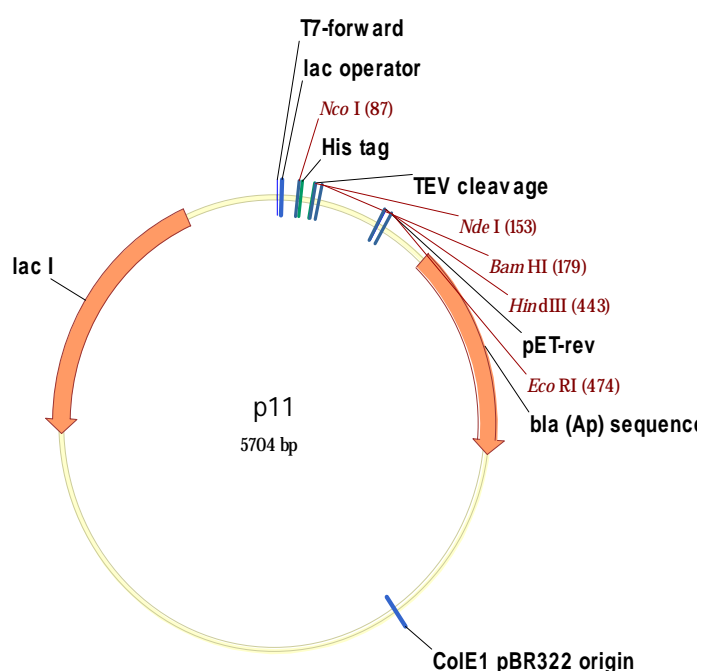


Vector information sheet.

Vector Name	p11
Source	Sujata Sharma, Toronto SGC
Sequence accession/link	(SGC)
Description	pET expression vector with His ₆ tag in 22-aa N-terminal fusion peptide, with TEV protease cleavage site.
Antibiotic resistance	amp
Promoter	T7 - lacO
Cloning	In-frame NdeI – BamHI.
Initiation codon	In vector
N-terminal fusion – seq.	MGSSHHHHHHSSGRENLYFQ*GH (* - TEV cleavage site)
N-terminal fusion – MW	2693.07 Da (including met). TEV cleavage removes 2367.65 Da.
Termination codons	In vector, after BamHI (in frame: GGA TCC TAA; adds gly-ser to the C-terminus) (Termination codon may be supplied in the insert)
C-terminal fusion – seq.	GS
C-terminal fusion – MW	144.14 Da
Protease cleavage	TEV
Additional features	
Preferred host	DE3 hosts: BL21, Rosetta, etc. MUST express T7 RNA polymerase.
5' sequencing primer	T7 promoter: TAATACGACTCACTATAGGG
3' sequencing primer	PET-rev. ATGTTTGACAGCTTATCATCGA NOTE: standard T7 terminator primer does not work!!!



Polylinker region

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5685                                     BglIII
                                         A GATCTCGATC
                                         T CTAGAGCTAG

                                     T7-forward
                                     ~~~~~~
5696 CCGCGAAATF AATACGACTC ACTATAGGGG AATTGTGAGC GGATAACAAT TCCCCTCTAG
GGCGCTTTAA TTATGCTGAG TGATATCCCC TTAACACTCG CCTATTGTTA AGGGGAGATC
                                         NcoI
                                         M G S S H H H H
52 AAATAATTTT GTTAACTTT AAGAAGGAGA TATACCATGG GCAGCAGCCA TCATCATCAT
TTTATTAATA CAAATTGAAA TTCTTCCTCT ATATGGTACC CGTCGTCGGT AGTAGTAGTA

                                         TEV
                                         ↓
                                         NdeI NheI
H H S S G R E N L Y F Q G H M A S L T G
112 CATCACAGCA GCGGCAGAGA AACTTGTAT TTCCAGGGCC ATATGGCTAG CTTGACTGGT
GTAGTGTCGT CGCCGTCTCT TTTGAACATA AAGGTCCCGG TATACCGATC GAACTGACCA
BamHI
G Q G S *
172 GGACAGGGAT CCTAATAACT AAGTAAACTA GTGCTGAGCA ATAAC TAGCA TAACCCCTTG
CCTGTCCCTA GGATTATTGA TTCATTTGAT CACGACTCGT TATTGATCGT ATTGGGGAAC

232 GGGCCTCTAA ACGGGTCTTG AGGGGTTTTT TGCTGAAAGG AGGAACTATA TCCGGATATC
CCCGGAGATT TGCCAGAAC TCCCAAAAA ACGACTTTCC TCCTTGATAT AGGCCTATAG

292 CCGCAAGAGG CCCGGCAGTA CCGGCATAAC CAAGCCTATG CCTACAGCAT CCAGGGTGAC
GGGCTTCTCC GGGCCGTCAT GGCCGTATTG GTTCGGATAC GGATGTCGTA GGTCCCCTG

352 GGTGCCGAGG ATGACGATGA GCGCATTGTT AGATTTTATA CACGGTGCCT GACTGCGTTA
CCACGGCTCC TACTGCTACT CGCGTAACAA TCTAAAGTAT GTGCCACGGA CTGACGCAAT

                                         ClaI
HindIII
412 GCAATTTAAC TGTGATAAC TACCGCATT AAGCTTATCG ATGATAAGCT GTCAAACATG
CGTTAAATG AACTATTG ATGGCGTAAT TTCGAATAGC TACTATTGCA CAGTTTGTAC
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                                         pET-rev

EcoRI
472 AGAATTC
TCTTAAG
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