

BLASTP 2.8.0+

Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schaffer, 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.

Reference for compositional score matrix adjustment: Stephen F. Altschul, John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schaffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", *FEBS J.* 272:5101-5109.

RID: CT2JBWCM01R

Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects

149,694,506 sequences; 54,860,295,172 total letters

Query= WP_007929940.1 MULTISPECIES: sulfonamide-resistant dihydropteroate synthase Sul1 [Actinobacteria]

Length=283

Score E

Sequences producing significant alignments:

(Bits) Value

| | | | |
|----------------|--|-----|-------|
| ACA34300.1 | dihydrofolate synthase 2 [Leucobacter komagatae] | 223 | 1e-71 |
| CZQ86650.1 | dihydropteroate synthase signature 2 [Trichococcus...] | 126 | 2e-33 |
| WP_014355480.1 | dihydropteroate synthase [Acetobacterium woodii] | 124 | 1e-32 |
| WP_050739642.1 | dihydropteroate synthase [Acetobacterium bakii] | 124 | 2e-32 |
| WP_086986002.1 | dihydropteroate synthase [Trichococcus collinsii] | 122 | 3e-32 |
| CZQ85205.1 | dihydropteroate synthase signature 2 [Trichococcus...] | 121 | 1e-31 |
| CZQ89210.1 | dihydropteroate synthase signature 2 [Trichococcus...] | 121 | 2e-31 |
| SFE72892.1 | dihydropteroate synthase [Trichococcus pasteurii] | 119 | 6e-31 |
| WP_069911287.1 | dihydropteroate synthase [Devosia insulae] | 119 | 1e-30 |
| WP_057081671.1 | dihydropteroate synthase [Bifidobacterium bifi...] | | |

119 2e-30
WP_086988369.1 dihydropteroate synthase [Trichococcus floccul...
118 2e-30
WP_013390177.1 dihydropteroate synthase [Bifidobacterium bifi...
119 2e-30
BBA47465.1 dihydropteroate synthase [Bifidobacterium bifidum ...
119 2e-30
WP_083546429.1 MULTISPECIES: dihydropteroate synthase [Tricho...
117 2e-30
WP_013363793.1 dihydropteroate synthase [Bifidobacterium bifi...
118 3e-30
WP_047298337.1 dihydropteroate synthase [Bifidobacterium bifi...
118 4e-30
WP_026394512.1 dihydropteroate synthase [Acetobacterium dehal...
117 4e-30
WP_034876901.1 dihydropteroate synthase [Bifidobacterium mouk...
117 6e-30
WP_101629030.1 dihydropteroate synthase [Bifidobacterium longum]
117 6e-30
WP_010081417.1 dihydropteroate synthase [Bifidobacterium longum]
117 7e-30
WP_032744530.1 dihydropteroate synthase [Bifidobacterium longum]
117 7e-30
WP_033499260.1 dihydropteroate synthase [Bifidobacterium adol...
117 7e-30
WP_034525832.1 dihydropteroate synthase [Bifidobacterium stel...
117 8e-30
WP_003808269.1 dihydropteroate synthase [Bifidobacterium adol...
117 9e-30
WP_086943467.1 dihydropteroate synthase [Trichococcus pasteurii]
116 9e-30
WP_049705597.1 dihydropteroate synthase [Devosia sp. H5989]
117 1e-29
WP_042990425.1 dihydropteroate synthase [Bifidobacterium adol...
117 1e-29
WP_033523224.1 dihydropteroate synthase [Bifidobacterium mery...
117 1e-29
WP_041777256.1 dihydropteroate synthase [Bifidobacterium adol...
116 2e-29
WP_065506906.1 dihydropteroate synthase [Bifidobacterium breve]
116 2e-29
WP_032746349.1 dihydropteroate synthase [Bifidobacterium longum]
116 2e-29
WP_053825171.1 dihydropteroate synthase [Bifidobacterium bifi...
116 2e-29
WP_055881405.1 dihydropteroate synthase [Devosia sp. Root105]
115 2e-29
WP_007053863.1 dihydropteroate synthase [Bifidobacterium longum]
116 2e-29
WP_077385559.1 dihydropteroate synthase [Bifidobacterium longum]
116 2e-29
BAF39192.1 dihydropteroate synthase 1 [Bifidobacterium adoles...
116 2e-29
WP_003814775.1 dihydropteroate synthase [Bifidobacterium bifi...

115 2e-29
WP_065445269.1 dihydropteroate synthase [Bifidobacterium longum]
115 3e-29
WP_065454755.1 dihydropteroate synthase [Bifidobacterium longum]
115 3e-29
AUD75228.1 Dihydropteroate synthase [Bifidobacterium breve]
115 3e-29
WP_100513572.1 dihydropteroate synthase [Bifidobacterium sp. ...]
115 3e-29
WP_014760561.1 dihydropteroate synthase [Bifidobacterium bifi...]
115 3e-29
WP_039774850.1 dihydropteroate synthase [Bifidobacterium adol...]
115 4e-29
WP_032736608.1 dihydropteroate synthase [Bifidobacterium longum]
115 4e-29
WP_033892007.1 dihydropteroate synthase [Bifidobacterium sagu...]
115 4e-29
WP_085379343.1 dihydropteroate synthase [Bifidobacterium adol...]
115 4e-29
CZQ91691.1 dihydropteroate synthase signature 1 [Trichococcus...]
115 4e-29
WP_047290331.1 dihydropteroate synthase [Bifidobacterium bifi...]
115 4e-29
BBA55689.1 dihydropteroate synthase [Bifidobacterium bifidum]
115 5e-29
KXS22994.1 dihydropteroate synthase [Bifidobacterium breve]
115 5e-29
WP_080867818.1 dihydropteroate synthase [Bifidobacterium breve]
115 5e-29
WP_032682980.1 dihydropteroate synthase [Bifidobacterium longum]
115 5e-29
EIJ22047.1 dihydropteroate synthase [Bifidobacterium longum s...]
115 5e-29
WP_026646441.1 dihydropteroate synthase [Bifidobacterium rumi...]
115 6e-29
WP_019728223.1 dihydropteroate synthase [Bifidobacterium breve]
114 6e-29
WP_025222047.1 dihydropteroate synthase [Bifidobacterium breve]
114 6e-29
WP_055996483.1 dihydropteroate synthase [Devosia sp. Root413D1]
114 6e-29
WP_025301383.1 dihydropteroate synthase [Bifidobacterium breve]
114 7e-29
WP_100510016.1 dihydropteroate synthase [Bifidobacterium sp. ...]
114 7e-29
AUD91812.1 Dihydropteroate synthase [Bifidobacterium breve]
114 9e-29
WP_085461798.1 dihydropteroate synthase [Bifidobacterium adol...]
114 9e-29
WP_065472186.1 dihydropteroate synthase [Bifidobacterium longum]
114 9e-29
CZQ85951.1 dihydropteroate synthase signature 2 [Trichococcus...]
114 9e-29
WP_100496241.1 dihydropteroate synthase [Bifidobacterium sp. ...]

114 9e-29
WP_015439115.1 dihydropteroate synthase [Bifidobacterium breve]
114 9e-29
WP_029679339.1 dihydropteroate synthase [Bifidobacterium longum]
114 1e-28
WP_021649768.1 dihydropteroate synthase [Bifidobacterium breve]
114 1e-28
WP_080784119.1 dihydropteroate synthase [Bifidobacterium breve]
114 1e-28
WP_077424703.1 dihydropteroate synthase [Bifidobacterium longum]
114 1e-28
WP_094667142.1 dihydropteroate synthase [Bifidobacterium myos...]
114 1e-28
WP_070372479.1 dihydropteroate synthase [Acetobacterium wieri...]
113 1e-28
WP_070122223.1 dihydropteroate synthase [Bifidobacterium adol...]
114 1e-28
WP_094730457.1 dihydropteroate synthase [Bifidobacterium hapali]
114 2e-28
WP_101621332.1 dihydropteroate synthase [Bifidobacterium parmae]
113 2e-28
WP_101626177.1 dihydropteroate synthase [Bifidobacterium impe...]
113 2e-28
OXS26090.1 dihydropteroate synthase [Acetobacterium sp. MES1]
113 2e-28
WP_077389951.1 dihydropteroate synthase [Bifidobacterium longum]
113 2e-28
WP_065436770.1 dihydropteroate synthase [Bifidobacterium longum]
113 2e-28
WP_013410667.1 dihydropteroate synthase [Bifidobacterium longum]
113 2e-28
WP_100493538.1 dihydropteroate synthase [Bifidobacterium sp. ...]
113 2e-28
WP_044089021.1 dihydropteroate synthase [Bifidobacterium reut...]
113 2e-28
WP_085382394.1 dihydropteroate synthase [Bifidobacterium adol...]
113 2e-28
WP_085381689.1 dihydropteroate synthase [Bifidobacterium adol...]
113 2e-28
PLS29794.1 dihydropteroate synthase [Bifidobacterium parmae]
113 3e-28
WP_060620656.1 dihydropteroate synthase [Bifidobacterium longum]
113 3e-28
KXS24820.1 dihydropteroate synthase [Bifidobacterium dentium]
113 3e-28
WP_056251287.1 dihydropteroate synthase [Devosia sp. Root436]
112 3e-28
WP_092184669.1 dihydropteroate synthase [Devosia sp. YR412]
112 3e-28
WP_100968037.1 dihydropteroate synthase [Bifidobacterium longum]
112 3e-28
ODS95184.1 dihydropteroate synthase [Devosia sp. SCN 66-27]
112 4e-28
WP_034518937.1 MULTISPECIES: dihydropteroate synthase [Bifido...

112 4e-28
 WP_003837180.1 dihydropteroate synthase [Bifidobacterium dent...
 112 4e-28
 WP_058594680.1 dihydropteroate synthase [Leucobacter chromiir...
 115 4e-28
 WP_003830054.1 dihydropteroate synthase [Bifidobacterium breve]
 112 5e-28
 KXS29119.1 dihydropteroate synthase [Bifidobacterium longum]
 112 6e-28
 WP_008782915.1 MULTISPECIES: dihydropteroate synthase [Bifido...
 112 6e-28
 WP_087033063.1 dihydropteroate synthase [Trichococcus palustris]
 111 6e-28
 WP_095346990.1 dihydropteroate synthase [Bifidobacterium longum]
 112 6e-28
 WP_011068790.1 dihydropteroate synthase [Bifidobacterium longum]
 112 7e-28
 WP_046138407.1 dihydropteroate synthase [Devosia epidermidihi...
 112 7e-28

ALIGNMENTS

>ACA34300.1 dihydrofolate synthase 2, partial (plasmid) [Leucobacter
 komagatae]
 Length=241

Score = 223 bits (569), Expect = 1e-71, Method: Compositional
 matrix adjust.
 Identities = 133/243 (55%), Positives = 169/243 (70%), Gaps = 2/243
 (1%)

Query 9
 FGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSDDVVDVGPAAASHDPARPVSPADEIRR 68
 FGI+N+T DSF D R L P A+ A +++ G+DV+D+GPA+S+PDA PVS
 EI R
 Sbjct 1
 FGIVNITSDFSFDGGRYLAPDAAIAQARKLMAEGADVIDLGPASSNPDAAPVSSDTEIAR 60

Query 69
 IAPLLDALSDQMHRVSIDSFQPETQRYALKRGVGYLNDIQGFDPALYPDIAEADCRLVV 128
 IAP+LDAL VS+DS+QP TQ YAL RGV YLNDI+GFPD A YP +A++
 +LVV
 Sbjct 61
 IAPVLDALKADGIPVSLDSYQPATQAYALSRGVAYLNDIRGFPDAAFYPQLAKSSAKLVV 120

Query 129
 MHSARQDGIATRTGHLRPEDALDEIVRFFEARVSALRRSGVAADRLILDPMGMFFLSPAP 188
 MHS Q DG A R D +D I FF+AR++AL +G+ +RL+LDPGMGMFFL
 AP
 Sbjct 121 MHSVQ-DGQADRR-
 EAPAGDIMDHIAAFFDARIAALTGAGIKRNRLVLDPMGMFFLGAAP 178

Query 189
 ETSLHVLNQLKLSALGLPLLVSRSRKSFLGATVGLPVKDLGPASLAAELHAIGNGADY 248
 ETSL VL+ +L+ LP+L+SRSRKSFL A G D+G A+LAAEL A

GAD+
Sbjct 179
ETSLSVLARFDELRLRFDLPVLLSVSRKSFLRALTGRGPGDVGAATLAAELAAAAGGADF 238

Query 249 VRT 251
+RT
Sbjct 239 IRT 241

>CZ086650.1 dihydropteroate synthase signature 2 [Trichococcus collinsii]
SDZ76153.1 dihydropteroate synthase [Trichococcus collinsii]
Length=277

Score = 126 bits (316), Expect = 2e-33, Method: Compositional matrix adjust.
Identities = 89/256 (35%), Positives = 136/256 (53%), Gaps = 19/256 (7%)

Query 2
LRSRVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSDDVVDVGAASHPDARPVS 61
L R + GILN+T DSF D A+ AIEM+ G+D++D+G ++ P

+S
Sbjct 12
LSQRSHIMGILNVTPDSFSDGGEWNTVEKAIHAHAEMVAEGADIIDIGGESTRPGHTQIS 71

Query 62 PADEIRRIAPLLDALSDQMHR-VSIDSFQPETQRYALKRGGVYLNDIQGFP-
DPALYPDI 119
+EI R+ P+++AL + +SID+++ R A + G+ +NDI G DP +

Sbjct 72
DEEEIARVVPIIEALKKAVDVPLSIDTYKSAVARAAACEAGIDIINDIWDGCKYDPEIAAVA 131

Query 120
AEADCRLVVMHSAQRDGIATRTGHLRPEDALDEIVRFFFEARVSALRRSGVAADRLLIDPG 179
AE D +++MH+ ++ A ED L ++ VSA GV +

+ILDPG
Sbjct 132 AEFDVPIILMHNREKSDYA-----FLIEDMLADLAESVRIAVSA-----
GVKRENIILDPG 182

Query 180 MGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSKSLGATVG-LPVK--
DLGPASLA 236
GF E +L+V+ +L++ + LG P+L+ SRK F+G +G LP K DLG

A+
Sbjct 183 CGF--GKTYEDNLNVVHHLKRF-
TELGYPVLLGTSRKRFIGTALGDLPFKERDLGTAATT 239

Query 237 AELHAIGNGADYVRTH 252
A I NGA R H
Sbjct 240 A--LGIMNGAQLFRVH 253

>WP_014355480.1 dihydropteroate synthase [Acetobacterium woodii]
AFA47877.1 dihydropteroate synthase FolP [Acetobacterium woodii DSM 1030]

Length=275

Score = 124 bits (311), Expect = 1e-32, Method: Compositional matrix adjust.

Identities = 82/253 (32%), Positives = 136/253 (54%), Gaps = 14/253 (6%)

Query 2

LRSRVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSVDVVDVGPAAASHPDARPVS 61
L V + GILN+T DSF D + ++ +M+ G+D++D+G ++ P

+S

Sbjct 10

LTHEVLIMGILNVTPDSFSDGGKFNTRDTSKQVEKMITDGADLIDLGGESTRPGHTQIS 69

Query 62 PADEIRRIAPLLDALSDQMHR-VSIDSFQPETQRYALKRGVGYLNDIQGFP-
DPALYPDI 119

A+EI R+AP+++A+ + +SID+++ ALK G +NDI GF DPAL

Sbjct 70

DAEEIDRVAPMIEAIRQRFDIPISIDTYKSAVGEAALKAGADLINDIWGFKYDPALAKVT 129

Query 120

AEADCRLVMHSAQRDGIATRGTGHLRPEDALDEIVRFFEARVSALRRSGVAADRLLIDPG 179
A+ V+MH+ HL + ++ R + + +GV+ D

+ILDPG

Sbjct 130 AKYKVPCLMHNRRN-----RNYDHL-----

MTDLNRDLQESIEIAINAGVSQDAIILDPG 180

Query 180

MGFFLSPAPETSLHVLSNLQKLKALGLPLLVSRSKFLGATVGLPVKDLGPASLAAEL 239
+GF A ++ V+++L+ L+ ALG P+L+ SRK F+G T+ LPV + +

+A +

Sbjct 181 IGFAKDYAQ--NMAVMNHLETLQ-

ALGYPIILLGTSRKGFIGLTLDPVTERVEGTVATTV 237

Query 240 HAINGADYVRTH 252

I GA +R H

Sbjct 238 IGIMKGASIIRVH 250

>WP_050739642.1 dihydropteroate synthase [Acetobacterium baki]

KNZ42351.1 dihydropteroate synthase [Acetobacterium baki]

Length=275

Score = 124 bits (310), Expect = 2e-32, Method: Compositional matrix adjust.

Identities = 78/253 (31%), Positives = 138/253 (55%), Gaps = 14/253 (6%)

Query 2

LRSRVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSVDVVDVGPAAASHPDARPVS 61
L + V + GILN+T DSF D + ++ +M+ G+D++D+G ++ P

PV

Sbjct 10

LDNCVVIMGILNVTPDSFSDGGKFNSLDTSLKHVEKMIHEGADIIDLGGESTRPGHEPVG 69

Query 62 PADEIRRIAPLLDALSDQMHR-VSIDSFQPETQRYALKRGGVGLNDIQGFP-
DPALYPDI 119

A EI R+ P+++A+ + +SID+++ + A+K G +ND+ GF D L
Sbjct 70
EAQEIDRVVPMIEAIRSRFDIPLSIDTYKSKVGE LAIKAGADLINDVWGFKRDLKLA EVT 129

Query 120
AEADCRLVVMHSAQRDGIATRTGHLRPEDALDEIVRFFFEARVSALRRSGVAADR LILDPG 179
A+ + V+MH+ RD + + + ++ EA ++ +GVA D+

+ILDPG
Sbjct 130 AKYEVPCVLMHN--RD-----
NQNYDHF MIDVCHDLEASIAIAVNAGVARDKIILDPG 180

Query 180
MGFFLSPAPETSLHVLSNLQKLK SALGLPLLVS VSRKSFLGATVGLPVKDLGPASLAAEL 239
+GF + + ++ ++ +L KL+ LG P+L+ SRK F+G T+ LPV + +

+A +
Sbjct 181 VGF--AKDYQLNMTMMKHLDKLQD-
LGFPIILLGTSRKGFIGITLDLPVTERIEGTVATTV 237

Query 240 HAIGNGADYVRTH 252
I GA +R H
Sbjct 238 MGIMKGASIIRVH 250

>WP_086986002.1 dihydropteroate synthase [Trichococcus collinsii]
Length=259

Score = 122 bits (307), Expect = 3e-32, Method: Compositional
matrix adjust.
Identities = 87/249 (35%), Positives = 133/249 (53%), Gaps = 19/249
(8%)

Query 9
FGILNLTEDSFFDESRR LDPAGAVTAAIEMLRVGS DVVDVGPAA SHPDARPVSPA DEIRR 68
GILN+T DSF D A+ AIEM+ G+D++D+G ++ P +S

+EI R
Sbjct 1
MGILNVTPDSFSDGGEWNTVEKAI AHAIEMVAEGADIIDIGGESTRPGHTQISDEEEIAR 60

Query 69 IAPLLDALSDQMHR-VSIDSFQPETQRYALKRGGVGLNDIQGFP-
DPALYPDIAEADCRL 126
+ P+++AL + +SID+++ R A + G+ +NDI G DP + AE

D +
Sbjct 61
VVPIIEALKKAVDVPLSIDTYKSAVARAA CEAGIDIINDIWGCKYDPEIAAVAAEF DVPI 120

Query 127
VVMHSAQRDGIATRTGHLRPEDALDEIVRFFFEARVSALRRSGVAADR LILDPGMGFFLSP 186
++MH+ ++ A ED L ++ VSA GV + +ILDPG GF

Sbjct 121 ILMHNREKSDYA-----FLIEDMLADLAESVRIAVSA-----
GVKRENIILDPGCGF--GK 169

Query 187 APETSLHVLSNLQKLKSALGLPLLVSRSRKSFLGATVG-LPVK--
DLGPASLAAELHAIG 243
E +L+V+ +L++ + LG P+L+ SRK F+G +G LP K DLG A+ A
I
Sbjct 170 TYEDNLNVVHHLKRF-TELGYPVLLGTSRKRFIGTALGDLPFKERDLGTAATTA--
LGIM 226

Query 244 NGADYVRTH 252
NGA R H
Sbjct 227 NGAQLFRVH 235

>CZQ85205.1 dihydropteroate synthase signature 2 [Trichococcus
flocculiformis]
SFH58580.1 dihydropteroate synthase [Trichococcus flocculiformis]
Length=277

Score = 121 bits (304), Expect = 1e-31, Method: Compositional
matrix adjust.
Identities = 90/256 (35%), Positives = 135/256 (53%), Gaps = 19/256
(7%)

Query 2
LRSRVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSVDVVDVGAASHPDARPVS 61
L R + GILN+T DSF D AV A+EM+ G+D++D+G ++ P
+S
Sbjct 12
LSQRSYIMGILNVTPDSFSDGGEWNTVEKAVAHALEMVADGADIIDIGGESTRPGHTQIS 71

Query 62 PADEIRRIAPLLDALSDQMHR-VSIDSFQPETQRYALKRGGVGLNDIQGF-
PDPALYPDI 119
+EI RI P+++AL + +SID+++ R A + GV +NDI G DP +
Sbjct 72
DEEEIARIVPVIEALKKAVDVPLSIDTYKSAVARAAACEAGVDIINDIWGCRYDPQIAAVA 131

Query 120
AEADCRLVVMHSAQRDGIATRGTGHLRPEDALDEIVRFFEARVSALRRSGVAADRILIDPG 179
A D +++MH+ ++ A ED L ++ VSA GV +
+ILDPG
Sbjct 132 ASFDVPIILMHNREKPDYA-----FLIEDMLTDLAESVRIAVSA-----
GVKRENIILDPG 182

Query 180 MGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSRKSFLGATVG-LPVK--
DLGPASLA 236
GF E +L+V+ +L++ + LG PLL+ SRK F+G +G +P K DLG
A+
Sbjct 183 CGF--GKTYEDNLNVVHHLKRF-
ADLGYPLLLGTSRKRFIGTALGDIPFKERDLGTAATT 239

Query 237 AELHAIGNGADYVRTH 252
A I NGA R H
Sbjct 240 A--LGIVNGAQIFRVH 253

>CZ089210.1 dihydropteroate synthase signature 2 [Trichococcus sp. ES5]

SHF49980.1 dihydropteroate synthase [Trichococcus flocculiformis]
Length=277

Score = 121 bits (303), Expect = 2e-31, Method: Compositional matrix adjust.

Identities = 89/256 (35%), Positives = 135/256 (53%), Gaps = 19/256 (7%)

Query 2

LRSRVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSVDVVDVGAASHPDARPVS 61
L R + GILN+T DSF D AV A+EM+ G+D++D+G ++ P

+S

Sbjct 12

LSQRSYIMGILNVTPDSFSDGGEWNTVEKAVAHALEMVADGADIIDIGGESTRPGHTQIS 71

Query 62 PADEIRRIAPLLDALSDQMHR-VSIDSFQPETQRYALKRGGVGLNDIQGF-
PDPALYPDI 119

+EI RI P+++AL + +SID+++ R A + G+ +NDI G DP +

Sbjct 72

DEEEIARIVPVIEALKKAVDVPLSIDTYKSAVARAAACEAGIDIINDIWIWCRYDPQIAAVA 131

Query 120

AEADCRLVVMHSAQRDGIATRTGHLRPEDALDEIVRFFEARVSALRRSGVAADRLILDPG 179
A D +++MH+ ++ A ED L ++ VSA GV +

+ILDPG

Sbjct 132 ASFDVPIILMHNREKPDYA-----FLIEDMLTDLAESVRIAVSA-----

GVKRENIILDPG 182

Query 180 MGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSRKSFLGATVG-LPVK--
DLGPASLA 236

GF E +L+V+ +L++ + LG PLL+ SRK F+G +G +P K DLG

A+

Sbjct 183 CGF--GKTYEDNLNVVHHLKRF-

ADLGYPLLLGTSRKRFIQTALGDIPFKERDLGTAATT 239

Query 237 AELHAIGNGADYVRTH 252

A I NGA R H

Sbjct 240 A--LGIVNGAQIFRVH 253

>SFE72892.1 dihydropteroate synthase [Trichococcus pasteurii]

SLM52671.1 dihydropteroate synthase signature 2 [Trichococcus pasteurii]
Length=277

Score = 119 bits (299), Expect = 6e-31, Method: Compositional matrix adjust.

Identities = 89/256 (35%), Positives = 135/256 (53%), Gaps = 19/256 (7%)

Query 2

LRSRVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSVDVVDVGAASHPDARPVS 61

L R + GILN+T DSF D AV A+EM+ G+D++D+G ++ P
 +S
 Sbjct 12
 LSKRSYIMGILNVTPDSFSDGGEWNTVEKAVAHALEMVADGADIIDIGGESTRPGHTQIS 71
 Query 62 PADEIRRIAPLLDALSDQMHR-VSIDSFQPETQRYALKRGGVGLNDIQGFP-
 DPALYPDI 119
 +EI RI P+++A+ + +SID+++ R A + GV +NDI G DP +
 Sbjct 72
 DEEEIARIVPVIEAVKKAVDVPLSIDTYKSAVARAAACEAGVDIINDIWGCKYDPEIAAVA 131
 Query 120
 AEADCRLVVMHSAQRDGIATRTRGHLRPEDALDEIVRFFEARVSALRRSGVAADRLILDPG 179
 A D +++MH+ ++ A ED L ++ VSA GV +
 +ILDPG
 Sbjct 132 AAFDVPPIILMHNREKPDYA-----FLIEDMLADLAESVRIAVSA-----
 GVKRENIILDPG 182
 Query 180 MGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSKSFGLGATVG-LPVK--
 DLGPASLA 236
 GF E +L+V+ +L++ + LG PLL+ SRK F+G +G +P K DLG
 A+
 Sbjct 183 CGF--GKTYEDNLNVVHHLKRF-
 ADLGYPLLLGTSRKRFIGTALGDVPFKGRDLGTAATT 239
 Query 237 AELHAIGNGADYVRTH 252
 A I NGA R H
 Sbjct 240 A--LGIVNGAQLFRVH 253

>WP_069911287.1 dihydropteroate synthase [Devosia insulae]
 OE029376.1 dihydropteroate synthase [Devosia insulae DS-56]
 Length=281

Score = 119 bits (298), Expect = 1e-30, Method: Compositional
 matrix adjust.
 Identities = 85/248 (34%), Positives = 132/248 (53%), Gaps = 14/248
 (6%)

Query 8
 VFGILNLTEDSFFDESRRDPAGAVTAAIEMLRVGSVDVVGPAASHDPARPVSPADEIR 67
 + GILN+T DSF D R A+ A ML G+D++D+G ++ P+A VS
 ADE+
 Sbjct 24
 LMGILNVTPDSFSDGGRFDVPAALAQARLMLAEGADIIDIGGESTRPEASEVSVADELA 83
 Query 68 RIAPLLDAL-SDQMHR-VSIDSFQPETQRYALKRGGVGLNDIQGFP-
 DPALYPDIAEADC 124
 R+ P ++AL +D + +SID+++ E A+ G +ND+ G +P +
 E
 Sbjct 84
 RVLPAIEALRADGIAAPISIDTYKAEVAERIAAAGATIINDVHGLQREPEVA AVATEHGA 143
 Query 125

RLVVMHSAQRDGIATRTGHLRPEDALDEIVRFFEARVSALRRSGVAADRILIDPGMGFFL 184
LVVMH + A TG D + E+ R+F+ + ++GVA DR++LDPG

GF

Sbjct 144 PLVVMHWDK----ARDTGR----
DVMAEMARYFDVTLADIADKAGVARDRIVLDPGFGFAK 195

Query 185

SPAPETSLHVLSNLQKLKSALGLPLLVSRSRKSFLGATVGLPKDLGPASLAAELHAIGN 244
S + + +L L +L ALG P+LV SRKS +G + +P + ++A +

Sbjct 196 SLS--ENYEILRRLPEL-
VALGFPVLVGTSRKSMIGKLLDVPASERLAGTVATSVLGYTA 252

Query 245 GADYVRTH 252

GA R H

Sbjct 253 GAHIFRVH 260

>WP_057081671.1 dihydropteroate synthase [Bifidobacterium bifidum]
CUN14007.1 dihydropteroate synthase [Bifidobacterium bifidum]
Length=290

Score = 119 bits (297), Expect = 2e-30, Method: Compositional
matrix adjust.

Identities = 90/280 (32%), Positives = 140/280 (50%), Gaps = 19/280
(7%)

Query 8

VFGILNLTEDSFFDESRRDPAGAVTAAIEMLRVGSDDVVDVGPAAASHPDARPVSPADEIR 67
+ G+LN+TEDSF D LDP A +ML G+D++D+G ++ P A+ VS

DE+

Sbjct 15

LMGVLNITEDSFSDDGLWLDPGKARDHGDDMLHAGADIIDIGAESTRPGAKRVSEKDELD 74

Query 68 RIAPLLDALSDQMHRVSIDSFQPETQRYALKRGGVGLNDIQGFP-
DPALYPDIAEADCRL 126

R+ AL VSID+ + + AL G +ND+ G D L +A+

DC

Sbjct 75

RVTGAAKALIAHGAVVSIDTTRSVAQAALNEGAQIINDVSGGRLDRDLPHVVADHDCLY 134

Query 127 VVMHSAQRDGIATRTGHLRPE-----

DALDEIVRFFEARVSALRRSGVAADRILIDP 178

+V H R +A G P+ D L ++ ++V A+ ++GVA +R

+I+DP

Sbjct 135 IVQH--

WRGWLKAGSKGGAAPDADTSHYEHDVLKDVYDELMSQVDAVLKAGVAPERVIIDP 192

Query 179 GMGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSRKSFLGAT-----VGLP-
VKDLGP 232

G+GF P E +L +L L K + G P+L+ SRK F+ A +G P +

D

Sbjct 193 GLGFS-KPGIEHNLPLLVGLDLFKRS-

GYPVLIGASRKRFVSAALNDAGIGEPTMDDRDN 250

Query 233 ASLAAELHAIGNGADYVRTHAPGDLRSAITFSETLAKFRS 272
A+ A +GA VR H R+A+T ++++
Sbjct 251 ATAALSALCAEHGAWAVRVHDMRRSRAALTIGSLWRQYQN 290

>WP_086988369.1 dihydropteroate synthase [Trichococcus
flocculiformis]
Length=259

Score = 118 bits (295), Expect = 2e-30, Method: Compositional
matrix adjust.
Identities = 88/249 (35%), Positives = 132/249 (53%), Gaps = 19/249
(8%)

Query 9
FGILNLTEDSFFDESRRDPAGAVTAAIEMLRVGSDDVDVGAASHDPARPVSPADEIRR 68
GILN+T DSF D AV A+EM+ G+D++D+G ++ P +S
+EI R
Sbjct 1
MGILNVTPDSFSDGGEWNTVEKAVAHALEMVADGADIIDIGGESTRPGHTQISDEEEIAR 60

Query 69 IAPLLDALSDQMHR-VSIDSFQPETQRYALKRGGVGLNDIQGF-
PDPALYPDIAEADCRL 126
I P+++AL + +SID+++ R A + GV +NDI G DP + A
D +
Sbjct 61
IVPVIEALKKAVDVPLSIDTYKSAVARAAACEAGVDIINDIWGCRYDPQIAAVAASFVPI 120

Query 127
VVMHSAQRDGIATRTRGHLRPEDALDEIVRFFEARVSALRRSGVAADRLILDPMGMFFLSP 186
++MH+ ++ A ED L ++ VSA GV + +ILDPG GF
Sbjct 121 ILMHNREKPDYA-----FLIEDMLTDLAESVRIAVSA-----
GVKRENIILDPGCGF--GK 169

Query 187 APETSLHVLSNLQKLKSALGLPLLVSRSRKSFLGATVG-LPVK--
DLGPASLAAELHAIG 243
E +L+V+ +L++ + LG PLL+ SRK F+G +G +P K DLG A+ A
I
Sbjct 170 TYEDNLNVVHHLKRF-ADLGYPPLLGTSRKRFIQTALGDIPFKERDLGTAATTA--
LGIV 226

Query 244 NGADYVRTH 252
NGA R H
Sbjct 227 NGAQIFRVH 235

>WP_013390177.1 dihydropteroate synthase [Bifidobacterium bifidum]
YP_003971513.1 dihydropteroate synthase [Bifidobacterium bifidum
PRL2010]
ADP36476.1 FolP Dihydropteroate synthase [Bifidobacterium bifidum
PRL2010]
KLN79105.1 FolP Dihydropteroate synthase [Bifidobacterium bifidum]
KLN82217.1 FolP dihydropteroate synthase [Bifidobacterium bifidum]
Length=290

Score = 119 bits (297), Expect = 2e-30, Method: Compositional matrix adjust.
Identities = 90/280 (32%), Positives = 140/280 (50%), Gaps = 19/280 (7%)

Query 8
VFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSVDVVGPAASHDPARPVSPADEIR 67
+ G+LN+TEDSF D LDP A +ML G+D++D+G ++ P A+ VS
DE+
Sbjct 15
LMGVLNITEDSFSDDGGLWLDPGKARDHGDDMLHAGADIIDIGAESTRPGAKRVSEKDELD 74

Query 68 RIAPLLDALSDQMHRVSIDSFQPETQRYALKRGVGYLNDIQGFP-
DPALYPDIAEADCRL 126
R+ AL VSID+ + + AL G +ND+ G D L +A+
DC
Sbjct 75
RVTGAALKALIAHGAVVSIDTTRSVAQAALNEGAQIINDVSGGRLDRDLPHVVADHDCLY 134

Query 127 VVMHSAQRDGIATRTGHLRPE-----
DALDEIVRFFEARVSALRRSGVAADRLILD 178
+V H R +A G P+ D L ++ ++V A+ ++GVA +R
+I+DP
Sbjct 135 IVQH--
WRGWLAGSKGGAAPDADTSHYEHDVLKDVYDELMSQVDAVLKAGVAPERVIIDP 192

Query 179 GMGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSRKSFLGAT-----VGLP-
VKDLGP 232
G+GF P E +L +L L K + G P+L+ SRK F+ A +G P +
D
Sbjct 193 GLGFS-KPGIEHNLPLLVGLDLFKRS-
GYPVLIGASRKRFSVAALNDAGIGEPTMDDRDN 250

Query 233 ASLAAELHAIGNGADYVRTHAPGDLRSAITFSETLAKFRS 272
A+ A +GA VR H R+A+T ++++
Sbjct 251 ATAALSALCAEHGAWAVRVHDVRRSRAALTIGSLWRQYQN 290

>BBA47465.1 dihydropteroate synthase [Bifidobacterium bifidum LMG 13195]
Length=290

Score = 119 bits (297), Expect = 2e-30, Method: Compositional matrix adjust.
Identities = 90/280 (32%), Positives = 140/280 (50%), Gaps = 19/280 (7%)

Query 8
VFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSVDVVGPAASHDPARPVSPADEIR 67
+ G+LN+TEDSF D LDP A +ML G+D++D+G ++ P A+ VS
DE+
Sbjct 15
LMGVLNITEDSFSDDGGLWLDPGKARDHGDDMLHAGADIIDIGAESTRPGAKRVSEKDELD 74

Query 68 RIAPLLDALSDQMHRVSIDSFQPETQRYALKRGGVGLNDIQGF-
DPALYPDIAEADCRL 126
R+ AL VSID+ + + AL G +ND+ G D L +A+

DC

Sbjct 75
RVTGAAKALIAHGAVVSIDTTRSVAQAALDEGAQIINDVSGRLDRDLPHVVADHDCLY 134

Query 127 VVMHSAQRDGIATRTRGHLRPE-----
DALDEIVRFFEARVSALRRSGVAADRILIDP 178
+V H R +A G P+ D L ++ ++V A+ ++GVA +R

+I+DP

Sbjct 135 IVQH--
WRGWLKAGSKGGAAPDADTSHYEHDVLDKDVYDELMSQVDAVLKAGVAPERI IIDP 192

Query 179 GMGFFLSPAPETSLHVLSNLQKLKLSALGLPLLVSRSRKSFLGAT-----VGLP-
VKDLGP 232
G+GF P E +L +L L K + G P+L+ SRK F+ A +G P +

D

Sbjct 193 GLGFS-KPGIEHNLPLLVLGLDLFKRS-
GYPVLIGASRKRFSVAALNDAGIGEPTMDDRDN 250

Query 233 ASLAAELHAIGNGADYVRTHAPGDLRSITFSETLAKFRS 272
A+ A +GA VR H R+A+T +++++

Sbjct 251 ATAALSALCAEHGAWAVRVHDVRRSRAALTIGSLWRQYQN 290

>WP_083546429.1 MULTISPECIES: dihydropteroate synthase
[Trichococcus]
Length=259

Score = 117 bits (294), Expect = 2e-30, Method: Compositional
matrix adjust.
Identities = 87/249 (35%), Positives = 132/249 (53%), Gaps = 19/249
(8%)

Query 9
FGILNLTEDSFFDESRRDPAGAVTAAIEMLRVGSVDVVGPAASHPDARPVSPADEIRR 68
GILN+T DSF D AV A+EM+ G+D++D+G ++ P +S

+EI R

Sbjct 1
MGILNVTPDSFSDGGEWNTVEKAVAHALEMVADGADIIDIGGESTRPGHTQISDEEEIAR 60

Query 69 IAPLLDALSDQMHR-VSIDSFQPETQRYALKRGGVGLNDIQGF-
PDPALYPDIAEADCRL 126
I P+++AL + +SID+++ R A + G+ +NDI G DP + A

D +

Sbjct 61
IVPVIEALKKAVDVPLSIDTYKSAVARAAACEAGIDIINDIWGCRYDPQIAAVAASFVPI 120

Query 127
VVMHSAQRDGIATRTRGHLRPEDALDEIVRFFEARVSALRRSGVAADRILIDPGMGFFLSP 186
++MH+ ++ A ED L ++ VSA GV + +ILDPG GF

Sbjct 121 ILMHNREKPDYA-----FLIEDMLTDLAESVRIAVSA-----

GVKRENIILDPGCGF--GK 169

Query 187 APETSLHVLSNLQKLKSALGLPLLVSRSKSFGLGATVG-LPVK--
DLGPASLAAELHAIG 243

E +L+V+ +L++ + LG PLL+ SRK F+G +G +P K DLG A+ A

I

Sbjct 170 TYEDNLNVVHHLKRF-ADLGYPLLLGTSRKRFIQTALGDIPFKERDLGTAATTA--
LGIV 226

Query 244 NGADYVRTH 252

NGA R H

Sbjct 227 NGAQIFRVH 235

>WP_013363793.1 dihydropteroate synthase [Bifidobacterium bifidum]
AD053591.1 Dihydropteroate synthase [Bifidobacterium bifidum S17]
CDB21893.1 dihydropteroate synthase [Bifidobacterium bifidum CAG:
234]

ERI83392.1 dihydropteroate synthase [Bifidobacterium bifidum ATCC
29521

= JCM 1255 = DSM 20456]

KFI43765.1 FolP Dihydropteroate synthase [Bifidobacterium bifidum]

BAQ98646.1 dihydropteroate synthase [Bifidobacterium bifidum ATCC
29521

= JCM 1255 = DSM 20456]

KLN76489.1 FolP Dihydropteroate synthase [Bifidobacterium bifidum]

KLN80026.1 FolP Dihydropteroate synthase [Bifidobacterium bifidum]

KLN84260.1 FolP Dihydropteroate synthase [Bifidobacterium bifidum]

KLN88624.1 FolP Dihydropteroate synthase [Bifidobacterium bifidum]

KLN90835.1 FolP Dihydropteroate synthase [Bifidobacterium bifidum]

KWZ81377.1 dihydropteroate synthase [Bifidobacterium bifidum]

KXS27988.1 dihydropteroate synthase [Bifidobacterium bifidum]

SFB95832.1 Dihydropteroate synthase [Bifidobacterium bifidum]

OKY90249.1 dihydropteroate synthase [Bifidobacterium sp. 56_9_plus]

OQM67463.1 dihydropteroate synthase [Bifidobacterium bifidum]

Length=290

Score = 118 bits (296), Expect = 3e-30, Method: Compositional
matrix adjust.

Identities = 90/280 (32%), Positives = 140/280 (50%), Gaps = 19/280
(7%)

Query 8

VFGILNLTEDSFFDESRRLDPAVATAAIEMLRVGSDDVVDVGPAAASHDPARPVSPADEIR 67

+ G+LN+TEDSF D LDP A +ML G+D++D+G ++ P A+ VS

DE+

Sbjct 15

LMGVLNITEDSFSDDGLWLDPGKARDHGDDMLHAGADIIDIGAESTRPGAKRVSEKDELD 74

Query 68 RIAPLLDALSDQMHRVSIDSFQPETQRYALKRGVGYLNDIQGFP-
DPALYPDIAEADCRL 126

R+ AL VSID+ + + AL G +ND+ G D L +A+

DC

Sbjct 75

RVTGAAKALIAHGAVVSIDTTRSVAQAALDEGAQIINDVSGGRLDRDLPHVVADHDCLY 134

Query 127 VVMHSAQRDGIATRTGHLRPE-----
DALDEIVRFFEARVSALRRSGVAADRLILDLP 178

+V H R +A G P+ D L ++ ++V A+ ++GVA +R
+I+DP

Sbjct 135 IVQH--
WRGWLKAGSKGGAAPDADTSHYEHDVLDKDVYDELMSQVDAVLKAGVAPERVIIDP 192

Query 179 GMGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSRKSFLGAT-----VGLP-
VKDLGP 232

G+GF P E +L +L L K + G P+L+ SRK F+ A +G P +
D

Sbjct 193 GLGFS-KPGIEHNLPLLVGLDLFKRS-
GYPVLIGASRKRFFVSAALNDAGIGEPTMDDRDN 250

Query 233 ASLAAELHAIGNGADYVRTHAPGDLRSAITFSETLAKFRS 272

A+ A +GA VR H R+A+T +++++
Sbjct 251 ATAALSALCAEHGAWAVRVHDVRRSRAALTIGSLWRQYQN 290

>WP_047298337.1 dihydropteroate synthase [Bifidobacterium bifidum]
KLN89647.1 FolP Dihydropteroate synthase [Bifidobacterium bifidum]
Length=290

Score = 118 bits (295), Expect = 4e-30, Method: Compositional
matrix adjust.

Identities = 90/280 (32%), Positives = 140/280 (50%), Gaps = 19/280
(7%)

Query 8
VFGILNLTEDSFFDESRRDPAGAVTAAIEMLRVGSVDVVGPAASHDPARPVSPADEIR 67

+ G+LN+TEDSF D LDP A +ML G+D++D+G ++ P A+ VS
DE+

Sbjct 15
LMGVLNITEDSFSDDGLWLDPGKARDHGDDMLHAGADIIDIGAESTRPGAKRVSEKDELD 74

Query 68 RIAPLLDALSDQMHRVSIDSFQPETQRYALKRGVGYLNDIQGFP-
DPALYPDIAEADCRL 126

R+ AL VSID+ + + AL G +ND+ G D L +A+
DC

Sbjct 75
RVTGAAKALIAYGAVVSIDTTRSVAQAALDEGAQIINDVSGGRLDRDLPHVVADHDCLY 134

Query 127 VVMHSAQRDGIATRTGHLRPE-----
DALDEIVRFFEARVSALRRSGVAADRLILDLP 178

+V H R +A G P+ D L ++ ++V A+ ++GVA +R
+I+DP

Sbjct 135 IVQH--
WRGWLKAGSKGGAAPDADTSHYEHDVLDKDVYDELMSQVDAVLKAGVAPERIIDP 192

Query 179 GMGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSRKSFLGAT-----VGLP-
VKDLGP 232

G+GF P E +L +L L K + G P+L+ SRK F+ A +G P +

D

Sbjct 193 GLGFS-KPGIEHNLPLLVGLDLFKRS-
GYPVLIGASRKRFVSAALNDAGIGEPTMDDRDN 250

Query 233 ASLAAELHAIGNGADYVRTHAPGDLRSAITFSETLAKFRS 272
A+ A +GA VR H R+A+T ++++
Sbjct 251 ATAALSALCAEHGAWAVRVHDVRRSRAALTIGSLWRQYQN 290

>WP_026394512.1 dihydropteroate synthase [Acetobacterium
dehalogenans]
Length=275

Score = 117 bits (294), Expect = 4e-30, Method: Compositional
matrix adjust.
Identities = 77/253 (30%), Positives = 133/253 (53%), Gaps = 14/253
(6%)

Query 2
LRSRVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSVDVVGPAASHDPARPVS 61
L +++ + GILN+T DSF D + + ++ +M+ G+D++D+G ++ P

+S

Sbjct 10
LTNQILIMGILNVTPDSFSDGGKFNNLDASLKQVEKMIADGADLIDLGGESTRPGHTQIS 69

Query 62 PADEIRRIAPLLDALSDQMHR-VSIDSFQPETQRYALKRGVGYLNDIQGFP-
DPALYPDI 119
+EI RI P++ A+ + +SID+++ AL+ G +NDI GF DP L

Sbjct 70
DEEEIDRIVPMITAIQKRFDIPISIDTYKGPVGAALQAGADMVNDIWFKYDPTLADVT 129

Query 120
AEADCRLVMHSAQRDGIATRTGHLRPEDALDEIVRFFEARVSALRRSGVAADRILIDPG 179
A V+MH+ HL + +I+ + + ++G++ D
+ILDPG

Sbjct 130 ARYQVPCVLMHNRNNQNYC----HL-----
ITDIISDLQESIDIALQAGISRDAIILDPG 180

Query 180
MGFFLSPAPETSLHVLSNLQKLKLSALGLPLLVSRSRKSFLGATVGLPVKDLGPASLAAEL 239
+GF A ++ + +L+ L+S LG PLL+ SRK F+G T+ LPV + +
+A +

Sbjct 181 IGFADYA--QNMETMHHLEALQS-
LGYPLLLGTSRKGFIGLTLDPVTERVEGTVATTV 237

Query 240 HAIGNGADYVRTH 252
I GA +R H

Sbjct 238 IGIMKGASIIRVH 250

>WP_034876901.1 dihydropteroate synthase [Bifidobacterium
moukalabense]
ETY70958.1 dihydropteroate synthase [Bifidobacterium moukalabense
DSM 27321]

Length=291

Score = 117 bits (294), Expect = 6e-30, Method: Compositional matrix adjust.

Identities = 87/278 (31%), Positives = 138/278 (50%), Gaps = 19/278 (7%)

Query 8

VFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSVDVVDVGPAAASHPDARPVSPADEIR 67
V G+LN+TEDSF D LPA A M+R G+D++D+G ++ P A+ VS

DE

Sbjct 16

VMGVNLTEDSFSDDGGLWLDPARAKAHGEAMMRQGADIIDIGAESTRPGAKRVSEEDERS 75

Query 68 RIAPLLDALSDQMHRVSIDSFQPETQRYALKRGVGYLNDIQGFDPALYPDI--
AEADCR 125 R+ +DAL + +SID+ + AL G +ND+ G A P + A

++C

Sbjct 76

RVLGAVDALIPEGAVLSIDTTRASVALAALDHGAQIINDVSGGRLDAELPHVVAHSECL 135

Query 126 LVVMHSAQRDGIATRTRGHLRPEDA-----

LDEIVRFFEARVSALRRSGVAADRLILD 178
+V H R +A G + D L+++ A+V A+ +GV ++

+I+DP

Sbjct 136 YIVQH--

WRGWLGAAGTVPDADTSVYANGVLNDVYDELMAQVDAVLAAGVGPEQVIIDP 193

Query 179 GMGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSRKSFLGATVGLP-----
VKDLGP 232 G+GF P E +L +L+ L++ +A G P+L+ SRK F+GA + +

D

Sbjct 194 GLGFS-KPGIEHNLPLLAGLERF-

NATGYPVLIGASRKRFGAMLAAGIDEPTMADKDN 251

Query 233 ASLAAELHAIGNGADYVRTHAPGDLRSAITFSETLAKF 270

A+ A + +GA VR H R A+ +

Sbjct 252 ATAAISALSAEHGAWVRVHDVAKTRDAVAIGSAWRAY 289

>WP_101629030.1 dihydropteroate synthase [Bifidobacterium longum]

PKY77274.1 dihydropteroate synthase [Bifidobacterium longum]

Length=291

Score = 117 bits (294), Expect = 6e-30, Method: Compositional matrix adjust.

Identities = 93/287 (32%), Positives = 141/287 (49%), Gaps = 27/287 (9%)

Query 4

SRVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSVDVVDVGPAAASHPDARPVSPA 63
+ V G+LN+TEDSF D LPA AV +M+ G+D++D+G ++ P A+

VS A

Sbjct 11

THTMVMGVLNITEDSFSDGGLWLDPAKAVQHGRDMMMAAGADIIDIGAESTRPGAKRVSEA 70

Query 64 DEIRRIAPLLDALSDQMHRVSIDSFQPETQRYALKRGGVYLNLDIQQFPDPALYPD-
IAEA 122

DE+ RI + L +SID+ + AL G +ND+ G A P

+A+

Sbjct 71

DELARITGAVKTLIPAGAVLSIDTTRASVAAAALSEGAQIINDVSGGTLDAELPHVVADH 130

Query 123 DCRLVVMH-----

SAQRDGIATRTGHLRPEDALDEIVRFFEARVSALRRSGVAADR 173

DC +V H A D + H D DE++R +V + +GV

+R

Sbjct 131 DCLYIVQHWRGWLVGSKGANPDQDTSVYEHGVLTDVHDELMR----

QVDGVLAAAGVKPER 186

Query 174 LILDPMGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSKSFGLGATV----
GLPVKDL 230

+I+DPG+GF P E +L +L+ L+ + A G P+L+ SRK F+ A + G

D

Sbjct 187 IIIDPGLGFS-KPGIEHNLPLLTGLETFR-

ATGYPLIGQSRKRFISAMLTGTGTAGAD- 243

Query 231 GPA-----SLAAELHAIG--NGADYVRTHAPGDLRSAITFSETLAKF 270

GP + A L A+ +GA VR H R+A+ T ++

Sbjct 244 GPTMAQRDDVTAALSALSAEHGAWAVRVHVDVAKSRAAVIAGNTWREY 290

>WP_010081417.1 dihydropteroate synthase [Bifidobacterium longum]
ACD99296.1 Dihydropteroate synthase [Bifidobacterium longum DJ010A]
KWZ92177.1 dihydropteroate synthase [Bifidobacterium longum]
Length=291

Score = 117 bits (293), Expect = 7e-30, Method: Compositional
matrix adjust.

Identities = 93/287 (32%), Positives = 141/287 (49%), Gaps = 27/287
(9%)

Query 4

SRVTVFGILNLTEDSFDESRRLLDPAGAVTAAIEMLRVGSVDVVDVGPAAASHPDARPVSPA 63

+ V G+LN+TEDSF D LDPA AV +M+ G+D++D+G ++ P A+

VS A

Sbjct 11

THTMVMGVLNITEDSFSDGGLWLDPAKAVQHGRDMMMAAGADIIDIGAESTRPGAKRVSEA 70

Query 64 DEIRRIAPLLDALSDQMHRVSIDSFQPETQRYALKRGGVYLNLDIQQFPDPALYPD-
IAEA 122

DE+ RI + L +SID+ + AL G +ND+ G A P

+A+

Sbjct 71

DELARITGAVKTLIPAGAVLSIDTTRASVAAAALSEGAQIINDVSGGTLDAELPHVVADH 130

Query 123 DCRLVVMH-----

SAQRDGIATRTGHLRPEDALDEIVRFFEARVSALRRSGVAADR 173

DC +V H A D + H D DE++R +V + +GV
+R
Sbjct 131 DCLYIVQHWRGWLVGSKGANPDQDTSVYEHGVLTDVHDELMR-----
QVDGVLAAAGVKPER 186

Query 174 LILDPMGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSKSFGLGATV---
GLPVKDL 230
+I+DPG+GF P E +L +L+ L+ + A G P+L+ SRK F+ A + G

D
Sbjct 187 IIIDPGLGFS-KPGIEHNLPLLTGLETFR-
ATGYPVLIGQSRKRFISAMLTGAGTAGAD- 243

Query 231 GPA-----SLAAELHAIG--NGADYVRTHAPGDLRSAITFSETLAKF 270
GP + A L A+ +GA VR H R+A+ T ++
Sbjct 244 GPTMAQRDDVTAALSALSAEHGAWAVRVHDVAKSRAAVIAGNTWREY 290

>WP_032744530.1 dihydropteroate synthase [Bifidobacterium longum]
KEY29142.1 dihydropteroate synthase [Bifidobacterium longum subsp.
infantis
EK3]
Length=291

Score = 117 bits (293), Expect = 7e-30, Method: Compositional
matrix adjust.
Identities = 94/289 (33%), Positives = 142/289 (49%), Gaps = 31/289
(11%)

Query 4
SRVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSVDVVGPAASHDPARPVSPA 63
SR V G+LN+TEDSF D LPA A +M+ G+D++D+G ++ P A+

V+ A
Sbjct 11
SRTMVMGVLNITEDSFSGGGLWLDPAKAAQHGRDMMMAAGADIIDIGAESTRPGAKRVAEA 70

Query 64 DEIRRIAPLLDALSDQMHRVSIDSFQPETQRYALKRGVGYLNDIQGFDPALYPD-
IAEA 122
DE+ RI + L +SID+ + AL G +ND+ G A P

+A+
Sbjct 71
DELARITGAVKTLIPAGAILSIDTTRASVAAAALSEGQTQIINDVSGGTLDAELPHVVADH 130

Query 123 DCRLVVMHSAQRDGIATRTG-----
HLRPEDALDEIVRFFEARVSALRRSGVAA 171
DC +V H R +A G H D DE++R +V +

+GV
Sbjct 131 DCLYIVQH--WRGWLAGSKGANPDQDTSVYEHGVLTDVHDELMR-----
QVDGVLAAAGVKP 184

Query 172 DRLILDPMGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSKSFGLGATV---
GLPVK 228
+R+I+DPG+GF P E +L +L+ L+ + A G P+L+ SRK F+ A + G

Sbjct 185 ERIIDPGLGFS-KPGIEHNLPLLTGLETFR-
ATGYPVLIGQSRKRFISAMLTEAGAAGA 242

Query 229 DLGPA-----SLAAELHAIG--NGADYVRTHAPGDLRSAITFSETLAKF 270
D GP + A L A+ +GA VR H R+A+ T ++
Sbjct 243 D-GPIMAQRDDVTAALSALSAEHGAWAVRVHVDVAKSRAAVIAGNTWREY 290

>WP_033499260.1 dihydropteroate synthase [Bifidobacterium
adolescentis]
KFI96588.1 dihydropteroate synthase 1 [Bifidobacterium stercoris
JCM 15918]
Length=292

Score = 117 bits (293), Expect = 7e-30, Method: Compositional
matrix adjust.
Identities = 87/283 (31%), Positives = 136/283 (48%), Gaps = 23/283
(8%)

Query 5
RVTVFGILNLTEDSFFDESRRDPAGAVTAAIEMLRVGSVDVVGPAASHPDARPVSPAD 64
R V G+LN+TEDSF D L P A M++ G+D++D+G ++ P A+
VS AD
Sbjct 13
RTLVMGVLNITEDSFS DGGLWLAPEAAKAHGEAMMKAGADIIDIGAESTRPGAKRVSEAD 72

Query 65
EIRRIAPLLDALSDQMHRVSDSFQPETQRYALKRGGVGLNDIQGFPDPALYPDIA--EA 122
E R+ +DAL + +SID+ + AL+ G +ND+ G P +
+
Sbjct 73
EKARVLGAVDALIPEGAVLSIDTTRASVALAALEHGAQIINDVSGGQLDRELPHVVADHS 132

Query 123 DCRLVVMHSAQR-----
DGIATRTGHLRPEDALDEIVRFFFEARVSALRRSGVAADR 173
DC +V H D +R H D DE++R +V A+ +GV
A++
Sbjct 133 DCLYIVQHWRGWLAGAAGNVPDADTSRYEHGVVNDVYDELMR-----
QVDAVLEAGVQAEQ 188

Query 174 LILDPGMGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSRKSFLG----
ATVGLPVKDL 230
+I+DPG+GF P E +L +L+ L + +A G P+L+ SRK F+G A G+
D+
Sbjct 189 VIIDPGLGFS-KPGVEHNLPILAALDRFNAA-
GYPVLIGASRKRFGVGSLLAGAGVTEPDM 246

Query 231 GP---ASLAAELHAIGNGADYVRTHAPGDLRSAITFSETLAKF 270
A+ A +G VR H R A+ ++
Sbjct 247 ASKDNATAAISALCTEHGVWAVRVHVDVAKSRDAVAVGNAWREY 289

>WP_034525832.1 dihydropteroate synthase [Bifidobacterium
stellenboschense]
KFJ01301.1 dihydropteroate synthase [Bifidobacterium
stellenboschense]

Length=294

Score = 117 bits (293), Expect = 8e-30, Method: Compositional matrix adjust.

Identities = 92/283 (33%), Positives = 144/283 (51%), Gaps = 30/283 (11%)

Query 8

VFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSDDVVDVGPAAASHDPARPVSPADEIR 67
V G+LN+TEDSF D LDP A M+ G+D++D+G ++ P A+ VS

DE+R

Sbjct 20

VMGVLNITEDSFSDDGGLWLDPRAAADHGRAMMAAGADIIDIGAESTRPGAKRVSEDELR 79

Query 68 RIAPLLDALSDQMHRVSIDSFQPETQRYALKRGVGYLNDIQGFP-

DPALYPDIAEADCRL 126

RI ++AL +SID+ + AL G +ND+ G D L +A+

DC

Sbjct 80

RITGAVEALIPAGATLSIDTTRASVAAAALDGGAQIINDVSGGTLDELPHVVADHDCLY 139

Query 127 VVMHSAQRDZIA-TRTG-----

HLRPEDALDEIVRFFEARVSALRRSGVAADRLI 175

+V H R +A ++TG H +D DE++R +V A+ +GVA

+R+I

Sbjct 140 IVQH--WRGWLKAGSKTGAPDADTSHYEHGVLQDVHDELMR-----

QVDAVLAAGVAPERII 193

Query 176 LDPGMGFLLSPAPETSLHVLSNLQKLKSALGLPLLVSRSKFLGAT-----
VGLPV 227

+DPG+GF P +L +L+ L + + A G P+L+ SRK F+ A V

+

Sbjct 194 IDPGLGFS-KPGIAHNLPLLGLDRFR-

ATGYPLVLIQSRKRFVTAIILDKAGFTDVTMAA 251

Query 228 KDLGPASLAAELHAIGNGADYVRTHAPGDLRSITFSETLAKF 270

+D A+ +A +GA VR H R+A+ +T ++

Sbjct 252 RDDATAAFSALCAE--HGAWAVRVHDVARSRAAVAVGDTWREY 292

>WP_003808269.1 dihydropteroate synthase [Bifidobacterium adolescentis]

EDN83746.1 dihydropteroate synthase [Bifidobacterium adolescentis L2-32]

CCY19839.1 dihydropteroate synthase [Bifidobacterium adolescentis CAG:119]

AII75842.1 dihydropteroate synthase 1 [Bifidobacterium adolescentis]

KLE28154.1 dihydropteroate synthase [Bifidobacterium adolescentis]

CUN79986.1 dihydropteroate synthase 1 [Bifidobacterium adolescentis]

CUN66354.1 dihydropteroate synthase 1 [Bifidobacterium adolescentis]

OQM57688.1 dihydropteroate synthase [Bifidobacterium adolescentis]

OSG94211.1 dihydropteroate synthase [Bifidobacterium adolescentis]
OSH02390.1 dihydropteroate synthase [Bifidobacterium adolescentis]
OSH04392.1 dihydropteroate synthase [Bifidobacterium adolescentis]
Length=292

Score = 117 bits (292), Expect = 9e-30, Method: Compositional
matrix adjust.
Identities = 87/283 (31%), Positives = 136/283 (48%), Gaps = 23/283
(8%)

Query 5
RVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSDDVVDVGPAAASHPDARPVSPAD 64
R V G+LN+TEDSF D L P A M++ G+D++D+G ++ P A+

VS AD

Sbjct 13
RTLVMGVLNLTEDSFFDSGGLWLAPEAAKAHGEAMMKAGADIIDIGAESTRPGAKRVSEAD 72

Query 65
EIRRIAPLLDALSDQMHRVSIDSFQPETQRYALKRGGVYLNDIQGFDPALYPDIA--EA 122
E R+ +DAL + +SID+ + AL+ G +ND+ G P +

+

Sbjct 73
EKARVLGAVDALIPEGAVLSIDTTRASVALAALEHGAQIINDVSGGQLDRELPHVVADHS 132

Query 123 DCRLVVMHSAQR-----
DGIATRTGHLRPEDALDEIVRFFEARVSALRRSGVAADR 173
DC +V H D +R H D DE++R +V A+ +GV

A++

Sbjct 133 DCLYIVQHWRGWLAGAAGNVPDADTSRYEHGVVNDVYDELMR-----
QVDAVLEAGVQAEQ 188

Query 174 LILDPMGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSKSFGLG---
ATVGLPVKDL 230
+I+DPG+GF P E +L +L+ L + +A G P+L+ SRK F+G A G+

D+

Sbjct 189 VIIDPGLGFS-KPGVEHNLPIAALDRFNAA-
GYPVLIGASRKRFGVGSLLAGAGVTEPDM 246

Query 231 GP---ASLAAELHAIGNGADYVRTHAPGDLRSITFSETLAKF 270
A+ A +G VR H R A+ ++

Sbjct 247 ASKDNATAAISALCAEHGVWAVRVHDVAKSRDAVAVGNWREY 289

>WP_086943467.1 dihydropteroate synthase [Trichococcus pasteurii]
Length=259

Score = 116 bits (290), Expect = 9e-30, Method: Compositional
matrix adjust.
Identities = 87/249 (35%), Positives = 131/249 (53%), Gaps = 19/249
(8%)

Query 9
FGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSDDVVDVGPAAASHPDARPVSPADEIRR 68
GILN+T DSF D AV A+EM+ G+D++D+G ++ P +S

+EI R
Sbjct 1
MGILNVTPDSFSDGGEWNTVEKAVAHALEMVADGADIIDIGGESTRPGHTQISDEEEIAR 60

Query 69 IAPLLDALSDQMR--VSIDSFQPETQRYALKRGGVGLNDIQGFP-
DPALYPDIAEADCRL 126
I P+++A+ + +SID+++ R A + GV +NDI G DP + A
D +

Sbjct 61
IVPVIEAVKKAVDVPLSIDTYKSAVARAAACEAGVDIINDIWGCKYDPEIAAVAAAFDVPI 120

Query 127
VVMHSAQRDGIATRTGHLRPEDALDEIVRFFEARVSALRRSGVAADRLILDPMGMFFLSP 186
++MH+ ++ A ED L ++ VSA GV + +ILDPG GF
Sbjct 121 ILMHNREKPDYA-----FLIEDMLADLAESVRIAVSA-----
GVKRENIILDPGCGF--GK 169

Query 187 APETSLHVLSNLQKLKSALGLPLLVSRSRKSFLGATVG--LPVK--
DLGPASLAAELHAIG 243
E +L+V+ +L++ LG PLL+ SRK F+G +G +P K DLG A+ A
I
Sbjct 170 TYEDNLNVVHHLKRFAD--LGYPLLLGTSRKRFIGTALGDVVPFKGRDLGTAATTA--
LGIV 226

Query 244 NGADYVRTH 252
NGA R H
Sbjct 227 NGAQLFRVH 235

>WP_049705597.1 dihydropteroate synthase [Devosia sp. H5989]
AKR56010.1 Dihydropteroate synthase [Devosia sp. H5989]
Length=287

Score = 117 bits (292), Expect = 1e-29, Method: Compositional
matrix adjust.
Identities = 83/249 (33%), Positives = 129/249 (52%), Gaps = 16/249
(6%)

Query 8
VFGILNLTEDSFFDESRRDPAGAVTAAIEMLRVGSVDVVGPAASHDPARPVSPADEIR 67
V GILN+T DSF D A+ A EM+ G+D++DVG ++ P VS
DE+
Sbjct 27
VMGILNVTPDSFSDGGDFAGVEAALAHAREMVAEGADIIDVGGESTRPGHEEVSQDELD 86

Query 68 RIAPLLDALSDQM--HRVSIDSFQPETQRYALKRGGVGLNDIQGFP-
DPALYPDIAEADC 124
R+ P+++AL D VSID+++ A++ G +ND+ G +P + A
+
Sbjct 87
RVVPVMEALRDAALDTLVSIDTYKALVADQAVQSGAAIINDVYGLQREPEIADVAALHNV 146

Query 125 RLVVMH-
SAQRDGIATRTGHLRPEDALDEIVRFFEARVSALRRSGVAADRLILDPMGMFF 183

GF ++ MH A RD RP +DE++R+FE + ++G+A DRLILDPG
Sbjct 147 PVIAMHWAARDPN-----RP--
LIDEMLRVFERTLEIASKAGIAKDRLILDPGFGF- 196

Query 184
LSPAPETSLHVLSNLQKLKSALGLPLLVSRSRKSFLGATVGLPKDLGPASLAAELHAIG 243
+ + + ++ +L LG P+L+ SRKS +G +G K+ +LA +

A
Sbjct 197 -GKSLQENYRLMQTFGRLE-
LGAPVLIGTSRKS MIGKLLGNEPKERLAGTLATTILAYA 254

Query 244 NGADYVRTH 252
GA R H
Sbjct 255 GGAHIFRVH 263

>WP_042990425.1 dihydropteroate synthase [Bifidobacterium
adolescentis]
KIM01708.1 dihydropteroate synthase [Bifidobacterium adolescentis]
OSG87519.1 dihydropteroate synthase [Bifidobacterium adolescentis]
Length=292

Score = 117 bits (292), Expect = 1e-29, Method: Compositional
matrix adjust.
Identities = 87/283 (31%), Positives = 136/283 (48%), Gaps = 23/283
(8%)

Query 5
RVTVFILNLTEDSFFDESRRDPAGAVTAAIEMLRVGSVDVVGPAASHDPARPVSPAD 64
R V G+LN+TEDSF D L P A M++ G+D++D+G ++ P A+

VS AD
Sbjct 13
RTLVMGVLNITEDSFS DGGLWLAPEAAKAHGEAMKAGADIIDIGAESTRPGAKRVSEAD 72

Query 65
EIRRIAPLLDALSDQMHRVSIDSFQPETQRYALKRGGVYLNDIQGFDPALYPDIA--EA 122
E R+ +DAL + +SID+ + AL+ G +ND+ G P +

+
Sbjct 73
EKARVLGAVDALIPEGAVLSIDTTRASVALAALEHGAQIINDVSGGQLDRELPHVVADHS 132

Query 123 DCRLVVMHSAQR-----
DGIATRTGHLRPEDALDEIVRFFEARVSALRRSGVAADR 173
DC +V H D +R H D DE++R +V A+ +GV

A++
Sbjct 133 DCLYIVQHWRGWLAGAAGDVPDADTSRYEHGVVNDVYDELMR-----
QVDAVLEAGVQAEQ 188

Query 174 LILDPGMGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSRKSFLG---
ATVGLPKDL 230
+I+DPG+GF P E +L +L+ L + +A G P+L+ SRK F+G A G+

D+
Sbjct 189 VIIDPGLGFS-KPGVEHNLPILAALDRFNAA-

GYPVLIGASRKRFVGSLLAGAGVTEPDM 246

Query 231 GP---ASLAAELHAIGNGADYVRTHAPGDLRSITFSETLAKF 270
A+ A +G VR H R A+ ++
Sbjct 247 ASKDNATAAISALCAEHGVAVRVHVDVAKSRDAVAVGNAREY 289

>WP_033523224.1 dihydropteroate synthase [Bifidobacterium merycicum]
KFI71188.1 dihydropteroate synthase [Bifidobacterium merycicum]
SHE69583.1 dihydropteroate synthase [Bifidobacterium merycicum DSM
6492]
Length=290

Score = 117 bits (292), Expect = 1e-29, Method: Compositional
matrix adjust.
Identities = 88/285 (31%), Positives = 140/285 (49%), Gaps = 22/285
(8%)

Query 5
RVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSVDVVGPAASHDPARPVSPAD 64
R V G+LN+TEDSF D LDP A +M+ G+D++D+G ++ P A+
VS AD
Sbjct 12
RTLVMGVLNITEDSFDGGLWLDPGKAAEHGRDMMATGADIIDIGAESTRPGAKRVSEAD 71

Query 65 EIRRIAPLLDALSDQMHRVSIDSFQPETQRYALKRGGVYLNDIQ-
GFPDPALYPDIAEAD 123
E+ RI ++AL + +SID+ + AL+ G +ND+ G D L
+A+ D
Sbjct 72
ELARIKGAVEALIEGAVLSIDTTRSSVAAGALELGAQIINDVSGGMLDKELPHVVADHD 131

Query 124 CRLVVM-----
HSAQRDGIATRTGHLRPEDALDEIVRFFFEARVSALRRSGVAADRL 174
C +V H + D +R H D DE++R +A ++A GV
R+
Sbjct 132 CLYIVQHWRGWLAGSHGSTPDADTSRYEHGVLADVRDELMRQVDAVIAA----
GVDPKRI 187

Query 175 ILDPGMGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSRKSFLGATVG-----
LPVK 228
I+DPG+GF P E +L +L+ L + G P+L+ SRK F+ A +
+ +
Sbjct 188 IIDPGLGFS-KPGVEHNLPLLGLDAF-
TGTGYPVLIGQSRKRFVSALLADAGFDRIDMD 245

Query 229 DLGPASLAAELHAIGNGADYVRTHAPGDLRSITFSETLAKFRSR 273
+ A+ A + +GA VR H R+A+ + + R
Sbjct 246 ERDNATAAISALSAEHGAWAVRVHVDVARAARAVAVGDARDYAKR 290

>WP_041777256.1 dihydropteroate synthase [Bifidobacterium
adolescentis]
OSG98699.1 dihydropteroate synthase [Bifidobacterium adolescentis]

Length=292

Score = 116 bits (291), Expect = 2e-29, Method: Compositional matrix adjust.

Identities = 87/283 (31%), Positives = 136/283 (48%), Gaps = 23/283 (8%)

Query 5
RVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSVDVVGPAASHPDARPVSPAD 64
R V G+LN+TEDSF D L P A M++ G+D++D+G ++ P A+

VS AD

Sbjct 13
RTLVMGVLNITEDSFSDDGGLWLAPEAAKAHGEAMMKAGADIIDIGAESTRPGAKRVSEAD 72

Query 65
EIRRIAPLLDALSDQMHRVSIDSFQPETQRYALKRGGVYLNDIQGFPDPALYPDIA--EA 122
E R+ +DAL + +SID+ + AL+ G +ND+ G P +

+

Sbjct 73
EKARVLGAVDALIPEGAVLSIDTTRASVALAALEHGAQIINDVSGGQLDRELPHVVADHS 132

Query 123 DCRLVVMHSAQR-----
DGIATRTGHLRPEDALDEIVRFFEARVSALRRSGVAADR 173
DC +V H D +R H D DE++R +V A+ +GV

A++

Sbjct 133 DCLYIVQHWRGWLAGAAGNVPDADTSRYEHGVVNDVYDELMR-----
QVDAVLEAGVQAEQ 188

Query 174 LILDPMGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSKSFGLG----
ATVGLPVKDL 230
+I+DPG+GF P E +L +L+ L + +A G P+L+ SRK F+G A G+

D+

Sbjct 189 VIIDPGLGFS-KPGVEHNLPIAALDRF-
NATGYPVLIGASRKRFVGSLLAGAGVTEPDM 246

Query 231 GP---ASLAAELHAIGNGADYVRTHAPGDLRSITFSETLAKF 270
A+ A +G VR H R A+ ++

Sbjct 247 ASKDNATAAISALCAEHGVWAVRVHDVAKSRDAVAVGNAWREY 289

>WP_065506906.1 dihydropteroate synthase [Bifidobacterium breve]
Length=291

Score = 116 bits (291), Expect = 2e-29, Method: Compositional matrix adjust.

Identities = 93/288 (32%), Positives = 141/288 (49%), Gaps = 29/288 (10%)

Query 4
SRVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSVDVVGPAASHPDARPVSPA 63
S V G+LN+TEDSF D LDPA A +M+ G+D++D+G ++ P A+

VS

Sbjct 11
SHTMVMGVLNITEDSFSDDGGLWLDPAKAAQHGRDMMMAAGADIIDIGAESTRPGAKRVSEE 70

Query 64 DEIRRIAPLLDALSDQMHRVSIDSFQPETQRYALKRGGVGLNDIQGFDPALYPD-
IAEA 122

DE+ RI ++AL +SID+ + AL G +ND+ G A P

IA+

Sbjct 71

DELARITGAVNALIPAGAVLSIDTTRASVAAAALDGGAQIINDVSGGTL DANLPHVIADH 130

Query 123 DCRLVVMHSAQRDGIATRTG-----

HLRPEDALDEIVRFFEARVSALRRSGVAA 171

DC +V H R +A G H D DE++R +V +

+GV

Sbjct 131 DCLYIVQH--WRGWLKAGSKGANPDQDTSVYEHGVLTDVHDELMR----

QVDGVLAAAGVKP 184

Query 172 DRLILDPMGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSRKSFLGA--

TVGLPVKD 229

+R+I+DPG+GF P+ E +L +L+ L+ + G P+L+ SRK F+ A T

V +

Sbjct 185 ERIIIDPGLGFS-KPSIEHNLPLLTGLETFRGT-

GYPVLIGQSRKRFISAMLTEAGAVGE 242

Query 230 LGPA-----SLAAELHAIG--NGADYVRTHAPGDLRSAITFSETLAKF 270

GP + A L A+ +GA VR H +A+ T ++

Sbjct 243 DGPTMAQRDDVTAALSALSAEHGAWAVRVHDVAKSHAAVIAGNTWRQY 290

>WP_032746349.1 dihydropteroate synthase [Bifidobacterium longum]
KEY21526.1 dihydropteroate synthase [Bifidobacterium longum subsp.
longum
17-1B]
Length=291

Score = 116 bits (290), Expect = 2e-29, Method: Compositional
matrix adjust.

Identities = 89/286 (31%), Positives = 137/286 (48%), Gaps = 25/286
(9%)

Query 4

SRVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSDDVVDVGPAAASHDPARPVSPA 63

+ V G+LN+TEDSF D LDPA A +M+ G+D++D+G ++ P A+

VS A

Sbjct 11

THTMVMGVLNITEDSFSDDGGLWLDPAKAAQHGRDMMMAAGADIIDIGAESTRPGAKRVSEA 70

Query 64 DEIRRIAPLLDALSDQMHRVSIDSFQPETQRYALKRGGVGLNDIQGFDPALYPD-
IAEA 122

DE+ RI + L +SID+ + AL G +ND+ G A P

+A+

Sbjct 71

DELARITGAVKTLIPAGAVLSIDTTRASVAAAALSEGAQIINDVSGGTLDAELPHVVADH 130

Query 123 DCRLVVMH-----

SAQRDGIATRTGHLRPEDALDEIVRFFEARVSALRRSGVAADR 173

DC VV H A D + H D DE++R +V + +GV
+R
Sbjct 131 DCLYVVQHWRGWLVGSKGANPDQDTSVYEHGVLTDVHDELMR-----
QVDGVLAAAGVKPER 186

Query 174
LILDPMGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSRKSFLGATV-----G 224
+I+DPG+GF P E +L +L+ L+ + A G P+L+ SRK F+ A +
G
Sbjct 187 IIIDPGLGFS-KPGIEHNLPLLTGLETFR-
ATGYPLVLIQSRKRFISAMLTGAGTAGADG 244

Query 225 LPVKDLGPASLAAELHAIGNGADYVRTHAPGDLRSITFSETLAKF 270
L + + A + +GA VR H R+A+ T ++
Sbjct 245 LTMAQRDDVTAALSALSAEHGAWAVRVHDVAKSRAAVIAGNTWREY 290

>WP_053825171.1 dihydropteroate synthase [Bifidobacterium bifidum]
ALE11915.1 Dihydropteroate synthase [Bifidobacterium bifidum]
Length=290

Score = 116 bits (290), Expect = 2e-29, Method: Compositional
matrix adjust.
Identities = 89/280 (32%), Positives = 139/280 (50%), Gaps = 19/280
(7%)

Query 8
VFGILNLTEDSFFDESRRDPAGAVTAAIEMLRVGSDDVVDVGPAAASHPDARPVSPADEIR 67
+ G+LN+TEDS D LDP A +ML G+D++D+G ++ P A+ VS
DE+
Sbjct 15
LMGVLNITEDSVSDGGLWLDPGKARDHGDDMLHAGADIIDIGAESTRPGAKRVSEKDELD 74

Query 68 RIAPLLDALSDQMHRVSIDSFQPETQRYALKRGGYLNDIQGFP-
DPALYPDIAEADCRL 126
R+ AL VSID+ + + AL G +ND+ G D L +A+
DC
Sbjct 75
RVTGAALKALIAHGAVVSIDTTRSVAQAALDEGAQIINDVSGGRLDRDLPHVVADHDCLY 134

Query 127 VVMHSAQRDGIATRGTGHLRPE-----
DALDEIVRFFEARVSALRRSGVAADRILIDP 178
+V H R +A G P+ D L ++ ++V A+ ++GVA +R
+I+DP
Sbjct 135 IVQH--
WRGWLKAGSKGGAAPDADTSHYEHDVLDKDVYDELMSQVDAVLKAGVAPERIIIDP 192

Query 179 GMGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSRKSFLGAT-----VGLP-
VKDLGP 232
G+GF P E +L +L L K + G P+L+ SRK F+ A +G P +
D
Sbjct 193 GLGFS-KPGIEHNLPLLVGLDLFKRS-
GYPVLIGASRKRFSVAALNDAGIGEPTMDDRDN 250

Query 233 ASLAAELHAIGNGADYVRTHAPGDLRSAITFSETLAKFRS 272
A+ A +GA VR H R+A+T +++++
Sbjct 251 ATAALSALCAEHGAWAVRVHDVRRSRAALTIGSLWRQYQN 290

>WP_055881405.1 dihydropteroate synthase [Devosia sp. Root105]
KQU96312.1 dihydropteroate synthase [Devosia sp. Root105]
Length=281

Score = 115 bits (289), Expect = 2e-29, Method: Compositional
matrix adjust.
Identities = 83/248 (33%), Positives = 131/248 (53%), Gaps = 14/248
(6%)

Query 8
VFGILNLTEDSFFDESRRDPAGAVTAAIEMLRVGSDDVVDVGPAAASHPDARPVSPADEIR 67
+ GILN+T DSF D R A+ A ML G+D++D+G ++ P A VS
ADE+
Sbjct 24
LMGILNVTPDSFSDGGRFDAAPAALAQARLMLAEGADIIDIGGESTRPGAEVSVADELT 83

Query 68 RIAPLLDAL-SDQMHR-VSIDSFQPETQRYALKRGVGYLNDIQGFP-
DPALYPDIAEADC 124
R+ P++ AL +D + +SID+++ E A+ G +ND+ G +P +
AE
Sbjct 84
RVLVPVIAALRADGITAPISIDTYKAEVAEQAIAAGATIINDVHGLQREPEVAAVAAEHGT 143

Query 125
RLVVMHSAQRDGIATRTGHLRPEDALDEIVRFFEARVSALRRSGVAADRILDPGMGFFL 184
LVVMH + A TG D + E+ R+F+ + ++GV DR++LDPG
GF
Sbjct 144 PLVVMHWDK----ARDTGR----
DVMAEMARYFDVTLDIADKAGVTRDRIVLDPGFGF-- 193

Query 185
SPAPETSLHVLSNLQKLKSALGLPLLVSRSRKSFLGATVGLPVKDLGPASLAAELHAIGN 244
+ + + +L L +L A+G P+LV SRKS +G + +P + ++A +
Sbjct 194 AKSLSENYEILRRLPEL-
VAMGFPVLVGTSRKSMIGKLLDMPANERLAGTIATSVLGYTA 252

Query 245 GADYVRTH 252
GA R H
Sbjct 253 GAHIFRVH 260

>WP_007053863.1 dihydropteroate synthase [Bifidobacterium longum]
EEI80776.1 dihydropteroate synthase [Bifidobacterium longum subsp.
longum
ATCC 55813]
BAJ67244.1 dihydropteroate synthase [Bifidobacterium longum subsp.
longum
JCM 1217]
EPE38573.1 Dihydropteroate synthase [Bifidobacterium longum D2957]

KFI62537.1 dihydropteroate synthase 1 [Bifidobacterium longum subsp. longum]
 AIW44191.1 dihydropteroate synthase [Bifidobacterium longum subsp. longum
 GT15]
 KHD95645.1 dihydropteroate synthase [Bifidobacterium longum subsp. longum]
 AL075193.1 dihydropteroate synthase [Bifidobacterium longum subsp. longum]
 KSA08440.1 dihydropteroate synthase [Bifidobacterium longum subsp. longum]
 KSA09168.1 dihydropteroate synthase [Bifidobacterium longum subsp. longum]
 A0L10901.1 dihydropteroate synthase [Bifidobacterium longum]
 SEB29401.1 Dihydropteroate synthase [Bifidobacterium longum]
 OJS82496.1 dihydropteroate synthase [Bifidobacterium longum subsp. longum]
 PKC83753.1 Dihydropteroate synthase [Bifidobacterium longum]
 PKD09814.1 Dihydropteroate synthase [Bifidobacterium longum]
 Length=291

Score = 116 bits (290), Expect = 2e-29, Method: Compositional matrix adjust.
 Identities = 93/287 (32%), Positives = 140/287 (49%), Gaps = 27/287 (9%)

Query 4
 SRVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSVDVVGPAASHDPARPVSPA 63
 + V G+LN+TEDSF D LPA A +M+ G+D++D+G ++ P A+

VS A
 Sbjct 11
 THTMVMGVLNITEDSFSDDGGLWLDPAKAAQHGRDMMMAAGADIIDIGAESTRPGAKRVSEA 70

Query 64 DEIRRIAPLLDALSDQMHRVSIDSFQPETQRYALKRGGVYLNLDIQQFPDPALYPD-
 IAEA 122
 DE+ RI + L +SID+ + AL G +ND+ G A P
 +A+

Sbjct 71
 DELARITGAVKTLIPAGAVLSIDTTRASVAAAALSEGAQIINDVSGGTLDAELPHVVADH 130

Query 123 DCRLVVMH-----
 SAQRDGIATRTGHLRPEDALDEIVRFFEARVSALRRSGVAADR 173
 DC VV H A D + H D DE++R +V + +GV
 +R

Sbjct 131 DCLYVVQHWRGWLVGSKGANPDQDTSVYEHGVLTDVHDELMR----
 QVDGVLAAAGVKPER 186

Query 174 LILDPMGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSRKSFLGATV---
 GLPVKDL 230
 +I+DPG+GF P E +L +L+ L+ + A G P+L+ SRK F+ A + G
 D

Sbjct 187 IIIDPGLGFS-KPGIEHNLPLLTGLETFR-
 ATGYVLIQSRKRFISAMLTGAGTAGAD- 243

Query 231 GPA-----SLAAELHAIG--NGADYVRTHAPGDLRSITFSETLAKF 270
GP + A L A+ +GA VR H R+A+ T ++
Sbjct 244 GPTMAQRDDVTAALSALSAEHGAWAVRVHVDVAKSRAAVIAGNTWREY 290

>WP_077385559.1 dihydropteroate synthase [Bifidobacterium longum]
Length=291

Score = 116 bits (290), Expect = 2e-29, Method: Compositional
matrix adjust.
Identities = 93/287 (32%), Positives = 140/287 (49%), Gaps = 27/287
(9%)

Query 4
SRVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSVDVVGPAASHDPARPVSPA 63
+ V G+LN+TEDSF D LDPA A +M+ G+D++D+G ++ P A+
VS A
Sbjct 11
THTMVMGVLNITEDSFSDDGGLWLDPAKAAQHGRDMMMAAGADIIDIGAESTRPGAKRVSEA 70

Query 64 DEIRRIAPLLDALSDQMHRVSI DSFQPETQRYALKRGVGYLNDIQGFDPALYPD-
IAEA 122
DE+ RI + L +SID+ + AL G +ND+ G A P
+A+
Sbjct 71
DELARITGAVKTLIPAGAVLSIDTTRASVAAAALSEGAQIINDVSGGTLDAELPHVVADH 130

Query 123 DCRLVVMH-----
SAQRDGIATRTGHLRPEDALDEIVRFFEARVSALRRSGVAADR 173
DC VV H A D + H D DE++R +V + +GV
+R
Sbjct 131 DCLYVVQHWRGWLVGSKGANPDQDTSVYEHGVLTDVHDELMR----
QVDGVLAAGVKPER 186

Query 174 LILDPMGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSKSF LGATV---
GLPVKDL 230
+I+DPG+GF P E +L +L+ L+ + A G P+L+ SRK F+ A + G
D
Sbjct 187 IIIDPGLGFS-KPGIEHNLPLLTGLETFR-
ATGYPLIGQSRKRFISAMLTGAGTAGAD- 243

Query 231 GPA-----SLAAELHAIG--NGADYVRTHAPGDLRSITFSETLAKF 270
GP + A L A+ +GA VR H R+A+ T ++
Sbjct 244 GPTMAQRDDVTAALSALSAEHGAWAVRVHVDVAKSRAAVIAGNTWREY 290

>BAF39192.1 dihydropteroate synthase 1 [Bifidobacterium adolescentis
ATCC
15703]
Length=299

Score = 116 bits (290), Expect = 2e-29, Method: Compositional
matrix adjust.
Identities = 87/283 (31%), Positives = 136/283 (48%), Gaps = 23/283

(8%)

Query 5
RVTVFILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSVDVVGPAASHDPARPVSPAD 64
R V G+LN+TEDSF D L P A M++ G+D++D+G ++ P A+

VS AD
Sbjct 20
RTLVMGVLNITEDSFS DGGLWLAPEAAKAHGEAMMKAGADIIDIGAESTRPGAKRVSEAD 79

Query 65
EIRRIAPLLDALSDQMHRVSI DSFQPETQRYALKRGGVYLNDIQGFDPALYPDIA--EA 122
E R+ +DAL + +SID+ + AL+ G +ND+ G P +

+
Sbjct 80
EKARVLGAVDALIPEGAVLSIDTTRASVALAALEHGAQIINDVSGGQLDRELPHVVADHS 139

Query 123 DCRLVVMHSAQR-----
DGIATRTGHLRPEDALDEIVRFFEARVSALRRSGVAADR 173
DC +V H D +R H D DE++R +V A+ +GV

A++
Sbjct 140 DCLYIVQHWRGWLAGAAGNVPDADTSRYEHGVVNDVYDELMR-----
QVDAVLEAGVQAEQ 195

Query 174 LILDPMGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSKFLG---
ATVGLPVKDL 230
+I+DPG+GF P E +L +L+ L + +A G P+L+ SRK F+G A G+

D+
Sbjct 196 VIIDPGLGFS-KPGVEHNLPILAALDRF-
NATGYPVLIGASRKRFVGSLLAGAGVTEPDM 253

Query 231 GP---ASLAAELHAIGNGADYVRTHAPGDLRSAITFSETLAKF 270
A+ A +G VR H R A+ ++
Sbjct 254 ASKDNATAAISALCAEHGVWAVRVHDVAKSRDAVAVGNWREY 296

>WP_003814775.1 dihydropteroate synthase [Bifidobacterium bifidum]
EFR51108.1 dihydropteroate synthase [Bifidobacterium bifidum NCIMB
41171]
EKE50939.1 dihydropteroate synthase [Bifidobacterium bifidum LMG
13195]
KLN84981.1 FolP Dihydropteroate synthase [Bifidobacterium bifidum
LMG 13195]
KXS26740.1 dihydropteroate synthase [Bifidobacterium bifidum]
KYJ84132.1 dihydropteroate synthase [Bifidobacterium bifidum]
OSP26627.1 dihydropteroate synthase [Bifidobacterium bifidum]
Length=290

Score = 115 bits (289), Expect = 2e-29, Method: Compositional
matrix adjust.
Identities = 89/280 (32%), Positives = 139/280 (50%), Gaps = 19/280
(7%)

Query 8
VFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSVDVVGPAASHDPARPVSPADEIR 67

+ G+LN+TEDSF D LDP A +ML G+D++D+G ++ P A+ VS
DE+
Sbjct 15
LMGVLNITEDSFSDGGLWLDPGKARDHGDDMLHAGADIIDIGAESTRPGAKRVSEKDELD 74

Query 68 RIAPLLDALSDQMHRVSIDSFQPETQRYALKRGGVGLNDIQGFP-
DPALYPDIAEADCRL 126
R+ AL VSID+ + + AL G +ND+ G D L +A+
DC
Sbjct 75
RVTGAALKALIAHGAVVSIDTTRSVAQAALDEGAQIINDVSGGRLDRDLPHVVADHDCLY 134

Query 127 VVMHSAQRDGIATRTGHLRPE-----
DALDEIVRFFEARVSALRRSGVAADRLILD 178
+V H R +A G P+ D L ++ ++V A+ ++ VA +R
+I+DP
Sbjct 135 IVQH--
WRGWLKAGSKGGAAPDADTSHYEHVLDKDVYDELMSQVDAVLKARVAPERIIDP 192

Query 179 GMGFFLSPAPETSLHVLSNLQKLKLSALGLPLLVSRSRKSFLGAT-----VGLP-
VKDLGP 232
G+GF P E +L +L L K + G P+L+ SRK F+ A +G P +
D
Sbjct 193 GLGFS-KPGIEHNLPLLVGLDMFKRS-
GYPVLIGASRKRFVSAALNDAGIGEPTMDDRDN 250

Query 233 ASLAAELHAIGNGADYVRTHAPGDLRSITFSETLAKFRS 272
A+ A +GA VR H R+A+T +++++
Sbjct 251 ATAALSALCAEHGAWAVRVHDVRRSRAALTIGSLWRQYQN 290

>WP_065445269.1 dihydropteroate synthase [Bifidobacterium longum]
Length=291

Score = 115 bits (289), Expect = 3e-29, Method: Compositional
matrix adjust.
Identities = 92/287 (32%), Positives = 140/287 (49%), Gaps = 27/287
(9%)

Query 4
SRVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSDDVVDVGPAAASHDPARPVSPA 63
+ V G+LN+TEDSF D LDPA A +M+ G+D++D+G ++ P A+
VS A
Sbjct 11
THTMVMGVLNITEDSFSDGGLWLDPAKAAQRGRDMMMAAGADIIDIGAESTRPGAKRVSEA 70

Query 64 DEIRRIAPLLDALSDQMHRVSIDSFQPETQRYALKRGGVGLNDIQGFPDPALYPD-
IAEA 122
DE+ RI + L +SID+ + AL G +ND+ G A P
+A+
Sbjct 71
DELARITGAVKTLIPAGAVLSIDTTRASVATAALSEGAQIINDVSGGTLDAELPHVVADH 130

Query 123 DCRLVVMH-----

SAQRDGIATRTGHLRPEDALDEIVRFFEARVSALRRSGVAADR 173
DC +V H A D + H D DE++R +V + +GV
+R
Sbjct 131 DCLYIVQHWRGWLVGSKGANPDQDTSVYEHGVLTDVHDELMR-----
QVDGVLAAGVKPER 186

Query 174 LILDPMGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSKFLGATV----
GLPVKDL 230
+I+DPG+GF P E +L +L+ L+ + A G P+L+ SRK F+ A + G
D
Sbjct 187 IIIDPGLGFS-KPGIEHNLPLLTGLETFR-
ATGYPVLIGQSRKRFISAMLTGAGTAGAD- 243

Query 231 GPA-----SLAAELHAIG--NGADYVRTHAPGDLRSAITFSETLAKF 270
GP + A L A+ +GA VR H R+A+ T ++
Sbjct 244 GPTMAQRDDVTAALSALSAEHGAWAVRVHDVAKSRAAVIAGNTWREY 290

>WP_065454755.1 dihydropteroate synthase [Bifidobacterium longum]
Length=291

Score = 115 bits (289), Expect = 3e-29, Method: Compositional
matrix adjust.
Identities = 93/287 (32%), Positives = 140/287 (49%), Gaps = 27/287
(9%)

Query 4
SRVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSVDVVGPAASHDPARPVSPA 63
+ V G+LN+TEDSF D LDPA A +M+ G+D++D+G ++ P A+
VS A
Sbjct 11
THTMVMGVLNITEDSFSGGGLWLDPAKAAQHGRDMMMAAGADIIDIGAESTRPGAKRVSEA 70

Query 64 DEIRRIAPLLDALSDQMHRVSIDSFQPETQRYALKRGGYLNDIQGFDPALYPD-
IAEA 122
DE+ RI + L +SID+ + AL G +ND+ G A P
+A+
Sbjct 71
DELARITGAVKTLIPAGAVLSIDTTRASVAAAALSEGAQIVNDVSGGTLDAELPHVVADH 130

Query 123 DCRLVVMH-----
SAQRDGIATRTGHLRPEDALDEIVRFFEARVSALRRSGVAADR 173
DC VV H A D + H D DE++R +V + +GV
+R
Sbjct 131 DCLYVVQHWRGWLVGSKGANPDQDTSVYEHGVLTDVHDELMR-----
QVDGVLAAGVKPER 186

Query 174 LILDPMGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSKFLGATV----
GLPVKDL 230
+I+DPG+GF P E +L +L+ L+ + A G P+L+ SRK F+ A + G
D
Sbjct 187 IIIDPGLGFS-KPGIEHNLPLLTGLETFR-
ATGYPVLIGQSRKRFISAMLTGAGTAGAD- 243

Query 231 GPA-----SLAAELHAIG--NGADYVRTHAPGDLRSITFSETLAKF 270
GP + A L A+ +GA VR H R+A+ T ++
Sbjct 244 GPTMAQRDDVTAALSALSAEHGAWAVRVHVDVAKSRAAVIAGNTWREY 290

>AUD75228.1 Dihydropteroate synthase [Bifidobacterium breve]
AUD87765.1 Dihydropteroate synthase [Bifidobacterium breve]
Length=291

Score = 115 bits (288), Expect = 3e-29, Method: Compositional
matrix adjust.
Identities = 92/288 (32%), Positives = 142/288 (49%), Gaps = 29/288
(10%)

Query 4
SRVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSVDVVGPAASHDPARPVSPA 63
S V G+LN+TEDSF D LDPA A +M+ G+D++D+G ++ P A+
VS
Sbjct 11
SHTMVMGVLNITEDSFSDDGGLWLDPAKAAQHGRDMMMAAGADIIDIGAESTRPGAKRVSEE 70

Query 64 DEIRRIAPLLDALSDQMHRVSIQSFQPETQRYALKRGGVGLNDIQGFPDPALYPD-
IAEA 122 DE+ RI ++AL +SID+ + AL G +ND+ G A P
IA+
Sbjct 71
DELARITGAVNALIPAGAVLSIDTTRASVAAAALDGGAQIINDVSGGTLNANLPHVIADH 130

Query 123 DCRLVVMHSAQRDGIATRTG-----
HLRPEDALDEIVRFFEARVSALRRSGVAA 171
DC +V H R +A G H D DE++R +V +
+GV
Sbjct 131 DCLYIVQH--WRGWLKSGKGANPDQDTSVYEHGVLTDVHDELMR-----
QVDDVLAAGVKP 184

Query 172 DRLILDPMGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSRKSFLGATVGL--
PVKD 229 +R+++DPG+GF P+ E +L +L+ L+ + A G P+L+ SRK F+ A +
+
Sbjct 185 ERIVIDPGLGFS-KPSIEHNLPLLTGLETFR-
ATGYPVLIGQSRKRFISAMLAEGASGE 242

Query 230 LGPA-----SLAAELHAIG--NGADYVRTHAPGDLRSITFSETLAKF 270
GP + A L A+ +GA VR H R+A+ T ++
Sbjct 243 NGPTMDQRDDVTAALSALSAEHGAWAVRVHVDVAKSRAAVITGNTWRQY 290

>WP_100513572.1 dihydropteroate synthase [Bifidobacterium sp. TRI 7]
PJM74691.1 dihydropteroate synthase [Bifidobacterium sp. TRI 7]
Length=293

Score = 115 bits (288), Expect = 3e-29, Method: Compositional
matrix adjust.
Identities = 92/285 (32%), Positives = 138/285 (48%), Gaps = 28/285

(10%)

Query 5
RVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSDDVVDVGPAAASHPDARPVSPAD 64
R V G+LN+TEDSF D LDP A ML G+D+VD+G ++ P A+

VS AD

Sbjct 15
RTLVMGVLNITEDSFFSDGGLWLDPAKAREHGAAMLDAAGADIVDIGAESTRPGAKRVSEAD 74

Query 65 EIRRIAPLLDALSDQMHRVSIDSFQPETQRYALKRGGVGLNDIQGFDPALYPD-
IAEAD 123
E+ R+ AL + +SID+ + AL G +ND+ G A P

+A+ D

Sbjct 75
ELARVTGATKALLEHGAVLSIDTTRASVAAAALDEGAQIINDVSGGTLDAELPHVVADHD 134

Query 124 CRLVMHSAQRDGIATRTGHLRPE-----
DALDEIVRFFEARVSALRRSGVAA 171
C +V H R +A G P+ D DE++R +V A+

+GV

Sbjct 135 CLYIVQH--WRGWLAGSKG-ATPDADTSVYHGGVLHDVRELMR-----
QVDAVLAAGVKP 187

Query 172
DRLILDPMGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSKFLGATVGL----- 225
+R+I+DPG+GF P E +L +L+ L+ + A G P+L+ SRK F+ A +

Sbjct 188 ERIIIDPGLGFS-KPGIEHNLPLLAGLETFR-
ATGYPVLIQSRKRFVSALLADAGFDEP 245

Query 226 PVKDLGPASLAAELHAIGNGADYVRTHAPGDLRSAITFSETLAKF 270
+ D A+ A +GA VR H R+A+ ++
Sbjct 246 TMDDRDNATAAFSALCAEHGAWAVRVHDVARSRAAVAVGNVWRRY 290

>WP_014760561.1 dihydropteroate synthase [Bifidobacterium bifidum]
AFL05010.1 dihydropteroate synthase [Bifidobacterium bifidum BGN4]
Length=290

Score = 115 bits (288), Expect = 3e-29, Method: Compositional
matrix adjust.

Identities = 89/280 (32%), Positives = 139/280 (50%), Gaps = 19/280
(7%)

Query 8
VFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSDDVVDVGPAAASHPDARPVSPADEIR 67
+ G+LN+TEDS D LDP A +ML G+D++D+G ++ P A+ VS

DE+

Sbjct 15
LMGVLNITEDSSSDGGLWLDPAKARDHGDDMLHAGADIIDIGAESTRPGAKRVSEKDELD 74

Query 68 RIAPLLDALSDQMHRVSIDSFQPETQRYALKRGGVGLNDIQGF-
DPALYPDIAEADCRL 126
R+ AL VSID+ + + AL G +ND+ G D L +A+

DC

Sbjct 75
RVTGAAKALIAHGAVVSIDTTRSVAQAALDEGAQIINDVSGGRLDRDLPHVVADHDCLY 134

Query 127 VVMHSAQRDGIATRTGHLRPE-----
DALDEIVRFFEARVSALRRSGVAADRLLIDP 178
+V H R +A G P+ D L ++ ++V A+ ++GVA +R
+I+DP

Sbjct 135 IVQH--
WRGWLKAGSKGGAEPDADTSHYEHDVLDKDVYDELMSQVDAVLKAGVAPERVIIDP 192

Query 179 GMGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSRKSFLGAT-----VGLP-
VKDLGP 232
G+GF P E +L +L L K + G P+L+ SRK F+ A +G P +
D

Sbjct 193 GLGFS-KPGIEHNLPLLVGLDLFKRS-
GYPVLIGASRKRFSVSAALNVAGIGEPTMDDRDN 250

Query 233 ASLAAELHAIGNGADYVRTHAPGDLRSAITFSETLAKFRS 272
A+ A +GA VR H R+A+T +++++
Sbjct 251 ATAALSALCAEHGAWAVRVHDVRRSRAALTIGSLWRQYQN 290

>WP_039774850.1 dihydropteroate synthase [Bifidobacterium
adolescentis]
AJE05414.1 dihydropteroate synthase 1 [Bifidobacterium
adolescentis]
CUN53000.1 dihydropteroate synthase 1 [Bifidobacterium
adolescentis]
OSG95197.1 dihydropteroate synthase [Bifidobacterium adolescentis]
Length=292

Score = 115 bits (288), Expect = 4e-29, Method: Compositional
matrix adjust.
Identities = 87/283 (31%), Positives = 136/283 (48%), Gaps = 23/283
(8%)

Query 5
RVTVFILNLTEDSFFDESRRDPAGAVTAAIEMLRVGSVDVVGPAASHDPARPVSPAD 64
R V G+LN+TEDSF D L P A M++ G+D++D+G ++ P A+

VS AD
Sbjct 13
RTLVMGVLNITEDSFDGGLWLAPEAAKAHGEAMMKAGADIIDIGAESTRPGAKRVSEAD 72

Query 65
EIRRIAPLLDALSDQMHRVSIDSFQPETQRYALKRGVGYLNDIQGFPDPALYPDIA--EA 122
E R+ +DAL + +SID+ + AL+ G +ND+ G P +
+

Sbjct 73
EKARVLGAVDALIPEGAVLSIDTTRASVALAALHGAQIINDVSGGQLDRELPHVVADHS 132

Query 123 DCRLVVMHSAQR-----
DGIATRTGHLRPEDALDEIVRFFEARVSALRRSGVAADR 173
DC +V H D +R H D DE++R +V A+ +GV
A++

Sbjct 133 DCLYIVQHWRGWLAGAAGNVPDADTSRYEHGVVNDVHDELMR-----
QVDAVLEAGVRAEQ 188

Query 174 LILDPMGMFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSRKSFLG----
ATVGLPVKDL 230
+I+DPG+GF P E +L +L+ L + +A G P+L+ SRK F+G A G+

D+

Sbjct 189 VIIDPGLGFS-KPGVEHNLPIAALDRFNAA-
GYPVLIGASRKRFVGSLLAGAGVTEPDM 246

Query 231 GP---ASLAAELHAIGNGADYVRTHAPGDLRSITFSETLAKF 270
A+ A +G VR H R A+ ++

Sbjct 247 ASKDNATAAISALCAEHGVAVRVHVDVAKSRDAVAVGNAWREY 289

>WP_032736608.1 dihydropteroate synthase [Bifidobacterium longum]
Length=291

Score = 115 bits (288), Expect = 4e-29, Method: Compositional
matrix adjust.

Identities = 94/289 (33%), Positives = 141/289 (49%), Gaps = 31/289
(11%)

Query 4
SRVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSDDVVDVGPAAASHDPARPVSPA 63
SR V G+LN+TEDS D LDPA A +M+ G+D++D+G ++ P A+

VS A

Sbjct 11
SRTMVMGVLNITEDSSSDGGLWLDPAKAAQHGRDMMMAAGADIIDIGAESTRPGAKRVSEA 70

Query 64 DEIRRIAPLLDALSDQMHRVSIDSFQPETQRYALKRGGYLNDIQGFDPALYPD-
IAEA 122

DE+ RI + L +SID+ + AL G +ND+ G A P
+A+

Sbjct 71
DELARITGAVKTLIPAGAILSIDTTRASVAAAALSEGAQIINDVSGGTLDAELPQVVADH 130

Query 123 DCRLVVMHSAQRDGIATRTG-----
HLRPEDALDEIVRFFEARVSALRRSGVAA 171

DC +V H R +A G H D DE++R +V +
+GV

Sbjct 131 DCLYIVQH--WRGWLKAGSKGANPDQDTSVYEHGVLTDVHDELMR-----
QVDGVLAAAGVKP 184

Query 172 DRLILDPMGMFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSRKSFLGATV----
GLPVK 228

+R+I+DPG+GF P E +L +L+ L+ + A G P+L+ SRK F+ A + G

Sbjct 185 ERIIIDPGLGFS-KPGIEHNLPLLTGLETFR-
ATGYVLIGQSRKRFISAMLTEAGAAGA 242

Query 229 DLGPA-----SLAAELHAIG--NGADYVRTHAPGDLRSITFSETLAKF 270
D GP + A L A+ +GA VR H R+A+ T ++

Sbjct 243 D-GPIMAQRDDVTAALSALSALAEHGAVRVHVDVAKSRAAVIAGNTWREY 290

>WP_033892007.1 dihydropteroate synthase [Bifidobacterium saguini]
KFI90997.1 Dihydropteroate synthase [Bifidobacterium saguini DSM
23967]
Length=290

Score = 115 bits (288), Expect = 4e-29, Method: Compositional
matrix adjust.
Identities = 91/286 (32%), Positives = 144/286 (50%), Gaps = 30/286
(10%)

Query 8
VFGILNLTEDSFFDESRRDPAGAVTAAIEMLRVGSVDVVGPAASHDPARPVSPADEIR 67
V G+LN+TEDSF D LPA A +M+ G+D++D+G ++ P A+ VS
DE++
Sbjct 15
VMGVNITEDSFSDDGGLWLDPAKAAQHGRDMMMAAGADIIDIGAESTRPGAKRVSEDELK 74

Query 68 RIAPLLDALSDQMHRVSIDSFQPETQRYALKRGVGYLNDIQGFP-
DPALYPDIAEADCRL 126
RI + AL +SID+ + AL+ G +ND+ G D L +A+
DC
Sbjct 75
RITGAVSALIPAGAVLSIDTTRASVACAALEGGAQIINDVSGGTLDRELPHVVADHDCLY 134

Query 127 VVMHSAQRDGIATRGTG-----
HLRPEDALDEIVRFFEARVSALRRSGVAADRLI 175
+V H R +A G H D DE++R +V + +GV
+R+I
Sbjct 135 IVQH--WRGWLKAGSKGVNPDQDTSVYEHGVLTDVHDELMR-----
QVDDVLAAGVKPERII 188

Query 176
LDPGMGFFLSPAPETSLHVLSNLQKLKLSALGLPLLVSVSRKSFLGATVG-----LPV 227
+DPG+GF P E +L +L+ L+ + A G P+L+ SRK F+ A +
+
Sbjct 189 IDPGLGFS-KPGIEHNLPLLAGLETFR-
ATGYPVLIGQSRKRFISAMLAEDGIDEPTMAQ 246

Query 228 KDLGPASLAAELHAIGNGADYVRTHAPGDLRSAITFSETLAKFRSR 273
+D A+L+A + +GA VR H R+A+ T ++ +R
Sbjct 247 RDDVTAALSAL--SAEHGAWAVRVHDVTKSRAAVIAGNTWRQYSAR 290

>WP_085379343.1 dihydropteroate synthase [Bifidobacterium
adolescentis]
OSG92753.1 dihydropteroate synthase [Bifidobacterium adolescentis]
Length=292

Score = 115 bits (288), Expect = 4e-29, Method: Compositional
matrix adjust.
Identities = 88/285 (31%), Positives = 137/285 (48%), Gaps = 27/285
(9%)

Query 5
RVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSVDVVDVGAASHDPARPVSPAD 64
R V G+LN+TEDSF D L P A M++ G+D++D+G ++ P A+

VS AD

Sbjct 13
RTLVMGVLNITEDSFDGGLWLAPEAAKAHGEAMMKAGADIIDIGAESTRPGAKRVSEAD 72

Query 65
EIRRIAPLLDALSDQMHRVSIIDSFQPETQRYALKRGGVYLNDIQGFPDPALYPDIA--EA 122
E R+ +DAL + +SID+ + AL+ G +ND+ G P +

+

Sbjct 73
EKARVLGAVDALIPEGAVLSIDTTRASVALAALEHGAQIINDVSGGQLDRELPHVVADHS 132

Query 123 DCRLVVMHSAQRDGIATRTG-----
HLRPEDALDEIVRFFEARVSALRRSGVAA 171
DC +V H R +A G H D DE++R +V A+

+GV A

Sbjct 133 DCLYIVQH--WRGWLAGAAGNVPDADTSCYEHGVVNDVHDELMR----
QVDAVLEAGVQA 186

Query 172 DRLILDPMGMFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSRKSFLG----
ATVGLPVK 228
+++I+DPG+GF P E +L +L+ L + +A G P+L+ SRK F+G A G

+

Sbjct 187 EQVIIDPGLGFS-KPGVEHNLPILAALDRFNAA-
GYPVLIGASRKRFGVGSLLAGAGVTEP 244

Query 229 DLGP---ASLAAELHAIGNGADYVRTHAPGDLRSAITFSETLAKF 270
D+ A+ A +G VR H R A+ ++

Sbjct 245 DMASKDNATAAISALCAEHGVWAVRVHDVAKSRDAVAVGNWREY 289

>CZ091691.1 dihydropteroate synthase signature 1 [Trichococcus
palustris]
SFL04062.1 dihydropteroate synthase [Trichococcus palustris]
Length=277

Score = 115 bits (287), Expect = 4e-29, Method: Compositional
matrix adjust.

Identities = 82/254 (32%), Positives = 130/254 (51%), Gaps = 15/254
(6%)

Query 2
LRSRVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSVDVVDVGAASHDPARPVS 61
L R + GILN+T DSF D AV AIEM+R G+D +D+G ++ P

+S

Sbjct 12
LSKRYSIMGILNVTPDSFSDGGEWNTLEAAVAHAIEMVVDGADFIDIGGESTRPGHTQIS 71

Query 62 PADEIRRIAPLLDALSDQMHR-VSIDSFQPETQRYALKRGGVYLNDIQGFP-
DPALYPDI 119
+EI RI P++ A+ + +S+D+++ R A + G+ +NDI G DP +

Sbjct 72

DEEEIARIVPVIKAVKAAVAVPLSVDTYKSAVARAAACEAGIDIINDIWGCKYDPEIAAVA 131

Query 120

AEADCRLVVMHSAQRDGIATRTGHLRPEDALDEIVRFFEARVSALRRSGVAADRLLIDPG 179

AE D +++MH+ + + ED + ++ ++A GV

+ILDPG

Sbjct 132 AEFDVPIILMHNRE-----AADYNFLIEDMIQDLSESMRIALAA-----

GVPRHNIILDPG 182

Query 180 MGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSRKSFLGATVG-

LPVKDLGPASLAAE 238

GF + E +L+V+ +L++ LG PLL++ SRK F+G +G P K+ +

A

Sbjct 183 CGF--AKTFEDNLNVIHHLRRFAD-

LGYPLLLATSRRKFIGTVLGDAPFKERDEGTAATT 239

Query 239 LHAIGNGADYVRTH 252

I NGA R H

Sbjct 240 ALGIMNGAHIFRVH 253

>WP_047290331.1 dihydropteroate synthase [Bifidobacterium bifidum]
KLN88250.1 FolP Dihydropteroate synthase [Bifidobacterium bifidum]
Length=290

Score = 115 bits (287), Expect = 4e-29, Method: Compositional matrix adjust.

Identities = 88/280 (31%), Positives = 138/280 (49%), Gaps = 19/280 (7%)

Query 8

VFGILNLTEDSFFDESRRDPAGAVTAAIEMLRVGSVDVVGPAASHDPARPVSPADEIR 67

+ G+LN+TEDS D LDP A +ML G+D++D+G ++ P A+ VS

DE+

Sbjct 15

LMGVLNITEDSVSDGGLWLDPGKARDHGDDMLHAGADIIDIGAESTRPGAKRVSEKDELD 74

Query 68 RIAPLLDALSDQMHRVSIDSFQPETQRYALKRGVGYLNDIQGFPDPALYPD-

IAEADCRL 126

R+ AL VSID+ + + AL G +ND+ G P +A+

DC

Sbjct 75

RVTGAAKALIAHGAVVSIDTTRSVAQAALNEGAQIINDVSGGRLGRDLPHVVADHDCLY 134

Query 127 VVMHSAQRDGIATRTGHLRPE-----

DALDEIVRFFEARVSALRRSGVAADRLLIDP 178

+V H R +A G P+ D L ++ ++V A+ ++GVA +R

+I+DP

Sbjct 135 IVQH--

WRGWLKAGSKGGGEPDADTSHYEHDVLDKDVYDELMSQVDAVLKAGVAPERVIIDP 192

Query 179 GMGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSRKSFLGAT-----VGLP-

VKDLGP 232

G+GF P E +L +L L K + G P+L+ SRK F+ A +G P +

D
Sbjct 193 GLGFS-KPGIEHNLPLLVGLDLFKRS-
GYPVLIGASRKRFVSAALNDAGIGEPTMDDRDN 250

Query 233 ASLAAELHAIGNGADYVRTHAPGDLRSAITFSETLAKFRS 272
A+ A +GA VR H R+A+T ++++
Sbjct 251 ATAALSALCAEHGAWAVRVHDVRRSRAALTIGSLWRQYQN 290

>BBA55689.1 dihydropteroate synthase [Bifidobacterium bifidum]
Length=290

Score = 115 bits (287), Expect = 5e-29, Method: Compositional
matrix adjust.
Identities = 89/280 (32%), Positives = 139/280 (50%), Gaps = 19/280
(7%)

Query 8
VFGILNLTEDSFFDESRRDPAGAVTAAIEMLRVGSDDVVDVGPAAASHDPARPVSPADEIR 67
+ G+LN+TEDS D LDP A +ML G+D++D+G ++ P A+ VS

DE+
Sbjct 15
LMGVLNITEDSSSDGGLWLDPGKARDHGDDMLHAGADIIDIGAESTRPGAKRVSEKDELD 74

Query 68 RIAPLLDALSDQMHRVSIDSFQPETQRYALKRGGVGLNDIQGFP-
DPALYPDIAEADCRL 126
R+ AL VSID+ + + AL G +ND+ G D L +A+

DC
Sbjct 75
RVTGAAKALIAHGAVVSIDTTRSVAQAALDEGAQIINDVSGGRLDRDLPHVVADHDCLY 134

Query 127 VVMHSAQRDGIATRTGHLRPE-----
DALDEIVRFFEARVSALRRSGVAADRLILDLP 178
+V H R +A G P+ D L ++ ++V A+ ++GVA +R
+I+DP

Sbjct 135 IVQH--
WRGWLKAGSKGGAAPDADTSHYEHDVLDKDYDELMSQVDAVLKAGVAPERVIIDP 192

Query 179 GMGFFLSPAPETSLHVLSNLQKLKLSALGLPLLVSRSRKSFLGAT-----VGLP-
VKDLGP 232
G+GF P E +L +L L K + G P+L+ SRK F+ A +G P +

D
Sbjct 193 GLGFS-KPGIEHNLPLLVGLDLFKRS-
GYPVLIGASRKRFVSAALNDAGIGEPTMDDRDN 250

Query 233 ASLAAELHAIGNGADYVRTHAPGDLRSAITFSETLAKFRS 272
A+ A +GA VR H R+A+T ++++
Sbjct 251 ATAALSALCAEHGAWAVRVHDVRRSRAALTIGSLWRQYQN 290

>KXS22994.1 dihydropteroate synthase [Bifidobacterium breve]
Length=291

Score = 115 bits (287), Expect = 5e-29, Method: Compositional

matrix adjust.

Identities = 91/288 (32%), Positives = 142/288 (49%), Gaps = 29/288 (10%)

Query 4

SRVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSVDVVDVGAASHPDARPVSPA 63
S V G+LN+TEDSF D LPA A +M+ G+D++D+G ++ P A+

VS

Sbjct 11

SHTMVMGVLNITEDSFSGGLWLDPAKAAQHGRDMMMAAGADIIDIGAESTRPGAKRVSEE 70

Query 64 DEIRRIAPLLDALSDQMHRVSIDSFQPETQRYALKRGGVYLNDIQGFDPALYPD-
IAEA 122

DE+ RI ++AL +SID+ + AL G +ND+ G A P

+A+

Sbjct 71

DELARITGAVNALIPAGAVLSIDTTRASVAAAALDGGAQIINDVSGGTLNANLPHVVADH 130

Query 123 DCRLVVMHSAQRDGIATRTG-----

HLRPEDALDEIVRFFEARVSALRRSGVAA 171

DC +V H R +A G H D DE++R +V +

+GV

Sbjct 131 DCLYIVQH--WRGWLKAGSKGANPDQDTSVYEHGVLTDVHDELMR----

QVDDVLAAGVKP 184

Query 172 DRLILDPMGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSRKSFLGATVGL--
PVKD 229

+R+++DPG+GF P+ E +L +L+ L+ + A G P+L+ SRK F+ A +

+

Sbjct 185 ERIVIDPGLGFS-KPSVEHNLPLLTGLETFR-

ATGYPVLIGSRKRFISAMLAEGASGE 242

Query 230 LGPA-----SLAAELHAIG--NGADYVRTHAPGDLRSITFSETLAKF 270
GP + A L A+ +GA VR H R+A+ T ++

Sbjct 243 NGPTMDQRDDVTAALSALSAEHGAWAVRVHVDVAKSRAAVITGNTWRQY 290

>WP_080867818.1 dihydropteroate synthase [Bifidobacterium breve]

0QM65039.1 dihydropteroate synthase [Bifidobacterium breve]

Length=292

Score = 115 bits (287), Expect = 5e-29, Method: Compositional
matrix adjust.

Identities = 93/290 (32%), Positives = 141/290 (49%), Gaps = 29/290 (10%)

Query 4

SRVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSVDVVDVGAASHPDARPVSPA 63
S V G+LN+TEDSF D LPA A +M+ G+D++D+G ++ P A+

VS

Sbjct 11

SHTMVMGVLNITEDSFSGGLWLDPAKAAQHGRDMMMAAGADIIDIGAESTRPGAKRVSEE 70

Query 64 DEIRRIAPLLDALSDQMHRVSIDSFQPETQRYALKRGGVYLNDIQGFDPALYPD-

IAEA 122 DE+ RI ++AL +SID+ + AL G +ND+ G A P

IA+
Sbjct 71
DELARITGAVNALIPAGAVLSIDTTRASVAAAALDGGAQIINDVSGGTLDANLPHVIADH 130

Query 123 DCRLVVMHSAQRDGIATRTG-----
HLRPEDALDEIVRFFEARVSALRRSGVAA 171
DC +V H R +A G H D DE++R +V +

+GV
Sbjct 131 DCLYIVQH--WRGWLKAGSKGAIPDQDTSVYEHGVLTDVHDELMR----
QVDGVLAAAGVKP 184

Query 172 DRLILDPMGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSRKSFLGA--
TVGLPVKD 229
+R+I+DPG+GF P+ E +L +L+ L+ + G P+L+ SRK F+ A T

V +
Sbjct 185 ERIIIDPGLGFS-KPSIEHNLPLLTGLETFRGT-
GYPVLIGQSRKRFISAMLTEAGAVGE 242

Query 230 LGPA-----SLAAELHAIG--NGADYVRTHAPGDLRSAITFSETLAKFRS 272
GP + A L A+ +GA VR H +A+ ++ S
Sbjct 243 DGPTMAQRDDVTAALSALSAEHGAWAVRVHDVAKSHA AVIAGNIWRQYLS 292

>WP_032682980.1 dihydropteroate synthase [Bifidobacterium longum]
KFI73711.1 dihydropteroate synthase [Bifidobacterium longum subsp.
suis]
AL073129.1 dihydropteroate synthase [Bifidobacterium longum subsp.
longum]
SD038494.1 Dihydropteroate synthase [Bifidobacterium longum]
PKD14212.1 Dihydropteroate synthase [Bifidobacterium longum]
Length=291

Score = 115 bits (287), Expect = 5e-29, Method: Compositional
matrix adjust.
Identities = 93/289 (32%), Positives = 141/289 (49%), Gaps = 31/289
(11%)

Query 4
SRVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSDDVVDVGPAAASHDPARPVSPA 63
+ V G+LN+TEDSF D LDPA A +M+ G+D++D+G ++ P A+

VS A
Sbjct 11
THTMVMGVLNITEDSFSDDGGLWLDPAKAAQHGRDMMMAAGADIIDIGAESTRPGAKRVSEA 70

Query 64 DEIRRIAPLLDALSDQMHRVSIDSFQPETQRYALKRGVGYLNDIQGFDPALYPD-
IAEA 122 DE+ RI + L +SID+ + AL G +ND+ G A P

+A+
Sbjct 71
DELVRITGAVKTLIPAGAILSIDTTRASVAAAALSEGAQIINDVSGGTLD AELPHVVADH 130

Query 123 DCRLVVMHSAQRDGIATRTG-----

HLRPEDALDEIVRFFFEARVSALRRSGVAA 171
 DC +V H R +A G H D DE++R +V +
 +GV
 Sbjct 131 DCLYIVQH--WRGWLAGSKGANPDQDTSVYEHGVLTDVHDELMR----
 QVDGVLAAAGVKP 184

Query 172 DRLILDPMGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSRKSFLGATV----
 GLPVK 228
 +R+I+DPG+GF P E +L +L+ L+ + A G P+L+ SRK F+ A + G
 Sbjct 185 ERIIIDPGLGFS-KPGIEHNLPLLTGLETFR-
 ATGYPVLIGQSRKRFISAMLTEAGAAGA 242

Query 229 DLGPA-----SLAAELHAIG--NGADYVRTHAPGDLRSAITFSETLAKF 270
 D GP + A L A+ +GA VR H R+A+ T ++
 Sbjct 243 D-GPIMAQRDDVTAALSALSAEHGAWAVRVHDVAKSRAAVIAGNTWREY 290

>EIJ22047.1 dihydropteroate synthase [Bifidobacterium longum subsp.
 longum
 35B]
 EIJ26900.1 dihydropteroate synthase [Bifidobacterium longum subsp.
 longum
 2-2B]
 Length=296

Score = 115 bits (287), Expect = 5e-29, Method: Compositional
 matrix adjust.
 Identities = 94/289 (33%), Positives = 141/289 (49%), Gaps = 31/289
 (11%)

Query 4
 SRVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSVDVVDVGPAAASHDPARPVSPA 63
 SR V G+LN+TEDS D LPA A +M+ G+D++D+G ++ P A+
 VS A
 Sbjct 16
 SRTMVMGVLNITEDSSSDGGLWLDPAKAAQHGRDMMMAAGADIIDIGAESTRPGAKRVSEA 75

Query 64 DEIRRIAPLLDALSDQMHRVSIDSFQPETQRYALKRGGVYLNLDIQQFPDPALYPD-
 IAEA 122
 DE+ RI + L +SID+ + AL G +ND+ G A P
 +A+
 Sbjct 76
 DELARITGAVKTLIPAGAILSIDTTRASVAAAALSEGAQIINDVSGGTLDAELPQVVADH 135

Query 123 DCRLVVMHSAQRDGIATRTG-----
 HLRPEDALDEIVRFFFEARVSALRRSGVAA 171
 DC +V H R +A G H D DE++R +V +
 +GV
 Sbjct 136 DCLYIVQH--WRGWLAGSKGANPDQDTSVYEHGVLTDVHDELMR----
 QVDGVLAAAGVKP 189

Query 172 DRLILDPMGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSRKSFLGATV----
 GLPVK 228
 +R+I+DPG+GF P E +L +L+ L+ + A G P+L+ SRK F+ A + G

Sbjct 190 ERIIIDPGLGFS-KPGIEHNLPLLTGLETFR-
ATGYVLIGQSRKRFISAMLTEAGAAGA 247

Query 229 DLGPA-----SLAAELHAIG--NGADYVRTHAPGDLRSAITFSETLAKF 270
D GP + A L A+ +GA VR H R+A+ T ++
Sbjct 248 D-GPIMAQRDDVTAALSALSAEHGAWAVRVHDVAKSRAAVIAGNTWREY 295

>WP_026646441.1 dihydropteroate synthase [Bifidobacterium ruminantium]
KFI87656.1 dihydropteroate synthase 1 [Bifidobacterium ruminantium]
Length=292

Score = 115 bits (287), Expect = 6e-29, Method: Compositional matrix adjust.
Identities = 91/286 (32%), Positives = 140/286 (49%), Gaps = 35/286 (12%)

Query 5
RVTVFILNLTEDSFFDESRRDPAGAVTAAIEMLRVGSVDVVGPAASHDPARPVSPAD 64
R V G+LN+TEDSF D LDPA A M++ G+D++D+G ++ P A+ V

AD
Sbjct 13
RTLVMGVLNITEDSFDGGLWLDPAAAKAHGEAMMKDGADIIDIGAESTRPGAKRVGEAD 72

Query 65 EIRRIAPLLDALSDQMHRVSIDSFQPETQRYALKRGGVYLNDIQGF-----
PDPALYPDIA 120
E R+ +DAL+ + +SID+ + AL+ G +ND+ G P +

D A
Sbjct 73
EKTRVLGAVDALAPEGAVLSIDTTRASVASAALEHGAQIINDVSGGQLDRELPHVVADYA 132

Query 121 EADCRLVMHSAQRDGIATRTG-----
HLRPEDALDEIVRFFEARVSALRRSGV 169
E+ +V H R +A G H D DE++R +V A+

+GV
Sbjct 133 ES--LYIVQH--WRGWLAGAAGNVPDADTSVYEHGVVRDVYDELMR-----
QVDAVLAAGV 184

Query 170
AADRLILDPMGMFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSRKSFLGATVG----- 224
A+++I+DPG+GF P E +L +L L + +A G P+L+ SRK F+GA +

Sbjct 185 RAEQIIIDPGLGFS-KPGVEHNLPIKALDRFNAA-
GYPVLIGASRKRFVVGALLADAGVD 242

Query 225 ---LPVKDLGPASLAAELHAIGNADYVRTHAPGDLRSAITFSETL 267
+ KD A+++A +GA VR H R A+

Sbjct 243 EPDMASKDNATAAISALCAE--HGAWAVRVHDVAKSRDAVAVGNAW 286

>WP_019728223.1 dihydropteroate synthase [Bifidobacterium breve]
EWH42066.1 Dihydropteroate synthase [Bifidobacterium breve 2L]
AHJ16152.1 Dihydropteroate synthase [Bifidobacterium breve 12L]
AUE05841.1 Dihydropteroate synthase [Bifidobacterium breve]

AUE21264.1 Dihydropteroate synthase [Bifidobacterium breve]
Length=291

Score = 114 bits (286), Expect = 6e-29, Method: Compositional
matrix adjust.
Identities = 91/288 (32%), Positives = 142/288 (49%), Gaps = 29/288
(10%)

Query 4
SRVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSVDVVDVGPAAASHPDARPVSPA 63
S V G+LN+TEDSF D LPA A +M+ G+D++D+G ++ P A+
VS

Sbjct 11
SHTMVMGVLNITEDSFS DGGLWLDPAKAAQHGRDMMMAAGADIIDIGAESTRPGAKRVSEE 70

Query 64 DEIRRIAPLLDALSDQMHRVSIDSFQPETQRYALKRGGVYLNDIQGFDPALYPD-
IAEA 122
DE+ RI ++AL +SID+ + AL G +ND+ G A P
+A+

Sbjct 71
DELARITGAVNALIPAGAVLSIDTTRASVAAAALDGGAQIINDVSGGTL DANLPHVVADH 130

Query 123 DCRLVVMHSAQRDGIATRTG-----
HLRPEDALDEIVRFFEARVSALRRSGVAA 171
DC +V H R +A G H D DE++R +V +
+GV

Sbjct 131 DCLYIVQH--WRGWLKAGSKGANPDQDTSVYEHGVLTDVHDELMR----
QVDDVLAAGVKP 184

Query 172 DRLILDPMGMFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSRKSFLGATVGL--
PVKD 229
+R+++DPG+GF P+ E +L +L+ L+ + A G P+L+ SRK F+ A +
+

Sbjct 185 ERIVIDPGLGFS-KPSIEHNLPLLTGLETFR-
ATGYVLIGQSRKRFISAMLAEGASGE 242

Query 230 LGPA-----SLAAELHAIG--NGADYVRTHAPGDLRSAITFSETLAKF 270
GP + A L A+ +GA VR H R+A+ T ++
Sbjct 243 NGPTMDQRDDVTAALSALSAEHGAWAVRVHDVAKSRAAVITGNTWRQY 290

>WP_025222047.1 dihydropteroate synthase [Bifidobacterium breve]
AHJ19861.1 Dihydropteroate synthase [Bifidobacterium breve JCM
7019]
KOA67036.1 dihydropteroate synthase [Bifidobacterium breve MCC
1605]
AUD77311.1 Dihydropteroate synthase [Bifidobacterium breve]
AUE03837.1 Dihydropteroate synthase [Bifidobacterium breve]
Length=292

Score = 114 bits (286), Expect = 6e-29, Method: Compositional
matrix adjust.
Identities = 93/290 (32%), Positives = 141/290 (49%), Gaps = 29/290
(10%)

Query 4
SRVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSDDVVDVGPAAASHPDARPVSPA 63
S V G+LN+TEDSF D LDPA A +M+ G+D++D+G ++ P A+

VS
Sbjct 11
SHTMVMGVLNITEDSFSDDGGLWLDPAKAAQHGRDMMMAAGADIIDIGAESTRPGAKRVSEE 70

Query 64 DEIRRIAPLLDALSDQMHRVSDSFQPETQRYALKRGGVYLNDIQGFDPALYPD-
IAEA 122 DE+ RI ++AL +SID+ + AL G +ND+ G A P

IA+
Sbjct 71
DELARITGAVNALIPAGAVLSIDTTRASVAAAALDGGAQIINDVSGGTLNPHVIADH 130

Query 123 DCRLVVMHSAQRDGIATRTG-----
HLRPEDALDEIVRFFEARVSALRRSGVAA 171
DC +V H R +A G H D DE++R +V +

+GV
Sbjct 131 DCLYIVQH--WRGWLKAGSKGANPDQDTSVYEHGVLTDVHDELMR----
QVDGVLAAGVKP 184

Query 172 DRLILDPMGMFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSRKSFLGA--
TVGLPVKD 229
+R+I+DPG+GF P+ E +L +L+ L+ + G P+L+ SRK F+ A T

V +
Sbjct 185 ERIIIDPGLGFS-KPSIEHNLPLLTGLETFRGT-
GYPVLIGQSRKRFISAMLTEAGAVGE 242

Query 230 LGPA-----SLAAELHAIG--NGADYVRTHAPGDLRSITFSETLAKFRS 272
GP + A L A+ +GA VR H +A+ ++ S
Sbjct 243 DGPTMAQRDDVTAALSALSAEHGAWAVRVHDVAKSHA AVIAGNIWRQYLS 292

>WP_055996483.1 dihydropteroate synthase [Devosia sp. Root413D1]
KQW81595.1 dihydropteroate synthase [Devosia sp. Root413D1]
Length=281

Score = 114 bits (286), Expect = 6e-29, Method: Compositional
matrix adjust.
Identities = 87/261 (33%), Positives = 136/261 (52%), Gaps = 14/261
(5%)

Query 8
VFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSDDVVDVGPAAASHPDARPVSPA
+ GILN+T DSF D R A+ A ML G+D++D+G ++ P A VS

ADE+
Sbjct 24
LMGILNVTPDSFSDGGRFDAAPAALAQARMLAEGADIIDIGGESTRPGAEVSVADELT 83

Query 68 RIAPLLDAL-SDQMHR-VSIDSFQPETQRYALKRGGVYLNDIQGF-
DPALYPDIAEADC 124
R+ P++ AL +D + +SID+++ E A+ G +ND+ G +P +

AE

Sbjct 84
RVLPVIAALRADGITAPISIDTYKAEVAEQIAAGATIINDVHGLQREPEVAVAVAEHGT 143

Query 125
RLVVMHSAQRDGIATRTGHLRPEDALDEIVRFFEARVSALRRSGVAADRLILDPMGFLL 184
LVVMH + A TG D + E+ R+F+ + ++GV DR++LDPG

GF
Sbjct 144 PLVVMHWDK----ARDTGR----
DVMAEMARYFDVTLADIADKAGVTRDRIVLDPGFGRFAK 195

Query 185
SPAPETSLHVLNLQKLKLSALGLPLLVSRSRKSFLGATVGLPVKDLGPASLAAELHAIGN 244
S + + +L L +L A+G P+LV SRKS +G + +P + ++A +

Sbjct 196 SLS--ENYEILRRLPEL-
VAMGFPVLVGTSRKSMIGKLLDMPNERLAGTIATSVLGYTA 252

Query 245 GADYVRTHAPGDLRSAITFSE 265
GA R H R A+ +E

Sbjct 253 GAHIFRVHDIRPNRDALRVAE 273

>WP_025301383.1 dihydropteroate synthase [Bifidobacterium breve]
AHJ17932.1 Dihydropteroate synthase [Bifidobacterium breve JCM
7017]
KOA56795.1 dihydropteroate synthase [Bifidobacterium breve MCC
1454]
KOA60024.1 dihydropteroate synthase [Bifidobacterium breve MCC
0305]
AUD81693.1 Dihydropteroate synthase [Bifidobacterium breve]
AUD83619.1 Dihydropteroate synthase [Bifidobacterium breve]
AUD85597.1 Dihydropteroate synthase [Bifidobacterium breve]
P0009024.1 Dihydropteroate synthase [Bifidobacterium breve]
Length=292

Score = 114 bits (286), Expect = 7e-29, Method: Compositional
matrix adjust.
Identities = 93/290 (32%), Positives = 141/290 (49%), Gaps = 29/290
(10%)

Query 4
SRVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSDDVVDVGPAAASHDPARPVSPA 63
S V G+LN+TEDSF D LDPA A +M+ G+D++D+G ++ P A+

VS
Sbjct 11
SHTMVMGVLNITEDSFSDDGGLWLDPAKAAQHGRDMMMAAGADIIDIGAESTRPGAKRVSEE 70

Query 64 DEIRRIAPLLDALSDQMHRVSIDSFQPETQRYALKRGGVGLNDIQGFDPALYPD-
IAEA 122
DE+ RI ++AL +SID+ + AL G +ND+ G A P

IA+
Sbjct 71
DELARITGAVNALIPAGAVLSIDTTRASVAAAALDGGAQIINDVSGGTLNANLPHVIADH 130

Query 123 DCRLVVMHSAQRDGIATRTG-----

HLRPEDALDEIVRFFFEARVSALRRSGVAA 171
DC +V H R +A G H D DE++R +V +
+GV
Sbjct 131 DCLYIVQH--WRGWLAGSKGANPDQDTSVYEHGVLTDVHDELMR-----
QVDGVLAAGVKP 184

Query 172 DRLILDPMGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSRKSFLGA--
TVGLPVKD 229
+R+I+DPG+GF P+ E +L +L+ L+ + G P+L+ SRK F+ A T
V +
Sbjct 185 ERIIIDPGLGFS-KPSIEHNLPLLTGLETFRGT-
GYPVLIGQSRKRFISAMLTEAGAVGE 242

Query 230 LGPA-----SLAAELHAIG--NGADYVRTHAPGDLRSAITFSETLAKFRS 272
GP + A L A+ +GA VR H +A+ ++ S
Sbjct 243 DGPTMAQRDDVTAALSALSAEHGAWAVRVHDVAKSHAAVIAGNIWRQYLS 292

>WP_100510016.1 dihydropteroate synthase [Bifidobacterium sp. TRE 1]
PJM73870.1 dihydropteroate synthase [Bifidobacterium sp. TRE 1]
Length=291

Score = 114 bits (286), Expect = 7e-29, Method: Compositional
matrix adjust.
Identities = 83/232 (36%), Positives = 121/232 (52%), Gaps = 22/232
(9%)

Query 4
SRVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSVDVVGPAASHDPARPVSPA 63
SR V G+LN+TEDSF D LDPA A +M+ G+D++D+G ++ P A+
VS
Sbjct 11
SRTLVMGVLNITEDSFSGGGLWLDPAKARRHGADMMADGADIIDIGAESTRPGAKRVSEE 70

Query 64 DEIRRIAPLLDALSDQMHRV-SIDSFQPETQRYALKRGGVYLNLDIQQGF-
DPALYPDIAE 121
DE+ RI + AL D V SID+ + AL G +ND+ G D L
+A+
Sbjct 71
DELTRITGAVTALIDHPGAVLSIDTTRASVAAAALDEGAQIINDVSGRRLDKELPHVVAD 130

Query 122 ADCRLVVMHSAQRDGIATRTGHLRPE-----
DALDEIVRFFFEARVSALRRSGV 169
DC +V H R +A G P+ D DE++R + ++A
GV
Sbjct 131 HDCLYIVQH--
WRGWLAGSHGGAAPDADTSHYEHGVLNDVRDELMRQVDDVIAA----GV 184

Query 170 AADRLILDPMGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSRKSFLGA
221
+R+++DPG+GF P E +L +L+ L K A G P+L+ SRK F+GA
Sbjct 185 RPERIVIDPGLGFS-KPGIEHNLPLLAGLA AFK-ATGYPVLIGQSRKRFIGA
234

>AUD91812.1 Dihydropteroate synthase [Bifidobacterium breve]
AUE19244.1 Dihydropteroate synthase [Bifidobacterium breve]
Length=291

Score = 114 bits (286), Expect = 9e-29, Method: Compositional
matrix adjust.
Identities = 91/288 (32%), Positives = 142/288 (49%), Gaps = 29/288
(10%)

Query 4
SRVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSVDVVGPAASHDPARPVSPA 63
S V G+LN+TEDSF D LDPA A +M+ G+D++D+G ++ P A+

VS
Sbjct 11
SHTMVMGVLNITEDSFSGGLWLDPAKAAQHGRDMMMAAGADIIDIGAESTRPGAKRVSEE 70

Query 64 DEIRRIAPLLDALSDQMHRVSIDSFQPETQRYALKRGGVYLNLDIQQFPDPALYPD-
IAEA 122
DE+ RI ++AL +SID+ + AL G +ND+ G A P

+A+
Sbjct 71
DELARITGAVNALIPAGAVLSIDTTRASVAAAALDGGAQIINDVSGGTLNANLPHVVADH 130

Query 123 DCRLVMHSAQRDGIATRTG-----
HLRPEDALDEIVRFFEARVSALRRSGVAA 171
DC +V H R +A G H D DE++R +V +

+GV
Sbjct 131 DCLYIVQH--WRGWLKAGSKGANPDQDTSVYEHGVLTDVHDELMR-----
QVDDVLAAGVKP 184

Query 172 DRLILDPMGMFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSRKSFLGATVGL--
PVKD 229
+R+++DPG+GF P+ E +L +L+ L+ + A G P+L+ SRK F+ A +

+
Sbjct 185 ERVVIDPGLGFS-KPSIEHNLPLLTGLETFR-
ATGYPLVIGQSRKRFISAMLAEGASGE 242

Query 230 LGPA-----SLAAELHAIG--NGADYVRTHAPGDLRSAITFSETLAKF 270
GP + A L A+ +GA VR H R+A+ T ++
Sbjct 243 NGPTMDQRDDVTAALSALSAEHGAWAVRVHDVAKSRAAVIAGNTRWQY 290

>WP_085461798.1 dihydropteroate synthase [Bifidobacterium
adolescentis]
OSG90301.1 dihydropteroate synthase [Bifidobacterium adolescentis]
Length=292

Score = 114 bits (286), Expect = 9e-29, Method: Compositional
matrix adjust.
Identities = 86/280 (31%), Positives = 135/280 (48%), Gaps = 23/280
(8%)

Query 8

VFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSVDVVDVGPAAASHPDARPVSPADEIR 67
V G+LN+TEDSF D L P A M++ G+D++D+G ++ P A+ VS

ADE

Sbjct 16

VMGVLNITEDSFSDDGGLWLAPEAAKAHGEAMMKAGADIIDIGAESTRPGAKRVSEADEKA 75

Query 68 RIAPLLDALSDQMHRVSIDSFQPETQRYALKRGVGYLNDIQGFPDPALYPDIA--
EADCR 125

R+ +DAL + +SID+ + AL+ G +ND+ G P +
+DC

Sbjct 76

RVLGAVDALIPEGAVLSIDTTRASVALAALEHGAQIINDVSGGQLDRELPHVVADHSDCL 135

Query 126 LVVMHSAQR-----

DGIATRTGHLRPEDALDEIVRFFEARVSALRRSGVAADRLIL 176

+V H D +R H D DE++R +V A+ +GV A+

++I+

Sbjct 136 YIVQHWRGWLAGAAGNVPDADTSRYEHGVVNDVHDELMR-----

QVDAVLEAGVQAEQVII 191

Query 177 DPGMGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSRKSFLG---

ATVGLPVKDLGP- 232

DPG+GF P E +L +L+ L + +A G P+L+ SRK F+G A G+ D
+

Sbjct 192 DPGLGFS-KPGVEHNLPILAALDRFNAA-

GYPVLIGASRKRFGVGSLLAGAGVTEPDMASK 249

Query 233 --ASLAAELHAIGNGADYVRTHAPGDLRSAITFSETLAKF 270

A+ A +G VR H R A+ ++

Sbjct 250 DNATAAISALCAEHGVWAVRVHDVAKSRDAVAVGNAWREY 289

>WP_065472186.1 dihydropteroate synthase [Bifidobacterium longum]
Length=291

Score = 114 bits (285), Expect = 9e-29, Method: Compositional
matrix adjust.

Identities = 93/289 (32%), Positives = 140/289 (48%), Gaps = 31/289
(11%)

Query 4

SRVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSVDVVDVGPAAASHPDARPVSPA 63

S V G+LN+TEDS D LDPA A +M+ G+D++D+G ++ P A+
VS A

Sbjct 11

SHTMVMGVLNITEDSVSDGGLWLDPAKAAQHGRDMMMAAGADIIDIGAESTRPGAKRVSEA 70

Query 64 DEIRRIAPLLDALSDQMHRVSIDSFQPETQRYALKRGVGYLNDIQGFPDPALYPD-
IAEA 122

DE+ RI + L +SID+ + AL G +ND+ G A P
+A+

Sbjct 71

DELARITGAVKTLISAGAILSIDTTRASVAAAALSEGAQIINDVSGGTLDAELPHVVADH 130

Query 123 DCRLVVMHSAQRDGIATRTG-----
 HLRPEDALDEIVRFFFEARVSALRRSGVAA 171
 DC +V H R +A G H D DE++R +V +
 +GV
 Sbjct 131 DCLYIVQH--WRGWLAGSKGANPDQDTSVYEHGVLTDVHDELMR-----
 QVDGVLAAAGVKP 184

Query 172 DRLILDPMGMFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSRKSFLGATV----
 GLPVK 228
 +R+I+DPG+GF P E +L +L+ L+ + A G P+L+ SRK F+ A + G
 Sbjct 185 ERIIIDPGLGFS-KPGIEHNLPLLTGLETFR-
 ATGYPLVIGSRKRFISAMLTEAGAAGA 242

Query 229 DLGPA-----SLAAELHAIG--NGADYVRTHAPGDLRSAITFSETLAKF 270
 D GP + A L A+ +GA VR H R+A+ T ++
 Sbjct 243 D-GPIMAQRDDVTAALSALSALAEHGAWAVRVHVDVAKSRAAVIAGNTWREY 290

>CZ085951.1 dihydropteroate synthase signature 2 [Trichococcus
 ilyis]
 SEJ69782.1 dihydropteroate synthase [Trichococcus sp. DSM 22150]
 Length=277

Score = 114 bits (284), Expect = 9e-29, Method: Compositional
 matrix adjust.
 Identities = 84/256 (33%), Positives = 133/256 (52%), Gaps = 19/256
 (7%)

Query 2
 LRSRVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSVDVVDVGAASHPDARPVS 61
 L R + GILN T DSF D AV A+EM+ G+D++D+G ++ P
 +S
 Sbjct 12
 LSQRSYIMGILNATPDSFSDGGEWNTAEKAVAHALEMVADGADIIDIGGESTRPGHVQIS 71

Query 62 PADEIRRIAPLLDALSDQMHR-VSIDSFQPETQRYALKRGVGYLNDIQGFP-
 DPALYPDI 119
 +EI R+ P++ A+ + +SID+++ R A + G+ +NDI G DP +
 Sbjct 72
 DEEEIARVVPIIKAVKAAVDVPLSIDTYKSAVARAAACEAGIDIINDIWGCKYDPEIAVVA 131

Query 120
 AEADCRLVVMHSAQRDGIATRTGHLRPEDALDEIVRFFFEARVSALRRSGVAADRLILDPG 179
 A + +++MH+ ++ A ED L+++ +A GV +
 +ILDPG
 Sbjct 132 AAFEVPIILMHNREKADYA-----FLIEDMLEDLAESVRIATAA-----
 GVKRENIILDPG 182

Query 180 MGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSRKSFLGATVG-LPVK--
 DLGPASLA 236
 GF + E +L+V+ L++ + LG PLL+ SRK F+G +G +P K DLG
 A+
 Sbjct 183 CGF--AKTYEDNLNVVHQLKRF-
 ADLGYPLLLGTSRKRFITGALGDIPFKERDLGTAATT 239

Query 237 AELHAIGNGADYVRTH 252
A I NGA R H
Sbjct 240 A--LGIVNGAQLFRVH 253

>WP_100496241.1 dihydropteroate synthase [Bifidobacterium sp. TRE D]
PJM79384.1 dihydropteroate synthase [Bifidobacterium sp. TRE D]
Length=290

Score = 114 bits (285), Expect = 9e-29, Method: Compositional
matrix adjust.
Identities = 87/283 (31%), Positives = 140/283 (49%), Gaps = 28/283
(10%)

Query 8
VFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSVDVVGPAASHDPARPVSPADEIR 67
V G+LN+T DSF D LPA A +M+ G+D++D+G ++ P A+ VS

DE+
Sbjct 15
VMGVLNITADSFSDGGLWLDPAKAAQHGRDMMAGADIIDIGAESTRPGAKRVSETDELT 74

Query 68 RIAPLLDALSDQMHRVSIDSFQPETQRYALKRGVGYLNDIQGFPDPALYPD-
IAEADCRL 126
RI ++ L +SID+ + AL+RG +ND+ G A P +A+

DC
Sbjct 75
RITGAVETLLPAGATLSIDTTRASVAAAALERGAQIINDVSGGTLDAELPHVVADYDCLY 134

Query 127 VVMHSAQRDGIATRTGHLRPEDA-----
LDEIVRFFEARVSALRRSGVAADRLILDPG 179
+V H R +A G +D L ++ +V + +GV +R+I

+DPG
Sbjct 135 IVQH--
WRGWLKAGSKGATPDQDTSVYEHGVLADVRDELHQVDGVLAAAGVKPERIIDPG 192

Query 180 MGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSKSFGLGATV---
GLPVKDL----- 230
+GF P E +L +L+ L+ + A G P+L+ SRK F+ A + G+ D+

Sbjct 193 LGFS-KPGIEHNLPLLAGLETFR-
ATGYPVLIGQSRKRFISAMLTAGGVADADMADRDNV 250

Query 231 --GPASLAAELHAIGNGADYVRTHAPGDLRSAITFSETLAKFR 271
G ++L AE +GA VR H R+A+ +++
Sbjct 251 TAGLSALCAE-----HGAWAVRVHDVAKSRAAVIAGNAWRRYQ 288

>WP_015439115.1 dihydropteroate synthase [Bifidobacterium breve]
ABE96165.1 Dihydropteroate synthase [Bifidobacterium breve UCC2003]
Length=291

Score = 114 bits (285), Expect = 9e-29, Method: Compositional
matrix adjust.
Identities = 91/270 (34%), Positives = 135/270 (50%), Gaps = 29/270

(11%)

Query 4
SRVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSVDVVGPAASHPDARPVSPA 63
S V G+LN+TEDSF D LDPA A +M+ G+D++D+G ++ P A+

VS

Sbjct 11
SHTMVMGVLNITEDSFS DGGLWLDPAKAAQHGRDMMMAAGADIIDIGAESTRPGAKRVSEE 70

Query 64 DEIRRIAPLLDALSDQMHRVSIDSFQPETQRYALKRGGVYLNLDIQQFPDPALYPD-
IAEA 122 DE+ RI ++AL +SID+ + AL G +ND+ G A P

IA+

Sbjct 71
DELARITGAVNALIPAGAVLSIDTTRASVAAAALDGGAQIINDVSGGTLNPHVIADH 130

Query 123 DCRLVVMHSAQRDGIATRTG-----
HLRPEDALDEIVRFFEARVSALRRSGVAA 171
DC +V H R +A G H D DE++R +V +

+GV

Sbjct 131 DCLYIVQH--WRGWLAGSKGANPDQDTSVYEHGVLTDVHDELMR-----
QVDGVLAAGVKP 184

Query 172 DRLILDPMGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSRKSFLGA--
TVGLPVKD 229
+R+I+DPG+GF P+ E +L +L+ L+ + G P+L+ SRK F+ A T

V +

Sbjct 185 ERIIIDPGLGFS-KPSIEHNLPLLTGLETFRGT-
GYPVLIGQSRKRFISAMLTEAGAVGE 242

Query 230 LGPA-----SLAAELHAIG--NGADYVRTH 252
GP + A L A+ +GA VR H
Sbjct 243 DGPTMAQRDDVTAALSALSAEHGAWAVRVH 272

>WP_029679339.1 dihydropteroate synthase [Bifidobacterium longum]
Length=291

Score = 114 bits (285), Expect = 1e-28, Method: Compositional
matrix adjust.

Identities = 93/289 (32%), Positives = 141/289 (49%), Gaps = 31/289
(11%)

Query 4
SRVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSVDVVGPAASHPDARPVSPA 63
+ V G+LN+TEDSF D LDPA A +M+ G+D++D+G ++ P A+

VS A

Sbjct 11
THTMVMGVLNITEDSFS DGGLWLDPAKAAQHGRDMMMAAGADIIDIGAESTRPGAKRVSEA 70

Query 64 DEIRRIAPLLDALSDQMHRVSIDSFQPETQRYALKRGGVYLNLDIQQFPDPALYPD-
IAEA 122 DE+ RI + L +SID+ + AL G +ND+ G A P

+A+

Sbjct 71
DELVRITGAVKTLIPAGAILSIDTTRASVAAAALSEGAQIINDVSGGTLDAELPHVVADH 130

Query 123 DCRLVVMHSAQRDGIATRTG-----
HLRPEDALDEIVRFFEARVSALRRSGVAA 171
DC +V H R +A G H D DE++R +V +
+GV

Sbjct 131 DCLYIVQH--WRGWLKAGSKGANPDQDTSVYEHGVLTDVHDELMR-----
QVDGVLAAAGVKP 184

Query 172 DRLILDPMGMFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSRKSFLGATV---
GLPVK 228
+R+I+DPG+GF P E +L +L+ L+ + A G P+L+ SRK F+ A + G

Sbjct 185 ERIIIDPGLGFS-KPGIEHNLPLLTGLETFR-
ATGYPVLIQSRKRFISAMLTEAGAAGA 242

Query 229 DLGPA-----SLAAELHAIG--NGADYVRTHAPGDLRSAITFSETLAKF 270
D GP + A L A+ +GA VR H R+A+ T ++

Sbjct 243 D-GPIMAQRDDVTAVLSALSAEHGAWAVRVHDVAKSRAAVIAGNTWREY 290

>WP_021649768.1 dihydropteroate synthase [Bifidobacterium breve]
ERI87299.1 dihydropteroate synthase [Bifidobacterium breve JCP7499]
EWH39267.1 Dihydropteroate synthase [Bifidobacterium breve 31L]
AHJ23522.1 Dihydropteroate synthase [Bifidobacterium breve 689b]
AHJ25292.1 Dihydropteroate synthase [Bifidobacterium breve S27]
KOA39427.1 dihydropteroate synthase [Bifidobacterium breve MCC
1094]
KOA45225.1 dihydropteroate synthase [Bifidobacterium breve MCC
0121]
KOA53197.1 dihydropteroate synthase [Bifidobacterium breve MCC
1340]
KOA65512.1 dihydropteroate synthase [Bifidobacterium breve MCC
1114]
KWZ84373.1 dihydropteroate synthase [Bifidobacterium breve]
SDK09910.1 Dihydropteroate synthase [Bifidobacterium breve]
PAC75530.1 dihydropteroate synthase [Bifidobacterium breve]
AUD99757.1 Dihydropteroate synthase [Bifidobacterium breve]
AUE01676.1 Dihydropteroate synthase [Bifidobacterium breve]
Length=292

Score = 114 bits (285), Expect = 1e-28, Method: Compositional
matrix adjust.
Identities = 92/290 (32%), Positives = 141/290 (49%), Gaps = 29/290
(10%)

Query 4
SRVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSVDVVGPAASHDPARPVSPA 63
S V G+LN+TEDSF D LPA A +M+ G+D++D+G ++ P A+

VS
Sbjct 11
SHTMVMGVLNITEDSFS DGGLWLDPAKAAQHGRDMMMAAGADIIDIGAESTRPGAKRVSEE 70

Query 64 DEIRRIAPLLDALSDQMHRVSIDSFQPETQRYALKRGVGYLNDIQGFDPALYPD-

IAEA 122 DE+ RI ++AL +SID+ + AL G +ND+ G A P
+A+
Sbjct 71 DELARITGAVNALIPAGAVLSIDTTRASVAAAALDGGAQIINDVSGGTLNANLPHVVADH 130

Query 123 DCRLVMHSAQRDGIATRTG-----
HLRPEDALDEIVRFFEARVSALRRSGVAA 171
DC +V H R +A G H D DE++R +V +
+GV
Sbjct 131 DCLYIVQH--WRGWLKAGSKGANPDQDTSVYEHGVLTDVHDELMR-----
QVDGVLAAAGVKP 184

Query 172 DRLILDPMGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSRKSFLGA--
TVGLPVKD 229
+R+I+DPG+GF P+ E +L +L+ L+ + G P+L+ SRK F+ A T
V +
Sbjct 185 ERIIIDPGLGFS-KPSIEHNLPLLTGLETFRGT-
GYPVLIGQSRKRFISAMLTEAGAVGE 242

Query 230 LGPA-----SLAAELHAIG--NGADYVRTHAPGDLRSAITFSETLAKFRS 272
GP + A L A+ +GA VR H +A+ ++ S
Sbjct 243 DGPTMAQRDDVTAALSALSAEHGAWAVRVHDVAKSHA AVIAGNIWRQYLS 292

>WP_080784119.1 dihydropteroate synthase [Bifidobacterium breve]
OQM47684.1 dihydropteroate synthase [Bifidobacterium breve]
Length=292

Score = 114 bits (285), Expect = 1e-28, Method: Compositional
matrix adjust.
Identities = 92/290 (32%), Positives = 141/290 (49%), Gaps = 29/290
(10%)

Query 4
SRVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSVDVVGPAASHPDARPVSPA 63
S V G+LN+TEDSF D LDPA A +M+ G+D++D+G ++ P A+
VS
Sbjct 11
SHTMVMGVLNITEDSFS DGGLWLDPAKAAQHGRDMMMAAGADIIDIGAESTRPGAKRVSEE 70

Query 64 DEIRRIAPLLDALSDQMHRVSIDSFQPETQRYALKRGVGYLNDIQGFDPALYPD-
IAEA 122 DE+ RI ++AL +SID+ + AL G +ND+ G A P
+A+
Sbjct 71 DELARITGAVNALIPAGAVLSIDTTRASVAAAALDGGAQIINDVSGGTLNANLPHVVADH 130

Query 123 DCRLVMHSAQRDGIATRTG-----
HLRPEDALDEIVRFFEARVSALRRSGVAA 171
DC +V H R +A G H D DE++R +V +
+GV
Sbjct 131 DCLYIVQH--WRGWLKAGSKGANPDQDTSIYEHGVLTDVHDELMR-----
QVDGVLAAAGVKP 184

Query 172 DRLILDPMGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSRKSFLGA--
TVGLPVKD 229

+R+I+DPG+GF P+ E +L +L+ L+ + G P+L+ SRK F+ A T

V +

Sbjct 185 ERIIIDPGLGFS-KPSIEHNLPLLTGLETFRGT-
GYPVLIGQSRKRFISAMLTEAGAVGE 242

Query 230 LGPA-----SLAAELHAIG--NGADYVRTHAPGDLRSAITFSETLAKFRS 272

GP + A L A+ +GA VR H +A+ ++ S

Sbjct 243 DGPTMAQRDDVTAALSALSAEHGAWAVRVHVDVAKSHA AVIAGNIWRQYLS 292

>WP_077424703.1 dihydropteroate synthase [Bifidobacterium longum]
Length=291

Score = 114 bits (285), Expect = 1e-28, Method: Compositional
matrix adjust.

Identities = 92/289 (32%), Positives = 141/289 (49%), Gaps = 31/289
(11%)

Query 4

SRVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSVDVVDVGPAAASHDPARPVSPA 63

+ V G+LN+TEDSF D LDPA A +M+ G+D++D+G ++ P A+

V+ A

Sbjct 11

THTMVMGVLNITEDSFSGGLWLDPAKAAQHGRDMMAAGADIIDIGAESTRPGAKRVAEA 70

Query 64 DEIRRIAPLLDALSDQMHRVSIDSFQPETQRYALKRGGYLNDIQGFDPALYPD-
IAEA 122

DE+ RI + L +SID+ + AL G +ND+ G A P

+A+

Sbjct 71

DELARITGAVKTLIPAGAILSIDTTRASVAAAALSEGAQIINDVSGGTLDAELPHVVADH 130

Query 123 DCRLVVMHSAQRDGIATRTG-----

HLRPEDALDEIVRFFFEARVSALRRSGVAA 171

DC +V H R +A G H D DE++R +V +

+GV

Sbjct 131 DCLYIVQH--WRGWLAGSKGANPDQDTSVYEHGVLTDVHDELMR-----

QVDGVLAAAGVKP 184

Query 172 DRLILDPMGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSRKSFLGATV----
GLPVK 228

+R+I+DPG+GF P E +L +L+ L+ + A G P+L+ SRK F+ A + G

Sbjct 185 ERIIIDPGLGFS-KPGIEHNLPLLTGLETFR-
ATGYPVLIGQSRKRFISAMLTEAGAAGA 242

Query 229 DLGPA-----SLAAELHAIG--NGADYVRTHAPGDLRSAITFSETLAKF 270

D GP + A L A+ +GA VR H R+A+ T ++

Sbjct 243 D-GPIMAQRDDVTAALSALSAEHGAWAVRVHVDVAKSRA AVIAGNTWREY 290

>WP_094667142.1 dihydropteroate synthase [Bifidobacterium myosotis]

OZG60824.1 dihydropteroate synthase [Bifidobacterium myosotis]
Length=294

Score = 114 bits (284), Expect = 1e-28, Method: Compositional
matrix adjust.

Identities = 91/288 (32%), Positives = 138/288 (48%), Gaps = 36/288
(13%)

Query 8
VFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSDDVVDVGPAAASHPDARPVSPADEIR 67
V G+LN+TEDSF D LDP A +M+ G+D++D+G ++ P A+ VS

DE R
Sbjct 17
VMGVLNITEDSFSDDGLWLDPKAAQHGRDMMMAAGADIIDIGAESTRPGAKRVSEDEHR 76

Query 68 RIAPLLDALSDQMHRVSIDSFQPETQRYALKRGVGYLNDIQGFDPALYPD-
IAEADCRL 126
RI ++AL +SID+ + AL+RG +ND+ G A P +A+

DC
Sbjct 77
RITGAVEALIPAGAVLSIDTTRASVAAAALERGAQIINDVSGGTLDAELPHVVADHDCLY 136

Query 127 VVMHSAQRDGIATRTG-----
HLRPEDALDEIVRFFEARVSALRRSGVAADRLI 175
+V H R +A G H D DE++R +V + +GV

+R+I
Sbjct 137 IVQH--WRGWLKAGSKGANPDQDTSVYEHGVLRDVHDELMR-----
QVDGVLAAAGVRPERII 190

Query 176
LDPGMGFFLSPAPETSLHVLSNLQKLKLSALGLPLLVSVSRKSFLGATVGLPVKD----- 229
+DPG+GF P +L +L+ L+ + A G P+L+ SRK F+ A + D

Sbjct 191 IDPGLGFS-KPGIGHNLPLLTGLETFR-
ATGYPVLIGQSRKRFISAMLAEGVDEPTMAD 248

Query 230 -----LGPASLAAELHAIGNGADYVRTHAPGDLRSITFSETLAKFRS 272
G +++ AE +GA VR H RSA+ +R

Sbjct 249 RDGVTAGLSAMCAE-----HGAWAVRVHDVAASRSAVIAGNVWRAYRQ 291

>WP_070372479.1 dihydropteroate synthase [Acetobacterium wieringae]
0FV69371.1 dihydropteroate synthase [Acetobacterium wieringae]
Length=275

Score = 113 bits (283), Expect = 1e-28, Method: Compositional
matrix adjust.

Identities = 78/254 (31%), Positives = 134/254 (53%), Gaps = 16/254
(6%)

Query 2
LRSRVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSDDVVDVGPAAASHPDARPV 61
L ++V + GILN+T DSF D + + ++ +M+ G+D++D+G ++ P

+S
Sbjct 10

LSNQVLIMGILNVTPDSFSDGGKFNNLDASLRQVEKMILDGADIIDLGGESTRPGHTKIS 69

Query 62 PADEIRRIAPLLDALSDQMHR-VSIDSFQPETQRYALKRGGVGLNDIQGFP-
DPALYPDI 119

A+EI R+ P+++A++ + +SID+++ AL G +NDI GF DP L
Sbjct 70
DAEEIERVPMIEAINQRFDIPISIDTYKGPVGAALAAGADMVNDIWGFKYDPTLADIT 129

Query 120
AEADCRLVVMHSAQRDGIATRTRGHLRPEDALDEIVRFFEARVSALRRSGVAADRLLIDPG 179

A+ V+MH+ RT + + +I + ++ +G++ D
+ILDPG
Sbjct 130 AQYQVPCVLMHN-----RTNQ-
NYHNLMTDINSDLQESINIALSAGISRDAIILDPG 180

Query 180 MGFFLSPAPET-
SLHVLSNLQKLKLSALGLPLLVSRSRKSFLGATVGLPVKDLGPASLAAE 238

+GF A ++H L +LQ LG P+L+ SRK F+G T+ LPV + +
+A
Sbjct 181 IGFAKDYAQNMETMHHLEDLQ----
TLGYPVLLGTSRKGFIGLTLDPVTERVEGTVATT 236

Query 239 LHAIGNGADYVRTH 252

+ I GA +R H
Sbjct 237 VIGIMKGASIIRVH 250

>WP_070122223.1 dihydropteroate synthase [Bifidobacterium
adolescentis]

OFA35872.1 dihydropteroate synthase [Bifidobacterium adolescentis]
OSG88808.1 Dihydropteroate synthase [Bifidobacterium adolescentis]
OSG97856.1 Dihydropteroate synthase [Bifidobacterium adolescentis]
Length=292

Score = 114 bits (284), Expect = 1e-28, Method: Compositional
matrix adjust.

Identities = 86/280 (31%), Positives = 135/280 (48%), Gaps = 23/280
(8%)

Query 8
VFGILNLTEDSFFDESRRDPAGAVTAAIEMLRVGSVDVVGPAASHPDARPVSPADEIR 67

V G+LN+TEDSF D L P A M++ G+D++D+G ++ P A+ VS
ADE
Sbjct 16
VMGVNLNITEDSFDGGLWLAPEAAKAHGEAMMKAGADIIDIGAESTRPGAKRVSEADEKA 75

Query 68 RIAPLLDALSDQMHRVSIDSFQPETQRYALKRGGVGLNDIQGFPDPALYPDIA--
EADCR 125

R+ +DAL + +SID+ + AL+ G +ND+ G P +
+DC
Sbjct 76
RVLGAVDALIPEGAVLSIDTTRASVALAALEHGAQIINDVSGGQLDRELPHVVADHSDCL 135

Query 126 LVMHSAQR-----

DGIATRTGHLRPEDALDEIVRFFEARVSALRRSGVAADRLIL 176
+V H D +R H D DE++R +V A+ +GV A+
++I+
Sbjct 136 YIVQHWRGWLAGAAGNVPDADTSRYEHGVNDVHDELMR-----
QVDAVLEAGVRAEQVII 191

Query 177 DPGMGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSRKSFLG---
ATVGLPVKDLGP- 232
DPG+GF P E +L +L+ L + +A G P+L+ SRK F+G A G+ D
+
Sbjct 192 DPGLGFS-KPGVEHNLPIAALDRFNAA-
GYPVLIGASRKRFGVGSLLAGAGVTEPDMASK 249

Query 233 --ASLAAELHAIGNGADYVRTHAPGDLRSITFSETLAKF 270
A+ A +G VR H R A+ ++
Sbjct 250 DNATAAISALCAEHGVWAVRVHDVAKSRDAVAVGNWREY 289

>WP_094730457.1 dihydropteroate synthase [Bifidobacterium hapali]
OZG63254.1 dihydropteroate synthase [Bifidobacterium hapali]
Length=288

Score = 114 bits (284), Expect = 2e-28, Method: Compositional
matrix adjust.
Identities = 77/226 (34%), Positives = 118/226 (52%), Gaps = 16/226
(7%)

Query 8
VFGILNLTEDSFFDESRRDPAGAVTAAIEMLRVGSVDVVGPAASHDPARPVSPADEIR 67
V G+LN+TEDSF D LDPA A + ML G+D++D+G ++ P A+ VS
ADE+
Sbjct 15
VMGVLNITEDSFSDDGLWLDPAKAREHGLAMLNDGADIIDIGAESTRPGAKRVSEADELS 74

Query 68 RIAPLLDALSDQMHRVSIDSFQPETQRYALKRGGVGLNDIQGFP-
DPALYPDIAEADCRL 126
R+ + AL +SID+ + AL+ G +ND+ G D L +A+
DC
Sbjct 75
RVTGAVKALIGGNTVLSIDTTRALVAAAALEDGAQIINDVSGGTLDKELPHVVADHDCLY 134

Query 127 VVM-----
HSAQRDGIATRTGHLRPEDALDEIVRFFEARVSALRRSGVAADRLILD 177
+V H A D + H D DE+++ +V A+ +GV +R
+I+D
Sbjct 135 IVQHWRGWLAGAHGATPDADTSHYEHGVLRDVYDELMQ-----
QVDAVLEAGVKPERIIID 190

Query 178 PGMGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSRKSFLGATV 223
PG+GF P E +L +L+ L + G P+L+ SRK F+ A +
Sbjct 191 PGLGFS-KPGIEHNLPLLAGLSTFEDT-GYPVLIGASRKRFGVSAVL 234

>WP_101621332.1 dihydropteroate synthase [Bifidobacterium parmae]

Length=290

Score = 113 bits (283), Expect = 2e-28, Method: Compositional matrix adjust.

Identities = 90/283 (32%), Positives = 142/283 (50%), Gaps = 30/283 (11%)

Query 8

VFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSDDVVDVGPAAASHPDARPVSPA 67
V G+LN+TEDSF D LDP A M+ G+D++D+G ++ P A+ VS

DE+

Sbjct 16

VMGVLNITEDSFSDDGGLWLDPRAAADHGRAMMAAGADIIDIGAESTRPGAKRVSEDELT 75

Query 68 RIAPLLDALSDQMHRVSIDSFQPETQRYALKRGVGYLNDIQGFP-

DPALYPDIAEADCRL 126

RI ++AL +SID+ + AL G +ND+ G D L +A+

DC

Sbjct 76

RITGAVEALIPAGATLSIDTTRASVAAAALDGGAQIINDVSGGTLDELPHVVADHDCLY 135

Query 127 VVMHSAQRDZIA-TRTG-----

HLRPEDALDEIVRFFEARVSALRRSGVAADRLI 175

+V H R +A ++TG H +D DE++R +V A+ +GVA

+R+I

Sbjct 136 IVQH--WRGWLAKGSKTGAPDADTSHYEHGVLQDVHDELMR-----

QVDAVLAAGVAPERII 189

Query 176 LDPGMGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSRKSFLGAT-----

VGLPV 227

+DPG+GF P +L +L+ L + + A G P+L+ SRK F+ A +

+

Sbjct 190 IDPGLGFS-KPGIAHNLPLLAGLDRFR-

ATGYVLIQSRKRFVTAILDKAGFTDITMDA 247

Query 228 KDLGPASLAAELHAIGNGADYVRTHAPGDLRSAITFSETLAKF 270

+D A+ +A +GA VR H R+A+ T ++

Sbjct 248 RDDATAAFSALCAE--HGAWAVRVHDVARSRAAVAVGNTWREY 288

>WP_101626177.1 dihydropteroate synthase [Bifidobacterium imperatoris]

PLS24383.1 dihydropteroate synthase [Bifidobacterium imperatoris]

Length=290

Score = 113 bits (283), Expect = 2e-28, Method: Compositional matrix adjust.

Identities = 90/290 (31%), Positives = 143/290 (49%), Gaps = 30/290 (10%)

Query 4

SRVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSDDVVDVGPAAASHPDARPVSPA 63

S V G+LN+TEDSF D LDPA A +M+ G+D++D+G ++ P A+

VS

Sbjct 11
SHTLVMGVLNITEDSFSDGGLWLDPAKAAQHGRDMMMAAGADIIDIGAESTRPGAKRVSEE 70

Query 64 DEIRRIAPLLDALSDQMHRVSIDSFQPETQRYALKRGGVGLNDIQGFP-
DPALYPDIAEA 122
DE++RI ++ L +SID+ + AL+ G +ND+ G D L

+A+

Sbjct 71
DELKRITGAVNTLIPAGAVLSIDTTRASVACAALEGGAQIINDVSGGTLDRPHVVADH 130

Query 123 DCRLVVMHSAQRDGIATRTG-----
HLRPEDALDEIVRFFEARVSALRRSGVAA 171
DC +V H R +A G H D DE++ +V +

+GV

Sbjct 131 DCLYIVQH--WRGWLKSGKANPDQDTSVYEHGVLTDVHDELMH----
QVDDVLAAGVKP 184

Query 172
DRLILDPMGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSKFLGATVG----- 224
+R+I+DPG+GF P E +L +L+ L+ + A G P+L+ SRK F+ A +

Sbjct 185 ERIIIDPGLGFS-KPGIEHNLPLLAGLETFR-
ATGYPVLIGQSRKRFISAMLAENGIDEP 242

Query 225 -LPVKDLGPASLAAELHAIGNGADYVRTHAPGDLRSAITFSETLAKFRSR 273
+ +D A+L+A + +GA VR H R+A+ T K+ +

Sbjct 243 TMAQRDDVTAALSAL--SAEHGAWAVRVHDAKSRRAAVIAGNTWRKYSEQ 290

>OX526090.1 dihydropteroate synthase [Acetobacterium sp. MES1]
Length=275

Score = 113 bits (282), Expect = 2e-28, Method: Compositional
matrix adjust.
Identities = 78/254 (31%), Positives = 134/254 (53%), Gaps = 16/254
(6%)

Query 2
LRSRVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSVDVVGPAASHDPARPVS 61
L ++V + GILN+T DSF D + + ++ +M+ G+D++D+G ++ P

+S

Sbjct 10
LSNQVLIMGILNVTPDSFSDGGKFNLDASLRQVEKMILDGADIIDLGGESTRPGHTQIS 69

Query 62 PADEIRRIAPLLDALSDQMHR-VSIDSFQPETQRYALKRGGVGLNDIQGFP-
DPALYPDI 119
A+EI R+ P+++A+ + +SID+++ AL G +NDI GF DP+L

Sbjct 70
DAEEIERVPMIEAIRQRFDIPISIDTYKGSVGAALAAGADMVNDIWFYKYPDLAEFT 129

Query 120
AEADCRLVVMHSAQRDGIATRTGHLRPEDALDEIVRFFEARVSALRRSGVAADRILDPG 179
A+ V+MH+ RT + + +I + ++ +G++ D

+ILDPG

Sbjct 130 AKYQVPCVLMHN-----RTNQ-

NYHNLMTDINGDLQESINIAVSAGISKDAIILDPG 180

Query 180 MGFFLSPAPET-
SLHVLSNLQKLKSALGLPLLVSRSRKSFLGATVGLPVKDLGPASLAAE 238
+GF A ++H L +LQ LG P+L+ SRK F+G T+ LPV + +
+A

Sbjct 181 IGFAKDYAQNMETMHHLEDLQ-----
TLGYPVLLGTSRKGFIGLTLDPVTERVEGTVATT 236

Query 239 LHAIGNGADYVRTH 252
+ I GA +R H

Sbjct 237 VIGIMKGASIIRVH 250

>WP_077389951.1 dihydropteroate synthase [Bifidobacterium longum]
Length=291

Score = 113 bits (283), Expect = 2e-28, Method: Compositional
matrix adjust.
Identities = 91/287 (32%), Positives = 140/287 (49%), Gaps = 27/287
(9%)

Query 4
SRVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSDDVVDVGPAAHPDARPVSPA 63
+ V G+LN+TEDSF D LDPA A +M+ G+D++D+G ++ P A+

V+ A
Sbjct 11
THTMVMGVLNITEDSFSDDGGLWLDPAKAAQHGRDMMMAAGADIIDIGAESTRPGAKRVAEA 70

Query 64 DEIRRIAPLLDALSDQMHRVSIDSFQPETQRYALKRGGYLNDIQGFDPALYPD-
IAEA 122
DE+ RI + L +SID+ + AL G +ND+ G A P

+A+
Sbjct 71
DELARITGAVKTLIPAGAILSIDTTRASVAAAALSEGAQIINDVSGGTLDAELPHVVADH 130

Query 123 DCRLVVMH-----
SAQRDGIATRTGHLRPEDALDEIVRFFEARVSALRRSGVAADR 173
DC +V H A D + H D DE++R +V + +GV

+R
Sbjct 131 DCLYIVQHWRGWLVGSKGANPDQDTSVYEHGVLTDVHDELMR-----
QVDGVLAAAGVKPER 186

Query 174 LILDPGMGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSRKSFLGATV---
GLPVKDL 230
+I+DPG+GF P E +L +L+ L+ + A G P+L+ SRK F+ A + G

D
Sbjct 187 IIIDPGLGFS-KPGIEHNLPLLTGLETFR-
ATGYPVLIGQSRKRFISAMLTEAGAAGAD- 243

Query 231 GPA-----SLAAELHAIG--NGADYVRTHAPGDLRSITFSETLAKF 270
GP + A L A+ +GA VR H R+A+ T ++
Sbjct 244 GPIMAQRDDVTAALSALSAEHGAWAVRVHDVAKSRAAVIAGNTWREY 290

>WP_065436770.1 dihydropteroate synthase [Bifidobacterium longum]
Length=291

Score = 113 bits (283), Expect = 2e-28, Method: Compositional
matrix adjust.
Identities = 78/230 (34%), Positives = 118/230 (51%), Gaps = 20/230
(9%)

Query 4
SRVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSVDVVDVGPAAASHPDARPVSPA 63
+ V G+LN+TEDSF D LDPA A +M+ G+D++D+G ++ P A+

VS A
Sbjct 11
THTMVMGVLNITEDSFS DGGLWLDPAKAAQHGRDMMMAAGADIIDIGAESTRPGAKRVSEA 70

Query 64 DEIRRIAPLLDALSDQMHRVSIDSFQPETQRYALKRGGVYLNLDIQQFPDPALYPD-
IAEA 122
DE+ RI + L +SID+ + AL G +ND+ G A P

+A+
Sbjct 71
DELARITGAVKTLIPAGAILSIDTTRASVAAAALSEGARIINDVSGGTLDAELPHVVADH 130

Query 123 DCRLVMHSAQRDGIATRTG-----
HLRPEDALDEIVRFFFEARVSALRRSGVAA 171
DC +V H R +A G H D DE++R +V +

+GV
Sbjct 131 DCLYIVQH--WRGWLKAGSKGANPDQDTSVYEHGVLTDVHDELMR-----
QVDGVLAAAGVKP 184

Query 172 DRLILDPMGMFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSRKSFLGA 221
+R+I+DPG+GF P E +L +L+ L+ + A G P+L+ SRK F+ A
Sbjct 185 ERIIIDPGLGFS-KPGIEHNPLLLTGLETFR-ATGYPVLIGQSRKRFISA 232

>WP_013410667.1 dihydropteroate synthase [Bifidobacterium longum]
ADQ02765.1 FolP [Bifidobacterium longum subsp. longum BBMN68]
Length=291

Score = 113 bits (283), Expect = 2e-28, Method: Compositional
matrix adjust.
Identities = 88/286 (31%), Positives = 136/286 (48%), Gaps = 25/286
(9%)

Query 4
SRVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSVDVVDVGPAAASHPDARPVSPA 63
+ V G+LN+TEDS D LDPA A +M+ G+D++D+G ++ P A+

VS A
Sbjct 11
THTMVMGVLNITEDSVSDGGLWLDPAKAAQHGRDMMMAAGADIIDIGAESTRPGAKRVSEA 70

Query 64 DEIRRIAPLLDALSDQMHRVSIDSFQPETQRYALKRGGVYLNLDIQQFPDPALYPD-
IAEA 122
DE+ RI + L +SID+ + AL G +ND+ G A P

+A+
Sbjct 71
DELARITGAVKTLIPAGAVLSIDTTRASVAAAALSEGAQIINDVSGGTLDAELPHVVADH 130

Query 123 DCRLVVMH-----
SAQRDGIATRTGHLRPEDALDEIVRFFEARVSALRRSGVAADR 173
DC VV H A D + H D DE++R +V + +GV

+R
Sbjct 131 DCLYVVQHWRGWLVGSKGANPDQDTSVYEHGVLTDVHDELMR-----
QVDGVLAAAGVKPER 186

Query 174
LILDPMGFLLSPAPETSLHVLSNLQKLKSALGLPLLVSRSKFLGATV-----G 224
+I+DPG+GF P E +L +L+ L+ + A G P+L+ SRK F+ A +

G
Sbjct 187 IIIDPGLGFS-KPGIEHNLPLLTGLETFR-
ATGYPVLIGQSRKRFISAMLTGAGTAGADG 244

Query 225 LPVKDLGPASLAAELHAIGNGADYVRTHAPGDLRSITFSETLAKF 270
L + + A + +GA VR H R+A+ T ++
Sbjct 245 LTMAQRDDVTAALSALSAEHGAWAVRVHDVAKSRAAVIAGNTWREY 290

>WP_100493538.1 dihydropteroate synthase [Bifidobacterium sp. TRE H]
PJM77959.1 dihydropteroate synthase [Bifidobacterium sp. TRE H]
Length=293

Score = 113 bits (283), Expect = 2e-28, Method: Compositional
matrix adjust.
Identities = 89/293 (30%), Positives = 147/293 (50%), Gaps = 30/293
(10%)

Query 4
SRVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSVDVVGPAASHDPARPVSPA 63
S+ V G+LN+TEDSF D LDP A +M+ G+D++D+G ++ P A+

VS
Sbjct 11
SQTLVMGVLNITEDSFSDDGGLWLDPPDKAAQHGRDMMMAAGADIIDIGAESTRPGAKRVSEE 70

Query 64 DEIRRIAPLLDALSDQMHRVSDSFQPETQRYALKRGVGYLNDIQGFP-
DPALYPDIAEA 122
DE++RI + AL +SID+ + AL+ G +ND+ G D L

+A+
Sbjct 71
DELKRITGAVHALVPAGAVLSIDTTRASVAAAALLEGGAQIINDVSGGTLDRELPHVVADH 130

Query 123 DCRLVVMHSAQRDGIATRTG-----
HLRPEDALDEIVRFFEARVSALRRSGVAA 171
DC +V H R +A G H D DE++R +V +

+G+
Sbjct 131 DCLYIVQH--WRGWLKAGSKGANPDQDTSVYEHGVLTDVHDELMR-----
QVDDVLAAGIKP 184

Query 172

DRLILDPMGFLLSPAPETSLHVLSNLQKLKSALGLPLLVSRSKFLGATVG----- 224
+R+I+DPG+GF P E +L +L+ L+ + A G P+L+ SRK F+ A +
Sbjct 185 ERIIIDPGLGFS-KPGIEHNLPLLAGLETFR-
ATGYPVLIGQSRKRFISAMLADNGITEP 242

Query 225 -LPVKDLGPASLAAELHAIGNGADYVRTHAPGDLRSAITFSETLAKFRSRNAR
276
+ +D A+L+A + +GA VR H R+A+ ++ +++A+
Sbjct 243 TMAQRDDVTAALSAL--SAEHGAWAVRVHDVAKSRAAVIAGNAWRQYSAQSAQ
293

>WP_044089021.1 dihydropteroate synthase [Bifidobacterium reuteri]
KFI86589.1 dihydropteroate synthase 1 [Bifidobacterium reuteri DSM
23975]
Length=288

Score = 113 bits (282), Expect = 2e-28, Method: Compositional
matrix adjust.
Identities = 93/283 (33%), Positives = 141/283 (50%), Gaps = 30/283
(11%)

Query 8
VFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSDDVDVGPAAASHDPARPVSPADEIR 67
V G+LN+TEDSF D LDP A +M+ G+D++D+G ++ P A+ VS
DE R
Sbjct 15
VMGVLNITEDSFSDDGGLWLDPKAAQHGRDMMMAAGADIIDIGAESTRPGAKRVSEDEHR 74

Query 68 RIAPLLDALSDQMHRVSIDSFQPETQRYALKRGVGYLNDIQGFDPALYPD-
IAEADCRL 126
RI + AL +SID+ + AL+ G +ND+ G A P +A+
DC
Sbjct 75
RITGAVSALIPAGAVLSIDTTRASVAAAALEGAQIINDVSGGTLDAELPHVVADHDCLY 134

Query 127 VVMHSAQRDGIATRTG-----
HLRPEDALDEIVRFFEARVSALRRSGVAADRLI 175
+V H R +A G H D DE++R +V A+ +GV
+R+I
Sbjct 135 IVQH--WRGWLKAGSKGANPDQDTSVYEHGVLIDVHDELMR-----
QVDAVLDAGVKPERII 188

Query 176
LDPGMGFLLSPAPETSLHVLSNLQKLKSALGLPLLVSRSKFLGATVG-----LPV 227
+DPG+GF P E +L +L+ L KL A G P+L+ SRK F+ A +
+
Sbjct 189 IDPGLGFS-KPGIEHNLPLLTGL-
KLFRAAGYPVLIGQSRKRFISAMLADAGISEPSMEQ 246

Query 228 KDLGPASLAAELHAIGNGADYVRTHAPGDLRSAITFSETLAKF 270
+D A+L+A + +GA VR H R+A+ T ++
Sbjct 247 RDDVTAALSAL--SAEHGAWAVRVHDVAKSRAAVIAGNTWRQY 287

>WP_085382394.1 dihydropteroate synthase [Bifidobacterium adolescentis]
OSH06033.1 dihydropteroate synthase [Bifidobacterium adolescentis]
Length=292

Score = 113 bits (282), Expect = 2e-28, Method: Compositional matrix adjust.
Identities = 86/283 (30%), Positives = 135/283 (48%), Gaps = 23/283 (8%)

Query 5
RVTVFILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSDDVVDVGPAAASHPDARPVSPAD 64
R V G+LN+TEDS D L P A M++ G+D++D+G ++ P A+
VS AD
Sbjct 13
RTLVMGVLNITEDSSSDGGLWLAPEAAKAHGEAMMKAGADIIDIGAESTRPGAKRVSEAD 72

Query 65
EIRRIAPLLDALSDQMHRVSIDSFQPETQRYALKRGGVYLNDIQGFDPALYPDIA--EA 122
E R+ +DAL + +SID+ + AL+ G +ND+ G P +
+
Sbjct 73
EKARVLGAVDALIPEGAVLSIDTTRASVALAALEHGAQIINDVSGGQLDRELPHVVADHS 132

Query 123 DCRLVVMHSAQR-----
DGIATRTGHLRPEDALDEIVRFFEARVSALRRSGVAADR 173
DC +V H D +R H D DE++R +V A+ +GV
A++
Sbjct 133 DCLYIVQHWRGWLAGAAGNVPDADTSRYEHGVVNDVYDELMR-----
QVDAVLEAGVQAEQ 188

Query 174 LILDPMGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSKSFGLG----
ATVGLPVKDL 230
+I+DPG+GF P E +L +L+ L + +A G P+L+ SRK F+G A G+
D+
Sbjct 189 VIIDPGLGFS-KPGVEHNLPIAALDRFNAA-
GYPVLIGASRKRFGVGSLLAGAGVTEPDM 246

Query 231 GP---ASLAAELHAIGNGADYVRTHAPGDLRSAITFSETLAKF 270
A+ A +G VR H R A+ ++
Sbjct 247 ASKDNATAAISALCAEHGVWAVRVHDVAKSRDAVAVGNAREY 289

>WP_085381689.1 dihydropteroate synthase [Bifidobacterium adolescentis]
OSH01388.1 dihydropteroate synthase [Bifidobacterium adolescentis]
Length=292

Score = 113 bits (282), Expect = 2e-28, Method: Compositional matrix adjust.
Identities = 86/283 (30%), Positives = 135/283 (48%), Gaps = 23/283 (8%)

Query 5
RVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSVDVVGPAASHDPARPVSPAD 64
R V G+LN+TEDS D L P A M++ G+D++D+G ++ P A+

VS AD

Sbjct 13
RTLVMGVLNITEDSSSDGGLWLAPEAAKAHGEAMMKAGADIIDIGAESTRPGAKRVSEAD 72

Query 65
EIRRIAPLLDALSDQMHRVSIDSFQPETQRYALKRGVGYLNDIQGFPDPALYPDIA--EA 122
E R+ +DAL + +SID+ + AL+ G +ND+ G P +

+

Sbjct 73
EKARVLGAVDALIPEGAVLSIDTTRASVALAALEHGAQIINDVSGGQLDRELPHVVADHS 132

Query 123 DCRLVVMHSAQR-----
DGIATRTGHLRPEDALDEIVRFFEARVSALRRSGVAADR 173
DC +V H D +R H D DE++R +V A+ +GV

A++

Sbjct 133 DCLYIVQHWRGWLAGAAGDVPDADTSRYEHGVVNDVYDELMR-----
QVDAVLEAGVQAEQ 188

Query 174 LILDPMGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSKFLG----
ATVGLPVKDL 230
+I+DPG+GF P E +L +L+ L + +A G P+L+ SRK F+G A G+

D+

Sbjct 189 VIIDPGLGFS-KPGVEHNLPILAALDRFNAA-
GYPVLIGASRKRFBVGSLLAGAGVTEPDM 246

Query 231 GP---ASLAAELHAIGNGADYVRTHAPGDLRSAITFSETLAKF 270
A+ A +G VR H R A+ ++

Sbjct 247 ASKDNATAAISALCAEHGVWAVRVHDAKSRDAVAVGNAWREY 289

>PLS29794.1 dihydropteroate synthase [Bifidobacterium parmae]
Length=311

Score = 113 bits (283), Expect = 3e-28, Method: Compositional
matrix adjust.

Identities = 90/283 (32%), Positives = 142/283 (50%), Gaps = 30/283
(11%)

Query 8
VFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSVDVVGPAASHDPARPVSPADEIR 67
V G+LN+TEDSF D LDP A M+ G+D++D+G ++ P A+ VS

DE+

Sbjct 37
VMGVLNITEDSFSDDGGLWLDPRAAADHGRAMMAAGADIIDIGAESTRPGAKRVSEDELT 96

Query 68 RIAPLLDALSDQMHRVSIDSFQPETQRYALKRGVGYLNDIQGFP-
DPALYPDIAEADCRL 126
RI ++AL +SID+ + AL G +ND+ G D L +A+

DC

Sbjct 97
RITGAVEALIPAGATLSIDTTRASVAAAALDGGGAQIINDVSGGTLDELPHVVADHDCLY 156

Query 127 VVMHSAQRDGIATRTRG-----
HLRPEDALDEIVRFFEARVSALRRSGVAADRLI 175
+V H R +A ++TG H +D DE++R +V A+ +GVA
+R+I

Sbjct 157 IVQH--WRGWLAGSKTGAPDADTSHYEHGVLQDVHDELMR-----
QVDAVLAAGVAPERII 210

Query 176 LDPGMGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSRKSFLGAT-----
VGLPV 227
+DPG+GF P +L +L+ L + + A G P+L+ SRK F+ A +

+
Sbjct 211 IDPGLGFS-KPGIAHNLPLLAGLDRFR-
ATGYVLIGQSRKRFVTAILDKAGFTDITMDA 268

Query 228 KDLGPASLAAELHAIGNGADYVRTHAPGDLRSAITFSETLAKF 270
+D A+ +A +GA VR H R+A+ T ++
Sbjct 269 RDDATAAFSALCAE--HGAWAVRVHDVARSRRAAVAVGNTWREY 309

>WP_060620656.1 dihydropteroate synthase [Bifidobacterium longum]
ALE09286.1 Dihydropteroate synthase [Bifidobacterium longum subsp.
infantis]
OQM70287.1 Dihydropteroate synthase [Bifidobacterium longum subsp.
infantis]
Length=291

Score = 113 bits (282), Expect = 3e-28, Method: Compositional
matrix adjust.
Identities = 92/289 (32%), Positives = 140/289 (48%), Gaps = 31/289
(11%)

Query 4
SRVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSVDVVGPAASHPDARPVSPA 63
+ V G+LN+TEDS D LDPA A +M+ G+D++D+G ++ P A+
VS A
Sbjct 11
THTMVMGVLNITEDSVSDGGLWLDPAKAAQHGRDMMMAAGADIIDIGAESTRPGAKRVSEA 70

Query 64 DEIRRIAPLLDALSDQMHRVSIDSFQPETQRYALKRGVGYLNDIQGFDPALYPD-
IAEA 122
DE+ RI + L +SID+ + AL G +ND+ G A P
+A+
Sbjct 71
DELARITGAVKTLIPAGAILSIDTTRASVAAAALSEGAQIINDVSGGTLDAELPHVVADH 130

Query 123 DCRLVVMHSAQRDGIATRTRG-----
HLRPEDALDEIVRFFEARVSALRRSGVAA 171
DC +V H R +A G H D DE++R +V +
+GV
Sbjct 131 DCLYIVQH--WRGWLAGSKGANPDQDTSVYEHGVLTDVHDELMR-----
QVDGVLAAGVKP 184

Query 172 DRLILDPMGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSRKSFLGATV----

GLPVK 228 +R+I+DPG+GF P E +L +L+ L+ + A G P+L+ SRK F+ A + G
Sbjct 185 ERIIIDPGLGFS-KPGIEHNLPLLTGLETFR-
ATGYPVLIGQSRKRFISAMLTEAGAAGA 242

Query 229 DLGPA-----SLAAELHAIG--NGADYVRTHAPGDLRSAITFSETLAKF 270
D GP + A L A+ +GA VR H R+A+ T ++
Sbjct 243 D-GPIMAQRDDVTAALSALSAEHGAWAVRVHDVAKSRAAVIVGNTWREY 290

>KXS24820.1 dihydropteroate synthase [Bifidobacterium dentium]
Length=292

Score = 113 bits (282), Expect = 3e-28, Method: Compositional
matrix adjust.
Identities = 87/278 (31%), Positives = 137/278 (49%), Gaps = 19/278
(7%)

Query 8
VFGILNLTEDSFFDESRRDPAGAVTAAIEMLRVGSVDVVGPAASHDPARPVSPADEIR 67
V G+LN+TEDSF D LDPA A T M++ G+D++D+G ++ P A+ VS

DE
Sbjct 17
VMGVLNITEDSFSDDGGLWLDPAKAKTHGEAMMKDGADIIDIGAESTRPGAKRVSEEDEKS 76

Query 68 RIAPLLDALSDQMHRVSIDSFQPETQRYALKRGGVGLNDIQGFDPALYPDIA--
EADCR 125
R+ +DAL + +SID+ + AL+ G +ND+ G A P +

+
Sbjct 77
RVLGAVDALVPEGAILSIDTTRASVASAALEHGAQIINDVSGGRLDAELPHVVADHPESL 136

Query 126 LVVMHSAQRDGIATRTHGLRPEDA-----
LDEIVRFFEARVSALRRSGVAADRLILD P 178
+V H R +A G++ D L+++ A+V A+ GV ++

+I+DP
Sbjct 137 YIVQH--
WRGWLAGAAGNVPDADTSVYANGVLNDVYDELMAQVDAVLSVGKPEQVIIDP 194

Query 179 GMGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSRKSFLGATVGL-----
PVKDLGP 232
G+GF P E +L +L+ L++ +A G P+LV SRK F+GA + +

D
Sbjct 195 GLGFS-KPGIEHNLPLLAGLERF-
NATGHPVLVGASRKRFIGAVLAAAGVSEPTMADRDN 252

Query 233 ASLAAELHAIGNGADYVRTHAPGDLRSAITFSETLAKF 270
A+ A + +GA VR H R AI +
Sbjct 253 ATAAISALSAEHGAWAVRVHDVARTRDAIAIGSAWRAY 290

>WP_056251287.1 dihydropteroate synthase [Devosia sp. Root436]
KQX42591.1 dihydropteroate synthase [Devosia sp. Root436]
Length=283

Score = 112 bits (281), Expect = 3e-28, Method: Compositional matrix adjust.
Identities = 88/267 (33%), Positives = 135/267 (51%), Gaps = 25/267 (9%)

Query 1
MLRSRVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSDDVVDVGPAASHPDARPV 60
 +L R V GILN+T DSF D + AGA+ +ML G+D++D+G ++ P
A PV
Sbjct 16
LLGQRPLVMGILNVTPDSFSDGGQHNRVAGALAHVRQMLAEGADIIDIGGESTRPGAAPV 75

Query 61 SPADEIRRIAPLLDALSDQ--
MHRVSIDSFQPETQRYALKRGVGYLNDIQGFPDPALYPD 118
 +E+ R+ P++DAL + +SID+++P A++ G +ND+ G
P+
Sbjct 76
GVQEELDRVMPVIDALIAEGITAPISIDTYKPLVADQAIQAGASIINDVHGLQG---APE 132

Query 119 IAEA----DCRLVVMHSAQ-
RDGIATRTGHLRPEDALDEIVRFFEARVSALRRSGVAADR 173
 +AE ++VMH RD A G ++ + ++ R+G+
DR
Sbjct 133 MAEVAALHGAPVIVMHWDNARDPAAPFIG-----
AVMDYLARSIAIAERAGLHRDR 183

Query 174
LILDPMGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSKSFGLGATVGLPVKDLGPA 233
 LILDPG GF S A L L L +L+ ALGLPLLV SRKS +G + ++
Sbjct 184 LILDPGFGFGKSLAENYQL--LDRLAELQ-
ALGLPLLVGTSRKSMIGKLLDNQPEERLAG 240

Query 234 SLAAELHAIGNGADYVRTHAPGDLRSA 260
 ++A + G R H D+R+A
Sbjct 241 TIATTVLGYIKGGHIFRVH---DVRRAA 264

>WP_092184669.1 dihydropteroate synthase [Devosia sp. YR412]
SEQ42521.1 dihydropteroate synthase [Devosia sp. YR412]
Length=287

Score = 112 bits (281), Expect = 3e-28, Method: Compositional matrix adjust.
Identities = 75/249 (30%), Positives = 128/249 (51%), Gaps = 10/249 (4%)

Query 7
TVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSDDVVDVGPAASHPDARPVSPADEI 66
 V GILN+T DSF D + A+ A +M+ G+D++D+G ++ P ++PV
+E+
Sbjct 22
CVMGILNVTPDSFSDGGQHDRVDAAMAHAHQMIAEGADIIDIGGESTRPGSQPVGVQEEL 81

Query 67 RRIAPLLDAL--
SDQMHRVSI DSFQPETQRYALKRGGVGLNDIQGFDPALYPDIAEADC 124
R+ P++ AL + +SID+++P A++ G +ND+ G D+A
Sbjct 82
DRVMPVIQALVAAGITTPLSIDTYKPLVADQAIQAGAAIINDVHGLQGADEMADVAALHQ 141

Query 125
RLVVMHSAQRDGIATRTRGHLRPEDALDEIVRFFEARVSALRRSGVAADRILDPGMGFFL 184
V++ Q+D P LD++ R+FE ++ ++G++ DRLILDPG
GF
Sbjct 142 VPVIVMHWQKD-----RDKFFP--
LLDDMRRYFERSIARAEQAGISRDLILDPGFGFGK 194

Query 185 SPAPETS-
LHVLSNLQKLKLSALGLPLLVSRSRKSFLGATVGLPVKDLGPASLAAELHAIG 243
+ + + L + +Q + LPLLV SRKS +G +G ++ ++AA +
Sbjct 195
TLSENYAILQQIGGIQHERWQQKPLLLVGCSRKSMIGKLLGNEPEERLAGTIAANVIGYL 254

Query 244 NGADYVRTH 252
NG R H
Sbjct 255 NGGHIFRVH 263

>WP_100968037.1 dihydropteroate synthase [Bifidobacterium longum]
PKC92892.1 Dihydropteroate synthase [Bifidobacterium longum]
PKC96401.1 Dihydropteroate synthase [Bifidobacterium longum]
Length=291

Score = 112 bits (281), Expect = 3e-28, Method: Compositional matrix adjust.
Identities = 92/289 (32%), Positives = 140/289 (48%), Gaps = 31/289 (11%)

Query 4
SRVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSVDVVDVGPAAASHPDARPVSPA 63
+ V G+LN+TEDS D LDPA A +M+ G+D++D+G ++ P A+
VS A
Sbjct 11
THTMVMGVLNITEDSVSDGGLWLDPAKAAQHGRDMMMAAGADIIDIGAESTRPGAKRVSEA 70

Query 64 DEIRRIAPLLDALSDQMHRVSI DSFQPETQRYALKRGGVGLNDIQGFDPALYPD-
IAEA 122
DE+ RI + L +SID+ + AL G +ND+ G A P
+A+
Sbjct 71
DELVRITGAVKTLIPAGAILSIDTTRASVAAAALSEGAQIINDVSGGTLDAELPHVVADH 130

Query 123 DCRLVVMHSAQRDGIATRTRG-----
HLRPEDALDEIVRFFEARVSALRRSGVAA 171
DC +V H R +A G H D DE++R +V +
+GV
Sbjct 131 DCLYIVQH--WRGWLKSGKGANPDQDTSVYEHGVLTDVHDELMR-----
QVDGVLAAGVKP 184

Query 172 DRLILDPMGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSRKSFLGATV---
 GLPVK 228
 +R+I+DPG+GF P E +L +L+ L+ + A G P+L+ SRK F+ A + G
 Sbjct 185 ERIIIDPGLGFS-KPGIEHNLPLLTGLETFR-
 ATGYPVLIGQSRKRFISAMLTGAGTAGA 242

Query 229 DLGPA-----SLAAELHAIG--NGADYVRTHAPGDLRSITFSETLAKF 270
 D GP + A L A+ +GA VR H R+A+ T ++
 Sbjct 243 D-GPTMAQRDDVTAALSALSAEHGAWAVRVHDVAKSRAAVIAGNTWREY 290

>ODS95184.1 dihydropteroate synthase [Devosia sp. SCN 66-27]
 OJX26605.1 dihydropteroate synthase [Devosia sp. 66-14]
 Length=284

Score = 112 bits (281), Expect = 4e-28, Method: Compositional
 matrix adjust.
 Identities = 87/255 (34%), Positives = 129/255 (51%), Gaps = 16/255
 (6%)

Query 2
 LRSRVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSDDVVDVGAASHPDARPVS 61
 L R + GILN+T DSF D R A+ A ML G+D++D+G ++ P A
 VS
 Sbjct 18
 LGRRARLMGILNVTPDSFSDGGRFDVPAALGQARRMLAEGADIIDIGGESTRPGAAEVS 77

Query 62 PADEIRRIAPLLDALSDQ--MHRVSIDSFQPETQRYALKRGGVGLNDIQGFP-
 DPALYPD 118
 ADE+ R+ P + AL + +SID+++ E A+ G +ND+ G +P
 L
 Sbjct 78
 AADELARVLPAAIALRADGIVAPISIDTYKAEVAEQAIAGATIINDVHGLQREPELAAV 137

Query 119 IAEADCRLVVMHSAQ-
 RDGIATRTHGLRPEDALDEIVRFFEARVSALRRSGVAADRLLD 177
 A L VVMH + RD A+R D + E+ R+FE + +GVA
 ++LD
 Sbjct 138 AASRGVPLVVMHWDKARD--ASR-----
 DVMAEMARYFEVTLRIADEAGVAPSGIVLD 188

Query 178
 PGMGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSRKSFLGATVGLPVKDLGPASLAA 237
 PG GF S + + +L L +L ALG P+LV SRKS +G + +P +
 ++A
 Sbjct 189 PGFGFAKSLS--ENYEILHRLPEL-
 VALGFVPLVGTSRKSMIGRLLDVPADERLAGTVAT 245

Query 238 ELHAINGADYVRTH 252
 + GA R H
 Sbjct 246 SVLGYTAGAHLFRVH 260

>WP_034518937.1 MULTISPECIES: dihydropteroate synthase
[Bifidobacterium]
ET098375.1 dihydropteroate synthase [Bifidobacterium sp. MSTE12]
Length=292

Score = 112 bits (281), Expect = 4e-28, Method: Compositional
matrix adjust.
Identities = 87/281 (31%), Positives = 137/281 (49%), Gaps = 19/281
(7%)

Query 5
RVTVF^GILNLTEDSFFDESRR^LDPAGAVTAAIEMLRVGS^DVVDV^GPAASH^PDAR^PVSPAD 64
 R V G+LN+TEDSF D L^DPA A M++ G+D++D+G ++ P A+

VS D
Sbjct 14
RTLVMGVLNITEDSFS^DGG^LWLDPAKAKAHGEAMMKDGADIIDIGAESTRPGAKRVSEED 73

Query 65
EIRRIAPLLDALSDQMHRVSIDSFQPETQRYALKR^GVG^LNDIQGFPDPALYPDIA--EA 122
 E R+ +DAL + +SID+ + AL+ G +ND+ G A P +

Sbjct 74
EKSRVLGAVDALVPEGAILSIDTTRASVASVALEHGAQIINDVSGGRLDAELPHVVADHP 133

Query 123 DCRLVMHSAQRDGIATRTGHLRPEDA-----
LDEIVRFFEARVSALRRSGVAADRLI 175
 + +V H R +A G++ D L+++ A+V A+ GV

+++I
Sbjct 134 E^SL^YI^VQ^H--
WRGWLAGAAGNVPDADTSVYANGVLNDVYDELMAQVDAVLSVGKPEQVI 191

Query 176 LDPGMGFFLSPAPETSLHVLSNLQKLKSALGLPLLVS^SSRKSFLGATVGL-----
PVKD 229
 +DPG+GF P E +L +L+ L++ +A G P+LV SRK F+GA +

+ D
Sbjct 192 IDPGLGFS-KPGIEHNLPLLAGLERF-
NATGHPVLVGASRKRFIGAVLAAAGVSEPTMAD 249

Query 230 LGPASLAAELHAIGNGADYVRTHAPGDLRS^AITFSETLAKF 270
 A+ A + +GA VR H R AI +

Sbjct 250 RDNATAAISALSAEHGAWAVRVHDVARTDAIAIGSAWRAY 290

>WP_003837180.1 dihydropteroate synthase [Bifidobacterium dentium]
EDT44426.1 dihydropteroate synthase [Bifidobacterium dentium ATCC
27678]

ADB09220.1 folP Dihydropteroate synthase [Bifidobacterium dentium
Bd1]

BAQ26519.1 dihydropteroate synthase [Bifidobacterium dentium JCM
1195 =

DSM 20436]
SEB76962.1 dihydropteroate synthase [Bifidobacterium dentium JCM
1195 =

DSM 20436]
Length=292

Score = 112 bits (281), Expect = 4e-28, Method: Compositional matrix adjust.
Identities = 87/281 (31%), Positives = 137/281 (49%), Gaps = 19/281 (7%)

Query 5
RVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSDDVVDVGAASHPDARPVSPAD 64
R V G+LN+TEDSF D LPA A M++ G+D++D+G ++ P A+
VS D
Sbjct 14
RTLVMGVLNITEDSFDGGLWLDPAKAKAHGEAMMKDGADIIDIGAESTRPGAKRVSEED 73

Query 65
EIRRIAPLLDALSDQMHRVSIIDSFQPETQRYALKRGVGYLNDIQGFDPALYPDIA--EA 122
E R+ +DAL + +SID+ + AL+ G +ND+ G A P +
Sbjct 74
EKSRVLGAVDALVPEGAILSIDTTRASVASAALEHGAQIINDVSGGRLDAELPHVVADHP 133

Query 123 DCRLVMHSAQRDGIATRTGHLRPEDA-----
LDEIVRFFEARVSALRRSGVAADRLI 175
+ +V H R +A G++ D L+++ A+V A+ GV
+++I
Sbjct 134 ESLYIVQH--
WRGWLAGAAGNVPDADTSVYANGVLNDVYDELMAQVDAVLSVGKPEQVI 191

Query 176 LDPGMGFLLSPAPETSLHVLSNLQKLKSALGLPLLVSRSRKSFLGATVGL-----
PVKD 229
+DPG+GF P E +L +L+ L++ +A G P+LV SRK F+GA +
+ D
Sbjct 192 IDPGLGFS-KPGIEHNLPLLAGLERF-
NATGHPVLVGASRKRFIGAVLAAAGVSEPTMAD 249

Query 230 LGPASLAAELHAIGNGADYVRTHAPGDLRSAITFSETLAKF 270
A+ A + +GA VR H R AI +
Sbjct 250 RDNATAAISALSAEHGAWAVRVHDVARTRDAIAIGSAWRAY 290

>WP_058594680.1 dihydropteroate synthase [Leucobacter chromiiresistens]
KTR81892.1 hypothetical protein NS354_11885 [Leucobacter chromiiresistens]
Length=424

Score = 115 bits (287), Expect = 4e-28, Method: Compositional matrix adjust.
Identities = 75/222 (34%), Positives = 123/222 (55%), Gaps = 14/222 (6%)

Query 9
FGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSDDVVDVGAASHPDARPVSPADEIRR 68
G+LN+T DSF D + A+ +E+ R+G+D+VDVG ++ P A PV
+DE R
Sbjct 1

MGVLNVTPDFSFDGGAYAEHDAIAHGVELARLGADLVVGGESTRPGAAPVRSSEDEQER 60

Query 69 IAPLLDALSDQMHRVSIIDSFQPETQRYALKRGGVGLNDIQ-
GFPDPALYPDIAEADCR-- 125

+ P++ AL+ + VS+D+ +T A++ G ++ND+ G DP + A+A

R

Sbjct 61

VLPVIRALASRSIGVSDTLHADTAHAAVEAGARWINDVSGGLHDPPEMLDAAADASRRGA 120

Query 126 --LVMHSAQRDGIATRTGHLRPE--

DALDEIVRFFEARVSALRRSGVAADRLILDPMGM 181

L++ H G+ GHLR + D + ++ R + R SA +GV R+

+LDPG+G

Sbjct 121 AGLIIGH---WRGVDP-

PGHLRSYADVSDVTRALKERASAAGAAGVDPGRIVLDPGLG 176

Query 182 FFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSRKSFLGATV 223

F + A +L+ L +++ ALG P+L+ SRK LG +

Sbjct 177 FDKTGA--QGWQLLAGLDEVR-ALGFPVLIGASRKRMLGEAI 215

>WP_003830054.1 dihydropteroate synthase [Bifidobacterium breve]
EFE88671.1 dihydropteroate synthase [Bifidobacterium breve DSM
20213 = JCM
1192]

KFI51697.1 Dihydropteroate synthase [Bifidobacterium breve]
BAR00571.1 dihydropteroate synthase [Bifidobacterium breve DSM
20213 = JCM
1192]

AUD67752.1 Dihydropteroate synthase [Bifidobacterium breve]
Length=292

Score = 112 bits (281), Expect = 5e-28, Method: Compositional
matrix adjust.

Identities = 92/290 (32%), Positives = 140/290 (48%), Gaps = 29/290
(10%)

Query 4

SRVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSVDVVGPAASHDPARPVSPA 63

S V G+LN+TEDS D LDPA A +M+ G+D++D+G ++ P A+

VS

Sbjct 11

SHTMVMGVLNITEDSLSDGGLWLDPAKAAQHGRDMMAAGADIIDIGAESTRPGAKRVSEE 70

Query 64 DEIRRIAPLLDALSDQMHRVSIIDSFQPETQRYALKRGGVGLNDIQGFPDPALYPD-
IAEA 122

DE+ RI ++AL +SID+ + AL G +ND+ G A P

IA+

Sbjct 71

DELARITGAVNALIPAGAVLSIDTTRASVAAAALDGGAQIINDVSGGTLNANLPHVIADH 130

Query 123 DCRLVMHSAQRDGIATRTG-----

HLRPEDALDEIVRFFEARVSALRRSGVAA 171

DC +V H R +A G H D DE++R +V +

+GV
Sbjct 131 DCLYIVQH--WRGWLKAGSKGANPDQDTSVYEHGVLTDVHDELMR-----
QVDGVLAAGVKP 184

Query 172 DRLILDPMGMFFLSPAPETSLHVLSNLQKLKLSALGLPLLVSRSRKSFLGA--
TVGLPVKD 229
+R+I+DPG+GF P+ E +L +L+ L+ + G P+L+ SRK F+ A T

V +
Sbjct 185 ERIIIDPGLGFS-KPSIEHNLPLLTGLETFRGT-
GYPVLIGQSRKRFISAMLTGAGTAGA 242

Query 230 LGPA-----SLAAELHAIG--NGADYVRTHAPGDLRSITFSETLAKFRS 272
GP + A L A+ +GA VR H +A+ ++ S
Sbjct 243 DGPTMAQRDDVTAALSALSAEHGAWAVRVHDVAKSHA AVIAGNIWRQYLS 292

>KXS29119.1 dihydropteroate synthase [Bifidobacterium longum]
Length=291

Score = 112 bits (280), Expect = 6e-28, Method: Compositional
matrix adjust.
Identities = 92/289 (32%), Positives = 140/289 (48%), Gaps = 31/289
(11%)

Query 4
SRVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSVDVVDVGPAAASHDPARPVSPA 63
+ V G+LN+TEDS D LDPA A +M+ G+D++D+G ++ P A+
VS A
Sbjct 11
THTMVMGVLNITEDSSSDGGLWLDPAKAAQHGRDMMMAAGADIIDIGAESTRPGAKRVSEA 70

Query 64 DEIRRIAPLLDALSDQMHRVSIDSFQPETQRYALKRGVGYLNDIQGFDPALYPD-
IAEA 122
DE+ RI + L +SID+ + AL G +ND+ G A P
+A+
Sbjct 71
DELVRITGAVKTLIPAGAILSIDTTRASVAAAALSEGAQIINDVSGGTLDAELPHVVADH 130

Query 123 DCRLVVMHSAQRDGIATRGT-----
HLRPEDALDEIVRFFEARVSALRRSGVAA 171
DC +V H R +A G H D DE++R +V +
+GV
Sbjct 131 DCLYIVQH--WRGWLKAGSKGANPDQDTSVYEHGVLTDVHDELMR-----
QVDGVLAAGVKP 184

Query 172 DRLILDPMGMFFLSPAPETSLHVLSNLQKLKLSALGLPLLVSRSRKSFLGATV---
GLPVK 228
+R+I+DPG+GF P E +L +L+ L+ + A G P+L+ SRK F+ A + G
Sbjct 185 ERIIIDPGLGFS-KPGIEHNLPLLTGLETFR-
ATGYPVLIGQSRKRFISAMLTGAGTAGA 242

Query 229 DLGPA-----SLAAELHAIG--NGADYVRTHAPGDLRSITFSETLAKF 270
D GP + A L A+ +GA VR H R+A+ T ++
Sbjct 243 D-GPTMAQRDDVTAALSALSAEHGAWAVRVHDVAKSRA AVIAGNTWREY 290

>WP_008782915.1 MULTISPECIES: dihydropteroate synthase
[Bifidobacterium]
EFV37870.1 dihydropteroate synthase [Bifidobacterium sp.
12_1_47BFAA]
PKC86636.1 Dihydropteroate synthase [Bifidobacterium longum]
PKC87768.1 Dihydropteroate synthase [Bifidobacterium longum]
Length=291

Score = 112 bits (280), Expect = 6e-28, Method: Compositional
matrix adjust.
Identities = 92/289 (32%), Positives = 140/289 (48%), Gaps = 31/289
(11%)

Query 4
SRVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSVDVVDVGPAAASHPDARPVSPA 63
+ V G+LN+TEDS D LDPA A +M+ G+D++D+G ++ P A+
VS A
Sbjct 11
THTMVMGVLNITEDSVSDGGLWLDPAKAAQHGRDMMMAAGADIIDIGAESTRPGAKRVSEA 70

Query 64 DEIRRIAPLLDALSDQMHRVSIIDSFQPETQRYALKRGGVYLNLDIQQFPDPALYPD-
IAEA 122
DE+ RI + L +SID+ + AL G +ND+ G A P
+A+
Sbjct 71
DELVRITGAVKTLIPAGAVLSIDTTRASVAAAALSEGAQIINDVSGGTLDAELPHVVADH 130

Query 123 DCRLVVMHSAQRDGIATRTG-----
HLRPEDALDEIVRFFEARVSALRRSGVAA 171
DC +V H R +A G H D DE++R +V +
+GV
Sbjct 131 DCLYIVQH--WRGWLKSGKGANPDQDTSVYEHGVLTDVHDELMR-----
QVDGVLAAGVKP 184

Query 172 DRLILDPMGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSRKSFLGATV----
GLPVK 228
+R+I+DPG+GF P E +L +L+ L+ + A G P+L+ SRK F+ A + G
Sbjct 185 ERIIIDPGLGFS-KPGIEHNLPLLTGLETFR-
ATGYPVLIGQSRKRFISAMLTEAGAAGA 242

Query 229 DLGPA-----SLAAELHAIG--NGADYVRTHAPGDLRSITFSETLAKF 270
D GP + A L A+ +GA VR H R+A+ T ++
Sbjct 243 D-GPIMAQRDDVTAALSALSAEHGAWAVRVHDVAKSRAAVIAGNTWREY 290

>WP_087033063.1 dihydropteroate synthase [Trichococcus palustris]
Length=259

Score = 111 bits (278), Expect = 6e-28, Method: Compositional
matrix adjust.
Identities = 80/247 (32%), Positives = 127/247 (51%), Gaps = 15/247
(6%)

Query 9
FGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSVVDVVGPAASHPDARPVSPADEIRR 68
GILN+T DSF D AV AIEM+R G+D +D+G ++ P +S

+EI R
Sbjct 1
MGILNVTPDSFSDGGEWNTLEAAVAHAIEMV RDGADFIDIGGESTRPGHTQISDEEEIAR 60

Query 69 IAPLLDALSDQMHR-VSIDSFQPETQRYALKRGGVGLNDIQGFP-
DPALYPDIAEADCRL 126
I P++ A+ + +S+D+++ R A + G+ +NDI G DP + AE

D +
Sbjct 61
IVPVIKAVKAAVAVPLSVDTYKSAVARAAACEAGIDIINDIWGCKYDPEIAAVAAEFDVPI 120

Query 127
VVMHSAQRDGIATRTRGHLRPEDALDEIVRFFEARVSALRRSGVAADRLILDPMGFFLSP 186
++MH+ + + ED + ++ ++A GV +ILDPG GF

+
Sbjct 121 ILMHNRE-----AADYNFLIEDMIQDLSESMRIALAA-----
GVPRHNIILDPGCGF--AK 169

Query 187 APETSLHVLSNLQKLKSALGLPLLVSRSRKSFLGATVG-
LPVKDLGPASLAAELHAIGNG 245
E +L+V+ +L++ LG PLL++ SRK F+G +G P K+ + A

I NG
Sbjct 170 TFEDNLNVIHHLRRFAD-
LGYPLLLATSRKRFI GTVLGDAPFKERDEGTAATTALGIMNG 228

Query 246 ADYVRTH 252
A R H
Sbjct 229 AHIFRVH 235

>WP_095346990.1 dihydropteroate synthase [Bifidobacterium longum]
PAK16983.1 dihydropteroate synthase [Bifidobacterium longum]
Length=291

Score = 112 bits (279), Expect = 6e-28, Method: Compositional
matrix adjust.
Identities = 91/287 (32%), Positives = 139/287 (48%), Gaps = 27/287
(9%)

Query 4
SRVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSVVDVVGPAASHPDARPVSPA 63
+ V G+LN+TEDS D LDPA A +M+ G+D++D+G ++ P A+

VS A
Sbjct 11
THTMVMGVLNITEDSSSDGGLWLDPAKAAQHGRDMMMAAGADIIDIGAESTRPGAKRVSEA 70

Query 64 DEIRRIAPLLDALSDQMHRVSIDSFQPETQRYALKRGGVGLNDIQGFPDPALYPD-
IAEA 122
DE+ RI + L +SID+ + AL G +ND+ G A P
+A+

Sbjct 71
DELARITGAVKTLIPAGAVLSIDTTRASVAAAALSEGAQIINDVSGGTLDAELPHVVADH 130

Query 123 DCRLVVMH-----
SAQRDGIATRTGHLRPEDALDEIVRFFEARVSALRRSGVAADR 173
DC +V H A D + H D DE++R +V + +GV
+R

Sbjct 131 DCLYIVQHWRGWLVGSKGANPDQDTSVYEHGVLTDVHDELMR-----
QVDGVLAAAGVKPER 186

Query 174 LILDPMGFFLSPAPETSLHVLSNLQKLKSALGLPLLVSRSKSFGLGATV---
GLPVKDL 230
+I+DPG+GF P E +L +L+ L+ + A G P+L+ SRK F+ A + G
D

Sbjct 187 IIIDPGLGFS-KPGIEHNLPLLTGLETFR-
ATGYPVLIQSRKRFISAMLTGAGTAGAD- 243

Query 231 GPA-----SLAAELHAIG--NGADYVRTHAPGDLRSITFSETLAKF 270
GP + A L A+ +GA VR H R+A+ T ++
Sbjct 244 GPTMAQRDDVTAALSALSAEHGAWAVRVHVDVAKSRAAVIAGNTWREY 290

>WP_011068790.1 dihydropteroate synthase [Bifidobacterium longum]
NP_696835.1 dihydropteroate synthase 1 [Bifidobacterium longum
NCC2705]
AAN25471.1 dihydropteroate synthase 1 [Bifidobacterium longum
NCC2705]
KEY33436.1 dihydropteroate synthase [Bifidobacterium longum subsp.
longum
EK13]
PKC77810.1 Dihydropteroate synthase [Bifidobacterium longum]
Length=291

Score = 112 bits (279), Expect = 7e-28, Method: Compositional
matrix adjust.
Identities = 91/289 (31%), Positives = 140/289 (48%), Gaps = 31/289
(11%)

Query 4
SRVTVFGILNLTEDSFFDESRRLLDPAGAVTAAIEMLRVGSDDVVDVGPAAASHPDARPVSPA 63
+ V G+LN+TEDSF D LDPA A +M+ G+ ++D+G ++ P A+
V+ A
Sbjct 11
THTMVMGVLNITEDSFSDDGGLWLDPAKAAQHGRDMMMAAGAAIIDIGAESTRPGAKRVAEA 70

Query 64 DEIRRIAPLLDALSDQMHRVSDSFQPETQRYALKRGGVYLNLDIQQFPDPALYPD-
IAEA 122
DE+ RI + L +SID+ + AL G +ND+ G A P
+A+

Sbjct 71
DELARITGAVKTLIPAGAVLSIDTTRASVAAAALSEGAQIINDVSGGTLDAELPHVVADH 130

Query 123 DCRLVVMHSAQRDGIATRTG-----
HLRPEDALDEIVRFFEARVSALRRSGVAA 171

DC +V H R +A G H D DE++R +V +
 +GV
 Sbjct 131 DCLYIVQH--WRGWLKSGGANPDQDTSVYEHGVLTDVHDELMR----
 QVDGVLAAGVKP 184
 Query 172 DRLILDPMGFLLSPAPETSLHVLSNLQKLKLSALGLPLLVSRSRKSFLGATV---
 GLPVK 228
 +R+I+DPG+GF P E +L +L+ L+ + A G P+L+ SRK F+ A + G
 Sbjct 185 ERIIIDPGLGFS-KPGIEHNLPLLTGLETFR-
 ATGYPVLIQSRKRFISAMLTGAGTAGA 242
 Query 229 DLGPA-----SLAAELHAIG--NGADYVRTHAPGDLRSITFSETLAKF 270
 D GP + A L A+ +GA VR H R+A+ T ++
 Sbjct 243 D-GPTMAQRDDVTAALSALSAEHGAWAVRVHDVAKSRAAVIAGNTWREY 290

>WP_046138407.1 dihydropteroate synthase [Devosia
 epidermidihirudinis]
 KKC39364.1 dihydropteroate synthase [Devosia epidermidihirudinis]
 Length=283

Score = 112 bits (279), Expect = 7e-28, Method: Compositional
 matrix adjust.
 Identities = 82/256 (32%), Positives = 131/256 (51%), Gaps = 16/256
 (6%)

Query 1
 MLRSRVTVFGILNLTEDSFFDESRRDPAGAVTAAIEMLRVGSDDVVDVGPAAASHPDARPV 60
 +L R V GILN+T DSF D + AV A M+ G+D++D+G ++ P
 A V
 Sbjct 16
 ILGQRALVMGILNVTPDSFSDGGQHNLINAVAHQAAMIADGADIIDIGGESTRPGAALV 75

Query 61 SPADEIRRIAPLLDAL--
 SDQMHRVSIDSFQPETQRYALKRGVGYLNDIQGFPDPALYPD 118
 S +E+ R+ P++DAL + +SIDS++P A++ G +ND+ G
 P+
 Sbjct 76
 SVQEELDRVMPVIDALVAAGITTPISIDSYKPLVADQAIQAGASIINDVHGLQGA---PE 132

Query 119 IAEADCRLVVMHSAQRDGIATRTGHLRPEDA--
 LDEIVRFFEARVSALRRSGVAADRLLIL 176
 +AE + +HS IA +R E + E+ R+FE ++ + GV
 +R+IL
 Sbjct 133 MAE-----IAALHSVPV--
 IAMHWDKVRDEAKPIIAEMARYFETTLALAKAVGVGRERIIL 186

Query 177
 DPMGMFFLSPAPETSLHVLSNLQKLKLSALGLPLLVSRSRKSFLGATVGLPVKDLGPASLA 236
 DPG GF S A + VL L +++ G+P+LV SRKS +G + +P +
 ++A
 Sbjct 187 DPGFGFGKSLA--ENYEVLRLETEVQPR-
 GMPILVGTSRKSMIGRLLDIPADERLAGTIA 243

Query 237 AELHAIGNGADYVRTH 252
+ G R H
Sbjct 244 TTVAGYLKGGHIFRVH 259

Database: All non-redundant GenBank CDS translations+PDB+SwissProt
+PIR+PRF

excluding environmental samples from WGS projects

Posted date: Mar 26, 2018 2:20 PM

Number of letters in database: 248,125,090

Number of sequences in database: 703,403

Lambda K H
0.321 0.137 0.392

Gapped

Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 703403

Number of Hits to DB: 48261

Number of extensions: 32

Number of successful extensions: 11

Number of sequences better than 100: 4

Number of HSP's better than 100 without gapping: 0

Number of HSP's gapped: 8

Number of HSP's successfully gapped: 4

Length of query: 283

Length of database: 248125090

Length adjustment: 118

Effective length of query: 165

Effective length of database: 165123536

Effective search space: 27245383440

Effective search space used: 27245383440

T: 21

A: 40

X1: 16 (7.4 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)

S1: 41 (20.4 bits)

S2: 61 (28.1 bits)

ka-blk-alpha gapped: 1.9

ka-blk-alpha ungapped: 0.7916

ka-blk-alpha_v gapped: 42.6028

ka-blk-alpha_v ungapped: 4.96466

ka-blk-sigma gapped: 43.6362