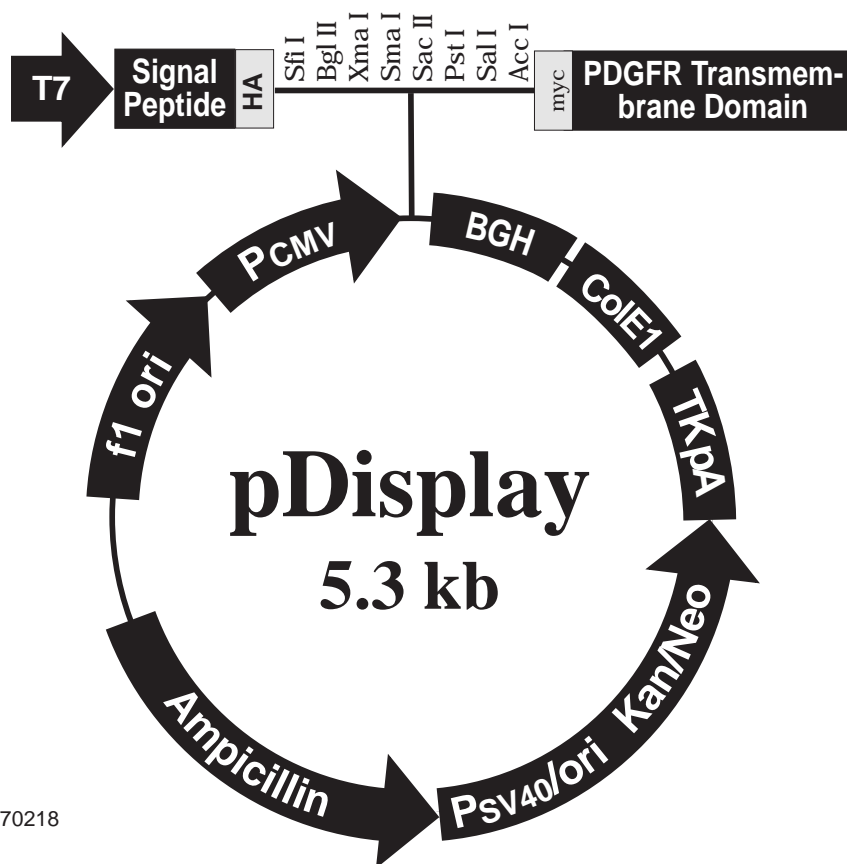


Comments for pDisplay:
5325 nucleotides



CMV promoter: bases 1-596
T7 promoter: bases 638-657
Murine Ig kappa-chain V-J2-C signal peptide: bases 737-799
Hemagglutinin A epitope: bases 800-826
Multiple Cloning Site: bases 827-873
myc epitope: bases 874-903
PDGFR transmembrane domain: bases 907-1056
Bovine growth hormone polyadenylation signal: bases 1069-1288
Col E1 origin: bases 1378-2051
Thymidine kinase polyadenylation site: bases 2458-2187
Neomycin/Kanamycin resistance gene: bases 3421-2366
SV40 origin and promoter: bases 3797-3456
Ampicillin resistance gene: bases 4736-3876
f1 origin: bases 5000-5099



The sequence of pDisplay has been compiled from information in sequence databases, published sequences, and other sources. This vector has not been completely sequenced. If you suspect an error in the sequence, please contact Invitrogen's Technical Services Department.

pDisplay
hCMV immediate early promoter
Ig k-chain signal sequence
Polylinker
Primer binding sites
Bovine growth hormone polyA



↓ 5' end of hCMV promoter/enhancer
1 GCGCGCGTTG ACATTGATTA TTGACTAGTT ATTAATAGTA ATCAATTACG GGGTCATTAG
61 TTCATAGCCC ATATATGGAG TTCCGCGTTA CATAACTTAC GGTAATGGC CCGCCTGGCT
121 GACCGCCCAA CGACCCCGC CCATTGACGT CAATAATGAC GTATGTTCCC ATAGTAACGC
181 CAATAGGGAC TTTCCATTGA CGTCAATGGG TGGACTATTT ACGGTAAACT GCCCACTTGG
241 CAGTACATCA AGTGTATCAT ATGCCAAGTA CGCCCCCTAT TGACGTCAAT GACGGTAAAT
301 GGCCCGCCTG GCATTATGCC CAGTACATGA CCTTATGGGA CTTTCCTACT TGGCAGTACA
361 TCTACGTATT AGTCATCGCT ATTACCATGG TGATGCGGTT TTGGCAGTAC ATCAATGGGC
421 GTGGATAGCG GTTTGACTCA CGGGGATTTC CAAGTCTCCA CCCCATTTGAC GTCAATGGGA
481 GTTTGTTTTG GCACCAAAAT CAACGGGACT TTCCAAAATG TCGTAACAAC TCCGCCCAT
541 TGACGCAAAT GGGCGGTAGG CGTGTACGGT GGGAGGTCTA TATAAGCAGA GCTCTCTGGC
601 TAACTAGAGA ACCCACTGCT TACTGGCTTA TCGAAATTAA TACGACTCAC TATAGGGAGA
661 CCCAAGCTTG GTACCGAGCT CGGATCCACT AGTAACGGCC GCCAGTGTGC TGGAAATTCGG
721 CTTGGGGATA TCCACC ATG GAG ACA GAC ACA CTC CTG CTA TGG GTA CTG CTG
Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu
hemagglutinin A epitope
773 CTC TGG GTT CCA GGT TCC ACT GGT GAC TAT CCA TAT GAT GTT CCA GAT
Leu Trp Val Pro Gly Ser Thr Gly Asp Tyr Pro Tyr Asp Val Pro Asp
821 TAT GCT GGG GCC CAGCCGGCCA GATCTCCCGG GATCCGCGG CTGCAGGTC GAC
Tyr Ala
874 GAA CAA AAA CTC ATC TCA GAA GAG GAT CTG AATGCTGTGG GCCAGGACAC
Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu ...
924 GCAGGAGGTC ATCGTGGTGC CACACTCCTT GCCCTTTAAG GTGGTGGTGA TCTCAGCCAT
984 CCTGGCCCTG GTGGTGCTCA CCATCATCTC CCTTATCATC CTCATCATGC TTTGGCAGAA
1044 GAAGCCACGT TAGGCGGCCG CTCGAGATCA GCCTCGACTG TGCCTTCTAG TTGCCAGCCA
1104 TCTGTTGTTT GCCCCTCCCC CGTGCCTTCC TTGACCCTGG AAGGTGCCAC TCCCACTGTC
1164 CTTTCCTAAT AAAATGAGGA