

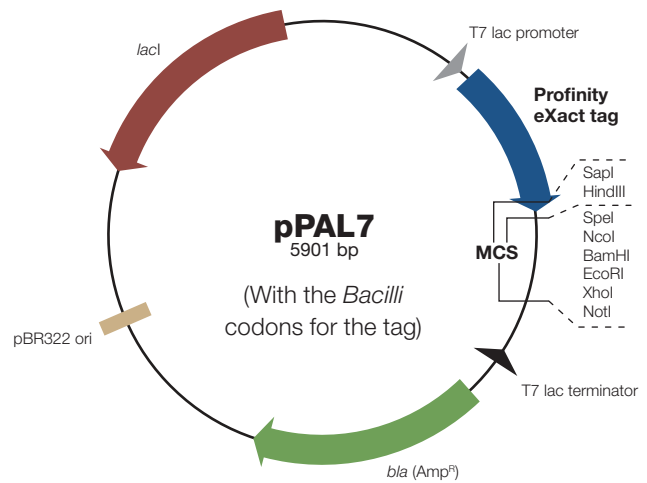
## The pPAL7 Vector Map and Plasmid Sequence

### The Profinity eXact pPAL7 Vector Enables *E. coli* Expression of Fusion Proteins with the Profinity eXact™ Tag

Precise fusions of the Profinity eXact tag to a protein of interest may be constructed with either the HindIII or SapI site. When using the HindIII site to insert a target gene, it is essential that the insertion contains the Profinity eXact tag's TG bases immediately downstream of the HindIII recognition site to restore the tag's terminal leucine. Similarly, if SapI is used, the tag must be fully restored by including AAGCTTTG upstream of the first codon of the target gene. A Thr-Ser spacer sequence may be created by cloning into the SpeI site; a longer spacer would be created by cloning into the other sites downstream of SpeI. RIC (restriction-independent cloning)-ready vector is available for precise fusion and high-throughput cloning. Finally, inserted genes must contain their own stop codon.

**Table 1. Features of pPAL7 expression vector.**

Feature	Position
T7lac promoter	1–17
Profinity eXact tag	92–316
MCS	
SpeI	318
NcoI	325
BamHI	333
EcoRI	345
XhoI	351
NotI	358
T7 terminator	413–460
<i>bla</i> (Amp <sup>R</sup> )	881–1,738
<i>Ori</i>	2,499
<i>lacI</i>	4,436–5,515



Profinity eXact pPAL7 vector.

### Cloning and Expression Region

T7 Promoter      lac Operator      XbaI  
 GCGAAATTAA TACGACTCAC TATAGGGGAA TTGTGAGCGG ATAACAATTC CCCTCTAGAA ATAATTTTGT TTAAC TTAA GAAGGAGATA  
Profinity eXact Tag

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NdeI  
 TACAT ATG GGA GGG AAA TCA AAC GGG GAA AAG AAA TAT ATT GTC GGG TTC AAA CAG GGC TTT AAG AGC TGC GCT AAG  
 Met Gly Gly Lys Ser Asn Gly Glu Lys Lys Tyr Ile Val Gly Phe Lys Gln Gly Phe Lys Ser Cys Ala Lys  
Profinity eXact Tag

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Profinity eXact Tag  
 AAG GAG GAT GTC ATT TCT GAA AAA GGC GGG AAA CTC CAA AAG TGC TTC AAA TAT GTA GAC GCA GCT AGC GCT ACA TTA  
 Lys Glu Asp Val Ile Ser Glu Lys Gly Gly Lys Leu Gln Lys Cys Phe Lys Tyr Val Asp Ala Ala Ser Ala Thr Leu  
Profinity eXact Tag

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SapI      HindIII  
 AAC GAA AAA GCT GTA GAA GAA TTG AAA AAA GAT CCG AGC GTC GCG TAC GTA GAA GAA GAC AAG CTC TTC AAA GCT TTG  
 Asn Glu Lys Ala Val Glu Glu Leu Lys Lys Asp Pro Ser Val Ala Tyr Val **Glu Glu Asp Lys Leu Phe Lys Ala Leu**  
Cleavage Recognition Sequence  
Profinity eXact Cleavage Site (FKAL)

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SpeI      NcoI      BamHI      EcoRI      XhoI      NotI  
 ACT AGT ACC ATG GCG GGA TCC GGC TGC GAA TTC CTC GAG GCG GCC GCA TAA GCCCGAAAGG AAGCTGAGTT GGCTGCTGCC  
 Thr Ser Thr Met Ala Gly Ser Gly Cys Glu Phe Leu Glu Ala Ala Ala Stop

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T7 Terminator  
 ACCGCTGAGC AATAACTAGC ATAACCCCTT GGGGCCCTCTA AACGGGTCTT GAGGGGTTTT TTGCTGAAAG GAGGAACTAT

1	TAATACGACT	CACTATAGGG	GAATTGTGAG	CGGATAACAA	TTCCCTCTA	GAATAATTT	TGTTTAACTT	TAAGAAGGAG	ATATACATAT	GGGAGGGAAA	TCAAACGGGG
111	AAAAGAAATA	TATTTGTCGGG	TTCAAACAGG	GCTTTAAGAG	CTGCGCTAAG	AAGGAGGATG	TCATTTCTGA	AAAAGGCGGG	AAACTCCAAA	AGTGCTTCAA	ATATGTAGAC
221	GCAGCTAGCG	CTACATTAAA	CGAAAAGCT	GTAGAAGAAT	TGAAAAAAGA	TCCGAGCGTC	CGGTACGTAG	AAGAAGACAA	GCTCTTCAA	GCTTTGACTA	GTACCATGGC
331	GGGATCCGG	TGCGAATTC	TCGAGGCGGC	CGCATAAGCC	CGAAAGGAAG	CTGAGTTGGC	TGCTGCCACC	GCTGAGCAAT	AACTAGCAT	ACCCCTTGGG	GCCTCTAAAC
441	GGGTCTTGA	GGGTTTTTGG	CTGAAGGAG	GAACATATCC	CGGATATCCC	GCAAGAGGCC	CGCGACTACC	GGCATAACCA	ACCCTATGCC	TACAGCATCC	TTGACGACGG
551	TGCCGAGGAT	GACGATGAGC	GCATTGTTAG	ATTTTCATACA	CGGTGCCTGA	CTGCGTTAGC	AATTTAACTG	TGATAAACTA	CGGCATAAA	GCCTATCGAT	GATAAGCTGT
661	CAAACATGAG	ATTTCTTGAA	GACGAAAGGG	CCTCGTGATA	CGCCTATTTT	TATAGGTTAA	TGTCATGATA	ATAATGGTFT	CTTAGACGTC	AGGTGGCACT	TTTCGGGGAA
771	ATGTGCGCGG	AACCCCTATP	TGTTTATTTT	TCTAAATACA	TTCAAATATG	TATCCGCTCA	TGAGACAATA	ACCCTGATAA	ATGCTTCAAT	AATATTGAAA	AAGGAAGAGT
881	ATGAGTATTC	AACATTTCCG	TGTCGCCCTT	ATTCCTTTT	TTGCGGCATT	TTGCCTTCT	GTTTTTGCTC	ACCCGAGAAC	GCTGGTGAAA	GTAAAAGATG	CTGAAGATCA
991	GTTGGGTGCA	CGATGGGTT	ACATCGAAT	GGATCTCAAC	AGCGGTGAAG	TCCTTGAGAG	TTTTTCGCCC	GAAGAACGTT	TTCCAATGAT	GAGCATTTTT	AAAGTTCTGC
1101	TATGTGGCGC	GGTATTATCC	CGTGTGACG	CCGGGCAAGA	GCAACTCGGT	CGCCGCATAC	ACTATTCTCA	GAATGACTTG	GTTGAGTACT	CACCACTGTC	AGAAAAGCAT
1211	CTTACGGATG	GCATGACAGT	AAGAGAATTA	TGCAGTGCTG	CCATAACCAT	GAGTGATAAC	ACTGCGGCCA	ACTTACTTCT	GACAAACGATC	GGAGGACCGA	AGGAGCTAAC
1321	CGCTTTTTTG	CACAACATGG	GGGATCATGT	AACTCGCCCT	GATCGTTGGG	AACCGGAGCT	GAATGAAGCC	ATACCAAACG	ACGAGCGTGA	CACCACGATG	CCTCGACCAA
1431	TGGCAACAAC	GTTCGCGAAA	CTATTAACCTG	GCGAACTACT	TACTCTAGCT	TCCGCGCAAC	AATTAATAGA	CTGGATGGAG	GCGGATAAAG	TTGACGAGCC	ACTTCTGGCC
1541	TCGGCCCTTC	CGGTGGGCTG	GTTTATTGCT	GATAAATCTG	GAGCCGGTGA	GCGTGGGTCT	CGCGGTATCA	TTGCGAGCACT	GGGGCCAGAT	GGTAAGCCCT	CCGCTATCGT
1651	AGTTATCTAC	ACGACGGGGA	GTCAGGCAAC	TATGGATGAA	CGAAATAGAC	AGATCGCTGA	TATAGGTGCC	TCACTGATTA	AGCATTTGTA	ACTGTCAGAC	CAAGTTTACT
1761	CATATATACT	TTAGATTGAT	TTAAAACCTC	ATTTTTAAT	TAAAAGGATC	TAGGTGAAGA	GCATTTTGA	TAATCTCATG	ACCAAAATCC	CTTAACGATG	GTTTTGCTTC
1871	CACTGAGCGT	CAGACCCCGT	AGAAAAGATC	AAAGGATCTT	CTTGAGATCC	TTTTTTTCTG	CGCGTAATCT	GCTGCTTGCA	AACAAAAAAA	CCACCGCTAC	CAGCGGTGTT
1981	TTGTTTGGCG	GATCAAGAGC	TACCAACTCT	TTTTCCGAAG	GTAAGTGGCT	TCAGCAGAGC	GCAGATACCA	AATACTGTCC	TTCTAGTGA	GCCGTAGTTA	GGCCACCACT
2091	TCAAAGACTC	TGTAGCACCG	CTACATATCC	TCGCTCTGCT	AATCCTGTTA	CCAGTGCGTG	CTGCCAGTGG	CGATAAGTCG	TGCTTACCG	GGTTGGACTC	AAGACGATAG
2201	TTACCGGATA	AGGCGCAGCG	GTCGGGCTGA	ACGGGGGGTT	CGTGACACCA	GCCCAGCTTG	GAGCGAACGA	CCTACACCGA	ACTGAGATAC	CTACAGCGTG	AGCTATGAGA
2301	AAGCGCCACG	CTTCCCGAAG	GGAGAAAGGC	GGACAGGTAT	CCGTTAAGCC	GCAGGCTCGG	AACAGGAGAG	CGCAGGAGGG	AGCTTCCAGG	GGGAAACGCG	TGGTATCTTT
2421	ATAGTCTGTG	GGGTTTFCG	CACCTCTGAC	TTGAGCGCTG	ATTTTTGTGA	TGCTCTCTG	GGGGCGGAGG	CCATATGAAA	AACGCGACGA	ACGCGCCCTT	TTTACGGTTT
2531	CTGGCCTTTT	GCTGGCCTTT	TGCTCACATG	TTCTTCTCTG	CGTTATCCCC	TGATCTGTG	GATAACCGTA	TTACCCGCTT	TGAGTGAGCT	GATACCGCTC	GCCGACGCGG
2641	AACGACCGAG	CGCAGCGAGT	CAGTGAGCGA	GGAAGCGGAA	GAGGCGCTGA	TGCGGTATTT	TCTCCTTACG	CATCTGTGCG	GTATTTTACA	CCGCATATAT	GGTGCACTCT
2751	CAGTACAATC	TGCTCTGATG	CGCATAGT	AAGCCAGTAT	ACACTCCGCT	ATCGCTACGT	GACTGGGTCA	TGGCTGCGCC	CCGACACCCG	CCAACACCCG	CTGACGCGCC
2861	CTGACGGGCT	TGCTGTCTCC	CGGCATCCGC	TTACAGACAA	GCTGTGACCC	TCTCCGGGAG	CTGCATGTGT	CAGAGGTTTT	CACCGTCACT	ACCGAAACGC	GCGAGGCGAG
2970	TGCGGTAAAG	CTCATCAGCG	TGGTCGTGAA	CGGATTCACA	GATGTCGCTG	TGTTTATCCG	CGTCCAGCTC	GTTGAGTTTC	TCCAGAAGCG	TTAATGTCTG	GCTTCTGATA
3081	AAGCGGGCCA	GGTTAAGGGC	GTTTTTTTTC	TGTTTGGTGA	CTGATCCGCT	CGTGAAGGG	GGATTTTGTG	TCATGGGGGT	AATGATACCG	AGGAAACGAG	GAGAGGCTGT
3191	CACGATACGG	GTTACTGATG	ATGAACATGC	CCGGTACTG	GAACGTTGTG	AGGGTAAACA	ACTGGCGGTA	TGGATGCGGC	GGGACCAGAG	AAAAATCACT	CAGGGTCAAT
3301	GCCAGCGCTT	CGTTAATACA	GATGTAGGTG	TTCCACAGGG	TAGCCAGCAG	CATCTGCGA	TGCAGATCCG	GAACATAATG	GTGACGGGCG	CTGACTCCG	CGTTTCCAGA
3411	CTTTACGAAA	CACGGAAACC	GAAGACCATT	CATGTTGTTG	CTCAGGTCGC	AGACGTTTTG	CAGCAGCAGT	CGCTTCACTG	TCGCTCGCGT	ATCGGTGATT	CATTCTGCTA
3521	ACCAGTAAGG	CAACCCCGCC	AGCCTAGCCG	GGTCTCAAC	GACAGGAGCA	CGATCATGCG	CACCCGTGGC	CAGGACCCAA	CGTGCCCCGA	GATGCGCCCG	GTGCGGCTGC
3631	TGGAGATGGC	GGAGCGGCTG	GATATGTCTC	GCCAAGGGTT	GGTTTGGCGA	TTACAGTTC	TCCCGAAGAA	TGATTTGGCT	CCAATCTTGG	GAGTGGTGA	TCCGTAGCG
3741	AGGTGCGCCG	GGCTTCCATT	CAGGTCGAGG	TGCGCCGCTG	CCATGACACG	GACGAAACAG	GACAAAGGTA	AGGCGCCGCG	AGGCGCCGCG	GAGCAATCCA	TGCCAACCCG
3851	TTCCATGTGC	TGCGCGAGGC	GGCATAAATC	GCCGTGACGA	TCAGCGGTCC	AGTGATCGAA	GTTAGGCTGG	TAAGAGCCCG	GAGCGATCCT	TGAAGCTGTC	CCTGATGGTC
2961	GTCATCTACC	TGCTGGGACA	GCATGGCCTG	CAACGCGGGC	ATCCGATGCG	CGCCGGAAGC	GAGAAGAATC	ATAATGGGGA	AGGCCATCCA	GCCTCGGCTC	GCGAACGCCA
4071	GCAAGACGTA	GCCAGCGCGG	TCGGCCGCCA	TGCGCGCGAT	AATGGCCTCG	TTCTCGCCGA	AACGTTTGGT	GGCGGGACCA	GTGACGAAGG	CTTGAGCGAG	GGCGTGCAAG
4181	ATTCGAATA	CCGCAAGCGA	CAGGCCGATC	ATCGTCGCGC	TCCAGCGAAA	GCGTCTCTCG	CCGAAAATGA	CCGACAGCGC	TGCCGGCACC	TGTCCTACGA	GTTGCATGAT
4291	AAAGAAGACA	GTCATAAGTG	CGGCGACGAT	AGTCATGCCC	CGCGCCACCG	GGAAGGAGCT	GACTGGGTTC	AAGGCTCTCA	AGGGCATCGG	TCGAGATCCC	GGTGCCTAAT
4401	GAGTGAGCTA	ACTTACATTA	ATTGCGTTG	GCTCACTGCG	CGTFTTCCAG	TCGGGAAACC	TGTCGTGCGA	GCTGCATTA	TGAATCGGCC	AACGCGCGGG	GAGAGGCGGT
4511	TTGCGTATTG	GGCGCCAGGG	TGTTTTTCT	TTTACCAGT	GAGACGGGCA	ACAGCTGATT	GCCCTTACC	GCCTGGCCCT	GAGAGAGTTG	CAGCAAGCGG	TCCACGCTGG
4621	TTTGCCCCAG	CAGGCGAAAA	TCCTGTTTGA	TGGTGGTTAA	CGGCGGGATA	TAACATGAGC	TGCTTCTGGT	ATCGTCGTAT	CCCACTACC	AGATATCCGC	ACCAACGCGC
4731	AGCCCGGACT	CGTAATGGC	GCGCATGGC	CCCAGCGCCA	TCTGATCGTT	GGCAACCAGC	ATCGCAGTGG	GAACGATGCC	CTCATTCAGC	ATTTGCATGG	TTTGTGAAA
4841	ACCGGACATG	GCATCCAGT	CGCCTTCCG	TTCCGCTATC	GGCTGAATTT	GATTGCGAGT	GAGATATTTA	TGCCAGCCAG	CCGACGCGAG	ACGCGCCGAG	ACGAACTTA
4951	ATGGGCCCCG	TAACAGCCCG	ATTTGCTGGT	GACCAATGCG	GACCAGATGC	TCCACGCCCA	GTCCGTACC	GTCTTATGG	GAGAAAATA	TACTGTGAT	GGGTGTCTGG
5061	TCAGAGACAT	CAAGAAATA	CGCGGAAACA	TTAGTGCAGG	CAGCTTCCAC	AGCAATGGCA	TCCTGTTTAT	CCAGCGGATA	GTAAATGATC	AGCCCACTGA	CGCGTTGCGC
5231	GAGAAGATTG	TGCACCGCGC	CTTTACAGGC	TTGACGCGCG	CTTCTGTTCA	CCATCGACAC	CACCACGCTG	GCACCCAGTT	GATCGGCGCG	AGATTTAATC	GCCGCGACAA
5171	TTTGGACGCG	CGGTGTCAGG	GCCAGACTGG	AGGTGGCAAC	GCCAAATCAG	AACGACTGTT	TGCCCGCCAG	TTGTTGTGCC	ACGCGGTTGG	GAATGTAATT	CAGCTCCGCC
5391	ATCGCGCTT	CCACTTTTTC	CGCGTTTTT	GCAGAAAGCT	GGCTGGCCCT	GTTTACCACG	CGGAAACCGG	TCTGATAAGA	GACACCGGCA	TACTCTGCGA	CATCGTATAA
5501	CGTTACTGGT	TTCACTTCA	CCACCCTGAA	TTGACTCTCT	TCCGGGCGCT	ATCATGCCAT	ACCCGGAAGG	GTTTTGCGCC	ATTCGATGGT	GTCCGGGATC	TCGACGCTCT
5611	CCCTTATGCG	ACTCTGCGAT	TAGGAAGCAG	CCCAGTAGTA	GTTTGGAGCC	GTTGAGCACC	CGCCCGCAA	GGAAATGGTG	ATGCAAGGAG	ATGGCGCCCA	ACAGTCCCCC
5721	GGCCAGGGGG	CTTCCACCA	TACCCACGCC	GAAACAAGCG	CTCATGAGCC	GAAAGTGGCG	AGCCGATCT	TCCCATCGG	TGATGTCCGC	GATATAGGGC	CCAGCAACCC
5831	CACCTGTGGC	GCCGGTGATG	CCGGCCACGA	TGCGTCCGGC	GTAGAGGATC	GAGATCTCGA	TCCCGGAAA	T			

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