

Protein Sequences

Tags and linkers underlined, mutations **bolded**, and fusions in respective colors.

>>1wa3

MHHHHHHGGMKMEELFKKHKIVAVLRANSVEEAKKALAVFEGGVHLIEITFTVPDADTVIKELSFLKEKGAIIGAGTV
TSVEQCRKAVESGAEFIVSPHLDEEISQFCKEKGVFYMPGVMTPTLVKAMKLGHTILKLFPGEVVGPQFVKAMKGFPP
NVKFPVPTGGVNLNDNVCEWFKAGVLAVGVGSALVKGTPDEVREKAKAFVEKIRGCTE

>>I3-01

MHHHHHHGGSGSGSGSGSMKMEELFKKHKIVAVLRANSVEEAKKALAVFLGGVHLIEITFTVPDADTVIKELSFLKE
MGAIIGAGTVTSVEQCRKAVESGAEFIVSPHLDEEISQFCKEKGVFYMPGVMTPTLVKAMKLGHTILKLFPGEVVGPQ
FVKAMKGFPPNVKFPVPTGGVNLNDNVCEWFKAGVLAVGVGSALVKGTP**VEVAEKAKAFVEKIRGCTE**

>>I3-01 (L33R)

MHHHHHHGGMKMEELFKKHKIVAVLRANSVEEAKKALAVFRGGVHLIEITFTVPDADTVIKELSFLKEMGAIIGAGTV
TSVEQCRKAVESGAEFIVSPHLDEEISQFCKEKGVFYMPGVMTPTLVKAMKLGHTILKLFPGEVVGPQFVKAMKGFPP
NVKFPVPTGGVNLNDNVCEWFKAGVLAVGVGSALVKGTPVEVAEKAKAFVEKIRGCTE

>>I3-01 (K129A)

MHHHHHHGGSGSGSGSGSMKMEELFKKHKIVAVLRANSVEEAKKALAVFLGGVHLIEITFTVPDADTVIKELSFLKE
MGAIIGAGTVTSVEQCRKAVESGAEFIVSPHLDEEISQFCKEKGVFYMPGVMTPTLVKAMKLGHTIL**AL**FPGEVVGPQ
FVKAMKGFPPNVKFPVPTGGVNLNDNVCEWFKAGVLAVGVGSALVKGTPVEVAEKAKAFVEKIRGCTE

>>T33-21 (12-mer)

A:MRITTKVGDKGSTRFLFGGEEVWKDSP^IIEANGTLDELTSFIGEAKHYVDEEMKGILEEIQNDIYKIMGEIGSKGKIE
GISEERIAWLLKLI^LLRMEMVNLKSFVLPGGTLES^AKLDVCRTIARRALRKVLTVTREFGIGAEAAAYLLALS^DLLFLL
ARVIEIEKNKLKEVRSGSGSGSSKGEELFTGVVPIILVELDGDVNGHKFSVRGEGEGDATNGKLT^LK^FICTTGKLPVPWP
TLVTT^LTYGVQCFARYPDHMKQHDFFKSAMPEGYVQERTISFKDDGTYKTRAEVKFEGDTLVNRIELK^GIDFKEDGNIL
GHKLEYNFN^SHNVYITADKQKNGIKANFKIRHNVEDGSVQLADHYQQNTPIGDGPVLLPDNHYLSTQSVLSKDPNEKRD
HMVLL^EFVTAAGITHGMDELY
B:M^PHLVIEATANLRLETSPGELLEQANKALFASGQFGEADIKSRFVTLEAYRQGTAAVERAYLHACLSILDGRDIATR
TLGASLCAVLAEAVAGGGE^EGVQVSVEVREMERLSYAKRVVARQRLEHHHHHH

>>T33-21 (24-mer)

A:MRITTKVGDKGSTRFLFGGEEVWKDSP^IIEANGTLDELTSFIGEAKHYVDEEMKGILEEIQNDIYKIMGEIGSKGKIE
GISEERIAWLLKLI^LLRMEMVNLKSFVLPGGTLES^AKLDVCRTIARRALRKVLTVTREFGIGAEAAAYLLALS^DLLFLL
ARVIEIEKNKLKEVRSGSGSGSSKGEELFTGVVPIILVELDGDVNGHKFSVRGEGEGDATNGKLT^LK^FICTTGKLPVPWP
TLVTT^LTYGVQCFARYPDHMKQHDFFKSAMPEGYVQERTISFKDDGTYKTRAEVKFEGDTLVNRIELK^GIDFKEDGNIL
GHKLEYNFN^SHNVYITADKQKNGIKANFKIRHNVEDGSVQLADHYQQNTPIGDGPVLLPDNHYLSTQSVLSKDPNEKRD
HMVLL^EFVTAAGITHGMDELY
B:M^PHLVIEATANLRLETSPGELLEQANKALFASGQFGEADIKSRFVTLEAYRQGTAAVERAYLHACLSILDGRDIATR
TLGASLCAVLAEAVAGGGE^EGVQVSVEVREMERLSYAKRVVARQRSKGEELFTGVVPIILVELDGDVNGHKFSVRGEGE

GDATNGKLTLLKFICTTGKLPVPWPTLVTTTLYGVQCFARYPDHMKQHDFFKSAMPEGYVQERTISFKDDGTYKTRAEVK
FEGDTLVNRIELKGIIDFKEDGNILGHKLEYNFNHSHNVYITADKQKNGIKANFKIRHNVEDGSQLADHYQQNTPIGDGP
VLLPDNHYLSTQSVLSKDPNEKRDMVLLLEFVTAAGITHGMDELYLEHHHHHH

>>I3-01 (ntGFP, 60-mer)

MHHHHHGGSSKGEELFTGVVPIILVELDGDVNGHKFSVRGEGEGDATNGKLTLLKFICTTGKLPVPWPTLVTTTLYGVQCF
ARYPDHMKQHDFFKSAMPEGYVQERTISFKDDGTYKTRAEVKFEGDTLVNRIELKGIIDFKEDGNILGHKLEYNFNHSHNV
YITADKQKNGIKANFKIRHNVEDGSQLADHYQQNTPIGDGPVLLPDNHYLSTQSVLSKDPNEKRDMVLLLEFVTAAGI
THGMDELYGGSSGGSSGGSSMKMEELFKKKHIVAVLRANSVEEAKKALAVFLGGVHLIEITFTVPDADTVIKELSFLK
EMGAIIGAGTVTSVEQCRKAVESGAEFIVSPHLDEEISQFCKEKGVFYMPGVMPTPELVKAMKLGHTILKLPGEVVG
QFVKAMKGFPPNVKVFVPTGGVNLNDVCEWFKAGVLAVGVGSALVKGTPVEVAEKAKAFVEKIRGCTE

>>I3-01 (ctGFP, 60-mer)

MHHHHHGGSSGGSSGGSSMKMEELFKKKHIVAVLRANSVEEAKKALAVFLGGVHLIEITFTVPDADTVIKELSFLKE
MGAIIGAGTVTSVEQCRKAVESGAEFIVSPHLDEEISQFCKEKGVFYMPGVMPTPELVKAMKLGHTILKLPGEVVG
FVKAMKGFPPNVKVFVPTGGVNLNDVCEWFKAGVLAVGVGSALVKGTPVEVAEKAKAFVEKIRGCTEGSGSGSGSSK
EELFTGVVPIILVELDGDVNGHKFSVRGEGEGDATNGKLTLLKFICTTGKLPVPWPTLVTTTLYGVQCFARYPDHMKQHDF
FKSAMPEGYVQERTISFKDDGTYKTRAEVKFEGDTLVNRIELKGIIDFKEDGNILGHKLEYNFNHSHNVYITADKQKNGI
ANFKIRHNVEDGSQLADHYQQNTPIGDGPVLLPDNHYLSTQSVLSKDPNEKRDMVLLLEFVTAAGITHGMDELY

>>I3-01 (nt/ctGFP, 120-mer)

MHHHHHGGSSKGEELFTGVVPIILVELDGDVNGHKFSVRGEGEGDATNGKLTLLKFICTTGKLPVPWPTLVTTTLYGVQCF
ARYPDHMKQHDFFKSAMPEGYVQERTISFKDDGTYKTRAEVKFEGDTLVNRIELKGIIDFKEDGNILGHKLEYNFNHSHNV
YITADKQKNGIKANFKIRHNVEDGSQLADHYQQNTPIGDGPVLLPDNHYLSTQSVLSKDPNEKRDMVLLLEFVTAAGI
THGMDELYGGSSGGSSGGSSMKMEELFKKKHIVAVLRANSVEEAKKALAVFLGGVHLIEITFTVPDADTVIKELSFLK
EMGAIIGAGTVTSVEQCRKAVESGAEFIVSPHLDEEISQFCKEKGVFYMPGVMPTPELVKAMKLGHTILKLPGEVVG
QFVKAMKGFPPNVKVFVPTGGVNLNDVCEWFKAGVLAVGVGSALVKGTPVEVAEKAKAFVEKIRGCTEGSGSGSGSSK
GEELFTGVVPIILVELDGDVNGHKFSVRGEGEGDATNGKLTLLKFICTTGKLPVPWPTLVTTTLYGVQCFARYPDHMKQHDF
FKSAMPEGYVQERTISFKDDGTYKTRAEVKFEGDTLVNRIELKGIIDFKEDGNILGHKLEYNFNHSHNVYITADKQKNGI
KANFKIRHNVEDGSQLADHYQQNTPIGDGPVLLPDNHYLSTQSVLSKDPNEKRDMVLLLEFVTAAGITHGMDELY

>>I3-01 (HB)

MHHHHHGGSSGGSSGGSSMKMEELFKKKHIVAVLRANSVEEAKKALAVFLGGVHLIEITFTVPDADTVIKELSFLKE
MGAIIGAGTVTSVEQCRKAVESGAEFIVSPHLDEEISQFCKEKGVFYMPGVMPTPELVKAMKLGHTILKLPGEVVG
FVKAMKGFPPNVKVFVPTGGVNLNDVCEWFKAGVLAVGVGSALVKGTPVEVAEKAKAFVEKIRGCTEGSGSGSGGTKEYEY
DIEELRKKLKEQNKEMEKLKEELKKMEKLPKSPIAKLLILQMKLLLLQIENLQMQITMLEILSKR