FIG. 1

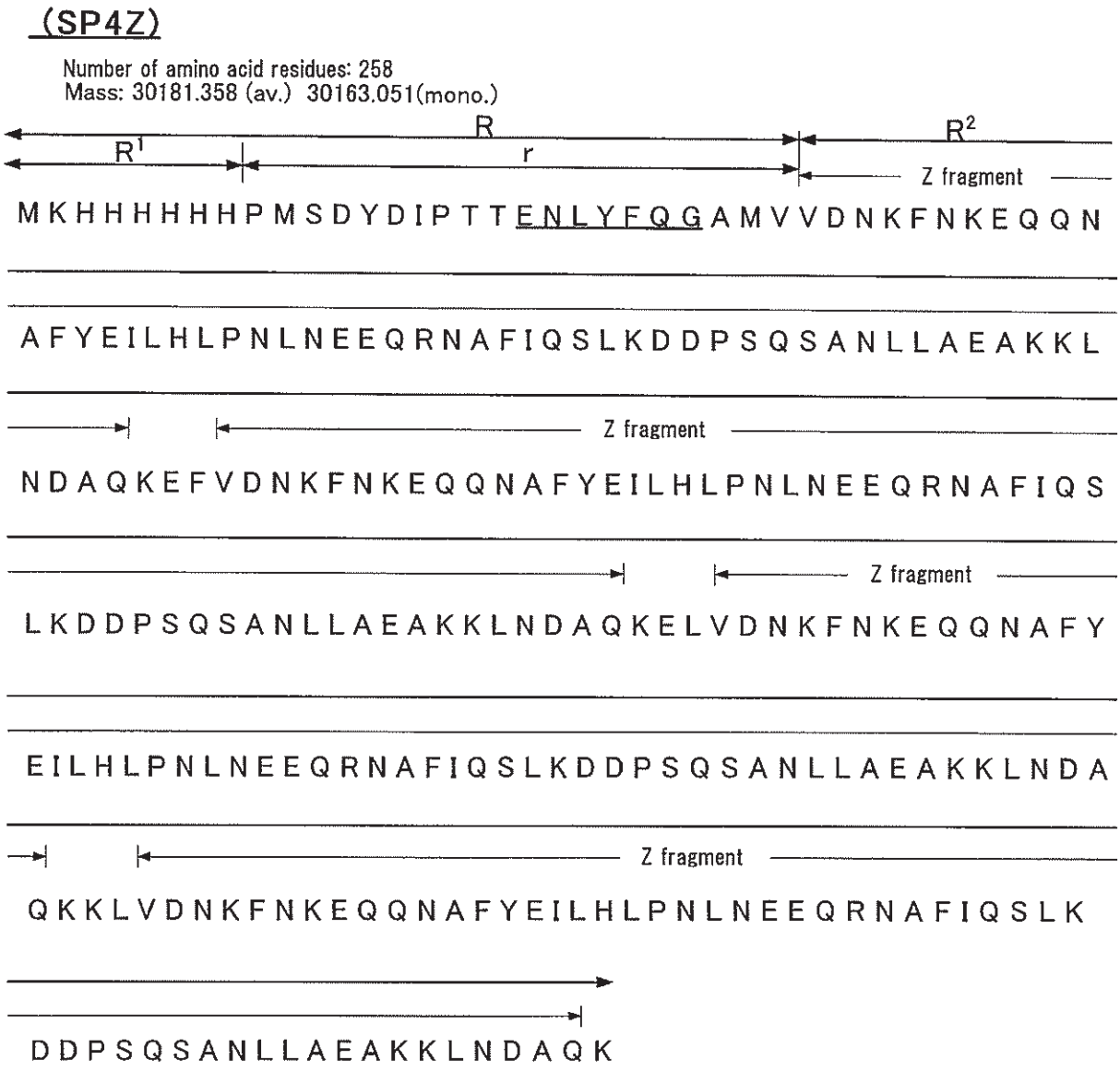

(SP4Z)
Number of amino acid residues: 258
Mass: 30181.358 (av.) 30163.051(mono.)
R
R1
r
R2
Z fragment
MKHHHHHHPMSDYDIPTTENLYFQGAMVVDNKFNKEQQN
AFYEILHLPNLNEEQRNAFIQSLKDDPSQSANLLAEAKKL
Z fragment
NDAQKEFVDNKFNKEQQNAFYEILHLPNLNEEQRNAFIQS
Z fragment
LKDDPSQSANLLAEAKKLNDAQKELVDNKFNKEQQNAFY
EILHLPNLNEEQRNAFIQSLKDDPSQSANLLAEAKKLNDA
Z fragment
QKKLVDNKFNKEQQNAFYEILHLPNLNEEQRNAFIQSLK
DDPSQSANLLAEAKKLNDAQK

FIG. 2

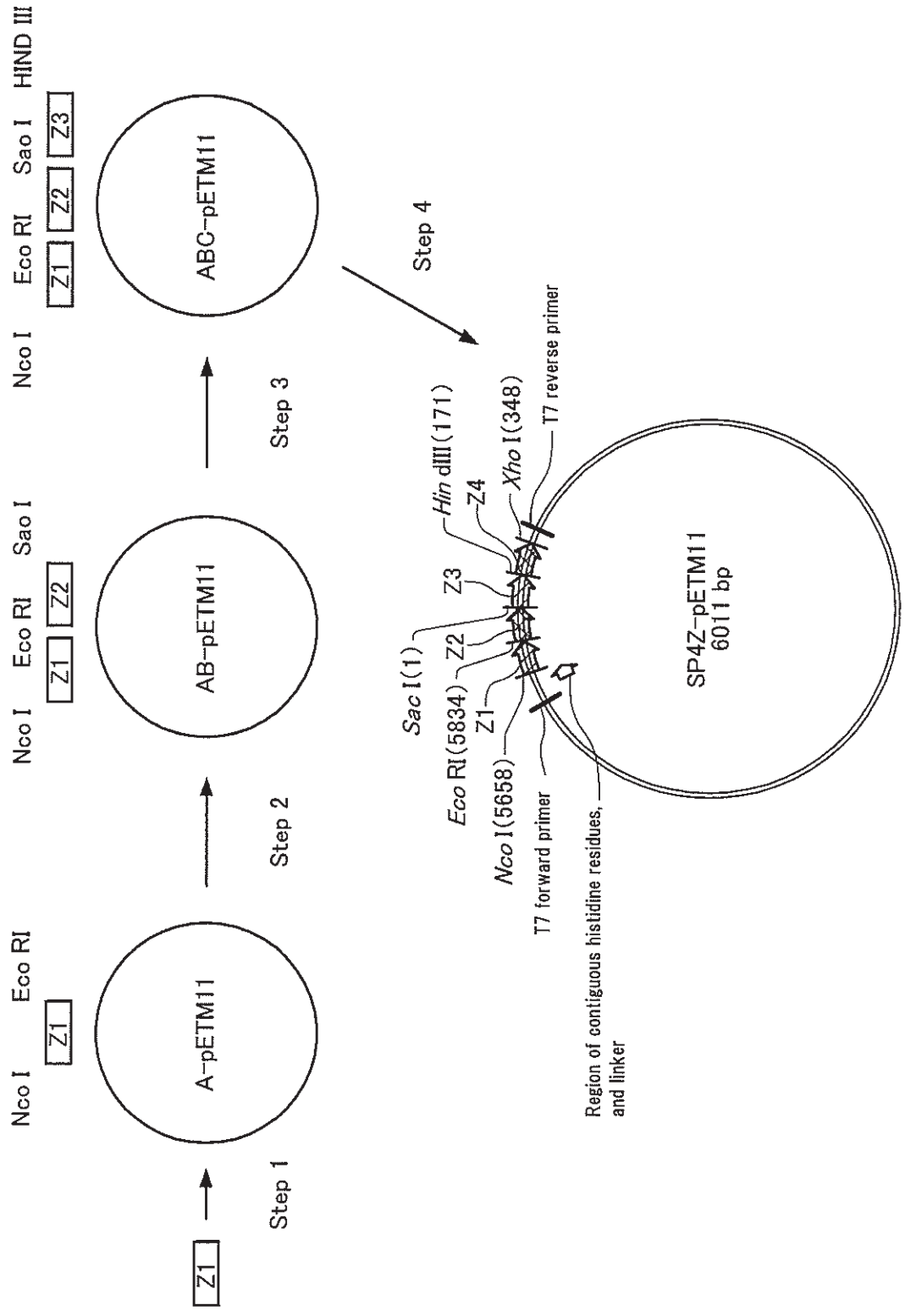
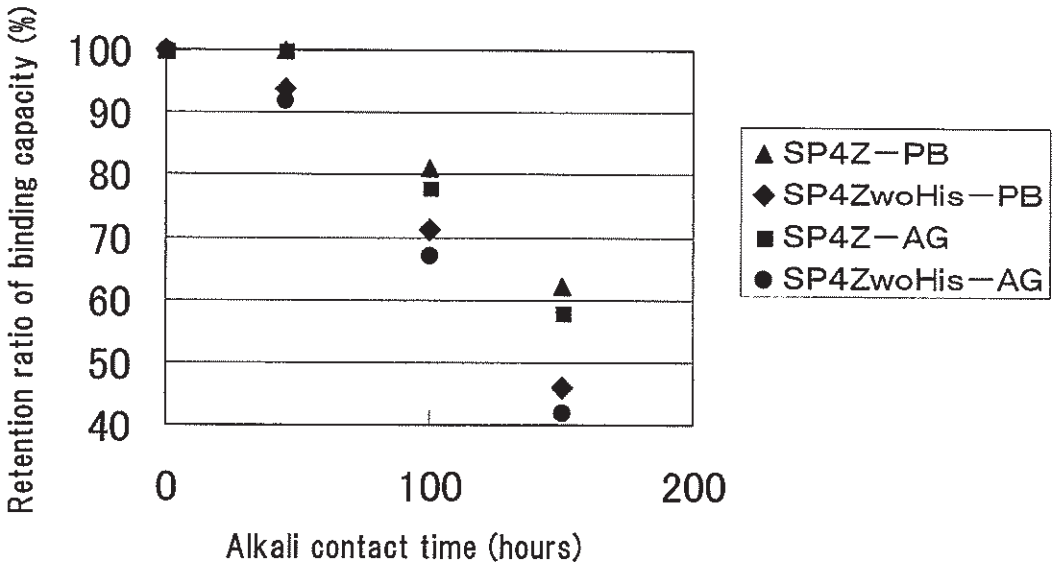

Nco I
Eco RI
Z1
A-pETM11
Step 1
Nco I
Eco RI
Sao I
Z1
Z2
AB-pETM11
Step 2
Nco I
Eco RI
Sao I
HIND III
Z1
Z2
Z3
ABC-pETM11
Step 3
Step 4
Sac I (1)
Z2
Z3
Hin dIII (171)
Z4
Xho I (348)
T7 reverse primer
Eco RI (5834)
Z1
Nco I (5658)
T7 forward primer
Region of contiguous histidine residues, and linker
SP4Z-pETM11
6011 bp

FIG. 3


Retention ratio of binding capacity (%)
100
90
80
70
60
50
40
0
100
200
Alkali contact time (hours)
▲ SP4Z−PB
◆ SP4ZwoHis−PB
■ SP4Z−AG
● SP4ZwoHis−AG