
HRP-NH-TCDD [0.1]
HRP-NH-ETU [0.1]
HRP-NH-TCDD [0.1]
HRP-NH-34K [0.1]
HRP-NH-Ac [0.1]
HRP-NH-Ac [1.0]

FIG.22

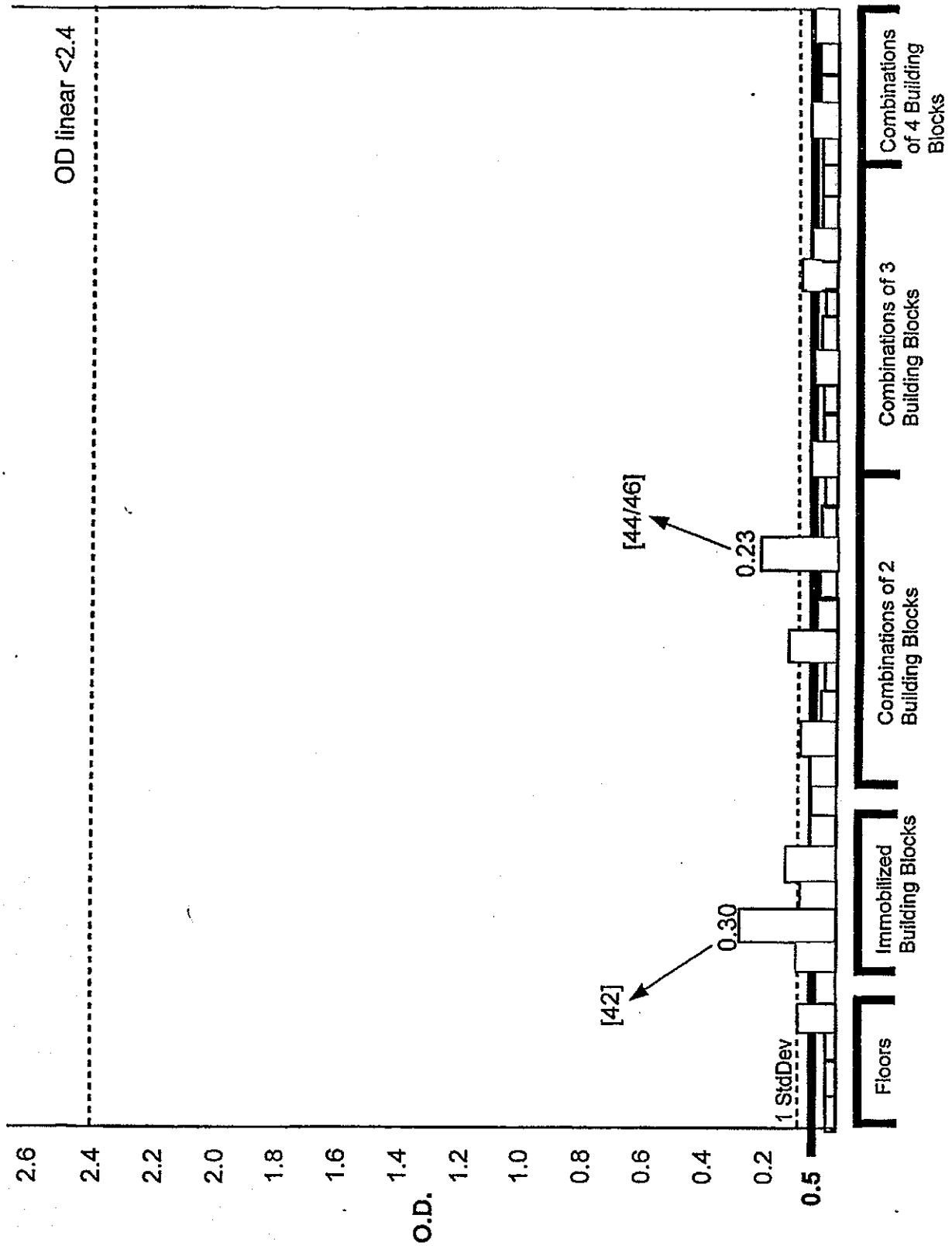

OD linear <2.4
[44/46]
0.23
[42]
0.30
1 StdDev
Floors
Immobilized Building Blocks
Combinations of 2 Building Blocks
Combinations of 3 Building Blocks
Combinations of 4 Building Blocks
O.D.
0.5
0.2
0.4
0.6
0.8
1.0
1.2
1.4
1.6
1.8
2.0
2.2
2.4
2.6

FIG.23

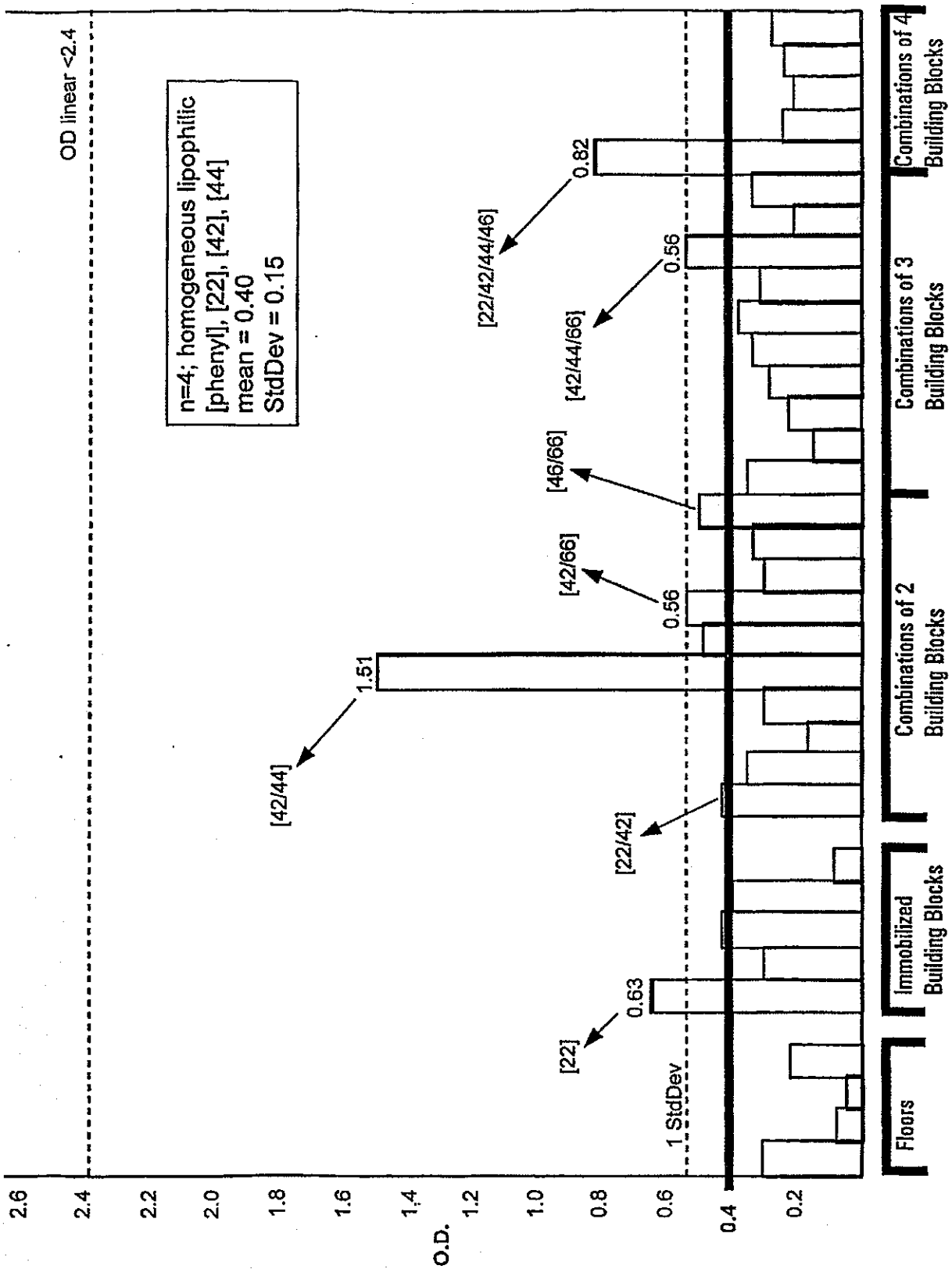

OD linear <2.4
n=4; homogeneous lipophilic
[phenyl], [22], [42], [44]
mean = 0.40
StdDev = 0.15
0.82
[22/42/44/46]
0.56
[42/44/66]
[46/66]
0.56
[42/66]
1.51
[42/44]
[22/42]
0.63
[22]
1 StdDev
O.D.
2.6
2.4
2.2
2.0
1.8
1.6
1.4
1.2
1.0
0.8
0.6
0.4
0.2
Combinations of 4 Building Blocks
Combinations of 3 Building Blocks
Combinations of 2 Building Blocks
Immobilized Building Blocks
Floors

FIG.24

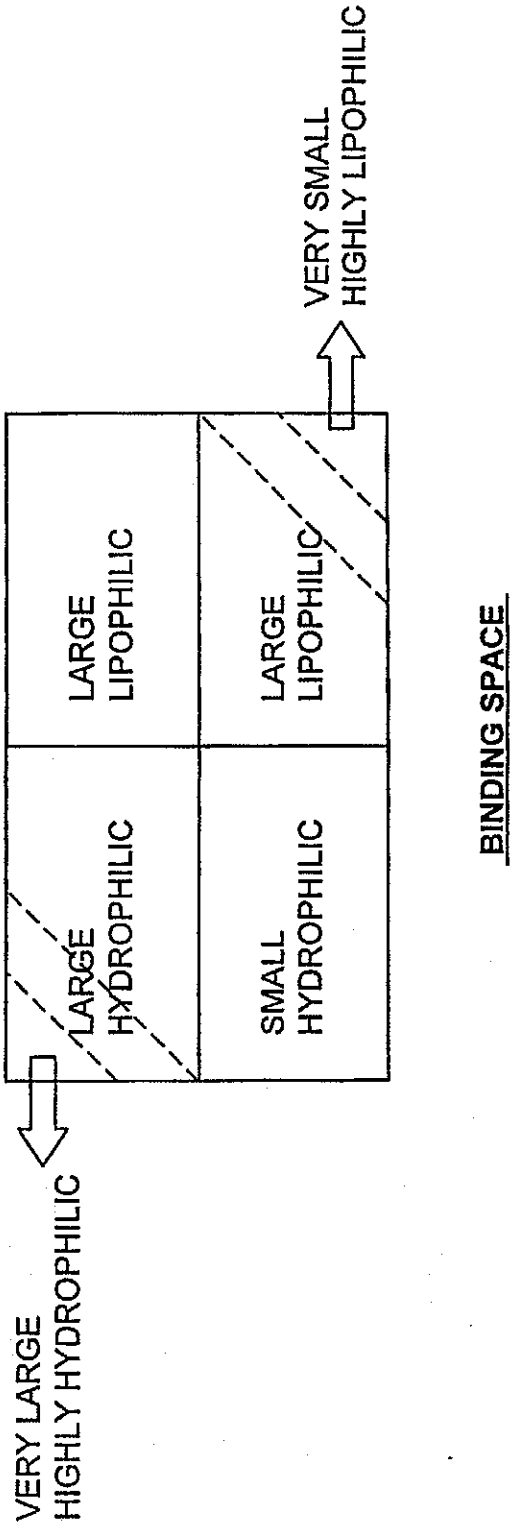

VERY SMALL
HIGHLY LIPOPHILIC
LARGE
LIPOPHILIC
LARGE
LIPOPHILIC
LARGE
HYDROPHILIC
SMALL
HYDROPHILIC
VERY LARGE
HIGHLY HYDROPHILIC
BINDING SPACE

FIG.25

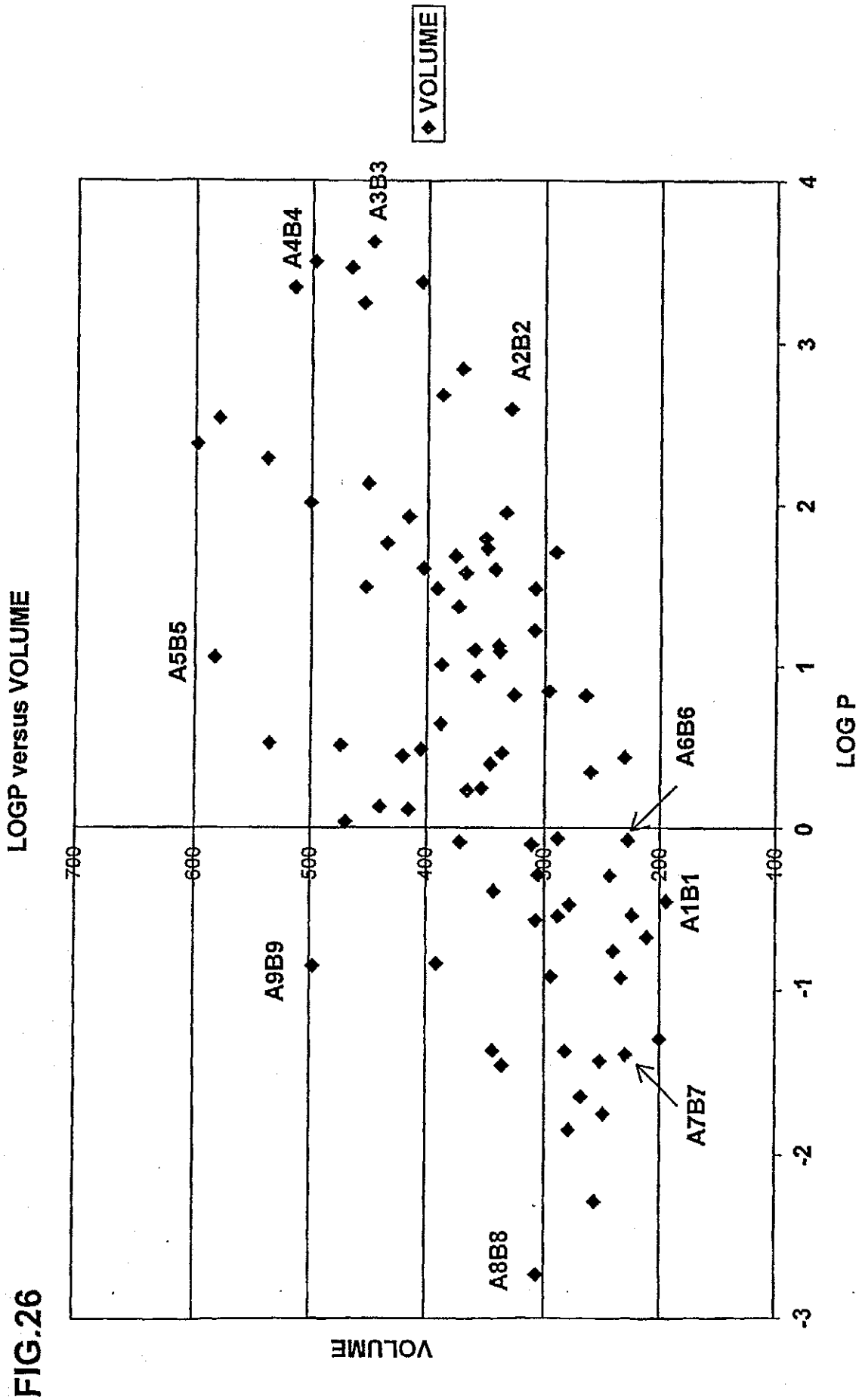

LOGP versus VOLUME
VOLUME
LOG P
A3B3
A4B4
A2B2
A5B5
A6B6
A1B1
A9B9
A7B7
A8B8
700
600
500
400
300
200
100
4
3
2
1
0
-1
-2
-3

FIG.26

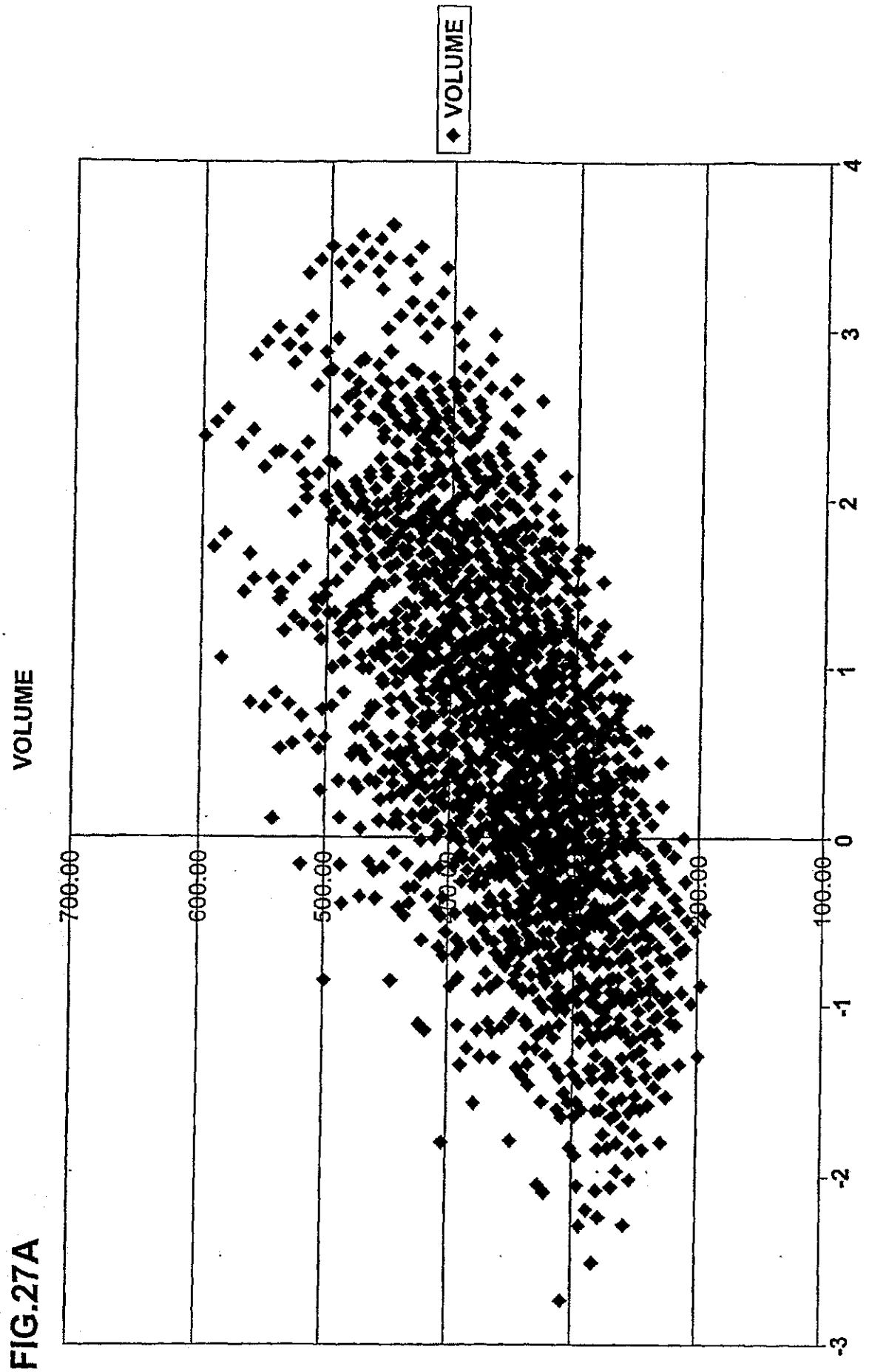

VOLUME
VOLUME
700.00
600.00
500.00
400.00
300.00
200.00
100.00
4
3
2
1
0
-1
-2
-3

FIG.27A

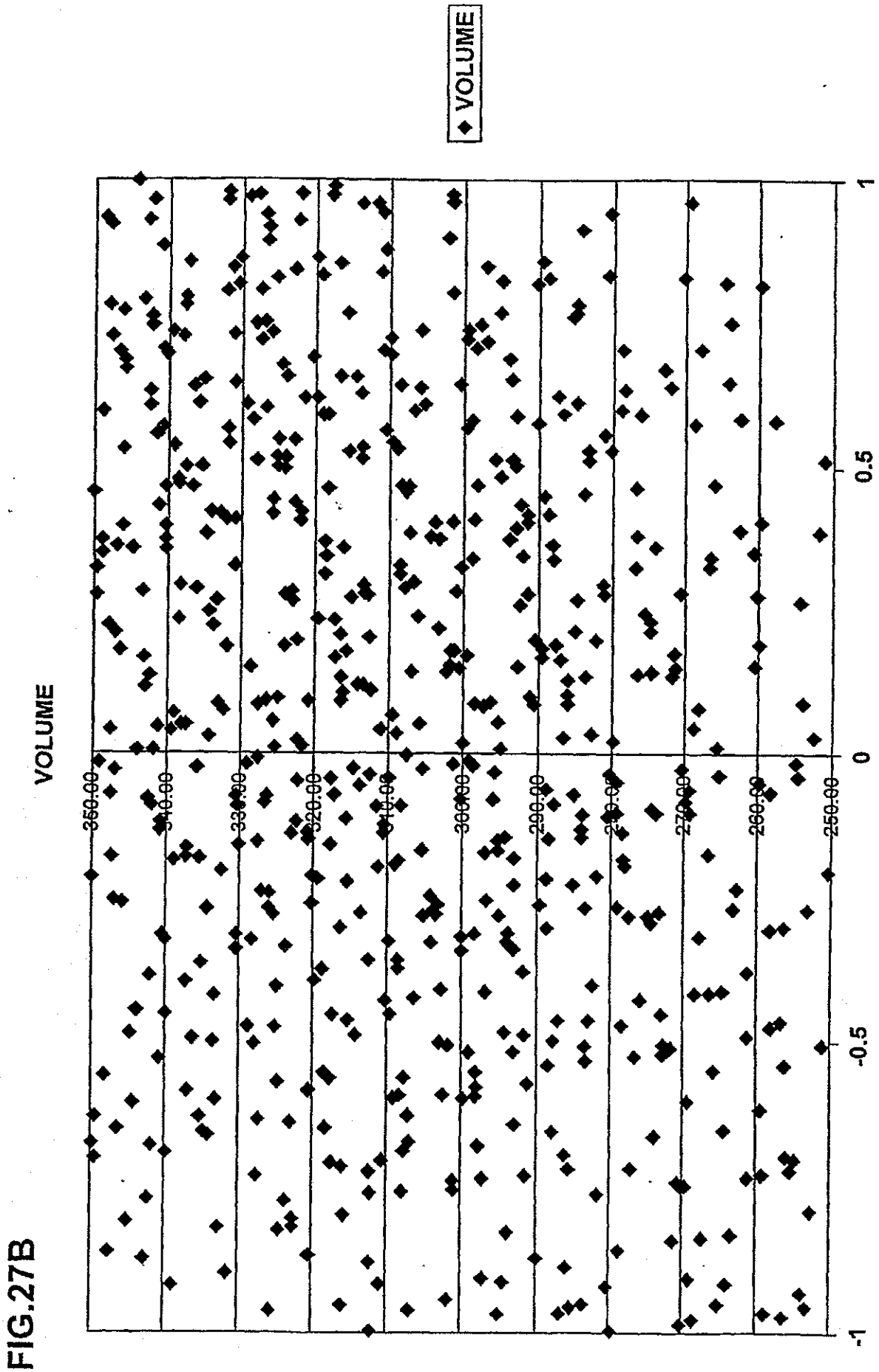

VOLUME
VOLUME
1
0.5
0
-0.5
-1
350.00
340.00
330.00
320.00
310.00
300.00
290.00
280.00
270.00
260.00
250.00

FIG.27B

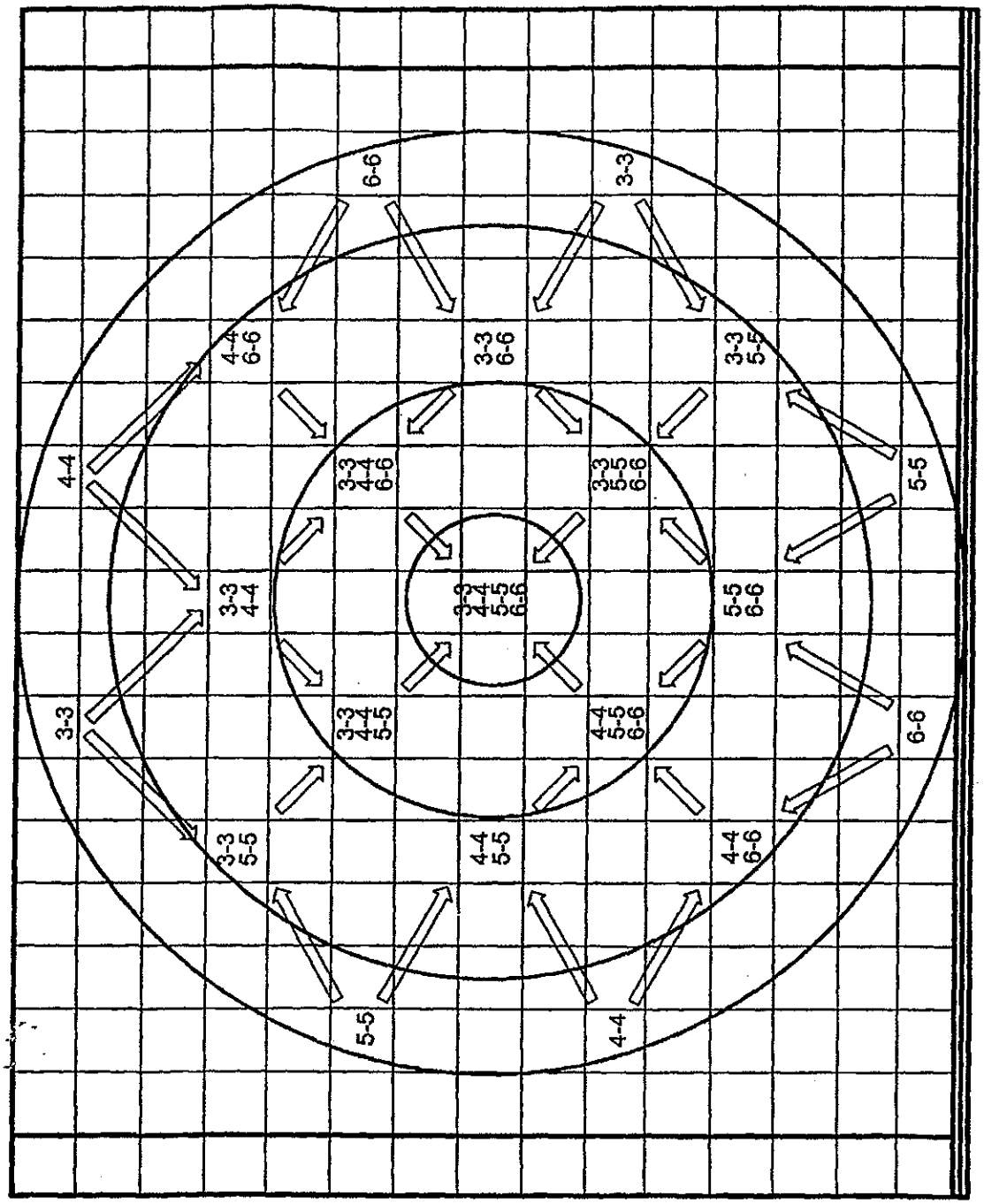

6-6
3-3
4-4 6-6
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3-3 4-4 5-5
4-4 5-5 6-6
6-6
3-3 5-5
4-4 5-5
4-4 6-6
5-5
4-4

FIG.28