



# results of BLAST

## BLASTX 2.2.10 [Oct-19-2004]

### Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1112675790-27548-25004277042.BLASTQ2

### Query=

(732 letters)

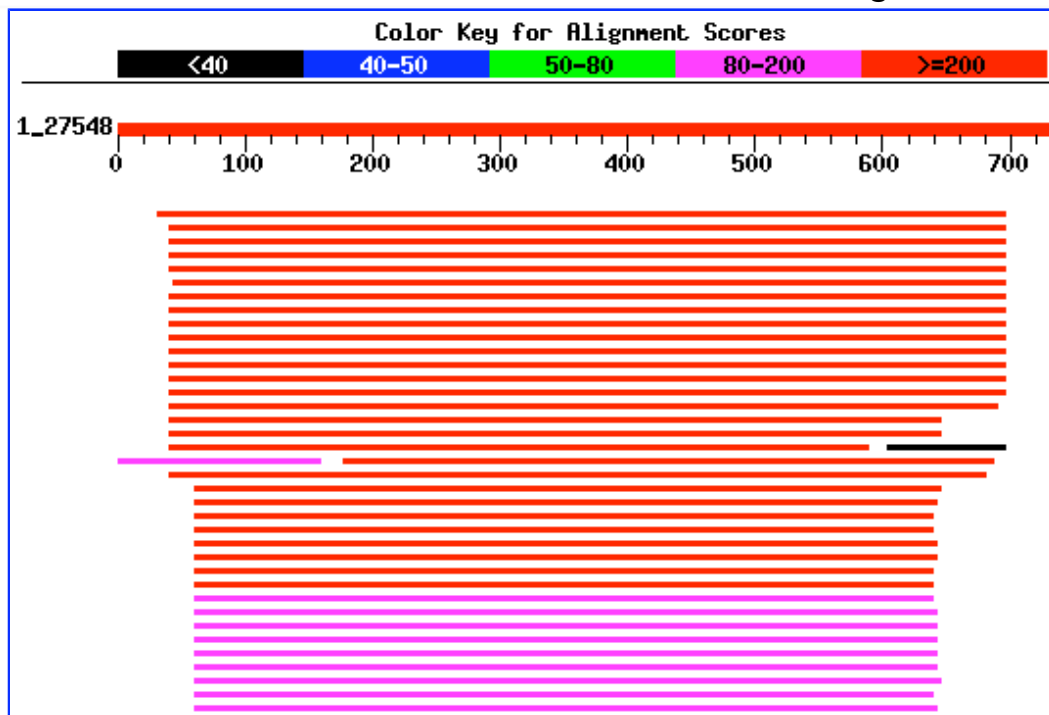
**Database:** All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples  
2,419,798 sequences; 819,541,351 total letters

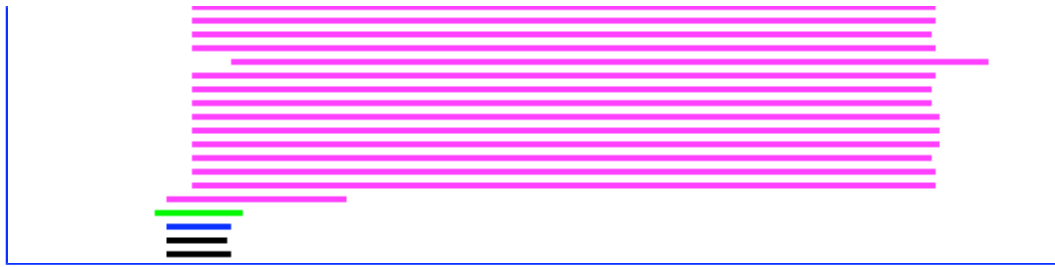
If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

## Distribution of 101 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments





### Related Structures

Sequences producing significant alignments:	Score (bits)	E Value	
<a href="#">gi 11934672 qb AAG41774.1</a> Cat [Promoter probe vector pPR9TT]	<a href="#">449</a>	e-125	
<a href="#">gi 38490699 qb AAR21679.1</a> chloramphenicol acetyltransferas...	<a href="#">446</a>	e-124	<b>G S</b>
<a href="#">gi 1480375 emb CAA67774.1</a> cat [Escherichia coli]	<a href="#">446</a>	e-124	
<a href="#">gi 303728 dbj BAA03718.1</a> PP-CAT [Photobacterium damsela...	<a href="#">446</a>	e-124	
<a href="#">gi 29421421 qb AAO48721.1</a> Cat [CRIM plasmid pLA1] >gi 1529...	<a href="#">445</a>	e-124	
<a href="#">gi 575451 qb AAC53603.1</a> chloramphenicol acetyltransferase	<a href="#">444</a>	e-124	
<a href="#">gi 2343026 qb AAB67677.1</a> choramphenicol acetyltransferase ...	<a href="#">444</a>	e-123	
<a href="#">gi 38347932 ref NP_941181.1</a> chloramphenicol acetyltransfer...	<a href="#">444</a>	e-123	<b>G</b>
<a href="#">gi 220940 dbj BAA03187.1</a> chloramphenicol acetyl transferas...	<a href="#">443</a>	e-123	
<a href="#">gi 20177832 sp P58777 CAT_KLESP</a> Chloramphenicol acetyltrans...	<a href="#">443</a>	e-123	
<a href="#">gi 13094143 dbj BAB32741.1</a> chloramphenicol acetyltransfera...	<a href="#">441</a>	e-123	
<a href="#">gi 9294793 qb AAF86675.1</a> chloramphenicol transacetylase [I...	<a href="#">441</a>	e-123	
<a href="#">gi 56387331 qb AAV86079.1</a> chloramphenicol acetyltransferas...	<a href="#">441</a>	e-123	
<a href="#">gi 15808712 qb AAL08441.1</a> chloramphenicol acetyltransferas...	<a href="#">437</a>	e-121	
<a href="#">gi 58252 emb CAA49282.1</a> cat mutant [synthetic construct]	<a href="#">432</a>	e-120	
<a href="#">gi 49659743 qb AAT68191.1</a> chloramphenicol acetyltransferas...	<a href="#">429</a>	e-119	
<a href="#">gi 15554330 qb AAL02033.1</a> chloramphenicol acetyl transfera...	<a href="#">426</a>	e-118	
<a href="#">gi 7384997 qb AAF61635.1</a> chloramphenicol acetyltransferase...	<a href="#">356</a>	e-102	
<a href="#">gi 47834500 qb AAT38899.1</a> chloramphenicol acetyltransferas...	<a href="#">348</a>	6e-95	
<a href="#">gi 79018 pir A24651</a> chloramphenicol O-acetyltransferase (E...	<a href="#">337</a>	1e-91	
<a href="#">gi 37526342 ref NP_929686.1</a> chloramphenicol acetyltransfer...	<a href="#">222</a>	9e-57	<b>G</b>
<a href="#">gi 1311280 pdb 1QCA</a> Quadruple Mutant Q92c, N146f, Y168f, ...	<a href="#">210</a>	3e-53	<b>S</b>
<a href="#">gi 43579 emb CAA37806.1</a> chloramphenicol acetyltransferase ...	<a href="#">204</a>	2e-51	
<a href="#">gi 19773454 dbj BAB86848.1</a> chloramphenicol acetyltransfera...	<a href="#">202</a>	9e-51	
<a href="#">gi 47025 emb CAA30695.1</a> unnamed protein product [Plasmid R...	<a href="#">200</a>	3e-50	<b>S</b>
<a href="#">gi 7007391 emb CAB75601.1</a> chloramphenicol acetyl transfera...	<a href="#">200</a>	3e-50	<b>G</b>
<a href="#">gi 56786625 qb AAW29416.1</a> CatA2 chloramphenicol acetyltran...	<a href="#">200</a>	4e-50	
<a href="#">gi 45758083 qb AAS76295.1</a> chloramphenicol acetyl transfera...	<a href="#">200</a>	4e-50	<b>G</b>
<a href="#">gi 34556025 emb CAD57199.1</a> chloramphenicol aminottransferas...	<a href="#">199</a>	5e-50	
<a href="#">gi 229747 pdb 1CLA</a> Type III Chloramphenicol Acetyltransfe...	<a href="#">199</a>	6e-50	<b>S</b>
<a href="#">gi 230967 pdb 4CLA</a> Type III Chloramphenicol Acetyltransfe...	<a href="#">199</a>	8e-50	<b>S</b>
<a href="#">gi 230457 pdb 2CLA</a> Chloramphenicol Acetyltransferase (E.C...	<a href="#">198</a>	1e-49	<b>S</b>
<a href="#">gi 493937 pdb 1CIA</a> Chloramphenicol Acetyltransferase (Typ...	<a href="#">197</a>	2e-49	<b>S</b>
<a href="#">gi 482596 pir A49793</a> chloramphenicol O-acetyltransferase (...)	<a href="#">194</a>	2e-48	
<a href="#">gi 477359 pir A48907</a> chloramphenicol O-acetyltransferase (...)	<a href="#">190</a>	3e-47	
<a href="#">gi 52081186 ref YP_079977.1</a> antibiotic resistance protein,...	<a href="#">190</a>	3e-47	<b>G</b>
<a href="#">gi 3132860 qb AAC16406.1</a> chloramphenicol acetyltransferase...	<a href="#">186</a>	7e-46	
<a href="#">gi 55233210 qb AAV48563.1</a> chloramphenicol acetyltransferas...	<a href="#">182</a>	6e-45	
<a href="#">gi 52143073 ref YP_083756.1</a> chloramphenicol acetyltransfer...	<a href="#">182</a>	1e-44	<b>G</b>
<a href="#">gi 49477664 ref YP_036506.1</a> chloramphenicol O-acetyltransf...	<a href="#">182</a>	1e-44	<b>G</b>
<a href="#">gi 47527702 ref YP_019051.1</a> chloramphenicol acetyltransfer...	<a href="#">180</a>	3e-44	<b>G</b>
<a href="#">gi 66525 pir XXBSCP</a> chloramphenicol O-acetyltransferase (E...	<a href="#">180</a>	4e-44	
<a href="#">gi 40433 emb CAA33203.1</a> unnamed protein product [Clostridi...	<a href="#">179</a>	6e-44	
<a href="#">gi 47565764 ref ZP_00236804.1</a> chloramphenicol acetyltransf...	<a href="#">177</a>	2e-43	

<a href="#">gi 42781506 ref NP_978753.1 </a>	chloramphenicol acetyltransfer...	<a href="#">174</a>	2e-42	<b>G</b>
<a href="#">gi 22775399 dbj BAC11901.1 </a>	chloramphenicol acetyltransfera...	<a href="#">172</a>	6e-42	
<a href="#">gi 1667472 qb AAB53259.1 </a>	chloramphenicol acetyltransferase...	<a href="#">172</a>	8e-42	
<a href="#">gi 257403 qb AAB23649.1 </a>	chloramphenicol acetyltransferase;...	<a href="#">172</a>	1e-41	
<a href="#">gi 29650179 qb AAO86060.1 </a>	chloramphenicol acetyltransferas...	<a href="#">172</a>	1e-41	
<a href="#">gi 66521 pir XXECC3</a>	chloramphenicol O-acetyltransferase (E...	<a href="#">167</a>	2e-40	
<a href="#">gi 32470483 ref NP_863168.1 </a>	chloramphenicol acetyltransfer...	<a href="#">165</a>	1e-39	
<a href="#">gi 46632 emb CAA26367.1 </a>	unnamed protein product [Staphyloc...	<a href="#">164</a>	2e-39	
<a href="#">gi 482777 pir A61152</a>	chloramphenicol O-acetyltransferase (...)	<a href="#">164</a>	2e-39	
<a href="#">gi 1053003 qb AAB48103.1 </a>	CAT protein [Staphylococcus aureu...	<a href="#">163</a>	5e-39	<b>G</b>
<a href="#">gi 46652 emb CAA43218.1 </a>	chlorAMPhenicol acetyltransferase ...	<a href="#">162</a>	6e-39	
<a href="#">gi 46537 emb CAA26631.1 </a>	unnamed protein product [Staphyloc...	<a href="#">162</a>	8e-39	
<a href="#">gi 482581 pir A49758</a>	chloramphenicol O-acetyltransferase (...)	<a href="#">162</a>	8e-39	
<a href="#">gi 30267509 qb AAP21696.1 </a>	chloramphenicol acetyltransferas...	<a href="#">161</a>	2e-38	<b>G</b>
<a href="#">gi 871403 emb CAA48475.1 </a>	chloramphenicol acetyltransferase...	<a href="#">161</a>	2e-38	
<a href="#">gi 80682 pir JQ0375</a>	chloramphenicol O-acetyltransferase (E...	<a href="#">160</a>	4e-38	
<a href="#">gi 2467233 emb CAA63522.1 </a>	chloramphenicol acetyltransferas...	<a href="#">159</a>	5e-38	
<a href="#">gi 56963743 ref YP_175474.1 </a>	chloramphenicol acetyltransfer...	<a href="#">156</a>	6e-37	<b>G</b>
<a href="#">gi 402660 emb CAA52904.1 </a>	chloramphenicol acetyltransferase...	<a href="#">155</a>	8e-37	
<a href="#">gi 21668300 emb CAC84275.1 </a>	chloramphenicol acetyl transfer...	<a href="#">150</a>	4e-35	
<a href="#">gi 152982 qb AAA26613.1 </a>	chloramphenicol acetyltransferase	<a href="#">150</a>	4e-35	
<a href="#">gi 1197553 qb AAA88776.1 </a>	inactive chloramphenicol acetyltr...	<a href="#">148</a>	1e-34	
<a href="#">gi 6460112 qb AAF11849.1 </a>	chloramphenicol acetyltransferase...	<a href="#">141</a>	2e-32	<b>G</b>
<a href="#">gi 15004764 ref NP_149224.1 </a>	Chloramphenicol O-acetyltransf...	<a href="#">134</a>	2e-30	<b>G</b>
<a href="#">gi 48837945 ref ZP_00294898.1 </a>	COG4845: Chloramphenicol O-a...	<a href="#">126</a>	6e-28	
<a href="#">gi 34328603 qb AAO63644.1 </a>	chloramphenicol acetyltransferas...	<a href="#">122</a>	1e-26	
<a href="#">gi 21228653 ref NP_634575.1 </a>	Acetyltransferase [Methanosarc...	<a href="#">119</a>	8e-26	<b>G</b>
<a href="#">gi 20090555 ref NP_616630.1 </a>	chloramphenicol O-acetyltransf...	<a href="#">117</a>	2e-25	<b>G</b>
<a href="#">gi 51245910 ref YP_065794.1 </a>	similar to chloramphenicol ace...	<a href="#">115</a>	1e-24	<b>G</b>
<a href="#">gi 28378460 ref NP_785352.1 </a>	chloramphenicol O-acetyltransf...	<a href="#">114</a>	2e-24	<b>G</b>
<a href="#">gi 28211102 ref NP_782046.1 </a>	chloramphenicol acetyltransfer...	<a href="#">112</a>	7e-24	<b>G</b>
<a href="#">gi 15893527 ref NP_346876.1 </a>	Chloramphenicol acetyltransfer...	<a href="#">102</a>	1e-20	<b>G</b>
<a href="#">gi 14571867 qb AAK67297.1 </a>	IGFII-GFP fusion protein [synthe...	<a href="#">93</a>	6e-18	
<a href="#">gi 228396 prf 1803436A</a>	envelope glycoprotein gp64	<a href="#">92</a>	1e-17	
<a href="#">gi 29338006 qb AAO75809.1 </a>	chloramphenicol acetyltransferas...	<a href="#">86</a>	7e-16	<b>G</b>
<a href="#">gi 671747 emb CAA59048.1 </a>	chloramphenicol transacetylase [s...	<a href="#">80</a>	7e-14	
<a href="#">gi 53713696 ref YP_099688.1 </a>	chloramphenicol acetyltransfer...	<a href="#">71</a>	3e-11	<b>G</b>
<a href="#">gi 60493401 emb CAH08187.1 </a>	putative chloramphenicol acetyl...	<a href="#">69</a>	9e-11	<b>G</b>
<a href="#">gi 29340433 qb AAO78225.1 </a>	chloramphenicol acetyltransferas...	<a href="#">67</a>	6e-10	<b>G</b>
<a href="#">gi 4768869 qb AAD29663.1 </a>	chloramphenicol acetyltransferase...	<a href="#">64</a>	4e-09	<b>G</b>
<a href="#">gi 53715861 ref YP_101853.1 </a>	chloramphenicol acetyltransfer...	<a href="#">60</a>	4e-08	<b>G</b>
<a href="#">gi 60495213 emb CAH10034.1 </a>	possible chloramphenicol acetyl...	<a href="#">60</a>	4e-08	<b>G</b>
<a href="#">gi 57102406 ref XP_542232.1 </a>	PREDICTED: similar to hypothet...	<a href="#">54</a>	3e-06	<b>G</b>
<a href="#">gi 208841 qb AAA72768.1 </a>	mutant pol polyprotein	<a href="#">53</a>	9e-06	
<a href="#">gi 553057 qb AAB58983.1 </a>	discoidin I-gamma	<a href="#">52</a>	2e-05	
<a href="#">gi 16331867 ref NP_442595.1 </a>	hypothetical protein slr0299 [...]	<a href="#">43</a>	0.007	<b>G</b>
<a href="#">gi 142639 qb AAA69838.1 </a>	chloramphenicol acetyltransferase ...	<a href="#">41</a>	0.036	
<a href="#">gi 209319 qb AAA72834.1 </a>	S19 ribosomal/chloramphenicol acet...	<a href="#">38</a>	0.30	
<a href="#">gi 208252 qb AAA72540.1 </a>	cat-cpxA fusion protein	<a href="#">36</a>	1.2	
<a href="#">gi 1061119 emb CAA53196.1 </a>	putative replicase [Grapevine vi...	<a href="#">35</a>	1.5	<b>G</b>
<a href="#">gi 54645516 qb EAL34254.1 </a>	GA21573-PA [Drosophila pseudoobs...	<a href="#">35</a>	2.6	
<a href="#">gi 142641 qb AAA22291.1 </a>	chloramphenicol acetyltransferase	<a href="#">34</a>	3.3	
<a href="#">gi 57106681 ref XP_543633.1 </a>	PREDICTED: similar to Transcri...	<a href="#">34</a>	4.4	<b>G</b>
<a href="#">gi 24582127 ref NP_608989.1 </a>	CG9144-PA [Drosophila melanoga...	<a href="#">34</a>	4.4	<b>G</b>
<a href="#">gi 46580550 ref YP_011358.1 </a>	chloramphenicol acetyltransfer...	<a href="#">34</a>	4.4	<b>G</b>
<a href="#">gi 60467793 qb EAL65809.1 </a>	putative protein kinase [Dictyos...	<a href="#">33</a>	9.7	

## Alignments

Get selected sequences

Select all

Deselect all

[>gi|11934672|qb|AAG41774.1|](#) Cat [Promoter probe vector pPR9TT]  
Length = 253

Score = 449 bits (1156), Expect = e-125  
Identities = 212/222 (95%), Positives = 214/222 (96%)  
Frame = +2

Query: 32 EAKMEKKITGYTTVDISQWHRKEHLEAFQSVAOCTYNQTVQLDITAFCLKTVKKNKHKFYF 211  
EAKMEKKITGYTTVDISQWHRKEH EAFQSVAOCTYNQTVQLDITAFCLKTVKKNKHKFYF  
Sbjct: 32 EAKMEKKITGYTTVDISQWHRKEHLEAFQSVAOCTYNQTVQLDITAFCLKTVKKNKHKFYF 91

Query: 212 AFIHILARLMNAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTEFFSSLWSEYHDDFRQFL 391  
AFIHILARLMNAHPE RMAMKDGELVIWDSVHPCYTVFHEQTEFFSSLWSEYHDDFRQFL  
Sbjct: 92 AFIHILARLMNAHPELRMAMKDGELVIWDSVHPCYTVFHEQTEFFSSLWSEYHDDFRQFL 151

Query: 392 HIYSQDVACYGENLAYFPKGFIEENFFVSANPWVSFTSFDLVANMDNFFAPVFTMGKYY 571  
HIYSQDVACYGENLAYFPKGFIEENFFVSANPWVSFTSFDLVANMDNFFAPVFTMGKYY  
Sbjct: 152 HIYSQDVACYGENLAYFPKGFIEENFFVSANPWVSFTSFDLVANMDNFFAPVFTMGKYY 211

Query: 572 TOGDKVLMPLAIQVHHAVCDGFHVGTNA\*\*IK\*YCDEWQOGGA 697  
TOGDKVLMPLAIQVHHAVCDGFHVG ++ YCDEWQOGGA  
Sbjct: 212 TOGDKVLMPLAIQVHHAVCDGFHVGRMLNELQOYCDEWQOGGA 253

[>gi|38490699|qb|AAR21679.1|](#) chloramphenicol acetyltransferase [BAC cloning vector pBAC-VM5]  
[gi|48391501|qb|AAT42373.1|](#) chloramphenicol acetyl transferase [Large-insert cloning vector  
pSMART VC]  
[gi|40795483|qb|AAR91463.1|](#) CatA1, formerly CAT1, chloramphenicol acetyl transferase  
[Klebsiella pneumoniae]  
[gi|56553585|qb|AAV97918.1|](#) Cm [Gateway destination plasmid pSAT6-NP-DEST-EGFP]  
[gi|56553566|qb|AAV97906.1|](#) Cm [Gateway destination plasmid pSAT6-DEST-EGFP-C1]  
[gi|56553558|qb|AAV97900.1|](#) Cm [Gateway destination plasmid pSAT6-DEST-EGFP-N1]  
[gi|29164971|qb|AAO65220.1|](#) Cat [Shuttle vector pBHC18mob2]  
[gi|29164962|qb|AAO65214.1|](#) Cat [Shuttle vector pBHC18]  
[gi|29164952|qb|AAO65207.1|](#) Cat [Expression vector pXK99CAT]  
[gi|29164946|qb|AAO65203.1|](#) Cat [Expression vector pXC99E]  
[gi|29164933|qb|AAO65193.1|](#) Cat [Shuttle expression vector pEC-XC99E]  
[gi|29242904|qb|AAO66603.1|](#) Cat [Shuttle vector pEC-C18mob2]  
[gi|29242886|qb|AAO66593.1|](#) Cat [Cloning vector pC19mob2]  
[gi|29242884|qb|AAO66592.1|](#) Cat [Cloning vector pC18mob2]  
[gi|32351267|qb|AAP75573.1|](#) chloramphenicol acetyl transferase [Cloning vector pFGC1008]  
[gi|9507572|ref|NP\\_052903.1|](#) **G** chloramphenicol acetyltransferase [Plasmid R100]  
[gi|31075618|qb|AAP42292.1|](#) chloramphenicol acetyltransferase [Cloning vector pHRS-9]  
[gi|54043015|qb|AAV28501.1|](#) chloramphenicol transacetylase [Cloning vector  
pUC18-mini-Tn7T-Tp-Gateway]  
[gi|54043007|qb|AAV28495.1|](#) chloramphenicol transacetylase [Cloning vector  
pUC18-mini-Tn7T-Gm-Gateway]  
[gi|18466598|ref|NP\\_569406.1|](#) **G** chloramphenicol acetyltransferase [Salmonella enterica subsp.  
enterica serovar Typhi str. CT18]  
[gi|52353991|qb|AAU44360.1|](#) chloramphenicol acetyl transferase [Cloning vector pSW27]  
[gi|52353989|qb|AAU44359.1|](#) chloramphenicol acetyl transferase [Cloning vector pSW26]  
[gi|52353987|qb|AAU44358.1|](#) chloramphenicol acetyl transferase [Cloning vector pSW24]

[gi|52353985|qb|AAU44357.1|](#) chloramphenicol acetyl transferase [Cloning vector pSW23T]  
[gi|52353983|qb|AAU44356.1|](#) chloramphenicol acetyl transferase [Cloning vector pSW23]  
[gi|30407694|qb|AAO61290.1|](#) CmR [BAC cloning vector pEBAC190G]  
[gi|60417430|emb|CAI59794.1|](#) chloramphenicol acetyltransferase [Shuttle promoter-probe vector pET2]

[gi|43769|emb|CAA23900.1|](#) **G** chloramphenicol acetyltransferase [Escherichia coli]  
[gi|29568875|qb|AAO84029.1|](#) chloramphenicol acetyl transferase [Expression vector pYPX145]  
[gi|29568871|qb|AAO84026.1|](#) catalase [Expression vector pYPX143]  
[gi|22595318|qb|AAN02502.1|](#) chloramphenicol resistance protein [Reporter vector pVA838]  
[gi|22595313|qb|AAN02498.1|](#) chloramphenicol resistance protein [Reporter vector pALH122]  
[gi|22595308|qb|AAN02494.1|](#) chloramphenicol resistance protein [Reporter vector pALH109]  
[gi|21667079|qb|AAM73894.1|](#) chloramphenicol acetyl transferase [Filamentous phage display vector c8-4]

[gi|21617576|qb|AAM66745.1|](#) chloramphenicol acetyltransferase [Cloning vector pMAK705]  
[gi|21552739|qb|AAM62302.1|](#) CmR [Binary vector pJawohl8-RNAi]  
[gi|21552737|qb|AAM62300.1|](#) CmR [Binary vector pJawohl8-RNAi]  
[gi|29150583|qb|AAO63170.1|](#) chloramphenicol-acetyl-transferase [Cloning vector pHRGFPTC]  
[gi|20804330|emb|CAD10260.1|](#) chloramphenicol acetyltransferase [Shuttle integration vector pPL]  
[gi|37496516|emb|CAD50591.1|](#) chloramphenicol acetyltransferase [Cloning vector pUVBAC]

[gi|16505914|emb|CAD09793.1|](#) **G** chloramphenicol acetyltransferase [Salmonella enterica subsp. enterica serovar Typhi str. CT18]  
[gi|57157729|dbj|BAD83835.1|](#) chloramphenicol acetyltransferase [Integration vector pCRA732]

[gi|43767|emb|CAA23899.1|](#) **G** amp [Escherichia coli]

[gi|3451550|emb|CAA74791.1|](#) **G** chloramphenicol marker [Escherichia coli]  
[gi|60594756|qb|AAX29980.1|](#) chloroamphenicol resistance protein [Cloning vector pHTSUB-106]  
[gi|60547282|qb|AAX23610.1|](#) chloramphenicol acetyl transferase [Cloning vector pEX18ApGW]  
[gi|50345955|qb|AAT74895.1|](#) chloramphenicol acetyl transferase [Anabaena transfer vector pRL2665b]

[gi|49176955|ref|YP\\_025721.1|](#) **G** chloramphenicol acetyltransferase [Escherichia coli]  
[gi|42556321|qb|AAS19750.1|](#) chloramphenicol acetyl transferase [Expression vector pFL506A]  
[gi|25988998|qb|AAN76304.1|](#) chloramphenicol acetyl transferase [his-3 integration vector pJHAM007]

[gi|3559833|emb|CAA07596.1|](#) chloramphenicol acetyl transferase [Cloning vector pEH3]  
[gi|3282101|qb|AAC25439.1|](#) chloramphenicol acetyltransferase [synthetic construct]  
[gi|60172113|qb|AAX14475.1|](#) chloramphenicol acetyltransferase [synthetic construct]  
[gi|60172027|qb|AAX14472.1|](#) chloramphenicol acetyltransferase [synthetic construct]  
[gi|60171998|qb|AAX14471.1|](#) chloramphenicol acetyltransferase [synthetic construct]  
[gi|60171879|qb|AAX14467.1|](#) chloramphenicol acetyltransferase [synthetic construct]  
[gi|7638141|qb|AAF65394.1|](#) chloramphenicol acetyl transferase [Binary vector pCAMBIA-2201]  
[gi|7638138|qb|AAF65392.1|](#) chloramphenicol acetyl transferase [Binary vector pCAMBIA-2200]  
[gi|7638060|qb|AAF65332.1|](#) chloramphenicol acetyl transferase [Binary vector pCAMBIA-1291Z]  
[gi|7638055|qb|AAF65328.1|](#) chloramphenicol acetyl transferase [Binary vector pCAMBIA-1281Z]  
[gi|7638050|qb|AAF65324.1|](#) chloramphenicol acetyl transferase [Binary vector pCAMBIA-1201]  
[gi|7638046|qb|AAF65321.1|](#) chloramphenicol acetyl transferase [Binary vector pCAMBIA-1200]  
[gi|4586831|dbj|BAA76493.1|](#) chloramphenicol acetyltransferase [Cloning vector pCHR8]  
[gi|2168167|dbj|BAA06211.1|](#) chloramphenicol acetyl transferase [Cloning vector pKF19c]  
[gi|2168166|dbj|BAA06209.1|](#) chloramphenicol acetyl transferase [Cloning vector pKF18c]  
[gi|2168165|dbj|BAA06207.1|](#) chloramphenicol acetyl transferase [Cloning vector pKF17c]  
[gi|1272692|dbj|BAA06205.1|](#) chloramphenicol acetyltransferase [Cloning vector pKF16c]  
[gi|992943|dbj|BAA06203.1|](#) chloramphenicol acetyltransferase [Cloning vector pKF399]  
[gi|992940|dbj|BAA06201.1|](#) chloramphenicol acetyltransferase [Cloning vector pKF398]  
[gi|992937|dbj|BAA06199.1|](#) chloramphenicol acetyltransferase [Cloning vector pKF397]  
[gi|1272694|dbj|BAA06197.1|](#) chloramphenicol acetyltransferase [Cloning vector pKF396]  
[gi|1107464|dbj|BAA13563.1|](#) chloramphenicol acetyltransferase [Cloning vector pHSG576]  
[gi|25006377|dbj|BAC23918.1|](#) chloramphenicol acetyl transferase [Cloning vector pHSG415r]  
[gi|25006372|dbj|BAC23914.1|](#) chloramphenicol acetyl transferase [Cloning vector pHSG415s]  
[gi|15721871|dbj|BAB68400.1|](#) unnamed protein product [Cloning vector pBAC-Lac]  
[gi|3953680|dbj|BAA34775.1|](#) chloramphenicol acetyltransferase [Cloning vector pTH19cs5]  
[gi|3953676|dbj|BAA34772.1|](#) chloramphenicol acetyltransferase [Cloning vector pTH19cs1]  
[gi|3953672|dbj|BAA34769.1|](#) chloramphenicol acetyltransferase [Cloning vector pTH19cr]  
[gi|3953668|dbj|BAA34766.1|](#) chloramphenicol acetyltransferase [Cloning vector pTH18cs5]  
[gi|3953664|dbj|BAA34763.1|](#) chloramphenicol acetyltransferase [Cloning vector pTH18cs1]

[gi|3970883|dbj|BAA34760.1|](#) chloramphenicol acetyltransferase [Cloning vector pTH18cr]  
[gi|1902896|dbj|BAA19464.1|](#) chloramphenicol acetyltransferase [Cloning vector pBEN70]  
[gi|1902778|dbj|BAA19238.1|](#) chloramphenicol-acetyltransferase [Cloning vector pBEN77]  
[gi|59800249|gb|AAx07430.1|](#) chloromphenicol resistance protein [Expression vector pHTSUB-105]  
[gi|59800244|gb|AAx07426.1|](#) chloromphenicol resistance protein [Expression vector pLuxR-wt]  
[gi|17066891|gb|AAA96237.2|](#) acetyltransferase [synthetic construct]  
[gi|938037|emb|CAA90483.1|](#) chloramphenicol acetyltransferase [synthetic construct]  
[gi|938045|emb|CAA90506.1|](#) chloramphenicol acetyltransferase [synthetic construct]  
[gi|938043|emb|CAA90482.1|](#) chloramphenicol acetyltransferase [synthetic construct]  
[gi|938040|emb|CAA90480.1|](#) chloramphenicol acetyltransferase [synthetic construct]  
[gi|58161|emb|CAA45754.1|](#) chloramphenicol acetyltransferase [synthetic construct]  
[gi|58164|emb|CAA45752.1|](#) chloramphenicol acetyltransferase [synthetic construct]  
[gi|29335743|emb|CAD83080.1|](#) chloramphenicol acetyl transferase [Transfection vector pBTdest]  
[gi|20975729|emb|CAD10280.1|](#) chloramphenicol acetyltransferase [Shuttle integration vector pPL]  
[gi|11061108|emb|CAC14451.1|](#) chloramphenicol acetyltransferase [Cloning vector pBPSCat2]  
[gi|8346632|emb|CAB93898.1|](#) chloramphenicol acetyltransferase [Artificial vector pLoxCat2]  
[gi|11061046|emb|CAC14436.1|](#) chloramphenicol acetyltransferase [Cloning vector pBRINTs-Cat2]  
[gi|5640092|emb|CAB51569.1|](#) chloramphenicol acetyltransferase [Expression vector pIVET]  
[gi|6562909|emb|CAB62546.1|](#) chloramphenicol acetyl transferase [Shuttle vector pXMJ19]  
[gi|6562905|emb|CAB62544.1|](#) chloramphenicol acetyl transferase [Shuttle vector pMJ1]  
[gi|3139057|gb|AAC16724.1|](#) chloramphenicol acetyltransferase [Cloning vector pCSOS-72]  
[gi|6010637|gb|AAF01200.1|](#) chloramphenicol acetyltransferase [Cloning vector pLM53]  
**G** [gi|47717948|gb|AAT37967.1|](#) chloramphenicol acetyltransferase [Escherichia coli]  
[gi|15004262|gb|AAK73768.1|](#) chloramphenicol acetyltransferase [Cloning vector pSB3616]  
[gi|3777574|gb|AAC64937.1|](#) chloramphenicol acetyl transferase [Cloning vector p34S-Cm2]  
[gi|58091859|gb|AAW65356.1|](#) chloramphenicol resistance protein [synthetic construct]  
[gi|58091843|gb|AAW65345.1|](#) chloramphenicol resistance protein [synthetic construct]  
[gi|1763645|gb|AAB39756.1|](#) chloramphenicol acetyl transferase [Cloning vector pBACE3.6]  
[gi|4704642|gb|AAD28188.1|](#) chloramphenicol-acetyl-transferase (CAT) [Cloning vector pBBR1-GFP]  
[gi|4585226|gb|AAD25335.1|](#) chloramphenicol acetyltransferase [Cloning vector pLM10]  
[gi|4545269|gb|AAD22469.1|](#) chloramphenicol acetyltransferase [Expression vector pCY216]  
[gi|47027949|gb|AAT08989.1|](#) chloramphenicol acetyl transferase [Chloramphenicol resistance FRT  
vector pFCM1]  
[gi|3138987|gb|AAD11461.1|](#) chloramphenicol acetyltransferase [synthetic construct]  
[gi|4165114|gb|AAD08688.1|](#) chloramphenicol acetyltransferase [Shuttle vector pCGL0482]  
[gi|40456279|gb|AAR86224.1|](#) CAT [Cloning vector pMK2017]  
[gi|40456275|gb|AAR86221.1|](#) CAT [Cloning vector pMK2016]  
[gi|40456272|gb|AAR86219.1|](#) CAT [Cloning vector pMK2010]  
[gi|46561797|gb|AAT01118.1|](#) chloramphenicol acetyl transferase [rpL23-fusion expression vector  
pScFV]  
[gi|46561793|gb|AAT01115.1|](#) chloramphenicol acetyl transferase [rpL23-fusion expression vector  
pSA]  
[gi|46561790|gb|AAT01113.1|](#) chloramphenicol acetyl transferase [Expression vector prpL23]  
[gi|46561785|gb|AAT01109.1|](#) chloramphenicol acetyl transferase [rpL23-fusion expression vector  
pGFP]  
[gi|46561781|gb|AAT01106.1|](#) chloramphenicol acetyl transferase [rpL23-fusion expression vector  
pmIL-6]  
[gi|46561777|gb|AAT01103.1|](#) chloramphenicol acetyl transferase [rpL23-fusion expression vector  
pyEF1A]  
**G** [gi|66520|pir|XXECC1](#) chloramphenicol O-acetyltransferase (EC 2.3.1.28) - Escherichia  
coli plasmids  
[gi|78087|pir|JQ0972](#) chloramphenicol O-acetyltransferase (EC 2.3.1.28) - Acinetobacter  
baumannii  
[gi|13958038|gb|AAK50772.1|](#) chloramphenicol acetyltransferase [Cloning vector pBT]  
[gi|45548774|gb|AAS67528.1|](#) chloramphenicol acetyltransferase [Cloning vector pDS132]  
[gi|1262898|gb|AAC53675.1|](#) chloramphenicol acetyl transferase  
[gi|1160360|gb|AAC53644.1|](#) chloramphenicol acetyltransferase  
[gi|984912|gb|AAC53621.1|](#) chloramphenicol acetyltransferase  
[gi|984909|gb|AAC53619.1|](#) chloramphenicol acetyltransferase  
[gi|984893|gb|AAC53608.1|](#) chloramphenicol acetyltransferase  
[gi|984890|gb|AAC53606.1|](#) chloramphenicol acetyltransferase  
[gi|595752|gb|AAC53600.1|](#) chloramphenicol acetyltransferase  
[gi|39754101|gb|AAR30558.1|](#) chloramphenicol acetyl transferase [Cloning vector pTARBAC2.1]

[gi|39754097|qb|AAR30555.1|](#) chloramphenicol acetyl transferase [Cloning vector pTARBAC1.3]  
[gi|45862534|qb|AAS79015.1|](#) chloramphenicol acyl transferase [Cloning vector pMCG161]  
[gi|32185271|qb|AAP73801.1|](#) chloramphenicol acetyltransferase [Shuttle vector pLEIIttd+KR''deltaORF]  
[gi|32140769|qb|AAP70042.1|](#) chloramphenicol acetyltransferase [Shuttle vector pLEIIttd+KR'']  
[gi|3135580|qb|AAC34783.1|](#) chloramphenicol acetyltransferase [Plasposon pTnMod-RCm]  
[gi|3551824|qb|AAC34780.1|](#) chloramphenicol acetyltransferase [Plasposon pTnMod-Cm'OTc]  
[gi|3135572|qb|AAC34777.1|](#) chloramphenicol acetyltransferase [Plasposon pTnMod-CmOTc]  
[gi|3135548|qb|AAC34761.1|](#) chloramphenicol acetyltransferase [Plasposon pTnMod-OCm']  
[gi|3135545|qb|AAC34759.1|](#) chloramphenicol acetyltransferase [Plasposon pTnMod-OCm]  
[gi|3135593|qb|AAC26205.1|](#) chloramphenicol acetyltransferase [Cloning vector p34S-Cm]  
[gi|45386993|qb|AAS60102.1|](#) chloramphenicol acetyltransferase [Cloning vector pSUP202]  
[gi|45384791|qb|AAS59438.1|](#) chloramphenicol acetyltransferase [Reporter vector pGSA1370]  
[gi|25246288|qb|AAN72828.1|](#) chloramphenicol acetyl transferase [Expression vector pIVETHP]  
[gi|25990175|qb|AAN74640.1|](#) chloramphenicol transferase [Cloning vector pCAT-3']  
[gi|4323383|qb|AAD16327.1|](#) chloramphenicol acetyltransferase [Cloning vector pVZ321]  
[gi|2293131|qb|AAB68658.1|](#) chloramphenicol acetyltransferase [unidentified cloning vector]  
[gi|10945617|qb|AAG24617.1|](#) chloramphenicol acetyltransferase [synthetic construct]  
[gi|4753685|emb|CAB42001.1|](#) chloramphenicol acetyl transferase [Corynebacterium glutamicum]  
[gi|1684863|qb|AAB36547.1|](#) chloramphenicol acetyl transferase [Cloning vector pRNA8]

[gi|51247237|pdb|1Q23|L](#)  Chain L, Crystal Structure Of Chloramphenicol Acetyltransferase I Complexed With Fusidic Acid At 2.18 A Resolution  
[gi|51247236|pdb|1Q23|K](#)  Chain K, Crystal Structure Of Chloramphenicol Acetyltransferase I Complexed With Fusidic Acid At 2.18 A Resolution  
[gi|51247235|pdb|1Q23|J](#)  Chain J, Crystal Structure Of Chloramphenicol Acetyltransferase I Complexed With Fusidic Acid At 2.18 A Resolution  
[gi|51247234|pdb|1Q23|I](#)  Chain I, Crystal Structure Of Chloramphenicol Acetyltransferase I Complexed With Fusidic Acid At 2.18 A Resolution  
[gi|51247233|pdb|1Q23|H](#)  Chain H, Crystal Structure Of Chloramphenicol Acetyltransferase I Complexed With Fusidic Acid At 2.18 A Resolution  
[gi|51247232|pdb|1Q23|G](#)  Chain G, Crystal Structure Of Chloramphenicol Acetyltransferase I Complexed With Fusidic Acid At 2.18 A Resolution  
[gi|51247231|pdb|1Q23|F](#)  Chain F, Crystal Structure Of Chloramphenicol Acetyltransferase I Complexed With Fusidic Acid At 2.18 A Resolution  
[gi|51247230|pdb|1Q23|E](#)  Chain E, Crystal Structure Of Chloramphenicol Acetyltransferase I Complexed With Fusidic Acid At 2.18 A Resolution  
[gi|51247229|pdb|1Q23|D](#)  Chain D, Crystal Structure Of Chloramphenicol Acetyltransferase I Complexed With Fusidic Acid At 2.18 A Resolution  
[gi|51247228|pdb|1Q23|C](#)  Chain C, Crystal Structure Of Chloramphenicol Acetyltransferase I Complexed With Fusidic Acid At 2.18 A Resolution  
[gi|51247227|pdb|1Q23|B](#)  Chain B, Crystal Structure Of Chloramphenicol Acetyltransferase I Complexed With Fusidic Acid At 2.18 A Resolution  
[gi|51247226|pdb|1Q23|A](#)  Chain A, Crystal Structure Of Chloramphenicol Acetyltransferase I Complexed With Fusidic Acid At 2.18 A Resolution  
[gi|49258461|pdb|1PD5|L](#)  Chain L, Crystal Structure Of E.Coli Chloramphenicol Acetyltransferase Type I At 2.5 Angstrom Resolution  
[gi|49258460|pdb|1PD5|K](#)  Chain K, Crystal Structure Of E.Coli Chloramphenicol Acetyltransferase Type I At 2.5 Angstrom Resolution  
[gi|49258459|pdb|1PD5|J](#)  Chain J, Crystal Structure Of E.Coli Chloramphenicol Acetyltransferase Type I At 2.5 Angstrom Resolution  
[gi|49258458|pdb|1PD5|I](#)  Chain I, Crystal Structure Of E.Coli Chloramphenicol Acetyltransferase Type I At 2.5 Angstrom Resolution  
[gi|49258457|pdb|1PD5|H](#)  Chain H, Crystal Structure Of E.Coli Chloramphenicol Acetyltransferase Type I At 2.5 Angstrom Resolution  
[gi|49258456|pdb|1PD5|G](#)  Chain G, Crystal Structure Of E.Coli Chloramphenicol Acetyltransferase Type I At 2.5 Angstrom Resolution  
[gi|49258455|pdb|1PD5|F](#)  Chain F, Crystal Structure Of E.Coli Chloramphenicol Acetyltransferase Type I At 2.5 Angstrom Resolution

[gi|49258454|pdb|1PD5|E](#) **GS** Chain E, Crystal Structure Of E.Coli Chloramphenicol Acetyltransferase Type I At 2.5 Angstrom Resolution

[gi|49258453|pdb|1PD5|D](#) **GS** Chain D, Crystal Structure Of E.Coli Chloramphenicol Acetyltransferase Type I At 2.5 Angstrom Resolution

[gi|49258452|pdb|1PD5|C](#) **GS** Chain C, Crystal Structure Of E.Coli Chloramphenicol Acetyltransferase Type I At 2.5 Angstrom Resolution

[gi|49258451|pdb|1PD5|B](#) **GS** Chain B, Crystal Structure Of E.Coli Chloramphenicol Acetyltransferase Type I At 2.5 Angstrom Resolution

[gi|49258450|pdb|1PD5|A](#) **GS** Chain A, Crystal Structure Of E.Coli Chloramphenicol Acetyltransferase Type I At 2.5 Angstrom Resolution

[gi|1197596|qb|AAA93352.1|](#) chloramphenicol acetyl transferase

[gi|208099|qb|AAA73140.1|](#) chloramphenicol acetyltransferase

[gi|208102|qb|AAA73138.1|](#) chloramphenicol acetyltransferase

[gi|209393|qb|AAA73022.1|](#) putative

[gi|209389|qb|AAA73021.1|](#) putative

[gi|209128|qb|AAA72304.1|](#) chloramphenicol resistance determinant

[gi|537614|qb|AAA67260.1|](#) chloramphenicol resistance

[gi|806887|qb|AAA66384.1|](#) chloramphenicol acetyltransferase

[gi|141789|qb|AAA62571.1|](#) CAT

[gi|450836|qb|AAA61619.1|](#) chloramphenicol acetyl methylase

[gi|9294790|qb|AAF86673.1|](#) chloramphenicol transacetylase [Integration vector pCD11PSK]

[gi|9294787|qb|AAF86671.1|](#) chloramphenicol transacetylase [Integration vector pCD11PKS]

[gi|3891864|pdb|1NOC|B](#) **GS** Chain B, Murine Inducible Nitric Oxide Synthase Oxygenase Domain (Delta 114) Complexed With Type I E. Coli Chloramphenicol Acetyl Transferase And Imidazole

[gi|12082332|dbj|BAB20666.1|](#) CAT [Cloning vector pCA24N]

[gi|141745|qb|AAA21891.1|](#) chloramphenicol acetyltransferase

[gi|50401834|sp|P62580|CAT\\_SALTI](#) Chloramphenicol acetyltransferase (CAT)

[gi|50401833|sp|P62579|CAT\\_ACTIBA](#) Chloramphenicol acetyltransferase (CAT)

[gi|50401832|sp|P62578|CAT\\_ACTIAN](#) Chloramphenicol acetyltransferase (CAT)

[gi|50401831|sp|P62577|CAT\\_ECOLI](#) **G** Chloramphenicol acetyltransferase (CAT)

[gi|223161|prf|0601249A](#) **G** transferase, chloramphenicol Ac

[gi|58186|emb|CAA46418.1|](#) CAT [Cloning vector pCAT-Basic]

[gi|58188|emb|CAA46415.1|](#) chloramphenicol acetyltransferase [Cloning vector pCAT-Control]

[gi|58194|emb|CAA46413.1|](#) chloramphenicol acetyltransferase [Cloning vector pCAT-Promoter]

[gi|58192|emb|CAA46412.1|](#) chloramphenicol acetyltransferase [Cloning vector pCAT-Enhancer]

[gi|5103171|dbj|BAA78807.1|](#) **G** chloramphenicol acetyltransferase [Plasmid R100]

Length = 219

Score = 446 bits (1148), Expect = e-124  
 Identities = 210/219 (95%), Positives = 212/219 (96%)  
 Frame = +2

Query: 41 MEKKITGYTTVDISQWHRKEHLEAFQSV AQCTYNQTVQLDITAF LKTVKKNKHKFYPAFI 220  
 MEKKITGYTTVDISQWHRKEH EAFQSV AQCTYNQTVQLDITAF LKTVKKNKHKFYPAFI

Sbjct: 1 MEKKITGYTTVDISQWHRKEHFEAFQSV AQCTYNQTVQLDITAF LKTVKKNKHKFYPAFI 60

Query: 221 HILARLMNAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTET FSSLWSEYHDDFRQFLHIY 400  
 HILARLMNAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTET FSSLWSEYHDDFRQFLHIY

Sbjct: 61 HILARLMNAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTET FSSLWSEYHDDFRQFLHIY 120

Query: 401 SQDVACYGENLAYFPKGF IENMFFVSANPWSF TSFDLNVANMDNFFAPVFTMGKYTQG 580  
 SQDVACYGENLAYFPKGF IENMFFVSANPWSF TSFDLNVANMDNFFAPVFTMGKYTQG

Sbjct: 121 SQDVACYGENLAYFPKGF IENMFFVSANPWSF TSFDLNVANMDNFFAPVFTMGKYTQG 180

Query: 581 DKVLMPLAIQVHHAVCDGFHVG TNA\*\*IK\*YCDEWQGGA 697  
 DKVLMPLAIQVHHAVCDGFHVG ++ YCDEWQGGA

Sbjct: 181 DKVLMPLAIQVHHAVCDGFHVGRMLNELQQY CDEWQGGA 219



>[gi|1480375|emb|CAA67774.1|](#) cat [Escherichia coli]  
Length = 219

Score = 446 bits (1147), Expect = e-124  
Identities = 210/219 (95%), Positives = 212/219 (96%)  
Frame = +2

Query: 41 MEKKITGYTTVDISQWHRKEHLEAFQSVACTYNTQTVQLDITAFKTVKKNKHKFYPAFI 220  
MEKKITGYTTVDISQWHRKEH EAFQSVACTYNTQTVQLDITAFKTVKKNKHKFYPAFI  
Sbjct: 1 MEKKITGYTTVDISQWHRKEHFEAFQSVACTYNTQTVQLDITAFKTVKKNKHKFYPAFI 60

Query: 221 HILARLMNAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTETTFSSLWSEYHDDFRQFLHIY 400  
HILARLMNAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTETTFSSLWSEYHDDFRQFLHIY  
Sbjct: 61 HILARLMNAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTETTFSSLWSEYHDDFRQFLHIY 120

Query: 401 SQDVACYGENLAYFPKGF IENMFFVSANPWSFTSFDLNVANMDNFFAPVFTMGKYYTQG 580  
SQDVACYGENLAYFPKGF IENMFFVSANPWSFTSFDLNVANMDNFFAPVFTMGKYYTQG  
Sbjct: 121 SQDVACYGENLAYFPKGF IENMFFVSANPWSFTSFDLNVANMDNFFAPVFTMGKYYTQG 180

Query: 581 DKVLMPLAIQVHHA VCDGFHVG TNA\*\*IK\*YCEWQGGGA 697  
DKVLMPLAIQVHHA VCDGFHVG ++ YCEWQGGGA  
Sbjct: 181 DKVLMPLAIQVHHA VCDGFHVGRILNELQQYCEWQGGGA 219

>[gi|303728|dbj|BAA03718.1|](#) PP-CAT [Photobacterium damsela subsp. piscicida]  
Length = 219

Score = 446 bits (1147), Expect = e-124  
Identities = 209/219 (95%), Positives = 212/219 (96%)  
Frame = +2

Query: 41 MEKKITGYTTVDISQWHRKEHLEAFQSVACTYNTQTVQLDITAFKTVKKNKHKFYPAFI 220  
MEKKITGYTTVDISQWHRKEH EAFQSVACTYNTQTVQLDITAFKTVKKNKHKFYPAFI  
Sbjct: 1 MEKKITGYTTVDISQWHRKEHFEAFQSVACTYNTQTVQLDITAFKTVKKNKHKFYPAFI 60

Query: 221 HILARLMNAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTETTFSSLWSEYHDDFRQFLHIY 400  
HILARLMNAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTETTFSSLWSEYHDDFRQFLHIY  
Sbjct: 61 HILARLMNAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTETTFSSLWSEYHDDFRQFLHIY 120

Query: 401 SQDVACYGENLAYFPKGF IENMFFVSANPWSFTSFDLNVANMDNFFAPVFTMGKYYTQG 580  
SQD+ACYGENLAYFPKGF IENMFFVSANPWSFTSFDLNVANMDNFFAPVFTMGKYYTQG  
Sbjct: 121 SQDIACYGENLAYFPKGF IENMFFVSANPWSFTSFDLNVANMDNFFAPVFTMGKYYTQG 180

Query: 581 DKVLMPLAIQVHHA VCDGFHVG TNA\*\*IK\*YCEWQGGGA 697  
DKVLMPLAIQVHHA VCDGFHVG ++ YCEWQGGGA  
Sbjct: 181 DKVLMPLAIQVHHA VCDGFHVGRMLNELQQYCEWQGGGA 219

>[gi|29421421|qb|AAO48721.1|](#) Cat [CRIM plasmid pLA1]  
[gi|15290654|qb|AAK94926.1|](#) chloramphenicol acetyltransferase [Template plasmid pSG76-CS]  
[gi|6467491|qb|AAF13162.1|](#) chloramphenicol-resistance protein [Integration vector pLOI2228]  
[gi|6467485|qb|AAF13159.1|](#) chloramphenicol-resistance protein [Integration vector pLOI2225]  
[gi|8346641|emb|CAB93904.1|](#) chloramphenicol acetyltransferase [Artificial vector pLoxCat4]  
[gi|8250018|emb|CAB93482.1|](#) chloramphenicol acetyltransferase [Cloning vector pBPRINT-TsCm]  
[gi|16209177|qb|AAL09912.1|](#) cat [CRIM plasmid pCAH63]  
[gi|16209173|qb|AAL09909.1|](#) cat [CRIM plasmid pCAH56]

[gi|1769882|emb|CAA71024.1|](#) chloramphenicol acetyltransferase [unidentified cloning vector]  
[gi|1769874|emb|CAA71019.1|](#) chloramphenicol acetyltransferase [unidentified cloning vector]  
[gi|475711|qb|AAA73425.1|](#) chloramphenicol acetyltransferase  
[gi|37930040|qb|AAP74500.1|](#) Cat [Cloning vector pLZ44]  
[gi|37930033|qb|AAP74498.1|](#) Cat [Cloning vector pLZ43]  
[gi|37930024|qb|AAP74496.1|](#) Cat [Cloning vector pLZ42]  
[gi|37930013|qb|AAP74494.1|](#) Cat [Cloning vector pLZ41]  
[gi|37930004|qb|AAP74492.1|](#) Cat [Cloning vector pKZ28]  
[gi|37929994|qb|AAP74490.1|](#) Cat [Cloning vector pKZ22]  
[gi|37929985|qb|AAP74488.1|](#) Cat [Cloning vector pKZ20]  
[gi|37929974|qb|AAP74486.1|](#) Cat [Cloning vector pKZ14]

Length = 219

Score = 445 bits (1144), Expect = e-124  
 Identities = 209/219 (95%), Positives = 212/219 (96%)  
 Frame = +2

Query: 41 MEKKITGYTTVDISQWHRKEHLEAFQSV AQCTYNQTVQLDITAF LKTVKKNKHKFYPAFI 220  
 MEKKITGYTTVDISQWHRKEH EAFQSV AQCTYNQTVQLDITAF LKTVKKNKHKFYPAFI  
 Sbjct: 1 MEKKITGYTTVDISQWHRKEHFEAFQSV AQCTYNQTVQLDITAF LKTVKKNKHKFYPAFI 60

Query: 221 HILARLMNAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTETFS S L WSEYHDDFRQFLHIY 400  
 HILARLMNAHP+FRMAMKDGELVIWDSVHPCYTVFHEQTETFS S L WSEYHDDFRQFLHIY  
 Sbjct: 61 HILARLMNAHPKFRMAMKDGELVIWDSVHPCYTVFHEQTETFS S L WSEYHDDFRQFLHIY 120

Query: 401 SQDVACYGENLAYFPKGF IENMFFVSANPWVSFTSFDLNVANMDNFFAPVFTMGKYYTQG 580  
 SQDVACYGENLAYFPKGF IENMFFVSANPWVSFTSFDLNVANMDNFFAPVFTMGKYYTQG  
 Sbjct: 121 SQDVACYGENLAYFPKGF IENMFFVSANPWVSFTSFDLNVANMDNFFAPVFTMGKYYTQG 180

Query: 581 DKVLMPLAIQVHHAVCDGFHVG TNA\*\*IK\*Y CDEWQGGGA 697  
 DKVLMPLAIQVHHAVCDGFHVG ++ Y CDEWQGGGA  
 Sbjct: 181 DKVLMPLAIQVHHAVCDGFHVG RMLNELQQY CDEWQGGGA 219

>[gi|575451|qb|AAC53603.1|](#) chloramphenicol acetyltransferase  
 Length = 220

Score = 444 bits (1143), Expect = e-124  
 Identities = 209/218 (95%), Positives = 211/218 (96%)  
 Frame = +2

Query: 44 EKKITGYTTVDISQWHRKEHLEAFQSV AQCTYNQTVQLDITAF LKTVKKNKHKFYPAFIH 223  
 EKKITGYTTVDISQWHRKEH EAFQSV AQCTYNQTVQLDITAF LKTVKKNKHKFYPAFIH  
 Sbjct: 3 EKKITGYTTVDISQWHRKEHFEAFQSV AQCTYNQTVQLDITAF LKTVKKNKHKFYPAFIH 62

Query: 224 ILARLMNAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTETFS S L WSEYHDDFRQFLHIYS 403  
 ILARLMNAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTETFS S L WSEYHDDFRQFLHIYS  
 Sbjct: 63 ILARLMNAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTETFS S L WSEYHDDFRQFLHIYS 122



Query: 404 QDVACYGENLAYFPKGF IENMFFVSANPWVSFTSFDLNVANMDNFFAPVFTMGKYYTQGD 583  
 QDVACYGENLAYFPKGF IENMFFVSANPWVSFTSFDLNVANMDNFFAPVFTMGKYYTQGD  
 Sbjct: 123 QDVACYGENLAYFPKGF IENMFFVSANPWVSFTSFDLNVANMDNFFAPVFTMGKYYTQGD 182

Query: 584 KVL MPLAIQVHHAVCDGFHVG TNA\*\*IK\*Y CDEWQGGGA 697  
 KVL MPLAIQVHHAVCDGFHVG ++ Y CDEWQGGGA  
 Sbjct: 183 KVL MPLAIQVHHAVCDGFHVG RMLNELQQY CDEWQGGGA 220

[gi|2343026|gb|AAB67677.1|](#) chloramphenicol acetyltransferase [Cloning vector pJB3Cm6]  
[gi|46309698|gb|AAS87172.1|](#) chloramphenicol acetyltransferase [Achromobacter xylosoxidans]  
[gi|14164987|gb|AAK55328.1|](#) chloramphenicol acetyltransferase [Cloning vector pALTER(R)\*-MAX]  
[gi|1399742|gb|AAB39977.1|](#) chloramphenicol acetyltransferase [Reporter vector  
 pCAT3-Promoter vector]  
[gi|1399739|gb|AAB39975.1|](#) chloramphenicol acetyltransferase [Reporter vector  
 pCAT3-Enhancer vector]  
[gi|1399736|gb|AAB39973.1|](#) chloramphenicol acetyltransferase [Reporter vector pCAT3-Control  
 vector]  
[gi|1399733|gb|AAB39971.1|](#) chloramphenicol acetyltransferase [Reporter vector pCAT3-Basic  
 vector]  
[gi|984931|gb|AAC53634.1|](#) chloramphenicol acetyltransferase  
[gi|984916|gb|AAC53624.1|](#) chloramphenicol acetyltransferase  
[gi|209080|gb|AAA72895.1|](#) chloramphenicol acetyltransferase  
 Length = 219

Score = 444 bits (1142), Expect = e-123  
 Identities = 209/219 (95%), Positives = 211/219 (96%)  
 Frame = +2

Query: 41 MEKKITGYTTVDISQWHRKEHLEAFQSV AQCTYNQTVQLDITAF LKTVKKNKHKFYPAFI 220  
 MEKKITGYTTVDISQWHRKEH EAFQSV AQCTYNQTVQLDITAF LKTVKKNKHKFYPAFI  
 Sbjct: 1 MEKKITGYTTVDISQWHRKEHFEAFQSV AQCTYNQTVQLDITAF LKTVKKNKHKFYPAFI 60  
  
 Query: 221 HILARLMNAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTET FSSLWSEYHDDFRQFLHIY 400  
 HILARLMNAHPE RMAMKDGELVIWDSVHPCYTVFHEQTET FSSLWSEYHDDFRQFLHIY  
 Sbjct: 61 HILARLMNAHPELRMAMKDGELVIWDSVHPCYTVFHEQTET FSSLWSEYHDDFRQFLHIY 120  
  
 Query: 401 SQDVACYGENLAYFPKGF IENMFFVSANPWSF TSFDLNVANMDNFFAPVFTMGKYTQG 580  
 SQDVACYGENLAYFPKGF IENMFFVSANPWSF TSFDLNVANMDNFFAPVFTMGKYTQG  
 Sbjct: 121 SQDVACYGENLAYFPKGF IENMFFVSANPWSF TSFDLNVANMDNFFAPVFTMGKYTQG 180  
  
 Query: 581 DKVLMPLAIQVHHAVCDGFHVG TNA\*\*IK\*YCDEWQGG A 697  
 DKVLMPLAIQVHHAVCDGFHVG ++ YCDEWQGG A  
 Sbjct: 181 DKVLMPLAIQVHHAVCDGFHVG RMLNELQQYCDEWQGG A 219

[gi|38347932|ref|NP\\_941181.1|](#)  chloramphenicol acetyltransferase [Serratia marcescens]  
[gi|38259409|emb|CAE51636.1|](#)  chloramphenicol acetyltransferase [Serratia marcescens]  
 Length = 219

Score = 444 bits (1142), Expect = e-123  
 Identities = 208/219 (94%), Positives = 212/219 (96%)  
 Frame = +2

Query: 41 MEKKITGYTTVDISQWHRKEHLEAFQSV AQCTYNQTVQLDITAF LKTVKKNKHKFYPAFI 220  
 MEKKITGYTTVDISQWHRKEH EAFQSV AQCTYNQTVQLDITAF LKTVKKNKHKFYPAFI  
 Sbjct: 1 MEKKITGYTTVDISQWHRKEHFEAFQSV AQCTYNQTVQLDITAF LKTVKKNKHKFYPAFI 60  
  
 Query: 221 HILARLMNAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTET FSSLWSEYHDDFRQFLHIY 400  
 HILARLMNAHPEFRMAMKDGELVIWDS+HPCYTVFHEQTET FSSLWSEYHDDFRQFLHIY  
 Sbjct: 61 HILARLMNAHPEFRMAMKDGELVIWDSIHPCYTVFHEQTET FSSLWSEYHDDFRQFLHIY 120  
  
 Query: 401 SQDVACYGENLAYFPKGF IENMFFVSANPWSF TSFDLNVANMDNFFAPVFTMGKYTQG 580  
 SQDVACYGENLAYFPKGF IENMFFVSANPWSF TSFDLNVANMDNFFAPVFTMGKYTQG  
 Sbjct: 121 SQDVACYGENLAYFPKGF IENMFFVSANPWSF TSFDLNVANMDNFFAPVFTMGKYTQG 180  
  
 Query: 581 DKVLMPLAIQVHHAVCDGFHVG TNA\*\*IK\*YCDEWQGG A 697  
 DKVLMPLAIQVHHAVCDGFHVG ++ YC+EWQGG A  
 Sbjct: 181 DKVLMPLAIQVHHAVCDGFHVG RMLNELQQYCNEWQGG A 219

[>gi|220940|dbj|BAA03187.1](#) chloramphenicol acetyl transferase [synthetic construct]  
Length = 219

Score = 443 bits (1140), Expect = e-123  
Identities = 209/219 (95%), Positives = 211/219 (96%)  
Frame = +2

Query: 41 MEKKITGYTTVDISQWHRKEHLEAFQSVQCTYNQTVQLDITAFLLKTVKKNKHKFYPAFI 220  
MEKKITGYTTVDISQWHRKEH EAFQSVQCTYNQTVQLDITAFLLKTVKKNKHKFYPAFI  
Sbjct: 1 MEKKITGYTTVDISQWHRKEHFEAFQSVQCTYNQTVQLDITAFLLKTVKKNKHKFYPAFI 60

Query: 221 HILARLMNAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTETFSWSEYHDDFRQFLHIY 400  
HILARLMNAH EFRMAMKDGELVIWDSVHPCYTVFHEQTETFSWSEYHDDFRQFLHIY  
Sbjct: 61 HILARLMNAHTEFRMAMKDGELVIWDSVHPCYTVFHEQTETFSWSEYHDDFRQFLHIY 120

Query: 401 SQDVACYGENLAYFPKGF IENMFFVSANPWSFTSFDLNVANMDNFFAPVFTMGKYYTQG 580  
SQDVACYGENLAYFPKGF IENMFFVSANPWSFTSFDLNVANMDNFFAPVFTMGKYYTQG  
Sbjct: 121 SQDVACYGENLAYFPKGF IENMFFVSANPWSFTSFDLNVANMDNFFAPVFTMGKYYTQG 180

Query: 581 DKVLMPLAIQVHHAVCDGFHVG TNA\*\*IK\*YCDEWQGGA 697  
DKVLMPLAIQVHHAVCDGFHVG ++ YCDEWQGGA  
Sbjct: 181 DKVLMPLAIQVHHAVCDGFHVGRMLNELQQYCDEWQGGA 219

[>gi|20177832|sp|P58777|CAT\\_KLESP](#) Chloramphenicol acetyltransferase (CAT)  
Length = 219

Score = 443 bits (1140), Expect = e-123  
Identities = 209/219 (95%), Positives = 211/219 (96%)  
Frame = +2

Query: 41 MEKKITGYTTVDISQWHRKEHLEAFQSVQCTYNQTVQLDITAFLLKTVKKNKHKFYPAFI 220  
MEKKITGYTTVDISQWHRKEH EAFQSVQCTYNQTVQLDITAFLLKTVKKNKHKFYPAFI  
Sbjct: 1 MEKKITGYTTVDISQWHRKEHFEAFQSVQCTYNQTVQLDITAFLLKTVKKNKHKFYPAFI 60

Query: 221 HILARLMNAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTETFSWSEYHDDFRQFLHIY 400  
HILARLMNAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTETFSWSEYHDDFRQFLHIY  
Sbjct: 61 HILARLMNAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTETFSWSEYHDDFRQFLHIY 120

Query: 401 SQDVACYGENLAYFPKGF IENMFFVSANPWSFTSFDLNVANMDNFFAPVFTMGKYYTQG 580  
SQDVACYGENLAYFPKGF IENMFFVSANPWSFTSFDLNVANMDNFFAPVFTMGKYYTQG  
Sbjct: 121 SQDVACYGENLAYFPKGF IENMFFVSANPWSFTSFDLNVANMDNFFAPVFTMGKYYTQG 180

Query: 581 DKVLMPLAIQVHHAVCDGFHVG TNA\*\*IK\*YCDEWQGGA 697  
DKVLMPLAIQVHHAVCDGFHVG ++ YCDEWQGGA  
Sbjct: 181 DKVLMPLAIQVHHAVCDGFHVGRMLNELQQYCDEWQGGA 219

[>gi|13094143|dbj|BAB32741.1](#) chloramphenicol acetyltransferase [Cloning vector pLCPVRGNR104]  
[gi|13094140|dbj|BAB32739.1](#) chloramphenicol acetyltransferase [Cloning vector pLCPV101]  
[gi|469222|dbj|BAA03490.1](#) chloramphenicol acetyl transferase [unidentified cloning vector]  
Length = 219

Score = 441 bits (1135), Expect = e-123

Identities = 208/219 (94%), Positives = 210/219 (95%)  
 Frame = +2

Query: 41 MEKKITGYTTVDISQWHRKEHLEAFQSVQCTYNQTVQLDITAFLLKTVKKNKHKFYPAFI 220  
 MEKKITGYTTVDISQWHRKEH EAFQSVQCTYNQTV LDITAFLLKTVKKNKHKFYPAFI  
 Sbjct: 1 MEKKITGYTTVDISQWHRKEHFEAFQSVQCTYNQTVHLDITAFLLKTVKKNKHKFYPAFI 60

Query: 221 HILARLMNAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTETFSWSEYHDDFRQFLHIY 400  
 HILARLMNAH EFRMAMKDGELVIWDSVHPCYTVFHEQTETFSWSEYHDDFRQFLHIY  
 Sbjct: 61 HILARLMNAHTEFRMAMKDGELVIWDSVHPCYTVFHEQTETFSWSEYHDDFRQFLHIY 120

Query: 401 SQDVACYGENLAYFPKGF IENMFFVSANPWSFTSFDLNVANMDNFFAPVFTMGKYYTQG 580  
 SQDVACYGENLAYFPKGF IENMFFVSANPWSFTSFDLNVANMDNFFAPVFTMGKYYTQG  
 Sbjct: 121 SQDVACYGENLAYFPKGF IENMFFVSANPWSFTSFDLNVANMDNFFAPVFTMGKYYTQG 180

Query: 581 DKVLMPLAIQVHHA VCDGFHVG TNA\*\*IK\*YCDEWQGGA 697  
 DKVLMPLAIQVHHA VCDGFHVG ++ YCDEWQGGA  
 Sbjct: 181 DKVLMPLAIQVHHA VCDGFHVGRMLNELQQYCDEWQGGA 219

[gi|9294793|qb|AAF86675.1](#) chloramphenicol transacetylase [Integration vector pCD11PZ1]  
 Length = 219

Score = 441 bits (1135), Expect = e-123  
 Identities = 208/219 (94%), Positives = 210/219 (95%)  
 Frame = +2

Query: 41 MEKKITGYTTVDISQWHRKEHLEAFQSVQCTYNQTVQLDITAFLLKTVKKNKHKFYPAFI 220  
 MEKKITGYTTVDISQWHRKEH EAFQSVQCTYNQTVQLDITAFLLKTVKKNKHKFYPAFI  
 Sbjct: 1 MEKKITGYTTVDISQWHRKEHFEAFQSVQCTYNQTVQLDITAFLLKTVKKNKHKFYPAFI 60

Query: 221 HILARLMNAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTETFSWSEYHDDFRQFLHIY 400  
 HILARLMNAHP RMAMKDGELVIWDSVHPCYTVFHEQTETFSWSEYHDDFRQFLHIY  
 Sbjct: 61 HILARLMNAHPXXRMAMKDGELVIWDSVHPCYTVFHEQTETFSWSEYHDDFRQFLHIY 120

Query: 401 SQDVACYGENLAYFPKGF IENMFFVSANPWSFTSFDLNVANMDNFFAPVFTMGKYYTQG 580  
 SQDVACYGENLAYFPKGF IENMFFVSANPWSFTSFDLNVANMDNFFAPVFTMGKYYTQG  
 Sbjct: 121 SQDVACYGENLAYFPKGF IENMFFVSANPWSFTSFDLNVANMDNFFAPVFTMGKYYTQG 180

Query: 581 DKVLMPLAIQVHHA VCDGFHVG TNA\*\*IK\*YCDEWQGGA 697  
 DKVLMPLAIQVHHA VCDGFHVG ++ YCDEWQGGA  
 Sbjct: 181 DKVLMPLAIQVHHA VCDGFHVGRMLNELQQYCDEWQGGA 219

[gi|56387331|qb|AAV86079.1](#) chloramphenicol acetyltransferase [Shuttle vector pNAK1]  
[gi|56912126|emb|CAI39220.1](#) chloramphenicol acetyltransferase [Escherichia coli]  
[gi|1906553|qb|AAC53699.1](#) chloramphenicol acetyl transferase [Cloning vector pNF2283]  
[gi|595746|qb|AAC53596.1](#) chloramphenicol acetyltransferase  
[gi|4323361|qb|AAD16307.1](#) chloramphenicol acetyltransferase [Cloning vector pVZ323]  
[gi|885957|qb|AAA70410.1](#) chloramphenicol acetyltransferase [Cloning vector pCG1408]  
[gi|595697|qb|AAA57080.1](#) chloramphenicol acetyltransferase  
 Length = 219

Score = 441 bits (1134), Expect = e-123  
 Identities = 209/219 (95%), Positives = 211/219 (96%)  
 Frame = +2

Query: 41 MEKKITGYTTVDISQWHRKEHLEAFQSVQCTYNQTVQLDITAFLLKTVKKNKHKFYPAFI 220

MEKKITGYTTVDISQ HRKEH EAFQSV AQCTYNQTVQLDITAF LKTVKKNKHKFYPAFI  
 Sbjct: 1 MEKKITGYTTVDISQSHRKEHFEAFQSV AQCTYNQTVQLDITAF LKTVKKNKHKFYPAFI 60

Query: 221 HILARLMNAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTET FSSLWSEYHDDFRQFLHIY 400  
 HILARLMNAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTET FSSLWSEYHDDFRQFLHIY  
 Sbjct: 61 HILARLMNAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTET FSSLWSEYHDDFRQFLHIY 120

Query: 401 SQDVACYGENLAYFPKGF IENMFFV SANPWSFTSFDLNVANMDNFFAPVFTMGKYTQG 580  
 SQDVACYGENLAYFPKGF IENMFFV SANPWSFTSFDLNVANMDNFFAPVFTMGKYTQG  
 Sbjct: 121 SQDVACYGENLAYFPKGF IENMFFV SANPWSFTSFDLNVANMDNFFAPVFTMGKYTQG 180

Query: 581 DKVLMPLAIQVHHA VCDGFHVG TNA\*\*IK\*YCDEWQGGA 697  
 DKVLMPLAIQVHHA VCDGFHVG ++ YCDEWQGGA  
 Sbjct: 181 DKVLMPLAIQVHHA VCDGFHVGRMLNELQQY CDEWQGGA 219

>[gi|15808712|qb|AAL08441.1](#) chloramphenicol acetyltransferase [Shigella flexneri 2a]  
 Length = 219

Score = 437 bits (1123), Expect = e-121  
 Identities = 206/219 (94%), Positives = 208/219 (94%)  
 Frame = +2

Query: 41 MEKKITGYTTVDISQWHRKEHLEAFQSV AQCTYNQTVQLDITAF LKTVKKNKHKFYPAFI 220  
 MEKKITGYTTVDISQWHRKEH EAFQSV AQCTYNQTVQLDITAF LKTVKKNKHKFYPAFI  
 Sbjct: 1 MEKKITGYTTVDISQWHRKEHFEAFQSV AQCTYNQTVQLDITAF LKTVKKNKHKFYPAFI 60

Query: 221 HILARLMNAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTET FSSLWSEYHDDFRQFLHIY 400  
 HILARLMNAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTET FSSLWSEYHDDFRQFLHIY  
 Sbjct: 61 HILARLMNAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTET FSSLWSEYHDDFRQFLHIY 120

Query: 401 SQDVACYGENLAYFPKGF IENMFFV SANPWSFTSFDLNVANMDNFFAPVFTMGKYTQG 580  
 S DVACYGENLAYFPK F ENM FV SANPWSFTSFDLNVANMDNFFAPVFTMGKYTQG  
 Sbjct: 121 SXDVACYGENLAYFPKXF XENMXFV SANPWSFTSFDLNVANMDNFFAPVFTMGKYTQG 180

Query: 581 DKVLMPLAIQVHHA VCDGFHVG TNA\*\*IK\*YCDEWQGGA 697  
 DKVLMPLAIQVHHA VCDGFHVG ++ YCDEWQGGA  
 Sbjct: 181 DKVLMPLAIQVHHA VCDGFHVGRMLNELQQY CDEWQGGA 219

>[gi|58252|emb|CAA49282.1](#) cat mutant [synthetic construct]  
 Length = 219

Score = 432 bits (1110), Expect = e-120  
 Identities = 205/217 (94%), Positives = 207/217 (95%)  
 Frame = +2

Query: 41 MEKKITGYTTVDISQWHRKEHLEAFQSV AQCTYNQTVQLDITAF LKTVKKNKHKFYPAFI 220  
 MEKKITGYTTVDISQWHRKEH EAFQSV AQCTYNQTVQLDITAF LKTVKKNKHKFYPAFI  
 Sbjct: 1 MEKKITGYTTVDISQWHRKEHFEAFQSV AQCTYNQTVQLDITAF LKTVKKNKHKFYPAFI 60

Query: 221 HILARLMNAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTET FSSLWSEYHDDFRQFLHIY 400  
 HILARLMNAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTET FSSLWSEYHDDFRQFLHIY  
 Sbjct: 61 HILARLMNAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTET FSSLWSEYHDDFRQFLHIY 120

Query: 401 SQDVACYGENLAYFPKGF IENMFFV SANPWSFTSFDLNVANMDNFFAPVFTMGKYTQG 580  
 SQDVACYGENLAYFPKGF IENMFFV SANPWSFTSFDLNVANMDNFFAPVFTMGKYTQG  
 Sbjct: 121 SQDVACYGENLAYFPKGF IENMFFV SANPWSFTSFDLNVANMDNFFAPVFTMGKYTQG 180

Query: 581 DKVLMPLAIQVHHAVCDGFHVG\*\*IK\*YCDEWQG 691  
 DKVLMPLAIQVHHAVCDGFHVG ++ YC QG  
 Sbjct: 181 DKVLMPLAIQVHHAVCDGFHVGRLNELQQYCSVDQG 217

>[gi|49659743|qb|AAT68191.1|](#) chloramphenicol acetyltransferase [Brucella expression vector pNSGroE]  
 Length = 232

Score = 429 bits (1102), Expect = e-119  
 Identities = 201/202 (99%), Positives = 201/202 (99%)  
 Frame = +2

Query: 41 MEKKITGYTTVDISQWHRKEHLEAFQSVACQTYNQT VQLDITAF LKTVKKNKHKFYPAFI 220  
 MEKKITGYTTVDISQWHRKEH EAFQSVACQTYNQT VQLDITAF LKTVKKNKHKFYPAFI  
 Sbjct: 1 MEKKITGYTTVDISQWHRKEHLEAFQSVACQTYNQT VQLDITAF LKTVKKNKHKFYPAFI 60

Query: 221 HILARLMNAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTET FSSLWSEYHDDFRQFLHIY 400  
 HILARLMNAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTET FSSLWSEYHDDFRQFLHIY  
 Sbjct: 61 HILARLMNAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTET FSSLWSEYHDDFRQFLHIY 120

Query: 401 SQDVACYGENLAYFPKGF IENMFFVSANPWSFTSFDLNVANMDNFFAPVFTMGKYTQG 580  
 SQDVACYGENLAYFPKGF IENMFFVSANPWSFTSFDLNVANMDNFFAPVFTMGKYTQG  
 Sbjct: 121 SQDVACYGENLAYFPKGF IENMFFVSANPWSFTSFDLNVANMDNFFAPVFTMGKYTQG 180

Query: 581 DKVLMPLAIQVHHAVCDGFHVG 646  
 DKVLMPLAIQVHHAVCDGFHVG  
 Sbjct: 181 DKVLMPLAIQVHHAVCDGFHVG 202

>[gi|15554330|qb|AAL02033.1|](#) chloramphenicol acetyl transferase [Template plasmid pKD3]  
 Length = 212

Score = 426 bits (1096), Expect = e-118  
 Identities = 200/202 (99%), Positives = 200/202 (99%)  
 Frame = +2

Query: 41 MEKKITGYTTVDISQWHRKEHLEAFQSVACQTYNQT VQLDITAF LKTVKKNKHKFYPAFI 220  
 MEKKITGYTTVDISQWHRKEH EAFQSVACQTYNQT VQLDITAF LKTVKKNKHKFYPAFI  
 Sbjct: 1 MEKKITGYTTVDISQWHRKEHLEAFQSVACQTYNQT VQLDITAF LKTVKKNKHKFYPAFI 60

Query: 221 HILARLMNAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTET FSSLWSEYHDDFRQFLHIY 400  
 HILARLMNAHPE RMAMKDGELVIWDSVHPCYTVFHEQTET FSSLWSEYHDDFRQFLHIY  
 Sbjct: 61 HILARLMNAHPELRMAMKDGELVIWDSVHPCYTVFHEQTET FSSLWSEYHDDFRQFLHIY 120

Query: 401 SQDVACYGENLAYFPKGF IENMFFVSANPWSFTSFDLNVANMDNFFAPVFTMGKYTQG 580  
 SQDVACYGENLAYFPKGF IENMFFVSANPWSFTSFDLNVANMDNFFAPVFTMGKYTQG  
 Sbjct: 121 SQDVACYGENLAYFPKGF IENMFFVSANPWSFTSFDLNVANMDNFFAPVFTMGKYTQG 180

Query: 581 DKVLMPLAIQVHHAVCDGFHVG 646  
 DKVLMPLAIQVHHAVCDGFHVG  
 Sbjct: 181 DKVLMPLAIQVHHAVCDGFHVG 202

[gi|7384997|gb|AAF61635.1](#) chloramphenicol acetyltransferase [Cloning vector pTG8]  
Length = 183

Score = 356 bits (914), Expect(2) = e-102  
Identities = 167/169 (98%), Positives = 167/169 (98%)  
Frame = +2

Query: 41 MEKKITGYTTVDISQWHRKEHLEAFQSV AQCTYNQTVQLDITAF LKTVKKNKHKFYPAFI 220  
MEKKITGYTTVDISQWHRKEH EAFQSV AQCTYNQTVQLDITAF LKTVKKNKHKFYPAFI  
Sbjct: 1 MEKKITGYTTVDISQWHRKEHFEAFQSV AQCTYNQTVQLDITAF LKTVKKNKHKFYPAFI 60

Query: 221 HILARLMNAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTETTFSSLWSEYHDDFRQFLHIY 400  
HILARLMNAHPE RMAMKDGELVIWDSVHPCYTVFHEQTETTFSSLWSEYHDDFRQFLHIY  
Sbjct: 61 HILARLMNAHPELRMAMKDGELVIWDSVHPCYTVFHEQTETTFSSLWSEYHDDFRQFLHIY 120

Query: 401 SQDVACYGENLAYFPKGF IENMFFVSANPWSF TSFDLNVANMDNFFAP 547  
SQDVACYGENLAYFPKGF IENMFFVSANPWSF TSFDLNVANMDNFFAP  
Sbjct: 121 SQDVACYGENLAYFPKGF IENMFFVSANPWSF TSFDLNVANMDNFFAP 169

Score = 37.7 bits (86), Expect(2) = e-102  
Identities = 15/15 (100%), Positives = 15/15 (100%)  
Frame = +3

Query: 546 PFSPWANIIRKATRC 590  
PFSPWANIIRKATRC  
Sbjct: 169 PFSPWANIIRKATRC 183

[gi|47834500|gb|AAT38899.1](#) chloramphenicol acetyltransferase [Salmonella enterica subsp.  
enterica serovar Pullorum]  
Length = 170

Score = 348 bits (894), Expect = 6e-95  
Identities = 162/170 (95%), Positives = 164/170 (96%)  
Frame = +2

Query: 179 TVKKNKHKFYPAFIHILARLMNAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTETTFSSLW 358  
TVKKNKHKFYPAFIHILARLMNAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTETTFSSLW  
Sbjct: 1 TVKKNKHKFYPAFIHILARLMNAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTETTFSSLW 60

Query: 359 SEYHDDFRQFLHIYSQDVACYGENLAYFPKGF IENMFFVSANPWSF TSFDLNVANMDNF 538  
SEYHDDFRQFLHIYSQDVACYGENLAYFPKGF IENMFFVSANPWSF TSFDLNVANMDNF  
Sbjct: 61 SEYHDDFRQFLHIYSQDVACYGENLAYFPKGF IENMFFVSANPWSF TSFDLNVANMDNF 120

Query: 539 FAPVFTMGKYYTQGDKVLMLPLAIQVHHA VCDGFHVGTNA\*\*IK\*YCDEWQ 688  
FAPVFTMGKYYTQGDKVLMLPLAIQVHHA VCDGFHVG ++ YCDEWQ  
Sbjct: 121 FAPVFTMGKYYTQGDKVLMLPLAIQVHHA VCDGFHVGRMLNELQQYCDEWQ 170

[gi|79018|pir|A24651](#) chloramphenicol O-acetyltransferase (EC 2.3.1.28) - Proteus  
mirabilis (strain PM13)  
[gi|115758|sp|P07641|CAT\\_PROMI](#) Chloramphenicol acetyltransferase (CAT)  
[gi|150883|gb|AA25655.1](#) chloramphenicol acetyltransferase (cat)



Length = 217


Score = 337 bits (865), Expect = 1e-91  
 Identities = 159/214 (74%), Positives = 183/214 (85%)  
 Frame = +2


Query: 41 MEKKITGYTTVDISQWHRKEHLEAFQSVAQCTYNQTVQLDITAFKTKVKKKHKFYPAFI 220  
 M+ K G VD+SQW RKEH EAFQS AQCT++QTVQLDIT+ LKTVK+N +KFYP FI  
 Sbjct: 1 MDTKRVGILVVDLSQWGRKEHFEAFQSFAQCTFSQTVQLDITSLKTVKQNGYKFYPTFI 60

Query: 221 HILARLMNAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTETFSSSLWSEYHDDFRQFLHIY 400  
 +I++ L+N H EFRMAMKDGELVIWDSV+P Y +FHEQTETFSSSLWS YH D +FL Y  
 Sbjct: 61 YIISLLVKNKHAEFRMAMKDGELVIWDSVNPVGYNIFHEQTETFSSSLWSYHKDINRFLKTY 120

Query: 401 SQDVACYGENLAYFPKGFIEINMFFVSANPWSFTSFDLNVANMDNFFAPVFTMGKYYTQG 580  
 S+D+A YG++LAYFPK FIEINMFFVSANPWSFTSF+LN+AN++NFFAPVFT+GKYYTQG  
 Sbjct: 121 SEDIAQYGDDLAYFPKFEINMFFVSANPWSFTSFNLNMANINNFFAPVFTIGKYYTQG 180

Query: 581 DKVLMPLAIQVHHAVCDGFHVG TNA\*\*IK\*YCDE 682  
 DKVLMPLAIQVHHAVCDGFHVG I+ YCDE  
 Sbjct: 181 DKVLMPLAIQVHHAVCDGFHVGRLLEIQYCYCDE 214

[gi|37526342|ref|NP\\_929686.1|](#)  chloramphenicol acetyltransferase (CATIII) [Photorhabdus luminescens subsp. laumondii TT01]

[gi|36785773|emb|CAE14823.1|](#)  chloramphenicol acetyltransferase (CATIII) [Photorhabdus luminescens subsp. laumondii TT01]

Length = 212


Score = 222 bits (565), Expect = 9e-57  
 Identities = 94/196 (47%), Positives = 146/196 (74%), Gaps = 1/196 (0%)  
 Frame = +2

Query: 62 YTTVDISQWHRKEHLEAFQSVAQCTYNQTVQLDITAFKTKVKKKHKFYPAFIHILARLM 241  
 Y+ VDI W RKEH +++V QC ++ T ++DIT L ++ + ++KFYP I++++ ++  
 Sbjct: 3 YSKVDIDLWDRKEHFLHYRNVVQCQGFSLTAKIDITHLLSSLVEKQYKFYPTMIYLISTVV 62

Query: 242 NAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTETFSSSLWSEYHDDFRQFLHIYSQDVACY 421  
 N++ EFRMA+KD EL++WD V+P YT+FH++TETFS++W+E++ D +F+ YS D Y  
 Sbjct: 63 NSYSEFRMAIKDEELIVWDGVPAYTIFHKETETFSAIWTEFNSDLAEFMKNYSADYETY 122

Query: 422 GENLAYFPKGFIEINMFFVSANPWSFTSFDLNVANMDNFFAPVFTMGKYYTQGDKVLMP 598  
 ++L +F K + EN F +S+ PWVSF F+LN+A++ ++F P+FTMGK+Y G++ +P  
 Sbjct: 123 KDDLCFFSKPELPHNFHISSVPWVSFDGFNLNMAVMDYFPPIFTMGKFYQNGNQTLPL 182

Query: 599 LAIQVHHAVCDGFHVG 646  
 LAIQVHHA CDGFHVG  
 Sbjct: 183 LAIQVHHATCDGFHVG 198

[gi|1311280|pdb|1OCA|](#)  Quadruple Mutant Q92c, N146f, Y168f, I172v Type Iii Cat Complexed With Fusidic Acid. Crystals Grown At Ph 6.3. X-Ray Data Collected At Room Temperature

Length = 213

Score = 210 bits (534), Expect = 3e-53  
 Identities = 96/195 (49%), Positives = 134/195 (68%), Gaps = 1/195 (0%)  
 Frame = +2

Query: 62 YTTVDISQWHRKEHLEAFQSVAQCTYNQTVQLDITAF LKTVKKNKHKFYPAFIHILARLM 241  
 YT D+ W R+EH E ++ C ++ T ++DIT K++ + +KFYP I+++A+ +  
 Sbjct: 3 YTKFDVKNWVRREHFEFVYRHLPCGFSLTSKIDITTLKSLDSDSAYKFYPMIYLIAQAV 62

Query: 242 NAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTETTFSSLWSEYHDDFRQFLHIYSQDVACY 421  
 N E RMA+KD EL++WDSV PC+TVFH++TETFS+L Y D QF+ Y + Y  
 Sbjct: 63 NQFDELIRMAIKDELIVWDSVDPCTVVFHQETETFSALSCPYSDDIDQFMVNYLSVMERY 122

Query: 422 GENLAYFPKGF I-ENMFFVSANPWSFTSFDLNVANMDNFFAPVFTMGKYYTQGDV LMP 598  
 + FP+G EN F+SA PWV+F SF+LNVAN +FFAPV TM KY +GD++L+P  
 Sbjct: 123 KSDTKLFPQGVTPENHLFISALPWVNFDSFNLNVANFTDFFAPVITMAKYQOEGDRLLLP 182

Query: 599 LAIQVHHAVCDGFHV 643  
 L++QVHHAVCDGFHV  
 Sbjct: 183 LSVQVHHAVCDGFHV 197

>[gi|43579|emb|CAA37806.1](#) chloramphenicol acetyltransferase [Haemophilus influenzae]  
[gi|97157|pir||S13399](#) chloramphenicol O-acetyltransferase (EC 2.3.1.28) - Haemophilus  
 influenzae  
[gi|115683|sp|P22616|CAT2\\_HAEIN](#) Chloramphenicol acetyltransferase II (CAT-II)  
 Length = 213

Score = 204 bits (519), Expect = 2e-51  
 Identities = 89/194 (45%), Positives = 136/194 (70%), Gaps = 1/194 (0%)  
 Frame = +2

Query: 62 YTTVDISQWHRKEHLEAFQSVAQCTYNQTVQLDITAF LKTVKKNKHKFYPAFIHILARLM 241  
 +T +D++ W+R+EH ++ +C ++ T +LDITAF + + +KFYP I++++R++  
 Sbjct: 3 FTRIDLNTWNRREHFALYRQOIKCGFSLTTLKLDITAFRTALAE TDYKFYPMIYLISR VV 62

Query: 242 NAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTETTFSSLWSEYHDDFRQFLHIYSQDVACY 421  
 N PEFRMAMKD L+ WD P +TVFH++TETFS+L+ Y D +F+ Y+ +A Y  
 Sbjct: 63 NQFPEFRMAMKDNALIYWDQTDVPVFTVVFHKETETFSALFCRYCPDISEFMAGYNAVMAEY 122

Query: 422 GENLAYFPKGF I-ENMFFVSANPWSFTSFDLNVANMDNFFAPVFTMGKYYTQGDV LMP 598  
 N A FP+G + EN +S+ PWVSF F+LN+ D++FAPVFTM K+ + ++VL+P  
 Sbjct: 123 QHNTALFPQALPENHLN ISSLPWVSFDGFNLNITGNDYFAPVFTMAKFOEDNRVLLP 182

Query: 599 LAIQVHHAVCDGFH 640  
 +++QVHHAVCDGFH  
 Sbjct: 183 VSVQVHHAVCDGFH 196

>[gi|19773454|dbj|BAB86848.1](#) chloramphenicol acetyltransferase [Photobacterium damsela sub:  
 piscicida]  
[gi|51507277|emb|CAF29026.1](#) chloramphenicol acetyltransferase II [Haemophilus influenzae]  
 Length = 213

Score = 202 bits (513), Expect = 9e-51  
 Identities = 88/194 (45%), Positives = 135/194 (69%), Gaps = 1/194 (0%)  
 Frame = +2

Query: 62 YTTVDISQWHRKEHLEAFQSVAQCTYNQTVQLDITAF LKTVKKNKHKFYPAFIHILARLM 241  
 +T +D++ W+R+EH ++ +C ++ T +LDITA + + +KFYP I++++R++  
 Sbjct: 3 FTRIDLNTWNRREHFALYRQOIKCGFSLTTLKLDITALRTALAE TDYKFYPMIYLISR VV 62

Query: 242 NAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTETFSSSLWSEYHDDFRQFLHIYSQDVACY 421  
 N PEFERMAMKD L+ WD P +TVFH++TETFS+L+ Y D +F+ Y+ +A Y  
 Sbjct: 63 NQFPEFRMAMKDNALIYWDQTPVFTVVFHKETETFSALFCRYCPDISEFMAGYNAVMAEY 122

Query: 422 GENLAYFPKGF I-ENMFFVSANPWVSFTSFDLNVANMDNFFAPVFTMGKYTQGDVLM 598  
 N A FP+G + EN +S+ PWVSF F+LN+ D++FAPVFTM K+ + ++VL+P  
 Sbjct: 123 QHNTALFPQALPENHLNSSLPWVSFDGFLNITGNDYFAPVFTMAKFOEDNRVLLP 182

Query: 599 LAIQVHHAVCDGFH 640  
 +++QVHHAVCDGFH  
 Sbjct: 183 VSVQVHHAVCDGFH 196

[gi|47025|emb|CAA30695.1|](#) unnamed protein product [Plasmid R387]  
[gi|66522|pir|XXEBCF](#) chloramphenicol O-acetyltransferase (EC 2.3.1.28) III - Shigella  
 flexneri plasmid R387  
[gi|230823|pdb|3CLA|](#) **S** Type III Chloramphenicol Acetyltransferase (CATIII) (E.C.2.3.1.28)  
 Complex With Chloramphenicol  
[gi|115686|sp|P00484|CAT3\\_ECOLI](#) Chloramphenicol acetyltransferase III (catIII)  
 Length = 213

Score = 200 bits (509), Expect = 3e-50  
 Identities = 92/195 (47%), Positives = 132/195 (67%), Gaps = 1/195 (0%)  
 Frame = +2

Query: 62 YTTVDISQWHRKEHLEAFQSV AQCTYNTQTVQLDITAF LKTVKKNKHKFYPAFIHILARLM 241  
 YT D+ W R+EH E ++ C ++ T ++DIT K++ + +KFYP I+++A+ +  
 Sbjct: 3 YTKFDVKNWVRREHFEFYRHRLPCGFSLTSKIDIT'TLKKSLDDSAYKFYPMIYLIAQAV 62

Query: 242 NAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTETFSSSLWSEYHDDFRQFLHIYSQDVACY 421  
 N E RMA+KD EL++WDSV P +TVFH++TETFS+L Y D QF+ Y + Y  
 Sbjct: 63 NQFDELRMAIKDELIVWDSVDPQFTVVFHQTETFSALSCPYSDDIDQFMVNYLSVMERY 122

Query: 422 GENLAYFPKGF I-ENMFFVSANPWVSFTSFDLNVANMDNFFAPVFTMGKYTQGDVLM 598  
 + FP+G EN +SA PWV+F SF+LNVAN ++FAP+ TM KY +GD++L+P  
 Sbjct: 123 KSDTKLFPQGVTPENHLNISALPWVNFDSFNLNVANFTDYFAPIITMAKYQOEGDRLLLP 182

Query: 599 LAIQVHHAVCDGFHV 643  
 L++QVHHAVCDGFHV  
 Sbjct: 183 LSVQVHHAVCDGFHV 197

[gi|7007391|emb|CAB75601.1|](#) **G** chloramphenicol acetyl transferase [uncultured eubacterium]  
[gi|12054888|emb|CAC20666.1|](#) **G** chloramphenicol O-acetyltransferase [Mannheimia haemolytica]  
[gi|18693102|emb|CAC85830.1|](#) **G** chloramphenicol acetyltransferase [Mannheimia varigena]  
[gi|32455905|ref|NP\\_862668.1|](#) **G** chloramphenicol acetyl transferase [uncultured eubacterium]  
[gi|18875441|ref|NP\\_573537.1|](#) **G** chloramphenicol acetyltransferase [Mannheimia varigena]  
[gi|12084929|ref|NP\\_073222.1|](#) **G** chloramphenicol O-acetyltransferase [Mannheimia haemolytica]  
 Length = 213

Score = 200 bits (509), Expect = 3e-50  
 Identities = 92/195 (47%), Positives = 132/195 (67%), Gaps = 1/195 (0%)  
 Frame = +2

Query: 62 YTTVDISQWHRKEHLEAFQSV AQCTYNTQTVQLDITAF LKTVKKNKHKFYPAFIHILARLM 241  
 YT D+ W R+EH E ++ C ++ T ++DIT K++ + +KFYP I+++A+ +

Sbjct: 3 YTKFDVKNWVRREHFYRHLPCGFSLSKIDITTLKSLDDSAKYFYPVMIYLIAQAV 62

Query: 242 NAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTETFSWSEYHDDFRQFLHIYSQDVACY 421  
 N E RMA+KD EL++WDSV P +TVFH++TETFS+L Y D QF+ Y + Y


Sbjct: 63 NQFDELRLMAIKDELIVWDSVDPQFTVVFHQETETFSALSCPYSDDIDQFMVNYLSVMERY 122

Query: 422 GENLAYFPKGF I-ENMFFVSANPWSFTSFDLNVANMDNFFAPVFTMGKYTQGDKVLMP 598  
 + FP+G EN +SA PWV+F SF+LNVAN ++FAP+ TM KY +GD++L+P

Sbjct: 123 KSDTKLFPQGVTPENHLNISALPWNFDSFNLNVANFTDYFAPITMAKYQOEGDRLLLP 182

Query: 599 LAIQVHHAVCDGFHV 643  
 L++QVHHAVCDGFHV

Sbjct: 183 LSVQVHHAVCDGFHV 197

 [>gi|56786625|qb|AAW29416.1|](#) CatA2 chloramphenicol acetyltransferase [Escherichia coli]  
[gi|41781|emb|CAA37805.1|](#) chloramphenicol acetyltransferase [Escherichia coli]  
[gi|95705|pir||S13398](#) chloramphenicol O-acetyltransferase (EC 2.3.1.28) - Escherichia coli plasmid pSa  
[gi|115682|sp|P22615|CAT2\\_ECOLI](#) Chloramphenicol acetyltransferase II (CAT-II)  
 Length = 213

Score = 200 bits (508), Expect = 4e-50  
 Identities = 88/194 (45%), Positives = 133/194 (68%), Gaps = 1/194 (0%)  
 Frame = +2

Query: 62 YTTVDISQWHRKEHLEAFQSV AQCTYNQTVQLDITAF LKTVKKNKHKFYPAFIHILARLM 241  
 +T +D++ W+R+EH ++ +C ++ T +LDITA + + +KFYP I++++R +

Sbjct: 3 FTTRIDLNTWNRREHFALYRQIQKCGFSLTTKLDITALRTALAE TGYKFYPLMIYLISR AV 62

Query: 242 NAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTETFSWSEYHDDFRQFLHIYSQDVACY 421  
 N PEFRMA+KD EL+ WD P +TVFH++TETFS+L Y D +F+ Y+ A Y




Sbjct: 63 NQFPEFRMALKDNELIYWDQSDPVFTVVFHKE TETFSALSCRYFPDLSEFMAGYNAVTA EY 122

Query: 422 GENLAYFPKGF I-ENMFFVSANPWSFTSFDLNVANMDNFFAPVFTMGKYTQGDKVLMP 598  
 + FP+G + EN +S+ PWVSF F+LN+ D++FAPVFTM K+ +GD+VL+P

Sbjct: 123 QHDTRLFPOGNLPENHLN ISSLPWVSFDGFNLNITGNDDYFAPVFTMAKFQOEGDRVLLP 182

Query: 599 LAIQVHHAVCDGFH 640  
 +++QVHHAVCDGFH

Sbjct: 183 VSVQVHHAVCDGFH 196

 [>gi|45758083|qb|AAS76295.1|](#)  chloramphenicol acetyl transferase II [Salmonella enterica su enterica serovar Choleraesuis]  
[gi|60115525|ref|YP\\_209316.1|](#)  chloramphenicol acetyl transferase II [Salmonella enterica sub enterica serovar Choleraesuis]  
 Length = 213

Score = 200 bits (508), Expect = 4e-50  
 Identities = 88/194 (45%), Positives = 133/194 (68%), Gaps = 1/194 (0%)  
 Frame = +2

Query: 62 YTTVDISQWHRKEHLEAFQSV AQCTYNQTVQLDITAF LKTVKKNKHKFYPAFIHILARLM 241  
 +T +D++ W+R+EH ++ +C ++ T +LDITA + K +KFYP I++++R +

Sbjct: 3 FTTRIDLNTWNRREHFALYRQIQKCGFSLTTKLDITALRTALAK TGYKFYPLMIYLISR AV 62

Query: 242 NAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTETFSWSEYHDDFRQFLHIYSQDVACY 421

N PEFERMAMKD EL+ W+ P +TVFH++TETFS+L Y D +F+ Y+ A Y  
 Sbjct: 63 NQFPPEFRMAMKDNELIYWEQSDPVFTVVFHKEETETFSALSCRYFPDLSEFMAGYNAVTAEY 122

Query: 422 GENLAYFPKGF I-ENMFFVSANPWVSFTSFDLNVANMDNFFAPVFTMGKYYTQGDVKLMP 598  
 + FP+G + EN +S+ PWVSF F+LN+ D++F+PVFTM K+ +GD+VL+P  
 Sbjct: 123 QHDTRLFPQGNL PENHLN ISSLPWVSFDGFNLNITGNDDYFSPVFTMAKFOQEGDRVLLP 182

Query: 599 LAIQVHHAVCDGFH 640  
 +++QVHHAVCDGFH  
 Sbjct: 183 VSVQVHHAVCDGFH 196

[>gi|34556025|emb|CAD57199.1|](#) chloramphenicol aminotransferase [*Aeromonas salmonicida*]  
 Length = 213


Score = 199 bits (507), Expect = 5e-50  
 Identities = 88/194 (45%), Positives = 133/194 (68%), Gaps = 1/194 (0%)  
 Frame = +2

Query: 62 YTTVDISQWHRKEHLEAFQSVAQCTYNQTVQLDITAF LKTVKKNKHKFYPAFIHILARLM 241  
 +T +D++ W+R+EH ++ +C ++ T +LDITA + + +KFYP I++++R +  
 Sbjct: 3 FTRIDLNTWNRREHF AFYRQOIKCGFSLT KLDITALRTALAE TGYKFYPLMIYLISR AV 62

Query: 242 NAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTETFS L WSEYHDDFRQFLHIYSQDVACY 421  
 N PEFERMA+KD EL+ WD P +TVFH++TETFS+L Y D +F+ Y+ A Y  
 Sbjct: 63 NQFPPEFRMALKDNE LIYWDQSDPVFTVVFHKEETETFSALSCRYFPDLSEFMAGYNAVTAEY 122

Query: 422 GENLAYFPKGF I-ENMFFVSANPWVSFTSFDLNVANMDNFFAPVFTMGKYYTQGDVKLMP 598  
 + FP+G + EN +S+ PWVSF F+LN+ D++FAPVFTM K+ +GD+VL+P  
 Sbjct: 123 QHDTRLFPQGNL PENHLN ISSLPWVSFDGFNLNITGNDDYFAPVFTMAKFOQEGDRVLLP 182

Query: 599 LAIQVHHAVCDGFH 640  
 +++QVHHAVCDGFH  
 Sbjct: 183 VSVQVHHAVCDGFH 196

[>gi|229747|pdb|1CLA|](#)  Type III Chloramphenicol Acetyltransferase (CATIII) (E.C.2.3.1.28)  
 (S148A Mutant) - Chloramphenicol Complex  
 Length = 213

Score = 199 bits (506), Expect = 6e-50  
 Identities = 91/195 (46%), Positives = 132/195 (67%), Gaps = 1/195 (0%)  
 Frame = +2

Query: 62 YTTVDISQWHRKEHLEAFQSVAQCTYNQTVQLDITAF LKTVKKNKHKFYPAFIHILARLM 241  
 YT D+ W R+EH E ++ C ++ T ++DIT K++ + +KFYP I++++A+ +  
 Sbjct: 3 YTKFDVKNWVRREHFEFYRHR LPCGFSLTSKIDIT T LKSLDSDSAYKFYPMIYLIAQAV 62

Query: 242 NAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTETFS L WSEYHDDFRQFLHIYSQDVACY 421  
 N E RMA+KD EL++WDSV P +TVFH++TETFS+L Y D QF+ Y + Y  
 Sbjct: 63 NQFDEL RMAIKDDELIVWDSVDPQFTVVFH QETETFSALSCPYSSDIDQFMVNYLSVMERY 122

Query: 422 GENLAYFPKGF I-ENMFFVSANPWVSFTSFDLNVANMDNFFAPVFTMGKYYTQGDVKLMP 598  
 + FP+G EN ++A PWV+F SF+LNVAN ++FAP+ TM KY +GD++L+P  
 Sbjct: 123 KSDTKLFPQGVTPENHLN IAALPWVNFDSFNLNVANF TDYFAP IITMAKYQOEGDRLLLP 182

Query: 599 LAIQVHHAVCDGFHV 643  
 L++QVHHAVCDGFHV

Sbjct: 183 LSVQVHHAVCDGFHV 197

[>gi|230967|pdb|4CLA|](#) **S** Type III Chloramphenicol Acetyltransferase (CATIII) (E.C.2.3.1.28)  
(Mutant With Leu 160 Replaced By Phe) (L160F) Complex  
With Chloramphenicol  
Length = 213

Score = 199 bits (505), Expect = 8e-50  
Identities = 91/195 (46%), Positives = 131/195 (67%), Gaps = 1/195 (0%)  
Frame = +2

Query: 62 YTTVDISQWHRKEHLEAFQSVACTYNTQTVQLDITAFKTKVKKKHKFYPAFIHILARLM 241  
YT D+ W R+EH E ++ C ++ T ++DIT K++ + +KFYP I+++A+ +

Sbjct: 3 YTKFDVKNWVRREHFYRHLPCGFSLTSKIDITTLKKSLLDSAYKFYPVMIYLIAQAV 62

Query: 242 NAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTETFSWLSEYHDDFRQFLHIYSQDVACY 421  
N E RMA+KD EL++WDSV P +TVFH++TETFS+L Y D QF+ Y + Y

Sbjct: 63 NQFDELRLMAIKDELIVWDSVDPQFTVVFHQETETFSALSCPYSDDIDQFMVNYLSVMERY 122

Query: 422 GENLAYFPKGF I-ENMFFVSANPWSFTSFDLNVANMDNFFAPVFTMGKYTQGDVLM 598  
+ FP+G EN +SA PWV+F SF+ NVAN ++FAP+ TM KY +GD++L+P

Sbjct: 123 KSDTKLFPQGVTPENHLNISALPWVNFDSFNFNANFTDYFAP IITMAKYQQEGDRLLLP 182

Query: 599 LAIQVHHAVCDGFHV 643  
L++QVHHAVCDGFHV

Sbjct: 183 LSVQVHHAVCDGFHV 197

[>gi|230457|pdb|2CLA|](#) **S** Chloramphenicol Acetyltransferase (E.C.2.3.1.28) (CATIII) (D199N  
Mutant)  
Length = 213

Score = 198 bits (504), Expect = 1e-49  
Identities = 91/195 (46%), Positives = 132/195 (67%), Gaps = 1/195 (0%)  
Frame = +2

Query: 62 YTTVDISQWHRKEHLEAFQSVACTYNTQTVQLDITAFKTKVKKKHKFYPAFIHILARLM 241  
YT D+ W R+EH E ++ C ++ T ++DIT K++ + +KFYP I+++A+ +

Sbjct: 3 YTKFDVKNWVRREHFYRHLPCGFSLTSKIDITTLKKSLLDSAYKFYPVMIYLIAQAV 62

Query: 242 NAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTETFSWLSEYHDDFRQFLHIYSQDVACY 421  
N E RMA+KD EL++WDSV P +TVFH++TETFS+L Y D QF+ Y + Y

Sbjct: 63 NQFDELRLMAIKDELIVWDSVDPQFTVVFHQETETFSALSCPYSDDIDQFMVNYLSVMERY 122

Query: 422 GENLAYFPKGF I-ENMFFVSANPWSFTSFDLNVANMDNFFAPVFTMGKYTQGDVLM 598  
+ FP+G EN +SA PWV+F SF+LNVAN ++FAP+ TM KY +GD++L+P

Sbjct: 123 KSDTKLFPQGVTPENHLNISALPWVNFDSFNLVANFTDYFAP IITMAKYQQEGDRLLLP 182

Query: 599 LAIQVHHAVCDGFHV 643  
L++QVHHAVC+GFHV

Sbjct: 183 LSVQVHHAVCNGFHV 197

[>gi|493937|pdb|1CIA|](#) **S** Chloramphenicol Acetyltransferase (Type Iii) (E.C.2.3.1.28) Mutant

With His 195 Replaced By Gln (H195q) (Engineered)  
Length = 213

Score = 197 bits (501), Expect = 2e-49  
Identities = 91/195 (46%), Positives = 131/195 (67%), Gaps = 1/195 (0%)  
Frame = +2

Query: 62 YTTVDISQWHRKEHLEAFQSVAQCTYNQTVQLDITAFKTVKKNKHKFYPAFIHILARLM 241  
YT D+ W R+EH E ++ C ++ T ++DIT K++ + +KFYP I+++A+ +  
Sbjct: 3 YTKFDVKNVWRREHFEFYRHLRPLCGFSLTSKIDITTLKKSLLDSAYKFYPMIYLIAQAV 62

Query: 242 NAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTETFSSSLWSEYHDDFRQFLHIYSQDVACY 421  
N E RMA+KD EL++WDSV P +TVFH++TETFS+L Y D QF+ Y + Y  
Sbjct: 63 NQFDELRLMAIKDDELIVWDSVDPQFTVVFHQETETFSALSFCYSSDIDQFMVNYLSVMERY 122

Query: 422 GENLAYFPKGF I-ENMFFVSANPWSFTSFDLNVANMDNFFAPVFTMGKYTQGDVLM 598  
+ FP+G EN +SA PWV+F SF+LNVAN ++FAP+ TM KY +GD++L+P  
Sbjct: 123 KSDTKLFPQGVTPENHLNISALPWNFDSFNLNVANFTDYFAPITMAKYQOEGDRLLLP 182

Query: 599 LAIQVHHA VCDGFHV 643  
L++QVH AVCDGFHV  
Sbjct: 183 LSVQVHQA VCDGFHV 197

>[gi|482596|pir||A49793](#) chloramphenicol O-acetyltransferase (EC 2.3.1.28) - Clostridium  
perfringens (strain CW531)  
[gi|115677|sp|P26825|CAT1\\_CLOPE](#) Chloramphenicol acetyltransferase (CAT)  
[gi|144744|qb|AAA23215.1|](#) ORF  
Length = 219

Score = 194 bits (493), Expect = 2e-48  
Identities = 84/196 (42%), Positives = 131/196 (66%), Gaps = 2/196 (1%)  
Frame = +2

Query: 62 YTTVDISQWHRKEHLEAFQSVAQCTYNQTVQLDITAFKTVKKNKHKFYPAFIHILARLM 241  
+ +DI W+RK + E + + +CTY+ T ++IT L+ +K K YP I+I+ ++  
Sbjct: 3 FNLIDIEDWNRKPYFEHYLNAVRCYSMTANIEITGLLEIKLKLKLYPTLIYIITTVV 62

Query: 242 NAHPEFRMAM-KDGELVIWDSVHPCYTVFHEQTETFSSSLWSEYHDDFRQFLHIYSQDVAC 418  
N H EFR + G+L WDS++P YTVFH+ ETFSS+W+EY ++F +F + Y +D+  
Sbjct: 63 NRHKEFRTCFDQKGLGYWDSMNPSYTVFHKDNETFSSIWTEYDENFPRFYNYLEDIRN 122

Query: 419 YGENLAYFPK-GFIENMFFVSANPWSFTSFDLNVANMDNFFAPVFTMGKYTQGDVLM 595  
Y + L + PK G N VS+ PWV+FT F+LN+ N + P+FT+GKY+ Q +K+L+  
Sbjct: 123 YSDVLFMPKTGEPANTINVSSIPWVNFTEGFLNIYNDATYLIPIFTLTKYFQDNKILL 182

Query: 596 PLAIQVHHA VCDGFHV 643  
P+++QVHHA VCDG+H+  
Sbjct: 183 PMSVQVHHA VCDGYHI 198

>[gi|477359|pir||A48907](#) chloramphenicol O-acetyltransferase (EC 2.3.1.28) - Clostridium  
butyricum  
[gi|926995|qb|AAA73865.1|](#) chloramphenicol acetyltransferase  
[gi|1345692|sp|Q02736|CAT\\_CLOBU](#) CHLORAMPHENICOL ACETYLTRANSFERASE (CAT)  
Length = 219

Score = 190 bits (483), Expect = 3e-47





Identities = 85/195 (43%), Positives = 127/195 (65%), Gaps = 2/195 (1%)  
 Frame = +2

Query: 62 YTTVDISQWHRKEHLEAFQSVAQCTYNQTVQLDITAFKTKVKKKHKFYPAFIHILARLM 241  
 + +DI+ W RK + E + + +CTY+ T ++IT L +K KFYP I+++A ++  
 Sbjct: 3 FNLIDINHWSRKPYPFEHYLNNVKCTYSMTANIEITDLLYEIKLKNIKFYPTLIYMIATVV 62

Query: 242 NAHPEFRMAMKD-GELVIWDSVHPCYTVFHEQTETFSSSLWSEYHDDFRQFLHIYSQDVAC 418  
 N H EFR+ G L WDS++P YT+FH++ ETFSS+W+EY+ F +F Y D+  
 Sbjct: 63 NNHKEFRICFDHKGSLGYWDSMNPSYTIHFHENETFSIWTENKSFLLRFYSYDYLDDIKN 122

Query: 419 YGENLAYFPKGF I-ENMFFVSANPWVSFTSFDLNVANMDNFFAPVFTMGKYTQGDKVL M 595  
 YG + + PK +N F VS+ PWVSFT F+LNV N + P+FT GKY+ Q +K+ +  
 Sbjct: 123 YGNIMKFTPKSNEPDNFTSVSSIPWVSFTGFNLNVYNEGTYLIPIFTAGKYFKQENKIFI 182

Query: 596 PLAIQVHHA VCDGFH 640  
 P++IQVHHA+CDG+H  
 Sbjct: 183 PISIQVHHAICDGYH 197

[>gi|52081186|ref|YP\\_079977.1|](#)  antibiotic resistance protein, methyltransferase [Bacillus licheniformis ATCC 14580]  
[gi|52004397|gb|AAU24339.1|](#)  antibiotic resistance protein, methyltransferase [Bacillus licheniformis ATCC 14580]  
[gi|52786569|ref|YP\\_092398.1|](#)  hypothetical protein BLi02835 [Bacillus licheniformis ATCC 14580]  
[gi|52349071|gb|AAU41705.1|](#)  putative protein [Bacillus licheniformis DSM 13]  
 Length = 216

Score = 190 bits (483), Expect = 3e-47  
 Identities = 82/197 (41%), Positives = 133/197 (67%), Gaps = 2/197 (1%)  
 Frame = +2

Query: 62 YTTVDISQWHRKEHLEAFQSVAQCTYNQTVQLDITAFKTKVKKKHKFYPAFIHILARLM 241  
 + T+++ W+RK + + + A+C+++ T +++T L +KK K K YPAFI+I++R++  
 Sbjct: 3 FQTIELDTWYRKS YFDHYMKEAKCSFSITANVNVNTNLLAVLKKKLLKLYPAFIYIVSRVI 62

Query: 242 NAHPEFRMAMKD-GELVIWDSVHPCYTVFHEQTETFSSSLWSEYHDDFRQFLHIYSQDVAC 418  
 ++ PEFR D G+L W+ +HPCY +FH+ +TFS+LW+EY DDF QF H Y D  
 Sbjct: 63 HSRPEFR TTFDDKGQLGYWEQMHPCYAIFHQDDQTF SALWTEYSDDFSQFYHQYLLDAER 122

Query: 419 YGENLAYFPKGF I-ENMFFVSANPWVSFTSFDLNVANMDNFFAPVFTMGKYTQGDKVL M 595  
 +G+ + K I N F VS+ PWV F++F+LN+ N ++ P+ T GKY+++G + +  
 Sbjct: 123 FGDKRGLWAKPDIPPNTFSVSSIPWVRFNSFNLNLNLDNSEHLL-PIITNGKYFSEGRETF L 181

Query: 596 PLAIQVHHA VCDGFHVG 646  
 P+++QVHHA VCDG+H G  
 Sbjct: 182 PVSLQVHHA VCDGYHAG 198

[>gi|3132860|gb|AAC16406.1|](#) chloramphenicol acetyltransferase [Shuttle vector pJIR1456]  
[gi|144780|gb|AAC36952.1|](#) chloramphenicol acetyltransferase [Shuttle vector pJIR750]  
[gi|3068601|gb|AAC14400.1|](#) chloramphenicol acetyltransferase [Neisseria meningitidis]  
[gi|7670741|gb|AAF66228.1|](#) CatD [Clostridium difficile]  
[gi|551138|gb|AAB51421.1|](#) CatP  
[gi|2117709|pir||I40797](#) chloramphenicol O-acetyltransferase (EC 2.3.1.28) - Clostridium perfringens transposon Tn4451  
[gi|208133|gb|AAA73115.1|](#) chloramphenicol acetyltransferase



[gi|115681|sp|P26826|CAT2\\_CLOPE](#) Chloramphenicol acetyltransferase (CAT)  
[gi|144741|qb|AAA23213.1|](#) chloramphenicol acetyltransferase  
 Length = 207

Score = 186 bits (471), Expect = 7e-46  
 Identities = 90/196 (45%), Positives = 128/196 (65%), Gaps = 2/196 (1%)  
 Frame = +2

Query: 62 YTTVDISQWHRKEHLEAFQSV AQCTYNQTVQLDITAF LKTVKKNKHKFYPAFIHILARLM 241  
 + +D + W+RKE+ + + + CTY+ TV++DIT +K+ K YPA ++ +A ++  
 Sbjct: 3 FEKIDKNSWNRKEYFDHYFASVPC TYSMTVKVDITQ----IKEKGMKLYPAMLYYIAMIV 58

Query: 242 NAHPEFRMAM-KDGELVIWDSVHPCYTVFHEQTET FSSLWSEYHDDFRQFLHIYSQDVAC 418  
 N H EFR A+ +DGEL I+D + P YT+FH TETFSSLW+E DF+ FL Y D  
 Sbjct: 59 NRHSEFERTAINQD GELGIYDEMIPSYTIFHNDTETFSSLWTECKSDFKSFLADYESDTQR 118

Query: 419 YGENLAYFPPK-GFIENMFFVSANPWSFTSFDLNVANMDNFFAPVFTMGKYYTQGDKVL M 595  
 YG N K EN+F VS PW +F F+LN+ ++ P+FTMGKYY + +K+++  
 Sbjct: 119 YGNNHRMEGKPNAPENIFNVSMIPWSTFDGFNLNLQKGYDYLLPIFTMGKYYKEDNKIIL 178

Query: 596 PLAIQVHHA VCDGFHV 643  
 PLAIQVHHA VCDGFHV+  
 Sbjct: 179 PLAIQVHHA VCDGFHI 194

[>gi|55233210|qb|AAV48563.1|](#) chloramphenicol acetyltransferase [Integrative depletion plasmid pID2]  
[gi|94633|pir|JQ0788](#) chloramphenicol O-acetyltransferase (EC 2.3.1.28) - Campylobacter coli plasmid pNR9589  
[gi|115754|sp|P22782|CAT\\_CAMCO](#) Chloramphenicol acetyltransferase (CAT)  
[gi|144189|qb|AAA23018.1|](#) chloramphenicol acetyltransferase (cat)  
 Length = 207



Score = 182 bits (463), Expect = 6e-45  
 Identities = 86/196 (43%), Positives = 129/196 (65%), Gaps = 2/196 (1%)  
 Frame = +2

Query: 62 YTTVDISQWHRKEHLEAFQSV AQCTYNQTVQLDITAF LKTVKKNKHKFYPAFIHILARLM 241  
 +T +DI+ W RKE+ + + CTY+ TV+LDI+ +KK+ K YP ++ + ++  
 Sbjct: 3 FTKIDINNWRKEYFDHYFGNTPCTYSMTVKLDISK----LKKDGKLYPTLLYGVTII 58

Query: 242 NAHPEFRMAM-KDGELVIWDSVHPCYTVFHEQTET FSSLWSEYHDDFRQFLHIYSQDVAC 418  
 N H EFR A+ ++G++ ++ + PCYTVFH++TETFSS+W+E+ D+ +FL Y +D+  
 Sbjct: 59 NRHEEFRTALDENGQVGFSEMLPCYTVFHKETETFSSIWTEFTADYTEFLQNYQKDIDA 118

Query: 419 YGENLAYFPPK-GFIENMFFVSANPWSFTSFDLNVANMDNFFAPVFTMGKYYTQGDKVL M 595  
 +GE + K EN F VS PW SF F+LN+ ++ P+FT GKYY +G K +  
 Sbjct: 119 FGERMGMSAKPNPPENTFPVSMIPWTSFEGFNLNLKKG YDYLLPIFTFGKYYEEGKYYI 178

Query: 596 PLAIQVHHA VCDGFHV 643  
 PL+IQVHHA VCDGFHV  
 Sbjct: 179 PLSIQVHHA VCDGFHV 194

[>gi|52143073|ref|YP\\_083756.1|](#)  chloramphenicol acetyltransferase [Bacillus cereus ZK]  
[gi|51976542|qb|AAU18092.1|](#)  chloramphenicol acetyltransferase [Bacillus cereus ZK]  
 Length = 216



Score = 182 bits (461), Expect = 1e-44  
 Identities = 81/196 (41%), Positives = 127/196 (64%), Gaps = 2/196 (1%)  
 Frame = +2

Query: 62 YTTVDISQWHRKEHLEAFQSV AQCTYNQTVQLDITAF LKTVKKNKHKFYPAFIHILARLM 241  
 + +D W+R+++ E + + +CT++ TV +DIT +K V + KFYP FI+I++R++  
 Sbjct: 3 FHVIDRENWNREQYFEHYLEL-KCTFSMTVNVDITLLIKKVHQKGIKFYPTFIYIISRII 61

Query: 242 NAHPEFRMAMKD-GELVIWDSVHPCYTVFHEQTETFS L WSEYHDDFRQFLHIYSQDVAC 418  
 N H EFR D G L W+ + P YT+FH+ ++FSS+W++Y DFR F Y +D+ C  
 Sbjct: 62 NKHKEFRTCFNDEGVLGYWEEMIPSYTIFHKDDKSFSSIWTDYSSDFRIFYKKEEDMRC 121

Query: 419 YGENLAYFPKGFIE-NMFFV SANPWVSFTSFDLNVANMDNFFAPVFTMGKYTQGDKVL M 595  
 Y F K I N+F +S PW SFT F+LN+ N F P+ T GKY+ + +K+++  
 Sbjct: 122 YASVHGLFTKENIPPNIFFISGIPWTSFTGFNLNINNDAGFLLPITCGKYFNEENKIML 181

Query: 596 PLAIQVHHAVCDGFHV 643  
 P+++QVHH+VCDG+HV  
 Sbjct: 182 PVSLQVHHSVCDGYHV 197

[gi|49477664|ref|YP\\_036506.1|](#)  chloramphenicol O-acetyltransferase [Bacillus thuringiensis konkukian str. 97-27]  
[gi|49329220|gb|AAAT59866.1|](#)  chloramphenicol O-acetyltransferase [Bacillus thuringiensis sero konkukian str. 97-27]  
 Length = 216







Score = 182 bits (461), Expect = 1e-44  
 Identities = 80/195 (41%), Positives = 127/195 (65%), Gaps = 2/195 (1%)  
 Frame = +2

Query: 62 YTTVDISQWHRKEHLEAFQSV AQCTYNQTVQLDITAF LKTVKKNKHKFYPAFIHILARLM 241  
 + +D W+R+++ E + + +CT++ TV +DIT +K V + KFYP FI+I++R++  
 Sbjct: 3 FHVIDRENWNREQYFEHYLEL-KCTFSMTVNVDITLLIKKVHQKGIKFYPTFIYIISRII 61

Query: 242 NAHPEFRMAMKD-GELVIWDSVHPCYTVFHEQTETFS L WSEYHDDFRQFLHIYSQDVAC 418  
 N H EFR D G L W+ + P YT+FH+ ++FSS+W++Y DFR F Y +DV C  
 Sbjct: 62 NKHKEFRTCFNDEGVLGYWEEMIPSYTIFHKDDKSFSSIWTDYSSDFRIFYKNEYEDVRC 121

Query: 419 YGENLAYFPKGFIE-NMFFV SANPWVSFTSFDLNVANMDNFFAPVFTMGKYTQGDKVL M 595  
 Y F K I N+F +S PW SFT F+LN+ N +F P+ T GKY+ + +K+++  
 Sbjct: 122 YASVHGLFTKENIPPNIFFISGIPWTSFTGFNLNINNDGDFLLPITCGKYFNEENKIML 181

Query: 596 PLAIQVHHAVCDGFH 640  
 P+++QVHH++CDG+H  
 Sbjct: 182 PVSLQVHHSICDGYH 196

[gi|47527702|ref|YP\\_019051.1|](#)  chloramphenicol acetyltransferase [Bacillus anthracis str. Ancestor']  
[gi|49185254|ref|YP\\_028506.1|](#)  chloramphenicol acetyltransferase [Bacillus anthracis str. Steinhilber]  
[gi|30262409|ref|NP\\_844786.1|](#)  chloramphenicol acetyltransferase [Bacillus anthracis str. Ames]  
[gi|21400282|ref|NP\\_656267.1|](#)  CAT, Chloramphenicol acetyltransferase [Bacillus anthracis str. Ames]  
[gi|30257040|gb|AAP26272.1|](#)  chloramphenicol acetyltransferase [Bacillus anthracis str. Ames]  
[gi|47502850|gb|AAAT31526.1|](#)  chloramphenicol acetyltransferase [Bacillus anthracis str. 'Ames']

Ancestor']

[gi|49179181|gb|AAT54557.1|](#) **G** chloramphenicol acetyltransferase [Bacillus anthracis str. Stern  
Length = 216

Score = 180 bits (457), Expect = 3e-44  
Identities = 80/196 (40%), Positives = 127/196 (64%), Gaps = 2/196 (1%)  
Frame = +2

Query: 62 YTTVDISQWHRKEHLEAFQSV AQCTYNQTVQLDITAF LKTVKKNKHKFYPAFIHILARLM 241  
+ +D W+R+++ E + + +CT++ TV +DIT +K V + KFYP FI+I++R++  
Sbjct: 3 FHVIDRENWNREQYFEHYLEL-KCTFSMTVNVDITLLIKKVHQKGIKIFYPTFIYIISRII 61

Query: 242 NAHPEFRMAMKD-GELVIWDSVHPCYTVFHEQTETFS LSWSEYHDDFRQFLHIYSQDVAC 418  
N H EFR D G L W+ + P YT+FH+ ++FSS+W++Y DFR F Y +D+ C  
Sbjct: 62 NKHKEFRCTCFNDEGVLGYWEEMIPSYTIFHKDDKSFSSIWTDYSSDFRIFYKNEYEDMRC 121

Query: 419 YGENLAYFPKGFIE-NMFFV SANPWVSFTSFDLNVANM DNFFAPVFTMGKYTQGDKVL M 595  
Y K I N+F +S PW SFT F+LN+ N +F P+ T GKY+ + +K+++  
Sbjct: 122 YASVHGLLTKENIPPNIFFISGIPWTSFTGFNLNINNDGDFLLPIITCGKYFNEENKIML 181

Query: 596 PLAIQVHHAVCDGFHV 643  
P+++QVHH+VCDG+HV  
Sbjct: 182 PVS LQVHHSVCDGYHV 197

[>gi|66525|pir||XVBSCP](#) chloramphenicol O-acetyltransferase (EC 2.3.1.28) - Bacillus  
pumilus  
[gi|115753|sp|P00487|CAT\\_BACPU](#) Chloramphenicol acetyltransferase (CAT) (Cat-86)  
[gi|551695|gb|AAA22289.1|](#) chloramphenicol acetyltransferase (ttg start codon)  
[gi|223844|prf||1002213A](#) acetyltransferase,chloramphenicol  
Length = 220

Score = 180 bits (456), Expect = 4e-44  
Identities = 82/202 (40%), Positives = 131/202 (64%), Gaps = 4/202 (1%)  
Frame = +2

Query: 92 RKEHLEAFQSV AQCTYNQTVQLDITAF LKTVKKNKHKFYPAFIHILARLMNAHPEFRMAM 271  
RKEH + ++ +C+Y+ + LDIT +K+ K K YP I++LAR + PEF RM  
Sbjct: 11 RKEHFHHYMTLFRCSYSLVINLDITKLHAILKEKLVYPVQIYLLARAVQKIPEFRMDQ 70

Query: 272 KDGELVIWDSVHPCYTVFHEQTETFS LSWSEYHDDFRQFLHIYSQDVACYGENLAYFPKG 451  
+ EL W+ +HP YT+ +++T+TFSS+W+ + ++F QF D+ + ++ FPK  
Sbjct: 71 VNDELGYWEILHPSYTI LNKETKTFSSIWTPFDENFAQFYKSCVADIEFSSKSSNLFPKP 130

Query: 452 FI-ENMFFV SANPWVSFTSFDLNVANM DNFFAPVFTMGKYTQGDKVL MPLAIQVHHAVC 628  
+ ENMF +S+ PW+ FTSF+LNV+ + + P+FT+GK+ + K+++P+AIQVHHAVC  
Sbjct: 131 HMPENMFNISSLPWIDF TSFNLNVSTDEAYLLPIFTIGKFKVEEGKIILPVAIQVHHAVC 190

Query: 629 DGFHVGTNA\*\*IK---\*YCDEW 685  
DG+H G ++ +CDEW  
Sbjct: 191 DGYHAGQYVEYLRWLIEHCDEW 212

[>gi|40433|emb|CAA33203.1|](#) unnamed protein product [Clostridium difficile]  
[gi|80496|pir||S04711](#) chloramphenicol O-acetyltransferase (EC 2.3.1.28) - Clostridium  
difficile  
[gi|115755|sp|P11504|CAT\\_CLODI](#) Chloramphenicol acetyltransferase (CAT)  
Length = 212


Score = 179 bits (454), Expect = 6e-44  
 Identities = 88/196 (44%), Positives = 126/196 (64%), Gaps = 2/196 (1%)  
 Frame = +2

Query: 62 YTTVDISQWHRKEHLEAFQSVAQCTYNQTVQLDITAFKTKVKKKHKFYPAFIHILARLM 241  
 + +D + W+RKE+ + + + CTY+ TV++DIT +K+ K YPA ++ +A ++  
 Sbjct: 3 FEKIDKNSWNRKEYFDHYFASVPCTYSMTVKVDITQ----IKEKGMKLYPAMLYIAMIIV 58

Query: 242 NAHPEFRMAM-KDGELVIWDSVHPCYTVFHEQTETFSSSLWSEYHDDFRQFLHIYSQDVAC 418  
 N H EFR A+ +DGEL I+D + P YT+FH TETFSSSLW+E DF+ FL Y D  
 Sbjct: 59 NRHSEFRTAINQDGELGIYDEMIPSYTIFHNDTETFSSSLWTECKSDFKSFADYSDTQR 118

Query: 419 YGENLAYFPK-GFIENMFFVSANPWVSFTSFDLNVANMDNFFAPVFTMGKYTQGDVKVLM 595  
 YG N K EN+F VS PW +F F+LN+ ++ P+FTMGK + +K+++  
 Sbjct: 119 YGNHRMEGKPNAPENIFNVSMIPWSTFDGFNLNLQKGYDYLIPIFTMGKIIKDKNKIIL 178

Query: 596 PLAIQVHHAVCDGFHV 643  
 PLAIQVHHAVCDGFH+  
 Sbjct: 179 PLAIQVHHAVCDGFHI 194

 [>gi|47565764|ref|ZP\\_00236804.1|](#) chloramphenicol acetyltransferase [Bacillus cereus G9241]  
[gi|47557400|qb|EAL15728.1|](#) chloramphenicol acetyltransferase [Bacillus cereus G9241]  
 Length = 216




Score = 177 bits (450), Expect = 2e-43  
 Identities = 78/195 (40%), Positives = 128/195 (65%), Gaps = 2/195 (1%)  
 Frame = +2

Query: 62 YTTVDISQWHRKEHLEAFQSVAQCTYNQTVQLDITAFKTKVKKKHKFYPAFIHILARLM 241  
 + +D W+R+++ E + + +CT++ TV +DIT ++ V + + KFYP FI+I++R++  
 Sbjct: 3 FHVIDRENWNRQYFEHYLEL-KCTFSLTVNVDITLLIEKVHQQEIKFYPTFIYIISRII 61

Query: 242 NAHPEFRMAMKD-GELVIWDSVHPCYTVFHEQTETFSSSLWSEYHDDFRQFLHIYSQDVAC 418  
 N H +FR D G L W+ + P YT+FH+ ++FSS+W++Y DFR F Y D+ C  
 Sbjct: 62 NKHKKFRCTCFNDEGVLGYWEEMIPSYTIFHKDDKSFSSIWTDYSSDFRTFYKNEYEDMRC 121

Query: 419 YGENLAYFPKGFIE-NMFFVSANPWVSFTSFDLNVANMDNFFAPVFTMGKYTQGDVKVLM 595  
 Y F K I N+F +S+ PW SFT F+LN+ N ++ P+ T GKY+ + +KV++  
 Sbjct: 122 YANVHGLFTKENIPNVFPISSIPWTSFTGFNLNINNDADYLLPIITCGKYFNEENKVIL 181

Query: 596 PLAIQVHHAVCDGFH 640  
 P+++QVHH+VCDG+H  
 Sbjct: 182 PVSLOVHHSVCDGYH 196

 [>gi|42781506|ref|NP\\_978753.1|](#)  chloramphenicol acetyltransferase [Bacillus cereus ATCC 109  
[gi|42737429|qb|AAS41361.1|](#)  chloramphenicol acetyltransferase [Bacillus cereus ATCC 10987]  
 Length = 216

Score = 174 bits (442), Expect = 2e-42  
 Identities = 77/195 (39%), Positives = 129/195 (66%), Gaps = 2/195 (1%)  
 Frame = +2

Query: 62 YTTVDISQWHRKEHLEAFQSVAQCTYNQTVQLDITAFKTKVKKKHKFYPAFIHILARLM 241  
 + +D +W+RK++ E + + +CT++ TV +DIT LK + + KFYP FI++++++  
 Sbjct: 3 FHVIDREKWNRRQYFEHYLKL-KCTFSMTVHVVDITRLLKELHQQGKIKFYVPVFIYLISKVV 61

Query: 242 NAHPEFRMAM-KDGELVIWDSVHPCYTVFHEQTETFSSSLWSEYHDDFRQFLHIYSQDVAC 418  
 N H EFR + ++G L W+ + P YT+FH+ ++FSS+W++Y DF F Y +D+  
 Sbjct: 62 NNHKEFRTSFNEEGALGYWEEMIPSYTIFHKDDKSFSSIWTDYSSDFHIFYRNYQEDMRL 121

Query: 419 YGENLAYFPKGFIE-NMFFVSANPWVSFTSFDLNVANMDNFFAPVFTMGKYTQGDVKVLM 595  
 Y F K I N+F +S+ PW SFT F+LN+ N +F P+ T GKY+ + +KV++  
 Sbjct: 122 YTNVHGLFTKENIPPVNFPISSIPWASFTGFNLNINNEGDFLLPIITCGKYFNEENKVML 181

Query: 596 PLAIQVHHA VCDGFH 640  
 P+++QVHH+VCDG+H  
 Sbjct: 182 PVS LQVHHSVCDGYH 196

>[gi|22775399|dbj|BAC11901.1](#) chloramphenicol acetyltransferase [Streptococcus suis]  
 Length = 216

Score = 172 bits (437), Expect = 6e-42  
 Identities = 76/197 (38%), Positives = 124/197 (62%), Gaps = 2/197 (1%)  
 Frame = +2

Query: 62 YTTVDISQWHRKEHLEAFQSVAQCTYNQTVQLDITAFKTVKKNKHKFYPAFIHILARLM 241  
 + +D+ W RKE + + Q T++ T ++DI+ + +K+ ++KFYPAF+ ++ R++  
 Sbjct: 3 FNKIDLDNWK RKEIFNH YLN-QQTF SITTEIDISVLYRNIKQKRYKFYPAFVFLVTRVI 61

Query: 242 NAHPEFRMAMK-DGELVIWDSVHPCYTVFHEQTETFSSSLWSEYHDDFRQFLHIYSQDVAC 418  
 N++ FR +GEL WD + P YT+F ++TFS +W+ +DF++F +Y DV  
 Sbjct: 62 NSNTAFRTGYNSEGELGYWDKLDPLYTIFDVSVKTFSGIWT PARNDFKEFYDLYLSDVEK 121

Query: 419 YGENLAYFPKGFIE-NMFFVSANPWVSFTSFDLNVANMDNFFAPVFTMGKYTQGDVKVLM 595  
 Y + FPK I EN F +S PW SFT F+LN+ N N+ P+ T GK+ +G+ + +  
 Sbjct: 122 YNGSGKLPKTP IPENAFSISIIIPWTSFTGFNLNINNNSNYLLPIITAGKFINKGNSIYL 181

Query: 596 PLAIQVHHA VCDGFHVG 646  
 PL++QVHH+VCDG+H G  
 Sbjct: 182 PLSLQVHHSVCDGYHAG 198

>[gi|1667472|gb|AAB53259.1](#) chloramphenicol acetyltransferase-TC [Lactobacillus reuteri]  
 Length = 238

Score = 172 bits (436), Expect = 8e-42  
 Identities = 78/197 (39%), Positives = 123/197 (62%), Gaps = 2/197 (1%)  
 Frame = +2

Query: 62 YTTVDISQWHRKEHLEAFQSVAQCTYNQTVQLDITAFKTVKKNKHKFYPAFIHILARLM 241  
 + +D+ W RKE + + Q T++ T ++DI+ + +K+ +KFYPAFI ++ R++  
 Sbjct: 3 FNKIDLDNWK RKEIFNH YLN-QQTF SITTEIDISVLYRNIKQEGYKFYPAFIFLVTRVI 61

Query: 242 NAHPEFRMAMK-DGELVIWDSVHPCYTVFHEQTETFSSSLWSEYHDDFRQFLHIYSQDVAC 418  
 N++ FR DGEL WD + P YT+F ++TFS +W+ +DF++F +Y DV  
 Sbjct: 62 NSNTAFRTGYNSDGELGYWDKLEPLYTIFDGVSKTFSGIWT SVKNDFKEFYDLYLSDVEK 121

Query: 419 YGENLAYFPKGFIE-NMFFVSANPWVSFTSFDLNVANMDNFFAPVFTMGKYTQGDVKVLM 595  
 Y + FPK I EN F +S PW SFT F+LN+ N N+ P+ T GK+ +G+ + +  
 Sbjct: 122 YNGSGKLPKTP IPENAFSLSIIPWTSFTGFNLNINNNSNYLLPIITAGKFINKGNSIYL 181

Query: 596 PLAIQVHHA VCDGFHVG 646

PL++QVHH+VCDG+H G

Sbjct: 182 PLSLQVHHSVCDGYHAG 198

[gi|257403|gb|AAB23649.1](#) chloramphenicol acetyltransferase; CAT [Listonella anguillarum]  
[gi|1345693|sp|P49417|CAT\\_VIBAN](#) Chloramphenicol acetyltransferase (CAT)  
 Length = 216

Score = 172 bits (435), Expect = 1e-41

Identities = 83/195 (42%), Positives = 119/195 (61%), Gaps = 2/195 (1%)

Frame = +2

Query: 62 YTTVDISQWHRKEHLEAFQSVACQCTYNQTVQLDITAFLLKTVKKNKHKFYPAFIHILARLM 241  
 + VD+ W RKE+ + CTY+ TV+LDIT T+K K K YPA ++ ++ ++

Sbjct: 3 FRLVDLKTWKRKEYFTHYFESVPCYTSMTVKLDIT----TIKTGKAKLYPALLYAVSTVV 58

Query: 242 NAHPEFRMAMKD-GELVIWDSVHPCYTVFHEQTETFFSSLWSEYHDDFRQFLHIYSQDVAC 418  
 N H EFRM + D G++ I+ + PCYT+F + TE FS++W+EY D+ +F Y +D+

Sbjct: 59 NRHEEFRTVDDGQIGIFSEMPCYTIFQKDTMFNSNIWTEYIGDYTEFCKQYKDMQQ 118

Query: 419 YGENLAYFPKGFIE-NMFFVSANPWVSFTSFDLNVANMDNFFAPVFTMGKYYTQGDKVL 595  
 YGEN K N F VS PW +F F+LN+ + P+FT G+YY + K +

Sbjct: 119 YGENKGMMAKPNPPVNTFPVSMIPWTTFEGFNLNQKGYGYLLPIFTFGRYYEENGGYWI 178

Query: 596 PLAIQVHHAHVCDGFH 640

PL+IQVHHAHVCDGFH

Sbjct: 179 PLSIQVHHAHVCDGFH 193

[gi|29650179|gb|AAO86060.1](#) chloramphenicol acetyltransferase [Cloning vector pNW33N]  
[gi|51493760|gb|AAU04871.1](#) chloramphenicol acetyltransferase [Bursa aurealis delivery vector  
 pBursa]  
[gi|30424555|gb|AAO24789.1](#) chloramphenicol acetyl transferase [Shuttle vector pSK5640]  
[gi|30424550|gb|AAO24785.1](#) chloramphenicol acetyl transferase [Shuttle vector pSK5632]  
[gi|30424544|gb|AAO24776.1](#) chloramphenicol acetyl transferase [Shuttle vector pSK5645]  
[gi|30424539|gb|AAO24781.1](#) chloramphenicol acetyl transferase [Shuttle vector pSK5630]  
[gi|60650126|dbj|BAD90928.1](#) chloramphenicol acetyltransferase [Cloning vector pND50]  
[gi|20804332|emb|CAD10262.1](#) chloramphenicol acetyltransferase [Shuttle integration vector pPL  
[gi|14211234|gb|AAK57387.1](#) chloramphenicol acetyl transferase [glnQ expression vector pAG200]  
[gi|14211232|gb|AAK57386.1](#) chloramphenicol acetyl transferase [glnQ allelic exchange vector  
 pAG101]  
[gi|46534|emb|CAA24586.1](#) unnamed protein product [Staphylococcus aureus]  
[gi|49036567|gb|AAT48879.1](#) chloramphenicol acetylase [Integration vector pDG3661]  
[gi|24898923|dbj|BAC23078.1](#) chloramphenicol acetyltransferase [transposable plasmid pSET8is]  
[gi|15553044|dbj|BAB64891.1](#) chloramphenicol acetyltransferase [Thermosensitive suicide vector  
 pSET6s]  
[gi|15553039|dbj|BAB64887.1](#) chloramphenicol acetyltransferase [Thermosensitive suicide vector  
 pSET5s]  
[gi|9309359|dbj|BAB03245.1](#) chloramphenicol acetyl transferase [Shuttle vector pSET3]  
[gi|9309349|dbj|BAB03237.1](#) chloramphenicol acetyl transferase [Shuttle vector pSET1]  
[gi|886841|emb|CAA59723.1](#) chloramphenicol acetyltransferase [synthetic construct]  
[gi|58001|emb|CAA35816.1](#) unnamed protein product [Cloning vector pBD64]  
[gi|20975731|emb|CAD10282.1](#) chloramphenicol acetyltransferase [Shuttle integration vector pPL  
[gi|5459336|emb|CAB50709.1](#) chloramphenicol acetyltransferase [Cloning vector pAMY-em1]  
[gi|5825494|gb|AAD53270.1](#) chloramphenicol acetyl transferase [Cloning vector pDC123]  
[gi|66523|pir|XXSACC](#) chloramphenicol O-acetyltransferase (EC 2.3.1.28) - Staphylococcus  
 aureus plasmids  
[gi|39726223|gb|AAR30052.1](#) chloramphenicol acetyltransferase [Integration vector pSac-Cm]

[gi|39726217|gb|AAR30048.1|](#) chloramphenicol acetyltransferase [Integration vector pGlt-Cm]  
[gi|39726211|gb|AAR30044.1|](#) chloramphenicol acetyltransferase [Integration vector pPyr-Cm]  
[gi|1277142|gb|AAC53695.1|](#) chloramphenicol-resistance protein  
[gi|32185270|gb|AAP73800.1|](#) chloramphenicol acetyltransferase [Shuttle vector  
 pLEIItD+KR''deltaORF]  
[gi|32140768|gb|AAP70041.1|](#) chloramphenicol acetyltransferase [Shuttle vector pLEIItD+KR'']  
[gi|7595744|gb|AAF64429.1|](#) chloramphenicolacetyltransferase [Enterococcus faecium]  
[gi|11545519|gb|AAG37889.1|](#) CAT [Tn10 delivery vector pHV1249]  
[gi|11545513|gb|AAG37884.1|](#) CAT [Tn10 delivery vector pHV1248]  
[gi|2342752|gb|AAB67758.1|](#) chloramphenicol acetyl transferase [Shuttle vector pSEmp18BBXM]  
[gi|1185567|gb|AAB40300.1|](#) chloramphenicol acetylase  
[gi|1185561|gb|AAB40295.1|](#) chloramphenicol acetylase  
[gi|10956142|ref|NP\\_040437.1|](#) hypothetical protein [Staphylococcus aureus]  
[gi|115680|sp|P00485|CAT1 STAAU](#) Chloramphenicol acetyltransferase (CAT)  
[gi|150547|gb|AAA92251.1|](#) chloramphenicol acetyltransferase  
 Length = 216

Score = 172 bits (435), Expect = 1e-41  
 Identities = 78/197 (39%), Positives = 123/197 (62%), Gaps = 2/197 (1%)  
 Frame = +2

Query: 62 YTTVDISQWHRKEHLEAFQSVAQCTYNQTVQLDITAFKTKVKKKHKFYPAFIHILARLM 241  
 + +D+ W RKE + + Q T++ T ++DI+ + +K+ +KFYPAFI ++ R++  
 Sbjct: 3 FNKIDLDNWKRKEIFNHLYLN-QQTFSTTEIDISVLYRNIKQEGYKFYPAFIFLVTRVI 61

Query: 242 NAHPEFRMAMK-DGELVIWDSVHPCYTVFHEQTETFSSSLWSEYHDDFRQFLHIYSQDVAC 418  
 N++ FR DGEL WD + P YT+F ++TFS +W+ +DF++F +Y DV  
 Sbjct: 62 NSNTAFRTGYNSDGELGYWDKLEPLYTIFDGVSKTFSGIWTPVKNDKFKEFYDLYLSDVEK 121

Query: 419 YGENLAYFPKGF I-ENMFFVSANPWSFSTFDLNVANMNDNFFAPVFTMGKYYTQGDKVL M 595  
 Y + FPK I EN F +S PW SFT F+LN+ N N+ P+ T GK+ +G+ + +  
 Sbjct: 122 YNGSGKLPKPTIPENAFSLSIIPWTSFTGFNLNINNNSNYLLPIITAGKFINKGNSIYL 181

Query: 596 PLAIQVHHAVCDGFHVG 646  
 PL++QVHH+VCDG+H G  
 Sbjct: 182 PLSLQVHHSVCDGYHAG 198

[>gi|66521|pir||XXECC3](#) chloramphenicol O-acetyltransferase (EC 2.3.1.28) III - Escherichia coli  
 Length = 203

Score = 167 bits (424), Expect = 2e-40  
 Identities = 85/196 (43%), Positives = 118/196 (60%), Gaps = 2/196 (1%)  
 Frame = +2

Query: 62 YTTVDISQWHRKEHLEAFQSVAQCTYNQTVQLDITAFKTKVKKKHKFYPAFIHILARLM 241  
 YT D+ W R+EH E + C + T ++DIT T+ K++H+ FI+++A+ +  
 Sbjct: 3 YTKFDVKNWVRREHFEFYVHFRXCXXSLTSKIDIT----TLFKDRHRLPCGFIYLIAQAV 58

Query: 242 NAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTETFSSSLWSEYHDDFRQFLHIYSQDVAC 421  
 N E RMA+ D +L++WDSV P +TVFH++TETFS+L Y D QF+ Y + Y  
 Sbjct: 59 NQFDELRLMAIADNQLIVWDSVDPQFTVVFHQTETFSALSCPYSDDIDQFMVNYLSVMERY 118

Query: 422 GENLAYFPKGF IENMFFVSANPWSFSTFDLNVANMNDNFFAPVFTMGKYYTQGDKVLMP- 598  
 N FP+G PWV+F SFDLNVAN DN M KY +GD++L+P  
 Sbjct: 119 KSNTLLFPQGVTPQNHINPLAPWVNFDSFDLNVANFDN-----MAKYQOEGDRLLLPL 171

Query: 599 -LAIQVHHAVCDGFHV 643  
 L++QVHHAVCDGFHV  
 Sbjct: 172 VLSVQVHHAVCDGFHV 187

Lambda	K	H
0.318	0.134	0.401

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 2419798

Number of Hits to DB: 251282219

Number of extensions: 6260536

Number of successful extensions: 19501

Number of sequences better than 10.0: 24

Number of HSP's better than 10.0 without gapping: 18961

Number of HSP's gapped: 19479

Number of HSP's successfully gapped: 24

Number of extra gapped extensions for HSPs above 10.0: 0

Length of query: 732

Length of database: 819541351

Length adjustment: 124

Effective length of query: 608

Effective length of database: 519486399

Effective search space: 315847730592

Effective search space used: 62338367880

T: 12

A: 40

X1: 16 ( 7.3 bits)

X2: 38 (15.0 bits)

X3: 64 (25.0 bits)

S1: 41 (22.0 bits)

S2: 73 (32.7 bits)