

57. E463K

>[ref|YP_627218.1](#) DNA gyrase subunit B [Helicobacter pylori HPAG1]
[gb|ABF84544.1](#) DNA gyrase subunit B [Helicobacter pylori HPAG1]
Length = 773

Score = 203 bits (516), Expect = 7e-51
Identities = 108/126 (85%), Positives = 109/126 (86%), Gaps = 1/126 (0%)
Frame = +1

Query: 22 KKIISVGTLP GKLTDCQSKDPLESEIFLVEGDSAGGSAKQGRDRVFQAILPLKGKILNV 201
KK SVGTLP GKLD CQSKDPLESEIFLVEGDSAGGSAKQGRDRVFQAILPLKGKILNV
Sbjct: 392 KKDNLVGTLP GKLADCQSKDPLESEIFLVEGDSAGGSAKQGRDRVFQAILPLKGKILNV 451

Query: 202 EKSHLSKILKSKEIKNMITAFGCGIQESFDIERLRYHKIIIMTDADVHGG-ISHLADDDFF 378
EKSHLSKILKS+EIKNMITAFGCGIQESFDIERLRYHKIIIMTDADV G I L FF
Sbjct: 452 EKSHLSKILKSEEIKNMITAFGCGIQESFDIERLRYHKIIIMTDADV D GSHIQTLTLM TFF 511

Query: 379 LSLFTP 396

P

Sbjct: 512 YRYLRP 517

53: D481E

>[ref|NP_207298.1](#) DNA gyrase subunit B [Helicobacter pylori 26695]
[sp|P55992.1|GYRB_HELPY](#) RecName: Full=DNA gyrase subunit B
[gb|AAD07566.1](#) DNA gyrase, sub B (gyrB) [Helicobacter pylori 26695]
Length = 773

Score = 262 bits (669), Expect = 1e-68
Identities = 131/132 (99%), Positives = 132/132 (100%)
Frame = +1

Query: 22 KDNLSVGTLP GKLADCQSKDPLESEIFLVEGDSAGGSAKQGRDRVFQAILPLKGKILNVE 201
KDNLSVGTLP GKLADCQSKDPLESEIFLVEGDSAGGSAKQGRDRVFQAILPLKGKILNVE
Sbjct: 393 KDNLSVGTLP GKLADCQSKDPLESEIFLVEGDSAGGSAKQGRDRVFQAILPLKGKILNVE 452

Query: 202 KSHLSKILKSEEIKNMITAFGCGIQESFEIERLRYHKIIIMTDADV D GSHIQTLTLM TFFY 381
KSHLSKILKSEEIKNMITAFGCGIQESF+IERLRYHKIIIMTDADV D GSHIQTLTLM TFFY
Sbjct: 453 KSHLSKILKSEEIKNMITAFGCGIQESFDIERLRYHKIIIMTDADV D GSHIQTLTLM TFFY 512

Query: 382 RYLRPLIEQGHV 417

RYLRPLIEQGHV

Sbjct: 513 RYLRPLIEQGHV 524

1.E483K

>[ref|NP_207298.1](#) DNA gyrase subunit B [Helicobacter pylori 26695]
[sp|P55992.1|GYRB_HELPY](#) RecName: Full=DNA gyrase subunit B
[gb|AAD07566.1](#) DNA gyrase, sub B (gyrB) [Helicobacter pylori 26695]
Length = 773

Score = 254 bits (649), Expect = 2e-66
Identities = 127/133 (95%), Positives = 131/133 (98%)
Frame = +3

Query: 9 TYRXDNLSVGTLP GKLADCQSKDPLESEIFLVEGDSAGGSAKQGRDRVFQAILPLKGKIL 188
T + DNLSVGTLP GKLADCQSKDPLESEIFLVEGDSAGGSAKQGRDRVFQAILPLKGKIL
Sbjct: 390 TRKKNLSVGTLP GKLADCQSKDPLESEIFLVEGDSAGGSAKQGRDRVFQAILPLKGKIL 449

Query: 189 NVEKSHLSKILKSEEIKNMITAFGCGIQESFDIKRLRYHKIIIMTDADV D GSHIQTLTLM T 368
NVEKSHLSKILKSEEIKNMITAFGCGIQESFDI+RLRYHKIIIMTDADV D GSHIQTLTLM T
Sbjct: 450 NVEKSHLSKILKSEEIKNMITAFGCGIQESFDIERLRYHKIIIMTDADV D GSHIQTLTLM T 509

Query: 369 FFYRYLRPLIDRG 407

FFYRYLRPLI++G

Sbjct: 510 FFYRYLRPLIEQG 522

65: D504P

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[gb|AAD07566.1](#) DNA gyrase, sub B (gyrB) [Helicobacter pylori 26695]
Length = 773

Score = 239 bits (610), Expect = 8e-62
Identities = 120/121 (99%), Positives = 120/121 (99%)
Frame = +2

Query: 56 KLADCQSKDPLESEIFLVEGDSAGGSAKQGRDRVFQAILPLKGKILNVEKSHLSKILKSE 235
KLADCQSKDPLESEIFLVEGDSAGGSAKQGRDRVFQAILPLKGKILNVEKSHLSKILKSE
Sbjct: 404 KLADCQSKDPLESEIFLVEGDSAGGSAKQGRDRVFQAILPLKGKILNVEKSHLSKILKSE 463

Query: 236 EIKNMITAFGCGIQESFDIERLRYHKIIIMTDADVDGSHIPTLLMTFFYRYLRPLIEQGH 415
EIKNMITAFGCGIQESFDIERLRYHKIIIMTDADVDGSHI TLLMTFFYRYLRPLIEQGH
Sbjct: 464 EIKNMITAFGCGIQESFDIERLRYHKIIIMTDADVDGSHIQTLTLLMTFFYRYLRPLIEQGH 523

Query: 416 V 418
V
Sbjct: 524 V 524

74 Q504R

>[ref|NP_207298.1](#) DNA gyrase subunit B [Helicobacter pylori 26695]
[sp|P55992.1|GYRB_HELPY](#) RecName: Full=DNA gyrase subunit B
[gb|AAD07566.1](#) DNA gyrase, sub B (gyrB) [Helicobacter pylori 26695]
Length = 773

Score = 256 bits (654), Expect = 7e-67
Identities = 129/132 (97%), Positives = 130/132 (98%)
Frame = +2

Query: 29 KGYLSVGTLPGLADCQSKDPLESEIFLVEGDSAGGSAKQGRDRVFQAILPLKGKILNVE 208
K LSVGTLPGLADCQSKDPLESEIFLVEGDSAGGSAKQGRDRVFQAILPLKGKILNVE
Sbjct: 393 KDNLSVGTLPGLADCQSKDPLESEIFLVEGDSAGGSAKQGRDRVFQAILPLKGKILNVE 452

Query: 209 KSHLSKILKSEEIKNMITAFGCGIQESFDIERLRYHKIIIMTDADVDGSHIRTLLMTFFY 388
KSHLSKILKSEEIKNMITAFGCGIQESFDIERLRYHKIIIMTDADVDGSHI+TLLMTFFY
Sbjct: 453 KSHLSKILKSEEIKNMITAFGCGIQESFDIERLRYHKIIIMTDADVDGSHIQTLTLLMTFFY 512

Query: 389 RYLRPLIEQGHV 424
RYLRPLIEQGHV
Sbjct: 513 RYLRPLIEQGHV 524

76. D394G

>[ref|NP_207298.1](#) DNA gyrase subunit B [Helicobacter pylori 26695]
[sp|P55992.1|GYRB_HELPY](#) RecName: Full=DNA gyrase subunit B
[gb|AAD07566.1](#) DNA gyrase, sub B (gyrB) [Helicobacter pylori 26695]
Length = 773

Score = 266 bits (679), Expect = 8e-70
Identities = 133/134 (99%), Positives = 134/134 (100%)
Frame = +1

Query: 19 REKDNLSVGTLPGKLADCQSKDPLESEIFLVEGDSAGGSAKQGRDRVFQAILPLKGKILN 198
R+KDNLSVGTLPGKLADCQSKDPLESEIFLVEGDSAGGSAKQGRDRVFQAILPLKGKILN
Sbjct: 391 RKKDNLSVGTLPGKLADCQSKDPLESEIFLVEGDSAGGSAKQGRDRVFQAILPLKGKILN 450

Query: 199 VEKSHLSKILKSEEIKNMITAFGCGIQESFDIERLRYHKIIIMTDADVDGSHIQTLMLTF 378
VEKSHLSKILKSEEIKNMITAFGCGIQESFDIERLRYHKIIIMTDADVDGSHIQTLMLTF
Sbjct: 451 VEKSHLSKILKSEEIKNMITAFGCGIQESFDIERLRYHKIIIMTDADVDGSHIQTLMLTF 510

Query: 379 FYRYLRPLIEQGHV 420
FYRYLRPLIEQGHV
Sbjct: 511 FYRYLRPLIEQGHV 524

99 K404R

>[ref|NP_207298.1|](#) DNA gyrase subunit B [Helicobacter pylori 26695]
[sp|P55992.1|GYRB_HELPY](#) RecName: Full=DNA gyrase subunit B
[gb|AAD07566.1|](#) DNA gyrase, sub B (gyrB) [Helicobacter pylori 26695]
Length = 773

Score = 210 bits (535), Expect(2) = 3e-60
Identities = 105/106 (99%), Positives = 106/106 (100%)
Frame = +2

Query: 41 GTLPGRLADCQSKDPLESEIFLVEGDSAGGSAKQGRDRVFQAILPLKGKILNVEKSHLSK 220
GTLPG+LADCQSKDPLESEIFLVEGDSAGGSAKQGRDRVFQAILPLKGKILNVEKSHLSK
Sbjct: 399 GTLPGLADCQSKDPLESEIFLVEGDSAGGSAKQGRDRVFQAILPLKGKILNVEKSHLSK 458

Query: 221 ILKSEEIKNMITAFGCGIQESFDIERLRYHKIIIMTDADVDGSHIQ 358
ILKSEEIKNMITAFGCGIQESFDIERLRYHKIIIMTDADVDGSHIQ
Sbjct: 459 ILKSEEIKNMITAFGCGIQESFDIERLRYHKIIIMTDADVDGSHIQ 504

124 D435V

>[ref|NP_207298.1|](#) DNA gyrase subunit B [Helicobacter pylori 26695]
[sp|P55992.1|GYRB_HELPY](#) RecName: Full=DNA gyrase subunit B
[gb|AAD07566.1|](#) DNA gyrase, sub B (gyrB) [Helicobacter pylori 26695]
Length = 773

Score = 190 bits (483), Expect = 4e-47
Identities = 100/124 (80%), Positives = 103/124 (83%)
Frame = +1

Query: 22 DNLSVGTLPGKLADCQSKDPLESEIFLVEGDSAGGSAKQGRVRFQAILPLKGKILNVEK 201
DNLSVGTLPGKLADCQSKDPLESEIFLVEGDSAGGSAKQGR RVFQAILPLKGKILNVEK
Sbjct: 394 DNLSVGTLPGKLADCQSKDPLESEIFLVEGDSAGGSAKQGRDRVFQAILPLKGKILNVEK 453