

a

Residue number	Domain description	GenBank accession number (matching residue numbers)
1-10	Src myristoylation motif	AAD13831.1 (1-10)
11-15	Linker	-
16-337	SARS2 M ^{Pro} with cognate N- and C-terminal cleavage sites	QNO91750.1 (3256-3577)
338-346	Linker	-
347-418	HIV-1 Tat	ACD75161.1 (1-72)
419-424	Linker	-
425-663	eGFP	AAB02576.1 (1-239)

Amino acid sequence:

MGSSKSKPKDGGGSSITSVAVLQSGFRKMAFSPGKVEGCMVQVTCGTTTLNGLWLDVVYQCPRHVICTSEDMLNPNYEDLLIRKSNHNFLVQAGNVQ
LRVIGHSMQNCVLLKLVDTANPKTPKYKRVRIQPGQTFVSVLACYNGSPSGVYQCAMPNFTIKGSFNLNGSCGVSFNFIDYDCVDFCYMHMELPTGV
HAGTDLEGNFYGPFVDRQTAQAAGTDTTITVNVLAWLYAAVINGDRWFLNRFNTLLNDFNLVAMKYNIEPLTQDHWVDILGPLSAQTGIAVLDMCASL
KELLQNGMNRITLGSALLEDEFPPFDVVRQCSGVTFQSAVKRTIKGTSGSGGMEPVDPRLEPWKHPGSQPKTACTNCYCKCCFHCQVCFITKA
LGISYGRKKRRRPPQGSQTHQVLSLQKPGSIATMVSKEELFTGVVPILEVELDGDVNGHKFSVSGEGEGDATYGLTLKFICTTGKLPVPWPTL
VTTLTYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGI DFKE DGNILGHKLEYNNSHNHYIMADKO
KNGIKVNFKIRHNIEDGSVQLADHYQQNTPIGDGPVLLPDNHLYLSTQSALS KDPNEKRDMVLEFVTAAGITLGMDELYK*

b

Nucleotide sequence:

AAGCTTGCCACCATGGGCAGCAGTAAGAGTAAACCGAAAGATGGAGCGGTGGGTCACTATCACCTCAGCTGTTTTGCAGTCTGGTTTTAGGAAAA
TGGCGTCCCCAGCGGTAAGTTGAAGGATGTATGGTCCAAGTAACTGTGGTACCCTACCTTAATGGGCTTTGGTTGGACGACGTAGTCTACTG
CCCCGCACAGTAATCTGCACTAGTGAGGATATGCTTAATCCCAATTACGAAGACCTTTTGATTCGGAAATCCAATCACAACTCCTGGTCCAAGCG
GGCAACGTCCAACCTCAGGGTTATTGGACATAGTATGCAGAATTGCGTACTGAAGCTCAAAGTCGATACTGCAAACCCCAAGACGCCCAAGTATAAAT
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TTACAGTGAATGTGCTCGCGTGGCTGTACGCAGCAGTCATAAACGGAGACAGGTGGTTTCTGAACCGATTTACGACGACTCTCAATGACTTCAACCT
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TGCGCGTCACTGAAGGAGCTTCCAAAATGGAATGAATGGGCGGACCATACTTGGTTCGGCACTCCTCGAAGATGAATTTACTCCATTTGACGTGG
TCAGACAATGCAGTGGGTCACTTCCAGAGTGCAGTGAAAAGAACAATCAAGGGTACC GGTCAGGGGCGAGGGGATGGAGCCAGTAGATCC
TAGACTAGAGCCCTGGAAGCATCCAGGAAGTCAGCCTAAAACCTGCTTGTACCAATTGCTATTGTAAAAAGTGTGCTTTCAATGCCAAGTTTGTTC
ATAACAAAAGCCTTAGGCATCTCCTATGGCAGGAAGAAGCGGAGACAGCGACGAAGACCTCCTCAAGGCAGTCAGACTCATCAAGTTTCTCTATCAA
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CCACAAGTTTACGGTGTCCGGCGAGGGCGAGGCGATGCCACCTACGGCAAGCTGACCTGAAGTTTCACTGCACCACCGGCAAGCTGCCCGTGCCC
TGGCCACCCTCGTGACCACCCTGACCTACGGCGTGCAGTGTTCAGCCGCTACCCCGACCACATGAAGCAGCAGACTTCTTCAAGTCCGCCATGC
CCGAAGGTACGTCCAGGAGCGACCATCTTCTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTGAGGGCGACACCCTGGTGAA
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GCCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACGGCAGCTGCAGCTCGCCGACCACTACCAGCAGAACA
CCCCATCGGCGACGGCCCCGTGCTGCTGCCGACAACCCTACCTGAGCACCCAGTCCGCCCTGAGCAAAGACCCCAACGAGAAGCGGATCACAT
GGTCTGTGGAGTTCGTGACCGCCCGGGATCACTCTCGGATGGACGAGTGTACAAGTAAAGCGGCCG