

SEQUENCE LISTING

<110> The Walter and Eliza Hall Institute of Medical Research

<120> Novel binding proteins

<130> 515053

<160> 22

<170> PatentIn version 3.5

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<212> PRT

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Ser	Ile	Ser	Pro	Ala	Gly	Ile	Thr	Thr	Tyr	Tyr	Arg	Asp	Ser	Val	Lys
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Gly

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His	Thr	Gly	Lys	Ser	Ser	Phe	Phe	Asp	Tyr
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Lys	Ala	Thr	Glu	Asn	Ile	Asn	Thr	Tyr	Leu	Ala
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Gln Gln His Asn Glu Tyr Pro Leu Thr
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Met Asp Phe Arg Leu Ser Leu Ala Phe Leu Val Leu Leu Ile Lys Ala
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Val Gln Cys Glu Val Glu Leu Val Glu Ser Gly Gly Asp Leu Val Gln
 20 25 30

Pro Gly Arg Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 35 40 45

Ser Asn Leu Ala Met Ala Trp Val Arg Gln Thr Pro Thr Lys Gly Leu
 50 55 60

Glu Trp Val Ala Ser Ile Ser Pro Ala Gly Ile Thr Thr Tyr Tyr Arg
 65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Arg Asn
 85 90 95

Thr Gln Tyr Leu Gln Met Asp Ser Leu Arg Ser Glu Asp Thr Ala Thr

100

105

110

Tyr Tyr Cys Ala Arg His Thr Gly Lys Ser Ser Phe Phe Asp Tyr Trp
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Gly Gln Gly Val Met Val Thr Val Ser Ser
 130 135

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Met Arg Val Gln Ile Gln Phe Leu Gly Leu Leu Leu Leu Trp Thr Ser
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Val Val Gln Cys Asp Val Gln Met Thr Gln Ser Pro Ser Tyr Leu Ala
 20 25 30

Ala Ser Pro Gly Glu Ser Val Ser Ile Ser Cys Lys Ala Thr Glu Asn
 35 40 45

Ile Asn Thr Tyr Leu Ala Trp Tyr Gln Ala Lys Pro Gly Lys Thr Thr
 50 55 60

Lys Leu Leu Leu Tyr Ser Gly Ser Thr Leu Gln Ser Gly Thr Pro Ser
 65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
 85 90 95

Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln His Asn
100 105 110

Glu Tyr Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
115 120 125

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Gly Val Ala Ala Pro Ala Asp
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Gly Val Ala Ala Pro
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120

tgtgcagcct caggattcac tttcagtaac ttagccatgg cctgggtccg ccagactcca
180

acgaagggtc tggagtgggt cgcattccatt agtcctgctg gtattaccac ctactatcga
240

gactccgtga agggccgatt cactatttcc agagataatg caagaaacac ccaatacttg
300

cagatggaca gtctgaggtc tgaggacacg gccacttatt actgtgccag acataccgga
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120

atcagttgca aggcaactga aaacattaac acatacttag cctgggtatca ggcgaaacct
180

gggaaaacga ctaagcttct tctctactct ggggtcaactt tgcaatctgg aactccatcg
240

agattcagtg gcagtgggtc tggaacagac ttcacgctca ccatcagcag cctggagcct
300

gaagattttg cagtctacta ctgtcaacaa cataatgaat accctctcac gttcggttct
360

g g g a c c a a g c t g g a g a t c a a a
381

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<223> mutated amino acid sequence of an epitope within the alpha1-
alpha2 loop
of Bak (P55X)

<220>

<221> misc_feature

<222> (5)..(5)

<223> Xaa can be any naturally occurring amino acid

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<211> 7

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alpha1-alpha2 loop of Bak (P55C)

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 alpha1-alpha2 loop of Bak (G51X)

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<400> 15

Xaa Val Ala Ala Pro Ala Asp
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Cys Val Ala Ala Pro Ala Asp
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<210> 17
 <211> 51
 <212> PRT
 <213> drosophila

<400> 17

Cys Tyr Ser Ala Arg Gly Gly Leu Asn Ile Leu Glu Leu Tyr Ser Ile
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Leu Glu Thr Arg Pro Pro His Glu Gly Leu Asn Ala Ser Asn Ala Arg
 20 25 30

Gly Ala Arg Gly Met Glu Thr Leu Tyr Ser Thr Arg Pro Leu Tyr Ser
 35 40 45

Leu Tyr Ser
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<400> 18

Thr Glu Glu Val Phe Arg Ser
 1 5

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<400> 19

Glu Glu Val Phe Arg
 1 5

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Tyr Val Phe Tyr Arg His Gln Gln
 1 5

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Glu	Gln	Glu	Ala	Glu	Gly	Val	Ala	Ala	Pro	Ala	Asp	Pro	Glu	Met	Val
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Thr	Leu	Pro	Leu	Gln	Pro	Ser	Ser
			20				

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Asp	Met	Arg	Pro	Glu	Ile	Trp	Ile	Ala	Gln	Glu	Leu	Arg	Arg	Ile	Gly
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Asp	Glu	Phe	Asn	Ala	Tyr	Tyr	Ala	Arg	Arg
			20					25	