

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	-
425-973	Firefly Luciferase	EU754723.1 (2-550)

Amino acid sequence:

MGSSKSKPKDGGGSSITS^{AVL}QSGFRKMAFPSPGKVEGCMVQVTCGTTTLNGLWLDVVYCPRHVICTSEDMLNPNYEDLLIRKSNHNFLVQAGNVQ
LRVIGHSMQNCV^{LK}LKVD^{TAN}PKTPKYK^{FVRI}QPGQ^{TS}SVLACYNGSPSGVYQCAMRPNFTIKGSFLNGSCG^{SVGF}NDYDCV^{SC}FCYMHMELPTGV
HAGTDLEGNFYGFV^{DR}QTAQAAGTDTIT^{VN}VLAWL^{YAAV}INGDRWFLNRF^{TTL}NDFNLVAMKYNYEPLTQ^{DH}V^{DL}GLPLSAQ^{TG}IAVLD^{MC}ASL
KELLQNGMNGRTIL^{GS}ALLEDEF^{TF}PFV^{VR}QCSG^{VT}FQSAVKRTIKGTGSGGSGGMEPVD^{PR}LEPWKHPGSQPKTACTN^{CY}CKKCCFHCQ^{VC}FITKA
LGLSYGRKRRRQRRRPPQGSQTHQVSLSKQPGSIATEDAKNIKKGPAPFYPLEDGTAGEQLHKAMKRYALVPGTIA^{FT}DAHIEVNI^{TY}AEYFEMSVR
LAEAMKRYGLN^{TN}HRI^{VV}CS^{NS}LQ^{FF}MPV^LGAL^{FI}GVA^{VAP}ANDI^{YNER}EL^{NS}MNI^{SQ}PT^{VV}FVSKKGLQKIL^{NV}QK^{KL}PIIQKI^{II}IMDSK^{TD}YQ
GFQSMY^{TF}V^{TS}HL^{PP}PGF^{NEY}DFV^{PE}SFDR^{DK}TIALIM^{NS}SGSTGLPK^{GVA}LPH^{RT}AC^{VR}FSHARD^{PI}FG^{NI}I^{IP}DTAIL^{SV}VP^{FF}HHG^{FG}M^{FT}TL^{GY}L
ICGFRV^{LM}YR^{FE}EEL^{FL}RL^{SD}YKI^{QS}ALL^{VPT}LF^{SFF}AKSTLID^{KY}DLS^{NL}HEIASGGAP^{LS}KEVGE^{AV}AKR^{FHL}PGIR^{QY}GL^{TET}TSAIL^{ITP}
EGDDKPGAVGK^{VV}FF^{EAK}V^{VD}L^{DT}GK^{TL}GV^{NQ}R^{GEL}CV^{RG}PM^{IS}GV^{VNN}PEAT^{NAL}ID^{KD}GW^{LH}SG^{DI}AY^{WDE}DE^{HE}FFI^{VDR}L^{KSL}I^{KY}K^{GY}Q^{VA}
PAELESILLQHPNIFDAGVAGL^{PDD}DAGEL^{PA}AV^{VV}LE^{HG}KTMTEKEIV^{DY}VAS^{QV}TTAK^{KL}R^{GG}V^VF^VDEV^{PK}GL^{TG}K^LDARKIRE^{IL}I^{KAK}KG^{SK}L*

b

Nucleotide sequence:

AAGCTTGCACCATGGGGCAGCAGTAAGAGTAAACCGAAAGATGGAGCGGTGGGTCA^{TCT}TATCACCTCAGCTGTTTTGCAGTCTGGTTTTAGGAAAA
TGGCGTCCCCAGCGGTAAGTGAAGGATGTATGGTCCAAGTAACTGTGGTACCCTACCTTAATGGGCTTTGGTGGACGACGTAGTCTACTG
CCCCCGACACGTAATCTGCAC^{TAG}TGAGGATATGCTTAATCCCAAT^{TAC}GAAGACCTTTTGATTCGGAAATCCAATCACA^{ACT}TCCTGGTCCAAAGCG
GGCAACGTCCA^{ACT}CAGGGTTAT^{TGG}CATAGTATGCGA^{ATT}TGCGTACTGAAGCTCAAAGTCGATACTGCAACCCCAAGACGCCCAAGTATAAAT
TCGTCCGAATCCAACCAAGCCAAACATTTCCGTAATTGGCTTGCATAAATGGAAGCCCCAGCGGTGTCTACCAATGTCAATGAGACCAAACTTAC
GATAAAGGGTTCATTTCTGAACGGCTCTTGGCTTCCGTTGGTTTTAATCGACTATGACTGTGTATCCTTTTGCTACATGCACCATATGGAAGTCC
CCTACCGGTGTCCACGCCGGTACAGATCTGGAAGGAAATTTCTACGGTCCGTTCTGTTGACCGGCAAAACCGCGCAAGCGGCTGGAACCGACACAACGA
TTACAGTGAATGTCTCGCTGGCTGTACGCAGCAGTCATAAACGGAGACAGGTGGTTCTGAACCGATTTACGACGACTCTCAATGACTTCAACCT
TGTTCCGATGAAGTACAAT^{TAC}GAGCCTC^{AC}CCAGACCATGTTGATATCCTGGTCCCTCAGTCCCAGACAGGGATCCGAGTCTCGATATG
TGCGGCTACTGAAGGAGCTTCCAAAATGGAATGAATGGCGGACCATACTGGTTCGGCACTCCTCGAAGATGAATTTACTCCATTTGACGTGG
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TAGACTAGAGCCTGGAAGCATCCAGGAAGTCAGCCTAAAAC^{TG}CTTGTACCAAT^{TGT}ATTTGTA^{AAA}AGTGTGTCTTTCATTTGCCAAGTTTGTTC
ATAACAAAAGCC^TTAGGCATCTCCTATGGCAGGAAGAAGCGGAGACAGCGACGAAGACCTCCTCAAGGCAGTCAGACTCATCAAGTTTCTCTATCAA
AGCAGCCGGGATCCATCGCCACCGAAGACGCCAAAACATAAAGAAAGGCCGGCGCCATTCATCCTCTAGAGGATGGAACCGCTGGAGAGCAACT
GCATAAGGCTATGAAGAGATACGCCCTGGTTCCTGGAACAAT^{TG}CTTTACAGATGCACATATCGAGGTGAACATCAGTACCGGGAATACTCGAA
ATGTCCGTTCCGTTGGCAGAAGTATGAACGATATGGGCTGAATACAAT^{CAC}AGAATCGTCGATGCAGTGA^{AA}ACTCTCTCAATTTCTTTATGC
CGGTGTTGGCGCGGTTATTTATCGGAGTTCGAGTTGCCCGCGGAACGACATTTATAATGAAGTGAAT^{TGC}TCAACAGTATGAACATTTCCGAGCC
TACCGTAGTGT^{TT}GT^{TT}CCAAAAGGGGTTGCAAAAATTTTGAACGTGCAAAAAAAT^{TAC}CAATAATCCAGAAAAT^{TAT}TATCATGGATTTCTAAA
ACGGATTACCAGGGATTCAGTGCATGTACACGTTCTGTCACATCTCATCTACCTCCCGGTTTTAATGAATACGATTTTGTACCAGAGTCTTTGATC
GTGACAAAACAAT^{TG}CACTGATAATGAAT^{CT}CTGGATCTACTGGGTTACCTAAGGGTGTGGCCCTCCGCATAGA^{ACT}GCCTGCGTCAGATTTCTC
GCATGCCAGAGATCCTATTTTGGCAATCAAATCATTCGGATACTCGGATTTAAGTGTGTTCATTTCCATCCATCAGGTTTTGGAATGTTACTACA
CTCGGATATTTGATATGTGGATTTCCAGTCTCTTAATGTATAGATTTGAAGAAGAGCTGTTTTTACGATCCCTT^{CAG}GATTACAAAAT^{TCAA}AGTG
CGTTGCTAGTACCAACCTATTTTCATCTCTCGCCAAAAGCACTCTGATTGACAAAATACGATTTATCTAATTTACACGAAAT^{TG}CTTCTGGGGCGC
ACCTCTTCGAAAGAAGTCGGGAAGCGGTTGCAAAACGCTTCCATCTCCAGGGATACGACAAGGATATGGGCTCACTGAGACTACATCAGCTATT
CTGATTAACCCGAGGGGATGATAAACCGGGCGCGTCCGTTAAAGTGTTCATTTTGAAGCGAAGTTGTGATCTGGATCCGGATACCGGAAAAACGC
TGGCGT^{TAA}TACAGAGGGCAAT^{TAT}GTGTGAGAGGACCTATGAT^{TAT}GTCCGGT^{TAT}GTAAACAATCCGGAAGCGACCAACGCCTT^{GAT}TGACAA
GGATGGATGGCTACATTTCTGGAGACATAGCTTACTGGGACGAAGACGAACACTTCTT^{CAT}AGTTGACCGCTTGAAGTCTTTAAT^{TAA}ATACAAAGGA
TATCAGGTGGCCCGCTGAAT^{TG}GAATCGATAT^{TGT}TACAACACCCCAACATCTTCGACGCGGGCGTGGCAGGTCTTCCGACGATGACGCCGGTG
AACTTCCCGCCCGTTGTGT^{TT}TGGAGCACGGAAGACGATGACGGA^{AAA}AGAGATCGTGGATTCGTCGCCAGTCAAGTAAACCCGCAAAAA
GTTGCGCGGAGGAGTTGT^{TT}TGTGAGCAGTACCGAAAGTCTTACCGGAAAAC^{TG}ACGCAAGAAAATCAGAGAGATCTCATAAAGGCCAAG
AAGGGCGAAAGTCCAAATTTGTAAGCGGCCG