

## pET30a/il3 sequence (with Parasitology sequencer, after cloned in DH5a)

ATACCGATAACAAGTTCCTCTAGAAAAATAATTTTGTCTTAACCTTTAAGAAGGAGATATACATATGCACCATCATCATCATCATCTTCTTC  
TGGTCTGGTGCCACGCGGTTCTGGTATGAAAGAAACCGCTGCTGCTAAATTCGAACGCCAGCACATGGACAGCCAGATCTGGGTACCG  
ACGACGACGACAAGCCATGGCTGATATCGGATCCGAATTCATGCCCGAACCAACAGATCAAAAACTAAAAAGTAATACAAATATTTAAT  
ATTTCAACGTCAGAGAAAGAATTACAAAAGGCGAATTGGAACCAACACCAATGTAACATTGAAAAGTGAAACAAAACACATCAACA  
CGATTACTTACATAGAAGTAATGAAGAACAAAAGAATAAATAGGAGACAAACAATTAATTAATCTTCGAAATTACCATCATTAACAT  
CATTTAGTATAGATCATATAAAGAAGCTTCGACGATTGAAATCTTTACCAATTTTAAACCAAGAATACAATAAAACAGAACATCACA  
AAAGAATCTAATTTATTATCGACATGATCATTTTCATATTTTCATAGGG

## Full pET30a/il3 sequence (software):

TGGCGAATGGGACGCGCCCTGTAGCGGCGCATTAAAGCGCGCGGGTGTGGTGGTTACGCGCAGCGTGACCGCTACACTTGCCAGCGCCC  
TAGCGCCCGCTCTTTCGCTTTCCTTCCCTTCTCGCCACGTTTCGCCGGCTTTCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTA  
GGGTTCGGAATTTAGTGCTTTACGGCACCTCGACCCCAAAAACTTGATTAGGGTGATGGTTACAGTAGTGGGCCATCGCCCTGATAGAC  
GGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGTGGACTCTTTGTTCCAACTGGAACAACACTCAACCCCTATCTCGGTCT  
ATTTCTTTTGATTTATAAGGGATTTTGCCGATTTTCGGCTATTGGTTAAAAAATGAGCTGATTTAACAAAAATTTAACCGGAATTTTAAC  
AAAAATTAACGTTTACAATTTTCAGGTGGCATTCTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTCTAAATACATTCAAA  
TATGTATCCGCTCATGAATTAATCTTAGAAAACTCATCGAGCATCAATGAACTGCAATTTATTCATATCAGGATTATCAATACCA  
TATTTTTGAAAAAGCCGTTTCTGTAATGAAGGAGAAAACTCACCGAGGCGAGTTCCATAGGATGGCAAGATCCTGGTATCGGTCTGCGAT  
TCCGACTCGTCCAACATCAATACAACCTATTAATTTCCCTCGTCAAAAATAAGGTTATCAAGTGAGAAATCACCATGAGTGACGACTG  
AATCCGGTGAGAATGGCAAAAGTTTATGCATTTCTTCCAGACTTGTTCACAGGCCAGCCATTACGCTCGTCATCAAAATCACTCGCA  
TCAACCAACCGTTATTCTATCTGATGATTGCGCCTGAGCGAGACGAAATACGCGATCGCTGTTAAAAGGACAATTACAAACAGGAATCGA  
ATGCAACCGCGCGCAGGAACACTGCCAGCGCATCAACAATATTTTACCTGAATCAGGATATCTTCTAATACCTGGAATCTGTTTTCC  
CGGGGATCGCAGTGGTGAGTAACCATGCATCATCAGGAGTACGGATAAAATGCTTGATGGTCGGAAGAGGCATAAATCCGTCAGCCAG  
TTTAGTCTGACCATCTCATCTGTAACATCATTTGGCAACGCTACTCTTTGCCATGTTTTCAGAAACAACCTCTGGCGCATCGGGCTTCCCAT  
CAATCGATAGATTGTGCGACCTGATTGCCCCGACATTATCGCGAGCCATTTATACCATATAAATCAGCATCCATGTTGGAATTTAATC  
GCGGCCCTAGAGCAAGACGTTTCCCGTTGAATATGGCTCATAACACCCCTTGTATTACTGTTTATGTAAGCAGACAGTTTTATTGTTTCAT  
GACCAAAATCCCTTAACGTGAGTTTTCGTTCCTGAGCGTCAGACCCGTTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTC  
TGCGCCTAATCTGCTGCTTTCGCAACAAAAAACCCCGCTACCCAGCGGTGGTTTGTGTTGCCGATCAAGAGCTTACCACTCTTTTTTCG  
AAGGTAACCTGCTTACGAGAGCGCAGATACCAAACTGTCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGC  
ACCGCTACATACCTCGCTCTGCTAATCCTGTTACAGTGGCTGCTGCCAGTGGCGATAAGTCGTGCTTACCGGGTTGGACTCAAGAC  
GATAGTTACCGGATAAGCGCGACGCGTTCGGCTGAACGGGGGTTCTCGTGCACACAGCCAGCTTGAGCGCAACGACCTACCGCAAGCTG  
AGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGCGGACAGGTATCCGGTAAGCGGCAGGGTTCGGAAC  
AGGAGAGCGCAGAGGGAGCTTCCAGGGGGAAACGCTTGGTATCTTTATAGTCTGTGCGGTTTCGCCACCTCTGACTTGAGCGTCGAT  
TTTTGTGATGCTCGTCAGGGGGCGGAGCCTATGGA AAAACGCCAGCAACGCGCCCTTTTTACGGTTCTTGGCCTTTTGCTGGCCTTTT  
GCTCAATGTTCTTTCTCGGTTATCCCTGATTTCTGTGGATACCCGTTATTACCGCTTTGAGTGAGCTGATACCGCTCCCGCAGCG  
AACGACCGAGCGCAGCGAGTCAGTGAGCGAGGAAGCGGAAGAGCGCTGATGCGGTATTTTCTCCTTACGCATCTGTGCGGTATTTTAC  
ACCGCATATATGGTGCACTCTCAGTACAATCTGCTCTGATGCCGATAGTTAAGCCAGTATACACTCCGCTATCGCTACGTGACTGGGT  
CATGGCTGCGCCCGACACCCGCCAACACCCGCTGACGCGCCCTGACGGGCTTGCTGCTGCCGCGCATCCGCTTACAGACAAGCTGTGA  
CCGCTCTCCGGGAGCTGTCATGTCAGAGTTTTTACCGTCACTACCGGAACGCGCGAGGCAGCTGCGGTAAAGCTCATCAGCTGGGTCG  
TGAAGCGATTTCAGATGTCTGCTGCTTATCCGCTCCAGCTCGTTGAGTTTCTCCAGAAGCGTTAATGTCTGGCTTCTGATAAAGCG  
GGCCTATGTTAAGGGCGGTTTTTTCTGTTTGGTCACTGATGCCCTCGGTGAAGGGGGATTTCTGTTTATGGGGGTAATGATACCGATGA  
ATGCGCGCGGACCGAGAAAAATCACTCAGGGTCAATGCCAGCGCTTCGTTAATACAGATGTAGGTGTTCCACAGGGTAGCCAGAGCA  
TCCTGCGATGCGATCCGGAACATAATGTTGCGAGGCGCTGACTTCCGCGTTTCCAGACTTACGAAACACGGAACCGGAAGACCATTC  
ATGTTGTTGCTCAGTTCGACAGCTTTTTCAGCAGCAGTCCGCTTACGTTCCGCTCGGTATCCGGTATTCTTGCTAACCAGTAAGG  
CAACCCCGCCAGCTTAGCCGGTCTCAACGACAGGACGATCATGCGCACCCGTTGGGGCCGCGCATGCCGGCGATAATGGCCGTCTT  
CTCGCCGAAACGTTTGGTGGCGGACAGTGACGAAGGCTTGAGCGAGGGCGTGCAAGATTCCGAATACCGCAAGCGACAGGCCGATCA  
TCGTCGCGCTCCAGCGAAAGCGGTCTTCGCCGAAATGACCCAGAGCGCTGCGCGCACCTGTCTACGAGTTGCATGATAAAGAAGACA  
GTCATAAGTGGCGGACGATAGTCATGCCCCGCGCCACCGGAAGGAGCTGACTGGGTGAAGGCTCTCAAGGGCATCGGTGAGATCC  
CGGTGCTAATGAGTGAGCTAACTTACATTAATGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCTGCGCAGCTGCATT  
AATGAATCGGCCAACCGCGGGGAGAGGCGGTTTTGCGTATTGGGCGCCAGGGTGGTTTTTCTTTTACCAGTGAGACGGGCAACAGCTG  
ATTGCCCTTACCAGCTGGCCCTGAGAGAGTTGCGAGCAAGCGGTCCAGCGCTGGTTTCCCGCAGCAGGCGAAATCCTGTTTGTAGGTGG  
TTAACGGCGGGATATAACATGAGCTGCTTTCGGTATCGTCTGATCCCACTACCGAGATGTCGCGACCAACGCGCAGCCCGGACTCGGTA  
ATGGCGCGCATTGGCCCGCAGCGCATCTGATCGTTGGCAACAGCATCGCAGTGGGAACGATGCCCTCATTCAGCATTTGCATGGTTTTG  
TTGAAAACCGGACATGGCACTCCAGTCGCTTCCCGTTCCGCTATCGGCTGAATTTGATTGCGAGTGAGATATTTATGCCAGCCAGCCA  
GACGCGAGACGCGCGGAGACGAACTTAATGGGCGCGCTTAACAGCGCGATTTGCTGGTGACCAATGCGACAGATGCTCCACGCGCCAGT  
CGCTACCGCTTTCATGGGAGAAAAATAACTGTTGATGGGTGTCTGGTCAGAGACATCAAGAAATAACGCCGGAACATTAGTGACAGGC  
AGCTTCCACAGCAATGGCATCTTGGTCACTCCAGCGGATAGTTAATGATCAGCCACTGACGCGTTGCGCGAGAAGATTGTGACCGCGCG  
CTTTACAGGCTTCGACGCGCGCTTCGTTCTACCATCGACACCACCGTGGCACCCAGTTGATCGGCGCGAGATTAAATCGCCGCGACA  
ATTTGCGACGGCGCGTGTCAGGGCCAGACTGGAGGTGGCAACGCCAATCAGCAACGACTGTTTGCCCGCCAGTTGTTGTGCCACGCGGTT  
GGGAATGTAATTCAGCTCCGCCATCGCCGCTTCCACTTTTCCCGGATTTTCGCGAGAAACGTGGCTGGCTTCACTACCGCGGAA  
CGGTCTGATAAGAGACACCGGCATACTCTGCGACATCGTATAACGTTACTGGTTTACATTACCAACCTGAATTGACTCTCTTCCGGG  
CGCTATCATGCCATACCGCGAAAGGTTTTGCGCCATTGATGTTGTCGGGATCTCGACGCTCTCCCTTATGCGACTCCGTCATTAGGA  
AGCAGCCAGTAGTAGTTGAGGCGGTTGAGCACCGCGCCGCAAGGAATGTTGATGCAAGGAGATGGCGCCCAACAGTCCCCCGGCC  
ACGGGCGCTGCCACCACCGCCGAAACAGCGCTTACGCCGGAAGTGGCGAGCCGATCTTCCCATCGGTGATGTTGCGCGAT  
ATAGGCGCCAGCAACCGCACCTGTGGCGCGGTGATGCCGGCCAGATGCGTCCGGCTAGAGGATCGAGATCGATCTCGATCCGCGCA

AATTAATACGACTCACTATAGGGGAATTGTGAGCGGATAACAATTCCCCTCTAGAAATAATTTTGTTAACTTTAAGAAGGAGATATAC  
 ATATGCACCATCATCATCATCTTCTTGGTCTGGTGCCACGCGGTCTTGGTATGAAAGAAACCGCTGCTGCTAAATTCGAACGCCAG  
 CACATGGACAGCCCAGATCTGGGTACCGACGACGACGACAAGGCCATGGGTGATATCGGATCCGAATTCATGCCCGAACCAACAGATCA  
 AAAACTAAAAGTAATACAAATATTTAATATTTCAACGTCAGAGAAAGAATTACAAAAGCGGAATTGGGAACCAACACCAAATGTAACAT  
 TGAAAAGTGAAACAAAACAACATCAACACGATTACTTACATAGAAGTAATGAAGAACAAAAGAATAAACTAGGAGACAAACAATTAATT  
 AATTCTTCGAAATTACCATCATTAACATCATTTAGTATAGATCATATAAAGAAGCTTCGACGATTGAAATCTTTACCAAATTTTAAAC  
 AGAATACAATAAAACAGAACATCAAAAAGAATCTAATTTATTATCGACATGATCATTTTCATATTTTCATAGGGAAACAAAAACTGCAG  
 CGGCCGCACTCGAGCACCACCACCACCACCCTGAGATCCGGCTGCTAACAAAGCCCGAAAGGAAGCTGAGTTGGCTGCTGCCACCGCT  
 GAGCAATAACTAGCATAACCCCTTGGGGCCTCTAAACGGGTCTTGAGGGGTTTTTTGCTGAAAGGAGGAACATATATCCGGAT

## Alignment between pET30a/il3 (a portion that was sequenced with our sequencer after being cloned in DH5α) and theoretical full sequence pET30a/il3 (software).

pET30ail3 sequencing	1		0
pET30ail3 complete	1	TGGCGAATGGGACGCGCCCTGTAGCGGCGCATTAAAGCGCGGCGGTGTGG	50
pET30ail3 sequencing	1		0
pET30ail3 complete	51	TGGTTACGCGCAGCGTGACCGCTACACTTGCCAGCGCCCTAGCGCCCGCT	100
pET30ail3 sequencing	1		0
pET30ail3 complete	101	CCTTTTCGCTTTCTTCCCTTCTTTCTCGCCACGTTCCGCCGGCTTTCCCCG	150
pET30ail3 sequencing	1		0
pET30ail3 complete	151	TCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCGATTTAGTGCTTTAC	200
pET30ail3 sequencing	1		0
pET30ail3 complete	201	GGCACCTCGACCCCAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGG	250
pET30ail3 sequencing	1		0
pET30ail3 complete	251	CCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTT	300
pET30ail3 sequencing	1		0
pET30ail3 complete	301	CTTTAATAGTGGACTCTTGTTCCAACTGGAACAACACTCAACCCTATCT	350
pET30ail3 sequencing	1		0
pET30ail3 complete	351	CGGTCTATTCTTTTGATTTATAAGGGATTTTGCCGATTTCGGCCTATTGG	400
pET30ail3 sequencing	1		0
pET30ail3 complete	401	TTAAAAATGAGCTGATTTAACAAAAATTTAACGCGAATTTTAACAAAAAT	450
pET30ail3 sequencing	1		0
pET30ail3 complete	451	ATTAACGTTTACAATTTCAAGTGGCACTTTTCGGGGAAATGTGCGCGGAA	500
pET30ail3 sequencing	1		0
pET30ail3 complete	501	CCCCTATTTGTTTATTTTCTAAATACATTCAAATATGTATCCGCTCATG	550
pET30ail3 sequencing	1		0
pET30ail3 complete	551	AATTAATTCTTAGAAAACTCATCGAGCATCAAATGAACTGCAATTTAT	600
pET30ail3 sequencing	1		0
pET30ail3 complete	601	TCATATCAGGATTATCAATACCATATTTTGAAGGAGCCGTTTCTGTAAT	650
pET30ail3 sequencing	1		0
pET30ail3 complete	651	GAAGGAGAAACTCACCGAGGAGTTCCATAGGATGGCAAGATCCTGGTA	700
pET30ail3 sequencing	1		0
pET30ail3 complete	701	TCGGTCTGCGATTCCGACTCGTCCAACATCAATACAACCTATTAATTTCC	750
pET30ail3 sequencing	1		0
pET30ail3 complete	751	CCTCGTCAAAAATAAGGTTATCAAGTGAGAAATCACCATGAGTGACGACT	800
pET30ail3 sequencing	1		0
pET30ail3 complete	801	GAATCCGGTGAGAATGGCAAAAGTTTATGCATTTCTTTCCAGACTTGTTTC	850
pET30ail3 sequencing	1		0
pET30ail3 complete	851	AACAGGCCAGCCATTACGCTCGTCATCAAAATCACTCGCATCAACCAAAC	900

pET30ail3 sequencing	1		0
pET30ail3 complete	901	CGTTATTCATTTCGTGATTGCGCCTGAGCGAGACGAAATACGCGATCGCTG	950
pET30ail3 sequencing	1		0
pET30ail3 complete	951	TTAAAAGGACAATTACAAACAGGAATCGAATGCAACCGGCGCAGGAACAC	1000
pET30ail3 sequencing	1		0
pET30ail3 complete	1001	TGCCAGCGCATCAACAATATTTTCACCTGAATCAGGATATTCTTCTAATA	1050
pET30ail3 sequencing	1		0
pET30ail3 complete	1051	CCTGGAATGCTGTTTTCCCGGGGATCGCAGTGGTGAGTAACCATGCATCA	1100
pET30ail3 sequencing	1		0
pET30ail3 complete	1101	TCAGGAGTACGGATAAAATGCTTGATGGTCGGAAGAGGCATAAATCCGT	1150
pET30ail3 sequencing	1		0
pET30ail3 complete	1151	CAGCCAGTTTAGTCTGACCATCTCATCTGTAACATCATTGGCAACGCTAC	1200
pET30ail3 sequencing	1		0
pET30ail3 complete	1201	CTTTGCCATGTTTCAGAAACAACTCTGGCGCATCGGGCTTCCCATACAAT	1250
pET30ail3 sequencing	1		0
pET30ail3 complete	1251	CGATAGATTGTGCGACCTGATTGCCCGACATTATCGCGAGCCCATTATA	1300
pET30ail3 sequencing	1		0
pET30ail3 complete	1301	CCCATATAAATCAGCATCCATGTTGGAATTTAATCGCGGCCTAGAGCAAG	1350
pET30ail3 sequencing	1		0
pET30ail3 complete	1351	ACGTTTCCCGTTGAATATGGCTCATAACACCCCTTGTATTACTGTTTATG	1400
pET30ail3 sequencing	1		0
pET30ail3 complete	1401	TAAGCAGACAGTTTTATTGTTTCATGACCAAAATCCCTTAACGTGAGTTTT	1450
pET30ail3 sequencing	1		0
pET30ail3 complete	1451	CGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGA	1500
pET30ail3 sequencing	1		0
pET30ail3 complete	1501	GATCCTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAACACC	1550
pET30ail3 sequencing	1		0
pET30ail3 complete	1551	GCTACCAGCGGTGGTTTGTGTTGCCGGATCAAGAGCTACCAACTCTTTTTC	1600
pET30ail3 sequencing	1		0
pET30ail3 complete	1601	CGAAGGTAACGGCTTCAGCAGAGCGCAGATACCAAATACTGTCTCTTCTA	1650
pET30ail3 sequencing	1		0
pET30ail3 complete	1651	GTGTAGCCGTAGTTAGGCCACCATTCAAGAACTCTGTAGCACCGCCTAC	1700
pET30ail3 sequencing	1		0
pET30ail3 complete	1701	ATACCTCGCTCTGCTAATCTGTACCAGTGGCTGCTGCCAGTGGCGATA	1750
pET30ail3 sequencing	1		0
pET30ail3 complete	1751	AGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCG	1800
pET30ail3 sequencing	1		0
pET30ail3 complete	1801	CAGCGGTCGGGCTGAACGGGGGTTTCGTGCACACAGCCAGCTTGGAGCG	1850
pET30ail3 sequencing	1		0
pET30ail3 complete	1851	AACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCG	1900
pET30ail3 sequencing	1		0
pET30ail3 complete	1901	CCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGG	1950
pET30ail3 sequencing	1		0
pET30ail3 complete	1951	GTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGAAACGCCTGGTA	2000
pET30ail3 sequencing	1		0
pET30ail3 complete	2001	TCTTTATAGTCTGTGCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTT	2050
pET30ail3 sequencing	1		0
pET30ail3 complete	2051	TGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCG	2100

pET30ail3 sequencing	1		0
pET30ail3 complete	2101	GCCTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTT	2150
pET30ail3 sequencing	1		0
pET30ail3 complete	2151	TCCTGCGTTATCCCTGATTCTGTGGATAACCGTATTACCGCCTTTGAGT	2200
pET30ail3 sequencing	1		0
pET30ail3 complete	2201	GAGCTGATACCGCTCGCCGACCCGAACGACCGAGCGCAGTCAGTG	2250
pET30ail3 sequencing	1		0
pET30ail3 complete	2251	AGCGAGGAAGCGGAAGAGCGCCTGATGCGGTATTTTCTCCTTACGCATCT	2300
pET30ail3 sequencing	1		0
pET30ail3 complete	2301	GTGCGGTATTTACACCGCATATATGGTGCACTCTCAGTACAATCTGCTC	2350
pET30ail3 sequencing	1		0
pET30ail3 complete	2351	TGATGCCGCATAGTTAAGCCAGTATACACTCCGCTATCGCTACGTGACTG	2400
pET30ail3 sequencing	1		0
pET30ail3 complete	2401	GGTCATGGCTGCGCCCCGACACCCGCCAACCCGCTGACGCGCCCTGAC	2450
pET30ail3 sequencing	1		0
pET30ail3 complete	2451	GGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCC	2500
pET30ail3 sequencing	1		0
pET30ail3 complete	2501	GGGAGCTGCATGTGTGAGAGGTTTTACCGTCATCACCGAAACGCGCGAG	2550
pET30ail3 sequencing	1		0
pET30ail3 complete	2551	GCAGCTGCGGTAAAGCTCATCAGCGTGGTCGTGAAGCGATTACAGATGT	2600
pET30ail3 sequencing	1		0
pET30ail3 complete	2601	CTGCCTGTTTCATCCGCTCCAGCTCGTTGAGTTTCTCCAGAAGCGTTAAT	2650
pET30ail3 sequencing	1		0
pET30ail3 complete	2651	GTCTGGCTTCTGATAAAGCGGGCCATGTTAAGGGCGGTTTTTCTGTTT	2700
pET30ail3 sequencing	1		0
pET30ail3 complete	2701	GGTCACTGATGCCCTCCGTGTAAGGGGGATTCTGTTTCATGGGGTAATGA	2750
pET30ail3 sequencing	1		0
pET30ail3 complete	2751	TACCGATGAAACGAGAGAGGATGCTCACGATACGGGTTACTGATGATGAA	2800
pET30ail3 sequencing	1		0
pET30ail3 complete	2801	CATGCCCGGTTACTGGAACGTTGTGAGGGTAAACAACCTGGCGGTATGGAT	2850
pET30ail3 sequencing	1		0
pET30ail3 complete	2851	GCGGCGGGACCAGAGAAAAATCACTCAGGGTCAATGCCAGCGCTTCGTTA	2900
pET30ail3 sequencing	1		0
pET30ail3 complete	2901	ATACAGATGTAGGTGTTCCACAGGGTAGCCAGCAGCATCCTGCGATGCAG	2950
pET30ail3 sequencing	1		0
pET30ail3 complete	2951	ATCCGGAACATAATGGTGCAGGGCGCTGACTCCGCGTTTCCAGACTTTA	3000
pET30ail3 sequencing	1		0
pET30ail3 complete	3001	CGAAACACGGAAACCGAAGACCATTTCATGTTGTTGCTCAGGTCGAGACG	3050
pET30ail3 sequencing	1		0
pET30ail3 complete	3051	TTTTGCAGCAGCAGTCGCTTCACGTTTCGCTCGCGTATCGGTGATTCATTC	3100
pET30ail3 sequencing	1		0
pET30ail3 complete	3101	TGCTAACCAGTAAGGCAACCCCGCCAGCCTAGCCGGGTCTCAACGACAG	3150
pET30ail3 sequencing	1		0
pET30ail3 complete	3151	GAGCACGATCATGCGCACCCGTGGGGCCGCCATGCCGGCGATAATGGCCT	3200
pET30ail3 sequencing	1		0
pET30ail3 complete	3201	GCTTCTCGCCGAAACGTTTGGTGGCGGGACCAAGTACGGAAGGCTTGAGCG	3250
pET30ail3 sequencing	1		0

pET30ail3 complete	3251	AGGGCGTGCAAGATTCCGAATACCGCAAGCGACAGGCCGATCATCGTCGC	3300
pET30ail3 sequencing	1		0
pET30ail3 complete	3301	GCTCCAGCGAAAGCGGTCTCGCCGAAAATGACCCAGAGCGCTGCCGGCA	3350
pET30ail3 sequencing	1		0
pET30ail3 complete	3351	CCTGTCTACGAGTTGCATGATAAAGAAGACAGTCATAAGTCCGGCGACG	3400
pET30ail3 sequencing	1		0
pET30ail3 complete	3401	ATAGTCATGCCCCGCGCCACCGGAAGGAGCTGACTGGGTGAAGGCTCT	3450
pET30ail3 sequencing	1		0
pET30ail3 complete	3451	CAAGGGCATCGGTTCGAGATCCCGGTGCCTAATGAGTGAGCTAATTACAT	3500
pET30ail3 sequencing	1		0
pET30ail3 complete	3501	TAATTGCGTTGCGCTCACTGCCCGCTTTCAGTCGGGAAACCTGTCGTGC	3550
pET30ail3 sequencing	1		0
pET30ail3 complete	3551	CAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGCGGTTTGCCTAT	3600
pET30ail3 sequencing	1		0
pET30ail3 complete	3601	TGGGCGCCAGGGTGGTTTTTCTTTTACCAGTGAGACGGGCAACAGCTGA	3650
pET30ail3 sequencing	1		0
pET30ail3 complete	3651	TTGCCCTTACCGCCTGGCCCTGAGAGAGTTGCAGCAAGCGGTCCACGCT	3700
pET30ail3 sequencing	1		0
pET30ail3 complete	3701	GGTTTGCCCCAGCAGGCGAAAATCCTGTTTGATGGTGGTTAACGGCGGGA	3750
pET30ail3 sequencing	1		0
pET30ail3 complete	3751	TATAACATGAGCTGTCTTCGGTATCGTCGTATCCCACTACCGAGATGTCC	3800
pET30ail3 sequencing	1		0
pET30ail3 complete	3801	GCACCAACGCGCAGCCCGGACTCGGTAATGGCGCGCATTGCGCCAGCGC	3850
pET30ail3 sequencing	1		0
pET30ail3 complete	3851	CATCTGATCGTTGGCAACCAGCATCGCAGTGGGAACGATGCCCTCATTCA	3900
pET30ail3 sequencing	1		0
pET30ail3 complete	3901	GCATTTGCATGTTTTGTTGAAAACCGGACATGGCACTCCAGTCGCCTTCC	3950
pET30ail3 sequencing	1		0
pET30ail3 complete	3951	CGTTCCGCTATCGGCTGAATTTGATTGCGAGTGAGATATTTATGCCAGCC	4000
pET30ail3 sequencing	1		0
pET30ail3 complete	4001	AGCCAGACGCAGACGCGCCGAGACAGAACTTAATGGGCCCCGCTAACAGCG	4050
pET30ail3 sequencing	1		0
pET30ail3 complete	4051	CGATTTGCTGGTGACCAATGCGACCAGATGCTCCACGCCAGTCGCGTA	4100
pET30ail3 sequencing	1		0
pET30ail3 complete	4101	CCGTCTTCATGGGAGAAAATAATACTGTTGATGGGTGTCTGGTCAGAGAC	4150
pET30ail3 sequencing	1		0
pET30ail3 complete	4151	ATCAAGAAATAACGCCGGAACATTAGTGCAGGCAGCTTCCACAGCAATGG	4200
pET30ail3 sequencing	1		0
pET30ail3 complete	4201	CATCCTGGTCATCCAGCGGATAGTTAATGATCAGCCCACTGACGCGTTGC	4250
pET30ail3 sequencing	1		0
pET30ail3 complete	4251	GCGAGAAGATTGTGCACCGCGCTTTACAGGCTTCGACGCCGCTTCGTTT	4300
pET30ail3 sequencing	1		0
pET30ail3 complete	4301	TACCATCGACACCACCACGCTGGCACCCAGTTGATCGGCGCGAGATTTAA	4350
pET30ail3 sequencing	1		0
pET30ail3 complete	4351	TCGCCGCGACAATTTGCGACGGCGCGTGCAGGGCCAGACTGGAGGTGGCA	4400
pET30ail3 sequencing	1		0
pET30ail3 complete	4401	ACGCCAATCAGCAACGACTGTTTGCCCGCCAGTTGTTGTGCCACGCGGTT	4450

pET30ail3 sequencing	1		0
pET30ail3 complete	4451	GGGAATGTAATTCAGTCTCGCCATCGCCGCTTCCACTTTTCCCGCGTTT	4500
pET30ail3 sequencing	1		0
pET30ail3 complete	4501	TCGCAGAAACGTGGCTGGCCTGGTTCACCACGCGGAAACGGTCTGATAA	4550
pET30ail3 sequencing	1		0
pET30ail3 complete	4551	GAGACACCGGCATACTCTGCGACATCGTATAACGTTACTGGTTTCACATT	4600
pET30ail3 sequencing	1		0
pET30ail3 complete	4601	CACCACCCTGAATTGACTCTCTTCCGGGCGCTATCATGCCATACCGCGAA	4650
pET30ail3 sequencing	1		0
pET30ail3 complete	4651	AGGTTTTGCGCCATTTCGATGGTGTCCGGGATCTCGACGCTCTCCCTTATG	4700
pET30ail3 sequencing	1		0
pET30ail3 complete	4701	CGACTCCTGCATTAGGAAGCAGCCAGTAGTAGGTTGAGCCGTTGAGCA	4750
pET30ail3 sequencing	1		0
pET30ail3 complete	4751	CCGCCCGCGCAAGGAATGGTGCATGCAAGGAGATGGCGCCCAACAGTCCC	4800
pET30ail3 sequencing	1		0
pET30ail3 complete	4801	CCGGCCACGGGGCCTGCCACCATACCCACGCCGAAACAAGCGCTCATGAG	4850
pET30ail3 sequencing	1		0
pET30ail3 complete	4851	CCCGAAGTGGCGAGCCCGATCTTCCCATCGGTGATGTCGGCGATATAGG	4900
pET30ail3 sequencing	1		0
pET30ail3 complete	4901	CGCCAGCAACCGCACCTGTGGCGCCGGTGATGCCGGCCACGATGCGTCCG	4950
pET30ail3 sequencing	1		0
pET30ail3 complete	4951	GCGTAGAGGATCGAGATCGATCTCGATCCCGCGAAATTAATACGACTCAC	5000
pET30ail3 sequencing	1	ATA	36
pET30ail3 complete	5001	TATAGGGGAATTGTGAGCGGATAACAAATTCCCTCTAGAAAATAATTTT	5048
pET30ail3 sequencing	37	GTTTAACTTTAAAGAGGAGATATACATATGCACCATCATCATCATTC	86
pET30ail3 complete	5049	GTTTAACTTTAAAGAGGAGATATACATATGCACCATCATCATCATTC	5098
pET30ail3 sequencing	87	TTCTGGTCTGGTGCCACGCGGTTCTGGTATGAAAGAAACCGCTGCTGCTA	136
pET30ail3 complete	5099	TTCTGGTCTGGTGCCACGCGGTTCTGGTATGAAAGAAACCGCTGCTGCTA	5148
pET30ail3 sequencing	137	AATTTCGAACGCCAGCAGCATGGACAGCCAGATCTGGGTACCGACGACGAC	186
pET30ail3 complete	5149	AATTTCGAACGCCAGCAGCATGGACAGCCAGATCTGGGTACCGACGACGAC	5198
pET30ail3 sequencing	187	GACAAGGCCATGGCTGATATCGGATCCGAATTCATGCCCGAACCAACAGA	236
pET30ail3 complete	5199	GACAAGGCCATGGCTGATATCGGATCCGAATTCATGCCCGAACCAACAGA	5248
pET30ail3 sequencing	237	TCAAAACTAAAAGTAATACAAATATTTAATATTTCAACGTCAGAGAAAG	286
pET30ail3 complete	5249	TCAAAACTAAAAGTAATACAAATATTTAATATTTCAACGTCAGAGAAAG	5298
pET30ail3 sequencing	287	AATTACAAAAGGCGAATTGGCAACCAACACCAATGTAACATTGAAAAGT	336
pET30ail3 complete	5299	AATTACAAAAGGCGAATTGGCAACCAACACCAATGTAACATTGAAAAGT	5348
pET30ail3 sequencing	337	GAAACAAAACAACATCAACACGATTACTTACATAGAAGTAATGAAGAACA	386
pET30ail3 complete	5349	GAAACAAAACAACATCAACACGATTACTTACATAGAAGTAATGAAGAACA	5398
pET30ail3 sequencing	387	AAAGAATAAACTAGGAGACAAACAATTAATTAATTCTTCGAAATTACCAT	436
pET30ail3 complete	5399	AAAGAATAAACTAGGAGACAAACAATTAATTAATTCTTCGAAATTACCAT	5448
pET30ail3 sequencing	437	CATTAACATCATTTAGTATAGATCATATAAAGAAGCTTCGACGATTGAAA	486
pET30ail3 complete	5449	CATTAACATCATTTAGTATAGATCATATAAAGAAGCTTCGACGATTGAAA	5498
pET30ail3 sequencing	487	TCTTTACCAAAATTTTAAACAGAAATACAATAAAACAGAAACATCACAAA	536
pET30ail3 complete	5499	TCTTTACCAAAATTTTAAACAGAAATACAATAAAACAGAAACATCACAAA	5547
pET30ail3 sequencing	537	AGAATCTAATTTATTATCGACATGATCATTTTCATATTTTCATAGGG	581
pET30ail3 complete	5548	AGAATCTAATTTATTATCGACATGATCATTTTCATATTTTCATAGGGAACAA	5597
pET30ail3 sequencing	582		581
pET30ail3 complete	5598	AAAACGTCAGCGCGCCGACTCGAGCACCACCACCACCACCAGATCC	5647

pET30ai13 sequencing	582		581
pET30ai13 complete	5648	GGCTGCTAACAAAGCCCGAAAGGAAGCTGAGTTGGCTGCTGCCACCGCTG	5697
pET30ai13 sequencing	582		581
pET30ai13 complete	5698	AGCAATAACTAGCATAACCCCTTGGGGCCTCTAAACGGGTCTTGAGGGGT	5747
pET30ai13 sequencing	582		581
pET30ai13 complete	5748	TTTTTGCTGAAAGGAGGAACATATCCGGAT	5778