

BLASTP 2.2.10 [Oct-19-2004]

Reference: Altschul, Stephen F., 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.

Query= gi|134104092|pdb|2CFS|A Chain A, Crystal Structure Of Human Pyridoxal 5'-Phosphate Phosphatase (298 letters)

Database: nr  
6,468,149 sequences; 2,207,775,278 total letters

Sequences producing significant alignments:	Score	E
	(bits)	Value
pdb 2CFS A Chain A, Crystal Structure Of Human Pyridoxal 5'-Phos... e-141	505	
ref NP_064711.1  pyridoxal (pyridoxine, vitamin B6) phosphatase ... e-140	501	
pdb 2CFR A Chain A, Crystal Structure Of Human Pyridoxal 5'-Phos... e-138	496	
pdb 2OYC A Chain A, Crystal Structure Of Human Pyridoxal Phospha... e-138	493	
ref NP_001030207.1  pyridoxal (pyridoxine, vitamin B6) phosphata... e-132	473	
gb AAI66563.1  Unknown (protein for MGC:188190) [Rattus norvegicus] e-130	468	
sp Q8VD52 PLPP_RAT Pyridoxal phosphate phosphatase (PLP phosphat... e-129	464	
ref NP_064667.2  pyridoxal phosphate phosphatase [Mus musculus] e-127	457	
ref XP_001376550.1  PREDICTED: similar to OTTHUMP00000042130 [Mo... e-109	399	
gb AAH69982.1  Pdxp protein [Mus musculus] 2e-094	349	
gb AAH09756.2  PDXP protein [Homo sapiens] 8e-085	317	
gb AAL37168.1 AF318578_1 reg I binding protein I [Rattus norvegi... 5e-079	297	
gb AAH58388.1  Pdxp protein [Mus musculus] 3e-078	295	
ref XP_689525.1  PREDICTED: hypothetical protein [Danio rerio] 1e-070	270	
emb CAG09614.1  unnamed protein product [Tetraodon nigroviridis] 8e-064	247	
ref NP_001025809.1  hypothetical protein LOC416559 [Gallus gallus] 2e-063	245	
emb CAG04471.1  unnamed protein product [Tetraodon nigroviridis] 2e-055	219	
ref NP_997891.1  hypothetical protein LOC792824 [Danio rerio] 5e-055	218	

gb AAH37010.1  Pdxp protein [Mus musculus]	214
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ref NP_080230.2  hypothetical protein LOC67078 [Mus musculus]	211
5e-053	
ref XP_001161839.1  PREDICTED: hypothetical protein isoform 4 [P...	210
8e-053	
ref XP_213235.3  PREDICTED: similar to pyridoxal (pyridoxine, vi...	210
8e-053	
dbj BAC86732.1  unnamed protein product [Homo sapiens]	210
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gb EDM03833.1  similar to RIKEN cDNA 1700012G19 gene (predicted)...	210
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ref XP_001088993.1  PREDICTED: SH3-domain binding protein 1 [Mac...	210
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ref XP_001084229.1  PREDICTED: similar to pyridoxal (pyridoxine,...	209
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ref XP_001234473.1  PREDICTED: similar to OTTHUMP00000042130 [Ga...	209
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ref NP_001035830.1  hypothetical protein LOC283871 [Homo sapiens]	207
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ref NP_001033261.1  hypothetical protein LOC538173 [Bos taurus]	206
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ref XP_001363637.1  PREDICTED: hypothetical protein [Monodelphis...	205
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ref XP_001162359.1  PREDICTED: hypothetical protein [Pan troglod...	204
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ref XP_538386.2  PREDICTED: similar to SH3-domain binding protei...	200
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ref XP_235500.4  PREDICTED: similar to SH3 domain-binding protei...	199
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ref XP_974660.1  PREDICTED: similar to CG5567-PA [Tribolium cast...	170
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ref XP_001732277.1  hypothetical protein MGL_0052 [Malassezia gl...	142
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ref XP_001353955.1  GA18976-PA [Drosophila pseudoobscura]	142
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emb CAL54968.1  phosphoglycolate phosphatase precursor (ISS) [Os...	141
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ref XP_001352722.1	GA16941-PA [Drosophila pseudoobscura]	119
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gb ABX00714.1	AT31245p [Drosophila melanogaster]	118
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ref YP_001222730.1  conserved hypothetical protein, putative hyd...	103
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ref YP_188107.1  hydrolase, haloacid dehalogenase-like family [S...	68
9e-010	
ref NP_718344.1  UMP phosphatase [Shewanella oneidensis MR-1]	68
9e-010	
ref XP_001526026.1  conserved hypothetical protein [Lodderomyces...	67
1e-009	
gb AAQ06974.1 AF496301_1 N-acetyl glucosamine catabolic protein ...	67
1e-009	
gb AAZ99810.1  Ptx16 [Pseudomonas syringae pv. phaseolicola]	67
1e-009	
ref YP_001356516.1  HAD-superfamily hydrolase, subfamily IIA [Ni...	67
1e-009	
ref YP_562847.1  UMP phosphatase [Shewanella denitrificans OS217]	67
1e-009	
ref YP_276422.1  hydrolase, HAD-superfamily, subfamily IIA [Pseu...	67
1e-009	
ref YP_151274.1  UMP phosphatase [Salmonella enterica subsp. ent...	67
1e-009	
ref NP_455242.1  UMP phosphatase [Salmonella enterica subsp. ent...	67
1e-009	
ref ZP_02946803.1  HAD-superfamily subfamily IIA hydrolase like ...	67
2e-009	
emb CAA61932.1  AraL protein [Bacillus subtilis]	67
2e-009	
ref NP_390755.1  arabinose operon protein L [Bacillus subtilis s...	67
2e-009	
ref XP_001674311.1  Hypothetical protein CBG18893 [Caenorhabditi...	66
3e-009	
ref NP_785726.1  sugar phosphatase of the HAD superfamily (putat...	66
3e-009	
ref YP_734510.1  UMP phosphatase [Shewanella sp. MR-4]	66
3e-009	
ref YP_750294.1  UMP phosphatase [Shewanella frigidimarina NCIMB...	66
3e-009	
dbj BAG26889.1  sugar phosphatase [Lactobacillus fermentum IFO 3...	66
3e-009	
ref YP_963806.1  UMP phosphatase [Shewanella sp. W3-18-1]	66
3e-009	
ref YP_738496.1  UMP phosphatase [Shewanella sp. MR-7]	66
3e-009	
emb CAJ75726.1  predicted sugar phosphatases of the HAD superfam...	65
4e-009	
ref YP_504259.1  HAD-superfamily subfamily IIA hydrolase, hypoth...	65
4e-009	
ref YP_001048126.1  HAD-superfamily hydrolase, subfamily IA, var...	65
6e-009	

ref|XP\_319146.4| AGAP010002-PA [Anopheles gambiae str. PEST] 65  
7e-009  
ref|NP\_687906.1| hydrolase, haloacid dehalogenase-like family [S... 64  
1e-008  
ref|NP\_504597.1| K08B12.3 [Caenorhabditis elegans] 64  
1e-008  
ref|XP\_001484781.1| hypothetical protein PGUG\_02510 [Pichia guil... 64  
2e-008  
emb|CAA06779.1| hypothetical protein [Acidianus ambivalens] 64  
2e-008  
ref|YP\_193358.1| n-acetylglucosamine catabolic protein [Lactobac... 64  
2e-008

>pdb|2CFS|A Chain A, Crystal Structure Of Human Pyridoxal 5'-Phosphate  
Phosphatase  
Length = 298

Score = 505 bits (1300), Expect = e-141  
Identities = 257/298 (86%), Positives = 257/298 (86%)

Query: 1 GAMARCERLRGAALRDVLGRAQGVLFD CDGVLWNGERAVPGAPPELLERLARAGKAALFVS 60  
GAMARCERLRGAALRDVLGRAQGVLFD CDGVLWNGERAVPGAPPELLERLARAGKAALFVS  
Sbjct: 1 GAMARCERLRGAALRDVLGRAQGVLFD CDGVLWNGERAVPGAPPELLERLARAGKAALFVS 60

Query: 61 NNSRRARPELALRFARLGFGLRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXX 120  
NNSRRARPELALRFARLGFGLRAEQLFSS PGPPDAPGAVFV  
Sbjct: 61 NNSRRARPELALRFARLGFGLRAEQLFSSALCAARLLRQLPGPPDAPGAVFVLGGEG 120

Query: 121 XXXXXXXXXXXXXXXXXXXXXXXXXXXXRVRAVLVG YDEHFSFAKLREACAHLRDPECLLVATDR 180  
RVRAVLVG YDEHFSFAKLREACAHLRDPECLLVATDR  
Sbjct: 121 RAELRAAGLRLAGDPSAGDGAAPRVRAVLVG YDEHFSFAKLREACAHLRDPECLLVATDR 180

Query: 181 DPWHPLSDGSRTPGTGSLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGD 240  
DPWHPLSDGSRTPGTGSLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGD  
Sbjct: 181 DPWHPLSDGSRTPGTGSLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGD 240

Query: 241 RLETDILFGHRCGMTTVLTLTGVSRL EEAQAYLAAGQHDLVPHYYVESIADLTEGLED 298  
RLETDILFGHRCGMTTVLTLTGVSRL EEAQAYLAAGQHDLVPHYYVESIADLTEGLED  
Sbjct: 241 RLETDILFGHRCGMTTVLTLTGVSRL EEAQAYLAAGQHDLVPHYYVESIADLTEGLED 298

>ref|NP\_064711.1| pyridoxal (pyridoxine, vitamin B6) phosphatase [Homo  
sapiens]  
Length = 296

Score = 501 bits (1290), Expect = e-140  
Identities = 255/296 (86%), Positives = 255/296 (86%)

Query: 3 MARCERLRGAALRDVLGRAQGVLFD CDGVLWNGERAVPGAPPELLERLARAGKAALFVSNN 62  
MARCERLRGAALRDVLGRAQGVLFD CDGVLWNGERAVPGAPPELLERLARAGKAALFVSNN  
Sbjct: 1 MARCERLRGAALRDVLGRAQGVLFD CDGVLWNGERAVPGAPPELLERLARAGKAALFVSNN 60

Query: 63 SRRARPELALRFARLGFGLRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXX 122  
SRRARPELALRFARLGFGLRAEQLFSS PGPPDAPGAVFV  
Sbjct: 61 SRRARPELALRFARLGFGLRAEQLFSSALCAARLLRQLPGPPDAPGAVFVLGGEG 120

Query: 123 XXXXXXXXXXXXXXXXXXXXXXXXXXXXRVRAVLVG YDEHFSFAKLREACAHLRDPECLLVATDRDP 182

RVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDP  
Sbjct: 121 ELRAAGLRLAGDPSAGDGAAPRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDP 180  
Query: 183 WHPLSDGSRTPGTGSLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDR 242  
WHPLSDGSRTPGTGSLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDR  
Sbjct: 181 WHPLSDGSRTPGTGSLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDR 240  
Query: 243 ETDILFGHRCGMTTVLTTLTGVSRLLEEAQAYLAAGQHDLVPHYYVESIADLTEGLED 298  
ETDILFGHRCGMTTVLTTLTGVSRLLEEAQAYLAAGQHDLVPHYYVESIADLTEGLED  
Sbjct: 241 ETDILFGHRCGMTTVLTTLTGVSRLLEEAQAYLAAGQHDLVPHYYVESIADLTEGLED 296

>pdb|2CFR|A Chain A, Crystal Structure Of Human Pyridoxal 5'-Phosphate  
Phosphatase  
Length = 298

Score = 496 bits (1276), Expect = e-138  
Identities = 253/298 (84%), Positives = 253/298 (84%)

Query: 1 GAMARCERLRGAALRDVLGRAQGVLFDCDGVWNGERAVPGAPPELLERLARAGKAALFVS 60  
GA ARCERLRGAALRDVLGRAQGVLFDCDGVWNGERAVPGAPPELLERLARAGKAALFVS  
Sbjct: 1 GAXARCERLRGAALRDVLGRAQGVLFDCDGVWNGERAVPGAPPELLERLARAGKAALFVS 60  
Query: 61 NNSRRARPELALRFARLGFGLRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXX 120  
NNSRRARPELALRFARLGFGLRAEQLFSS PGPPDAPGAVFV  
Sbjct: 61 NNSRRARPELALRFARLGFGLRAEQLFSSALCAARLLRQLPGPPDAPGAVFVLGGEG 120  
Query: 121 XXXXXXXXXXXXXXXXXXXXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDR 180  
RVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDR  
Sbjct: 121 RAELRAAGLRLAGDPSAGDGAAPRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDR 180  
Query: 181 DPWHPLSDGSRTPGTGSLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGD 240  
DPWHPLSDGSRTPGTGSLAAAVETASGRQALVVGKPSPY FECITENFSIDPARTL VGD  
Sbjct: 181 DPWHPLSDGSRTPGTGSLAAAVETASGRQALVVGKPSPYXFECITENFSIDPARTLXVGD 240  
Query: 241 RLETDILFGHRCGMTTVLTTLTGVSRLLEEAQAYLAAGQHDLVPHYYVESIADLTEGLED 298  
RLETDILFGHRCG TTVLTTLTGVSRLLEEAQAYLAAGQHDLVPHYYVESIADLTEGLED  
Sbjct: 241 RLETDILFGHRCGXTTVLTTLTGVSRLLEEAQAYLAAGQHDLVPHYYVESIADLTEGLED 298

>pdb|20YC|A Chain A, Crystal Structure Of Human Pyridoxal Phosphate  
Phosphatase  
Length = 306

Score = 493 bits (1270), Expect = e-138  
Identities = 251/297 (84%), Positives = 253/297 (85%)

Query: 2 AMARCERLRGAALRDVLGRAQGVLFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSN 61  
++ARCERLRGAALRDVLGRAQGVLFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSN  
Sbjct: 2 SLARCERLRGAALRDVLGRAQGVLFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSN 61  
Query: 62 NSRRARPELALRFARLGFGLRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXX 121  
NSRRARPELALRFARLGFGLRAEQLFSS PGPPDAPGAVFV  
Sbjct: 62 NSRRARPELALRFARLGFGLRAEQLFSSALCAARLLRQLPGPPDAPGAVFVLGGEG 121  
Query: 122 XXXXXXXXXXXXXXXXXXXXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDR 181  
RVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDR

Sbjct: 122 AELRAAGLRLAGDPSAGDGAAPRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRD 181  
Query: 182 PWHPLSDGSRTPGTGSLLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDR 241  
PWHPLSDGSRTPGTGSLLAAAVETASGRQALVVGKPSPY FECITENFSIDPARTL VGDR  
Sbjct: 182 PWHPLSDGSRTPGTGSLLAAAVETASGRQALVVGKPSPYXFECITENFSIDPARTLXVGDR 241  
Query: 242 LETDILFGHRCGTTVLTLTGVSRLLEEAQAYLAAGQHDLVPHYYVESIADLTEGLED 298  
LETDILFGHRCG TTVLTLTGVSRLLEEAQAYLAAGQHDLVPHYYVESIADLTEGLED  
Sbjct: 242 LETDILFGHRCGXTTVLTLTGVSRLLEEAQAYLAAGQHDLVPHYYVESIADLTEGLED 298

>ref|NP\_001030207.1| pyridoxal (pyridoxine, vitamin B6) phosphatase [Bos taurus]

Length = 296

Score = 473 bits (1216), Expect = e-132  
Identities = 240/296 (81%), Positives = 247/296 (83%)

Query: 3 MARCERLRGAALRDVLGRAQGVLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNN 62  
MARCERLRGAALRDV+GRAQGVLFDC+GVWNGERAVPGAPELLERLA+AGKA LFVSNN  
Sbjct: 1 MARCERLRGAALRDVVGRAQGVLFDCNGVWNGERAVPGAPELLERLAQAGKATLFVSNN 60  
Query: 63 SRRARPELALRFARLGFGLRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXX 122  
SRRARPELALRFARLGFGLR+EQLFSS GPPD GAVFV  
Sbjct: 61 SRRARPELALRFARLGFGLRSEQLFSSALCAARLLRQRLGPPDTPQGAVFVVLGGEGLR 120  
Query: 123 XXXXXXXXXXXXXXXXXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDP 182  
RVRAVLVGYDEHFSFAKL EACAHLRDP+CLLVATDRDP  
Sbjct: 121 ELRAAGLRLAGDPSDPAAPRVRAVLVGYDEHFSFAKLSEACAHLRDPDCLLVATDRDP 180  
Query: 183 WHPLSDGSRTPGTGSLLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRL 242  
WHPLSDGSRTPGTGSLLAAAVETASGRQALVVGKPSPYMFECITE+FS+DP RPLMVGDR  
Sbjct: 181 WHPLSDGSRTPGTGSLLAAAVETASGRQALVVGKPSPYMFECITEHFSVDPGRTLMVGDRL 240  
Query: 243 ETDILFGHRCGTTVLTLTGVSRLLEEAQAYLAAGQHDLVPHYYVESIADLTEGLED 298  
ETDILFGHRCGTTVLTLTGVS LEEAQAYLAAGQHDLVPHYYVESIADL EGLED  
Sbjct: 241 ETDILFGHRCGTTVLTLTGVSLEEAQAYLAAGQHDLVPHYYVESIADLMEGLED 296

>gb|AAI66563.1| Unknown (protein for MGC:188190) [Rattus norvegicus]

Length = 292

Score = 468 bits (1205), Expect = e-130  
Identities = 239/296 (80%), Positives = 248/296 (83%), Gaps = 4/296 (1%)

Query: 3 MARCERLRGAALRDVLGRAQGVLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNN 62  
MARCERLRGAALRDVLG+AQGVLFDCDGVWNGER VPGAPELL+RLA+AGKA LFVSNN  
Sbjct: 1 MARCERLRGAALRDVLGQAQGVLFDCDGVWNGERIVPGAPELLQRLAQAGKATLFVSNN 60  
Query: 63 SRRARPELALRFARLGFGLRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXX 122  
SRRARPELALRFARLGF GLRAE+LFSS PGPPDAPGAVFV  
Sbjct: 61 SRRARPELALRFARLGFGLRAEELFSSAVCAARLLRQRLPGPPDAPGAVFVVLGGEGLR 120  
Query: 123 XXXXXXXXXXXXXXXXXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDP 182  
RVRAVLVGYDEHFSFAKL EACAHLRDP+CLLVATDRDP  
Sbjct: 121 ELRAAGLRLAGDPGDDP----RVRAVLVGYDEHFSFAKLTEACAHLRDPDCLLVATDRDP 176

Query: 183 WHPLSDGSRTPGTGSLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRL 242  
WHPL+DGSRTPTGTGSLAAAVETASGRQALVVGKPSPYMF+CITE+FS+DPAR LMVGDRL  
Sbjct: 177 WHPLTDGSRTPGTGSLAAAVETASGRQALVVGKPSPYMFQCITEDFSVDPARMLMVGDRL 236

Query: 243 ETDILFGHRCGMTTTLTGTGVSRLLEEAQAYLAAGQHDLVPHYYVESIADLTEGLED 298  
ETDILFGHRCGMTTTLTGTGVS LEEAQAYLAAGQHDLVPHYYVESIADL EGGLEL  
Sbjct: 237 ETDILFGHRCGMTTTLTGTGVSLEEAQAYLAAGQHDLVPHYYVESIADLMEGLEL 292

>sp|Q8VD52|PLPP\_RAT Pyridoxal phosphate phosphatase (PLP phosphatase) (Reg I-binding

protein 1)  
Length = 309

Score = 464 bits (1194), Expect = e-129  
Identities = 237/294 (80%), Positives = 246/294 (83%), Gaps = 4/294 (1%)

Query: 3 MARCERLRGAALRDVLGRAQGVLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNN 62  
MARCERLRGAALRDVLG+AQGVLFDCDGVWNGER VPGAPELL+RLA+AGKA LFVSNN  
Sbjct: 1 MARCERLRGAALRDVLGQAQGVLFDCDGVWNGERIVPGAPELLQRLAQAGKATLFVSNN 60

Query: 63 SRRARPELALRFARLGFGLRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXX 122  
SRRARPELALRFARLGF GLRAE+LFSS PGPPDAPGAVFV  
Sbjct: 61 SRRARPELALRFARLGFGLRAEELFSSAVCAARLLRQLRPGPPDAPGAVFVVLGGGLRA 120

Query: 123 XXXXXXXXXXXXXXXXXXXXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRDPCELLVATDRDP 182  
RVRAVLVGYDEHFSFAKL EACAHLRDP+CLLVATDRDP  
Sbjct: 121 ELRAAGLRLAGDPGDDP----RVRAVLVGYDEHFSFAKLTEACAHLRDPCELLVATDRDP 176

Query: 183 WHPLSDGSRTPGTGSLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRL 242  
WHPL+DGSRTPTGTGSLAAAVETASGRQALVVGKPSPYMF+CITE+FS+DPAR LMVGDRL  
Sbjct: 177 WHPLTDGSRTPGTGSLAAAVETASGRQALVVGKPSPYMFQCITEDFSVDPARMLMVGDRL 236

Query: 243 ETDILFGHRCGMTTTLTGTGVSRLLEEAQAYLAAGQHDLVPHYYVESIADLTEGL 296  
ETDILFGHRCGMTTTLTGTGVS LEEAQAYLAAGQHDLVPHYYVESIADL EGL  
Sbjct: 237 ETDILFGHRCGMTTTLTGTGVSLEEAQAYLAAGQHDLVPHYYVESIADLMEGLEL 290

>ref|NP\_064667.2| pyridoxal phosphate phosphatase [Mus musculus]  
Length = 292

Score = 457 bits (1175), Expect = e-127  
Identities = 235/296 (79%), Positives = 243/296 (82%), Gaps = 4/296 (1%)

Query: 3 MARCERLRGAALRDVLGRAQGVLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNN 62  
MARCERLRGAALRDVLG+AQGVLFDCDGVWNGER VPGAPELL+RLARAGK LFVSNN  
Sbjct: 1 MARCERLRGAALRDVLGQAQGVLFDCDGVWNGERIVPGAPELLQRLARAGKNTLFVSNN 60

Query: 63 SRRARPELALRFARLGFGLRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXX 122  
SRRARPELALRFARLGF GLRAEQLFSS GPPDA GAVFV  
Sbjct: 61 SRRARPELALRFARLGFAGLRAEQLFSSALCAARLLRQLRSGPPDASGAVFVVLGGGLRA 120

Query: 123 XXXXXXXXXXXXXXXXXXXXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRDPCELLVATDRDP 182  
RVRAVLVGYDE FSF++L EACAHLRDP+CLLVATDRDP  
Sbjct: 121 ELRAAGLRLAGDPGEDP----RVRAVLVGYDEQFSFRLTEACAHLRDPCELLVATDRDP 176

Query: 183 WHPLSDGSRTPGTGSLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRL 242

WHPLSDGSRTPGTGS LAAAVETASGRQALVVGKPSPYMF+CITE+FS+DPARTLMVGDRL  
Sbjct: 177 WHPLSDGSRTPGTGS LAAAVETASGRQALVVGKPSPYMFQCITEDFSVDPARTLMVGDRL 236

Query: 243 ETDILFGHRCGM TTVLTLTGVSRL EEAQAYLAAGQHDLVPHYYVESIADLTEGLED 298

ETDILFGHRCGM TTVLTLTGVS LEEAQAYL AGQ DLVPHYYVESIADL EGLED

Sbjct: 237 ETDILFGHRCGM TTVLTLTGVS SLEEAQAYLTAGQRDLVPHYYVESIADLMEGLED 292

>ref|XP\_001376550.1| PREDICTED: similar to OTTHUMP00000042130 [Monodelphis domestica]

Length = 289

Score = 399 bits (1025), Expect = e-109

Identities = 211/295 (71%), Positives = 224/295 (75%), Gaps = 7/295 (2%)

Query: 3 MARCERLRGAALRDVLGRAQGVLFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNN 62

MA CERL G ALR++L R QGVLFDCDGVWNGE AV GAPELLERL R GKAALFVSNN

Sbjct: 1 MAVCERLGGNALRELLARTQGVLFDCDGVWNGELAVTGAPELLERLGRGGKAALFVSNN 60

Query: 63 SRRARPELALRFARLGFGLRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXX 122

SRR+ ELA RFARLGF G+ AEQLFSS P P PGAVFV

Sbjct: 61 SRRSVEELAAARFARLGFGRVAAEQLFSSALCAARLLRQRLRPRCP-PGAVFVLGGEGLRG 119

Query: 123 XXXXXXXXXXXXXXXXXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDP 182

VRAVLVGYDEHF+FAKL EACAHLRDP+CLLVATD DP

Sbjct: 120 ELRAAGLRLAGDEPGP-----VRAVLVGYDEHFTFAKLSEACAHLRDPDCLLVATDVDP 173

Query: 183 WHPLSDGSRTPGTGS LAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRL 242

WHPLSDG TPGTGS LAAAVETASGRQALVVGKPS YMFECITE F +DPARTLMVGDRL

Sbjct: 174 WHPLSDGR TTPGTGS LTA AVETASGRQALVVGKPS TYMFECITERFGVDPARTLMVGDRL 233

Query: 243 ETDILFGHRCGM TTVLTLTGVSRL EEAQAYLAAGQHDLVPHYYVESIADLTEGLE 297

ETDILFGHRCG+TTVLTLTGVSRL E+AQAYLAAG+ +LVPHYYV+S+ADL GLE

Sbjct: 234 ETDILFGHRCGLTTVLTLTGVSRL EEAQAYLAAGKPELVPHYYVDSVADLMAGLE 288

>gb|AAH69982.1| Pdxp protein [Mus musculus]

Length = 233

Score = 349 bits (895), Expect = 2e-094

Identities = 181/237 (76%), Positives = 187/237 (78%), Gaps = 4/237 (1%)

Query: 62 NSRRARPELALRFARLGFGLRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXX 121

NSRRARPELALRFARLGF GLRAEQLFSS GPPDA GAVFV

Sbjct: 1 NSRRARPELALRFARLGFAGLRAEQLFSSALCAARLLRQRLSGPPDASGAVFVLGGEGLR 60

Query: 122 XXXXXXXXXXXXXXXXXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRD 181

RVRAVLVGYDE FSF++L EACAHLRDP+CLLVATDRD

Sbjct: 61 AELRAAGLRLAGDPGEDP----RVRAVLVGYDEQFSFRLTEACAHLRDPDCLLVATDRD 116

Query: 182 PWHPLSDGSRTPGTGS LAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRL 241

PWHPLSDGSRTPGTGS LAAAVETASGRQALVVGKPSPYMF+CITE+FS+DPARTLMVGDRL

Sbjct: 117 PWHPLSDGSRTPGTGS LAAAVETASGRQALVVGKPSPYMFQCITEDFSVDPARTLMVGDRL 176

Query: 242 LETDILFGHRCGM TTVLTLTGVSRL EEAQAYLAAGQHDLVPHYYVESIADLTEGLED 298

LETDILFGHRCGM TTVLTLTGVS LEEAQAYL AGQ DLVPHYYVESIADL EGLED

Sbjct: 177 LETDILFGHRCGM TTVLTLTGVS SLEEAQAYLTAGQRDLVPHYYVESIADLMEGLED 233

>gb|AAH09756.2| PDXP protein [Homo sapiens]  
Length = 176

Score = 317 bits (811), Expect = 8e-085  
Identities = 155/155 (100%), Positives = 155/155 (100%)

Query: 144 RVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGSGLAAAVE 203  
RVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGSGLAAAVE  
Sbjct: 22 RVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGSGLAAAVE 81

Query: 204 TASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMTTVLTLTG 263  
TASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMTTVLTLTG  
Sbjct: 82 TASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMTTVLTLTG 141

Query: 264 SRLEEAQAYLAAGQHDLVPHYYVESIADLTEGLED 298  
SRLEEAQAYLAAGQHDLVPHYYVESIADLTEGLED  
Sbjct: 142 SRLEEAQAYLAAGQHDLVPHYYVESIADLTEGLED 176

>gb|AAL37168.1|AF318578\_1 reg I binding protein I [Rattus norvegicus]  
Length = 204

Score = 297 bits (761), Expect = 5e-079  
Identities = 144/153 (94%), Positives = 149/153 (97%)

Query: 144 RVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGSGLAAAVE 203  
RVRAVLVGYDEHFSFAKL EACAHLRDP+CLLVATDRDPWHPL+DGSRTPGTGSGLAAAVE  
Sbjct: 33 RVRAVLVGYDEHFSFAKLTEACAHLRDPDCLLVATDRDPWHPLTDGSRTPGTGSGLAAAVE 92

Query: 204 TASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMTTVLTLTG 263  
TASGRQALVVGKPSPYMF+CITE+FS+DPAR LMVGDRLDILFGHRCGMTTVLTLTG  
Sbjct: 93 TASGRQALVVGKPSPYMFQCITEDFSVDPARMLMVGDRLDILFGHRCGMTTVLTLTG 152

Query: 264 SRLEEAQAYLAAGQHDLVPHYYVESIADLTEGL 296  
S LEEAQAYLAAGQHDLVPHYYVESIADL EGL  
Sbjct: 153 SSLEEAQAYLAAGQHDLVPHYYVESIADLMEGL 185

>gb|AAH58388.1| Pdxp protein [Mus musculus]  
Length = 157

Score = 295 bits (755), Expect = 3e-078  
Identities = 143/155 (92%), Positives = 149/155 (96%)

Query: 144 RVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGSGLAAAVE 203  
RVRAVLVGYDE FSF++L EACAHLRDP+CLLVATDRDPWHPLSDGSRTPGTGSGLAAAVE  
Sbjct: 3 RVRAVLVGYDEQFSFRLTEACAHLRDPDCLLVATDRDPWHPLSDGSRTPGTGSGLAAAVE 62

Query: 204 TASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMTTVLTLTG 263  
TASGRQALVVGKPSPYMF+CITE+FS+DPARTLMVGDRLDILFGHRCGMTTVLTLTG  
Sbjct: 63 TASGRQALVVGKPSPYMFQCITEDFSVDPARTLMVGDRLDILFGHRCGMTTVLTLTG 122

Query: 264 SRLEEAQAYLAAGQHDLVPHYYVESIADLTEGLED 298  
S LEEAQAYL AGQ DLVPHYYVESIADL EGLED  
Sbjct: 123 SSLEEAQAYLTAGQRDLVPHYYVESIADLMEGLED 157



>ref|XP\_689525.1| PREDICTED: hypothetical protein [Danio rerio]  
Length = 308

Score = 270 bits (689), Expect = 1e-070  
Identities = 146/300 (48%), Positives = 181/300 (60%), Gaps = 7/300 (2%)

Query: 6 CERLRGAALRDVLRGAVQVLFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNRR 65  
C LRGA +RD+L VLFDCDGV+WNGE AV GAPE++ L + GK FV+NN R  
Sbjct: 8 CVALRGAQIRDLLDAKHNVLFDCDGVWNGETAVAGAPEVVSLLKQRGKRVFFVTNNCTR 67

Query: 66 ARPELALRFARLGFGLRAEQLFSSX--XXXXXXXXXXXXPGPPDA--PGAVFVXXXXXXXX 121  
R +F+RLGF + E++FSS G A G V  
Sbjct: 68 PRENYVQKFSRLGFADVAEEEEIFSSAYCSAAYLRDVARLQGVYAIGGGVVKELRDAGV 127

Query: 122 XXXXXXXXXXXXXXXXXXXXXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRD 181  
VRAVLVGYDE F+F KL +AC +LRD ECL +ATD D  
Sbjct: 128 PVVEEPAEQEETSINCPDPDVRRAVLVGYDESFTFMKLAKACCYLRLDAECLFLATDPD 187

Query: 182 PWHPLSDGSRTPGTGLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDR 241  
PWHPL G TPG+GSL AA+ETAS R+A V+GKPS +MF+CI+ F +DP+R+LM+GDR  
Sbjct: 188 PWHPLRGGIRITPGSGSLTAALETASSRKATVIGKPSRFMFDCISSQFDLDPSSLMIGDR 247

Query: 242 LETDILFGHRCGMMTTLTTLTGVSRLLEEAQAY---LAAGQHDLVPHYYVESIADLTEGLED 298  
LETDILFG CG++TVLTLTGVS L+EAQ Y + Q D P + VES+AD + LE+  
Sbjct: 248 LETDILFGSNCGLSTVLTTLTGVSSTLDEAQRYSQSPKDCAPDFVVEVADFLQVLEE 307

>emb|CAG09614.1| unnamed protein product [Tetraodon nigroviridis]  
Length = 302

Score = 247 bits (630), Expect = 8e-064  
Identities = 134/296 (45%), Positives = 174/296 (58%), Gaps = 14/296 (4%)

Query: 6 CERLRGAALRDVLRGAVQVLFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNRR 65  
C+++ GA +R +L +LFDGCDGV+WNGE+A+ GA ++ L R GK +FV+NN R  
Sbjct: 10 CQKIGGAQIRSLLAAKDFILFDCDGVWNGEKAIAGAVAVVSSLIRLGKNVFFVTNNCTR 69

Query: 66 ARPELALRFARLGFGLRAEQLFSSXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXX 125  
R +F RLGF + EQ+FSS G VFV  
Sbjct: 70 PRENYVHKFCRLGFTDVMLEQIFSSSYCSALYL RDVV----QVRGQVFVIGCDGLRRELQ 125

Query: 126 XXX-----XXXXXXXXXXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATD 179  
V+AVLVG+D+ +F KL +A +LRDP+CL +ATD  
Sbjct: 126 EAGVPCLEDADEPNATIFDCALAPDVKAVLVGHDDKMTFLKAKASCYLRLDPDCLFLATD 185

Query: 180 RDPWHPLSDGSRTPGTGLAAAVETASGRQALVVGKPSPYMFECITENFS-IDPARTLMV 238  
DPWHPLS G PG+GSL AA+E ASGR+A V+GKPS +MFECI+ FS +DPA+ LM+  
Sbjct: 186 NDPWHPLSSGRILPGSGSLTAALEVASGRKATVIGKPSRFMFECISSQFSGVDPAQCLMI 245

Query: 239 GDRLETDILFGHRCGMMTTLTTLTGVSRLLEEAQAY---LAAGQHDLVPHYYVESIAD 291  
GDRL+TD+LFG CG+ TVLTLTGVS++EEAQ Y LVP Y V++IAD  
Sbjct: 246 GDRLQTDMLFGSNCGLDTVLTTLTGVSQMEEAQEYSNSQLTSHRSLVPDYVVDTIAD 301

>ref|NP\_001025809.1| hypothetical protein LOC416559 [Gallus gallus]

Length = 312

Score = 245 bits (626), Expect = 2e-063

Identities = 144/307 (46%), Positives = 172/307 (56%), Gaps = 15/307 (4%)

Query: 5 RCERLRGAALRDVLGRAQGVLFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNSR 64  
RC RL G R VL +LFDGCDGVW GE A+ GAP L RLA AGK +V+NNS  
Sbjct: 8 RCRRLEGETARAVLANVDTLFDCDGVWLRGEAALSGAPAALGRLAAAGKRLCYVTNNS 67

Query: 65 RARPELALRFARLGFGLRAEQLFSSXXXXXXXXXXXXP-----GPPDAPGAVFVX 115  
R R + RLGf +F S P GP A A  
Sbjct: 68 RTRVAYTEKLRRLGFPPAEPRHVFGSAFCAARYLRQALPPGAAAYVLGGP--ALSAELEA 125

Query: 116 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHL-RDPECL 174  
VRAVLVG+DEHFS+AKL +A +L R P+CL  
Sbjct: 126 AGIPHLGPGPAALPGPAPADWAQAPLEPAVRAVLVGFDEHFSYAKLCQALRYLLRGPDC 185

Query: 175 LVATDRDPWHPLSDGSRTPGTGLAAAVETASGRQALVVGKPSPYMFECITENFSIDPAR 234  
LV T+RD PL GS PGTG L AVETA+ R+AL+VGKPS Y+F+C+ F IDPAR  
Sbjct: 186 LVGTNRDNRPLLEGGSAIPGTGCLVKAVETAAREALIVGKPSRYIFDCVASEFDIDPAR 245

Query: 235 TLMVGDRLLETDILFGHRCGMTTVLTTLTGVSRLLEEQAAYLAA---GQHDLPVPHYVESIAD 291  
T+MVGDRl+TDIL G+ CG+TT+LTLTGVS LEE + + + + LVP YYV+SIAD  
Sbjct: 246 TIMVGDRLDITDILMGNTCGLTLLTLTGVSRLLEEVRGHQESDCPARQGLVPDYVDSIAD 305

Query: 292 LTEGLE 298  
L LED  
Sbjct: 306 LLPAL 312

>emb|CAG04471.1| unnamed protein product [Tetraodon nigroviridis]  
Length = 315

Score = 219 bits (557), Expect = 2e-055

Identities = 124/307 (40%), Positives = 168/307 (54%), Gaps = 18/307 (5%)

Query: 4 ARCERLRGAALRDVLGRAQGVLFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNS 63  
A+C RL GA ++ +L VLFDCDGV+W G++A+PGAP+++ L + GK FV+NNS  
Sbjct: 13 AKCVRLNGALIKQLLDSVDSVLFDCDGVWIRGDQAIIPGAPQVINLLKQKGVHFFVTNNS 72

Query: 64 RRARPELALRFARLGFGLRAEQLFSSXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXX 123  
+ R A + A LGF + E++F + G V++  
Sbjct: 73 TKTRKMYADKMASLGFN-VSEEEIFGTAYCCARYLKSVC----GLEGKVYLIGSPAMEQE 127

Query: 124 XXXXXXXXXXXXXXXXXXXXXXXR-----VRAVLVGYDEHFSFAKLREACAHLRDPEC 173  
V+AV+VG+DEHFS+ KL A +L  
Sbjct: 128 LEAVGIRQTGAGPDLIAGKQNDWANVALDPEVKAVVVGDFEHSYMKLNRLALQYLSQRGS 187

Query: 174 LLVATDRDPWHPLSDGSRTPGTGLAAAVETASGRQALVVGKPSPYMFECITENFSIDPA 233  
L V T+RD PL +G PGTG L AVETA+ RQA VGKPS YMF+C+ F ++P  
Sbjct: 188 LFVGTNRDTRLPLEEGRAVPGTGCLLQAVETAQRQAHTVKGKPSHYMFCVASQFPVEPG 247

Query: 234 RTL MVGDRLLETDILFGHRCGMTTVLTTLTGVSRLLEEQAAYLAAG---QHDLPVPHYVESIA 290  
R LMVGDRL+TDIL G CG+ T+LTLTGVS L +A+ + A+G + +VP YYVESIA  
Sbjct: 248 RCLMVGDRLDITDILLGSNCGLRLLTLTGVSRLADAEHRASGCPQRQAMVPDYVESIA 307

Query: 291 DLTEGLE 297

D+ L+  
Sbjct: 308 DVLPALQ 314

>ref|NP\_997891.1| hypothetical protein LOC792824 [Danio rerio]  
Length = 306

Score = 218 bits (554), Expect = 5e-055  
Identities = 124/309 (40%), Positives = 168/309 (54%), Gaps = 18/309 (5%)

Query: 2 AMARCERLRGAALRDVLGRAQGVLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSN 61  
A ++C RL GA R +L VLFDCDGV+W G++A+PGAPE++ L + GK FV+N  
Sbjct: 2 AASKCVRLNGALSRQLLDSVDCVLFDCDGVWIRGDQAIPGAPEVINSLKKHGKQVFFVTN 61

Query: 62 NSRRARPELALRFARLGFGLRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXX 121  
NS + R A + +LGF A+++F + G V++  
Sbjct: 62 NSTKTRQMYADKLGKLGFDAA-ADEVFGTAYCSAQYLKNVCK----LDGKVYLIGSKAMK 116

Query: 122 XXXXXXXX-----XXXXXXXXXXXXXXXXRVRVAVLVGYDEHFSFAKLREACAHLRDP 171  
V+AVLVG+DEHFS+ KL A +L DP  
Sbjct: 117 QELEEVIQIPVGVGPDILISGVQIDWANVPLDQEVQAVLVGFDEHFSYMKLNRLQYLCDP 176

Query: 172 ECLLVATDRDPWHPLSDGSRTPGTGLAAAVETASGRQALVVGKPSPYMFECITENFSID 231  
+C V T+ D PL G PGTG L AVETA+ RQA VVGKPS +MFEC+ F++  
Sbjct: 177 DCQFVGTNTDTRLPLEGGKAVPGTGCLLRVETAAQRQAQVVGKPSNFMFECVASQFNLK 236

Query: 232 PARTLMVGDRLLETDILFGHRCGMTTVLTLTGVSRLLEEAQAYLAA---GQHDLVPHYYVES 288  
P R LMVGDRL+TDI+ G CG+ T+LTLTGVS + EA+A + +VP YY++S  
Sbjct: 237 PQRCLMVGDRLDITDMLGNSNCGKLTLLTLTGVSSTVAEAEANQKSECPQKQRMVPDYYIDS 296

Query: 289 IADLTEGLE 297  
IAD+ L+  
Sbjct: 297 IADILPALQ 305

>gb|AAH37010.1| Pdxp protein [Mus musculus]  
Length = 117

Score = 214 bits (545), Expect = 6e-054  
Identities = 106/113 (93%), Positives = 109/113 (96%)

Query: 186 LSDGSRTPGTGLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLLETD 245  
LSDGSRTPGTGLAAAVETASGRQALVVGKPSPYMF+CITE+FS+DPARTLMVGDRLLETD  
Sbjct: 5 LSDGSRTPGTGLAAAVETASGRQALVVGKPSPYMFQCITEDFSVDPARTLMVGDRLLETD 64

Query: 246 ILFGHRCGMTTVLTLTGVSRLLEEAQAYLAAGQHDLVPHYYVESIADLTEGLED 298  
ILFGHRCGMTTVLTLTGVS LEEAQAYL AGQ DLVPHYYVESIADL EGLED  
Sbjct: 65 ILFGHRCGMTTVLTLTGVSRLLEEAQAYLTAGQRDLVPHYYVESIADLMEGLED 117

>ref|NP\_080230.2| hypothetical protein LOC67078 [Mus musculus]  
Length = 321

Score = 211 bits (537), Expect = 5e-053  
Identities = 123/313 (39%), Positives = 166/313 (53%), Gaps = 16/313 (5%)

Query: 1 GAMARCERLRGAALRDVLGRAQGVLFDCDGVWNGERAVPGAPELLERLARAGKAALFVS 60

G ARC RL + +L +LFDCDGVW GE AVPGAPE L L GK F++  
 Sbjct: 8 GDEARCVRLSAERAKLLLAEVDTLLFDCDGVWLRGETAVPGAPELTRALRARGKRLGFIT 67  
 Query: 61 NNSRRARPELALRFARLGFGLRAEQ----LFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXX 116  
 NNS + R A + RLGF GG + +F + G PD V  
 Sbjct: 68 NNSKTRTAYAEKLRRLGFGGPVGPEAGLEVFGTAYCSALYLRQLAGVPDPKAYVLGSP 127  
 Query: 117 XXXXXXXXXXXXXXXXXXXXXXXXXXXXR-----VRAVLVGYDEHFSFAKLREACAH 167  
 VRAV+VG+D HFS+ KL +A +  
 Sbjct: 128 ALAAELEAVGVTSVGVGPDVHLHGDGPSDWLAVPLEPDVRAVVVGFDPHFSYMKLTKAVRY 187  
 Query: 168 LRDPECLLVATDRDPWHPLSDGSRTPGTGSLAAAVETASGRQALVVGKPSYMFECITEN 227  
 L+ P+CLLV T+ D PL +G GTG L AVE A+ RQA ++GKPS ++F+C+++  
 Sbjct: 188 LQQPDCLLVGTNMDNRLPLENGRFIAGTGCLVRAVEMAAQRQADIIGKPSRFIFDCVSQE 247  
 Query: 228 FSIDPARTLMVGDRLLETDILFGHRCGMTTTLTGTGVSRLAEAQAYLAAG---QHDLVPHY 284  
 + I+P RT+MVGDR L+TDIL G C + T+LTLTGVS LE+ ++ + + +VP +  
 Sbjct: 248 YGINPERTVMVGDRLDITDILLGSTCSLKTILTTLTGVSLELVKSNQESDCMFKKKMVPDF 307  
 Query: 285 YVESIADLTEGLE 297  
 YV+SIADL L+  
 Sbjct: 308 YVDSIADLLPALQ 320

>ref|XP\_001161839.1| PREDICTED: hypothetical protein isoform 4 [Pan  
 troglodytes]  
 Length = 669

Score = 210 bits (535), Expect = 8e-053  
 Identities = 107/114 (93%), Positives = 109/114 (95%), Gaps = 1/114 (0%)

Query: 185 PLSDGSRTPGTGSLAAAVETASGRQALVVGKPSYMFECITENFSIDPARTLMVGDRLLET 244  
 P+ D +R TGSLAAAVETASGRQALVVGKPSYMFECITENFSIDPARTLMVGDRLLET  
 Sbjct: 557 PVEDMARR-STGSLAAAVETASGRQALVVGKPSYMFECITENFSIDPARTLMVGDRLLET 615  
 Query: 245 DILFGHRCGMTTTLTGTGVSRLAEAQAYLAAGQHDLVPHYVESIADLTEGLE 298  
 DILFGHRCGMTTTLTGTGVSRLAEAQAYLAAGQHDLVPHYVESIADLTEGLE  
 Sbjct: 616 DILFGHRCGMTTTLTGTGVSRLAEAQAYLAAGQHDLVPHYVESIADLTEGLE 669

>ref|XP\_213235.3| PREDICTED: similar to pyridoxal (pyridoxine, vitamin B6)  
 phosphatase [Rattus norvegicus]  
 Length = 418

Score = 210 bits (535), Expect = 8e-053  
 Identities = 122/313 (38%), Positives = 165/313 (52%), Gaps = 16/313 (5%)

Query: 1 GAMARCERLRGAALRDVLGRAQGVLFDCDGVWNGERAVPGAPELLERLARAGKAALFVS 60  
 G RC RL + +L +LFDCDGVW GE AVPGAPE L L GK F++  
 Sbjct: 105 GDEVRCVRLSAERAKLLLAEVDTLLFDCDGVWLRGETAVPGAPELTRALRARGKRLGFIT 164  
 Query: 61 NNSRRARPELALRFARLGFGLRAEQ----LFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXX 116  
 NNS + R A + RLGF GG + +F + G PD V  
 Sbjct: 165 NNSKTRTAYAEKLRRLGFGGPVGPEAGLEVFGTAYCSALYLRQLAGVPDPKAYVLGSP 224  
 Query: 117 XXXXXXXXXXXXXXXXXXXXXXXXXXXXR-----VRAVLVGYDEHFSFAKLREACAH 167  
 VRAV+VG+D HFS+ KL +A +

Sbjct: 225 ALAAELEAVGVTSVGVGPDVHLHGDGSPDWLAVPLEPDVRAVVVGFDPHFSYMKLTKAVRY 284  
Query: 168 LRDPECLLVATDRDPWHPLSDGSRTPGTGSLLAAAVETASGRQALVVGKPSPYMFECITEN 227  
L+ P+CLLV T+ D PL +G GTG L AVE A+ RQA ++GKPS ++F+C+++  
Sbjct: 285 LQQPDCLLVGTNMDNRLPLENGRFIAGTGCLVRAVEMAAQRQADIIGKPSRFIFDCVSQE 344  
Query: 228 FSIDPARTLMVGDRLLETDILFGHRCGTTVLTTLTGVSRLLEEAQAYLAAG---QHDLVPHY 284  
+ I+P RT+MVGDR+TDIL G C + T+LTLTGVS LE+ ++ + + +VP +  
Sbjct: 345 YGINPERTVMVGDRLDITDILLGSTCSLKTILTTLTGVSLEEDVKSQESDCMFKKKMVPDF 404  
Query: 285 YVESIADLTEGLE 297  
YV+SIADL L+  
Sbjct: 405 YVDSIADLLPALQ 417

>dbj|BAC86732.1| unnamed protein product [Homo sapiens]  
Length = 605

Score = 210 bits (535), Expect = 8e-053  
Identities = 107/114 (93%), Positives = 109/114 (95%), Gaps = 1/114 (0%)

Query: 185 PLSDGSRTPGTGSLLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLLET 244  
P+ D +R TGSLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLLET  
Sbjct: 493 PVEDMARR-STGSLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLLET 551  
Query: 245 DILFGHRCGTTVLTTLTGVSRLLEEAQAYLAAGQHDLVPHYVESIADLTEGLED 298  
DILFGHRCGTTVLTTLTGVSRLLEEAQAYLAAGQHDLVPHYVESIADLTEGLED  
Sbjct: 552 DILFGHRCGTTVLTTLTGVSRLLEEAQAYLAAGQHDLVPHYVESIADLTEGLED 605

>gb|EDM03833.1| similar to RIKEN cDNA 1700012G19 gene (predicted) [Rattus  
norvegicus]  
Length = 321

Score = 210 bits (535), Expect = 8e-053  
Identities = 122/313 (38%), Positives = 165/313 (52%), Gaps = 16/313 (5%)

Query: 1 GAMARCERLRGAALRDVLGRAQGVLFDCDGVWNGERAVPGAPELLERLARAGKAALFVS 60  
G RC RL + +L +LFDGCDGVW GE AVPGAPE L L GK F++  
Sbjct: 8 GDEVRCVRLSAERAKLLLAEVDTLLFDGCDGVWLRGETAVPGAPETLRALRARGKRLGFIT 67  
Query: 61 NNSRRARPELALRFARLGFGLRAEQ----LFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXX 116  
NNS + R A + RLGFGL + +F + G PD V  
Sbjct: 68 NNSKTRTAYAEKLRRLGFGLPMPGPEAGLEVFGTAYCSALYLRQLAGVDPKAYVLGSP 127  
Query: 117 XXXXXXXXXXXXXXXXXXXXXXXXXXXXR-----VRAVLVGYDEHFSFAKLREACAH 167  
VRAV+VG+D HFS+ KL +A +  
Sbjct: 128 ALAAELEAVGVTSVGVGPDVHLHGDGSPDWLAVPLEPDVRAVVVGFDPHFSYMKLTKAVRY 187  
Query: 168 LRDPECLLVATDRDPWHPLSDGSRTPGTGSLLAAAVETASGRQALVVGKPSPYMFECITEN 227  
L+ P+CLLV T+ D PL +G GTG L AVE A+ RQA ++GKPS ++F+C+++  
Sbjct: 188 LQQPDCLLVGTNMDNRLPLENGRFIAGTGCLVRAVEMAAQRQADIIGKPSRFIFDCVSQE 247  
Query: 228 FSIDPARTLMVGDRLLETDILFGHRCGTTVLTTLTGVSRLLEEAQAYLAAG---QHDLVPHY 284  
+ I+P RT+MVGDR+TDIL G C + T+LTLTGVS LE+ ++ + + +VP +  
Sbjct: 248 YGINPERTVMVGDRLDITDILLGSTCSLKTILTTLTGVSLEEDVKSQESDCMFKKKMVPDF 307

Query: 285 YVESIADLTEGLE 297  
YV+SIADL L+  
Sbjct: 308 YVDSIADLLPALQ 320

>ref|XP\_001088993.1| PREDICTED: SH3-domain binding protein 1 [Macaca mulatta]  
Length = 757

Score = 210 bits (534), Expect = 1e-052  
Identities = 106/114 (92%), Positives = 109/114 (95%), Gaps = 1/114 (0%)

Query: 185 PLSDGSRTPGTGSLSAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRL 244  
P+ D +R TGSLSAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRL  
Sbjct: 645 PVEDMARR-STGSLSAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRL 703

Query: 245 DILFGHRCGMTTVLTTLTGVSRLLEEAQAYLAAGQHDLVPHYYVESIADLTEGLED 298  
DILFGHRCGMTTVLTTLTGVSRLLEEAQAYLAAGQHDLVPHYYVES+ADLTEGLED  
Sbjct: 704 DILFGHRCGMTTVLTTLTGVSRLLEEAQAYLAAGQHDLVPHYYVESVADLTEGLED 757

>ref|XP\_001084229.1| PREDICTED: similar to pyridoxal (pyridoxine, vitamin B6)  
phosphatase [Macaca mulatta]  
Length = 453

Score = 209 bits (532), Expect = 2e-052  
Identities = 125/314 (39%), Positives = 166/314 (52%), Gaps = 18/314 (5%)

Query: 1 GAMARCERLRGAALRDVLGRAQGVLFDCDGVWNGERAVPGAPELLERLARAGKAALFVS 60  
G ARC RL + +L +LFDGCVLW GE AVPGAPE L L GK F++  
Sbjct: 140 GDDARCVRLSAERAQALLADVDTLLFDGCVLWVGETAVPGAPEALRALRARGKRLGFIT 199

Query: 61 NNSRRARPELALRFARLGFGLRAE----QLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXX 116  
NNS + R A + RLGFGL ++F + G P AP A +  
Sbjct: 200 NNSKTRAAEAELRRLGFGLPAGPGAGLEVFGTAYCTALYLSQRLAGAP-APKAYVLGS 258

Query: 117 XXXXXXXXXXXXXXXXXXXX-----XXXXXXXXRVRAVLVGYDEHFSFAKLREACA 166  
VRVAV+VG+D HFS+ KL +A  
Sbjct: 259 PALAAELEAVGVTSVGVGPEPLQEGPGDWLHAPLEPDVRAVVVGFDPHFSYMKLTKALR 318

Query: 167 HLRDPECLLVATDRDPWHPLSDGSRTPGTGSLSAAAVETASGRQALVVGKPSPYMFECITE 226  
+L+ P+CLLV T+ D PL +G GTG L AVE A+ RQA ++GKPS ++F+C+++  
Sbjct: 319 YLQQPDCLLVGTNMDNRLPLENGRFIAGTGCLVRAVEMAAQRQADIIGKPSRFIFDCVQS 378

Query: 227 NFSIDPARTLMVGDRLTDILFGHRCGMTTVLTTLTGVSRLLEEA---QAYLAAGQHDLVPH 283  
+ I+P RT+MVGDR+TDIL G CG+ T+LTLTGVS L + Q + +VP  
Sbjct: 379 EYGINPERTVMVGDRLDITDILLGVTCGLKILTTLTGVSRLLEEAQAYLAAGQHDLVPH 438

Query: 284 YVESIADLTEGLE 297  
+YV+SIADL L+  
Sbjct: 439 FYVDSIADLLPALQ 452

>ref|XP\_001234473.1| PREDICTED: similar to OTTHUMP00000042130 [Gallus gallus]  
Length = 196

Score = 209 bits (531), Expect = 2e-052  
Identities = 114/196 (58%), Positives = 126/196 (64%), Gaps = 7/196 (3%)

Query: 3 MARCERLRGAALRDVLGRAQGVLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNN 62  
 MA C RL GAALR+VLG AQG+LFDCDGVW GE AVPGAPELLERL R GKAALFVSNN  
 Sbjct: 1 MASCRRLSGAALREVLGSAQGLLFDCDGVWAGESAVPGAPELLERLQRGGKAALFVSNN 60

Query: 63 SRRARPELALRFARLGFGLRAEQLFSSXXXXX----XXXXXXXXPGPPDAPGAVFVXXXX 118  
 SRR+ EL LRF+RLGF G+RAE +FSS G A G VFV  
 Sbjct: 61 SRRSVAEELRFSRLGFRGVRAEHVFSSALCSALFLRQHLLSGGAGDSSAVGRVFFV---L 117

Query: 119 XXXXXXXXXXXXXXXXXXXXXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVAT 178  
 +V AVLVGYD+ F+FAKL +ACA+LRDP C+LVAT  
 Sbjct: 118 GGEGLRGEVRDAGLRLVGEQAEQVHAVLVGYDDQFTFAKLAQACAYLRDPRCMLVAT 177

Query: 179 DRDPWHPLSDGSRTPG 194  
 D DPWHPLSDG RTPG  
 Sbjct: 178 DPDPWHPLSDGQRTPG 193

>ref|NP\_001035830.1| hypothetical protein LOC283871 [Homo sapiens]  
 Length = 321

Score = 207 bits (528), Expect = 5e-052  
 Identities = 125/314 (39%), Positives = 165/314 (52%), Gaps = 18/314 (5%)

Query: 1 GAMARCERLRGAALRDVLGRAQGVLFDCDGVWNGERAVPGAPELLERLARAGKAALFVS 60  
 G ARC RL + +L +LFDCDGVW GE AVPGAPE L L GK F++  
 Sbjct: 8 GDDARCVRLSAERAQALLADVDTLLFDCDGVWLRGETAVPGAPEALRALRARGKRLGFIT 67

Query: 61 NNSRRARPELALRFARLGFGLRAE----QLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXX 116  
 NNS + R A + RLGF GG ++F + G P AP A +  
 Sbjct: 68 NNSKTRAAYA EKLRRLGFGG PAGPGASLEVFGTAYCTALYLRQLAGAP-APKAYVLGS 126

Query: 117 XXXXXXXXXXXXXXXXXXXXXXXX-----XXXXXXXXRVRAVLVGYDEHFSFAKLREACA 166  
 VRAV+VG+D HFS+ KL +A  
 Sbjct: 127 PALAAELEAVGVASVGVGPEPLQEGPGDWLHAPLEPDVRAVVVGFDPHFSYMKLTKALR 186

Query: 167 HLRDPECLLVATDRDPWHPLSDGSRTPGTGLSAAAVETASGRQALVVGKPSPYMFECITE 226  
 +L+ P CLLV T+ D PL +G GTG L AVE A+ RQA ++GKPS ++F+C+++  
 Sbjct: 187 YLQQPGCLLVGTNMDNRLPLENGRFIAGTGCLVRAVEMAAQRQADIIGKPSRFIFDCVSO 246

Query: 227 NFSIDPARTLMVGDRLDILFGHRCGTTVLTTLTGVSRL EEA---QAYLAAGQHDLVPH 283  
 + I+P RT+MVGDR L+TDIL G CG+ T+LTLTGVS L + Q + +VP  
 Sbjct: 247 EYGINPERTVMVGDRLDITDILLGATCGLKILTTLTGVS TLGDVKNNQESDCVSKKKMVPD 306

Query: 284 YYVESIADLTEGLE 297  
 +YV+SIADL L+  
 Sbjct: 307 FYVDSIADLLPALQ 320

>ref|NP\_001033261.1| hypothetical protein LOC538173 [Bos taurus]  
 Length = 321

Score = 206 bits (525), Expect = 1e-051  
 Identities = 122/314 (38%), Positives = 165/314 (52%), Gaps = 18/314 (5%)

Query: 1 GAMARCERLRGAALRDVLGRAQGVLFDCDGVWNGERAVPGAPELLERLARAGKAALFVS 60  
 G RC RL + +L +LFDCDGVW GE AVPGAPE L L GK F++

Sbjct: 8 GDDGRCVRLNAERAQALLADVDTLLFDCDGVLRGETAVPGAPETLTALRARGKRLAFIT 67

Query: 61 NNSRRARPELALRFARLGFGLRA----EQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXX 116  
 NNS + R A + LGFG ++F + GPP AP A +

Sbjct: 68 NNSKKTREAYA EKLRCLGFGAPAGPDAGREVFGTAYCTALYLRQLTGPP-APKAYVLGS 126

Query: 117 XXXXXXXXXXXXXXXXXXXX-----XXXXXXXXXRVRAVLVGYDEHFSFAKLREACA 166  
 VRAV+VG+D HFS+ KL +A

Sbjct: 127 VALAAELEAVGVSCVGVGPEPLLGDGPGAWLDAPLEPDVRAVVVGFDPHFSYMKLTKAVR 186

Query: 167 HLRDPECLLVATDRDPWHPLSDGSRTPGTGS LAAAVETASGRQALVVGKPSPYMFECITE 226  
 +L+ P+CLLV T+ D PL +G GTG L AVE A+ RQA ++GKPS ++F+C+++

Sbjct: 187 YLQQPDCLLVGTNMDNRLPLENGRFIAGTGCLVRAVEMAAQRQADIIGKPSRFIFDCVSQ 246

Query: 227 NFSIDPARTLMVGDRLDILFGHRCGM TTVLTLTGVSRL EEAQAYLAA---GQHDLVPH 283  
 + I P RT+MVGDR L+TDIL G CG+ T+LTLTGVS L + ++ + + +VP

Sbjct: 247 EYGIHPERTVMVGDRLD T DILLGVTCGLKTILTLTGVS SLRDVKS NQESDCMAKKKMVPD 306

Query: 284 YYVESIADLTEGLE 297  
 +YV+SIADL L+

Sbjct: 307 FYVDSIADLLPALQ 320

>ref|XP\_001363637.1| PREDICTED: hypothetical protein [Monodelphis domestica]  
 Length = 322

Score = 205 bits (522), Expect = 3e-051  
 Identities = 126/316 (39%), Positives = 163/316 (51%), Gaps = 19/316 (6%)

Query: 1 GAMARCERLRGAALRDVLGRAQGVLFDCDGVWNGERAVPGAPELLERLARAGKAALFVS 60  
 G RC RL + +L +LFD CDGV LW GE AVPGAPE L L GK FV+

Sbjct: 8 GDDGRCVRLSADRAQTLLADVDTLLFDCDGVLRGETAVPGAPEALNALRAQKRLGFVT 67

Query: 61 NNSRRARPELALRFARLGF----GGLRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXX 116  
 NNS + R A + RLGF G ++F + G P +V

Sbjct: 68 NNSKKTREAYA EKLRCLGFGGPGAGLEVFGTAYCAALYLRQRLEGG-GVPAKAYVLG 126

Query: 117 XXXXXXXXXXXXXXXXXXXX-----XXXXXXRVRAVLVGYDEHFSFAKLREAC 165  
 V AV+VG+D HFS+AKL +A

Sbjct: 127 SPALAAELEAVGIESVGVGPEPLHG VGP GDWLAEP L DSGV GAVVVGFDPHFSYAKLTKAV 186

Query: 166 AHLRDPECLLVATDRDPWHPLSDGSRTPGTGS LAAAVETASGRQALVVGKPSPYMFECIT 225  
 +L+ P CLLV T+ D PL GS GTG L AVE A+ RQA ++GKPS ++F+C+

Sbjct: 187 RYLQQPGCLLVGTNMDNRLPLEGGSYIAGTGCLVRAVEMAAQRQAEIIGKPSRFIFDCVA 246

Query: 226 ENFSIDPARTLMVGDRLDILFGHRCGM TTVLTLTGVSRL EEA---QAYLAAGQHDLP 282  
 + F ++P RT+MVGDR L+TDIL G CG+ T+LTLTGVS LE+ Q + + +VP

Sbjct: 247 KEFGLNPERTVMVGDRLD T DILLGVTCGLKTILTLTGVS SLEDVKG NQESDCSHRKKMVP 306

Query: 283 HYYVESIADLTEGLE 298  
 +YV+SIADL LED

Sbjct: 307 DFYVDSIADLIPALE 322

>ref|XP\_001162359.1| PREDICTED: hypothetical protein [Pan troglodytes]  
 Length = 321



Score = 204 bits (520), Expect = 5e-051  
Identities = 124/314 (39%), Positives = 164/314 (52%), Gaps = 18/314 (5%)

Query: 1 GAMARCERLRGAALRDVLGRAQGVLFDCDGVWNGERAVPGAPELLERLARAGKAALFVS 60  
G ARC RL + +L +LFDCDGVW GE AVPGAPE L L GK F++  
Sbjct: 8 GDDARCVRLSAERAQALLADVDTLLFDCDGVWLRGETAVPGAPEALRALRARGKRLGFIT 67

Query: 61 NNSRRARPELALRFARLGFGLRAE----QLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXX 116  
NNS + R A + RLGFGG ++F + P AP A +  
Sbjct: 68 NNSKTRAAAYAEKLRRLGFGGPAGPGASLEVFGTAYCTALYLRQLASAP-APKAYVLGS 126

Query: 117 XXXXXXXXXXXXXXXXXXXX-----XXXXXXXXRVRAVLVGYDEHFSFAKLREACA 166  
VRAV+VG+D HFS+ KL +A  
Sbjct: 127 PALAELEAVGVASVGVGPEPLQEGPGDWLHAPLEPDVRAVVVGFDPHFSYMKLTALR 186

Query: 167 HLRDPECLLVATDRDPWHPLSDGSRTPGTGSLAAAVETASGRQALVVGKPSPYMFECITE 226  
+L+ P CLLV T+ D PL +G GTG L AVE A+ RQA ++GKPS ++F+C+++  
Sbjct: 187 YLQQPGCLLVGTNMDNRLPLENGRFIAGTGCLVRAVEMAAQRQADIIGKPSRFIFDCVSO 246

Query: 227 NFSIDPARTLMVGDRLLETDILFGHRCGMTTTLTLTGVSRLLEE---QAYLAAGQHDLVPH 283  
+ I+P RT+MVGDR+TDIL G CG+ T+LTLTGVS L + Q + +VP  
Sbjct: 247 EYGINPERTVMVGDRLDTDILLGVTGCLKTILTLTGVSTLGDVKNQESDCVSKKMPD 306

Query: 284 YYVESIADLTEGLE 297  
+YV+SIADL L+  
Sbjct: 307 FYVDSIADLLPALQ 320

>ref|XP\_538386.2| PREDICTED: similar to SH3-domain binding protein 1 (3BP-1)  
[Canis familiaris]  
Length = 703

Score = 200 bits (509), Expect = 9e-050  
Identities = 101/114 (88%), Positives = 106/114 (92%), Gaps = 1/114 (0%)

Query: 185 PLSDGSRTPGTGSLLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLLET 244  
P D +R TGSLAAAVE ASGRQALVVGKPSPYMFECITE+FS+DPARTLMVGDRLLET  
Sbjct: 591 PAEDMARR-STGSLAAAVEIASGRQALVVGKPSPYMFECITEHFSVDPARTLMVGDRLLET 649

Query: 245 DILFGHRCGMTTTLTLTGVSRLLEEQAAYLAAGQHDLVPHYYVESIADLTEGLED 298  
DILFGHRCGMTT+LTLTGVSRLLEEQAAYLA+GQHDLVPHYYVESIADL EGLED  
Sbjct: 650 DILFGHRCGMTTLLTLTGVSRLLEEQAAYLASGQHDLVPHYYVESIADLMEGLED 703

>ref|XP\_235500.4| PREDICTED: similar to SH3 domain-binding protein 1 (3BP-1)  
[Rattus norvegicus]  
Length = 664

Score = 199 bits (506), Expect = 2e-049  
Identities = 99/113 (87%), Positives = 104/113 (92%)

Query: 186 LSDGSRTPGTGSLLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLLET 245  
L++ TGSLAAAVETASGRQALVVGKPSPYMF+CITE+FS+DPAR LMVGDRLLET  
Sbjct: 552 LAEDMTRKSTGSLAAAVETASGRQALVVGKPSPYMFQCITEDFSVDPARMLMVGDRLLET 611

Query: 246 ILFGHRCGTTVLTTLTGVSRLLEEAQAYLAAGQHDLVPHYYVESIADLTEGLED 298  
ILFGHRCGTTVLTTLTGVS LEEAQAYLAAGQHDLVPHYYVESIADL EGLED  
Sbjct: 612 ILFGHRCGTTVLTTLTGVSLEEAQAYLAAGQHDLVPHYYVESIADLMEGLED 664

>ref|XP\_001516666.1| PREDICTED: hypothetical protein, partial  
[Ornithorhynchus anatinus]  
Length = 109

Score = 190 bits (482), Expect = 1e-046  
Identities = 93/109 (85%), Positives = 101/109 (92%)

Query: 190 SRTPGTGSLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLTDILFG 249  
+RTPGTGSL AAVETASGRQALVVGKPS YMFECITE F +DPARTLMVGDRLTDILFG  
Sbjct: 1 ARTPGTGSLLAAAVETASGRQALVVGKPSYMFECITERFDVDPARTLMVGDRLTDILFG 60

Query: 250 HRCGTTVLTTLTGVSRLLEEAQAYLAAGQHDLVPHYYVESIADLTEGLED 298  
HRCG+TTVLTTLTGVS+LEEAQAY+A+G+ DLVP YYV+SIADL GLED  
Sbjct: 61 HRCGLTTVLTTLTGVSQLEEAQAYMASGRPDLVPDYVDSIADLIAGLED 109

>ref|XP\_974660.1| PREDICTED: similar to CG5567-PA [Tribolium castaneum]  
Length = 305

Score = 170 bits (430), Expect = 1e-040  
Identities = 97/283 (34%), Positives = 148/283 (52%), Gaps = 20/283 (7%)

Query: 24 VLFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNRRARPELALRFARLGFGLR 83  
VLFDCDGVW + G+ ++ RL GK FV+NNS + R E A++ R+ F +  
Sbjct: 24 VLFDCDGVWLDNEPISGSVPVNRRLRELGKRIFVTNNSTKMRNEFAVKAKRMNFN-IE 82

Query: 84 AEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXX-----XX 132  
+++ S+ D +V+V  
Sbjct: 83 TDEIISTAYLAAAYLKNM-----DFKQSVYVVGSRGITQELDAVGIKHYGVGPDLVQNAL 137

Query: 133 XXXXXXXXXXXXRVRAVLVGYDEHFSFAKLREACALHRDPECLLVATDRDPWHPLSDGSRT 192  
V AV+VGYDEHFS+ K+ +A ++L +P CL +AT+ D P+S  
Sbjct: 138 VHVIENFQMESDVGAVIVGYDEHFSYVKMMKAASYLNNPNCLFIATNTDERFPMSTDLVI 197

Query: 193 PGTGSLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLTDILFGHRC 252  
PGTG++ +AVET + R +VVGKP+PY+ + + + + I P RTLM+GDR+ TDIL G RC  
Sbjct: 198 PGTGAIWSAVETCAQRSPVVGKPNPYIVDDLIKKYGIVPKRTLMIGDRVNTDILLGTRC 257

Query: 253 GMTTVLTTLTGVSRLLEEAQAYLAAGQ---HDLVPHYYVESIADL 292  
G T+L L+GV+ L+EA A + + ++V +Y+E + D+  
Sbjct: 258 GFQTLVLVLSGVTTLKEAVALKNSHKKEDKEMVADFYLEKLGDI 300

>ref|XP\_309300.4| AGAP011350-PA [Anopheles gambiae str. PEST]  
Length = 322

Score = 164 bits (415), Expect = 7e-039  
Identities = 101/299 (33%), Positives = 142/299 (47%), Gaps = 23/299 (7%)

Query: 9 LRGAALRDVLGRAQGVLFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNRRARP 68  
L A ++ L VL DCDGV+W +PGAPE++ R GK FV+NNS + RP  
Sbjct: 28 LSPAIEIKQWLDSFDTVLTDCDGVIVVDNPNLPGAPEVINRFIANGKCLFFVTNNSTKTRP 87

Query: 69 ELALRFARLGF-----GLRAEQLFSSXXXXXXXXXXXXXPGPPDAPGAVFVXXXXX 119  
E + +LGF A Q S G AV +  
Sbjct: 88 EFVEKAVKLGFNVTIDNIIISTAYLAAQYLKSVGFSKTVYITIGSTGITKELDAVGIRHIGI 147

Query: 120 XXXXXXXXXXXXXXXXXXXXXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATD 179  
V AV+VG+DEHFSF K+ +A ++L +P+ + + T+  
Sbjct: 148 GPDTIQGSLADTVASFVDPDP----VSAVIVGFDEHFSFVKMMKAASYLNNPDVIFIGTN 203

Query: 180 RDPWHPLSDGSRTPGTGSLLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVG 239  
D P+ D PGTGS+ A+ T S R+ +V+GKP+P++ E I + +DPARTLM+G  
Sbjct: 204 TDERFPMPDRV-IPGTGSIVQAMVTCSEREPIVMGKPNPHICEIIRREYDVPARTLMIG 262

Query: 240 DRLETDILFGHRCGMMTTVLTTLTGVSRLAEAQAYLAAGQHD-----LVPHYYVESIADL 292  
DR TDIL G C T+L TG+ + E+ Y GQ + LVP Y+ + DL  
Sbjct: 263 DRCNTDILLGKNCDFQTLLEVETGIHKAEDIAKY---GQSEDPAVRALVPDVYLPKLGDL 318

>emb|CAQ09782.1| pyridoxal (pyridoxine, vitamin B6) phosphatase [Homo sapiens]

Length = 79

Score = 162 bits (410), Expect = 3e-038  
Identities = 79/79 (100%), Positives = 79/79 (100%)

Query: 220 MFECITENFSIDPARTLMVGDRLDILFGHRCGMMTTVLTTLTGVSRLAEAQAYLAAGQHD 279  
MFECITENFSIDPARTLMVGDRLDILFGHRCGMMTTVLTTLTGVSRLAEAQAYLAAGQHD  
Sbjct: 1 MFECITENFSIDPARTLMVGDRLDILFGHRCGMMTTVLTTLTGVSRLAEAQAYLAAGQHD 60

Query: 280 LVPHYYVESIADLTEGLE 298  
LVPHYYVESIADLTEGLE  
Sbjct: 61 LVPHYYVESIADLTEGLE 79

>ref|NP\_001062708.1| Os09g0261300 [Oryza sativa (japonica cultivar-group)]  
Length = 325

Score = 154 bits (388), Expect = 9e-036  
Identities = 93/293 (31%), Positives = 147/293 (50%), Gaps = 14/293 (4%)

Query: 9 LRGAALRDVLGRAQGVLFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARP 68  
L A R ++ LFDCDGV+W G++ + G PE L+ L + GK +FV+NNSR++R  
Sbjct: 32 LTADAARSLVDSVDAFLFDCDGVWIKGQQLIEGVPETLDLLRKMGGKLVFVTNNSRKSRR 91

Query: 69 ELALRFARLGFGLRAEQLFSSXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXX- 127  
+ A +F LG + E++F+S P V  
Sbjct: 92 QYAKKFRALGLE-VTEEEIFTSSFAAAMFLKLNNSPEKKVYVVGEDGILEELRLAGFEC 150

Query: 128 -----XXXXXXXXXXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRD-PECLLVATD 179  
V AV+VG D++F++ K++ A +R+ P CL +AT+  
Sbjct: 151 LGGPEDGKKNILLEANFYFEHDKSVGAVIVGLDQYFNYYKMQYASLCIRENPGCLFIATN 210

Query: 180 RDPWHPLSDGSRTPGTGSLLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVG 239  
RDP ++ PG G++ AAV + ++ +VVGKPS ++ + + ++F+++ +R MVG  
Sbjct: 211 RDPTGHMTSVQEWPGAGTMVAAVSCSVQKEPIVVGKPSFLMDFLLKSFNLETSRMCMVG 270

Query: 240 DRLETDILFGHRCGMMTTVLTTLTGVSRLAEAQAYLAAGQHDLVPHYYVESIADL 292

DRL+TDILFG G T+L L+GV+ L E Q + + P Y S+ DL  
Sbjct: 271 DRLDTDILFGQNTGCKTLLVLSGVTTLPQLQ----DASNTIHPDLYTNSVYDL 319

>dbj|BAD29554.1| putative phosphoglycolate phosphatase precursor [Oryza sativa

Japonica Group]  
Length = 303

Score = 154 bits (388), Expect = 9e-036  
Identities = 93/293 (31%), Positives = 147/293 (50%), Gaps = 14/293 (4%)

Query: 9 LRGAALRDVLGRAQGVLFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARP 68  
L A R ++ LFDCDGV+W G++ + G PE L+ L + GK +FV+NNSR++R  
Sbjct: 10 LTADAARSLVDSVDAFLFDCDGVWIKGDQLIEGVPETLDLLRKMGGKLVFVTNNSRKSRR 69  
Query: 69 ELALRFARLGFGLRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXX- 127  
+ A +F LG + E++F+S P V  
Sbjct: 70 QYAKKFRALGLE-VTEEEIFTSSFAAAMFLKLNNSPEKKVYVVGEDGILEELRLAGFEC 128  
Query: 128 -----XXXXXXXXXXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRD-PECLLVATD 179  
V AV+VG D++F++ K++ A +R+ P CL +AT+  
Sbjct: 129 LGGPEDGKKNILLEANFYFEHDKSVGAVIVGLDQYFNYYKMQYASLCIRENPGCLFIATN 188  
Query: 180 RDPWHPLSDGSRTPGTGLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVG 239  
RDP ++ PG G++ AAV + ++ +VVGKPS ++ + + ++F+++ +R MVG  
Sbjct: 189 RDPTGHMTSVQEWPGAGTMVAAVSCSVQKEPIVVGKPSFLMDFLLKSFNLETSRMCVMG 248  
Query: 240 DRLETDILFGHRCGMTTVLTLTGVSRLLEEQAAYLAAGQHDLVPHYYVESIADL 292  
DRL+TDILFG G T+L L+GV+ L E Q + + P Y S+ DL  
Sbjct: 249 DRLDTDILFGQNTGCKTLLVLSGVTTLPQLQ----DASNTIHPDLYTNSVYDL 297

>ref|XP\_853602.1| PREDICTED: similar to pyridoxal (pyridoxine, vitamin B6)  
phosphatase [Canis familiaris]  
Length = 323

Score = 153 bits (386), Expect = 2e-035  
Identities = 77/156 (49%), Positives = 109/156 (69%), Gaps = 3/156 (1%)

Query: 145 VRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGLAAAVET 204  
VRAV+VG+D HFS+ KL +A +L+ P CLLV T+ D PL +G GTG L AVE  
Sbjct: 167 VRAVVVGFDPHFSYMKLTKAVRYLQQPGCLLVGTNMDNRLPLENGRFIAGTGCLVRAVEM 226  
Query: 205 ASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMTTVLTLTGVS 264  
A+ RQA ++GKPS ++F+C+++ + I+P RT+MVGDRD+TDIL G CG+ T+LTLTGVS  
Sbjct: 227 AAQRQADIIGKPSRFIFDCVSEQEYGINPERTVMVGDRLDILLGVTCGLKTIILTTLTGVS 286  
Query: 265 RLEEAQAYLAA---GQHDLVPHYYVESIADLTEGLE 297  
L + ++ + + +VP +YV+SIADL L+  
Sbjct: 287 TLGDVKSNDQESDCMSKMKMVPDFYVDSIADLLPALQ 322

>ref|XP\_001498171.1| PREDICTED: hypothetical protein [Equus caballus]  
Length = 233

Score = 152 bits (384), Expect = 3e-035

Identities = 77/156 (49%), Positives = 108/156 (69%), Gaps = 3/156 (1%)

Query: 145 VRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGLAAAVET 204  
VRAV+VG+D HFS+ KL +A +L+ P CLLV T+ D PL +G GTG L AVE  
Sbjct: 77 VRAVVVGFDPHFSYMKLTKAVRYLQQPGCLLVGTNMDNRLPLENGRFIAGTGCLVRAVEM 136

Query: 205 ASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMTTVLTLTGVS 264  
AS RQA ++GKPS ++F+C+++ + I+P RT+MVGDRD+TDIL G CG+ T+LTLTGVS  
Sbjct: 137 ASQRQADIIGKPSRFIFDCVSEQEYGINPERTVMVGDRLDITDILLGVTCGLKTLTLTGVS 196

Query: 265 RLEEAQAYLAA---GQHDLVPHYYVESIADLTEGLE 297  
L + ++ + + +VP +YV+SIAD L+  
Sbjct: 197 TLGDVKSQESDCMSKKTVPDFYVDSIADFLPALQ 232

>ref|XP\_504528.1| hypothetical protein [Yarrowia lipolytica]  
Length = 299

Score = 150 bits (379), Expect = 1e-034  
Identities = 92/284 (32%), Positives = 131/284 (46%), Gaps = 16/284 (5%)

Query: 25 LFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLRA 84  
LFDCDGVW G +P PE L+ L GK +FV+NNS ++R +F + G +  
Sbjct: 22 LFDCDGVWQGNHLLPHVPETLQLLRDNGKRLIFVTNNSKSRQAYTKKFEKFGIK-VNK 80

Query: 85 EQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXX-----XXXXXXXXXXXXX 134  
E++F S P D V  
Sbjct: 81 EEIFGSAYSAAVYLQKVVKFPKDKKVLVVGGETGLEEELTEAGIPWLGATDAAYNRVADDE 140

Query: 135 XXXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPG 194  
+ AVL G D H ++ K+ A L+DPE L +AT+ D +P S G PG  
Sbjct: 141 ALSSIVRDKSIGAVLCGLDFHINYKIANALIQLQDPETLFLATNIDSTYP-SHGKLLPG 199

Query: 195 TGLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGM 254  
G++ +ET+SGR+ + +GKPS M +CI F DP++ MVGDRL TD+ FG G+  
Sbjct: 200 AGTIVGTLETSSGRKPVALGKPSQAMMDCIKAQFEFDPKACMVGDRDNTDMRFGEEGGL 259

Query: 255 TTVLTLTGVSRLLEEAQAYLAAGQHDLVPHYYVESIADLTEGLED 298  
T+ L+GV E + A + P YY + + DL E L++  
Sbjct: 260 GTLFLVLSGVDTEESIKKEDAVAK----PKYYADKLGDLYELLKN 299

>ref|XP\_001419146.1| predicted protein [Ostreococcus lucimarinus CCE9901]  
Length = 308

Score = 147 bits (371), Expect = 9e-034  
Identities = 90/301 (29%), Positives = 147/301 (48%), Gaps = 22/301 (7%)

Query: 4 ARCERLRGAALRDVLGRAQGVLFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNS 63  
A+ RL+ + +++++ + +FDCDGV+W G+ + G PE LE L GK +FV+NNS  
Sbjct: 10 AKANRLQEKS AQELVDATETFIFDCDGVWIKGDSLIEGVPETLELLRSMGKRLIFVTNNS 69

Query: 64 RRARPELALRFARLGFGLRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXX 123  
++R +F LG + AE++FSS D +V  
Sbjct: 70 TKSRAGYTKKFESLGLK-VNAEEIFSSSFAAAAYLESI-----DFKKKAYVVGETGILEE 123

Query: 124 X-----XXXXXXXXXXXXXXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRD-P 171

V AV+VG+D + ++ K++ A +R+ P

Sbjct: 124 LDGVGIKHIGGESDAGKQVTLASGELMHHDDEDVGAVIVGFDRNINYYKIQYATLCIRENP 183

Query: 172 ECLLVATDRDPWHPLSDGSRTPGTGLAAAVETASGRQALVVGKPSPYMFECITENFSID 231  
 C+ +AT+ D L+D G GS+ A++ ++ R+ +VVGKP+ +M + I F I

Sbjct: 184 GCMFIATNTDAVTHLTDAQEWAGNGSMVGAIKGSTKREPIVVGKPAAFMLDYIANKFQIR 243

Query: 232 PARTLMVGDRLDILFGHRCGMMTTVLTLTGVSRLLEEAQAYLAAGQHDLVPHYYVESIAD 291  
 + MVGDRL+TDILFG+ G+ T+L L+GV+ + L + + + P YY + +AD

Sbjct: 244 KDQITMVGDRDLDTDILFGNDGGLNTMLVLSGVT----TKDMLCSDDNTIAPTYTDLKAD 299

Query: 292 L 292  
 L

Sbjct: 300 L 300

>ref|XP\_001660159.1| 4-nitrophenylphosphatase [Aedes aegypti]  
 Length = 317

Score = 145 bits (366), Expect = 3e-033  
 Identities = 87/278 (31%), Positives = 130/278 (46%), Gaps = 14/278 (5%)

Query: 24 VLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNRRARPELALRFARLGF--- 80  
 VL DCDGV+W +P A +++ +L GK FV+NNS + RPE + +LGF

Sbjct: 41 VLTDCDGVIVVDNDTLPHATDVINKLIENGKQLFFVTNNSTKTRPEFVAKSVKLGFNVG 100

Query: 81 -----GLRAEQLFSSXXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXX 134  
 A Q + G AV +

Sbjct: 101 DNIISTAYLAAQYLKNIGFSKKVYVVGSTGITRELDVAVGIQHTGIGPDVLGGSLADAVHN 160

Query: 135 XXXXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPG 194  
 V AV+VG+DEHF+F K+ +A ++L P+ + + T+ D P+ D PG

Sbjct: 161 FTPDP----EVGAVIVGFDEHFNFIKMMKAASYLDKPDVIFIGTNTDERFPMPD-CVIPG 215

Query: 195 TGSLLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGM 254  
 TGS+ AV T + R+ V+GKP+ ++ + + + + +DP+RTLM+GDRL TDIL G CG

Sbjct: 216 TGSIVNAVTTCAERKPTVMGKPNKHICDILQKEYKVDPSRTLMIGDRLNTDILLGKNCGF 275

Query: 255 TTVLTLTGVSRLLEEAQAYLAAGQHDLVPHYYVESIADL 292  
 T+L TG+ + + A VP Y + DL

Sbjct: 276 QTLLVETGIHKAADFSQTEDAEIKQCVPDVYTSKLGDL 313

>ref|XP\_001752953.1| predicted protein [Physcomitrella patens subsp. patens]  
 Length = 313

Score = 144 bits (362), Expect = 1e-032  
 Identities = 87/278 (31%), Positives = 138/278 (49%), Gaps = 16/278 (5%)

Query: 25 LFDGCDGVWNGERAVPGAPELLERLARAGKAALFVSNNRRARPELALRFARLGFGLRA 84  
 +FDGCDGV+W G+ + G PE L+ L GK +FV+NNS ++R + +F LG + A

Sbjct: 32 IFDCDGVIVKGDLSLIDGVPETLDMLRSMGKRLVFTVNNSTKSRKQYGGKFFESLGLS-VSA 90

Query: 85 EQLFSSXXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXXXR 144  
 E++F + P D +

Sbjct: 91 EEIF-ASSFAAAAYLKSMKFPTDKKVIYIIGEAGIQLELKQAGINYYIGGPEDGDKRIDLTP 149

Query: 145 -----VRAVLVGYDEHFSFAKLREACAHLRD-PECLLVATDRDPWHPLSDGSRTPG 194  
V AV+VG+D + ++ KL+ A +R+ P C+ +AT+ D L+D G  
Sbjct: 150 GQLMEHDHDVAVVGVGFDRLNYYKLQYATLCIRENPGCMFIATNCDAVIHLTDAQEWAG 209

Query: 195 TGSLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGM 254  
GS+ A++ ++ ++ LVVGKPS +M +C+ F+I ++ MVGDRL+TDILFG G  
Sbjct: 210 GGSMVGAIKGSTKKEPLVVGKPSFMMDCCLASEFNKTSQICMVGDRDLTDILFGQNGGC 269

Query: 255 TTVLTLTGVSRLLEEAQAYLAAGQHDLVPHYVVEESIADL 292  
T+L L+GV+ LE Q + ++ + P +Y I+DL  
Sbjct: 270 ATLLVLSGVTTLETLQ----SSENKIQPDFYTNKISDL 303

>ref|XP\_001696217.1| phosphoglycolate phosphatase [Chlamydomonas reinhardtii]  
Length = 347

Score = 144 bits (362), Expect = 1e-032  
Identities = 97/284 (34%), Positives = 136/284 (47%), Gaps = 20/284 (7%)

Query: 24 VLFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLR 83  
++FDCDGVW G + APE L+ R GK L FV+NNS ++R +F+ LG +  
Sbjct: 64 LIFDCDGVWLRGSEIIHNAPEALKEFRRQKRLLFVTNNSKSRAGYVAKFSSLGLE-VA 122

Query: 84 AEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXX----- 131  
AE++ SS GP + V  
Sbjct: 123 AEEIVSSSYCAAAYLTSQGFPGGSRPCSKVLLLGWSGVEQELEQAGIPYVGGRAKLVPP 182

Query: 132 --XXXXXXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRD-PECLLVATDRDPWHPLSD 188  
V AV+VG+D +FS+++L A HLR+ P CLLVAT+ D +  
Sbjct: 183 MDDLAMKALKVDPDVGAVVGVGDPNFSYSRLVYASIHRELPGCLLVATNMDCADHIGG 242

Query: 189 GSRTPGTGSLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILF 248  
G PGTG L AVETASG A+ V K ++ + + ++PA T +VGDR++TDI  
Sbjct: 243 GRMMPGTGGLVKAVETASGVSANVAKGGEWLLPYLCRTYGLEPAHTAIVGDRMDTDIHL 302

Query: 249 GHRCGMTTVLTLTGVSRLLEEAQAYLAAGQHDLVPHYVVEESIADL 292  
G + G+ T L LTGV+ L+ + L A +H P V S+A L  
Sbjct: 303 GRQGGLFTCLPLTGVTTLKRLEG-LPASEH---PDVVVRSVAQL 342

>dbj|BAA97552.1| N-glyceraldehyde-2-phosphotransferase-like [Arabidopsis thaliana]  
Length = 289

Score = 144 bits (362), Expect = 1e-032  
Identities = 86/268 (32%), Positives = 137/268 (51%), Gaps = 18/268 (6%)

Query: 25 LFDGCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLRA 84  
+FDGCDGV+W G++ + G PE L+ L GK +FV+NNS ++R + +F LG +  
Sbjct: 30 IFDCDGVWIKGDKLIEGVPETLDMLRAKGRKLVFVTNNSKSRKQYGKFFETLGLN-VNE 88

Query: 85 EQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 144  
E++F+S P D V  
Sbjct: 89 EEIFASSFAAAAYLQSIN-FPKDKKVYVI-----GEEGILKELELAGFQYLGGP 136

Query: 145 VRAVLVGYDEHFSFAKLREACAHLRD-PECLLVATDRDPWHPLSDGSRTPGTGSLAAAVE 203  
V AV+VG+D +F++ K++ +R+ P CL +AT+RD L+D G GS+ A+

Sbjct: 137 VGAVVVGFDYFNYYKIQYGTLCIRENPGCLFIATNRDAVTHLTDAQEWAGGGSMV GALV 196

Query: 204 TASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLTDILFGHRCGM TTVLTLTG V 263  
 ++ R+ LVVGKPS +M + + + F I ++ MVGDRL+TDILFG G T+L L+GV

Sbjct: 197 GSTQREPLVVGKPSFMMDYLADKFGIQKSQICMVGDRLD TDILFGQNGGCKTLLVLSGV 256

Query: 264 SRLEEAQAYLAAGQHDLVPHYVYESIAD 291  
 + + + L + ++ + P +Y I+D

Sbjct: 257 TSI----SMLESPENKIQPDFYTSKISD 280

>ref|XP\_001732277.1| hypothetical protein MGL\_0052 [Malassezia globosa CBS 7966]

Length = 320

Score = 142 bits (359), Expect = 2e-032  
 Identities = 101/301 (33%), Positives = 134/301 (44%), Gaps = 37/301 (12%)

Query: 25 LFD CDGVLWNGERAVPGAPELLERLARAGKAALFVSNNSRRARPELALRFARLGF GGLRA 84  
 LFD CDGVLW+G +PG +L GK LFVSNN+ ++R L R +G G R

Sbjct: 27 LFD CDGVLW SGP TVLPGVVSFFRKLRE R GKRILFVSNNASKSRRTLLERINAMGIDG-RE 85

Query: 85 EQLFSSXXXXXXXXXXXXXXXXPGPPD-----APGAVFVXXXXXXXXXXXXXXXXX 128  
 +++FSS P D A G ++

Sbjct: 86 DEVFSSAYATAAYLKDVLRFP TDRKAYVVG MNGLEDEL DANGIQYIGGTDEQDCQGLDGL 145

Query: 129 XXXXXXXXXXXXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRDPE-----CLL 175  
 V AV+ G D FS+ KL +A ++ P C

Sbjct: 146 DFSPLASKDALDPS--VA AVVCGIDTKFSYRKLAKAFRYITRPGAEGEVRAGEQNGGCHF 203

Query: 176 VATDRDPWHPLSDGSRTPGTGSLAAAVETASGRQALVVGKPSPYMFECITENFSIDPART 235  
 V T+ D P S+G PG G++ ++ +SGR +VVGKP M + I F+ D +RT

Sbjct: 204 VCTNEDVTFPSSEGL-FPGAGAVWKG IQVSSGRDPIVVGKPHQPMIDTIFARFAFDKSR T 262

Query: 236 LMVGDRLTDILFGHRCGM TTVLTLTGVSRL EEAQAYLAAGQHDLVPHYVYESIADLTEG 295  
 LMVGDRL+TDI FG R G+ T+L LTG+S LE A AA VP Y V + DL

Sbjct: 263 LMVGDRLD TDIAFGQRGGIDTLLVLTGISTLEHVHASDAAA----VPTYVVNGLCDLDTA 318

Query: 296 L 296  
 L

Sbjct: 319 L 319

>ref|XP\_001353955.1| GA18976-PA [Drosophila pseudoobscura]

Length = 320

Score = 142 bits (358), Expect = 3e-032  
 Identities = 90/282 (31%), Positives = 133/282 (47%), Gaps = 10/282 (3%)

Query: 24 VLFDCDGVLWNGERAVPGAPELLERLARAGKAALFVSNNSRRARPELALRFARLGF GGLR 83  
 V+ DCDGVLW RA+ GA ++ K F +NNS + R EL + +GF

Sbjct: 40 VITDCDGVLWVYGRAIDGAVSVINL F KSMRKN IYFCTNNSTKTREELLKKAQNMGFSITE 99

Query: 84 AEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 143  
 E + ++ G+ +

Sbjct: 100 GEIISTAHATAAYLKKRNFEKRVYVIGSDGITKELDAVGIGHTGCGPDPMKGTMAETTKI 159



Query: 144 RVR----AVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGSLA 199  
 ++ AV+VG+DEHFSF K+ +A ++L DP CL +AT+ D P+ D PG+G  
 Sbjct: 160 QLETDIGAVVVGFDHFSFPMKASSYLNDPNCLFIATNTDERFPM-DNMVVPVSGGCFV 218

Query: 200 AAVETASGRQALVVGKPSYMFECITENF--SIDPARTLMVGDRLDILFGHRCGTTV 257  
 A+ET + R A V+GKP+P + E + + IDPARTLM+GDR TDIL G CG T+  
 Sbjct: 219 RAIETCAERTAKVIGKPNPAICEVLLQKEIGRIDPARTLMIGDRANTDILLGFNCGFQTL 278

Query: 258 LTLTGVSRLLEEAQAYLAAGQHD---LVPHYYVESIADLTEGL 296  
 L TGV +L + + + + + L+P Y+ + DL L  
 Sbjct: 279 LVGTGVHQLSDVERWKKSKDLEDKKLIPDMYLPKLGDLLPAL 320

>emb|CAL54968.1| phosphoglycolate phosphatase precursor (ISS) [Ostreococcus tauri]

Length = 342

Score = 141 bits (356), Expect = 5e-032  
 Identities = 89/301 (29%), Positives = 145/301 (48%), Gaps = 22/301 (7%)

Query: 4 ARCERLRGAALRDVLRGQGVLFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNN 63  
 A+ RL + + ++ + +FDCDGV+W G+ + G PE L+ L GK +FV+NNS  
 Sbjct: 44 AKASRLGESEAKALVDATETFIIFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNN 103

Query: 64 RRARPELALRFARLFGGLRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXX 123  
 ++R +F LG + AE++FSS D +V  
 Sbjct: 104 TKSRAGYTKKFESLGLK-VNAEEIFSSSFAAAAYLESI-----DFKKKAYVIGETGILEE 157

Query: 124 X-----XXXXXXXXXXXXXXXXXXXXRVRVAVLVGYDEHFSFAKLREACAHLRD-P 171  
 V AV+VG+D + ++ K++ A +R+ P  
 Sbjct: 158 LDNVGVKHIGGESDADKQVTLKSGELMHHEDEDVGAVIVGFDRNINYYKIQYATLCIRENP 217

Query: 172 ECLLVATDRDPWHPLSDGSRTPGTGSLAAAVETASGRQALVVGKPSYMFECITENFSID 231  
 C+ +AT+ D L+D G GS+ A++ ++ R+ +VVGKP+ +M + I F+I  
 Sbjct: 218 GCMFIATNTDAVTHLTDAQEWAGNGSMVGAIKGSTKREPIVVGKPAAFMLDYIANKFNIR 277

Query: 232 PARTLMVGDRLDILFGHRCGTTVTLTLTGVSRLLEEAQAYLAAGQHDLVPHYYVESIAD 291  
 + MVGDRL+TDILFG+ G+ T+L L+GV+ E L + + + P Y + +AD  
 Sbjct: 278 KDQITMVGDRDLTDILFGNDGGLNTLLVLSGVTTKE----MLCSDDNNTIAPTNYTDKLDLAD 333

Query: 292 L 292  
 L  
 Sbjct: 334 L 334

>gb|EAY94644.1| hypothetical protein OsI\_015877 [Oryza sativa (indica cultivar-group)]

Length = 372

Score = 140 bits (352), Expect = 1e-031  
 Identities = 89/307 (28%), Positives = 143/307 (46%), Gaps = 22/307 (7%)

Query: 3 MARCERLRGAALRD---VLGRAQGVLFDCDGVWNGERAVPGAPPELLERLARAGKAALFV 59  
 MA + A L D ++ + +FDCDGV+W G++ + G PE L+ L GK +FV  
 Sbjct: 61 MAAAGAVPAKLEDADALIDSVETFIIFDCDGVWNGERAVPGAPPELLERLARAGKAALFV 120

Query: 60 SNNRRARPELALRFARLFGGLRAEQLFSSXXXXXXXXXXXXXXXXPGPP----- 106

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      +NNS ++R +   +F LG      E  SS      P
Sbjct: 121 TNNSTKSRKQYGKKFETLGLNVNEEEIFASSFAAAAYLQSIDFPKDKKVVYVIGEDGILKE 180

Query: 107 -DAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXRVRAVLVGYDEHFSFAKLREAC 165
      + G  ++                                V AV+VG+D +F++ K++
Sbjct: 181 LELAGFQYLGGPSDGDKKIELKPGFYMEHDKDVTTIPTLVGAVVVGFDTRYFNYYKQYGT 240

Query: 166 AHLRD-PECLLVATDRDPWHPLSDGSRTPGTGSLAAAVETASGRQALVVGKPSPYMFECI 224
      +R+ P CL +AT+RD   L+D      G GS+  A+  ++ ++ LVVGKPS +M + +
Sbjct: 241 LCIRENPGCLFIATNRDAVTHLTDAQEWAGGGSMVGAILGSTKQEPLVVGKPSFMMDYL 300

Query: 225 TENFSIDPARTLMVGDRLDILFGHRCGMTTVLTLTGVSRLEEAQAYLAAGQHDLVPHY 284
      + F I  ++  MVGDRL+TDILFG   G  T+L L+GV+ ++      L +  + + P +
Sbjct: 301 AKKFGITTSQICMVGDRDLTDILFGQNGGCKTLLVLSGVTSVQ----MLQSPDNSIQPDF 356

Query: 285 YVESIAD 291
      Y   I+D
Sbjct: 357 YTNQISD 363

```

>ref|XP\_001758778.1| predicted protein [Physcomitrella patens subsp. patens]  
Length = 369

Score = 139 bits (349), Expect = 3e-031  
Identities = 86/280 (30%), Positives = 134/280 (47%), Gaps = 20/280 (7%)

```

Query: 25  LFDCDGVLWNGERAVPGAPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLRA 84
      +FDCDGV+W G+  + G PE L+ L   GK  +FV+NNS ++R +   +F LG
Sbjct: 89  IFDCDGVIIWKGDLSLIEGVPETLDMLRSMGKRLVFVTNNSTKSRKQYGKKFESLGLSVSEE 148

Query: 85  EQLFSSXXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXX----- 133
      E  SS      P      V++
Sbjct: 149 EIFASSFAAAAYLKSIFPSDKK----VYIIGEAGIQLELQAGINYYIGGPEDGDKRIDL 204

Query: 134 XXXXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRD-PECLLVATDRDPWHPLSDGSRT 192
      V AV+VG+D +  ++ KL+  A   +R+ P C+ +AT+ D   L+D
Sbjct: 205 APGQLMEHDHDVAVVVGFDRYLNYKLYATLCIRENPGCMFIATNCDAVTHLTDAQEW 264

Query: 193 PGTGSLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRC 252
      G GS+  A++ ++ ++ LVVGKPS +M + +   F+I  ++  MVGDRL+TDILFG
Sbjct: 265 AGGGSVMGAIKSTKKEPLVVGKPSFMMDYLAASEFNIKTSQICMVGDRDLTDILFGQNG 324

Query: 253 GMTTVLTLTGVSRLEEAQAYLAAGQHDLVPHYVESIADL 292
      G  T+L L+GV+ LE  Q   +  ++ + P +Y   I+DL
Sbjct: 325 GCATLLVLSGVTTLETLQ----SPENKIQPDFYTTKISDL 360

```

>gb|EAZ31186.1| hypothetical protein OsJ\_014669 [Oryza sativa (japonica  
cultivar-group)]  
Length = 372

Score = 139 bits (349), Expect = 3e-031  
Identities = 84/282 (29%), Positives = 134/282 (47%), Gaps = 19/282 (6%)

```

Query: 25  LFDCDGVLWNGERAVPGAPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLRA 84
      +FDCDGV+W G++ + G PE L+ L   GK  +FV+NNS ++R +   +F LG
Sbjct: 86  IFDCDGVIIWKGDKLDIGVPETLDMLRSGKRLVFVTNNSTKSRKQYGKKFETLGLNVNEE 145

```

Query: 85 EQLFSSXXXXXXXXXXXXPGPP-----DAPGAVFVXXXXXXXXXXXXXXXXX 130  
 E SS P + G ++  
 Sbjct: 146 EIFASSFAAAAYLQSIDFPKDKKVVYVIGEDGILKELELAGFQYLGGPSDGDKKIELKPGF 205

Query: 131 XXXXXXXXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRD-PECLLVATDRDPWHPLSDG 189  
 V AV+VG+D +F++ K++ +R+ P CL +AT+RD L+D  
 Sbjct: 206 YMEHDKDVTTIPTLVGAVVVGFDRYFNYYKVQYGTLCIRENPGCLFIATNRDAVTHLTDA 265

Query: 190 SRTPGTGSLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLTDILFG 249  
 G GS+ A+ ++ ++ LVVGKPS +M + + + F I ++ MVDRL+TDILFG  
 Sbjct: 266 QEWAGGSMVGAILGSTKQEPLVVGKPSFMMDYLAKKFGITTSQICMVGDRDLTDILFG 325

Query: 250 HRCGTTTLTGTGVSRLAEAQAYLAAGQHDLVPHYVYESIAD 291  
 G T+L L+GV+ ++ L + + + P +Y I+D  
 Sbjct: 326 QNGGCKTLLVLSGVTSVQ----MLQSPDNSIQPDFYTNQISD 363

>ref|NP\_199587.1| ATPK5 (Arabidopsis thaliana serine/threonine protein kinase 5);

phosphoglycolate phosphatase  
 Length = 301

Score = 138 bits (348), Expect = 4e-031  
 Identities = 87/283 (30%), Positives = 139/283 (49%), Gaps = 15/283 (5%)

Query: 25 LFDCDGVLWNGERAVPGAPPELLERLARAGKAALFVSNNRRARPELALRFARLGFGLRA 84  
 LFDCDGV+W GE + G + L+ + GK +FV+NNS ++R + A +F LG +  
 Sbjct: 22 LFDCDGVIIWKGETLIDGVSQTLDLIRSKGKNVVFVTNNSVKSRRQYAEKFRSLGVTSITQ 81

Query: 85 EQLFSSXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXX-----XXXXX 135  
 +++FSS P D V  
 Sbjct: 82 DEIFSSSFAAAMYKLVNN-FPKDKKVVYVIGGEGVLEELQIAGFTGLGGPEDGEKKAQWKS 140

Query: 136 XXXXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRD-PECLLVATDRDPWHPLSDGSRTPG 194  
 V AV+VG D + ++ KL+ +R+ P CL +AT+RD ++D PG  
 Sbjct: 141 NSLFEHDKSVGAVVVGLDPNINYYKLQYGTLCVRENPGCLFIATNRDAVGHMTDLQEWPG 200

Query: 195 TGSLLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLTDILFGHRCGM 254  
 G + AA+ ++ R+ +VVGKPS +M + + + F + +R MVDRL+TDILFG G  
 Sbjct: 201 AGCMVAAMCGSTEREPIVVGKPSFMDFLLQKFGTETSRMCMVGDRDLTDILFGQNAGC 260

Query: 255 TTVLTLTGTGVSRLAEAQAYLAAGQHDLVPHYVYESIADLTEGLE 297  
 T+L LTGV+ +++ L + + P YY +++D+ + +E  
 Sbjct: 261 KTLVLVLTGVT----SESLLDKGNKIEPDYYTSTVSDIIKLME 299

>dbj|BAB11323.1| 4-nitrophenylphosphatase-like protein [Arabidopsis thaliana]  
 Length = 311

Score = 138 bits (348), Expect = 4e-031  
 Identities = 87/283 (30%), Positives = 139/283 (49%), Gaps = 15/283 (5%)

Query: 25 LFDCDGVLWNGERAVPGAPPELLERLARAGKAALFVSNNRRARPELALRFARLGFGLRA 84  
 LFDCDGV+W GE + G + L+ + GK +FV+NNS ++R + A +F LG +  
 Sbjct: 22 LFDCDGVIIWKGETLIDGVSQTLDLIRSKGKNVVFVTNNSVKSRRQYAEKFRSLGVTSITQ 81

Query: 85 EQLFSSXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXX-----XXXXX 135  
+++FSS P D V  
Sbjct: 82 DEIFSSSFAAAMYLVKVN--FPKDKKVYVIGGEGVLEELQIAGFTGLGGPEDGEKKAQWKS 140

Query: 136 XXXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRD-PECLLVATDRDPWHPLSDGSRTPG 194  
V AV+VG D + ++ KL+ +R+ P CL +AT+RD ++D PG  
Sbjct: 141 NSLFEHDKSVGAVVVGLDPNINYYKLYGTLCVRENPGCLFIATNRDAVGHMTDLQEWPG 200

Query: 195 TGS�AAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGM 254  
G + AA+ ++ R+ +VVGKPS +M + + + F + +R MVDRL+TDILFG G  
Sbjct: 201 AGCMVAAMCGSTEREPIVVGKPSFMMDFLLQKFGTETSRMCMVGDRLDILFGQONAGC 260

Query: 255 TTVLTLTGVSRLLEEAQAYLAAGQHDLVPHYYVESIADLTEGLE 297  
T+L LTGV+ +++ L + + P YY +++D+ + +E  
Sbjct: 261 KTLVLVLTGVT----SESLLDKGNKIEPDYTTSTVSDIIKLME 299

>emb|CAO48346.1| unnamed protein product [Vitis vinifera]  
Length = 362

Score = 138 bits (347), Expect = 5e-031  
Identities = 86/284 (30%), Positives = 133/284 (46%), Gaps = 12/284 (4%)

Query: 16 DVLGRAQGVLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNRRARPELALRFA 75  
+++ + +FDCDGV+W G+ + G PE L+ L GK +FV+NNS ++R + +F  
Sbjct: 74 ELIDSVETFIFFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNRRARPELALRFA 133

Query: 76 RLGFGGLRAEQLFSSXXXXXXXXXXXXPGPP-----DAPGAVFVXXXXXXXXXXXXXXXXX 128  
LG E SS P D  
Sbjct: 134 TLGLSVSEEEIFASSFAAAAYLKSINFPKDKKVYVIGEDGILKELELAGFEYLGPPEDGG 193

Query: 129 XXXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRD-PECLLVATDRDPWHPLS 187  
V AV+VG+D +F++ K++ +R+ P CL +AT+RD L+  
Sbjct: 194 KKIELKPGFLMEHDENVGAVVVGFDRYFNYYKIQYGTLCIRENPGCLFIATNRDAVTHLT 253

Query: 188 DGSRTPGTGS�AAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDIL 247  
D G GS+ A+ ++ R+ LVVGKPS +M + + F I ++ MVDRL+TDIL  
Sbjct: 254 DAQEWAGGSMVGGALAGSTQREPLVVGKPSFMMDYLANKFGILKSQICMVDRLDIL 313

Query: 248 FGHRCGMMTTVLTLTGVSRLLEEAQAYLAAGQHDLVPHYYVESIAD 291  
FG G T+L L+GV+ L + L + + + P +Y I+D  
Sbjct: 314 FGQNGGCKTLLVLSGVTSL----SMLQSPNNSIQPDFYTSKISD 353

>ref|NP\_198495.1| phosphoglycolate phosphatase, putative [Arabidopsis thaliana]  
Length = 362

Score = 138 bits (347), Expect = 5e-031  
Identities = 86/279 (30%), Positives = 134/279 (48%), Gaps = 20/279 (7%)

Query: 25 LFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNRRARPELALRFARLFGGLRA 84  
+FDCDGV+W G++ + G PE L+ L GK +FV+NNS ++R + +F LG  
Sbjct: 83 IFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNRRARPELALRFARLFGGLRA 142

Query: 85 EQLFSSXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 144  
E SS P V+V



V AV+VG+D +F++ K++ +R+ P

Sbjct: 181 LELAGFYQLGGPSDGDKKIELKPGFYMEHDKDVGAVVVGFDYRFNYYKVQYGTLCIRENP 240

Query: 172 ECLLVATDRDPWHPLSDGSRTPGTGLAAAVETASGRQALVVGKPSPYMFECITENFSID 231  
 CL +AT+RD L+D G GS+ A+ ++ ++ LVVGKPS +M + + + F I

Sbjct: 241 GCLFIATNRDAVTHLTDAQEWAGGSMVGGAILGSTKQEPLVVGKPSFMMDYLAKKFGIT 300

Query: 232 PARTLMVGDRLDILFGHRCGMMTTVLTLTGVSRLLEEAQAYLAAGQHDLVPHYYVESIAD 291  
 ++ MVGDRL+TDILFG G T+L L+GV+ ++ L + + + P +Y I+D

Sbjct: 301 TSQICMVGDRDLTDILFGQNGGCKTLLVLSGVTSVQ---MLQSPDNSIQPDFYTNQISD 356

>ref|XP\_001838048.1| hypothetical protein CC1G\_07538 [Coprinopsis cinerea okayama7#130]

Length = 301

Score = 137 bits (345), Expect = 9e-031  
 Identities = 86/277 (31%), Positives = 131/277 (47%), Gaps = 15/277 (5%)

Query: 25 LFDCDGVLWNGERAVPGAPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLRA 84  
 LFDCDGVLW G+ + GA E+L+ L R K +FV+NN+ ++R +F LG

Sbjct: 22 LFDCDGVLWRGDHLLDGAVEVLDLLRRRNKKVVFVTNNATKSRRSYKSKFDDLGVFA-HV 80

Query: 85 EQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 144  
 ++++ S P V

Sbjct: 81 DEIYGSAYAAAVYISSVIKLPKTKKVVYVIGMAGLEELQNEGITILGGTDPADNTLESFN 140

Query: 145 -----VRAVLVGYDEHFSFAKLREACAHL-RDPECLLVATDRDPWHPLSDGSRTPG 194  
 V AV+ G D ++ KL +A +L + +CL +AT+ D +P S G PG

Sbjct: 141 LADFVRDPDVGAVVCGLDTKINYTKLSKAFQYLLHNQDCLFIATNEDSTYPSSHGL-LPG 199

Query: 195 TGSLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGM 254  
 GS++A + A G+ + GKP+ M +CI + DP RT+MVGDRL TDILFG G+

Sbjct: 200 AGSISAPLRCALGKNPICTGKPASTMLDCAKAKVNFDPKRTIMVGDRLNTDILFGQNGGL 259

Query: 255 TTVLTLTGVSRLLEEAQAYLAAGQHDLVPHYYVESIAD 291  
 T+L LTG++++ + Q A+ +VP + E++ D

Sbjct: 260 ATLLVLTGITKVTDIQGNAS---PIVPDFVTEALGD 293

>gb|ABK96026.1| unknown [Populus trichocarpa]

Length = 304

Score = 136 bits (343), Expect = 2e-030  
 Identities = 89/291 (30%), Positives = 136/291 (46%), Gaps = 20/291 (6%)

Query: 14 LRDVLGRAQGVLFDCDGVLWNGERAVPGAPELLERLARAGKAALFVSNNSRRARPELALR 73  
 +R + + LFDCDGV+W G++ + G + L+ L GK +FV+NNS ++R + A +

Sbjct: 16 IRSLFESVEAFLFDCDGVIVKGDKLIDGVSQTLDWLRSKGKLVFVTNNSLKSRIQYAKK 75

Query: 74 FARLGFGLRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXX 133  
 F LG E SS P V+V

Sbjct: 76 FHSLGISVAEDEFSSSFAAAMYLVNFPQEKK---VYVIGGEGILEELQLAGYTGLG 131

Query: 134 XXXXXXXXXXXX-----RRAVLVGYDEHFSFAKLREACAHLRD-PECLLVATDRD 181  
 V AV+VG D ++ KL+ +R+ P CL +AT+RD

Sbjct: 132 GPEDGEKRVELKPNPFEHDKSVGAVVVGIDPRINYYKLYGTLCIRENPGCLFIATNRD 191

Query: 182 PWHPLSDGSRTPGTGSLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDR 241  
++D PG GS+ AA+ ++ R+ +VVGKPS +M + + + F I+ ++ MVGDR  
Sbjct: 192 AVGHMTDLQEWPGAGSMVAAMCGSTEREPIVVGKPSFMMDFLLQKFHINTSKMCMVGDR 251

Query: 242 LETDILFGHRCGMTTTLTGTGVSRLLEEAQAYLAAGQHDLVPHYVYESIADL 292  
L+TDILFG G T+L L+GV+ Q L + + P YY ++DL  
Sbjct: 252 LDTDILFGQNAGCKTLLVLSGVT----TQTTLRDPSNSVQPDYYTSQVSDL 298

>ref|XP\_393558.1| PREDICTED: similar to CG5567-PA [*Apis mellifera*]  
Length = 307

Score = 136 bits (343), Expect = 2e-030  
Identities = 79/279 (28%), Positives = 128/279 (45%), Gaps = 8/279 (2%)

Query: 24 VLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNRRARPELALRFARLGFGLR 83  
VL DCDGVLW + +PE +++L GK +++NN+ + R E + L +  
Sbjct: 24 VLSDCDGVWRETEVIQNSPETVKKLKLKELGKFFYITNNNTKTRAEFLKCCNDLNYDATI 83

Query: 84 AEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 143  
E + +S G+V +  
Sbjct: 84 DEIVCTSFLAAVYLKEKEFNKKVYVVGSVGIGKELEAVGIQHYGSGPDIIEGDEVELVKN 143

Query: 144 -----RVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGSL 198  
V AV++G+D+ FSF K+ +A +L DP + T+ D P ++ PGTG  
Sbjct: 144 FKPDPEVGAVVIGFDKDFSFPKIVKAVTYLNDPNVHFIGTNNNDIERPSPSANKFPGTGCF 203

Query: 199 AAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLETDILFGHRCGMTTTL 258  
+E A R A+++GKP ++ E IT+ + ++P RTLM+GD TDIL G RCG T++  
Sbjct: 204 IKNIEAACNRSAVILGKPESFVSEYITKKYGLNPERTLMIGDNCNTDILLGKRCGFKTLV 263

Query: 259 TLTGVSRLLEEAQAYLAAGQHDLVPHYVYESIADLTE 294  
LTG++ +E A ++ ++P YY + D+ E  
Sbjct: 264 VLTGITTQNDIENMNASDINTKNLIIPDYANELGDILE 302

>ref|NP\_001053167.1| Os04g0490800 [*Oryza sativa* (japonica cultivar-group)]  
Length = 365

Score = 136 bits (343), Expect = 2e-030  
Identities = 84/275 (30%), Positives = 131/275 (47%), Gaps = 12/275 (4%)

Query: 25 LFDGCDGVWNGERAVPGAPELLERLARAGKAALFVSNNRRARPELALRFARLGFGLRA 84  
+FDCDGV+W G++ + G PE L+ L GK +FV+NNS ++R + +F LG  
Sbjct: 86 IFDCDGVVIWKGDKLIDGVPETLDMLRSKGRKLVFVTNNSTKSRKQYGGKFFETLGLNVNEE 145

Query: 85 EQLFSSXXXXXXXXXXXXXXXXPGPP-----DAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 137  
E SS P D  
Sbjct: 146 EIFASSFAAAAYLQSIDFPKDKKVYVIGEDGILKELELAGFQYLGGPSDGDKKIELKPGF 205

Query: 138 XXXXXXRVRAVLVGYDEHFSFAKLREACAHLRD-PECLLVATDRDPWHPLSDGSRTPGTG 196  
V AV+VG+D +F++ K++ +R+ P CL +AT+RD L+D G G  
Sbjct: 206 YMEHDKDVGAVVVGFDYFNYKQYGTLCIRENPGCLFIATNRDAVTHLTDAQEWAGGG 265

Query: 197 SLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLETDILFGHRCGMTT 256  
S+ A+ ++ ++ LVVGKPS +M + + + F I ++ MVGDRL+TDILFG G T

Sbjct: 266 SMVGAILGSTKQEPLVVGKPFSTFMMDYLAKKFGITTSQICMVGDRDLDTDILFGQNGGCKT 325

Query: 257 VLTLTGVSRLLEEAQAYLAAGQHDLVPHYYVESIAD 291

+L L+GV+ ++ L + + + P +Y I+D

Sbjct: 326 LLVLSGVTSVQ----MLQSPDNSIQPDFYTNQISD 356

>ref|XP\_001193132.1| PREDICTED: hypothetical protein [Strongylocentrotus purpuratus]

Length = 306

Score = 136 bits (342), Expect = 2e-030

Identities = 70/157 (44%), Positives = 99/157 (63%), Gaps = 4/157 (2%)

Query: 145 VRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRT-PGTGSLAAAVE 203

V V+VG+D++FSF KL +A ++L+ P + + T+ D P+ + PGTGSL VE

Sbjct: 150 VNGVVVGFQYFYSFMKLLKAASYLKRPNVFIGTNIQQFPMRNSSELIMPGTGS�VRPVE 209

Query: 204 TASGRQALVVGKPSPYMFECITENFSDPARTLMVGDRLLETDLFGHRCGMTTVLTLTG 263

AS R A +GKPS +MFECI E F ++P RT+M+GDRL TDIL G CG+ T+ LTGV

Sbjct: 210 VASNRTATTLGKPSKFMFECIQEKFDVNPQRTIMIGDRLNTDILLGKNCGLKTLAVLTGV 269

Query: 264 SRLEEAQAYLAA---GQHDLVPHYYVESIADLTEGLE 297

+ EE + + + +LVP Y+ESI L + L+

Sbjct: 270 TSEEEILGFQSEKEKERELVPDLYIESIGHLGKLLD 306

Score = 69.3 bits (168), Expect = 3e-010

Identities = 30/77 (38%), Positives = 47/77 (61%)

Query: 3 MARCERLRGAALRDVLGRAQGVLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNN 62

MA C +L ++++L +L DCDGVW+ A PGA E + +L GK +FV+NN

Sbjct: 1 MATCRKLTQLMKELLDSDIDTILLDCDGVWHSNMAFPGAETINKLRSMGKQPIFVTNN 60

Query: 63 SRRARPELALRFARLGF 79

S ++R + +F ++GF

Sbjct: 61 STKSRLQYQEKFTKMGF 77

>dbj|BAC42546.1| putative p-nitrophenylphosphatase [Arabidopsis thaliana]

Length = 309

Score = 135 bits (341), Expect = 3e-030

Identities = 85/279 (30%), Positives = 133/279 (47%), Gaps = 20/279 (7%)

Query: 25 LFDGCDGVWNGERAVPGAPELLERLARAGKAALFVSNNSSRRARPELALRFARLGFGLRA 84

+ DCDGV+W G++ + G PE L+ L GK +FV+NNS ++R + +F LG

Sbjct: 30 ILDCDGVWIKGDKLIEGVPETLDMLRAKGRKLVFVTNNSTKSRKQYGGKFETLGLNVNEE 89

Query: 85 EQLFSSXXXXXXXXXXXXXXXXPPDAPGVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXR 144

E SS P V+V

Sbjct: 90 EIFASSFAAAAYLQSFNPKDKK----VYVIGEEGILKELELAGFYQLGGPDDGKRQIEL 145

Query: 145 -----VRAVLVGYDEHFSFAKLREACAHLRD-PECLLVATDRDPWHPLSDGSRT 192

V AV+VG+D +F++ K++ +R+ P CL +AT+RD L+D

Sbjct: 146 KPGFLMEHDHVDGAVVVGFDYFYNYKIYGTLCIRENPGCLFIATNRDAVTHLTDAQEW 205



Query: 193 PGTGSLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRC 252  
G GS+ A+ ++ R+ LVVGKPS +M + + + F I ++ MVGDRL+TDILFG  
Sbjct: 206 AGGGSVMGALVGSTQREPLVVGKPSFMMDYLDKFGIQKSQICMVGDRDLTDILFGQNG 265

Query: 253 GMTTVLTLTGVSRLLEEAQAYLAAGQHDLVPHYYVESIAD 291  
G T+L L+GV+ + + L + ++ + P +Y I+D  
Sbjct: 266 GCKTLLVLSGVTSI----SMLESPENKIQPDFYTSKISD 300

>gb|ABK95024.1| unknown [Populus trichocarpa]  
Length = 371

Score = 135 bits (339), Expect = 4e-030  
Identities = 89/298 (29%), Positives = 139/298 (46%), Gaps = 14/298 (4%)

Query: 2 AMARCERLRGAALRDVLRGQGVLFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSN 61  
A A + L+ A +++ + +FDCDGV+W G++ + G P+ L+ L GK +FV+N  
Sbjct: 71 ASAAAQPLKNAD--ELIDSVETFI FDCDGVWNGERAVPGAPPELLERLARAGKAALFVSN 128

Query: 62 NSRRARPELALRFARLGFGLRAEQLFSSXXXXXXXXXXXXXPGPP-----DAPGAVFV 114  
NS ++R + +F LG E SS P D  
Sbjct: 129 NSTKSRKQYKGFETLGLDVSEEEIFASSFAAAAYLKSIDFPKDKKVYVVGEDGILKELE 188

Query: 115 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXRVRAVLVGYDEHFSFAKLREACALRD-PEC 173  
V AV+VG+D +F++ K++ +R+ P C  
Sbjct: 189 LAGFQYLGPEDEGGKIELKPGFLMEHDKDVGAVVVGFDYFNYYKVQYGTLCIRENPGC 248

Query: 174 LLVATDRDPWHPLSDGSRTPGTGLAAAVETASGRQALVVGKPSPYMFECITENFSIDPA 233  
L +AT+RD L+D G GS+ A ++ R+ LVVGKPS +M + + F I +  
Sbjct: 249 LFIATNRDAVTHLTDAQEWAGGSMVGA FVGSTQREPLVVGKPSFMMDYLAN KFGILKS 308

Query: 234 RTL MVGDRLDILFGHRCGMTTVLTLTGVSRLLEEAQAYLAAGQHDLVPHYYVESIAD 291  
+ MVGDRL+TDILFG G T+L L+GV+ L + L + + + P +Y I+D  
Sbjct: 309 QICMVGDRDLTDILFGQNGGCKTLLVLSGVTSL----SMLQSPGNSIQPDFYTNKISD 362

>emb|CA063941.1| unnamed protein product [Vitis vinifera]  
Length = 306

Score = 134 bits (338), Expect = 6e-030  
Identities = 89/298 (29%), Positives = 138/298 (46%), Gaps = 12/298 (4%)

Query: 2 AMARCERLRGAALRDVLRGQGVLFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSN 61  
A A E L R +L + LFDCDGV+W G++ + G E L+ L GK +FV+N  
Sbjct: 8 AKAPELLSPQNARLLLDSTEAFLFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSN 67

Query: 62 NSRRARPELALRFARLGFGLRAEQLFSSXXXXXXXXXXXXXPGPPDA-----PGAV--FV 114  
NS ++R + A +F LG E SS P G +  
Sbjct: 68 NSSKSRQYAEKFNSLGI AVSEDEIFSSSFAAAMFLKVNDFPQEKKVYVIGGEGILEELQ 127

Query: 115 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXRVRAVLVGYDEHFSFAKLREACALRD-PEC 173  
V AV+VG D + ++ KL+ +R+ P C  
Sbjct: 128 LAGFTGLGPEDEGKKTVELKSNCFFEHDKSVGAVVVGIDPYINYYKLQYGTLCIRENPGC 187

Query: 174 LLVATDRDPWHPLSDGSRTPGTGLAAAVETASGRQALVVGKPSPYMFECITENFSIDPA 233  
L +AT+ D ++D PG G + A+ +++ ++ +VVGKPS +M + + + + I+ +

Sbjct: 188 LFIATNLDAVGHMTDLQEWPGAGCMVGAISSSTEKKPMVVGKPKSTFMDFLLQKYHINTS 247  
Query: 234 RTLMVGDRLLETDILFGHRCGMTTVLTLTGVSRLLEEAQAYLAAGQHDLVPHYYVESIAD 291  
+ MVGDRL+TDILFG G T+L L+GV+ QA L + + P YY ++D  
Sbjct: 248 KMCMVGDRLDITDILFGQNAGCKTLLVLSGVT----TQAILQDPSNKIQPDYYTSKLS 301

>ref|XP\_001604657.1| PREDICTED: similar to 4-nitrophenylphosphatase [Nasonia vitripennis]  
Length = 306

Score = 134 bits (338), Expect = 6e-030  
Identities = 82/275 (29%), Positives = 125/275 (45%), Gaps = 6/275 (2%)

Query: 24 VLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNRRARPELALRFARLGFGLR 83  
VL DCDGVW + + E++ GK +V+NNS + R E A + L F  
Sbjct: 24 VLTDCDGVWMMEMTPLYHSAEVMNTFQELGKRVFYVTNNSTKTREEFAEKCKLLNFKASE 83

Query: 84 AEQLFSSXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX- 142  
L +S G +  
Sbjct: 84 ENILCTSHLAANYLKNISFNRKVYVIGKSGISQELDAQGIEHVGLGPDVTEGDELDFK 143

Query: 143 ----XRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGSL 198  
V AV+VG+D HFS+ K+ +A + D + T+ D P + R PG G  
Sbjct: 144 FKPDSEVGVVVGFDHRHFSYQKIVKAATYAYDKNIHFICTNPDVERPSPNTIRYPGAGCF 203

Query: 199 AAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLLETDILFGHRCGMTTVL 258  
+A+E + R A++VGKP P++ E I + + +DPARTLM+GD L TDIL G RCG TT+L  
Sbjct: 204 LSAIEKIAKRSAIIVGKPEPFVSEVIKKYGVDPARTLMIGDNLNTDILLGQRCGFTTLL 263

Query: 259 TLTGVSRLLEEAQAYLAAGQHDLVPHYYVESIADL 292  
++G++ EE A ++P++Y + ++D+  
Sbjct: 264 VMGGITTPPEELASIKKNPKGSPILPNFYADQLSDI 298

>ref|XP\_001703502.1| phosphoglycolate phosphatase 1 [Chlamydomonas reinhardtii]  
Length = 330

Score = 134 bits (338), Expect = 6e-030  
Identities = 88/303 (29%), Positives = 144/303 (47%), Gaps = 50/303 (16%)

Query: 16 DVLGRAQGVLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNRRARPELALRFA 75  
++L + + +FDCDGV+W G++ + G PE L+ L GK FV+NNS ++R +F  
Sbjct: 41 ELLKKVECFIFDCDGVWGLGDKVIEGVPETLDMLRGMGKKVFFVTNNSTKSRAGYMSKQ 100

Query: 76 RLGFGGLRAEQLFSSXXXXXXXXXXXX-----PGPPDAPG 110  
LG ++AE+++SS GP DA  
Sbjct: 101 SLGLN-VKAEIYSSSYAAAAYLESINFNKKVYVIGETGILEELDLKIRHVGGPGDADK 159

Query: 111 AVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRD 170  
V + V AV+VG+D + ++ K++ A +R+  
Sbjct: 160 KVTLKSGEFMEHDH-----VGAVVVGFDVRYVNYKIQYATLCIRE 200

Query: 171 -PECLLVATDRDPWHPLSDGSRTPGTGSLAAAVETASGRQALVVGKPSPYMFECITENFS 229  
P C+ +AT+RD L+D G GS+ A+ ++ R+ +VVGKPS +M + I+ +  
Sbjct: 201 NPGCMFIATNRDAVTHLTDAQEWAGNGSMVGAIVGSKREPIVVGKPSDFMLKNISASLG 260

Query: 230 IDPARTLMVGDRLLETDILFGHRCGMTTTLTGTGVSRLLEEAQAYLAAGQHDLVPHYYVESI 289  
+ P + MVDRL+TDI+FG G+ T L L+GV+ E L + + + P + + S+  
Sbjct: 261 LRPDQIAMVGDRLDITDIMFGKNGGLATALVLSGVTTPE---VLNSPDNKVHPDFVLNSL 316

Query: 290 ADL 292  
DL  
Sbjct: 317 PDL 319

>ref|XP\_001520582.1| PREDICTED: hypothetical protein [Ornithorhynchus anatinus]

Length = 131

Score = 134 bits (336), Expect = 1e-029  
Identities = 66/106 (62%), Positives = 79/106 (74%)

Query: 3 MARCERLRGAALRDVLGRAQGVLFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNN 62  
MA C+ L G ALR+V+GR+QG+LFDCDGVW+GER VPGAPPELL+RL R GKAA FVSNN  
Sbjct: 1 MAGCKALSGGALREVVGSRQILFDCDGVWNGERAVPGAPPELLDRLGRGGKAAFFVSNN 60

Query: 63 SRRARPELALRFARLGFGLRAEQLFSSXXXXXXXXXXXXXXXXPGPPDA 108  
SRR+R +L RF+RLGF G+ AE+LFSS GP +A  
Sbjct: 61 SRRSRQDLQRRFSRLGFRGVAAERLFSSALCSALLLRHRLGPN 106

>dbj|BAA98057.1| 4-nitrophenylphosphatase-like [Arabidopsis thaliana]  
Length = 389

Score = 133 bits (335), Expect = 1e-029  
Identities = 81/255 (31%), Positives = 123/255 (48%), Gaps = 16/255 (6%)

Query: 25 LFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNRRARPELALRFARLGFGLRA 84  
+FDCDGV+W G++ + G PE L+ L GK +FV+NNS ++R + +F LG  
Sbjct: 83 IFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNRRARPELALRFARLGFGLRA 142

Query: 85 EQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXXXR 144  
E SS P V+V  
Sbjct: 143 EIFASSFAAAAYLQSFNPKDKK----VYVIGEEGILKELELAGFQYLGPPDDGKRQIEL 198

Query: 145 -----VRAVLVGYDEHFSFAKLREACAHLRD-PECLLVATDRDPWHPLSDGSRT 192  
V AV+VG+D +F++ K++ +R+ P CL +AT+RD L+D  
Sbjct: 199 KPGFLMEHDHDVAVVGVDFRYFNYYKIQYGTLCIRENPGCLFIATNRDAVTHLTDAQEW 258

Query: 193 PGTGSLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLLETDILFGHRC 252  
G GS+ A+ ++ R+ LVVGKPS +M + + + F I ++ MVDRL+TDILFG  
Sbjct: 259 AGGGSMVGVGALVSTQREPLVVGKPSFMMMDYLADKFGIQKSQICMVDRLDITDILFGQNG 318

Query: 253 GMTTTLTGTGVSRL 267  
G T+L L+G++ L+  
Sbjct: 319 GCKTLLVLSGITNLQ 333

>ref|XP\_001895356.1| haloacid dehalogenase-like hydrolase family protein [Brugia malayi]

Length = 301

Score = 132 bits (333), Expect = 2e-029  
Identities = 87/303 (28%), Positives = 136/303 (44%), Gaps = 18/303 (5%)

Query: 8 RLRGAALRDVLRGQGVLFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNSRRAR 67  
R++ A ++ LFD DGVLW + +PGA + L L AGK ++NNS +  
Sbjct: 3 RVQQADGHQLISSFDSFLFDADGVLWLDLDTXLPGAADFLRHLVSAGKNVFILTNSTKTL 62

Query: 68 PELALRFARLGFGLRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXX----- 118  
+ + R+GF L + + S P V++  
Sbjct: 63 DDYVNKCKRIGFDMLSDDHILSPAKVLAHILAKEKSDLP-----VYIVGSSGLQRELKKE 117

Query: 119 ---XXXXXXXXXXXXXXXXXXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRDPECLL 175  
+VRAV+V +D H S+ K+ A ++  
Sbjct: 118 GIESFGTGPDLVESYTNVESIQQMDISRKVRVVVSDIHLSPKIMRAANYINQAGVRF 177

Query: 176 VATDRDPWHPLS-DGSRTPGTGLAAAVETASGRQALVVGKPSPYMFECITENFSIDPAR 234  
AT+ DP P G PG+G AV+TA+G++ +V+GKPS MFE I E F++ +  
Sbjct: 178 YATNPDPRLPGPVPGVVIPGSGVSMRAVQTAAGKEPVVIGKPSKTMFEYIKERFNLKAEK 237

Query: 235 TLMVGDRLDILFGHRCGTTVLTTLTGVSRLEEAQAYLAAGQHDLVPHYYVESIADLTE 294  
+++ GD ETDI FGH G+T+VL TGV L + + + G D +P++Y S+ L +  
Sbjct: 238 SVIFGDSCETDIKFGHVNGLTSVLVGTGVHDLNKVEEFKXGYKDFIPNFYTPSLKVLFD 297

Query: 295 GLE 297  
L+  
Sbjct: 298 ILQ 300

>ref|XP\_001885204.1| predicted protein [Laccaria bicolor S238N-H82]  
Length = 303

Score = 131 bits (330), Expect = 5e-029  
Identities = 83/277 (29%), Positives = 128/277 (46%), Gaps = 15/277 (5%)

Query: 25 LFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLRA 84  
LFDCDGVW G+ + G E+L L K +FV+NN+ ++R +F +LG  
Sbjct: 22 LFDCDGVWLRGDELIDGVVEVLHMLRCLKKQVVVFTNNATKSRKSYKTKFDQLGVEA-HV 80

Query: 85 EQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXX-----XXXXXXXXXXXXXXXXXXXX 135  
+++F S P V  
Sbjct: 81 DEIFGSAYASAVYLSVIKLPKTKKVYVIGMGGLEELRDEGISYLGGTDPADNTLETFS 140

Query: 136 XXXXXXXXRVRAVLVGYDEHFSFAKLREACAHL-RDPECLLVATDRDPWHPLSDGSRTPG 194  
V AV+ G D ++ KL +A +L R+P C +AT+ D +P +DG PG  
Sbjct: 141 LANFTLDPDVAAVVCGLDLDTQINYTEKLSKAFQYLTRNPGCHFATNEDSTYPGADGL-LPG 199

Query: 195 TGSLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGM 254  
GS++A + A+GR + GKPS M +C+ + D RT+M+GDRL TDILFG G+  
Sbjct: 200 AGSISAPLRYAAGRAPICTGKPSNTMLDCVKAKINFDTERTIMIGDRLNTDILFGQNGGL 259

Query: 255 TTVLTLTGVSRLEEAQAYLAAGQHDLVPHYYVESIAD 291  
+T+L LTG++ + A+ +VP + +++ D  
Sbjct: 260 STLLVLTGITEEADITGPYAS---PIVPDFVTQALGD 293

>gb|ABK24589.1| unknown [Picea sitchensis]  
Length = 372

Score = 131 bits (330), Expect = 5e-029  
Identities = 84/287 (29%), Positives = 138/287 (48%), Gaps = 16/287 (5%)

Query: 16 DVLGRAQGVLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNSRRARPELALRFA 75  
+++ + +FDCDGV+W G+ + G PE L+ L GK +FV+NNS ++R + +F  
Sbjct: 84 ELINSVETFIFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNSRRARPELALRFA 143

Query: 76 RLFGGLRAEQLFSSXXXXXXXXXXXXXXXXXPGPPDAP----GAVFVXXXXXXXXXXXXXXXXXXXX 131  
LG + E++F+S P D G V +  
Sbjct: 144 TLGLT-VGEEEIFASSFAAAAYLKSID-FPQDKKVYVIGEVGILKELELAGFKYLGGPDD 201

Query: 132 XXXXXXXX-----XXXXRVRAVLVGYDEHFSFAKLREACAHLRD-PECLLVATDRDPWHP 185  
V AV+VG+D + ++ K++ +R+ P CL +AT+ D  
Sbjct: 202 GDRRIELKPGFLLQDKEVGAVVVGFDYVNYKIQYGTLCIRENPGCLFIATNCDVAVTH 261

Query: 186 LSDGSRTPGTGSLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDLETD 245  
L+D G GS+ A+ ++ + +VVGKPS +M + +++ F I ++ MVGDRL+TD  
Sbjct: 262 LTDAQEWAGGSMVGLRGSTQKDPVVGKPSYMFECITENFSIDPARTLMVGDRLDLETD 321

Query: 246 ILFGHRCGMTTTLTLTGVSRLAEAQAYLAAGQHDLVPHYYVESIADL 292  
ILFG G T+L L+GV+ L L + + P +Y ++DL  
Sbjct: 322 ILFGQNGGCKTLLVLSGVTTL----PMLQNPNSNIQPDFYTNKVSIDL 364

>ref|XP\_568941.1| 4-nitrophenylphosphatase [Cryptococcus neoformans var. neoformans

JEC21]  
Length = 312

Score = 130 bits (328), Expect = 8e-029  
Identities = 88/286 (30%), Positives = 132/286 (46%), Gaps = 23/286 (8%)

Query: 25 LFDCDGVWNGERAVPGAPELLERLARAGKAA-----LFVSNNSRRARPELALRFAR 76  
L DCDGVL++G++ V G +L L + GKA +FV+NN+ ++R +L F +  
Sbjct: 23 LLDCDGVLYHGKQVVEGVRTVLNMLRKKGKAQRFELGKKIIFVTNNATKSRRKLKETFQDQ 82

Query: 77 LGFGGLRAEQLFSSXXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXX-- 134  
LG ++ F S P D VF  
Sbjct: 83 LGLNA-SIDECFGSAYASAVYISEVLNFPKDKKVYVFGEEGLEEELDQCGIAHCGGSDPV 141

Query: 135 -----XXXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPL 186  
+ AVL G+D ++ KL +A +LR+PEC L+ T+ DP P  
Sbjct: 142 DREFKAPIDFTVFKADDSIGAVLCGFDSWINYQKLAKAMTYLRNPECKLILTNTDPTFP- 200

Query: 187 SDGSRTPGTGSLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDLETDI 246  
+ G PG+GSL+ + AS R+ LV+GKP+ M + I + DP+R LMVGD L TDI  
Sbjct: 201 THGDVFPGSGSLSIPIVNASKRKPLVIGKPNKMMMDAILAHMFDPSRALMVGDNLATDI 260

Query: 247 LFGHRCGMTTTLTLTGVSRLAEAQAYLAAGQHDLVPHYYVESIADL 292  
FG + T+L + GV++ E+ +++VP + S DL  
Sbjct: 261 AFGRNSKIRTLVVMGGVTKYEQV---FGENPNEVVPDLVMNSFGDL 303

>ref|XP\_001674235.1| Hypothetical protein CBG09323 [Caenorhabditis briggsae AF16]

Length = 335

Score = 130 bits (327), Expect = 1e-028  
Identities = 84/282 (29%), Positives = 130/282 (46%), Gaps = 15/282 (5%)

Query: 25 LFD CDGVLWNGERAVPGAPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLR- 83  
+FD DGVLW GE +PG+P L++ L + K + ++NN+ ++R A + A+LG+ +  
Sbjct: 50 IFDADGVLWLGESVMPGSPRLIDYLVKHNKQIIIVLTNNATKSRAVYAKKLAKLGYNSSKM 109

Query: 84 -----AEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXX 131  
A+ L S G D + +  
Sbjct: 110 NKNLNVNPAAVVADTLHRSGLDGKRVYLIGEQLRDEMDELGIEYFGHGPEKKQNEEAGS 169

Query: 132 XXXXXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSR 191  
V AV+VGY++HF + K+ +A +LR+ L VAT+ D P +  
Sbjct: 170 GAFMYDIKLEE-NVGAVVVGYEKHFYTKMMKAANYLREEGVLFVATNEDETCPGNPEV 228

Query: 192 T-PGTGSLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGH 250  
P G + AA+ ASGR L VGKP F I ++I+P+RT+M+GDR TD+ FG  
Sbjct: 229 VIPDAGPIVAAIRCASGRDPLTVGKPCPAFNYIKRKWNINPSRTMMIGDRNTDVKFGR 288

Query: 251 RCGMTTVLTLTGVSRLLEEAQAYLAAGQHDLVPHYYVESIADL 292  
GM T+L L+G ++E+ + D+VP Y + L  
Sbjct: 289 DHGMKTLVLVSGCHQIEDIIENQMNERDDMVPDYVAPCLGAL 330

>ref|XP\_761126.1| hypothetical protein UM04979.1 [Ustilago maydis 521]  
Length = 697

Score = 130 bits (326), Expect = 1e-028  
Identities = 88/305 (28%), Positives = 136/305 (44%), Gaps = 35/305 (11%)

Query: 16 DVLGRAQGVLFDCDGLWNGERAVPGAPELLERLARAGKAALFVSNNSRRARPELALRFA 75  
++L + LFD CDGVLW+G+ +P +L++L + GK+ +FV+NN+ ++R +FA  
Sbjct: 396 ELLSKYDTFLFDCDGLWNGEITPHVVSVLQKLRQRGKSVIFVTNNASKSRQTYLKKFA 455

Query: 76 RLGFGGLRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVF-----VXXXXXXXX 121  
+ +++FSS P D V +  
Sbjct: 456 SMNIQA-SLDEVFSSSYASAVYLKVKLNFADPKVYVIGMHGIEEELDAENILHCGGTDA 514

Query: 122 XXXXXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRDPE----- 172  
+V AV+ G+D H S+ KL +A HL P  
Sbjct: 515 QDNKFLPALDFGSLQTDEAIDPKVAVVCGFDMHMSYLKLAFAFKHLTRPGFDGPEVEAEG 574

Query: 173 ----CLLVATDRDPWHPLSDGSRTPGTGSLAAAVETASGRQALVVGKPSPYMFECITENF 228  
C + T+ D P + G PG GSL+A + ++ R +VGKP M +CI  
Sbjct: 575 MGGGCHFILTNDSTFP-AKGGPWPAGSLSAPLIFSTKRTPTIVGKPKMLDCIIATK 633

Query: 229 SIDPARTLMVGDRLDILFGHRCGMTTVLTLTGVSRLLEEAQAYLAAGQH-DLVPHYYVE 287  
DP R +MVGDR L TDI F G+ ++L LTG+S+ +E + G H +P Y ++  
Sbjct: 634 QFDPKRAIMVGDRLNTDIEFAKAGGIASMLVLTGISKRDEIE-----GPHAKTIPDY LID 688

Query: 288 SIADL 292  
S+ DL  
Sbjct: 689 SLGDL 693

>ref|XP\_957212.1| 4-nitrophenylphosphatase [Neurospora crassa OR74A]

Length = 306

Score = 130 bits (326), Expect = 1e-028

Identities = 102/310 (32%), Positives = 141/310 (45%), Gaps = 29/310 (9%)

Query: 3 MARCERLRG--AALRDVLGRAQGVLFDCDGVWNGERAVPGAPELLERLARAGKAALFVS 60  
MA+ + L G AA+ + + + LFDCDGVW+GE G E L E L GK +FV+  
Sbjct: 1 MAQPKYLSGDVAINEFIDKFDVFLFDCDGVWLSGEHVFEFVVETLELLRSRGKKTVFVT 60

Query: 61 NNSRRARPELALRFARLGFGLRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXX 120  
NNS ++RPE +F LG E S+ PP VFV  
Sbjct: 61 NNSTKSRPEYKKKFEGLGIPADEDEIFGSAYSSAIYISRILKLAPPK--NKVFVIGEAGI 118

Query: 121 XXXXXXXX-----XXXXXXXXXXXXXXXXXRVRAVLVGYDEHFSFAKLREA 164  
V VLVG D H ++ KL A  
Sbjct: 119 EQELTTENIPFIGGTDPSFRRDVTVEDFNGLADGSLNPEVGCVLVGLDWHINYLKLSHA 178

Query: 165 CAHLRDPECLLVATDRDPWHPLSDGSRTPGTGSLAAAVETASGRQALVVGKPSPYMFECI 224  
+LR L AT+ D P+++ PG GS++ + +G++ + +GKPS M + I  
Sbjct: 179 YQYLRRGAVFL-ATNVDSTFPMMNNF-FPGAGSISVPLVHMTGQEPVALGKPSQAMMDAI 236

Query: 225 TENFSIDPARTLMVGDRLDILFG--HRCGMTTTLTGTGVSRLAEAQAYLAAGQHDLVP 282  
F +D ART MVDRL TDI FG R G T+ LTGV++ E+ +A A VP  
Sbjct: 237 EGKFHLDRARTCMVGDRLNTDIKFGIEGRG-LTAVLTGVNKKEDWEAADAVA----VP 291

Query: 283 HYYVESIADL 292  
+YV+ ++DL  
Sbjct: 292 SFYVDKLSDL 301

>ref|NP\_504509.1| K09H11.7 [Caenorhabditis elegans]

Length = 322

Score = 129 bits (324), Expect = 2e-028

Identities = 83/282 (29%), Positives = 131/282 (46%), Gaps = 15/282 (5%)

Query: 25 LFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNNSRRARPELALRFARLGFGLR- 83  
+FD DGVLW GE +PG+P L++ L + K + ++NN+ ++R A + A+LG+ +  
Sbjct: 33 IFDADGVWLVGESVMPGSPRLIDYLVKHNKQIIVLTNNATKSRVYAKKLAKLGYNSSKM 92

Query: 84 -----AEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXX 131  
A+ L + G D + +  
Sbjct: 93 NKNLNVNPAAVVADTLHRAGLDGKRVYLIGEQLRDEMDELGIEYFGHGPEKKQDEADGS 152

Query: 132 XXXXXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSR 191  
V AV+VGY++HF + K+ +A +LR+ L VAT+ D P +  
Sbjct: 153 GAFMYDIKLEE-NVGAVVGYEKHFYVMMKASNYLREEGVLFVATNEDETCGPNPEV 211

Query: 192 T-PGTGSLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGH 250  
P G + AA++ ASGR L VGKP F I ++I+P+RT+M+GDR TD+ FG  
Sbjct: 212 VIPDAGPIVAAIKCASGRDPLTVGKPCPTAFNYIKRKNINPSRTMMIGDRTNTDVKFGR 271

Query: 251 RCGMTTTLTGTGVSRLAEAQAYLAAGQHDLVPHYYVESIADL 292  
GM T+L L+G ++E+ + D+VP Y + L  
Sbjct: 272 DHGMKTLVLVSGCHQIEDIIENQMNERDDMVPDYVAPCLGAL 313

>ref|NP\_504512.1| F44E7.2 [Caenorhabditis elegans]  
Length = 335

Score = 129 bits (323), Expect = 3e-028  
Identities = 83/282 (29%), Positives = 131/282 (46%), Gaps = 15/282 (5%)

Query: 25 LFDCDGVLVNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLR- 83  
+FD DGVLW GE +PG+P L++ L + K + ++NN+ ++R A + A+LG+ +  
Sbjct: 50 IFDADGVWLWLGESVMPGSPRLIDYLVKHNKQIIIVLTNNATKSRAVYAKKLAKLGYNSSKM 109

Query: 84 -----AEQLFSSXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXX 131  
A+ L + G D + +  
Sbjct: 110 NKNLNVNPAAVVADTLHRAGLDGKRVYLIGEQLRDEMDELGIEYFGHGPEKKQDEADGS 169

Query: 132 XXXXXXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSR 191  
V AV+VGY++HF + K+ +A +LR+ L VAT+ D P +  
Sbjct: 170 GAFMYDIKLEE-NVGAVVVGYEKHFYIKMMKASNYLREEGVLFVATNEDETCPGNPEV 228

Query: 192 T-PGTGSLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGH 250  
P G + AA++ ASGR L VGKP F I ++I+P+RT+M+GDR TD+ FG  
Sbjct: 229 VIPDAGPIVAAIKCASGRDPLTVGKPCPAFNYIKRKWNINPSRTMMIGDRTNTDVKFGR 288

Query: 251 RCGMTTVLTLTGVSRLAEAQAYLAAGQHDLVPHYVESIADL 292  
GM T+L L+G ++E+ + D+VP Y + L  
Sbjct: 289 DHGKMTLLVLSGCHQIEDIIENQMNERDDMVPDYVAPCLGAL 330

>ref|NP\_504511.1| C53A3.2 [Caenorhabditis elegans]  
Length = 349

Score = 129 bits (323), Expect = 3e-028  
Identities = 82/274 (29%), Positives = 129/274 (47%), Gaps = 15/274 (5%)

Query: 25 LFDCDGVLVNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLR- 83  
+FD DGVLW GE +PG+P L++ L + K + ++NN+ ++R A + A+LG+ +  
Sbjct: 60 IFDADGVWLWLGESVMPGSPRLIDYLVKHNKQIIIVLTNNATKSRAVYAKKLAKLGYNSSKM 119

Query: 84 -----AEQLFSSXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXX 131  
A+ L + G D + +  
Sbjct: 120 NKNLNVNPAAVVADTLHRAGLDGKRVYLIGEQLRDEMDELGIEYFGHGPEKKQDEADGS 179

Query: 132 XXXXXXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSR 191  
V AV+VGY++HF + K+ +A +LR+ L VAT+ D P +  
Sbjct: 180 GAFMYDIKLEE-NVGAVVVGYEKHFYVMMKASNYLREEGVLFVATNEDETCPGNPEV 238

Query: 192 T-PGTGSLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGH 250  
P G + AA++ ASGR L VGKP F I ++I+P+RT+M+GDR TD+ FG  
Sbjct: 239 VIPDAGPIVAAIKCASGRDPLTVGKPCPAFNYIKRKWNINPSRTMMIGDRTNTDVKFGR 298

Query: 251 RCGMTTVLTLTGVSRLAEAQAYLAAGQHDLVPHY 284  
GM T+L L+G ++E+ + D+VP Y  
Sbjct: 299 DHGKMTLLVLSGCHQIEDIIENQMNERDDMVPDY 332

>ref|XP\_777337.1| hypothetical protein CNBB1390 [Cryptococcus neoformans var.  
neoformans B-3501A]  
Length = 308



Score = 128 bits (321), Expect = 5e-028  
Identities = 88/288 (30%), Positives = 129/288 (44%), Gaps = 15/288 (5%)

```
Query: 15 RDVLGRAQGVLFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRF 74
          R ++ A LFDCDGVL+ G + A LL+ L +GK +FV+NNS ++R +L F
Sbjct: 20 RQLVDSADTFLFDCDGVFLFLTGTQLTENAKVLLDMLRSSGKKVIFVTNNSTKSRRQLKAHF 79

Query: 75 ARLGFGGLRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXX 134
          LG E+ F S P D VF
Sbjct: 80 DSLGLDA-SLEECFGSAYASAVYLSEVLKFPKDKKVYVFGHEGIEEELDEVGIAHIGGSD 138

Query: 135 -----XXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWH 184
          V AVL G D ++ K+ +A +L +PEC L+ T+ D
Sbjct: 139 PEDREFTPPIDYSHYSPDPSVGAVLCGADNWINWKKITKAVIYLHNPECRLILTNPDATF 198

Query: 185 PLSDGSRTPGTGSLLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLLET 244
          P+ GS P GS++A + A+ + +V+GKPS M + + + I+PART+M+GD L T
Sbjct: 199 PIG-GSLFPAAGSMSAPIVYAAKQTPVIGKPSKTMMDAVIAHHHINPARTIMIGDNLHT 257

Query: 245 DILFGHRCGMTTTLTGTGVSRLLEEAQAYLAAGQHDLVPHYYVESIADL 292
          DI FG G+ T+L + GV++ E +VP Y + DL
Sbjct: 258 DIEFGINSGIRTLVVMGGVTKYE---YIYGENPSPVVPTYVINRAGDL 302
```

>ref|XP\_568933.1| 4-nitrophenylphosphatase [Cryptococcus neoformans var. neoformans

JEC21]  
Length = 308

Score = 127 bits (320), Expect = 7e-028  
Identities = 88/288 (30%), Positives = 129/288 (44%), Gaps = 15/288 (5%)

```
Query: 15 RDVLGRAQGVLFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRF 74
          R ++ A LFDCDGVL+ G + A LL+ L +GK +FV+NNS ++R +L F
Sbjct: 20 RQLVDSADTFLFDCDGVFLFLTGTQLTENAKVLLDMLRSSGKKVIFVTNNSTKSRRQLKAHF 79

Query: 75 ARLGFGGLRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXX 134
          LG E+ F S P D VF
Sbjct: 80 DSLGLDA-SLEECFGSAYASAVYLSEVLKFPKDKKVYVFGHEGIEEELDEVGIAHIGGSD 138

Query: 135 -----XXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWH 184
          V AVL G D ++ K+ +A +L +PEC L+ T+ D
Sbjct: 139 PEDREFTPPIDYSHYSPDPSVGAVLCGADNWINWKKITKAVIYLHNPECRLILTNPDATF 198

Query: 185 PLSDGSRTPGTGSLLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLLET 244
          P+ GS P GS++A + A+ + +V+GKPS M + + + I+PART+M+GD L T
Sbjct: 199 PIG-GSLFPAAGSMSAPIVYAAKQTPVIGKPSKTMMDAVIAHHHINPARTIMIGDNLHT 257

Query: 245 DILFGHRCGMTTTLTGTGVSRLLEEAQAYLAAGQHDLVPHYYVESIADL 292
          DI FG G+ T+L + GV++ E +VP Y + DL
Sbjct: 258 DIEFGINSGIRTLVVMGGVTKYE---YIYGENPSPVVPTYVINRAGDL 302
```

>ref|NP\_649015.2| CG5567 CG5567-PA [Drosophila melanogaster]  
Length = 330

Score = 127 bits (319), Expect = 9e-028  
Identities = 62/151 (41%), Positives = 96/151 (63%), Gaps = 4/151 (2%)

Query: 145 VRAVLVGYDEHFSFAKLREACALRDPECLLVATDRDPWHPLSDGSRTPGTGSLAAAVET 204  
+ AV+VG+DEHFSF K+ +A ++L DPECL VAT+ D P+ + PG+GS A++T  
Sbjct: 169 IGAVVVGFDHFSFPMKMMKAASYLNDPECLFVATNTDERFMPN-MIVPGSGSFVRAIQT 227

Query: 205 ASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGTTVLTGTGVS 264  
+ R +V+GKP+P + E + IDP+RTLM+GDR TDIL G CG T+L +G+  
Sbjct: 228 CAERDPVVIGKPNPAICESLVTEKKIDPSRTLMIGDRANTDILLGFNCGFQTLVGVSGIH 287

Query: 265 RLEEAQAYLAA---GQHDLVPHYYVESIADL 292  
+L++ + + + + L+P Y+ + DL  
Sbjct: 288 QLKDVERWKLSQDPEEKKLIPDVYLPKLGDL 318

Score = 51.2 bits (121), Expect = 8e-005  
Identities = 26/71 (36%), Positives = 40/71 (56%)

Query: 9 LRGAALRDVLGRAQGVLFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARP 68  
L A + + L V+ DCDGVW +A+ G+ +++ +L GK+ F +NNS + R  
Sbjct: 27 LSSAKVTEWLAGFDSVITDCDGVWLIYQALEGSVDVMNQLKGMGKSIYFCTNNSTKTRS 86

Query: 69 ELALRFARLGF 79  
EL + LGF  
Sbjct: 87 ELLKKGVELGF 97

>ref|NP\_596255.1| 4-nitrophenylphosphatase (PMID 1645660)  
[Schizosaccharomyces pombe  
972h-]  
Length = 298

Score = 127 bits (319), Expect = 9e-028  
Identities = 86/281 (30%), Positives = 127/281 (45%), Gaps = 17/281 (6%)

Query: 25 LFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLRA 84  
LFDCDGVW+G + +PG + ++ L GK +FVSNNS ++R + G +  
Sbjct: 22 LFDCDGVWWSGSKPIPGVTDTMKLLRSLGKQIIFVSNNSTKSRETYMNKINEHGIAA-KL 80

Query: 85 EQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXXXR 144  
E+++ S P D V  
Sbjct: 81 EEIYPSAYSATYVKKVVKLPADKKVFLGEAGIEDELDRVGVVAHIGGTDPSSLRRALASE 140

Query: 145 -----VRAVLVGYDEHFSFAKLREACALRDPECLLVATDRDPWHPLSDGSRTPG 194  
V AVL G D H ++ K A +L+DP C + T++D P ++G PG  
Sbjct: 141 DVEKIGPDPSVGAVLCGMDMHVTYLYKCMFQYLQDPNCAFLLTNQDSTFP-TNGKFLPG 199

Query: 195 TGSLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGM 254  
+G+++ + ++GRQ ++GKP M E I N + D + VGDR L TDI F +  
Sbjct: 200 SGAISYPLIFSTGRQPKILGKPYDEMMEAIIANVNFDRKKACFVGDR LNTDIQFAKNSNL 259

Query: 255 -TTVLTGTGVSRLLEEAQAYLAAGQHDLVPHYYVESIADLTE 294  
++L LTGVS+ EE + +VP YYVES+A L E  
Sbjct: 260 GGSLLVLTGTGVSKEEE----ILEKDAPVVPDYVESLAKLAE 296

>ref|XP\_001742750.1| predicted protein [Monosiga brevicollis MX1]  
Length = 301

Score = 127 bits (318), Expect = 1e-027  
Identities = 91/302 (30%), Positives = 138/302 (45%), Gaps = 21/302 (6%)

Query: 12 AALRDVLGRAQGVLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNRRARPELA 71  
A R ++ + +FDCDGV+W G + G + L+ L R GK F++NNS + R  
Sbjct: 5 AQCRALESTKLFVFDGVIWRGATLIDGVADALDGLRRHGKRVAFITNNSTKTRANFV 64

Query: 72 LRFARLGFGLRAEQLFSSXXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXX 131  
+F LG + + ++SS D V+V  
Sbjct: 65 KKFHGLGLTWVERDDVWSSASAAAAYLTQRAK--LDKSRKVYVVGQSGLCEELCEAGYTV 122

Query: 132 XXXXXXXXXXXXX-----RVRAVLVGYDEHFSFAKLREACAHLRD-PECLLVATDR 180  
V AV+VG+D ++ KL A R+ +CL +AT+R  
Sbjct: 123 LGGPDDEGSSVFPVPERFEVDPAVGAVVVGFDRAINYYKLAYATMCARENKDCLFLATNR 182

Query: 181 DPWHPLSDGSRTPGTGLAAAVETASGRQALVVGKPSPYMFECI--TENFSIDPARTLMV 238  
D L+D PG G++ AA+ETA GR V GKPSP++ + + D A +MV  
Sbjct: 183 DAITHLNDEQEFPGGTMVAALETAIGRAPEVAGKPSPFLLVDALYAFHGLDRDSAHAVMV 242

Query: 239 GDRLETDILFGHRCGTTTLTGTGVSRLLEEAQAYLAAGQ--HDLVPHYVYESIADLTEGL 296  
GDRL+TDI+FG+ M T+L ++GV+R Q+++ A Q D P Y S+ L + L  
Sbjct: 243 GDRLDTDIIFGNTNNMATLLVMSGVTR----QSHVDATQPGEDDYPTYIAPSLKLLADTL 298

Query: 297 ED 298  
+  
Sbjct: 299 AE 300

>ref|XP\_001603048.1| PREDICTED: similar to ENSANGP00000018510 [Nasonia vitripennis]  
Length = 304

Score = 127 bits (318), Expect = 1e-027  
Identities = 59/153 (38%), Positives = 97/153 (63%)

Query: 145 VRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGLAAAVET 204  
V AV+VG+D+HFS+ KL +A + D + T+ D P + + PG G A+E  
Sbjct: 150 VGAVVVGFDKHFSSYPKLVKAATYAHDRGNHFIGTNPDFERPSPNENLFPAGCYLLAIEA 209

Query: 205 ASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLLETDILFGHRCGTTTLTGTGS 264  
A+GR+A+V+GKP P++ E I + + ++PARTLM+GD L TDIL G RCG TT+L ++G++  
Sbjct: 210 AAGRKAVVLGKPEPFVSELIRKKYGVNPARTLMIGDNLSTDILLGKRCGFTLLVMSGIT 269

Query: 265 RLEEAQAYLAAGQHDLVPHYVYESIADLTEGLE 297  
EE + + ++P +Y + ++D+ + L+  
Sbjct: 270 TKEELEKQRDSPNSILPDFYADQLSDVLDCLQ 302

Score = 49.3 bits (116), Expect = 3e-004  
Identities = 20/47 (42%), Positives = 30/47 (63%)

Query: 24 VLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNRRARPEL 70

VL DCDGVLW + + G+PE + R +GK +++NN+ + R EL  
Sbjct: 24 VLSDCDGVWREKEVIKSPETVARFKESGKKFFYITNNNCKTRAE L 70

>ref|NP\_982763.1| ABL184Wp [Ashbya gossypii ATCC 10895]  
Length = 309

Score = 126 bits (317), Expect = 2e-027  
Identities = 92/296 (31%), Positives = 126/296 (42%), Gaps = 18/296 (6%)

Query: 12 AALRDVLRGAVQGVLFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELA 71  
A + L + LFDCDGVW G +P E L L GK FV+NNS ++R A  
Sbjct: 14 AGVHSFLDQYDTFLFDCDGVWLGTHLLPLVKETLAMLTAKGKQLYFVTNNSTKSRAAYA 73

Query: 72 LRFARLGFGLRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGA-----VFVXXXX 118  
+FA G + EQ+F+S P A +  
Sbjct: 74 KKFASFGIT-VGVEQIFTSSYAAALHVRDELRLAPGADKIWVFGAAGIQDELQLMGYETM 132

Query: 119 XXXXXXXXXXXXXXXXXXXXXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVAT 178  
VRAV+ G D H ++ +L +L+ PE VAT  
Sbjct: 133 GGADERLDAPFAADASPFLEGGLDPAVRAVAGLDTHLNYHRLSVTLQYLQQPEVAFVAT 192

Query: 179 DRDPWHPLSDGSRTPGTGSLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMV 238  
+ D P G + PG G++ + TASGR+ GKP+ M + I +D RT MV  
Sbjct: 193 NLDNTLP-QKGLKLPAGATMIQCLVTASGREPQACGKPNQNMMLKSIVAATGLDRTRTCMV 251

Query: 239 GDRLETDILFGHRCGTTVLTLTGVSRLAEAQAYLAAGQHDLVPHYYVESIADLTE 294  
GDRL TD+ FG G+ T+L LTG+ EA A + +H P YY + + L E  
Sbjct: 252 GDRLNTDMRFGADGGLGTLVLVLTGIE--TEAGALAPSAEHP-QPAYYADKLGSLYE 304

>ref|XP\_001674234.1| Hypothetical protein CBG09325 [Caenorhabditis briggsae AF16]  
Length = 348

Score = 125 bits (315), Expect = 3e-027  
Identities = 84/282 (29%), Positives = 130/282 (46%), Gaps = 16/282 (5%)

Query: 25 LFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLR- 83  
+FD DGVLW GE +PG+P L++ L + K + ++NN+ ++R A + A+LG+ +  
Sbjct: 60 IFDADGVWLGESVMPGSPRLIDYLVKH-KQIIVLTNNATKSRAVYAKKLAKLGYNSSKM 118

Query: 84 -----AEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXX 131  
A+ L S G D + +  
Sbjct: 119 NKNLNVNPAAVVADTLHRSGLDGKRVYLIGEQLRDEMDELGIEYFGHGPEKKQNEEAGS 178

Query: 132 XXXXXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSR 191  
V AV+VGY++HF + K+ +A +LR+ L VAT+ D P +  
Sbjct: 179 GAFMYDIKLEE-NVGAVVGYEKHFYTKMMKAANYLREEGVLFVATNEDETCPGNPEV 237

Query: 192 T-PGTGSLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLTDILFGH 250  
P G + AA+ ASGR L VGKP F I ++I+P+RT+M+GDR TD+ FG  
Sbjct: 238 VIPDAGPIVAAIRCASGRDPLTVGKPTPAFNYIKRKNINPSRTMMIGDRNTDVKFGR 297

Query: 251 RCGMTTVLTLTGVSRLAEAQAYLAAGQHDLVPHYYVESIADL 292  
GM T+L L+G ++E+ + D+VP Y + L  
Sbjct: 298 DHGKMTLLVLSGCHQIEDIIENQMNERDDMVPDYVAPCLGAL 339

>ref|XP\_001354807.1| GA13927-PA [Drosophila pseudoobscura]  
Length = 313

Score = 125 bits (313), Expect = 5e-027  
Identities = 94/284 (33%), Positives = 130/284 (45%), Gaps = 10/284 (3%)

Query: 18 LGRAQGVLFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNRRARPELALRFARL 77  
+G VL D DGVLW+ E VP A + L RAGK FV+NNS R + F +L  
Sbjct: 23 VGSFDRVLSIDIDGVLWSMEYTVPRAVDGYAALQRAGKEVSFVTNNSVRTMEQCLRHFEKL 82

Query: 78 GFGGLRAEQLFSSXXXXXXXXXXXXXXXXXPGP----PDAP-GAVFVXXXXXXXXXXXXXXXXXXXX 132  
G + + G AP AV  
Sbjct: 83 GLQVAPEQVWHPAQSIIVLYLRDIQFEGLIYIIASAPFKAVLREAGFQLLDGPNFIEESY 142

Query: 133 XXXXXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHL-RDPECLLVATDRDPWHPLSDGSR 191  
VRVAV++ D + + KL A +L R+PECLL+ D P++ G  
Sbjct: 143 QSLAKTIFDHQPVRVAVIIDVDFNLTSPKLLRAHMYLMRNPECLLIGGATDRLLPVAKGVN 202

Query: 192 TPGTGSGLAAAVETASGRQALVVGKPSPYMFECITENFSI-DPARTLMVGDRLDILFGH 250  
G G A+ + ASGRQA+ +GKP + E + ++ I+P R LMVGD L DI FG  
Sbjct: 203 IIGPGPFASILVEASGRQAVTLGKPGRELGELLIKHLKIAEPQRVLMVGDMLAQDIQFGR 262

Query: 251 RCGMTTVLTLTGVSRLAEAQAYLAAGQHDLVPHYYVESIADLTE 294  
+CG T+L L+G LE+ QA + DL+P YY +S+AD+ +  
Sbjct: 263 QCGFQTLVLVLSGGCSLEQLQAETSP---DLLPDYYADSVADVAQ 303

>ref|XP\_638376.1| hypothetical protein DDBDRAFT\_0186160 [Dictyostelium discoideum  
AX4]  
Length = 303

Score = 124 bits (310), Expect = 1e-026  
Identities = 85/279 (30%), Positives = 127/279 (45%), Gaps = 18/279 (6%)

Query: 25 LFDCDGVWNGERAVPGAPPELLERLARA-GKAALFVSNNRRARPELALRFARLGFGLR 83  
+FDCDGVLW + VPGA E L L + GK L FV+NNS + R + +  
Sbjct: 26 IFDCDGVLWIADTIVPGA IETLNYLRQTLGKILFVTNNSTKTRQQFLEKIKSFNIEAFI 85

Query: 84 AEQLFSSXXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 143  
E SS P VF+  
Sbjct: 86 DEVYSSYGAAYLNQINFPKETK---VFIIGEHGLEKELNDQNFKTIKEINKLKDGLD 142

Query: 144 RVR-----AVLVGYDEHFSFAKLREACAHLRDPE-CLLVATDRDPWHPLSDGSRTP 193  
V+ AV+VG D +F K A +++ E CL +AT+ D +P+ + P  
Sbjct: 143 SVQNTAIDKDVGAIVGMDTQLTFQKATYAHMCIKEIEGCLFIATNPDTSYVKNKTLTP 202

Query: 194 GTGSLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCG 253  
G GS+ A ++T++G + + +GKP + + I + +++P RTL VGDRL+TDI F G  
Sbjct: 203 GAGSIVAMIQTSTGVKIPITIGKPETLLLDVILKKDNLNPRTLFGDRLDITDIAFAVNGG 262

Query: 254 MTTVLTLTGVSRLAEAQAYLAAGQHDLVPHYYVESIADL 292  
+ ++L LTG+S+L E + P+YY +IADL  
Sbjct: 263 IRSLLVLTGISKLNEINNI----DSKINPNYYTNTIADL 297

>ref|XP\_001908284.1| unnamed protein product [Podospora anserina]  
Length = 308

Score = 123 bits (308), Expect = 2e-026  
Identities = 93/298 (31%), Positives = 132/298 (44%), Gaps = 25/298 (8%)

Query: 12 AALRDVLGRAQGVLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNRRARPELA 71  
AA+ + + R L DCDGV+W+GE G E L E L GK +FV+NNS ++R E  
Sbjct: 12 AAINEFIDRFDFVLLDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNRRARPELA 71

Query: 72 LRFARLGFGLRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXX 131  
+F LG E S+ PP VFV  
Sbjct: 72 KKFTGLGIPSDVEEIFGSAYSASVYISRILKLAPPK--NKVFVIGEAGIEHELSENVPF 129

Query: 132 XXXX-----XXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRDPECLL 175  
V VLVG D H ++ KL A +LR +  
Sbjct: 130 IGGTDPAFRRDVTPEDFKGLADGSLLDPEVGCVLVGLDFHINYLLKLSHALQYLRRG-AIF 188

Query: 176 VATDRDPWHPLSDGSRTPGTGLAAAVETASGRQALVVGKPSPYMFECITENFSIDPART 235  
+AT+ D P+S G PG GS++ + ++G++ + +GKPS M + + F D RT  
Sbjct: 189 LATNVDSTFPM SHGF-FPGAGSMSMPLVYSTGQKPVALGKPSQAMMDAVEGKFQFDRERT 247

Query: 236 LMVGDRLETDILFGHRCGM-TTVLTLTGVSRL EEAQAYLAAGQHDLVPHYYVESIADL 292  
MVGDR L+TDI FG + T+ LTGVS+ E +A A VP +YV+ ++D+  
Sbjct: 248 CMVGDRDLTDIKFGIEGKLGGLTAVLTGVSQKEHWEAADA---VPAFYVDKLSDI 301

>ref|XP\_001521615.1| PREDICTED: hypothetical protein, partial  
[Ornithorhynchus anatinus]  
Length = 117

Score = 120 bits (302), Expect = 9e-026  
Identities = 60/108 (55%), Positives = 80/108 (74%), Gaps = 3/108 (2%)

Query: 193 PGTGSLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLETDILFGHRC 252  
PGTG L AVETA+ R+A V+GKPS ++FEC+++ + +DPARTLMVGDR L+TDIL G C  
Sbjct: 9 PGTGCLVRVAVETAARAEVIGKPSRFIFECVSQEYGLDPARTLMVGDR L+TDILGATC 68

Query: 253 GMTTVLTLTGVSRL EEAQAYLAAG---QHDLVPHYYVESIADLTEGLE 297  
G+ T+LTLTGVS L E ++ + + +VP +YVESIADL L+  
Sbjct: 69 GLRLLTLTGVSLLGEVESCRRSDCPTRRKMVPDFYVESIADLLPALQ 116

>ref|XP\_001273643.1| 4-nitrophenylphosphatase, putative [Aspergillus clavatus  
NRRL 1]  
Length = 333

Score = 120 bits (300), Expect = 1e-025  
Identities = 89/305 (29%), Positives = 133/305 (43%), Gaps = 35/305 (11%)

Query: 16 DVLGRAQGVLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNRRARPELALRFA 75  
++L R LFD CDGV+W+G+ + GA E ++ L R GK L FV+NN+ R+R L +F  
Sbjct: 15 EILNRYDTWLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNRRARPELALRFA 74

Query: 76 RLGFGGLRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVF-----VXXXXXXXX 121  
RLG +++ SS P D V +

Sbjct: 75 RLGISASE-DEIVSSAFAAAGYLKDVLFKPADRKVYVMGEGIEAELDAVGILHCGGTSP 133

Query: 122 XXXXXXXXXXXXXXXXXXXXXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHL----- 168  
V AVL G+D H ++AKL +A HL

Sbjct: 134 EDNQFLPANDYSPLQSEGAIDPSVGAFLCGFDMHMNYAKLCKAFKHLTREGAQGPVLAGE 193

Query: 169 RDPECLLVATDRDPWHPLSDGSRTPGTGSLAAAVETASGRQALVVGKPSPYMFECITENF 228  
+ C + T+ D P G PG+GSLA + A+ R+ ++VGKP M + + +

Sbjct: 194 QGGGCHFLLTNDKVV PAL-GEPWPGSGSLATPLIAATKREPIIVGKPHAPMLDMVKSLY 252

Query: 229 SIDPARTLMVGDRLDILFGHRCGMTTVLTTLTGVSRL EEAQAYLAAGQHDLVPHYYVES 288  
ID R++ VGD L TDILF + ++L LTGV+ + Q + + P Y ++

Sbjct: 253 QID EKRSIFVGDNLHTDILFAK DGNIDSLLVLTGVTTERDCQ-----EEGIWPSYIIQG 306

Query: 289 IADLT 293  
I+ LT

Sbjct: 307 ISALT 311

>ref|XP\_001848163.1| 4-nitrophenylphosphatase [Culex pipiens  
quinquefasciatus]  
Length = 306

Score = 119 bits (298), Expect = 3e-025  
Identities = 59/151 (39%), Positives = 91/151 (60%), Gaps = 4/151 (2%)

Query: 145 VRAVLVGYDEHFSFAKLREACAHLRDPPECLLVATDRDPWHPLSDGSRTPGTGSLAAAVET 204  
V AV+VG+DEHFSF K+ +A ++L + E + + T+ D P+ D PGTGS+ AV T

Sbjct: 153 VGAVIVGFDEHFSFVKMMKAASYLNNQEVI FIGTNTDERFPMPD-CVIPGTGSIVNAVTT 211

Query: 205 ASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMTTVLTTLTGVS 264  
+ R V+GKP+ ++ + + + +DP RTLM+GDR TDIL G CG T+L TG+

Sbjct: 212 CAERPPTVMGKPNKHICDILQOEYKVDPERTLMIGDRCNTDILLGKNCGFKTLLVETGIH 271

Query: 265 RLEEAQAYLAAGQHD---LVPHYVVE SIADL 292  
+ E+ + + + + LVP Y + DL

Sbjct: 272 KAEDIEKWAQSEDEETRRLVDPVYAGKLGDL 302

Score = 59.7 bits (143), Expect = 2e-007  
Identities = 27/71 (38%), Positives = 40/71 (56%)

Query: 9 LRGAALRDVLGRAQGVLFDCDGV LWNGERAVPGAPELLERLARAGKAALFVSNNRRARP 68  
L A ++D +G VL DCDGV+W +P A +++ + GK FV+NNS + RP

Sbjct: 12 LSPA EIKDWVGSFDTVLTDCDGV IVDNNTLPQATDVINKFIENGKQLFFVTNNSTKTRP 71

Query: 69 ELALRFARLGF 79  
E + +LGF

Sbjct: 72 EFVTKAVKLG F 82

>ref|XP\_001352722.1| GA16941-PA [Drosophila pseudoobscura]  
Length = 320

Score = 119 bits (298), Expect = 3e-025  
Identities = 83/288 (28%), Positives = 127/288 (44%), Gaps = 9/288 (3%)

Query: 14 LRDVLGRAQGVLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNRRARPELALR 73  
 +R +L +++ DGVW +A+ GA + L GK + +NNS + L +  
 Sbjct: 25 VRQLLKTFTDITIVYAADGVWLRHGQALTGAADTFNALRAMGKNSFICTNNSSEASCALTKK 84

Query: 74 FARLGFGLRAEQLFSSXXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXX 133  
 LGF E L S+ G +  
 Sbjct: 85 AHSGLFLIAENEILSSAQALARYMRERKFNRKVYIVGGQGIKDELQVGIESLPLDLAST 144

Query: 134 XXXXXXXXXXXR-----VRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLS 187  
 + V AV VG D + KL +A +LRDP L +AT+RD P++  
 Sbjct: 145 QENSMVDQVQKMYLDANVGAVAVGMDLGLNVLKLTKASIYLRDPRTLFLATNRDRAFPVA 204

Query: 188 DGSRTPGTGS LAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDIL 247  
 + PG G + AA++ + R GKPSY+ + I+P RTL+VGD + TD+  
 Sbjct: 205 ADRQVPGAGVVVAIQAVAKRAPFTCGKPSYVCSHLIRQGVIEPERTLLVGD TMYTDMQ 264

Query: 248 FGHRCGTTVLTTLTGVSRL EEAQAYLAAGQ---HDLVPHYVVE SIADL 292  
 FG+ CG T+L TGVS L++ + LA+ Q + +P Y+ ++DL  
 Sbjct: 265 FGYNCGFHTLLVGTGVSSLQDVRHALASKQAIAYQQIPDLYLHRLSDL 312

>gb|ABX00714.1| AT31245p [Drosophila melanogaster]  
 Length = 327

Score = 118 bits (296), Expect = 4e-025  
 Identities = 83/278 (29%), Positives = 122/278 (43%), Gaps = 9/278 (3%)

Query: 24 VLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNRRARPELALRFARLGFGLR 83  
 ++FD +GVLW+ + + A E L GK A +NNS + + +GF +  
 Sbjct: 41 IIFDGNVWLSHGKVL E NAAETFNALRAMGKKAFICTNNSVTSVEGICKYAQEMGFLVAK 100

Query: 84 AEQLFSSXXXXXXXXXXXXXP-----GPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 137  
 E L S G + +  
 Sbjct: 101 NEILSSVQTLAKFMKEKKFKKKCYVVGQIVDELKLVGIESLPLDHSSLQGF SMPDHIH 160

Query: 138 XXXXXXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGS 197  
 V AV+VG D+ F+ KL +AC +LRD E + VAT RD P + G P G  
 Sbjct: 161 SIYLDPNVAVVVGSDKDFNTIKLTKACCYL RDSEVMFVATSRDAALPAAPGRMVPSAGV 220

Query: 198 LAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGTTV 257  
 + AA++ AS R GKP+PYM + + I P RTL++GD + TDIL G++CG T+  
 Sbjct: 221 MVAIQAASQRMPFTCGKPNPYMCIDL MQGVIQPDRTLIIGDTMCTDILLGYKCGFQTL 280

Query: 258 LTLTGVSRL E---EAQAYLAAGQHDLVPHYVVE SIADL 292  
 L TGV+ + EAQ A + VP Y+ +++L  
 Sbjct: 281 LVGTGVNSYQDAIEAQGSKAPLLYQVPDLYMPKLSNL 318

>ref|NP\_728791.1| CG32487 CG32487-PA [Drosophila melanogaster]  
 Length = 320

Score = 118 bits (296), Expect = 4e-025  
 Identities = 83/278 (29%), Positives = 122/278 (43%), Gaps = 9/278 (3%)

Query: 24 VLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNRRARPELALRFARLGFGLR 83  
 ++FD +GVLW+ + + A E L GK A +NNS + + +GF +



Sbjct: 34 IIFDGNGLVLSHGKVLNAAETFNALRAMGKKAFICTNNSVTSVEGICKYAQEMGFLVAK 93

Query: 84 AEQLFSSXXXXXXXXXXXXXP-----GPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXX 137  
 E L S G + +

Sbjct: 94 NEILSSVQTLAKFMKEKKFKKKCYVVGQGIVDELKLVGIESLPLDHSSLQGFSSMPDHIH 153

Query: 138 XXXXXXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGS 197  
 V AV+VG D+ F+ KL +AC +LRD E + VAT RD P + G P G

Sbjct: 154 SIYLDPNVGA VVGSDKDFNTIKLTKACCYL RDSEVMFVATSRDAALPAAPGRMVPSAGV 213

Query: 198 LAAAVETASGRQALVVGKPSPYMFECITENF SIDPARTLMVGDRL ETDILFGHRCGM TTV 257  
 + AA++ AS R GKP+PYM + + I P RTL++GD + TDIL G++CG T+

Sbjct: 214 MVA AIQAASQRMPFTCGKPNPYMCIDL MQKGV IQPDR TLIIGDTMCTDILLGYKCGFQTL 273

Query: 258 LTLTGVSRL E---EAQAYLAAGQHDLVPHYYVESIADL 292  
 L TGV+ + EAQ A + VP Y+ +++L

Sbjct: 274 LVGTGVNSYQDAIEAQGSKAPLLYQQVPDLYMPKLSNL 311

>ref|XP\_001270852.1| 4-nitrophenylphosphatase [Aspergillus clavatus NRRL 1]  
 Length = 306

Score = 118 bits (295), Expect = 6e-025  
 Identities = 88/299 (29%), Positives = 134/299 (44%), Gaps = 27/299 (9%)

Query: 14 LRDVLGRAQGVLFDCDGV LWNGERAVPGAP ELLERLARAGKAALFVSNNRRARPELALR 73  
 +++ L R LFDCDGV LW+G+ PG E LE L GK +FV+NNS ++R + +

Sbjct: 15 IKEFLDRFDVFLFDCDGV LWSGDLVYPGT VETLEMLRSNGKQVVFVTNNSTKSRADYRKK 74

Query: 74 FARLGFGLRAEQLFSSXXXXXXXXXXXXXPGPP-----DAPGAVFVXX 116  
 +LG E++FSS P + F+

Sbjct: 75 LEKLGIPS-STEEIFSSSYSASIYISRILKLPENKRKVFIIGETGIEQELETENVPFIGG 133

Query: 117 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLV 176  
 V VLVG D H ++ KL A +++ L

Sbjct: 134 TDPAYRRDVTTEDYKLITSGDSSLIDPEVGVVLVGLDRHINYLKLALAYHYVVKRGAVFL- 192

Query: 177 ATDRDPWHPLSDGSRTPGTGS LAAAVETASGRQALVVGKPSPYMFECITENF SIDPARTL 236  
 AT+ D +P ++G+ PG GS++A + G++ + +GKP+ M + I F D +RT

Sbjct: 193 ATNIDSTYP-NEGALFPGAGSMSAPLIMMLGQEPVSLGKPNQAMMDAIEGKFKFDRSRTC 251

Query: 237 MVGDRLETDILFGHRCGM-TTVLTLTGVSRL EEAQAYLAAGQHDLVPHYYVESIADLTE 294  
 MVGDR+ TDI FG + T+ LTGVS E+ +LA P Y++ ++DL +

Sbjct: 252 MVGDRVNTDIRFGVEGKLGGLTGLVLTGVSTKED---FLAGPTR---PAIYLDKLSDLLD 304

>ref|YP\_001431946.1| phosphoglycolate phosphatase [Roseiflexus castenholzii  
 DSM 13941]  
 Length = 259

Score = 117 bits (294), Expect = 7e-025  
 Identities = 89/272 (32%), Positives = 124/272 (45%), Gaps = 24/272 (8%)

Query: 25 LFDCDGV LWNGERAVPGAP ELLERLARAGKAALFVSNNRRARPELALRFARLGFGLRA 84  
 +FD DG ++ G+ +PGA E + RL AG +F+SNN R R + A + LG +

Sbjct: 10 IFDL DGTVYLG DALLPGAAEAITRLRAAGSKVVFLSNNPTRTRAQYAAKLTALGIPTMAD 69

Query: 85 EQLFSSXXXXXXXXXXXXPGPPDAPGA-VFVXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 143  
 E + SS +APG+ VFV  
 Sbjct: 70 EVINSSYVMVRWLLA-----EAPGSRVVFVVGEPPLCDELRTAGFDLADDADG----- 116

Query: 144 RVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGSLAAAVE 203  
 VR V+ +D F++ KL+ A +R VAT+ D + P G P ++ AA+E  
 Sbjct: 117 -VRFVIASFDRFTFYRKLQIAFDAIR-AGARFVATNPDRYCPTPTGGE-PDAAAMIAAIE 173

Query: 204 TASGRQA-LVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMTTTLTLTG 262  
 + +VVGKPS M + I E + PA+ L+VGDRLDIL G GM T LTLTG  
 Sbjct: 174 ACTAHPVEVVVGKPSPIVQTIETLRLPPAQCLVVGDRLETDIAMGRAAGMATALTLTG 233

Query: 263 VSRLEEAQAYLAAGQHDLVPHYYVESIADLTE 294  
 A A + + P Y +ES+ L E  
 Sbjct: 234 -----ATDRRALAEATIQPDYVIESLGALIE 259

>ref|XP\_001352721.1| GA16942-PA [Drosophila pseudoobscura]  
 Length = 308

Score = 117 bits (294), Expect = 7e-025  
 Identities = 81/291 (27%), Positives = 128/291 (43%), Gaps = 8/291 (2%)

Query: 14 LRDVLGRAQGVLFDCDGLWNGERAVPGAPPELLERLARAGKAALFVSNNRRARPELALR 73  
 +R L + V+FD DGVLW+ R + GA E + +G+ L +N+S +LA +  
 Sbjct: 17 VRQWLTTIESVIFDADGVLWHLNRPINGAVETFNMIKSSGRQVLVATNHSGLLTKDLAAK 76

Query: 74 FARLGFGLRAEQLFSSXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXX 133  
 + G+ + L S+ G +  
 Sbjct: 77 AQQFGYEIQEEQILSSALSVARFLSAKGFKKKAYIVGESAIVDELAKENICFSVSGKEKL 136

Query: 134 XX-----XXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSD 188  
 V AV++G DE F+ K+ A ++L++P+ L + T D +P+  
 Sbjct: 137 LKPMEQFAKDMYLDHEVGAVIIGKDESFNVPKIIIRASSYLQEPKVLFLGTCLDTAYPVGK 196

Query: 189 GSRTPGTGLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILF 248  
 G G++ AAV+ +GR L++GKP+P M E + + + TLMVGD L TDILF  
 Sbjct: 197 NRMIVGAGAMVAAVKAITGRMPLILGKPNPLMVEQLLQCGVLKRESTLMVGD TLYTDILF 256

Query: 249 GHRCGMTTTLTLTGVSRLLEEAQAYLAAGQH---DLVPHYYVESIADLTEGL 296  
 CG ++ TGVS L+E + H D++P Y+ S+ L E L  
 Sbjct: 257 ASNCGFQSLFVGTGVSTLKEVRQICNDEGHKVDMPDLYLPSLGHFLREFL 307

>gb|AAB51111.1| 4-nitrophenylphosphatase  
 Length = 292

Score = 116 bits (291), Expect = 2e-024  
 Identities = 81/277 (29%), Positives = 127/277 (45%), Gaps = 12/277 (4%)

Query: 24 VLFDCDGLWNGERAVPGAPPELLERLARAGKAALFVSNNRRARPELALRFARLGFGLR 83  
 VLF D DGVLW G+ VPGAPE+ ++L G V+NN R E+A R GF +  
 Sbjct: 7 VLF DADGVLWCGDNLVPGAPEVFDKLRMGINPYLVTTNNPTSTRNEIANRLMGKGFNRIP 66

Query: 84 AEQLFSSXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 143  
 + + S+ G D VF+  
 Sbjct: 67 DDMIVSAGYVTTQYLLSM--GFSDQRRKVFIIIGEQLINEMRNNGVNALGVDDFPDELA 124

Query: 144 RVR-----AVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGS 197  
++ AV+V D ++ KL + + + LL+ T+ D PL G P S  
Sbjct: 125 TLKIDEDILAVVVALDRTLTYRKLAIIGNRIVVENDALLIGTNCDCALPLGHGVFVVDAMS 184

Query: 198 LAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLLETDILFGHRCGMTTV 257  
A++++SGR+A+++GKPS MFE + + +D + +MVG D+ +TDI F G +  
Sbjct: 185 NILALQSSSGRKAIMLGKPSKLMFEPLKKTGLDASEAIMVGDQFKTDIQFAKNIGARST 244

Query: 258 LTLTGVSRLLEEQAAYLAAGQHDLVPHYYVESIADLTE 294  
+ LTGV+ ++ +AA +L P Y ES+ D+ +  
Sbjct: 245 IVLTGVTTKDD----VAAINPELKPDPYVKESVRDIPD 277

>ref|XP\_001297981.1| haloacid dehalogenase-like hydrolase family protein  
[Trichomonas  
vaginalis G3]  
Length = 282

Score = 115 bits (288), Expect = 4e-024  
Identities = 70/262 (26%), Positives = 116/262 (44%), Gaps = 4/262 (1%)

Query: 24 VLFDCDGLWNGERAVPGAPELLERLARAGKAALFVSNNRRARPELALRFARLGFGLR 83  
V FD +GVLW+ +PGA E++ + + G + ++NN+ ++ + RF + G+  
Sbjct: 6 VCFDGEGLVWHAGEPIPGASEVINEITKLYRPIVITNNASKSVEQYYQRFQKSGYNSFE 65

Query: 84 AEQLFSSXXXXXXXXXXXXPGPPDAP----GAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 139  
+ +S P+ G  
Sbjct: 66 MSDVITSAAAVGTYLQKIGLDKPNRKIFVIGTAGFVSQRLQLHLQVITTADFDGIEFHTM 125

Query: 140 XXXXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGS 199  
V AV+VG E F++ L A + + + +L++ + D +P + PG +L+  
Sbjct: 126 ELDPSVCAVVVGSSEFTYRHLAIATRVIENDAILISANPDNSYPYNPKVLVPGAHALS 185

Query: 200 AAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLLETDILFGHRCGMTTVLT 259  
++ ASGRQ +VGK P +FE I ID + M+GDRL TDI F G+ ++L  
Sbjct: 186 VSISVASGRQPKIVGKPDPKVFEAIPGYKDIDIKNSWMIGDRLNTDIAFAKNVGLKSILV 245

Query: 260 LTGVSRLLEEQAAYLAAGQHDLV 281  
LTGVS+ +E +A + D V  
Sbjct: 246 LTGVSKRDECEALSFEKPDFV 267

>ref|NP\_728790.1| CG32488 CG32488-PA [Drosophila melanogaster]  
Length = 307

Score = 114 bits (286), Expect = 6e-024  
Identities = 81/290 (27%), Positives = 129/290 (44%), Gaps = 7/290 (2%)

Query: 14 LRDVLGRAQGVLFDCDGLWNGERAVPGAPELLERLARAGKAALFVSNNRRARPELALR 73  
+R L + V+ D DGVLW+ +A+ GA + + G+ +SNNS +R E+A +  
Sbjct: 17 VRQWLSTFESVILDADGVLWHFASKAIDGAVDTFNYMNTTGRKIFIIISNNSEISRQEMADK 76

Query: 74 FARLGFGLRAEQLFSSXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 133  
G L SS G V  
Sbjct: 77 AKGFGIEIKEDNVLTSFSCANFLAVKNFQKKVFMGEKGVHFELEKFGICSLKMSEKLE 136

Query: 134 XXXXXXXXXXXR----VRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDG 189  
V AV+VG DE F+ AKL ++L +P+ + + T D +P+ +  
Sbjct: 137 KPMHEFVTELELDPDVGAVIVGRDEGFNMAKLVRTGSYLLNPDVIFLGTCLDAAYPIGNN 196

Query: 190 SRTPGTGSLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFG 249  
G G+ AA++ +GR LV+GKP+P+M + ++ +I P TLMVGD L+TD+ F  
Sbjct: 197 RVMVGAGATLAAMKAYTGRSPLVLGKPNPMMASTLMQSGAIKPETTLMVGDTLQTDMHFA 256

Query: 250 HRCGMTTVLTLTGVSRLLEEAQAYLAAG---QHDLVPHYYVESIADLTEGL 296  
CG +++ +GV+ +E Q + G + LVP Y+ S+ + E L  
Sbjct: 257 SNCGFQSLMVGSGVNTPKVEVQIIEEGDPKKKILVPDITYLPSLGHMLEFL 306

>dbj|BAB26698.1| unnamed protein product [Mus musculus]  
Length = 122

Score = 114 bits (285), Expect = 8e-024  
Identities = 56/116 (48%), Positives = 81/116 (69%), Gaps = 3/116 (2%)

Query: 185 PLSDGSRTPGTGSLLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFG 244  
PL +G GTG L AVE A+ RQA ++GKPS ++F+C+++ + I+P RT+MVGDRDL+T  
Sbjct: 6 PLENGRFIAGTGCLVRAVEMAAQRQADIIGKPSRFIFDCVSQEYGINPERTVMVGDRLDILFG 65

Query: 245 DILFGHRCGMTTVLTLTGVSRLLEEAQAYLAAG---QHDLVPHYYVESIADLTEGLE 297  
DIL G C + T+LTLTGVS LE+ ++ + + +VP +YV+SIADL L+  
Sbjct: 66 DILLGSTCSLKTILTTLTGVSLEEDVKSQESDCMFKKKMVPDFYVDSIADLLPALQ 121

>ref|NP\_902914.1| N-acetylglucosamine metabolism protein [Chromobacterium violaceum  
ATCC 12472]  
Length = 315

Score = 114 bits (285), Expect = 8e-024  
Identities = 74/272 (27%), Positives = 121/272 (44%), Gaps = 19/272 (6%)

Query: 21 A QGVLFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRFARLGF 80  
++ ++ D DGV++ G++ +PGA E ++RL LF+++NN+ + +L L+ LG  
Sbjct: 58 SKSIISDMDGVIYRGKQLIPGAREFIQRLIDTQTPFLFLTNNAEQTPLDLRLKLEGLGIS 117

Query: 81 GLRAEQLFSSXXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 140  
GL + +S P A V  
Sbjct: 118 GLTEDNFITSAMATAMFLKSQTRKA--MPTAYVVGAGLINELYNVGFSISESHPDY--- 172

Query: 141 XXXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGSLAA 200  
V+V + FSF ++++A + D + T+ D P+ G P G+L A  
Sbjct: 173 -----VVAKSQTFSEFIKKAVERFI-DQAKFIGTNPDMIDPIEGGGYEPAAAGTLLA 224

Query: 201 AVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMTTVLTL 260  
A+E A+GR+ +VGKP+ M T + P +M+GDR++TDI+ G GM+T L L  
Sbjct: 225 AIEAATGRKPYIVGKPNLMMMLATRKLGVHPEEAVMIGDRMDTDIVGGLEAGMSTALVL 284

Query: 261 TGVSRLLEEAQAYLAAGQHDLVPHYYVESIADL 292  
+GVS + Q P Y +S+AD+  
Sbjct: 285 SGVSSRASME-----QFPYQPDYVFDVADI 310

>ref|YP\_001277074.1| phosphoglycolate phosphatase [Roseiflexus sp. RS-1]  
Length = 268

Score = 114 bits (284), Expect = 1e-023  
Identities = 88/282 (31%), Positives = 123/282 (43%), Gaps = 24/282 (8%)

Query: 18 LGRAQGVLFDGCDGVLWNGERAVPGAPPELLERLARAGKAALFVSNNRRARPELALRFARL 77  
L R +FD DG ++ G+ +PGA E + RL G LF+SNN R R + A + L  
Sbjct: 3 LPRYSAYVFDLDGTIYLGDALLPGAAETIARLRTGGSKVLFLSNNPTRTRAQYAAKLTAL 62

Query: 78 GFGGLRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGA-VFVXXXXXXXXXXXXXXXXXXXXX 136  
G E + SS +APG+ +FV  
Sbjct: 63 GIPTTPDEVINSSYVMVRWLRA-----EAPGSRIFVIGEQLCDELAAGFDLATDAG 115

Query: 137 XXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTG 196  
V+ V+ +D F++ KL+ A +R VAT+ D + P G P  
Sbjct: 116 G-----VQFVIASFDRFTFTYRKLQIAFDAIR-AGARFVATNPDRYCPTPTGGE-PDAA 166

Query: 197 SLAAAVETASGRQA-LVVGKPSPYMFECITENFSIDPARTLMVGDRLLETDILFGHRCGMT 255  
++ AA+E + +VVGKPS M + + + P R LMVGDRLLETDI+ G GM  
Sbjct: 167 AIIAAIEACTSHPVEVVVGKPSIMARTVADILQLPPERCLMVGDRLLETDIVMGRTAGMA 226

Query: 256 TVLTLTGVSRLAEAQAYLAAGQHDLVPHYVYESIADLTEGLE 297  
T LTLTG A A + P Y +ES+ +L E  
Sbjct: 227 TALTLTG-----ATDRCALINSPVQPDYVIESVGELIRQTE 262

>dbj|BAG29888.1| putative phosphatase [Kocuria rhizophila DC2201]  
Length = 348

Score = 113 bits (283), Expect = 1e-023  
Identities = 86/278 (30%), Positives = 120/278 (43%), Gaps = 18/278 (6%)

Query: 17 VLGRAQGVLFDGCDGVLWNGERAVPGAPPELLERLARAGKAALFVSNNRRARPELALRFAR 76  
++ R +L D DGV++ G A+ GAPE LER+ +G++ ++V+NN+ R +A  
Sbjct: 18 LIERFDALLCDLDGVVYAGPHAIAGAPEALERVRASGRSVVYVTNNASRPPSAVAEHITS 77

Query: 77 LGFGGLRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXX 136  
LG + S+ PG  
Sbjct: 78 LGAPTAVENVVSSAQAAAALLAERLQPG-----ARVLVTGSSALAEVVRGVGLV 126

Query: 137 XXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTG 196  
R AV+ G+D H + +L EA L D L AT+ D P G PG G  
Sbjct: 127 PVTSQEDRPVAVVQGFDPHLGWEQLAEAAFTLADDSVLWCATNTDRTIPKERGI-APGNG 185

Query: 197 SLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLLETDILFGHRCGMTT 256  
+L AAV A+GR+ LV GKP +F E + R +VGDRL+TDIL H GM +  
Sbjct: 186 TLVAVAEATGREPLVAGKPEAPIFREGAER--VGARRPAVVGDRDLTDILGAHHAGMDS 243

Query: 257 VLTLTGVSRLAEAQAYLAAGQHDLVPHYVYESIADLTE 294  
+ LTGV R A AA + P Y + S+ L E  
Sbjct: 244 IQVLTGVDRPASVLAARAAER----PTYLLGSLTQLFE 277

>gb|EAZ43959.1| hypothetical protein OsJ\_027442 [Oryza sativa (japonica  
cultivar-group)]  
Length = 316

Score = 113 bits (283), Expect = 1e-023  
Identities = 83/301 (27%), Positives = 133/301 (44%), Gaps = 61/301 (20%)

Query: 9 LRGAALRDVLGRAQGVLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNSRRARP 68  
L A R ++ LFDCDGV+W G++ + G PE L+ L + GK +FV+NNSR++R  
Sbjct: 10 LTADAARSLVDSVDAFLFDCDGVWIKGDLIEGVPETLDLLRKMGGKLVFVTNNSRKSRR 69

Query: 69 ELALRFARLGFGLRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXX 128  
+ A +F LG + E++F+S P V+V  
Sbjct: 70 QYAKKFRALGL-EVTEEEIFTSSFAAAMFLKLNNSPEK---KVYV-----VGEDG 116

Query: 129 XXXXXXXXXXXXXXXXXXXRVRAVLVGYDEHFSFAKL-----REACAHLRD----- 170  
V AV+VG D++F++ K+ + A R+  
Sbjct: 117 ILEELRLAGFECLGGPVGAVIVGLDQYFNYYKMQVMAQQANGVQGAAGEKREWGQGFQ 176

Query: 171 -----PECLLVAT-----DRDPWHPLSDGSRTPGTGLSLAA 200  
LL+AT +RDP ++ PG G++ A  
Sbjct: 177 LLLIPVAASDLLLIATVNRLLLYASLCIRENPGCLFIATNRDPTGHMTSVQEWPGAGTMVA 236

Query: 201 AVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLTDILFGHRCGMTTVLTL 260  
AV + ++ +VVGKPS ++ + + ++F+++ +R MVDRL+TDILFG G T+L L  
Sbjct: 237 AVSCSVQKEPIVVGKPSFLMDFLLKSFNLETSRMCMVGDRLDTDILFGQNTGCKTLLVL 296

Query: 261 T 261  
+  
Sbjct: 297 S 297

>ref|NP\_572760.1| CG15739 CG15739-PA [Drosophila melanogaster]  
Length = 308

Score = 113 bits (283), Expect = 1e-023  
Identities = 78/285 (27%), Positives = 127/285 (44%), Gaps = 21/285 (7%)

Query: 24 VLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLR 83  
V+ D DGVLW E+++P A + L + GK F++NNS R + FA++G +  
Sbjct: 25 VVSDIDGVLWTFEQSIPRAADGYAALEQMGKHLTFLTNNNSVRTSEQCVKLFKIGMQ-VH 83

Query: 84 AEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXX-----XX 132  
EQ++ G +++  
Sbjct: 84 PEQIWHPAKSIVSYLQSIK-----FEGLIYIIASQSFKTVLREAGFQLLDGPNFIEESY 138

Query: 133 XXXXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRT 192  
VRAV++ D + + K+ A +LR PEC+L+ D P++  
Sbjct: 139 ASLAEHIFGKEPVRAVIDVDFNLTSPKILRAHLYLRHPECMLIEGATDRLLPVAKEVNI 198

Query: 193 PGTGLSLAAAVETASGRQALVVGKPSPYMFECITENFSI-DPARTLMVGDRLTDILFGHR 251  
G G+ A+ + ASG+Q + +GKP + + + E++ I P+R LM+GD L D+ FG +  
Sbjct: 199 VGPGAFASILVEASGKQPITLKGKPRELGDLLVEHYQIVQPSRVLMIQDMLAQDVSFGRQ 258

Query: 252 CGMTTVLTLTGVSRLLEEQAAYLAAGQHDLVPHYYVESIADLTEGL 296  
CG T+L L+G EE LA +P YY +S+AD+ + L  
Sbjct: 259 CGFQTLVLSGGCSKEE---LLAETDPQRIPTYADSVADVAQML 300

>ref|XP\_001304315.1| haloacid dehalogenase-like hydrolase family protein  
[Trichomonas vaginalis G3]  
Length = 295

Score = 112 bits (281), Expect = 2e-023  
Identities = 81/282 (28%), Positives = 125/282 (44%), Gaps = 12/282 (4%)

Query: 22 QGVLFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNRRARPELALRFARLGFGG 81  
+ VLFD DGVLW G + +P AP+ +++L G V+NN R +A + GF  
Sbjct: 5 KNVLFADAGVLWVGKKTIPAAPDAIQKLRMGLNVFVVTNNPTHTRQAIADKMMGRGFKN 64

Query: 82 LRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 141  
+ + + S+ G + VFV  
Sbjct: 65 ITKDMIVSAGYVTAQFLVSK--GFTNQKRKVFVVGKGLIQEMRDNGINAIGVDDLPDDP 122

Query: 142 XXRVR-----AVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGT 195  
++ A +V D ++ KL + + + +L+ T+ D PL +G P  
Sbjct: 123 IENLKLDP SILACVVALDMTLYRKLAI GNRVVVENDAMLIGTNC DNALPLGNGVFPDA 182

Query: 196 GSLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLLETDILFGHRCGMT 255  
A+E +SGR+A+V+GKPS MFE + +D TLMVGDRL TDILF G  
Sbjct: 183 FPNILALENSSGRKAIVLGKPSPLMFEPLHTVRGLDVGETLMVGDRLNTDILFSKNIGSR 242

Query: 256 TVLTLTGVSRL EEAQAYLAAGQHDLVPHYYVESIADLTEGLE 297  
L LTG++ E+A + + P+Y +SI ++ E +E  
Sbjct: 243 GCLVLTGITTREDAMSVPEER----PNYICQSIGNIPELVE 280

>ref|XP\_001240453.1| hypothetical protein CIMG\_07616 [Coccidioides immitis RS]  
Length = 306

Score = 112 bits (281), Expect = 2e-023  
Identities = 88/302 (29%), Positives = 130/302 (43%), Gaps = 28/302 (9%)

Query: 13 ALRDVLGRAQGVLFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNRRARPELAL 72  
A++D + + LFDCDGVW+G+ G E LE L GK +FV+NNS ++R +  
Sbjct: 12 AIKDFIDKFDVFLFDCDGVWVSGDIVFKGTVETLEMLRSKQVVFVTNNSTKSRLDYKK 71

Query: 73 RFARLGFGGLRAEQLFSSXXXXXXXXXXXXXXXXPGPPD-----APGAVFVX 115  
+ +LG E++FSS PP+ A ++  
Sbjct: 72 KLDKLGVPATH-EEIFSSSYSAAVYISRILNLPNKRKVFVAIGETGIEQELQAENIQYIG 130

Query: 116 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRDPECLL 175  
V VLVG D H ++ K+ A ++R +  
Sbjct: 131 ATDPAYRRDITPEDYSKIAAGDSSLLDPEVGVVVLVGLDFHINYLKISLAYHYIRRG-AIF 189

Query: 176 VATDRDPWHPLSDGSRTPGTGS LAAA-VETASGRQALVVGKPSPYMFECITENFSIDPAR 234  
+AT+ D P + GS PG G+++A + G + +GKPS M + F D R  
Sbjct: 190 LATNIDSTLP-NAGSLFPGAGTISAPLIRMLGGIEPTSLGKPSPEMMMAVEGKFKFD RRR 248

Query: 235 TLMVGDRLLETDILFGHRCGM-TTVLTLTGVSRL EEAQAYLAAGQHDLVPHYYVESIADLT 293  
MVGDR L+TDI FG G+ T+ LTGV + + L P YV+++ DL  
Sbjct: 249 ACMVGDRLD TDIRFGIEGGLGGTLGVLTGVCSKADFET-----ATLPPMAYVDTLGDLL 302

Query: 294 EG 295

G  
Sbjct: 303 NG 304

>ref|XP\_001658123.1| 4-nitrophenylphosphatase [Aedes aegypti]  
Length = 315

Score = 112 bits (279), Expect = 4e-023  
Identities = 84/292 (28%), Positives = 125/292 (42%), Gaps = 23/292 (7%)

Query: 24 VLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNRRARPELALRFARLGFGLR 83  
++ DCDGV+WN +PG E L+ L + GK F+SNN R E +F++L G+  
Sbjct: 27 IMSDCDGVVWNFTGPIPGVDEALQLLKQNGKCLAFISNNGMRTMDEYREKFSKL---GIE 83

Query: 84 AEQLFSSXXXXXXXXXXXXXPGPPDA-----PGAVFVXXXXXXXXXXXXXXXXX 128  
+++ DA G +  
Sbjct: 84 SQEHDIVHPALTTVKYLKSVNMQDAVYCIQTEVFKNYLRSEGFTVLDGPTEERLPDGGGAN 143

Query: 129 XXXXXXXXXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHL-RDPECLLVATDRDPWHPLS 187  
V AV+V D + S + L +A +L R+P+CLL+ D PL  
Sbjct: 144 AVRTFASYFTDTSGPVAVGVVDIDVNVSLSHLMKAKCYLDRNPDCLLLVGATDYVIPLG 203

Query: 188 DGSRTPGTGLAAAVETASGRQALVVGKPSYMFECITENFSI-DPARTLMVGDRLTDI 246  
D G G +E A+GR+ALV+GKP + E I E F + P RTL +GD L D+  
Sbjct: 204 DNMDVIGPGYFIDILEKATGRRALVLGKPGQALSEFILEQFHVTQPRTLFIGDMLPQDM 263

Query: 247 LFGHRCGMTTVLTTLTGVSRLLEEAQAYLAAGQHDLVPHYYVESIADLTEGLED 298  
FG RCG VL L+G + A + + P++Y +S AD + +D  
Sbjct: 264 GFGARCGFQKVLMLSGGT---TKAMMFAHNKPEELPNFYADSFADFIQLYKD 312

>ref|XP\_001658125.1| 4-nitrophenylphosphatase [Aedes aegypti]  
Length = 318

Score = 112 bits (279), Expect = 4e-023  
Identities = 83/290 (28%), Positives = 128/290 (44%), Gaps = 18/290 (6%)

Query: 24 VLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNRRARPELALRFARLGFGLR 83  
++ DCDGV+W+ +P + L+ L + GK F+SNN R E +F +LG  
Sbjct: 29 IMSDCDGVVWHFTGPIPNVDKALQLLKQKGLAFISNNGMRTMEEYKQKFLKLGIPSHE 88

Query: 84 AEQLFSSXXXXXXXXXXXXXPGPPDA-----PGAVFVXXXXXXXXXXXXXXXXX 131  
E + + G V +  
Sbjct: 89 LEIVHPALTTVRYLKAINMQDAVYCIATEVFKDYLRNEGYVVLDPTEQFSDDRAADSVR 148

Query: 132 XXXXXXXXXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHL-RDPECLLVATDRDPWHPL-SDG 189  
+V AV++ D + S A L A +L R+P+CLL+A D PL S+G  
Sbjct: 149 VFTEYFEETDSPKVGAVVMDLDCNVSLAHLMRACCYLQRNPDCLLLAGATDYIVPLGSNG 208

Query: 190 SRTPGTGLAAAVETASGRQALVVGKPSYMFECITENFSI-DPARTLMVGDRLTDILF 248  
G G +E A+GR+ALV+GKP + + I E F++ P RTL +GD L D+ F  
Sbjct: 209 RDVIGPGYFLEMLERATGREALVLGKPGQALAQFILEQFNVTQPRTLFIGDMLMQDMGF 268

Query: 249 GHRCGMTTVLTTLTGVSRLLEEAQAYLAAGQHDLVPHYYVESIADLTEGLED 298  
G RCG +L L+G + LE +A+ + + P +Y +S AD + +D  
Sbjct: 269 GSRCGFQKLLLLSGGTTLEMLKAH---NKPEELPDFYADSFADFIQLYQD 315



>ref|XP\_001658124.1| 4-nitrophenylphosphatase [Aedes aegypti]  
Length = 318

Score = 111 bits (277), Expect = 7e-023  
Identities = 82/290 (28%), Positives = 127/290 (43%), Gaps = 18/290 (6%)

Query: 24 VLFDCDGVLWNGERAVPGAPELLERLARAGKAALFVSNNRRARPELALRFARLGFGGLR 83  
++ DCDGV+W+ +P + L+ L + GK F+SNN R E +F +LG  
Sbjct: 29 IMSDCDGVVWHFTGPIPNVDKALKLLKQKGGKLAFLISNNGMRTMEEYKQKFLKLGIPSHE 88

Query: 84 AEQLFSSXXXXXXXXXXXXPGPPDA-----PGAVFVXXXXXXXXXXXXXXXXXXXX 131  
E + + G V +  
Sbjct: 89 LEIVHPALTTVRYLKAINMQDAVYCIATEVFKDYLRNEGYVVLDGPTEQFSDDRAADSVR 148

Query: 132 XXXXXXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHL-RDPECLLVATDRDPWHPL-SDG 189  
+V AV++ D + S A L A +L R+P+CLL+A D PL SDG  
Sbjct: 149 VFTEYFEETDSPKVGAVVMDMDCNVSLAHLMRACQYLQRNPDCLLLAGATDYIVPLGSDG 208

Query: 190 SRTPGTGLAAAVETASGRQALVVGKPSPYMFECITENFSI-DPARTLMVGDRLLETDILF 248  
G G +E A+GR+ALV+GKP + + + E F++ P +TL +GD L D+ F  
Sbjct: 209 RDVIGPGYFLEMLERATGREALVLGKPGQALAQFVLEQFNVTQPKKTLFIGDMLMQDMGF 268

Query: 249 GHRCGTTVLTTLTGVSRLAEAQAYLAAGQHDLVPHYYVESIADLTEGLED 298  
G RCG +L L+G + LE +A+ + + +P +Y +S AD + D  
Sbjct: 269 GSRCGFQKLLLLSGGTTLEMLKAH---NKPEELPDFYADSFADFIQLYRD 315

>ref|XP\_001221893.1| hypothetical protein CHGG\_05798 [Chaetomium globosum CBS  
148.51]  
Length = 294

Score = 110 bits (275), Expect = 1e-022  
Identities = 90/285 (31%), Positives = 124/285 (43%), Gaps = 29/285 (10%)

Query: 30 GVLWNGERAVPGAPELLERLARAGKAALFVSNNRRARPELALRFARLGFGGLRAEQLFS 89  
GV+W+G+ G PE LE L GK +FV+NNS ++R E +F LG E++F  
Sbjct: 15 GVIWSDGHVFEVGPETLEYLRSRGKKVVFVTNNSTKSREEYLKKTGLGIPS-DVEEIFG 73

Query: 90 SXXXXXXXXXXXXPGPPDAP-GAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX----- 135  
S P AP VFV  
Sbjct: 74 SAYSSAIYISRILQLP--APKNKVFVLGEAGIEHELSENVPFIGGTDPAFRRDITPEDW 131

Query: 136 ---XXXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRT 192  
V VL G D H ++ KL A +LR L AT+ D P++  
Sbjct: 132 KGIADGSHLSDVGVVLAGLDLHINYLKLSHALQYLRRGAVFL-ATNTDSTFPMNHNF-F 189

Query: 193 PGTGLSAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLLETDILFG--H 250  
PG GS++ + +G+Q L +GKPS M + + F +D ART MVDRL TDI FG  
Sbjct: 190 PGAGSISMPLOYMTGQQPLALGKPSQAMMDAVEGKFRDRARTCMVDRLNTDIKFGVEG 249

Query: 251 RCGMTTVLTTLTGVSRLAEAQAYLAAGQHDLVPHYYVESIADLTEG 295  
R G T+ LTGVS++ + +A VP +Y + ++DL G  
Sbjct: 250 RLG-GTLAVLTGVSKVADWEAEDPVA----VPAFYADKLSDLRAG 289

>ref|XP\_001382554.1| p-nitrophenyl phosphatase [Pichia stipitidis CBS 6054]

Length = 308

Score = 110 bits (274), Expect = 2e-022  
Identities = 88/298 (29%), Positives = 126/298 (42%), Gaps = 24/298 (8%)

Query: 14 LRDVLGRAQGVLFDGVLWNGERAVPGAPELLERLARAGKAALFVSNNSRRARPELALR 73  
++ +LG+ LFDCDGVW G+ +P PE L L K +FV+NNS ++R + +  
Sbjct: 11 VQSLGQYDYFLFDGVLWLGHDHLLPHVPETLNLLKEHRKTVIFVTNNSTKSRDDYLKK 70

Query: 74 FARLGFGLRAEQLFSSXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXX 133  
F +LG G+ +++F S P + V  
Sbjct: 71 FQKLGISGITKDEVFGSSYASAVYIDKILKLPKEKKVWVLGEEGIEKELKELGYTTVGG 130

Query: 134 XXXXXXXXXXXX-----RVRVAVLVGYDEHFSFAKLREACAHL-RDPECL-LVAT 178  
V AVL G + ++ KL +L +D + L +AT  
Sbjct: 131 DPVLVQDGVAFDPEHPHLVELDEVDGAVLAGLTLNLNLYLKLSITMQYLLKDNKSLPFIAT 190

Query: 179 DRDPWHPLSDGSRTPGTGSAAAVETASGRQA-LVVGKPSPYMFECITEN---FSIDPAR 234  
+ D P S G G GS+ V ASGRQ V GKP+ M I + P R  
Sbjct: 191 NIDSTFP-SKGKLLIGAGSIIETVAFASGRQPDVCGKPNQSMNNSIKADNPGLRETPKR 249

Query: 235 TLMVGDRLDILFGHRCGTTVLTLTGVSRLLEEAQAYLAAGQHDLVPHYYVESIADL 292  
LM+GDRL TD+ FG G+ T+L LTG+ E + + D+ P YY + DL  
Sbjct: 250 GLMIGDRLNTDMKFGRDGGLDTLVLTGI----ETEENVLQPKDVAPTYYYASKLGD 303

>ref|XP\_001263607.1| 4-nitrophenylphosphatase [Neosartorya fischeri NRRL 181]  
Length = 318

Score = 109 bits (272), Expect = 3e-022  
Identities = 87/299 (29%), Positives = 129/299 (43%), Gaps = 27/299 (9%)

Query: 14 LRDVLGRAQGVLFDGVLWNGERAVPGAPELLERLARAGKAALFVSNNSRRARPELALR 73  
+++ L + LFDCDGVW+G+ PG E LE L GK +FV+NNS ++R + +  
Sbjct: 27 IKEFLDKFDVFLFDGVLWVSGDHLFPGTVETLEMLRSNGKQVVFVTNNSTKSRADYKKK 86

Query: 74 FARLGFGLRAEQLFSSXXXXXXXXXXXXPGPPD-----APGAVFVXX 116  
+LG E+++FSS P + F+  
Sbjct: 87 LEKLGIPST-TEEIFSSYSASIIYISRIKLPENKRKVFVIGETGIEQELQTENVPFIGG 145

Query: 117 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXRVRVAVLVGYDEHFSFAKLREACAHLRDPECLLV 176  
V VLVG D H ++ KL A +++ L  
Sbjct: 146 TDPAYRREVRPDDYKLIAGDPSLLDPEVGVVVLVGLDFHNLNLYLKLALAYHYIKRGAVFL- 204

Query: 177 ATDRDPWHPLSDGSRTPGTGSAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTL 236  
AT+ D P S G+ PG GS++A + G + + +GKP+ M + I F D +RT  
Sbjct: 205 ATNIDSTLPNS-GTLFPGAGSMSAPLIMMLGEEPVSLGKPNQAMMDAIEGKFKFDRSRTC 263

Query: 237 MVGDRLDILFGHRCGM-TTVLTLTGVSRLLEEAQAYLAAGQHDLVPHYYVESIADLTE 294  
MVGDR TDI FG + T+ LTGVS E+ +L + P Y++ ++D E  
Sbjct: 264 MVGDRLDILFGHRCGM-TTVLTLTGVSRLLEEAQAYLAAGQHDLVPHYYVESIADLTE 294

>ref|XP\_746320.1| 4-nitrophenylphosphatase [Aspergillus fumigatus Af293]  
Length = 331

Score = 109 bits (272), Expect = 3e-022

Identities = 83/284 (29%), Positives = 123/284 (43%), Gaps = 33/284 (11%)

Query: 16 DVLGRAQGVLFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNRRARPELALRFA 75  
 ++L R LFDCDGV+W+G+ A GA + ++ L GK +FV+NN+ R+R L +F  
 Sbjct: 15 ELLCRYDTWLFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNRRARPELALRFA 74

Query: 76 RLGFGGLRAEQLFSSXXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXX----- 127  
 RL +++ SS P D VFV  
 Sbjct: 75 RLRIAASE-DEIVSSSFAAAVYLKEVLKFPADRK--VFVMGMEGVEAELDAVHIKRCGGT 131

Query: 128 -----XXXXXXXXXXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHL-RDPE----- 172  
 V AV+ G+D H ++ KL +A +L RD  
 Sbjct: 132 GPEDNKFLAANDYSSLAGEEAIDPSVGAVVCGFDMHMNYGKLCCKAFKYLTRDGAQGPVLA 191

Query: 173 -----CLLVATDRDPWHPLSDGSRTPGTGSLAAAVETASGRQALVVGKPSPYMFECITE 226  
 C + T+ D P G PG GSL + ++ R +V+GKP M + +  
 Sbjct: 192 GETGGGCHFILTNDKVPAL-GELWPGAGSLVTPLIAS TKRNPIVIGKPHAPMLD TVKS 250

Query: 227 NFSIDPARTLMVGDRLDILFGHRCGMTTTLTGTGVSRLLEEAQ 270  
 ++IDP RT+ VGD L TDILF + ++L LTGV++ E+ Q  
 Sbjct: 251 LYNIDPTRTIFVGDNLYTDILFAREGRVDSLLVLTGVTKEEDCQ 294

>ref|XP\_001353954.1| GA18982-PA [Drosophila pseudoobscura]  
 Length = 313

Score = 109 bits (272), Expect = 3e-022  
 Identities = 90/308 (29%), Positives = 129/308 (41%), Gaps = 26/308 (8%)

Query: 9 LRGAALRDVLGRAQGVLFDCDGVWNGERAVPGAPPELLERLARA-GKAALFVSNNRRAR 67  
 L G + + L VL D DG +W + A+ GA +L L GK ++NN + R  
 Sbjct: 12 LSGEQVSEWLRSFDTVLSGDGDIWQDDTAIEGAAAVLNALQNQFGKRVYLITNNGLKTR 71

Query: 68 PELALRFARLGFGGLRAEQLFSSXXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXX 127  
 EL R RLG F + +Q S P VFV  
 Sbjct: 72 RELFERAQLRGFQ-VPNDQHIIISPTATIVDHLKQLPDFDSTKHKV FVVGNA AIGRELQAN 130

Query: 128 XXXXXXXX-----XXXXXXXXRVRAVLVGYDEHFSFAKLREACAHL- 168  
 V AV+VG+DEHFS+ K+ A L  
 Sbjct: 131 GIDSYGAGEEEPLPMGEKWQDFALREFTKPEAADNVGAVVVGWDEHFSYCKMARASHILC 190

Query: 169 RDPECLLVATDRDPWHPLSDGSRTPGTGSLAAAVETASGRQALVVGKPSPYMFECITENF 228  
 R+ + T+RD H PGT + A +E +GR+AL +GKPS P + E + ++  
 Sbjct: 191 RINGSSAFLVTNRDAVHKYP-ALCIPGTA AFVAGIEACAGREALEMGKPSPVVLEPLIQSG 249

Query: 229 SIDPARTLMVGDRLDILFGHRCGMTTTLTGTGVSRLLEEAQAYLAAGQHDLVPHYYVES 288  
 ++ P RTLM+GD + DI F CGM ++L TG +L+ Q + Q DL Y+  
 Sbjct: 250 ALRPERTLMIGDCPKIDIAFARNCGMSLLVGTGYSYQLDILQNGSLPQPDL----YLPR 305

Query: 289 IADLTEGL 296  
 + DL + L  
 Sbjct: 306 LGDLLQFL 313

>ref|ZP\_02733637.1| N-acetylglucosamine-6-phosphatase or p-nitrophenyl  
 phosphatase  
 [Gemmata obscuriglobus UQM 2246]

Length = 282

Score = 108 bits (271), Expect = 3e-022  
Identities = 82/272 (30%), Positives = 120/272 (44%), Gaps = 23/272 (8%)

Query: 23 GVLFD CDGVLWNGERAVPGAPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGL 82  
G L D DGVL+ G +PGA + L F++NNS+R R ++ R RLG +  
Sbjct: 10 GFLIDMDGVLVYRGTDLIPGADRFVRELRE RDIPFRFLTNN SQRTTRRDVVARLVRLGLD-V 68

Query: 83 RAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 142  
E +F+S PG G +V  
Sbjct: 69 EEEHVFTSAMATARFLAQKPG-----GTAYVIGEGGLLTALHQHGYAVVDHDPDY---- 119

Query: 143 XRVRVAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGSAAAV 202  
V+VG F+ +L E+ + L+AT+ DP P +G R PG G+ A +  
Sbjct: 120 -----VVVGEGRTFNL-ELVESAVRMILGGAKLIATNMDPNCPTQNGIR-PGCGAFVALL 172

Query: 203 ETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMTTVLTLTG 262  
ETA+G +A VGKPS M + + +T M+GD +ETDIL G + G TVL L+G  
Sbjct: 173 ETATGVKAFSVGKPSVMMRAARKELGLTTDQTTMIGDTMETDILGGVQLGFHTVLVLSG 232

Query: 263 VSRLEEAQAYLAAGQHDLVPHYYVESIADLTE 294  
++ E+ Y + P V S+A+L +  
Sbjct: 233 GTKAEDLPRYAYS-----PETVVPSLAELAD 258

>ref|NP\_143780.1| hypothetical protein PH1952 [Pyrococcus horikoshii OT3]  
Length = 263

Score = 108 bits (271), Expect = 3e-022  
Identities = 75/246 (30%), Positives = 114/246 (46%), Gaps = 12/246 (4%)

Query: 24 VLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLR 83  
++FD DGVL+ G RA+PG EL+E L G F++NNS + + ++G  
Sbjct: 4 IIFDMDGVLVYRGNR AIPGVRELIEFLKERGIPFAFLTNNSTKTPEMYREKLLKMG I---- 59

Query: 84 AEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 143  
+ SS PG +FV  
Sbjct: 60 --DVSSSIIITSGLATRLYMSKHLDPGKIFVIGGEGLVKEMQALGWGIVTLDEARQGSWK 117

Query: 144 RVRVAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGSAAAVE 203  
V+ V+VG D ++ KL+ A +R+ + T+ D P +G PG GS+ AA++  
Sbjct: 118 EVKHVVVGLDPLDLYEKLKYATLAIRN-GATFIGTNPDPATLPGEEGI-YPGAGSIIAALK 175

Query: 204 TASGRQALVVGKPSPYMFECITENFSIDPARTL-MVGDRLDILFGHRCGMTTVLTLTG 262  
A+ + +++GKP+ M+E + E F P L MVDRL+TDI F + GM ++ LTG  
Sbjct: 176 VATNVEPIIIIGKPNEMPEVREMFM---PGEELWVVDRLDTDIAFAKKFGMKAIMVLTG 232

Query: 263 VSRLEE 268  
VS LE+  
Sbjct: 233 VSSLED 238

>gb|AAH83113.1| 1700012G19Rik protein [Mus musculus]  
Length = 217

Score = 108 bits (270), Expect = 4e-022

Identities = 70/202 (34%), Positives = 89/202 (44%), Gaps = 13/202 (6%)

Query: 1 GAMARCERLRGAALRDVLGRAQGVLFDCDGVWNGERAVPGAPELLERLARAGKAALFVS 60  
 G ARC RL + +L +LFDCDGVW GE AVPGAPE L L GK F++  
 Sbjct: 8 GDEARCVRLSAERAKLLLAEVDTLLFDCDGVWLRGETAVPGAPETLRALRARGKRLGFIT 67

Query: 61 NNSRRARPELALRFARLGFGG----LRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXX 116  
 NNS + R A + RLGFGG ++F + G PD V  
 Sbjct: 68 NNSKTRTAYAEKLRRLGFGGPGVPEAGLEVFGTAYCSALYLRQLAGVDPKAYVLGSP 127

Query: 117 XXXXXXXXXXXXXXXXXXXX-----XXXXXXXXXXRVRAVLVGYDEHFSFAKLREACAH 167  
 VRAV+VG+D HFS+ KL +A +  
 Sbjct: 128 ALAAELEAVGVTSVGVGPDVHLHGDGPSDWLAVPLEPDVRAVVVGFDPHFSYMKLTKAVRY 187

Query: 168 LRDPECLLVATDRDPWHPLSDG 189  
 L+ P+CLLV T+ D PL +G  
 Sbjct: 188 LQQPDCLLVGTNMDNRLPLENG 209

>ref|YP\_001636398.1| HAD-superfamily hydrolase, subfamily IIA [Chloroflexus  
 aurantiacus  
 J-10-f1]  
 Length = 264

Score = 108 bits (270), Expect = 4e-022  
 Identities = 87/278 (31%), Positives = 125/278 (44%), Gaps = 24/278 (8%)

Query: 20 RAQGVLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNSRRARPELALRFARLGF 79  
 R G +FD DG ++ G+ +PGA ELL L R G+ F+SNN + R + A R RLG  
 Sbjct: 6 RYDGYIFDLGTIYLGDILLPGAELLHTLRREGRRVTFLSNNPTKTRRQYAERLQRLGI 65

Query: 80 GGLRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGA-VFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 138  
 E + SS +APGA +FV  
 Sbjct: 66 AADEHEIVNSSAVMVEWLLA-----NAPGASLFVVGEAPLIGELEAAGFPLSEKPG-- 116

Query: 139 XXXXXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGSL 198  
 + V+ +D F++ KL+ A +R LVAT+ D + P+ G P ++  
 Sbjct: 117 -----EIAFVVASFDRTFTYRKLQIAFDAIR-AGARLVATNPDRFCVPVGGGE-PDAAAI 169

Query: 199 AAAVETASG-RQALVVGKPSPYMFECITENFSIDPARTLMVGDRLTDILFGHRCGTTV 257  
 AA+E + R ++VGKPS M +T + P R ++VGDR L TDI G GM T  
 Sbjct: 170 IAAIEACTDTRCEVIVGKPSIMARTVTNLIGLPPERICIIVGDR LMTDIAMGVTAGMDTA 229

Query: 258 LTLTGVSRLLEEAQAYLAAGQHDLVPHYVYESIADLTEG 295  
 L LTG S+ + + + P Y +E I +L G  
 Sbjct: 230 LVLTGDSQRADLE-----RSPYQPTYVLERIDELIGG 261

>ref|XP\_001818366.1| hypothetical protein [Aspergillus oryzae RIB40]  
 Length = 306

Score = 108 bits (269), Expect = 6e-022  
 Identities = 88/300 (29%), Positives = 128/300 (42%), Gaps = 27/300 (9%)

Query: 11 GAALRDVLGRAQGVLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNSRRARPEL 70  
 G +R+ + + LFDCDGVW+G+ PG E LE L GK +FV+NNS ++R +  
 Sbjct: 12 GEGIREFIDKFDVFLFDCDGVWSGDHIFPGTNETLELLRSRGKQVVFVTNNSTKSRADY 71

Query: 71 ALRFARLGFGLRAEQLFSSXXXXXXXXXXXXXPGPPD-----APGAVF 113  
+ LG E++FSS P + + F  
Sbjct: 72 QKKLDSLGLIPST-TEEIFSSSYSASIYISRIQLPENKRKVFVLGETGIEQELRSENVPF 130

Query: 114 VXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRDPEC 173  
+ V VLVG D H ++ KL A ++R  
Sbjct: 131 IGGTDPAYRRDITPEDYKRIAAGDPELLDPEVGVVLVGLDFHINYLKLSLAFHYVRRGAV 190

Query: 174 LLVATDRDPWHPLSDGSRTPGTGLAAAVETASGRQALVVGKPSPYMFECITENFSIDPA 233  
L AT+ D P S G+ PG GS++A + A G++ + +GKP+ M + I F D  
Sbjct: 191 FL-ATNIDSTLPNS-GTFFPGAGSVSAPLIMALGKEPVS LGKPNQAMMDAIEGKFRFRDRN 248

Query: 234 RTL MVGDRLETDILFGHRCGM-TTVLTLTGVSRL EEAQAYLAAGQHDLVPHYYVESIADL 292  
R MVGDR TDI FG + T+ LTGVS E+ + P Y++ ++DL  
Sbjct: 249 RACMVGDRLTDIRFGLEGKLGGLTGLVLTGVSSKEDFET-----GPTRPLAYLDKLSDL 302

>ref|XP\_001540463.1| conserved hypothetical protein [Ajellomyces capsulatus NAM1]

Length = 307

Score = 107 bits (268), Expect = 8e-022  
Identities = 89/302 (29%), Positives = 129/302 (42%), Gaps = 28/302 (9%)

Query: 12 AALRDVLGRAQGVLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNRRARPELA 71  
A +++ L + LFDCDGV LW+G+ G E LE L + GK +FV+NNS ++R +  
Sbjct: 13 AGIQEFLNKFVFLFDCDGVWNGDITFEGETVETLEMLRQKQKQIIFVTNNSTKSRADYK 72

Query: 72 ALRFARLGFGLRAEQLFSSXXXXXXXXXXXXXPGPPD-----APGAVFV 114  
+ LG E++F+S P + A F+  
Sbjct: 73 KKLESLGIPA-DIEEIFTSSYSASIYISRIITLPQNKQKVFVLGETGIEQELNAENVPI 131

Query: 115 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRDPECL 174  
V VL G D H ++ KL A +LR  
Sbjct: 132 GGTDPTYRRDISPHDFGQIATGDPSIIDPEVGVVLVGLDFHINYLKLLALAYHYLRRGAVF 191

Query: 175 LVATDRDPWHPLSDGSRTPGTGLAAA-VETASGRQALVVGKPSPYMFECITENFSIDPA 233  
L AT+ D P + GS PG G+++A + G++ + +GKPS M + I F +  
Sbjct: 192 L-ATNTDVTL P-NAGSFFPGAGTISAPLIRMLGGKEPVALGKPSQAMMDAIEGKFKLQRH 249

Query: 234 RTL MVGDRL+TDI FG G+ T+ LTGV+ + G L P YV+ + DL  
Sbjct: 250 RACMVGDRLDTRFVGI EGGGLTGLAVLTGVN----TKVDFTTG--PLRPTAYVDGLKDL 303

Query: 293 TE 294  
E  
Sbjct: 304 LE 305

>ref|XP\_001267455.1| 4-nitrophenylphosphatase, putative [Neosartorya fischeri NRRL 181]

Length = 335

Score = 107 bits (268), Expect = 8e-022  
Identities = 84/306 (27%), Positives = 131/306 (42%), Gaps = 39/306 (12%)

Query: 16 DVLGRAQGVLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNRRARPELALRFA 75  
 ++L R LFDCDGV+W+G+ A+ GA + L GK +FV+NN+ R+R L +F  
 Sbjct: 15 ELLYRYDTWLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNRRARPELALRFA 74

Query: 76 RLGFGGLRAEQLFSSXXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXX----- 127  
 RL +++ SS P D VFV  
 Sbjct: 75 RLRIAASE-DEIVSSSSAAAVYLKEVLKFPADRK--VFVMGMEGVEAELDVVNIKRCGGT 131

Query: 128 -----XXXXXXXXXXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRDPE----- 172  
 V AV+ G+D H ++AKL +A +L  
 Sbjct: 132 CPEDNKFLAANDYSSLAGEEAIDPSVAVCGFDMHMNYAKLCKAFKYLTRREGAQQGPVLA 191

Query: 173 -----CLLVATDRDPWHPLSDGSRTPGTGLSAAAVETASGRQALVVGKPSPYMFECITE 226  
 C + T+ D P G PG+GSLA + ++ R +V+GKP M + +  
 Sbjct: 192 GETGGGCHFILTNDKVPAL-GELWPGSGSLATPLIASTKRNPVIGKPHAPMLDVTKS 250

Query: 227 NFSIDPARTLMVGDRLDILFGHRCGTTVLTTLTGVSRLEEAQAYLAAGQHDLVPHYYV 286  
 ++ID R++ VGD L TDILF + ++L LTGV++ E+ Q + P +  
 Sbjct: 251 LYNIDQNRSIFVGDNLHTDILFARDGSIDSLVLTGVTKEEDCQT-----EGIWPTFIT 304

Query: 287 ESIADL 292  
 +SI+++  
 Sbjct: 305 QSISNI 310

>ref|NP\_127281.1| hypothetical 4-nitrophenylphosphatase. [Pyrococcus abyssi GE5]

Length = 262

Score = 107 bits (268), Expect = 8e-022

Identities = 72/245 (29%), Positives = 116/245 (47%), Gaps = 11/245 (4%)

Query: 24 VLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNRRARPELALRFARLGFGGLR 83  
 ++FD DGV++ G + +PGA E++E L LF++NNS + +G +  
 Sbjct: 4 IIFDMDGVIYRGNKPIPGAKEVIEFLKGNVRFVLTNNSTKTPEMYREKLLNMGID-VP 62

Query: 84 AEQLFSSXXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 143  
 AE + +S P PG VF+  
 Sbjct: 63 AEIIVTSGLATRIYMEKHYP-----PGKVFIIIGRGLIVEMKKGWEIISLEEAKRGKWR 117

Query: 144 RVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGLSAAAVE 203  
 + V+VG D ++ KL+ A +R+ L + T+ D P +G PG GS+ AA++  
 Sbjct: 118 EIDYVVVGLDPELTYEKLKYATLAIRNG-ALFIGTNPDTTFPGEEGIY-PGAGSIIAALK 175

Query: 204 TASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGTTVLTTLTGV 263  
 ++ ++ +++GKP+ M+E I E P MVDRL+TDI+F R GM ++ LTGV  
 Sbjct: 176 ASTEKEPIIIGKPNRPMYEVKERC---PGEMWVGDRLDTIIFAKRFGMKAIMVLTGV 232

Query: 264 SRLEE 268  
 LE+  
 Sbjct: 233 HSLED 237

>ref|ZP\_02839909.1| HAD-superfamily hydrolase, subfamily IIA [Arthrobacter chlorophenolicus A6]

Length = 335

Score = 107 bits (266), Expect = 1e-021  
Identities = 87/276 (31%), Positives = 125/276 (45%), Gaps = 19/276 (6%)

Query: 17 VLGRAQGVLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNSRRARPELALRFAR 76  
++ R +L D DGV++ G A+PGA E L++LA G +V+NN+ R+ E+A  
Sbjct: 6 LISRFDALLSDLGDVYAGPHAIPGAVESLQQLAGVGVGLGYVTNNASRSPA EVAHLRE 65

Query: 77 LGFGGLRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXX 136  
LG EQ+ SS APG+ +  
Sbjct: 66 LG-APAEDEQVSSSQAAADLLASRL-----APGSKVLITGSPALAHEIELVGLTPVFGQ 119

Query: 137 XXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTG 196  
AV+ G++ + L EA A++ L VAT+ D P + G PG G  
Sbjct: 120 DEEPV-----AVVQGFNPGIGWKDLAEA-AYVVSAGALWVATNTDMSIPQARGI-APGNG 172

Query: 197 SLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMMT 256  
+L AAV A+GR LV GKP +F + + R L+VGDRL+TDIL G+ G T  
Sbjct: 173 TLVAAVTAATGRTPLVAGKPEAPLFHSAAKRLGAE--RPLVVGDRDLTDILGGNNAGFAT 230

Query: 257 VLTLTGVSRLLEEQAAYLAAGQHDLVPHYVYESIADL 292  
LTGV LE A +A + P Y + +++DL  
Sbjct: 231 AAVLTGVDLTLESILATRSAER----PDYIIGALS DL 262

>ref|NP\_578161.1| putative sugar-catabolism phosphotransferase [Pyrococcus  
furiosus  
DSM 3638]  
Length = 273

Score = 107 bits (266), Expect = 1e-021  
Identities = 77/274 (28%), Positives = 126/274 (45%), Gaps = 16/274 (5%)

Query: 24 VLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLR 83  
++FD DGV L+ G + GA E++E L G F++NNS + R ++G +  
Sbjct: 5 IVFDMDGVLVYRGNTPIEGAREVIEFLKEKGKIFAFALTNNSTKTPEMYRERLLKMGID-VP 63

Query: 84 AEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 143  
A+ + +S PG +FV  
Sbjct: 64 ADSIITSGLATRIYMKKHFE-----PGKIFVIGGRGLVEEMEKLGWGIVSVEEAREGIWK 118

Query: 144 RVRVAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGSLAAAVE 203  
V+ V+VG D ++ KL+ +R+ + T+ D +P +G PG GS+ AA+E  
Sbjct: 119 EVKYVVVGLDPELTYEKLKYGTLAIRNG-AEFIGTNPDRTPGEEGIY-PGAGSIIAALE 176

Query: 204 TASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMMTTLTLTG 263  
A+ ++ L++GKP+ M+E + E + MVDRL+TDILF + GM ++ LTGV  
Sbjct: 177 AATDKKPLIIGKPNPEMYEVLREK--LGEGEVWVGDRLDILFAKKFGMKAIMVLTGV 234

Query: 264 SRLEEAQAAYLAAGQHDLVPHYVYESIADLTEGLE 297  
L + + + D+ P + SI +L E L+  
Sbjct: 235 HSLSDIE-----KSDIKPDLVLPSEIKELLEYLK 262

>ref|XP\_001528050.1| conserved hypothetical protein [Lodderomyces  
elongisporus NRRL  
YB-4239]  
Length = 309



Score = 106 bits (264), Expect = 2e-021  
Identities = 87/304 (28%), Positives = 130/304 (42%), Gaps = 24/304 (7%)

Query: 10 RGAALRDVLGRAQGVLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNRRARPE 69  
R AL ++ + LFDCDGV+W G+ +P E LE L K +FV+NNS ++R +  
Sbjct: 8 RKQALDLIVDKYDYFLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNRRARPE 67

Query: 70 LALRFARLFGGGLRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXX 129  
+F ++G + +LF S P D V  
Sbjct: 68 YLKKFEKMGIKNVNKLLELFGSAYATAIYIDKILKLPKDKHVWVLGEEGIETELKEVGYKT 127

Query: 130 XXXXXXXXXXXXXXXX-----XRVRAVLVGDEHFSFAKLREACAHL-RDPECL- 174  
+V AV+ G ++ KL +L +D + L  
Sbjct: 128 LGGTDAKLEEDGINFNPNPILDNLDSQVGAVVCGLTFKINYLKLSMTMQYLLKDNKTLTP 187

Query: 175 LVATDRDPWHPLSDGSRTPGTGSAAAVETASGRQA-LVVGKPSPYMFECITENF---SI 230  
+AT+ D P+ G G GS+ +V ASGRQ + GKP+ M + +  
Sbjct: 188 FIATNIDSTFPMK-GKLLIGAGSVIESVAYASGRQPDAICGKPNQSMMDAVKAQLPGLKE 246

Query: 231 DPARTLMVGDRLLETDILFGHRCGMTTVLTLTGVSRLLEEAQAYLAAGQHDLVPHYYVESIA 290  
+P R LMVGDRL TD+ FG G+ T+L LTG+ + ++ L AG+ P YY + +  
Sbjct: 247 NPKRGLMVGDRLENTDMKFGDRDGLDGLTLLVLTGIETEDNVKS-LKAGE---APTYYADKLG 302

Query: 291 DLTE 294  
DL E  
Sbjct: 303 DLYE 306

>ref|NP\_279720.1| AraL [Halobacterium sp. NRC-1]  
Length = 288

Score = 106 bits (264), Expect = 2e-021  
Identities = 86/273 (31%), Positives = 124/273 (45%), Gaps = 22/273 (8%)

Query: 21 AQGVLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNRRARPELALRFARLFGFG 80  
A GVLFD DG ++ G+ VPGA ++ L AG F+SN + R + LG  
Sbjct: 29 ADGVLFDLDTIYVGDALVPGAAAADGLRAAGVGVGFLSNKAIERRDAFVSKLDGLGVP 88

Query: 81 GLRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 140  
+ + ++ PG +VFV  
Sbjct: 89 ADESA-ILNAASIAASYLARHPGE-----SVFVVGEPPLFEELAAHGVATTTDPG---- 138

Query: 141 XXXRVRAVLVGDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGSAA 200  
R +LV D F + L +A + D +AT+ D P++ G P S+  
Sbjct: 139 ---RADVLLVSMDDHDFDYDTLTDAFNAV-DEGTPFLATNPDRTCPVA-GGEVPDCASVMG 193

Query: 201 AVETASGRQA-LVVGKPSPYMFECITENFSIDPARTLMVGDRLLETDILFGHRCGMTTVLT 259  
A+E A+GR V+GKPS E T+ + AR +MVGDR+ETDI G+R GMTTVL  
Sbjct: 194 AIEGATGRSLDRVLGKPSVAVEAATDLLGVPLARCVMVGDRIETDIEMGNRAGMTTVLV 253

Query: 260 LTGVSRLLEEAQAYLAAGQHDLVPHYYVESIADL 292  
L+GV+ A LAA D+ P + ++S++DL  
Sbjct: 254 LSGVT----DDAALAAS--DVEPDHVIDSVSDL 280

>ref|YP\_001363890.1| HAD-superfamily hydrolase, subfamily IIA [Kineococcus radiotolerans  
SRS30216]  
Length = 259

Score = 106 bits (264), Expect = 2e-021  
Identities = 78/270 (28%), Positives = 120/270 (44%), Gaps = 23/270 (8%)

Query: 25 LFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLRA 84  
L D DGVL + E A+PGA E L+RL + + L ++NNS +LA R +R G +  
Sbjct: 11 LTDMDGVLVHEEHALPGAAEFLQRLVDSRRFLVLTNNSIFTPRDLAARLSRSGIE-VPE 69

Query: 85 EQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXXR 144  
E +++S PG G+ +V  
Sbjct: 70 ESIWTSALATADFLARQLPG-----GSAYVIGESGLTTALHEAGYILTDTDPDY----- 118

Query: 145 VRAVLVGYDEHFSFAKLREACALHRDPECLLVATDRDPWHPLSDGSRTPGTGSAAVET 204  
V++G +SF + +A L + +AT+ D P +GS P TGS+AA +  
Sbjct: 119 ---VVLGETRTYSFEAITKAI-RLVEAGARFIATNPDATGPSKEGS-LPATGSVAALITR 173

Query: 205 ASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGM TTVLTLTGVS 264  
A+G + VGKP+P MF T M+GDR++TD++ G G+ T L LTG +  
Sbjct: 174 ATGAEPYFVGKPNPMMFRSAMNRIQAHSETTAMIGDRMDTDVVAGIEAGLRTFLVLTGST 233

Query: 265 RLEEAQAYLAAGQHDLVPHYYVESIADLTE 294  
+ E+ + + PH V+ I DL +  
Sbjct: 234 KREQVRRF-----PFQPHRVVDGIGDLVD 257

>ref|XP\_001545741.1| hypothetical protein BC1G\_15715 [Botryotinia fuckeliana B05.10]  
Length = 319

Score = 105 bits (263), Expect = 3e-021  
Identities = 94/315 (29%), Positives = 131/315 (41%), Gaps = 43/315 (13%)

Query: 12 AALRDVLGRAQGVLFDCDGVWNGERAVPGAPELLERLARAG-----KA 55  
+A+ + + LFDCDGVW+G+ PG E LE L G K  
Sbjct: 12 SAINHFIDQFDVFLFDCDGVWWSGDHIFPGTVETLELLRSKALPKSRLIALLRNTNGKK 71

Query: 56 ALFVSNNSRRARPELALRFARLGFGLRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAP-GAVFV 114  
+FV+NNS ++R E + LG +++F S P AP VFV  
Sbjct: 72 VVFVTNNSTKSRTYQKLTALGIPS-NVDEIFGSAYSSAIYISRILKLP--APKNKVFV 128

Query: 115 XXXXXXXXXXXXXXXXXXXXXXXX-----XXXXXXXXRVRAVLVGYDEHFSF 158  
V VL G D H ++  
Sbjct: 129 LGESGIETELKTEGVEFIGGTDPAYRRDITPEDYKGIADGSLDDDDVGVVLAGLDFHINY 188

Query: 159 AKLREACALHRDPECLLVATDRDPWHPLSDGSRTPGTGSAAVETASGRQALVVGKPS 218  
KL A +LR L AT+ D P S+ + PG GS++ + G++ +GKP+  
Sbjct: 189 LKLCHAYHYLRRGAVFL-ATNTDSTLP-SNHTFFPGAGSISIPLINMIGKEPTALGKPNQ 246

Query: 219 YMFECITENFSIDPARTLMVGDRLDILFGHRCGM-TTVLTLTGVSRLLEEAQAYLAAGQ 277  
M + I F D +T MVGDRL TDI FG + T+ LTGVS+ EE +A A  
Sbjct: 247 AMMDSIEGKFQFDRKKTICMVGDRLENTDIKFGIEGKLGGLTAVLTGVSKKEEWEAENA--- 303

Query: 278 HDLVPHYVESIADL 292

+VP YYV+ ++DL  
Sbjct: 304 -PVVPAYYVDKLSDL 317

>ref|ZP\_01516436.1| HAD-superfamily hydrolase, subfamily IIA [Chloroflexus  
aggregans

DSM 9485]  
Length = 263

Score = 105 bits (263), Expect = 3e-021  
Identities = 83/274 (30%), Positives = 122/274 (44%), Gaps = 22/274 (8%)

Query: 20 RAQGVLFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNRRARPELALRFARLGF 79  
R G +FD DG ++ G+ +PG ELL L R G+ +F+SNN + R + A R RLG  
Sbjct: 6 RYDGYIFDLTGTYLGDILLPGVAELLATLRREGRRIVFLSNNPTKTRRQYAERLRLGI 65

Query: 80 GGLRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXX 139  
E + +S PG P +FV  
Sbjct: 66 DADEHE-IVNSSAVMVEWLLANAPGAP-----LFVVGEAPLIGELEAAGFPLSERPG--- 116

Query: 140 XXXXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGLA 199  
+ V+ +D F++ KL+ A +R LVAT+ D + P+ G P ++  
Sbjct: 117 ----EIAFVVASFDRFTFTYRKLQIAFDAIR-AGARLVATNPDRFCVPPGGGE-PDAAAI 170

Query: 200 AAVETASG-RQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMTTVL 258  
AA+E + R ++VVGKPS M ++ ++ P R ++VGDRL TDI G GM T L  
Sbjct: 171 AAIEACTDTRCEVIVGKPSPI MARTVSRLINLPPERCIIVGDRLMTDIAMGITAGMDTAL 230

Query: 259 TLTGVSRLLEEAQAYLAAGQHDLVPHYYVESIADL 292  
LTG SR + + P Y +E I +L  
Sbjct: 231 VLTGDSRRADLE-----HSSYRPTYVLERIDEL 258

>emb|CAI64354.1| conserved hypothetical protein [uncultured archaeon]  
Length = 253

Score = 105 bits (263), Expect = 3e-021  
Identities = 81/277 (29%), Positives = 123/277 (44%), Gaps = 27/277 (9%)

Query: 18 LGRAQGVLFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNRRARPELALRFARL 77  
+ R + D DGV+++G +PGA E +ERL +G +F++NN+ R R +A R +  
Sbjct: 1 MNRPAVYILDLDGVVYHGRTVIPGASESIERLRSSGCRVVFLTNATRTREAIARRLVDM 60

Query: 78 GFGGLRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXX 137  
G + + S+ +V++  
Sbjct: 61 GIPCDAGDVISSAYAA-----SVYIKEKYSSTIYPVGEQGLVEELER 103

Query: 138 XXXXXRVRA--VLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGT 195  
A V+ G D F++ KL A L +AT+ D P G PG  
Sbjct: 104 AGHIINEQDADYVAVGLDREFTYKLRALDLLMSGAGF-IATNTDAMLPTHEHGF-LPGA 161

Query: 196 GSLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMT 255  
GS+ AA++ ASG VVGK+ + + + + + +MVGDRLETDIL G R GM  
Sbjct: 162 GSMVAAIQAASGVVDPVVGKPNKPIDVLLREYGMRSSEECVMVGDRLDILAGIRGGMQ 221

Query: 256 TVLTLTGVSRLLEEAQAYLAAGQHDLVPHYYVESIADL 292  
TVL LTG S +E+ ++ + P ++SIADL

Sbjct: 222 TVLVLTGASGIEDIES-----SGIRPDAVLDSIADL 252

>ref|NP\_868759.1| N-acetylglucosamine-6-phosphatase or p-nitrophenyl phosphatase

[Rhodopirellula baltica SH 1]

Length = 283

Score = 105 bits (263), Expect = 3e-021

Identities = 79/272 (29%), Positives = 121/272 (44%), Gaps = 23/272 (8%)

Query: 23 GVLFDGCDGVLWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGL 82  
G L D DGV++ G +PGA + ++ L R LF++NNS+R R ++ + R+G +

Sbjct: 5 GFLIDMDGVIYRGSELIPGADQFIDVLIRQDIPFLFLTNNRTRRDVQTKLHRMGIF-V 63

Query: 83 RAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 142  
+F+ P G ++

Sbjct: 64 EESHIFTCAMATARFLAKLKPN-----GTAYIIGEGGLLQAMHQNGFSIVDHSDF----- 114

Query: 143 XRVRVAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGLAAAV 202  
V+VG + L A + L+AT+ DP P +G+R PG G+ A +

Sbjct: 115 -----VVVGEGRITITLNALESVDMILGG-AKLIATNLDPSCPTKNGTR-PGCGATVAYL 167

Query: 203 ETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGTTVLTLTG 262  
E +GR+A VGKPS M + + ++T+MVG D +ETDIL G + G TVLTL+G

Sbjct: 168 EAVTGRKAFSVGKPSPIIMRAARKELKLATSQTMVGDVDMETDILGGVQMGYRTVLTLSG 227

Query: 263 VSRLEEAQAYLAAGQHDLVPHYYVESIADLTE 294  
+ E+ GQ P V+SIA+L +

Sbjct: 228 GTNKED-----LGQFAYGPDVIVDSIAELCD 253

>ref|XP\_453922.1| unnamed protein product [Kluyveromyces lactis]  
Length = 309

Score = 105 bits (262), Expect = 4e-021

Identities = 87/298 (29%), Positives = 123/298 (41%), Gaps = 21/298 (7%)

Query: 12 AALRDVLRAGQVLFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELA 71  
+A + + + LFDCDGVW G +P E L E L GK LFV+NNS ++R +

Sbjct: 15 SATEEFVQKFDTFDFDCDGVWLGSHLLPLVETLEYLKSLGKQLLFVTNNSTKRSQYV 74

Query: 72 LRFARLGFGLRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGA-----VFVXXX 117  
+FA GFG + +Q+F+S P +

Sbjct: 75 KKFA--GFGIEVTEDQIFTSGYASALYVRDFLKLTPGQDRVWIFGENGIKEELNIMGFDT 132

Query: 118 XXXXXXXXXXXXXXXXXXXXXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVA 177  
+V+ V+ G D ++ +L +LR PE VA

Sbjct: 133 SGGNDPRLDEPFDVATSPFLKDGLDDQVKCVIAGLDTKINYHRLAITLQYLRKPEVHFVA 192

Query: 178 TDRDPWHPLSDGSRTPGTGLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLM 237  
T+ D P G PG GS ++ AS R GKP+ M I + +D ++ M

Sbjct: 193 TNIDSTFP-QKGLILPGAGSAINLSYASDRTPACGKPNLMLNNAIVKAKGLDRSKCCM 251

Query: 238 VGDRLETDILFGHRCGM-TTVLTLTGVSRLLEEAQAYLAAGQHDLVPHYYVESIADLTE 294  
VGDR L TDI FG G+ T+L LTG+ E A L + P YY + +L E

Sbjct: 252 VGDR LNTDIKFGETGGLGGTLLVLTGIEETEERA--LDNTHGNPSPKYYT SKLGNLYE 306

>ref|YP\_074615.1| hypothetical protein STH786 [Symbiobacterium thermophilum IAM

14863]  
Length = 257

Score = 105 bits (261), Expect = 5e-021  
Identities = 82/274 (29%), Positives = 114/274 (41%), Gaps = 22/274 (8%)

Query: 20 RAQGVLFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRFARLGF 79  
R G +FD DG L+ G+ A+PGAPE L L R G F+SN A + RLG  
Sbjct: 3 RYAGYVFDL DGTLYLGDHAIPGAPETLAELRRRGARIAFLSNKPIEPAASYAAKLNRLLGI 62

Query: 80 GGLRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 139  
E + SS APGA  
Sbjct: 63 QAAVEEVINSSIVMARYLSRT-----APGA-----RVYLIGEEPLAEELRKRGRIRIV 109

Query: 140 XXXXRVRVAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGSLA 199  
V+V +D F++ KL +A +R+ +AT D P+ G G +  
Sbjct: 110 ADPLDCEYVVVSWDRQFTYQKLNLDALQAIRNG-ARFIATHPDRTCPVP-GGEVADVGGMI 167

Query: 200 AAVETASGRQA-LVVGKPSPYMFECITENFSIDPARTLMVGDRLTDILFGHRCGMTTVL 258  
AVE +G++ L+ GKPS P + + P + +MVGDRLET D+ G GM T L  
Sbjct: 168 GAVEGVTGKKVELITGKPSPI TVQEAMNLLGLPPDQCIMVGDRLTDMRMGREAGMATAL 227

Query: 259 TLTGVSRL EEAQAYLAAGQHDLVPHYYVESIADL 292  
LTGV+R E+ ++ P Y +ES+ L  
Sbjct: 228 VLTGVTRREQVES-----SPWKPDYVLESVRGL 255

>ref|XP\_714670.1| p-nitrophenyl phosphatase [Candida albicans SC5314]  
Length = 321

Score = 105 bits (261), Expect = 5e-021  
Identities = 78/303 (25%), Positives = 130/303 (42%), Gaps = 21/303 (6%)

Query: 17 VLGRAQGVLFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRFAR 76  
+L + L DCDGV+W E+ +P + L+ L + K FV+NNS ++R +F  
Sbjct: 19 ILSQFDNFLIDCDGVIWLSEQLLPKINQFLQFLTNNKFTFVTNNSSKSRQSYVTKFKN 78

Query: 77 LGFGGLRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAV-----FVXXXXXXXXXXXXXXXXXXXX 128  
LG G+ +Q++++ P + + +  
Sbjct: 79 LGKDGVTIDQIYTTGYSAVLQLKKMGILPGEKIWVLGDEGIEDELLSEGYIPLGGSNELL 138

Query: 129 XXXXXXXXXXXXXXXXXXXRVRVAVLVGYDEHFSFAKLREACAHL--RDPECLLVATDRDPWHPL 186  
VRVAV+ G +F++ ++ +L D + T+ D +P  
Sbjct: 139 NQSWSDKNPLLIIDPEVRAVIAGSTLNFNYMRIATT LQYLMHNDKTL PFIGTNGDRNYPG 198

Query: 187 SDGSRTPGTGSLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLTDI 246  
S+G P GS+ + +S R + VGKP + E I N D ++T+M+GD L +DI  
Sbjct: 199 SNGLTLPAGGSMVEY MAYSSQRDYVNVGKPD TTTLAETILANTGYDKSKTIMIGDTLYSDI 258

Query: 247 LFGHRC-----GMTTVLTLTGVSRL EEAQAYLAAGQ-----HDLVPHYYVESIADLTEG 295  
FG+ G T+L L+GV+ EE + + LVP YY++S+ L E  
Sbjct: 259 KFGNEAQLGGDNGSGTLLVLSGVTDKEELTNTVNIARETKQGQSLVPRYYIDS LTKLIEL 318

Query: 296 LED 298  
LE+  
Sbjct: 319 LEE 321

>ref|XP\_001867828.1| 4-nitrophenylphosphatase [Culex pipiens  
quinquefasciatus]  
Length = 304

Score = 104 bits (260), Expect = 6e-021  
Identities = 82/275 (29%), Positives = 118/275 (42%), Gaps = 10/275 (3%)

Query: 24 VLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLR 83  
VL DCDGVLW +PG L L AGK +++NNS R+ + + LG  
Sbjct: 27 VLTDCDGVWLTWFEPVPGVAGLTGLLAAGKTIRYITNNSVRSLASYSACLRTLGVTLDP 86

Query: 84 AEQLFSSXXXXXXXXXXXXPG-----PPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXX 138  
A+ + + G D+ V  
Sbjct: 87 ADLIHPAKSIVGHLKSINFRGLIYCLGTDSFKDVLREGGFVVDGPNELQENFREIIGT 146

Query: 139 XXXXXRVRAVLVGYDEHFSFAKLREACAHLR-DPECLLVATDRDPWHPLSDGSRTPGTGS 197  
VRAV+V D + ++ KL A +L+ DP CLLVA D G G G  
Sbjct: 147 VDDRAPVRAVVVDVFNVNYPKLLRAEFYKTDPTCLLVAGATDRVLNTGRGFNLIGPGR 206

Query: 198 LAAAVETASGRQALVVGKPSPYMFECITENFSI-DPARTLMVGDRLDILFGHRCGMMT 256  
+E ++GR+A+V+GKP + + + + I DP R LMVGD +E D+ FG RCG  
Sbjct: 207 FLDILERSTGRKAIVLGKPGVGLARQVLKEYGIRDPGRVLMVGDMMEQDVAFGSRCGFQR 266

Query: 257 VLTLTGVSRLLEEAQAYLAAGQHDLVPHYYVESIAD 291  
+L L+G + E+ + VP YY +S+AD  
Sbjct: 267 LLVLSGGASRED---MMKEADGACVPDYYADSLAD 298

>ref|XP\_458157.1| hypothetical protein DEHA0C11924g [Debaryomyces hanseni  
CBS767]  
Length = 308

Score = 104 bits (260), Expect = 6e-021  
Identities = 86/292 (29%), Positives = 128/292 (43%), Gaps = 24/292 (8%)

Query: 25 LFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLRA 84  
+FDCDGVW G+ +P E L+ L +A K LFV+NNS ++R +F +LG G+  
Sbjct: 22 IFDCDGVWLGDHLLPHICETLDLLKANKTVLFVTNNSTKSRDAYLSKFDKLGVLGITK 81

Query: 85 EQLFSSXXXXXXXXXXXXPGPPDAPGAVF-----VXXXXXXXXXXXXXXXXXXXX 131  
++F S P + V  
Sbjct: 82 SEVFGSSYASAVYIDKILKLPKNKKIWLVEEGIERELHELGYTTIGGTDPTLVEHGVHF 141

Query: 132 XXXXXXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHL-RDPECL-LVATDRDPWHPLSDG 189  
V AV+ G + ++ KL +L +D + + +AT+ D P+ G  
Sbjct: 142 DHDHPLLTELDDVAVVTGLTFNLNLYKLSITMQYLLKDNKSIPFIATNIDSTFPMK-G 200

Query: 190 SRTPGTGS LAAAVETASGRQA-LVVGKPSPYMFECITENF---SIDPARTLMVGDRLD 245  
G GS+ V ASGRQ + GKP+ M I ++ S +P+R LM+GDRL TD  
Sbjct: 201 KLLIGAGSIIETVAFASGRQPDICGKPNQSMNNSIKADYPGLSSNPSRGLMIGDRLNTD 260

Query: 246 ILFGHRCGMMTTLTLTGVSRLLEEAQAYLAAGQHDLVPHYYVESIADLTEGLE 297

+ FG G+ T+L LTG+ E QA L+ P +Y + + DL E L+  
Sbjct: 261 MKFGRDGGGLDTRLVLTGI---ESEQAVLSQST-STAPTHYADKLGDLYELLK 308

>ref|XP\_001690570.1| phosphoglycolate phosphatase [Chlamydomonas reinhardtii]  
Length = 304

Score = 104 bits (259), Expect = 8e-021  
Identities = 73/274 (26%), Positives = 120/274 (43%), Gaps = 11/274 (4%)

Query: 25 LFDGCDGVLWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLRA 84  
+FD DG LW G +PGA E +E L K FV+NN+ ++R A + +G +A  
Sbjct: 20 VFDLDGTLWKGSTLIPGAKEFIELLRYYNKKVFFVTNNATKSRATNAAKLTAMGINATQA 79

Query: 85 EQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXXXR 144  
E SS G +  
Sbjct: 80 EMYTSSFAAAAYLKAI SFNKKAYVIGEEGLVEELTAVGVQCVGGPAHRGVEVDWSQAEPH 139

Query: 145 VR-----AVLVGYDEHFSFAKLREACAHLRDP-CLLVATDRDPWHPLSDGSRTPGTGS 197  
V AV+VG D + S+ KL+ A L + + C+ +A + D S G G+  
Sbjct: 140 VEVDPEVGAVVVGLDRYISYYKLQYATLCLANNDSCMFLACNTDARGHFSQAQEWAGAGT 199

Query: 198 LAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLTDILFGHRCGTTV 257  
+ AA+ +S R+ +++GKP+ ++ + + + +T++VGDRL+TDIL+G + G T  
Sbjct: 200 MVAALIGSSEREPMLLGKPFILDLHCATHQVARDKTIVVGDRLDLDILWGIQNGAGTC 259

Query: 258 LTLTGVSRLLEEAQAYLAAGQHDLVPHYYVESIAD 291  
L+GV+ ++A L A + + P Y+ I D  
Sbjct: 260 CVLSGVT----SEAQLLAESNKVHPKLYMSDIGD 289

>ref|XP\_001482125.1| hypothetical protein PGUG\_05888 [Pichia guilliermondii  
ATCC 6260]  
Length = 310

Score = 104 bits (259), Expect = 8e-021  
Identities = 86/288 (29%), Positives = 120/288 (41%), Gaps = 23/288 (7%)

Query: 25 LFDGCDGVLWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLRA 84  
LFDGCDGVLW G+ +P E L+ L K +FV+NNS ++R + +F +LG G++  
Sbjct: 22 LFDGCDGVLWLDGHDHILPFVKETDLLKSLDKRVIFVTNNSTKSRKDYRGKFEKLGIPGIE 81

Query: 85 EQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX- 134  
++F S P D V  
Sbjct: 82 NEIFGSSYALAVYVDKILKLPKDKKVVVLGETGIERELQELGYATVGGSDPKLDETGILP 141

Query: 135 --XXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHL-RDPECL-LVATDRDPWHPLSDGS 190  
V AV+ G ++ KL +L +D + + +AT+ D P+ G  
Sbjct: 142 ADSEAVNNLDPEVGAVVAGLTLVNYIKLSATMQYLLKDNKSIPFIATNIDSTFPMK-GK 200

Query: 191 RTPGTGSLAAAVETASGRQA-LVVGKPSPYMFECI---TENFSIDPARTLMVGDRLTDI 246  
G GSL +V ASGRQ V GKP+ M I + P R LMVGDRL TD+  
Sbjct: 201 LMIGAGSLIESVAYASGRQPDVAVCGKPNQAMMNSIKAANPDQAKPGRGLMVGDRLNTDM 260

Query: 247 LFGHRCGTTVLTTLTGVSRLLEEAQAYLAAGQHDLVPHYYVESIADLTE 294  
FG G+ T+L LTG+ E + L + P YY I D+ E  
Sbjct: 261 KFGRDGGLDTRLVLTGI----ETEESLQQLDPNEAPTYASKIGDIYE 304

>ref|YP\_001544363.1| HAD-superfamily hydrolase, subfamily IIA [Herpetosiphon aurantiacus

ATCC 23779]  
Length = 266

Score = 104 bits (259), Expect = 8e-021  
Identities = 85/274 (31%), Positives = 115/274 (41%), Gaps = 17/274 (6%)

Query: 24 VLFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNRRARPELALRFARLGFGLR 83  
VL D DGVL G +PGA EL L R G ++NNS + A LG +  
Sbjct: 10 VLLDMDGVLHRGGEILPGAAELTTVLDRLGLGYACLTTNNSSQLPATFARHLQDLGVA-IA 68

Query: 84 AEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 143  
E + +S P  
Sbjct: 69 PEHVITSSTATATLLRTRYP-----QGTRLLAIGMDGIQSSLFADRYFVSAET 116

Query: 144 RVRVAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGLAAAVE 203  
V AV+VG D + ++A+L+ A LR +AT+ D P +G PG GS+ AA+  
Sbjct: 117 DVAAVVGVDFNLTYARLKTATLALR-AGAAFIATNSDRTPAPEGL-IPGAGSIVAALA 174

Query: 204 TASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMTTTLTLTG 263  
AS V+GKP P MFE + F + +TLMVGDRL+TDI R G+ T +GV  
Sbjct: 175 AASDCTPEVIGKPEPAMFEAALQLFGVTAEQTLVGDRLDIDIAGAQRVGIATAFVSGSV 234

Query: 264 SRLEEAQAYLAAGQHDLVPHYVYESIADLTEGLE 297  
+++AQA+ A DLV +A L G E  
Sbjct: 235 HSMQQAQAWQPA--IDLVADDLAGILALLRAGRE 266

>ref|XP\_714090.1| p-nitrophenyl phosphatase [Candida albicans SC5314]  
Length = 308

Score = 104 bits (259), Expect = 8e-021  
Identities = 82/300 (27%), Positives = 124/300 (41%), Gaps = 24/300 (8%)

Query: 14 LRDVLGRAQGVLFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNRRARPELALR 73  
+ +L + LFDGCDGVW G+ +P PE + L K +FV+NNS ++R + +  
Sbjct: 11 VNQLLDKYDYFLFDGCDGVWLGHDLLPSIPEAISLLRSKNKQVIFVTNNSTKSRNDYLK 70

Query: 74 FARLGFGLRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVF-----VXXXXXX 120  
F +LG + ++F S P D V  
Sbjct: 71 FEKLGIPDISKQEIFGSSYASAIKILKLPKDKKVVVLGKIEQELHELGYTTVGG 130

Query: 121 XXXXXXXXXXXXXXXXXXXXXXXXXXXRVRVAVLVGYDEHFSFAKLREACAHL-RDPECL-LVAT 178  
V VL G + ++ KL +L +D + + +AT  
Sbjct: 131 DPDLISSGVDFDSNDPRLNKLNDVGCVLGVLVFNLYLKLSTLQYLLKDKKTIPFIAT 190

Query: 179 DRDPWHPLSDGSRTPGTGLAAAVETASGRQA-LVVGKPSPYMFECITENF---SIDPAR 234  
+ D P ++G G GS+ V ASGRQ + GKP+ M I +F P R  
Sbjct: 191 NIDSTFP-ANGKLLIGAGSIIETVFSASGRQPEAICGKPNQSMNSIKADFPDLGKTPKR 249

Query: 235 TLMVGDRLDILFGHRCGMTTTLTLTGVSRLLEEAQAYLAAGQHDLVPHYVYESIADLTE 294  
LM+GDRL TD+ FG G+ T+L LTG+ E ++ + P YY+ + D E  
Sbjct: 250 GLMIGDRLNTDMKFGDRDGLDGLTLLVLTGIETEENVKSL----NENETPTYIINKLGFHE 305



>ref|XP\_001688766.1| AGAP005972-PA [Anopheles gambiae str. PEST]  
Length = 320

Score = 103 bits (258), Expect = 1e-020  
Identities = 83/302 (27%), Positives = 119/302 (39%), Gaps = 22/302 (7%)

Query: 9 LRGAALRDVLGRAQGVLFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARP 68  
L A R L ++ DCDGVLWN +PG + L+ L GK F+SNN R  
Sbjct: 15 LSKAERRQFLHSFDTLMSDCDGVWLNFTGPIPGVDKALQLLRTDGKKLAFISNNGMRTME 74

Query: 69 ELALRFARLGFGLRAEQLFSSXXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXX 128  
E +F LG L E + + DA +  
Sbjct: 75 EYQKKFHSLGIDALEEEIVHPALTTVHYLKSIRM---RDAVYICIGTEVFKDYLRKAGFKV 131

Query: 129 XXXXXXXXXXXXXXXXXXXRVRAVLVGYDEH-----FSFAKLREACAHL-RDPEC 173  
+VR +++H S L +A +L RDP C  
Sbjct: 132 LDGPKERFPDSREANQVRVYSDYFEQHGPKVGAVVIDIDVNLSQLHLMKAKCYLERDPNC 191

Query: 174 LLVATDRDPWHPLSDGSRTPGTGLAAAVETASGRQALVVGKPSPYMFECITENFSI-DP 232  
+ +A D PL G G +E +GR+AL++GKP + + + E F I +P  
Sbjct: 192 VFIAGATDYIIPLDSSMDVIGPGYFIDILERTTGRKALILGKPGKALAQQVLEQFQITEP 251

Query: 233 ARTLMVGDRLDILFGHRCGTTVLTLTGVSRLAEAQAYLAAGQHDLVPHYYVESIADL 292  
R L VGD + D+ FG CG +L L+G + A LA + +P+YY +S AD  
Sbjct: 252 KRVLFVGDMMPPQDMGFGTECGFQKLLMLSGGT---PKDALLAQTDPNQLPNYYADSFADF 308

Query: 293 TE 294  
E  
Sbjct: 309 IE 310

STOPSTART

>ref|XP\_001384338.2| p-Nitrophenyl phosphatase [Pichia stipitis CBS 6054]  
Length = 320

Score = 103 bits (258), Expect = 1e-020  
Identities = 78/300 (26%), Positives = 127/300 (42%), Gaps = 24/300 (8%)

Query: 17 VLGRAQGVLFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRFAR 76  
+L + LFDCDGV+W E+ + G + LE L + GK FV+NNS ++R E +F+  
Sbjct: 19 LLEKYDNFLFDCDGVWLDEKIIIEGVKDTLEFLKKNKKFAFVTNNSKSRQEYLAKFSS 78

Query: 77 LGFGLRAEQLFSSXXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXX 136  
LG G+ + +F + P + ++V  
Sbjct: 79 LGIQGVTKDHIFPTCYAAVQALES DLQVPKSK--IWVLGDSGIEDELEEAGYIPVGGTD 136

Query: 137 XXXXXXR-----VRAVLVGYDEHFSFAKLREACAHL--RDPECLLVATDRDPW 183  
R V+AV+VG + F++ ++ +L ++ + + D  
Sbjct: 137 ARLNQAFRADHEFLTVDPEVQAVVVGSTKEFNMYRIASTLQYLLWKNKTIPFIGCNIDRS 196

Query: 184 HPLSDGSRTPGTGLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRL 243  
+P +G P GS+ ++ + R + VGKPS E I D +RTL MVGD L  
Sbjct: 197 YPGPNGLILPAGGSVVNYMQYTADRDFINVGKPSKVFLEAILAKNGFDRSRTL MVGDTLY 256

Query: 244 TDILFGHRC----GTTVLTLTGVSRLAEAQAYLAAGQH-----DLVPHYYVESIADLTE 294  
TDI FG+ G ++L LTG + E +L H ++P Y + S+ D +  
Sbjct: 257 TDIKFGNDGQLGEGCGSLLVLTGGTTPEYLHQFLQNPNNHYDEGESMIPSYVIRSLGDFVD 316

>ref|YP\_001222730.1| conserved hypothetical protein, putative hydrolase  
[Clavibacter  
michiganensis subsp. michiganensis NCPPB 382]  
Length = 346

Score = 103 bits (258), Expect = 1e-020  
Identities = 82/271 (30%), Positives = 122/271 (45%), Gaps = 18/271 (6%)

Query: 24 VLFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLR 83  
+L D DGV++ G ++P A + L R A G +++NN+ R +A + LG +  
Sbjct: 18 ILADLDGVVYAGPDSIPHAVDALNRAAGDGIRLGYITNNASRTDASVAEHLSSLGLT-VA 76

Query: 84 AEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 143  
E + +S P A V V  
Sbjct: 77 PEDVVTSPQAALRLLADRVP----AGSTVLVVG DGLVHELEKAGYVVTRSTEDSPA--- 129

Query: 144 RVRVAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGLAAAVE 203  
AV+ G+ +A+L EA L DP+ + VAT+ D P++ G PG G+L +AV  
Sbjct: 130 ---AVVQGFSPDVGWAQLAEAAFALADPDVWVWATNTDWTIPVARGI-APGNGTLVSAVH 185

Query: 204 TASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLTDILFGHRCGMTTVLTLTG 263  
TA GR +V GKP +F+ E F D R + +GDRL+TDIL R GM +V LTG+  
Sbjct: 186 TAVGRLPVVAGKPETPIFDVARERF--DAQRPVFLGDRLDLDILGATRAGMASVHVLTGI 243

Query: 264 SRLEEAQAYLAAGQHDLVPHYYVESIADLTE 294  
R ++ L A + D P + +E + L E  
Sbjct: 244 DRAKQ----LLAAEEDQRPTFILEHLGQLHE 270

>ref|XP\_001658126.1| 4-nitrophenylphosphatase [Aedes aegypti]  
Length = 319

Score = 103 bits (258), Expect = 1e-020  
Identities = 80/301 (26%), Positives = 125/301 (41%), Gaps = 23/301 (7%)

Query: 15 RDVLGRAQGVLFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRF 74  
R L ++ DCDGV+W+ +PG + L L + GK F+SNN R E +F  
Sbjct: 23 RQFLDSFDTIMSDCDGVWDFIGPIPGVDKALPLLKKGKLLAFISNNGMRTMEEYKQKF 82

Query: 75 ARLGFGLRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAV-----FVXXXXX 119  
+L G+ + +L DA V +  
Sbjct: 83 LKL---GIPSHELDIVHPALTTVRYLKAINMTDAVYCVATEVFKDYLRNEQYTVLDGPDD 139

Query: 120 XXXXXXXXXXXXXXXXXXXXXXXXXXXXRVAVLVGYDEHFSFAKLREACAHL-RDPECLLVAT 178  
RV AV++ D + S A L + +L R+P+C+L+A  
Sbjct: 140 RFADERAADSVRVFTDFFTESDSPRVGAVVLDIDVNISLAHLMKVKCYLERNPDCILIAG 199

Query: 179 DRDPWHPLSDGSRTPGTGLAAAVETASGRQALVVGKPSPYMFECITENFSID-PARTLM 237  
D PL D G G +E A+GR+AL++GKP + + + E F++ P R L  
Sbjct: 200 ATDYIVPLGDRMDVIGPGYFIDILERATGREALILGKPGQALADVFLEQFNVKRKRVL 259

Query: 238 VGDRLTDILFGHRCGMTTVLTLTLTGVSRLLEEAQAYLAAGQHDLVPHYYVESIADLTEGLE 297  
+GD L D+ F CG +L L+G + L+ +A Q +P +Y+ S AD + +  
Sbjct: 260 IGDMLPQDMGFASLCGFQKLLMLSGGTTLDMVRQAQVPAQ---LPDFYMNSFADFIQLYK 316

Query: 298 D 298  
D  
Sbjct: 317 D 317

>ref|YP\_001709982.1| hypothetical protein CMS1244 [Clavibacter michiganensis subsp.

sepedonicus]  
Length = 346

Score = 102 bits (255), Expect = 2e-020  
Identities = 79/271 (29%), Positives = 124/271 (45%), Gaps = 18/271 (6%)

Query: 24 VLFDCDGVLWNGERAVPGAPELLERLARAGKAALFVSNNRRARPELALRFARLGFGLR 83  
+L D DGV++ G ++P A + L R A G +++NN+ R +A + LG +  
Sbjct: 18 ILADLDGVVYAGPDSIPHAVDALNRAAGDGIRLGYITNNASRTDASVAEHLSSLGLT-VA 76

Query: 84 AEQLFSSXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 143  
E + +S P G++ +  
Sbjct: 77 PEDVVTSPQAALRLLADRVPV-----GSIVLVVGGEGLVHELEKAGYVVTRSTDD----- 126

Query: 144 RVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGLAAAVE 203  
+ AV+ G+ +A+L EA L DP+ + VAT+ D P++ G PG G+L +AV  
Sbjct: 127 QPAAVVQGFSPVEVGWAQLAEAAAFALADPDVWVWATNTDWTIPVARGI-APNGTLVSAVH 185

Query: 204 TASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDLETDILFGHRCGTTVLTLTGV 263  
TA GR +V GKP +F+ E F + R + +GDRL+TDIL R GM +V LTG+  
Sbjct: 186 TAVGRLPVVAGKPETPIFDVARERFGAE--RPVFLGDRLDLETDILGATRAGMASVHVLTGI 243

Query: 264 SRLEEAQAYLAAGQHDLVPHYYVESIADLTE 294  
R ++ L A + D P + +E + L E  
Sbjct: 244 DRAKQ----LLAAEEDQRPTFILEHLGQLHE 270

>ref|YP\_953017.1| HAD-superfamily hydrolase, subfamily IIA [Mycobacterium vanbaalenii

PYR-1]  
Length = 271

Score = 102 bits (255), Expect = 2e-020  
Identities = 77/259 (29%), Positives = 115/259 (44%), Gaps = 17/259 (6%)

Query: 14 LRDVLGRAQGVLFDCDGVLWNGERAVPGAPELLERLARAGKAALFVSNNRRARPELALR 73  
L DV Q L D DGV L E A+PGA E L+RL + L ++NNS +LA R  
Sbjct: 12 LDDVRSTPQCWLTDMDGVLVREEHALPGAAEFLQRLIDRERPFLVLTNNSIFTPRDLAAR 71

Query: 74 FARLGFGLLRAEQLFSSXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXX 133  
AR G + +++S PG G+ +V  
Sbjct: 72 LARSGLA-VPENAIWTSALATAGFLADQLPG-----GSAYVIGEAGLTTALHEAGYTLTD 125

Query: 134 XXXXXXXXXXXRVRVAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRT 193  
V++G +SF +A L +AT+ D P ++G P  
Sbjct: 126 IDPDF-----VVLGETRITYSFEAITKA-VRLILGGARFIATNPDVGTGSAEGP-LP 174

Query: 194 GTGSLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDLETDILFGHRCG 253  
TGS+AA + A+GR+ VGKP+P MF T+MVGDR++TD++ G G  
Sbjct: 175 ATGSVAAMITKATGREPYFVGKPNPMMFRSALNRIEAHSESTVMVGDRLDMDTDDVAGIEAG 234

Query: 254 MTTVLTLTGVSRLLEEAQAY 272  
+ T+L LTG + +++ + Y  
Sbjct: 235 LETILVLTGSTTIDDVERY 253

>ref|YP\_001159837.1| HAD-superfamily hydrolase, subfamily IIA [Salinispora tropica  
CNB-440]  
Length = 259

Score = 102 bits (254), Expect = 3e-020  
Identities = 80/273 (29%), Positives = 115/273 (42%), Gaps = 23/273 (8%)

Query: 22 QGVLFDCDGLWNGERAVPGAPELLERLARAGKAALFVSNNRRARPELALRFARLGFGG 81  
Q L D DGVL + + VPGAPE + RL +G+ L ++NNS +L R R+G  
Sbjct: 8 QSWLTDMDGVLVHEGQPVPGAPEFIARLRSSGRPFVLVTNNSIYTPRDLQARLVRMGLD- 66

Query: 82 LRAEQLFSSXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 141  
+ ++SS PG G +V  
Sbjct: 67 VPESAIWSSALATAQFLADQRPG-----GTAYVIGEAGLTTALHAVGYVLSDFAPDY--- 118

Query: 142 XXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGLAAA 201  
V++G +SF + A + D + T+ D P +G+ P GS+AA  
Sbjct: 119 -----VVLGETRYSFEAITRAIRLINDG-ARFICTNPDVTGSPMEGA-LPAAGSVAAM 170

Query: 202 VETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMTTVLTLT 261  
V A+G + VGKP+P M T M+GDR++TDIL G G+ T+L LT  
Sbjct: 171 VSKATGVEPYFVGKPNPMMRSALNTIDAHSESTAMIGDRMDTDILCGLEAGLETILVLT 230

Query: 262 GVSRLLEEAQAYLAAGQHDLVPHYYVESIADLTE 294  
G+S EA+ Y P V S+ADL +  
Sbjct: 231 GISSRTEAERY-----PYRPSRIVGSVADLID 257

>ref|YP\_446001.1| pyridoxal phosphate phosphatase [Salinibacter ruber DSM 13855]  
Length = 260

Score = 102 bits (253), Expect = 4e-020  
Identities = 80/269 (29%), Positives = 112/269 (41%), Gaps = 26/269 (9%)

Query: 24 VLFDCDGLWNGERAVPGAPELLERLARAGKAALFVSNNRRARPELALRFARLGFGG 83  
+L D DGV++ G+R +PGA L RL G F++N+ R R E+ R RLG  
Sbjct: 9 LLLDLGDVVVYVGDRLLPGARRALRRLRERGTTLRFLTNDPRPTRDEVVARLERLGVAAASV 68

Query: 84 AEQLFSSXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 143  
E + +  
Sbjct: 69 QEVVTCGWSTAV-----CLREAGLASAYVVGSDGLRRELDRAGVRGTDGN 113

Query: 144 RVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGLAAAVE 203  
AV+VG DE S+ ++ A +R VAT+ DP P +G P TG++ AAV  
Sbjct: 114 EAEAVVVGCDCECVSPHIKRAARLIRKG-ARFVATNDDPTFPTPEGP-APATGTIVA AAVR 171

Query: 204 TASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMTTVLTLTG 263  
ASG VVGKP P MFE + DPA +MVGDR+TDI R GM+ +L G  
Sbjct: 172 AASGTAPHVVGKPHPAMFEALGD--RDPAAAVMVGDRLDTDIRGARRMGMSALLLRGD 229

Query: 264 SRLEEAQAYLAAGQHDLVPHYYVESIADL 292  
R + + ++ P + S++DL  
Sbjct: 230 ERPQHET-----EVTDPDRVITSLSDL 251

>ref|ZP\_01129603.1| N-acetylglucosamine metabolism protein [marine  
actinobacterium  
PHSC20C1]  
Length = 258

Score = 102 bits (253), Expect = 4e-020  
Identities = 81/270 (30%), Positives = 120/270 (44%), Gaps = 27/270 (10%)

Query: 25 LFDCDGVLWNGERAVPGAPPELLERLARAGKAALFVSNNRRARPELALRFARLGFGLRA 84  
L D DGVL + VPGA ELL++ + K L ++NNS +L+ ARL GL  
Sbjct: 11 LTDMDGVLVHENHPVPGAAELLKQWRKEDKPYLVLTNNSIFTPRDLS---ARLKASGLDV 67

Query: 85 EQ--LFSSXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 142  
+ +++S PG G+ FV  
Sbjct: 68 PESAIWTSALATADFLKEQIPG-----GSAFVIGEAGITTALHEAGFIMTETDPDY---- 118

Query: 143 XRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGSAAV 202  
V++G ++SF + +A + + +AT+ D P +DG P TG++AA +  
Sbjct: 119 -----VVIGETRNYSFESITKAIRLIGNGS-RFIATNPDATGPSADGP-LPATGAVAALI 171

Query: 203 ETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMTTVLTLTG 262  
A+GR+ +VGKP+P MF T M+GDR++TDI+ G G+ TVL LTG  
Sbjct: 172 TKATGREPYIVGKPNPMMFRSALNKIGAHSETTGMIGDRMDTDIVAGIEAGLHTVLVLTG 231

Query: 263 VSRLEEAQAYLAAGQHDLVPHYYVESIADL 292  
+S E Y PH + S+ADL  
Sbjct: 232 ISDQREIDRY-----PFRPHEVLNSVADL 255

>ref|ZP\_02930896.1| N-acetylglucosamine-6-phosphatase or p-nitrophenyl  
phosphatase  
[Verrucomicrobium spinosum DSM 4136]  
Length = 302

Score = 101 bits (252), Expect = 5e-020  
Identities = 72/278 (25%), Positives = 114/278 (41%), Gaps = 22/278 (7%)

Query: 20 RAQGVLFDCDGVLWNGERAVPGAPPELLERLARAGKAALFVSNNRRARPELALRFARLGF 79  
+ +G+L D DGV++ +P A E + L + +FV+NNS +L ++ + LG  
Sbjct: 3 QTKGLLIDMDGVIYRENHLLPRAAEFVHFLIESATPFVVTNNSAPTPELTVVKLSHLGI 62

Query: 80 GGLRAEQLFSSXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 139  
GL +++ A F+  
Sbjct: 63 SGLSVRHFYTAAMNT-----AEFLAGTHPCCTAFVMGDAGLNLALQKAG 106

Query: 140 XXXXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGSAA 199  
+R V E + L + LVAT+ D W P+ + PG G+LA  
Sbjct: 107 IPNDSIRPTYVVVVGEGMQSTEKLSKAHELLERGARLVATNPDNWCPVKNEVTRPGAGALA 166

Query: 200 AAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMTTVLT 259  
A +E ++G++A +GKP+PYMF+ +MVG D +ETDI GM L

Sbjct: 167 AYLEASTGQRAYFLGKPNPYMFQRRARLLQRRTEEVMMVGD<sup>T</sup>METDIRGAIEVGMQACLV 226

Query: 260 LTGVSRL<sup>E</sup>EAAQAYLAAGQHDLVPHYYVESIADL<sup>T</sup>EGLE 297

LTG +RLE+ G + P +E + DL + L+

Sbjct: 227 LTGSTRLED-----LGNVYVQPTCVLEGVGDLLDELK 258

>ref|XP\_001581765.1| HAD-superfamily hydrolase, subfamily IIA containing protein

[*Trichomonas vaginalis* G3]

Length = 282

Score = 101 bits (252), Expect = 5e-020

Identities = 66/249 (26%), Positives = 108/249 (43%), Gaps = 4/249 (1%)

Query: 24 VLFDCDGV<sup>L</sup>WNGERAVPGAP<sup>E</sup>LLERLARAGKAALFVSNNSRRARPELALRFARLGF<sup>G</sup>GLR 83  
V FD +GV+W G V GA E++ + + G A+ V+NN+ ++ + RF + G+

Sbjct: 6 VCFDGE<sup>G</sup>VIWYGGYPVEGAN<sup>E</sup>IIGDIRKLG<sup>Y</sup>RAVCVTNNASKSVQ<sup>Y</sup>LERFQKSGYT<sup>N</sup>FN 65

Query: 84 AEQLFSSXXXXXXXXXXXXXXXXPGPPDAP----GAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 139

E + +S P G

Sbjct: 66 EEDVITSARSVGIYLVKARFNKPG<sup>R</sup>KV<sup>F</sup>IGTAGFVSQ<sup>L</sup>RSYNLNIVIAADYDGLDI<sup>H</sup>SM 125

Query: 140 XXXXRVR<sup>A</sup>VLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGT<sup>G</sup>SLA 199

V AV+VG E FS+ L A ++ + + LL++ + D +P + P +LA

Sbjct: 126 DIDPEVCAVVVGSSEEF<sup>S</sup>YRHLTIASRYVIENDALLISANPDDNYPYNHDVLVPA<sup>A</sup>HALA 185

Query: 200 AAVETASGRQALVVGK<sup>P</sup>SPYMFECITENFSIDPARTLMVGD<sup>R</sup>LETDILFGHRCG<sup>M</sup>TTVLT 259

+ A+ L +GKP MFE I + ID A + ++GDRL TD+ F G+ ++L

Sbjct: 186 ECIAAATNHTTLALGK<sup>P</sup>QKSMFEAIPGSDKIDRAHSWII<sup>G</sup>DRLATDVKFAKTAGLRSILV 245

Query: 260 LTGVSRL<sup>E</sup>E 268

LTGV++ E+

Sbjct: 246 LTGVTK<sup>K</sup>ED 254

>ref|YP\_639140.1| HAD-superfamily hydrolase, subfamily IIA [*Mycobacterium* sp. MCS]

Length = 257

Score = 101 bits (252), Expect = 5e-020

Identities = 75/248 (30%), Positives = 111/248 (44%), Gaps = 17/248 (6%)

Query: 25 L<sup>F</sup>DCDGV<sup>L</sup>WNGERAVPGAP<sup>E</sup>LLERLARAGKAALFVSNNSRRARPELALRFARLGF<sup>G</sup>GLRA 84  
L D DGVL E A+PGA E L RL + L ++NNS +LA R AR G +

Sbjct: 9 LTDMDGVLVREEHALPGA<sup>E</sup>FLARLVERERPF<sup>L</sup>VLTNNSIFT<sup>P</sup>RD<sup>L</sup>AARLARSGLI-VPE 67

Query: 85 EQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXXXR 144

E +++S PG G+ +V

Sbjct: 68 EAIWTSALATATFLSDQLPG-----GSAYVIGEAGLTTALHEAGYTLTDVGP<sup>D</sup>F----- 116

Query: 145 VRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGT<sup>G</sup>SLAAAVET 204

V++G +SF + +A L +AT+ D P ++G P TGS+AA +

Sbjct: 117 ---VVLGETRTYSFEAITKA-VRLILGGARFIATNP<sup>D</sup>V<sup>T</sup>GPSAEGP-LPATGSVAAMITK 171

Query: 205 ASGRQALVVGK<sup>P</sup>SPYMFECITENFSIDPARTLMVGD<sup>R</sup>LETDILFGHRCG<sup>M</sup>TTVLT<sup>L</sup>TGVS 264

A+GR+ VGK<sup>P</sup>+P MF T+MVGD<sup>R</sup>++TD++ G G+ T+L LTG +

Sbjct: 172 ATGREPYFVGKPNPMMFRSALNRIEAHSEGTVMVGDRMDTDVVAGIEAGLETILVLTGST 231

Query: 265 RLEEAQAY 272

+E+ + Y

Sbjct: 232 TIEDVERY 239

>ref|YP\_001070234.1| HAD-superfamily hydrolase, subfamily IIA [Mycobacterium sp. JLS]

Length = 257

Score = 101 bits (251), Expect = 7e-020

Identities = 75/248 (30%), Positives = 111/248 (44%), Gaps = 17/248 (6%)

Query: 25 LFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLRA 84  
L D DGVL E A+PGA E L RL + L ++NNS +LA R AR G +

Sbjct: 9 LTDMDGVLVREEHALPGAAEFLARLVERERPFLVLTNNSIFTPRDLAARLARSGLI-VPE 67

Query: 85 EQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXXXR 144  
E +++S PG G+ +V

Sbjct: 68 EAIWTSALATATFLGDQLPG-----GSAYVIGEAGLTTALHEAGYTLTDVGPDF----- 116

Query: 145 VRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGLAAAVET 204  
V++G +SF + +A L +AT+ D P ++G P TGS+AA +

Sbjct: 117 ---VVLGETRTYSFEAITKA-VRLILGGARFIATNPVDTGPSAEGP-LPATGSVAAMITK 171

Query: 205 ASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLTDILFGHRCGMTTVLTLTGVS 264  
A+GR+ VGKP+P MF T+MVGDR++TD++ G G+ T+L LTG +

Sbjct: 172 ATGREPYFVGKPNPMMFRSALNRIEAHSEGTVMVGDRMDTDVVAGIEAGLETILVLTGST 231

Query: 265 RLEEAQAY 272

+E+ + Y

Sbjct: 232 TIEDVERY 239

>ref|YP\_702198.1| possible N-acetylglucosamine metabolism protein [Rhodococcus sp.

RHA1]

Length = 276

Score = 101 bits (251), Expect = 7e-020

Identities = 73/248 (29%), Positives = 107/248 (43%), Gaps = 17/248 (6%)

Query: 25 LFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLRA 84  
L D DGVL + E VPGA L L +G + ++NNS R +L R R G +

Sbjct: 13 LMDMDGVLVHEEHLVPGADLFLAELRESGTPFIVLTNNSIRTTPRDLRARLLRTGLD-IPE 71

Query: 85 EQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXXXR 144  
E +++S PG G+ +V

Sbjct: 72 ESIWTSALATATFLASQRP-----GSAYVVGESGLTTALHDIGYVLTNDPDY----- 120

Query: 145 VRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGLAAAVET 204  
V++G +SF + A L + +AT+ DP P +GS P TGS+AA +

Sbjct: 121 ---VVLGETRTYSFEAITAI-RLVEKGARFIATNPDPDTPGSRREGS-LPATGSVAALISR 175

Query: 205 ASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLTDILFGHRCGMTTVLTLTGVS 264  
A+GR VGKP+ M A TLM+GDR++TDI+ G G+ T+L LTG+S

Sbjct: 176 ATGRDPYYVVGKPNALMMRSALRAIGAHSANTLMIGDRMDTDIVCGLEAGLQTLVLTGIS 235

Query: 265 RLEEAQAY 272

+ + +

Sbjct: 236 TRDSVELF 243

>ref|XP\_386894.1| hypothetical protein FG06718.1 [Gibberella zeae PH-1]  
Length = 292

Score = 101 bits (251), Expect = 7e-020

Identities = 80/274 (29%), Positives = 114/274 (41%), Gaps = 21/274 (7%)

Query: 12 AALRDVLRGAVGVLFDGVLWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELA 71  
AA+ + + + L DCDGVLW+G+ G PE + L GK +FV+NNS ++R E

Sbjct: 13 AAINFIDKFDVFLLDGVLWSDGHVYEGVPETINFLRSKGRVVFVTNNSTKSRDEYL 72

Query: 72 LRFARLGFGLRAEQLFSSXXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXX----- 118  
+ LG + + SS P+ VF+

Sbjct: 73 KKLTGLGIPSEKDDVFGSSYSAAIYIARILKL--PEGKRKVFIIIGESGIEQELDSEGVPH 130

Query: 119 ---XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRDPECLL 175  
V AVL G D H ++ K A +++ L

Sbjct: 131 IGGTEEAFFRRDITNDDFKGIADGSLLDPEVGAVLCGLDYHVNYLKYAHAMHYVVKRGATFL 190

Query: 176 VATDRDPWHPLSDGSRTPGTGLAAAVETASGRQALVVGKPSPYMFECITENFSIDPART 235  
AT+ D P+ G GS V A+G+Q L +GKPS M + + F +D ART

Sbjct: 191 -ATNVDSTLPMHNNFFL-GAGSCHIPVVHATGQQPLALGKPSQAMMDAVEGKQFLDRART 248

Query: 236 LMVGDRLETDILFGHRCGM-TTVLTLTGVSRL EE 268

MVGDR L TDI FG + T+ LTGV++ E+

Sbjct: 249 CMVGDRLENTDIKFGIEGKLGGLTLHVLTVGNKKED 282

>ref|ZP\_01855903.1| N-acetylglucosamine-6-phosphatase or p-nitrophenyl  
phosphatase

[Planctomyces maris DSM 8797]

Length = 263

Score = 100 bits (250), Expect = 9e-020

Identities = 78/264 (29%), Positives = 119/264 (45%), Gaps = 23/264 (8%)

Query: 29 DGVLWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLRAEQLF 88  
DGV++ G + GA + L + +F++NNS+R R ++ + +R+G + E +F

Sbjct: 2 DGVIYRGTDLIDGAVGFINELKKRDLPFMFLTNNNSQRTRRDVVTKLSRMGIT-VGEEHIF 60

Query: 89 SSXXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXRVRAV 148  
+ P G +V V

Sbjct: 61 TCAMATARFLAQSKPN-----GTAYVIGEGGLLHALHRNGYSIVDHPDY-----V 106

Query: 149 LVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGLAAAVETASGR 208  
+VG +F + EA + + L+AT+ DP P +G R PG G++ A +E A+ +

Sbjct: 107 VVGEGRSMNFEMI-EAAVRMIENGAKLIATNMDPNCPTQNGPR-PGCGAIVAMLEAATKK 164

Query: 209 QALVVGKPSPYMFECITENFSIDPARTLMVGDRLETDILFGHRCGMTTVLTLTGVSRL EE 268  
QA VGKPS M + I A+T M+GD +ETDIL G G +VL L+G + L +

Sbjct: 165 QAFVSVGKPSVMMRSARQELGISSAQTTMIGDTMETDILGGVEMGYRSVLVLSGGTALS 224



Query: 269 AQAYLAAGQHDLVPHYYVESIADL 292  
+ A Q DLV V+SIADL  
Sbjct: 225 LANF--AYQPDLV----VDSIADL 242

>ref|XP\_001654244.1| 4-nitrophenylphosphatase [Aedes aegypti]  
Length = 317

Score = 100 bits (250), Expect = 9e-020  
Identities = 55/156 (35%), Positives = 86/156 (55%), Gaps = 5/156 (3%)

Query: 145 VRAVLVGYDEHFSFAKLREACALHR-DPECLLVATDRDPWHPLSDGSRTPGTGSLAAAVE 203  
V+AV++ YD +F++ KL A +L+ DPEC+L+A D W P+ G G +E  
Sbjct: 156 VKAVVIDYDYNFNYPKLMRAELYLKSDEPECILIAAGGTDHWTPIRQKVVNIGPGHFVDILE 215

Query: 204 TASGRQALVVGKPSPYMFECITENFSI-DPARTLMVGDRLDILFGHRCGMTTVLTLTG 262  
A+GR+A+ +GKP + + E + + D R L VGD + D+ FG G T+L LTG  
Sbjct: 216 KATGRKAIGLKGKPLQLGVQLMEQYGVQDSQRVLVFGDTIAQDVAFGKVGAFQTLVLTG 275

Query: 263 VSRLEEAQAYLAAGQHDLVPHYYVESIADLTEGLED 298  
+++ + + D+ P YY ES ADL + + D  
Sbjct: 276 GTKMSDV---MKLSGRDIAPDYTESFADLRKVIND 308

Score = 38.1 bits (87), Expect = 0.74  
Identities = 19/55 (34%), Positives = 26/55 (47%)

Query: 24 VLFDCDGVLWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRFARLG 78  
V DCDGVLWN + G + L K ++VSNNS R + ++G  
Sbjct: 30 VFTDCDGVLWNRYEPIEGVGAAIGTLKSLDKHVYVSNNSIRTFENYRKQLQKMG 84

>ref|YP\_001538043.1| HAD-superfamily hydrolase, subfamily IIA [Salinispora arenicola  
CNS-205]  
Length = 259

Score = 100 bits (249), Expect = 1e-019  
Identities = 78/270 (28%), Positives = 114/270 (42%), Gaps = 23/270 (8%)

Query: 25 LFDGCDGVLWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLRA 84  
L D DGVL + + VPGAPE + RL +G+ L ++NNS +L R R+G +  
Sbjct: 11 LTDMDGVLVHEGQPVPGAPEFVARLRSSGRPFVLVLTNNSIYTPRDLQARLVRMGLD-VPE 69

Query: 85 EQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXXXR 144  
++SS PG G +V  
Sbjct: 70 SAIWSSALATAQFLADQRP-----GTAYVIGEAGLTTALHAVGYVLSDFAPDY----- 118

Query: 145 VRAVLVGYDEHFSFAKLREACALHRDPECLLVATDRDPWHPLSDGSRTPGTGSLAAAVET 204  
V++G +SF + +A + D + T+ D P +G+ P GS+AA +  
Sbjct: 119 ---VVLGETRRTYSFEAITKAIRLINDG-ARFICTNPDVTGSPVEGA-LPAAGSVAAMISK 173

Query: 205 ASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMTTVLTLTGVS 264  
A+G VGKP+P M T M+GDR++TDIL G G+ T+L LTG+S  
Sbjct: 174 ATGVDPYFVVGKPNPMMRSALNTIDAHSSESTAMIGDRMDTDILCGLEAGLETILVLTGIS 233

Query: 265 RLEEAQAYLAAGQHDLVPHYYVESIADLTE 294  
EA+ Y P V S+ADL +  
Sbjct: 234 SRAEAERY-----PYRPSRIVASVADLID 257

>ref|XP\_001662402.1| 4-nitrophenylphosphatase [Aedes aegypti]  
Length = 304

Score = 100 bits (249), Expect = 1e-019  
Identities = 78/281 (27%), Positives = 118/281 (41%), Gaps = 10/281 (3%)

Query: 24 VLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNRRARPELALRFARLGFGLR 83  
V+ DCDGVLW +PG E L+ L GK +++NNS R A +F LG  
Sbjct: 27 VICDCDGVWLTVDPIPGVGEALKTLQTHGKTLRYITNNSVRTFDHYAAQFRTLGITLTP 86

Query: 84 AEQLFSSXXXXXXXXXXXXPG-----PPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXX 138  
++ + + G V +  
Sbjct: 87 SDIIHPALAIVRHLKSIHFEGFLIFCLATQPFKNVLINAGFELTEGPDQPLEESFKKIIAT 146

Query: 139 XXXXRVRAVLVGYDEHFSFAKLREACAHLR-DPECLLVATDRDPWHPLSDGSRTPGTGS 197  
VRAV++ D + ++ KL A +L+ DP+CLL+A D G G  
Sbjct: 147 VHDRAPVRAVIDVDFNINYPKLLRAELYLKNDPKCLLIAGATDKVLHARKDFNLIGPGH 206

Query: 198 LAAAVETASGRQALVVGKPSPYMFECITENFSI-DPARTLMVGDRLTDILFGHRCGMMT 256  
+E ++GR+A V+GKP + + + F I D R L VGD LE D++F RCG  
Sbjct: 207 FLDVLEQSTGRKATVLGKPGKELANLVGDIFGIEDRGRVLFVGDMLEQDMVFASRCGFHK 266

Query: 257 VLTLTGVSRLEEAQAYLAAGQHDLVPHYYVESIADLTEGLE 297  
+L L+G + ++ L + VP YY + + DLT+ E  
Sbjct: 267 MLVLSGGASKDD--MLQERDVERVPDYYADRLEDLTKLFE 304

>ref|YP\_001546134.1| HAD-superfamily hydrolase, subfamily IIA [Herpetosiphon  
aurantiacus  
ATCC 23779]  
Length = 257

Score = 100 bits (248), Expect = 2e-019  
Identities = 76/271 (28%), Positives = 117/271 (43%), Gaps = 23/271 (8%)

Query: 22 QGVLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNRRARPELALRFARLGFGLR 81  
+ VL D DGVL +G + +PGAPE L RL +G+ L ++NNS +L R AR+G  
Sbjct: 8 RAVLCDMDGVLVHGAQIIPGAPEFLGRRLRASGRKFLVLTNNSIYTPRDLQARLARIGLP- 66

Query: 82 LRAEQLFSSXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 141  
L E +++S P G FV  
Sbjct: 67 LEIEDIYTSALATAKFLDSQRPN-----GTAFVIGEAGLTNALYDVGYTMTHEHPDY--- 118

Query: 142 XXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGS 201  
V++G +SF ++ +A + L+ T+ D P S+ P G++ A  
Sbjct: 119 -----VVIGETTSYSFERITQAVRFVAAGS-RLIGTNPDVSGP-SERGILPACGAVVAL 170

Query: 202 VETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLTDILFGHRCGMMTTLTLT 261  
+ A+ +A VGKP+P M A +M+GDR++TDI+ G GM T L L+  
Sbjct: 171 IRAATNAEAYFVGKPNPVMRTALRTIDSHAAEAMMIGDRMDTDIIGGTESGMRTALVLS 230

Query: 262 GVSRLEEAQAYLAAGQHDLVPHYYVESIADL 292  
G+ +A+ Y P +ES+A+L  
Sbjct: 231 GMMTRLDAERY-----PYRPTAIIESVAEL 255

>ref|ZP\_01088472.1| N-acetylglucosamine-6-phosphatase or p-nitrophenyl  
phosphatase  
[Blastopirellula marina DSM 3645]  
Length = 286

Score = 100 bits (248), Expect = 2e-019  
Identities = 77/276 (27%), Positives = 119/276 (43%), Gaps = 23/276 (8%)

Query: 23 GVLFDGVLWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGL 82  
G L D DGV++ G + + GA + L + LF++NNS+R R ++A + R+G +  
Sbjct: 4 GFLIDMDGVIYRGSQQLIDGADRFIATLKKKQIPFLFLTNNQRTRRDVAAKLFMRGID-V 62

Query: 83 RAEQLFSSXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 142  
+++F+ PG G FV  
Sbjct: 63 DEDRIFTCAMATARFLAKQKPG-----GTAFVIGEGGLHNALHRNGYAIVDHAPDY---- 113

Query: 143 XRVRVAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGLAAAV 202  
V+VG + L A + D L+AT+ DP P G+R+ G G+ + +  
Sbjct: 114 -----VVVGEARSITLMLDAAVQMVLDG-AQLIATNLDPNCPTKSGTRS-GCGATVSFI 166

Query: 203 ETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGTTVLTTLTG 262  
E A+G+ A VGKPS M + T+M+GD +ETDIL + G LTL+G  
Sbjct: 167 EKATGKTAFSVGKPSVMMRSAQWELGVRSWETVMIGDTMETDILGAVQMGYYATLTLTG 226

Query: 263 VSRLEEAQAYLAAGQHDLVPHYYVESIADLTEGLED 298  
SR E+ +Y P + S+ DL E +E+  
Sbjct: 227 GSRAEDLPSYA-----FRPDRVINSVVDLIEDIEN 256

>ref|ZP\_00996235.1| putative N-acetyl-glucosamine catabolism protein  
[Janibacter sp.  
HTCC2649]  
Length = 266

Score = 100 bits (248), Expect = 2e-019  
Identities = 77/268 (28%), Positives = 117/268 (43%), Gaps = 23/268 (8%)

Query: 25 LFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLRA 84  
L D DGV L + E A+PGA + +E L AG+ L ++NNS +L R G +  
Sbjct: 11 LTDMGVLVHEEHAIPGAADFIEALKAAGRPFVLVLTNNSIYTARDLRARLLASGID-VPE 69

Query: 85 EQLFSSXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXXR 144  
+ +++S P G +V +  
Sbjct: 70 DSIWTSAMATAQFLADQRPS-----GTAYVVGEGGLTTALHDVGYILTSR-----K 115

Query: 145 VRVAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGLAAAVET 204  
V++G +SF ++ +A L D +AT+ D P +G P TGS+AA +  
Sbjct: 116 PDYVVLGETRTYSFEQITQAI-RLIDKGARFIATNPVSGPSPEGI-LPATGSVAALITA 173

Query: 205 ASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGTTVLTTLTGVS 264  
A+GRQ VGKP+P M T M+GDR++TD++ G G+ TVL LTG +  
Sbjct: 174 ATGRQPYVVGKPNPLMMRSALNRLDAHSETTAMIGDRMDTDVVSGLAAGLRTVLVLTGST 233

Query: 265 RLEEAQAYLAAGQHDLVPHYYVESIADL 292  
R ++ + + P V+SIADL  
Sbjct: 234 RPDQVELF-----PYRPTAVVDSIADL 255

>ref|YP\_946359.1| putative sugar phosphatase/hydrolase of the HAD superfamily  
[Arthrobacter aurescens TC1]  
Length = 289

Score = 99.8 bits (247), Expect = 2e-019  
Identities = 77/270 (28%), Positives = 117/270 (43%), Gaps = 23/270 (8%)

Query: 25 LFDGCDGVLWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLRA 84  
L D DGVL + +A+PGA EL++R K L ++NNS +LA ARL GL  
Sbjct: 37 LTDMGDLVHENQAIPGAAELIQRWVDTSKRFLVLTNNSIFTPRDLA---ARLRASGLEV 93

Query: 85 --EQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 142  
E +++S A +  
Sbjct: 94 PEENIWTSALATAQFLKDQVQSSDSGNRAYTIGEAGLTTALHEAGFILTDTPDF----- 148

Query: 143 XRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGLAAAV 202  
V++G +SF + A H+ +AT+ D P DG P TG++AA +  
Sbjct: 149 -----VVLGETRRTYSFEAITMAVRHIL-AGARFIATNPDATGPSKDGPM-PATGAIAAMI 201

Query: 203 ETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMTTVLTTLTG 262  
A+GR+ +VGKP+P MF T M+GDR++TDI+ G G+ TVL L+G  
Sbjct: 202 TKATGREPYIVGKPNPMMFRSAMNQIDAHSETTAMIGDRMDTDIVAGMEAGLHTVVLVLSG 261

Query: 263 VSRLEEAQAYLAAGQHDLVPHYYVESIADL 292  
+++ EE ++ P+ + S+ADL  
Sbjct: 262 ITQREEIVSF-----PFRPNQILNSVADL 285

>ref|YP\_184147.1| predicted sugar phosphatase, HAD superfamily [Thermococcus  
kodakarensis KOD1]  
Length = 268

Score = 99.8 bits (247), Expect = 2e-019  
Identities = 72/278 (25%), Positives = 123/278 (44%), Gaps = 15/278 (5%)

Query: 20 RAQGVLFDCDGLWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRFARLGF 79  
R G++FD DGV++ G + GA E++E L LF++NNS R + +G  
Sbjct: 3 RKIGIIFDMDGVIYRGSEPIGAKIEVIEFLKERKIPFLFLTNNSTRDPAMYREKLLSMGI 62

Query: 80 GGLRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 139  
+ + + +S PG VFV  
Sbjct: 63 D-VPEDVIVTSGLATRLYMEKHFE-----PGEVFIIGGKGLLREMERLGGVVSLEDARK 116

Query: 140 XXXXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGLA 199  
R++ V+VG D ++ KL+ +R+ + T+ D +P +G PG G++  
Sbjct: 117 GAWKRIKHVVVGLDPELTYEKLKYGTLAIRNGASF-IGTNPDTTYPAEGLY-PGAGAI 174

Query: 200 AAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMTTVLT 259  
AA+ ++ R+ +++GKP+ +E + + D MVGDRL+TDI F R GM ++  
Sbjct: 175 AALRASTDREPVIIGKPNPAYEVVKDKLG-DVEELWMVGDRLDTDIAFAKRFGMKAIMV 233

Query: 260 LTGVSRLLEEAQAYLAAGQHDLVPHYYVESIADLTEGLE 297  
LTGVS L++ + + P+ + +L LE  
Sbjct: 234 LTGVSTLKD-----VAESGIKPNLVLDPVDELKRYLE 265

>ref|XP\_754783.1| 4-nitrophenylphosphatase [Aspergillus fumigatus Af293]  
Length = 324

Score = 99.8 bits (247), Expect = 2e-019  
Identities = 87/317 (27%), Positives = 131/317 (41%), Gaps = 45/317 (14%)

Query: 14 LRDVLGRAQGVLFDCDGVWNGERAVPGAPELLERLA-----RAGKA 55  
+++ L + LFDCDGVW+G+ PG E LE L + GK  
Sbjct: 15 IKEFLDKFDVFLFDCDGVWNGDHLFPGTVETLEMLRSNGMLAPAGEKVRARDSYQLGKQ 74

Query: 56 ALFVSNNRRARPELALRFARLGFGLRAEQLFSSXXXXXXXXXXXXXXXXPGPPD----- 107  
+FV+NNS ++R + + +LG E++FSS P +  
Sbjct: 75 VVFVTNNSTKSRADYKKKLEKLGIPST-TEEIFSSSYSASIIYISRILKLPENKRKVFVIG 133

Query: 108 -----APGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXRVRAVLVGYDEHFSF 158  
F+ V VLVG D H ++  
Sbjct: 134 ETGIEQELQTENVFIGGTDPAYRREVRPDDYKLIAAGDPSLLDPEVGVVVLVGLDFHLNY 193

Query: 159 AKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGSAAVETASGRQALVVGKPS 218  
KL A +++ L AT+ D P S G+ PG GS++A + G + +GKP+  
Sbjct: 194 LKLALAYHYIKRGAVFL-ATNIDSTLPNS-GALFPGAGSMSAPLIMMLGEEPVSLGKPNQ 251

Query: 219 YMFECITENFSIDPARTLMVGDRLETDILFGHRCGM-TTVLTLTGVSRLLEEAQAYLAAGQ 277  
M + I F D +RT MVGDR TDI FG + T+ LTGVS ++ +L  
Sbjct: 252 AMMDAIEGKFKFDRSRTCMVGDRANTDIRFGLEGKLGGTGLGVLTGVSSKDD---FLTG-- 306

Query: 278 HDLVPHYVESIADLTE 294  
+ P Y++ ++DL E  
Sbjct: 307 -PIRPSVYLDKLSDLLE 322

>ref|XP\_001354639.1| GA15426-PA [Drosophila pseudoobscura]  
Length = 305

Score = 99.8 bits (247), Expect = 2e-019  
Identities = 77/282 (27%), Positives = 113/282 (40%), Gaps = 11/282 (3%)

Query: 24 VLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNRRARPELALRFARLGFGLR 83  
V+ DCDGV+W +PG + L AGK FVSNNR R + +F +G +  
Sbjct: 25 VISDCDGVVWMLVWIPGTGAAVNALKSAGKQIKFVSNNRFRTDEQYMAKFKHIGANNVH 84

Query: 84 AEQLFSSXXXXXXXXXXXXXXXXPGPP-----DAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXX 138  
+ + PG +  
Sbjct: 85 DDDVHPVKTIVRYLKKHRPGQVYSLMSLEANETLRKQGIDFESLQVKEHLTAASLVDH 144

Query: 139 XXXXXRVRAVLVGYDEHFSFAKLREACAHLRDPE-CLLVATDRDPWHPLSDGSRTPGTGS 197  
V AVL S+ +L +A HL+ E C L+A D PL++ G  
Sbjct: 145 LSIDKPVGAVLFDIHLDMSYVELAKAIRHLQONEDCQLIAGGSDVIMPLAENLVAGFFD 204

Query: 198 LAAAVETASGRQALVVGKPSYMFECITENFSI-DPARTLMVGDRLETDILFGHRCGTT 256  
V+ + R+A +GKPS + E E F I DP R + +GD L D+ FG CG +  
Sbjct: 205 FLEHVKRYTQREATFLGKPSILGEMFEMFEITDPKRCIFIGDTLVQDVQFGKSCGYQS 264

Query: 257 VLTLTGVSRLLEEAQAYLAAGQHDLVPHYYVESIADLTEGLED 298  
+L L+G E+ + D P YY +S+AD T+ L++  
Sbjct: 265 LLVLSGCLTKED----MFNAPVDAQPDYYADSLADFTQLLQN 302

>ref|YP\_001623967.1| HAD-superfamily hydrolase, subfamily IIA [Renibacterium salmoninarum ATCC 33209]  
Length = 342

Score = 99.4 bits (246), Expect = 3e-019  
Identities = 86/282 (30%), Positives = 125/282 (44%), Gaps = 19/282 (6%)

Query: 11 GAALRDVLGRAQGVLFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPEL 70  
G +LG VL D DGV++ G +A+PGA E LE + + G +++NN+ R +  
Sbjct: 11 GMNTSSLLGFEFDAVLSDLGDVVYAGAQAIPGAVEALEAVEKLGIGLYITNNASRTPDAV 70

Query: 71 ALRFARLGFGLRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXX 130  
A LG A+Q+F S G + V  
Sbjct: 71 AEHLRELG-APATAQQVFGSARA-----GAGLLADRLAVGSKVLVIGSAALADEV 119

Query: 131 XXXXXXXXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGS 190  
+ AV+ G+ + L EA A + L VAT+ D P++ G  
Sbjct: 120 AAKGFLLVDGAADQPDVAVIQGFSPELGWKDLAEA-AFAINAGALWVATNTDLTIPVARGI 178

Query: 191 RTPGTGSLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGH 250  
PG GSL AAV A LV GKP MF + ++ R L++GDRL+TDIL G+  
Sbjct: 179 -APNGSLVAAVAQAVNVAPLVAGKPEATMFLAAK--ALKARRPLVIGDRDLDTDILGGN 235

Query: 251 RCGMTTTLTLTGVSRLLEEAQAYLAAGQHDLVPHYYVESIADL 292  
M+T L LTG+ + AQ+ LAA + P+Y +E++ L  
Sbjct: 236 NAQMSTALVLTGI---DTAQSALAARTSER-PNYLLENLFGL 273

>ref|YP\_886791.1| HAD-superfamily protein hydrolase, subfamily protein IIA [Mycobacterium smegmatis str. MC2 155]  
Length = 258

Score = 99.4 bits (246), Expect = 3e-019  
Identities = 75/256 (29%), Positives = 112/256 (43%), Gaps = 17/256 (6%)

Query: 17 VLGRAQGVLFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRFAR 76  
V AQ L D DGV L E A+PGA E L+ L + L ++NNS +LA R AR  
Sbjct: 2 VRSHAQCWLTDMDGVLVREEHALPGAAEFLQTLVDKERPFLVLTNNSIFTPRDLAARLAR 61

Query: 77 LGFGGLRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXX 136  
G + +++S PG G+ +V  
Sbjct: 62 SGLT-VPESSIWTSALATAAFLDGLPG-----GSAYVIGEAGLTTALHEVGYTLTDVEP 115

Query: 137 XXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTG 196  
V++G +SF + A + +AT+ D P ++G P TG  
Sbjct: 116 DF-----VVLGETRTRYSFEAITRAIRLILGG-ARFIATNPDVTGPSAEGP-LPATG 164

Query: 197 SLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMTT 256  
S+AA + A+GR+ VGKP+P MF T+MVGDR++TD++ G G+ T  
Sbjct: 165 SVAAMITKATGREPYFVGKPNPMMFRSALNRIEHAHSENTVMVGDRMDTDVVAGIEAGLDT 224

Query: 257 VLTLTGVSRLLEEAQAY 272  
+L LTG + +E+ + Y  
Sbjct: 225 ILVLTGSTAVEDIERY 240

>ref|YP\_572850.1| HAD-superfamily hydrolase, subfamily IIA [Chromohalobacter  
salexigens DSM 3043]  
Length = 257

Score = 99.4 bits (246), Expect = 3e-019  
Identities = 75/270 (27%), Positives = 119/270 (44%), Gaps = 23/270 (8%)

Query: 25 LFDGCDGVLWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLRA 84  
L D DGVL + A+PGA EL+++ G L ++NNS +L+ R RLG +  
Sbjct: 10 LTDMDGVLIGEDHALPGAVELIDQWRANGTPFLVLTNNSIYTPRDLRSARLNRLGIN-VPE 68

Query: 85 EQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXXXR 144  
++L++S PG G+ FV  
Sbjct: 69 DRLWTSALATAAFLRDQAPG-----GSAFVIGEAGLTTAIHEAGFVMTDVPDF----- 117

Query: 145 VRVAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGSAAAVET 204  
V++G +SF + A L + +AT+ D P +G P TG++AA +  
Sbjct: 118 ---VVLGETRSYSFEAITRAI-RLINAGARFIATNPDVTGPSPEGP-LPATGAVAALITA 172

Query: 205 ASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMMTTVLTLTGVS 264  
A+ R+ VGKP+P MF RT M+GDR++TD++ G G+ TVL +TG++  
Sbjct: 173 ATKREPYVVGKPNPMMFRSAMNKLGTHSERTGMIGDRMDTDVIAGIEAGLHTVLVMTGIA 232

Query: 265 RLEEAQAYLAAGQHDLVPHYYVESIADLTE 294  
+ + Y P ++S+A+L E  
Sbjct: 233 TRGDLERY-----PFRPREIIDSVAELLE 256

>gb|AAU14865.1| plastid phosphoglycolate phosphatase [Bigelowiella natans]  
Length = 405

Score = 99.0 bits (245), Expect = 4e-019  
Identities = 63/246 (25%), Positives = 108/246 (43%), Gaps = 5/246 (2%)

Query: 24 VLFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLR 83  
++ D DGVLW G+R P L+R G LFV+NN+ ++R + ++ ++G +  
Sbjct: 126 IILDQDGVWLRGDRVFPSTLPSLQFRDLGIRVLFVTNNAAKSREQYVEKWKVGLLEITK 185

Query: 84 AEQLFSSXXXXXXXXXXXXXXXXPGP----PDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 139  
E + +S G D + +  
Sbjct: 186 NEIVPASYMAAAYLESIKFQKILFIGDEGTRLELQGHGFELVEVPKEATTMSNQELANF 245

Query: 140 XXXXRVRAVLVGYDEHFSFAKLREACAHLRDPE-CLLVATDRDPWHPLSDGSRTPGTGS 198  
V+AV++ +D +F++ KL A +LR E C V T+ D L + PGTG +  
Sbjct: 246 QLDSEVKAVVLAHDPNFYRKLAIATQYLRSNEDCHFVVTNMDAGDMLDNQRFMPGTGGM 305

Query: 199 AAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMMTTVL 258  
A A+ + +GR + GK ++ + + + + P+ + VGDRL+TDI G + T +  
Sbjct: 306 ADAITSTTGRVPVNTGKGGDFLLPFLMKKYGVKPSSEMMCVGDRLDTDIALGRQANCKTAM 365

Query: 259 TLTGVS 264  
TGV+

Sbjct: 366 PFTGVT 371

>ref|YP\_445614.1| protein nagD [Salinibacter ruber DSM 13855]  
Length = 260

Score = 99.0 bits (245), Expect = 4e-019  
Identities = 79/270 (29%), Positives = 113/270 (41%), Gaps = 23/270 (8%)

Query: 25 LFD CDGVLWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLRA 84  
L D DGVL + E +PGA E +ERL L ++NNS R +L+ R AR G A  
Sbjct: 12 LLDMDGVLVHEEVVLPGAQEFIERLREKELPFLVLTNNSIYTRRDL SARLARAGLDVPEA 71

Query: 85 EQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXXR 144  
+ S+ A G +  
Sbjct: 72 KIWTSAVATAQFLSNQAPEASAYAVGEAGLT TALHEVGYTLTDADPDF----- 119

Query: 145 VRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGS LAAAVET 204  
V++G +SF + A L + +AT+ D P DG P TGS+AA +  
Sbjct: 120 ---VVLGETRTYSFQHIT-AAVRLIEQGARFIATNP DVTGSPDGP-LPATGSVAALIRE 174

Query: 205 ASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRL ETDILFGHRCGMTT VLT LTGVS 264  
A+G++ VGKP+P M A T M GDR++TD++ G G+TT L L+G +  
Sbjct: 175 ATGQKPYFVGKPNPIMIRSALNQIEAHSATTAMAGDRMDTDVMAGMEAGLT THLVLSGST 234

Query: 265 RLEEAQAYLAAGQHDLVPHYVVE SIADLTE 294  
R EE + P+ VESI++L E  
Sbjct: 235 RREEISDFAYR-----PNNVVE SISELIE 258

>ref|YP\_831008.1| HAD-superfamily hydrolase, subfamily IIA [Arthrobacter sp.  
FB24]  
Length = 330

Score = 98.6 bits (244), Expect = 5e-019  
Identities = 83/284 (29%), Positives = 124/284 (43%), Gaps = 22/284 (7%)

Query: 9 LRGAALRDVLGRAQGVLFDCDGV LWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARP 68  
+ GA+L + R +L D DGVL++ G A+PGA E L +LA +V+NN+ R  
Sbjct: 1 MSGASL---ISRFDALLSDLDGVVYAGPHAI PGAVEALRQLAGIDVGLGYVTNNASRTPA 57

Query: 69 ELALRFARLGFGLRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXX 128  
++A LG A+ + SS G +  
Sbjct: 58 QVAHLRELGAPAEDAQVSSQAAGELLA-----GLLPAGARVLVTGSPALAH 106

Query: 129 XXXXXXXXXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSD 188  
+ AV+ G++ + L EA +++ L VAT+ D P +  
Sbjct: 107 EVELVGLTPVHSAKEKPVAVVQGFNPEIGWKDLAE A-SYVIAGGALWVATNTDMSIPQAR 165

Query: 189 GSRTPGTGS LAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRL ETDILF 248  
G PG G+L AAV A+G+Q LV GKP +F + + + R L+VGDR L+TDIL  
Sbjct: 166 GM-APGNGLVA AVAAATGQQPLVAGKPEAPLFR TAAKRLTSE--RPLVVGDR LDTDILG 222

Query: 249 GHRCGMTT VLT LTGVS RLEEAQAYLAAGQHDLVPHYVVE SIADL 292  
G+ G TV LTGV E A A + P + + ++DL  
Sbjct: 223 GNNAGFATVAVLTGVDTRESILAARTAER----PDFLINDLSDL 262



>ref|NP\_010045.1| Alkaline phosphatase specific for p-nitrophenyl phosphate, involved in dephosphorylation of histone II-A and casein; Pho13p [Saccharomyces cerevisiae]  
Length = 312

Score = 98.2 bits (243), Expect = 6e-019  
Identities = 80/293 (27%), Positives = 122/293 (41%), Gaps = 21/293 (7%)

Query: 15 RDVLGRAQGVLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNSRRARPELALRF 74  
++ L + LFDGCVLW G +A+P E+L L + GK +FV+NNS ++R +F  
Sbjct: 18 QEFLDKYDTFLFDGCVLWLGSQLPYTLEILNLLKQLGKQLIFVTNNSTKSRLAYTKKF 77

Query: 75 ARLGFGGLRAEQLFSSXXXXXXXXXXXXXXXXXPGPPDAPGA-VFVXXXXXXXXXXXXXXXXXXXX 133  
A G ++ EQ+F+S P VF  
Sbjct: 78 ASFGI-DVKEEQIFTSGYASAVYIRDFLKLPKDKVWVFGESGIGEELKLMGYESLGGA 136

Query: 134 XXXXXXXXXXXRVRAVLV-----GYDEHFSFAKLREACAHLRDPECLLVATDRD 181  
LV G D ++ +L +L+ V T+ D  
Sbjct: 137 DSRLDTPFDAAKSPFLVNLGDKDVSCVIAGLDTKVNYHRLAVTLQYLQKDSVHFVGTNVD 196

Query: 182 PWHPLSDGSRTPGTGSLAAAVETASGRQALVVGKPSYMFECITENFSIDPARTLMVGDR 241  
P G PG GS+ ++ +S R+ GKP+ M I F++D ++ MVGDR  
Sbjct: 197 STFP-QKGYTFPGAGSMIESLAFSSNRRPSYCGKPNQNMNSIISAFNLDRSKCCMVGDR 255

Query: 242 LETDILFGHRCGM-TTVLTLTGVSRLLEEAQAYLAAGQHDLV-PHYVVEESIADL 292  
L TD+ FG G+ T+L L+G+ E A HD P +Y++ + D+  
Sbjct: 256 LNTDMKFGVEGGLGGTLLVLSGIETEERALKI----SHDYPRPKFYIDKLGDI 304

>ref|XP\_001858497.1| pyridoxal phosphate phosphatase [Culex pipiens quinquefasciatus]  
Length = 310

Score = 97.8 bits (242), Expect = 8e-019  
Identities = 78/288 (27%), Positives = 118/288 (40%), Gaps = 22/288 (7%)

Query: 24 VLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLR 83  
VL DCDGVLW + G + L AGK +FVSNN ++ + A LG  
Sbjct: 22 VLTDCDGVWLTNLEPLEGTDRAIRALKDAGKRVPVFSNNGAKSLDSYQKQIAGLGHSAE 81

Query: 84 AEQLFSSXXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXX----- 134  
+ ++ + D G +F  
Sbjct: 82 DDIVYPAISVVRYLQSI-----DFKGLIFAICSKTFMDILRKAGYEVISGPNPLPESV 135

Query: 135 --XXXXXXXXRVRAVLVGYDEHFSFAKLREACAHLR-DPECLLVATDRDPWHPLSDGSR 191  
V+AV+ D +F+ KL A +L+ DP CLLVA P ++  
Sbjct: 136 DIIVSTIDDKLPVKAVIFDNDNFNHNHMKLFRAEYLKNDPNCLLVAGAISPRIFVTPQVD 195

Query: 192 TPGTGLSAAAVETASGRQALVVGKPSYMFECITENFSIDP-ARTLMVGDRLETDILFGH 250  
G + +E ++ R+A+++GKPSP + E + + I R L VGD + D+ FG  
Sbjct: 196 VTGMSQYLSVLEQSTDRKAVILGKPSRLAEQLKNHLKITQNRVLFVGDVDMIAQDVTFGR 255

Query: 251 RCGMTTVLTLTGVSRLLEEAQAYLAAGQHDLVPHYVVEESIADLTEGLED 298  
G T+L L+G + LE +A G VP +Y +S ADL ++D  
Sbjct: 256 AAGFQTLVLSGGTSLMVEALSNNGN---VPDFYTDSFADLDRLIQD 300

>ref|YP\_947413.1| putative haloacid dehalogenase-like hydrolase [Arthrobacter  
aureus TC1]  
Length = 328

Score = 97.4 bits (241), Expect = 1e-018  
Identities = 81/269 (30%), Positives = 115/269 (42%), Gaps = 19/269 (7%)

Query: 24 VLFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNRRARPELALRFARLGFGLR 83  
VL D DGV++ G A+PGA E L+RL G +V+NN+ R ++A LG  
Sbjct: 12 VLSLDLGVVYAGPHAIPGAVESLQRLETVGVGLGYVTNNASRTPAQVAHLRELG-APAE 70

Query: 84 AEQLFSSXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 143  
Q+ SS P A V +  
Sbjct: 71 DHQVVSSSQAGELLASMLP----AGAHVLITGSAALAHEIELAGLKPVHSAAESPV--- 123

Query: 144 RVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGLAAAVE 203  
AV+ G++ + L EA +++ + AT+ D P + G PG G+L AAV  
Sbjct: 124 ---AVVQGFNPEIGWKDLAEA-SYVVAGGAMWFATNTDMSIPQARGM-APGNGLVAAVA 178

Query: 204 TASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMTTTLTLTG 263  
A+G+ LV GKP +F + D R L+VGDRL+TDIL G+R G T LTGV  
Sbjct: 179 AATGKTPLVAGKPEAPLFHAAAKRLKAD--RPLVVGDRDLTDILGGNRAGFATAAVLTGV 236

Query: 264 SRLEEAQAYLAAGQHDLVPHYVESIADL 292  
+ + A + D P Y + +A L  
Sbjct: 237 ----DTTHTIIAARTDERPDYLLADLAGL 261

>ref|ZP\_01514347.1| HAD-superfamily hydrolase, subfamily IIA [Chloroflexus  
aggregans  
DSM 9485]  
Length = 269

Score = 97.4 bits (241), Expect = 1e-018  
Identities = 77/249 (30%), Positives = 114/249 (45%), Gaps = 17/249 (6%)

Query: 22 QGVLFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNRRARPELALRFARLGF 81  
+ VLF D DGV L+ G+ +PG +L + L A +NN+ + A + A +G  
Sbjct: 8 RAVLFDMDGVLYRQTPPLPGVADLWQFLHDHQIAFACATNNASMTPOQYAAKLAAMGIV- 66

Query: 82 LRAEQLFSSXXXXXXXXXXXXPGPPDAPGA-VFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 140  
L A+++ +S P PG VFV  
Sbjct: 67 LPADRVITSAQATALYLRDHYF-----PGTRVFVGMQGLRAALFADGYFVEDDDAP--- 118

Query: 141 XXXRVRVAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGLAA 200  
V+ G D ++ +L+ A H+R ++T+ D P +G PG G+++AA  
Sbjct: 119 -----ELVVQGADFTLTYERLKRATLHIRRG-ARFISTNPDRTPFPSEEG-IPGAGAI 171

Query: 201 AVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMTTTLTL 260  
A+ A+ LV+GKP+P MF + P+ TL+VGDRL+TDI GM +VL L  
Sbjct: 172 ALTAATDVSPVLVIGKPAPT MFLIGAKMLDAPPSATLVVGDRLDITDIAGAIAGMPSVLVL 231

Query: 261 TGVSRLAEA 269  
TGVS +EEA  
Sbjct: 232 TGVSTVEEA 240

>ref|YP\_001275664.1| HAD-superfamily hydrolase, subfamily IIA [Roseiflexus sp. RS-1]

Length = 265

Score = 97.1 bits (240), Expect = 1e-018

Identities = 73/247 (29%), Positives = 101/247 (40%), Gaps = 15/247 (6%)

Query: 18 LGRAQGVLFDCDGVLWNGERAVPGAPELLERLARAGKAALFVSNNRRARPELALRFARL 77  
L R V+FD DGVL+ G RA+PG ELL G +NN+ + + A +  
Sbjct: 5 LNRFTAVIFDMDGVLRYGSRALPGVNELLALFDARGVIYACCTNNATMTPAQYEAklaAM 64

Query: 78 GFGGLRAEQLFSSXXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXX 137  
G A + SS G VFV  
Sbjct: 65 GIRMPAARIVTSSVATRRWLETQAPRGT-----GVFVIGMDGLRSALFDDGYFVEDDEHP 119

Query: 138 XXXXXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGS 197  
V+VG D ++ +LR+AC +R + T+ D P DG PG G+  
Sbjct: 120 AF-----VVVGMDFEVTYRRLRKA CLLIR-AGARFIGTNPDTTFPAEDGI-VPGCCGA 169

Query: 198 LAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMTTV 257  
L A + ++ + V+GKP P MF E D RTL +GDRL+TDI G+ +  
Sbjct: 170 LLALLRVSTETEPFVIGKPGPTMFRAAIEILGADATRTLTLIGDRLDTDIAGARAAGLASA 229

Query: 258 LTLTGVS 264  
L LTGV+  
Sbjct: 230 LVLTGVT 236

>ref|YP\_001041311.1| HAD-superfamily hydrolase, subfamily IIA [Staphylothermus marinus F1]

Length = 262

Score = 97.1 bits (240), Expect = 1e-018

Identities = 65/250 (26%), Positives = 115/250 (46%), Gaps = 17/250 (6%)

Query: 22 QGVLFDCDGVLWNGERAVPGAPELLERLARAGKAALFVSNNRRARPELALRFARLGFGG 81  
+GV+ D DGV+W GE+ + E +++L ++G +++SNN+ R+R E + R G  
Sbjct: 3 KGVIIIDLGVVWRGEKPLKNNIEAIKLEKSLKIIYLSNNATRSRIEYVYKIRRYGLKA 62

Query: 82 LRAEQLFSSXXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 141  
+ S+ + +F+  
Sbjct: 63 SEKNVINSAFAAAQYIVE-----NGGSNIFIIGEAGLYYECTKAGLLPVTIGTPA--- 112

Query: 142 XRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGS LAAA 201  
+ VLVG D ++ KL A +R+ +A + D P+ + PG GS+ A  
Sbjct: 113 ----QHVLVGLDRFVTYNKLLYATELIRNG-AKFIAANTDKTFPV-ENRLDPGAGSIVAF 166

Query: 202 VETASGRQA-LVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMTTVLTL 260  
+E ++G++ ++GKP+P++ + + L+VGDRD+TDIL G CG T+L L  
Sbjct: 167 LEASTGKKPDAIIGKPNWILDALRMNGLSRKDV LIVGDRLDTDILLGINCGADTLLVL 226

Query: 261 TGVSRLLEEAQ 270  
TGV+ +E+ +  
Sbjct: 227 TGVNSIEDIE 236

>ref|YP\_001431753.1| HAD-superfamily hydrolase, subfamily IIA [Roseiflexus castenholzii

DSM 13941]  
Length = 265

Score = 97.1 bits (240), Expect = 1e-018  
Identities = 73/247 (29%), Positives = 101/247 (40%), Gaps = 15/247 (6%)

Query: 18 LGRAQGVLFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRFARL 77  
L VLF D DGVL+ G +A+PG ELL L G +NN+ + + AR+  
Sbjct: 5 LNHFTAVLFDMDGVLYRGSQALPGVSELLALLDSRGVTYACCTNNATMTPAQYEAKLARM 64

Query: 78 GFGGLRAEQLFSSXXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXX 137  
G + + SS G VFV  
Sbjct: 65 GIHMPASRIVTSSVATRRWLETQASRGT-----GVFVIGMDGLRSALFDDGYFVEDEEHP 119

Query: 138 XXXXXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGS 197  
V+VG D ++ +LR+AC +R V T+ D P DG PG G+  
Sbjct: 120 AF-----VVVGMDFEVTYRRLRKA CLLIR-AGARFVGTNPDTTFPAEDGI-VPGCGA 169

Query: 198 LAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMTTV 257  
L A + ++ + ++GKP P MF E D RTL +GDRL+TDI G+  
Sbjct: 170 LLALLRVSTETEPFIIGKPGPTMFHSAIEILGADATRTLTLIGDRLDTDIAGARAAGLAGA 229

Query: 258 LTLTGVS 264  
L LTGV+  
Sbjct: 230 LVLTGVT 236

>ref|XP\_001850558.1| pyridoxal phosphate phosphatase [Culex pipiens quinquefasciatus]

Length = 325

Score = 96.7 bits (239), Expect = 2e-018  
Identities = 60/153 (39%), Positives = 87/153 (56%), Gaps = 5/153 (3%)

Query: 144 RVRAVLVGYDEHFSFAKLREACAHL-RDPECLLVATDRDPWHPLSDGSRTPGTGS LAAAV 202  
+V AV++ D + S A L +A +L R+P+CLL+A D PL G G +  
Sbjct: 161 KVGAVVMDIDVNI SLAHLMKAKCYLQRNPDCLLIAGATDYIVPLDTSMDVVGPGYFIEVL 220

Query: 203 ETASGRQALVVGKPSPYMFECITENFSID-PARTLMVGDRLDILFGHRCGMTTVLTLT 261  
E +SGR+ALV+GKP + + I + F++ P RTL VGD L D+ FG RCG +L L+  
Sbjct: 221 ERSSGRKALVLGKPGQALADFIELDQFNVTRPERTLFVGDMLPQDMGFGTRCGFQKLLMLS 280

Query: 262 GVSRL EEAQAYLAAGQHDLVPHYYVESIADLTE 294  
G + LE LA + + +PHYY +S AD +  
Sbjct: 281 GGTTLE---MMLAHQKPEELPHYYADSYADFIQ 310

Score = 49.7 bits (117), Expect = 2e-004  
Identities = 24/64 (37%), Positives = 32/64 (50%)

Query: 15 RDVLGRAQGVLFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRF 74  
R L +L DCDGV+WN +P + L+ L GK F+SNN R E +F

Sbjct: 20 RTFLNSFDTILSDCDGVVWNFTGPIPDVDQALQLLKHQKQVAFISNNGMRTMAEYKHKF 79

Query: 75 ARLG 78  
+LG

Sbjct: 80 HQLG 83

>emb|CAA44597.1| p-nitrophenylphosphatase [Schizosaccharomyces pombe]  
Length = 269

Score = 96.7 bits (239), Expect = 2e-018  
Identities = 58/151 (38%), Positives = 85/151 (56%), Gaps = 6/151 (3%)

Query: 145 VRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGLAAAVET 204  
V AVL G D H ++ K A +L+DP C + T++D P ++G PG+G+++ +

Sbjct: 122 VGAVLCGMDMHVTYLKYCMAFYQLQDPNCAFLLTNQDSTFP-TNGKFLPGSGAISYPLIF 180

Query: 205 ASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGM-TTVLTLTGTV 263  
++GRQ ++GKP M E I N + D + VGDRL TDI F + ++L LTGV

Sbjct: 181 STGRQPKILGKPYDEMMEAIIANVNFDRKKACFVGDRLENTDIQFAKNSNLGGSLLVLTGV 240

Query: 264 SRLEEAQAYLAAGQHDLVPHYYVESIADLTE 294

S+ EE + +VP YYVES+A L E

Sbjct: 241 SKEEE----ILEKDAPVVPDYVESLAKLAE 267

>ref|YP\_001626526.1| haloacid dehalogenase-like hydrolase [Renibacterium  
salmoninarum  
ATCC 33209]  
Length = 264

Score = 96.3 bits (238), Expect = 2e-018  
Identities = 73/268 (27%), Positives = 115/268 (42%), Gaps = 23/268 (8%)

Query: 25 LFDGCDGVLWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLRA 84  
L D DGVL + +AVPGA EL++R K L ++NNS +L R G +

Sbjct: 16 LTDMDGVLVHENQAVPGASELIQRWVDTSKRFLVLTNNSIYTPRDLRARLRASGLE-IPE 74

Query: 85 EQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXXXR 144  
E +++S P G FV

Sbjct: 75 ENIWTSALATAEFLKSQMPA-----GKAFVIGEAGLTTALHEAGFILTDQNPDY----- 123

Query: 145 VRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGLAAAVET 204  
V++G ++SF + +A + D +AT+ D P +G P TG++AA +

Sbjct: 124 ---VVLGETRNYSFEAITQAIRLIGDG-ARFIATNPDATGPSKEGPM-PATGAIAALITK 178

Query: 205 ASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGM-TTVLTLTGVS 264  
A+ R+ +VGKP+P MF T M+GDR++TDI+ G G+ TVL +TG++

Sbjct: 179 ATNREPYIVGKPNPMMFRSAMNQIEAHSETTAMIGDRMDTDIIAGMEAGLHTVLVMTGIT 238

Query: 265 RLEEAQAYLAAGQHDLVPHYYVESIADL 292

+ + + P ++S+ADL

Sbjct: 239 QPGDVDTF-----PFRPDQTLDSVADL 260

>ref|XP\_001024155.2| haloacid dehalogenase-like hydrolase family protein  
[Tetrahymena

thermophila SB210]  
Length = 291

Score = 96.3 bits (238), Expect = 2e-018  
Identities = 65/284 (22%), Positives = 122/284 (42%), Gaps = 14/284 (4%)

Query: 14 LRDVLGRAQGVLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNRRARPELALR 73  
L ++ + + FD DGV WNG + A + ++L + GK F++NNS R+R +  
Sbjct: 12 LLELKDKYKAFFFDMDGVWNGSHKIQNAIDTYQQLKKEGKQCFFITNNSRSRKTYVEK 71

Query: 74 FARLGFGLRAEQLFSSXXXXXXXXXXXXPGPPDA-----PGAVFVXXXXXXXXXX 124  
LG E++F++ P  
Sbjct: 72 LRALGVE-TEEERVFAASSIAAYYIKNNLPNVKCKYVVGKGCICEELANYGIDYIWSNEH 130

Query: 125 XXXXXXXXXXXXXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWH 184  
V AV+VG + F++A + A +++++ +AT+ D +  
Sbjct: 131 HNQSKEMTADEFENLKL DSEVGAVVVGINYE FNYAMMAYASSYIQNG-AKFIATNEDKYI 189

Query: 185 PLSDGSRTPGTGS LAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRL 244  
++ G + PG G++ A+ + L+ GKP+ ++ + + ++I+ + +M+GD L+T  
Sbjct: 190 -MAGGKKMPGGGTIVNAIAFGCDTRPLITGKPN SFVVDLLCNQYNINKSEAIMIGDNLDT 248

Query: 245 DILFGHRCGMTTTLTGTGVSRL EEAQAYLAAGQHDLVPHYVYVES 288  
DI G G+ T+L +TGV+ +E + VP YY +S  
Sbjct: 249 DIALGQNAGLDTLLVMTGVT--DENLLKKTVEEGLFVPTY YADS 290

>ref|YP\_056630.1| predicted sugar phosphatase/hydrolase [Propionibacterium  
acnes

KPA171202]  
Length = 272

Score = 96.3 bits (238), Expect = 2e-018  
Identities = 73/270 (27%), Positives = 116/270 (42%), Gaps = 23/270 (8%)

Query: 25 LFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNRRARPELALRFARLGFGLRA 84  
L D DGV L + VPGA +L+ R K L ++NNS +LA R G +  
Sbjct: 24 LTDMDGVLVHENHEVPGASDLINRWVDTSKRFLVLTNNSIFTPRDLAARMQASGLT-VPE 82

Query: 85 EQLFSSXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 144  
+ +++S PG ++V  
Sbjct: 83 DNIWTSALATAHFLADQQPG-----ARLYVIGEAGLTALHEAGFILTDIDPDY----- 131

Query: 145 VRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGS LAAAVET 204  
V++G +SF + A + D + T+ D P +G P TG++AA +E  
Sbjct: 132 ---VVLGETRTYSFEAITRAVRFIVDG-ARFICTNP DATGPSKEGP-LPATGAVAAMIEA 186

Query: 205 ASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRL ETDILFGHRCGMTTTLTGTGVS 264  
AS + +VGKP+P MF T M+GDR++TD++ G G+ TVL L+G++  
Sbjct: 187 ASKHKPYIVGKPNPMMFRSALNRIEAHSETTAMIGDRMDTDMVAGMEAGLLTVLVLSGIT 246

Query: 265 RLEEAQAYLAAGQHDLVPHYVYVESIADLTE 294  
+ EE + Q+ P+ ++S+ADL E  
Sbjct: 247 KREEVE-----QYPYRPNIIILDSVADLNE 270

>ref|YP\_001221224.1| putative N-acetylglucosamine-6-phosphate deacetylase  
[Clavibacter  
michiganensis subsp. michiganensis NCPPB 382]  
Length = 265

Score = 95.9 bits (237), Expect = 3e-018  
Identities = 73/250 (29%), Positives = 113/250 (45%), Gaps = 21/250 (8%)

Query: 25 LFDCDGVLWNGERAVPGAPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLRA 84  
L D DGVL + +A+PGA L+++ GK L ++NNS +L+ ARL GL  
Sbjct: 11 LTDMDGVLVHENQALPGAAALIQQWQDQGKPFVLVTNNSIFTPRDLS---ARLRASGLHV 67

Query: 85 --EQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 142  
E +++S PG G+ FV  
Sbjct: 68 PEESIWTSALATAAFLEQQMPG-----GSAFVIGEAGLTTALHEAGFIMTDT----- 114

Query: 143 XRVRVAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGLAAAV 202  
+ V++G ++SF + A L + +AT+ D P ++G P TG++ A +  
Sbjct: 115 -KPDFVIVIGETRNYSEAITRAI-RLINGGARYIATNPDATGPSAEGV-LPATGAVLALI 171

Query: 203 ETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMTTTLTLTG 262  
A+G++ +VGKP+P MF T M+GDR++TDI+ G G+ TVL LTG  
Sbjct: 172 SKATGKEPYIVGKPNPMMFRSALNKIGAHSESTGMIGDRMDTDIIAGIEAGLHTVLVLTG 231

Query: 263 VSRLEEAQAY 272  
+S E + Y  
Sbjct: 232 ISDRAEIERY 241

>ref|YP\_063093.1| N-acetylglucosamine metabolism protein [Leifsonia xyli  
subsp. xyli  
str. CTCB07]  
Length = 267

Score = 95.9 bits (237), Expect = 3e-018  
Identities = 70/248 (28%), Positives = 108/248 (43%), Gaps = 17/248 (6%)

Query: 25 LFDCDGVLWNGERAVPGAPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLRA 84  
L D DGVL + +A+PGAP L+++ G L ++NNS +LA R G +  
Sbjct: 13 LTDMDGVLVHENKALPGAPALIQQWRDQGTGPFVLVTNNSIYTPRDLAARLRASGLD-VPE 71

Query: 85 EQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXXXR 144  
E +++S PG G+V+V  
Sbjct: 72 ESIWTSALATADFLRQONPG-----GSVYVIGEAGLTTALHEAGFIMTETNPDY----- 120

Query: 145 VRVAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGLAAAVET 204  
V+VG +SF + +A L +AT+ D P ++G P TG++ A +  
Sbjct: 121 ---VVVGETRSYSFDAITKAI-RLIGKGARFIATNPDATGPSAEGP-LPATGAVTAMITK 175

Query: 205 ASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMTTTLTLTGVS 264  
A+G + V+GKP+P MF T M+GDR++TD++ G G+ T+L LTG+S  
Sbjct: 176 ATGMKPYVIGKPNPMMFRSALNRIGAHSENTAMIGDRMDTDVVAGIEAGLHTILVLTGIS 235

Query: 265 RLEEAQAY 272  
E Y  
Sbjct: 236 DQAEIDLY 243

>gb|ABC72335.1| signal-transducing histidine kinase [uncultured haloarchaeon]  
Length = 267

Score = 95.9 bits (237), Expect = 3e-018  
Identities = 75/269 (27%), Positives = 115/269 (42%), Gaps = 23/269 (8%)

Query: 25 LFDCDGVLWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLRA 84  
L D DGV L + A+ GA + +L + + L ++NN+ R +LA R + +G +  
Sbjct: 16 LIDMDGVLIRDDDALSGAESFIHQKQERQFLVLTNNAIYTRDLAARLSDVGLT-IPE 74

Query: 85 EQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXXR 144  
E++++S P DA V  
Sbjct: 75 ERIWTSAVATAQFVSNQMP---DASAYVI-----GEAGLKTALHDVGYTLTG TN 120

Query: 145 VRVAVLVGYDEHFSFAKLREACALRDPECLLVATDRDPWHPLSDGSRTPGTGSLAAAVET 204  
V++G +SF + A L + + T+ D P ++G P TGS+AA +  
Sbjct: 121 PDFVVLGESRTYSFQ NIT-AAVRLVNQGARFIVTNP DATAPSAEGP-LPATGSVAALITE 178

Query: 205 ASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMTTVLTLTGVS 264  
A+G++ VGKP+P M T MVDGDR++TD++ G G+TT L LTG +  
Sbjct: 179 ATGKEPYFVGKPNPIMIRSALNKLGAHKSSTAMVGD RMDTDVVAGIEAGLTTYLVLTGST 238

Query: 265 RLEEAQAYLAAGQHDLVPHYYVESIADLT 293  
E+ Y PH VESIA+LT  
Sbjct: 239 DREDVSEYAYR-----PHRIVESIAELT 261

>ref|YP\_830014.1| HAD-superfamily hydrolase, subfamily IIA [Arthrobacter sp.  
FB24]  
Length = 276

Score = 95.9 bits (237), Expect = 3e-018  
Identities = 74/268 (27%), Positives = 113/268 (42%), Gaps = 19/268 (7%)

Query: 25 LFDCDGVLWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLRA 84  
L D DGV L + + +PGA EL++R K L ++NNS +LA R G +  
Sbjct: 24 LTDMDGVLVHENQPIPGAELIQRWVDTSKRFLVLTNNSIFTPRDLAARLRSSGLE-IPE 82

Query: 85 EQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXXR 144  
E +++S G A +  
Sbjct: 83 ENIWTSALATAQFLKQVGRSDSGNRAYTIGEAGLTTALHEAGFILTDQNPDF----- 135

Query: 145 VRVAVLVGYDEHFSFAKLREACALRDPECLLVATDRDPWHPLSDGSRTPGTGSLAAAVET 204  
V++G +SF + A L + +AT+ D P DG P TG++AA +  
Sbjct: 136 ---VVLGETRTYSFEAITMAI-RLILAGARFIATNP DATGPSKDGPM-PATGAIAALITK 190

Query: 205 ASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMTTVLTLTGVS 264  
A+GR+ +VGKP+P MF T M+GDR++TDI+ G G+ TVL L+G++  
Sbjct: 191 ATGREPYIVGKPNPMMFRSAMNQIDAHSETTAMIGDRMDTDIIAGMEAGLHTVLVLSGIT 250

Query: 265 RLEEAQAYLAAGQHDLVPHYYVESIADL 292  
++ AY P+ + S+ADL  
Sbjct: 251 HKDDIAAY-----PFRPNQILNSVADL 272

>ref|XP\_001400325.1| hypothetical protein An02g11970 [Aspergillus niger]



Length = 268

Score = 95.5 bits (236), Expect = 4e-018  
Identities = 72/248 (29%), Positives = 105/248 (42%), Gaps = 23/248 (9%)

Query: 12 AALRDVLGRAQGVLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNSRRARPELA 71  
A +++ L + LFDCDGVW+G+ PG E LE L R GK +FV+NNS ++R +  
Sbjct: 25 AGIQEFLDKFDVFLFDCDGVWNGDHLFPGTNETLEMLRRKKGQVVFVTNNSTKSRADYN 84

Query: 72 LRFARLGFGLRAEQLFSSXXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXX----- 126  
+ LG E++FSS PP+ VFV  
Sbjct: 85 KKLTAALGIPS-NTEEIFSSSYSASIIYISRILSLPPN-KRKVFVIGETGIEQELASENVPF 142

Query: 127 -----XXXXXXXXXXXXXXXXXXXXRVRVAVLVGYDEHFSFAKLREACAHLRDPE 172  
V VLVG D H ++ KL A ++R  
Sbjct: 143 IGGTDPAYRRDITPEDYKDIAGDSSTLLDPEVGVVVLVGLDFHINYFKLALAYHYIR-RG 201

Query: 173 CLLVATDRDPWHPLSDGSRTPGTGLAAAVETASGRQALVVGKPSPYMFECITENFSIDP 232  
+ +AT+ D P + G+ PG GS++A + G++ +GKP+ M + I F D  
Sbjct: 202 AVFLATNIDSTLP-NSGTLPFGAGSMSAPLIMMLGKEPTSLGKPNQAMMDAIEGKFRFDR 260

Query: 233 ARTLMVGD 240  
+R MVGD  
Sbjct: 261 SRACMVGD 268

>ref|YP\_001635630.1| HAD-superfamily hydrolase, subfamily IIA [Chloroflexus aurantiacus  
J-10-fl]  
Length = 273

Score = 95.5 bits (236), Expect = 4e-018  
Identities = 84/276 (30%), Positives = 122/276 (44%), Gaps = 24/276 (8%)

Query: 22 QGVLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGG 81  
+ VLFD DGVL+ G+ +PG +L + L A +NN+ + + A +G  
Sbjct: 13 RAVLFDMDGVLYRGQTPLPGVSDLFQFLTEQQIAFACATNNASMTPOQYEAKLAAMGIT- 71

Query: 82 LRAEQLFSSXXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 141  
L A+++ +S P A VFV  
Sbjct: 72 LPADRVITSAQATARYLRDQYP----AGTRVFFVGMQGLREALFADGYFVEDDQSPDL-- 125

Query: 142 XXRVAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGLAAA 201  
V+ G D ++ +L+ A H+R ++T+ D P +G PG G++AAA  
Sbjct: 126 -----VVQGADFTLTYDRLKRATLHIRRG-ARFISTNPDRTPFPSEEGL-IPGAGAVAAA 177

Query: 202 VETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDLETDILFGHRCGTTVLTLT 261  
+ A+ LV+GKPS MF PA+TL+VGDRL+TDI M +VL LT  
Sbjct: 178 LSAATDVTPLVIGKPSPTMFLIGATLLGATPAQTLVVGDRDLDTDIAGAIANMPSVLVLT 237

Query: 262 GVSRLAEAQAYLAAGQHDLVPHYYVESIADLTEGLE 297  
GVS L A+A + DL+ +ADL E LE  
Sbjct: 238 GVSTL--AEATTGPIRPDLI-----VADLPELLE 264

>gb|ABY48803.1| Hypothetical protein K02D10.1c [Caenorhabditis elegans]  
Length = 299

Score = 94.7 bits (234), Expect = 7e-018  
Identities = 52/140 (37%), Positives = 79/140 (56%), Gaps = 1/140 (0%)

Query: 146 RAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLS-DGSRTPGTGSGLAAAVET 204  
+AV+ YD HFS+ K+ +A +L+DP + T++D P G PG+G+ +AAV  
Sbjct: 152 KAVVCSYDAHFSYPKIMKASNYLQDPSVEYLVTNQDYTFPGVPVPGVVIPGSGATSAAVTA 211

Query: 205 ASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLLETDILFGHRCGMTTVLTLTGVS 264  
+GR V GKP M + + +DP RT+M GDRL+TDI+FG+ G ++V TGV  
Sbjct: 212 VTGRDPKVFVGKPHKPMADFLLRRAHVDPKRTVMFGDRLDTDIMFGNANGFSSVWMPGTGVH 271

Query: 265 RLEEAQAYLAAGQHDLVPHY 284  
+ + GQ D +P +  
Sbjct: 272 TIVDIHNAKEKGLDRIPTF 291

Score = 47.8 bits (112), Expect = 0.001  
Identities = 27/75 (36%), Positives = 38/75 (50%), Gaps = 1/75 (1%)

Query: 16 DVLGRAQGVLFDCDGVWNGERAVPGAPPELLERLARAGKAALFV-SNNSRRARPELALRF 74  
++L LFD DGVLW G+ VPGA E + L +FV +NNS + + +  
Sbjct: 10 ELLANYDTFLFDADGVLTGDI PVPGAIEWINLLLEDPSKKVFLVLTNNSTKTLEQYMKKI 69

Query: 75 ARLGFGGLRAEQFLS 89  
+LGFG L + S  
Sbjct: 70 EKLGFHGLGRNNVIS 84

>ref|YP\_289818.1| HAD-superfamily hydrolase, subfamily IIA [Thermobifida fusca YX]  
Length = 269

Score = 94.7 bits (234), Expect = 7e-018  
Identities = 70/248 (28%), Positives = 104/248 (41%), Gaps = 17/248 (6%)

Query: 25 LFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGGLRA 84  
L D DGVL E VPGA + + L G + ++NNS +L R R G +  
Sbjct: 10 LMDMDGVLVREEHLVPGADQFVAELRANGTRFMVLTNNSIYTPRDLRARLLRSGLD-IPE 68

Query: 85 EQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXR 144  
E +++S PG G+ +V  
Sbjct: 69 ESIWTSALATARFLQEQRPG-----GSAYVIGESGLTTALHNAGYVLTDSDPDY----- 117

Query: 145 VRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGSGLAAAVET 204  
V++G +SF + A L + +AT+ D P +GS P TG++AA +E  
Sbjct: 118 ---VVLGETRTYSFEAITRAI-RLVENGARFIATNPDEKGPSREGS-LPATGAVAALIEK 172

Query: 205 ASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLLETDILFGHRCGMTTVLTLTGVS 264  
A+GR VGKP+P M T+M+GDR++TD+ G GM T+L LTG+S  
Sbjct: 173 ATGRSPYYVVGKPNPLMMRSALRTLGAHSENTVMIGDRMDTDVRSGLEAGMKTILVLTGIS 232

Query: 265 RLEEAQAY 272  
A+ +  
Sbjct: 233 DASTAERF 240

>ref|YP\_001709025.1| putative N-acetylglucosamine-6-phosphate deacetylase  
[Clavibacter  
michiganensis subsp. sepedonicus]  
Length = 265

Score = 94.4 bits (233), Expect = 9e-018  
Identities = 72/250 (28%), Positives = 113/250 (45%), Gaps = 21/250 (8%)

Query: 25 LFDGCDGVLWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLRA 84  
L D DGVL + +A+PGA L+++ GK L ++NNS +L+ ARL GL  
Sbjct: 11 LTDMGDLVHENQALPGAAALIQQWQDQGKPFVLVLTNNSIFTPRDLS---ARLRASGLHV 67

Query: 85 EQ--LFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 142  
+ +++S PG G+ FV  
Sbjct: 68 PESAIWTSALATAAFLEQQMPG-----GSAFVIGEAGLTTALHEAGFIMTDT----- 114

Query: 143 XRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGSAAAV 202  
+ V++G ++SF + A L + +AT+ D P ++G P TG++ A +  
Sbjct: 115 -KPDYVVIGETRNYSFEAITRAI-RLINGGARYIATNPDATGPSAEGV-LPATGAVLALI 171

Query: 203 ETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMTTTLTLTG 262  
A+G++ +VGKP+P MF T M+GDR++TDI+ G G+ TVL LTG  
Sbjct: 172 SKATGKEPYIVGKPNPMMFRSALNKIGAHSESTGMIGDRMDTDIIAGIEAGLHTVLVLTG 231

Query: 263 VSRLEEAQAY 272  
+S E + Y  
Sbjct: 232 ISDRAEIERY 241

>gb|AAM49997.1| RE47284p [Drosophila melanogaster]  
Length = 305

Score = 94.4 bits (233), Expect = 9e-018  
Identities = 74/282 (26%), Positives = 114/282 (40%), Gaps = 11/282 (3%)

Query: 24 VLFDCDGLWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLR 83  
V+ DCDGV+W +P + L AGK FVSNNS R+ + +F +G ++  
Sbjct: 25 VISDCDGVVWLLVWIPNTGAAVNALKAAGKQIKFVSNNSFRSEEDYMEKFRHIGAKNVQ 84

Query: 84 AEQLFSSXXXXXXXXXXXXXXXXPGPP-----DAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 138  
+ + PG +  
Sbjct: 85 EDDIVHPVKTIVRYLKKHKPGERVYSLMSLEANETLRKHNIEFESLQVKEHLTAASLVDH 144

Query: 139 XXXXXRVRAVLVGYDEHFSFAKLREACAHLRD-PECLLVATDRDPWHPLSDGSRTPGTGS 197  
V AVL S+ +L +A HL++ +C L+A D PL++ G  
Sbjct: 145 LAIEKPVGAVLFDIHLDSLVELAKAIRHLQENDDCQLIAGGSDVIMPLAENLNVAGFFD 204

Query: 198 LAAAVETASGRQALVVGKPSPYMFECITENFSI-DPARTLMVGDRLDILFGHRCGMTT 256  
V+ + R+A +GKPS + E E F I D R + +GD L D+ FG CG +  
Sbjct: 205 FLEHVKRYTQREATFLGKPSILGEMFEMFEIRDCKRCIFIGDTLVQDVQFGKACGFQS 264

Query: 257 VLTLTGVSRLLEEAQAYLAAGQHDLVPHYYVESIADLTEGLED 298  
+L L+G E+ + + P YY +S+AD T+ LE+  
Sbjct: 265 LLVLSGCLTKED----MLNAPVEAQPDIYADSLADFTQLLEN 302

>ref|NP\_570021.1| CG2680 CG2680-PA [Drosophila melanogaster]  
Length = 336

Score = 94.4 bits (233), Expect = 9e-018  
Identities = 74/282 (26%), Positives = 114/282 (40%), Gaps = 11/282 (3%)

Query: 24 VLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLR 83  
V+ DCDGV+W +P + L AGK FVSNNS R+ + +F +G ++  
Sbjct: 56 VISDCDGVVWLLVGWIPNTGAAVNALKAAGKQIKFVSNNSFRSEEDYMEKFRHIGAKNVQ 115

Query: 84 AEQLFSSXXXXXXXXXXXXPGPP-----DAPGAVFVXXXXXXXXXXXXXXXXXXXX 138  
+ + PG +  
Sbjct: 116 EDDIVHPVKTIIVRYLKKHKPGERVYSLMSLEANETLRKHNIEFESLQVKEHLTAASLVDH 175

Query: 139 XXXXXRVRAVLVGYDEHFSFAKLREACALHRD-PECLLVATDRDPWHPLSDGSRTPGTGS 197  
V AVL S+ +L +A HL++ +C L+A D PL++ G  
Sbjct: 176 LAIEKPVGAVLFDIHLDSLVELAKAIRHLQENDDCQLIAGGSDVIMPLAENLNVAGFFD 235

Query: 198 LAAAVETASGRQALVVGKPSPYMFECITENFSI-DPARTLMVGDRLETDILFGHRCGMMT 256  
V+ + R+A +GKPS + E E F I D R + +GD L D+ FG CG +  
Sbjct: 236 FLEHVKRYTQREATFLGKPSILGEMFEMFEIRDCKRCIFIGDTLVQDVQFGKACGFQS 295

Query: 257 VLTLTGVSRLAEAQAYLAAGQHDLVPHYVYESIADLTEGLED 298  
+L L+G E+ + + P YY +S+AD T+ LE+  
Sbjct: 296 LLVLSGCLTKED----MLNAPVEAQPDIYADSLADFTQLLEN 333

>emb|CAB56540.1| p-nitrophenylphosphatase [Saccharomyces cerevisiae]  
Length = 312

Score = 94.4 bits (233), Expect = 9e-018  
Identities = 80/293 (27%), Positives = 124/293 (42%), Gaps = 21/293 (7%)

Query: 15 RDVLGRAQGVLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNSRRARPELALRF 74  
++ L + LFDCDGVW G +A+P E+L+ L + GK +FV+NNS ++R +F  
Sbjct: 18 QEFLDKYDTFLFDCDGVWLGSQLPYTLEILDLLKQLGKQLIFVTNNSTKSRLAYTKKF 77

Query: 75 ARLGFGLRAEQLFSSXXXXXXXXXXXXPGPPDAPGA-VFVXXXXXXXXXXXXXXXXXXXX 133  
A G ++ EQ+F+S P VF  
Sbjct: 78 ASFGI-DVKEEQIFTSGYAPAVYIRDFLKLQPGKDKVWVFGESGIGEELKLMGYESLGG 136

Query: 134 XXXXXXXXXXXRVRAVLV-GYDEHFS-----FAKLREACALHRDPECLLVATDRD 181  
LV G D+ S + +L +L+ V T+ D  
Sbjct: 137 DSRLDTPFDDAKSPFLVNLGDKDVCVIAGLDTKVNYHRLAVTLQYLQKDSVHFVGTNVD 196

Query: 182 PWHPLSDGSRTPGTGSLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDR 241  
P G PG GS+ ++ +S R+ GKP+ M I F++D ++ MVGDR  
Sbjct: 197 STFP-QKGYTFPGAGSMIESLAFSSNRRPSYCGKPNQNMNSIISAFNLDRSKCCMVGDR 255

Query: 242 LETDILFGHRCGM-TTVLTLTGVSRLAEAQAYLAAGQHDLV-PHYVYESIADL 292  
L TD+ FG G+ T+L L+G+ E + HD P +Y++ + D+  
Sbjct: 256 LNTDMKFGVEGGLGGTLLVLSGI----ETEERTLKISHDYPRPKFYIDKLGDI 304

>ref|NP\_627072.1| N-acetylglucosamine-6-phosphate deacetylase [Streptomyces  
coelicolor A3(2)]  
Length = 259

Score = 94.4 bits (233), Expect = 9e-018  
Identities = 75/270 (27%), Positives = 117/270 (43%), Gaps = 23/270 (8%)

```
Query: 25  LFDCDGVLVNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLRA 84
           L D DGVL + +PGA ++RL +GK L ++NNS +L R R+G +
Sbjct: 11  LTDMDGVLIHEGVPIPGADAFIKRLRDSGKPFVLVTNNSIYTPRDLHARLRMGLE-VPI 69

Query: 85  EQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXXR 144
           E +++S PG G+ +V
Sbjct: 70  ESIWTSALATAQFLEDQRP-----GSAYVIGEAGLTTALHDIGYILTDHDPDY----- 118

Query: 145 VRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGS�AAVET 204
           V++G +SF + +A L + + T+ D P ++G P TG++AA +
Sbjct: 119 ---VVLGETRRTYSFEAMTKA-VRLINAGARFICTNPDETGPSTEGP-LPATGAVAALITK 173

Query: 205 ASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMTTTLTGTGS 264
           A+G+Q GKP+P M + M+GDR++TD+L G GM T L LTG++
Sbjct: 174 ATGKQPYFAGKPNPLMMRTGLNAIGAHSETSAMIGDRMDDVLAGMEAGMOTFLVLTGLT 233

Query: 265 RLEEAQAYLAAGQHDLVPHYYVESIADLTE 294
           R E+ + + P V+SIADL E
Sbjct: 234 RPEQVENF-----PYRPSQVVDSIADLVE 257
```

>ref|ZP\_02945756.1| HAD-superfamily hydrolase, subfamily IIA [Micrococcus luteus NCTC 2665]  
Length = 276

Score = 93.6 bits (231), Expect = 1e-017  
Identities = 81/249 (32%), Positives = 105/249 (42%), Gaps = 14/249 (5%)

```
Query: 23  GVLFDGCDGVLVNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGL 82
           G+L D DGV++ G A+ GA E L L G FV+NN+ RA +A LG
Sbjct: 11  GLLCDLDGVVYAGGGAIAGAVETLSTLQEQGVVPGFVTNNASRAPESVAEHLRTLGVPA- 69

Query: 83  RAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 142
           A Q+F S G V V
Sbjct: 70  EAGQVFGSAPAGVDLLEETLGR---RTGRVLVVGSAYLRAVVEERGYEVVASAAQCPD-- 124

Query: 143 XRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGS�AAV 202
           AV+ G+D +A L EA +R VAT+ D P ++G PG G+L AV
Sbjct: 125 ----AVIQGFDPLGWADLAEAAAYAVR-AGATWVATNLDTSIPRAEGI-APGNALVEAV 178

Query: 203 ETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMTTTLTGT 262
           A+G + GKP P +F E + AR L+VGDRL+TDI G+ G TVL LTG
Sbjct: 179 GRATGTAPVAAGKPEPRLFRTAAEALGL--ARPLVVGDRLDITDIRGGNAAGFDTVLVLTG 236

Query: 263 VSRLEEAQA 271
           + E A A
Sbjct: 237 IDTRETAAA 245
```

>ref|XP\_001617155.1| phosphoglycolate phosphatase precursor, putative [Plasmodium vivax SaI-1]

Length = 314

Score = 93.6 bits (231), Expect = 1e-017  
Identities = 49/147 (33%), Positives = 89/147 (60%), Gaps = 3/147 (2%)

Query: 145 VRAVLVGDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGSAAVET 204  
V AV+V D + ++ K++ A + + + + +++D + + GTGS+ A+VE  
Sbjct: 169 VGAVVVAIDFNINYYKIQYAHLCINELDAEFIVSNKDATANFTSKQKWAGTGSVVASVEA 228

Query: 205 ASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMTTVLTGTGVS 264  
S ++ V+GKP+ +M E + ++ +IDP++ +MVGDR+TDI F C + +VL +GV+  
Sbjct: 229 VSLKKPTVLGKPNLFMIENVLKDNLIDPSKVVMVGDRDLDTDISFAKNCNIKSVLVSSGVT 288

Query: 265 RLEEAQAYLAAGQHDLVPHYYVESIAD 291  
+A YL ++ P Y+++SIAD  
Sbjct: 289 ---DANIYLNHNHLNIQPDYFMKSIAD 312

Score = 63.2 bits (152), Expect = 2e-008  
Identities = 27/66 (40%), Positives = 41/66 (62%)

Query: 22 QGVLFDCDGLWNGERAVPGAPPELLERLARAGKAALFVSNNRRARPELALRFARLGFGG 81  
+ FDCDGLW G + GA E++ +L +A K F++NNS ++R L +F +LGFG  
Sbjct: 36 EAFFFDCDGLWNGEVIQGAVEVINKLVKANKQIYFITNNSIKSRATLLEKFHQLGFGL 95

Query: 82 LRAEQL 87  
+ E +  
Sbjct: 96 TKKENI 101

>ref|YP\_001102845.1| HAD-superfamily hydrolase, subfamily IIA  
[Saccharopolyspora  
erythraea NRRL 2338]  
Length = 264

Score = 93.6 bits (231), Expect = 1e-017  
Identities = 77/274 (28%), Positives = 114/274 (41%), Gaps = 23/274 (8%)

Query: 25 LFDCDGLWNGERAVPGAPPELLERLARAGKAALFVSNNRRARPELALRFARLGFGGLRA 84  
L D DGVL + E VPGA L L + +NNS +L R R G +  
Sbjct: 10 LMDMDGLVHEEHMVPGADTFNLALREHDIPFMVFTNNSIYTPRDLRARLHRTGLD-VPE 68

Query: 85 EQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXXXR 144  
E +++S PG G+ FV  
Sbjct: 69 EAIWTSALATAQFLEKQRPG-----GSAFVVGESGLTTALHNIGYVLTDRPDY----- 117

Query: 145 VRAVLVGDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGSAAVET 204  
V++G +SF + +A L + +AT+ D P +G+ P TG++AA +E  
Sbjct: 118 ---VILGETRTYSFEAITKAI-RLVEGGARFIATNPDEKGPSREGT-LPATGAVAALIER 172

Query: 205 ASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMTTVLTGTGVS 264  
+GR VGKP+P M + TLM+GDR++TD+ G G+ T+L L+G+S  
Sbjct: 173 VTGRAPYYVVGKPNPLMMRSALRQLGVHSENTLMIGDRMDTDVRSGLSGLQTILVLSGIS 232

Query: 265 RLEEAQAYLAAGQHDLVPHYYVESIADLTEGLED 298  
A+ + P V SIADL E ++D

Sbjct: 233 DEHTAELF-----PYRPTKVVRSIADLIEHVKD 260

>gb|AAC38756.1| putative N-glyceraldehyde-2-phosphotransferase [Streptococcus pneumoniae]  
Length = 277

Score = 93.6 bits (231), Expect = 1e-017  
Identities = 68/273 (24%), Positives = 118/273 (43%), Gaps = 21/273 (7%)

Query: 25 LFD CDGVLWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLRA 84  
LFD DG ++ +R G ELL+ + G +F++NNS ++ + + RLG R  
Sbjct: 24 LFDMDGTIYEEDRLFEGTLELLDYIHNIGGEYIFITNNSKSVVDYVEKVNRLGIKAER- 82

Query: 85 EQLFSSXXXXXXXXXXXXXP-GPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 143  
+ F+S P G F+  
Sbjct: 83 DNFF TSAQATIVYIKENYPKSKVY CQGTKFLIKELSDAGIDVTEQVSAD----- 131

Query: 144 RVRVAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGLAAAVE 203  
+ VLVG+D + K+R C L + +AT+ D P+S G P GS+ +  
Sbjct: 132 -IDVVLVGFDELTSDKIRNTCEILSTKDVPIATNPDIRCPVSFGF-IPDCGSICDMIS 189

Query: 204 TASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLTDILFGHRCGMTTVLTLTG 263  
+ R+ + +GKP P M + + + + T+++GDRL TDI+ G G+T+V LTG  
Sbjct: 190 KSVDRKPVYIGKPEPTMVDIVRKKLNYSLFETVVI GDRLYTDIMTGINAGVTSVCVLTGE 249

Query: 264 SRLEEAQAYLAAGQHDLVPHYYVESIADLTEGL 296  
+ + + Q Q + P Y +++ ++ +G+  
Sbjct: 250 ATVNDIQ-----QDSIKPTYTFKNVKEMWKG I 276

>ref|YP\_482968.1| HAD-superfamily hydrolase, subfamily IIA [Frankia sp. CcI3]  
Length = 301

Score = 93.6 bits (231), Expect = 1e-017  
Identities = 74/274 (27%), Positives = 117/274 (42%), Gaps = 23/274 (8%)

Query: 22 QGVLFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRFARLGF 81  
+ L D DGVL + E +PGA L + AG L ++NNS +L+ R A G  
Sbjct: 7 ENYLIDMDGVLVHEEHP I PGADAFLAGIGEAGLGLVLTNNSIYTARDLSARLAGAGLT- 65

Query: 82 LRAEQLFSSXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 141  
+ E++++S P G+ +V  
Sbjct: 66 IPPERIWTSALATALFLHTQRPR-----GSAYVVG EAGLTTALHDIGYVLSDRSPDY--- 117

Query: 142 XXRVAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGLAAA 201  
V++G +SF + +A +RD +AT+ DP P +G P TG++AA  
Sbjct: 118 -----VVLGETRTYSFEAITKAVRLVRDG-ARFIATNPDP TGPSVEGL-LPATGAVAAM 169

Query: 202 VETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLTDILFGHRCGMTTVLTLT 261  
+ A+G VGKP+P M S T+++GDR++TD++ G GM TVL L+  
Sbjct: 170 ITRATGVTPYFVGKPNPLMMSALNTLSAHSETTVVIGDRMDTDVVAGLEAGMDTVLVLS 229

Query: 262 GVSRLLEEAQAYLAAGQHDLVPHYYVESIADLTEG 295  
G++ + + + P V+SIA L G  
Sbjct: 230 GITSITDVDRF-----PYRPTAIVDSIAQLPVG 257

>ref|YP\_327037.1| probable sugar phosphatase [Natronomonas pharaonis DSM 2160]

Length = 261

Score = 93.6 bits (231), Expect = 1e-017

Identities = 77/276 (27%), Positives = 114/276 (41%), Gaps = 22/276 (7%)

Query: 23 GVLFD CDGVLWNGERAVPGAPPELLERLARAGKAALFVSNNRRARPELALRFARLGFGL 82  
G + D DG ++ G +PGA + RL G +F SNN ++R A R + LG +  
Sbjct: 5 GAVL DLDGTIYRGSELLPGAAA VRRRLRELGIRPVFFSNNPTKRSR SAYADRLSELGID-V 63

Query: 83 RAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 142  
E + S+ GA+F+

Sbjct: 64 GPESVLSAGTVTTRFLADEH-----GDGAI FLVGD DGLRRQFEAAGLHVVEEATAAD--- 115

Query: 143 XRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGLAAAV 202  
++V + + F + L L TD D P G PG+G++ AV

Sbjct: 116 ----VLVSWTDKFDYGDLLAGYRALNSG-ATFYGTDPDR LIPAESGM-APGSGAI INAV 169

Query: 203 ETASGRQ-ALVVGKPSPYMFECITENFSIDPARTLMVGDRL ETDILFGHRCGMTTVLTLT 261  
GR+ A ++GKPS P R L++GDRL+TDI G GMTTVL T

Sbjct: 170 GGVVGREPAKILGKPSPEARAAALSALDAPPERCLVIGDR LDTDIALGAAAGMTTVLVET 229

Query: 262 GVSRL EEAQAYLAAGQHDLVPHYYVESIADLTEGLE 297  
G+ +A+A + G+ P Y +ES+A+L + LE

Sbjct: 230 GI----DAEADI--GESR RTPDYVIESLAELEQVLE 259

>ref|YP\_001179034.1| HAD-superfamily hydrolase, subfamily IIA  
[Caldicellulosiruptor

saccharolyticus DSM 8903]

Length = 279

Score = 93.6 bits (231), Expect = 1e-017

Identities = 71/282 (25%), Positives = 125/282 (44%), Gaps = 16/282 (5%)

Query: 16 DVLGRAQGVLFDCD GVLWNGERAVPGAPPELLERLARAGKAALFVSNNRRARPELALRFA 75  
+VL + L D DG ++ G+R G+ E ++ L K LF++NNS ++ + + +

Sbjct: 7 EVLSKVDLFLLDMDGTIYLGDR LFEGSREFVQLLKENK EFLFLTNNSSKSSDDYLK KLS 66

Query: 76 RLGFGGLRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 135  
++G + E L +S D AV

Sbjct: 67 KMGIE-IAKENLLTSGQATAIYLKSI-----DQRS AV---SAYVVGTQSLKDELKSFGIN 117

Query: 136 XXXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGT 195  
V ++VG+D ++ KL +AC +R L AT+ D PL G P

Sbjct: 118 VVGSIEKEDVDYLIVGFDTELT YKLLLDACKLIRKGV PFL-ATNPDLVCPLDGGEYIPDC 176

Query: 196 GSLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRL ETDILFGHRCGMT 255  
GS+ +E A+ ++ L +GKPS + + I++ +++ ++ M+GDRL TDI + GM

Sbjct: 177 GSICIMLENATKKKPLFIGKPSIIIVDVISKFKNVEKSKIAMIGDR LYTDIKMANDNGMI 236

Query: 256 TVLTLTGVSRL EEAQAYLAAGQHDLVPHYYVESIADLTEGLE 297  
++L L+G + E+ + + + P SI D+ E L+

Sbjct: 237 SILVLSGETTYEDVEKF-----QVKPTLIYNSIKDIYEDLK 272



>ref|YP\_001420195.1| hypothetical protein RBAM\_005720 [Bacillus  
amyloliquefaciens FZB42]  
Length = 411

Score = 93.2 bits (230), Expect = 2e-017  
Identities = 64/234 (27%), Positives = 114/234 (48%), Gaps = 19/234 (8%)

Query: 25 LFD CDGVLWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLRA 84  
LFD DGV++ G++A+PGA L+RL KA F++N+ R + R +LG  
Sbjct: 10 LFDLDGVIYIGDKALPGAVASLKRLEEKKAIRFLTNDPCVTRETIVKRLHKLGISI-SI 68

Query: 85 EQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXXXR 144  
+++F++ A V +  
Sbjct: 69 DEVFTAGW-----ATADYLVSEGIKKAYILGNDQLKSEIQKAGIDLTEDQ 113

Query: 145 VRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGSAAAVET 204  
AV++G+D++ +F + +A +R +A + D P ++G P TG++ AAV+T  
Sbjct: 114 AEAVVIGWDQNITFQDVHKAVNLIRCGASF-IAANGDKTFPAANGP-APATGAIVA AVKT 171

Query: 205 ASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLLET DILFGHRCGM TTVL 258  
A+ ++ +++GKP+ +FE + E+F D R +M+GD ETDI+ ++ G+T+VL  
Sbjct: 172 AAAKEPIIIGKPASSIFEKVLESFE-DKERCVMIGDTPETDIVGANQIGITSVL 224

>ref|YP\_658016.1| putative N-acetyl-glucosamine catabolism protein  
[Haloquadratum  
walsbyi DSM 16790]  
Length = 263

Score = 93.2 bits (230), Expect = 2e-017  
Identities = 72/273 (26%), Positives = 115/273 (42%), Gaps = 23/273 (8%)

Query: 25 LFD CDGVLWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLRA 84  
L D DGV L + A+PG+ + + +L + L ++NN+ R +LA + +G +  
Sbjct: 12 LIDMDGVLIRDDTALPGSEDFIHQLREQKRQFLVLTNNAIYTRDLAAHLSEVGIN-IPE 70

Query: 85 EQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXXXR 144  
+++++S P DA V  
Sbjct: 71 DRIWTSAVATAQFVSNQMP---DASAYVI-----GEAGLKTALHDVGYTLTSTN 116

Query: 145 VRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGSAAAVET 204  
V++G +SF + EA L + + T+ D P ++G P TGS+AA +  
Sbjct: 117 PDFVVLGESRTYSFQNITEA-VRLVNQGARFIVTNP DATAPSAEGP-LPATGSVAALITE 174

Query: 205 ASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLLET DILFGHRCGM TTVLTLTGVS 264  
A+G+ VGKP+P M T MVGDR++TD++ G G+ T L LTG +  
Sbjct: 175 ATGKNPYFVGKPNPIMIRSALNRLGAHKSSTAMVGD RMDTDVVAGIEAGLITYLVLTGST 234

Query: 265 RLEEAQAYLAAGQHDLVPHYYVESIADLTEGLE 297  
++ Y P+ VESIADL +E  
Sbjct: 235 NRQDVSEYAYR-----PNKIVESIADLMGTIE 261

>emb|CAI34063.2| putative phosphotransferase [Streptococcus pneumoniae]  
Length = 277

Score = 93.2 bits (230), Expect = 2e-017  
Identities = 66/272 (24%), Positives = 115/272 (42%), Gaps = 19/272 (6%)

Query: 25 LFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNRRARPELALRFARLGFGLRA 84  
LFD DG ++ +R G ELL+ + G +F++NNS ++ + + RLG R  
Sbjct: 24 LFDMDGTIYEEDRLFEGTLELLDYIHNIGGEYIFITNNSKSVVDYVEKVNRLGIKAER- 82

Query: 85 EQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXXR 144  
+ F+S P  
Sbjct: 83 DNFF TSAQATIVYIKENYP-----KSKVYCQGTKSLIKELSDAGIDVTEQVSAD 131

Query: 145 VRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGSLAAAVET 204  
+ VLVG+D + K+R C L + +AT+ D P+S G P GS+ +  
Sbjct: 132 IDVVLVGFDTLTSKIRNTCEILSTKDAPFIATNPDIRCPVSFGF-IPDCGSICDMISK 190

Query: 205 ASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMTTTLTGVS 264  
+ R+ + +GKP P M + + + + T+++GDRL TDI+ G G+T+V LTG +  
Sbjct: 191 SVDREPVYIGKPEPTMVDIVRKKLNYSLFETVVIGDRLYTDIMTGINAGVTSVCVLTGEA 250

Query: 265 RLEEAQAYLAAGQHDLVPHYYVESIADLTEGL 296  
+ + Q Q + P Y +++ ++ +G+  
Sbjct: 251 TVNDIQ-----QGSIKPTYTFKNVKEMWKGI 276

>ref|NP\_444200.1| p-nitrophenyl phosphatase [Halobacterium sp. NRC-1]  
Length = 257

Score = 93.2 bits (230), Expect = 2e-017  
Identities = 73/253 (28%), Positives = 100/253 (39%), Gaps = 19/253 (7%)

Query: 22 QGVLFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNRRARPELALRFARLGFGL 81  
+GV+ D DG + G+ +PGA + L A LF++NN R E A R LG  
Sbjct: 4 RGVVLDLDTGLRGTLLPGAKAGVAALREHADAVLFLTNNPMRPASEHAARLEGLGVDA 63

Query: 82 LRAEQLFSSXXXXXXXXXXXXXXXXPGP--PDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXX 139  
E L ++ P A A +  
Sbjct: 64 TPGEVLTATDATITYLQRSHDGAAVYPIAADAITTLRAAGVAITADPVAAD----- 115

Query: 140 XXXXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGSLA 199  
V+ G+D F F L+ A D LV TD D P +DG++ PG+G++  
Sbjct: 116 -----VVVAGFDPAFGFQDLQAAVDAFADGTTALVGTDPDITIPAADGAK-PGSGAIV 167

Query: 200 AAVETASGRQA-LVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMTTTL 258  
AV + R V+GKPS + + PA L+VGDR +TD+ G GMTT L  
Sbjct: 168 QAVAGVAERDPDAVLGKPSSETTARLAVDRLGVPPAECLVVGDRPDTDVALGAAAGMTTAL 227

Query: 259 TLTGVSRLLEEAQA 271  
TGV A A  
Sbjct: 228 VRTGVDAATPAHA 240

>emb|CAM57980.1| para nitrophenyl phosphate phosphatase [Plasmodium falciparum]  
Length = 322

Score = 92.8 bits (229), Expect = 3e-017  
Identities = 47/148 (31%), Positives = 89/148 (60%), Gaps = 3/148 (2%)

Query: 145 VRAVLVGYDEHFSSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGLAAAVET 204  
 + AV+VG D + ++ K++ A + + +AT++D + + GTG++ +++E  
 Sbjct: 177 IGAVVVGIDFNINYYKIQYAQLCINELNAEFIATNKDATGNFTSKQKWAGTGAIVSSIEA 236

Query: 205 ASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMTTVLTLTGVS 264  
 S ++ +VVGKP+ YM E + ++ +I ++ +M+GDRLETDI F C + ++L TGV+  
 Sbjct: 237 VSLKKPIVVGKPNVYMIENVLKDLNIHHSKVVMIIGDRLETDIHFACNKNISILVSTGVT 296

Query: 265 RLEEAQAYLAAGQHDLVPHYYVESIADL 292  
 A YL ++ P Y+++SI++L  
 Sbjct: 297 ---NANIYLNHNSLNIHPDYFMKSISEL 321

Score = 60.5 bits (145), Expect = 1e-007  
 Identities = 25/62 (40%), Positives = 39/62 (62%)

Query: 26 FDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNRRARPELALRFARLGFGLRAE 85  
 FDCDGVW+G + G+ E++ L R GK F++NNS ++R +F +LGF ++ E  
 Sbjct: 48 FDCDGVWLNHGNELIEGSIEVINYLREGKVVYFITNNSTKSRASFLEKFKLGFNTVKRE 107

Query: 86 QL 87  
 +  
 Sbjct: 108 HI 109

>ref|ZP\_01834510.1| NagD protein [Streptococcus pneumoniae SP23-BS72]  
 Length = 275

Score = 92.8 bits (229), Expect = 3e-017  
 Identities = 66/272 (24%), Positives = 115/272 (42%), Gaps = 19/272 (6%)

Query: 25 LFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNRRARPELALRFARLGFGLRA 84  
 LFD DG ++ +R G ELL+ + G +F++NNS ++ + + RLG R  
 Sbjct: 22 LFDMDGTIYEEDRLFEGTLELLDYIHNIGGEYIFITNNSKSVVDYVEKVNRLGIKAER- 80

Query: 85 EQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXXXR 144  
 + F+S P  
 Sbjct: 81 DNFF TSAQATIVYIKENYP-----KSKVYCQGTKSLIKELSDAGIDVTEQVSAD 129

Query: 145 VRAVLVGYDEHFSSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGLAAAVET 204  
 + VLVG+D + K+R C L + +AT+ D P+S G P GS+ +  
 Sbjct: 130 IDVVLVGFDTELTSDKIRNTCEILSTKDVFPFIATNPDIRCPVSFGF-IPDCGSICDMISK 188

Query: 205 ASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMTTVLTLTGVS 264  
 + R+ + +GKP P M + + + + T+++GDRL TDI+ G G+T+V LTG +  
 Sbjct: 189 SVDRKPVYIGKPEPTMVDIVRKKLNYSLFETVVIGDRLYTDIMTGINAGVTSVCVLTGEA 248

Query: 265 RLEEAQAYLAAGQHDLVPHYYVESIADLTEGL 296  
 + + Q Q + P Y +++ ++ +G+  
 Sbjct: 249 TVNDIQ-----QDSIKPTYTFKNVKEMWKG I 274

>ref|XP\_001349053.1| 4-nitrophenylphosphatase, putative [Plasmodium falciparum 3D7]  
 Length = 322

Score = 92.8 bits (229), Expect = 3e-017  
Identities = 47/148 (31%), Positives = 89/148 (60%), Gaps = 3/148 (2%)

Query: 145 VRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGSAAVET 204  
+ AV+VG D + ++ K++ A + + +AT++D + + GTG++ +++E  
Sbjct: 177 IGAVVVGIDFNINYYKIQYAQLCINELNAEFIATNKDATGNFTSKQKWAGTGAIVSSIEA 236

Query: 205 ASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMTTVLTLTGVS 264  
S ++ +VVGKP+ YM E + ++ +I ++ +M+GDRLETDI F C + ++L TGV+  
Sbjct: 237 VSLKKPIVVGKPNVYMIENVLKDLNIHHSKVVMIIGDRLETDIHFACNKNIKSILVSTGVT 296

Query: 265 RLEEAQAYLAAGQHDLVPHYYVESIADL 292  
A YL ++ P Y+++SI++L  
Sbjct: 297 ---NANIYLNHNSLNIHPDYFMKSISEL 321

Score = 60.5 bits (145), Expect = 1e-007  
Identities = 25/62 (40%), Positives = 39/62 (62%)

Query: 26 FD CDGVLWNGERAVPGAPPELLERLARAGKAALFVSNNRRARPELALRFARLGFGLRAE 85  
FD CDGVLW+G + G+ E++ L R GK F++NNS ++R +F +LGF ++ E  
Sbjct: 48 FD CDGVLWHGNELIEGSIEVINYLREGKQVYFITNNSKSRASFLEKFHKLGFNTVVKRE 107

Query: 86 QL 87  
+  
Sbjct: 108 HI 109

>gb|AAC69537.1| Cps23fN [Streptococcus pneumoniae]  
Length = 277

Score = 92.8 bits (229), Expect = 3e-017  
Identities = 66/272 (24%), Positives = 115/272 (42%), Gaps = 19/272 (6%)

Query: 25 LFDCDGVLWNGERAVPGAPPELLERLARAGKAALFVSNNRRARPELALRFARLGFGLRA 84  
LFD DG ++ +R G ELL+ + G +F++NNS ++ + + RLG R  
Sbjct: 24 LFDMDGTIYEEDRLFEGTLELLDYIHNIGGEYIFITNNSKSVVDYVEKVNRLGIKAER- 82

Query: 85 EQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXXR 144  
+ F+S P  
Sbjct: 83 DNFF TSAQATIVYIKENYP-----KSKVYCQGTKSLIKELSDAGIDVTEQVSAD 131

Query: 145 VRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGSAAVET 204  
+ VLVG+D + K+R C L + +AT+ D P+S G P GS+ +  
Sbjct: 132 IDVVLVGFDTLSTDKIRNTCEILSTKDVPF IATNPDIRCPVSFGF-IPDCGSICDMISK 190

Query: 205 ASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMTTVLTLTGVS 264  
+ R+ + +GKP P M + + + + T+++GDRL TDI+ G G+T+V LTG +  
Sbjct: 191 SIDRKPVIYIGKPEPTMVDIVRKKLNYSLFETVIGDRLYTDIMTGINAGVTSVCVLTGEA 250

Query: 265 RLEEAQAYLAAGQHDLVPHYYVESIADLTEGL 296  
+ + Q Q + P Y +++ ++ +G+  
Sbjct: 251 TVNDIQ-----QDSIKPTYTFKNVKEMWKG I 276

>emb|CAI33824.1| putative phosphotransferase [Streptococcus pneumoniae]  
Length = 277

Score = 92.8 bits (229), Expect = 3e-017  
Identities = 66/272 (24%), Positives = 115/272 (42%), Gaps = 19/272 (6%)

Query: 25 LFD CDGVLWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLRA 84  
LFD DG ++ +R G ELL+ + G +F++NNS ++ + + RLG R  
Sbjct: 24 LFDMDGTIYEEDRLFEGTLELLDYIHNIGGEYIFITNNSKSVVDYVEKVNRLGIKAER- 82

Query: 85 EQLFSSXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXXXR 144  
+ F+S P  
Sbjct: 83 DNFF TSAQATIVYIKENYP-----KSKVYCQGTKSLIKELSDAGIDVTEQVSAD 131

Query: 145 VRAVLVG YDEHFSFAKLREAC AHLRDPECLLVATDRDPWHPLSDGSRTPGTGSLAAAVET 204  
+ VLVG+D + K+R C L + +AT+ D P+S G P GS+ +  
Sbjct: 132 IDVVLVGFDTELTSDKIRNTCEILSTKDVPIATNPDIRCPVSFGF-IPDCGSICDMISK 190

Query: 205 ASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGTTVLTLTGVS 264  
+ R+ + +GKP P M + + + + T+++GDRL TDI+ G G+T+V LTG +  
Sbjct: 191 SVDRKPVYIGKPEPTMVDIVRKKLNYSLFETVVIGDRLYTDIMTGINAGVTSVCVLTGEA 250

Query: 265 RLEEAQAYLAAGQHDLVPHYVYESIADLTEGL 296  
+ + Q Q + P Y +++ ++ +G+  
Sbjct: 251 TVNDIQ-----QDSIKPTYTFKNVKEMWKGI 276

>emb|CAI33847.1| putative phosphotransferase [Streptococcus pneumoniae]  
Length = 283

Score = 92.8 bits (229), Expect = 3e-017  
Identities = 66/272 (24%), Positives = 115/272 (42%), Gaps = 19/272 (6%)

Query: 25 LFD CDGVLWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLRA 84  
LFD DG ++ +R G ELL+ + G +F++NNS ++ + + RLG R  
Sbjct: 30 LFDMDGTIYEEDRLFEGTLELLDYIHNIGGEYIFITNNSKSVVDYVEKVNRLGIKAER- 88

Query: 85 EQLFSSXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXXXR 144  
+ F+S P  
Sbjct: 89 DNFF TSAQATIVYIKENYP-----KSKVYCQGTKSLIKELSDAGIDVTEQVSAD 137

Query: 145 VRAVLVG YDEHFSFAKLREAC AHLRDPECLLVATDRDPWHPLSDGSRTPGTGSLAAAVET 204  
+ VLVG+D + K+R C L + +AT+ D P+S G P GS+ +  
Sbjct: 138 IDVVLVGFDTELTSDKIRNTCEILSTKDVPIATNPDIRCPVSFGF-IPDCGSICDMISK 196

Query: 205 ASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGTTVLTLTGVS 264  
+ R+ + +GKP P M + + + + T+++GDRL TDI+ G G+T+V LTG +  
Sbjct: 197 SVDRKPVYIGKPEPTMVDIVRKKLNYSLFETVVIGDRLYTDIMTGINAGVTSVCVLTGEA 256

Query: 265 RLEEAQAYLAAGQHDLVPHYVYESIADLTEGL 296  
+ + Q Q + P Y +++ ++ +G+  
Sbjct: 257 TVNDIQ-----QDSIKPTYTFKNVKEMWKGI 282

>ref|YP\_001536774.1| HAD-superfamily hydrolase, subfamily IIA [Salinispora arenicola  
CNS-205]

Length = 340

Score = 92.4 bits (228), Expect = 3e-017  
Identities = 81/272 (29%), Positives = 117/272 (43%), Gaps = 20/272 (7%)

Query: 24 VLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNRRARPELALRFARLGFGLR 83  
V+FD DGV++ +R +PGA E + +L G+A + +NN+ R E+A +G R  
Sbjct: 16 VVFDLDGVIYLVDRPIPGAVEAVSQLHADGQAVAYATNNASRRSSEVADLLTGMGIAA-R 74

Query: 84 AEQLFSSXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 143  
E++ +S P G+ +  
Sbjct: 75 PEEVLTSAAAAQLLRERYP-----EGSQILVVGAEALRAEIRAAGLTPVTRADDGPV-- 127

Query: 144 RVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGLAAAVE 203  
AV+ GY + L EA +R VAT+ D P G PG G+L AAV  
Sbjct: 128 ---AVVQGYGPQVGWTDLAEAAVAVRGG-ATWVATNTDRTLPSGRGP-LPGNGALVAAVR 182

Query: 204 TASGRQA-LVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMTTVLTLTG 262  
T+ GR ++VGKP+P +F + R L+VGDRL+TDI R G+ ++L LTG  
Sbjct: 183 TSLGRGPDVIVGKPAPELFAAAARR--VPAGRALVVGDRDLTDIEGAVRAGLDSLLVLTG 240

Query: 263 VSRLEEAQAYLAAGQHDLVPHYYVESIADLTE 294  
VS + E L A P Y +A L E  
Sbjct: 241 VSDVAE----LLAAPPQRRPTYVSVDLAGLFE 268

>ref|YP\_001512677.1| HAD-superfamily hydrolase, subfamily IIA [Alkaliphilus oremlandii OhILAs]  
Length = 263

Score = 92.4 bits (228), Expect = 3e-017  
Identities = 65/270 (24%), Positives = 119/270 (44%), Gaps = 19/270 (7%)

Query: 25 LFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNRRARPELALRFARLGFGLRA 84  
L D DG ++ G+ + GA + LE + GK +F++NNS +++ + +RLG A  
Sbjct: 11 LLDMDGTIYLGDELIDGAKKFLETIKNGKRYIFLTNNSKSKESYVEKLSRLGIEA-SA 69

Query: 85 EQLFSSXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXXR 144  
E++F+S G  
Sbjct: 70 EEVFTSGEATTMYLKKEKEG-----AKIYLLGTAALAEAFIQAGFVLEKERHKD 118

Query: 145 VRVAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGLAAAVET 204  
+ V++G+D ++ KL AC ++ + +AT D PL + P G++AA +E  
Sbjct: 119 IDYVVLGFDTTLTYEKLWAAACEYIAEG-VEYIATHPDFNCPLPNDKFMPPDAGAMAALIEA 177

Query: 205 ASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMTTVLTLTGVS 264  
++G++ V+GKP+ + E I + ++ +MVGDR L TDI G G+ + L +G +  
Sbjct: 178 STGKKPKVIGKPNKEVVESIALKYGLNKEDMVMVGDRLYTDIKTGKNAGIASALVYSGET 237

Query: 265 RLEEAQAYLAAGQHDLVPHYYVESIADLTE 294  
+ E+ + + ++ Y SI D+ +  
Sbjct: 238 KEEDYK-----KSEIRADYVFNSIKDMID 261

>gb|AAP76302.1| putative glyceraldehyde-2-phosphotransferase [Streptococcus pneumoniae]

Length = 277

Score = 92.4 bits (228), Expect = 3e-017  
Identities = 66/272 (24%), Positives = 115/272 (42%), Gaps = 19/272 (6%)

```
Query: 25  LFDCDGVLWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLRA 84
          LFD DG ++ +R  G  ELL+ +  G  +F++NNS ++ +  +  RLG  R
Sbjct: 24  LFDMDGTIYEEDRLFEGTLELLDYIHNIGGEYIFITNNSKSVVDYVEKVNRLGIKAER- 82

Query: 85  EQLFSSXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXXXR 144
          +  F+S                               P
Sbjct: 83  DNFF TSAQATIVYIKENYP-----KSKVYCQGTKSLIKELSDAGIDVTEQVSAD 131

Query: 145 VRAVLVGYDEHF SFAKLREAC AHLR DPECLLVATDRDPWHPLSDGSRTPGTGSLAAAVET 204
          +  VLVG+D  +  K+R  C  L  +  +AT+ D  P+S G  P  GS+  +
Sbjct: 132 IDVVLVGFDTELTSDKIRNTCEILSTKDIPFIATNPDIRCPVSFGF-IPDCGSICDMISK 190

Query: 205 ASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRL ETDILFGHRCGMTTVLTLTGVS 264
          +  R+ + +GKP P M + + + +  T+++GDRL TDI+ G  G+T+V  LTG +
Sbjct: 191 SVDRKPVYIGKPEPTMVDIVRKKLNYS LFETVVIGDRLYTDIMTGINAGVTSVCVLTGEA 250

Query: 265 RLEEAQAYLAAGQHDLVPHYYVESIADLTEGL 296
          + + Q      Q  + P Y  +++ ++ +G+
Sbjct: 251 TVNDIQ-----QGSIKPTYTFKNVKEMWKGI 276
```

>emb|CAI33398.1| putative phosphotransferase [Streptococcus pneumoniae]  
Length = 283

Score = 92.4 bits (228), Expect = 3e-017  
Identities = 66/272 (24%), Positives = 115/272 (42%), Gaps = 19/272 (6%)

```
Query: 25  LFDCDGVLWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLRA 84
          LFD DG ++ +R  G  ELL+ +  G  +F++NNS ++ +  +  RLG  R
Sbjct: 30  LFDMDGTIYEEDRLFEGTLELLDYIHNIGGEYIFITNNSKSVVDYVEKVNRLGIKAER- 88

Query: 85  EQLFSSXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXXXR 144
          +  F+S                               P
Sbjct: 89  DNFF TSAQATIVYIKENYP-----KSKVYCQGTKSLIKELSDAGIDVTEQVSAD 137

Query: 145 VRAVLVGYDEHF SFAKLREAC AHLR DPECLLVATDRDPWHPLSDGSRTPGTGSLAAAVET 204
          +  VLVG+D  +  K+R  C  L  +  +AT+ D  P+S G  P  GS+  +
Sbjct: 138 IDVVLVGFDTELTSDKIRNTCEILSTKDIPFIATNPDIRCPVSFGF-IPDCGSICDMISK 196

Query: 205 ASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRL ETDILFGHRCGMTTVLTLTGVS 264
          +  R+ + +GKP P M + + + +  T+++GDRL TDI+ G  G+T+V  LTG +
Sbjct: 197 SVDRKPVYIGKPEPTMVDIVRKKLNYS LFETVVIGDRLYTDIMTGINAGVTSVCVLTGEA 256

Query: 265 RLEEAQAYLAAGQHDLVPHYYVESIADLTEGL 296
          + + Q      Q  + P Y  +++ ++ +G+
Sbjct: 257 TVNDIQ-----QGSIKPTYTFKNVKEMWKGI 282
```

>emb|CAI33352.1| putative phosphotransferase [Streptococcus pneumoniae]  
Length = 277

Score = 92.4 bits (228), Expect = 3e-017

Identities = 66/272 (24%), Positives = 115/272 (42%), Gaps = 19/272 (6%)

```
Query: 25  LFDCDGVLWNGERAVPGAPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLRA 84
          LFD DG ++ +R  G  ELL+ +  G  +F++NNS ++ +  +  RLG  R
Sbjct: 24  LFDMDGTIYEEDRLFEGTLELLDYIHNIGGEYIFITNNSKSVVDYVEKVNRLGIKAER- 82

Query: 85  EQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXXR 144
          +  F+S                               P
Sbjct: 83  DNFFTSAQATIVYIKENYP-----KSKVYCQGTKSLIKELSDAGIDVTEQVSAD 131

Query: 145  VRAVLVGYDEHFSSFAKLREACALHRDPECLLVATDRDPWHPLSDGSRTPGTGSLAAAVET 204
          +  VLVG+D  +  K+R  C  L  +  +AT+ D  P+S  G  P  GS+  +
Sbjct: 132  IDVVLVGFDELTSDKIRNTCEILSTKDVPIATNPDIRCPVSFGF-IPDCGSICDMISK 190

Query: 205  ASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMTTTLTGVS 264
          +  R+ +  +GKP  P  M  +  +  +  +  T+++GDRL  TDI+  G  G+T+V  LTG  +
Sbjct: 191  SVDRKPVYIGKPEPTMVDIVRKKLNYSLFETVVIGDRLYTDIMTGINAGVTSVCVLTGEA 250

Query: 265  RLEEAQAYLAAGQHDLVPHYYVESIADLTEGL 296
          +  +  Q  Q  +  P  Y  +++  ++  +G+
Sbjct: 251  TVNDIQ-----QGSIKPTYTFKNVKEMWKGI 276
```

>ref|YP\_001826211.1| putative N-acetylglucosamine metabolism protein  
[Streptomyces  
griseus subsp. griseus NBRC 13350]  
Length = 284

Score = 92.0 bits (227), Expect = 4e-017  
Identities = 74/270 (27%), Positives = 113/270 (41%), Gaps = 23/270 (8%)

```
Query: 25  LFDCDGVLWNGERAVPGAPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLRA 84
          L  D  DGVL  +  +PGA  ++RL  +G  L  ++NNS  +L  R  R+G  +
Sbjct: 11  LTDMDGVLIHEGTPIPGADAFIKRLRDSGLPFLVLTNNSIYTARDLHARLKRMGDL-VPV 69

Query: 85  EQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXXR 144
          E  +++S                               PG  G  +V
Sbjct: 70  ENIWTSALATAQFLDDQRPG-----GTAYVIGEAGLTTALHDIGYVLTDHDPDY----- 118

Query: 145  VRAVLVGYDEHFSSFAKLREACALHRDPECLLVATDRDPWHPLSDGSRTPGTGSLAAAVET 204
          V++G  +SF  L  +A  L  +  +  T+  D  P  ++G  P  TGS+AA  +
Sbjct: 119  ---VVLGETRTYSFEALTKAI-RLINAGARFICTNPDETGPSAEGP-LPATGSVAALITK 173

Query: 205  ASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMTTTLTGVS 264
          A+G+  GKP+P  M  +  M+GDR++TD+L  G  GM  T  L  LTG++
Sbjct: 174  ATGKDPYFAGKPNPLMMRTGLNAIGAHSETSAMIGDRMDTDVLAGLEAGMQTFLVLTGLT 233

Query: 265  RLEEAQAYLAAGQHDLVPHYYVESIADLTE 294
          +  +  Y  P  +  VESIADL  +
Sbjct: 234  TVADVDRY-----PFGPSHVVESIADLVD 257
```

>ref|XP\_462491.1| hypothetical protein DEHA0G23100g [Debaryomyces hansenii  
CBS767]  
Length = 317

Score = 92.0 bits (227), Expect = 4e-017



Identities = 72/287 (25%), Positives = 123/287 (42%), Gaps = 18/287 (6%)

Query: 25 LFDCDGVLWNGERAVPGAPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLRA 84  
 LFDCDGV+W E+ +PG +E L K +FV+NNS ++R +F RLGF G+

Sbjct: 29 LFDCDGVWLDEKLIPGVLSTIEYLQSKNKRYVFTNNSKSRQNYVEKFQRLGFKGITK 88

Query: 85 EQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 144  
 + ++ + P + V

Sbjct: 89 DMIYPTCYAATFNLKEHLKVPEGSKIWVLGDSGIEDELREANYIPVGGTDDRLNAPFDPH 148

Query: 145 -----VRAVLVGYDEHFSFAKLREACAHL-RDPECL-LVATDRDPWHPLSDGSRT 193  
 V+AV+VG + F++ ++ +L D + + + D +P SDG P

Sbjct: 149 HELLLKVDPDVKAVVVGSTKDFNYMRIALTLLQYLLHDNKSIPFIGANIDRSYP-SDGLILP 207

Query: 194 GTGSLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCG 253  
 GS+ ++ + R + VGKPS + + I E+ D +T+MVG D L TDI FG+

Sbjct: 208 AGGSVVNYMQYTADRDFINVGKPSSTLLDVIHLSRFDKKTKIMVGD TLYTDIKFGNDGQ 267

Query: 254 M-TTVLTLTGVSRLAEAQAAYLAAG-----QHDLVPHYYVESIADLTE 294  
 + ++L +G + + +L ++P Y+ES D+ +

Sbjct: 268 LANSLLVFSGGTTKQYFDHFLTTSYKQEETKSMIPLCYIESFGDIID 314

>ref|YP\_061321.1| 4-nitrophenylphosphatase [Leifsonia xyli subsp. xyli str. CTCB07]

Length = 337

Score = 92.0 bits (227), Expect = 4e-017  
Identities = 80/274 (29%), Positives = 118/274 (43%), Gaps = 22/274 (8%)

Query: 24 VLFDCDGVLWNGERAVPGAPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLR 83  
 +L D DGV++ G A+P A E L R A + +++NN+ R +A LG LR

Sbjct: 18 ILADLDGVVYKGPDAIPHAVESLNRAAETTRVG-YITNNASRTAVSVAGHLTELG---LR 73

Query: 84 AEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 143  
 E PP A V

Sbjct: 74 VEPTDVVTSPQAAVRLLSQQVPPGATVLVVG DGLVDEVRKGGFGVTRSAEDDPA----- 128

Query: 144 RVRRAVLVGYDEHFSFAKLREACAHLR---DPECLLVATDRDPWHPLSDGSRTPGTGLAA 200  
 AV+ G+ + +L EA L+ D E +AT+ D P++ G PG G+L +

Sbjct: 129 ---AVIQGFAPDVGWTQLAEAAFALQGR TDAERPWIATNIDWTIPVARGV-APGNGLTVS 184

Query: 201 AVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGTTVLT 260  
 AV TA+GR +V GKP +F F+ AR L +GDRL+TD+L +R G+ +VL L

Sbjct: 185 AVHTAAGRLPMVAGKPEVAIFAEAVARFAA--ARPLFIGDRLD TDVLGANRAGIDSVLVL 242

Query: 261 TGVSRLAEAQAAYLAAGQHDLVPHYYVESIADLTE 294  
 TG+ R ++ L A D P Y ++ + L +

Sbjct: 243 TGIDRAKQ---LIAADADSRPAYILDDLRLGLAQ 272

>ref|NP\_244295.1| p-nitrophenyl phosphatase [Bacillus halodurans C-125]  
Length = 259

Score = 92.0 bits (227), Expect = 4e-017  
Identities = 76/279 (27%), Positives = 114/279 (40%), Gaps = 22/279 (7%)

Query: 20 RAQGVLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNRRARPELALRFARLGF 79  
R G L D DG ++ G + A +++L + + LFV+NNS ++ +A +  
Sbjct: 3 RYSGFLIDLDTMYRGSEVITEAVAFVKQLEKQSASYLFVTNNSTKSPETVATLLKSMDV 62

Query: 80 GGLRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 139  
+ E +F+S FV  
Sbjct: 63 PATK-EHVFTSSMAMASYLTRTKE-----FVRAFVIGEEGLLESLKESGMMVSEDE 112

Query: 140 XXXXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGSLA 199  
V++G D S+ KL +A ++R + T+ D P G PG GSLA  
Sbjct: 113 QPDY---VVMGLDRAISYEKLAKAATYVRQGAKFFI-TNGDAALPTEKGLM-PGNGLA 166

Query: 200 AAVETASGRQALVVGKPSPYMFEICITENFSIDPARTLMVGDRLDILFGHRCGMMTTVLT 259  
A V T +G + VVGKPS + E + TL++GD +TDIL G G+ T+L  
Sbjct: 167 AVVATTTGVKPFVVGKPSPIIIIEEALKRLGTTKEETLLIGDNYDITDILAGIHAGIDTLLV 226

Query: 260 LTGVSRLLEEQAAYLAAGQHDLVPHYYVESIADLTEGLED 298  
TGV+ E A Q + P Y ES+AD +E+  
Sbjct: 227 HTGVTTKE-----ALKQKEAQPTYTCESLADWQRSIEE 259

>ref|XP\_001300390.1| HAD-superfamily hydrolase, subfamily IIA containing protein

[Trichomonas vaginalis G3]  
Length = 303

Score = 91.7 bits (226), Expect = 6e-017  
Identities = 67/277 (24%), Positives = 111/277 (40%), Gaps = 13/277 (4%)

Query: 22 QGVLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNRRARPELALRFARLGF 81  
+ +L D DG +W PG PE + + + G A + +SNNS R R A + G  
Sbjct: 6 KAILLDVDGTIWKAGTVFPGVPEAISEMRKMGLAVIILSNSSRDRAHFVAKVLSKGIAN 65

Query: 82 LRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 141  
L +F++ G  
Sbjct: 66 LSKNDVFTAGYTCALKMKED-----GIRSALVYGVGLKEELDHIGIQTYTFKTLNE 117

Query: 142 XXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGSLAAA 201  
+ A+ V + F + L ++ +C + + D + ++ G G GS+ A  
Sbjct: 118 IRHLDAIIVCNLTFDYDHLCRIATIVKDYCKIYGANPDTSNIVA-GKTICGAGSMVAT 176

Query: 202 VETASGRQALVVGKPSPYMFEICITENFSIDPARTLMVGDRLDILFGHRCGMMTTVLT 261  
+ T +G+ +GKPS + + N I +MVGDR+ TDI FG R G+ T+ LT  
Sbjct: 177 IATLAGKLEANLGKPSPELIPILSNIKIAKEEMIMVGDRIPTDIEFGARNGLKTIFVLT 236

Query: 262 GVSRLLEEQAAYLAAGQHDLVPHYYVESIADLTEGLED 298  
GV R + ++ A + P Y + S+AD+ L++  
Sbjct: 237 GVDRNTKIESLDPA----IRPTYILPSLADVPSLLKE 269

>ref|YP\_001158747.1| HAD-superfamily hydrolase, subfamily IIA [Salinispora tropica

CNB-440]  
Length = 340

Score = 91.7 bits (226), Expect = 6e-017  
Identities = 81/256 (31%), Positives = 114/256 (44%), Gaps = 18/256 (7%)

Query: 24 VLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLR 83  
V+FD DGV++ ++ +PGA E + +L +A + +NN+ R E+A +G  
Sbjct: 16 VIFDLGVIYLVDPQIPGAIEAVRQLHAEERAVAYATNNASRRSSEVADLLTGMGIAA-G 74

Query: 84 AEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 143  
E++ +S P A + V  
Sbjct: 75 PEEVLTSAAAAAELLRERHP----AGTQILVVGAEALRAEIRAAGLTPVTQAEDGPV--- 127

Query: 144 RVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGLAAAVE 203  
AV+ GY +A L EA A +R VAT+ D P G PG G+L AAV  
Sbjct: 128 ---AVVQGYGPQVGWADLAEATAAIRGG-ATWVATNTDRTLPSKRGP-LPGNGALVAVR 182

Query: 204 TASGRQA-LVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMTTTLTLTG 262  
A GR LVVGKP+P +F + S R L+VGDRL+TDI R G+ ++L LTG  
Sbjct: 183 IALGRDPLVVGKPAPELFVAASRRAS--GGRALVVGDRDLDTIAGAVRAGLDSLVLTLTG 240

Query: 263 VSRLEEAQAYLAAGQH 278  
VS + E A AA +H  
Sbjct: 241 VSDVAELLA--AAPEH 254

>ref|XP\_660574.1| hypothetical protein AN2970.2 [Aspergillus nidulans FGSC A4]

Length = 282

Score = 91.7 bits (226), Expect = 6e-017

Identities = 83/290 (28%), Positives = 121/290 (41%), Gaps = 25/290 (8%)

Query: 12 AALRDVLGRAQGVLFDCDGVWNGERAVPGAPELLERLARAG---KAALFVSNNSRRARP 68  
A +++ L + LFDCDGVW+G+ PG E LE L G K +F S+ S  
Sbjct: 14 AGIKEFLDKFDVFLFDCDGVWWSGDHLFPGETVETLELLRSRGNPKKEEIFSSSYSA---- 69

Query: 69 ELALRFARLGFGLRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXX 128  
++ +R+ ++F P F+  
Sbjct: 70 --SIYISRILNLPANKRKVFLVGETGIEQELRSENVP-----FIGGTDPSYRRDITAE 120

Query: 129 XXXXXXXXXXXXXXXXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSD 188  
V VLVG D H ++ KL A ++R L AT+ D P S  
Sbjct: 121 DYKLIAAGDESLLDPEVGVVVLVGLDFHLNLYKLALAYHYIRRGAVFL-ATNIDSTLPNS- 178

Query: 189 GSRTPGTGLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILF 248  
G+ PG G+++A + GR + +GKP+ M + I F +D AR MVGDR TDI F  
Sbjct: 179 GTLFPAGTVSAPLILMVGDRDPVALGKPNQAMMDAIEGKFLDRARACMVGDRANTDIRF 238

Query: 249 GHRCGM-TTVLTLTGVSRLLEEAQAYLAAGQHDLVPHYVYESIADLTEGLE 297  
G + T+ LTGVS E+ + P Y++ ++DL E E  
Sbjct: 239 GLEGNLGGTLGVLTGVSSKEDFVEGVVR-----PSAYLDKLSDLLLEAAE 282

>ref|ZP\_02273939.1| NagD protein [Fusobacterium nucleatum subsp. polymorphum ATCC

10953]

Length = 264

Score = 91.3 bits (225), Expect = 7e-017

Identities = 70/275 (25%), Positives = 123/275 (44%), Gaps = 23/275 (8%)

Query: 25 LFD CDGVLWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLRA 84  
 L D DG ++ G + GA E LE+L +F++NNS + + + +LG R  
 Sbjct: 11 LLDMDGTIYLGNELIDGAKEFLEKLEKKNIRYIFLTNNSSKNKDRYVEKLNKLGIEAHR- 69

Query: 85 EQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXXXR 144  
 E +FSS G VF+  
 Sbjct: 70 EDVFSSGEATTIYLNKQKKG-----AKVFLLGTDLEDEFEKAGFELVKERNK-----N 118

Query: 145 VRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGSLAAAVET 204  
 + V++G+D ++ KL AC ++ + VAT D PL +G P G++ A ++  
 Sbjct: 119 IDFVVLGFDTTLTYEKLWIACEYIANG-VEYVATHPDFNCPLENGKFMPDAGAMMAFIKA 177

Query: 205 ASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMTTVLTGTGVS 264  
 ++ ++ +V+GKP+ ++ + I E +++ + MVDRL TDI G G+T++L ++G +  
 Sbjct: 178 STEKEPIVIGKPNKHIIDAIIEKYNLKKSELAMVGDRLYTDIRTGIDNGLTSILVMSGET 237

Query: 265 --RLEEAQAYLAAGQHDLVPHYYVESIADLTEGLE 297  
 ++ E Y P Y +S+ +L E +E  
 Sbjct: 238 DKKMLEETIY-----KPDYVFDVSVKELKEKIE 264

>ref|ZP\_02596858.1| 4-nitrophenylphosphatase (p-nitrophenylphosphate phosphohydrolase)  
 [Bacillus cereus H3081.97]  
 Length = 254

Score = 90.9 bits (224), Expect = 1e-016  
 Identities = 67/251 (26%), Positives = 106/251 (42%), Gaps = 17/251 (6%)

Query: 22 QGVLFDCDGLWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLRA 81  
 +G L D DG ++ GE + A + ++ L G L FV+NNS R ++A + R  
 Sbjct: 3 KGYLIDLDTMYRGEEQIEEASDFVKALGERGIPYLFVTNNSTRKPEQVAEKLVRFDIPA 62

Query: 82 LRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 141  
 +AEQ+F++ ++  
 Sbjct: 63 -KAEQVFTTSMATANF-----IYERKQDATVYMIGEGLHDALVEKGFELV 107

Query: 142 XXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGSLAAA 201  
 V+VG D ++ KL +AC +R+ ++T+ D P G PG GSL +  
 Sbjct: 108 DENPDFVVVGLDRDITYEKLAKACLAVRNG-ATFISTNGDIAIPTERGL-LPGNGSLTSV 165

Query: 202 VETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMTTVLTGT 261  
 V ++G + +GKP + E + I+ LMVGD +TDIL G GM T+L T  
 Sbjct: 166 VAVSTGVDPIFIGKPEIIMEQALKLLGIEKNEALMVGDNYDITDILAGINAGMHTLLVHT 225

Query: 262 GVSRLLEEAQAY 272  
 GV+ +E+ Y  
 Sbjct: 226 GVTTVEKLTLEY 236

>ref|ZP\_02539488.1| 4-nitrophenylphosphatase (p-nitrophenylphosphate phosphohydrolase)  
 [Bacillus cereus W]  
 Length = 254

Score = 90.9 bits (224), Expect = 1e-016

Identities = 67/251 (26%), Positives = 106/251 (42%), Gaps = 17/251 (6%)

Query: 22 QGVLFDCDGVLWNGERAVPGAPELLERLARAGKAALFVSNNRRARPELALRFARLGFGG 81  
 +G L D DG ++ GE + A + ++ L G LFV+NNS R ++A + R  
 Sbjct: 3 KGYLIDL DGTMYRGEEQIEEASDFVKALGERGIPYLFVTNNSTRKPEQVAEKLVRFDIPA 62

Query: 82 LRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 141  
 +AEQ+F++ ++  
 Sbjct: 63 -KAEQVFTTSMATANF-----IYERKQDATVYMIGEEGLHDALVEKGFELV 107

Query: 142 XXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGLAAA 201  
 V+VG D ++ KL +AC +R+ ++T+ D P G PG GSL +  
 Sbjct: 108 DENPDFVVVGLDRDITYEKLAKACLAVRNG-ATFISTNGDIAIPTERGL-LPGNGSLTSV 165

Query: 202 VETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGTTVLTLT 261  
 V ++G + +GKP + E + I+ LMVGD +TDIL G GM T+L T  
 Sbjct: 166 VAVSTGVNPIFIGKPESIIMEQALKVLGIEKNEALMVGDNYDITDILAGINAGMHTLLVHT 225

Query: 262 GVSRLLEEAQAY 272  
 GV+ +E+ Y  
 Sbjct: 226 GVTTVEKLTEY 236

>ref|YP\_897195.1| hydrolase, haloacid dehalogenase-like family, possible  
 4-nitrophenylphosphatase [Bacillus thuringiensis str. Al  
 Hakam]  
 Length = 254

Score = 90.9 bits (224), Expect = 1e-016  
 Identities = 67/251 (26%), Positives = 106/251 (42%), Gaps = 17/251 (6%)

Query: 22 QGVLFDCDGVLWNGERAVPGAPELLERLARAGKAALFVSNNRRARPELALRFARLGFGG 81  
 +G L D DG ++ GE + A + ++ L G LFV+NNS R ++A + R  
 Sbjct: 3 KGYLIDL DGTMYRGEEQIEEASDFVKALGERGIPYLFVTNNSTRKPEQVAEKLVRFDIPA 62

Query: 82 LRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 141  
 +AEQ+F++ ++  
 Sbjct: 63 -KAEQVFTTSMATANF-----IYERKQDATVYMIGEEGLHDALVEKGFELV 107

Query: 142 XXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGLAAA 201  
 V+VG D ++ KL +AC +R+ ++T+ D P G PG GSL +  
 Sbjct: 108 DENPDFVVVGLDRDITYEKLAKACLAVRNG-ATFISTNGDIAIPTERGL-LPGNGSLTSV 165

Query: 202 VETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGTTVLTLT 261  
 V ++G + +GKP + E + I+ LMVGD +TDIL G GM T+L T  
 Sbjct: 166 VAVSTGVNPIFIGKPESIIMEQALKVLGIEKNEALMVGDNYDITDILAGINAGMHTLLVHT 225

Query: 262 GVSRLLEEAQAY 272  
 GV+ +E+ Y  
 Sbjct: 226 GVTTVEKLTEY 236

>ref|YP\_086257.1| 4-nitrophenylphosphatase (p-nitrophenylphosphate  
 phosphohydrolase)  
 [Bacillus cereus E33L]  
 Length = 254

Score = 90.9 bits (224), Expect = 1e-016  
Identities = 67/251 (26%), Positives = 106/251 (42%), Gaps = 17/251 (6%)

```
Query: 22 QGVLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNRRARPELALRFARLGFGG 81
      +G L D DG ++ GE + A + ++ L G LFV+NNS R ++A + R
Sbjct: 3 KGYLIDL DGTMYRGEEQIEEASDFVKALGERGIPYLFVTNNSTRKPEQVAEKLVRFDIPA 62

Query: 82 LRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 141
      +AEQ+F++ ++
Sbjct: 63 -KAEQVFTTSMATANF-----IYERKQDATVYMIGEEGLHDALVEKGFELV 107

Query: 142 XXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGLAAA 201
      V+VG D ++ KL +AC +R+ ++T+ D P G PG GSL +
Sbjct: 108 DENPDFVVVGLDRDITYEKLAKACLAVRNG-ATFISTNGDIAIPTERGL-LPGNGSLTSV 165

Query: 202 VETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMTTVLTLT 261
      V ++G + +GKP + E + I+ LMVGD +TDIL G GM T+L T
Sbjct: 166 VAVSTGVDPIFIGKPESIIMEQALKVLGIEKNEALMVGDNYDITDILAGINAGMHTLLVHT 225

Query: 262 GVSRL EEAQAY 272
      GV+ +E+ Y
Sbjct: 226 GVTTVEKLT EY 236
```

>ref|NP\_834630.1| 4-nitrophenylphosphatase [Bacillus cereus ATCC 14579]  
Length = 254

Score = 90.9 bits (224), Expect = 1e-016  
Identities = 67/251 (26%), Positives = 106/251 (42%), Gaps = 17/251 (6%)

```
Query: 22 QGVLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNRRARPELALRFARLGFGG 81
      +G L D DG ++ GE + A + ++ L G LFV+NNS R ++A + R
Sbjct: 3 KGYLIDL DGTMYRGEEQIEEASDFVKALGERGIPYLFVTNNSTRKPEQVAEKLVRFDIPA 62

Query: 82 LRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 141
      +AEQ+F++ ++
Sbjct: 63 -KAEQVFTTSMATANF-----IYERKQDATVYMIGEEGLHDALVEKGFELV 107

Query: 142 XXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGLAAA 201
      V+VG D ++ KL +AC +R+ ++T+ D P G PG GSL +
Sbjct: 108 DENPDFVVVGLDRDITYEKLAKACLAVRNG-ATFISTNGDIAIPTERGL-LPGNGSLTSV 165

Query: 202 VETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMTTVLTLT 261
      V ++G + +GKP + E + I+ LMVGD +TDIL G GM T+L T
Sbjct: 166 VAVSTGVDPIFIGKPESIIMEQALKVLGIEKNEALMVGDNYDITDILAGINAGMHTLLVHT 225

Query: 262 GVSRL EEAQAY 272
      GV+ +E+ Y
Sbjct: 226 GVTTVEKLT EY 236
```

>ref|YP\_743385.1| HAD-superfamily subfamily IIA hydrolase like protein  
[Alkalilimnicola ehrlichei MLHE-1]  
Length = 260

Score = 90.9 bits (224), Expect = 1e-016  
Identities = 79/250 (31%), Positives = 106/250 (42%), Gaps = 42/250 (16%)

Query: 23 GVLFDGCDGVLWNGERAVPGAPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGG 82  
 G+L D GVL+ G A+PGAPE ++RL +G A F +N SR R LA + RLGF +  
 Sbjct: 8 GLLLDIGGVLYQGAEALPGAPEAMQRLRASGLALRFATNTSRTTRAALAEKLGRLGF-DV 66

Query: 83 RAEQLFSSXXXXXXXXXXXXXPGP-----PDAPGAVFVXXXXXXXXXXXXXXXXXXXX 133  
 AE++F++ P PD G  
 Sbjct: 67 AAEEIFTAPLAAVQTIRERGLRPLLLVHPDLGPDLTG----- 103

Query: 134 XXXXXXXXXXXRVRAVLVG-YDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRT 192  
 AVL+G EHF + L A L + LL A R+ + DG +  
 Sbjct: 104 -----FPDGPPDAVLIGDAGEHFDYRGLNRAFRLMEGAPLL-ALARNRYFREQDG-LS 155

Query: 193 PGTGSLAAAVETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRC 252  
 G AA+E ASG A V GKP+P F E + P R LMVGD +E+D++  
 Sbjct: 156 LDVGPVFAALEYASGVAAEVYKPPAPGFFREAAEALGVAPERLLMVGDDVESDVIGALDA 215

Query: 253 GMTTVLTLTG 262  
 G+ L TG  
 Sbjct: 216 GLQAALVRTG 225

>ref|ZP\_00237712.1| HAD-superfamily subfamily IIA hydrolase, TIGR01457  
 [Bacillus cereus  
 G9241]  
 Length = 254

Score = 90.9 bits (224), Expect = 1e-016  
 Identities = 67/251 (26%), Positives = 106/251 (42%), Gaps = 17/251 (6%)

Query: 22 QGVLFDCDGLWNGERAVPGAPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGG 81  
 +G L D DG ++ GE + A + ++ L G LFV+NNS R ++A + R  
 Sbjct: 3 KGYLIDLDTMYRGEEQIEEASDFVKALGERGIPYLFVTNNSTRKPEQVAEKLVRFDIPA 62

Query: 82 LRAEQLFSSXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 141  
 +AEQ+F++ ++  
 Sbjct: 63 -KAEQVFTTSMATANF-----IYERKQDATVYMIGEGLHDALVEKGFELV 107

Query: 142 XXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGSLAAA 201  
 V+VG D ++ KL +AC +R+ ++T+ D P G PG GSL +  
 Sbjct: 108 DENPDFVVVGLDRDITYEKLAKACLAVRNG-ATFISTNGDIAIPTERGL-LPGNGSLTSV 165

Query: 202 VETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMTTVLTLT 261  
 V ++G + +GKP + E + I+ LMVGD +TDIL G GM T+L T  
 Sbjct: 166 VAVSTGVDPIFIGKPEIIMEQALKVLGIEKDEALMVGDNVDTDILAGINAGMHTLLVHT 225

Query: 262 GVSRLLEEQAAY 272  
 GV+ +E+ Y  
 Sbjct: 226 GVTTVEKLTEY 236

>ref|XP\_001328825.1| haloacid dehalogenase-like hydrolase family protein  
 [Trichomonas  
 vaginalis G3]  
 Length = 275

Score = 90.5 bits (223), Expect = 1e-016

Identities = 67/271 (24%), Positives = 113/271 (41%), Gaps = 9/271 (3%)

Query: 24 VLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLR 83  
 +L D DGV+W + + GA + L R+ + G + V+NN + R + + +LG G  
 Sbjct: 8 LLLDGDGVIWIDNQPIKGAIDALNRIRKLGVRLLVLTNNCSKTREQYLKQLEKLGQGF 67

Query: 84 AEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 143  
 E +FSS + VFV  
 Sbjct: 68 VEDVFSSGFATAKYLQH-----NNIHKVFCVCGFDGLMQELSQHGIIEVHNMKTDPEPQPA 121

Query: 144 RVRVAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGLAAAVE 203  
 AV+V E S A + +++ L+ T+ DP P++ G G+G+ A E  
 Sbjct: 122 E--AVIVSKSESLSHADISRGIYIKNFGAKLIGTNPDPNPFMAGGILICGSGACVRAFE 179

Query: 204 TASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGTTVLTTLTG 263  
 A + A V+GKP+ MF+ + + +MVGDR+ TDI F + G ++L L+G+  
 Sbjct: 180 VAVNQDATVIGKPNKPMFDTVLLTLGVTKDDVVMVGDRLDIAFASQNGARSILVLSGI 239

Query: 264 SRLEEAQAYLAAGQHDLVPHYYVESIADLTE 294  
 ++ Y + + H + +AD+ E  
 Sbjct: 240 DTRDDVLKYPEQDRPTWI-HPSLVEVADMFE 269

>ref|ZP\_02580578.1| 4-nitrophenylphosphatase (p-nitrophenylphosphate phosphohydrolase)  
 [Bacillus cereus B4264]  
 Length = 254

Score = 90.1 bits (222), Expect = 2e-016  
 Identities = 67/251 (26%), Positives = 106/251 (42%), Gaps = 17/251 (6%)

Query: 22 QGVLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLR 81  
 +G L D DG ++ GE + A + ++ L G LFV+NNS R ++A + R  
 Sbjct: 3 KGYLIDLDTMYRGEEQIEEASDFVKALGERGIPYLFVTNNSTRKPEQVAEKLVRFDILA 62

Query: 82 LRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 141  
 +AEQ+F++ ++  
 Sbjct: 63 -KAEQVFTTSMATANF-----IYERKQDATVYMIGEEGLHDALVEKGFELV 107

Query: 142 XXRVAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGLAAA 201  
 V+VG D ++ KL +AC +R+ ++T+ D P G PG GSL +  
 Sbjct: 108 DENPDFVVVGLDRDITYEKLAKACLAVRNG-ATFISTNGDIAIPTERGL-LPGNGSLTSV 165

Query: 202 VETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGTTVLTTLT 261  
 V ++G + +GKP + E + I+ LMVGD +TDIL G GM T+L T  
 Sbjct: 166 VAVSTGVDPIFIGKPESIIMEQALKVLGIEKNEALMVGDNYDITDILAGINAGMHTLLVHT 225

Query: 262 GVSRLLEEAQAY 272  
 GV+ +E+ Y  
 Sbjct: 226 GVTTVEKLTEY 236

>ref|NP\_738155.1| hypothetical protein CE1545 [Corynebacterium efficiens YS-314]  
 Length = 331

Score = 90.1 bits (222), Expect = 2e-016



Identities = 78/270 (28%), Positives = 118/270 (43%), Gaps = 21/270 (7%)

```
Query: 24 VLFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLR 83
      +L D DG +W G RA+ A ++ + AG ++V+NN+ RA +A + +G
Sbjct: 10 LLLDLDTIWEQGRAIDDA---VDAITGAGLPVVVVTNNASRAPEAVAEQLRIGLDSAT 66

Query: 84 AEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 143
      A+ + +S P A V++
Sbjct: 67 ADDVMTSAQAAVIMASEKIP----AGSPVYILGTESFRDLARDAGFRVVDSDADD----- 116

Query: 144 RVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGLAAAVE 203
      R AVL G++ +A+L EA + + L A++ D P+ G G GS+ AAV
Sbjct: 117 RPVAVLHGHNPATGWAQLSEAALSIHNG-ALYFASNLDTTLPMERGLHV-GNGSMVAADV 174

Query: 204 TASGRQALVVGKPSYMFECITENFSIDPARTLMVGDRLDILFGHRCGMTTTLTGTG 263
      +A+G GKP P MF + + AR L+VGDRL+TDI G+ GM T LTGV
Sbjct: 175 SATGVTPEAAGKPGPAMFFKAAQQ--VASARPLVVGDRDLTDIAGGNAAGMDTFQVLTGV 232

Query: 264 SRLEEAQAYLAAGQHDLPVPHYYVESIADLT 293
      S A GQ P + +++ADL+
Sbjct: 233 SG-HYALLTAVPGQR---PDFIADTLADLS 258
```

>ref|ZP\_00995567.1| putative hydrolase [Janibacter sp. HTCC2649]  
Length = 302

Score = 90.1 bits (222), Expect = 2e-016  
Identities = 75/254 (29%), Positives = 104/254 (40%), Gaps = 17/254 (6%)

```
Query: 17 VLGRAQGVLFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRFAR 76
      ++ R ++ D DGV++ G+ AVP A +E L+ G F +NN+ R ++A R
Sbjct: 3 LVDRYDAIVCDLDGVVYRGDPAVPHA---VEALSAVGVPIQFATNNASRPPSQVADHLRR 59

Query: 77 LGFGGLRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXX 136
      LG SS PG
Sbjct: 60 LGLDIANDAVATSSQAAAWLTRHLEPG-----AAVLAIGGEGVAEALRESGFV 108

Query: 137 XXXXXXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTG 196
      AV+ GY + S L +A A+ L +AT+ D P +DG PG G
Sbjct: 109 PVTSDVDEPAAVVQGYGPNVSATDLAQA-AYAVQRGALWMATNTDHTLPTADGY-APGNG 166

Query: 197 SLAAAVETASGR-QALVVGKPSYMFECITENFSIDPARTLMVGDRLDILFGHRCGMT 255
      +L AV A GR LV GKP ++ E + P R L +GDRLETDI H GM
Sbjct: 167 ALVLAVGAAVGRGPELVAGKPDEPLYLMCAERLGVPPNRVLAIGDRLETDIEGAHAGMD 226

Query: 256 TVLTLTGVSRLAEA 269
      ++L LTGV + +A
Sbjct: 227 SLLVLTGVHGVRDA 240
```

>ref|ZP\_02586935.1| 4-nitrophenylphosphatase (p-nitrophenylphosphate  
phosphohydrolase)  
[Bacillus cereus G9842]  
Length = 254

Score = 89.7 bits (221), Expect = 2e-016  
Identities = 67/251 (26%), Positives = 105/251 (41%), Gaps = 17/251 (6%)

Query: 22 QGVLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGG 81  
 +G L D DG ++ GE + A + ++ L G LFV+NNS R ++A + R  
 Sbjct: 3 KGYLIDLDTMYRGEEQIEEASDFVKALGERGIPYLFVTNNSRTRKPEQVAEKLVRFDIPA 62

Query: 82 LRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 141  
 +AEQ+F++ ++  
 Sbjct: 63 -KAEQVFTTSMATANF-----IYERKQDATVYMIGEEGLHDALVEKGFELV 107

Query: 142 XXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGSLAAA 201  
 V+VG D ++ KL +AC +R+ ++T+ D P G PG GSL +  
 Sbjct: 108 DENPDFVVGGLDRDITYEKLAKACLAVRNG-ATFISTNGDIAIPTERGL-LPGNGSLTSV 165

Query: 202 VETASGRQALVVGKPSYMFECITENFSIDPARTLMVGDRLDILFGHRCGTTVLTLT 261  
 V ++G + +GKP + E + I LMVGD +TDIL G GM T+L T  
 Sbjct: 166 VAVSTGVDPIFIGKPESIIMEQALKVLGIGKDEALMVGDNYDITDILAGVNAGMHTLLVHT 225

Query: 262 GVSRLLEEAQAY 272  
 GV+ +E+ Y  
 Sbjct: 226 GVTTVEKLTEY 236

>ref|YP\_716338.1| N-acetylglucosamine-6-phosphate deacetylase [Frankia alni ACN14a]

Length = 308

Score = 89.7 bits (221), Expect = 2e-016  
 Identities = 72/274 (26%), Positives = 117/274 (42%), Gaps = 23/274 (8%)

Query: 22 QGVLFDCDGVWNGERAVPGAPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGG 81  
 + L D DGVL + E + GA + + AG L ++NNS +L+ R +R G  
 Sbjct: 24 ENYLIDMDGVLVHEEHPIAGADAFIAGVIAAGLGFLVLTNNSIYTARDLSARLSRSGLE- 82

Query: 82 LRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 141  
 + E++++S PG G+ +V  
 Sbjct: 83 IPPERIWTSALATALFLHTQRPG-----GSAYVVGEGALTTALHDIGYVLSOSSPDY--- 134

Query: 142 XXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGSLAAA 201  
 V++G +SF + A +RD +AT+ DP P +G P TG++AA  
 Sbjct: 135 -----VVLGETRTYSFEAITRAVRLVRDG-ARFIATNPDPDTPGPSVEGL-LPATGAVAAM 186

Query: 202 VETASGRQALVVGKPSYMFECITENFSIDPARTLMVGDRLDILFGHRCGTTVLTLT 261  
 + A+G VGKP+P M S T+++GDR++TD++ G GM TVL L+  
 Sbjct: 187 ITKATGVTPYFVGKPNPLMMSALNTLSAHSETTVVIGDRMDTDVVAGLEAGMDTVLVLS 246

Query: 262 GVSRLLEEAQAYLAAGQHDLVPHYYVESIADLTEG 295  
 G++ + + + P V+SIA + G  
 Sbjct: 247 GITTHADIERF-----PYRPSAVVDSIARVPVG 274

>emb|CAL57687.1| p-Nitrophenyl phosphatase (ISS) [Ostreococcus tauri]  
 Length = 427

Score = 89.4 bits (220), Expect = 3e-016  
 Identities = 63/160 (39%), Positives = 91/160 (56%), Gaps = 10/160 (6%)

Query: 145 VRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGSLAAAVET 204

V AV+VG D F+FAKL A ++ + VAT+ D + G PG G+L AV T  
 Sbjct: 210 VGAVVVGSDSKFTFAKLAYASLQIQRG-AMFVATNPDAGDLVGPGLY-PGAGALVNAVAT 267  
 Query: 205 ASGRQA-LVVGKPSPYMFECITENFSIDPARTLMVGDRLLETDILFGHRCGMT-TVLTLTG 262  
 A G+Q + GKPS +M E + ++ +ID +RTL++GDRL+TDI FG T L LTG  
 Sbjct: 268 ACGKQPEIYCGKPSFMLELLKDHANIDLSRTLVIQDRLDLDIAFGKAGNAALTALVLTG 327  
 Query: 263 VSRLEEAQAYLAAGQHD-----LVPHYYVESIADLTEGLE 297  
 V+ +++ A+ + D +P V S+A+L GLE  
 Sbjct: 328 VTEIDDVNAWAERAETDPAAAAALPDRIVGSLAELC-GLE 366

Score = 60.1 bits (144), Expect = 2e-007  
 Identities = 27/63 (42%), Positives = 37/63 (58%)

Query: 23 GVLFDGCDGVLWNGERAVPGAPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGL 82  
 GV+ DCDGV+W+G+R +PGA +E L GK FV+NNS + R A + LG  
 Sbjct: 61 GVVLDGCDGVIWHGDRILIPGARAAIESLRARGKRVFFVTNNSTKTREHYAQLNALGIEAS 120  
 Query: 83 RAE 85  
 + E  
 Sbjct: 121 KYE 123

>ref|NP\_847375.1| phosphatase,haloacid dehalogenase family [Bacillus  
 anthracis str.  
 Ames]  
 Length = 254

Score = 89.4 bits (220), Expect = 3e-016  
 Identities = 66/251 (26%), Positives = 106/251 (42%), Gaps = 17/251 (6%)

Query: 22 QGVLFDGCDGVLWNGERAVPGAPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGL 81  
 +G L D DG ++ GE + A + ++ L G L FV+NNS R ++A + R  
 Sbjct: 3 KGYLIDLDTMYRGEEQIEEASDFVKALGERGIPYLFVTNNSTRKPEQVAEKLVRFDIPA 62  
 Query: 82 LRAEQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 141  
 +AEQ+F++ ++  
 Sbjct: 63 -KAEQVFTTSMATANF-----IYERKQDATVYMIGEEGLHDALVEKGFELV 107  
 Query: 142 XXRVRAVLVGYDEHFSFAKLREACAHLRDPECLLVATDRDPWHPLSDGSRTPGTGLAAA 201  
 V+VG D ++ KL +AC +R+ ++T+ D P G PG GSL +  
 Sbjct: 108 DENPDFVVVGLDRDITYEKLAKACLAVRNG-ATFISTNGDIAIPTERGL-LPGNGSLTSV 165  
 Query: 202 VETASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLLETDILFGHRCGMTTVLTLT 261  
 V ++G + +GKP + E + I+ L+VGD +TDIL G GM T+L T  
 Sbjct: 166 VAVSTGVDPIFIGKPESIIMEQALKVLGIEKNEALIVGDNYDITDILAGINAGMHTLLVHT 225  
 Query: 262 GVSRLLEAQAY 272  
 GV+ +E+ Y  
 Sbjct: 226 GVTTVEKLTEY 236

>sp|P46351|YTH1\_PANTH Uncharacterized 45.4 kDa protein in thiaminase I  
 5'region  
 Length = 413

Score = 89.4 bits (220), Expect = 3e-016  
Identities = 69/238 (28%), Positives = 102/238 (42%), Gaps = 18/238 (7%)

```
Query: 25  LFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLRA 84
          LFD DGV++ G  A+PGA E LERL  GK  F++NN  R + A R  RLG  +
Sbjct: 10  LFDLDGVIYVGPEALPGAVEALERLRSGGKTIRFLTNNPCMTREQTAARLNRLGIEAAKD 69

Query: 85  EQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXXR 144
          E + S                               G+V+V
Sbjct: 70  EVISSGWATACCLRERRA-----GSVYVLGDEHLERECRDAGLDIVDVNAA----- 115

Query: 145 VRAVLVGYDEHFSFAKLREACALHRDPECLLVATDRDPWHPLSDGSRTPGTGSAAAVET 204
          AV+VG+ + + ++ A  + +  +AT+ D  P  DG  G+  A++
Sbjct: 116 -EAVVVGWSDDLTLRDIQSAVTRIANG-AQFIATNADWSFPGPDGPM-AVGTAVEAIKM 172

Query: 205 ASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMTTTLTGT 262
          ASG+  +VGKP PYMF  ++  D +R +M GD  + DI  HR G++ VL  +G
Sbjct: 173 ASGKTPYIVGKPYPYMFRQALQHVE-DWSRAVMFGDTPDADIAGAHRIGISAVLISSG 229
```

>ref|YP\_922443.1| HAD-superfamily hydrolase, subfamily IIA [Nocardioides sp. JS614]

Length = 268

Score = 89.4 bits (220), Expect = 3e-016  
Identities = 75/270 (27%), Positives = 111/270 (41%), Gaps = 23/270 (8%)

```
Query: 25  LFDCDGVWNGERAVPGAPPELLERLARAGKAALFVSNNSRRARPELALRFARLGFGLRA 84
          L D DGVL + E  +PGA E +E L  + +  L ++NNS  +L R  G  +
Sbjct: 13  LTDMDGVLVHEEVPIPGAQEFIEALKASQRRFLVLTNNSIFTPRDLRARLLGSGID-VPE 71

Query: 85  EQLFSSXXXXXXXXXXXXXXXXPGPPDAPGAVFVXXXXXXXXXXXXXXXXXXXXXXXXXXXXR 144
          E +++S                               P  G  +V
Sbjct: 72  EAIWTSALATAQFLDDQRPR-----GTAYVVGEAGLTALHDIGYVMTDRDPDY----- 120

Query: 145 VRAVLVGYDEHFSFAKLREACALHRDPECLLVATDRDPWHPLSDGSRTPGTGSAAAVET 204
          V++G  +SF + A  L  +AT+ D  P  G  P TGS+AA + T
Sbjct: 121 ---VVLGETRTYSFEAITRAI-RLVAAGARFIATNPDASGPSQQGM-LPATGSVAALIST 175

Query: 205 ASGRQALVVGKPSPYMFECITENFSIDPARTLMVGDRLDILFGHRCGMTTTLTGTGS 264
          A+GR+  +GKP+P M  T+MVGDR++TDI+ G  G+ T+L  TG  +
Sbjct: 176 ATGRRPYFIGKPNPLMMRSALNRLEAHSETTMVVGDRMDTDIISGLEAGLRTILVTTGST 235

Query: 265 RLEEAQAYLAAGQHDLVPHYVYESIADLTE 294
          R E+  +  P  V+S+ADL E
Sbjct: 236 RPEQVSTF-----PYRPTRVVDSVADLLE 259
```

Database: nr  
Posted date: Apr 28, 2008 6:58 PM  
Number of letters in database: 997,030,366  
Number of sequences in database: 2,969,608

Database: C:\Genomics\blast\databases\nr.01  
Posted date: Apr 28, 2008 7:40 PM  
Number of letters in database: 997,186,050

Number of sequences in database: 2,813,524

Database: C:\Genomics\blast\databases\nr.02

Posted date: Apr 28, 2008 8:00 PM

Number of letters in database: 213,558,862

Number of sequences in database: 685,017

Lambda	K	H
0.322	0.138	0.419

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 1,143,521,583

Number of Sequences: 6468149

Number of extensions: 42454060

Number of successful extensions: 106594

Number of sequences better than 10.0: 500

Number of HSP's better than 10.0 without gapping: 837

Number of HSP's successfully gapped in prelim test: 283

Number of HSP's that attempted gapping in prelim test: 104631

Number of HSP's gapped (non-prelim): 1849

length of query: 298

length of database: 2,207,775,278

effective HSP length: 133

effective length of query: 165

effective length of database: 1,347,511,461

effective search space: 222339391065

effective search space used: 222339391065

T: 11

A: 40

X1: 16 ( 7.4 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)

S1: 41 (21.9 bits)

S2: 78 (34.7 bits)