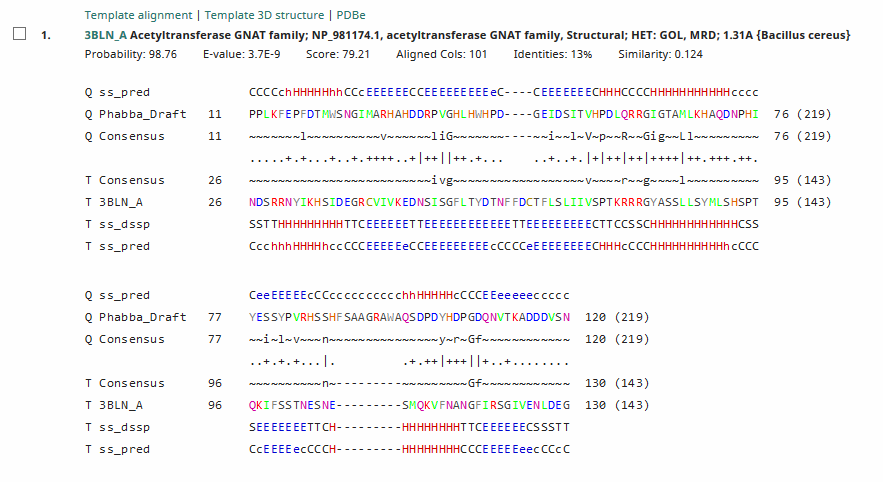
<https://toolkit.tuebingen.mpg.de/#/jobs/6362589> (6 Aug 2017 – 20? Aug 2017)



[](http://www.ebi.ac.uk/pdbe/entry/pdb/3bln/protein/1)

Query Phabba\_Draft gp83

Match\_columns 219

No\_of\_seqs 255 out of 2822

Neff 8.12084

Searched\_HMMs 106131

Date Sun Aug 6 22:52:39 2017

Command hhsearch -cpu 8 -i ../results/full.a3m -d /cluster/toolkit/production/databases/hh-suite/mmcif70/pdb70 -d /cluster/toolkit/production/databases/hh-suite/scope70/scope -d /cluster/toolkit/production/databases/hh-suite/pfama/pfama -d /cluster/toolkit/production/databases/hh-suite/NCBI\_CD/NCBI\_CD -o ../results/6362589.hhr -oa3m ../results/6362589.a3m -p 20 -Z 250 -loc -z 1 -b 1 -B 250 -ssm 2 -sc 1 -seq 1 -dbstrlen 10000 -norealign -maxres 32000 -contxt /cluster/toolkit/production/bioprogs/tools/hh-suite-build/data/context\_data.crf

No Hit Prob E-value P-value Score SS Cols Query HMM Template HMM

1 3BLN\_A Acetyltransferase GNAT 98.8 3.7E-09 3.5E-14 79.2 13.1 101 11-120 26-130 (143)

2 d1q2ya\_ d.108.1.1 (A:) Probabl 98.7 3.8E-09 3.5E-14 79.2 12.2 117 1-126 18-137 (140)

3 3FNC\_B Putative acetyltransfer 98.7 7.2E-09 6.8E-14 78.9 13.8 102 16-126 51-157 (163)

4 3FNC\_A Putative acetyltransfer 98.7 7.2E-09 6.8E-14 78.9 13.8 102 16-126 51-157 (163)

5 1Q2Y\_A similar to hypothetical 98.7 4.6E-09 4.3E-14 78.4 12.1 117 1-126 18-137 (140)

6 d3fncb1 d.108.1.0 (B:1-160) au 98.7 8.5E-09 8E-14 78.6 13.6 102 16-126 48-154 (160)

7 d2fiaa1 d.108.1.1 (A:1-157) Pr 98.7 8.1E-09 7.7E-14 78.3 12.8 96 11-115 36-139 (157)

8 2FIA\_A acetyltransferase; Acet 98.7 9.3E-09 8.7E-14 78.4 13.1 99 7-114 32-138 (162)

9 2FIA\_B acetyltransferase; Acet 98.7 9.3E-09 8.7E-14 78.4 13.1 99 7-114 32-138 (162)

10 1B87\_A AMINOGLYCOSIDE N6'-ACET 98.6 6.6E-09 6.3E-14 85.1 12.3 105 1-114 20-158 (181)

11 1N71\_B (6')-Ii; AMINOGLYCOSIDE 98.6 8.2E-09 7.8E-14 84.6 12.7 110 1-119 20-163 (180)

12 d2atra1 d.108.1.1 (A:1-137) Pr 98.6 1.3E-08 1.3E-13 75.8 12.8 93 16-117 32-129 (137)

13 d1n71b\_ d.108.1.1 (B:) Aminogl 98.6 9.5E-09 8.9E-14 84.0 12.6 110 1-119 20-163 (179)

14 d4m85a1 d.108.1.0 (A:1-182) au 98.6 1.4E-08 1.3E-13 79.9 13.2 91 16-115 39-171 (182)

15 d2fiwa1 d.108.1.1 (A:0-157) Pr 98.6 8.7E-09 8.2E-14 78.5 11.7 96 16-120 51-146 (158)

16 4YFJ\_B Aminoglycoside 3'-N-ace 98.6 1.8E-08 1.7E-13 79.5 13.7 114 2-124 50-177 (182)

17 4W83\_A AAC(3')-Ib (E.C.2.3.1.6 98.6 1.8E-08 1.7E-13 79.5 13.7 114 2-124 50-177 (182)

18 2FIW\_A GCN5-related N-acetyltr 98.6 9.6E-09 9E-14 80.2 11.9 96 16-120 53-148 (172)

19 4E0A\_B BH1408 protein; Structu 98.6 1.7E-08 1.6E-13 77.0 13.1 110 6-124 33-161 (164)

20 d2ae6d\_ d.108.1.1 (D:) automat 98.6 1.8E-08 1.7E-13 76.2 12.9 100 7-115 28-138 (157)

21 4M85\_B Uncharacterized protein 98.6 1.5E-08 1.4E-13 79.5 12.9 101 15-124 41-183 (186)

22 4M85\_A Uncharacterized protein 98.6 1.5E-08 1.4E-13 79.5 12.9 101 15-124 41-183 (186)

23 2OH1\_D Acetyltransferase, GNAT 98.6 8.3E-09 7.9E-14 79.4 11.2 91 15-114 55-166 (179)

24 2OH1\_A Acetyltransferase, GNAT 98.6 8.3E-09 7.9E-14 79.4 11.2 91 15-114 55-166 (179)

25 2OZH\_A Hypothetical protein XC 98.6 8.8E-09 8.3E-14 78.4 11.1 108 11-128 31-142 (142)

26 2ATR\_A acetyltransferase, GNAT 98.6 1.6E-08 1.5E-13 75.1 12.2 100 8-116 24-128 (138)

27 d3ld2a1 d.108.1.0 (A:1-158) au 98.6 1.6E-08 1.5E-13 76.6 12.3 92 15-115 37-138 (158)

28 3JVN\_A Acetyltransferase (E.C. 98.6 1.7E-08 1.6E-13 77.3 12.5 103 16-127 45-164 (166)

29 d1s5kb\_ d.108.1.1 (B:) Aminogl 98.6 1E-08 9.8E-14 75.9 10.7 106 1-115 16-138 (144)

30 2AE6\_A acetyltransferase, GNAT 98.6 2.1E-08 2E-13 76.5 12.7 101 6-115 34-145 (166)

31 2AE6\_D acetyltransferase, GNAT 98.6 2.1E-08 2E-13 76.5 12.7 101 6-115 34-145 (166)

32 2K5T\_A Uncharacterized protein 98.6 1.1E-08 1E-13 75.0 10.7 84 23-115 35-124 (128)

33 4F6A\_A BH1408 protein; Structu 98.6 2.9E-08 2.7E-13 74.3 12.9 105 2-115 29-152 (156)

34 2R1I\_A GCN5-related N-acetyltr 98.6 1.1E-08 1E-13 78.9 10.8 92 16-116 59-162 (172)

35 1YVK\_D hypothetical protein BS 98.6 2E-08 1.9E-13 79.6 12.4 100 12-120 26-132 (163)

36 5F47\_B aminoglycoside acetyltr 98.6 2.3E-08 2.1E-13 75.1 12.2 102 8-118 38-153 (157)

37 1CJW\_A TRANSFERASE + COA-S-ACE 98.6 3.2E-08 3E-13 75.7 13.0 110 8-126 31-162 (166)

38 d1tiqb1 d.108.1.1 (B:2-172) Pr 98.6 2.4E-08 2.3E-13 76.3 12.3 99 13-120 44-158 (171)

39 2PC1\_A Acetyltransferase, GNAT 98.6 2.1E-08 2E-13 80.7 12.5 92 16-116 62-173 (201)

40 5JPH\_C Acetyltransferase SACOL 98.6 9.9E-09 9.3E-14 77.9 10.0 107 1-116 20-130 (144)

41 2I6C\_A putative acetyltransfer 98.6 3.6E-08 3.4E-13 75.0 13.1 103 4-115 28-140 (160)

42 d1cjwa\_ d.108.1.1 (A:) Seroton 98.6 3.3E-08 3.1E-13 75.6 12.9 110 8-126 31-162 (166)

43 d2jdda\_ d.108.1.1 (A:) Probabl 98.6 2E-08 1.9E-13 76.0 11.6 117 1-126 14-140 (145)

44 d4f0ya\_ d.108.1.0 (A:) automat 98.6 2.2E-08 2E-13 74.2 11.5 98 16-122 31-145 (145)

45 d1yvka1 d.108.1.1 (A:5-155) Hy 98.5 2.7E-08 2.5E-13 77.1 12.4 94 12-114 22-122 (151)

46 4CRY\_B ASPARTATE 1-DECARBOXYLA 98.5 1.5E-08 1.4E-13 76.1 10.7 90 23-121 35-130 (137)

47 d2ge3b\_ d.108.1.1 (B:) automat 98.5 2.8E-08 2.7E-13 75.6 12.3 91 15-114 41-142 (163)

48 4L8A\_A Uncharacterized protein 98.5 3.4E-08 3.2E-13 75.3 12.7 102 5-115 31-142 (162)

49 d1y7rb\_ d.108.1.1 (B:) Hypothe 98.5 3E-08 2.8E-13 74.4 12.2 102 7-118 20-129 (133)

50 PF12568.7 ; DUF3749 ; Acetyltr 98.5 2.9E-08 2.8E-13 72.9 11.8 96 11-115 23-128 (129)

51 d4oaea1 d.108.1.1 (A:1-159) Pu 98.5 4.3E-08 4.1E-13 74.1 13.0 105 2-115 26-140 (159)

52 d4e2aa\_ d.108.1.0 (A:) automat 98.5 2.8E-08 2.6E-13 75.9 11.9 101 15-124 46-162 (170)

53 d1u6ma1 d.108.1.1 (A:4-189) Pu 98.5 3.6E-08 3.4E-13 77.1 12.8 105 10-123 28-181 (186)

54 3EXN\_A Probable acetyltransfer 98.5 2.5E-08 2.3E-13 75.9 11.6 91 23-122 60-157 (160)

55 3NE7\_A ACETYLTRANSFERASE; COEN 98.5 2.2E-08 2E-13 76.1 11.2 78 27-113 65-148 (159)

56 3DSB\_B Putative acetyltransfer 98.5 3.7E-08 3.5E-13 74.4 12.3 96 15-119 42-153 (157)

57 1S5K\_A aminoglycoside 6'-N-ace 98.5 1.7E-08 1.6E-13 77.7 10.7 107 1-116 37-160 (165)

58 4EVY\_A Aminoglycoside N(6')-ac 98.5 3.1E-08 2.9E-13 76.3 12.0 97 11-116 47-160 (166)

59 2FL4\_A spermine/spermidine ace 98.5 2.6E-08 2.5E-13 75.0 11.3 79 27-114 48-134 (149)

60 4QUS\_B Acetyltransferase YpeA 98.5 4.1E-08 3.9E-13 73.6 12.3 107 1-116 17-131 (149)

61 1Z4E\_A transcriptional regulat 98.5 4.1E-08 3.9E-13 73.1 12.2 105 2-115 30-149 (153)

62 d1yx0a1 d.108.1.1 (A:1-149) Hy 98.5 3.9E-08 3.6E-13 74.1 12.1 102 16-126 35-147 (149)

63 d1z4eb\_ d.108.1.1 (B:) Transcr 98.5 3.6E-08 3.4E-13 72.8 11.7 105 2-115 27-146 (150)

64 1YX0\_A hypothetical protein ys 98.5 3.3E-08 3.1E-13 76.2 11.9 111 16-135 35-156 (159)

65 d1y9kc\_ d.108.1.1 (C:) automat 98.5 4.2E-08 4E-13 75.5 12.4 96 10-114 19-121 (150)

66 1U6M\_C acetyltransferase, GNAT 98.5 4.7E-08 4.5E-13 78.1 13.1 98 15-121 40-182 (199)

67 3T9Y\_A Acetyltransferase, GNAT 98.5 3.7E-08 3.5E-13 73.4 11.7 92 15-115 39-146 (150)

68 3FYN\_A Integron gene cassette 98.5 2.9E-08 2.7E-13 77.8 11.6 93 15-116 58-165 (176)

69 5IB0\_E Uncharacterized protein 98.5 3.3E-08 3.1E-13 72.4 11.3 95 16-119 33-135 (137)

70 d1wwzb\_ d.108.1.1 (B:) Hypothe 98.5 3.6E-08 3.4E-13 74.2 11.8 92 15-115 41-146 (157)

71 1Y7R\_B hypothetical protein SA 98.5 4.3E-08 4E-13 73.4 12.1 101 8-118 21-129 (133)

72 3LD2\_D Putative acetyltransfer 98.5 3.9E-08 3.6E-13 79.2 12.6 95 15-118 71-175 (197)

73 3LD2\_B Putative acetyltransfer 98.5 3.9E-08 3.6E-13 79.2 12.6 95 15-118 71-175 (197)

74 2GE3\_A probable acetyltransfer 98.5 4.6E-08 4.4E-13 74.8 12.5 95 15-118 47-152 (170)

75 2GE3\_B probable acetyltransfer 98.5 4.6E-08 4.4E-13 74.8 12.5 95 15-118 47-152 (170)

76 d2x7ba\_ d.108.1.0 (A:) automat 98.5 5.1E-08 4.8E-13 73.5 12.5 101 11-120 25-146 (156)

77 d4r9mc\_ d.108.1.0 (C:) automat 98.5 5.1E-08 4.8E-13 74.7 12.7 91 16-115 42-143 (168)

78 4MBU\_A Similar to N-acetyltran 98.5 3E-08 2.8E-13 75.6 11.3 84 23-115 51-145 (166)

79 4MBU\_B Similar to N-acetyltran 98.5 3E-08 2.8E-13 75.6 11.3 84 23-115 51-145 (166)

80 1TIQ\_B Protease synthase and s 98.5 5E-08 4.7E-13 76.0 12.7 99 13-120 45-159 (180)

81 3I9S\_D Integron cassette prote 98.5 5E-08 4.7E-13 77.0 12.8 99 9-116 50-168 (183)

82 3I9S\_B Integron cassette prote 98.5 5E-08 4.7E-13 77.0 12.8 99 9-116 50-168 (183)

83 d4mbub\_ d.108.1.0 (B:) automat 98.5 4.5E-08 4.3E-13 74.4 12.0 90 17-115 42-142 (162)

84 3WR7\_C Spermidine N1-acetyltra 98.5 5.6E-08 5.3E-13 74.8 12.6 91 16-115 42-143 (170)

85 3WR7\_B Spermidine N1-acetyltra 98.5 5.6E-08 5.3E-13 74.8 12.6 91 16-115 42-143 (170)

86 1WWZ\_A hypothetical protein PH 98.5 3.8E-08 3.6E-13 74.1 11.4 92 15-115 43-148 (159)

87 PF13527.6 ; Acetyltransf\_9 ; A 98.5 2.8E-08 2.6E-13 72.2 10.3 81 22-111 42-133 (133)

88 2KCW\_A Uncharacterized acetylt 98.5 3.2E-08 3E-13 74.6 10.9 96 16-123 41-137 (147)

89 1YR0\_A phosphinothricin acetyl 98.5 4.5E-08 4.2E-13 76.1 12.0 91 15-114 44-146 (175)

90 d3fixd\_ d.108.1.0 (D:) automat 98.5 3.1E-08 2.9E-13 75.1 10.9 78 27-113 63-146 (157)

91 1Y9K\_B IAA acetyltransferase ( 98.5 5.2E-08 4.9E-13 75.3 12.3 97 15-120 27-130 (157)

92 1Y9K\_A IAA acetyltransferase ( 98.5 5.2E-08 4.9E-13 75.3 12.3 97 15-120 27-130 (157)

93 2AJ6\_A hypothetical protein MW 98.5 5.9E-08 5.5E-13 75.5 12.6 91 16-115 54-154 (159)

94 d2fe7a1 d.108.1.1 (A:3-158) Pr 98.5 2.9E-08 2.8E-13 75.0 10.7 84 23-115 47-142 (156)

95 5T7D\_D Phosphinothricin N-acet 98.5 5.8E-08 5.4E-13 76.4 12.7 91 16-115 54-155 (189)

96 5T7E\_D Phosphinothricin N-acet 98.5 5.8E-08 5.4E-13 76.4 12.7 91 16-115 54-155 (189)

97 2DXQ\_A Acetyltransferase; acet 98.5 4.4E-08 4.2E-13 72.8 11.5 93 15-116 39-146 (150)

98 d1yr0b\_ d.108.1.0 (B:) automat 98.5 5.1E-08 4.8E-13 73.9 12.0 92 15-115 41-144 (163)

99 d1xebg\_ d.108.1.1 (G:) Hypothe 98.5 2.2E-08 2.1E-13 75.5 9.9 85 23-116 45-136 (147)

100 d4j3gc\_ d.108.1.0 (C:) automat 98.5 4.8E-08 4.5E-13 73.9 11.7 91 16-115 41-143 (162)

101 1UFH\_B YYCN protein; alpha and 98.5 4.2E-08 4E-13 76.9 11.7 91 16-115 69-176 (180)

102 5HGZ\_A N-alpha-acetyltransfera 98.5 6.5E-08 6.1E-13 81.5 13.6 99 11-118 37-166 (243)

103 d2fl4a1 d.108.1.1 (A:1-146) Pr 98.5 3.8E-08 3.6E-13 73.5 10.9 79 27-114 47-133 (146)

104 1TIQ\_A Protease synthase and s 98.5 6.2E-08 5.9E-13 75.5 12.5 99 13-120 45-159 (180)

105 1S3Z\_B aminoglycoside 6'-N-ace 98.5 3.3E-08 3.1E-13 76.2 10.7 107 1-116 37-160 (165)

106 d1ufhb\_ d.108.1.1 (B:) Putativ 98.5 3.9E-08 3.7E-13 73.6 10.9 84 23-115 56-150 (154)

107 d3i9sd\_ d.108.1.0 (D:) automat 98.5 4.8E-08 4.6E-13 73.9 11.4 92 16-116 38-145 (160)

108 3F5B\_A Aminoglycoside N(6')ace 98.5 8.3E-08 7.8E-13 74.9 13.0 110 8-126 43-168 (182)

109 2OB0\_C Human MAK3 homolog; ace 98.5 7.6E-08 7.2E-13 74.6 12.7 99 11-118 30-140 (170)

110 2OB0\_A Human MAK3 homolog; ace 98.5 7.6E-08 7.2E-13 74.6 12.7 99 11-118 30-140 (170)

111 1XEB\_A PA0115, Acyl-CoA N-acyl 98.5 2.5E-08 2.3E-13 75.7 9.8 85 23-116 47-138 (150)

112 3OWC\_A Probable acetyltransfer 98.5 9E-08 8.5E-13 75.2 13.2 105 2-115 38-158 (188)

113 3D8P\_B acetyltransferase of GN 98.5 4.7E-08 4.4E-13 74.1 11.3 93 15-116 42-143 (163)

114 3D8P\_A acetyltransferase of GN 98.5 4.7E-08 4.4E-13 74.1 11.3 93 15-116 42-143 (163)

115 PF09390.9 ; DUF1999 ; Protein 98.5 2E-08 1.9E-13 78.9 9.5 89 15-113 43-150 (155)

116 4E2A\_B Putative acetyltransfer 98.5 5.7E-08 5.4E-13 79.0 12.4 100 15-123 82-197 (207)

117 1YK3\_F Hypothetical protein Rv 98.5 7.4E-08 7E-13 77.7 13.0 110 15-133 79-210 (210)

118 1MK4\_A Hypothetical protein yq 98.5 5.7E-08 5.3E-13 74.0 11.6 83 24-115 41-132 (157)

119 4PV6\_A N-terminal acetyltransf 98.5 5.4E-08 5.1E-13 75.5 11.7 88 24-120 49-143 (162)

120 4PV6\_H N-terminal acetyltransf 98.5 5.4E-08 5.1E-13 75.5 11.7 88 24-120 49-143 (162)

121 3EFA\_A Putative Acetyltransfer 98.5 3.2E-08 3E-13 74.0 10.1 88 23-119 45-136 (147)

122 3F8K\_A Protein acetyltransfera 98.4 1E-07 9.7E-13 72.9 13.1 103 12-124 39-146 (160)

123 d1yk3e\_ d.108.1.1 (E:) Hypothe 98.4 5.1E-08 4.8E-13 77.5 11.8 103 15-126 68-192 (196)

124 d4kvxb\_ d.108.1.0 (B:) automat 98.4 5.9E-08 5.5E-13 72.9 11.5 91 15-114 28-134 (152)

125 d4nsqa1 d.108.1.0 (A:493-652) 98.4 7.7E-08 7.2E-13 75.6 12.5 100 6-114 30-136 (160)

126 3DR8\_B yncA (E.C.2.3.1.-); Sal 98.4 7.1E-08 6.7E-13 74.2 12.1 89 17-114 46-145 (174)

127 4R3L\_A Uncharacterized N-acety 98.4 7E-08 6.6E-13 75.4 12.2 96 16-120 40-156 (173)

128 5ICV\_A N-alpha-acetyltransfera 98.4 7.7E-08 7.2E-13 74.8 12.3 96 11-115 32-158 (180)

129 PF17013.4 ; Acetyltransf\_15 ; 98.4 6.4E-08 6E-13 80.8 12.4 94 21-123 30-144 (204)

130 2R7H\_B Putative D-alanine N-ac 98.4 6.3E-08 5.9E-13 74.8 11.7 97 15-120 53-165 (177)

131 d1y9wb\_ d.108.1.1 (B:) Probabl 98.4 1E-07 9.6E-13 72.0 12.5 108 10-126 21-136 (140)

132 3H4Q\_A putative acetyltransfer 98.4 5.2E-08 4.9E-13 79.1 11.7 96 16-122 59-174 (188)

133 5JTF\_A Phosphinothricin N-acet 98.4 6.4E-08 6.1E-13 79.0 12.3 91 16-115 45-146 (207)

134 d3dr6b\_ d.108.1.1 (B:) automat 98.4 7.8E-08 7.3E-13 73.7 11.9 89 17-114 44-143 (169)

135 2JLM\_E PUTATIVE PHOSPHINOTHRIC 98.4 8E-08 7.6E-13 75.0 12.2 98 9-115 40-154 (182)

136 2JLM\_D PUTATIVE PHOSPHINOTHRIC 98.4 8E-08 7.6E-13 75.0 12.2 98 9-115 40-154 (182)

137 3DR6\_C yncA (E.C.2.3.1.-); ace 98.4 7.8E-08 7.4E-13 73.8 11.9 89 17-114 46-145 (174)

138 2J8M\_B ACETYLTRANSFERASE PA486 98.4 7.7E-08 7.3E-13 73.9 11.8 91 16-115 43-146 (172)

139 d1mk4b1 d.108.1.1 (B:1-156) Hy 98.4 6.5E-08 6.1E-13 73.7 11.3 84 24-116 40-132 (156)

140 3EO4\_C Uncharacterized protein 98.4 7E-08 6.6E-13 74.8 11.6 99 15-122 54-161 (164)

141 3EO4\_D Uncharacterized protein 98.4 7E-08 6.6E-13 74.8 11.6 99 15-122 54-161 (164)

142 3MGD\_A Predicted acetyltransfe 98.4 4.5E-08 4.2E-13 74.1 10.3 92 16-116 40-146 (157)

143 3MGD\_B Predicted acetyltransfe 98.4 4.5E-08 4.2E-13 74.1 10.3 92 16-116 40-146 (157)

144 4XNH\_C Yeast Saccharomyces cer 98.4 5.9E-08 5.6E-13 75.2 11.2 84 23-115 57-154 (176)

145 2Q0Y\_A GCN5-related N-acetyltr 98.4 5.3E-08 5E-13 72.7 10.5 97 15-120 41-153 (153)

146 2CY2\_A probable acetyltransfer 98.4 7E-08 6.6E-13 74.3 11.5 97 15-120 44-157 (174)

147 1WK4\_B ttk003001606; ttk003001 98.4 7E-08 6.6E-13 74.3 11.5 97 15-120 44-157 (174)

148 3LOD\_A Putative acyl-CoA N-acy 98.4 7.6E-08 7.2E-13 74.1 11.7 100 18-126 41-149 (162)

149 2JDD\_A GLYPHOSATE N-ACETYLTRAN 98.4 6.3E-08 6E-13 73.0 11.0 117 1-126 15-141 (146)

150 3EY5\_A Acetyltransferase-like, 98.4 4.6E-08 4.3E-13 78.0 10.7 102 16-126 41-154 (181)

151 2QEC\_A Histone acetyltransfera 98.4 8.6E-08 8.1E-13 77.0 12.3 106 19-135 55-204 (204)

152 4J3G\_A GCN5-related N-acetyltr 98.4 5.4E-08 5.1E-13 76.8 10.9 92 15-115 63-166 (185)

153 4JWP\_A GCN5-related N-acetyltr 98.4 5.4E-08 5.1E-13 76.8 10.9 92 15-115 63-166 (185)

154 4LX9\_A Uncharacterized N-acety 98.4 9.7E-08 9.1E-13 73.2 12.1 89 23-120 49-156 (167)

155 d2euib\_ d.108.1.1 (B:) automat 98.4 1.1E-07 1E-12 71.1 12.0 99 15-122 35-149 (150)

156 d3bj7b\_ d.108.1.1 (B:) automat 98.4 5.2E-08 4.9E-13 75.1 10.6 82 23-113 48-148 (165)

157 2FE7\_B probable N-acetyltransf 98.4 8E-08 7.6E-13 73.4 11.5 91 16-115 50-152 (166)

158 1ON0\_D similar to hypothetical 98.4 7.3E-08 6.9E-13 72.1 11.1 84 23-115 58-152 (158)

159 2QML\_A BH2621 protein; Structu 98.4 1.3E-07 1.2E-12 74.7 13.0 103 15-126 58-181 (198)

160 3PP9\_C Putative streptothricin 98.4 1.3E-07 1.2E-12 74.9 12.9 104 11-123 60-172 (187)

161 3PP9\_A Putative streptothricin 98.4 1.3E-07 1.2E-12 74.9 12.9 104 11-123 60-172 (187)

162 4FD4\_A Putative uncharacterize 98.4 7.1E-08 6.7E-13 78.6 11.7 91 17-116 51-189 (217)

163 1YGH\_B PROTEIN (GCN5) (2.3.1.4 98.4 1.5E-07 1.4E-12 73.2 13.0 96 10-114 30-134 (164)

164 4QC6\_B Bifunctional AAC/APH (E 98.4 1E-07 9.5E-13 73.9 12.0 95 11-114 39-159 (179)

165 d1wk4a\_ d.108.1.1 (A:) Probabl 98.4 8.7E-08 8.2E-13 73.8 11.5 97 15-120 44-157 (174)

166 1Y9W\_B Acetyltransferase; Baci 98.4 1.6E-07 1.5E-12 70.9 12.8 108 10-126 21-136 (140)

167 5HMN\_A aminoglycoside acetyltr 98.4 1.2E-07 1.1E-12 71.3 11.9 92 15-115 42-149 (159)

168 5HMN\_B aminoglycoside acetyltr 98.4 1.2E-07 1.1E-12 71.3 11.9 92 15-115 42-149 (159)

169 1YVO\_B conserved hypothetical 98.4 9.7E-08 9.1E-13 73.4 11.6 101 15-124 42-155 (172)

170 4KVX\_B N-terminal acetyltransf 98.4 8.6E-08 8.1E-13 72.6 11.2 92 15-115 29-136 (156)

171 4KVM\_F N-terminal acetyltransf 98.4 8.6E-08 8.1E-13 72.6 11.2 92 15-115 29-136 (156)

172 1M4I\_A Aminoglycoside 2'-N-ace 98.4 5.1E-08 4.8E-13 76.9 10.3 83 24-116 46-139 (181)

173 5IX3\_A Diamine N-acetyltransfe 98.4 1.2E-07 1.1E-12 73.4 12.1 92 15-115 42-144 (168)

174 4E8O\_B Aac(6')-Ih protein (E.C 98.4 1E-07 9.5E-13 73.4 11.6 92 16-116 52-161 (167)

175 d4ygoe\_ d.108.1.0 (E:) automat 98.4 1.2E-07 1.1E-12 73.1 12.1 91 16-115 41-143 (167)

176 d2vi7b\_ d.108.1.0 (B:) automat 98.4 1.1E-07 1E-12 72.3 11.7 92 15-115 41-145 (164)

177 d1yghb\_ d.108.1.1 (B:) Catalyt 98.4 1.8E-07 1.7E-12 72.8 13.0 96 10-114 30-134 (164)

178 1Z4R\_A General control of amin 98.4 1.4E-07 1.3E-12 75.3 12.6 100 7-115 34-140 (168)

179 5H86\_A Histone acetyltransfera 98.4 1.4E-07 1.3E-12 75.3 12.6 100 7-115 34-140 (168)

180 1VHS\_A similar to phosphinothr 98.4 7.8E-08 7.4E-13 74.9 11.0 91 15-114 42-144 (175)

181 d3r9gb\_ d.108.1.0 (B:) automat 98.4 1.3E-07 1.2E-12 72.4 12.0 93 15-116 49-155 (173)

182 d5dwnc\_ d.108.1.0 (C:) automat 98.4 1.3E-07 1.2E-12 73.5 12.1 92 15-115 41-146 (178)

183 4LUA\_A Uncharacterized protein 98.4 9.8E-08 9.3E-13 73.3 11.3 91 16-115 42-145 (167)

184 3C26\_A Putative acetyltransfer 98.4 1.2E-07 1.1E-12 82.3 13.0 99 15-122 50-154 (266)

185 d1vhsb1 d.108.1.1 (B:2-163) Pu 98.4 7.9E-08 7.5E-13 72.9 10.4 91 16-115 40-142 (162)

186 d2i79e\_ d.108.1.0 (E:) automat 98.4 1.3E-07 1.2E-12 72.5 11.7 92 15-115 44-148 (168)

187 3D3S\_A L-2,4-diaminobutyric ac 98.4 9.6E-08 9.1E-13 76.3 11.3 92 15-115 56-158 (189)

188 3D3S\_C L-2,4-diaminobutyric ac 98.4 9.6E-08 9.1E-13 76.3 11.3 92 15-115 56-158 (189)

189 2EUI\_D Probable acetyltransfer 98.4 1.3E-07 1.3E-12 70.8 11.4 93 15-116 35-143 (153)

190 3ZJ0\_A ACETYLTRANSFERASE; TRAN 98.4 6.4E-08 6E-13 78.8 10.4 83 23-114 54-193 (206)

191 2VI7\_B ACETYLTRANSFERASE PA137 98.4 1.5E-07 1.4E-12 73.1 12.1 91 16-115 47-150 (177)

192 2VI7\_C ACETYLTRANSFERASE PA137 98.4 1.5E-07 1.4E-12 73.1 12.1 91 16-115 47-150 (177)

193 d1yrec\_ d.108.1.1 (C:) automat 98.4 1.5E-07 1.4E-12 73.3 12.1 95 12-115 39-148 (182)

194 d1yvoa1 d.108.1.1 (A:4-172) Hy 98.4 1.1E-07 1E-12 72.7 11.0 91 16-115 40-143 (169)

195 2I79\_C Acetyltransferase, GNAT 98.4 1.4E-07 1.3E-12 72.5 11.6 92 15-115 47-151 (172)

196 2I79\_E Acetyltransferase, GNAT 98.4 1.4E-07 1.3E-12 72.5 11.6 92 15-115 47-151 (172)

197 4MI4\_C Spermidine n1-acetyltra 98.4 1.4E-07 1.3E-12 76.1 12.1 92 15-115 67-170 (197)

198 4NXY\_A Acyl-CoA synthetase; Ly 98.4 7.1E-08 6.7E-13 76.7 10.3 91 15-115 78-184 (194)

199 3FIX\_D N-ACETYLTRANSFERASE; N- 98.4 7.9E-08 7.4E-13 76.4 10.5 78 27-113 89-172 (183)

200 d1m4db\_ d.108.1.1 (B:) Aminogl 98.3 7.7E-08 7.3E-13 75.7 10.2 82 24-115 41-133 (176)

201 3QB8\_A A654L protein; GNAT N-A 98.3 9E-08 8.5E-13 78.0 10.9 93 15-116 45-170 (197)

202 d2ganb\_ d.108.1.1 (B:) Hypothe 98.3 1.1E-07 1E-12 75.8 11.1 83 23-115 65-169 (181)

203 2VEZ\_A PUTATIVE GLUCOSAMINE 6- 98.3 1.1E-07 1.1E-12 75.8 11.3 91 16-118 85-189 (190)

204 2VXK\_A GLUCOSAMINE 6-PHOSPHATE 98.3 1.1E-07 1.1E-12 75.8 11.3 91 16-118 85-189 (190)

205 3EG7\_B Spermidine n1-acetyltra 98.3 1.6E-07 1.5E-12 73.0 11.8 92 15-115 46-149 (176)

206 3PZJ\_B Probable acetyltransfer 98.3 1.5E-07 1.4E-12 75.5 12.1 91 16-115 80-183 (209)

207 3PZJ\_A Probable acetyltransfer 98.3 1.5E-07 1.4E-12 75.5 12.1 91 16-115 80-183 (209)

208 5DWM\_C Phosphinothricin N-acet 98.3 1.9E-07 1.8E-12 75.1 12.6 91 16-115 50-154 (187)

209 5DWN\_A Phosphinothricin N-acet 98.3 1.9E-07 1.8E-12 75.1 12.5 91 16-115 50-154 (187)

210 d3fb3a\_ d.108.1.0 (A:) automat 98.3 7.2E-08 6.7E-13 70.9 9.3 80 27-115 49-138 (142)

211 4H89\_A GCN5-related N-acetyltr 98.3 1.2E-07 1.1E-12 72.8 10.8 87 23-118 58-156 (173)

212 3JUW\_A Probable GnaT-family ac 98.3 1.7E-07 1.6E-12 71.8 11.7 93 15-116 48-163 (175)

213 3JUW\_C Probable GnaT-family ac 98.3 1.7E-07 1.6E-12 71.8 11.7 93 15-116 48-163 (175)

214 5K9N\_B Polyamine N acetyltrans 98.3 1.3E-07 1.2E-12 76.5 11.4 92 16-116 51-188 (216)

215 5K9N\_A Polyamine N acetyltrans 98.3 1.1E-07 1.1E-12 76.8 11.0 92 16-116 51-188 (216)

216 PF08444.9 ; Gly\_acyl\_tr\_C ; Ar 98.3 4.7E-08 4.4E-13 67.8 7.6 82 27-118 1-85 (89)

217 1QSM\_A HISTONE ACETYLTRANSFERA 98.3 1E-07 9.8E-13 71.8 10.1 80 27-115 54-147 (152)

218 2Q7B\_A Acetyltransferase, GNAT 98.3 1.6E-07 1.5E-12 74.9 11.5 93 15-116 59-162 (181)

219 d2jlmb1 d.108.1.0 (B:7-182) au 98.3 2.2E-07 2.1E-12 72.2 12.0 92 15-115 44-148 (176)

220 1VKC\_B putative acetyl transfe 98.3 2.6E-07 2.4E-12 71.6 12.3 91 15-115 49-154 (158)

221 d2zxva\_ d.108.1.0 (A:) automat 98.3 1.9E-07 1.8E-12 73.1 11.7 91 15-115 51-153 (188)

222 3R95\_A MccE protein; Microcin 98.3 2.3E-07 2.2E-12 72.5 12.1 92 15-115 63-168 (188)

223 3R9F\_A MccE protein; Microcin 98.3 2.3E-07 2.2E-12 72.5 12.1 92 15-115 63-168 (188)

224 5K04\_B Uncharacterized protein 98.3 2.3E-07 2.2E-12 72.0 12.0 91 15-114 30-135 (170)

225 d4jxqa\_ d.108.1.0 (A:) automat 98.3 2.1E-07 2E-12 73.0 11.8 91 16-115 43-146 (185)

226 3GY9\_A GCN5-related N-acetyltr 98.3 1.8E-07 1.7E-12 70.4 10.9 86 23-119 47-139 (150)

227 4FD7\_B Putative uncharacterize 98.3 1.4E-07 1.3E-12 77.5 11.2 92 15-116 75-210 (238)

228 3FBU\_B Acetyltransferase, GNAT 98.3 1.5E-07 1.5E-12 73.2 10.8 84 23-115 56-147 (168)

229 d1bo4b\_ d.108.1.1 (B:) Aminogl 98.3 2.7E-07 2.6E-12 67.4 11.5 87 11-106 36-136 (136)

230 d1z9ua\_ d.108.1.0 (A:) automat 98.3 2.8E-07 2.7E-12 71.9 12.2 91 15-114 50-154 (175)

231 5K18\_B Uncharacterized protein 98.3 3E-07 2.8E-12 73.6 12.5 95 15-118 30-139 (188)

232 2REE\_A CurA (E.C.2.3.1.38, 4.1 98.3 4.1E-07 3.8E-12 74.3 13.5 99 11-118 38-189 (224)

233 2REF\_B CurA (E.C.2.3.1.38, 4.1 98.3 4.1E-07 3.8E-12 74.3 13.5 99 11-118 38-189 (224)

234 2B5G\_A Diamine acetyltransfera 98.3 1E-07 9.6E-13 74.2 9.5 78 27-113 54-150 (171)

235 3I3G\_B N-acetyltransferase; TR 98.3 1.4E-07 1.3E-12 72.7 10.1 80 27-115 68-157 (161)

236 3FB3\_B N-acetyltransferase; tr 98.3 1.4E-07 1.3E-12 72.7 10.1 80 27-115 68-157 (161)

237 1QSO\_C HISTONE ACETYLTRANSFERA 98.3 1.5E-07 1.4E-12 70.4 10.0 80 27-115 51-144 (149)

238 d1qsoa\_ d.108.1.1 (A:) Histone 98.3 1.5E-07 1.4E-12 70.4 10.0 80 27-115 51-144 (149)

239 3IGR\_B Ribosomal-protein-S5-al 98.3 1.7E-07 1.6E-12 73.5 10.7 80 27-115 69-160 (184)

240 5NNR\_E N-terminal acetyltransf 98.3 3.3E-07 3.1E-12 74.8 12.7 90 16-114 30-144 (195)

241 5NNP\_B N-terminal acetyltransf 98.3 3.3E-07 3.1E-12 74.8 12.7 90 16-114 30-144 (195)

242 5ISV\_A Ornithine aminotransfer 98.3 2.1E-07 2E-12 72.4 11.1 80 27-115 42-127 (165)

243 4U9V\_B NatD; Acetyltransferase 98.3 2.4E-07 2.3E-12 73.7 11.6 98 12-118 68-179 (197)

244 1GHE\_B ACETYLTRANSFERASE (E.C. 98.3 2.4E-07 2.2E-12 71.5 11.3 89 16-114 51-152 (177)

245 1GHE\_A ACETYLTRANSFERASE (E.C. 98.3 2.4E-07 2.2E-12 71.5 11.3 89 16-114 51-152 (177)

246 2B4B\_B Diamine acetyltransfera 98.3 1.4E-07 1.3E-12 73.2 10.0 84 23-115 50-152 (171)

247 4JXQ\_A Acetyltransferase (E.C. 98.3 3.1E-07 2.9E-12 72.1 12.0 91 16-115 44-147 (186)

248 2G3A\_A acetyltransferase; acet 98.3 2.2E-07 2.1E-12 71.2 10.9 91 27-126 54-148 (152)

249 PF13673.6 ; Acetyltransf\_10 ; 98.3 4.1E-07 3.9E-12 67.1 11.8 90 13-113 17-111 (127)

250 4UA3\_B NatD (Naa40p); Acetyltr 98.3 3.4E-07 3.2E-12 72.5 12.0 95 10-113 59-166 (194)

No 1

>3BLN\_A Acetyltransferase GNAT family; NP\_981174.1, acetyltransferase GNAT family, Structural; HET: GOL, MRD; 1.31A {Bacillus cereus}

Probab=98.76 E-value=3.7e-09 Score=79.21 Aligned\_cols=101 Identities=13% Similarity=0.124 Sum\_probs=0.0 Template\_Neff=12.300

Q ss\_pred CCCCchHHHHHhhCCcEEEEEECCEEEEEEEEEeC----CEEEEEEECHHHCCCCHHHHHHHHHHHccccCeeEEEEEcC

Q Phabba\_Draft 11 PPLKFEPFDTMWSNGIMARHAHDDRPVGHLHWHPD----GEIDSITVHPDLQRRGIGTAMLKHAQDNPHIYESSYPVRHS 86 (219)

Q Consensus 11 ~~~~~~~l~~~~~~~~~~v~~~~~~liG~~~~~~~----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~~~i~l~v~~~ 86 (219)

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T Consensus 26 ~~~~~~~~~~~~~~~~~~~~~~~~~ivg~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~~~~~~ 105 (143)

T 3BLN\_A 26 NDSRRNYIKHSIDEGRCVIVKEDNSISGFLTYDTNFFDCTFLSLIIVSPTKRRRGYASSLLSYMLSHSPTQKIFSSTNES 105 (143)

T ss\_dssp SSTTHHHHHHHHHTTCEEEEEETTEEEEEEEEEEEETTEEEEEEEEECTTCCSSCHHHHHHHHHHHHCSSSEEEEEEETT

T ss\_pred CcchhhHHHHhccCCCEEEEEeCCEEEEEEEEEcCCCCeEEEEEEEECHHHcCCCHHHHHHHHHHhcCCCCcEEEEecCC

Q ss\_pred CcccccccccchhHHHHHcCCCEEeeeeeccccc

Q Phabba\_Draft 87 SHFSAAGRAWAQSDPDYHDPGDQNVTKADDDVSN 120 (219)

Q Consensus 87 n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~ 120 (219)

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T Consensus 106 n~---------~~~~~~~~~Gf~~~~~~~~~~~~ 130 (143)

T 3BLN\_A 106 NE---------SMQKVFNANGFIRSGIVENLDEG 130 (143)

T ss\_dssp CH---------HHHHHHHHTTCEEEEEECSSSTT

T ss\_pred CH---------HHHHHHHHCCCEEEEEeecCCcC

No 2

>d1q2ya\_ d.108.1.1 (A:) Probable acetyltransferase YjcF {Bacillus subtilis [TaxId: 1423]}

Probab=98.73 E-value=3.8e-09 Score=79.19 Aligned\_cols=117 Identities=15% Similarity=0.159 Sum\_probs=0.0 Template\_Neff=12.100

Q ss\_pred CCccccCCCCCCCCchHHHHHhhCCcEEEEEECCEEEEEEEEEeC---CEEEEEEECHHHCCCCHHHHHHHHHHHccccC

Q Phabba\_Draft 1 MHQAGANGDLPPLKFEPFDTMWSNGIMARHAHDDRPVGHLHWHPD---GEIDSITVHPDLQRRGIGTAMLKHAQDNPHIY 77 (219)

Q Consensus 1 ~~~~~~~~~~~~~~~~~l~~~~~~~~~~v~~~~~~liG~~~~~~~---~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~~ 77 (219)

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T Consensus 18 l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ivg~~~~~~~~~~~~i~~~~v~~~~r~~g~~~~l~~~~~~~~~~~ 97 (140)

T d1q2ya\_ 18 VREEVFVKEQNVPAEEEIDELENESEHIVVYDGEKPVGAGRWRMKDGYGKLERICVLKSHRSAGVGGIIMKALEKAAADG 97 (140)

T ss\_dssp HHHCCCCCCSCCCTTTTCCTTGGGSEEEEEEETTEEEEEEEEEEETTEEEEEEEECCGGGTTTTHHHHHHHHHHHHHHHT

T ss\_pred HhHHHhcccCCCChHHHHHHHhcCceEEEEEECCEEEEEEEEEEECCEEEEEEEEEcHHHCCCCHHHHHHHHHHHHHHhC

Q ss\_pred eeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeeeccccccceEEe

Q Phabba\_Draft 78 ESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDVSNWGYTAM 126 (219)

Q Consensus 78 ~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~~~~~~~ 126 (219)

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T Consensus 98 ~~~~~~~~~n~---------~~~~~~~k~Gf~~~~~~~~~~~~~~~~~~ 137 (140)

T d1q2ya\_ 98 GASGFILNAQT---------QAVPFYKKHGYRVLSEKEFLDAGIPHLQM 137 (140)

T ss\_dssp TCCSEEEEEEG---------GGHHHHHHTTCEESCSCCEESSSSEEEEE

T ss\_pred CCCEEEEecCH---------HHHHHHHHCCCEEeceeeeecCCCeeEEe

No 3

>3FNC\_B Putative acetyltransferase; GNAT, RimI, Acetyltransferase, Listeria innocua; HET: MLI, EDO; 1.75A {Listeria innocua}

Probab=98.72 E-value=7.2e-09 Score=78.88 Aligned\_cols=102 Identities=18% Similarity=0.260 Sum\_probs=0.0 Template\_Neff=12.600

Q ss\_pred hHHHHHhhCCcEEEEEECCEEEEEEEEEeC----CEEEEEEECHHHCCCCHHHHHHHHHHHcccc-CeeEEEEEcCCccc

Q Phabba\_Draft 16 EPFDTMWSNGIMARHAHDDRPVGHLHWHPD----GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI-YESSYPVRHSSHFS 90 (219)

Q Consensus 16 ~~l~~~~~~~~~~v~~~~~~liG~~~~~~~----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~-~~i~l~v~~~n~~~ 90 (219)

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T Consensus 51 ~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~i~~~~v~~~~r~~G~~~~l~~~~~~~~~~~~~~~~~~~~~n~-- 128 (163)

T 3FNC\_B 51 ETLHNRISATPFAVLEQADKVIGFANFIELEKGKSELAAFYLLPEVTQRGLGTELLEVGMTLFHVPLPMFVNVEKGNE-- 128 (163)

T ss\_dssp HHHHHHHHHSCEEEEEETTEEEEEEEEEEETTTEEEEEEEEECGGGTTSSHHHHHHHHHHHHHTCCSCEEEEEETTCH--

T ss\_pred HHHHhhhhcCCEEEEEeCCeEEEEEEEEEccCCeEEEEEEEECHHHcCCCHHHHHHHHHHHHccCCccEEEEEeCCCH--

Q ss\_pred ccccccchhHHHHHcCCCEEeeeeeccccccceEEe

Q Phabba\_Draft 91 AAGRAWAQSDPDYHDPGDQNVTKADDDVSNWGYTAM 126 (219)

Q Consensus 91 ~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~~~~~~~ 126 (219)

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T Consensus 129 -------~~~~~~~~~Gf~~~~~~~~~~~~~~~~~~ 157 (163)

T 3FNC\_B 129 -------TAIHFYKAKGFVQVEEFTEDFYGYPLETI 157 (163)

T ss\_dssp -------HHHHHHHHTTCEEEEEEEEEETTEEEEEE

T ss\_pred -------HHHHHHHHCCCEEeeEeeeccCCeeeeEe

No 4

>3FNC\_A Putative acetyltransferase; GNAT, RimI, Acetyltransferase, Listeria innocua; HET: EDO, MLI; 1.75A {Listeria innocua}

Probab=98.72 E-value=7.2e-09 Score=78.88 Aligned\_cols=102 Identities=18% Similarity=0.260 Sum\_probs=0.0 Template\_Neff=12.600

Q ss\_pred hHHHHHhhCCcEEEEEECCEEEEEEEEEeC----CEEEEEEECHHHCCCCHHHHHHHHHHHcccc-CeeEEEEEcCCccc

Q Phabba\_Draft 16 EPFDTMWSNGIMARHAHDDRPVGHLHWHPD----GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI-YESSYPVRHSSHFS 90 (219)

Q Consensus 16 ~~l~~~~~~~~~~v~~~~~~liG~~~~~~~----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~-~~i~l~v~~~n~~~ 90 (219)

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T Consensus 51 ~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~i~~~~v~~~~r~~G~~~~l~~~~~~~~~~~~~~~~~~~~~n~-- 128 (163)

T 3FNC\_A 51 ETLHNRISATPFAVLEQADKVIGFANFIELEKGKSELAAFYLLPEVTQRGLGTELLEVGMTLFHVPLPMFVNVEKGNE-- 128 (163)

T ss\_dssp HHHHHHHHHSCEEEEEETTEEEEEEEEEEEETTEEEEEEEEECGGGCSSSHHHHHHHHHHHHTTCCSSEEEEEETTCH--

T ss\_pred HHHHhhhhcCCEEEEEeCCeEEEEEEEEEccCCeEEEEEEEECHHHcCCCHHHHHHHHHHHHccCCccEEEEEeCCCH--

Q ss\_pred ccccccchhHHHHHcCCCEEeeeeeccccccceEEe

Q Phabba\_Draft 91 AAGRAWAQSDPDYHDPGDQNVTKADDDVSNWGYTAM 126 (219)

Q Consensus 91 ~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~~~~~~~ 126 (219)

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T Consensus 129 -------~~~~~~~~~Gf~~~~~~~~~~~~~~~~~~ 157 (163)

T 3FNC\_A 129 -------TAIHFYKAKGFVQVEEFTEDFYGYPLETI 157 (163)

T ss\_dssp -------HHHHHHHHTTCEEEEEEEEEETTEEEEEE

T ss\_pred -------HHHHHHHHCCCEEeeEeeeccCCeeeeEe

No 5

>1Q2Y\_A similar to hypothetical proteins; GCN5-related N-acetyltransferase superfamily fold, NYSGXRC; 2.0A {Bacillus subtilis} SCOP: d.108.1.1

Probab=98.71 E-value=4.6e-09 Score=78.39 Aligned\_cols=117 Identities=15% Similarity=0.159 Sum\_probs=0.0 Template\_Neff=12.300

Q ss\_pred CCccccCCCCCCCCchHHHHHhhCCcEEEEEECCEEEEEEEEEeC---CEEEEEEECHHHCCCCHHHHHHHHHHHccccC

Q Phabba\_Draft 1 MHQAGANGDLPPLKFEPFDTMWSNGIMARHAHDDRPVGHLHWHPD---GEIDSITVHPDLQRRGIGTAMLKHAQDNPHIY 77 (219)

Q Consensus 1 ~~~~~~~~~~~~~~~~~l~~~~~~~~~~v~~~~~~liG~~~~~~~---~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~~ 77 (219)

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T Consensus 18 l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ivg~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~~ 97 (140)

T 1Q2Y\_A 18 VREEVFVKEQNVPAEEEIDELENESEHIVVYDGEKPVGAGRWRMKDGYGKLERICVLKSHRSAGVGGIIMKALEKAAADG 97 (140)

T ss\_dssp HHHCCCCCCSCCCTTTTCCTTGGGSEEEEEEETTEEEEEEEEEEETTEEEEEEEECCGGGTTTTHHHHHHHHHHHHHHHT

T ss\_pred HhHHHhcccCCCChHHHHHHHhcCceEEEEEECCEEEEEEEEEEeCCEEEEEEEEEcHHHCCCCHHHHHHHHHHHHHHhC

Q ss\_pred eeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeeeccccccceEEe

Q Phabba\_Draft 78 ESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDVSNWGYTAM 126 (219)

Q Consensus 78 ~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~~~~~~~ 126 (219)

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T Consensus 98 g~~~~~~~~~~---------~~~~~~~~~Gf~~~~~~~~~~~~~~~~~~ 137 (140)

T 1Q2Y\_A 98 GASGFILNAQT---------QAVPFYKKHGYRVLSEKEFLDAGIPHLQM 137 (140)

T ss\_dssp TCCSEEEEEEG---------GGHHHHHHTTCEESCSCCEESSSSEEEEE

T ss\_pred CCCEEEEeccH---------HHHHHHHHCCCEEeceeeeecCCceeEEe

No 6

>d3fncb1 d.108.1.0 (B:1-160) automated matches {Listeria innocua [TaxId: 272626]}

Probab=98.70 E-value=8.5e-09 Score=78.57 Aligned\_cols=102 Identities=18% Similarity=0.260 Sum\_probs=0.0 Template\_Neff=12.400

Q ss\_pred hHHHHHhhCCcEEEEEECCEEEEEEEEEeC----CEEEEEEECHHHCCCCHHHHHHHHHHHcccc-CeeEEEEEcCCccc

Q Phabba\_Draft 16 EPFDTMWSNGIMARHAHDDRPVGHLHWHPD----GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI-YESSYPVRHSSHFS 90 (219)

Q Consensus 16 ~~l~~~~~~~~~~v~~~~~~liG~~~~~~~----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~-~~i~l~v~~~n~~~ 90 (219)

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T Consensus 48 ~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~i~~~~v~~~~r~~G~g~~l~~~~~~~~~~~~~~~~~~~~~n~-- 125 (160)

T d3fncb1 48 ETLHNRISATPFAVLEQADKVIGFANFIELEKGKSELAAFYLLPEVTQRGLGTELLEVGMTLFHVPLPMFVNVEKGNE-- 125 (160)

T ss\_dssp HHHHHHHHHSCEEEEEETTEEEEEEEEEEETTTEEEEEEEEECGGGTTSSHHHHHHHHHHHHHTCCSCEEEEEETTCH--

T ss\_pred HHHHHHhcCCCEEEEEeCCEEEEEEEEEEecCCeEEEEEEEECHHHcCCChhHHHHHHHHHHccCCCcEEEEEecCCH--

Q ss\_pred ccccccchhHHHHHcCCCEEeeeeeccccccceEEe

Q Phabba\_Draft 91 AAGRAWAQSDPDYHDPGDQNVTKADDDVSNWGYTAM 126 (219)

Q Consensus 91 ~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~~~~~~~ 126 (219)

.+.++|+++||+..+.......+......

T Consensus 126 -------~~~~~~~~~Gf~~~~~~~~~~~~~~~~~~ 154 (160)

T d3fncb1 126 -------TAIHFYKAKGFVQVEEFTEDFYGYPLETI 154 (160)

T ss\_dssp -------HHHHHHHHTTCEEEEEEEEEETTEEEEEE

T ss\_pred -------HHHHHHHHCCCEEeeeeeecccCcceeee

No 7

>d2fiaa1 d.108.1.1 (A:1-157) Probable acetyltransferase EF1919 {Enterococcus faecalis [TaxId: 1351]}

Probab=98.68 E-value=8.1e-09 Score=78.26 Aligned\_cols=96 Identities=7% Similarity=0.078 Sum\_probs=0.0 Template\_Neff=12.500

Q ss\_pred CCCCchHHHHHhhCCcEEEEEECCEEEEEEEEEeC-----CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEE

Q Phabba\_Draft 11 PPLKFEPFDTMWSNGIMARHAHDDRPVGHLHWHPD-----GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYP 82 (219)

Q Consensus 11 ~~~~~~~l~~~~~~~~~~v~~~~~~liG~~~~~~~-----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~ 82 (219)

.....+.+...+....++++..+++++|++.+... ..+..++|+|++|++|+|+.|++.+++.+.+ ..+.+.

T Consensus 36 ~~~~~~~~~~~~~~~~~~~~~~~~~~iG~~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~i~~~ 115 (157)

T d2fiaa1 36 DYPSQGDIQEDITKKRLYLLVHEEMIFSMATFCMEQEQDFVWLKRFATSPNYIAKGYGSLLFHELEKRAVWEGRRKMYAQ 115 (157)

T ss\_dssp SSSCHHHHHHHHHTTCEEEEEETTEEEEEEEEEECTTCSEEEEEEEEECGGGTTTTHHHHHHHHHHHHHHTTTCCEEEEE

T ss\_pred CCCChHHHHHHhccCcEEEEEECCeEEEEEEEEeccCCCEEEEEEEEeCHHHcCCCHHHHHHHHHHHHHHHhCCCEEEEE

Q ss\_pred EEcCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 83 VRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 83 v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

+...|. .+.++|+++||+..+...

T Consensus 116 ~~~~n~---------~~~~~~~~~Gf~~~~~~~ 139 (157)

T d2fiaa1 116 TNHTNH---------RMIRFFESKGFTKIHESL 139 (157)

T ss\_dssp EETTCH---------HHHHHHHHTTCEEEEEEC

T ss\_pred eecCCH---------HHHHHHHhcCCEEEeeee

No 8

>2FIA\_A acetyltransferase; Acetyltransferase, structural genomics, PSI, Protein; 2.6A {Enterococcus faecalis} SCOP: d.108.1.1

Probab=98.67 E-value=9.3e-09 Score=78.36 Aligned\_cols=99 Identities=7% Similarity=0.071 Sum\_probs=0.0 Template\_Neff=12.500

Q ss\_pred CCCCCCCCchHHHHHhhCCcEEEEEECCEEEEEEEEEeC-----CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---Ce

Q Phabba\_Draft 7 NGDLPPLKFEPFDTMWSNGIMARHAHDDRPVGHLHWHPD-----GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YE 78 (219)

Q Consensus 7 ~~~~~~~~~~~l~~~~~~~~~~v~~~~~~liG~~~~~~~-----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~ 78 (219)

.........+.+...+....++++..+|+++|++.+... ..+..+.|+|++|++|+|+.|+..+++.+.+ ..

T Consensus 32 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ivG~~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~~g~~~ 111 (162)

T 2FIA\_A 32 QWTKDYPSQGDIQEDITKKRLYLLVHEEMIFSMATFCMEQEQDFVWLKRFATSPNYIAKGYGSLLFHELEKRAVWEGRRK 111 (162)

T ss\_dssp CCCSSSSCHHHHHHHHHTTCEEEEEETTEEEEEEEEEECTTCSEEEEEEEEECGGGTTTTHHHHHHHHHHHHHHTTTCCE

T ss\_pred cCCCCCCCHHHHHHHHhcCCEEEEEECCeEEEEEEEeecccCCEEEEEEEEeCHhHCCCCHHHHHHHHHHHHHHHcCCCE

Q ss\_pred eEEEEEcCCcccccccccchhHHHHHcCCCEEeeee

Q Phabba\_Draft 79 SSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKA 114 (219)

Q Consensus 79 i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~ 114 (219)

+.+.+...|. .+.++|+++||+..+..

T Consensus 112 ~~~~~~~~n~---------~~~~~~~~~Gf~~~~~~ 138 (162)

T 2FIA\_A 112 MYAQTNHTNH---------RMIRFFESKGFTKIHES 138 (162)

T ss\_dssp EEEEEETTCH---------HHHHHHHHTTCEEEEEE

T ss\_pred EEEEeecCCH---------HHHHHHHhcCCEEeeEE

No 9

>2FIA\_B acetyltransferase; Acetyltransferase, structural genomics, PSI, Protein; 2.6A {Enterococcus faecalis} SCOP: d.108.1.1

Probab=98.67 E-value=9.3e-09 Score=78.36 Aligned\_cols=99 Identities=7% Similarity=0.071 Sum\_probs=0.0 Template\_Neff=12.500

Q ss\_pred CCCCCCCCchHHHHHhhCCcEEEEEECCEEEEEEEEEeC-----CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---Ce

Q Phabba\_Draft 7 NGDLPPLKFEPFDTMWSNGIMARHAHDDRPVGHLHWHPD-----GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YE 78 (219)

Q Consensus 7 ~~~~~~~~~~~l~~~~~~~~~~v~~~~~~liG~~~~~~~-----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~ 78 (219)

.........+.+...+....++++..+|+++|++.+... ..+..+.|+|++|++|+|+.|+..+++.+.+ ..

T Consensus 32 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ivG~~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~~g~~~ 111 (162)

T 2FIA\_B 32 QWTKDYPSQGDIQEDITKKRLYLLVHEEMIFSMATFCMEQEQDFVWLKRFATSPNYIAKGYGSLLFHELEKRAVWEGRRK 111 (162)

T ss\_dssp CCCSSTTCHHHHHHHHHTTCEEEECSSSCCCEEEEEECCTTCSEEEEEEEEECHHHHTTTHHHHHHHHHHHHHHTTTCCE

T ss\_pred cCCCCCCCHHHHHHHHhcCCEEEEEECCeEEEEEEEeecccCCEEEEEEEEeCHhHCCCCHHHHHHHHHHHHHHHcCCCE

Q ss\_pred eEEEEEcCCcccccccccchhHHHHHcCCCEEeeee

Q Phabba\_Draft 79 SSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKA 114 (219)

Q Consensus 79 i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~ 114 (219)

+.+.+...|. .+.++|+++||+..+..

T Consensus 112 ~~~~~~~~n~---------~~~~~~~~~Gf~~~~~~ 138 (162)

T 2FIA\_B 112 MYAQTNHTNH---------RMIRFFESKGFTKIHES 138 (162)

T ss\_dssp EEEEEETTCH---------HHHHHHHHHTCEEEEEE

T ss\_pred EEEEeecCCH---------HHHHHHHhcCCEEeeEE

No 10

>1B87\_A AMINOGLYCOSIDE N6'-ACETYLTRANSFERASE TYPE 1; AMINOGLYCOSIDE 6'-N-ACETYLTRANSFERASE, ANTIBIOTIC RESISTANCE, ACETYL; HET: ACO; 2.7A {Enterococcus faecium} SCOP: d.108.1.1

Probab=98.65 E-value=6.6e-09 Score=85.07 Aligned\_cols=105 Identities=13% Similarity=0.107 Sum\_probs=0.0 Template\_Neff=8.400

Q ss\_pred CCccccCCCCCCCCchHHHHHhhCCc-EEEEEECCEEEEEEEEEeC-----CEEEEEEECHHHCCCCHHHHHHHHHHHcc

Q Phabba\_Draft 1 MHQAGANGDLPPLKFEPFDTMWSNGI-MARHAHDDRPVGHLHWHPD-----GEIDSITVHPDLQRRGIGTAMLKHAQDNP 74 (219)

Q Consensus 1 ~~~~~~~~~~~~~~~~~l~~~~~~~~-~~v~~~~~~liG~~~~~~~-----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~ 74 (219)

++.......+.....+.+..+++... ++++.+++++||++.+... .++..++|.|++|++|+|++|++.+++.+

T Consensus 20 l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~iVG~~~~~~~~~~~~~~i~~~~v~~~~rg~Gig~~l~~~~~~~~ 99 (181)

T 1B87\_A 20 LLRLTWPEEYGDSSAEEVEEMMNPERIAVAAVDQDELVGFIGAIPQYGITGWELHPLVVESSRRKNQIGTRLVNYLEKEV 99 (181)

T ss\_dssp HHHHHCTTTCSTTHHHHHHHHTCTTSEEEEEEETTEEEEEEEEEEEETTTEEEEEEEEECTTSTTSSHHHHHHHHHHHHH

T ss\_pred HHhhhCCcccCCCCHHHHHHHhCCCeEEEEEEeCCEEEEEEEEEecCCcceEEEEEEEECHHHCCCCHHHHHHHHHHHHH

Q ss\_pred cc---CeeEEEEEcCC-------------------------cccccccccchhHHHHHcCCCEEeeee

Q Phabba\_Draft 75 HI---YESSYPVRHSS-------------------------HFSAAGRAWAQSDPDYHDPGDQNVTKA 114 (219)

Q Consensus 75 ~~---~~i~l~v~~~n-------------------------~~~~~~~~~~~~~~~y~r~Gf~~~~~~ 114 (219)

.. ..+.+.+...| . .+.+||+|+||+..+..

T Consensus 100 ~~~g~~~i~~~~~~~n~~~~~~~~~~~~~~~~~~~~~~~~~~---------~~~~~y~k~Gf~~~~~~ 158 (181)

T 1B87\_A 100 ASRGGITIYLGTDDLDHGTTLSQTDLYEHTFDKVASIQNLRE---------HPYEFYEKLGYKIVGVL 158 (181)

T ss\_dssp HHTTCCEEEEEEECCSSCBTTSSSCTTSSHHHHHHTCCBSSC---------CTHHHHHHTTCEEEEEE

T ss\_pred HHCCCcEEEEEecCCCCCcccccccccccccccccccccccc---------CcHHHHHHCCcEEEEEe

No 11

>1N71\_B (6')-Ii; AMINOGLYCOSIDE 6'-N-ACETYLTRANSFERASE, ANTIBIOTIC RESISTANCE, COENZYME; HET: COA, SO4; 1.8A {Enterococcus faecium} SCOP: d.108.1.1

Probab=98.65 E-value=8.2e-09 Score=84.56 Aligned\_cols=110 Identities=13% Similarity=0.101 Sum\_probs=0.0 Template\_Neff=8.100

Q ss\_pred CCccccCCCCCCCCchHHHHHhhCCc-EEEEEECCEEEEEEEEEeC-----CEEEEEEECHHHCCCCHHHHHHHHHHHcc

Q Phabba\_Draft 1 MHQAGANGDLPPLKFEPFDTMWSNGI-MARHAHDDRPVGHLHWHPD-----GEIDSITVHPDLQRRGIGTAMLKHAQDNP 74 (219)

Q Consensus 1 ~~~~~~~~~~~~~~~~~l~~~~~~~~-~~v~~~~~~liG~~~~~~~-----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~ 74 (219)

+........+.....+.+...+.... ++++.+++++||++.+... .++..++|+|++|++|+|+.|++.+++.+

T Consensus 20 l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~iVG~~~~~~~~~~~~~~i~~~~v~~~~r~~G~g~~l~~~~~~~~ 99 (180)

T 1N71\_B 20 LLRLTWPEEYGDSSAEEVEEMMNPERIAVAAVDQDELVGFIGAIPQYGITGWELHPLVVESSRRKNQIGTRLVNYLEKEV 99 (180)

T ss\_dssp HHHHHCTTTSSTTHHHHHHHTTCTTSEEEEEEETTEEEEEEEEEEEETTTEEEEEEEEECGGGCSSSHHHHHHHHHHHHH

T ss\_pred HHhhcCccccCCCCHHHHHHHhCCccEEEEEEeCCEEEEEEEEEecCCCceEEEEEEEECHHHCCCCHHHHHHHHHHHHH

Q ss\_pred cc---CeeEEEEEcCC-------------------------cccccccccchhHHHHHcCCCEEeeeeecccc

Q Phabba\_Draft 75 HI---YESSYPVRHSS-------------------------HFSAAGRAWAQSDPDYHDPGDQNVTKADDDVS 119 (219)

Q Consensus 75 ~~---~~i~l~v~~~n-------------------------~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~ 119 (219)

+. ..+.+.+...| . .+.+||+|+||+..+.+.....

T Consensus 100 ~~~g~~~i~l~~~~~n~~~~~~~~~~~~~~~~~~~~~~~~~~---------~~~~~y~k~Gf~~~~~~~~~~~ 163 (180)

T 1N71\_B 100 ASRGGITIYLGTDDLDHGTTLSQTDLYEHTFDKVASIQNLRE---------HPYEFYEKLGYKIVGVLPNANG 163 (180)

T ss\_dssp HHTTCCEEEEEEECSSSCBTTSSSCTTSSHHHHHHTCCBSSC---------CTHHHHHTTTCEEEEEETTTTS

T ss\_pred HHCCCCEEEEEecCCCCCcccccccccccccccchhhccccc---------ccHHHHHHcCcEEEEEEeCCCC

No 12

>d2atra1 d.108.1.1 (A:1-137) Probable acetyltransferase SP0256 {Pneumococcus (Streptococcus pneumoniae) [TaxId: 1313]}

Probab=98.64 E-value=1.3e-08 Score=75.78 Aligned\_cols=93 Identities=20% Similarity=0.231 Sum\_probs=0.0 Template\_Neff=12.200

Q ss\_pred hHHHHHhhCCc-EEEEEECCEEEEEEEEEeC----CEEEEEEECHHHCCCCHHHHHHHHHHHccccCeeEEEEEcCCccc

Q Phabba\_Draft 16 EPFDTMWSNGI-MARHAHDDRPVGHLHWHPD----GEIDSITVHPDLQRRGIGTAMLKHAQDNPHIYESSYPVRHSSHFS 90 (219)

Q Consensus 16 ~~l~~~~~~~~-~~v~~~~~~liG~~~~~~~----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~~~i~l~v~~~n~~~ 90 (219)

+.+........ .+++.++|++||++.+... ..+..++|+|++|++|+|+.|++.+++.+............|.

T Consensus 32 ~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~i~~~~v~~~~r~~G~~~~l~~~~~~~~~~~~~~~~~~~~n~-- 109 (137)

T d2atra1 32 EMLEQALSHSLVIYLALDGDAVVGLIRLVGDGFSSVFVQDLIVLPSYQRQGIGSSLMKEALGNFKEAYQVQLATEETE-- 109 (137)

T ss\_dssp CHHHHHHTSCSEEEEEEETTEEEEEEEEEECSSSEEEEEEEEECTTSCSSSHHHHHHHHHHGGGTTCSEEECCCCCCH--

T ss\_pred HHHHHHHhcCcEEEEEEcCCeEEEEEEEEcCCCcEEEEEEEEECHHHccCCHHHHHHHHHHHhccceeEEEEEEcCcH--

Q ss\_pred ccccccchhHHHHHcCCCEEeeeeecc

Q Phabba\_Draft 91 AAGRAWAQSDPDYHDPGDQNVTKADDD 117 (219)

Q Consensus 91 ~~~~~~~~~~~~y~r~Gf~~~~~~~~~ 117 (219)

.+.++|+++||+..+.....

T Consensus 110 -------~~~~~~~~~Gf~~~~~~~~~ 129 (137)

T d2atra1 110 -------KNVGFYRSMGFEILSTYDCT 129 (137)

T ss\_dssp -------HHHHHHHHTTCCCGGGGTCC

T ss\_pred -------HHHHHHHHcCcEEEeeeecc

No 13

>d1n71b\_ d.108.1.1 (B:) Aminoglycoside 6'-N-acetyltransferase {Enterococcus faecium [TaxId: 1352]}

Probab=98.63 E-value=9.5e-09 Score=84.02 Aligned\_cols=110 Identities=13% Similarity=0.109 Sum\_probs=0.0 Template\_Neff=8.400

Q ss\_pred CCccccCCCCCCCCchHHHHHhhCCc-EEEEEECCEEEEEEEEEeC-----CEEEEEEECHHHCCCCHHHHHHHHHHHcc

Q Phabba\_Draft 1 MHQAGANGDLPPLKFEPFDTMWSNGI-MARHAHDDRPVGHLHWHPD-----GEIDSITVHPDLQRRGIGTAMLKHAQDNP 74 (219)

Q Consensus 1 ~~~~~~~~~~~~~~~~~l~~~~~~~~-~~v~~~~~~liG~~~~~~~-----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~ 74 (219)

+........+.....+.+...+.... ++++.+++++||++.+... .++..++|+|++|++|+|+.|++.+++.+

T Consensus 20 l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~iVG~~~~~~~~~~~~~~i~~~~v~~~~r~~Gig~~l~~~~~~~~ 99 (179)

T d1n71b\_ 20 LLRLTWPEEYGDSSAEEVEEMMNPERIAVAAVDQDELVGFIGAIPQYGITGWELHPLVVESSRRKNQIGTRLVNYLEKEV 99 (179)

T ss\_dssp HHHHHCTTTSSTTHHHHHHHTTCTTSEEEEEEETTEEEEEEEEEEEETTTEEEEEEEEECGGGCSSSHHHHHHHHHHHHH

T ss\_pred HHHhhCCcccCCCCHHHHHHHcCCCcEEEEEEeCCEEEEEEEEEecCCcceEEEEEEEECHHHCCCCHHHHHHHHHHHHH

Q ss\_pred cc---CeeEEEEEc-----------------------CC--cccccccccchhHHHHHcCCCEEeeeeecccc

Q Phabba\_Draft 75 HI---YESSYPVRH-----------------------SS--HFSAAGRAWAQSDPDYHDPGDQNVTKADDDVS 119 (219)

Q Consensus 75 ~~---~~i~l~v~~-----------------------~n--~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~ 119 (219)

.. ..+.+.+.. .| . .+.+||+|+||+..+......+

T Consensus 100 ~~~~~~~i~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~n~~~---------~~~~~y~k~Gf~~~~~~~~~~g 163 (179)

T d1n71b\_ 100 ASRGGITIYLGTDDLDHGTTLSQTDLYEHTFDKVASIQNLRE---------HPYEFYEKLGYKIVGVLPNANG 163 (179)

T ss\_dssp HHTTCCEEEEEEECSSSCBTTSSSCTTSSHHHHHHTCCBSSC---------CTHHHHHTTTCEEEEEETTTTS

T ss\_pred HHCCCCEEEEEecCCCCCcccccccccccccccchhhccccc---------chHHHHHHcCcEEEEEeeCCCC

No 14

>d4m85a1 d.108.1.0 (A:1-182) automated matches {Staphylococcus aureus [TaxId: 158878]}

Probab=98.63 E-value=1.4e-08 Score=79.89 Aligned\_cols=91 Identities=13% Similarity=0.136 Sum\_probs=0.0 Template\_Neff=11.900

Q ss\_pred hHHHHHhhCC-------cEEEEEECCEEEEEEEEEe---------------------------------C--CEEEEEEE

Q Phabba\_Draft 16 EPFDTMWSNG-------IMARHAHDDRPVGHLHWHP---------------------------------D--GEIDSITV 53 (219)

Q Consensus 16 ~~l~~~~~~~-------~~~v~~~~~~liG~~~~~~---------------------------------~--~~i~~l~V 53 (219)

+.+...+... .++++.+++++||++.+.. . .++..++|

T Consensus 39 ~~~~~~~~~~~~~~~~~~~~v~~~~~~ivG~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~i~~~~V 118 (182)

T d4m85a1 39 DAIEKSCVDATYRTFYQHILVYEVENKVAGCIISYSGENELKYEKAWELLDLPEEIKQYGTPLPVKEAKDDEYYIETIAT 118 (182)

T ss\_dssp HHHHHHHHSSCCTTCGGGEEEEEETTEEEEEEEEEEGGGHHHHHHGGGGSCCCHHHHTTCCSCCSCCSCTTCEEEEEEEE

T ss\_pred HHHHHHhcCCCcccceecEEEEEECCeEEEEEEEEcCCchhhHHHHHHHhcccHHHHhhCCCCCCCCCCCCeEEEEEEEe

Q ss\_pred CHHHCCCCHHHHHHHHHHHccccCeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 54 HPDLQRRGIGTAMLKHAQDNPHIYESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 54 ~p~~R~~Gig~~Ll~~~~~~~~~~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

+|++|++|||++|++.+++.+....+.+.+...|. .+.++|+|+||+..+...

T Consensus 119 ~p~~r~~Gig~~l~~~~~~~~~~~~i~~~~~~~n~---------~~~~~y~k~Gf~~~~~~~ 171 (182)

T d4m85a1 119 FAAYRGRGIATKLLTSLLESNTHVKWSLNCDINNE---------AALKLYKKVGFISDGQIE 171 (182)

T ss\_dssp CGGGTTSSHHHHHHHHHHHTCTTSCEEEEEETTCH---------HHHHHHHHTTCEEEEEEE

T ss\_pred CHHHCCCCHHHHHHHHHHHhcCCCeeEEEEEeCCH---------HHHHHHHhcCCEEeeEEE

No 15

>d2fiwa1 d.108.1.1 (A:0-157) Probable N-acetyltransferase RPA1999 {Rhodopseudomonas palustris [TaxId: 1076]}

Probab=98.63 E-value=8.7e-09 Score=78.51 Aligned\_cols=96 Identities=17% Similarity=0.219 Sum\_probs=0.0 Template\_Neff=12.300

Q ss\_pred hHHHHHhhCCcEEEEEECCEEEEEEEEEeCCEEEEEEECHHHCCCCHHHHHHHHHHHccccCeeEEEEEcCCcccccccc

Q Phabba\_Draft 16 EPFDTMWSNGIMARHAHDDRPVGHLHWHPDGEIDSITVHPDLQRRGIGTAMLKHAQDNPHIYESSYPVRHSSHFSAAGRA 95 (219)

Q Consensus 16 ~~l~~~~~~~~~~v~~~~~~liG~~~~~~~~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~~~i~l~v~~~n~~~~~~~~ 95 (219)

..+........++++..++++||++.+....++..+.|+|++|++|+|++|++.+++.+....+.......|.

T Consensus 51 ~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~v~~~~r~~G~~~~l~~~~~~~~~~~~~~~~~~~~n~------- 123 (158)

T d2fiwa1 51 AKFAARLSGQLTLIATLQGVPVGFASLKGPDHIDMLYVHPDYVGRDVGTTLIDALEKLAGARGALILTVDASD------- 123 (158)

T ss\_dssp HHHHHHHHTSEEEEEEETTEEEEEEEEETTTEEEEEEECGGGCSSSHHHHHHHHHHHHHHTTTCSEEEEEECT-------

T ss\_pred HHHHHHccCceEEEEEeCCceEEEEEeecCcEEEEEEECHHHCCCCHHHHHHHHHHHHHHhCCCeEEEEeCCh-------

Q ss\_pred cchhHHHHHcCCCEEeeeeeccccc

Q Phabba\_Draft 96 WAQSDPDYHDPGDQNVTKADDDVSN 120 (219)

Q Consensus 96 ~~~~~~~y~r~Gf~~~~~~~~~~~~ 120 (219)

.+.++|+++||+..+.......+

T Consensus 124 --~~~~~~~~~Gf~~~~~~~~~~~~ 146 (158)

T d2fiwa1 124 --NAAEFFAKRGYVAKQRNTVSING 146 (158)

T ss\_dssp --TTHHHHHTTTCEEEEEEEEEETT

T ss\_pred --HHHHHHHHCCcEEcceeEEeeCC

No 16

>4YFJ\_B Aminoglycoside 3'-N-acetyltransferase; GNAT FOLD, ANTIBIOTIC RESISTANCE, STRUCTURAL; HET: SO4; 2.2A {Pseudomonas aeruginosa}

Probab=98.62 E-value=1.8e-08 Score=79.53 Aligned\_cols=114 Identities=12% Similarity=-0.009 Sum\_probs=0.0 Template\_Neff=11.700

Q ss\_pred CccccCCCCCCCCchHHHHHhhCCc--EEEEEECCEEEEEEEEEeC---------CEEEEEEECHHHCCCCHHHHHHHHH

Q Phabba\_Draft 2 HQAGANGDLPPLKFEPFDTMWSNGI--MARHAHDDRPVGHLHWHPD---------GEIDSITVHPDLQRRGIGTAMLKHA 70 (219)

Q Consensus 2 ~~~~~~~~~~~~~~~~l~~~~~~~~--~~v~~~~~~liG~~~~~~~---------~~i~~l~V~p~~R~~Gig~~Ll~~~ 70 (219)

+.............+.+...+..+. ++++.+++++||++.+... ..+..++|+|++||+|+|+.|++.+

T Consensus 50 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ivG~~~~~~~~~~~~~~~~~~i~~~~v~p~~rg~Gig~~ll~~~ 129 (182)

T 4YFJ\_B 50 FEDIPTYSDRQPTNEYLANLLHSETFIALAAFDRGTAIGGLAAYVLPKFEQARSEIYIYDLAVASSHRRLGVATALISHL 129 (182)

T ss\_dssp TTCHHHHTTTCCCHHHHHHHHHCTTEEEEEEESSSSEEEEEEEEEEECSSSSCEEEEEEEEEECGGGTTSSHHHHHHHHH

T ss\_pred ccCCCCCCCCCCcHHHHHHHhcCCCEEEEEEEeCCeEEEEEEEEEccchhcCCcEEEEEEEEECHHHCCCCHHHHHHHHH

Q ss\_pred HHcccc---CeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeeeccccccceE

Q Phabba\_Draft 71 QDNPHI---YESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDVSNWGYT 124 (219)

Q Consensus 71 ~~~~~~---~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~~~~~ 124 (219)

++.+++ ..+.+.+...|. .+.++|+|+||+..+........+...

T Consensus 130 ~~~~~~~g~~~i~~~~~~~n~---------~~~~~~~k~Gf~~~~~~~~~~~~~~~~ 177 (182)

T 4YFJ\_B 130 KRVAVELGAYVIYVQADYGDD---------PAVALYTKLGVREDVMHFDIDPRTATH 177 (182)

T ss\_dssp HHHHHHHTCCEEEEEECTTCH---------HHHHHHHHHSEEEEEEEEEECTTSCC-

T ss\_pred HHHHHHcCCCEEEEEEeCCCH---------HHHHHHHHcCCEEeEEEeEeccccccC

No 17

>4W83\_A AAC(3')-Ib (E.C.2.3.1.60); aminoglycoside acetyltransferase, GNAT fold, antibiotic; HET: PE3, COA; 2.05A {Pseudomonas aeruginosa}

Probab=98.62 E-value=1.8e-08 Score=79.53 Aligned\_cols=114 Identities=12% Similarity=-0.009 Sum\_probs=0.0 Template\_Neff=11.700

Q ss\_pred CccccCCCCCCCCchHHHHHhhCCc--EEEEEECCEEEEEEEEEeC---------CEEEEEEECHHHCCCCHHHHHHHHH

Q Phabba\_Draft 2 HQAGANGDLPPLKFEPFDTMWSNGI--MARHAHDDRPVGHLHWHPD---------GEIDSITVHPDLQRRGIGTAMLKHA 70 (219)

Q Consensus 2 ~~~~~~~~~~~~~~~~l~~~~~~~~--~~v~~~~~~liG~~~~~~~---------~~i~~l~V~p~~R~~Gig~~Ll~~~ 70 (219)

+.............+.+...+..+. ++++.+++++||++.+... ..+..++|+|++||+|+|+.|++.+

T Consensus 50 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ivG~~~~~~~~~~~~~~~~~~i~~~~v~p~~rg~Gig~~ll~~~ 129 (182)

T 4W83\_A 50 FEDIPTYSDRQPTNEYLANLLHSETFIALAAFDRGTAIGGLAAYVLPKFEQARSEIYIYDLAVASSHRRLGVATALISHL 129 (182)

T ss\_dssp TTCHCCCCCTCCCHHHHHHHHHCTTEEEEEEEETTEEEEEEEEEEEECSSSSCEEEEEEEEEECGGGTTSSHHHHHHHHH

T ss\_pred ccCCCCCCCCCCcHHHHHHHhcCCCEEEEEEEeCCeEEEEEEEEEccchhcCCcEEEEEEEEECHHHCCCCHHHHHHHHH

Q ss\_pred HHcccc---CeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeeeccccccceE

Q Phabba\_Draft 71 QDNPHI---YESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDVSNWGYT 124 (219)

Q Consensus 71 ~~~~~~---~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~~~~~ 124 (219)

++.+++ ..+.+.+...|. .+.++|+|+||+..+........+...

T Consensus 130 ~~~~~~~g~~~i~~~~~~~n~---------~~~~~~~k~Gf~~~~~~~~~~~~~~~~ 177 (182)

T 4W83\_A 130 KRVAVELGAYVIYVQADYGDD---------PAVALYTKLGVREDVMHFDIDPRTATH 177 (182)

T ss\_dssp HHHHHHHTCCEEEEEEETTCH---------HHHHHHHHHSEEEEEEEEEECTTCCC-

T ss\_pred HHHHHHcCCCEEEEEEeCCCH---------HHHHHHHHcCCEEeEEEeEeccccccC

No 18

>2FIW\_A GCN5-related N-acetyltransferase:Aminotransferase, class-II; alpha-beta-alpha sandwich, GCN4-related acetyltransferase, Structural; HET: ACO; 2.35A {Rhodopseudomonas palustris} SCOP: d.108.1.1

Probab=98.62 E-value=9.6e-09 Score=80.20 Aligned\_cols=96 Identities=17% Similarity=0.219 Sum\_probs=0.0 Template\_Neff=11.800

Q ss\_pred hHHHHHhhCCcEEEEEECCEEEEEEEEEeCCEEEEEEECHHHCCCCHHHHHHHHHHHccccCeeEEEEEcCCcccccccc

Q Phabba\_Draft 16 EPFDTMWSNGIMARHAHDDRPVGHLHWHPDGEIDSITVHPDLQRRGIGTAMLKHAQDNPHIYESSYPVRHSSHFSAAGRA 95 (219)

Q Consensus 16 ~~l~~~~~~~~~~v~~~~~~liG~~~~~~~~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~~~i~l~v~~~n~~~~~~~~ 95 (219)

..+........++++..+|++||++.+....++..+.|+|++|++|+|+.|++.+++.+....+...+...|.

T Consensus 53 ~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~v~~~~r~~G~~~~l~~~~~~~~~~~~~~~~~~~~n~------- 125 (172)

T 2FIW\_A 53 AKFAARLSGQLTLIATLQGVPVGFASLKGPDHIDMLYVHPDYVGRDVGTTLIDALEKLAGARGALILTVDASD------- 125 (172)

T ss\_dssp HHHHHHHHTSEEEEEEETTEEEEEEEEETTTEEEEEEECGGGCSSSHHHHHHHHHHHHHHTTTCSEEEEEECT-------

T ss\_pred HHHHHHhcCCEEEEEEECCEEEEEEEEecCcEEEEEEECHHhCCCCHHHHHHHHHHHHHHHCCCcEEEEecCh-------

Q ss\_pred cchhHHHHHcCCCEEeeeeeccccc

Q Phabba\_Draft 96 WAQSDPDYHDPGDQNVTKADDDVSN 120 (219)

Q Consensus 96 ~~~~~~~y~r~Gf~~~~~~~~~~~~ 120 (219)

.+.++|+|+||+..+......++

T Consensus 126 --~~~~~~~k~Gf~~~~~~~~~~~g 148 (172)

T 2FIW\_A 126 --NAAEFFAKRGYVAKQRNTVSING 148 (172)

T ss\_dssp --TTHHHHHTTTCEEEEEEEEEETT

T ss\_pred --HHHHHHHHCCCEEeeeceeEECC

No 19

>4E0A\_B BH1408 protein; Structural Genomics, PSI-Biology, Protein Structure; HET: GOL, PO4; 1.801A {Bacillus halodurans}

Probab=98.62 E-value=1.7e-08 Score=77.01 Aligned\_cols=110 Identities=12% Similarity=0.068 Sum\_probs=0.0 Template\_Neff=12.500

Q ss\_pred cCCCCCCCCchHHHHHhhCCc--EEEEEECCEEEEEEEEEe----------C----CEEEEEEECHHHCCCCHHHHHHHH

Q Phabba\_Draft 6 ANGDLPPLKFEPFDTMWSNGI--MARHAHDDRPVGHLHWHP----------D----GEIDSITVHPDLQRRGIGTAMLKH 69 (219)

Q Consensus 6 ~~~~~~~~~~~~l~~~~~~~~--~~v~~~~~~liG~~~~~~----------~----~~i~~l~V~p~~R~~Gig~~Ll~~ 69 (219)

..........+.+...+..+. ++++.+++++||++.+.. . ..+..++|+|++|++|+|+.|++.

T Consensus 33 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~vg~~~~~~~~~~~~~~~~~~~~~~~i~~~~v~~~~r~~g~g~~l~~~ 112 (164)

T 4E0A\_B 33 FRSNEPTLNPSRFQAAVQGEKSTVLVFVDEREKIGAYSVIHLVQTPLLPTMQQRKTVYISDLCVDETRRGGGIGRLIFEA 112 (164)

T ss\_dssp BCCCSSSSCHHHHHHHHHCSSEEEEEEECTTSCEEEEEEEEEEEECCCSSBCCEEEEEEEEEEECGGGTTSSHHHHHHHH

T ss\_pred ccCCCCCCCHHHHHHHHhCCCeEEEEEEcCCCeEEEEEEEEeecCCCCCcccCCCEEEEEEEEECHHHCCCCHHHHHHHH

Q ss\_pred HHHcccc---CeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeeeccccccceE

Q Phabba\_Draft 70 AQDNPHI---YESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDVSNWGYT 124 (219)

Q Consensus 70 ~~~~~~~---~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~~~~~ 124 (219)

+++.++. ..+.+.+...|. .+.++|+|+||+..+........+..+

T Consensus 113 ~~~~~~~~g~~~i~~~~~~~n~---------~~~~~~~k~Gf~~~~~~~~~~~~~~~~ 161 (164)

T 4E0A\_B 113 IISYGKAHQVDAIELDVYDFND---------RAKAFYHSLGMRCQKQTMELPLLEHHH 161 (164)

T ss\_dssp HHHHHHHTTCSEEEEEEETTCH---------HHHHHHHHTTCEEEEEEEEEECC----

T ss\_pred HHHHHHHCCCCEEEEEEeCCCH---------HHHHHHHhcCCEEeeeecccCCccCCC

No 20

>d2ae6d\_ d.108.1.1 (D:) automated matches {Enterococcus faecalis [TaxId: 226185]}

Probab=98.61 E-value=1.8e-08 Score=76.19 Aligned\_cols=100 Identities=21% Similarity=0.310 Sum\_probs=0.0 Template\_Neff=12.600

Q ss\_pred CCCCCCCCchHHHHHhhCCcEEEEEECCEEEEEEEEEeC--------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc--

Q Phabba\_Draft 7 NGDLPPLKFEPFDTMWSNGIMARHAHDDRPVGHLHWHPD--------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI-- 76 (219)

Q Consensus 7 ~~~~~~~~~~~l~~~~~~~~~~v~~~~~~liG~~~~~~~--------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~-- 76 (219)

.....+.....+........++++.+++++||++.+... ..+..++|+|++|++|+|+.|+..+.+.++.

T Consensus 28 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~~g 107 (157)

T d2ae6d\_ 28 PAEIQPLSLAAYQEKMKDETIFVAISGQQLAGFIEVHPPTSLAAHQKQWLLSIGVSPDFQDQGIGGSLLSYIKDMAEISG 107 (157)

T ss\_dssp -------CHHHHHHHTTTCEEEEEESSSSEEEEEEEECSSSCGGGTTEEEEEEEECSTTTTSSHHHHHHHHHHHHHHHHT

T ss\_pred CcccCccCHHHHHHhcCCCeEEEEEeCCEEEEEEEEeCCCcchhhccEEEEEEEeCHHHCCCCHHHHHHHHHHHHHHHhC

Q ss\_pred -CeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 77 -YESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 77 -~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

..+.+.+...|. .+.++|+++||+..+...

T Consensus 108 ~~~i~~~~~~~n~---------~~~~~~~~~Gf~~~~~~~ 138 (157)

T d2ae6d\_ 108 IHKLSLRVMATNQ---------EAIRFYEKHGFVQEAHFK 138 (157)

T ss\_dssp CCEEEEEEETTCH---------HHHHHHHHTTCEEEEEEE

T ss\_pred CCEEEEEEEeCCH---------HHHHHHHHCCCEEEEEec

No 21

>4M85\_B Uncharacterized protein; GNAT fold, acetyltransferase, transferase; 2.0A {Staphylococcus aureus subsp. aureus}

Probab=98.61 E-value=1.5e-08 Score=79.47 Aligned\_cols=101 Identities=11% Similarity=0.086 Sum\_probs=0.0 Template\_Neff=12.200

Q ss\_pred chHHHHHhhCC-------cEEEEEECCEEEEEEEEEeCC-----------------------------------EEEEEE

Q Phabba\_Draft 15 FEPFDTMWSNG-------IMARHAHDDRPVGHLHWHPDG-----------------------------------EIDSIT 52 (219)

Q Consensus 15 ~~~l~~~~~~~-------~~~v~~~~~~liG~~~~~~~~-----------------------------------~i~~l~ 52 (219)

.+.+...+... .++++.++|++||++.+.... ++..++

T Consensus 41 ~~~~~~~~~~~~~~~~~~~~~v~~~~~~ivG~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~i~~~~ 120 (186)

T 4M85\_B 41 LDAIEKSCVDATYRTFYQHILVYEVENKVAGCIISYSGENELKYEKAWELLDLPEEIKQYGTPLPVKEAKDDEYYIETIA 120 (186)

T ss\_dssp HHHHHHHHHSSCCTTCGGGEEEEEETTEEEEEEEEEEGGGHHHHHHGGGGSCCCHHHHTTCCSCCSCCSCTTSEEEEEEE

T ss\_pred HHHHHHHhcCCCcccceecEEEEEECCEEEEEEEEEcCcchhhHHHHHHHccCcHHHHhhCCCccCCCCCCCeEEEEEEE

Q ss\_pred ECHHHCCCCHHHHHHHHHHHccccCeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeeeccccccceE

Q Phabba\_Draft 53 VHPDLQRRGIGTAMLKHAQDNPHIYESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDVSNWGYT 124 (219)

Q Consensus 53 V~p~~R~~Gig~~Ll~~~~~~~~~~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~~~~~ 124 (219)

|+|++||+|+|+.|++.+++.+....+.+.+...|. .+.++|+++||+..+........+...

T Consensus 121 v~~~~r~~Gi~~~l~~~~~~~~~~~~i~~~v~~~n~---------~~~~~~~~~Gf~~~~~~~~~~~~~~~~ 183 (186)

T 4M85\_B 121 TFAAYRGRGIATKLLTSLLESNTHVKWSLNCDINNE---------AALKLYKKVGFISDGQIELYKHMYHHL 183 (186)

T ss\_dssp ECGGGTTSCHHHHHHHHHHHHBSSSCEEEEEETTCH---------HHHHHHHHTTCEEEEEEEETTEEEEEE

T ss\_pred ECHHHCCCCHHHHHHHHHHHhCCCCeeEEeccCCCH---------HHHHHHHHcCCeeeeEEEechhhceee

No 22

>4M85\_A Uncharacterized protein; GNAT fold, acetyltransferase, transferase; 2.0A {Staphylococcus aureus subsp. aureus}

Probab=98.61 E-value=1.5e-08 Score=79.47 Aligned\_cols=101 Identities=11% Similarity=0.086 Sum\_probs=0.0 Template\_Neff=12.200

Q ss\_pred chHHHHHhhCC-------cEEEEEECCEEEEEEEEEeCC-----------------------------------EEEEEE

Q Phabba\_Draft 15 FEPFDTMWSNG-------IMARHAHDDRPVGHLHWHPDG-----------------------------------EIDSIT 52 (219)

Q Consensus 15 ~~~l~~~~~~~-------~~~v~~~~~~liG~~~~~~~~-----------------------------------~i~~l~ 52 (219)

.+.+...+... .++++.++|++||++.+.... ++..++

T Consensus 41 ~~~~~~~~~~~~~~~~~~~~~v~~~~~~ivG~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~i~~~~ 120 (186)

T 4M85\_A 41 LDAIEKSCVDATYRTFYQHILVYEVENKVAGCIISYSGENELKYEKAWELLDLPEEIKQYGTPLPVKEAKDDEYYIETIA 120 (186)

T ss\_dssp HHHHHHHHHSSCCTTCGGGEEEEEETTEEEEEEEEEEGGGHHHHHHGGGGSCCCHHHHTTCCSCCSCCSCTTCEEEEEEE

T ss\_pred HHHHHHHhcCCCcccceecEEEEEECCEEEEEEEEEcCcchhhHHHHHHHccCcHHHHhhCCCccCCCCCCCeEEEEEEE

Q ss\_pred ECHHHCCCCHHHHHHHHHHHccccCeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeeeccccccceE

Q Phabba\_Draft 53 VHPDLQRRGIGTAMLKHAQDNPHIYESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDVSNWGYT 124 (219)

Q Consensus 53 V~p~~R~~Gig~~Ll~~~~~~~~~~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~~~~~ 124 (219)

|+|++||+|+|+.|++.+++.+....+.+.+...|. .+.++|+++||+..+........+...

T Consensus 121 v~~~~r~~Gi~~~l~~~~~~~~~~~~i~~~v~~~n~---------~~~~~~~~~Gf~~~~~~~~~~~~~~~~ 183 (186)

T 4M85\_A 121 TFAAYRGRGIATKLLTSLLESNTHVKWSLNCDINNE---------AALKLYKKVGFISDGQIELYKHMYHHL 183 (186)

T ss\_dssp ECGGGTTSSHHHHHHHHHHHTCTTSCEEEEEETTCH---------HHHHHHHHTTCEEEEEEEETTEEEEEE

T ss\_pred ECHHHCCCCHHHHHHHHHHHhCCCCeeEEeccCCCH---------HHHHHHHHcCCeeeeEEEechhhceee

No 23

>2OH1\_D Acetyltransferase, GNAT family; YP\_013287.1, acetyltransferase GNAT family, Structural; HET: UNL, EDO; 1.46A {Listeria monocytogenes str. 4b}

Probab=98.61 E-value=8.3e-09 Score=79.41 Aligned\_cols=91 Identities=13% Similarity=0.007 Sum\_probs=0.0 Template\_Neff=12.800

Q ss\_pred chHHHHHhhCCcEEEEEE-CCEEEEEEEEE-----------------eCCEEEEEEECHHHCCCCHHHHHHHHHHHcccc

Q Phabba\_Draft 15 FEPFDTMWSNGIMARHAH-DDRPVGHLHWH-----------------PDGEIDSITVHPDLQRRGIGTAMLKHAQDNPHI 76 (219)

Q Consensus 15 ~~~l~~~~~~~~~~v~~~-~~~liG~~~~~-----------------~~~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~ 76 (219)

.+.+...+....++++.. ++++||++.+. ...++..++|+|++|++|+|+.|++.+++.+..

T Consensus 55 ~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~v~~~~r~~Gi~~~l~~~~~~~~~~ 134 (179)

T 2OH1\_D 55 VHNIEQRIELGEVALFETEAGALAGAMIIRKTPSDWDTDLWEDLAIDKAYYLHRIMVSRAFSGISLSKQMIYFAEKLGIE 134 (179)

T ss\_dssp CTTHHHHHHTTCEEEEEETTCCEEEEEEEESSCCHHHHHHHGGGGGSCEEEEEEEEECGGGCSSCHHHHHHHHHHHHHHH

T ss\_pred HHHHHHhhhcCeEEEEEcCCCeEEEEEEEEeCCCccCccccchhhccCeEEEEEEEECHHHCCCCHHHHHHHHHHHHHHH

Q ss\_pred ---CeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeee

Q Phabba\_Draft 77 ---YESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKA 114 (219)

Q Consensus 77 ---~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~ 114 (219)

..+.+.+...|. .+.++|+++||+..+..

T Consensus 135 ~~~~~i~~~~~~~n~---------~~~~~~~~~Gf~~~~~~ 166 (179)

T 2OH1\_D 135 MSVPFIRLDCIESNE---------TLNQMYVRYGFQFSGKK 166 (179)

T ss\_dssp TTCCEEEEEEETTCH---------HHHHHHHHHTCEEEEEE

T ss\_pred cCCCEEEEEecCCCH---------HHHHHHHHcCcEEecee

No 24

>2OH1\_A Acetyltransferase, GNAT family; YP\_013287.1, acetyltransferase GNAT family, Structural; HET: UNL, EDO; 1.46A {Listeria monocytogenes str. 4b}

Probab=98.61 E-value=8.3e-09 Score=79.41 Aligned\_cols=91 Identities=13% Similarity=0.007 Sum\_probs=0.0 Template\_Neff=12.800

Q ss\_pred chHHHHHhhCCcEEEEEE-CCEEEEEEEEE-----------------eCCEEEEEEECHHHCCCCHHHHHHHHHHHcccc

Q Phabba\_Draft 15 FEPFDTMWSNGIMARHAH-DDRPVGHLHWH-----------------PDGEIDSITVHPDLQRRGIGTAMLKHAQDNPHI 76 (219)

Q Consensus 15 ~~~l~~~~~~~~~~v~~~-~~~liG~~~~~-----------------~~~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~ 76 (219)

.+.+...+....++++.. ++++||++.+. ...++..++|+|++|++|+|+.|++.+++.+..

T Consensus 55 ~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~v~~~~r~~Gi~~~l~~~~~~~~~~ 134 (179)

T 2OH1\_A 55 VHNIEQRIELGEVALFETEAGALAGAMIIRKTPSDWDTDLWEDLAIDKAYYLHRIMVSRAFSGISLSKQMIYFAEKLGIE 134 (179)

T ss\_dssp CTTHHHHHHTTCEEEEECTTCCEEEEEEEESSCCHHHHHHHGGGTTSCEEEEEEEEECGGGTTSCHHHHHHHHHHHHHHH

T ss\_pred HHHHHHhhhcCeEEEEEcCCCeEEEEEEEEeCCCccCccccchhhccCeEEEEEEEECHHHCCCCHHHHHHHHHHHHHHH

Q ss\_pred ---CeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeee

Q Phabba\_Draft 77 ---YESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKA 114 (219)

Q Consensus 77 ---~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~ 114 (219)

..+.+.+...|. .+.++|+++||+..+..

T Consensus 135 ~~~~~i~~~~~~~n~---------~~~~~~~~~Gf~~~~~~ 166 (179)

T 2OH1\_A 135 MSVPFIRLDCIESNE---------TLNQMYVRYGFQFSGKK 166 (179)

T ss\_dssp TTCCEEEEEEETTCH---------HHHHHHHHTTCEEEEEE

T ss\_pred cCCCEEEEEecCCCH---------HHHHHHHHcCcEEecee

No 25

>2OZH\_A Hypothetical protein XCC2953; Structural genomics, Joint Center for; HET: SO4, EDO; 1.4A {Xanthomonas campestris pv. campestris}

Probab=98.61 E-value=8.8e-09 Score=78.42 Aligned\_cols=108 Identities=11% Similarity=0.089 Sum\_probs=0.0 Template\_Neff=11.400

Q ss\_pred CCCCchHHHHHhhCCcEEEEEECCEEEEEEEEEeC----CEEEEEEECHHHCCCCHHHHHHHHHHHccccCeeEEEEEcC

Q Phabba\_Draft 11 PPLKFEPFDTMWSNGIMARHAHDDRPVGHLHWHPD----GEIDSITVHPDLQRRGIGTAMLKHAQDNPHIYESSYPVRHS 86 (219)

Q Consensus 11 ~~~~~~~l~~~~~~~~~~v~~~~~~liG~~~~~~~----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~~~i~l~v~~~ 86 (219)

++...+.+...++...++++..++++||++.+... ..+..++|+|++|++|+|..|++.+++.+....+..... .

T Consensus 31 ~~~~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~v~~~~r~~g~g~~l~~~~~~~~~~~~~~~~~~-~ 109 (142)

T 2OZH\_A 31 KDIPLALVQRAIDHSLCFGGFVDGRQVAFARVISDYATFAYLGDVFVLPEHRGRGYSKALMDAVMAHPDLQGLRRFSL-A 109 (142)

T ss\_dssp TTCCHHHHHHHHHTSEEEEEEETTEEEEEEEEEECSSSEEEEEEEEECGGGTTSSHHHHHHHHHHHCGGGSSCSEEEC-C

T ss\_pred hcCCHHHHHHHHhcCcEEEEEECCEEEEEEEEEeCCCCeEEEEEEEECHHHCCCCHHHHHHHHHHhcHHhCCCCEEEE-e

Q ss\_pred CcccccccccchhHHHHHcCCCEEeeeeeccccccceEEecC

Q Phabba\_Draft 87 SHFSAAGRAWAQSDPDYHDPGDQNVTKADDDVSNWGYTAMGE 128 (219)

Q Consensus 87 n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~~~~~~~~~ 128 (219)

|. .+.++|+++||+.++................

T Consensus 110 n~---------~~~~~~~~~Gf~~~~~~~~~~~~~~~~~~~~ 142 (142)

T 2OZH\_A 110 TS---------DAHGLYARYGFTPPLFPQSLMERYVPGLYST 142 (142)

T ss\_dssp CS---------SCHHHHHTTTCCSCSSGGGCCCCCCTTTTCC

T ss\_pred cc---------chHHHHHHcCCccCccCccccccccccccCC

No 26

>2ATR\_A acetyltransferase, GNAT family; MCSG, structural genomics, Streptococcus pneumoniae; 2.01A {Streptococcus pneumoniae} SCOP: d.108.1.1

Probab=98.60 E-value=1.6e-08 Score=75.11 Aligned\_cols=100 Identities=19% Similarity=0.173 Sum\_probs=0.0 Template\_Neff=12.400

Q ss\_pred CCCCCCCchHHHHHhhCCc-EEEEEECCEEEEEEEEEeC----CEEEEEEECHHHCCCCHHHHHHHHHHHccccCeeEEE

Q Phabba\_Draft 8 GDLPPLKFEPFDTMWSNGI-MARHAHDDRPVGHLHWHPD----GEIDSITVHPDLQRRGIGTAMLKHAQDNPHIYESSYP 82 (219)

Q Consensus 8 ~~~~~~~~~~l~~~~~~~~-~~v~~~~~~liG~~~~~~~----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~~~i~l~ 82 (219)

....+...+.+......+. ++++.++|++||++.+... ..+..++|+|++|++|+|+.|++.+++.+........

T Consensus 24 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ivG~~~~~~~~~~~~~~~~~~v~~~~r~~gi~~~l~~~~~~~~~~~~~~~~ 103 (138)

T 2ATR\_A 24 WTNYTHQTEMLEQALSHSLVIYLALDGDAVVGLIRLVGDGFSSVFVQDLIVLPSYQRQGIGSSLMKEALGNFKEAYQVQL 103 (138)

T ss\_dssp CCC-----CHHHHHHTSCSEEEEEEETTEEEEEEEEEECSSSEEEEEEEEECTTSCSSSHHHHHHHHHHGGGTTCSEEEC

T ss\_pred CCCccccHHHHHHHHhCCcEEEEEEcCCeEEEEEEEEcCCCcEEEEEEEEECHHHCCCCHHHHHHHHHHHHHHHhccEEE

Q ss\_pred EEcCCcccccccccchhHHHHHcCCCEEeeeeec

Q Phabba\_Draft 83 VRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADD 116 (219)

Q Consensus 83 v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~ 116 (219)

....|. .+.++|+++||+..+....

T Consensus 104 ~~~~n~---------~~~~~~~~~Gf~~~~~~~~ 128 (138)

T 2ATR\_A 104 ATEETE---------KNVGFYRSMGFEILSTYDC 128 (138)

T ss\_dssp CCCCCH---------HHHHHHHHTTCCCGGGGTC

T ss\_pred EeCCCh---------hhHHHHHhcCCeEeccccc

No 27

>d3ld2a1 d.108.1.0 (A:1-158) automated matches {Streptococcus mutans [TaxId: 210007]}

Probab=98.60 E-value=1.6e-08 Score=76.62 Aligned\_cols=92 Identities=18% Similarity=0.115 Sum\_probs=0.0 Template\_Neff=12.600

Q ss\_pred chHHHHHhhCCcEEEEEECCEEEEEEEEEeC--------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc--CeeEEEEE

Q Phabba\_Draft 15 FEPFDTMWSNGIMARHAHDDRPVGHLHWHPD--------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI--YESSYPVR 84 (219)

Q Consensus 15 ~~~l~~~~~~~~~~v~~~~~~liG~~~~~~~--------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~--~~i~l~v~ 84 (219)

............++++.+++++||++.+... ..+..+.|+|++|++|+|+.|++.+++.+.+ ..+.+.+.

T Consensus 37 ~~~~~~~~~~~~~~~~~~~~~ivG~~~~~~~~~~~~~~~~~~~~~~v~~~~r~~gi~~~l~~~~~~~~~~~~~~~~~~~~ 116 (158)

T d3ld2a1 37 DQIIQKFESNTHFLVAKIKDKIVGVLDYSSLYPFPSGQHIVTFGIAVAEKERRKGIGRALVQIFLNEVKSDYQKVLIHVL 116 (158)

T ss\_dssp HHHHHHHTTTCEEEEEEESSCEEEEEEEEESCSSGGGTTEEEEEEEECGGGTTSSHHHHHHHHHHHHHTTTCSEEEEEEE

T ss\_pred HHHHHHHhcCceEEEEEECCeEEEEEEEEEecCCCCCceEEEEEEEECHHHcCCCHHHHHHHHHHHHHHhcCCeEEEEEe

Q ss\_pred cCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 85 HSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 85 ~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

..|. .+.++|+++||+..+...

T Consensus 117 ~~n~---------~~~~~~~~~Gf~~~~~~~ 138 (158)

T d3ld2a1 117 SSNQ---------EAVLFYKKLGFDLEARLT 138 (158)

T ss\_dssp TTCH---------HHHHHHHHTTCEEEEEEE

T ss\_pred cCCH---------HHHHHHHHcCCEEEEEec

No 28

>3JVN\_A Acetyltransferase (E.C.2.3.1.-); alpha-beta protein, Structural Genomics, PSI-2; 2.61A {Vibrio fischeri}

Probab=98.60 E-value=1.7e-08 Score=77.25 Aligned\_cols=103 Identities=13% Similarity=0.076 Sum\_probs=0.0 Template\_Neff=12.500

Q ss\_pred hHHHHHhhCCc--EEEEEECCEEEEEEEEE------------eCCEEEEEEECHHHCCCCHHHHHHHHHHHcccc---Ce

Q Phabba\_Draft 16 EPFDTMWSNGI--MARHAHDDRPVGHLHWH------------PDGEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YE 78 (219)

Q Consensus 16 ~~l~~~~~~~~--~~v~~~~~~liG~~~~~------------~~~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~ 78 (219)

+.+...+.... ++++..+|++||++.+. ....+..++|+|++|++|+|+.|++.+++.+++ ..

T Consensus 45 ~~~~~~~~~~~~~~~~~~~~~~ivG~~~~~~~~~~~~~~~~~~~~~i~~~~v~~~~r~~G~~~~l~~~~~~~~~~~g~~~ 124 (166)

T 3JVN\_A 45 KSIARYLDDPECMVYVAEMDDVIIGFITGHFCELISTVSKLVMMATIDELYIEKEYRREGVAEQLMMRIEQELKDYGVKE 124 (166)

T ss\_dssp CCHHHHHHCTTEEEEEEESSSSEEEEEEEEEEEECCSSSCCEEEEEEEEEEECTTTCSSSHHHHHHHHHHHHHHTTTCSE

T ss\_pred HHHHHHHhCCCeeEEEEEECCeEEEEEEEEEehhhhhhhhcceEEEEEEEEeCHHHhCCCHHHHHHHHHHHHHHHCCCCE

Q ss\_pred eEEEEEcCCcccccccccchhHHHHHcCCCEEeeeeeccccccceEEec

Q Phabba\_Draft 79 SSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDVSNWGYTAMG 127 (219)

Q Consensus 79 i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~~~~~~~~ 127 (219)

+.+.+...|. .+.++|+++||+..+.+........+....

T Consensus 125 i~~~~~~~n~---------~~~~~~~~~Gf~~~~~~~~~~~~~~~~~~~ 164 (166)

T 3JVN\_A 125 IFVEVWDFNK---------GALEFYNKQGLNEHIHYLRKPLNRLEHHHH 164 (166)

T ss\_dssp EEECCC--CC---------BC----------------------------

T ss\_pred EEEEEecccH---------HHHHHHHhCCCeEEEEEEecchhccccCCC

No 29

>d1s5kb\_ d.108.1.1 (B:) Aminoglycoside N-acetyltransferase AAC(6')-IY {Salmonella enteritidis [TaxId: 149539]}

Probab=98.59 E-value=1e-08 Score=75.86 Aligned\_cols=106 Identities=12% Similarity=0.083 Sum\_probs=0.0 Template\_Neff=12.900

Q ss\_pred CCccccCCCCCCCCchHHHHHhhCCc--EEEEEECCEEEEEEEEE------------eCCEEEEEEECHHHCCCCHHHHH

Q Phabba\_Draft 1 MHQAGANGDLPPLKFEPFDTMWSNGI--MARHAHDDRPVGHLHWH------------PDGEIDSITVHPDLQRRGIGTAM 66 (219)

Q Consensus 1 ~~~~~~~~~~~~~~~~~l~~~~~~~~--~~v~~~~~~liG~~~~~------------~~~~i~~l~V~p~~R~~Gig~~L 66 (219)

+..............+.+...+..+. ++++.++|++||++.+. ....+..++|+|++|++|+|+.|

T Consensus 16 l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~v~~~~~~ivg~~~~~~~~~~~~~~~~~~~~~i~~~~v~~~~r~~g~~~~l 95 (144)

T d1s5kb\_ 16 LRKQLWPGHPDDAHLADGEEILQADHLASFIAMADGVAIGFADASIRHDYVNGCDSSPVVFLEGIFVLPSFRQRGVAKQL 95 (144)

T ss\_dssp HHHHC----------CHHHHHHHCSSEEEEEEEETTEEEEEEEEEEECSCCTTCCSSSEEEEEEEEECGGGCSSSHHHHH

T ss\_pred HHHHHCCCCCChhhHHhHHHHhhhcCccEEEEEeCCEEEEEEEEEEecccCCCcCCCCEEEEEeeEECHHHCCCCHHHHH

Q ss\_pred HHHHHHcccc---CeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 67 LKHAQDNPHI---YESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 67 l~~~~~~~~~---~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

++.+.+.+.. ..+.+.+...|. .+.++|+++||+..+...

T Consensus 96 ~~~~~~~~~~~~~~~~~~~~~~~n~---------~~~~~~~~~Gf~~~~~~~ 138 (144)

T d1s5kb\_ 96 IAAVQRWGTNKGCREMASDTSPENT---------ISQKVHQALGFEETERVI 138 (144)

T ss\_dssp HHHHHHHHHTTTCSEEEEEECTTCH---------HHHHHHHHTTCEEEEEEE

T ss\_pred HHHHHHHHHHCCCCEEEEeCCCCCh---------HHHHHHHHcCCeEeEEEE

No 30

>2AE6\_A acetyltransferase, GNAT family (E.C.2.3.-.-); GCN5-related N-acetyltransferase (GNAT), alpha-beta, Structural; HET: GOL; 2.19A {Enterococcus faecalis} SCOP: d.108.1.1

Probab=98.59 E-value=2.1e-08 Score=76.53 Aligned\_cols=101 Identities=21% Similarity=0.309 Sum\_probs=0.0 Template\_Neff=12.600

Q ss\_pred cCCCCCCCCchHHHHHhhCCcEEEEEECCEEEEEEEEEeC--------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc-

Q Phabba\_Draft 6 ANGDLPPLKFEPFDTMWSNGIMARHAHDDRPVGHLHWHPD--------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI- 76 (219)

Q Consensus 6 ~~~~~~~~~~~~l~~~~~~~~~~v~~~~~~liG~~~~~~~--------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~- 76 (219)

......+.....+........++++.+++++||++.+... .++..+.|+|++|++|+|+.|++.+++.++.

T Consensus 34 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~~ 113 (166)

T 2AE6\_A 34 TPAEIQPLSLAAYQEKMKDETIFVAISGQQLAGFIEVHPPTSLAAHQKQWLLSIGVSPDFQDQGIGGSLLSYIKDMAEIS 113 (166)

T ss\_dssp --------CCSHHHHHTTSSEEEEEEETTEEEEEEEEECSSSCGGGTTEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHH

T ss\_pred CchhcCcccHHHHHHHhcCCcEEEEEeCCEEEEEEEEeCCcchhhcceEEEEEEEEChhhCCCCHHHHHHHHHHHHHHhh

Q ss\_pred --CeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 77 --YESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 77 --~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

..+.+.+...|. .+.++|+++||+..+...

T Consensus 114 g~~~i~~~~~~~n~---------~~~~~~~~~Gf~~~~~~~ 145 (166)

T 2AE6\_A 114 GIHKLSLRVMATNQ---------EAIRFYEKHGFVQEAHFK 145 (166)

T ss\_dssp TCCEEEEEEETTCH---------HHHHHHHHTTCEEEEEEE

T ss\_pred CCCEEEEEEEeCCH---------HHHHHHHHCCCeEEEEec

No 31

>2AE6\_D acetyltransferase, GNAT family (E.C.2.3.-.-); GCN5-related N-acetyltransferase (GNAT), alpha-beta, Structural; HET: GOL; 2.19A {Enterococcus faecalis} SCOP: d.108.1.1

Probab=98.59 E-value=2.1e-08 Score=76.53 Aligned\_cols=101 Identities=21% Similarity=0.309 Sum\_probs=0.0 Template\_Neff=12.600

Q ss\_pred cCCCCCCCCchHHHHHhhCCcEEEEEECCEEEEEEEEEeC--------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc-

Q Phabba\_Draft 6 ANGDLPPLKFEPFDTMWSNGIMARHAHDDRPVGHLHWHPD--------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI- 76 (219)

Q Consensus 6 ~~~~~~~~~~~~l~~~~~~~~~~v~~~~~~liG~~~~~~~--------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~- 76 (219)

......+.....+........++++.+++++||++.+... .++..+.|+|++|++|+|+.|++.+++.++.

T Consensus 34 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~~ 113 (166)

T 2AE6\_D 34 TPAEIQPLSLAAYQEKMKDETIFVAISGQQLAGFIEVHPPTSLAAHQKQWLLSIGVSPDFQDQGIGGSLLSYIKDMAEIS 113 (166)

T ss\_dssp --------CHHHHHHHTTTCEEEEEESSSSEEEEEEEECSSSCGGGTTEEEEEEEECSTTTTSSHHHHHHHHHHHHHHHH

T ss\_pred CchhcCcccHHHHHHHhcCCcEEEEEeCCEEEEEEEEeCCcchhhcceEEEEEEEEChhhCCCCHHHHHHHHHHHHHHhh

Q ss\_pred --CeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 77 --YESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 77 --~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

..+.+.+...|. .+.++|+++||+..+...

T Consensus 114 g~~~i~~~~~~~n~---------~~~~~~~~~Gf~~~~~~~ 145 (166)

T 2AE6\_D 114 GIHKLSLRVMATNQ---------EAIRFYEKHGFVQEAHFK 145 (166)

T ss\_dssp TCCEEEEEEETTCH---------HHHHHHHHTTCEEEEEEE

T ss\_pred CCCEEEEEEEeCCH---------HHHHHHHHCCCeEEEEec

No 32

>2K5T\_A Uncharacterized protein yhhK; N-acetyl transferase, CoA, bound ligand; HET: COA; NMR {Escherichia coli K12}

Probab=98.58 E-value=1.1e-08 Score=75.02 Aligned\_cols=84 Identities=15% Similarity=0.121 Sum\_probs=0.0 Template\_Neff=12.400

Q ss\_pred hCCcEEEEEECCEEEEEEEEEeC---CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEEEcCCccccccccc

Q Phabba\_Draft 23 SNGIMARHAHDDRPVGHLHWHPD---GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPVRHSSHFSAAGRAW 96 (219)

Q Consensus 23 ~~~~~~v~~~~~~liG~~~~~~~---~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v~~~n~~~~~~~~~ 96 (219)

....++++..+++++|++.+... ..+..++|+|++|++|+|+.|++.+++.+.+ ..+.+.+...|.

T Consensus 35 ~~~~~~~~~~~~~~vg~~~~~~~~~~~~i~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~i~~~~~~~n~-------- 106 (128)

T 2K5T\_A 35 DNHRIYAARFNERLLAAVRVTLSGTEGALDSLRVREVTRRRGVGQYLLEEVLRNNPGVSCWWMADAGVEDRG-------- 106 (128)

T ss\_dssp SSEEEEEEEETTEEEEEEEEEEETTEEEEEEEEECTTCSSSSHHHHHHHHHHHHSCSCCEEEECCTTCSTHH--------

T ss\_pred CCccEEEEEECCEEEEEEEEEeCCCccceEEEEECHHHccCCHHHHHHHHHHHhCccCCeeEEEEeeccchH--------

Q ss\_pred chhHHHHHcCCCEEeeeee

Q Phabba\_Draft 97 AQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 97 ~~~~~~y~r~Gf~~~~~~~ 115 (219)

.+.++|+++||+..+.+.

T Consensus 107 -~~~~~~~~~Gf~~~~~~~ 124 (128)

T 2K5T\_A 107 -VMTAFMQALGFTTQQGGW 124 (128)

T ss\_dssp -HHHHHHHHHTCEECSSSE

T ss\_pred -HHHHHHHHCCCEeccCce

No 33

>4F6A\_A BH1408 protein; Structural Genomics, PSI-Biology, Protein Structure; HET: UNL; 2.009A {Bacillus halodurans}

Probab=98.57 E-value=2.9e-08 Score=74.32 Aligned\_cols=105 Identities=12% Similarity=0.102 Sum\_probs=0.0 Template\_Neff=13.000

Q ss\_pred CccccCCCCCCCCchHHHHHhhCCc--EEEEEECCEEEEEEEEEe----------C----CEEEEEEECHHHCCCCHHHH

Q Phabba\_Draft 2 HQAGANGDLPPLKFEPFDTMWSNGI--MARHAHDDRPVGHLHWHP----------D----GEIDSITVHPDLQRRGIGTA 65 (219)

Q Consensus 2 ~~~~~~~~~~~~~~~~l~~~~~~~~--~~v~~~~~~liG~~~~~~----------~----~~i~~l~V~p~~R~~Gig~~ 65 (219)

..............+.+...++.+. ++++.+++++||++.+.. . .++..++|+|++|++|+|+.

T Consensus 29 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~vg~~~~~~~~~~~~~~~~~~~~~~~i~~~~v~~~~r~~g~~~~ 108 (156)

T 4F6A\_A 29 RGDIFRSNEPTLNPSRFQAAVQGEKSTVLVFVDEREKIGAYSVIHLVQTPLLPTMQQRKTVYISDLCVDETRRGGGIGRL 108 (156)

T ss\_dssp CTTTBCCCSSSSCHHHHHHHHHCSSEEEEEEECTTSCEEEEEEEEEEEECCCSSBCCEEEEEEEEEEECGGGTTSSHHHH

T ss\_pred ccccccCCCCCCCHHHHHHHHcCCCeEEEEEEcCCCeEEEEEEEEccCCCCCCcccCCcEEEEEEEEeCHHHCCCCHHHH

Q ss\_pred HHHHHHHcccc---CeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 66 MLKHAQDNPHI---YESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 66 Ll~~~~~~~~~---~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

|+..+++.++. ..+.+.+...|. .+.++|+++||+..+...

T Consensus 109 l~~~~~~~~~~~g~~~i~~~~~~~n~---------~~~~~~~~~Gf~~~~~~~ 152 (156)

T 4F6A\_A 109 IFEAIISYGKAHQVDAIELDVYDFNE---------RAKRFYHSLGMRCQKQTM 152 (156)

T ss\_dssp HHHHHHHHHHHTTCSEEEEEEETTCH---------HHHHHHHHTTCEEEEEEE

T ss\_pred HHHHHHHHHHHCCCCEEEEEEeCCCH---------HHHHHHHHcCCeEeeeee

No 34

>2R1I\_A GCN5-related N-acetyltransferase; YP\_831484.1, Putative acetyltransferase, Arthrobacter sp.; HET: GOL, EDO; 1.65A {Arthrobacter sp.}

Probab=98.57 E-value=1.1e-08 Score=78.89 Aligned\_cols=92 Identities=13% Similarity=0.118 Sum\_probs=0.0 Template\_Neff=12.400

Q ss\_pred hHHHHHhhCCcEEEEEECCEEEEEEEEEeC---------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEE

Q Phabba\_Draft 16 EPFDTMWSNGIMARHAHDDRPVGHLHWHPD---------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPV 83 (219)

Q Consensus 16 ~~l~~~~~~~~~~v~~~~~~liG~~~~~~~---------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v 83 (219)

..+...+.+..++++..++++||++.+... ..+..++|+|++|++|+|+.|++.+.+.++. ..+.+.+

T Consensus 59 ~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~i~~~~v~~~~r~~Gi~~~l~~~~~~~~~~~~~~~i~~~~ 138 (172)

T 2R1I\_A 59 SRLSHLLAGEDVVVLLAGEPPTGLAVLSFRPNVWYPGPVAILDELYVRPGRRGHRLGSALLAASCGLVRSRGGALLEINV 138 (172)

T ss\_dssp HHHHHHTTSSSEEEEEETTTTCEEEEEEEECCTTCSSCEEEEEEEECCSSHHHHHHHHHHHHHHHHHHHHTTCCEEEEEE

T ss\_pred HHHHHHhcCCCEEEEEeCCCceEEEEEEECCCccCCCCEEEEEEEEEChHHcCCCHHHHHHHHHHHHHHhcCCCEEEEEe

Q ss\_pred EcCCcccccccccchhHHHHHcCCCEEeeeeec

Q Phabba\_Draft 84 RHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADD 116 (219)

Q Consensus 84 ~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~ 116 (219)

...|. .+.++|+++||+..+....

T Consensus 139 ~~~n~---------~~~~~~~~~Gf~~~~~~~~ 162 (172)

T 2R1I\_A 139 DGEDT---------DARRFYEARGFTNTEPNGT 162 (172)

T ss\_dssp ETTCH---------HHHHHHHTTTCBSSCTTCC

T ss\_pred cCCCH---------HHHHHHHHCCCeeCCCCCc

No 35

>1YVK\_D hypothetical protein BSU33890; alphs-beta protein, Structural Genomics, PSI; HET: COA; 3.01A {Bacillus subtilis subsp. subtilis str. 168} SCOP: d.108.1.1

Probab=98.57 E-value=2e-08 Score=79.62 Aligned\_cols=100 Identities=18% Similarity=0.106 Sum\_probs=0.0 Template\_Neff=10.200

Q ss\_pred CCCchHHHHHhhCCcEEEEEECCEEEEEEEEEeC----CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEEE

Q Phabba\_Draft 12 PLKFEPFDTMWSNGIMARHAHDDRPVGHLHWHPD----GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPVR 84 (219)

Q Consensus 12 ~~~~~~l~~~~~~~~~~v~~~~~~liG~~~~~~~----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v~ 84 (219)

....+.+...+.++.++++.+++++||++.+... ..+..++|+|++|++|++++|++.+.+.+.. ..+.+.+.

T Consensus 26 ~~~~~~~~~~~~~~~~~~~~~~~~ivG~~~~~~~~~~~~~i~~~~v~~~~r~~Gi~~~Ll~~~~~~~~~~~~~~i~~~~~ 105 (163)

T 1YVK\_D 26 DPSKDIVDEYLERGECYTAWAGDELAGVYVLLKTRPQTVEIVNIAVKESLQKKGFGKQLVLDAIEKAKKLGADTIEIGTG 105 (163)

T ss\_dssp CCCHHHHHHHHHHSEEEEEEETTEEEEEEEEEECSTTEEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHTTCSEEEEEEE

T ss\_pred CCChHHHHHHHhcCCeEEEEECCeEEEEEEEEECCCCEEEEEEEEECHHHCCCCHHHHHHHHHHHHHHHcCCCEEEEEcc

Q ss\_pred cCCcccccccccchhHHHHHcCCCEEeeeeeccccc

Q Phabba\_Draft 85 HSSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDVSN 120 (219)

Q Consensus 85 ~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~ 120 (219)

..|. .+.++|+++||+..+........

T Consensus 106 ~~n~---------~~~~~~~~~Gf~~~~~~~~~~~~ 132 (163)

T 1YVK\_D 106 NSSI---------HQLSLYQKCGFRIQAIDHDFFLR 132 (163)

T ss\_dssp TTCH---------HHHHHHHHTTCEEEEEETTHHHH

T ss\_pred CCCH---------HHHHHHHHCCCEEEEEehhhchh

No 36

>5F47\_B aminoglycoside acetyltransferase HMB0020; GNAT fold, GCN5-N-acetyltransferase fold, acetyltransferase; HET: TRE; 1.497A {uncultured bacterium}

Probab=98.57 E-value=2.3e-08 Score=75.14 Aligned\_cols=102 Identities=13% Similarity=0.065 Sum\_probs=0.0 Template\_Neff=12.900

Q ss\_pred CCCCCCCchHHHHHhhCCc--EEEEEECCEEEEEEEEEeC---------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc

Q Phabba\_Draft 8 GDLPPLKFEPFDTMWSNGI--MARHAHDDRPVGHLHWHPD---------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI 76 (219)

Q Consensus 8 ~~~~~~~~~~l~~~~~~~~--~~v~~~~~~liG~~~~~~~---------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~ 76 (219)

........+.+...+..+. ++++.++|++||++.+... ..+..++|+|++|++|+++.|++.+++.+..

T Consensus 38 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~vg~~~~~~~~~~~~~~~~~~i~~~~v~~~~r~~g~~~~l~~~~~~~~~~ 117 (157)

T 5F47\_B 38 KNFSIPDSEHLQKLLNQNNFYVFVALLENKIVGGLTSYVLEQYYSEKPLAYIYDLAVDTNWQRQGIGKKLITATNQFYTE 117 (157)

T ss\_dssp SSCCCCCHHHHHHHHHCTTEEEEEEEETTEEEEEEEEEEECCSSCSSCEEEEEEEEECGGGCSSSHHHHHHHHHHHHHHH

T ss\_pred cCCCCCcHHHHHHHHccCCeEEEEEEeCCEEEEEEEEEEeecccCCCCEEEEEEEEEChhHcCCCHHHHHHHHHHHHHHH

Q ss\_pred ---CeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeeeccc

Q Phabba\_Draft 77 ---YESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDV 118 (219)

Q Consensus 77 ---~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~ 118 (219)

..+.+.+...|. .+.++|+++||+..+......

T Consensus 118 ~~~~~~~~~~~~~n~---------~~~~~~~~~Gf~~~~~~~~~~ 153 (157)

T 5F47\_B 118 KGFEEVFVQADKVDD---------YALDFYRSTKPTAEEQVVHFY 153 (157)

T ss\_dssp TTCSEEEEEEETTCH---------HHHHHHTTSCCSEEEEEEEEE

T ss\_pred cCCCEEEEEeecCCh---------HHHHHHHhcCCccccceeeee

No 37

>1CJW\_A TRANSFERASE + COA-S-ACETYL TRYPTAMINE; N-ACETYL TRANSFERASE, TRANSFERASE; HET: COT; 1.8A {Ovis aries} SCOP: d.108.1.1

Probab=98.56 E-value=3.2e-08 Score=75.73 Aligned\_cols=110 Identities=15% Similarity=0.111 Sum\_probs=0.0 Template\_Neff=12.500

Q ss\_pred CCCCCCCchHHHHHhhCCc--EEEEEECCEEEEEEEEEeC-------------------CEEEEEEECHHHCCCCHHHHH

Q Phabba\_Draft 8 GDLPPLKFEPFDTMWSNGI--MARHAHDDRPVGHLHWHPD-------------------GEIDSITVHPDLQRRGIGTAM 66 (219)

Q Consensus 8 ~~~~~~~~~~l~~~~~~~~--~~v~~~~~~liG~~~~~~~-------------------~~i~~l~V~p~~R~~Gig~~L 66 (219)

....++..+.+...+.... ++++.+++++||++.+... ..+..++|+|++||+|+|+.|

T Consensus 31 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~~~~~~~~~~~i~~~~v~p~~r~~G~~~~l 110 (166)

T 1CJW\_A 31 SGNCPLNLDEVQHFLTLCPELSLGWFVEGRLVAFIIGSLWDEERLTQESLALHRPRGHSAHLHALAVHRSFRQQGKGSVL 110 (166)

T ss\_dssp HSCCSCCHHHHHHHHHHCGGGEEEEEETTEEEEEEEEEEECSSSCCGGGGGCCCTTCCEEEEEEEEECTTSTTSSHHHHH

T ss\_pred cCCCCCCHHHHHHHHHhCCCcEEEEEECCEEEEEEEEEecccccCCHHHHhhcCCCCceEEEEEEEeCHHHhcCCHHHHH

Q ss\_pred HHHHHHccc-cCeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeeeccccccceEEe

Q Phabba\_Draft 67 LKHAQDNPH-IYESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDVSNWGYTAM 126 (219)

Q Consensus 67 l~~~~~~~~-~~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~~~~~~~ 126 (219)

++.+++.+. ...+...+...|. .+.++|+++||+..+.............+

T Consensus 111 ~~~~~~~~~~~~~~~~~~~~~n~---------~~~~~~~~~Gf~~~~~~~~~~~~~~~~~~ 162 (166)

T 1CJW\_A 111 LWRYLHHVGAQPAVRRAVLMCED---------ALVPFYQRFGFHPAGPCAIVVGSLTFTEM 162 (166)

T ss\_dssp HHHHHHHHHTSTTCCEEEEEECG---------GGHHHHHTTTEEEEEECSCCBTTBCCEEE

T ss\_pred HHHHHHHHhcCccceEEEEEecc---------chHHHHHHcCCeeceeeeeEeccchheee

No 38

>d1tiqb1 d.108.1.1 (B:2-172) Protease synthase and sporulation negative regulatory protein PaiA {Bacillus subtilis [TaxId: 1423]}

Probab=98.56 E-value=2.4e-08 Score=76.28 Aligned\_cols=99 Identities=17% Similarity=0.137 Sum\_probs=0.0 Template\_Neff=12.800

Q ss\_pred CCchHHHHHhhCCc--EEEEEECCEEEEEEEEEeC-----------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---

Q Phabba\_Draft 13 LKFEPFDTMWSNGI--MARHAHDDRPVGHLHWHPD-----------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI--- 76 (219)

Q Consensus 13 ~~~~~l~~~~~~~~--~~v~~~~~~liG~~~~~~~-----------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~--- 76 (219)

+..+.+...+.... ++++..+|++||++.+... .++..++|+|++|++|+|+.|++.+.+.++.

T Consensus 44 ~~~~~~~~~~~~~~~~~~~~~~~~~ivG~~~~~~~~~~~~~~~~~~~~~~~~~v~~~~r~~G~~~~l~~~~~~~~~~~~~ 123 (171)

T d1tiqb1 44 FNTEQLEKELSNMSSQFFFIYFDHEIAGYVKVNIDDAQSEEMGAESLEIERIYIKNSFQKHGLGKHLLNKAIEIALERNK 123 (171)

T ss\_dssp SCHHHHHHHHHCTTEEEEEEEETTEEEEEEEEEEGGGSSSCCCTTEEEEEEEEECGGGCSSSHHHHHHHHHHHHHHHTTC

T ss\_pred cCHHHHHHHHhcCceeEEEEEeCCeEEEEEEEEeCcccccccCCCEEEEEEEEECHHHcCCCHHHHHHHHHHHHHHHcCC

Q ss\_pred CeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeeeccccc

Q Phabba\_Draft 77 YESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDVSN 120 (219)

Q Consensus 77 ~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~ 120 (219)

..+.+.+...|. .+.++|+++||+..+........

T Consensus 124 ~~i~~~~~~~n~---------~~~~~~~~~Gf~~~~~~~~~~~~ 158 (171)

T d1tiqb1 124 KNIWLGVWEKNE---------NAIAFYKKMGFVQTGAHSFYMGD 158 (171)

T ss\_dssp SEEEEEEETTCH---------HHHHHHHHTTCEEEEEEEEEETT

T ss\_pred CEEEEEEEcCcH---------HHHHHHHHcCCEEecceEEecCC

No 39

>2PC1\_A Acetyltransferase, GNAT family; NP\_688560.1, acetyltransferase GNAT family, Structural; HET: SO4; 1.28A {Streptococcus agalactiae 2603V/R}

Probab=98.56 E-value=2.1e-08 Score=80.74 Aligned\_cols=92 Identities=12% Similarity=0.010 Sum\_probs=0.0 Template\_Neff=11.500

Q ss\_pred hHHHHHhhCCcEEEEEECCEEEEEEEE--------------------EeCCEEEEEEECHHHCCCCHHHHHHHHHHHccc

Q Phabba\_Draft 16 EPFDTMWSNGIMARHAHDDRPVGHLHW--------------------HPDGEIDSITVHPDLQRRGIGTAMLKHAQDNPH 75 (219)

Q Consensus 16 ~~l~~~~~~~~~~v~~~~~~liG~~~~--------------------~~~~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~ 75 (219)

..+...+....++++..+|++||++.+ ....++..++|+|++||+|+|+.|++.+++.+.

T Consensus 62 ~~~~~~~~~~~~~v~~~~~~ivG~~~~~~~~~~~~~~~~~~~~~~~~~~~~~i~~~~v~p~~r~~Gig~~l~~~~~~~~~ 141 (201)

T 2PC1\_A 62 NDIIDDILNGYAWVGIEDGMLATYAAVIDGHEEVYDAIYEGKWLHDNHRYLTFHRIAISNQFRGRGLAQTFLQGLIEGHK 141 (201)

T ss\_dssp HHHHHHHHHTCEEEEEETTEEEEEEEEEEECCGGGGGCBSSCCSSCCSCEEEEEEEEECSTTCSSHHHHHHHHHHHHHSC

T ss\_pred HHHHHHhhcCcEEEEEECCeEEEEEEEEcCCchhhhhhhccccccCCCCeEEEEEEEECHHHCCCCHHHHHHHHHHHhcC

Q ss\_pred cCeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeeec

Q Phabba\_Draft 76 IYESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADD 116 (219)

Q Consensus 76 ~~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~ 116 (219)

...+.+.+...|. .+.+||+++||+..+....

T Consensus 142 ~~~~~~~~~~~n~---------~~~~~~~~~Gf~~~~~~~~ 173 (201)

T 2PC1\_A 142 GPDFRCDTHEKNV---------TMQHILNKLGYQYCGKVPL 173 (201)

T ss\_dssp CSEEEEEECTTCH---------HHHHHHHHTTCEEEEEECS

T ss\_pred CCcEEEEEeCCCH---------HHHHHHHHcCcEEEEEeec

No 40

>5JPH\_C Acetyltransferase SACOL1063 (E.C.2.3.1.-); acetyltransferase, Gcn5-related N-acetyltransferase, GNAT, protein; HET: COA, MSE; 1.46A {Staphylococcus aureus}

Probab=98.56 E-value=9.9e-09 Score=77.90 Aligned\_cols=107 Identities=11% Similarity=0.048 Sum\_probs=0.0 Template\_Neff=11.700

Q ss\_pred CCccccCCCCCCCCchHHHHHhhCCcEEEEEECCEEEEEEEEEeC----CEEEEEEECHHHCCCCHHHHHHHHHHHcccc

Q Phabba\_Draft 1 MHQAGANGDLPPLKFEPFDTMWSNGIMARHAHDDRPVGHLHWHPD----GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI 76 (219)

Q Consensus 1 ~~~~~~~~~~~~~~~~~l~~~~~~~~~~v~~~~~~liG~~~~~~~----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~ 76 (219)

|.....................+...++++.+++++||++.+... ..+..++|+|++|++|+|+.|++.+++.+..

T Consensus 20 l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~vg~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~ 99 (144)

T 5JPH\_C 20 IRKKVFVEEQGIPEESEIDEYESESIHLIGYDNGQPVATARIRPINETTVKIERVAVMKSHRGQGMGRMLMQAVESLAKD 99 (144)

T ss\_dssp HHCCCCCCCTCCCHHHHSCTTTTTSEEEEEEETTEEEEEEEEEESSSSEEEEEEEEECGGGTTSSHHHHHHHHHHHHHHH

T ss\_pred HHHHhhccCCCCCccccccccCCCeEEEEEEECCeEEEEEEEEEcCCCeEEEEEEEECHhHCCCCHHHHHHHHHHHHHHH

Q ss\_pred CeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeeec

Q Phabba\_Draft 77 YESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADD 116 (219)

Q Consensus 77 ~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~ 116 (219)

..+...+...|. .+.++|+++||+..+....

T Consensus 100 ~~~~~~~~~~n~---------~~~~~~~~~Gf~~~~~~~~ 130 (144)

T 5JPH\_C 100 EGFYVATMNAQC---------HAIPFYESLNFKMRGNIFL 130 (144)

T ss\_dssp TTCCEEEEEEEG---------GGHHHHHHTTCEEEEEEEE

T ss\_pred cCCeEEEEecch---------hhHHHHHhCCCEEecceee

No 41

>2I6C\_A putative acetyltransferase; acetyltransferase, GNAT family, structural genomic; HET: EPE, SO4; 1.3A {Pseudomonas aeruginosa} SCOP: d.108.1.1

Probab=98.55 E-value=3.6e-08 Score=74.99 Aligned\_cols=103 Identities=11% Similarity=0.080 Sum\_probs=0.0 Template\_Neff=12.500

Q ss\_pred cccCCCCCCCCchHHHHHhhCCc-EEEEEECCEEEEEEEEEeC-----CEEEEEEECHHHCCCCHHHHHHHHHHHcccc-

Q Phabba\_Draft 4 AGANGDLPPLKFEPFDTMWSNGI-MARHAHDDRPVGHLHWHPD-----GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI- 76 (219)

Q Consensus 4 ~~~~~~~~~~~~~~l~~~~~~~~-~~v~~~~~~liG~~~~~~~-----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~- 76 (219)

........+...+.+...+..+. ++++.+++++||++.+... ..+..+.|+|++|++|+|+.|+..+++.+..

T Consensus 28 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~~ 107 (160)

T 2I6C\_A 28 YCYPKAIWPFSVAQLAAAIAERRGSTVAVHDGQVLGFANFYQWQHGDFCALGNMMVAPAARGLGVARYLIGVMENLAREQ 107 (160)

T ss\_dssp HHCTTCCSSCCHHHHHHHHHHSEEEEEEEETTEEEEEEEEEEEETTTEEEEEEEEECGGGTTTTHHHHHHHHHHHHHHHH

T ss\_pred hhCCCCCCCCCHHHHHHHHHhCCcEEEEEECCEEEEEEEEEEecCCCeEEEEeEEECHHHCCCcHHHHHHHHHHHHHHHH

Q ss\_pred ---CeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 77 ---YESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 77 ---~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

..+.+.+...|. .+.++|+++||+..+...

T Consensus 108 ~~~~~~~~~~~~~n~---------~~~~~~~~~Gf~~~~~~~ 140 (160)

T 2I6C\_A 108 YKARLMKISCFNANA---------AGLLLYTQLGYQPRAIAE 140 (160)

T ss\_dssp HCCSEEEEEEETTCH---------HHHHHHHHTTCEEEEEEE

T ss\_pred hcCCeEEEEEecCCH---------HHHHHHHHcCCeEeEeee

No 42

>d1cjwa\_ d.108.1.1 (A:) Serotonin N-acetyltranferase {Sheep (Ovis aries) [TaxId: 9940]}

Probab=98.55 E-value=3.3e-08 Score=75.63 Aligned\_cols=110 Identities=15% Similarity=0.111 Sum\_probs=0.0 Template\_Neff=12.500

Q ss\_pred CCCCCCCchHHHHHhhCCc--EEEEEECCEEEEEEEEEeC-------------------CEEEEEEECHHHCCCCHHHHH

Q Phabba\_Draft 8 GDLPPLKFEPFDTMWSNGI--MARHAHDDRPVGHLHWHPD-------------------GEIDSITVHPDLQRRGIGTAM 66 (219)

Q Consensus 8 ~~~~~~~~~~l~~~~~~~~--~~v~~~~~~liG~~~~~~~-------------------~~i~~l~V~p~~R~~Gig~~L 66 (219)

....++..+.+...+.... ++++.++|++||++.+... ..+..++|+|++||+|+|+.|

T Consensus 31 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ivG~~~~~~~~~~~~~~~~~~~~~~~~~~~~i~~~~v~~~~r~~G~~~~l 110 (166)

T d1cjwa\_ 31 SGNCPLNLDEVQHFLTLCPELSLGWFVEGRLVAFIIGSLWDEERLTQESLALHRPRGHSAHLHALAVHRSFRQQGKGSVL 110 (166)

T ss\_dssp HSCCSCCHHHHHHHHHHCGGGEEEEEETTEEEEEEEEEEECSSSCCGGGGGCCCTTCCEEEEEEEEECTTSTTSSHHHHH

T ss\_pred cCCCCCCHHHHHHHHhhCCCcEEEEEECCEEEEEEEEEecccccCCHHHHHhcCCCCCeEEEEEEEeCHHHccCCHHHHH

Q ss\_pred HHHHHHccc-cCeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeeeccccccceEEe

Q Phabba\_Draft 67 LKHAQDNPH-IYESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDVSNWGYTAM 126 (219)

Q Consensus 67 l~~~~~~~~-~~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~~~~~~~ 126 (219)

+..+++.+. ...+...+...|. .+.++|+++||+..+..........+..+

T Consensus 111 ~~~~~~~~~~~~~~~~~~~~~n~---------~~~~~~~~~Gf~~~~~~~~~~~~~~~~~~ 162 (166)

T d1cjwa\_ 111 LWRYLHHVGAQPAVRRAVLMCED---------ALVPFYQRFGFHPAGPCAIVVGSLTFTEM 162 (166)

T ss\_dssp HHHHHHHHHTSTTCCEEEEEECG---------GGHHHHHTTTEEEEEECSCCBTTBCCEEE

T ss\_pred HHHHHHHHhcCCcccEEEEEecc---------chHHHHHHcCCeeceeeeeEECCccceeh

No 43

>d2jdda\_ d.108.1.1 (A:) Probable acetyltransferase YitI {Bacillus licheniformis [TaxId: 1402]}

Probab=98.55 E-value=2e-08 Score=75.98 Aligned\_cols=117 Identities=9% Similarity=0.037 Sum\_probs=0.0 Template\_Neff=11.900

Q ss\_pred CCccccCCCCCCCCchHHHHHhhCCcEEEEEECCEEEEEEEEE----------eCCEEEEEEECHHHCCCCHHHHHHHHH

Q Phabba\_Draft 1 MHQAGANGDLPPLKFEPFDTMWSNGIMARHAHDDRPVGHLHWH----------PDGEIDSITVHPDLQRRGIGTAMLKHA 70 (219)

Q Consensus 1 ~~~~~~~~~~~~~~~~~l~~~~~~~~~~v~~~~~~liG~~~~~----------~~~~i~~l~V~p~~R~~Gig~~Ll~~~ 70 (219)

++........+...............++++.+++++||++.+. ....+..++|+|++|++|+|+.|++.+

T Consensus 14 l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~vg~~~~~~~~~~~~~~~~~~~i~~~~v~~~~r~~g~~~~l~~~~ 93 (145)

T d2jdda\_ 14 LRHRILRPNQPIEACMFESDLLRGAFHLGGYYGGKLISIASFHQAEHSELQGQKQYQLRGMATLEGYREQKAGSSLIKHA 93 (145)

T ss\_dssp HCCCCCCTTSCGGGGSCGGGGSTTCEEEEEEETTEEEEEEEEEECCCTTSCCSSEEEEEEEEECTTSTTSSHHHHHHHHH

T ss\_pred eeeeeecCCCChhheeehhhccCCcEEEEEEECCEEEEEEEEEEcCccccCCCcEEEEEEEEECHHHCCCCHHHHHHHHH

Q ss\_pred HHccccCeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeeeccccccceEEe

Q Phabba\_Draft 71 QDNPHIYESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDVSNWGYTAM 126 (219)

Q Consensus 71 ~~~~~~~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~~~~~~~ 126 (219)

++.+....+...+...|. .+.++|+++||+..+.+...........+

T Consensus 94 ~~~~~~~~~~~~~~~~n~---------~~~~~~~~~Gf~~~~~~~~~~~~~~~~~~ 140 (145)

T d2jdda\_ 94 EEILRKRGADLLWCNART---------SASGYYKKLGFSEQGEVFDTPPVGPHILM 140 (145)

T ss\_dssp HHHHHHTTCCEEEEEEEG---------GGHHHHHHTTCEEEEEEEECTTSCEEEEE

T ss\_pred HHHHHHCCCCEEEEeeCh---------hHHHHHHHhCcEEeeEEeecCCCCceEEE

No 44

>d4f0ya\_ d.108.1.0 (A:) automated matches {Acinetobacter haemolyticus [TaxId: 29430]}

Probab=98.55 E-value=2.2e-08 Score=74.24 Aligned\_cols=98 Identities=16% Similarity=0.138 Sum\_probs=0.0 Template\_Neff=12.900

Q ss\_pred hHHHHHhhCCc--EEEEEECCEEEEEEEEE------------eCCEEEEEEECHHHCCCCHHHHHHHHHHHcccc---Ce

Q Phabba\_Draft 16 EPFDTMWSNGI--MARHAHDDRPVGHLHWH------------PDGEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YE 78 (219)

Q Consensus 16 ~~l~~~~~~~~--~~v~~~~~~liG~~~~~------------~~~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~ 78 (219)

+.+...+.... ++++.+++++||++.+. ....+..++|+|++|++|+++.|++.+.+.+.. ..

T Consensus 31 ~~~~~~~~~~~~~~~~~~~~~~~vg~~~~~~~~~~~~~~~~~~~~~i~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~ 110 (145)

T d4f0ya\_ 31 QEMHQLLAEKYALQLLAYSDHQAIAMLEASIRFEYVNGTETSPVGFLEGIYVLPAHRRSGVATMLIRQAEVWAKQFSCTE 110 (145)

T ss\_dssp HHHHHHHTCTTEEEEEEEETTEEEEEEEEEEECSCCTTCCSSSEEEEEEEEECGGGTTSSHHHHHHHHHHHHHHTTTCCE

T ss\_pred HHHHHHHhhcCceEEEEEcCCeEEEEEEEEEeecccCCCCCCcEEEEEEEEECHHHcCCCHHHHHHHHHHHHHHHCCCCE

Q ss\_pred eEEEEEcCCcccccccccchhHHHHHcCCCEEeeeeeccccccc

Q Phabba\_Draft 79 SSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDVSNWG 122 (219)

Q Consensus 79 i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~~~ 122 (219)

+.+.+...|. .+.++|+++||+..+.+........

T Consensus 111 ~~~~~~~~n~---------~~~~~~~~~Gf~~~~~~~~~~~~l~ 145 (145)

T d4f0ya\_ 111 FASDAALDNV---------ISHAMHRSLGFQETEKVVYFSKKID 145 (145)

T ss\_dssp EEEEEETTCH---------HHHHHHHTTTCEEEEEEEEEEEECC

T ss\_pred EEEEeecccH---------HHHHHHHHcCcEEcceEEEeeecCC

No 45

>d1yvka1 d.108.1.1 (A:5-155) Hypothetical protein YvbK (BSu33890) {Bacillus subtilis [TaxId: 1423]}

Probab=98.55 E-value=2.7e-08 Score=77.10 Aligned\_cols=94 Identities=18% Similarity=0.116 Sum\_probs=0.0 Template\_Neff=11.000

Q ss\_pred CCCchHHHHHhhCCcEEEEEECCEEEEEEEEEeC----CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEEE

Q Phabba\_Draft 12 PLKFEPFDTMWSNGIMARHAHDDRPVGHLHWHPD----GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPVR 84 (219)

Q Consensus 12 ~~~~~~l~~~~~~~~~~v~~~~~~liG~~~~~~~----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v~ 84 (219)

....+.+...+.+..++++..+|++||++.+... ..+..+.|+|++|++|+|+.|++.+.+.+.. ..+.+.+.

T Consensus 22 ~~~~~~~~~~~~~~~~~~~~~~~~ivG~~~~~~~~~~~~~i~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~~~~~~~ 101 (151)

T d1yvka1 22 DPSKDIVDEYLERGECYTAWAGDELAGVYVLLKTRPQTVEIVNIAVKESLQKKGFGKQLVLDAIEKAKKLGADTIEIGTG 101 (151)

T ss\_dssp CCCHHHHHHHHHHSEEEEEEETTEEEEEEEEEECSTTEEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHTTCSEEEEEEE

T ss\_pred CCChHHHHHHHhcCCEEEEEECCEEEEEEEEEECCCCEEEEEEEEECHHHCCCCHHHHHHHHHHHHHHHcCCCEEEEEcC

Q ss\_pred cCCcccccccccchhHHHHHcCCCEEeeee

Q Phabba\_Draft 85 HSSHFSAAGRAWAQSDPDYHDPGDQNVTKA 114 (219)

Q Consensus 85 ~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~ 114 (219)

..|. .+.++|+++||+..+..

T Consensus 102 ~~n~---------~~~~~~~~~Gf~~~~~~ 122 (151)

T d1yvka1 102 NSSI---------HQLSLYQKCGFRIQAID 122 (151)

T ss\_dssp TTCH---------HHHHHHHHTTCEEEEEE

T ss\_pred CCCH---------HHHHHHHHCCCEEEEec

No 46

>4CRY\_B ASPARTATE 1-DECARBOXYLASE (E.C.4.1.1.11), PANZ; LYASE, COENZYME A, RADIATION DAMAGE; HET: ACO; 1.61A {ESCHERICHIA COLI K-12}

Probab=98.55 E-value=1.5e-08 Score=76.14 Aligned\_cols=90 Identities=16% Similarity=0.129 Sum\_probs=0.0 Template\_Neff=11.800

Q ss\_pred hCCcEEEEEECCEEEEEEEEEeC---CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEEEcCCccccccccc

Q Phabba\_Draft 23 SNGIMARHAHDDRPVGHLHWHPD---GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPVRHSSHFSAAGRAW 96 (219)

Q Consensus 23 ~~~~~~v~~~~~~liG~~~~~~~---~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v~~~n~~~~~~~~~ 96 (219)

....++++..++++||++.+... .++..++|+|++|++|+|+.|++.+++.+.+ ..+.+.+...|.

T Consensus 35 ~~~~~~~~~~~~~~vG~~~~~~~~~~~~i~~~~v~~~~r~~gi~~~l~~~~~~~~~~~~~~~i~~~~~~~~~-------- 106 (137)

T 4CRY\_B 35 DNHRIYAARFNERLLAAVRVTLSGTEGALDSLRVREVTRRRGVGQYLLEEVLRNNPGVSCWWMADAGVEDRG-------- 106 (137)

T ss\_dssp TTEEEEEEEETTEEEEEEEEEEETTEEEEEEEEECGGGTTSSHHHHHHHHHHHTCTTCCEEEEECTTCSCHH--------

T ss\_pred CCeEEEEEEECCEEEEEEEEEeCCCeEEEEEEEECHHHCCCCHHHHHHHHHHHhCCCCCeeEEEecCcCCch--------

Q ss\_pred chhHHHHHcCCCEEeeeeecccccc

Q Phabba\_Draft 97 AQSDPDYHDPGDQNVTKADDDVSNW 121 (219)

Q Consensus 97 ~~~~~~y~r~Gf~~~~~~~~~~~~~ 121 (219)

.+.++|+++||+..+.+......+

T Consensus 107 -~~~~~~~~~Gf~~~~~~~~~~~~~ 130 (137)

T 4CRY\_B 107 -VMTAFMQALGFTAQQGGWEKCSGL 130 (137)

T ss\_dssp -HHHHHHHHTTCEEETTEEEEC---

T ss\_pred -HHHHHHHHcCCEEecCCcccCCCC

No 47

>d2ge3b\_ d.108.1.1 (B:) automated matches {Agrobacterium tumefaciens [TaxId: 358]}

Probab=98.55 E-value=2.8e-08 Score=75.62 Aligned\_cols=91 Identities=14% Similarity=0.154 Sum\_probs=0.0 Template\_Neff=12.600

Q ss\_pred chHHHHHhhCCc-EEEEEECCEEEEEEEEEeC-------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEE

Q Phabba\_Draft 15 FEPFDTMWSNGI-MARHAHDDRPVGHLHWHPD-------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPV 83 (219)

Q Consensus 15 ~~~l~~~~~~~~-~~v~~~~~~liG~~~~~~~-------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v 83 (219)

.+.+........ ++++..+|+++|++.+... ..+..++|+|++|++|+|+.|++.+++.++. ..+.+.+

T Consensus 41 ~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~~g~~~i~~~~ 120 (163)

T d2ge3b\_ 41 RAFVLDMIENDHPQFVAIADGDVIGWCDIRRQDRATRAHCGTLGMGILPAYRNKGLGARLMRRTLDAAHEFGLHRIELSV 120 (163)

T ss\_dssp HHHHHHHHHTTCCEEEEEETTEEEEEEEEEECSSTTTTTEEEEEEEECGGGCSSSHHHHHHHHHHHHHHHHTCSEEEEEE

T ss\_pred HHHHHHhhcCCCcEEEEEECCeEEEEEEEEeCCCcccceEEEEEEEeCHHHCCCCHHHHHHHHHHHHHHHhCCCEEEEEE

Q ss\_pred EcCCcccccccccchhHHHHHcCCCEEeeee

Q Phabba\_Draft 84 RHSSHFSAAGRAWAQSDPDYHDPGDQNVTKA 114 (219)

Q Consensus 84 ~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~ 114 (219)

...|. .+.++|+++||+..+..

T Consensus 121 ~~~n~---------~~~~~~~~~Gf~~~~~~ 142 (163)

T d2ge3b\_ 121 HADNA---------RAIALYEKIGFAHEGRA 142 (163)

T ss\_dssp ETTCH---------HHHHHHHHHTCEEEEEE

T ss\_pred ECCCH---------HHHHHHHHcCCeEEEEe

No 48

>4L8A\_A Uncharacterized protein; Structural Genomics, PSI-Biology, Midwest Center; HET: COA, SO4, EDO, 1VP; 1.2A {Pseudomonas aeruginosa}

Probab=98.54 E-value=3.4e-08 Score=75.29 Aligned\_cols=102 Identities=11% Similarity=0.088 Sum\_probs=0.0 Template\_Neff=12.500

Q ss\_pred ccCCCCCCCCchHHHHHhhCCc-EEEEEECCEEEEEEEEEeC-----CEEEEEEECHHHCCCCHHHHHHHHHHHcccc--

Q Phabba\_Draft 5 GANGDLPPLKFEPFDTMWSNGI-MARHAHDDRPVGHLHWHPD-----GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI-- 76 (219)

Q Consensus 5 ~~~~~~~~~~~~~l~~~~~~~~-~~v~~~~~~liG~~~~~~~-----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~-- 76 (219)

.......+...+.+...+..+. ++++..+|++||++.+... ..+..++|+|++|++|+|+.|+..+++.+..

T Consensus 31 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ivG~~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~ 110 (162)

T 4L8A\_A 31 CYPKAIWPFSVAQLAAAIAERRGSTVAVHDGQVLGFANFYQWQHGDFCALGNMMVAPAARGLGVARYLIGVMENLAREQY 110 (162)

T ss\_dssp HCTTSCSSCCHHHHHHHHHHSEEEEEEEETTEEEEEEEEEEEETTTEEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHHH

T ss\_pred cCCCCcCCCCHHHHHHHHhcCCcEEEEEECCEEEEEEEEEEecCCCEEEEEEEEECHHHCCCcHHHHHHHHHHHHHHHHh

Q ss\_pred --CeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 77 --YESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 77 --~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

..+.+.+...|. .+.++|+++||+..+...

T Consensus 111 ~~~~~~~~~~~~n~---------~~~~~~~~~Gf~~~~~~~ 142 (162)

T 4L8A\_A 111 KARLMKISCFNANA---------AGLLLYTQLGYQPRAIAE 142 (162)

T ss\_dssp CCSEEEEEEETTCH---------HHHHHHHHTTCEEEEEEE

T ss\_pred cCCEEEEEeecccH---------HHHHHHHHcCCceeeeee

No 49

>d1y7rb\_ d.108.1.1 (B:) Hypothetical protein SA2161 {Staphylococcus aureus [TaxId: 1280]}

Probab=98.54 E-value=3e-08 Score=74.41 Aligned\_cols=102 Identities=17% Similarity=0.126 Sum\_probs=0.0 Template\_Neff=11.600

Q ss\_pred CCCCCCCCchHHHHHhhCCc-EEEEEECCEEEEEEEEEeC----CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---Ce

Q Phabba\_Draft 7 NGDLPPLKFEPFDTMWSNGI-MARHAHDDRPVGHLHWHPD----GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YE 78 (219)

Q Consensus 7 ~~~~~~~~~~~l~~~~~~~~-~~v~~~~~~liG~~~~~~~----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~ 78 (219)

.....+...+.+...+.+.. ++++.+++++||++.+... ..+..+.|+|++|++|+|+.|++.+++.+.. ..

T Consensus 20 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~vg~~~~~~~~~~~~~i~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~ 99 (133)

T d1y7rb\_ 20 NAGMSPKTREAAEKGLPNALFTVTLYDKDRLIGMGRVIGDGGTVFQIVDIAVLKSYQGQAYGSLIMEHIMKYIKNVSVES 99 (133)

T ss\_dssp HTTCCCCCHHHHHHHGGGCSEEEEEEETTEEEEEEEEEECSSSEEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHHCCTT

T ss\_pred hCCCCcCCHHHHHhcCCcceEEEEEEeCCeEEEEEEEEeCCCeEEEEEEEEEChhhCCCCHHHHHHHHHHHHHHhCCCce

Q ss\_pred eEEEEEcCCcccccccccchhHHHHHcCCCEEeeeeeccc

Q Phabba\_Draft 79 SSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDV 118 (219)

Q Consensus 79 i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~ 118 (219)

+.+.+...+. +.++|+++||+..+......

T Consensus 100 ~~~~~~~~~~----------~~~~~~~~Gf~~~~~~~~~~ 129 (133)

T d1y7rb\_ 100 VYVSLIADYP----------ADKLYVKFGFMPTEPDSGGM 129 (133)

T ss\_dssp CEEEEEEEGG----------GHHHHHHTTCEECTTTEEEE

T ss\_pred EEEEEecCCc----------hHHHHHHcCCEECCCccccc

No 50

>PF12568.7 ; DUF3749 ; Acetyltransferase (GNAT) domain

Probab=98.54 E-value=2.9e-08 Score=72.86 Aligned\_cols=96 Identities=14% Similarity=0.221 Sum\_probs=0.0 Template\_Neff=12.400

Q ss\_pred CCCCchHHHHHhhCCc-EEEEEECCEEEEEEEEEeC-----CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEE

Q Phabba\_Draft 11 PPLKFEPFDTMWSNGI-MARHAHDDRPVGHLHWHPD-----GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSY 81 (219)

Q Consensus 11 ~~~~~~~l~~~~~~~~-~~v~~~~~~liG~~~~~~~-----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l 81 (219)

.....+.+...+++.. ++++..++++||++.+... ..+..++|+|++|++|+++.|++.+.+.+.. ..+..

T Consensus 23 ~~~~~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~~~~ 102 (129)

T Q2NWW2\_SODGM/2 23 PAVDIDALQQQFTDSFALFAARFNDRLLAAVQVELDAAWGEGRLMGLRVRPETRRRGVGLYLVNETRRQMPDIVSWWLSN 102 (129)

T ss\_pred ccCCHHHHHHhhhcCceEEEEEECCEEEEEEEEEecCCcCcEEEEEEEECHHHCCCCHHHHHHHHHHHhCccCCceEEEE

Q ss\_pred EEEc-CCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 82 PVRH-SSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 82 ~v~~-~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

.+.. .|. .+.++|+++||+..+...

T Consensus 103 ~~~~~~n~---------~~~~~~~~~Gf~~~~~~~ 128 (129)

T Q2NWW2\_SODGM/2 103 QQPLEDAA---------LMGKFMSACGFYEEPDGW 128 (129)

T ss\_pred eccCCCcH---------HHHHHHHHcCCEeCCCCC

No 51

>d4oaea1 d.108.1.1 (A:1-159) Putative acetyltransferase PA4794 {Pseudomonas aeruginosa [TaxId: 287]}

Probab=98.54 E-value=4.3e-08 Score=74.14 Aligned\_cols=105 Identities=10% Similarity=0.034 Sum\_probs=0.0 Template\_Neff=12.700

Q ss\_pred CccccCCCCCCCCchHHHHHhhC-CcEEEEEECCEEEEEEEEEeC-----CEEEEEEECHHHCCCCHHHHHHHHHHHccc

Q Phabba\_Draft 2 HQAGANGDLPPLKFEPFDTMWSN-GIMARHAHDDRPVGHLHWHPD-----GEIDSITVHPDLQRRGIGTAMLKHAQDNPH 75 (219)

Q Consensus 2 ~~~~~~~~~~~~~~~~l~~~~~~-~~~~v~~~~~~liG~~~~~~~-----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~ 75 (219)

..........+...+.+...+.. ..++++..++++||++.+... ..+..+.|+|++|++|+|..|+..+++.+.

T Consensus 26 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~ 105 (159)

T d4oaea1 26 LFYAYPKAIWPFSVAQLAAAIAERRGSTVAVHDGQVLGFANFYQWQHGDFCALGNMMVAPAARGLGVARYLIGVMENLAR 105 (159)

T ss\_dssp HHHHCTTCCSSCCHHHHHHHHHHSEEEEEEEETTEEEEEEEEEEEETTTEEEEEEEEECGGGTTSSHHHHHHHHHHHHHH

T ss\_pred hcccCCcccCCCCHHHHHHHHHhcCCeEEEEECCEEEEEEEEEEeecCCeEEEEEEEECHHHCCCCHHHHHHHHHHHHHH

Q ss\_pred c----CeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 76 I----YESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 76 ~----~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

. ..+.+.+...|. .+.++|+++||+..+...

T Consensus 106 ~~~~~~~~~~~~~~~n~---------~~~~~~~k~Gf~~~~~~~ 140 (159)

T d4oaea1 106 EQYKARLMKISAFNANA---------AGLLLATQLGYQPRAIAE 140 (159)

T ss\_dssp HHHCCSEEEEEEETTCH---------HHHHHHHHTTCEEEEEEE

T ss\_pred HhhhcceEEEEEeCCCH---------HHHHHHHHcCCeeeEeec

No 52

>d4e2aa\_ d.108.1.0 (A:) automated matches {Streptococcus mutans [TaxId: 1309]}

Probab=98.53 E-value=2.8e-08 Score=75.87 Aligned\_cols=101 Identities=16% Similarity=0.084 Sum\_probs=0.0 Template\_Neff=12.800

Q ss\_pred chHHHHHhhCCc--EEEEEECCEEEEEEEE-----------EeCCEEEEEEECHHHCCCCHHHHHHHHHHHcccc---Ce

Q Phabba\_Draft 15 FEPFDTMWSNGI--MARHAHDDRPVGHLHW-----------HPDGEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YE 78 (219)

Q Consensus 15 ~~~l~~~~~~~~--~~v~~~~~~liG~~~~-----------~~~~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~ 78 (219)

.+.+........ ++++..++++||++.+ .....+..++|+|++||+|+|+.|+..+++.+.. ..

T Consensus 46 ~~~~~~~~~~~~~~~~~~~~~~~ivG~~~~~~~~~~~~~~~~~~~~i~~~~v~~~~r~~g~~~~l~~~~~~~~~~~g~~~ 125 (170)

T d4e2aa\_ 46 LSVLKLELDDKESETYFILMSGKAAGFLKVNWGSSQTEQVLEDAFEIQRLYILKAYQGLGLGKQLFEFALERAQISGLSW 125 (170)

T ss\_dssp HHHHHHHHHCTTEEEEEEEETTEEEEEEEEEEGGGSSSCCSSSEEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHHTCSE

T ss\_pred HHHHHHhhcCCCceEEEEEECCeEEEEEEEEeccccccccccceEEEEEEEECHHHCCCCHHHHHHHHHHHHHHHcCCCE

Q ss\_pred eEEEEEcCCcccccccccchhHHHHHcCCCEEeeeeeccccccceE

Q Phabba\_Draft 79 SSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDVSNWGYT 124 (219)

Q Consensus 79 i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~~~~~ 124 (219)

+.+.+...|. .+.++|+|+||+..+......+.....

T Consensus 126 i~~~~~~~n~---------~~~~~~~k~Gf~~~~~~~~~~~~~~~~ 162 (170)

T d4e2aa\_ 126 VWLGVWEKNV---------KAQLLYAKYGFEQFSKHSFFVGNKVDT 162 (170)

T ss\_dssp EEEEEETTCH---------HHHHHHHHTTCEEEEEEEEEETTEEEE

T ss\_pred EEEEEecCCH---------HHHHHHHHhCcEEeeeeeEEeCCeeee

No 53

>d1u6ma1 d.108.1.1 (A:4-189) Putative acetyltransferase EF0945 {Enterococcus faecalis [TaxId: 1351]}

Probab=98.53 E-value=3.6e-08 Score=77.06 Aligned\_cols=105 Identities=16% Similarity=0.152 Sum\_probs=0.0 Template\_Neff=12.400

Q ss\_pred CCCCCchHHHHHhhC-----------CcEEEEEECCEEEEEEEEEeC---------------------------------

Q Phabba\_Draft 10 LPPLKFEPFDTMWSN-----------GIMARHAHDDRPVGHLHWHPD--------------------------------- 45 (219)

Q Consensus 10 ~~~~~~~~l~~~~~~-----------~~~~v~~~~~~liG~~~~~~~--------------------------------- 45 (219)

..+...+.+...+.. ..++++.+++++||++.+...

T Consensus 28 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~v~~~~~~ivG~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ 107 (186)

T d1u6ma1 28 LEEVSEEQMIDLLAEATAYPTYRYGYQRILVYEHAGEVAGIAVGYPAEDEKIIDEPLREVFKKHGLAEDVRLFIEEETLP 107 (186)

T ss\_dssp GGTSCHHHHHHHHHHHHTSTTSTTCGGGEEEEEETTEEEEEEEEEEGGGTTTSSHHHHHHHHHTTSCTTCCCCCCCCCCT

T ss\_pred hcCCCHHHHHHHHHHHccCCccccCeeEEEEEEECCeEEEEEEEeeccChhhcchhHHHHHHHcCCchhHHHHhccCCCC

Q ss\_pred --CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeeeccccc

Q Phabba\_Draft 46 --GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDVSN 120 (219)

Q Consensus 46 --~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~ 120 (219)

.++..++|+|++|++|+|+.|++.+++.++. ..+.+.+...|. .+.++|+++||+..+........

T Consensus 108 ~~~~i~~~~v~p~~r~~G~~~~l~~~~~~~~~~~g~~~~~~~~~~~n~---------~~~~~~~~~Gf~~~~~~~~~~~~ 178 (186)

T d1u6ma1 108 NEWYLDTISVDERFRGMGIGSKLLDALPEVAKASGKQALGLNVDFDNP---------GARKLYASKGFKDVTTMTISGHL 178 (186)

T ss\_dssp TEEEEEEEEECGGGTTSSHHHHHHHTHHHHHHTTTCSEEEEEEETTCH---------HHHHHHHTTTCEEEEEEEETTEE

T ss\_pred CcEEEEEEEECHHHCCCCHHHHHHHHHHHHHHHcCCCeEEEEeeCCCH---------HHHHHHHhCCcEEEEEEeeCCce

Q ss\_pred cce

Q Phabba\_Draft 121 WGY 123 (219)

Q Consensus 121 ~~~ 123 (219)

+.+

T Consensus 179 ~~~ 181 (186)

T d1u6ma1 179 YNH 181 (186)

T ss\_dssp EEE

T ss\_pred eee

No 54

>3EXN\_A Probable acetyltransferase; acetyltransferase, GCN5-related N-acetyltransferase, MCSG, PSI; HET: ACO; 1.8A {Thermus thermophilus}

Probab=98.53 E-value=2.5e-08 Score=75.89 Aligned\_cols=91 Identities=14% Similarity=0.116 Sum\_probs=0.0 Template\_Neff=12.500

Q ss\_pred hCCcEEEEEECCEEEEEEEEEeC------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc-CeeEEEEEcCCcccccccc

Q Phabba\_Draft 23 SNGIMARHAHDDRPVGHLHWHPD------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI-YESSYPVRHSSHFSAAGRA 95 (219)

Q Consensus 23 ~~~~~~v~~~~~~liG~~~~~~~------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~-~~i~l~v~~~n~~~~~~~~ 95 (219)

....++++.+++++||++.+... ..+..++|+|++|++|+|+.|++.+++.+.. ..+.+.+...|.

T Consensus 60 ~~~~~~~~~~~~~ivG~~~~~~~~~~~~~~~i~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~i~~~~~~~n~------- 132 (160)

T 3EXN\_A 60 PRRRAFLLFLGQEPVGYLDAKLGYPEAEDATLSLLLIREDHQGRGLGRQALERFAAGLDGVRRLYAVVYGHNP------- 132 (160)

T ss\_dssp TTEEEEEEEETTEEEEEEEEEETCSSTTCEEEEEEEECGGGTTSSHHHHHHHHHHHTCTTCCEEEEEEESSCH-------

T ss\_pred ccccEEEEEECCEEEEEEEEecCCCccCeEEEEEEEECHhhCCCCHHHHHHHHHHHhcCCCcEEEEEEeCCCH-------

Q ss\_pred cchhHHHHHcCCCEEeeeeeccccccc

Q Phabba\_Draft 96 WAQSDPDYHDPGDQNVTKADDDVSNWG 122 (219)

Q Consensus 96 ~~~~~~~y~r~Gf~~~~~~~~~~~~~~ 122 (219)

.+.++|+++||+..+........+.

T Consensus 133 --~~~~~~~~~Gf~~~~~~~~~~~~~~ 157 (160)

T 3EXN\_A 133 --KAKAFFQAQGFRYVKDGGPTLTWYV 157 (160)

T ss\_dssp --HHHHHHHHTTCEEEEECSTTEEEEE

T ss\_pred --HHHHHHHHcCCEEeecCCceeeeee

No 55

>3NE7\_A ACETYLTRANSFERASE; COENZYME A, STRUCTURAL GENOMICS, MCSG; HET: COA; 2.3A {Thermoplasma acidophilum}

Probab=98.53 E-value=2.2e-08 Score=76.10 Aligned\_cols=78 Identities=15% Similarity=0.166 Sum\_probs=0.0 Template\_Neff=12.500

Q ss\_pred EEEEEECCEEEEEEEEEeC---CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEEEcCCcccccccccchhH

Q Phabba\_Draft 27 MARHAHDDRPVGHLHWHPD---GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPVRHSSHFSAAGRAWAQSD 100 (219)

Q Consensus 27 ~~v~~~~~~liG~~~~~~~---~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v~~~n~~~~~~~~~~~~~ 100 (219)

++++..++++||++.+... ..+..++|+|++|++|+|+.|++.+++.++. ..+.+.+...|. .+.

T Consensus 65 ~~~~~~~~~~iG~~~~~~~~~~~~i~~~~v~~~~r~~g~~~~l~~~~~~~~~~~g~~~i~~~~~~~n~---------~~~ 135 (159)

T 3NE7\_A 65 FLGAFADSTLIGFIELKIIANKAELLRLYLKPEYTHKKIGKTLLLEAEKIMKKKGILECRLYVHRQNS---------VGF 135 (159)

T ss\_dssp EEEEEETTEEEEEEEEEEETTEEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHTTCCEEEEEEETTCH---------HHH

T ss\_pred EEEEEeCCeEEEEEEEEEeCCeEEEEEEEeCHHHCCCcHHHHHHHHHHHHHHHcCCcEEEEEEeCCCh---------hHH

Q ss\_pred HHHHcCCCEEeee

Q Phabba\_Draft 101 PDYHDPGDQNVTK 113 (219)

Q Consensus 101 ~~y~r~Gf~~~~~ 113 (219)

++|+++||+..+.

T Consensus 136 ~~~~k~Gf~~~~~ 148 (159)

T 3NE7\_A 136 SFYYKNGFKVEDT 148 (159)

T ss\_dssp HHHHTTTCEEEEE

T ss\_pred HHHHHCCCEEEee

No 56

>3DSB\_B Putative acetyltransferase; APC60368.2, acetyltransferase, Clostridium difficile 630; HET: BET, SO4; 1.48A {Clostridium difficile}

Probab=98.53 E-value=3.7e-08 Score=74.36 Aligned\_cols=96 Identities=10% Similarity=0.055 Sum\_probs=0.0 Template\_Neff=12.700

Q ss\_pred chHHHHHhhCC---cEEEEEECCEEEEEEEEEeC---------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc----Ce

Q Phabba\_Draft 15 FEPFDTMWSNG---IMARHAHDDRPVGHLHWHPD---------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI----YE 78 (219)

Q Consensus 15 ~~~l~~~~~~~---~~~v~~~~~~liG~~~~~~~---------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~----~~ 78 (219)

.+.+....... .++++..+|++||++.+... ..+..+.|+|++|++|+|+.|++.+++.+.+ ..

T Consensus 42 ~~~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~~ 121 (157)

T 3DSB\_B 42 TKGVKALLLDERKGKYHVYTVFDKVVAQIMYTYEWSDWRNGNFLWIQSVYVDKEYRRKGIFNYLFNYIKNICDKDENIVG 121 (157)

T ss\_dssp HHHHHHHHTCGGGCEEEEEEETTEEEEEEEEEEEEETTTTEEEEEEEEEEECGGGCSSSHHHHHHHHHHHHHHTCTTEEE

T ss\_pred chhHHHHHhccCCCcEEEEEECCEEEEEEEEEecCccccCCcEEEEEEEEECHHHhcCCHHHHHHHHHHHHhhcCCCCcE

Q ss\_pred eEEEEEcCCcccccccccchhHHHHHcCCCEEeeeeecccc

Q Phabba\_Draft 79 SSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDVS 119 (219)

Q Consensus 79 i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~ 119 (219)

+.+.+...|. .+.++|+++||+..+...+.+.

T Consensus 122 i~~~~~~~n~---------~~~~~~~~~Gf~~~~~~~~~~~ 153 (157)

T 3DSB\_B 122 MRLYVEKENI---------NAKATYESLNMYECDYNMYEYE 153 (157)

T ss\_dssp EEEEEETTCT---------THHHHHHHTTEEECSEEEEEEC

T ss\_pred EEEEEecCCH---------HHHHHHHhCCceEcceeeceee

No 57

>1S5K\_A aminoglycoside 6'-N-acetyltransferase (E.C.2.3.1.82); GNAT, N-acetyltransferase, acetyltransferase, aminoglycoside, CoA; HET: SO4, COA; 2.4A {Salmonella enteritidis} SCOP: d.108.1.1

Probab=98.52 E-value=1.7e-08 Score=77.65 Aligned\_cols=107 Identities=12% Similarity=0.069 Sum\_probs=0.0 Template\_Neff=12.200

Q ss\_pred CCccccCCCCCCCCchHHHHHhhCCc--EEEEEECCEEEEEEEEE------------eCCEEEEEEECHHHCCCCHHHHH

Q Phabba\_Draft 1 MHQAGANGDLPPLKFEPFDTMWSNGI--MARHAHDDRPVGHLHWH------------PDGEIDSITVHPDLQRRGIGTAM 66 (219)

Q Consensus 1 ~~~~~~~~~~~~~~~~~l~~~~~~~~--~~v~~~~~~liG~~~~~------------~~~~i~~l~V~p~~R~~Gig~~L 66 (219)

+..............+.+...+.... ++++.++|++||++.+. ....+..++|+|++|++|+|+.|

T Consensus 37 l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ivG~~~~~~~~~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l 116 (165)

T 1S5K\_A 37 LRKQLWPGHPDDAHLADGEEILQADHLASFIAMADGVAIGFADASIRHDYVNGCDSSPVVFLEGIFVLPSFRQRGVAKQL 116 (165)

T ss\_dssp HHHHHSTTCCHHHHHHHHHHHHHCTTEEEEEEEETTEEEEEEEEEEECSCCTTCSSSSEEEEEEEEECGGGCSSSHHHHH

T ss\_pred HHHHHCCCCCChhhHHhHHHHhhcCCceEEEEEECCEEEEEEEEEEecccCCCCCCCCEEEEEEEEECHHHcCCCHHHHH

Q ss\_pred HHHHHHcccc---CeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeeec

Q Phabba\_Draft 67 LKHAQDNPHI---YESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADD 116 (219)

Q Consensus 67 l~~~~~~~~~---~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~ 116 (219)

++.+++.+++ ..+.+.+...|. .+.++|+++||+..+....

T Consensus 117 l~~~~~~~~~~~~~~~~~~~~~~n~---------~~~~~~~~~Gf~~~~~~~~ 160 (165)

T 1S5K\_A 117 IAAVQRWGTNKGCREMASDTSPENT---------ISQKVHQALGFEETERVIF 160 (165)

T ss\_dssp HHHHHHHHHHTTCSEEEEEECTTCH---------HHHHHHHHTTCEEEEEEEE

T ss\_pred HHHHHHHHHhcCCCEEEeecCCCCH---------HHHHHHHHcCCeEeEEEEE

No 58

>4EVY\_A Aminoglycoside N(6')-acetyltransferase type 1 (E.C.2.3.1.82); Center for Structural Genomics of; HET: TOY; 1.768A {Acinetobacter haemolyticus}

Probab=98.52 E-value=3.1e-08 Score=76.31 Aligned\_cols=97 Identities=15% Similarity=0.136 Sum\_probs=0.0 Template\_Neff=12.200

Q ss\_pred CCCCchHHHHHhhCCc--EEEEEECCEEEEEEEEEeC------------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc

Q Phabba\_Draft 11 PPLKFEPFDTMWSNGI--MARHAHDDRPVGHLHWHPD------------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI 76 (219)

Q Consensus 11 ~~~~~~~l~~~~~~~~--~~v~~~~~~liG~~~~~~~------------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~ 76 (219)

.+...+.+...+..+. ++++.++|++||++.+... ..+..++|+|++|++|+|+.|++.+++.+..

T Consensus 47 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~~~~i~~~~v~~~~r~~G~~~~l~~~~~~~~~~ 126 (166)

T 4EVY\_A 47 EASHLQEMHQLLAEKYALQLLAYSDHQAIAMLEASIRFEYVNGTETSPVGFLEGIYVLPAHRRSGVATMLIRQAEVWAKQ 126 (166)

T ss\_dssp HHHHHHHHHHHHTCTTEEEEEEEETTEEEEEEEEEEECSCCTTCSSSSEEEEEEEEECGGGTTSSHHHHHHHHHHHHHHH

T ss\_pred ccccHHHHHHHhhhcceeEEEEEeCCeEEEEEEEEEecccCCCCcCCCEEEEEEEEECHHHCCCCHHHHHHHHHHHHHHH

Q ss\_pred ---CeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeeec

Q Phabba\_Draft 77 ---YESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADD 116 (219)

Q Consensus 77 ---~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~ 116 (219)

..+.+.+...|. .+.++|+++||+..+....

T Consensus 127 ~~~~~i~~~~~~~n~---------~~~~~~~~~Gf~~~~~~~~ 160 (166)

T 4EVY\_A 127 FSCTEFASDAALDNV---------ISHAMHRSLGFQETEKVVY 160 (166)

T ss\_dssp TTCCEEEEEEETTCH---------HHHHHHHHTTCEEEEEEEE

T ss\_pred CCCCeEEeeeeccCH---------HHHHHHHHcCCeEeeeEEE

No 59

>2FL4\_A spermine/spermidine acetyltransferase; Spermine/spermidine acetyltransferase, Structural Genomics, PSI; 1.6A {Enterococcus faecalis} SCOP: d.108.1.1

Probab=98.52 E-value=2.6e-08 Score=74.99 Aligned\_cols=79 Identities=13% Similarity=0.013 Sum\_probs=0.0 Template\_Neff=12.400

Q ss\_pred EEEEEECCEEEEEEEEEeC----CEEEEEEECHHHCCCCHHHHHHHHHHHcccc----CeeEEEEEcCCcccccccccch

Q Phabba\_Draft 27 MARHAHDDRPVGHLHWHPD----GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI----YESSYPVRHSSHFSAAGRAWAQ 98 (219)

Q Consensus 27 ~~v~~~~~~liG~~~~~~~----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~----~~i~l~v~~~n~~~~~~~~~~~ 98 (219)

++++.++|++||++.+... ..+..+.|+|++|++|+|+.|++.+++.+.+ ..+.+.+...|. .

T Consensus 48 ~~~~~~~~~~vG~~~~~~~~~~~~~i~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~~~~~~~~~~n~---------~ 118 (149)

T 2FL4\_A 48 SAGIYDGNQLIGYAMYGRWQDGRVWLDRFLIDQRFQGQGYGKAACRLLMLKLIEKYQTNKLYLSVYDTNS---------S 118 (149)

T ss\_dssp EEEEEETTEEEEEEEEEECTTSCEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHHSSCSEEEEEECTTCH---------H

T ss\_pred EEEEEeCCEEEEEEEEEEecCCcEEEEEEEECHhhCCCCHHHHHHHHHHHHHHHHhCCCeEEEEEECCCH---------H

Q ss\_pred hHHHHHcCCCEEeeee

Q Phabba\_Draft 99 SDPDYHDPGDQNVTKA 114 (219)

Q Consensus 99 ~~~~y~r~Gf~~~~~~ 114 (219)

+.++|+++||+..+..

T Consensus 119 ~~~~~~~~Gf~~~~~~ 134 (149)

T 2FL4\_A 119 AIRLYQQLGFVFNGEL 134 (149)

T ss\_dssp HHHHHHHTTCEEEEEE

T ss\_pred HHHHHHhcCcEEEEEe

No 60

>4QUS\_B Acetyltransferase YpeA (E.C.2.3.1.-); predicted acyltransferase, acyl-CoA N-acyltransferase domain; HET: EDO, PO4; 1.28A {Escherichia coli str. K-12 substr. MG1655}

Probab=98.52 E-value=4.1e-08 Score=73.58 Aligned\_cols=107 Identities=14% Similarity=0.083 Sum\_probs=0.0 Template\_Neff=12.600

Q ss\_pred CCccccCCCCCCCCchHHHHHhhCCc--EEEEEECCEEEEEEEEEeC---CEEEEEEECHHHCCCCHHHHHHHHHHHccc

Q Phabba\_Draft 1 MHQAGANGDLPPLKFEPFDTMWSNGI--MARHAHDDRPVGHLHWHPD---GEIDSITVHPDLQRRGIGTAMLKHAQDNPH 75 (219)

Q Consensus 1 ~~~~~~~~~~~~~~~~~l~~~~~~~~--~~v~~~~~~liG~~~~~~~---~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~ 75 (219)

+................+........ ++++..++++||++.+... ..+..+.|+|++|++|+|+.|++.+++.+.

T Consensus 17 l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~ 96 (149)

T 4QUS\_B 17 LWERCDLLRPWNDPEMDIERKMNHDVSLFLVAEVNGDVVGTVMGGYDGHRGSAYYLGVHPEFRGRGIANALLNRLEKKLI 96 (149)

T ss\_dssp HHHHTTCCBTTBCHHHHHHHHHHHCCTTEEEEEETTEEEEEEEEEECSSCEEEEEEEECGGGTTSSHHHHHHHHHHHHHH

T ss\_pred HHHhcCCCCCCCCcchhHHHHhcCCCeEEEEEEeCCEEEEEEEEEEcCCCceEEEEEECHHHCCCCHHHHHHHHHHHHHH

Q ss\_pred c---CeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeeec

Q Phabba\_Draft 76 I---YESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADD 116 (219)

Q Consensus 76 ~---~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~ 116 (219)

+ ..+.+.+...|. .+.++|+++||+..+....

T Consensus 97 ~~~~~~i~~~~~~~n~---------~~~~~~~~~Gf~~~~~~~~ 131 (149)

T 4QUS\_B 97 ARGCPKIQINVPEDND---------MVLGMYERLGYEHADVLSL 131 (149)

T ss\_dssp HTTCCEEEEEEETTCH---------HHHHHHHHTTCEECSCEEE

T ss\_pred HCCCCEEEEEecCCCH---------HHHHHHHHhCCeEeEEEEe

No 61

>1Z4E\_A transcriptional regulator; NYSGXRC target T2017, GNAT fold; 2.0A {Bacillus halodurans} SCOP: d.108.1.1

Probab=98.52 E-value=4.1e-08 Score=73.09 Aligned\_cols=105 Identities=13% Similarity=0.155 Sum\_probs=0.0 Template\_Neff=13.100

Q ss\_pred CccccCCCCCCCCchHHHHHhhCCc--EEEEEECCEEEEEEEEEeC----------CEEEEEEECHHHCCCCHHHHHHHH

Q Phabba\_Draft 2 HQAGANGDLPPLKFEPFDTMWSNGI--MARHAHDDRPVGHLHWHPD----------GEIDSITVHPDLQRRGIGTAMLKH 69 (219)

Q Consensus 2 ~~~~~~~~~~~~~~~~l~~~~~~~~--~~v~~~~~~liG~~~~~~~----------~~i~~l~V~p~~R~~Gig~~Ll~~ 69 (219)

..............+.+........ ++++..++++||++.+... ..+..++|+|++|++|+|+.|++.

T Consensus 30 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~~i~~~~v~~~~r~~g~~~~l~~~ 109 (153)

T 1Z4E\_A 30 KRERYEKPLPVSYVRAFKEIKKDKNNELIVACNGEEIVGMLQVTFTPYLTYQGSWRATIEGVRTHSAARGQGIGSQLVCW 109 (153)

T ss\_dssp GTCCCCSSCCHHHHHHHHHHHHCTTEEEEEEEETTEEEEEEEEEEEECSHHHHCEEEEEEEEEECTTSTTSSHHHHHHHH

T ss\_pred ccccccCCCCcchHHHHHHHhcCCCceEEEEEcCCeEEEEEEEEecccccccCCeEEEEEEEEECHHHcCCCHHHHHHHH

Q ss\_pred HHHcccc---CeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 70 AQDNPHI---YESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 70 ~~~~~~~---~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

+++.++. ..+.+.+...|. .+.++|+++||+..+...

T Consensus 110 ~~~~~~~~~~~~~~~~~~~~n~---------~~~~~~~~~Gf~~~~~~~ 149 (153)

T 1Z4E\_A 110 AIERAKERGCHLIQLTTDKQRP---------DALRFYEQLGFKASHEGL 149 (153)

T ss\_dssp HHHHHHHTTEEEEEEEEETTCT---------THHHHHHHHTCEEEEEEE

T ss\_pred HHHHHHHcCCCEEEEEeCCCCH---------HHHHHHHHcCCEEeccee

No 62

>d1yx0a1 d.108.1.1 (A:1-149) Hypothetical protein YsnE {Bacillus subtilis [TaxId: 1423]}

Probab=98.51 E-value=3.9e-08 Score=74.07 Aligned\_cols=102 Identities=17% Similarity=0.049 Sum\_probs=0.0 Template\_Neff=12.400

Q ss\_pred hHHHHHhhCCc--EEEEEECCEEEEEEEEEeC----CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEEEc-

Q Phabba\_Draft 16 EPFDTMWSNGI--MARHAHDDRPVGHLHWHPD----GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPVRH- 85 (219)

Q Consensus 16 ~~l~~~~~~~~--~~v~~~~~~liG~~~~~~~----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v~~- 85 (219)

..+...+..+. ++++.+++++||++.+... ..+..+.|+|++|++|+++.|+..+++.+.. ..+.+.+..

T Consensus 35 ~~~~~~~~~~~~~~~~~~~~~~ivG~~~~~~~~~~~~~i~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~~~~~~~~~ 114 (149)

T d1yx0a1 35 ALGLEKLRGPEITFWSAWEGDELAGCGALKELDTRHGEIKSMRTSASHLRKGVAKQVLQHIIEEAEKRGYERLSLETGSM 114 (149)

T ss\_dssp CSCHHHHSSSSCEEEEEECSSSEEEEEEEEEEETTEEECCCCCCSTTTCCSCHHHHHHHHHHHHHHHHTCSCEECCCSSC

T ss\_pred hhhHHHhcCCCeEEEEEEeCCeEEEEEEEEECCCCeEEEEEEEECHHHcCCCHHHHHHHHHHHHHHHcCCCEEEEEecCC

Q ss\_pred -CCcccccccccchhHHHHHcCCCEEeeeeeccccccceEEe

Q Phabba\_Draft 86 -SSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDVSNWGYTAM 126 (219)

Q Consensus 86 -~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~~~~~~~ 126 (219)

.|. .+.++|+++||+..+.+...........+

T Consensus 115 ~~n~---------~~~~~~~~~Gf~~~~~~~~~~~~~~~~~~ 147 (149)

T d1yx0a1 115 ASFE---------PARKLYESFGFQYCEPFADYGEDPNSVFM 147 (149)

T ss\_dssp TTHH---------HHHHHHHTTSEEECCCCTTSCCCTTCCCE

T ss\_pred CCCH---------HHHHHHHHcCcEEeecccCCCCCcccccc

No 63

>d1z4eb\_ d.108.1.1 (B:) Transcriptional regulator BH1968 {Bacillus halodurans [TaxId: 86665]}

Probab=98.51 E-value=3.6e-08 Score=72.78 Aligned\_cols=105 Identities=13% Similarity=0.155 Sum\_probs=0.0 Template\_Neff=13.300

Q ss\_pred CccccCCCCCCCCchHHHHHhhCCc--EEEEEECCEEEEEEEEEeC----------CEEEEEEECHHHCCCCHHHHHHHH

Q Phabba\_Draft 2 HQAGANGDLPPLKFEPFDTMWSNGI--MARHAHDDRPVGHLHWHPD----------GEIDSITVHPDLQRRGIGTAMLKH 69 (219)

Q Consensus 2 ~~~~~~~~~~~~~~~~l~~~~~~~~--~~v~~~~~~liG~~~~~~~----------~~i~~l~V~p~~R~~Gig~~Ll~~ 69 (219)

+........+....+.+........ ++++..++++||++.+... ..+..++|+|++|++|+++.|++.

T Consensus 27 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ivg~~~~~~~~~~~~~~~~~~~i~~~~v~~~~r~~g~~~~l~~~ 106 (150)

T d1z4eb\_ 27 KRERYEKPLPVSYVRAFKEIKKDKNNELIVACNGEEIVGMLQVTFTPYLTYQGSWRATIEGVRTHSAARGQGIGSQLVCW 106 (150)

T ss\_dssp GTCCCCSSCCHHHHHHHHHHHHCTTEEEEEEEETTEEEEEEEEEEEECSHHHHCEEEEEEEEEECTTSTTSSHHHHHHHH

T ss\_pred cchhccCCCCccHHHHHHHHccCCCCeEEEEEcCCcEEEEEEEEeCCCcccCCceEEEEEEEEeCHHHcCCCHHHHHHHH

Q ss\_pred HHHcccc---CeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 70 AQDNPHI---YESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 70 ~~~~~~~---~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

+++.+.+ ..+.+.+...|. .+.++|+++||+..+...

T Consensus 107 ~~~~~~~~~~~~~~~~~~~~n~---------~~~~~~~~~Gf~~~~~~~ 146 (150)

T d1z4eb\_ 107 AIERAKERGCHLIQLTTDKQRP---------DALRFYEQLGFKASHEGL 146 (150)

T ss\_dssp HHHHHHHTTCSEEEEEEETTCT---------THHHHHHTTTCEEEEEEE

T ss\_pred HHHHHHHhCCcEEEEEecCCCH---------HHHHHHHHhCcEEecccc

No 64

>1YX0\_A hypothetical protein ysnE; NESG, GFT NMR, Structral Genomics; NMR {Bacillus subtilis subsp. subtilis str. 168} SCOP: d.108.1.1

Probab=98.51 E-value=3.3e-08 Score=76.19 Aligned\_cols=111 Identities=16% Similarity=0.045 Sum\_probs=0.0 Template\_Neff=11.800

Q ss\_pred hHHHHHhhCCc--EEEEEECCEEEEEEEEEeC----CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEEEc-

Q Phabba\_Draft 16 EPFDTMWSNGI--MARHAHDDRPVGHLHWHPD----GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPVRH- 85 (219)

Q Consensus 16 ~~l~~~~~~~~--~~v~~~~~~liG~~~~~~~----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v~~- 85 (219)

+.+........ ++++.++|++||++.+... ..+..+.|+|++|++|+|+.|++.+++.++. ..+.+.+..

T Consensus 35 ~~~~~~~~~~~~~~~~~~~~~~ivG~~~~~~~~~~~~~i~~~~v~~~~r~~Gi~~~l~~~~~~~~~~~~~~~i~~~~~~~ 114 (159)

T 1YX0\_A 35 ALGLEKLRGPEITFWSAWEGDELAGCGALKELDTRHGEIKSMRTSASHLRKGVAKQVLQHIIEEAEKRGYERLSLETGSM 114 (159)

T ss\_dssp CSCHHHHSSSSCEEEEEECSSSEEEEEEEEEEETTEEECCCCCCSTTTCCSCHHHHHHHHHHHHHHHHTCSCEECCCSSC

T ss\_pred HhhHHHHcCCCeEEEEEEeCCeEEEEEEEEEcCCCeEEEEEEEECHHHccCCHHHHHHHHHHHHHHHcCCcEEEEEcCCC

Q ss\_pred -CCcccccccccchhHHHHHcCCCEEeeeeeccccccceEEecCCCCCCCc

Q Phabba\_Draft 86 -SSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDVSNWGYTAMGEEGYTPLH 135 (219)

Q Consensus 86 -~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~~~~~~~~~~~~~~~~ 135 (219)

.|. .+.++|+++||+..+..................+....

T Consensus 115 ~~n~---------~~~~~~~~~Gf~~~~~~~~~~~~~~~~~~~~~~~~~~~ 156 (159)

T 1YX0\_A 115 ASFE---------PARKLYESFGFQYCEPFADYGEDPNSVFMTKKLLEHHH 156 (159)

T ss\_dssp TTHH---------HHHHHHHTTSEEECCCCTTSCCCTTCCCEEECC-----

T ss\_pred cCCH---------HHHHHHHHcCCEEcccccccCCCcceehhccchhhccc

No 65

>d1y9kc\_ d.108.1.1 (C:) automated matches {Bacillus cereus [TaxId: 226900]}

Probab=98.51 E-value=4.2e-08 Score=75.52 Aligned\_cols=96 Identities=21% Similarity=0.178 Sum\_probs=0.0 Template\_Neff=11.300

Q ss\_pred CCCCCchHHHHHhhCCcEEEEEECCEEEEEEEEEeC----CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEE

Q Phabba\_Draft 10 LPPLKFEPFDTMWSNGIMARHAHDDRPVGHLHWHPD----GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYP 82 (219)

Q Consensus 10 ~~~~~~~~l~~~~~~~~~~v~~~~~~liG~~~~~~~----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~ 82 (219)

..+...+.+...+....++++..+|+++|++.+... ..+..++|+|++|++|+|..|++.+.+.+.. ..+.+.

T Consensus 19 ~~~~~~~~~~~~~~~~~~~~~~~~~~~vg~~~~~~~~~~~~~i~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~~~~~ 98 (150)

T d1y9kc\_ 19 LADPSERQIATYVQRGLTYVAKQGGSVIGVYVLLETRPKTMEIMNIAVAEHLQGKGIGKKLLRHAVETAKGYGMSKLEVG 98 (150)

T ss\_dssp HHCCCHHHHHHHHHHSEEEEEEETTEEEEEEEEEECSTTEEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHTTCSEEEEE

T ss\_pred hcCCCHHHHHHHhhcCeEEEEEECCEEEEEEEEEECCCCeEEEEEEEECHHHCCCCHHHHHHHHHHHHHHHCCCCEEEEE

Q ss\_pred EEcCCcccccccccchhHHHHHcCCCEEeeee

Q Phabba\_Draft 83 VRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKA 114 (219)

Q Consensus 83 v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~ 114 (219)

+...|. .+.++|+++||+..+..

T Consensus 99 ~~~~n~---------~~~~~~~~~Gf~~~~~~ 121 (150)

T d1y9kc\_ 99 TGNSSV---------SQLALYQKCGFRIFSID 121 (150)

T ss\_dssp EETTCH---------HHHHHHHHTTCEEEEEE

T ss\_pred cCCCCH---------HHHHHHHHCCCEEEEec

No 66

>1U6M\_C acetyltransferase, GNAT family; acetyltransferase, GNAT family, Structural Genomics; HET: SO4; 2.4A {Enterococcus faecalis} SCOP: d.108.1.1

Probab=98.51 E-value=4.7e-08 Score=78.14 Aligned\_cols=98 Identities=15% Similarity=0.151 Sum\_probs=0.0 Template\_Neff=11.800

Q ss\_pred chHHHHHhhCC-------cEEEEEECCEEEEEEEEEeCC-----------------------------------EEEEEE

Q Phabba\_Draft 15 FEPFDTMWSNG-------IMARHAHDDRPVGHLHWHPDG-----------------------------------EIDSIT 52 (219)

Q Consensus 15 ~~~l~~~~~~~-------~~~v~~~~~~liG~~~~~~~~-----------------------------------~i~~l~ 52 (219)

..++...+... .++++.++|++||++.+.... ++..++

T Consensus 40 ~~~~~~~~~~~~~~~~~~~~~v~~~~g~ivG~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~i~~~~ 119 (199)

T 1U6M\_C 40 IDLLAEATAYPTYRYGYQRILVYEHAGEVAGIAVGYPAEDEKIIDEPLREVFKKHGLAEDVRLFIEEETLPNEWYLDTIS 119 (199)

T ss\_dssp HHHHHHHTTSTTSTTCGGGEEEEEETTEEEEEEEEEEGGGGGTTTHHHHHHHHHTTCCSSCCCCCCCCCCTTEEEEEEEE

T ss\_pred HHHHHHHhcCCccCCceEEEEEEEECCeEEEEEEEeeCCCchhcchhHHHHHHHcCchHHHHHHhcccCCCCeEEEEEEE

Q ss\_pred ECHHHCCCCHHHHHHHHHHHcccc---CeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeeecccccc

Q Phabba\_Draft 53 VHPDLQRRGIGTAMLKHAQDNPHI---YESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDVSNW 121 (219)

Q Consensus 53 V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~~ 121 (219)

|+|++|++|+|+.|++.+++.+.+ ..+.+.+...|. .+.++|+++||+..+........+

T Consensus 120 v~p~~rg~Gig~~l~~~~~~~~~~~g~~~~~~~~~~~n~---------~~~~~y~~~Gf~~~~~~~~~~~~~ 182 (199)

T 1U6M\_C 120 VDERFRGMGIGSKLLDALPEVAKASGKQALGLNVDFDNP---------GARKLYASKGFKDVTTMTISGHLY 182 (199)

T ss\_dssp ECGGGTTSSHHHHHHHTHHHHHHHTTCSEEEEEEETTCH---------HHHHHHHHTTCEEEEEEECSSCEE

T ss\_pred ECHHHCCCCHHHHHHHHHHHHHHHcCCCeEEEEEECCCH---------HHHHHHHhcCCEEEEEeecCCcch

No 67

>3T9Y\_A Acetyltransferase, GNAT family; PSI-BIOLOGY, Structural genomics, Midwest center; HET: PGE; 2.0A {Staphylococcus aureus}

Probab=98.51 E-value=3.7e-08 Score=73.42 Aligned\_cols=92 Identities=11% Similarity=0.161 Sum\_probs=0.0 Template\_Neff=12.900

Q ss\_pred chHHHHHhhCCc--EEEEEECCEEEEEEEEEeC---------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeE

Q Phabba\_Draft 15 FEPFDTMWSNGI--MARHAHDDRPVGHLHWHPD---------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESS 80 (219)

Q Consensus 15 ~~~l~~~~~~~~--~~v~~~~~~liG~~~~~~~---------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~ 80 (219)

.+.+........ ++++..++++||++.+... ..+..++|+|++|++|+|+.|+..+++.+++ ..+.

T Consensus 39 ~~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~i~ 118 (150)

T 3T9Y\_A 39 KKRLKKITNHDDYFLLLLIKENKIIGLSGMCKMMFYEKNAEYMRILAFVIHSEFRKKGYGKRLLADSEEFSKRLNCKAIT 118 (150)

T ss\_dssp HHHHHHHHTSTTEEEEEEEETTEEEEEEEEEEEECSSSSCEEEEEEEEEECGGGCSSSHHHHHHHHHHHHHHHTTCSCEE

T ss\_pred HHHHHHHhcCCCEEEEEEEECCEEEEEEEeeehhccCCccceEEEEEEEECHHHccCCHHHHHHHHHHHHHHHcCCcEEE

Q ss\_pred EEEEcCCcccccccccch--hHHHHHcCCCEEeeeee

Q Phabba\_Draft 81 YPVRHSSHFSAAGRAWAQ--SDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 81 l~v~~~n~~~~~~~~~~~--~~~~y~r~Gf~~~~~~~ 115 (219)

+.+...|. . +.++|+++||+..+...

T Consensus 119 ~~~~~~n~---------~~~~~~~~~~~Gf~~~~~~~ 146 (150)

T 3T9Y\_A 119 LNSGNRNE---------RLSAHKLYSDNGYVSNTSGF 146 (150)

T ss\_dssp ECCCCCC---------------------CCCCCCCCC

T ss\_pred EEeCCccc---------HHHHHHHHHhCCCeecccee

No 68

>3FYN\_A Integron gene cassette protein HFX\_CASS3; Integron Cassette Protein, Mobile Metagenome; 1.449A {uncultured bacterium}

Probab=98.51 E-value=2.9e-08 Score=77.82 Aligned\_cols=93 Identities=17% Similarity=0.214 Sum\_probs=0.0 Template\_Neff=11.800

Q ss\_pred chHHHHHhhC---CcEEEEEECCEEEEEEEEEe-----C----CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---Cee

Q Phabba\_Draft 15 FEPFDTMWSN---GIMARHAHDDRPVGHLHWHP-----D----GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YES 79 (219)

Q Consensus 15 ~~~l~~~~~~---~~~~v~~~~~~liG~~~~~~-----~----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i 79 (219)

.+.+...+.. ..++++..+|++||++.+.. . ..+..++|+|++|++|+|++|++.+++.+.. ..+

T Consensus 58 ~~~~~~~~~~~~~~~~~~~~~~~~ivG~~~~~~~~~~~~~~~~~~i~~~~v~~~~r~~G~~~~l~~~~~~~~~~~g~~~i 137 (176)

T 3FYN\_A 58 IRAFKALLGKPDLGRIWLIAEGTESVGYIVLTLGFSMEYGGLRGFVDDFFVRPNARGKGLGAAALQTVKQGCCDLGVRAL 137 (176)

T ss\_dssp HHHHHHHHHCGGGEEEEEEEETTEEEEEEEEEEEEETTTTEEEEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHTTCCCE

T ss\_pred HHHHHHHhcCCCCceEEEEEeCCcEEEEEEEEeccCccccCceEEEEEEEeCHHHCCCCHHHHHHHHHHHHHHHcCCCEE

Q ss\_pred EEEEEcCCcccccccccchhHHHHHcCCCEEeeeeec

Q Phabba\_Draft 80 SYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADD 116 (219)

Q Consensus 80 ~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~ 116 (219)

.+.+...|. .+.++|+++||+..+....

T Consensus 138 ~~~~~~~n~---------~~~~~~~k~Gf~~~~~~~~ 165 (176)

T 3FYN\_A 138 LVETGPEDH---------PARGVYSRAGFEESGRMLL 165 (176)

T ss\_dssp ECCCC-----------------HHHHTTCCCCCCCCC

T ss\_pred EEecCCCCh---------HHHHHHHHCCCeEeeeeec

No 69

>5IB0\_E Uncharacterized protein PA4534; Acetyl transferase, TRANSFERASE; HET: ACO, GOL; 1.65A {Pseudomonas aeruginosa (strain ATCC 15692 / PAO1 / 1C / PRS 101 / LMG 12228)}

Probab=98.51 E-value=3.3e-08 Score=72.38 Aligned\_cols=95 Identities=16% Similarity=0.141 Sum\_probs=0.0 Template\_Neff=13.000

Q ss\_pred hHHHHHh--hCCcEEEEEECCEEEEEEEEEeC---CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEEEcCC

Q Phabba\_Draft 16 EPFDTMW--SNGIMARHAHDDRPVGHLHWHPD---GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPVRHSS 87 (219)

Q Consensus 16 ~~l~~~~--~~~~~~v~~~~~~liG~~~~~~~---~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v~~~n 87 (219)

+.+...+ ....++++.++++++|++.+... ..+..+.|+|++|++|+++.|++.+++.+++ ..+.+.+...|

T Consensus 33 ~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~i~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~i~~~~~~~n 112 (137)

T 5IB0\_E 33 PFFLAYLQRNPGLSLLVETEGEVIACLMAGHDGRRGYLQHLVVDPGYRGLGLARRMLDEVLARLAREGIGKSHVFVLDAA 112 (137)

T ss\_dssp HHHHHHHHHSTTTSEEEEETTEEEEEEEEEECSSCEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHTTCCCEEEEEETTC

T ss\_pred HHHHHHHhcCCCcEEEEEECCeEEEEEEEeecCcEEEEEEEEEChhhCCCCHHHHHHHHHHHHHHHCCCCEEEEEEeCch

Q ss\_pred cccccccccchhHHHHHcCCCEEeeeeecccc

Q Phabba\_Draft 88 HFSAAGRAWAQSDPDYHDPGDQNVTKADDDVS 119 (219)

Q Consensus 88 ~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~ 119 (219)

. .+.++|+++||+..+.....+.

T Consensus 113 ~---------~~~~~~~~~Gf~~~~~~~~~~~ 135 (137)

T 5IB0\_E 113 E---------EAQAFWRAQSDWERRKDIQVFS 135 (137)

T ss\_dssp H---------HHHHHHHTCTTEEECCSEEEEE

T ss\_pred H---------HHHHHHHhcccceecceeEEee

No 70

>d1wwzb\_ d.108.1.1 (B:) Hypothetical protein PH1933 {Pyrococcus horikoshii [TaxId: 53953]}

Probab=98.51 E-value=3.6e-08 Score=74.25 Aligned\_cols=92 Identities=20% Similarity=0.174 Sum\_probs=0.0 Template\_Neff=12.800

Q ss\_pred chHHHHHh--hCCcEEEEEECCEEEEEEEEEe----------CCEEEEEEECHHHCCCCHHHHHHHHHHHcccc--CeeE

Q Phabba\_Draft 15 FEPFDTMW--SNGIMARHAHDDRPVGHLHWHP----------DGEIDSITVHPDLQRRGIGTAMLKHAQDNPHI--YESS 80 (219)

Q Consensus 15 ~~~l~~~~--~~~~~~v~~~~~~liG~~~~~~----------~~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~--~~i~ 80 (219)

.+.+.... ....++++..+|++||++.+.. ...+..++|+|++|++|+|..|++.+++.+.. ..+.

T Consensus 41 ~~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~~i~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~~ 120 (157)

T d1wwzb\_ 41 RNYIKWCWKKASDGFFVAKVGDKIVGFIVCDKDWFSKYEGRIVGAIHEFVVDKKFQGKGIGRKLLITCLDFLGKYNDTIE 120 (157)

T ss\_dssp HHHHHHHHHHHGGGEEEEEETTEEEEEEEEEEEEEETTTTEEEEEEEEEEECGGGTTSSHHHHHHHHHHHHHTTTCSEEE

T ss\_pred HHHHHHHhhcccccEEEEEECCEEEEEEEEecccccccccceEEEEEEEEECHHhCCCCHHHHHHHHHHHHHHhcCCEEE

Q ss\_pred EEEEcCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 81 YPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 81 l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

+.+...|. .+.++|+++||+..+...

T Consensus 121 ~~~~~~n~---------~~~~~~~~~Gf~~~~~~~ 146 (157)

T d1wwzb\_ 121 LWVGEKNY---------GAMNLYEKFGFKKVGKSG 146 (157)

T ss\_dssp EEEETTCH---------HHHHHHHHTTCEEEEEET

T ss\_pred EEEecCCc---------hhHHHHHHcCCEEeecCc

No 71

>1Y7R\_B hypothetical protein SA2161; Structural Genomics, hypothetical protein, Protein; HET: PO4; 1.7A {Staphylococcus aureus} SCOP: d.108.1.1

Probab=98.50 E-value=4.3e-08 Score=73.40 Aligned\_cols=101 Identities=16% Similarity=0.115 Sum\_probs=0.0 Template\_Neff=11.700

Q ss\_pred CCCCCCCchHHHHHhhCCc-EEEEEECCEEEEEEEEEeC----CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---Cee

Q Phabba\_Draft 8 GDLPPLKFEPFDTMWSNGI-MARHAHDDRPVGHLHWHPD----GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YES 79 (219)

Q Consensus 8 ~~~~~~~~~~l~~~~~~~~-~~v~~~~~~liG~~~~~~~----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i 79 (219)

....+...+.+...+.+.. ++++.++++++|++.+... ..+..++|+|++|++|+|+.|++.+++.+.. ..+

T Consensus 21 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~vg~~~~~~~~~~~~~i~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~~ 100 (133)

T 1Y7R\_B 21 AGMSPKTREAAEKGLPNALFTVTLYDKDRLIGMGRVIGDGGTVFQIVDIAVLKSYQGQAYGSLIMEHIMKYIKNVSVESV 100 (133)

T ss\_dssp TTCCCCCHHHHHHHGGGCSEEEEEEETTEEEEEEEEEECSSSEEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHHCCTTC

T ss\_pred cCCCccCHHHHHhcCCccEEEEEEEeCCeEEEEEEEEeCCCeEEEEEEEEEChhhCCCCHHHHHHHHHHHHHHhcCCCeE

Q ss\_pred EEEEEcCCcccccccccchhHHHHHcCCCEEeeeeeccc

Q Phabba\_Draft 80 SYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDV 118 (219)

Q Consensus 80 ~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~ 118 (219)

.+.+...|. +.++|+++||+..+......

T Consensus 101 ~~~~~~~~~----------~~~~~~~~Gf~~~~~~~~~~ 129 (133)

T 1Y7R\_B 101 YVSLIADYP----------ADKLYVKFGFMPTEPDSGGM 129 (133)

T ss\_dssp EEEEEEEGG----------GHHHHHHTTCEECTTTEEEE

T ss\_pred EEEEecCCc----------hHHHHHHcCCEEcCCCcCcc

No 72

>3LD2\_D Putative acetyltransferase; putative acetyltransferase, TRANSFERASE; HET: COA; 2.5A {Streptococcus mutans}

Probab=98.50 E-value=3.9e-08 Score=79.22 Aligned\_cols=95 Identities=18% Similarity=0.117 Sum\_probs=0.0 Template\_Neff=11.300

Q ss\_pred chHHHHHhhCCcEEEEEECCEEEEEEEEEeC--------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc--CeeEEEEE

Q Phabba\_Draft 15 FEPFDTMWSNGIMARHAHDDRPVGHLHWHPD--------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI--YESSYPVR 84 (219)

Q Consensus 15 ~~~l~~~~~~~~~~v~~~~~~liG~~~~~~~--------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~--~~i~l~v~ 84 (219)

.........+..++++..++++||++.+... ..+..++|+|++|++|+|++|++.+++.++. ..+.+.+.

T Consensus 71 ~~~~~~~~~~~~~~v~~~~~~ivG~~~~~~~~~~~~~~~~~~~~~~v~p~~r~~Gig~~ll~~~~~~a~~~~~~~~~~~~ 150 (197)

T 3LD2\_D 71 DQIIQKFESNTHFLVAKIKDKIVGVLDYSSLYPFPSGQHIVTFGIAVAEKERRKGIGRALVQIFLNEVKSDYQKVLIHVL 150 (197)

T ss\_dssp HHHHHHHHTTCEEEEEEETTEEEEEEEEEESCSSGGGTTEEEEEEEECGGGTTSSHHHHHHHHHHHHHTTTCSEEEEEEE

T ss\_pred HHHHHHhccCcEEEEEEeCCEEEEEEEEEEccCCCCCcEEEEEEEEECHHHCCCChHHHHHHHHHHHHhhcCCEEEEEEe

Q ss\_pred cCCcccccccccchhHHHHHcCCCEEeeeeeccc

Q Phabba\_Draft 85 HSSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDV 118 (219)

Q Consensus 85 ~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~ 118 (219)

..|. .+.++|+++||+..+......

T Consensus 151 ~~n~---------~~~~~~~k~Gf~~~~~~~~~~ 175 (197)

T 3LD2\_D 151 SSNQ---------EAVLFYKKLGFDLEARLTKQF 175 (197)

T ss\_dssp TTCH---------HHHHHHHHTTCEEEEEEEEEE

T ss\_pred cCCH---------HHHHHHHHcCCEEEEEeeccE

No 73

>3LD2\_B Putative acetyltransferase; putative acetyltransferase, TRANSFERASE; HET: COA; 2.5A {Streptococcus mutans}

Probab=98.50 E-value=3.9e-08 Score=79.22 Aligned\_cols=95 Identities=18% Similarity=0.117 Sum\_probs=0.0 Template\_Neff=11.300

Q ss\_pred chHHHHHhhCCcEEEEEECCEEEEEEEEEeC--------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc--CeeEEEEE

Q Phabba\_Draft 15 FEPFDTMWSNGIMARHAHDDRPVGHLHWHPD--------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI--YESSYPVR 84 (219)

Q Consensus 15 ~~~l~~~~~~~~~~v~~~~~~liG~~~~~~~--------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~--~~i~l~v~ 84 (219)

.........+..++++..++++||++.+... ..+..++|+|++|++|+|++|++.+++.++. ..+.+.+.

T Consensus 71 ~~~~~~~~~~~~~~v~~~~~~ivG~~~~~~~~~~~~~~~~~~~~~~v~p~~r~~Gig~~ll~~~~~~a~~~~~~~~~~~~ 150 (197)

T 3LD2\_B 71 DQIIQKFESNTHFLVAKIKDKIVGVLDYSSLYPFPSGQHIVTFGIAVAEKERRKGIGRALVQIFLNEVKSDYQKVLIHVL 150 (197)

T ss\_dssp HHHHHHHTTTCEEEEEEETTEEEEEEEEEESCSSGGGTTEEEEEEEECGGGTTSSHHHHHHHHHHHHHTTTCSEEEEEEE

T ss\_pred HHHHHHhccCcEEEEEEeCCEEEEEEEEEEccCCCCCcEEEEEEEEECHHHCCCChHHHHHHHHHHHHhhcCCEEEEEEe

Q ss\_pred cCCcccccccccchhHHHHHcCCCEEeeeeeccc

Q Phabba\_Draft 85 HSSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDV 118 (219)

Q Consensus 85 ~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~ 118 (219)

..|. .+.++|+++||+..+......

T Consensus 151 ~~n~---------~~~~~~~k~Gf~~~~~~~~~~ 175 (197)

T 3LD2\_B 151 SSNQ---------EAVLFYKKLGFDLEARLTKQF 175 (197)

T ss\_dssp TTCH---------HHHHHHHHTTCEEEEEEEEEE

T ss\_pred cCCH---------HHHHHHHHcCCEEEEEeeccE

No 74

>2GE3\_A probable acetyltransferase; acetyltransferase, Agrobacterium tumefaciens, Structural genomics; HET: ACO; 2.25A {Agrobacterium tumefaciens} SCOP: d.108.1.1

Probab=98.50 E-value=4.6e-08 Score=74.81 Aligned\_cols=95 Identities=16% Similarity=0.174 Sum\_probs=0.0 Template\_Neff=12.700

Q ss\_pred chHHHHHhhCCc-EEEEEECCEEEEEEEEEeC-------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEE

Q Phabba\_Draft 15 FEPFDTMWSNGI-MARHAHDDRPVGHLHWHPD-------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPV 83 (219)

Q Consensus 15 ~~~l~~~~~~~~-~~v~~~~~~liG~~~~~~~-------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v 83 (219)

.+.+........ ++++..++++||++.+... ..+..++|+|++|++|+|+.|++.+++.++. ..+.+.+

T Consensus 47 ~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~i~~~~ 126 (170)

T 2GE3\_A 47 RAFVLDMIENDHPQFVAIADGDVIGWCDIRRQDRATRAHCGTLGMGILPAYRNKGLGARLMRRTLDAAHEFGLHRIELSV 126 (170)

T ss\_dssp HHHHHHHHHTTCCEEEEEETTEEEEEEEEEECCSTTTTTEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHHTCCEEEEEE

T ss\_pred HHHHHHHhhCCCCEEEEEECCEEEEEEEEEecCCCCCcEEEEEEEEECHHHCCCCHHHHHHHHHHHHHHHhCCCEEEEEE

Q ss\_pred EcCCcccccccccchhHHHHHcCCCEEeeeeeccc

Q Phabba\_Draft 84 RHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDV 118 (219)

Q Consensus 84 ~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~ 118 (219)

...|. .+.++|+++||+..+......

T Consensus 127 ~~~n~---------~~~~~~~~~Gf~~~~~~~~~~ 152 (170)

T 2GE3\_A 127 HADNA---------RAIALYEKIGFAHEGRARDAV 152 (170)

T ss\_dssp ETTCH---------HHHHHHHHHTCEEEEEEEEEE

T ss\_pred eCCCH---------HHHHHHHHcCCeEEEecCCce

No 75

>2GE3\_B probable acetyltransferase; acetyltransferase, Agrobacterium tumefaciens, Structural genomics; HET: ACO; 2.25A {Agrobacterium tumefaciens} SCOP: d.108.1.1

Probab=98.50 E-value=4.6e-08 Score=74.81 Aligned\_cols=95 Identities=16% Similarity=0.174 Sum\_probs=0.0 Template\_Neff=12.700

Q ss\_pred chHHHHHhhCCc-EEEEEECCEEEEEEEEEeC-------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEE

Q Phabba\_Draft 15 FEPFDTMWSNGI-MARHAHDDRPVGHLHWHPD-------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPV 83 (219)

Q Consensus 15 ~~~l~~~~~~~~-~~v~~~~~~liG~~~~~~~-------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v 83 (219)

.+.+........ ++++..++++||++.+... ..+..++|+|++|++|+|+.|++.+++.++. ..+.+.+

T Consensus 47 ~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~i~~~~ 126 (170)

T 2GE3\_B 47 RAFVLDMIENDHPQFVAIADGDVIGWCDIRRQDRATRAHCGTLGMGILPAYRNKGLGARLMRRTLDAAHEFGLHRIELSV 126 (170)

T ss\_dssp HHHHHHHHHTTCCEEEEEETTEEEEEEEEEECSSTTTTTEEEEEEEECGGGCSSSHHHHHHHHHHHHHHHHTCSEEEEEE

T ss\_pred HHHHHHHhhCCCCEEEEEECCEEEEEEEEEecCCCCCcEEEEEEEEECHHHCCCCHHHHHHHHHHHHHHHhCCCEEEEEE

Q ss\_pred EcCCcccccccccchhHHHHHcCCCEEeeeeeccc

Q Phabba\_Draft 84 RHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDV 118 (219)

Q Consensus 84 ~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~ 118 (219)

...|. .+.++|+++||+..+......

T Consensus 127 ~~~n~---------~~~~~~~~~Gf~~~~~~~~~~ 152 (170)

T 2GE3\_B 127 HADNA---------RAIALYEKIGFAHEGRARDAV 152 (170)

T ss\_dssp ETTCH---------HHHHHHHHHTCEEEEEEEEEE

T ss\_pred eCCCH---------HHHHHHHHcCCeEEEecCCce

No 76

>d2x7ba\_ d.108.1.0 (A:) automated matches {Sulfolobus solfataricus [TaxId: 273057]}

Probab=98.50 E-value=5.1e-08 Score=73.53 Aligned\_cols=101 Identities=19% Similarity=0.139 Sum\_probs=0.0 Template\_Neff=12.700

Q ss\_pred CCCCchHHHHHhhCCc--EEEEEECCEEEEEEEEE---------------eCCEEEEEEECHHHCCCCHHHHHHHHHHHc

Q Phabba\_Draft 11 PPLKFEPFDTMWSNGI--MARHAHDDRPVGHLHWH---------------PDGEIDSITVHPDLQRRGIGTAMLKHAQDN 73 (219)

Q Consensus 11 ~~~~~~~l~~~~~~~~--~~v~~~~~~liG~~~~~---------------~~~~i~~l~V~p~~R~~Gig~~Ll~~~~~~ 73 (219)

.....+.+...+.... ++++..++++||++.+. ....+..++|+|++||+|+|+.|++.+++.

T Consensus 25 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~ig~~~~~~~~~~~~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~ 104 (156)

T d2x7ba\_ 25 ENYPYYFFVEHLKEYGLAFFVAIVDNSVVGYIMPRIEWGFSNIKQLPSLVRKGHVVSIAVLEEYRRKGIATTLLEASMKS 104 (156)

T ss\_dssp CCCCHHHHHHHHHHHGGGCEEEEETTEEEEEEEEEEEEEECSSCSSCCEEEEEEEEEEEECGGGTTSSHHHHHHHHHHHH

T ss\_pred CCCCchhhhhHhhhcCceEEEEEECCeEEEEEeeeeccccccccccchhhceEEEEEEEeCHHHccCCHHHHHHHHHHHH

Q ss\_pred ccc----CeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeeeccccc

Q Phabba\_Draft 74 PHI----YESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDVSN 120 (219)

Q Consensus 74 ~~~----~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~ 120 (219)

+.. ..+.+.+...|. .+.++|+++||+..+.....+..

T Consensus 105 ~~~~~~~~~~~~~~~~~n~---------~~~~~~~~~Gf~~~~~~~~~~~~ 146 (156)

T d2x7ba\_ 105 MKNDYNAEEIYLEVRVSNY---------PAIALYEKLNFKKVKVLKGYYAD 146 (156)

T ss\_dssp HHHTTCCSEEEEEEETTCH---------HHHHHHHHTTCEEEEEETTCSTT

T ss\_pred HHhhcCCCEEEEEEEcCCh---------HHHHHHHHcCCEEEEEechhhcC

No 77

>d4r9mc\_ d.108.1.0 (C:) automated matches {Escherichia coli [TaxId: 83333]}

Probab=98.50 E-value=5.1e-08 Score=74.75 Aligned\_cols=91 Identities=16% Similarity=0.109 Sum\_probs=0.0 Template\_Neff=12.500

Q ss\_pred hHHHHHh--hCCcEEEEEECCEEEEEEEEEeC-----CEEEEEEECHHHCCCCHHHHHHHHHHHcccc----CeeEEEEE

Q Phabba\_Draft 16 EPFDTMW--SNGIMARHAHDDRPVGHLHWHPD-----GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI----YESSYPVR 84 (219)

Q Consensus 16 ~~l~~~~--~~~~~~v~~~~~~liG~~~~~~~-----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~----~~i~l~v~ 84 (219)

+.+...+ ....++++..+|++||++.+... ..+..+.|+|++|++|+|++|++.+++.+.+ ..+.+.+.

T Consensus 42 ~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~~v~~~~r~~G~~~~l~~~~~~~~~~~~~~~~i~~~~~ 121 (168)

T d4r9mc\_ 42 DLYDKHIHDQSERRFVVECDGEKAGLVELVEINHVHRRAEFQIIISPEYQGKGLATRAAKLAMDYGFTVLNLYKLYLIVD 121 (168)

T ss\_dssp HHHHHTTTCTTCEEEEEEETTEEEEEEEEEEEETTTTEEEEEEEECGGGCSSSHHHHHHHHHHHHHHHTSCCSEEEEEEE

T ss\_pred HHHHHHccCCCcceEEEEECCEEEEEEEEEEeeCCCcEEEEEEEECHHHCCCCHHHHHHHHHHHHhchhcCccEEEEEEc

Q ss\_pred cCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 85 HSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 85 ~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

..|. .+.++|+++||+..+...

T Consensus 122 ~~n~---------~~~~~~~~~Gf~~~~~~~ 143 (168)

T d4r9mc\_ 122 KENE---------KAIHIYRKLGFSVEGELM 143 (168)

T ss\_dssp TTCH---------HHHHHHHHHTCEEEEEEE

T ss\_pred CCCH---------HHHHHHHHcCCEEEEEEe

No 78

>4MBU\_A Similar to N-acetyltransferase; N-acetyltransferase, transferase; HET: PO4; 2.15A {Staphylococcus aureus subsp. aureus}

Probab=98.50 E-value=3e-08 Score=75.57 Aligned\_cols=84 Identities=11% Similarity=0.026 Sum\_probs=0.0 Template\_Neff=12.700

Q ss\_pred hCCcEEEEEECCEEEEEEEEEeC--------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEEEcCCcccc

Q Phabba\_Draft 23 SNGIMARHAHDDRPVGHLHWHPD--------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPVRHSSHFSA 91 (219)

Q Consensus 23 ~~~~~~v~~~~~~liG~~~~~~~--------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v~~~n~~~~ 91 (219)

....++++..+|++||++.+... ..+..++|+|++|++|+|+.|++.+.+.+++ ..+.+.+...|.

T Consensus 51 ~~~~~~~~~~~~~ivG~~~~~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~~g~~~i~~~~~~~n~--- 127 (166)

T 4MBU\_A 51 NHEPIFVFEENGSVLGFATFGSFRPWPAYQYTIEHSIYVDASARGKGIASQLLQRLIVEAKAKGYRTLVAGIDASNE--- 127 (166)

T ss\_dssp TTCCEEEEEETTEEEEEEEEEESSSSGGGTTEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHTTCSEEEEEEETTCH---

T ss\_pred CCCCeEEEEeCCcEEEEEEEeecCCCCccceEEEEEEEECHHHCCCChHHHHHHHHHHHHHHCCCCEEEEEeeCCCH---

Q ss\_pred cccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 92 AGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 92 ~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

.+.++|+++||+..+...

T Consensus 128 ------~~~~~~~~~Gf~~~~~~~ 145 (166)

T 4MBU\_A 128 ------ASIKLHQKFNFKHAGTLT 145 (166)

T ss\_dssp ------HHHHHHHHTTCEEEEEEE

T ss\_pred ------HHHHHHHhCCcEEeeEee

No 79

>4MBU\_B Similar to N-acetyltransferase; N-acetyltransferase, transferase; HET: PO4; 2.15A {Staphylococcus aureus subsp. aureus}

Probab=98.50 E-value=3e-08 Score=75.57 Aligned\_cols=84 Identities=11% Similarity=0.026 Sum\_probs=0.0 Template\_Neff=12.700

Q ss\_pred hCCcEEEEEECCEEEEEEEEEeC--------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEEEcCCcccc

Q Phabba\_Draft 23 SNGIMARHAHDDRPVGHLHWHPD--------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPVRHSSHFSA 91 (219)

Q Consensus 23 ~~~~~~v~~~~~~liG~~~~~~~--------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v~~~n~~~~ 91 (219)

....++++..+|++||++.+... ..+..++|+|++|++|+|+.|++.+.+.+++ ..+.+.+...|.

T Consensus 51 ~~~~~~~~~~~~~ivG~~~~~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~~g~~~i~~~~~~~n~--- 127 (166)

T 4MBU\_B 51 NHEPIFVFEENGSVLGFATFGSFRPWPAYQYTIEHSIYVDASARGKGIASQLLQRLIVEAKAKGYRTLVAGIDASNE--- 127 (166)

T ss\_dssp TTCCEEEEEETTEEEEEEEEEESSSSGGGTTEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHTTCSEEEEEEETTCH---

T ss\_pred CCCCeEEEEeCCcEEEEEEEeecCCCCccceEEEEEEEECHHHCCCChHHHHHHHHHHHHHHCCCCEEEEEeeCCCH---

Q ss\_pred cccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 92 AGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 92 ~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

.+.++|+++||+..+...

T Consensus 128 ------~~~~~~~~~Gf~~~~~~~ 145 (166)

T 4MBU\_B 128 ------ASIKLHQKFNFKHAGTLT 145 (166)

T ss\_dssp ------HHHHHHHHTTCEEEEEEE

T ss\_pred ------HHHHHHHhCCcEEeeEee

No 80

>1TIQ\_B Protease synthase and sporulation negative; alpha-beta protein, Structural Genomics, PSI; HET: COA, DTT; 1.9A {Bacillus subtilis} SCOP: d.108.1.1

Probab=98.50 E-value=5e-08 Score=76.02 Aligned\_cols=99 Identities=17% Similarity=0.152 Sum\_probs=0.0 Template\_Neff=12.300

Q ss\_pred CCchHHHHHhhCCc--EEEEEECCEEEEEEEEEeCC-----------EEEEEEECHHHCCCCHHHHHHHHHHHcccc---

Q Phabba\_Draft 13 LKFEPFDTMWSNGI--MARHAHDDRPVGHLHWHPDG-----------EIDSITVHPDLQRRGIGTAMLKHAQDNPHI--- 76 (219)

Q Consensus 13 ~~~~~l~~~~~~~~--~~v~~~~~~liG~~~~~~~~-----------~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~--- 76 (219)

+..+.+...+.... ++++..+|++||++.+.... .+..++|+|++|++|+|+.|++.+++.+++

T Consensus 45 ~~~~~~~~~~~~~~~~~~~~~~~~~ivG~~~~~~~~~~~~~~~~~~~~i~~~~v~~~~r~~Gi~~~l~~~~~~~~~~~~~ 124 (180)

T 1TIQ\_B 45 FNTEQLEKELSNMSSQFFFIYFDHEIAGYVKVNIDDAQSEEMGAESLEIERIYIKNSFQKHGLGKHLLNKAIEIALERNK 124 (180)

T ss\_dssp SCHHHHHHHHHCTTEEEEEEEETTEEEEEEEEEEGGGSSSCCCTTEEEEEEEEECGGGCSSSHHHHHHHHHHHHHHHTTC

T ss\_pred cCHHHHHHHHhcCcceEEEEEECCEEEEEEEEEccccccccccCCEEEEEEEEECHHHCCCCHHHHHHHHHHHHHHHcCC

Q ss\_pred CeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeeeccccc

Q Phabba\_Draft 77 YESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDVSN 120 (219)

Q Consensus 77 ~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~ 120 (219)

..+.+.+...|. .+.++|+++||+..+.....+..

T Consensus 125 ~~i~~~~~~~n~---------~~~~~~~k~Gf~~~~~~~~~~~~ 159 (180)

T 1TIQ\_B 125 KNIWLGVWEKNE---------NAIAFYKKMGFVQTGAHSFYMGD 159 (180)

T ss\_dssp SEEEEEEETTCH---------HHHHHHHHTTCEEEEEEEEEETT

T ss\_pred CEEEEEEEcCCH---------HHHHHHHHcCCEEEEEEEEEeCC

No 81

>3I9S\_D Integron cassette protein; Integron cassette protein, Vibrio cholerae; HET: SO4; 2.2A {Vibrio cholerae}

Probab=98.49 E-value=5e-08 Score=76.98 Aligned\_cols=99 Identities=11% Similarity=0.144 Sum\_probs=0.0 Template\_Neff=11.800

Q ss\_pred CCCCCCchHHHHHhhC--------CcEEEEEECCEEEEEEEEEeC---------CEEEEEEECHHHCCCCHHHHHHHHHH

Q Phabba\_Draft 9 DLPPLKFEPFDTMWSN--------GIMARHAHDDRPVGHLHWHPD---------GEIDSITVHPDLQRRGIGTAMLKHAQ 71 (219)

Q Consensus 9 ~~~~~~~~~l~~~~~~--------~~~~v~~~~~~liG~~~~~~~---------~~i~~l~V~p~~R~~Gig~~Ll~~~~ 71 (219)

.......+.+...+.. ..++++..++++||++.+... ..+..++|+|++|++|+|+.|++.++

T Consensus 50 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ivG~~~~~~~~~~~~~~~~~~i~~~~v~~~~r~~G~~~~l~~~~~ 129 (183)

T 3I9S\_D 50 GDKAASEQDLANYLSHQVFSEHSGVKVIAAVEHDKVLGFATYTIMFPAPKLSGQMYMKDLFVSSSARGKGIGLQLMKHLA 129 (183)

T ss\_dssp GGGCCCHHHHHHHCCCCCTSTTCCCEEEEEEETTEEEEEEEEEEECCCTTTCEEEEEEEEEECGGGTTSCHHHHHHHHHH

T ss\_pred CCCcCCHHHHHHHHhhcccCCCCCcEEEEEEeCCcEEEEEEEEEcCCCcccCCcEEEEEEEECHHHCCCCHHHHHHHHHH

Q ss\_pred Hcccc---CeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeeec

Q Phabba\_Draft 72 DNPHI---YESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADD 116 (219)

Q Consensus 72 ~~~~~---~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~ 116 (219)

+.+.. ..+.+.+...|. .+.++|+++||+..+....

T Consensus 130 ~~~~~~g~~~i~~~~~~~n~---------~~~~~~~~~Gf~~~~~~~~ 168 (183)

T 3I9S\_D 130 TIAITHNCQRLDWTAESTNP---------TAGKFYKSIGASLIREKEY 168 (183)

T ss\_dssp HHHHHTTEEEEEEEEETTCH---------HHHHHHHHTTCEECTTEEE

T ss\_pred HHHHHcCCCEEEEEeeccCH---------HHHHHHHhcCCEEEceeEe

No 82

>3I9S\_B Integron cassette protein; Integron cassette protein, Vibrio cholerae; HET: SO4; 2.2A {Vibrio cholerae}

Probab=98.49 E-value=5e-08 Score=76.98 Aligned\_cols=99 Identities=11% Similarity=0.144 Sum\_probs=0.0 Template\_Neff=11.800

Q ss\_pred CCCCCCchHHHHHhhC--------CcEEEEEECCEEEEEEEEEeC---------CEEEEEEECHHHCCCCHHHHHHHHHH

Q Phabba\_Draft 9 DLPPLKFEPFDTMWSN--------GIMARHAHDDRPVGHLHWHPD---------GEIDSITVHPDLQRRGIGTAMLKHAQ 71 (219)

Q Consensus 9 ~~~~~~~~~l~~~~~~--------~~~~v~~~~~~liG~~~~~~~---------~~i~~l~V~p~~R~~Gig~~Ll~~~~ 71 (219)

.......+.+...+.. ..++++..++++||++.+... ..+..++|+|++|++|+|+.|++.++

T Consensus 50 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ivG~~~~~~~~~~~~~~~~~~i~~~~v~~~~r~~G~~~~l~~~~~ 129 (183)

T 3I9S\_B 50 GDKAASEQDLANYLSHQVFSEHSGVKVIAAVEHDKVLGFATYTIMFPAPKLSGQMYMKDLFVSSSARGKGIGLQLMKHLA 129 (183)

T ss\_dssp GGGCCCHHHHHHHCCCCCSSTTCCCEEEEEEETTEEEEEEEEEEESCCTTTCEEEEEEEEEECGGGTTSCHHHHHHHHHH

T ss\_pred CCCcCCHHHHHHHHhhcccCCCCCcEEEEEEeCCcEEEEEEEEEcCCCcccCCcEEEEEEEECHHHCCCCHHHHHHHHHH

Q ss\_pred Hcccc---CeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeeec

Q Phabba\_Draft 72 DNPHI---YESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADD 116 (219)

Q Consensus 72 ~~~~~---~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~ 116 (219)

+.+.. ..+.+.+...|. .+.++|+++||+..+....

T Consensus 130 ~~~~~~g~~~i~~~~~~~n~---------~~~~~~~~~Gf~~~~~~~~ 168 (183)

T 3I9S\_B 130 TIAITHNCQRLDWTAESTNP---------TAGKFYKSIGASLIREKEY 168 (183)

T ss\_dssp HHHHHTTEEEEEEEEETTCH---------HHHHHHHHTTCEECTTEEE

T ss\_pred HHHHHcCCCEEEEEeeccCH---------HHHHHHHhcCCEEEceeEe

No 83

>d4mbub\_ d.108.1.0 (B:) automated matches {Staphylococcus aureus [TaxId: 158878]}

Probab=98.49 E-value=4.5e-08 Score=74.42 Aligned\_cols=90 Identities=10% Similarity=-0.013 Sum\_probs=0.0 Template\_Neff=12.600

Q ss\_pred HHHHHhhCCcEEEEEECCEEEEEEEEEeC--------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEEEc

Q Phabba\_Draft 17 PFDTMWSNGIMARHAHDDRPVGHLHWHPD--------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPVRH 85 (219)

Q Consensus 17 ~l~~~~~~~~~~v~~~~~~liG~~~~~~~--------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v~~ 85 (219)

..........++++.++|++||++.+... ..+..++|+|++|++|+|+.|++.+++.+.+ ..+.+.+..

T Consensus 42 ~~~~~~~~~~~~v~~~~~~~vG~~~~~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~~g~~~i~~~~~~ 121 (162)

T d4mbub\_ 42 FETKQRNHEPIFVFEENGSVLGFATFGSFRPWPAYQYTIEHSIYVDASARGKGIASQLLQRLIVEAKAKGYRTLVAGIDA 121 (162)

T ss\_dssp HHHHHHTTCCEEEEEETTEEEEEEEEEESSSSGGGTTEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHTTCSEEEEEEET

T ss\_pred HHHhccCCCCeEEEEeCCeEEEEEEEeecCCCCccceEEEEEEEECHHHCCCCHHHHHHHHHHHHHHHcCCCEEEEEeeC

Q ss\_pred CCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 86 SSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 86 ~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

.|. .+.++|+++||+..+...

T Consensus 122 ~n~---------~~~~~~~~~Gf~~~~~~~ 142 (162)

T d4mbub\_ 122 SNE---------ASIKLHQKFNFKHAGTLT 142 (162)

T ss\_dssp TCH---------HHHHHHHHTTCEEEEEEE

T ss\_pred CCH---------HHHHHHHhcCcEEeEEEE

No 84

>3WR7\_C Spermidine N1-acetyltransferase; alpha and beta, TRANSFERASE; HET: SPD, COA; 2.5A {Escherichia coli}

Probab=98.49 E-value=5.6e-08 Score=74.83 Aligned\_cols=91 Identities=16% Similarity=0.109 Sum\_probs=0.0 Template\_Neff=12.400

Q ss\_pred hHHHHHh--hCCcEEEEEECCEEEEEEEEEeC-----CEEEEEEECHHHCCCCHHHHHHHHHHHcccc----CeeEEEEE

Q Phabba\_Draft 16 EPFDTMW--SNGIMARHAHDDRPVGHLHWHPD-----GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI----YESSYPVR 84 (219)

Q Consensus 16 ~~l~~~~--~~~~~~v~~~~~~liG~~~~~~~-----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~----~~i~l~v~ 84 (219)

+.+.... ....++++..+|++||++.+... ..+..++|+|++||+|+|+.|++.+++.+.. ..+.+.+.

T Consensus 42 ~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~~i~~~~~ 121 (170)

T 3WR7\_C 42 DLYDKHIHDQSERRFVVECDGEKAGLVELVEINHVHRRAEFQIIISPEYQGKGLATRAAKLAMDYGFTVLNLYKLYLIVD 121 (170)

T ss\_dssp HHHHHHTTCTTCEEEEEEETTEEEEEEEEEEEETTTTEEEEEEEECGGGTTSSHHHHHHHHHHHCCCCCSCCSEEEEEEE

T ss\_pred HHHHHhccCCcceEEEEEECCEEEEEEEEEEcccccCEEEEEEEECHHHCCCCHHHHHHHHHHHHhhhHcCccEEEEEEe

Q ss\_pred cCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 85 HSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 85 ~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

..|. .+.++|+++||+..+...

T Consensus 122 ~~n~---------~~~~~~~~~Gf~~~~~~~ 143 (170)

T 3WR7\_C 122 KENE---------KAIHIYRKLGFSVEGELM 143 (170)

T ss\_dssp TTCH---------HHHHHHHHHTCEEEEEEE

T ss\_pred cCCH---------HHHHHHHHcCCeEEEEee

No 85

>3WR7\_B Spermidine N1-acetyltransferase; alpha and beta, TRANSFERASE; HET: SPD, COA; 2.5A {Escherichia coli}

Probab=98.49 E-value=5.6e-08 Score=74.83 Aligned\_cols=91 Identities=16% Similarity=0.109 Sum\_probs=0.0 Template\_Neff=12.400

Q ss\_pred hHHHHHh--hCCcEEEEEECCEEEEEEEEEeC-----CEEEEEEECHHHCCCCHHHHHHHHHHHcccc----CeeEEEEE

Q Phabba\_Draft 16 EPFDTMW--SNGIMARHAHDDRPVGHLHWHPD-----GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI----YESSYPVR 84 (219)

Q Consensus 16 ~~l~~~~--~~~~~~v~~~~~~liG~~~~~~~-----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~----~~i~l~v~ 84 (219)

+.+.... ....++++..+|++||++.+... ..+..++|+|++||+|+|+.|++.+++.+.. ..+.+.+.

T Consensus 42 ~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~~i~~~~~ 121 (170)

T 3WR7\_B 42 DLYDKHIHDQSERRFVVECDGEKAGLVELVEINHVHRRAEFQIIISPEYQGKGLATRAAKLAMDYGFTVLNLYKLYLIVD 121 (170)

T ss\_dssp HHHHHHTTCTTCEEEEEEETTEEEEEEEEEEEETTTTEEEEEEEECGGGTTSSHHHHHHHHHHHCCCCCSCCSEEEEEEE

T ss\_pred HHHHHhccCCcceEEEEEECCEEEEEEEEEEcccccCEEEEEEEECHHHCCCCHHHHHHHHHHHHhhhHcCccEEEEEEe

Q ss\_pred cCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 85 HSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 85 ~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

..|. .+.++|+++||+..+...

T Consensus 122 ~~n~---------~~~~~~~~~Gf~~~~~~~ 143 (170)

T 3WR7\_B 122 KENE---------KAIHIYRKLGFSVEGELM 143 (170)

T ss\_dssp TTCH---------HHHHHHHHTTCEEEEEEE

T ss\_pred cCCH---------HHHHHHHHcCCeEEEEee

No 86

>1WWZ\_A hypothetical protein PH1933; structural genomics, Pyrococcus horikoshii OT3; HET: ACO; 1.75A {Pyrococcus horikoshii} SCOP: d.108.1.1

Probab=98.48 E-value=3.8e-08 Score=74.08 Aligned\_cols=92 Identities=21% Similarity=0.208 Sum\_probs=0.0 Template\_Neff=12.900

Q ss\_pred chHHHHHhhCCc--EEEEEECCEEEEEEEEEeC----------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc--CeeE

Q Phabba\_Draft 15 FEPFDTMWSNGI--MARHAHDDRPVGHLHWHPD----------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI--YESS 80 (219)

Q Consensus 15 ~~~l~~~~~~~~--~~v~~~~~~liG~~~~~~~----------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~--~~i~ 80 (219)

.+.+........ ++++..++++||++.+... ..+..++|+|++|++|+|+.|++.+++.+.. ..+.

T Consensus 43 ~~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~~i~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~~ 122 (159)

T 1WWZ\_A 43 RNYIKWCWKKASDGFFVAKVGDKIVGFIVCDKDWFSKYEGRIVGAIHEFVVDKKFQGKGIGRKLLITCLDFLGKYNDTIE 122 (159)

T ss\_dssp HHHHHHHHHHHGGGEEEEEETTEEEEEEEEEEEEEETTTTEEEEEEEEEEECGGGTTSSHHHHHHHHHHHHHHTTCSEEE

T ss\_pred HHHHHHHhhhcCCcEEEEEECCEEEEEEEEehhHhcccCCceEEEEEEEEECHHHCCCCHHHHHHHHHHHHHHhcCCEEE

Q ss\_pred EEEEcCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 81 YPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 81 l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

+.+...|. .+.++|+++||+..+...

T Consensus 123 ~~~~~~n~---------~~~~~~~~~Gf~~~~~~~ 148 (159)

T 1WWZ\_A 123 LWVGEKNY---------GAMNLYEKFGFKKVGKSG 148 (159)

T ss\_dssp EEEETTCH---------HHHHHHHHTTCEEEEEET

T ss\_pred EEeeccch---------hhHHHHHHcCCEEccccc

No 87

>PF13527.6 ; Acetyltransf\_9 ; Acetyltransferase (GNAT) domain

Probab=98.48 E-value=2.8e-08 Score=72.22 Aligned\_cols=81 Identities=20% Similarity=0.261 Sum\_probs=0.0 Template\_Neff=13.100

Q ss\_pred hhCCcEEEEEECCEEEEEEEEEeC-----------CEEEEEEECHHHCCCCHHHHHHHHHHHccccCeeEEEEEcCCccc

Q Phabba\_Draft 22 WSNGIMARHAHDDRPVGHLHWHPD-----------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHIYESSYPVRHSSHFS 90 (219)

Q Consensus 22 ~~~~~~~v~~~~~~liG~~~~~~~-----------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~~~i~l~v~~~n~~~ 90 (219)

.....++++..+++++|++.+... .++..++|+|++|++|+|+.|++.+.+.+....+...+...|.

T Consensus 42 ~~~~~~~~~~~~~~~vg~~~~~~~~~~~~~~~~~~~~i~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~~~~~~n~-- 119 (133)

T A0M2X1\_GRAFK/2 42 FGSSVILIAKEDNKIVGVRAFMRWQWQHGDKKYHALRAVDTATHPNHQGKGIFKKLTLRAVDFSRSNDDNFIFNTPNE-- 119 (133)

T ss\_pred cCCccEEEEEECCEEEEEEEEEEceeecccceeeEEEEEEEEECHhhCCCCHHHHHHHHHHHHHhcCCCcEEEEcCCc--

Q ss\_pred ccccccchhHHHHHcCCCEEe

Q Phabba\_Draft 91 AAGRAWAQSDPDYHDPGDQNV 111 (219)

Q Consensus 91 ~~~~~~~~~~~~y~r~Gf~~~ 111 (219)

.+.++|+++||+.+

T Consensus 120 -------~~~~~~~~~Gf~~~ 133 (133)

T A0M2X1\_GRAFK/2 120 -------QSRPGYLKMGWEQV 133 (133)

T ss\_pred -------cchhHHHhcCcEEC

No 88

>2KCW\_A Uncharacterized acetyltransferase yjaB (E.C.2.3.1.-); GNAT fold, Acyltransferase, Transferase; NMR {Escherichia coli}

Probab=98.48 E-value=3.2e-08 Score=74.64 Aligned\_cols=96 Identities=18% Similarity=0.279 Sum\_probs=0.0 Template\_Neff=12.200

Q ss\_pred hHHHHHhhCCcEEEEEE-CCEEEEEEEEEeCCEEEEEEECHHHCCCCHHHHHHHHHHHccccCeeEEEEEcCCccccccc

Q Phabba\_Draft 16 EPFDTMWSNGIMARHAH-DDRPVGHLHWHPDGEIDSITVHPDLQRRGIGTAMLKHAQDNPHIYESSYPVRHSSHFSAAGR 94 (219)

Q Consensus 16 ~~l~~~~~~~~~~v~~~-~~~liG~~~~~~~~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~~~i~l~v~~~n~~~~~~~ 94 (219)

+.+........++++.. +|++||++.+.. ..+..++|+|++|++|+|+.|++.+++.++. +.+.+...|.

T Consensus 41 ~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~-~~~~~~~v~~~~r~~G~~~~l~~~~~~~~~~--~~~~~~~~n~------ 111 (147)

T 2KCW\_A 41 DLVRSFLPEAPLWVAVNERDQPVGFMLLSG-QHMDALFIDPDVRGCGVGRVLVEHALSMAPE--LTTNVNEQNE------ 111 (147)

T ss\_dssp HHHHTTTTTSCCEEEEETTSCEEEEEEEET-TEEEEEEECHHHCCCCCHHHHHHHHHHHCTT--CEEEEETTCH------

T ss\_pred HHHHHhCCCCCEEEEECCCCcEEEEEEEec-cceeeEEECHhhCCCCHHHHHHHHHHHHchh--cceeeecCCh------

Q ss\_pred ccchhHHHHHcCCCEEeeeeeccccccce

Q Phabba\_Draft 95 AWAQSDPDYHDPGDQNVTKADDDVSNWGY 123 (219)

Q Consensus 95 ~~~~~~~~y~r~Gf~~~~~~~~~~~~~~~ 123 (219)

.+.++|+++||+..+..........+

T Consensus 112 ---~~~~~~~k~Gf~~~~~~~~~~~~~~~ 137 (147)

T 2KCW\_A 112 ---QAVGFYKKVGFKVTGRSEVDDLGKPY 137 (147)

T ss\_dssp ---HHHHHHHHHTEEEEEECSSSSSSCSC

T ss\_pred ---hHHHHHHHcCCEEeecccccccCCcc

No 89

>1YR0\_A phosphinothricin acetyltransferase (E.C.2.3.1.-); Structural Genomics, Protein Structure Initiative; HET: SO4; 2.0A {Agrobacterium tumefaciens str.} SCOP: d.108.1.1

Probab=98.48 E-value=4.5e-08 Score=76.08 Aligned\_cols=91 Identities=18% Similarity=0.108 Sum\_probs=0.0 Template\_Neff=12.200

Q ss\_pred chHHHHHhhCCc-EEEEEECCEEEEEEEEEeC--------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEE

Q Phabba\_Draft 15 FEPFDTMWSNGI-MARHAHDDRPVGHLHWHPD--------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYP 82 (219)

Q Consensus 15 ~~~l~~~~~~~~-~~v~~~~~~liG~~~~~~~--------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~ 82 (219)

.+.+........ ++++..++++||++.+... ..+..++|+|++|++|+|+.|++.+++.++. ..+.+.

T Consensus 44 ~~~~~~~~~~~~~~~v~~~~~~iiG~~~~~~~~~~~~~~~~~~~~~~v~~~~r~~gi~~~l~~~~~~~~~~~~~~~i~~~ 123 (175)

T 1YR0\_A 44 KDWFAARTSRGFPVIVAILDGKVAGYASYGDWRAFDGYRHTREHSVYVHKDARGHGIGKRLMQALIDHAGGNDVHVLIAA 123 (175)

T ss\_dssp HHHHHHHHHHTCCEEEEEETTEEEEEEEEEESSSSGGGTTEEEEEEEECTTSTTSSHHHHHHHHHHHHHHTTTCCEEEEE

T ss\_pred HHHHHhccCCCccEEEEEeCCeEEEEEEEeccccccCCceEEEEEEEECHHHCCCCHHHHHHHHHHHHHccCCeeEEEEE

Q ss\_pred EEcCCcccccccccchhHHHHHcCCCEEeeee

Q Phabba\_Draft 83 VRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKA 114 (219)

Q Consensus 83 v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~ 114 (219)

+...|. .+.++|+++||+..+..

T Consensus 124 ~~~~n~---------~~~~~~~~~Gf~~~~~~ 146 (175)

T 1YR0\_A 124 IEAENT---------ASIRLHESLGFRVVGRF 146 (175)

T ss\_dssp EETTCH---------HHHHHHHHTTCEEEEEE

T ss\_pred eecCCH---------HHHHHHHHcCCEEEEEe

No 90

>d3fixd\_ d.108.1.0 (D:) automated matches {Thermoplasma acidophilum [TaxId: 2303]}

Probab=98.48 E-value=3.1e-08 Score=75.11 Aligned\_cols=78 Identities=15% Similarity=0.166 Sum\_probs=0.0 Template\_Neff=12.500

Q ss\_pred EEEEEECCEEEEEEEEEeC---CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEEEcCCcccccccccchhH

Q Phabba\_Draft 27 MARHAHDDRPVGHLHWHPD---GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPVRHSSHFSAAGRAWAQSD 100 (219)

Q Consensus 27 ~~v~~~~~~liG~~~~~~~---~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v~~~n~~~~~~~~~~~~~ 100 (219)

++++.+++++||++.+... ..+..+.|+|++|++|+++.|++.+++.++. ..+.+.+...|. .+.

T Consensus 63 ~~~~~~~~~iiG~~~~~~~~~~~~i~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~i~~~~~~~n~---------~~~ 133 (157)

T d3fixd\_ 63 FLGAFADSTLIGFIELKIIANKAELLRLYLKPEYTHKKIGKTLLLEAEKIMKKKGILECRLYVHRQNS---------VGF 133 (157)

T ss\_dssp EEEEEETTEEEEEEEEEEETTEEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHHTCCEEEEEEETTCH---------HHH

T ss\_pred EEEEEeCCeEEEEEEEEEeCCeEEEEEEEEChhhCCCcHHHHHHHHHHHHHHHcCCcEEEEEEeCCCH---------HHH

Q ss\_pred HHHHcCCCEEeee

Q Phabba\_Draft 101 PDYHDPGDQNVTK 113 (219)

Q Consensus 101 ~~y~r~Gf~~~~~ 113 (219)

++|+++||+..+.

T Consensus 134 ~~~~~~Gf~~~~~ 146 (157)

T d3fixd\_ 134 SFYYKNGFKVEDT 146 (157)

T ss\_dssp HHHHTTTCEEEEC

T ss\_pred HHHHHCCCEEEec

No 91

>1Y9K\_B IAA acetyltransferase (E.C.2.3.1.-); structural genomics, Midwest Center for; 2.39A {Bacillus cereus ATCC 14579} SCOP: d.108.1.1

Probab=98.48 E-value=5.2e-08 Score=75.33 Aligned\_cols=97 Identities=22% Similarity=0.173 Sum\_probs=0.0 Template\_Neff=11.500

Q ss\_pred chHHHHHhhCCcEEEEEECCEEEEEEEEEeC----CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEEEcCC

Q Phabba\_Draft 15 FEPFDTMWSNGIMARHAHDDRPVGHLHWHPD----GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPVRHSS 87 (219)

Q Consensus 15 ~~~l~~~~~~~~~~v~~~~~~liG~~~~~~~----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v~~~n 87 (219)

.+.+...++...++++.+++++||++.+... ..+..+.|+|++|++|+++.|++.+++.+.. ..+.+.+...|

T Consensus 27 ~~~~~~~~~~~~~~~~~~~~~~vg~~~~~~~~~~~~~i~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~i~~~~~~~n 106 (157)

T 1Y9K\_B 27 ERQIATYVQRGLTYVAKQGGSVIGVYVLLETRPKTMEIMNIAVAEHLQGKGIGKKLLRHAVETAKGYGMSKLEVGTGNSS 106 (157)

T ss\_dssp HHHHHHHHHHSEEEEEEETTEEEEEEEEEECSTTEEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHTTCSEEEEEEETTC

T ss\_pred HHHHHHHhhcCeEEEEEECCEEEEEEEEEeCCCCeEEEEEEEECHHHCCCCHHHHHHHHHHHHHHHCCCCEEEEEeCCCC

Q ss\_pred cccccccccchhHHHHHcCCCEEeeeeeccccc

Q Phabba\_Draft 88 HFSAAGRAWAQSDPDYHDPGDQNVTKADDDVSN 120 (219)

Q Consensus 88 ~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~ 120 (219)

. .+.++|+++||+..+.....+..

T Consensus 107 ~---------~~~~~~~~~Gf~~~~~~~~~~~~ 130 (157)

T 1Y9K\_B 107 V---------SQLALYQKCGFRIFSIDFDYFSK 130 (157)

T ss\_dssp H---------HHHHHHHHTTCEEEEEETTTTTT

T ss\_pred H---------HHHHHHHHcCCEEEEEecceecC

No 92

>1Y9K\_A IAA acetyltransferase (E.C.2.3.1.-); structural genomics, Midwest Center for; 2.39A {Bacillus cereus ATCC 14579} SCOP: d.108.1.1

Probab=98.48 E-value=5.2e-08 Score=75.33 Aligned\_cols=97 Identities=22% Similarity=0.173 Sum\_probs=0.0 Template\_Neff=11.500

Q ss\_pred chHHHHHhhCCcEEEEEECCEEEEEEEEEeC----CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEEEcCC

Q Phabba\_Draft 15 FEPFDTMWSNGIMARHAHDDRPVGHLHWHPD----GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPVRHSS 87 (219)

Q Consensus 15 ~~~l~~~~~~~~~~v~~~~~~liG~~~~~~~----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v~~~n 87 (219)

.+.+...++...++++.+++++||++.+... ..+..+.|+|++|++|+++.|++.+++.+.. ..+.+.+...|

T Consensus 27 ~~~~~~~~~~~~~~~~~~~~~~vg~~~~~~~~~~~~~i~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~i~~~~~~~n 106 (157)

T 1Y9K\_A 27 ERQIATYVQRGLTYVAKQGGSVIGVYVLLETRPKTMEIMNIAVAEHLQGKGIGKKLLRHAVETAKGYGMSKLEVGTGNSS 106 (157)

T ss\_dssp HHHHHHHHHHSEEEEEECSSSEEEEEEEEECSTTEEEEEEEEECGGGCSSSHHHHHHHHHHHHHHHTTCSEEEEEEETTC

T ss\_pred HHHHHHHhhcCeEEEEEECCEEEEEEEEEeCCCCeEEEEEEEECHHHCCCCHHHHHHHHHHHHHHHCCCCEEEEEeCCCC

Q ss\_pred cccccccccchhHHHHHcCCCEEeeeeeccccc

Q Phabba\_Draft 88 HFSAAGRAWAQSDPDYHDPGDQNVTKADDDVSN 120 (219)

Q Consensus 88 ~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~ 120 (219)

. .+.++|+++||+..+.....+..

T Consensus 107 ~---------~~~~~~~~~Gf~~~~~~~~~~~~ 130 (157)

T 1Y9K\_A 107 V---------SQLALYQKCGFRIFSIDFDYFSK 130 (157)

T ss\_dssp H---------HHHHHHHHTTCEEEEEETTHHHH

T ss\_pred H---------HHHHHHHHcCCEEEEEecceecC

No 93

>2AJ6\_A hypothetical protein MW0638; Structural genomics, Joint Center for; HET: UNL; 1.63A {Staphylococcus aureus subsp. aureus} SCOP: d.108.1.1

Probab=98.48 E-value=5.9e-08 Score=75.48 Aligned\_cols=91 Identities=14% Similarity=0.089 Sum\_probs=0.0 Template\_Neff=11.300

Q ss\_pred hHHHHHhh--CCcEEEEEECCEEEEEEEEEeC-----CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEEEc

Q Phabba\_Draft 16 EPFDTMWS--NGIMARHAHDDRPVGHLHWHPD-----GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPVRH 85 (219)

Q Consensus 16 ~~l~~~~~--~~~~~v~~~~~~liG~~~~~~~-----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v~~ 85 (219)

+.+...+. ...++++.+++++||++.+... ..+..++|+|++|++|+|+.|++.+++.++. ..+.+.+..

T Consensus 54 ~~~~~~~~~~~~~~~~~~~~~~ivG~~~~~~~~~~~~~~i~~~~v~~~~r~~G~~~~l~~~~~~~~~~~g~~~i~~~~~~ 133 (159)

T 2AJ6\_A 54 EMICSRLEHTNDKIYIYENEGQLIAFIWGHFSNEKSMVNIELLYVEPQFRKLGIATQLKIALEKWAKTMNAKRISNTIHK 133 (159)

T ss\_dssp HHHHHHHHSSSEEEEEEEETTEEEEEEEEEEETTTTEEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHTTCSCCCCC---

T ss\_pred HHHHHhhcccCCeEEEEEECCcEEEEEEEEEcCccceEEEEEEEECHHHCCCCHHHHHHHHHHHHHHhCCCcEEEEEEec

Q ss\_pred CCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 86 SSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 86 ~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

.|. .+.++|+++||+..+...

T Consensus 134 ~n~---------~~~~~~~k~Gf~~~~~~~ 154 (159)

T 2AJ6\_A 134 NNL---------PMISLNKDLGYQVSHVKM 154 (159)

T ss\_dssp ------------------------------

T ss\_pred CcH---------HHHHHHHHcCCEEEEEEE

No 94

>d2fe7a1 d.108.1.1 (A:3-158) Probable N-acetyltransferase PA0478 {Pseudomonas aeruginosa [TaxId: 287]}

Probab=98.48 E-value=2.9e-08 Score=74.98 Aligned\_cols=84 Identities=14% Similarity=0.144 Sum\_probs=0.0 Template\_Neff=12.600

Q ss\_pred hCCcEEEEEECCEEEEEEEEEe---------CCEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEEEcCCccc

Q Phabba\_Draft 23 SNGIMARHAHDDRPVGHLHWHP---------DGEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPVRHSSHFS 90 (219)

Q Consensus 23 ~~~~~~v~~~~~~liG~~~~~~---------~~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v~~~n~~~ 90 (219)

....++++.+++++||++.+.. ...+..++|+|++|++|+|+.|++.+.+.+++ ..+.+.+...|.

T Consensus 47 ~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~~~~~~~~~n~-- 124 (156)

T d2fe7a1 47 SPTRALMCLSEGRPIGYAVFFYSYSTWLGRNGIYLEDLYVTPEYRGVGAGRRLLRELAREAVANDCGRLEWSVLDWNQ-- 124 (156)

T ss\_dssp CSEEEEEEEETTEEEEEEEEEEEEETTTTEEEEEEEEEEECGGGCC--HHHHHHHHHHHHHHHTTCSEEEEEEETTCH--

T ss\_pred CCeEEEEEEeCCceEEEEEEEEcccccccceeEEEEEeeeCHHHCCCCHHHHHHHHHHHHHHHCCCCEEEEEEEecCH--

Q ss\_pred ccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 91 AAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 91 ~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

.+.++|+++||+..+...

T Consensus 125 -------~~~~~~~~~Gf~~~~~~~ 142 (156)

T d2fe7a1 125 -------PAIDFYRSIGALPQDEWV 142 (156)

T ss\_dssp -------HHHHHHHHTTCEECTTEE

T ss\_pred -------HHHHHHHhcCCeecceeE

No 95

>5T7D\_D Phosphinothricin N-acetyltransferase (E.C.2.3.1.183); Gcn5-related N-acetyltransferases Phosphinothricin-deactivating activity, TRANSFERASE; HET: ACO, ACT; 1.4A {Streptomyces hygroscopicus}

Probab=98.48 E-value=5.8e-08 Score=76.41 Aligned\_cols=91 Identities=13% Similarity=0.041 Sum\_probs=0.0 Template\_Neff=12.200

Q ss\_pred hHHHHHhhCCcEEEEEECCEEEEEEEEEeC--------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEEE

Q Phabba\_Draft 16 EPFDTMWSNGIMARHAHDDRPVGHLHWHPD--------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPVR 84 (219)

Q Consensus 16 ~~l~~~~~~~~~~v~~~~~~liG~~~~~~~--------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v~ 84 (219)

..+........++++..+|++||++.+... ..+..++|+|++|++|+|+.|++.+++.++. ..+.+.+.

T Consensus 54 ~~~~~~~~~~~~~v~~~~~~~vG~~~~~~~~~~~~~~~~~~~~~~v~~~~r~~gi~~~l~~~~~~~~~~~~~~~i~~~~~ 133 (189)

T 5T7D\_D 54 DDLVRLRERYPWLVAEVDGEVAGIAYAGPWKARNAYDWTAESTVYVSPRHQRTGLGSTLYTHLLKSLEAQGFKSVVAVIG 133 (189)

T ss\_dssp HHHHHHTTTSCEEEEEETTEEEEEEEEEESSSSGGGTTEEEEEEEECTTSTTSSHHHHHHHHHHHHHHHHTCSEEEEEEE

T ss\_pred HHHHHhhhcCCEEEEEECCeEEEEEEEEeccccccCCeeEEEEEEECHHHCCCCHHHHHHHHHHHHHHHCCCCEEEEEEe

Q ss\_pred cCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 85 HSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 85 ~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

..|. .+.++|+++||+..+...

T Consensus 134 ~~n~---------~~~~~~~~~Gf~~~~~~~ 155 (189)

T 5T7D\_D 134 LPND---------PSVRMHEALGYAPRGMLR 155 (189)

T ss\_dssp SSCH---------HHHHHHHHTTCEEEEEEE

T ss\_pred CCCc---------hHHHHHHHcCCeeeeEEE

No 96

>5T7E\_D Phosphinothricin N-acetyltransferase (E.C.2.3.1.183); Phosphinothricin-deactivating activity GCN5-Related N-Acetyltransferases, TRANSFERASE; HET: PPQ, COA, BNG; 1.8A {Streptomyces hygroscopicus}

Probab=98.48 E-value=5.8e-08 Score=76.41 Aligned\_cols=91 Identities=13% Similarity=0.041 Sum\_probs=0.0 Template\_Neff=12.200

Q ss\_pred hHHHHHhhCCcEEEEEECCEEEEEEEEEeC--------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEEE

Q Phabba\_Draft 16 EPFDTMWSNGIMARHAHDDRPVGHLHWHPD--------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPVR 84 (219)

Q Consensus 16 ~~l~~~~~~~~~~v~~~~~~liG~~~~~~~--------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v~ 84 (219)

..+........++++..+|++||++.+... ..+..++|+|++|++|+|+.|++.+++.++. ..+.+.+.

T Consensus 54 ~~~~~~~~~~~~~v~~~~~~~vG~~~~~~~~~~~~~~~~~~~~~~v~~~~r~~gi~~~l~~~~~~~~~~~~~~~i~~~~~ 133 (189)

T 5T7E\_D 54 DDLVRLRERYPWLVAEVDGEVAGIAYAGPWKARNAYDWTAESTVYVSPRHQRTGLGSTLYTHLLKSLEAQGFKSVVAVIG 133 (189)

T ss\_dssp HHHHHHTTTSCEEEEEETTEEEEEEEEEESSSSGGGTTEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHHTCSEEEEEEE

T ss\_pred HHHHHhhhcCCEEEEEECCeEEEEEEEEeccccccCCeeEEEEEEECHHHCCCCHHHHHHHHHHHHHHHCCCCEEEEEEe

Q ss\_pred cCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 85 HSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 85 ~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

..|. .+.++|+++||+..+...

T Consensus 134 ~~n~---------~~~~~~~~~Gf~~~~~~~ 155 (189)

T 5T7E\_D 134 LPND---------PSVRMHEALGYAPRGMLR 155 (189)

T ss\_dssp SSCH---------HHHHHHHHTTCEEEEEEE

T ss\_pred CCCc---------hHHHHHHHcCCeeeeEEE

No 97

>2DXQ\_A Acetyltransferase; acetyltransferase, Structural Genomics, PSI-2, Protein; HET: PO4; 1.8A {Agrobacterium tumefaciens str.}

Probab=98.48 E-value=4.4e-08 Score=72.82 Aligned\_cols=93 Identities=14% Similarity=0.133 Sum\_probs=0.0 Template\_Neff=13.000

Q ss\_pred chHHHHHhhCCc--EEEEEECCEEEEEEEEEeC----------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---Cee

Q Phabba\_Draft 15 FEPFDTMWSNGI--MARHAHDDRPVGHLHWHPD----------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YES 79 (219)

Q Consensus 15 ~~~l~~~~~~~~--~~v~~~~~~liG~~~~~~~----------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i 79 (219)

.+.+...+.... ++++.+++++||++.+... ..+..++|+|++|++|+|+.|++.+++.++. ..+

T Consensus 39 ~~~~~~~~~~~~~~~~~~~~~~~ivG~~~~~~~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~~g~~~~ 118 (150)

T 2DXQ\_A 39 GAVFAAMLAQPGLTIFVATENGKPVATATLLIVPNLTRAARPYAFIENVVTLEARRGRGYGRTVVRHAIETAFGANCYKV 118 (150)

T ss\_dssp HHHHHHHHHSTTEEEEEEEETTEEEEEEEEEEECCSHHHHCCEEEEEEEECCGGGTTSSHHHHHHHHHHHHHHHTTCSEE

T ss\_pred HHHHHHHhhCCCEEEEEEEeCCcEEEEEEEEEecCcccCCCCEEEEEEEEECHhhcCCCHHHHHHHHHHHHHHhCCCCEE

Q ss\_pred EEEEEcCCcccccccccchhHHHHHcCCCEEeeeeec

Q Phabba\_Draft 80 SYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADD 116 (219)

Q Consensus 80 ~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~ 116 (219)

.+.+...|. .+.++|+++||+..+....

T Consensus 119 ~~~~~~~n~---------~~~~~~~~~Gf~~~~~~~~ 146 (150)

T 2DXQ\_A 119 MLLTGRHDP---------AVHAFYESCGFVQNKTGFQ 146 (150)

T ss\_dssp EEEECCCCH---------HHHHHHHHTTCEEEEEEEE

T ss\_pred EEEEeCCCH---------HHHHHHHhcCcEeccccee

No 98

>d1yr0b\_ d.108.1.0 (B:) automated matches {Agrobacterium tumefaciens [TaxId: 176299]}

Probab=98.48 E-value=5.1e-08 Score=73.87 Aligned\_cols=92 Identities=17% Similarity=0.109 Sum\_probs=0.0 Template\_Neff=12.800

Q ss\_pred chHHHHHhhCCc-EEEEEECCEEEEEEEEEeC--------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEE

Q Phabba\_Draft 15 FEPFDTMWSNGI-MARHAHDDRPVGHLHWHPD--------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYP 82 (219)

Q Consensus 15 ~~~l~~~~~~~~-~~v~~~~~~liG~~~~~~~--------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~ 82 (219)

.+.+........ ++++..++++||++.+... ..+..++|+|++|++|+|+.|++.+++.+.. ..+.+.

T Consensus 41 ~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~~g~~~i~~~ 120 (163)

T d1yr0b\_ 41 KDWFAARTSRGFPVIVAILDGKVAGYASYGDWRAFDGYRHTREHSVYVHKDARGHGIGKRLMQALIDHAGGNDVHVLIAA 120 (163)

T ss\_dssp HHHHHHHHHTTCCEEEEEETTEEEEEEEEEESSSSGGGTTEEEEEEEECTTSTTSSHHHHHHHHHHHHHHTTTCCEEEEE

T ss\_pred HHHHHhcccCCccEEEEEECCeEEEEEEEeecccccCCccEEEEEEEECHHHcCCCHHHHHHHHHHHHHccCCceEEEEE

Q ss\_pred EEcCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 83 VRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 83 v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

+...|. .+.++|+++||+..+...

T Consensus 121 ~~~~n~---------~~~~~~~~~Gf~~~~~~~ 144 (163)

T d1yr0b\_ 121 IEAENT---------ASIRLHESLGFRVVGRFS 144 (163)

T ss\_dssp EETTCH---------HHHHHHHTTTCEEEEEEE

T ss\_pred eeccCH---------HHHHHHHHcCCEEEEEec

No 99

>d1xebg\_ d.108.1.1 (G:) Hypothetical protein PA0115 {Pseudomonas aeruginosa [TaxId: 287]}

Probab=98.48 E-value=2.2e-08 Score=75.52 Aligned\_cols=85 Identities=12% Similarity=0.068 Sum\_probs=0.0 Template\_Neff=12.200

Q ss\_pred hCCcEEEEEECCEEEEEEEEEeC------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc-CeeEEEEEcCCcccccccc

Q Phabba\_Draft 23 SNGIMARHAHDDRPVGHLHWHPD------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI-YESSYPVRHSSHFSAAGRA 95 (219)

Q Consensus 23 ~~~~~~v~~~~~~liG~~~~~~~------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~-~~i~l~v~~~n~~~~~~~~ 95 (219)

....++++.+++++||++.+... ..+..++|+|++||+|+|++|++.+++.+.+ ......+...|.

T Consensus 45 ~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~~~v~~~~rg~G~~~~l~~~~~~~~~~~~~~~~~~~~~n~------- 117 (147)

T d1xebg\_ 45 GDTHHLMAWRDGQLLAYLRLLDPVRHEGQVVIGRVVSSSAARGQGLGHQLMERALQAAERLWLDTPVYLSAQA------- 117 (147)

T ss\_dssp TTCEEEEEECSSCEEEEEEEECGGGTTTCEEEEEEEECSTTTTSSHHHHHHHHHHHHHHHHTTTCCEEEEEEG-------

T ss\_pred CCEEEEEEEECCeEEEEEEEEcCCCCCCEEEEEEEEECHHHCCCCHHHHHHHHHHHHHHHcCCCccEEEecCH-------

Q ss\_pred cchhHHHHHcCCCEEeeeeec

Q Phabba\_Draft 96 WAQSDPDYHDPGDQNVTKADD 116 (219)

Q Consensus 96 ~~~~~~~y~r~Gf~~~~~~~~ 116 (219)

.+.++|+++||+..+....

T Consensus 118 --~~~~~~~~~Gf~~~~~~~~ 136 (147)

T d1xebg\_ 118 --HLQAYYGRYGFVAVTEVYL 136 (147)

T ss\_dssp --GGHHHHHTTTCEEEEEEEE

T ss\_pred --HHHHHHHHcCCEEccceec

No 100

>d4j3gc\_ d.108.1.0 (C:) automated matches {Brucella melitensis [TaxId: 359391]}

Probab=98.47 E-value=4.8e-08 Score=73.95 Aligned\_cols=91 Identities=13% Similarity=0.114 Sum\_probs=0.0 Template\_Neff=12.800

Q ss\_pred hHHHHHhhCCc-EEEEEECCEEEEEEEEEeC--------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEE

Q Phabba\_Draft 16 EPFDTMWSNGI-MARHAHDDRPVGHLHWHPD--------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPV 83 (219)

Q Consensus 16 ~~l~~~~~~~~-~~v~~~~~~liG~~~~~~~--------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v 83 (219)

.++........ ++++..+|++||++.+... ..+..++|+|++||+|+|+.|++.+++.+.+ ..+.+.+

T Consensus 41 ~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~~g~~~~~~~~ 120 (162)

T d4j3gc\_ 41 QWLENRNRDGFPVLVAEREGQVVGYASYGPFRPFEGFRHSSELSVYVASNARGGGIGRTLLAELIEEARERKVHVLIAGI 120 (162)

T ss\_dssp HHHHHHHHHTCCEEEEEETTEEEEEEEEEESCSSGGGTTEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHTTCCEEEEEE

T ss\_pred HHHHhccCCCCcEEEEEeCCeEEEEEEEeeccCccCCCeeeEEEEEECHhhCCCCHHHHHHHHHHHHHHHCCCCEEEEEe

Q ss\_pred EcCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 84 RHSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 84 ~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

...|. .+.++|+++||+..+...

T Consensus 121 ~~~n~---------~~~~~~~~~Gf~~~~~~~ 143 (162)

T d4j3gc\_ 121 EAGNA---------ASIALHRSQGFEECGTLK 143 (162)

T ss\_dssp ETTCH---------HHHHHHHHTTCEEEEEEE

T ss\_pred eCCCH---------HHHHHHHHcCcEEeeeec

No 101

>1UFH\_B YYCN protein; alpha and beta, fold, acetyltransferase; 2.2A {Bacillus subtilis subsp. subtilis str. 168} SCOP: d.108.1.1

Probab=98.47 E-value=4.2e-08 Score=76.87 Aligned\_cols=91 Identities=14% Similarity=0.143 Sum\_probs=0.0 Template\_Neff=12.000

Q ss\_pred hHHHHHhh------CCcEEEEE-ECCEEEEEEEEEeC-------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---Ce

Q Phabba\_Draft 16 EPFDTMWS------NGIMARHA-HDDRPVGHLHWHPD-------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YE 78 (219)

Q Consensus 16 ~~l~~~~~------~~~~~v~~-~~~~liG~~~~~~~-------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~ 78 (219)

+.+...+. ...++++. ++|++||++.+... ..+..++|+|++|++|+|++|++.+++.+++ ..

T Consensus 69 ~~~~~~~~~~~~~~~~~~~~~~~~~~~ivG~~~~~~~~~~~~~~~~i~~~~v~p~~r~~Gig~~l~~~~~~~~~~~g~~~ 148 (180)

T 1UFH\_B 69 QVFTDLLPRGLETPHHHLWSLKLNEKDIVGWLWIHAEPEHPQQEAFIYDFGLYEPYRGKGYAKQALAALDQAARSMGIRK 148 (180)

T ss\_dssp HHHHHHCTTGGGCTTEEEEEEEEETTEEEEEEEEECCTTCTTCEEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHHTCCE

T ss\_pred HHHHHhcccCCCCCCeeEEEEEEcCCcEEEEEEEEeCCCCcccceEEEEEEECHhhCCCchHHHHHHHHHHHHHHcCCCE

Q ss\_pred eEEEEEcCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 79 SSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 79 i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

+.+.+...|. .+.++|+|+||+..+...

T Consensus 149 i~~~~~~~n~---------~~~~~~~k~Gf~~~~~~~ 176 (180)

T 1UFH\_B 149 LSLHVFAHNQ---------TARKLYEQTGFQETDVVM 176 (180)

T ss\_dssp EEECCCTTCH---------HHHHHHHHTTCCCCCCCC

T ss\_pred EEEEEecCCH---------HHHHHHHHcCCEEeeeee

No 102

>5HGZ\_A N-alpha-acetyltransferase 60 (E.C.2.3.1.48,2.3.1.88); N-terminal acetylation, Complex, NATs, Protein; HET: ACO, MLA; 1.383A {Homo sapiens}

Probab=98.47 E-value=6.5e-08 Score=81.54 Aligned\_cols=99 Identities=14% Similarity=0.038 Sum\_probs=0.0 Template\_Neff=10.400

Q ss\_pred CCCCchHHHHHhhCCc--EEEEEECCEEEEEEEEEeCC-----------------------EEEEEEECHHHCCCCHHHH

Q Phabba\_Draft 11 PPLKFEPFDTMWSNGI--MARHAHDDRPVGHLHWHPDG-----------------------EIDSITVHPDLQRRGIGTA 65 (219)

Q Consensus 11 ~~~~~~~l~~~~~~~~--~~v~~~~~~liG~~~~~~~~-----------------------~i~~l~V~p~~R~~Gig~~ 65 (219)

..+...++.....+.. ++++..+|++||++.+.... ++..++|+|++|++|+|++

T Consensus 37 ~~~~~~~~~~~~~~~~~~~~v~~~~g~iVG~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~i~~l~V~~~~r~~Gig~~ 116 (243)

T 5HGZ\_A 37 IEYPDSWYRDITSNKKFFSLAATYRGAIVGMIVAEIKNRTKIHKEDGDILASNFSVDTQVAYILSLGVVKEFRKHGIGSL 116 (243)

T ss\_dssp SCCCHHHHHHHHHCTTEEEEEEEETTEEEEEEEEEEEEGGGSCGGGTTSSCTTSCTTCEEEEEEEEEECGGGTTSSHHHH

T ss\_pred CCCCHHHHHHHhcCCCeEEEEEEECCeEEEEEEEEEecccccchhcccchhccCCCCCcEEEEEEEEECHHHcCCCHHHH

Q ss\_pred HHHHHHHcc---cc---CeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeeeccc

Q Phabba\_Draft 66 MLKHAQDNP---HI---YESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDV 118 (219)

Q Consensus 66 Ll~~~~~~~---~~---~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~ 118 (219)

|++.+++.+ +. ..+++.+...|. .+.++|+++||+..+.....+

T Consensus 117 Ll~~~~~~~~~~~~~g~~~i~~~~~~~n~---------~~~~~y~~~GF~~~~~~~~~~ 166 (243)

T 5HGZ\_A 117 LLESLKDHISTTAQDHCKAIYLHVLTTNN---------TAINFYENRDFKQHHYLPYYY 166 (243)

T ss\_dssp HHHHHHHHHHHHHTTTEEEEEEEEETTCH---------HHHHHHHTTTCEEEEEEEEEE

T ss\_pred HHHHHHHHHhhccccCCCEEEEEEEcCCH---------HHHHHHHhCCcEEEEeecCeE

No 103

>d2fl4a1 d.108.1.1 (A:1-146) Probable spermine/spermidine acetyltransferase EF1086 {Enterococcus faecalis [TaxId: 1351]}

Probab=98.47 E-value=3.8e-08 Score=73.53 Aligned\_cols=79 Identities=13% Similarity=0.013 Sum\_probs=0.0 Template\_Neff=12.600

Q ss\_pred EEEEEECCEEEEEEEEEeC----CEEEEEEECHHHCCCCHHHHHHHHHHHcccc----CeeEEEEEcCCcccccccccch

Q Phabba\_Draft 27 MARHAHDDRPVGHLHWHPD----GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI----YESSYPVRHSSHFSAAGRAWAQ 98 (219)

Q Consensus 27 ~~v~~~~~~liG~~~~~~~----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~----~~i~l~v~~~n~~~~~~~~~~~ 98 (219)

++++..+|++||++.+... ..+..++|+|++|++|+++.|++.+++.+.+ ..+.+.+...|. .

T Consensus 47 ~~~~~~~~~ivG~~~~~~~~~~~~~i~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~~~~~~~~~~n~---------~ 117 (146)

T d2fl4a1 47 SAGIYDGNQLIGYAMYGRWQDGRVWLDRFLIDQRFQGQGYGKAACRLLMLKLIEKYQTNKLYLSVYDTNS---------S 117 (146)

T ss\_dssp EEEEEETTEEEEEEEEEECTTSCEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHHSSCSEEEEEECTTCH---------H

T ss\_pred EEEEEcCCeEEEEEEEEEecCCeEEEEEeEECHHHCCCCHHHHHHHHHHHHHHHhhcCCeEEEEEecCCH---------H

Q ss\_pred hHHHHHcCCCEEeeee

Q Phabba\_Draft 99 SDPDYHDPGDQNVTKA 114 (219)

Q Consensus 99 ~~~~y~r~Gf~~~~~~ 114 (219)

+.++|+++||+..+..

T Consensus 118 ~~~~~~~~Gf~~~~~~ 133 (146)

T d2fl4a1 118 AIRLYQQLGFVFNGEL 133 (146)

T ss\_dssp HHHHHHHTTCEEEEEE

T ss\_pred HHHHHHHcCCEEEeEe

No 104

>1TIQ\_A Protease synthase and sporulation negative; alpha-beta protein, Structural Genomics, PSI; HET: COA, DTT; 1.9A {Bacillus subtilis} SCOP: d.108.1.1

Probab=98.47 E-value=6.2e-08 Score=75.46 Aligned\_cols=99 Identities=17% Similarity=0.152 Sum\_probs=0.0 Template\_Neff=12.300

Q ss\_pred CCchHHHHHhhCCc--EEEEEECCEEEEEEEEEeCC-----------EEEEEEECHHHCCCCHHHHHHHHHHHcccc---

Q Phabba\_Draft 13 LKFEPFDTMWSNGI--MARHAHDDRPVGHLHWHPDG-----------EIDSITVHPDLQRRGIGTAMLKHAQDNPHI--- 76 (219)

Q Consensus 13 ~~~~~l~~~~~~~~--~~v~~~~~~liG~~~~~~~~-----------~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~--- 76 (219)

+..+.+...+.... ++++..+|++||++.+.... .+..++|+|++|++|+|+.|++.+++.++.

T Consensus 45 ~~~~~~~~~~~~~~~~~~~~~~~~~ivG~~~~~~~~~~~~~~~~~~~~i~~~~v~~~~r~~G~~~~l~~~~~~~~~~~g~ 124 (180)

T 1TIQ\_A 45 FNTEQLEKELSNMSSQFFFIYFDHEIAGYVKVNIDDAQSEEMGAESLEIERIYIKNSFQKHGLGKHLLNKAIEIALERNK 124 (180)

T ss\_dssp SSHHHHHHHHHCTTEEEEEEEETTEEEEEEEEEEGGGSSSCCCTTEEEEEEEEECGGGCSSSHHHHHHHHHHHHHHHTTC

T ss\_pred cCHHHHHHHhhcCCeeEEEEEECCEEEEEEEEEecchhchhhcCCEEEEEEEEECHHHCCCCHHHHHHHHHHHHHHHcCC

Q ss\_pred CeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeeeccccc

Q Phabba\_Draft 77 YESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDVSN 120 (219)

Q Consensus 77 ~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~ 120 (219)

..+.+.+...|. .+.++|+++||+..+.....+..

T Consensus 125 ~~i~~~~~~~n~---------~~~~~~~k~Gf~~~~~~~~~~~~ 159 (180)

T 1TIQ\_A 125 KNIWLGVWEKNE---------NAIAFYKKMGFVQTGAHSFYMGD 159 (180)

T ss\_dssp SEEEEEEETTCH---------HHHHHHHHTTCEEEEEEEEEETT

T ss\_pred CEEEEEEEcCCH---------HHHHHHHHcCCEEecceeEEeCC

No 105

>1S3Z\_B aminoglycoside 6'-N-acetyltransferase (E.C.2.3.1.82); GNAT, N-acetyltransferase, acetyltransferase, aminoglycoside, CoA; HET: COA, RIO, SO4; 2.0A {Salmonella enteritidis} SCOP: d.108.1.1

Probab=98.46 E-value=3.3e-08 Score=76.22 Aligned\_cols=107 Identities=12% Similarity=0.069 Sum\_probs=0.0 Template\_Neff=12.100

Q ss\_pred CCccccCCCCCCCCchHHHHHhhCCc--EEEEEECCEEEEEEEEE------------eCCEEEEEEECHHHCCCCHHHHH

Q Phabba\_Draft 1 MHQAGANGDLPPLKFEPFDTMWSNGI--MARHAHDDRPVGHLHWH------------PDGEIDSITVHPDLQRRGIGTAM 66 (219)

Q Consensus 1 ~~~~~~~~~~~~~~~~~l~~~~~~~~--~~v~~~~~~liG~~~~~------------~~~~i~~l~V~p~~R~~Gig~~L 66 (219)

+..............+.+........ ++++.++|++||++.+. ....+..++|+|++|++|+|+.|

T Consensus 37 l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ivG~~~~~~~~~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l 116 (165)

T 1S3Z\_B 37 LRKQLWPGHPDDAHLADGEEILQADHLASFIAMADGVAIGFADASIRHDYVNGCDSSPVVFLEGIFVLPSFRQRGVAKQL 116 (165)

T ss\_dssp HHHHHCTTSCHHHHHHHHHHHHHCTTEEEEEEEETTEEEEEEEEEEECSCCTTCCSSSEEEEEEEEECGGGCSSSHHHHH

T ss\_pred HHHHHCCCCCChhhhHhHHHHhhcCCcEEEEEEECCEEEEEEEEEEecccCCCCCCCCEEEEEEEEECHHHcCCCHHHHH

Q ss\_pred HHHHHHcccc---CeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeeec

Q Phabba\_Draft 67 LKHAQDNPHI---YESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADD 116 (219)

Q Consensus 67 l~~~~~~~~~---~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~ 116 (219)

++.+++.++. ..+.+.+...|. .+.++|+++||+..+....

T Consensus 117 ~~~~~~~~~~~~~~~i~~~~~~~n~---------~~~~~~~~~Gf~~~~~~~~ 160 (165)

T 1S3Z\_B 117 IAAVQRWGTNKGCREMASDTSPENT---------ISQKVHQALGFEETERVIF 160 (165)

T ss\_dssp HHHHHHHHHHTTCSEEEEEECTTCH---------HHHHHHHHTTCEEEEEEEE

T ss\_pred HHHHHHHHHhcCCcEEEEecCCCCH---------HHHHHHHHhCCEEeEEEEE

No 106

>d1ufhb\_ d.108.1.1 (B:) Putative acetyltransferase YycN {Bacillus subtilis [TaxId: 1423]}

Probab=98.46 E-value=3.9e-08 Score=73.62 Aligned\_cols=84 Identities=14% Similarity=0.107 Sum\_probs=0.0 Template\_Neff=12.900

Q ss\_pred hCCcEEEEEE-CCEEEEEEEEEeC-------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEEEcCCcccc

Q Phabba\_Draft 23 SNGIMARHAH-DDRPVGHLHWHPD-------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPVRHSSHFSA 91 (219)

Q Consensus 23 ~~~~~~v~~~-~~~liG~~~~~~~-------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v~~~n~~~~ 91 (219)

....++++.. ++++||++.+... ..+..++|+|++||+|+|+.|++.+++.+++ ..+.+.+...|.

T Consensus 56 ~~~~~~~~~~~~~~ivG~~~~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~~g~~~i~~~~~~~n~--- 132 (154)

T d1ufhb\_ 56 PHHHLWSLKLNEKDIVGWLWIHAEPEHPQQEAFIYDFGLYEPYRGKGYAKQALAALDQAARSMGIRKLSLHVFAHNQ--- 132 (154)

T ss\_dssp TTEEEEEEEEETTEEEEEEEEECCTTCTTCEEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHHTCCEEEECCCTTCH---

T ss\_pred CCEEEEEEEeCCCcEEEEEEEEeCCCCccceEEEEEEEeCHhhCCCCHHHHHHHHHHHHHHhCCCCEEEEEEEcCCH---

Q ss\_pred cccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 92 AGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 92 ~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

.+.++|+|+||+..+...

T Consensus 133 ------~~~~~~~k~Gf~~~~~~~ 150 (154)

T d1ufhb\_ 133 ------TARKLYEQTGFQETDVVM 150 (154)

T ss\_dssp ------HHHHHHHHTTCCCCCCCC

T ss\_pred ------HHHHHHHHcCCeEeEEee

No 107

>d3i9sd\_ d.108.1.0 (D:) automated matches {Vibrio cholerae [TaxId: 666]}

Probab=98.46 E-value=4.8e-08 Score=73.95 Aligned\_cols=92 Identities=12% Similarity=0.164 Sum\_probs=0.0 Template\_Neff=12.700

Q ss\_pred hHHHHHh----hCCcEEEEEECCEEEEEEEEEeC---------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---Cee

Q Phabba\_Draft 16 EPFDTMW----SNGIMARHAHDDRPVGHLHWHPD---------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YES 79 (219)

Q Consensus 16 ~~l~~~~----~~~~~~v~~~~~~liG~~~~~~~---------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i 79 (219)

+.+.... ....++++..+|++||++.+... ..+..++|+|++|++|+++.|++.+++.+.+ ..+

T Consensus 38 ~~~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~i 117 (160)

T d3i9sd\_ 38 NYLSHQVFSEHSGVKVIAAVEHDKVLGFATYTIMFPAPKLSGQMYMKDLFVSSSARGKGIGLQLMKHLATIAITHNCQRL 117 (160)

T ss\_dssp HHCCCCCTSTTCCCEEEEEEETTEEEEEEEEEEECCCTTTCEEEEEEEEEECGGGTTSCHHHHHHHHHHHHHHHTTEEEE

T ss\_pred HHHHhhccccCCceEEEEEEECCeEeEEEEEEEecCCcccCCeeEEEEEEECHHHCCCCHHHHHHHHHHHHHHhCCCCEE

Q ss\_pred EEEEEcCCcccccccccchhHHHHHcCCCEEeeeeec

Q Phabba\_Draft 80 SYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADD 116 (219)

Q Consensus 80 ~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~ 116 (219)

.+.+...|. .+.++|+++||+..+....

T Consensus 118 ~~~~~~~n~---------~~~~~~~~~Gf~~~~~~~~ 145 (160)

T d3i9sd\_ 118 DWTAESTNP---------TAGKFYKSIGASLIREKEY 145 (160)

T ss\_dssp EEEEETTCH---------HHHHHHHHTTCEECTTEEE

T ss\_pred EEEecCCCH---------HHHHHHHHcCCEEecceeE

No 108

>3F5B\_A Aminoglycoside N(6')acetyltransferase; APC60744, aminoglycoside N(6')acetyltransferase, Legionella pneumophila; HET: FMT; 2.0A {Legionella pneumophila subsp. pneumophila}

Probab=98.46 E-value=8.3e-08 Score=74.91 Aligned\_cols=110 Identities=11% Similarity=0.013 Sum\_probs=0.0 Template\_Neff=12.300

Q ss\_pred CCCCCCCchHHHHHhhC----CcEEEEEECCEEEEEEEEE----------eCCEEEEEEECHHHCCCCHHHHHHHHHHHc

Q Phabba\_Draft 8 GDLPPLKFEPFDTMWSN----GIMARHAHDDRPVGHLHWH----------PDGEIDSITVHPDLQRRGIGTAMLKHAQDN 73 (219)

Q Consensus 8 ~~~~~~~~~~l~~~~~~----~~~~v~~~~~~liG~~~~~----------~~~~i~~l~V~p~~R~~Gig~~Ll~~~~~~ 73 (219)

....+...+.+...+.. ..++++.++|++||++.+. ....+..+.|+|++|++|+|+.|++.+++.

T Consensus 43 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~~i~~~~v~~~~r~~Gi~~~l~~~~~~~ 122 (182)

T 3F5B\_A 43 GDGLSNTIKDLHEFLNDGKPWATHWIAYDNEIPFAYLITSEIEKSEEYPDGAVTLDLFICRLDYIGKGLSVQMIHEFILS 122 (182)

T ss\_dssp HHHHHHHHHHHHHHHTTSCCSSEEEEEEETTEEEEEEEEEEECSCSSCTTCEEEEEEEECSGGGCCHHHHHHHHHHHHHH

T ss\_pred CCCCchhHHHHHHHHhcCCCceeEEEEEECCeEEEEEEEEecCCCcCCCCCeEEEEEEEeCHHHCCCCHHHHHHHHHHHH

Q ss\_pred ccc--CeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeeeccccccceEEe

Q Phabba\_Draft 74 PHI--YESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDVSNWGYTAM 126 (219)

Q Consensus 74 ~~~--~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~~~~~~~ 126 (219)

++. ..+.+.+...|. .+.++|+++||+..+.............+

T Consensus 123 ~~~~~~~~~~~~~~~n~---------~~~~~~~~~Gf~~~~~~~~~~~~~~~~~m 168 (182)

T 3F5B\_A 123 QFSDTKIVLINPEISNE---------RAVHVYKKAGFEIIGEFIASWHPVPHYKM 168 (182)

T ss\_dssp HCTTCSEEEECCBTTCH---------HHHHHHHHHTCEEEEEEEETTEEEEEEEE

T ss\_pred HcCCCCeEEEecccccH---------HHHHHHHHcCCEEEeeeEecCCccceeee

No 109

>2OB0\_C Human MAK3 homolog; acetyltransferase, Structural Genomics Consortium, SGC; HET: ACO; 1.8A {Homo sapiens}

Probab=98.46 E-value=7.6e-08 Score=74.57 Aligned\_cols=99 Identities=18% Similarity=0.127 Sum\_probs=0.0 Template\_Neff=12.100

Q ss\_pred CCCCchHHHHHhhCCc-EEEEEECCEEEEEEEEEeC-------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc----Ce

Q Phabba\_Draft 11 PPLKFEPFDTMWSNGI-MARHAHDDRPVGHLHWHPD-------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI----YE 78 (219)

Q Consensus 11 ~~~~~~~l~~~~~~~~-~~v~~~~~~liG~~~~~~~-------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~----~~ 78 (219)

.......+........ ++++..++++||++.+... .++..++|+|++|++|+|..|++.+++.+.. ..

T Consensus 30 ~~~~~~~~~~~~~~~~~~~~~~~~~~ivG~~~~~~~~~~~~~~~~i~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~~ 109 (170)

T 2OB0\_C 30 VSYNDKFYKDVLEVGELAKLAYFNDIAVGAVCCRVDHSQNQKRLYIMTLGCLAPYRRLGIGTKMLNHVLNICEKDGTFDN 109 (170)

T ss\_dssp SCCCHHHHHHHTTSGGGEEEEEETTEEEEEEEEEEEEETTEEEEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHHCCCSE

T ss\_pred CCcchHHHHHHhhccCeEEEEEeCCeEEEEEEEEEcCCcCCcEEEEEEEEECHHHcCCChHHHHHHHHHHHHHHcCCCCE

Q ss\_pred eEEEEEcCCcccccccccchhHHHHHcCCCEEeeeeeccc

Q Phabba\_Draft 79 SSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDV 118 (219)

Q Consensus 79 i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~ 118 (219)

+.+.+...|. .+.++|+++||+..+......

T Consensus 110 ~~~~~~~~n~---------~~~~~~~~~Gf~~~~~~~~~~ 140 (170)

T 2OB0\_C 110 IYLHVQISNE---------SAIDFYRKFGFEIIETKKNYY 140 (170)

T ss\_dssp EEEEEETTCH---------HHHHHHHHTTCEEEEEETTCC

T ss\_pred EEEEEEeCCH---------HHHHHHHHcCCEEEEEeecee

No 110

>2OB0\_A Human MAK3 homolog; acetyltransferase, Structural Genomics Consortium, SGC; HET: ACO; 1.8A {Homo sapiens}

Probab=98.46 E-value=7.6e-08 Score=74.57 Aligned\_cols=99 Identities=18% Similarity=0.127 Sum\_probs=0.0 Template\_Neff=12.100

Q ss\_pred CCCCchHHHHHhhCCc-EEEEEECCEEEEEEEEEeC-------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc----Ce

Q Phabba\_Draft 11 PPLKFEPFDTMWSNGI-MARHAHDDRPVGHLHWHPD-------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI----YE 78 (219)

Q Consensus 11 ~~~~~~~l~~~~~~~~-~~v~~~~~~liG~~~~~~~-------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~----~~ 78 (219)

.......+........ ++++..++++||++.+... .++..++|+|++|++|+|..|++.+++.+.. ..

T Consensus 30 ~~~~~~~~~~~~~~~~~~~~~~~~~~ivG~~~~~~~~~~~~~~~~i~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~~ 109 (170)

T 2OB0\_A 30 VSYNDKFYKDVLEVGELAKLAYFNDIAVGAVCCRVDHSQNQKRLYIMTLGCLAPYRRLGIGTKMLNHVLNICEKDGTFDN 109 (170)

T ss\_dssp SCCCHHHHHHHTTSGGGEEEEEETTEEEEEEEEEEEEETTEEEEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHHCCCSE

T ss\_pred CCcchHHHHHHhhccCeEEEEEeCCeEEEEEEEEEcCCcCCcEEEEEEEEECHHHcCCChHHHHHHHHHHHHHHcCCCCE

Q ss\_pred eEEEEEcCCcccccccccchhHHHHHcCCCEEeeeeeccc

Q Phabba\_Draft 79 SSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDV 118 (219)

Q Consensus 79 i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~ 118 (219)

+.+.+...|. .+.++|+++||+..+......

T Consensus 110 ~~~~~~~~n~---------~~~~~~~~~Gf~~~~~~~~~~ 140 (170)

T 2OB0\_A 110 IYLHVQISNE---------SAIDFYRKFGFEIIETKKNYY 140 (170)

T ss\_dssp EEEEEETTCH---------HHHHHHHHTTCEEEEEETTCC

T ss\_pred EEEEEEeCCH---------HHHHHHHHcCCEEEEEeecee

No 111

>1XEB\_A PA0115, Acyl-CoA N-acyltransferase, APC22065; Midwest Center for Structural Genomics; 2.35A {Pseudomonas aeruginosa} SCOP: d.108.1.1

Probab=98.46 E-value=2.5e-08 Score=75.69 Aligned\_cols=85 Identities=12% Similarity=0.032 Sum\_probs=0.0 Template\_Neff=12.100

Q ss\_pred hCCcEEEEEECCEEEEEEEEEeC------CEEEEEEECHHHCCCCHHHHHHHHHHHccccCeeE-EEEEcCCcccccccc

Q Phabba\_Draft 23 SNGIMARHAHDDRPVGHLHWHPD------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHIYESS-YPVRHSSHFSAAGRA 95 (219)

Q Consensus 23 ~~~~~~v~~~~~~liG~~~~~~~------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~~~i~-l~v~~~n~~~~~~~~ 95 (219)

....++++.+++++||++.+... ..+..++|+|++||+|+|+.|++.+++.+...... ..+...|.

T Consensus 47 ~~~~~~~~~~~~~ivG~~~~~~~~~~~~~~~i~~~~v~~~~r~~G~~~~l~~~~~~~~~~~~~~~~~~~~~n~------- 119 (150)

T 1XEB\_A 47 GDTHHLMAWRDGQLLAYLRLLDPVRHEGQVVIGRVVSSSAARGQGLGHQLMERALQAAERLWLDTPVYLSAQA------- 119 (150)

T ss\_dssp TTCEEEEEEETTEEEEEEEEECSTTTTTCEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHHHTTCCEEEEEES-------

T ss\_pred CCEEEEEEEeCCeEEEEEEEEcCccCCCeEEEEEEEECHHHCCCCHHHHHHHHHHHHHHHcCCCCCEEEeccH-------

Q ss\_pred cchhHHHHHcCCCEEeeeeec

Q Phabba\_Draft 96 WAQSDPDYHDPGDQNVTKADD 116 (219)

Q Consensus 96 ~~~~~~~y~r~Gf~~~~~~~~ 116 (219)

.+.++|+++||+..+....

T Consensus 120 --~~~~~~~~~Gf~~~~~~~~ 138 (150)

T 1XEB\_A 120 --HLQAYYGRYGFVAVTEVYL 138 (150)

T ss\_dssp --TTHHHHHTTTEEECSCCEE

T ss\_pred --HHHHHHHHcCcEEcceeec

No 112

>3OWC\_A Probable acetyltransferase; Structural Genomics, PSI-Biology, Protein Structure; HET: COA, EDO; 1.9A {Pseudomonas aeruginosa}

Probab=98.46 E-value=9e-08 Score=75.25 Aligned\_cols=105 Identities=17% Similarity=0.190 Sum\_probs=0.0 Template\_Neff=12.200

Q ss\_pred CccccCCCCCCCCchHHHHHhhC-------CcEEEEEECCEEEEEEEEEeC-----CEEEEEEECHHHCCCCHHHHHHHH

Q Phabba\_Draft 2 HQAGANGDLPPLKFEPFDTMWSN-------GIMARHAHDDRPVGHLHWHPD-----GEIDSITVHPDLQRRGIGTAMLKH 69 (219)

Q Consensus 2 ~~~~~~~~~~~~~~~~l~~~~~~-------~~~~v~~~~~~liG~~~~~~~-----~~i~~l~V~p~~R~~Gig~~Ll~~ 69 (219)

..........+...+.+...+.. ..++++..++++||++.+... ..+..++|+|++|++|+|+.|++.

T Consensus 38 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ivG~~~~~~~~~~~~~~i~~~~v~~~~r~~gi~~~l~~~ 117 (188)

T 3OWC\_A 38 VQWAGPALRHPLSLEQMHEDLAESRRRPPLRLLWSACRDDQVIGHCQLLFDRRNGVVRLARIVLAPSARGQGLGLPMLEA 117 (188)

T ss\_dssp HHHHCTTCCSSCCGGGGHHHHHHHHSSSCSEEEEEEEETTEEEEEEEEEEETTTTEEEEEEEEECGGGTTSSCHHHHHHH

T ss\_pred eecccCCCCCCCCHHHHHHHHHHHccCCCccEEEEEEeCCeEEEEEEEEecCCCCeEEEEEEEECHHHCCCChHHHHHHH

Q ss\_pred HHHcc-cc---CeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 70 AQDNP-HI---YESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 70 ~~~~~-~~---~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

+++.+ +. ..+.+.+...|. .+.++|+++||+..+...

T Consensus 118 ~~~~~~~~~~~~~i~~~~~~~n~---------~~~~~~~~~Gf~~~~~~~ 158 (188)

T 3OWC\_A 118 LLAEAFADADIERVELNVYDWNA---------AARHLYRRAGFREEGLRR 158 (188)

T ss\_dssp HHHHHHHSTTCCEEEEEEETTCH---------HHHHHHHHTTCEEEEEEE

T ss\_pred HHHHHHHcCCCCEEEEEEecCCH---------HHHHHHHHcCCeEEEEEe

No 113

>3D8P\_B acetyltransferase of GNAT family; NP\_373092.1, acetyltransferase of GNAT family; HET: ACT, EDO; 2.2A {Staphylococcus aureus subsp. aureus Mu50}

Probab=98.46 E-value=4.7e-08 Score=74.08 Aligned\_cols=93 Identities=11% Similarity=0.030 Sum\_probs=0.0 Template\_Neff=12.800

Q ss\_pred chHHHHHhhCCc-EEEEEEC-CEEEEEEEEEeC----CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEEEc

Q Phabba\_Draft 15 FEPFDTMWSNGI-MARHAHD-DRPVGHLHWHPD----GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPVRH 85 (219)

Q Consensus 15 ~~~l~~~~~~~~-~~v~~~~-~~liG~~~~~~~----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v~~ 85 (219)

............ ++++..+ +++||++.+... ..+..+.|+|++|++|+++.|++.+++.+.. ..+.+.+..

T Consensus 42 ~~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~~~~~~~~ 121 (163)

T 3D8P\_B 42 ENIEHNYLNSGGQFWLAINNHQNIVGTIGLIRLDNNMSALKKMFVDKGYRNLKIGKKLLDKVIMTCKEQNIDGIYLGTID 121 (163)

T ss\_dssp GCHCCCCCTTTCEEEEEECTTCCEEEEEEEEECSTTEEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHTTCCEEEEEECT

T ss\_pred HHHHHHhcccCCEEEEEECCCCCEEEEEEEEEcCCCeEEEEEEEEChhhcCCCHHHHHHHHHHHHHHHCCCCeEEEEecc

Q ss\_pred CCcccccccccchhHHHHHcCCCEEeeeeec

Q Phabba\_Draft 86 SSHFSAAGRAWAQSDPDYHDPGDQNVTKADD 116 (219)

Q Consensus 86 ~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~ 116 (219)

.|. .+.++|+++||+..+....

T Consensus 122 ~n~---------~~~~~~~~~Gf~~~~~~~~ 143 (163)

T 3D8P\_B 122 KFI---------SAQYFYSNNGFREIKRGDL 143 (163)

T ss\_dssp TSH---------HHHHHHHTTTCEEECGGGS

T ss\_pred cch---------hHHHHHHhCCcEEeeeCCC

No 114

>3D8P\_A acetyltransferase of GNAT family; NP\_373092.1, acetyltransferase of GNAT family; HET: EDO, ACT; 2.2A {Staphylococcus aureus subsp. aureus Mu50}

Probab=98.46 E-value=4.7e-08 Score=74.08 Aligned\_cols=93 Identities=11% Similarity=0.030 Sum\_probs=0.0 Template\_Neff=12.800

Q ss\_pred chHHHHHhhCCc-EEEEEEC-CEEEEEEEEEeC----CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEEEc

Q Phabba\_Draft 15 FEPFDTMWSNGI-MARHAHD-DRPVGHLHWHPD----GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPVRH 85 (219)

Q Consensus 15 ~~~l~~~~~~~~-~~v~~~~-~~liG~~~~~~~----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v~~ 85 (219)

............ ++++..+ +++||++.+... ..+..+.|+|++|++|+++.|++.+++.+.. ..+.+.+..

T Consensus 42 ~~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~~~~~~~~ 121 (163)

T 3D8P\_A 42 ENIEHNYLNSGGQFWLAINNHQNIVGTIGLIRLDNNMSALKKMFVDKGYRNLKIGKKLLDKVIMTCKEQNIDGIYLGTID 121 (163)

T ss\_dssp GCHCCCCCTTTCEEEEEECTTCCEEEEEEEEECSTTEEEEEEEEECGGGTTTTHHHHHHHHHHHHHHHTTCCEEEEEECT

T ss\_pred HHHHHHhcccCCEEEEEECCCCCEEEEEEEEEcCCCeEEEEEEEEChhhcCCCHHHHHHHHHHHHHHHCCCCeEEEEecc

Q ss\_pred CCcccccccccchhHHHHHcCCCEEeeeeec

Q Phabba\_Draft 86 SSHFSAAGRAWAQSDPDYHDPGDQNVTKADD 116 (219)

Q Consensus 86 ~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~ 116 (219)

.|. .+.++|+++||+..+....

T Consensus 122 ~n~---------~~~~~~~~~Gf~~~~~~~~ 143 (163)

T 3D8P\_A 122 KFI---------SAQYFYSNNGFREIKRGDL 143 (163)

T ss\_dssp TCH---------HHHHHHHHTTCEEECGGGS

T ss\_pred cch---------hHHHHHHhCCcEEeeeCCC

No 115

>PF09390.9 ; DUF1999 ; Protein of unknown function (DUF1999)

Probab=98.46 E-value=2e-08 Score=78.91 Aligned\_cols=89 Identities=11% Similarity=0.089 Sum\_probs=0.0 Template\_Neff=10.300

Q ss\_pred chHHHHHhhCCcEEEEEECCEEEEEEEEEeC-------CEEEEEEECHHHCCC---CHHHHHHHHHHHcccc---Cee--

Q Phabba\_Draft 15 FEPFDTMWSNGIMARHAHDDRPVGHLHWHPD-------GEIDSITVHPDLQRR---GIGTAMLKHAQDNPHI---YES-- 79 (219)

Q Consensus 15 ~~~l~~~~~~~~~~v~~~~~~liG~~~~~~~-------~~i~~l~V~p~~R~~---Gig~~Ll~~~~~~~~~---~~i-- 79 (219)

...+...++...++++..+++++|++.+... .++..++|+|++|++ |||+.|++.+++.+++ ..+

T Consensus 43 ~~~~~~~~~~~~~~v~~~~~~ivG~~~~~~~~~~~~~~~~i~~l~V~p~~r~~~~~Gig~~Ll~~~~~~a~~~g~~~i~l 122 (155)

T F0RM83\_DEIPM/1 43 LGALKFYERTDHSFVAVRDGAVAGMVLAQSVWQGDKPIVLVRTLLTDPALPEALRAEVYSGLLRALFKSAYDTAVYEVHF 122 (155)

T ss\_pred HHHHHHHhcCCcEEEEEECCEEEEEEEEEEEecCCCcEEEEEEEEEChhhCccccCCHHHHHHHHHHHHHHHcCCcEEEE

Q ss\_pred ----EEEEEcCCcccccccccchhHHHHHcCCCEEeee

Q Phabba\_Draft 80 ----SYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTK 113 (219)

Q Consensus 80 ----~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~ 113 (219)

.+.+...|. .+..+ +++||+..+.

T Consensus 123 ~~~~~l~~~~~~~---------~~~~~-~~~Gf~~~~~ 150 (155)

T F0RM83\_DEIPM/1 123 VPHRRWPLAADLG---------DVRRL-GDYGVRYLGS 150 (155)

T ss\_pred ecCCCCCccCCch---------HHHHH-HhcceEEeee

No 116

>4E2A\_B Putative acetyltransferase; Alpha Beta, Alpha and Beta; 2.0A {Streptococcus mutans}

Probab=98.45 E-value=5.7e-08 Score=78.99 Aligned\_cols=100 Identities=15% Similarity=0.075 Sum\_probs=0.0 Template\_Neff=11.200

Q ss\_pred chHHHHHhhCCc--EEEEEECCEEEEEEEEEe---------C--CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---Ce

Q Phabba\_Draft 15 FEPFDTMWSNGI--MARHAHDDRPVGHLHWHP---------D--GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YE 78 (219)

Q Consensus 15 ~~~l~~~~~~~~--~~v~~~~~~liG~~~~~~---------~--~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~ 78 (219)

...+...+.... ++++.+++++||++.+.. . ..+..++|+|++|++|+|+.|++.+++.++. ..

T Consensus 82 ~~~~~~~~~~~~~~~~~~~~~~~iVG~~~~~~~~~~~~~~~~~~~~i~~~~v~~~~rg~Gi~~~ll~~~~~~~~~~g~~~ 161 (207)

T 4E2A\_B 82 LSVLKLELDDKESETYFILMSGKAAGFLKVNWGSSQTEQVLEDAFEIQRLYILKAYQGLGLGKQLFEFALERAQISGLSW 161 (207)

T ss\_dssp HHHHHHHHHCTTEEEEEEEETTEEEEEEEEEEGGGSSSCCSSSEEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHHTCSE

T ss\_pred HHHHhHhhcCCCceEEEEEECCeEEEEEEEEeCccCcccccCceEEEEEEEECHHHCCCCHHHHHHHHHHHHHHHcCCCE

Q ss\_pred eEEEEEcCCcccccccccchhHHHHHcCCCEEeeeeeccccccce

Q Phabba\_Draft 79 SSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDVSNWGY 123 (219)

Q Consensus 79 i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~~~~ 123 (219)

+.+.+...|. .+.++|+++||+..+......+....

T Consensus 162 i~~~~~~~n~---------~~~~~~~k~Gf~~~~~~~~~~~~~~~ 197 (207)

T 4E2A\_B 162 VWLGVWEKNV---------KAQLLYAKYGFEQFSKHSFFVGNKVD 197 (207)

T ss\_dssp EEEEEETTCH---------HHHHHHHHTTCEEEEEEEEEETTEEE

T ss\_pred EEEEEecCCH---------HHHHHHHHcCCEEeeeEEEEeCCEEe

No 117

>1YK3\_F Hypothetical protein Rv1347c/MT1389; acyltransferase, GCN5-related fold, Structural Genomics; HET: BOG; 2.2A {Mycobacterium tuberculosis} SCOP: d.108.1.1

Probab=98.45 E-value=7.4e-08 Score=77.68 Aligned\_cols=110 Identities=10% Similarity=0.029 Sum\_probs=0.0 Template\_Neff=11.800

Q ss\_pred chHHHHHhhCCc--EEEEEECCEEEEEEEE---------------EeCCEEEEEEECHHHCCCCHHHHHHHHHHHccc--

Q Phabba\_Draft 15 FEPFDTMWSNGI--MARHAHDDRPVGHLHW---------------HPDGEIDSITVHPDLQRRGIGTAMLKHAQDNPH-- 75 (219)

Q Consensus 15 ~~~l~~~~~~~~--~~v~~~~~~liG~~~~---------------~~~~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~-- 75 (219)

.+.+...+.... ++++..++++||++.+ .....+..++|+|++||+|+|+.|++.+++.+.

T Consensus 79 ~~~~~~~~~~~~~~~~v~~~~~~~vG~~~~~~~~~~~~~~~~~~~~~~~~i~~~~v~~~~r~~Gi~~~ll~~~~~~~~~~ 158 (210)

T 1YK3\_F 79 RQHLNAQLEGTYSLPLIGSWHGTDGGYLELYWAAKDLISHYYDADPYDLGLHAAIADLSKVNRGFGPLLLPRIVASVFAN 158 (210)

T ss\_dssp HHHHHHHHHSSSEEEEEEEETTEEEEEEEEEEGGGBGGGGSSCCCTTCEEEEEEESCHHHHHTTHHHHHHHHHHHHHHHH

T ss\_pred HHHHHHHhcCCccccEEEEECCeEEEEEEEEehhHhhhhhccCCCccceEEEEEEeCHHHcCCChHHHHHHHHHHHHHcC

Q ss\_pred c---CeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeeeccccccceEEecCCCCCC

Q Phabba\_Draft 76 I---YESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDVSNWGYTAMGEEGYTP 133 (219)

Q Consensus 76 ~---~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~~~~~~~~~~~~~~ 133 (219)

. ..+.+.+...|. .+.++|+++||+..+....................+

T Consensus 159 ~~~~~~i~~~~~~~n~---------~~~~~~~k~GF~~~~~~~~~~~~~~~~~~~~~~~~~ 210 (210)

T 1YK3\_F 159 EPRCRRIMFDPDHRNT---------ATRRLCEWAGCKFLGEHDTTNRRMALYALEAPTTAA 210 (210)

T ss\_dssp CTTCCEEEECCBTTCH---------HHHHHHHHTTCEEEEEEEETTEEEEEEEEECCCCC-

T ss\_pred CCCccEEEEcccCCCH---------HHHHHHHHcCCEEEEEEECCCceEEEEEEccCCcCC

No 118

>1MK4\_A Hypothetical protein yqjY; alpha-beta-alpha sandwich, Structural Genomics, PSI; 1.7A {Bacillus subtilis} SCOP: d.108.1.1

Probab=98.45 E-value=5.7e-08 Score=73.98 Aligned\_cols=83 Identities=13% Similarity=0.051 Sum\_probs=0.0 Template\_Neff=12.300

Q ss\_pred CCcEEEEEECCEEEEEEEEEeC------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEEEcCCccccccc

Q Phabba\_Draft 24 NGIMARHAHDDRPVGHLHWHPD------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPVRHSSHFSAAGR 94 (219)

Q Consensus 24 ~~~~~v~~~~~~liG~~~~~~~------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v~~~n~~~~~~~ 94 (219)

...++++..+++++|++.+... ..+..++|+|++|++|+|+.|++.+++.+.. ..+.+.+...|.

T Consensus 41 ~~~~~~~~~~~~ivG~~~~~~~~~~~~~~~i~~~~v~~~~r~~g~~~~l~~~~~~~~~~~g~~~i~~~~~~~n~------ 114 (157)

T 1MK4\_A 41 QDTSFITSEHNSMTGFLIGFQSQSDPETAYIHFSGVHPDFRKMQIGKQLYDVFIETVKQRGCTRVKCVTSPVNK------ 114 (157)

T ss\_dssp GGGCEEEESSSSEEEEEEEEECSSSTTEEEEEEEEECTTSCHHHHHHHHHHHHHHHHHTTTCCEEEEEECTTCH------

T ss\_pred CCCeEEEEeCCeEEEEEEEEeCCCCCCeEEEEEEEECHHHCCCCHHHHHHHHHHHHHHHCCCCEEEEEEcCCCc------

Q ss\_pred ccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 95 AWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 95 ~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

.+.++|+++||+..+...

T Consensus 115 ---~~~~~~~k~Gf~~~~~~~ 132 (157)

T 1MK4\_A 115 ---VSIAYHTKLGFDIEKGTK 132 (157)

T ss\_dssp ---HHHHHHHHTTCEECCCSE

T ss\_pred ---hHHHHHHHcCCEEeeEee

No 119

>4PV6\_A N-terminal acetyltransferase complex subunit [ARD1]; N-terminal acetyltransferase, transferase; HET: COA, ACO; 3.32A {Thermoplasma volcanium}

Probab=98.45 E-value=5.4e-08 Score=75.51 Aligned\_cols=88 Identities=15% Similarity=0.085 Sum\_probs=0.0 Template\_Neff=11.600

Q ss\_pred CCcEEEEEECCEEEEEEEEEeC----CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEEEcCCccccccccc

Q Phabba\_Draft 24 NGIMARHAHDDRPVGHLHWHPD----GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPVRHSSHFSAAGRAW 96 (219)

Q Consensus 24 ~~~~~v~~~~~~liG~~~~~~~----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v~~~n~~~~~~~~~ 96 (219)

...++++..+|++||++.+... ..+..++|+|++|++|+|+.|++.+.+.+++ ..+.+.+...|.

T Consensus 49 ~~~~~~~~~~~~ivG~~~~~~~~~~~~~i~~~~v~~~~r~~gig~~l~~~~~~~~~~~g~~~i~~~~~~~n~-------- 120 (162)

T 4PV6\_A 49 PESFMVYTVAGSVVGFIVGSKYSRTEARILLFAVDERFRRMGVGSALMDAFLSLCREQNMLSVRLEVRTDND-------- 120 (162)

T ss\_dssp GGGCEEEESSSCEEEEEEEEESSSSEEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHTTCCEEEEEEESSCH--------

T ss\_pred CCceEEEEECCEEEEEEEEEecCCCEEEEEEEEECHHHCCCCHHHHHHHHHHHHHHHCCCcEEEEEEecCCH--------

Q ss\_pred chhHHHHHcCCCEEeeeeeccccc

Q Phabba\_Draft 97 AQSDPDYHDPGDQNVTKADDDVSN 120 (219)

Q Consensus 97 ~~~~~~y~r~Gf~~~~~~~~~~~~ 120 (219)

.+.++|+++||+..+........

T Consensus 121 -~~~~~~~~~Gf~~~~~~~~~~~~ 143 (162)

T 4PV6\_A 121 -EAIRFYKKYGFVITAMLPNYYSD 143 (162)

T ss\_dssp -HHHHHHHHTTCEEEEEETTCSTT

T ss\_pred -HHHHHHHHcCCEEEEEEehhhcC

No 120

>4PV6\_H N-terminal acetyltransferase complex subunit [ARD1]; N-terminal acetyltransferase, transferase; HET: COA, ACO; 3.32A {Thermoplasma volcanium}

Probab=98.45 E-value=5.4e-08 Score=75.51 Aligned\_cols=88 Identities=15% Similarity=0.085 Sum\_probs=0.0 Template\_Neff=11.600

Q ss\_pred CCcEEEEEECCEEEEEEEEEeC----CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEEEcCCccccccccc

Q Phabba\_Draft 24 NGIMARHAHDDRPVGHLHWHPD----GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPVRHSSHFSAAGRAW 96 (219)

Q Consensus 24 ~~~~~v~~~~~~liG~~~~~~~----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v~~~n~~~~~~~~~ 96 (219)

...++++..+|++||++.+... ..+..++|+|++|++|+|+.|++.+.+.+++ ..+.+.+...|.

T Consensus 49 ~~~~~~~~~~~~ivG~~~~~~~~~~~~~i~~~~v~~~~r~~gig~~l~~~~~~~~~~~g~~~i~~~~~~~n~-------- 120 (162)

T 4PV6\_H 49 PESFMVYTVAGSVVGFIVGSKYSRTEARILLFAVDERFRRMGVGSALMDAFLSLCREQNMLSVRLEVRTDND-------- 120 (162)

T ss\_dssp TTTCEEEEETTEEEEEEEEEESSSSEEEEEEEEECGGGGGGTHHHHHHHHHHHHHHHTTCCEEEEEEETTCH--------

T ss\_pred CCceEEEEECCEEEEEEEEEecCCCEEEEEEEEECHHHCCCCHHHHHHHHHHHHHHHCCCcEEEEEEecCCH--------

Q ss\_pred chhHHHHHcCCCEEeeeeeccccc

Q Phabba\_Draft 97 AQSDPDYHDPGDQNVTKADDDVSN 120 (219)

Q Consensus 97 ~~~~~~y~r~Gf~~~~~~~~~~~~ 120 (219)

.+.++|+++||+..+........

T Consensus 121 -~~~~~~~~~Gf~~~~~~~~~~~~ 143 (162)

T 4PV6\_H 121 -EAIRFYKKYGFVITAMLPNYYSD 143 (162)

T ss\_dssp -HHHHHHHHTTCEEEEEETTCSTT

T ss\_pred -HHHHHHHHcCCEEEEEEehhhcC

No 121

>3EFA\_A Putative Acetyltransferase; acetyltransferase, Lactobacillus plantarum, Structural Genomics; HET: FMT; 2.423A {Lactobacillus plantarum WCFS1}

Probab=98.45 E-value=3.2e-08 Score=74.00 Aligned\_cols=88 Identities=14% Similarity=0.119 Sum\_probs=0.0 Template\_Neff=12.600

Q ss\_pred hCCcEEEEEECCEEEEEEEEEeC----CEEEEEEECHHHCCCCHHHHHHHHHHHccccCeeEEEEEcCCcccccccccch

Q Phabba\_Draft 23 SNGIMARHAHDDRPVGHLHWHPD----GEIDSITVHPDLQRRGIGTAMLKHAQDNPHIYESSYPVRHSSHFSAAGRAWAQ 98 (219)

Q Consensus 23 ~~~~~~v~~~~~~liG~~~~~~~----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~~~i~l~v~~~n~~~~~~~~~~~ 98 (219)

....++++..++++||++.+... ..+..++|+|++||+|+|+.|++.+++.+....+.......|. .

T Consensus 45 ~~~~~~~~~~~~~~vG~~~~~~~~~~~~~i~~~~v~~~~r~~G~~~~l~~~~~~~~~~~~~~~~~~~~n~---------~ 115 (147)

T 3EFA\_A 45 QCEYAVLYLQPDLPITTLRLEPQADHVMRFGRVCTRKAYRGHGWGRQLLTAAEEWATQRGFTHGEIHGEL---------T 115 (147)

T ss\_dssp TCCEEEEEEETTEEEEEEEEEECSTTEEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHTTCCEEEEEEEG---------G

T ss\_pred CCeEEEEEecCCcEEEEEEEEECCCceEEEEEEEECHHHCCCChHHHHHHHHHHHHHHCCCCEEEEeccH---------H

Q ss\_pred hHHHHHcCCCEEeeeeecccc

Q Phabba\_Draft 99 SDPDYHDPGDQNVTKADDDVS 119 (219)

Q Consensus 99 ~~~~y~r~Gf~~~~~~~~~~~ 119 (219)

+.++|+++||+..+......+

T Consensus 116 ~~~~~~~~Gf~~~~~~~~~~g 136 (147)

T 3EFA\_A 116 AQRFYELCGYRVTAGPYDEDG 136 (147)

T ss\_dssp GHHHHHHTTCEEEECCCCBTT

T ss\_pred HHHHHHhcCeEEecceeCCCC

No 122

>3F8K\_A Protein acetyltransferase; GCN5-related N-acetyltransferase, TRANSFERASE; HET: COA; 1.84A {Sulfolobus solfataricus P2}

Probab=98.45 E-value=1e-07 Score=72.94 Aligned\_cols=103 Identities=20% Similarity=0.161 Sum\_probs=0.0 Template\_Neff=12.200

Q ss\_pred CCCchHHHHHhhCCc--EEEEEECCEEEEEEEEEeCCEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEEEcC

Q Phabba\_Draft 12 PLKFEPFDTMWSNGI--MARHAHDDRPVGHLHWHPDGEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPVRHS 86 (219)

Q Consensus 12 ~~~~~~l~~~~~~~~--~~v~~~~~~liG~~~~~~~~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v~~~ 86 (219)

....+.+...+.... ++++.+++++||++.+...... .++|+|++|++|+|+.|++.+++.+.. ..+.+.+...

T Consensus 39 ~~~~~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~-~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~~~~~~~~~ 117 (160)

T 3F8K\_A 39 RITEEDAKKIASNEDHVTFLAEVDGKVVGEASLHKDGEF-SLVVHRNYRTLGIGTLLVKTLIEEAKKSGLSTVKFYTLPE 117 (160)

T ss\_dssp HTC-----------CEEEEEEEETTEEEEEEEEETTSBE-EEEECGGGTTSSHHHHHHHHHHHHHHHTTCSEEEEEECTT

T ss\_pred cCCHHHHHHHhcCCCeEEEEEEECCEEEEEEEEEECCEE-EEEECHHHcCCCHHHHHHHHHHHHHHHCCCCEEEEEecCC

Q ss\_pred CcccccccccchhHHHHHcCCCEEeeeeeccccccceE

Q Phabba\_Draft 87 SHFSAAGRAWAQSDPDYHDPGDQNVTKADDDVSNWGYT 124 (219)

Q Consensus 87 n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~~~~~ 124 (219)

|. .+.++|+++||+..+............

T Consensus 118 n~---------~~~~~~~~~Gf~~~~~~~~~~~~~~~~ 146 (160)

T 3F8K\_A 118 NT---------PMIKIGRKLGFKMRFYEDEVYGEMRLT 146 (160)

T ss\_dssp CH---------HHHHHHHHHTCEEEECSSCEEEEEECC

T ss\_pred CH---------HHHHHHHHcCCEEEEEecceeeeeEee

No 123

>d1yk3e\_ d.108.1.1 (E:) Hypothetical protein Rv1347c/MT1389 {Mycobacterium tuberculosis [TaxId: 1773]}

Probab=98.45 E-value=5.1e-08 Score=77.45 Aligned\_cols=103 Identities=11% Similarity=0.041 Sum\_probs=0.0 Template\_Neff=12.000

Q ss\_pred chHHHHHhhCCc--EEEEEECCEEEEEEEE---------------EeCCEEEEEEECHHHCCCCHHHHHHHHHHHccc--

Q Phabba\_Draft 15 FEPFDTMWSNGI--MARHAHDDRPVGHLHW---------------HPDGEIDSITVHPDLQRRGIGTAMLKHAQDNPH-- 75 (219)

Q Consensus 15 ~~~l~~~~~~~~--~~v~~~~~~liG~~~~---------------~~~~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~-- 75 (219)

.+.+...+.... ++++..++++||++.+ .....+..++|+|++||+|||++|++.+++.+.

T Consensus 68 ~~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~~~~~~~i~~~~v~~~~r~~Gig~~l~~~~~~~~~~~ 147 (196)

T d1yk3e\_ 68 RQHLNAQLEGTYSLPLIGSWHGTDGGYLELYWAAKDLISHYYDADPYDLGLHAAIADLSKVNRGFGPLLLPRIVASVFAN 147 (196)

T ss\_dssp HHHHHHHHHSSSEEEEEEEETTEEEEEEEEEEGGGBGGGGSSCCCTTCEEEEEEESCHHHHHTTCHHHHHHHHHHHHHHH

T ss\_pred HHHHHHHhcCCccccEEEEECCEEEEEEEEEecchhhHhhhccCCCCceEEEEEEeCHHHcCCChHHhHHHHHHHHHHhc

Q ss\_pred c---CeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeeeccccccceEEe

Q Phabba\_Draft 76 I---YESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDVSNWGYTAM 126 (219)

Q Consensus 76 ~---~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~~~~~~~ 126 (219)

. ..+.+.+...|. .+.+||+++||+..+..............

T Consensus 148 ~~~~~~i~~~~~~~n~---------~~~~~~~~~Gf~~~~~~~~~~~~~~~~~~ 192 (196)

T d1yk3e\_ 148 EPRCRRIMFDPDHRNT---------ATRRLCEWAGCKFLGEHDTTNRRMALYAL 192 (196)

T ss\_dssp CTTCCEEEECCBTTCH---------HHHHHHHHTTCEEEEEEECSSCEEEEEEE

T ss\_pred CCCccEEEEcCCCCCH---------HHHHHHHHcCCEEEEEEecCCceEEEEEE

No 124

>d4kvxb\_ d.108.1.0 (B:) automated matches {Schizosaccharomyces pombe [TaxId: 284812]}

Probab=98.45 E-value=5.9e-08 Score=72.85 Aligned\_cols=91 Identities=18% Similarity=0.091 Sum\_probs=0.0 Template\_Neff=12.700

Q ss\_pred chHHHHHhhCCc-EEEEEE-CCEEEEEEEEEeC---------CEEEEEEECHHHCCCCHHHHHHHHHHHccc-c---Cee

Q Phabba\_Draft 15 FEPFDTMWSNGI-MARHAH-DDRPVGHLHWHPD---------GEIDSITVHPDLQRRGIGTAMLKHAQDNPH-I---YES 79 (219)

Q Consensus 15 ~~~l~~~~~~~~-~~v~~~-~~~liG~~~~~~~---------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~-~---~~i 79 (219)

..++........ ++++.+ ++++||++.+... .++..++|+|++|++|+|+.|++.+++.+. . ..+

T Consensus 28 ~~~~~~~~~~~~~~~~~~~~~~~ivg~~~~~~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~~~ 107 (152)

T d4kvxb\_ 28 KYYLYHAISWPMLSYVATDPKGRVVGYVLAKMEEEPKDGIPHGHITSVSVMRSYRHLGLAKRLMVQSQRAMVEVYGAKYM 107 (152)

T ss\_dssp HHHHHHHHTSTTSCEEEECTTSCEEEEEEEEECSSCGGGCCEEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHHHCCSEE

T ss\_pred HHHHHHhhcCCeEEEEEECCCCcEEEEEEEEEccCcCCCCcEEEEEEEEECHHHccCCHHHHHHHHHHHHHHHHhCCCEE

Q ss\_pred EEEEEcCCcccccccccchhHHHHHc-CCCEEeeee

Q Phabba\_Draft 80 SYPVRHSSHFSAAGRAWAQSDPDYHD-PGDQNVTKA 114 (219)

Q Consensus 80 ~l~v~~~n~~~~~~~~~~~~~~~y~r-~Gf~~~~~~ 114 (219)

.+.+...|. .+.++|++ +||+..+..

T Consensus 108 ~~~~~~~n~---------~~~~~~~~~~Gf~~~~~~ 134 (152)

T d4kvxb\_ 108 SLHVRKSNR---------AAIHLYRDTLQFDVQGIE 134 (152)

T ss\_dssp EEEEETTCH---------HHHCCCCCCSCCEEEEEE

T ss\_pred EEEEEecCH---------HHHHHHHhccCcEEEEeh

No 125

>d4nsqa1 d.108.1.0 (A:493-652) automated matches {Human (Homo sapiens) [TaxId: 9606]}

Probab=98.45 E-value=7.7e-08 Score=75.62 Aligned\_cols=100 Identities=16% Similarity=0.127 Sum\_probs=0.0 Template\_Neff=10.700

Q ss\_pred cCCCCCCCCchHHHHHhhCCc--EEEEEECCEEEEEEEEEeC-----CEEEEEEECHHHCCCCHHHHHHHHHHHccccCe

Q Phabba\_Draft 6 ANGDLPPLKFEPFDTMWSNGI--MARHAHDDRPVGHLHWHPD-----GEIDSITVHPDLQRRGIGTAMLKHAQDNPHIYE 78 (219)

Q Consensus 6 ~~~~~~~~~~~~l~~~~~~~~--~~v~~~~~~liG~~~~~~~-----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~~~ 78 (219)

.....+....+++........ ++++..++++||++.+... ..+..++|+|++||+|+|+.|+..+++.+....

T Consensus 30 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~i~~~~v~~~~rg~G~~~~l~~~~~~~~~~~~ 109 (160)

T d4nsqa1 30 FSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQVKGYGTHLMNHLKEYHIKHD 109 (160)

T ss\_dssp HHHHCTTSCHHHHHHHHTCTTEEEEEEEETTEEEEEEEEEEETTTTEEEEEEEEECGGGCSSSHHHHHHHHHHHHHHHHT

T ss\_pred hhcCCCCCCHHHHHHHhcCCCccEEEEEECCEEEEEEEEEEcCCCCeEEEEEEEEChHHcCCCHHHHHHHHHHHHHHHCC

Q ss\_pred eEEEEEcCCcccccccccchhHHHHHcCCCEEeeee

Q Phabba\_Draft 79 SSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKA 114 (219)

Q Consensus 79 i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~ 114 (219)

+...+...|. .+.++|+++||+..+..

T Consensus 110 ~~~~~~~~n~---------~~~~~~~~~Gf~~~~~~ 136 (160)

T d4nsqa1 110 ILNFLTYADE---------YAIGYFKKQGFSKEIKI 136 (160)

T ss\_dssp CCEEEEEECT---------TSHHHHHHTTCBSSCCS

T ss\_pred CcEEEEcCCH---------HHHHHHHHCCCEEeeee

No 126

>3DR8\_B yncA (E.C.2.3.1.-); Salmonella essential gene IDP0086 acetyltransferase; HET: ACO, ACT; 1.95A {Salmonella typhimurium}

Probab=98.44 E-value=7.1e-08 Score=74.23 Aligned\_cols=89 Identities=15% Similarity=0.040 Sum\_probs=0.0 Template\_Neff=12.600

Q ss\_pred HHHHHhhCCcEEEEEECCEEEEEEEEEeC--------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEEEc

Q Phabba\_Draft 17 PFDTMWSNGIMARHAHDDRPVGHLHWHPD--------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPVRH 85 (219)

Q Consensus 17 ~l~~~~~~~~~~v~~~~~~liG~~~~~~~--------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v~~ 85 (219)

..........++++..++++||++.+... ..+..+.|+|++|++|+|+.|++.+++.++. ..+.+.+..

T Consensus 46 ~~~~~~~~~~~~~~~~~~~ivG~~~~~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~~~~~~~~ 125 (174)

T 3DR8\_B 46 YEARQLLGYPVLVSEENGVVTGYASFGDWRSFDGFRYTVEHSVYVHPAHQGKGLGRKLLSRLIDEARRCGKHVMVAGIES 125 (174)

T ss\_dssp HHHHHHTTCCEEEEEETTEEEEEEEEEESSSSGGGTTEEEEEEEECTTSCSSSHHHHHHHHHHHHHHHTTCSEEEEEEET

T ss\_pred HHHHHhhCCCEEEEeeCCeEEEEEEEEeecccCCCceEEEEEEEECHHHCCCCHHHHHHHHHHHHHHHcCCCEEEEEEec

Q ss\_pred CCcccccccccchhHHHHHcCCCEEeeee

Q Phabba\_Draft 86 SSHFSAAGRAWAQSDPDYHDPGDQNVTKA 114 (219)

Q Consensus 86 ~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~ 114 (219)

.|. .+.++|+++||+..+..

T Consensus 126 ~n~---------~~~~~~~~~Gf~~~~~~ 145 (174)

T 3DR8\_B 126 QNA---------ASIRLHHSLGFTVTAQM 145 (174)

T ss\_dssp TCH---------HHHHHHHHTTCEEEEEE

T ss\_pred CCH---------HHHHHHHHcCCeEEEEc

No 127

>4R3L\_A Uncharacterized N-acetyltransferase SSO0209 (E.C.2.3.1.-), N-terminal; Protein-substrate complex, GNAT domain, N-acetyltransferase; HET: COA; 1.839A {Sulfolobus solfataricus P2}

Probab=98.44 E-value=7e-08 Score=75.42 Aligned\_cols=96 Identities=20% Similarity=0.135 Sum\_probs=0.0 Template\_Neff=11.800

Q ss\_pred hHHHHHhhCCc--EEEEEECCEEEEEEEEE---------------eCCEEEEEEECHHHCCCCHHHHHHHHHHHcccc--

Q Phabba\_Draft 16 EPFDTMWSNGI--MARHAHDDRPVGHLHWH---------------PDGEIDSITVHPDLQRRGIGTAMLKHAQDNPHI-- 76 (219)

Q Consensus 16 ~~l~~~~~~~~--~~v~~~~~~liG~~~~~---------------~~~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~-- 76 (219)

..+...+.+.. ++++.++|++||++.+. ...++..++|+|++|++|+|+.|++.+++.+.+

T Consensus 40 ~~~~~~~~~~~~~~~v~~~~~~~vG~~~~~~~~~~~~~~~~~~~~~~~~~~~~~v~~~~rg~G~~~~l~~~~~~~~~~~~ 119 (173)

T 4R3L\_A 40 YFFVEHLKEYGLAFFVAIVDNSVVGYIMPRIEWGFSNIKQLPSLVRKGHVVSIAVLEEYRRKGIATTLLEASMKSMKNDY 119 (173)

T ss\_dssp HHHHHHHHHHGGGCEEEEETTEEEEEEEEEEEEEECSSCSSCCEEEEEEEEEEEECGGGCSSSHHHHHHHHHHHHHHHHH

T ss\_pred hhhhHHhhcCCeEEEEEEECCeEEEEEEeEEecCCCCcccchhhcCceEEEEEEeCHHHhcCCHHHHHHHHHHHHHHhhc

Q ss\_pred --CeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeeeccccc

Q Phabba\_Draft 77 --YESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDVSN 120 (219)

Q Consensus 77 --~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~ 120 (219)

..+.+.+...|. .+.++|+++||+..+.....+..

T Consensus 120 ~~~~~~~~~~~~n~---------~~~~~~~~~Gf~~~~~~~~~~~~ 156 (173)

T 4R3L\_A 120 NAEEIYLEVRVSNY---------PAIALYEKLNFKKVKVLKGYYAD 156 (173)

T ss\_dssp CCSEEEEEEETTCH---------HHHHHHHHTTCEEEEEETTCSTT

T ss\_pred CCCEEEEEEEcccH---------HHHHHHHHcCCEEEEEeccccCC

No 128

>5ICV\_A N-alpha-acetyltransferase 60 (E.C.2.3.1.48,2.3.1.88), MET-LYS-ALA-VAL-LIG; Transferase, Acetylation, GNAT, NAT; HET: 1XE; 1.53A {Homo sapiens}

Probab=98.44 E-value=7.7e-08 Score=74.80 Aligned\_cols=96 Identities=15% Similarity=0.060 Sum\_probs=0.0 Template\_Neff=12.400

Q ss\_pred CCCCchHHHHHhhCCc--EEEEEECCEEEEEEEEE-----------------------eCCEEEEEEECHHHCCCCHHHH

Q Phabba\_Draft 11 PPLKFEPFDTMWSNGI--MARHAHDDRPVGHLHWH-----------------------PDGEIDSITVHPDLQRRGIGTA 65 (219)

Q Consensus 11 ~~~~~~~l~~~~~~~~--~~v~~~~~~liG~~~~~-----------------------~~~~i~~l~V~p~~R~~Gig~~ 65 (219)

.....+++........ ++++.++|++||++.+. ....+..++|+|++|++|+++.

T Consensus 32 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~i~~~~v~p~~r~~g~~~~ 111 (180)

T 5ICV\_A 32 IEYPDSWYRDITSNKKFFSLAATYRGAIVGMIVAEIKNRTKIHKEDGDILASNFSVDTQVAYILSLGVVKEFRKHGIGSL 111 (180)

T ss\_dssp SCCCHHHHHHHHHCTTEEEEEEEETTEEEEEEEEEEEEGGGSCGGGTTTTTTCCCTTCEEEEEEEEEECGGGTTSSHHHH

T ss\_pred CCCCchHHHHhccCCCcEEEEEEECCeEEEEEEEEEccCcccccCCCccccccCCCCccEEEEEEEEECHHHcCCCHHHH

Q ss\_pred HHHHHHHcc---cc---CeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 66 MLKHAQDNP---HI---YESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 66 Ll~~~~~~~---~~---~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

|++.+++.+ +. ..+.+.+...|. .+.++|+++||+..+...

T Consensus 112 l~~~~~~~~~~~~~~~~~~i~~~~~~~n~---------~~~~~~~~~Gf~~~~~~~ 158 (180)

T 5ICV\_A 112 LLESLKDHISTTAQDHCKAIYLHVLTTNN---------TAINFYENRDFKQHHYLP 158 (180)

T ss\_dssp HHHHHHHHHHHHSTTTEEEEEEEEETTCH---------HHHHHHHTTTCEEEEEEE

T ss\_pred HHHHHHHHHhhhHHhcCCEEEEEEEcCCH---------HHHHHHHhCCCeEeeccc

No 129

>PF17013.4 ; Acetyltransf\_15 ; Putative acetyl-transferase

Probab=98.44 E-value=6.4e-08 Score=80.79 Aligned\_cols=94 Identities=12% Similarity=0.056 Sum\_probs=0.0 Template\_Neff=8.600

Q ss\_pred HhhCCcEEEEEECCEEEE--EEEEEeC-------------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEE

Q Phabba\_Draft 21 MWSNGIMARHAHDDRPVG--HLHWHPD-------------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYP 82 (219)

Q Consensus 21 ~~~~~~~~v~~~~~~liG--~~~~~~~-------------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~ 82 (219)

.......+++..++++|| ++.+... ..+..++|+|++||+|||++|++.+++.++. ..+.+.

T Consensus 30 ~~~~~~~~~i~~~~~iVG~~~~~l~~~~~~~~~~~~~~~~~~i~~l~V~p~yrgqGig~~Ll~~~~~~~~~~g~~~i~l~ 109 (204)

T A9CS30\_ENTBH/3 30 LFKNTYRYIILDKTQFVGGVNTKIVYVKYHSFWKTTNIKSAIIYDFCIDKKYRKQGLAYKLLNFAVSNLKRHKIKLLALH 109 (204)

T ss\_pred ccccCCEEEEEECCeEEEEEEEEEEEcccccccCCcCCceEEEEEEEECHHHCCCCHHHHHHHHHHHHHHhCCCcEEEEE

Q ss\_pred EEcCC---cccccccccchhHHHHHcCCCEEeeeeeccccccce

Q Phabba\_Draft 83 VRHSS---HFSAAGRAWAQSDPDYHDPGDQNVTKADDDVSNWGY 123 (219)

Q Consensus 83 v~~~n---~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~~~~ 123 (219)

+...| . .+.+||+++||+..+..........+

T Consensus 110 ~~~~N~~~~---------~a~~fY~k~GF~~~~~~~~~~~~~~~ 144 (204)

T A9CS30\_ENTBH/3 110 LNAADKSMP---------ISSYIYYKLGFKQFCWCRSSFEDFIG 144 (204)

T ss\_pred eecCCCCCc---------HHHHHHHHcCCEEEEEEecCCcccee

No 130

>2R7H\_B Putative D-alanine N-acetyltransferase of GNAT; PUTATIVE ACETYLTRANSFERASE OF THE GNAT; HET: ETX; 1.85A {Desulfovibrio desulfuricans subsp. desulfuricans str.}

Probab=98.44 E-value=6.3e-08 Score=74.76 Aligned\_cols=97 Identities=16% Similarity=0.112 Sum\_probs=0.0 Template\_Neff=12.600

Q ss\_pred chHHHHHh-----hCCcEEEEEECCEEEEEEEEEeC------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeE

Q Phabba\_Draft 15 FEPFDTMW-----SNGIMARHAHDDRPVGHLHWHPD------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESS 80 (219)

Q Consensus 15 ~~~l~~~~-----~~~~~~v~~~~~~liG~~~~~~~------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~ 80 (219)

.+.+...+ ....++++..++++||++.+... ..+..+.|+|++|++|+|++|++.+++.+++ ..+.

T Consensus 53 ~~~~~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~~~v~~~~r~~G~~~~l~~~~~~~~~~~~~~~~~ 132 (177)

T 2R7H\_B 53 QELVDEHLMHGAACGYHFVFATEDDDMAGYACYGPTPATEGTYDLYWIAVAPHRQHSGLGRALLAEVVHDVRLTGGRLLF 132 (177)

T ss\_dssp HHHHHHHHHTSGGGCCEEEEEEETTEEEEEEEEEECTTCSSEEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHTTCCEEE

T ss\_pred HHHHHHHHHhccccCcEEEEEecCCCeEEEEEEEecCCCCCeEEEEEEEEChhHcCCcHHHHHHHHHHHHHHHcCCCEEE

Q ss\_pred EEEEc--CCcccccccccchhHHHHHcCCCEEeeeeeccccc

Q Phabba\_Draft 81 YPVRH--SSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDVSN 120 (219)

Q Consensus 81 l~v~~--~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~ 120 (219)

+.+.. .|. .+.++|+++||+..+........

T Consensus 133 ~~~~~~~~n~---------~~~~~~~~~Gf~~~~~~~~~~~~ 165 (177)

T 2R7H\_B 133 AETSGIRKYA---------PTRRFYERAGFSAEAVLKAFYRA 165 (177)

T ss\_dssp EEEECSGGGH---------HHHHHHHHTTCEEEEEEEEEEET

T ss\_pred EEeecccccH---------HHHHHHHHcCCeEEEEEEccccC

No 131

>d1y9wb\_ d.108.1.1 (B:) Probable acetyltransferase BC2806 {Bacillus cereus [TaxId: 1396]}

Probab=98.44 E-value=1e-07 Score=72.03 Aligned\_cols=108 Identities=11% Similarity=0.066 Sum\_probs=0.0 Template\_Neff=11.700

Q ss\_pred CCCCCchHHHHHhh---CCcEEEEEE-CCEEEEEEEEEeC---CEEEEEEECHHHCCCCHHHHHHHHHHHcccc-CeeEE

Q Phabba\_Draft 10 LPPLKFEPFDTMWS---NGIMARHAH-DDRPVGHLHWHPD---GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI-YESSY 81 (219)

Q Consensus 10 ~~~~~~~~l~~~~~---~~~~~v~~~-~~~liG~~~~~~~---~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~-~~i~l 81 (219)

+.++..+.+...+. ...++++.. +|++||++.+... ..+..++|+|++|++|+|+.|+..+++.+.. ....+

T Consensus 21 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~v~~~~rg~g~g~~l~~~~~~~~~~~~~~~~ 100 (140)

T d1y9wb\_ 21 VIQYNMSILTDEVKQPMEEVSLVVKNEEGKIFGGVTGTMYFYHLHIDFLWVDESVRHDGYGSQLLHEIEGIAKEKGCRLI 100 (140)

T ss\_dssp HHHHHHHHSCGGGCCCCEEEEEEEECTTSCEEEEEEEEEETTEEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHTTCSEE

T ss\_pred hhhcchhhcHHHhcCChhccEEEEEeCCCcEEEEEEEEEeeceEEEEEEEEChhhCCCCHHHHHHHHHHHHHHHcCCCEE

Q ss\_pred EEEcCCcccccccccchhHHHHHcCCCEEeeeeeccccccceEEe

Q Phabba\_Draft 82 PVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDVSNWGYTAM 126 (219)

Q Consensus 82 ~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~~~~~~~ 126 (219)

.+...|. .+.++|+++||+..+.......+.....+

T Consensus 101 ~~~~~n~---------~~~~~~~~~Gf~~~~~~~~~~~~~~~~~~ 136 (140)

T d1y9wb\_ 101 LLDSFSF---------QAPEFYKKHGYREYGVVEDHPKGHSQHFF 136 (140)

T ss\_dssp EEEEEGG---------GCHHHHHHTTCEEEEEETTSSTTCCEEEE

T ss\_pred EEEecCc---------cHHHHHHHCCCEEEEEEeCCCCCceEEEE

No 132

>3H4Q\_A putative acetyltransferase; NP\_371943.1, putative acetyltransferase, Structural Genomics; HET: P33; 2.5A {Staphylococcus aureus subsp. aureus Mu50}

Probab=98.43 E-value=5.2e-08 Score=79.10 Aligned\_cols=96 Identities=11% Similarity=0.065 Sum\_probs=0.0 Template\_Neff=10.200

Q ss\_pred hHHHHHhhCCcEEEEEECCEEEEEEEEEe-----------------CCEEEEEEECHHHCCCCHHHHHHHHHHHcccc--

Q Phabba\_Draft 16 EPFDTMWSNGIMARHAHDDRPVGHLHWHP-----------------DGEIDSITVHPDLQRRGIGTAMLKHAQDNPHI-- 76 (219)

Q Consensus 16 ~~l~~~~~~~~~~v~~~~~~liG~~~~~~-----------------~~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~-- 76 (219)

+.+...+.+..++++.+++++||++.+.. ...+..++|+|++ +|+|++|++.+++.+++

T Consensus 59 ~~~~~~~~~~~~~v~~~~~~~vG~~~~~~~~~~~~~~~~~~~~~~~~~~i~~l~v~p~~--kGig~~L~~~~~~~a~~~g 136 (188)

T 3H4Q\_A 59 EHFEEDIAKDYLYVLEENDKIYGFIVVDQDQAEWYDDIDWPVNREGAFVIHRLTGSKEY--KGAATELFNYVIDVVKARG 136 (188)

T ss\_dssp HHHHHHHHTTCEEEEEETTEEEEEEEEESCCCGGGGGSCCSSCCTTCEEEEEEECCSSC--TTHHHHHHHHHHHHHHHTT

T ss\_pred HHHHHHHhcCcEEEEEECCEEEEEEEEECCCchhcccCCCCcCcCCcEEEEEEEeCccc--CCHHHHHHHHHHHHHHHCC

Q ss\_pred -CeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeeeccccccc

Q Phabba\_Draft 77 -YESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDVSNWG 122 (219)

Q Consensus 77 -~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~~~ 122 (219)

..+.+.+...|. .+.+||+++||+..+........+.

T Consensus 137 ~~~i~l~~~~~N~---------~a~~~y~k~GF~~~~~~~~~~~~~~ 174 (188)

T 3H4Q\_A 137 AEVILTDTFALNK---------PAQGLFAKFGFHKVGEQLMEYPPYD 174 (188)

T ss\_dssp CCEEEEEGGGSCG---------GGTHHHHHTTCEEC-----------

T ss\_pred CCEEEEeeeCCCH---------HHHHHHHHcCcEEEEEEeeecCCCC

No 133

>5JTF\_A Phosphinothricin N-acetyltransferase, putative; N-acetyltransferase, Pseudomonas putida, TRANSFERASE; 2.156A {Pseudomonas putida}

Probab=98.43 E-value=6.4e-08 Score=79.05 Aligned\_cols=91 Identities=13% Similarity=-0.037 Sum\_probs=0.0 Template\_Neff=10.900

Q ss\_pred hHHHHHhhCCcEEEEEECCEEEEEEEEE--------eCCEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEEE

Q Phabba\_Draft 16 EPFDTMWSNGIMARHAHDDRPVGHLHWH--------PDGEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPVR 84 (219)

Q Consensus 16 ~~l~~~~~~~~~~v~~~~~~liG~~~~~--------~~~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v~ 84 (219)

..+........++++.++|++||++.+. ....+..++|+|++||+|+|++|++.+++.++. ..+.+.+.

T Consensus 45 ~~~~~~~~~~~~~v~~~~g~ivG~~~~~~~~~~~~~~~~~~~~~~v~p~~rg~Gig~~ll~~~~~~~~~~g~~~i~~~~~ 124 (207)

T 5JTF\_A 45 ERISTTLQTYPYLVAVREGRVVGYAYASQHRARAAYRWAVDVTVYVAEGQRRSGIARQLYDVLLPVLKRLGYRSAYAGIA 124 (207)

T ss\_dssp HHHHHHTTTSCEEEEESSSSEEEEEEEEESSSSGGGTTEEEEEEEECSSSCTTTHHHHHHHHHHHHHHTTTCCEEEEEEE

T ss\_pred HHHHHhhhhCCEEEEEECCEEEEEEEEEccccccccccEEEEEEEECHHHcCCCHHHHHHHHHHHHHHHhCCCEEEEEee

Q ss\_pred cCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 85 HSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 85 ~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

..|. .+.++|+++||+..+...

T Consensus 125 ~~n~---------~~~~~~~~~GF~~~~~~~ 146 (207)

T 5JTF\_A 125 LPNE---------GSVGLHERLGFQHIGTFP 146 (207)

T ss\_dssp ECCH---------HHHHHHHHHTCEEEEEEE

T ss\_pred CCCH---------HhHHHHHHcCCEEEEEEC

No 134

>d3dr6b\_ d.108.1.1 (B:) automated matches {Salmonella typhimurium [TaxId: 90371]}

Probab=98.43 E-value=7.8e-08 Score=73.66 Aligned\_cols=89 Identities=15% Similarity=0.040 Sum\_probs=0.0 Template\_Neff=12.600

Q ss\_pred HHHHHhhCCcEEEEEECCEEEEEEEEEeC--------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEEEc

Q Phabba\_Draft 17 PFDTMWSNGIMARHAHDDRPVGHLHWHPD--------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPVRH 85 (219)

Q Consensus 17 ~l~~~~~~~~~~v~~~~~~liG~~~~~~~--------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v~~ 85 (219)

..........++++..++++||++.+... ..+..++|+|++|++|+|+.|++.+++.++. ..+.+.+..

T Consensus 44 ~~~~~~~~~~~~~~~~~~~ivG~~~~~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~i~~~~~~ 123 (169)

T d3dr6b\_ 44 YEARQLLGYPVLVSEENGVVTGYASFGDWRSFDGFRYTVEHSVYVHPAHQGKGLGRKLLSRLIDEARRCGKHVMVAGIES 123 (169)

T ss\_dssp HHHHHHTTCCEEEEEETTEEEEEEEEEESSSSGGGTTEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHTTCSEEEEEEET

T ss\_pred HHHhHhhCCCEEEEEECCeEEEEEEeccccccCCCceEEEEEEEECHHHCCCCHHHHHHHHHHHHHHHcCCcEEEEEEec

Q ss\_pred CCcccccccccchhHHHHHcCCCEEeeee

Q Phabba\_Draft 86 SSHFSAAGRAWAQSDPDYHDPGDQNVTKA 114 (219)

Q Consensus 86 ~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~ 114 (219)

.|. .+.++|+++||+..+..

T Consensus 124 ~n~---------~~~~~~~~~Gf~~~~~~ 143 (169)

T d3dr6b\_ 124 QNA---------ASIRLHHSLGFTVTAQM 143 (169)

T ss\_dssp TCH---------HHHHHHHHTTCEEEEEE

T ss\_pred CCH---------HHHHHHHHcCCeEEEEe

No 135

>2JLM\_E PUTATIVE PHOSPHINOTHRICIN N-ACETYLTRANSFERASE; PHOSPHINOTHRICIN, ACETYLTRANSFERASE, TRANSFERASE, METHIONINE SULFOXIMINE; HET: PEG, ACT, AZI; 2.35A {ACINETOBACTER BAYLYI}

Probab=98.43 E-value=8e-08 Score=74.98 Aligned\_cols=98 Identities=11% Similarity=0.071 Sum\_probs=0.0 Template\_Neff=12.300

Q ss\_pred CCCCCCchHHHHHhhC-----CcEEEEEE-CCEEEEEEEEEeC--------CEEEEEEECHHHCCCCHHHHHHHHHHHcc

Q Phabba\_Draft 9 DLPPLKFEPFDTMWSN-----GIMARHAH-DDRPVGHLHWHPD--------GEIDSITVHPDLQRRGIGTAMLKHAQDNP 74 (219)

Q Consensus 9 ~~~~~~~~~l~~~~~~-----~~~~v~~~-~~~liG~~~~~~~--------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~ 74 (219)

...+...+.+...+.. ..++++.. ++++||++.+... .++..++|+|++|++|+|+.|++.+++.+

T Consensus 40 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~~~~~v~~~~r~~G~~~~l~~~~~~~~ 119 (182)

T 2JLM\_E 40 DYKPRSKESMAAWFATKRQNNFPIIGAVNEVGQLLGFASWGSFRAFPAYKYTVEHSVYIHKDYRGLGLSKHLMNELIKRA 119 (182)

T ss\_dssp CSSCCCTTHHHHHHHHHHTTTCCEEEEECTTCCEEEEEEEEESSSSGGGTTEEEEEEEECGGGTTSSHHHHHHHHHHHHH

T ss\_pred cCCCCCHHHHHHHHHhcccCCCCEEEEEeCCCcEEEEEEEEecCCCcccceEEEEEEEEChhhCCCChHHHHHHHHHHHH

Q ss\_pred cc---CeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 75 HI---YESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 75 ~~---~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

+. ..+.+.+...|. .+.++|+++||+..+...

T Consensus 120 ~~~~~~~~~~~~~~~n~---------~~~~~~~~~Gf~~~~~~~ 154 (182)

T 2JLM\_E 120 VESEVHVMVGCIDATNV---------ASIQLHQKLGFIHSGTIQ 154 (182)

T ss\_dssp HHTTCCEEEEEEETTCH---------HHHHHHHHTTCEEEEEEE

T ss\_pred HHCCCcEEEEEeeCCCH---------HHHHHHHHcCCEEeEEEE

No 136

>2JLM\_D PUTATIVE PHOSPHINOTHRICIN N-ACETYLTRANSFERASE; PHOSPHINOTHRICIN, ACETYLTRANSFERASE, TRANSFERASE, METHIONINE SULFOXIMINE; HET: AZI, ACT, PEG; 2.35A {ACINETOBACTER BAYLYI}

Probab=98.43 E-value=8e-08 Score=74.98 Aligned\_cols=98 Identities=11% Similarity=0.071 Sum\_probs=0.0 Template\_Neff=12.300

Q ss\_pred CCCCCCchHHHHHhhC-----CcEEEEEE-CCEEEEEEEEEeC--------CEEEEEEECHHHCCCCHHHHHHHHHHHcc

Q Phabba\_Draft 9 DLPPLKFEPFDTMWSN-----GIMARHAH-DDRPVGHLHWHPD--------GEIDSITVHPDLQRRGIGTAMLKHAQDNP 74 (219)

Q Consensus 9 ~~~~~~~~~l~~~~~~-----~~~~v~~~-~~~liG~~~~~~~--------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~ 74 (219)

...+...+.+...+.. ..++++.. ++++||++.+... .++..++|+|++|++|+|+.|++.+++.+

T Consensus 40 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~~~~~v~~~~r~~G~~~~l~~~~~~~~ 119 (182)

T 2JLM\_D 40 DYKPRSKESMAAWFATKRQNNFPIIGAVNEVGQLLGFASWGSFRAFPAYKYTVEHSVYIHKDYRGLGLSKHLMNELIKRA 119 (182)

T ss\_dssp CSSCCCHHHHHHHHHHHHHTTCCEEEEEETTCCEEEEEEEEESSSSGGGTTEEEEEEEECGGGTTSSHHHHHHHHHHHHH

T ss\_pred cCCCCCHHHHHHHHHhcccCCCCEEEEEeCCCcEEEEEEEEecCCCcccceEEEEEEEEChhhCCCChHHHHHHHHHHHH

Q ss\_pred cc---CeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 75 HI---YESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 75 ~~---~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

+. ..+.+.+...|. .+.++|+++||+..+...

T Consensus 120 ~~~~~~~~~~~~~~~n~---------~~~~~~~~~Gf~~~~~~~ 154 (182)

T 2JLM\_D 120 VESEVHVMVGCIDATNV---------ASIQLHQKLGFIHSGTIQ 154 (182)

T ss\_dssp HHTTCCEEEEEEETTCH---------HHHHHHHHTTCEEEEEEE

T ss\_pred HHCCCcEEEEEeeCCCH---------HHHHHHHHcCCEEeEEEE

No 137

>3DR6\_C yncA (E.C.2.3.1.-); acetyltransferase, CSGID target, essential gene; HET: EDO; 1.75A {Salmonella typhimurium}

Probab=98.43 E-value=7.8e-08 Score=73.84 Aligned\_cols=89 Identities=15% Similarity=0.040 Sum\_probs=0.0 Template\_Neff=12.700

Q ss\_pred HHHHHhhCCcEEEEEECCEEEEEEEEEeC--------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEEEc

Q Phabba\_Draft 17 PFDTMWSNGIMARHAHDDRPVGHLHWHPD--------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPVRH 85 (219)

Q Consensus 17 ~l~~~~~~~~~~v~~~~~~liG~~~~~~~--------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v~~ 85 (219)

..........++++..++++||++.+... ..+..++|+|++|++|+|++|++.+++.+++ ..+.+.+..

T Consensus 46 ~~~~~~~~~~~~~~~~~~~ivG~~~~~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~~~~~~~~ 125 (174)

T 3DR6\_C 46 YEARQLLGYPVLVSEENGVVTGYASFGDWRSFDGFRYTVEHSVYVHPAHQGKGLGRKLLSRLIDEARRCGKHVMVAGIES 125 (174)

T ss\_dssp HHHHHHHTCCEEEEEETTEEEEEEEEEESSSSGGGTTEEEEEEEECTTSCSSSHHHHHHHHHHHHHHHTTCSEEEEEEET

T ss\_pred HHHHHhcCCCEEEEeeCCeEEEEEEEeeecccCCCceEEEEEEEECHHHCCCCHHHHHHHHHHHHHHHcCCcEEEEEEec

Q ss\_pred CCcccccccccchhHHHHHcCCCEEeeee

Q Phabba\_Draft 86 SSHFSAAGRAWAQSDPDYHDPGDQNVTKA 114 (219)

Q Consensus 86 ~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~ 114 (219)

.|. .+.++|+++||+..+..

T Consensus 126 ~n~---------~~~~~~~~~Gf~~~~~~ 145 (174)

T 3DR6\_C 126 QNA---------ASIRLHHSLGFTVTAQM 145 (174)

T ss\_dssp TCH---------HHHHHHHTTTCEEEEEE

T ss\_pred CCH---------HHHHHHHHcCCeEEEEc

No 138

>2J8M\_B ACETYLTRANSFERASE PA4866 FROM P. AERUGINOSA; GCN5 FAMILY, PHOSPHINOTHRICIN, METHIONINE SULFONE; HET: GOL, AZI; 1.44A {PSEUDOMONAS AERUGINOSA}

Probab=98.42 E-value=7.7e-08 Score=73.90 Aligned\_cols=91 Identities=13% Similarity=0.102 Sum\_probs=0.0 Template\_Neff=12.600

Q ss\_pred hHHHHHhhCCc-EEEEEE-CCEEEEEEEEE--------eCCEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEE

Q Phabba\_Draft 16 EPFDTMWSNGI-MARHAH-DDRPVGHLHWH--------PDGEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYP 82 (219)

Q Consensus 16 ~~l~~~~~~~~-~~v~~~-~~~liG~~~~~--------~~~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~ 82 (219)

.++........ ++++.. ++++||++.+. ....+..++|+|++|++|+|+.|++.+++.++. ..+.+.

T Consensus 43 ~~~~~~~~~~~~~~~~~~~~~~iiG~~~~~~~~~~~~~~~~~~~~~~v~~~~r~~G~~~~l~~~~~~~~~~~~~~~i~~~ 122 (172)

T 2J8M\_B 43 AWFDARARQGYPILVASDAAGEVLGYASYGDWRPFEGFRGTVEHSVYVRDDQRGKGLGVQLLQALIERARAQGLHVMVAA 122 (172)

T ss\_dssp HHHHHHHHHTCCEEEEECTTCCEEEEEEEEESSSSGGGTTEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHTTCCEEEEE

T ss\_pred HHHHHHHhcCCcEEEEECCCCcEEEEEEEEeccccCCCCcEEEEEEEEcHHHCCCcHHHHHHHHHHHHHHHCCCCEEEEE

Q ss\_pred EEcCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 83 VRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 83 v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

+...|. .+.++|+++||+..+...

T Consensus 123 ~~~~n~---------~~~~~~~~~Gf~~~~~~~ 146 (172)

T 2J8M\_B 123 IESGNA---------ASIGLHRRLGFEISGQMP 146 (172)

T ss\_dssp EETTCH---------HHHHHHHTTTCEEEEEEE

T ss\_pred EecCCH---------HHHHHHHHcCCEEEEEec

No 139

>d1mk4b1 d.108.1.1 (B:1-156) Hypothetical protein YqiY {Bacillus subtilis [TaxId: 1423]}

Probab=98.42 E-value=6.5e-08 Score=73.73 Aligned\_cols=84 Identities=13% Similarity=0.051 Sum\_probs=0.0 Template\_Neff=12.200

Q ss\_pred CCcEEEEEECCEEEEEEEEEeC------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEEEcCCccccccc

Q Phabba\_Draft 24 NGIMARHAHDDRPVGHLHWHPD------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPVRHSSHFSAAGR 94 (219)

Q Consensus 24 ~~~~~v~~~~~~liG~~~~~~~------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v~~~n~~~~~~~ 94 (219)

...++++..++++||++.+... ..+..++|+|++|++|+|+.|+..+++.+.. ..+.+.+...|.

T Consensus 40 ~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~i~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~i~~~~~~~n~------ 113 (156)

T d1mk4b1 40 QDTSFITSEHNSMTGFLIGFQSQSDPETAYIHFSGVHPDFRKMQIGKQLYDVFIETVKQRGCTRVKCVTSPVNK------ 113 (156)

T ss\_dssp GGGCEEEEETTEEEEEEEEEECSSSTTEEEEEEEEECTTSCHHHHHHHHHHHHHHHHHTTTCCEEEEEECTTCH------

T ss\_pred CCCeEEEEeCCeEEEEEEEEecCCCCCEEEEEEEEECHHHCCCCHHHHHHHHHHHHHHHcCCCEEEEEEcCCCH------

Q ss\_pred ccchhHHHHHcCCCEEeeeeec

Q Phabba\_Draft 95 AWAQSDPDYHDPGDQNVTKADD 116 (219)

Q Consensus 95 ~~~~~~~~y~r~Gf~~~~~~~~ 116 (219)

.+.++|+++||+..+....

T Consensus 114 ---~~~~~~~~~Gf~~~~~~~~ 132 (156)

T d1mk4b1 114 ---VSIAYHTKLGFDIEKGTKT 132 (156)

T ss\_dssp ---HHHHHHHHTTCEECCCSEE

T ss\_pred ---HHHHHHHHcCcEEEeeeec

No 140

>3EO4\_C Uncharacterized protein MJ1062; APC60792.2,MJ\_1062,Methanocaldococcus jannaschii DSM 2661, structural; HET: MES, PG6, EDO; 2.19A {Methanocaldococcus jannaschii}

Probab=98.42 E-value=7e-08 Score=74.78 Aligned\_cols=99 Identities=11% Similarity=-0.022 Sum\_probs=0.0 Template\_Neff=11.800

Q ss\_pred chHHHHHhhCCcEEEEEECC--EEEEEEEEEeC----CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEEEc

Q Phabba\_Draft 15 FEPFDTMWSNGIMARHAHDD--RPVGHLHWHPD----GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPVRH 85 (219)

Q Consensus 15 ~~~l~~~~~~~~~~v~~~~~--~liG~~~~~~~----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v~~ 85 (219)

..+.........++++..++ ++||++.+... .++..++|+|++||+|||+.|++.+++.+.. ..+.+.+..

T Consensus 54 ~~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~i~~~~v~~~~rg~Gig~~l~~~~~~~~~~~~~~~i~~~~~~ 133 (164)

T 3EO4\_C 54 SWWMSRENRVDWIILLRENNTIRKVGSVNVSQLNTDNPEIGILIGEFFLWGKHIGRHSVSLVLKWLKNIGYKKAHARILE 133 (164)

T ss\_dssp HHHHTCCSEEEEEEEEEETTEEEEEEEEEEECTTSSSCEEEEEECSGGGTTSSHHHHHHHHHHHHHHHHTCSEEEEEEET

T ss\_pred HHHHhhcCCCCEEEEEEeCCCcceEEEEEEEeCCCCCceEEEEEeCHHHCCCCHHHHHHHHHHHHHHHcCCCEEEEEeec

Q ss\_pred CCcccccccccchhHHHHHcCCCEEeeeeeccccccc

Q Phabba\_Draft 86 SSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDVSNWG 122 (219)

Q Consensus 86 ~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~~~ 122 (219)

.|. .+.++|+++||+..+........+.

T Consensus 134 ~n~---------~~~~~~~~~Gf~~~~~~~~~~~~~~ 161 (164)

T 3EO4\_C 134 NNI---------RSIKLFESLGFKKTKKGRENEWIYE 161 (164)

T ss\_dssp TCH---------HHHHHHHHTTCEEEEECSTTEEEEE

T ss\_pred cCH---------HHHHHHHHcCCEEEEeecccceEEE

No 141

>3EO4\_D Uncharacterized protein MJ1062; APC60792.2,MJ\_1062,Methanocaldococcus jannaschii DSM 2661, structural; HET: PG6, EDO, MES; 2.19A {Methanocaldococcus jannaschii}

Probab=98.42 E-value=7e-08 Score=74.78 Aligned\_cols=99 Identities=11% Similarity=-0.022 Sum\_probs=0.0 Template\_Neff=11.800

Q ss\_pred chHHHHHhhCCcEEEEEECC--EEEEEEEEEeC----CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEEEc

Q Phabba\_Draft 15 FEPFDTMWSNGIMARHAHDD--RPVGHLHWHPD----GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPVRH 85 (219)

Q Consensus 15 ~~~l~~~~~~~~~~v~~~~~--~liG~~~~~~~----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v~~ 85 (219)

..+.........++++..++ ++||++.+... .++..++|+|++||+|||+.|++.+++.+.. ..+.+.+..

T Consensus 54 ~~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~i~~~~v~~~~rg~Gig~~l~~~~~~~~~~~~~~~i~~~~~~ 133 (164)

T 3EO4\_D 54 SWWMSRENRVDWIILLRENNTIRKVGSVNVSQLNTDNPEIGILIGEFFLWGKHIGRHSVSLVLKWLKNIGYKKAHARILE 133 (164)

T ss\_dssp HHHHHCCSEEEEEEEEEETTEEEEEEEEEEECTTSSSCEEEEEECCGGGTTSSHHHHHHHHHHHHHHHHTCCEEEEEEET

T ss\_pred HHHHhhcCCCCEEEEEEeCCCcceEEEEEEEeCCCCCceEEEEEeCHHHCCCCHHHHHHHHHHHHHHHcCCCEEEEEeec

Q ss\_pred CCcccccccccchhHHHHHcCCCEEeeeeeccccccc

Q Phabba\_Draft 86 SSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDVSNWG 122 (219)

Q Consensus 86 ~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~~~ 122 (219)

.|. .+.++|+++||+..+........+.

T Consensus 134 ~n~---------~~~~~~~~~Gf~~~~~~~~~~~~~~ 161 (164)

T 3EO4\_D 134 NNI---------RSIKLFESLGFKKTKKGRENEWIYE 161 (164)

T ss\_dssp TCH---------HHHHHHHTTTCEEEEECSTTEEEEE

T ss\_pred cCH---------HHHHHHHHcCCEEEEeecccceEEE

No 142

>3MGD\_A Predicted acetyltransferase; Structural Genomics, PSI-2, Protein Structure; HET: ACO; 1.9A {Clostridium acetobutylicum}

Probab=98.42 E-value=4.5e-08 Score=74.06 Aligned\_cols=92 Identities=16% Similarity=0.167 Sum\_probs=0.0 Template\_Neff=12.600

Q ss\_pred hHHHHHhhCCc--EEEEEECCEEEEEEEEEe----------C---CEEEEEEECHHHCCCCHHHHHHHHHHHccccCeeE

Q Phabba\_Draft 16 EPFDTMWSNGI--MARHAHDDRPVGHLHWHP----------D---GEIDSITVHPDLQRRGIGTAMLKHAQDNPHIYESS 80 (219)

Q Consensus 16 ~~l~~~~~~~~--~~v~~~~~~liG~~~~~~----------~---~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~~~i~ 80 (219)

+.+...+..+. ++++.+++++||++.+.. . ..+..++|+|++|++|+|+.|++.+++.+++..+.

T Consensus 40 ~~~~~~~~~~~~~~~v~~~~~~~vG~~~~~~~~~~~~~~~~~~~~~~i~~~~v~~~~r~~g~~~~l~~~~~~~~~~~g~~ 119 (157)

T 3MGD\_A 40 RYFNNKLANNLLVEWIAEENNQIIATAAIAFIDFPPTYTNKTGRKGYITNMYTEPTSRGNGIATGMLDRLVNEAKERNIH 119 (157)

T ss\_dssp HHHHHHHHTTSEEEEEEEETTEEEEEEEEEEEECCCBTTBTTCEEEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHTTCC

T ss\_pred HHHHHHhhcCceEEEEEEeCCeEEEEEEEEEcCCCccccccCCCEEEEEEEEECHHHCCCCHHHHHHHHHHHHHHHCCCc

Q ss\_pred EEEEcCCcccccccccchhHHHHHcCCCEEeeeeec

Q Phabba\_Draft 81 YPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADD 116 (219)

Q Consensus 81 l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~ 116 (219)

......|. .+.++|+++||+..+....

T Consensus 120 ~i~~~~~~---------~~~~~~~~~Gf~~~~~~~~ 146 (157)

T 3MGD\_A 120 KICLVASK---------LGRPVYKKYGFQDTDEWLE 146 (157)

T ss\_dssp CEEECCCT---------THHHHHHHHTCCCCTTCCC

T ss\_pred EEEEEEcC---------CChhHHHhcCcEecchHHH

No 143

>3MGD\_B Predicted acetyltransferase; Structural Genomics, PSI-2, Protein Structure; HET: ACO; 1.9A {Clostridium acetobutylicum}

Probab=98.42 E-value=4.5e-08 Score=74.06 Aligned\_cols=92 Identities=16% Similarity=0.167 Sum\_probs=0.0 Template\_Neff=12.600

Q ss\_pred hHHHHHhhCCc--EEEEEECCEEEEEEEEEe----------C---CEEEEEEECHHHCCCCHHHHHHHHHHHccccCeeE

Q Phabba\_Draft 16 EPFDTMWSNGI--MARHAHDDRPVGHLHWHP----------D---GEIDSITVHPDLQRRGIGTAMLKHAQDNPHIYESS 80 (219)

Q Consensus 16 ~~l~~~~~~~~--~~v~~~~~~liG~~~~~~----------~---~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~~~i~ 80 (219)

+.+...+..+. ++++.+++++||++.+.. . ..+..++|+|++|++|+|+.|++.+++.+++..+.

T Consensus 40 ~~~~~~~~~~~~~~~v~~~~~~~vG~~~~~~~~~~~~~~~~~~~~~~i~~~~v~~~~r~~g~~~~l~~~~~~~~~~~g~~ 119 (157)

T 3MGD\_B 40 RYFNNKLANNLLVEWIAEENNQIIATAAIAFIDFPPTYTNKTGRKGYITNMYTEPTSRGNGIATGMLDRLVNEAKERNIH 119 (157)

T ss\_dssp HHHHHHHHTTSEEEEEEEETTEEEEEEEEEEEECCCBTTBTTCEEEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHTTCC

T ss\_pred HHHHHHhhcCceEEEEEEeCCeEEEEEEEEEcCCCccccccCCCEEEEEEEEECHHHCCCCHHHHHHHHHHHHHHHCCCc

Q ss\_pred EEEEcCCcccccccccchhHHHHHcCCCEEeeeeec

Q Phabba\_Draft 81 YPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADD 116 (219)

Q Consensus 81 l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~ 116 (219)

......|. .+.++|+++||+..+....

T Consensus 120 ~i~~~~~~---------~~~~~~~~~Gf~~~~~~~~ 146 (157)

T 3MGD\_B 120 KICLVASK---------LGRPVYKKYGFQDTDEWLE 146 (157)

T ss\_dssp CEECCCCT---------TTHHHHHHHTCCCCSCCCC

T ss\_pred EEEEEEcC---------CChhHHHhcCcEecchHHH

No 144

>4XNH\_C Yeast Saccharomyces cerevisiae Naa15, Yeast; N-terminal acetyltransferase, bisubstrate, inositol hexaxisphosphate; HET: ACO, I6P, CMC; 2.1A {Saccharomyces cerevisiae}

Probab=98.42 E-value=5.9e-08 Score=75.16 Aligned\_cols=84 Identities=18% Similarity=0.154 Sum\_probs=0.0 Template\_Neff=12.400

Q ss\_pred hCCcEEEEEECCEEEEEEEEEeC-----------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEEEcCCc

Q Phabba\_Draft 23 SNGIMARHAHDDRPVGHLHWHPD-----------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPVRHSSH 88 (219)

Q Consensus 23 ~~~~~~v~~~~~~liG~~~~~~~-----------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v~~~n~ 88 (219)

....++++..++++||++.+... ..+..++|+|++|++|+|+.|++.+++.+.. ..+.+.+...|.

T Consensus 57 ~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~~~i~~~~v~~~~r~~G~~~~l~~~~~~~~~~~~~~~i~~~~~~~n~ 136 (176)

T 4XNH\_C 57 DVHFTQMAYYSEIPVGGLVAKLVPKKQNELSLKGIQIEFLGVLPNYRHKSIGSKLLKFAEDKCSECHQHNVFVYLPAVDD 136 (176)

T ss\_dssp CCEEEEEEEETTEEEEEEEEEEECC--CCSSCCEEEEEEEEECGGGCSSSHHHHHHHHHHHHHHHTTCCEEEEEEETTCH

T ss\_pred CceeEEEEEECCeEEEEEEEEEccccCcccccceEEEEEEEEChhhCCCcHHHHHHHHHHHHHHHcCCceEEEEEeCCCH

Q ss\_pred ccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 89 FSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 89 ~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

.+.++|+++||+..+...

T Consensus 137 ---------~~~~~~~~~Gf~~~~~~~ 154 (176)

T 4XNH\_C 137 ---------LTKQWFIAHGFEQVGETV 154 (176)

T ss\_dssp ---------HHHHHHHHTTCEEEEEEE

T ss\_pred ---------HHHHHHHHcCCeEeeEee

No 145

>2Q0Y\_A GCN5-related N-acetyltransferase; YP\_295895.1, Acetyltransferase (GNAT) family, GCN5-related; HET: FMT; 1.8A {Ralstonia eutropha JMP134}

Probab=98.42 E-value=5.3e-08 Score=72.68 Aligned\_cols=97 Identities=19% Similarity=0.227 Sum\_probs=0.0 Template\_Neff=13.000

Q ss\_pred chHHHHHhhCCc--EEEEEECCEEEEEEEEEeC--------------CEEEEEEECHHHCCCCHHHHHHHHHHHccccCe

Q Phabba\_Draft 15 FEPFDTMWSNGI--MARHAHDDRPVGHLHWHPD--------------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHIYE 78 (219)

Q Consensus 15 ~~~l~~~~~~~~--~~v~~~~~~liG~~~~~~~--------------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~~~ 78 (219)

.+.+...+..+. ++++.+++++||.+.+... ..+..+.|+|++|++|+|++|++.+++.++...

T Consensus 41 ~~~~~~~~~~~~~~~~v~~~~~~~ig~~~~~~~~~~~~~~~~~~~~~~~~~~~~v~~~~r~~G~~~~l~~~~~~~~~~~~ 120 (153)

T 2Q0Y\_A 41 RDWLLPRLADGSYFGWVMEEGGAPLAGIGLMVIEWPPHPSHPLQDKRGYILNLYVDPSHRERGIGQALMNRAEAEFAERG 120 (153)

T ss\_dssp HHHHHHHHHHTSSEEEEEEETTEEEEEEEEEEEECCCBTTBTTCSEEEEEEEEEECGGGCSSSHHHHHHHHHHHHHHHTT

T ss\_pred HHHHHHHhhCCCEEEEEEEeCCceEEEEEEEEecCCCCCCCCCCCceEEEEEEEeCHhHCCCCHHHHHHHHHHHHHHHcC

Q ss\_pred eEEEEEcCCcccccccccchhHHHHHcCCCEEeeeeeccccc

Q Phabba\_Draft 79 SSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDVSN 120 (219)

Q Consensus 79 i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~ 120 (219)

+...+...|. .+.++|+++||+..+.+.....+

T Consensus 121 ~~~~~~~~n~---------~~~~~~~~~Gf~~~~~~~~~~~g 153 (153)

T 2Q0Y\_A 121 IAFAVLHATE---------MGQPLYARMGWSPTTEMSKPIAG 153 (153)

T ss\_dssp CCCEEECCCT---------TTHHHHHHTTCCCCCCCCCCSCC

T ss\_pred CCEEEEEecc---------ccHHHHHhcCCccccccccccCC

No 146

>2CY2\_A probable acetyltransferase; STRUCTURAL GENOMICS, UNKNOWN FUNCTION, NPPSFA; HET: ACO; 2.0A {Thermus thermophilus} SCOP: d.108.1.1

Probab=98.42 E-value=7e-08 Score=74.28 Aligned\_cols=97 Identities=18% Similarity=0.200 Sum\_probs=0.0 Template\_Neff=12.600

Q ss\_pred chHHHHHhhCC----cEEEEEE-CCEEEEEEEEEeC---------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---C

Q Phabba\_Draft 15 FEPFDTMWSNG----IMARHAH-DDRPVGHLHWHPD---------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---Y 77 (219)

Q Consensus 15 ~~~l~~~~~~~----~~~v~~~-~~~liG~~~~~~~---------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~ 77 (219)

.+.+...+... .++++.+ +|+++|++.+... ..+..++|+|++|++|+|++|++.+++.+.+ .

T Consensus 44 ~~~~~~~~~~~~~~~~~~v~~~~~~~~vG~~~~~~~~~~~~~~~~~~i~~~~v~~~~r~~g~~~~l~~~~~~~~~~~g~~ 123 (174)

T 2CY2\_A 44 AERWAQRLKTPTWPGRLFVAESESGEVVGFAAFGPDRASGFPGYTAELWAIYVLPTWQRKGLGRALFHEGARLLQAEGYG 123 (174)

T ss\_dssp HHHHHHHHHCTTCCCEEEEEECTTSCEEEEEEEEECCSCSCTTCCEEEEEEEECGGGCSSSHHHHHHHHHHHHHHHTTCC

T ss\_pred HHHHHHHhcCCCCCceEEEEEcCCCCEEEEEEEEeCCCCCCCCCceEEEEEEECHHHCCCCHHHHHHHHHHHHHHHCCCc

Q ss\_pred eeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeeeccccc

Q Phabba\_Draft 78 ESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDVSN 120 (219)

Q Consensus 78 ~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~ 120 (219)

.+.+.+...|. .+.++|+++||+..+........

T Consensus 124 ~v~~~~~~~n~---------~~~~~~~k~Gf~~~~~~~~~~~~ 157 (174)

T 2CY2\_A 124 RMLVWVLKENP---------KGRGFYEHLGGVLLGEREIELGG 157 (174)

T ss\_dssp EEEEEEETTCH---------HHHHHHHHTTCEEEEEEEEEETT

T ss\_pred ceEEEEecCCH---------HHHHHHHHcCcEEEceEEEEeCC

No 147

>1WK4\_B ttk003001606; ttk003001606, STRUCTURAL GENOMICS, RIKEN Structural; HET: MES; 2.8A {Thermus thermophilus} SCOP: d.108.1.1

Probab=98.42 E-value=7e-08 Score=74.28 Aligned\_cols=97 Identities=18% Similarity=0.200 Sum\_probs=0.0 Template\_Neff=12.600

Q ss\_pred chHHHHHhhCC----cEEEEEE-CCEEEEEEEEEeC---------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---C

Q Phabba\_Draft 15 FEPFDTMWSNG----IMARHAH-DDRPVGHLHWHPD---------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---Y 77 (219)

Q Consensus 15 ~~~l~~~~~~~----~~~v~~~-~~~liG~~~~~~~---------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~ 77 (219)

.+.+...+... .++++.+ +|+++|++.+... ..+..++|+|++|++|+|++|++.+++.+.+ .

T Consensus 44 ~~~~~~~~~~~~~~~~~~v~~~~~~~~vG~~~~~~~~~~~~~~~~~~i~~~~v~~~~r~~g~~~~l~~~~~~~~~~~g~~ 123 (174)

T 1WK4\_B 44 AERWAQRLKTPTWPGRLFVAESESGEVVGFAAFGPDRASGFPGYTAELWAIYVLPTWQRKGLGRALFHEGARLLQAEGYG 123 (174)

T ss\_dssp HHHHHHHHHCTTCCCEEEEEECSSSCEEEEEEEEECCSCCCTTCCEEEEEEEECGGGCSSSHHHHHHHHHHHHHTTTTCC

T ss\_pred HHHHHHHhcCCCCCceEEEEEcCCCCEEEEEEEEeCCCCCCCCCceEEEEEEECHHHCCCCHHHHHHHHHHHHHHHCCCc

Q ss\_pred eeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeeeccccc

Q Phabba\_Draft 78 ESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDVSN 120 (219)

Q Consensus 78 ~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~ 120 (219)

.+.+.+...|. .+.++|+++||+..+........

T Consensus 124 ~v~~~~~~~n~---------~~~~~~~k~Gf~~~~~~~~~~~~ 157 (174)

T 1WK4\_B 124 RMLVWVLKENP---------KGRGFYEHLGGVLLGEREIELGG 157 (174)

T ss\_dssp EEEEEEETTCH---------HHHHHHHTTTCEEEEEEEEEETT

T ss\_pred ceEEEEecCCH---------HHHHHHHHcCcEEEceEEEEeCC

No 148

>3LOD\_A Putative acyl-CoA N-acyltransferase; acyl-CoA N-acyltransferase, structural genomics, PSI2; 2.5A {Klebsiella pneumoniae subsp. pneumoniae}

Probab=98.42 E-value=7.6e-08 Score=74.12 Aligned\_cols=100 Identities=13% Similarity=0.108 Sum\_probs=0.0 Template\_Neff=12.000

Q ss\_pred HHHHhhCCcEEEEEE--CCEEEEEEEEEeC----CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEEEcCCc

Q Phabba\_Draft 18 FDTMWSNGIMARHAH--DDRPVGHLHWHPD----GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPVRHSSH 88 (219)

Q Consensus 18 l~~~~~~~~~~v~~~--~~~liG~~~~~~~----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v~~~n~ 88 (219)

.........++++.. +|++||++.+... .++..+.|+|++|++|+++.|++.+.+.+.. ..+.+.+...|.

T Consensus 41 ~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~~~~~~~~~n~ 120 (162)

T 3LOD\_A 41 LSQLPPQTVIALAIRSPQGEAVGCGAIVLSEEGFGEMKRVYIDPQHRGQQLGEKLLAALEAKARQRDCHTLRLETGIHQH 120 (162)

T ss\_dssp GGTSCGGGEEEEEEECSSCCEEEEEEEEECTTSEEEEEEEEECTTSCSSSHHHHHHHHHHHHHHTTTCCEEEEEEETTCH

T ss\_pred hhhCCCCCeEEEEEECCCCCEEEEEEEEEccCCcEEEEEEEECHHHCCCCHHHHHHHHHHHHHHhCCCCEEEEEecCCcH

Q ss\_pred ccccccccchhHHHHHcCCCEEeeeeeccccccceEEe

Q Phabba\_Draft 89 FSAAGRAWAQSDPDYHDPGDQNVTKADDDVSNWGYTAM 126 (219)

Q Consensus 89 ~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~~~~~~~ 126 (219)

.+.++|+++||+..+.............+

T Consensus 121 ---------~~~~~~~~~Gf~~~~~~~~~~~~~~~~~~ 149 (162)

T 3LOD\_A 121 ---------AAIALYTRNGYQTRCAFAPYQPDPLSVFM 149 (162)

T ss\_dssp ---------HHHHHHHHTTCEEECCCTTCCCCSSEEEE

T ss\_pred ---------HHHHHHHHCCCEEeeccccCCCCcceEEe

No 149

>2JDD\_A GLYPHOSATE N-ACETYLTRANSFERASE; GNAT, GLYPHOSATE, TRANSFERASE, N-ACETYLTRANSFERASE; HET: ACO, 3PG; 1.6A {BACILLUS LICHENIFORMIS} SCOP: d.108.1.1

Probab=98.42 E-value=6.3e-08 Score=72.96 Aligned\_cols=117 Identities=9% Similarity=0.037 Sum\_probs=0.0 Template\_Neff=12.200

Q ss\_pred CCccccCCCCCCCCchHHHHHhhCCcEEEEEECCEEEEEEEEE----------eCCEEEEEEECHHHCCCCHHHHHHHHH

Q Phabba\_Draft 1 MHQAGANGDLPPLKFEPFDTMWSNGIMARHAHDDRPVGHLHWH----------PDGEIDSITVHPDLQRRGIGTAMLKHA 70 (219)

Q Consensus 1 ~~~~~~~~~~~~~~~~~l~~~~~~~~~~v~~~~~~liG~~~~~----------~~~~i~~l~V~p~~R~~Gig~~Ll~~~ 70 (219)

+.+.......................++++.+++++||++.+. ....+..++|+|++|++|++..|+..+

T Consensus 15 l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ivg~~~~~~~~~~~~~~~~~~~i~~~~v~~~~r~~g~~~~l~~~~ 94 (146)

T 2JDD\_A 15 LRHRILRPNQPIEACMFESDLLRGAFHLGGYYGGKLISIASFHQAEHSELQGQKQYQLRGMATLEGYREQKAGSSLIKHA 94 (146)

T ss\_dssp HCCCCCCTTSCGGGGSCGGGGSTTCEEEEEEETTEEEEEEEEEECCCTTSCCSSEEEEEEEEECTTSTTSSHHHHHHHHH

T ss\_pred hHhhhcCCCCCccceeeccccccCceEEEEEECCEEEEEEEEEecccchhcCCCEEEEEEEEeCHHHccCChHHHHHHHH

Q ss\_pred HHccccCeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeeeccccccceEEe

Q Phabba\_Draft 71 QDNPHIYESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDVSNWGYTAM 126 (219)

Q Consensus 71 ~~~~~~~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~~~~~~~ 126 (219)

++.+....+...+...|. .+.++|+++||+..+.............+

T Consensus 95 ~~~~~~~~~~~~~~~~n~---------~~~~~~~~~Gf~~~~~~~~~~~~~~~~~~ 141 (146)

T 2JDD\_A 95 EEILRKRGADLLWCNART---------SASGYYKKLGFSEQGEVFDTPPVGPHILM 141 (146)

T ss\_dssp HHHHHHTTCCEEEEEEEG---------GGHHHHHHTTCEEEEEEEECTTSCEEEEE

T ss\_pred HHHHHHCCCCEEEEecCh---------hhHHHHHHhCcEEeeeEecCCCCCceEEE

No 150

>3EY5\_A Acetyltransferase-like, GNAT family; structural genomics, APC60148, acetyltransferase, GNAT; HET: SO4; 2.15A {Bacteroides thetaiotaomicron}

Probab=98.41 E-value=4.6e-08 Score=77.96 Aligned\_cols=102 Identities=18% Similarity=0.141 Sum\_probs=0.0 Template\_Neff=11.100

Q ss\_pred hHHHHHhhCCcEEEEEECCEEEEEEEEEeC---CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEEEcCCcc

Q Phabba\_Draft 16 EPFDTMWSNGIMARHAHDDRPVGHLHWHPD---GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPVRHSSHF 89 (219)

Q Consensus 16 ~~l~~~~~~~~~~v~~~~~~liG~~~~~~~---~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v~~~n~~ 89 (219)

...........++++.+++++||++.+... ..+..++|+|++||+|+|+.|++.+++.++. ..+.+.+...|.

T Consensus 41 ~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~v~p~~r~~Gig~~l~~~~~~~~~~~~~~~i~~~~~~~n~- 119 (181)

T 3EY5\_A 41 REYTDRIGNFHNNIIFDDDLPIGFITYWDFDEFYYVEHFATNPALRNGGYGKRTLEHLCEFLKRPIVLEVERPVEEMAK- 119 (181)

T ss\_dssp HHHHHHCTTEEEEEEEETTEEEEEEEEEECSSCEEEEEEEECGGGTTSSHHHHHHHHHHHHCCSCEEEEECCTTSHHHH-

T ss\_pred HHHHHHhcCceEEEEEeCCeEEEEEEEEEcCCEEEEEEEEECHHHcCCCHHHHHHHHHHHHhcCCCeeEEeCChHHHHH-

Q ss\_pred cccccccchhHHHHHcCCCEEeeeeec------cccccceEEe

Q Phabba\_Draft 90 SAAGRAWAQSDPDYHDPGDQNVTKADD------DVSNWGYTAM 126 (219)

Q Consensus 90 ~~~~~~~~~~~~~y~r~Gf~~~~~~~~------~~~~~~~~~~ 126 (219)

.+.++|+++||+..+...+ ......+..+

T Consensus 120 --------~~~~~~~k~GF~~~~~~~~~~~~~~~~~~~~~~~~ 154 (181)

T 3EY5\_A 120 --------RRINFYQRHGFTLWEKDYYQPPYKEGDDFLPMYLM 154 (181)

T ss\_dssp --------HHHHHHHHTTCEEEEEEEEECCSSTTSCCEEEEEE

T ss\_pred --------HHHHHHHHCCCEEceeceecCCccCCCCcccEEEE

No 151

>2QEC\_A Histone acetyltransferase HPA2 and related; NP\_600742.1, histone acetyltransferase HPA2 and; HET: EDO; 1.9A {Corynebacterium glutamicum ATCC 13032}

Probab=98.41 E-value=8.6e-08 Score=76.96 Aligned\_cols=106 Identities=15% Similarity=0.135 Sum\_probs=0.0 Template\_Neff=11.800

Q ss\_pred HHHhhCCcEEEEEE-CCEEEEEEEEEeCC-------------------------------------------EEEEEEEC

Q Phabba\_Draft 19 DTMWSNGIMARHAH-DDRPVGHLHWHPDG-------------------------------------------EIDSITVH 54 (219)

Q Consensus 19 ~~~~~~~~~~v~~~-~~~liG~~~~~~~~-------------------------------------------~i~~l~V~ 54 (219)

........++++.+ ++++||++.+.... ++..++|+

T Consensus 55 ~~~~~~~~~~v~~~~~~~ivG~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~v~ 134 (204)

T 2QEC\_A 55 KQYAVAGNIDVARDSEGEIVGVALWDRPDGNHSAKDQAAMLPRLVSIFGIKAAQVAWTDLSSARFHPKFPHWYLYTVATS 134 (204)

T ss\_dssp CCCHHHEEEEEEECTTSCEEEEEEEECCC------------CCHHHHHC-CCC---------CTTSCSSCCEEEEEEEEC

T ss\_pred HHHcccCEEEEEeCCCCCEEEEEEEECCCCCCcHHHHHhhHHHHHHHhCCchHHHHHHHHHHhhhCCCCCeEEEEEEEEC

Q ss\_pred HHHCCCCHHHHHHHHHHHccccCeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeeeccccccceEEecCCCCCCC

Q Phabba\_Draft 55 PDLQRRGIGTAMLKHAQDNPHIYESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDVSNWGYTAMGEEGYTPL 134 (219)

Q Consensus 55 p~~R~~Gig~~Ll~~~~~~~~~~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~~~~~~~~~~~~~~~ 134 (219)

|++||+|+|+.|++.+++.++...+.+.. .|. .+.++|+++||+..+......+......+-.....+.

T Consensus 135 p~~rg~Gig~~Ll~~~~~~a~~~~~~~~~--~n~---------~~~~~y~k~GF~~~~~~~~~~~~~~~~~~~~~~~~~~ 203 (204)

T 2QEC\_A 135 SSARGTGVGSALLNHGIARAGDEAIYLEA--TST---------RAAQLYNRLGFVPLGYIPSDDDGTPELAMWKPPAMPT 203 (204)

T ss\_dssp GGGTTSSHHHHHHHHHHHHHTTSCEEEEE--SSH---------HHHHHHHHTTCEEEEEECCSSCSSCEEEEEECCCCCC

T ss\_pred HHHCCCCHHHHHHHHHHHhhhcCCcEEEE--ecH---------HHHHHHHHcCcEEeEeecCCCCCCcccccccCCCCCC

Q ss\_pred c

Q Phabba\_Draft 135 H 135 (219)

Q Consensus 135 ~ 135 (219)

.

T Consensus 204 ~ 204 (204)

T 2QEC\_A 204 V 204 (204)

T ss\_dssp C

T ss\_pred C

No 152

>4J3G\_A GCN5-related N-acetyltransferase (E.C.2.3.1.-); SSGCID, Seattle Structural Genomics Center; HET: EDO, SO4; 1.75A {Brucella melitensis biovar Abortus}

Probab=98.41 E-value=5.4e-08 Score=76.78 Aligned\_cols=92 Identities=13% Similarity=0.113 Sum\_probs=0.0 Template\_Neff=11.900

Q ss\_pred chHHHHHhhCCc-EEEEEECCEEEEEEEEEeC--------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEE

Q Phabba\_Draft 15 FEPFDTMWSNGI-MARHAHDDRPVGHLHWHPD--------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYP 82 (219)

Q Consensus 15 ~~~l~~~~~~~~-~~v~~~~~~liG~~~~~~~--------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~ 82 (219)

..++........ ++++..+|++||++.+... ..+..+.|+|++||+|+|++|++.+++.+++ ..+.+.

T Consensus 63 ~~~~~~~~~~~~~~~v~~~~~~ivG~~~~~~~~~~~~~~~~~~~~~~v~~~~r~~G~~~~l~~~~~~~~~~~g~~~i~~~ 142 (185)

T 4J3G\_A 63 HQWLENRNRDGFPVLVAEREGQVVGYASYGPFRPFEGFRHSSELSVYVASNARGGGIGRTLLAELIEEARERKVHVLIAG 142 (185)

T ss\_dssp HHHHHHHHHHTCCEEEEEETTEEEEEEEEEESSSSGGGTTEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHTTCCEEEEE

T ss\_pred HHHHHhccCCCCCEEEEEeCCEEEEEEEEeecCCccCCcceEEEEEEECcccCCCCHHHHHHHHHHHHHHHCCCcEEEEE

Q ss\_pred EEcCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 83 VRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 83 v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

+...|. .+.++|+++||+..+...

T Consensus 143 ~~~~n~---------~~~~~~~~~Gf~~~~~~~ 166 (185)

T 4J3G\_A 143 IEAGNA---------ASIALHRSQGFEECGTLK 166 (185)

T ss\_dssp EETTCH---------HHHHHHHHTTCEEEEEEE

T ss\_pred eeCCCH---------HHHHHHHHCCCEEceeeh

No 153

>4JWP\_A GCN5-related N-acetyltransferase (E.C.2.3.1.-); SSGCID, Ribosomal-protein-alanine N-acetyltransferase, Acetyl CoA; HET: ACO; 2.0A {Brucella abortus}

Probab=98.41 E-value=5.4e-08 Score=76.78 Aligned\_cols=92 Identities=13% Similarity=0.113 Sum\_probs=0.0 Template\_Neff=11.900

Q ss\_pred chHHHHHhhCCc-EEEEEECCEEEEEEEEEeC--------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEE

Q Phabba\_Draft 15 FEPFDTMWSNGI-MARHAHDDRPVGHLHWHPD--------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYP 82 (219)

Q Consensus 15 ~~~l~~~~~~~~-~~v~~~~~~liG~~~~~~~--------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~ 82 (219)

..++........ ++++..+|++||++.+... ..+..+.|+|++||+|+|++|++.+++.+++ ..+.+.

T Consensus 63 ~~~~~~~~~~~~~~~v~~~~~~ivG~~~~~~~~~~~~~~~~~~~~~~v~~~~r~~G~~~~l~~~~~~~~~~~g~~~i~~~ 142 (185)

T 4JWP\_A 63 HQWLENRNRDGFPVLVAEREGQVVGYASYGPFRPFEGFRHSSELSVYVASNARGGGIGRTLLAELIEEARERKVHVLIAG 142 (185)

T ss\_dssp HHHHHHHHHTTCCEEEEEETTEEEEEEEEEESSSSGGGTTEEEEEEEECTTSTTSSHHHHHHHHHHHHHHHTTCCEEEEE

T ss\_pred HHHHHhccCCCCCEEEEEeCCEEEEEEEEeecCCccCCcceEEEEEEECcccCCCCHHHHHHHHHHHHHHHCCCcEEEEE

Q ss\_pred EEcCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 83 VRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 83 v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

+...|. .+.++|+++||+..+...

T Consensus 143 ~~~~n~---------~~~~~~~~~Gf~~~~~~~ 166 (185)

T 4JWP\_A 143 IEAGNA---------ASIALHRSQGFEECGTLK 166 (185)

T ss\_dssp EETTCH---------HHHHHHHHTTCEEEEEEE

T ss\_pred eeCCCH---------HHHHHHHHCCCEEceeeh

No 154

>4LX9\_A Uncharacterized N-acetyltransferase SSO0209 (E.C.2.3.1.-); transferase, amino-terminal acetyltransferase, GNAT fold; HET: ACO; 1.98A {Sulfolobus solfataricus}

Probab=98.41 E-value=9.7e-08 Score=73.15 Aligned\_cols=89 Identities=20% Similarity=0.159 Sum\_probs=0.0 Template\_Neff=12.500

Q ss\_pred hCCcEEEEEECCEEEEEEEEEe---------------CCEEEEEEECHHHCCCCHHHHHHHHHHHcccc----CeeEEEE

Q Phabba\_Draft 23 SNGIMARHAHDDRPVGHLHWHP---------------DGEIDSITVHPDLQRRGIGTAMLKHAQDNPHI----YESSYPV 83 (219)

Q Consensus 23 ~~~~~~v~~~~~~liG~~~~~~---------------~~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~----~~i~l~v 83 (219)

....++++..+|++||++.+.. ..++..++|+|++||+|+|+.|++.+.+.+.. ..+.+.+

T Consensus 49 ~~~~~~~~~~~~~ivG~~~~~~~~~~~~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~~~~~~~ 128 (167)

T 4LX9\_A 49 YGLAFFVAIVDNSVVGYIMPRIEWGFSNIKQLPSLVRKGHVVSIAVLEEYRRKGIATTLLEASMKSMKNDYNAEEIYLEV 128 (167)

T ss\_dssp HGGGCEEEEETTEEEEEEEEEEEEEECSSCSSCCEEEEEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHTTCCSEEEEEE

T ss\_pred cCCeEEEEEECCEEEEEEEeEEeccCCCcccCchhhcccceEEEEeCHHHccCCHHHHHHHHHHHHHHhhcCCCEEEEEE

Q ss\_pred EcCCcccccccccchhHHHHHcCCCEEeeeeeccccc

Q Phabba\_Draft 84 RHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDVSN 120 (219)

Q Consensus 84 ~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~ 120 (219)

...|. .+.++|+++||+..+.....+..

T Consensus 129 ~~~n~---------~~~~~~~~~Gf~~~~~~~~~~~~ 156 (167)

T 4LX9\_A 129 RVSNY---------PAIALYEKLNFKKVKVLKGYYAD 156 (167)

T ss\_dssp ETTCH---------HHHHHHHHTTCEEEEEETTCSTT

T ss\_pred eccch---------HHHHHHHhCCcEEEEEecccccC

No 155

>d2euib\_ d.108.1.1 (B:) automated matches {Pseudomonas aeruginosa, PA01 [TaxId: 208964]}

Probab=98.41 E-value=1.1e-07 Score=71.09 Aligned\_cols=99 Identities=12% Similarity=0.112 Sum\_probs=0.0 Template\_Neff=12.800

Q ss\_pred chHHHHHhhCCc--EEEEEE--CCEEEEEEEEEeC---------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---Ce

Q Phabba\_Draft 15 FEPFDTMWSNGI--MARHAH--DDRPVGHLHWHPD---------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YE 78 (219)

Q Consensus 15 ~~~l~~~~~~~~--~~v~~~--~~~liG~~~~~~~---------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~ 78 (219)

.+.+...+.+.. ++++.. ++++||++.+... ..+..++|+|++|++|+++.|++.+++.+.. ..

T Consensus 35 ~~~~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~i~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~ 114 (150)

T d2euib\_ 35 RKFLEKRLRRKESVIYLALADEEDRLLGFCQLYPSFSSLSLKRVWILNDIYVAEEARRQLVADHLLQHAKQMARETHAVR 114 (150)

T ss\_dssp HHHHHHHHHHTCSEEEEEECC---CEEEEEEEEEEEETTTTEEEEEEEEEEECTTSCSSHHHHHHHHHHHHHHHHTTEEE

T ss\_pred HHHHHHHHhCCCceEEEEEEcCCCcEEEEEEEEecCCccccccEEEEEEEEECHHHcCCCHHHHHHHHHHHHHHHcCCcE

Q ss\_pred eEEEEEcCCcccccccccchhHHHHHcCCCEEeeeeeccccccc

Q Phabba\_Draft 79 SSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDVSNWG 122 (219)

Q Consensus 79 i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~~~ 122 (219)

+.+.+...|. .+.++|+++||+..+..........

T Consensus 115 ~~~~~~~~n~---------~~~~~~~~~Gf~~~~~~~~~~~~~~ 149 (150)

T d2euib\_ 115 MRVSTSVDNE---------VAQKVYESIGFREDQEFKNYTLPIS 149 (150)

T ss\_dssp EEECCBC-CH---------HHHHHHHTTTCEECCSEEEEEEECC

T ss\_pred EEEEeecCCH---------HHHHHHHHcCCeeecceEEEeccCC

No 156

>d3bj7b\_ d.108.1.1 (B:) automated matches {Mouse (Mus musculus) [TaxId: 10090]}

Probab=98.41 E-value=5.2e-08 Score=75.12 Aligned\_cols=82 Identities=16% Similarity=0.110 Sum\_probs=0.0 Template\_Neff=12.100

Q ss\_pred hCCcEEEEEE--------CCEEEEEEEEEeC--------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEE

Q Phabba\_Draft 23 SNGIMARHAH--------DDRPVGHLHWHPD--------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPV 83 (219)

Q Consensus 23 ~~~~~~v~~~--------~~~liG~~~~~~~--------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v 83 (219)

....++++.. ++++||++.+... .++..++|+|++|++|+|+.|++.+++.++. ..+.+.+

T Consensus 48 ~~~~~~v~~~~~~~~~~~~~~ivG~~~~~~~~~~~~~~~~~i~~~~v~~~~r~~Gi~~~l~~~~~~~~~~~g~~~i~~~~ 127 (165)

T d3bj7b\_ 48 PFYHCLVAEVPKEHWTPEGHSIVGFAMYYFTYDPWIGKLLYLEDFFVMSDYRGFGIGSEILKNLSQVAMKCRCSSMHFLV 127 (165)

T ss\_dssp CSCEEEEEECCGGGCCTTCCCEEEEEEEEEEEETTTEEEEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHTTCSEEEECC

T ss\_pred CceEEEEEEeccccCCCCCCcEEEEEEEEEccCccccceEEEEEEEECHHHCCCCHHHHHHHHHHHHHHHCCCCEEEEEE

Q ss\_pred EcCCcccccccccchhHHHHHcCCCEEeee

Q Phabba\_Draft 84 RHSSHFSAAGRAWAQSDPDYHDPGDQNVTK 113 (219)

Q Consensus 84 ~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~ 113 (219)

...|. .+.++|+++||+..+.

T Consensus 128 ~~~n~---------~~~~~~~~~Gf~~~~~ 148 (165)

T d3bj7b\_ 128 AEWNE---------PSINFYKRRGASDLSS 148 (165)

T ss\_dssp BTTCH---------HHHHHHHTTTCEEC--

T ss\_pred ecCCH---------HHHHHHHHcCCEeccc

No 157

>2FE7\_B probable N-acetyltransferase; Structural genomics, N-acetyltransferase, Pseudomonas aeruginosa; 2.0A {Pseudomonas aeruginosa UCBPP-PA14} SCOP: d.108.1.1

Probab=98.41 E-value=8e-08 Score=73.36 Aligned\_cols=91 Identities=13% Similarity=0.109 Sum\_probs=0.0 Template\_Neff=12.600

Q ss\_pred hHHHHHhhCCcEEEEEECCEEEEEEEEEeC---------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEE

Q Phabba\_Draft 16 EPFDTMWSNGIMARHAHDDRPVGHLHWHPD---------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPV 83 (219)

Q Consensus 16 ~~l~~~~~~~~~~v~~~~~~liG~~~~~~~---------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v 83 (219)

..+........++++.+++++||++.+... ..+..++|+|++|++|+|+.|++.++..++. ..+.+.+

T Consensus 50 ~~~~~~~~~~~~~~~~~~~~ivG~~~~~~~~~~~~~~~~~~i~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~i~~~~ 129 (166)

T 2FE7\_B 50 RSLFAEGSPTRALMCLSEGRPIGYAVFFYSYSTWLGRNGIYLEDLYVTPEYRGVGAGRRLLRELAREAVANDCGRLEWSV 129 (166)

T ss\_dssp HHHTSTTCSEEEEEEEESSSEEEEEEEEEEEETTTTEEEEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHTTCSEEEEEE

T ss\_pred HHHHhcCCCcEEEEEEECCeEEEEEEEEEcccccccCceEEEEEEEECHHHCCCCHHHHHHHHHHHHHHHCCCCEEEEEE

Q ss\_pred EcCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 84 RHSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 84 ~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

...|. .+.++|+++||+..+...

T Consensus 130 ~~~n~---------~~~~~~~~~Gf~~~~~~~ 152 (166)

T 2FE7\_B 130 LDWNQ---------PAIDFYRSIGALPQDEWV 152 (166)

T ss\_dssp ETTCH---------HHHHHHHHTTCEECTTEE

T ss\_pred ecCCH---------HHHHHHHhcCCcccceEE

No 158

>1ON0\_D similar to hypothetical proteins; structural genomics, alpha-beta protein with; HET: SO4; 2.2A {Bacillus subtilis} SCOP: d.108.1.1

Probab=98.41 E-value=7.3e-08 Score=72.15 Aligned\_cols=84 Identities=14% Similarity=0.107 Sum\_probs=0.0 Template\_Neff=13.100

Q ss\_pred hCCcEEEEEE-CCEEEEEEEEEeC-------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEEEcCCcccc

Q Phabba\_Draft 23 SNGIMARHAH-DDRPVGHLHWHPD-------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPVRHSSHFSA 91 (219)

Q Consensus 23 ~~~~~~v~~~-~~~liG~~~~~~~-------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v~~~n~~~~ 91 (219)

....++++.. +++++|++.+... ..+..+.|+|++|++|+|+.|++.+++.+.. ..+.+.+...|.

T Consensus 58 ~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~~g~~~i~~~~~~~n~--- 134 (158)

T 1ON0\_D 58 PHHHLWSLKLNEKDIVGWLWIHAEPEHPQQEAFIYDFGLYEPYRGKGYAKQALAALDQAARSMGIRKLSLHVFAHNQ--- 134 (158)

T ss\_dssp TTEEEEEEESSTTCEEEEEEEECCTTCTTCEEEEEEEEECTTSCSSSHHHHHHHHHHHHHHHTTCCEEEECCCTTCH---

T ss\_pred CCeeEEEEEeCCCCEEEEEEEEeCCCCCCceEEEEEEEeCHhhCCCChHHHHHHHHHHHHHHCCCCEEEEEEecCCH---

Q ss\_pred cccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 92 AGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 92 ~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

.+.++|+++||+..+...

T Consensus 135 ------~~~~~~~~~Gf~~~~~~~ 152 (158)

T 1ON0\_D 135 ------TARKLYEQTGFQETDVVM 152 (158)

T ss\_dssp ------HHHHHHHHTTCCCCCCCC

T ss\_pred ------HHHHHHHHcCCEEEEEEe

No 159

>2QML\_A BH2621 protein; Structural genomics, Joint Center for; HET: GOL; 1.55A {Bacillus halodurans}

Probab=98.41 E-value=1.3e-07 Score=74.68 Aligned\_cols=103 Identities=10% Similarity=-0.025 Sum\_probs=0.0 Template\_Neff=12.400

Q ss\_pred chHHHHHhhCCc--EEEEEECCEEEEEEEEE---------------eCCEEEEEEECHHHCCCCHHHHHHHHHHHcccc-

Q Phabba\_Draft 15 FEPFDTMWSNGI--MARHAHDDRPVGHLHWH---------------PDGEIDSITVHPDLQRRGIGTAMLKHAQDNPHI- 76 (219)

Q Consensus 15 ~~~l~~~~~~~~--~~v~~~~~~liG~~~~~---------------~~~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~- 76 (219)

.+.+........ ++++..++++||++.+. ....+..++++|++|++|+|+.|++.+++.+.+

T Consensus 58 ~~~~~~~~~~~~~~~~v~~~~~~~vG~~~~~~~~~~~~~~~~~~~~~~~~i~~~~~~~~~r~~Gi~~~l~~~~~~~~~~~ 137 (198)

T 2QML\_A 58 KKHLQTFLNDDHQTLMVGAINGVPMSYWESYWVKEDIIANYYPFEEHDQGIHLLIGPQEYLGQGLIYPLLLAIMQQKFQE 137 (198)

T ss\_dssp HHHHHHHHTCTTEEEEEEEETTEEEEEEEEEEGGGSGGGGGSCCCTTCEEEEEEECSGGGSSSSTHHHHHHHHHHHHHTS

T ss\_pred HHHHHHHhcCCCCcEEEEEECCEEEEEEEEEecChhHHhhcCCCCcccEEEEEEEcCHHHcCCChHHHHHHHHHHHHhhC

Q ss\_pred ---CeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeeeccccccceEEe

Q Phabba\_Draft 77 ---YESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDVSNWGYTAM 126 (219)

Q Consensus 77 ---~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~~~~~~~ 126 (219)

..+.+.+...|. .+.++|+++||+..+..............

T Consensus 138 ~~~~~i~~~~~~~n~---------~~~~~~~~~Gf~~~~~~~~~~~~~~~~~~ 181 (198)

T 2QML\_A 138 PDTNTIVAEPDRRNK---------KMIHVFKKCGFQPVKEVELPDKIGLLMKC 181 (198)

T ss\_dssp TTCCEEEECCBTTCH---------HHHHHHHHTTCEEEEEEECSSCEEEEEEE

T ss\_pred CCcCeEEEEecCCCH---------HHHHHHHHcCCEEeeeeeCCCceeEEEEE

No 160

>3PP9\_C Putative streptothricin acetyltransferase; Putative Streptothricin Acetyltransferase, Toxin Production; HET: ACO, PO4; 1.6A {Bacillus anthracis}

Probab=98.41 E-value=1.3e-07 Score=74.93 Aligned\_cols=104 Identities=11% Similarity=0.040 Sum\_probs=0.0 Template\_Neff=11.800

Q ss\_pred CCCCchHHHHHhhC--CcEEEEEECCEEEEEEEEEeC----CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEE

Q Phabba\_Draft 11 PPLKFEPFDTMWSN--GIMARHAHDDRPVGHLHWHPD----GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSY 81 (219)

Q Consensus 11 ~~~~~~~l~~~~~~--~~~~v~~~~~~liG~~~~~~~----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l 81 (219)

.+...+.+...... ..++++..++++||++.+... ..+..+.|+|++|++|+++.|++.+++.+.. ..+.+

T Consensus 60 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~i~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~i~~ 139 (187)

T 3PP9\_C 60 NDNEELVYNEYINKPNQIIYIALLHNQIIGFIVLKKNWNNYAYIEDITVDKKYRTLGVGKRLIAQAKQWAKEGNMPGIML 139 (187)

T ss\_dssp --CCCCCGGGGTTCSSEEEEEEEETTEEEEEEEEEECTTSSEEEEEEEECGGGCSSSHHHHHHHHHHHHHHHTTCCEEEE

T ss\_pred CCCcHHHHHHHhcCCCeEEEEEEECCEEEEEEEEEEcCCcEEEEEEEEECHHHCCCCHHHHHHHHHHHHHHhCCCCEEEE

Q ss\_pred EEEcCCcccccccccchhHHHHHcCCCEEeeeeeccccccce

Q Phabba\_Draft 82 PVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDVSNWGY 123 (219)

Q Consensus 82 ~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~~~~ 123 (219)

.+...|. .+.++|+++||+..+...........

T Consensus 140 ~~~~~n~---------~~~~~~~~~Gf~~~~~~~~~~~~~~~ 172 (187)

T 3PP9\_C 140 ETQNNNV---------AACKFYEKCGFVIGGFDFLVYKGLNM 172 (187)

T ss\_dssp EEETTCH---------HHHHHHHHTTCEEEEEESSGGGGTC-

T ss\_pred EeeCCCH---------HHHHHHHHCCCEEEEEEEEEecCCCC

No 161

>3PP9\_A Putative streptothricin acetyltransferase; Putative Streptothricin Acetyltransferase, Toxin Production; HET: ACO, PO4; 1.6A {Bacillus anthracis}

Probab=98.41 E-value=1.3e-07 Score=74.93 Aligned\_cols=104 Identities=11% Similarity=0.040 Sum\_probs=0.0 Template\_Neff=11.800

Q ss\_pred CCCCchHHHHHhhC--CcEEEEEECCEEEEEEEEEeC----CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEE

Q Phabba\_Draft 11 PPLKFEPFDTMWSN--GIMARHAHDDRPVGHLHWHPD----GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSY 81 (219)

Q Consensus 11 ~~~~~~~l~~~~~~--~~~~v~~~~~~liG~~~~~~~----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l 81 (219)

.+...+.+...... ..++++..++++||++.+... ..+..+.|+|++|++|+++.|++.+++.+.. ..+.+

T Consensus 60 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~i~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~i~~ 139 (187)

T 3PP9\_A 60 NDNEELVYNEYINKPNQIIYIALLHNQIIGFIVLKKNWNNYAYIEDITVDKKYRTLGVGKRLIAQAKQWAKEGNMPGIML 139 (187)

T ss\_dssp ----CCCGGGGSSCSSEEEEEEEETTEEEEEEEEEECTTSCEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHTTCCEEEE

T ss\_pred CCCcHHHHHHHhcCCCeEEEEEEECCEEEEEEEEEEcCCcEEEEEEEEECHHHCCCCHHHHHHHHHHHHHHhCCCCEEEE

Q ss\_pred EEEcCCcccccccccchhHHHHHcCCCEEeeeeeccccccce

Q Phabba\_Draft 82 PVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDVSNWGY 123 (219)

Q Consensus 82 ~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~~~~ 123 (219)

.+...|. .+.++|+++||+..+...........

T Consensus 140 ~~~~~n~---------~~~~~~~~~Gf~~~~~~~~~~~~~~~ 172 (187)

T 3PP9\_A 140 ETQNNNV---------AACKFYEKCGFVIGGFDFLVYKGLNM 172 (187)

T ss\_dssp EEETTCH---------HHHHHHHHTTCEEEEEESSGGGGTCS

T ss\_pred EeeCCCH---------HHHHHHHHCCCEEEEEEEEEecCCCC

No 162

>4FD4\_A Putative uncharacterized protein (E.C.2.3.1.87 ; GNAT, transferase; HET: GOL; 1.95A {Aedes aegypti}

Probab=98.40 E-value=7.1e-08 Score=78.63 Aligned\_cols=91 Identities=11% Similarity=0.031 Sum\_probs=0.0 Template\_Neff=11.500

Q ss\_pred HHHHHhhCCcEEEEEEC--CEEEEEEEEE---------------------------------------------eCCEEE

Q Phabba\_Draft 17 PFDTMWSNGIMARHAHD--DRPVGHLHWH---------------------------------------------PDGEID 49 (219)

Q Consensus 17 ~l~~~~~~~~~~v~~~~--~~liG~~~~~---------------------------------------------~~~~i~ 49 (219)

.......++.++++.++ |++||++.+. ...++.

T Consensus 51 ~~~~~~~~~~~~v~~~~~~~~ivG~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~ 130 (217)

T 4FD4\_A 51 FSLSFVEQGTVVVAEDSAAKKFIGVSIAGPIQPGDPDAMVEEAATTETKKWGDILKLLALLERTADVCGRYGLEKAYHVH 130 (217)

T ss\_dssp HHHTTTTTTCEEEEEETTTTEEEEEEEEEEECTTHHHHHHHHHHHSSCHHHHHHHHHHHHHHHHHCHHHHHTCSCEEEEE

T ss\_pred HHHHHHhcCeEEEEEeCCCCeEEEEEEEeeeCCCCchhhHHhhhhcCChhHHHHHHHHHHHHhccChhHhhCCCceEEEE

Q ss\_pred EEEECHHHCCCCHHHHHHHHHHHcccc-CeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeeec

Q Phabba\_Draft 50 SITVHPDLQRRGIGTAMLKHAQDNPHI-YESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADD 116 (219)

Q Consensus 50 ~l~V~p~~R~~Gig~~Ll~~~~~~~~~-~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~ 116 (219)

.++|+|++||+|+|++|++.+++.+++ ....+.+..+|. .+.++|+|+||+..+...+

T Consensus 131 ~l~V~~~~rg~G~g~~ll~~~~~~a~~~g~~~~~~~~~n~---------~~~~~~~k~GF~~~~~~~~ 189 (217)

T 4FD4\_A 131 ILAVDPTYRGHSLGQRLLQFQMDLSKKLGFKAISGDFTSV---------FSVKLAEKLGMECISQLAL 189 (217)

T ss\_dssp EEEECTTSCSSCHHHHHHHHHHHHHHHHTCSEEEEEECSH---------HHHHHHHHTTCEEEEEEEG

T ss\_pred EEEEChhhCCCcHHHHHHHHHHHHHHHhCCCEEEEEcCCH---------HHHHHHHHcCCEEEEEEEh

No 163

>1YGH\_B PROTEIN (GCN5) (2.3.1.48); TRANSCRIPTIONAL REGULATION, HISTONE ACETYLATION, N-ACETYLTRANSFERASE; HET: GOL; 1.9A {Saccharomyces cerevisiae} SCOP: d.108.1.1

Probab=98.40 E-value=1.5e-07 Score=73.17 Aligned\_cols=96 Identities=19% Similarity=0.194 Sum\_probs=0.0 Template\_Neff=11.600

Q ss\_pred CCCCCchHHHHHhhCCc---EEEEEECCEEEEEEEEEeC-----CEEEEEEECHHHCCCCHHHHHHHHHHHcccc-CeeE

Q Phabba\_Draft 10 LPPLKFEPFDTMWSNGI---MARHAHDDRPVGHLHWHPD-----GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI-YESS 80 (219)

Q Consensus 10 ~~~~~~~~l~~~~~~~~---~~v~~~~~~liG~~~~~~~-----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~-~~i~ 80 (219)

.+....+.+...+.... ++++..++++||++.+... ..+..++|+|++|++|+|++|++.+++.+.. ....

T Consensus 30 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~i~~~~v~~~~r~~G~g~~l~~~~~~~~~~~~~~~ 109 (164)

T 1YGH\_B 30 LPKMPKEYIARLVYDRSHLSMAVIRKPLTVVGGITYRPFDKREFAEIVFCAISSTEQVRGYGAHLMNHLKDYVRNTSNIK 109 (164)

T ss\_dssp CTTSCHHHHHHHHHCTTCEEEEEEETTTEEEEEEEEEEEGGGTEEEEEEEEECTTCCCTTHHHHHHHHHHHHHHHHSCCC

T ss\_pred CCCCCHHHHHHHhhcCCCcEEEEEEeCCEEEEEEEEEEcCccCEEEEEEEEECHHHCCCCHHHHHHHHHHHHHhhcCCCE

Q ss\_pred EEEEcCCcccccccccchhHHHHHcCCCEEeeee

Q Phabba\_Draft 81 YPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKA 114 (219)

Q Consensus 81 l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~ 114 (219)

..+...|. .+.++|+++||+..+..

T Consensus 110 ~~~~~~n~---------~~~~~~~~~Gf~~~~~~ 134 (164)

T 1YGH\_B 110 YFLTYADN---------YAIGYFKKQGFTKEITL 134 (164)

T ss\_dssp EEEEEECG---------GGHHHHHHTTCBSSCCS

T ss\_pred EEEEecch---------HHHHHHHHCCCEEeEEe

No 164

>4QC6\_B Bifunctional AAC/APH (E.C.2.3.1.-, 2.7.1.-); antibiotic resistance, GNAT family, acetyltransferase; HET: FMT, 30N, KAN; 1.3A {Staphylococcus warneri}

Probab=98.40 E-value=1e-07 Score=73.93 Aligned\_cols=95 Identities=13% Similarity=0.145 Sum\_probs=0.0 Template\_Neff=12.500

Q ss\_pred CCCCchHHHHHhhCC-----cEEEEEECCEEEEEEEEEeC-----------------CEEEEEEECHHHCCCCHHHHHHH

Q Phabba\_Draft 11 PPLKFEPFDTMWSNG-----IMARHAHDDRPVGHLHWHPD-----------------GEIDSITVHPDLQRRGIGTAMLK 68 (219)

Q Consensus 11 ~~~~~~~l~~~~~~~-----~~~v~~~~~~liG~~~~~~~-----------------~~i~~l~V~p~~R~~Gig~~Ll~ 68 (219)

.+...+.+...+... .++++..++++||++.+... ..+..++|+|++|++|+|++|++

T Consensus 39 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~~~~~~~~~i~~~~v~~~~r~~g~~~~l~~ 118 (179)

T 4QC6\_B 39 KKYTLESLKKHYTEPWEDEVFRVIIEYNNVPIGYGQIYKMYDELYTDYHYPKTDEIVYGMDQFIGEPNYWSKGIGTRYIK 118 (179)

T ss\_dssp CCCCSCC-CCGGGCCCSSCEEEEEEEETTEEEEEEEEEECCHHHHHHHTCCCCSSCEEEEEEEESCGGGTTSSHHHHHHH

T ss\_pred CCCCHHHHHHHccCCccccceEEEEEECCEEEEEEEEEEcccccccccCCCCCCccEEEeeEEEeChhhcCCCHHHHHHH

Q ss\_pred HHHHccc-c---CeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeee

Q Phabba\_Draft 69 HAQDNPH-I---YESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKA 114 (219)

Q Consensus 69 ~~~~~~~-~---~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~ 114 (219)

.+++.+. . ..+.+.+...|. .+.++|+++||+..+..

T Consensus 119 ~~~~~~~~~~g~~~i~~~~~~~n~---------~~~~~~~~~Gf~~~~~~ 159 (179)

T 4QC6\_B 119 LIFEFLKKERNANAVILDPHKNNP---------RAIRAYQKSGFRIIEDL 159 (179)

T ss\_dssp HHHHHHHHHHCCCEEEECCBTTCH---------HHHHHHHHHTCEEEEEE

T ss\_pred HHHHHHHHhcCCCEEEEeccCCCH---------HHHHHHHHcCCEEEEEe

No 165

>d1wk4a\_ d.108.1.1 (A:) Probable acetyltransferase TTHA1209 {Thermus thermophilus [TaxId: 274]}

Probab=98.40 E-value=8.7e-08 Score=73.76 Aligned\_cols=97 Identities=18% Similarity=0.200 Sum\_probs=0.0 Template\_Neff=12.600

Q ss\_pred chHHHHHhhCC----cEEEEEE-CCEEEEEEEEEeC---------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---C

Q Phabba\_Draft 15 FEPFDTMWSNG----IMARHAH-DDRPVGHLHWHPD---------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---Y 77 (219)

Q Consensus 15 ~~~l~~~~~~~----~~~v~~~-~~~liG~~~~~~~---------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~ 77 (219)

.+.+...+... .++++.. +|+++|++.+... ..+..++|+|++|++|+|+.|+..+++.+++ .

T Consensus 44 ~~~~~~~~~~~~~~~~~~v~~~~~~~~vG~~~~~~~~~~~~~~~~~~i~~~~v~~~~r~~g~~~~l~~~~~~~~~~~g~~ 123 (174)

T d1wk4a\_ 44 AERWAQRLKTPTWPGRLFVAESESGEVVGFAAFGPDRASGFPGYTAELWAIYVLPTWQRKGLGRALFHEGARLLQAEGYG 123 (174)

T ss\_dssp HHHHHHHHSCTTCCCEEEEEECTTCCEEEEEEEEECCSCCCTTCCEEEEEEEECGGGCSSSHHHHHHHHHHHHHHHTTCS

T ss\_pred HHHHHHHhcCCCCCceEEEEECCCCCEEEEEEEeeccCCCCCCCceEEEEEEECHHhCCCCHHHHHHHHHHHHHHHCCCc

Q ss\_pred eeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeeeccccc

Q Phabba\_Draft 78 ESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDVSN 120 (219)

Q Consensus 78 ~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~ 120 (219)

.+.+.+...|. .+.++|+++||+..+........

T Consensus 124 ~i~~~~~~~n~---------~~~~~~~~~Gf~~~~~~~~~~~~ 157 (174)

T d1wk4a\_ 124 RMLVWVLKENP---------KGRGFYEHLGGVLLGEREIELGG 157 (174)

T ss\_dssp EEEEEEESSCH---------HHHHHHHHTTCEEEEEEEEEETT

T ss\_pred eeEEEEeCCCH---------HHHHHHHHcCcEEEceEEEEeCC

No 166

>1Y9W\_B Acetyltransferase; Bacillus cereus, acetyltransferase, Structural Genomics; 1.9A {Bacillus cereus} SCOP: d.108.1.1

Probab=98.40 E-value=1.6e-07 Score=70.91 Aligned\_cols=108 Identities=11% Similarity=0.066 Sum\_probs=0.0 Template\_Neff=11.700

Q ss\_pred CCCCCchHHHHHhh---CCcEEEEEE-CCEEEEEEEEEeC---CEEEEEEECHHHCCCCHHHHHHHHHHHcccc-CeeEE

Q Phabba\_Draft 10 LPPLKFEPFDTMWS---NGIMARHAH-DDRPVGHLHWHPD---GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI-YESSY 81 (219)

Q Consensus 10 ~~~~~~~~l~~~~~---~~~~~v~~~-~~~liG~~~~~~~---~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~-~~i~l 81 (219)

+.++..+.+...+. ...++++.. +|++||++.+... ..+..+.|+|++||+|+|+.|+..+++.+.. ....+

T Consensus 21 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~v~~~~rg~g~~~~l~~~~~~~~~~~~~~~i 100 (140)

T 1Y9W\_B 21 VIQYNMSILTDEVKQPMEEVSLVVKNEEGKIFGGVTGTMYFYHLHIDFLWVDESVRHDGYGSQLLHEIEGIAKEKGCRLI 100 (140)

T ss\_dssp HHHHHHHHSCGGGCCCCEEEEEEEECTTSCEEEEEEEEEETTEEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHTTCSEE

T ss\_pred hhhcCHhHhHHHhcCCccccEEEEEecCCeEEEEEEEEEeceEEEEEEEEEChhhCCCCHHHHHHHHHHHHHHHcCCCEE

Q ss\_pred EEEcCCcccccccccchhHHHHHcCCCEEeeeeeccccccceEEe

Q Phabba\_Draft 82 PVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDVSNWGYTAM 126 (219)

Q Consensus 82 ~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~~~~~~~ 126 (219)

.+...|. .+.++|++.||+..+.......+.....+

T Consensus 101 ~~~~~n~---------~~~~~~~~~Gf~~~~~~~~~~~g~~~~~~ 136 (140)

T 1Y9W\_B 101 LLDSFSF---------QAPEFYKKHGYREYGVVEDHPKGHSQHFF 136 (140)

T ss\_dssp EEEEEGG---------GCHHHHHHTTCEEEEEETTSSTTCCEEEE

T ss\_pred EEEecCc---------cHHHHHHHCCCEEEEEEcCCCCCccEEEE

No 167

>5HMN\_A aminoglycoside acetyltransferase HMB0005; GNAT FOLD, GCN5-N-ACETYLTRANSFERASE FOLD, ACETYLTRANSFERASE; HET: COA, PG4; 2.018A {uncultured bacterium}

Probab=98.39 E-value=1.2e-07 Score=71.25 Aligned\_cols=92 Identities=15% Similarity=0.035 Sum\_probs=0.0 Template\_Neff=13.000

Q ss\_pred chHHHHHhhCCc--EEEEEECCEEEEEEEEEeC---------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeE

Q Phabba\_Draft 15 FEPFDTMWSNGI--MARHAHDDRPVGHLHWHPD---------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESS 80 (219)

Q Consensus 15 ~~~l~~~~~~~~--~~v~~~~~~liG~~~~~~~---------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~ 80 (219)

..+......... ++++..++++||++.+... ..+..+.|+|++|++|+|+.|++.+++.+.. ..+.

T Consensus 42 ~~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~i~~~~v~~~~r~~g~~~~l~~~~~~~~~~~g~~~~~ 121 (159)

T 5HMN\_A 42 GAYSRRLLESDYFIALAALEYGEIVGGLAAYELKKFEQERSEIYIYDLAVAKAHRRRGIATALIEKLKELGAARGAYVIF 121 (159)

T ss\_dssp HHHHHHHHHSSSEEEEEEEETTEEEEEEEEEEEECSSSSCEEEEEEEEEECGGGCSSSHHHHHHHHHHHHHHHHTCCEEE

T ss\_pred hhHHHHHhhcCcEEEEEEeccCcEEEEEEEEEeccccCCCcEEEEEEEEECHHHCCCCHHHHHHHHHHHHHHhCCCcEEE

Q ss\_pred EEEEc--CCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 81 YPVRH--SSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 81 l~v~~--~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

+.+.. .|. .+.++|+++||+..+...

T Consensus 122 ~~~~~~~~n~---------~~~~~~~~~Gf~~~~~~~ 149 (159)

T 5HMN\_A 122 VQADTAIEDE---------PAIALYSKLGVREEVLHF 149 (159)

T ss\_dssp EEEECSGGGH---------HHHHHHHHHSEEEEEEEE

T ss\_pred EEecccCCCc---------hHHHHHHHcCCeEEEEEE

No 168

>5HMN\_B aminoglycoside acetyltransferase HMB0005; GNAT FOLD, GCN5-N-ACETYLTRANSFERASE FOLD, ACETYLTRANSFERASE; HET: COA, PG4; 2.018A {uncultured bacterium}

Probab=98.39 E-value=1.2e-07 Score=71.25 Aligned\_cols=92 Identities=15% Similarity=0.035 Sum\_probs=0.0 Template\_Neff=13.000

Q ss\_pred chHHHHHhhCCc--EEEEEECCEEEEEEEEEeC---------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeE

Q Phabba\_Draft 15 FEPFDTMWSNGI--MARHAHDDRPVGHLHWHPD---------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESS 80 (219)

Q Consensus 15 ~~~l~~~~~~~~--~~v~~~~~~liG~~~~~~~---------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~ 80 (219)

..+......... ++++..++++||++.+... ..+..+.|+|++|++|+|+.|++.+++.+.. ..+.

T Consensus 42 ~~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~i~~~~v~~~~r~~g~~~~l~~~~~~~~~~~g~~~~~ 121 (159)

T 5HMN\_B 42 GAYSRRLLESDYFIALAALEYGEIVGGLAAYELKKFEQERSEIYIYDLAVAKAHRRRGIATALIEKLKELGAARGAYVIF 121 (159)

T ss\_dssp HHHHHHHHHSSSEEEEEEEETTEEEEEEEEEEEECSSSSCEEEEEEEEEECGGGCSSSHHHHHHHHHHHHHHHTTEEEEE

T ss\_pred hhHHHHHhhcCcEEEEEEeccCcEEEEEEEEEeccccCCCcEEEEEEEEECHHHCCCCHHHHHHHHHHHHHHhCCCcEEE

Q ss\_pred EEEEc--CCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 81 YPVRH--SSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 81 l~v~~--~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

+.+.. .|. .+.++|+++||+..+...

T Consensus 122 ~~~~~~~~n~---------~~~~~~~~~Gf~~~~~~~ 149 (159)

T 5HMN\_B 122 VQADTAIEDE---------PAIALYSKLGVREEVLHF 149 (159)

T ss\_dssp EEEECSGGGH---------HHHHHHHHHSEEEEEEEE

T ss\_pred EEecccCCCc---------hHHHHHHHcCCeEEEEEE

No 169

>1YVO\_B conserved hypothetical protein (E.C.2.3.-.-); Hypothetical protein, structural genomics, hypothetical; 1.9A {Pseudomonas aeruginosa} SCOP: d.108.1.1

Probab=98.39 E-value=9.7e-08 Score=73.36 Aligned\_cols=101 Identities=14% Similarity=0.075 Sum\_probs=0.0 Template\_Neff=12.600

Q ss\_pred chHHHHHhhCCc-EEEEEE-CCEEEEEEEEEeC--------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEE

Q Phabba\_Draft 15 FEPFDTMWSNGI-MARHAH-DDRPVGHLHWHPD--------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSY 81 (219)

Q Consensus 15 ~~~l~~~~~~~~-~~v~~~-~~~liG~~~~~~~--------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l 81 (219)

...+........ ++++.. ++++||++.+... ..+..++|+|++|++|+|+.|++.+++.++. ..+.+

T Consensus 42 ~~~~~~~~~~~~~~~~~~~~~~~ivG~~~~~~~~~~~~~~~~~~~~~~v~~~~r~~gi~~~l~~~~~~~~~~~g~~~i~~ 121 (172)

T 1YVO\_B 42 QAWFDTRARQGYPILVASDAAGEVLGYASYGDWRPFEGFRGTVEHSVYVRDDQRGKGLGVQLLQALIERARAQGLHVMVA 121 (172)

T ss\_dssp HHHHHHHHHHTCCEEEEECTTCCEEEEEEEEESSSSGGGTTEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHTTCCEEEE

T ss\_pred HHHHHHhhhcCCcEEEEECCCCCEEEEEEeCCCccCCCcccEEEEEEEECHHHCCCCHHHHHHHHHHHHHHHCCCCEEEE

Q ss\_pred EEEcCCcccccccccchhHHHHHcCCCEEeeeeeccccccceE

Q Phabba\_Draft 82 PVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDVSNWGYT 124 (219)

Q Consensus 82 ~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~~~~~ 124 (219)

.+...|. .+.++|+++||+..+.........+..

T Consensus 122 ~~~~~n~---------~~~~~~~~~Gf~~~~~~~~~~~~~g~~ 155 (172)

T 1YVO\_B 122 AIESGNA---------ASIGLHRRLGFEISGQMPQVGQKFGRW 155 (172)

T ss\_dssp EEETTCH---------HHHHHHHHTTCEEEEEEEEEEEETTEE

T ss\_pred EeecCCH---------HHHHHHHHcCCEEEEEeceeEeeCCEE

No 170

>4KVX\_B N-terminal acetyltransferase A complex catalytic; acetyltransferase, transferase; HET: ACO; 2.0A {Schizosaccharomyces pombe}

Probab=98.39 E-value=8.6e-08 Score=72.60 Aligned\_cols=92 Identities=18% Similarity=0.120 Sum\_probs=0.0 Template\_Neff=12.500

Q ss\_pred chHHHHHhhCCc-EEEEEE-CCEEEEEEEEE---------eCCEEEEEEECHHHCCCCHHHHHHHHHHHccc-c---Cee

Q Phabba\_Draft 15 FEPFDTMWSNGI-MARHAH-DDRPVGHLHWH---------PDGEIDSITVHPDLQRRGIGTAMLKHAQDNPH-I---YES 79 (219)

Q Consensus 15 ~~~l~~~~~~~~-~~v~~~-~~~liG~~~~~---------~~~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~-~---~~i 79 (219)

..++......+. ++++.+ ++++||++.+. ....+..+.|+|++|++|+++.|++.+++.+. . ..+

T Consensus 29 ~~~~~~~~~~~~~~~~~~~~~~~ivg~~~~~~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~~~ 108 (156)

T 4KVX\_B 29 KYYLYHAISWPMLSYVATDPKGRVVGYVLAKMEEEPKDGIPHGHITSVSVMRSYRHLGLAKRLMVQSQRAMVEVYGAKYM 108 (156)

T ss\_dssp HHHHHHHHTSTTSCEEEECTTSCEEEEEEEEECSSCGGGCCEEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHHHCCSEE

T ss\_pred HHHHHHhcccceeEEEEECCCCcEEEEEEEEecCCCCCCCcEEEEEEEEECHHHccCCHHHHHHHHHHHHHHHHhCCCEE

Q ss\_pred EEEEEcCCcccccccccchhHHHHHc-CCCEEeeeee

Q Phabba\_Draft 80 SYPVRHSSHFSAAGRAWAQSDPDYHD-PGDQNVTKAD 115 (219)

Q Consensus 80 ~l~v~~~n~~~~~~~~~~~~~~~y~r-~Gf~~~~~~~ 115 (219)

.+.+...|. .+.++|++ +||+..+...

T Consensus 109 ~~~~~~~n~---------~~~~~~~k~~Gf~~~~~~~ 136 (156)

T 4KVX\_B 109 SLHVRKSNR---------AAIHLYRDTLQFDVQGIES 136 (156)

T ss\_dssp EEEEETTCH---------HHHCCCCCCSCCEEEEEET

T ss\_pred EEEEEecCH---------HHHHHHHhccCceEEEecc

No 171

>4KVM\_F N-terminal acetyltransferase A complex subunit; Acetyltransferase, TPR repeats, amino-terminal acetylation; HET: 1XE, CL, SO4; 2.597A {Schizosaccharomyces pombe}

Probab=98.39 E-value=8.6e-08 Score=72.60 Aligned\_cols=92 Identities=18% Similarity=0.120 Sum\_probs=0.0 Template\_Neff=12.500

Q ss\_pred chHHHHHhhCCc-EEEEEE-CCEEEEEEEEE---------eCCEEEEEEECHHHCCCCHHHHHHHHHHHccc-c---Cee

Q Phabba\_Draft 15 FEPFDTMWSNGI-MARHAH-DDRPVGHLHWH---------PDGEIDSITVHPDLQRRGIGTAMLKHAQDNPH-I---YES 79 (219)

Q Consensus 15 ~~~l~~~~~~~~-~~v~~~-~~~liG~~~~~---------~~~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~-~---~~i 79 (219)

..++......+. ++++.+ ++++||++.+. ....+..+.|+|++|++|+++.|++.+++.+. . ..+

T Consensus 29 ~~~~~~~~~~~~~~~~~~~~~~~ivg~~~~~~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~~~ 108 (156)

T 4KVM\_F 29 KYYLYHAISWPMLSYVATDPKGRVVGYVLAKMEEEPKDGIPHGHITSVSVMRSYRHLGLAKRLMVQSQRAMVEVYGAKYM 108 (156)

T ss\_dssp HHHHHHHHHSTTSCEEEECTTCCEEEEEEEEECSSCGGGCCCEEEEEEEECGGGCSSSHHHHHHHHHHHHHHHHHCCSEE

T ss\_pred HHHHHHhcccceeEEEEECCCCcEEEEEEEEecCCCCCCCcEEEEEEEEECHHHccCCHHHHHHHHHHHHHHHHhCCCEE

Q ss\_pred EEEEEcCCcccccccccchhHHHHHc-CCCEEeeeee

Q Phabba\_Draft 80 SYPVRHSSHFSAAGRAWAQSDPDYHD-PGDQNVTKAD 115 (219)

Q Consensus 80 ~l~v~~~n~~~~~~~~~~~~~~~y~r-~Gf~~~~~~~ 115 (219)

.+.+...|. .+.++|++ +||+..+...

T Consensus 109 ~~~~~~~n~---------~~~~~~~k~~Gf~~~~~~~ 136 (156)

T 4KVM\_F 109 SLHVRKSNR---------AAIHLYRDTLQFDVQGIES 136 (156)

T ss\_dssp EEEEETTCH---------HHHHHHTTTSCCEEEEEET

T ss\_pred EEEEEecCH---------HHHHHHHhccCceEEEecc

No 172

>1M4I\_A Aminoglycoside 2'-N-acetyltransferase (E.C.2.3.1.-); COA BINDING MOTIF, TRANSFERASE; HET: PAP, COA, KAN; 1.5A {Mycobacterium tuberculosis} SCOP: d.108.1.1

Probab=98.39 E-value=5.1e-08 Score=76.91 Aligned\_cols=83 Identities=16% Similarity=0.123 Sum\_probs=0.0 Template\_Neff=11.700

Q ss\_pred CCcEEEEEECCEEEEEEEEEe-----------CCEEEEEEECHHHCCCCHHHHHHHHHHHccccCeeEEEEEcCCccccc

Q Phabba\_Draft 24 NGIMARHAHDDRPVGHLHWHP-----------DGEIDSITVHPDLQRRGIGTAMLKHAQDNPHIYESSYPVRHSSHFSAA 92 (219)

Q Consensus 24 ~~~~~v~~~~~~liG~~~~~~-----------~~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~~~i~l~v~~~n~~~~~ 92 (219)

...++++.++|++||++.+.. ..++..++|+|++||+|+|+.|++.+++.+++ .+.+.+...|.

T Consensus 46 ~~~~~~~~~~~~ivG~~~~~~~~~~~~~~~~~~~~i~~~~v~~~~rg~Gi~~~l~~~~~~~~~~-~~~~~~~~~n~---- 120 (181)

T 1M4I\_A 46 GGMHALIWHHGAIIAHAAVIQRRLIYRGNALRCGYVEGVAVRADWRGQRLVSALLDAVEQVMRG-AYQLGALSSSA---- 120 (181)

T ss\_dssp SSEEEEEEETTEEEEEEEEEEEEEEETTEEEEEEEEEEEEECGGGTTSSHHHHHHHHHHHHHHH-HCSEEEEECCT----

T ss\_pred CCcEEEEEECCEEEEEEEEEEeeeeeCCceeEEEEEEEEEECHHHCCCCHHHHHHHHHHHHHhh-cCcEEEEcCCH----

Q ss\_pred ccccchhHHHHHcCCCEEeeeeec

Q Phabba\_Draft 93 GRAWAQSDPDYHDPGDQNVTKADD 116 (219)

Q Consensus 93 ~~~~~~~~~~y~r~Gf~~~~~~~~ 116 (219)

.+.++|+++||+.......

T Consensus 121 -----~~~~~y~~~Gf~~~~~~~~ 139 (181)

T 1M4I\_A 121 -----RARRLYASRGWLPWHGPTS 139 (181)

T ss\_dssp -----TTHHHHHHTTCEECCSCEE

T ss\_pred -----HHHHHHHhCCceecCCCeE

No 173

>5IX3\_A Diamine N-acetyltransferase (E.C.2.3.1.57); N-acetyltransferase, GNATs, SPEG, Staphylococcus aureus; 1.81A {Staphylococcus aureus}

Probab=98.39 E-value=1.2e-07 Score=73.36 Aligned\_cols=92 Identities=12% Similarity=0.045 Sum\_probs=0.0 Template\_Neff=12.100

Q ss\_pred chHHHHHhhCCc--EEEEEECCEEEEEEEEEeC-----CEEEEEEECHHHCCCCHHHHHHHHHHHcccc----CeeEEEE

Q Phabba\_Draft 15 FEPFDTMWSNGI--MARHAHDDRPVGHLHWHPD-----GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI----YESSYPV 83 (219)

Q Consensus 15 ~~~l~~~~~~~~--~~v~~~~~~liG~~~~~~~-----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~----~~i~l~v 83 (219)

.+.+........ ++++..++++||++.+... .....+.|+|++|++|+|+.|++.+++.+.+ ..+.+.+

T Consensus 42 ~~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~ll~~~~~~~~~~~~~~~~~~~~ 121 (168)

T 5IX3\_A 42 QHLFDKHLLDESERRFIVEDENQVVGIVELVEINYIHRNCEIQIIIKPEFSGKGYAKFAFEKAIIYAFNILNMHKIYLYV 121 (168)

T ss\_dssp HHHHHHTTTCTTCEEEEEEESSCEEEEEEEEEEETTTTEEEEEEEECGGGTTSSHHHHHHHHHHHCCCCCSCCSEEEEEE

T ss\_pred HHHHHHccCCccccEEEEEeCCeEEEEEEEEEeecCCCeEEEEEEECHHHCCCCHHHHHHHHHHHHHHHHcCcCEEEEEE

Q ss\_pred EcCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 84 RHSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 84 ~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

...|. .+.++|+++||+..+...

T Consensus 122 ~~~n~---------~~~~~~~~~Gf~~~~~~~ 144 (168)

T 5IX3\_A 122 DADNK---------KAIHIYESEGFKTEGLLK 144 (168)

T ss\_dssp ETTCH---------HHHHHHHHTTCEEEEEEE

T ss\_pred eCCCH---------HHHHHHHHCCCeEEEEEe

No 174

>4E8O\_B Aac(6')-Ih protein (E.C.2.3.1.-); antibiotic resistance, Center for Structural; 2.138A {Acinetobacter baumannii}

Probab=98.39 E-value=1e-07 Score=73.38 Aligned\_cols=92 Identities=13% Similarity=0.125 Sum\_probs=0.0 Template\_Neff=12.300

Q ss\_pred hHHHHHhhCCc--EEEEEEC-CEEEEEEEEEeC------------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---C

Q Phabba\_Draft 16 EPFDTMWSNGI--MARHAHD-DRPVGHLHWHPD------------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---Y 77 (219)

Q Consensus 16 ~~l~~~~~~~~--~~v~~~~-~~liG~~~~~~~------------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~ 77 (219)

+.+...+.... ++++..+ +++||++.+... ..+..++|+|++|++|+|+.|++.+++.+.. .

T Consensus 52 ~~~~~~~~~~~~~~~~~~~~~~~ivG~~~~~~~~~~~~~~~~~~~~~i~~~~v~p~~r~~g~~~~l~~~~~~~~~~~g~~ 131 (167)

T 4E8O\_B 52 QEMRQLITQAHRLQLLAYTDTQQAIAMLEASIRYEYVNGTQTSPVAFLEGIFVLPEYRRSGIATGLVQQVEIWAKQFACT 131 (167)

T ss\_dssp HHHHHHTTCTTEEEEEEECTTCCEEEEEEEEEECSCCTTCSSSSEEEEEEEEECGGGGGGTHHHHHHHHHHHHHHHTTCC

T ss\_pred HHHHHHhhccCeEEEEEEeCCCcEEEEEEEEEeeccCCCCCCCCEEEEEEEEeCHHHhCCCHHHHHHHHHHHHHHHcCCc

Q ss\_pred eeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeeec

Q Phabba\_Draft 78 ESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADD 116 (219)

Q Consensus 78 ~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~ 116 (219)

.+.+.+...|. .+.++|+++||+..+....

T Consensus 132 ~i~~~~~~~n~---------~~~~~~~~~Gf~~~~~~~~ 161 (167)

T 4E8O\_B 132 EFASDAALDNQ---------ISHAMHQALGFHETERVVY 161 (167)

T ss\_dssp EEEEEEETTCH---------HHHHHHHHTTCEEEEEEEE

T ss\_pred EEEEeeecccH---------HHHHHHHHcCCeeceeEEE

No 175

>d4ygoe\_ d.108.1.0 (E:) automated matches {Vibrio cholerae [TaxId: 666]}

Probab=98.39 E-value=1.2e-07 Score=73.09 Aligned\_cols=91 Identities=12% Similarity=0.095 Sum\_probs=0.0 Template\_Neff=12.200

Q ss\_pred hHHHHHhhCCc--EEEEEE-CCEEEEEEEEEeC-----CEEEEEEECHHHCCCCHHHHHHHHHHHcccc----CeeEEEE

Q Phabba\_Draft 16 EPFDTMWSNGI--MARHAH-DDRPVGHLHWHPD-----GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI----YESSYPV 83 (219)

Q Consensus 16 ~~l~~~~~~~~--~~v~~~-~~~liG~~~~~~~-----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~----~~i~l~v 83 (219)

+.+........ ++++.. +|++||++.+... ..+..++|+|++|++|+|+.|++.+++.+.. ..+.+.+

T Consensus 41 ~~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~ll~~~~~~~~~~~~~~~i~~~~ 120 (167)

T d4ygoe\_ 41 ELYNKHIHDNAERRFVVEDAQKNLIGLVELIEINYIHRSAEFQIIIAPEHQGKGFARTLINRALDYSFTILNLHKIYLHV 120 (167)

T ss\_dssp HHHHHHTTCCSCEEEEEEETTCCEEEEEEEEEEETTTTEEEEEEEECGGGTTSSCHHHHHHHHHHCCCCCSCCSEEEEEE

T ss\_pred HHHHHhcCCCCceEEEEEeCCCcEEEEEEEEEeeCCCCEEEEEEEECHHhCCCcHHHHHHHHHHHHHHHHcCCCEEEEEE

Q ss\_pred EcCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 84 RHSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 84 ~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

...|. .+.++|+++||+..+...

T Consensus 121 ~~~n~---------~~~~~~~~~Gf~~~~~~~ 143 (167)

T d4ygoe\_ 121 AVENP---------KAVHLYEECGFVEEGHLV 143 (167)

T ss\_dssp ETTCH---------HHHHHHHHTTCEEEEEEE

T ss\_pred EcCCH---------HHHHHHHHcCCEEEEEee

No 176

>d2vi7b\_ d.108.1.0 (B:) automated matches {Pseudomonas aeruginosa [TaxId: 287]}

Probab=98.39 E-value=1.1e-07 Score=72.31 Aligned\_cols=92 Identities=12% Similarity=0.093 Sum\_probs=0.0 Template\_Neff=12.700

Q ss\_pred chHHHHHhhCCc--EEEEEECCEEEEEEEEEeC-------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc----CeeEE

Q Phabba\_Draft 15 FEPFDTMWSNGI--MARHAHDDRPVGHLHWHPD-------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI----YESSY 81 (219)

Q Consensus 15 ~~~l~~~~~~~~--~~v~~~~~~liG~~~~~~~-------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~----~~i~l 81 (219)

.+.+........ ++++..+++++|++.+... ..+..+.|+|++|++|+|+.|++.+++.+.. ..+.+

T Consensus 41 ~~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~~i~~ 120 (164)

T d2vi7b\_ 41 RKRLHDSADDDRLLILVALHQGDVIGSASLEQHPRIRRSHSGSIGMGVAVAWQGKGVGSRLLGELLDIADNWMNLRRVEL 120 (164)

T ss\_dssp HHHHHTC-CCTTEEEEEEEETTEEEEEEEEEECSSGGGTTEEECTTCCEESSTTSSHHHHHHHHHHHHHHHTSCCSEEEE

T ss\_pred HHHHhhccCCCceEEEEEEeCCcEEEEEEEeecCccccccEEEEEEEEcHHHCCCCHHHHHHHHHHHHHHHhcCCCEEEE

Q ss\_pred EEEcCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 82 PVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 82 ~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

.+...|. .+.++|+++||+..+...

T Consensus 121 ~~~~~n~---------~~~~~~~~~Gf~~~~~~~ 145 (164)

T d2vi7b\_ 121 TVYTDNA---------PALALYRKFGFETEGEMR 145 (164)

T ss\_dssp EEETTCH---------HHHHHHHHTTCEEEEEEE

T ss\_pred EEecCCH---------HHHHHHHHhCCeEEEEec

No 177

>d1yghb\_ d.108.1.1 (B:) Catalytic domain of GCN5 histone acetyltransferase {Baker's yeast (Saccharomyces cerevisiae) [TaxId: 4932]}

Probab=98.39 E-value=1.8e-07 Score=72.81 Aligned\_cols=96 Identities=19% Similarity=0.194 Sum\_probs=0.0 Template\_Neff=11.600

Q ss\_pred CCCCCchHHHHHhhCCc---EEEEEECCEEEEEEEEEeC-----CEEEEEEECHHHCCCCHHHHHHHHHHHcccc-CeeE

Q Phabba\_Draft 10 LPPLKFEPFDTMWSNGI---MARHAHDDRPVGHLHWHPD-----GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI-YESS 80 (219)

Q Consensus 10 ~~~~~~~~l~~~~~~~~---~~v~~~~~~liG~~~~~~~-----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~-~~i~ 80 (219)

.+....+.+...+.... ++++..++++||++.+... ..+..++|+|++|++|+|++|++.+++.+.. ....

T Consensus 30 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~i~~~~v~~~~r~~G~g~~l~~~~~~~~~~~~~~~ 109 (164)

T d1yghb\_ 30 LPKMPKEYIARLVYDRSHLSMAVIRKPLTVVGGITYRPFDKREFAEIVFCAISSTEQVRGYGAHLMNHLKDYVRNTSNIK 109 (164)

T ss\_dssp CTTSCHHHHHHHHHCTTCEEEEEEETTTEEEEEEEEEEEGGGTEEEEEEEEECTTCCCTTHHHHHHHHHHHHHHHHSCCC

T ss\_pred CCCCCHHHHHHHhhcCCCcEEEEEEeCCEEEEEEEEEEcCccCEEEEEEEEECHHHCCCCHHHHHHHHHHHHHhhcCCCE

Q ss\_pred EEEEcCCcccccccccchhHHHHHcCCCEEeeee

Q Phabba\_Draft 81 YPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKA 114 (219)

Q Consensus 81 l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~ 114 (219)

..+...|. .+.++|+++||+..+..

T Consensus 110 ~~~~~~n~---------~~~~~~~~~Gf~~~~~~ 134 (164)

T d1yghb\_ 110 YFLTYADN---------YAIGYFKKQGFTKEITL 134 (164)

T ss\_dssp EEEEEECG---------GGHHHHHHTTCBSSCCS

T ss\_pred EEEEecch---------HHHHHHHHCCCEEeEEe

No 178

>1Z4R\_A General control of amino acid; GCN5, Acetyltransferase, SGC, Structural Genomics; HET: ACO; 1.74A {Homo sapiens} SCOP: d.108.1.1

Probab=98.38 E-value=1.4e-07 Score=75.28 Aligned\_cols=100 Identities=17% Similarity=0.156 Sum\_probs=0.0 Template\_Neff=10.200

Q ss\_pred CCCCCCCCchHHHHHhhCCc--EEEEEECCEEEEEEEEEeC-----CEEEEEEECHHHCCCCHHHHHHHHHHHccccCee

Q Phabba\_Draft 7 NGDLPPLKFEPFDTMWSNGI--MARHAHDDRPVGHLHWHPD-----GEIDSITVHPDLQRRGIGTAMLKHAQDNPHIYES 79 (219)

Q Consensus 7 ~~~~~~~~~~~l~~~~~~~~--~~v~~~~~~liG~~~~~~~-----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~~~i 79 (219)

....+....+.+...+..+. ++++..++++||++.+... ..+..++|+|++|++|||+.|+..+.+.+....+

T Consensus 34 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~i~~~~v~p~~r~~Gig~~l~~~~~~~~~~~g~ 113 (168)

T 1Z4R\_A 34 SHQLPRMPKEYIARLVFDPKHKTLALIKDGRVIGGICFRMFPTQGFTEIVFCAVTSNEQVKGYGTHLMNHLKEYHIKHNI 113 (168)

T ss\_dssp HHHCTTSCHHHHHHHHTCTTCEEEEEEETTEEEEEEEEEEETTTTEEEEEEEEECGGGCSSSHHHHHHHHHHHHHHHTTC

T ss\_pred ccCCCCCcHHHHHHHhhCCCCcEEEEEECCEEEEEEEEEEecCCCeEEEEEEEECHHHCCCCHHHHHHHHHHHHHHHCCC

Q ss\_pred EEEEEcCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 80 SYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 80 ~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

...+..+|. .+.++|+++||+..+...

T Consensus 114 ~~~~~~~n~---------~s~~~~~k~Gf~~~~~~~ 140 (168)

T 1Z4R\_A 114 LYFLTYADE---------YAIGYFKKQGFSKDIKVP 140 (168)

T ss\_dssp CEEEEEECG---------GGHHHHHHTTEESCCCSC

T ss\_pred CEEEEcCCH---------HHHHHHHHCCCEEeEecc

No 179

>5H86\_A Histone acetyltransferase KAT2A (E.C.2.3.1.48); Gcn5, Coenzyme A, transferase; HET: BCO; 2.08A {Homo sapiens}

Probab=98.38 E-value=1.4e-07 Score=75.28 Aligned\_cols=100 Identities=17% Similarity=0.156 Sum\_probs=0.0 Template\_Neff=10.200

Q ss\_pred CCCCCCCCchHHHHHhhCCc--EEEEEECCEEEEEEEEEeC-----CEEEEEEECHHHCCCCHHHHHHHHHHHccccCee

Q Phabba\_Draft 7 NGDLPPLKFEPFDTMWSNGI--MARHAHDDRPVGHLHWHPD-----GEIDSITVHPDLQRRGIGTAMLKHAQDNPHIYES 79 (219)

Q Consensus 7 ~~~~~~~~~~~l~~~~~~~~--~~v~~~~~~liG~~~~~~~-----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~~~i 79 (219)

....+....+.+...+..+. ++++..++++||++.+... ..+..++|+|++|++|||+.|+..+.+.+....+

T Consensus 34 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~i~~~~v~p~~r~~Gig~~l~~~~~~~~~~~g~ 113 (168)

T 5H86\_A 34 SHQLPRMPKEYIARLVFDPKHKTLALIKDGRVIGGICFRMFPTQGFTEIVFCAVTSNEQVKGYGTHLMNHLKEYHIKHNI 113 (168)

T ss\_dssp HHHSTTSCHHHHHHHHTCTTCEEEEEEETTEEEEEEEEEEETTTTEEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHTTC

T ss\_pred ccCCCCCcHHHHHHHhhCCCCcEEEEEECCEEEEEEEEEEecCCCeEEEEEEEECHHHCCCCHHHHHHHHHHHHHHHCCC

Q ss\_pred EEEEEcCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 80 SYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 80 ~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

...+..+|. .+.++|+++||+..+...

T Consensus 114 ~~~~~~~n~---------~s~~~~~k~Gf~~~~~~~ 140 (168)

T 5H86\_A 114 LYFLTYADE---------YAIGYFKKQGFSKDIKVP 140 (168)

T ss\_dssp CEEEEEECG---------GGHHHHHHTTEESSCCSC

T ss\_pred CEEEEcCCH---------HHHHHHHHCCCEEeEecc

No 180

>1VHS\_A similar to phosphinothricin acetyltransferase; structural genomics, unknown function; 1.8A {Bacillus subtilis} SCOP: d.108.1.1

Probab=98.38 E-value=7.8e-08 Score=74.86 Aligned\_cols=91 Identities=11% Similarity=0.011 Sum\_probs=0.0 Template\_Neff=12.100

Q ss\_pred chHHHHHhhCCcEEEEEE-CCEEEEEEEEEeC--------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEE

Q Phabba\_Draft 15 FEPFDTMWSNGIMARHAH-DDRPVGHLHWHPD--------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYP 82 (219)

Q Consensus 15 ~~~l~~~~~~~~~~v~~~-~~~liG~~~~~~~--------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~ 82 (219)

...+........++++.. ++++||++.+... .....++|+|++|++|+|+.|++.+++.++. ..+.+.

T Consensus 42 ~~~~~~~~~~~~~~v~~~~~~~~vG~~~~~~~~~~~~~~~~~~~~~~v~~~~r~~Gi~~~l~~~~~~~~~~~~~~~i~~~ 121 (175)

T 1VHS\_A 42 MEWFSGHTESRPLYVAEDENGNVAAWISFETFYGRPAYNKTAEVSIYIDEACRGKGVGSYLLQEALRIAPNLGIRSLMAF 121 (175)

T ss\_dssp HHHHHTCCSSSCEEEEECTTSCEEEEEEEEESSSSGGGTTEEEEEEEECGGGCSSSHHHHHHHHHHHHGGGGTCSEEEEE

T ss\_pred HHHHcccCCCCCEEEEECCCCCEEEEEEEEecCCccCCCceEEEEEEECHHHCCCCHHHHHHHHHHHHHHHcCCCEEEEE

Q ss\_pred EEcCCcccccccccchhHHHHHcCCCEEeeee

Q Phabba\_Draft 83 VRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKA 114 (219)

Q Consensus 83 v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~ 114 (219)

+...|. .+.++|+++||+..+..

T Consensus 122 ~~~~n~---------~~~~~~~~~Gf~~~~~~ 144 (175)

T 1VHS\_A 122 IFGHNK---------PSLKLFEKHGFAEWGLF 144 (175)

T ss\_dssp EETTCH---------HHHHHHHHTTCEEEEEE

T ss\_pred EeCCCh---------HHHHHHHHcCCEEEEee

No 181

>d3r9gb\_ d.108.1.0 (B:) automated matches {Escherichia coli [TaxId: 562]}

Probab=98.38 E-value=1.3e-07 Score=72.41 Aligned\_cols=93 Identities=8% Similarity=-0.040 Sum\_probs=0.0 Template\_Neff=12.800

Q ss\_pred chHHHHHh-----hCCcEEEEEECCEEEEEEEEEeC-----CEEEEEEECHHHCCCCHHHHHHHHHHHcccc----CeeE

Q Phabba\_Draft 15 FEPFDTMW-----SNGIMARHAHDDRPVGHLHWHPD-----GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI----YESS 80 (219)

Q Consensus 15 ~~~l~~~~-----~~~~~~v~~~~~~liG~~~~~~~-----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~----~~i~ 80 (219)

...+.... ....++++..+|++||++.+... .....+.|+|++|++|+|+.|++.+++.+.. ..+.

T Consensus 49 ~~~~~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~~i~ 128 (173)

T d3r9gb\_ 49 VSFIEQSMIDNQNEKALILFIKYKTKIAGVVSFNIIDHANKTAYIGYWLGANFQGKGIVTNAINKLIQEYGDSGVIKRFV 128 (173)

T ss\_dssp HHHHHHHHHHHHHTSCEEEEEEETTEEEEEEEEEEEETTTTEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHTTSCSEEE

T ss\_pred HHHHHHHhhhccccceEEEEEEeCCEEEEEEEeEEeeCCCCcEEEEEEeChhhcCCCHHHHHHHHHHHHHHhcCCccEEE

Q ss\_pred EEEEcCCcccccccccchhHHHHHcCCCEEeeeeec

Q Phabba\_Draft 81 YPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADD 116 (219)

Q Consensus 81 l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~ 116 (219)

+.+...|. .+.++|+++||+..+....

T Consensus 129 ~~~~~~n~---------~~~~~~~~~Gf~~~~~~~~ 155 (173)

T d3r9gb\_ 129 IKCIVDNK---------KSNATALRCGFTLEGVLQK 155 (173)

T ss\_dssp EEEETTCH---------HHHHHHHHTTCEEEEEEEE

T ss\_pred EEeecCCH---------HHHHHHHHCCCEEEEEEec

No 182

>d5dwnc\_ d.108.1.0 (C:) automated matches {Brucella ovis [TaxId: 444178]}

Probab=98.38 E-value=1.3e-07 Score=73.45 Aligned\_cols=92 Identities=17% Similarity=0.129 Sum\_probs=0.0 Template\_Neff=12.400

Q ss\_pred chHHHHHhhCCc-EEEEEECCEEEEEEEEEeC--------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEE

Q Phabba\_Draft 15 FEPFDTMWSNGI-MARHAHDDRPVGHLHWHPD--------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYP 82 (219)

Q Consensus 15 ~~~l~~~~~~~~-~~v~~~~~~liG~~~~~~~--------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~ 82 (219)

.+.+........ ++++..+|++||++.+... ..+..++|+|++|++|+|+.|++.+++.++. ..+.+.

T Consensus 41 ~~~~~~~~~~~~~~~~~~~~~~~iG~~~~~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~~g~~~~~~~ 120 (178)

T d5dwnc\_ 41 AKRFAAFADQGFPILVAEADGRVLGYAYASYFRVRPAYRWLAEDSIYIAPDAKGQGIGKLLLRELIARISALGFRQLLAV 120 (178)

T ss\_dssp HHHHHHHHHHTCCEEEEEETTEEEEEEEEEESCCSGGGTTEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHTTCSEEEEE

T ss\_pred HHHHHHHhhCCCcEEEEEeCCeEEEEEEEEecccCcccceEEEEEEEECHhHCCCCHHHHHHHHHHHHHHHcCCCEEEEE

Q ss\_pred EE--cCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 83 VR--HSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 83 v~--~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

+. ..|. .+.++|+++||+..+...

T Consensus 121 ~~~~~~n~---------~~~~~~~~~Gf~~~~~~~ 146 (178)

T d5dwnc\_ 121 IGDGEHNI---------GSVKLHESLGFTHCGRIE 146 (178)

T ss\_dssp ETTTTTCH---------HHHHHHHHTTCEEEEEEE

T ss\_pred ecCCCCCH---------HHHHHHHHcCCEEEeeec

No 183

>4LUA\_A Uncharacterized protein; NAT\_SF, acetyltransferase, transferase; 1.6001A {Staphylococcus aureus subsp. aureus}

Probab=98.38 E-value=9.8e-08 Score=73.28 Aligned\_cols=91 Identities=3% Similarity=-0.095 Sum\_probs=0.0 Template\_Neff=12.400

Q ss\_pred hHHHHHhhC--Cc--EEEEEECCEEEEEEEEEeCCE------EEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEE

Q Phabba\_Draft 16 EPFDTMWSN--GI--MARHAHDDRPVGHLHWHPDGE------IDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYP 82 (219)

Q Consensus 16 ~~l~~~~~~--~~--~~v~~~~~~liG~~~~~~~~~------i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~ 82 (219)

+.+...+.. .. ++++..++++||++.+..... +..+.+.+++||+|+|++|++.+++.++. ..+.+.

T Consensus 42 ~~~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~~~~~~~~r~~G~~~~l~~~~~~~~~~~~~~~~~~~ 121 (167)

T 4LUA\_A 42 TLIHDILNQGSPKCIVFGCYENETLIATAALEQIRYVGKEHKSLIKYNFVTNNDKSINSELINFIINYARQNNYESLLTS 121 (167)

T ss\_dssp HHHHHHHC----CEEEEEEEETTEEEEEEEEEEEC----CCEEEEEEEEEGGGCHHHHHHHHHHHHHHHHHTTCSEEEEE

T ss\_pred HHHHHHHhcCCCCeEEEEEEeCCeEEEEEEEEEeeecCccceEEEEEEecccCCCCHHHHHHHHHHHHHHhCCceEEEEE

Q ss\_pred EEcCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 83 VRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 83 v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

+...|. .+.++|+++||+..+...

T Consensus 122 ~~~~n~---------~~~~~~~~~Gf~~~~~~~ 145 (167)

T 4LUA\_A 122 IVSNNI---------GAKVFYSALGFDILGFEK 145 (167)

T ss\_dssp EETTCH---------HHHHHHHHTTCEEEEEEE

T ss\_pred EEcCCH---------HHHHHHHHcCCEEEEecc

No 184

>3C26\_A Putative acetyltransferase Ta0821; NP\_394282.1, A Putative Acetyltransferase, Acetyltransferase; HET: EDO, NO3; 2.0A {Thermoplasma acidophilum DSM 1728}

Probab=98.37 E-value=1.2e-07 Score=82.34 Aligned\_cols=99 Identities=15% Similarity=0.106 Sum\_probs=0.0 Template\_Neff=8.500

Q ss\_pred chHHHHHhhCCcEEEEEECCEEEEEEEEEeC----CEEEEEEECHHHCCCCHHHHHHHHHHHcccc--CeeEEEEEcCCc

Q Phabba\_Draft 15 FEPFDTMWSNGIMARHAHDDRPVGHLHWHPD----GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI--YESSYPVRHSSH 88 (219)

Q Consensus 15 ~~~l~~~~~~~~~~v~~~~~~liG~~~~~~~----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~--~~i~l~v~~~n~ 88 (219)

...+........++++..++++||++.+... ..+..++|+|++|++|+|++|++.+++.++. ..+.+.+...|.

T Consensus 50 ~~~~~~~~~~~~~~v~~~~g~iVG~i~~~~~~~~~~~i~~l~V~p~~rgkGig~~L~~~~~~~a~~~~~~i~~~~~~~N~ 129 (266)

T 3C26\_A 50 DKVIERWVNDGSVYVLRVSGRPVATIHMEKLPDGSVMLGGLRVHPEYRGSRLGMSIMQETIQFLRGKTERLRSAVYSWNE 129 (266)

T ss\_dssp HHHHHHHHHTTCEEEEEETTEEEEEEEEEECTTSCEEEEEEEECGGGTTSSHHHHHHHHHHHHHBTTBSEEEEEEETTCH

T ss\_pred HHHHHHHhcCCeEEEEEECCEEEEEEEEEECCCCeEEEEEEEECHHHCCCCHHHHHHHHHHHHHhhcCCeEEEEEECCCH

Q ss\_pred ccccccccchhHHHHHcCCCEEeeeeeccccccc

Q Phabba\_Draft 89 FSAAGRAWAQSDPDYHDPGDQNVTKADDDVSNWG 122 (219)

Q Consensus 89 ~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~~~~~ 122 (219)

.+.++|+|+||+..+..........

T Consensus 130 ---------~a~~~~~k~GF~~~~~~~~~~~~~g 154 (266)

T 3C26\_A 130 ---------PSLRLVHRLGFHQVEEYPIYTFQGG 154 (266)

T ss\_dssp ---------HHHHHHHHHTCEEEEEEEEEEEEEC

T ss\_pred ---------HHHHHHHHcCCEEEEEEcceeccCC

No 185

>d1vhsb1 d.108.1.1 (B:2-163) Putative phosphinothricin acetyltransferase YwnH {Bacillus subtilis [TaxId: 1423]}

Probab=98.37 E-value=7.9e-08 Score=72.93 Aligned\_cols=91 Identities=11% Similarity=0.003 Sum\_probs=0.0 Template\_Neff=12.700

Q ss\_pred hHHHHHhhCCcEEEEEE-CCEEEEEEEEEeC--------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEE

Q Phabba\_Draft 16 EPFDTMWSNGIMARHAH-DDRPVGHLHWHPD--------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPV 83 (219)

Q Consensus 16 ~~l~~~~~~~~~~v~~~-~~~liG~~~~~~~--------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v 83 (219)

..+........++++.. ++++||++.+... .....+.|+|++|++|+|++|++.+++.+.. ..+.+.+

T Consensus 40 ~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~~g~~~i~~~~ 119 (162)

T d1vhsb1 40 EWFSGHTESRPLYVAEDENGNVAAWISFETFYGRPAYNKTAEVSIYIDEACRGKGVGSYLLQEALRIAPNLGIRSLMAFI 119 (162)

T ss\_dssp HHHHTCCSSSCEEEEECTTSCEEEEEEEEESSSSGGGTTEEEEEEEECTTTSSSSHHHHHHHHHHHHGGGGTCSEEEEEE

T ss\_pred HHHccCCCCCCEEEEECCCCCEEEEEEEeccCCCCcccceEEEEEEECHHHCCCCHHHHHHHHHHHHHHHhCCCEEEEEE

Q ss\_pred EcCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 84 RHSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 84 ~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

...|. .+.++|+++||+..+...

T Consensus 120 ~~~n~---------~~~~~~~~~Gf~~~~~~~ 142 (162)

T d1vhsb1 120 FGHNK---------PSLKLFEKHGFAEWGLFP 142 (162)

T ss\_dssp ESSCH---------HHHHHHHHTTCEEEEEEE

T ss\_pred eCCCH---------HHHHHHHHCCCeEeeccC

No 186

>d2i79e\_ d.108.1.0 (E:) automated matches {Streptococcus pneumoniae [TaxId: 170187]}

Probab=98.36 E-value=1.3e-07 Score=72.48 Aligned\_cols=92 Identities=12% Similarity=0.029 Sum\_probs=0.0 Template\_Neff=12.500

Q ss\_pred chHHHHHhhCCc--EEEEEECCEEEEEEEEEeC-------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc----CeeEE

Q Phabba\_Draft 15 FEPFDTMWSNGI--MARHAHDDRPVGHLHWHPD-------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI----YESSY 81 (219)

Q Consensus 15 ~~~l~~~~~~~~--~~v~~~~~~liG~~~~~~~-------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~----~~i~l 81 (219)

...+......+. ++++..+|++||++.+... .....++|+|++|++|+|++|++.+++.+.. ..+.+

T Consensus 44 ~~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~~i~~ 123 (168)

T d2i79e\_ 44 EIFLNKQASSDNQITLLAFLNGKIAGIVNITADQRKRVRHIGDLFIVIGKRYWNNGLGSLLLEEAIEWAQASGILRRLQL 123 (168)

T ss\_dssp HHHHHHHHHCSSCEEEEEEETTEEEEEEEEECCCSTTTTTEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHHSSCCEEEE

T ss\_pred HHHHHHcCCCCCcEEEEEEECCeEEEEEEEEecccccceeEEEEEEEECHHHcCCCHHHHHHHHHHHHHHHcCCeEEEEE

Q ss\_pred EEEcCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 82 PVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 82 ~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

.+...|. .+.++|++.||+..+...

T Consensus 124 ~~~~~n~---------~~~~~~~~~Gf~~~~~~~ 148 (168)

T d2i79e\_ 124 TVQTRNQ---------AAVHLYQKHGFVIEGSQE 148 (168)

T ss\_dssp EEETTCH---------HHHHHHHHTTCEEEEEEE

T ss\_pred EeccCCH---------HHHHHHHHCCCEEEEEEe

No 187

>3D3S\_A L-2,4-diaminobutyric acid acetyltransferase (E.C.2.3.1.178); alpha-beta-alpha sandwich, Structural Genomics, PSI-2; HET: SO4, GOL, DAB; 1.87A {Bordetella parapertussis 12822}

Probab=98.36 E-value=9.6e-08 Score=76.29 Aligned\_cols=92 Identities=12% Similarity=0.052 Sum\_probs=0.0 Template\_Neff=11.400

Q ss\_pred chHHHHHhhCCc-EEEEEE-CCEEEEEEEEEeC------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEE

Q Phabba\_Draft 15 FEPFDTMWSNGI-MARHAH-DDRPVGHLHWHPD------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPV 83 (219)

Q Consensus 15 ~~~l~~~~~~~~-~~v~~~-~~~liG~~~~~~~------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v 83 (219)

...+........ ++++.. +|++||++.+... .++..++|+|++|++|+|..|++.+++.+.. ..+.+.+

T Consensus 56 ~~~~~~~~~~~~~~~~~~~~~~~iiG~~~~~~~~~~~~~~~i~~~~v~~~~r~~G~~~~l~~~~~~~~~~~~~~~i~~~~ 135 (189)

T 3D3S\_A 56 YAYLLLCEHHAHTCVVAESPGGRIDGFVSAYLLPTRPDVLFVWQVAVHSRARGHRLGRAMLGHILERQECRHVRHLETTV 135 (189)

T ss\_dssp HHHHHHHHHCGGGCEEEECTTSCEEEEEEEEECSSCTTEEEEEEEEECGGGTTSCHHHHHHHHHHHSGGGTTCCEEEEEE

T ss\_pred HHHHHHhhcCCcEEEEEECCCCcEEEEEEEEECCCCCCEEEEEEEEECHHHCCCCHHHHHHHHHHHHHHhhCCCEEEEEc

Q ss\_pred EcCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 84 RHSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 84 ~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

...|. .+.++|+++||+..+.+.

T Consensus 136 ~~~n~---------~~~~~~~~~Gf~~~~~~~ 158 (189)

T 3D3S\_A 136 GPDNQ---------ASRRTFAGLAGERGAHVS 158 (189)

T ss\_dssp CTTCH---------HHHHHHHHHHHTTTCEEE

T ss\_pred CCCCH---------HHHHHHHhcCcEEeeeee

No 188

>3D3S\_C L-2,4-diaminobutyric acid acetyltransferase (E.C.2.3.1.178); alpha-beta-alpha sandwich, Structural Genomics, PSI-2; HET: GOL, SO4, DAB; 1.87A {Bordetella parapertussis 12822}

Probab=98.36 E-value=9.6e-08 Score=76.29 Aligned\_cols=92 Identities=12% Similarity=0.052 Sum\_probs=0.0 Template\_Neff=11.400

Q ss\_pred chHHHHHhhCCc-EEEEEE-CCEEEEEEEEEeC------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEE

Q Phabba\_Draft 15 FEPFDTMWSNGI-MARHAH-DDRPVGHLHWHPD------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPV 83 (219)

Q Consensus 15 ~~~l~~~~~~~~-~~v~~~-~~~liG~~~~~~~------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v 83 (219)

...+........ ++++.. +|++||++.+... .++..++|+|++|++|+|..|++.+++.+.. ..+.+.+

T Consensus 56 ~~~~~~~~~~~~~~~~~~~~~~~iiG~~~~~~~~~~~~~~~i~~~~v~~~~r~~G~~~~l~~~~~~~~~~~~~~~i~~~~ 135 (189)

T 3D3S\_C 56 YAYLLLCEHHAHTCVVAESPGGRIDGFVSAYLLPTRPDVLFVWQVAVHSRARGHRLGRAMLGHILERQECRHVRHLETTV 135 (189)

T ss\_dssp HHHHHHHHHCGGGCEEEECTTSCEEEEEEEEEETTEEEEEEEEEEEECGGGTTSCHHHHHHHHHHTSGGGTTCCEEEEEE

T ss\_pred HHHHHHhhcCCcEEEEEECCCCcEEEEEEEEECCCCCCEEEEEEEEECHHHCCCCHHHHHHHHHHHHHHhhCCCEEEEEc

Q ss\_pred EcCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 84 RHSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 84 ~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

...|. .+.++|+++||+..+.+.

T Consensus 136 ~~~n~---------~~~~~~~~~Gf~~~~~~~ 158 (189)

T 3D3S\_C 136 GPDNQ---------ASRRTFAGLAGERGAHVS 158 (189)

T ss\_dssp CGGGT---------THHHHHHHHHHHTTCCEE

T ss\_pred CCCCH---------HHHHHHHhcCcEEeeeee

No 189

>2EUI\_D Probable acetyltransferase; transferase, dimer, T1065, Structural Genomics; 2.8A {Pseudomonas aeruginosa PAO1} SCOP: d.108.1.1

Probab=98.36 E-value=1.3e-07 Score=70.82 Aligned\_cols=93 Identities=13% Similarity=0.149 Sum\_probs=0.0 Template\_Neff=12.800

Q ss\_pred chHHHHHhhCCc--EEEEE--ECCEEEEEEEEEeC---------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---Ce

Q Phabba\_Draft 15 FEPFDTMWSNGI--MARHA--HDDRPVGHLHWHPD---------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YE 78 (219)

Q Consensus 15 ~~~l~~~~~~~~--~~v~~--~~~~liG~~~~~~~---------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~ 78 (219)

.+.+...+.... ++++. ++++++|++.+... ..+..+.|+|++|++|++..|+..+++.++. ..

T Consensus 35 ~~~~~~~~~~~~~~~~~~~~~~~~~~iG~~~~~~~~~~~~~~~~~~i~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~ 114 (153)

T 2EUI\_D 35 RKFLEKRLRRKESVIYLALADEEDRLLGFCQLYPSFSSLSLKRVWILNDIYVAEEARRQLVADHLLQHAKQMARETHAVR 114 (153)

T ss\_dssp HHHHHHHHHHTCCEEEEEECTTSCCEEEEEEEEEEEETTTTEEEEEEEEEEECTTSCHHHHHHHHHHHHHHHHHHTTCSE

T ss\_pred HHHHHHHhhCccceEEEEEeCCCCeEEEEEEEEecCcccccccEEEEEEEEECHHHccCCHHHHHHHHHHHHHHHcCCcE

Q ss\_pred eEEEEEcCCcccccccccchhHHHHHcCCCEEeeeeec

Q Phabba\_Draft 79 SSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADD 116 (219)

Q Consensus 79 i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~ 116 (219)

+.+.+...|. .+.++|+++||+..+....

T Consensus 115 i~~~~~~~n~---------~~~~~~~~~Gf~~~~~~~~ 143 (153)

T 2EUI\_D 115 MRVSTSVDNE---------VAQKVYESIGFREDQEFKN 143 (153)

T ss\_dssp EEEEEESSCH---------HHHHHHHHTTCEECCSEEE

T ss\_pred EEEEEecCCH---------HHHHHHHHcCCEEccceEE

No 190

>3ZJ0\_A ACETYLTRANSFERASE; TRANSFERASE, O-GLCNAC HAT, HISTONE ACETYLTRANSFERASE; HET: ACO; 1.8A {OCEANICOLA GRANULOSUS}

Probab=98.36 E-value=6.4e-08 Score=78.77 Aligned\_cols=83 Identities=14% Similarity=0.139 Sum\_probs=0.0 Template\_Neff=11.100

Q ss\_pred hCCcEEEEEECCEEEEEEEEE------------------------------------------------------eCCEE

Q Phabba\_Draft 23 SNGIMARHAHDDRPVGHLHWH------------------------------------------------------PDGEI 48 (219)

Q Consensus 23 ~~~~~~v~~~~~~liG~~~~~------------------------------------------------------~~~~i 48 (219)

....++++.++|++||++.+. ....+

T Consensus 54 ~~~~~~v~~~~~~ivG~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~i 133 (206)

T 3ZJ0\_A 54 APDFAFVLEDAEGVCGYLLGAPDTLSFQHFLEKEWLPPLRAGLTDPGPDPAAWQGSDWARDAIHRPPALPPIDLAAYPAH 133 (206)

T ss\_dssp CGGGEEEEEETTEEEEEEEEESCHHHHHHHCCCCCHHHHHTTCCCCCSCTTSCCTTHHHHHHHHSCCCCCSSCTTTSCEE

T ss\_pred CCCcEEEEEeCCcEEEEEEEecChHHHHHHHHHcchHhHHhcCCCCCCChhhccCcHHHHHHhhCCCCCCCcccccCceE

Q ss\_pred EEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeee

Q Phabba\_Draft 49 DSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKA 114 (219)

Q Consensus 49 ~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~ 114 (219)

..++|+|++||+|+|++|++.+++.+.. ..+.+.+...|. .+.++|+++||+..+..

T Consensus 134 ~~~~v~p~~rg~Gig~~l~~~~~~~~~~~g~~~i~~~~~~~n~---------~~~~~~~k~GF~~~~~~ 193 (206)

T 3ZJ0\_A 134 GHIDLLPRAQGRGVGSRAMDHLEAALAAAGAPGMHLQVSPENP---------RALGFYEHRGFRELCRS 193 (206)

T ss\_dssp EEEEECGGGCSSSHHHHHHHHHHHHHHHTTCCEEEEEECTTCH---------HHHHHHHHTTCEEEEEC

T ss\_pred EEEEeCHHhCCCCHHHHHHHHHHHHHHHCCCCeEEEEeCCCCH---------HHHHHHHHcCCEEeecC

No 191

>2VI7\_B ACETYLTRANSFERASE PA1377; GNAT, GCN5 FAMILY, TRANSFERASE, N-ACETYLTRANSFERASE; HET: GOL, SO4, AZI; 2.25A {PSEUDOMONAS AERUGINOSA}

Probab=98.36 E-value=1.5e-07 Score=73.09 Aligned\_cols=91 Identities=12% Similarity=0.106 Sum\_probs=0.0 Template\_Neff=12.300

Q ss\_pred hHHHHHhhCCc--EEEEEECCEEEEEEEEEeC-------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc----CeeEEE

Q Phabba\_Draft 16 EPFDTMWSNGI--MARHAHDDRPVGHLHWHPD-------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI----YESSYP 82 (219)

Q Consensus 16 ~~l~~~~~~~~--~~v~~~~~~liG~~~~~~~-------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~----~~i~l~ 82 (219)

..+........ ++++..+|++||++.+... .....++|+|++|++|+|+.|++.+++.+.. ..+.+.

T Consensus 47 ~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~~~~v~~~~r~~G~~~~ll~~~~~~~~~~~g~~~i~~~ 126 (177)

T 2VI7\_B 47 KRLHDSADDDRLLILVALHQGDVIGSASLEQHPRIRRSHSGSIGMGVAVAWQGKGVGSRLLGELLDIADNWMNLRRVELT 126 (177)

T ss\_dssp HHHHTC-CCTTEEEEEEEETTEEEEEEEEEECSSGGGTTEEECTTCCEESSTTSSHHHHHHHHHHHHHHHTSCCSEEEEE

T ss\_pred HHHHhcCCCCceEEEEEEeCCcEEEEEEEEecCccCccceEEEEEEEcHHHCCCCHHHHHHHHHHHHHHHccCCCEEEEE

Q ss\_pred EEcCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 83 VRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 83 v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

+...|. .+.++|+++||+..+...

T Consensus 127 ~~~~n~---------~~~~~~~~~Gf~~~~~~~ 150 (177)

T 2VI7\_B 127 VYTDNA---------PALALYRKFGFETEGEMR 150 (177)

T ss\_dssp EETTCH---------HHHHHHHHTTCEEEEEEE

T ss\_pred EecCCH---------HHHHHHHHcCCeEEEEee

No 192

>2VI7\_C ACETYLTRANSFERASE PA1377; GNAT, GCN5 FAMILY, TRANSFERASE, N-ACETYLTRANSFERASE; HET: SO4, AZI, GOL; 2.25A {PSEUDOMONAS AERUGINOSA}

Probab=98.36 E-value=1.5e-07 Score=73.09 Aligned\_cols=91 Identities=12% Similarity=0.106 Sum\_probs=0.0 Template\_Neff=12.300

Q ss\_pred hHHHHHhhCCc--EEEEEECCEEEEEEEEEeC-------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc----CeeEEE

Q Phabba\_Draft 16 EPFDTMWSNGI--MARHAHDDRPVGHLHWHPD-------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI----YESSYP 82 (219)

Q Consensus 16 ~~l~~~~~~~~--~~v~~~~~~liG~~~~~~~-------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~----~~i~l~ 82 (219)

..+........ ++++..+|++||++.+... .....++|+|++|++|+|+.|++.+++.+.. ..+.+.

T Consensus 47 ~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~~~~v~~~~r~~G~~~~ll~~~~~~~~~~~g~~~i~~~ 126 (177)

T 2VI7\_C 47 KRLHDSADDDRLLILVALHQGDVIGSASLEQHPRIRRSHSGSIGMGVAVAWQGKGVGSRLLGELLDIADNWMNLRRVELT 126 (177)

T ss\_dssp HHHHHC-CCTTEEEEEEEETTEEEEEEEEEECSSGGGTTEEECTTCCEESSTTSSHHHHHHHHHHHCCCCCSCCSEEEEE

T ss\_pred HHHHhcCCCCceEEEEEEeCCcEEEEEEEEecCccCccceEEEEEEEcHHHCCCCHHHHHHHHHHHHHHHccCCCEEEEE

Q ss\_pred EEcCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 83 VRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 83 v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

+...|. .+.++|+++||+..+...

T Consensus 127 ~~~~n~---------~~~~~~~~~Gf~~~~~~~ 150 (177)

T 2VI7\_C 127 VYTDNA---------PALALYRKFGFETEGEMR 150 (177)

T ss\_dssp EETTCH---------HHHHHHHHTTCEEEEEEE

T ss\_pred EecCCH---------HHHHHHHHcCCeEEEEee

No 193

>d1yrec\_ d.108.1.1 (C:) automated matches {Pseudomonas aeruginosa, PA01 [TaxId: 208964]}

Probab=98.36 E-value=1.5e-07 Score=73.31 Aligned\_cols=95 Identities=9% Similarity=0.024 Sum\_probs=0.0 Template\_Neff=12.400

Q ss\_pred CCCchHHHHHhhC-----CcEEEEEECCEEEEEEEEEeC------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc----

Q Phabba\_Draft 12 PLKFEPFDTMWSN-----GIMARHAHDDRPVGHLHWHPD------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---- 76 (219)

Q Consensus 12 ~~~~~~l~~~~~~-----~~~~v~~~~~~liG~~~~~~~------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---- 76 (219)

+...+.+...+.. ..++++..++++||++.+... ..+..++|+|++|++|+|+.|++.+++.+..

T Consensus 39 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~i~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~ 118 (182)

T d1yrec\_ 39 PTRPDWYRQSLAEQREGRALPLAVRLGVQLVGTTRFAEFLPALPACEIGWTWLDQAQHGSGLNRMIKYLMLKHAFDNLRM 118 (182)

T ss\_dssp TTSHHHHHHHHHHHHTTSEEEEEEEETTEEEEEEEEEEEETTTTEEEEEEEEECGGGTTTTHHHHHHHHHHHCCCCCSCC

T ss\_pred CCCHHHHHHHHHhhhcCCcceEEEEeCCEEEEEEEEEEeeCcCCeEEEEEEEeCHHHccccHHHHHHHHHHHHHHHhcCc

Q ss\_pred CeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 77 YESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 77 ~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

..+.+.+...|. .+.++|+++||+..+...

T Consensus 119 ~~i~~~~~~~n~---------~~~~~~~~~Gf~~~~~~~ 148 (182)

T d1yrec\_ 119 VRVQLSTAASNL---------RAQGAIDKLGAQREGVLR 148 (182)

T ss\_dssp SEEEEEEETTCH---------HHHHHHHHHTCEEEEEEE

T ss\_pred cEEEEEEeccCH---------HHHHHHHHcCCeEEEEEe

No 194

>d1yvoa1 d.108.1.1 (A:4-172) Hypothetical protein PA4866 {Pseudomonas aeruginosa [TaxId: 287]}

Probab=98.36 E-value=1.1e-07 Score=72.75 Aligned\_cols=91 Identities=14% Similarity=0.091 Sum\_probs=0.0 Template\_Neff=12.700

Q ss\_pred hHHHHHhhCCc-EEEEEE-CCEEEEEEEEEeC--------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEE

Q Phabba\_Draft 16 EPFDTMWSNGI-MARHAH-DDRPVGHLHWHPD--------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYP 82 (219)

Q Consensus 16 ~~l~~~~~~~~-~~v~~~-~~~liG~~~~~~~--------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~ 82 (219)

.++........ ++++.. ++++||++.+... .++..++|+|++||+|+|+.|++.+++.++. ..+.+.

T Consensus 40 ~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~~g~~~i~~~ 119 (169)

T d1yvoa1 40 AWFDTRARQGYPILVASDAAGEVLGYASYGDWRPFEGFRGTVEHSVYVRDDQRGKGLGVQLLQALIERARAQGLHVMVAA 119 (169)

T ss\_dssp HHHHHHHHHTCCEEEEECTTCCEEEEEEEEESSSSGGGTTEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHTTCCEEEEE

T ss\_pred HHHHHhHhcCCcEEEEECCCCCEEEEEeeccceecCCcceEEEEEEEECHhhCCCcHHHHHHHHHHHHHHHCCCCEEEEE

Q ss\_pred EEcCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 83 VRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 83 v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

+...|. .+.++|+++||+..+...

T Consensus 120 ~~~~n~---------~~~~~~~~~Gf~~~~~~~ 143 (169)

T d1yvoa1 120 IESGNA---------ASIGLHRRLGFEISGQMP 143 (169)

T ss\_dssp EETTCH---------HHHHHHHHTTCEEEEEEE

T ss\_pred eeCCCH---------HHHHHHHHcCCEEEEEcc

No 195

>2I79\_C Acetyltransferase, GNAT family; acetyltransferase, GNAT family, acetyl Coenzyme; HET: ACO; 2.1A {Streptococcus pneumoniae}

Probab=98.36 E-value=1.4e-07 Score=72.51 Aligned\_cols=92 Identities=12% Similarity=0.029 Sum\_probs=0.0 Template\_Neff=12.600

Q ss\_pred chHHHHHhhCCc--EEEEEECCEEEEEEEEEeC-------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc----CeeEE

Q Phabba\_Draft 15 FEPFDTMWSNGI--MARHAHDDRPVGHLHWHPD-------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI----YESSY 81 (219)

Q Consensus 15 ~~~l~~~~~~~~--~~v~~~~~~liG~~~~~~~-------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~----~~i~l 81 (219)

..++........ ++++..+|++||++.+... .....+.|+|++|++|+|++|++.+++.+.. ..+.+

T Consensus 47 ~~~~~~~~~~~~~~~~v~~~~~~~vG~~~~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~~i~~ 126 (172)

T 2I79\_C 47 EIFLNKQASSDNQITLLAFLNGKIAGIVNITADQRKRVRHIGDLFIVIGKRYWNNGLGSLLLEEAIEWAQASGILRRLQL 126 (172)

T ss\_dssp HHHHHHHHHCSSCEEEEEEETTEEEEEEEEECCCSTTTTTEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHHSSCCEEEE

T ss\_pred HHHHHHccCCCCeEEEEEEECCEEEEEEEEEecchhccceEEEEEEEECHHHhcCCHHHHHHHHHHHHHHHhCCccEEEE

Q ss\_pred EEEcCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 82 PVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 82 ~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

.+...|. .+.++|+++||+..+...

T Consensus 127 ~~~~~n~---------~~~~~~~~~Gf~~~~~~~ 151 (172)

T 2I79\_C 127 TVQTRNQ---------AAVHLYQKHGFVIEGSQE 151 (172)

T ss\_dssp EEETTCH---------HHHHHHHHTTCEEEEEEE

T ss\_pred EEccCCH---------HHHHHHHHcCcEEEEEec

No 196

>2I79\_E Acetyltransferase, GNAT family; acetyltransferase, GNAT family, acetyl Coenzyme; HET: ACO; 2.1A {Streptococcus pneumoniae}

Probab=98.36 E-value=1.4e-07 Score=72.51 Aligned\_cols=92 Identities=12% Similarity=0.029 Sum\_probs=0.0 Template\_Neff=12.600

Q ss\_pred chHHHHHhhCCc--EEEEEECCEEEEEEEEEeC-------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc----CeeEE

Q Phabba\_Draft 15 FEPFDTMWSNGI--MARHAHDDRPVGHLHWHPD-------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI----YESSY 81 (219)

Q Consensus 15 ~~~l~~~~~~~~--~~v~~~~~~liG~~~~~~~-------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~----~~i~l 81 (219)

..++........ ++++..+|++||++.+... .....+.|+|++|++|+|++|++.+++.+.. ..+.+

T Consensus 47 ~~~~~~~~~~~~~~~~v~~~~~~~vG~~~~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~~i~~ 126 (172)

T 2I79\_E 47 EIFLNKQASSDNQITLLAFLNGKIAGIVNITADQRKRVRHIGDLFIVIGKRYWNNGLGSLLLEEAIEWAQASGILRRLQL 126 (172)

T ss\_dssp HHHHHHHHHCSSCEEEEEEETTEEEEEEEEECCCSTTTTTEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHHSSCCEEEE

T ss\_pred HHHHHHccCCCCeEEEEEEECCEEEEEEEEEecchhccceEEEEEEEECHHHhcCCHHHHHHHHHHHHHHHhCCccEEEE

Q ss\_pred EEEcCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 82 PVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 82 ~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

.+...|. .+.++|+++||+..+...

T Consensus 127 ~~~~~n~---------~~~~~~~~~Gf~~~~~~~ 151 (172)

T 2I79\_E 127 TVQTRNQ---------AAVHLYQKHGFVIEGSQE 151 (172)

T ss\_dssp EEETTCH---------HHHHHHHHTTCEEEEEEE

T ss\_pred EEccCCH---------HHHHHHHHcCcEEEEEec

No 197

>4MI4\_C Spermidine n1-acetyltransferase; Structural Genomics, NIAID, National Institute; HET: SPM; 1.848A {Vibrio cholerae O1 biovar El tor}

Probab=98.35 E-value=1.4e-07 Score=76.10 Aligned\_cols=92 Identities=13% Similarity=0.097 Sum\_probs=0.0 Template\_Neff=11.200

Q ss\_pred chHHHHHhhCCc--EEEEEE-CCEEEEEEEEEeC-----CEEEEEEECHHHCCCCHHHHHHHHHHHccc-c---CeeEEE

Q Phabba\_Draft 15 FEPFDTMWSNGI--MARHAH-DDRPVGHLHWHPD-----GEIDSITVHPDLQRRGIGTAMLKHAQDNPH-I---YESSYP 82 (219)

Q Consensus 15 ~~~l~~~~~~~~--~~v~~~-~~~liG~~~~~~~-----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~-~---~~i~l~ 82 (219)

.+.+...+.... ++++.+ +|++||++.+... ..+..++|+|++|++|+|+.|++.+++.+. . ..+.+.

T Consensus 67 ~~~~~~~~~~~~~~~~~~~~~~~~ivG~~~~~~~~~~~~~~~~~~~v~~~~rg~Gig~~ll~~~~~~~~~~~g~~~i~~~ 146 (197)

T 4MI4\_C 67 EELYNKHIHDNAERRFVVEDAQKNLIGLVELIEINYIHRSAEFQIIIAPEHQGKGFARTLINRALDYSFTILNLHKIYLH 146 (197)

T ss\_dssp HHHHHHTTTCTTCEEEEEEETTCCEEEEEEEEEEETTTTEEEEEEEECGGGTTSSCHHHHHHHHHHCCCCCSCCSEEEEE

T ss\_pred HHHHHHhcccCCCCeEEEEeCCCcEEEEEEEEEeecCCCEEEEEEEECHHHCCCCHHHHHHHHHHHHHHHhcCCCEEEEE

Q ss\_pred EEcCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 83 VRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 83 v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

+...|. .+.++|+++||+..+...

T Consensus 147 ~~~~n~---------~~~~~~~~~GF~~~~~~~ 170 (197)

T 4MI4\_C 147 VAVENP---------KAVHLYEECGFVEEGHLV 170 (197)

T ss\_dssp EETTCH---------HHHHHHHHTTCEEEEEEE

T ss\_pred EecCCH---------HHHHHHHHcCCEEEEEEe

No 198

>4NXY\_A Acyl-CoA synthetase; Lysine Acetyltransferase, AMP-Forming Acetate:CoA Ligase; 1.449A {Streptomyces lividans}

Probab=98.35 E-value=7.1e-08 Score=76.68 Aligned\_cols=91 Identities=12% Similarity=0.151 Sum\_probs=0.0 Template\_Neff=11.900

Q ss\_pred chHHHHHhhCCcEEEEEECCEEEEEEEEE-------------eCCEEEEEEECHHHCCCCHHHHHHHHHHHcccc---Ce

Q Phabba\_Draft 15 FEPFDTMWSNGIMARHAHDDRPVGHLHWH-------------PDGEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YE 78 (219)

Q Consensus 15 ~~~l~~~~~~~~~~v~~~~~~liG~~~~~-------------~~~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~ 78 (219)

...+........++++..++++||++.+. ....+ .++|+|++|++|+++.|++.+++.+.. ..

T Consensus 78 ~~~~~~~~~~~~~~v~~~~~~~vG~~~~~~~~~~~~~~~~~~~~~~i-~~~v~~~~r~~G~~~~l~~~~~~~~~~~g~~~ 156 (194)

T 4NXY\_A 78 HRFTHHDFVDRVGLAATIGGEFIATVRYDRIGAGGTPATAPADEAEV-AFLVQDAHQGRGVASALLEHIAAVARERGIRR 156 (194)

T ss\_dssp HHHHCCCSSSEEEEEEEETTEEEEEEEEEEECTTSSBCCTTCCEEEE-EEEECGGGTTSSHHHHHHHHHHHHHHHTTCCE

T ss\_pred HHHhcCCCCcceEEEEEECCEEEEEEEEEecCCCCCCCCCCCCEEEE-EEEECHHHCCCCHHHHHHHHHHHHHHHCCCCE

Q ss\_pred eEEEEEcCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 79 SSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 79 i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

+.+.+...|. .+.++|+++||+..+...

T Consensus 157 ~~~~~~~~n~---------~~~~~~~~~Gf~~~~~~~ 184 (194)

T 4NXY\_A 157 FAAEVLPANN---------KMIKVFMDAGYTQKRSFE 184 (194)

T ss\_dssp EEEEECTTCH---------HHHHHHHHTTCEEECCSS

T ss\_pred EEEEeeccCH---------HHHHHHHHcCCeEEEEcc

No 199

>3FIX\_D N-ACETYLTRANSFERASE; N-ACETYLTRANSFERASE, TERMOPLASMA ACIDOPHILUM, STRUCTURAL GENOMICS; 2.3A {Thermoplasma acidophilum}

Probab=98.35 E-value=7.9e-08 Score=76.39 Aligned\_cols=78 Identities=15% Similarity=0.166 Sum\_probs=0.0 Template\_Neff=11.400

Q ss\_pred EEEEEECCEEEEEEEEEeC---CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEEEcCCcccccccccchhH

Q Phabba\_Draft 27 MARHAHDDRPVGHLHWHPD---GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPVRHSSHFSAAGRAWAQSD 100 (219)

Q Consensus 27 ~~v~~~~~~liG~~~~~~~---~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v~~~n~~~~~~~~~~~~~ 100 (219)

++++..++++||++.+... ..+..++|+|++|++|+|+.|++.+++.++. ..+.+.+...|. .+.

T Consensus 89 ~~v~~~~~~ivG~~~~~~~~~~~~i~~~~v~~~~r~~G~~~~l~~~~~~~~~~~g~~~i~~~~~~~n~---------~~~ 159 (183)

T 3FIX\_D 89 FLGAFADSTLIGFIELKIIANKAELLRLYLKPEYTHKKIGKTLLLEAEKIMKKKGILECRLYVHRQNS---------VGF 159 (183)

T ss\_dssp EEEEEETTEEEEEEEEEEETTEEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHHTCCEEEEEEETTCH---------HHH

T ss\_pred EEEEecCCceEEEEEEEEeCCeEEEEEEEeChhhcCCcHHHHHHHHHHHHHHHcCCCEEEEEEEcCCh---------hHH

Q ss\_pred HHHHcCCCEEeee

Q Phabba\_Draft 101 PDYHDPGDQNVTK 113 (219)

Q Consensus 101 ~~y~r~Gf~~~~~ 113 (219)

++|+++||+..+.

T Consensus 160 ~~~~~~Gf~~~~~ 172 (183)

T 3FIX\_D 160 SFYYKNGFKVEDT 172 (183)

T ss\_dssp HHHHTTTCEEEEC

T ss\_pred HHHHHCCCEEEec

No 200

>d1m4db\_ d.108.1.1 (B:) Aminoglycoside 2'-N-acetyltransferase {Mycobacterium tuberculosis [TaxId: 1773]}

Probab=98.35 E-value=7.7e-08 Score=75.69 Aligned\_cols=82 Identities=16% Similarity=0.135 Sum\_probs=0.0 Template\_Neff=11.600

Q ss\_pred CCcEEEEEECCEEEEEEEEEeC-----------CEEEEEEECHHHCCCCHHHHHHHHHHHccccCeeEEEEEcCCccccc

Q Phabba\_Draft 24 NGIMARHAHDDRPVGHLHWHPD-----------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHIYESSYPVRHSSHFSAA 92 (219)

Q Consensus 24 ~~~~~v~~~~~~liG~~~~~~~-----------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~~~i~l~v~~~n~~~~~ 92 (219)

...++++.+++++||++.+... ..+..++|+|++|++|+|+.|++.+++.+++ .+.+.+...|.

T Consensus 41 ~~~~~~~~~~~~ivg~~~~~~~~~~~~~~~~~~~~i~~~~v~p~~r~~Gi~~~l~~~~~~~~~~-~~~~~~~~~n~---- 115 (176)

T d1m4db\_ 41 GGMHALIWHHGAIIAHAAVIQRRLIYRGNALRCGYVEGVAVRADWRGQRLVSALLDAVEQVMRG-AYQLGALSSSA---- 115 (176)

T ss\_dssp SSEEEEEEETTEEEEEEEEEEEEEEETTEEEEEEEEEEEEECGGGCSSSHHHHHHHHHHHHHHH-HCSEEEEECCT----

T ss\_pred CCcEEEEEECCEEEEEEEEEeeeeeeCCCceeEEEEEEEEECHHHCCCcHHHHHHHHHHHHHhh-CCeEEEEeCCH----

Q ss\_pred ccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 93 GRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 93 ~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

.+.++|+++||+..+...

T Consensus 116 -----~~~~~~~~~Gf~~~~~~~ 133 (176)

T d1m4db\_ 116 -----RARRLYASRGWLPWHGPT 133 (176)

T ss\_dssp -----TTHHHHHHTTCEECCSCE

T ss\_pred -----HHHHHHHhcceeecCCCc

No 201

>3QB8\_A A654L protein; GNAT N-Acetyltransferase, Acetyltransferase, CoA, Spermine; HET: COA, IMD; 1.5A {Paramecium bursaria Chlorella virus 1}

Probab=98.35 E-value=9e-08 Score=78.03 Aligned\_cols=93 Identities=12% Similarity=0.072 Sum\_probs=0.0 Template\_Neff=10.500

Q ss\_pred chHHHHHhhCCcEEEEEE-CCEEEEEEEEEeC-------------------------------CEEEEEEECHHHCCCCH

Q Phabba\_Draft 15 FEPFDTMWSNGIMARHAH-DDRPVGHLHWHPD-------------------------------GEIDSITVHPDLQRRGI 62 (219)

Q Consensus 15 ~~~l~~~~~~~~~~v~~~-~~~liG~~~~~~~-------------------------------~~i~~l~V~p~~R~~Gi 62 (219)

...+...+..+.++++.. +++++|++.+... ..+..++|.|++||+|+

T Consensus 45 ~~~~~~~~~~~~~~~~~~~~~~iiG~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~i~~~~v~p~~r~~Gl 124 (197)

T 3QB8\_A 45 QNIMKQCVDYGHSFAFVDADDNIKAQILNIPYDAYENMHYGNIRETDPMFDLFGNLDSYTPDDKCLYVFAIGSEVTGKGL 124 (197)

T ss\_dssp HHHHHHHHHTTCCEEEECTTCCEEEEEEEEEHHHHHTCCCCCCGGGHHHHHHHHGGGGSCCSSCEEEEEEEEESSCSSSH

T ss\_pred HHHHHHHHhhCCcEEEECCCCCEEEEEeeCccccccccccccccccChhHHHHhhhhhcCCCCCEEEEEEECHHhCCCCH

Q ss\_pred HHHHHHHHHHccccCee-EEEEEcCCcccccccccchhHHHHHcCCCEEeeeeec

Q Phabba\_Draft 63 GTAMLKHAQDNPHIYES-SYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADD 116 (219)

Q Consensus 63 g~~Ll~~~~~~~~~~~i-~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~ 116 (219)

|++|+..+++.++...+ .+.+...|. .+.++|+++||+..+...+

T Consensus 125 g~~L~~~~~~~~~~~g~~~v~~~~~n~---------~~~~~y~k~GF~~~~~~~~ 170 (197)

T 3QB8\_A 125 ATKLLKKTIEESSSHGFKYIYGDCTNI---------ISQNMFEKHGFETVGSVKY 170 (197)

T ss\_dssp HHHHHHHHHHHHHHTTCCEEEEEECSH---------HHHHHHHHTTCEEEEEEES

T ss\_pred HHHHHHHHHHHHHhcCCCEEEEEcCCH---------HHHHHHHHCCCEEEEEEec

No 202

>d2ganb\_ d.108.1.1 (B:) Hypothetical protein PH0736 {Pyrococcus horikoshii [TaxId: 53953]}

Probab=98.35 E-value=1.1e-07 Score=75.75 Aligned\_cols=83 Identities=18% Similarity=0.232 Sum\_probs=0.0 Template\_Neff=11.200

Q ss\_pred hCCcEEEEEECCEEEEEEEEEeC-------------------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeE

Q Phabba\_Draft 23 SNGIMARHAHDDRPVGHLHWHPD-------------------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESS 80 (219)

Q Consensus 23 ~~~~~~v~~~~~~liG~~~~~~~-------------------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~ 80 (219)

....++++..+|++||++.+... .++..++|+|++||+|+|+.|+..+++.++. ..+.

T Consensus 65 ~~~~~~v~~~~~~ivG~~~~~~~~~~~~~~~~~~~~~~~~~~~~i~~~~v~p~~r~~Gl~~~l~~~~~~~~~~~~~~~~~ 144 (181)

T d2ganb\_ 65 EFDELYTYQKDNRIIGTIALVYKRIKEKGIWWVPEELMNEKVGLIEFFVVDPEFQGKGIGSTLLEFAVKRLRSLGKDPYV 144 (181)

T ss\_dssp CCSEEEEEEETTEEEEEEEEECSSGGGSCCCSSCGGGCSTTEEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHTTCEEEE

T ss\_pred ccceEEEEEECCeEEEEEEEEecchhhcCceeccHHHccCcEEEEEEEEECHHHCCCCHHHHHHHHHHHHHHHCCCCeEE

Q ss\_pred EEEEcCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 81 YPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 81 l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

+ +...|. .+.++|+++||+..+...

T Consensus 145 ~-~~~~n~---------~~~~~~~~~Gf~~~~~~~ 169 (181)

T d2ganb\_ 145 V-TFPNLE---------AYSYYYMKKGFREIMRYK 169 (181)

T ss\_dssp E-ECGGGS---------HHHHHHHHTTEEEEEECS

T ss\_pred E-EcCChh---------HHHHHHHHCCcEEEEEec

No 203

>2VEZ\_A PUTATIVE GLUCOSAMINE 6-PHOSPHATE ACETYLTRANSFERASE (E.C.2.3.1.4); TRANSFERASE, ACYLTRANSFERASE, GLUCOSAMINE-6-PHOSPHATE N-ACETYLTRANSFERASE (GNA1); HET: G6P, ACO; 1.45A {ASPERGILLUS FUMIGATUS}

Probab=98.34 E-value=1.1e-07 Score=75.85 Aligned\_cols=91 Identities=14% Similarity=0.124 Sum\_probs=0.0 Template\_Neff=11.500

Q ss\_pred hHHHHHhhCCcEEEEEE-CCEEEEEEEEEeC----------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEE

Q Phabba\_Draft 16 EPFDTMWSNGIMARHAH-DDRPVGHLHWHPD----------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSY 81 (219)

Q Consensus 16 ~~l~~~~~~~~~~v~~~-~~~liG~~~~~~~----------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l 81 (219)

..+........++++.+ ++++||++.+... .++..++|+|++||+|+|++|++.+++.+.+ ..+.+

T Consensus 85 ~~~~~~~~~~~~~~~~~~~~~ivG~~~~~~~~~~~~~~~~~~~i~~~~v~p~~rg~Glg~~l~~~~~~~~~~~g~~~i~~ 164 (190)

T 2VEZ\_A 85 EWIRARSDEYYLLVVCDGEGRIVGTGSLVVERKFIHSLGMVGHIEDIAVEKGQQGKKLGLRIIQALDYVAEKVGCYKTIL 164 (190)

T ss\_dssp HHHHTTTTTEEEEEEECTTSCEEEEEEEEEEECSHHHHCEEEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHHTCSEEEC

T ss\_pred HHHHHhccCCEEEEEECCCCcEEEEEEEEEeccccccCCcEEEEEEEEECHHHCCCCHHHHHHHHHHHHHHHhCCCEEEE

Q ss\_pred EEEcCCcccccccccchhHHHHHcCCCEEeeeeeccc

Q Phabba\_Draft 82 PVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDV 118 (219)

Q Consensus 82 ~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~ 118 (219)

.+...|. ++|+|+||+..+.....+

T Consensus 165 ~~~~~n~------------~~~~k~Gf~~~~~~~~~~ 189 (190)

T 2VEZ\_A 165 DCSEANE------------GFYIKCGFKRAGLEMAHY 189 (190)

T ss\_dssp CCCGGGH------------HHHHHTTCCCCCCCCCCC

T ss\_pred EeecccH------------HHHHHcCcEEcceeeecc

No 204

>2VXK\_A GLUCOSAMINE 6-PHOSPHATE ACETYLTRANSFERASE (E.C.2.3.1.4); KINETICS, UDP-GLCNAC, TRANSFERASE, INHIBITOR DESIGN; HET: COA, 16G; 1.8A {ASPERGILLUS FUMIGATUS}

Probab=98.34 E-value=1.1e-07 Score=75.85 Aligned\_cols=91 Identities=14% Similarity=0.124 Sum\_probs=0.0 Template\_Neff=11.500

Q ss\_pred hHHHHHhhCCcEEEEEE-CCEEEEEEEEEeC----------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEE

Q Phabba\_Draft 16 EPFDTMWSNGIMARHAH-DDRPVGHLHWHPD----------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSY 81 (219)

Q Consensus 16 ~~l~~~~~~~~~~v~~~-~~~liG~~~~~~~----------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l 81 (219)

..+........++++.+ ++++||++.+... .++..++|+|++||+|+|++|++.+++.+.+ ..+.+

T Consensus 85 ~~~~~~~~~~~~~~~~~~~~~ivG~~~~~~~~~~~~~~~~~~~i~~~~v~p~~rg~Glg~~l~~~~~~~~~~~g~~~i~~ 164 (190)

T 2VXK\_A 85 EWIRARSDEYYLLVVCDGEGRIVGTGSLVVERKFIHSLGMVGHIEDIAVEKGQQGKKLGLRIIQALDYVAEKVGCYKTIL 164 (190)

T ss\_dssp HHHHTTTTTEEEEEEECTTSCEEEEEEEEEEECSHHHHCEEEEEEEEEECGGGCSSSHHHHHHHHHHHHHHHHTCSEEEC

T ss\_pred HHHHHhccCCEEEEEECCCCcEEEEEEEEEeccccccCCcEEEEEEEEECHHHCCCCHHHHHHHHHHHHHHHhCCCEEEE

Q ss\_pred EEEcCCcccccccccchhHHHHHcCCCEEeeeeeccc

Q Phabba\_Draft 82 PVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDV 118 (219)

Q Consensus 82 ~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~ 118 (219)

.+...|. ++|+|+||+..+.....+

T Consensus 165 ~~~~~n~------------~~~~k~Gf~~~~~~~~~~ 189 (190)

T 2VXK\_A 165 DCSEANE------------GFYIKCGFKRAGLEMAHY 189 (190)

T ss\_dssp CCCTTTH------------HHHHHTTCCCCCCCCCCC

T ss\_pred EeecccH------------HHHHHcCcEEcceeeecc

No 205

>3EG7\_B Spermidine n1-acetyltransferase; structural genomics, Spermidine n1-acetyltransferase, IDP01616; HET: MSE; 2.38A {Vibrio cholerae}

Probab=98.34 E-value=1.6e-07 Score=72.96 Aligned\_cols=92 Identities=13% Similarity=0.097 Sum\_probs=0.0 Template\_Neff=12.300

Q ss\_pred chHHHHHhhCCc--EEEEEE-CCEEEEEEEEEeC-----CEEEEEEECHHHCCCCHHHHHHHHHHHccc-c---CeeEEE

Q Phabba\_Draft 15 FEPFDTMWSNGI--MARHAH-DDRPVGHLHWHPD-----GEIDSITVHPDLQRRGIGTAMLKHAQDNPH-I---YESSYP 82 (219)

Q Consensus 15 ~~~l~~~~~~~~--~~v~~~-~~~liG~~~~~~~-----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~-~---~~i~l~ 82 (219)

...+........ ++++.. +|++||++.+... ..+..++|+|++|++|+|+.|++.+++.+. . ..+.+.

T Consensus 46 ~~~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~~v~~~~r~~gi~~~l~~~~~~~~~~~~~~~~i~~~ 125 (176)

T 3EG7\_B 46 EELYNKHIHDNAERRFVVEDAQKNLIGLVELIEINYIHRSAEFQIIIAPEHQGKGFARTLINRALDYSFTILNLHKIYLH 125 (176)

T ss\_dssp HHHHHHHTTCCSCEEEEEECTTCCEEEEEEEEEEETTTTEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHTSCCSEEEEE

T ss\_pred HHHHHHhcccCCceeEEEEcCCCCEEEEEEEEEeccccCEEEEEEEECHHHCCCcHHHHHHHHHHHHHHHhcCCcEEEEE

Q ss\_pred EEcCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 83 VRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 83 v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

+...|. .+.++|+++||+..+...

T Consensus 126 ~~~~n~---------~~~~~~~~~Gf~~~~~~~ 149 (176)

T 3EG7\_B 126 VAVENP---------KAVHLYEECGFVEEGHLV 149 (176)

T ss\_dssp EETTCH---------HHHHHHHHTTCEEEEEEE

T ss\_pred EeCCCH---------HHHHHHHHcCCEEEEEee

No 206

>3PZJ\_B Probable acetyltransferases (E.C.2.3.1.-); MCSG, PSI-2, Structural Genomics, Protein; 1.85A {Chromobacterium violaceum}

Probab=98.34 E-value=1.5e-07 Score=75.55 Aligned\_cols=91 Identities=13% Similarity=0.080 Sum\_probs=0.0 Template\_Neff=12.000

Q ss\_pred hHHHHHhhCCc--EEEEEE--CCEEEEEEEEEeC------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEE

Q Phabba\_Draft 16 EPFDTMWSNGI--MARHAH--DDRPVGHLHWHPD------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYP 82 (219)

Q Consensus 16 ~~l~~~~~~~~--~~v~~~--~~~liG~~~~~~~------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~ 82 (219)

+.+........ ++++.. +|++||++.+... ..+..++|+|++|++|+|+.|++.+++.+.+ ..+.+.

T Consensus 80 ~~~~~~~~~~~~~~~~~~~~~~~~ivG~~~~~~~~~~~~~~~i~~~~v~~~~r~~Gi~~~l~~~~~~~~~~~g~~~i~~~ 159 (209)

T 3PZJ\_B 80 TWLALTVAQSDTALYVVCAKDSDQALGFLGYRQMVQAHGAIEIGHVNFSPALRRTRLATEAVFLLLKTAFELGYRRCEWR 159 (209)

T ss\_dssp HHHHHHHTSTTCEEEEEEC--CCCEEEEEEEEEEETTTTEEEEEEEEECTTTCC--HHHHHHHHHHHHHHHTTCSEEEEE

T ss\_pred HHHHHHhhcCCcEEEEEEECCCCcEEEEEEEEEeecCccEEEEEEEEeCHHHcCCCHHHHHHHHHHHHHHHcCCCEEEEE

Q ss\_pred EEcCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 83 VRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 83 v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

+...|. .+.++|+++||+..+...

T Consensus 160 ~~~~n~---------~~~~~~~~~Gf~~~~~~~ 183 (209)

T 3PZJ\_B 160 CDSRNA---------ASAAAARRFGFQFEGTLR 183 (209)

T ss\_dssp EETTCH---------HHHHHHHHHTCEEEEEEE

T ss\_pred EcCCCH---------HHHHHHHHcCCEEEEEEE

No 207

>3PZJ\_A Probable acetyltransferases (E.C.2.3.1.-); MCSG, PSI-2, Structural Genomics, Protein; 1.85A {Chromobacterium violaceum}

Probab=98.34 E-value=1.5e-07 Score=75.55 Aligned\_cols=91 Identities=13% Similarity=0.080 Sum\_probs=0.0 Template\_Neff=12.000

Q ss\_pred hHHHHHhhCCc--EEEEEE--CCEEEEEEEEEeC------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEE

Q Phabba\_Draft 16 EPFDTMWSNGI--MARHAH--DDRPVGHLHWHPD------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYP 82 (219)

Q Consensus 16 ~~l~~~~~~~~--~~v~~~--~~~liG~~~~~~~------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~ 82 (219)

+.+........ ++++.. +|++||++.+... ..+..++|+|++|++|+|+.|++.+++.+.+ ..+.+.

T Consensus 80 ~~~~~~~~~~~~~~~~~~~~~~~~ivG~~~~~~~~~~~~~~~i~~~~v~~~~r~~Gi~~~l~~~~~~~~~~~g~~~i~~~ 159 (209)

T 3PZJ\_A 80 TWLALTVAQSDTALYVVCAKDSDQALGFLGYRQMVQAHGAIEIGHVNFSPALRRTRLATEAVFLLLKTAFELGYRRCEWR 159 (209)

T ss\_dssp HHHHHHHHSTTCEEEEEEETTCCCCCEEEEEEEEEGGGTEEEEEEEEECTTTTTSHHHHHHHHHHHHHHHHTTCSEEEEE

T ss\_pred HHHHHHhhcCCcEEEEEEECCCCcEEEEEEEEEeecCccEEEEEEEEeCHHHcCCCHHHHHHHHHHHHHHHcCCCEEEEE

Q ss\_pred EEcCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 83 VRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 83 v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

+...|. .+.++|+++||+..+...

T Consensus 160 ~~~~n~---------~~~~~~~~~Gf~~~~~~~ 183 (209)

T 3PZJ\_A 160 CDSRNA---------ASAAAARRFGFQFEGTLR 183 (209)

T ss\_dssp EETTCH---------HHHHHHHHHTCEEEEEEE

T ss\_pred EcCCCH---------HHHHHHHHcCCEEEEEEE

No 208

>5DWM\_C Phosphinothricin N-acetyltransferase (E.C.2.3.1.-); SSGCID, Brucella ovis, brucellosis, Phosphinothricin; HET: GOL, EDO, IMD; 1.45A {Brucella ovis (strain ATCC 25840 / 63/290 / NCTC 10512)}

Probab=98.34 E-value=1.9e-07 Score=75.14 Aligned\_cols=91 Identities=18% Similarity=0.139 Sum\_probs=0.0 Template\_Neff=10.800

Q ss\_pred hHHHHHhhCCc-EEEEEECCEEEEEEEEEeC--------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEE

Q Phabba\_Draft 16 EPFDTMWSNGI-MARHAHDDRPVGHLHWHPD--------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPV 83 (219)

Q Consensus 16 ~~l~~~~~~~~-~~v~~~~~~liG~~~~~~~--------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v 83 (219)

+.+........ ++++..++++||++.+... ..+..++|.|++|++|+|+.|++.+++.+++ ..+.+.+

T Consensus 50 ~~~~~~~~~~~~~~v~~~~~~ivG~~~~~~~~~~~~~~~~~~~~~~v~p~~r~~Gi~~~ll~~~~~~~~~~g~~~i~~~~ 129 (187)

T 5DWM\_C 50 KRFAAFADQGFPILVAEADGRVLGYAYASYFRVRPAYRWLAEDSIYIAPDAKGQGIGKLLLRELIARISALGFRQLLAVI 129 (187)

T ss\_dssp HHHHHHHHHTCCEEEEEETTEEEEEEEEEESCCSGGGTTEEEEEEEECTTCTTSCHHHHHHHHHHHHHHHTTCSEEEEEE

T ss\_pred HHHHHHhCCCCCEEEEEECCEEEEEEEEEeccCchhccEEEEEEEEECHHHCCCCHHHHHHHHHHHHHHHCCCCEEEEEe

Q ss\_pred E--cCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 84 R--HSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 84 ~--~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

. ..|. .+.++|+++||+..+...

T Consensus 130 ~~~~~n~---------~~~~~~~~~Gf~~~~~~~ 154 (187)

T 5DWM\_C 130 GDGEHNI---------GSVKLHESLGFTHCGRIE 154 (187)

T ss\_dssp TTTTTCH---------HHHHHHHHTTCEEEEEEE

T ss\_pred cCCCcch---------hHHHHHHhcCCEEEEEEe

No 209

>5DWN\_A Phosphinothricin N-acetyltransferase (E.C.2.3.1.-); SSGCID, Brucella ovis, brucellosis, Phosphinothricin; HET: ACO; 1.95A {Brucella ovis (strain ATCC 25840 / 63/290 / NCTC 10512)}

Probab=98.34 E-value=1.9e-07 Score=75.14 Aligned\_cols=91 Identities=18% Similarity=0.139 Sum\_probs=0.0 Template\_Neff=10.800

Q ss\_pred hHHHHHhhCCc-EEEEEECCEEEEEEEEEeC--------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEE

Q Phabba\_Draft 16 EPFDTMWSNGI-MARHAHDDRPVGHLHWHPD--------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPV 83 (219)

Q Consensus 16 ~~l~~~~~~~~-~~v~~~~~~liG~~~~~~~--------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v 83 (219)

+.+........ ++++..++++||++.+... ..+..++|.|++|++|+|+.|++.+++.+++ ..+.+.+

T Consensus 50 ~~~~~~~~~~~~~~v~~~~~~ivG~~~~~~~~~~~~~~~~~~~~~~v~p~~r~~Gi~~~ll~~~~~~~~~~g~~~i~~~~ 129 (187)

T 5DWN\_A 50 KRFAAFADQGFPILVAEADGRVLGYAYASYFRVRPAYRWLAEDSIYIAPDAKGQGIGKLLLRELIARISALGFRQLLAVI 129 (187)

T ss\_dssp HHHHHHHHHTCCEEEEEETTEEEEEEEEEESCCSGGGTTEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHTTCCEEEEEE

T ss\_pred HHHHHHhcCCCCEEEEEECCEEEEEEEEEeccCChhccEEEEEEEEECHHHCCCCHHHHHHHHHHHHHHHCCCCEEEEEe

Q ss\_pred E--cCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 84 R--HSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 84 ~--~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

. ..|. .+.++|+++||+..+...

T Consensus 130 ~~~~~n~---------~~~~~~~~~Gf~~~~~~~ 154 (187)

T 5DWN\_A 130 GDGEHNI---------GSVKLHESLGFTHCGRIE 154 (187)

T ss\_dssp TTTTTCH---------HHHHHHHHTTCEEEEEEE

T ss\_pred cCCCccH---------HHHHHHHhCCCEEEEEEe

No 210

>d3fb3a\_ d.108.1.0 (A:) automated matches {Trypanosome (Trypanosoma brucei) [TaxId: 5691]}

Probab=98.34 E-value=7.2e-08 Score=70.86 Aligned\_cols=80 Identities=21% Similarity=0.267 Sum\_probs=0.0 Template\_Neff=13.100

Q ss\_pred EEEEEECCEEEEEEEEEeC----------CEEEEEEECHHHCCCCHHHHHHHHHHHccccCeeEEEEEcCCccccccccc

Q Phabba\_Draft 27 MARHAHDDRPVGHLHWHPD----------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHIYESSYPVRHSSHFSAAGRAW 96 (219)

Q Consensus 27 ~~v~~~~~~liG~~~~~~~----------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~~~i~l~v~~~n~~~~~~~~~ 96 (219)

++++..++++||++.+... .++..++|+|++|++|+|+.|++.+++.++...+...+...|.

T Consensus 49 ~~~~~~~~~~vg~~~~~~~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~~~~~~~~-------- 120 (142)

T d3fb3a\_ 49 VFCHQPTGRIVGSASLMIQPKFTRGGRAVGHIEDVVVDPSYRGAGLGKALIMDLCEISRSKGCYKVILDSSE-------- 120 (142)

T ss\_dssp EEEETTTTEEEEEEEEEEEECSSGGGCEEEEEEEEEECTTTTTSSHHHHHHHHHHHHHHHTTCSEEEEEECT--------

T ss\_pred EEEEcCCCCEEEEEEEEEcccccCCCceEEEEEEEEECHHHCCCChHHHHHHHHHHHHHhCCCcEEEEcCCc--------

Q ss\_pred chhHHHHHcCCCEEeeeee

Q Phabba\_Draft 97 AQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 97 ~~~~~~y~r~Gf~~~~~~~ 115 (219)

.+.++|+++||+..+...

T Consensus 121 -~~~~~~~~~Gf~~~~~~~ 138 (142)

T d3fb3a\_ 121 -KSLPFYEKLGFRAHERQM 138 (142)

T ss\_dssp -TTHHHHHTTTCEEEEEEE

T ss\_pred -chHHHHHHcCceeccccc

No 211

>4H89\_A GCN5-related N-acetyltransferase; N-Acyltransferase superfamily, Structural Genomics, PSI-Biology; 1.37A {Kribbella flavida}

Probab=98.34 E-value=1.2e-07 Score=72.77 Aligned\_cols=87 Identities=14% Similarity=0.158 Sum\_probs=0.0 Template\_Neff=12.700

Q ss\_pred hCCcEEEEEE-CCEEEEEEEEEeC-------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEE-EEcCCccc

Q Phabba\_Draft 23 SNGIMARHAH-DDRPVGHLHWHPD-------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYP-VRHSSHFS 90 (219)

Q Consensus 23 ~~~~~~v~~~-~~~liG~~~~~~~-------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~-v~~~n~~~ 90 (219)

....++++.. ++++||++.+... ..+..+.|+|++|++|+|+.|++.+++.+.. ..+.+. +...|.

T Consensus 58 ~~~~~~~~~~~~~~ivG~~~~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~~~~~~~~~~n~-- 135 (173)

T 4H89\_A 58 PQSRTTVAVDADGTVLGSANMYPNRPGPGAHVASASFMVAAAARGRGVGRALCQDMIDWAGREGFRAIQFNAVVETNT-- 135 (173)

T ss\_dssp CCCEEEEEECTTCCEEEEEEEEESSSGGGTTEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHTTCSEEEEEEEETTCH--

T ss\_pred CCccEEEEEccCCcEEEEEEEecCCCCCCceEEEEEEEECHHHcCCCHHHHHHHHHHHHHHHcCCeEEEEEEEecCCH--

Q ss\_pred ccccccchhHHHHHcCCCEEeeeeeccc

Q Phabba\_Draft 91 AAGRAWAQSDPDYHDPGDQNVTKADDDV 118 (219)

Q Consensus 91 ~~~~~~~~~~~~y~r~Gf~~~~~~~~~~ 118 (219)

.+.++|+++||+..+......

T Consensus 136 -------~~~~~~~~~Gf~~~~~~~~~~ 156 (173)

T 4H89\_A 136 -------VAVKLWQSLGFRVIGTVPEAF 156 (173)

T ss\_dssp -------HHHHHHHHTTCEEEEEEEEEE

T ss\_pred -------HHHHHHHHcCCEEEEeccccc

No 212

>3JUW\_A Probable GnaT-family acetyltransferase; structural genomics, APC60242, GnaT family; HET: SO4; 2.11A {Bordetella pertussis}

Probab=98.33 E-value=1.7e-07 Score=71.84 Aligned\_cols=93 Identities=9% Similarity=-0.071 Sum\_probs=0.0 Template\_Neff=12.800

Q ss\_pred chHHHHHhh-------CCcEEEEEE--CCEEEEEEEEE----------eCCEEEEEEECHHHCCCCHHHHHHHHHHHccc

Q Phabba\_Draft 15 FEPFDTMWS-------NGIMARHAH--DDRPVGHLHWH----------PDGEIDSITVHPDLQRRGIGTAMLKHAQDNPH 75 (219)

Q Consensus 15 ~~~l~~~~~-------~~~~~v~~~--~~~liG~~~~~----------~~~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~ 75 (219)

...+..... ....+++.. ++++||++.+. .......++|+|++|++|+|+.|++.+++.+.

T Consensus 48 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ivG~~~~~~~~~~~~~~~~~~~~~~~~v~~~~r~~G~~~~l~~~~~~~~~ 127 (175)

T 3JUW\_A 48 QAWLRLCARQGMWDAYACGFYYLLDPVSGEMRGEAGFQFRRRGFGPGFDNHPEAAWAVASAHQGRGLAAEAMQALLAHHD 127 (175)

T ss\_dssp HHHHHHHHHHHHHHHHSCCEEEEECTTTCCEEEEEEEECCCCSSCTTTTTSCEEEEEECGGGTTSSHHHHHHHHHHHHHH

T ss\_pred HHHHHHHHHhccccccCceEEEEEeCCCCCeeEEEEEEeeccCCCCCCCCCeeEEEEeCHHHCCCCHHHHHHHHHHHHHH

Q ss\_pred c----CeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeeec

Q Phabba\_Draft 76 I----YESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADD 116 (219)

Q Consensus 76 ~----~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~ 116 (219)

. ..+.+.+...|. .+.++|+++||+..+....

T Consensus 128 ~~~~~~~~~~~~~~~n~---------~~~~~~~~~Gf~~~~~~~~ 163 (175)

T 3JUW\_A 128 RSSGRQRVVALIARSNL---------PSLRLAERLGFRGYSDVAF 163 (175)

T ss\_dssp HHHTSCCEEEEEETTCH---------HHHHHHHHTTCEEEEEEEE

T ss\_pred HcCCCcEEEEEEeCCcH---------HHHHHHHHhCCeEEEEEee

No 213

>3JUW\_C Probable GnaT-family acetyltransferase; structural genomics, APC60242, GnaT family; HET: SO4; 2.11A {Bordetella pertussis}

Probab=98.33 E-value=1.7e-07 Score=71.84 Aligned\_cols=93 Identities=9% Similarity=-0.071 Sum\_probs=0.0 Template\_Neff=12.800

Q ss\_pred chHHHHHhh-------CCcEEEEEE--CCEEEEEEEEE----------eCCEEEEEEECHHHCCCCHHHHHHHHHHHccc

Q Phabba\_Draft 15 FEPFDTMWS-------NGIMARHAH--DDRPVGHLHWH----------PDGEIDSITVHPDLQRRGIGTAMLKHAQDNPH 75 (219)

Q Consensus 15 ~~~l~~~~~-------~~~~~v~~~--~~~liG~~~~~----------~~~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~ 75 (219)

...+..... ....+++.. ++++||++.+. .......++|+|++|++|+|+.|++.+++.+.

T Consensus 48 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ivG~~~~~~~~~~~~~~~~~~~~~~~~v~~~~r~~G~~~~l~~~~~~~~~ 127 (175)

T 3JUW\_C 48 QAWLRLCARQGMWDAYACGFYYLLDPVSGEMRGEAGFQFRRRGFGPGFDNHPEAAWAVASAHQGRGLAAEAMQALLAHHD 127 (175)

T ss\_dssp HHHHHHHHHHHHHHHHSCCEEEEECTTTCCEEEEEEEECCCCSSCTTTTTSCEEEEEECGGGTTSSHHHHHHHHHHHHHH

T ss\_pred HHHHHHHHHhccccccCceEEEEEeCCCCCeeEEEEEEeeccCCCCCCCCCeeEEEEeCHHHCCCCHHHHHHHHHHHHHH

Q ss\_pred c----CeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeeec

Q Phabba\_Draft 76 I----YESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADD 116 (219)

Q Consensus 76 ~----~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~ 116 (219)

. ..+.+.+...|. .+.++|+++||+..+....

T Consensus 128 ~~~~~~~~~~~~~~~n~---------~~~~~~~~~Gf~~~~~~~~ 163 (175)

T 3JUW\_C 128 RSSGRQRVVALIARSNL---------PSLRLAERLGFRGYSDVAF 163 (175)

T ss\_dssp HC---CCEEEEEETTCH---------HHHHHHHHTTCEEEEEEEE

T ss\_pred HcCCCcEEEEEEeCCcH---------HHHHHHHHhCCeEEEEEee

No 214

>5K9N\_B Polyamine N acetyltransferase (E.C.2.3.1.-); Polyamine N acetyltransferase, agmatine, N; 2.3A {Drosophila melanogaster}

Probab=98.33 E-value=1.3e-07 Score=76.53 Aligned\_cols=92 Identities=17% Similarity=0.130 Sum\_probs=0.0 Template\_Neff=11.900

Q ss\_pred hHHHHHhhCCcEEEEEECCEEEEEEEEEeC---------------------------------------------CEEEE

Q Phabba\_Draft 16 EPFDTMWSNGIMARHAHDDRPVGHLHWHPD---------------------------------------------GEIDS 50 (219)

Q Consensus 16 ~~l~~~~~~~~~~v~~~~~~liG~~~~~~~---------------------------------------------~~i~~ 50 (219)

+.+........++++..+|++||++.+... .++..

T Consensus 51 ~~~~~~~~~~~~~v~~~~~~ivG~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ 130 (216)

T 5K9N\_B 51 EFLLSNVPFGTCFVALHEGRIVAAVVAGPKDSHEPEHMAEEARKYAGGKWGSILHLLSAVETATDVCRRFSVPSCLHVHA 130 (216)

T ss\_dssp HHHHTTGGGTCCEEEEETTEEEEEEEEEEECTTHHHHHHHHHHHHTTSHHHHHHHHHHHHHHHHCHHHHTTCSCEEEEEE

T ss\_pred HHHHhhCCcCeEEEEEeCCcEEEEEEecCCCCCCchHHHHHHHHhcCchHHHHHHHHHHHHhhcchHHhcCCCceEEEEE

Q ss\_pred EEECHHHCCCCHHHHHHHHHHHcccc-CeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeeec

Q Phabba\_Draft 51 ITVHPDLQRRGIGTAMLKHAQDNPHI-YESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADD 116 (219)

Q Consensus 51 l~V~p~~R~~Gig~~Ll~~~~~~~~~-~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~ 116 (219)

++|+|++||+|+|+.|++.+++.+.+ ..-.+.+...|. .+.++|+++||+..+....

T Consensus 131 ~~v~~~~rg~Gig~~ll~~~~~~~~~~g~~~~~~~~~n~---------~s~~~~~k~Gf~~~~~~~~ 188 (216)

T 5K9N\_B 131 LGVDPQLRGRNLGGRLMETVAQRGRDLGHQLVSVDCTSV---------YSARLVQRLGYQLINTLRY 188 (216)

T ss\_dssp EEECGGGTTSCHHHHHHHHHHHHHHHTTCCEEEEEECSH---------HHHHHHHHTTCEEEEEEEG

T ss\_pred EEeCHHHCCCCHHHHHHHHHHHHHHHhCCCEEEEEcCcH---------HHHHHHHHcCCEEEEEEec

No 215

>5K9N\_A Polyamine N acetyltransferase (E.C.2.3.1.-); Polyamine N acetyltransferase, agmatine, N; 2.3A {Drosophila melanogaster}

Probab=98.33 E-value=1.1e-07 Score=76.84 Aligned\_cols=92 Identities=16% Similarity=0.091 Sum\_probs=0.0 Template\_Neff=11.900

Q ss\_pred hHHHHHhhCCcEEEEEECCEEEEEEEE---------------------------------------------EeCCEEEE

Q Phabba\_Draft 16 EPFDTMWSNGIMARHAHDDRPVGHLHW---------------------------------------------HPDGEIDS 50 (219)

Q Consensus 16 ~~l~~~~~~~~~~v~~~~~~liG~~~~---------------------------------------------~~~~~i~~ 50 (219)

+.+........++++..+|++||++.+ ....++..

T Consensus 51 ~~~~~~~~~~~~~v~~~~~~ivG~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ 130 (216)

T 5K9N\_A 51 EFLLSNVPFGTCFVALHEGRIVAAVVAGPKDSHEPEHMAEEARKYAGGKWGSILHLLSAVETATDVCRRFSVPSCLHVHA 130 (216)

T ss\_dssp HHHHTTGGGTCCEEEEETTEEEEEEEEEEECTTHHHHHHHHHHHHTTSHHHHHHHHHHHHHHHHCHHHHTTCSCEEEEEE

T ss\_pred HHHHhhCCcCcEEEEEeCCcEEEEEEecCCCCCChhHHHHHHHHhcCchHHHHHHHHHHHHHhhhHHHhcCCCcEEEEEE

Q ss\_pred EEECHHHCCCCHHHHHHHHHHHcccc-CeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeeec

Q Phabba\_Draft 51 ITVHPDLQRRGIGTAMLKHAQDNPHI-YESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADD 116 (219)

Q Consensus 51 l~V~p~~R~~Gig~~Ll~~~~~~~~~-~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~ 116 (219)

++|+|++||+|||+.|++.+++.+.+ ....+.+...|. .+.++|+++||+..+...+

T Consensus 131 ~~v~~~~rg~Gig~~ll~~~~~~~~~~g~~~i~~~~~n~---------~s~~~~~k~Gf~~~~~~~~ 188 (216)

T 5K9N\_A 131 LGVDPQLRGRNLGGRLMETVAQRGRDLGHQLVSVDCTSV---------YSARLVQRLGYQLINTLRY 188 (216)

T ss\_dssp EEECGGGTTSCHHHHHHHHHHHHHHHHTCCEEEEEECSH---------HHHHHHHHTTCEEEEEEEG

T ss\_pred EEeCHHHCCCCHHHHHHHHHHHHHHHhCCCEEEEEcCCH---------HHHHHHHHCCCEEEEEEec

No 216

>PF08444.9 ; Gly\_acyl\_tr\_C ; Aralkyl acyl-CoA:amino acid N-acyltransferase, C-terminal region

Probab=98.33 E-value=4.7e-08 Score=67.83 Aligned\_cols=82 Identities=11% Similarity=0.018 Sum\_probs=0.0 Template\_Neff=11.800

Q ss\_pred EEEEEECCEEEEEEEEEeCCEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEEEcCCcccccccccchhHHHH

Q Phabba\_Draft 27 MARHAHDDRPVGHLHWHPDGEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPVRHSSHFSAAGRAWAQSDPDY 103 (219)

Q Consensus 27 ~~v~~~~~~liG~~~~~~~~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v~~~n~~~~~~~~~~~~~~~y 103 (219)

++++..+++++|++.+.....+..+.|+|++|++|++..|++.+++.+.. . +.+.+...|. .+.++|

T Consensus 1 ~~~~~~~~~~vg~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~-~~~~~~~~~~---------~~~~~~ 70 (89)

T GLYAT\_PONAB/20 1 CCLLGPEGTPVCWDLMDQTGEMRMAGTLPEYRLHGLVTYVIYSHAQKLGKLGFP-VYSHVDYSNE---------AMQKMS 70 (89)

T ss\_pred CeeeCCCCCEEEEEEECCCceEEEEEECHHHccCcHHHHHHHHHHHHHHHcCCC-EEEEecCCCH---------HHHHHH

Q ss\_pred HcCCCEEeeeeeccc

Q Phabba\_Draft 104 HDPGDQNVTKADDDV 118 (219)

Q Consensus 104 ~r~Gf~~~~~~~~~~ 118 (219)

+++||+..+.....+

T Consensus 71 ~~~Gf~~~~~~~~~~ 85 (89)

T GLYAT\_PONAB/20 71 YTLQHVPIPRSWNQW 85 (89)

T ss\_pred HhcCCeecCCceeee

No 217

>1QSM\_A HISTONE ACETYLTRANSFERASE HPA2 (E.C.2.3.1.48); PROTEIN-ACETYL COENZYME A COMPLEX, ACETYLTRANSFERASE; HET: ACO; 2.4A {Saccharomyces cerevisiae} SCOP: d.108.1.1

Probab=98.32 E-value=1e-07 Score=71.82 Aligned\_cols=80 Identities=14% Similarity=0.201 Sum\_probs=0.0 Template\_Neff=12.500

Q ss\_pred EEEEEE--CCEEEEEEEEEeC---------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEEEcCCccccc

Q Phabba\_Draft 27 MARHAH--DDRPVGHLHWHPD---------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPVRHSSHFSAA 92 (219)

Q Consensus 27 ~~v~~~--~~~liG~~~~~~~---------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v~~~n~~~~~ 92 (219)

++++.+ +|++||++.+... ..+..++|+|++|++|+++.|++.+++.++. ..+.+.+...|.

T Consensus 54 ~~~~~~~~~~~ivG~~~~~~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~~~~~~~~~n~---- 129 (152)

T 1QSM\_A 54 AAVAVESSSEKIIGMINFFNHMTTWDFKDKIYINDLYVDENSRVKGAGGKLIQFVYDEADKLGTPSVYWCTDESNH---- 129 (152)

T ss\_dssp EEEEEESSSCCEEEEEEEEEECCTTCSSCEEEEEEEEECGGGCSSSHHHHHHHHHHHHHHHTTCCCEEEEEETTCH----

T ss\_pred EEEEEecCCCcEEEEEEEEecCCccCccCeEEEEEEEECHHHCCCCHHHHHHHHHHHHHHHhCCCEEEEEecCCCH----

Q ss\_pred ccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 93 GRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 93 ~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

.+.++|+++||+..+...

T Consensus 130 -----~~~~~~~~~Gf~~~~~~~ 147 (152)

T 1QSM\_A 130 -----RAQLLYVKVGYKAPKILY 147 (152)

T ss\_dssp -----HHHHHHHHHEEECSEEEE

T ss\_pred -----HHHHHHHHcCCccceEEE

No 218

>2Q7B\_A Acetyltransferase, GNAT family; NP\_689019.1, acetyltransferase (GNAT) family, Structural; HET: FLC; 2.0A {Streptococcus agalactiae 2603V/R}

Probab=98.32 E-value=1.6e-07 Score=74.92 Aligned\_cols=93 Identities=10% Similarity=0.123 Sum\_probs=0.0 Template\_Neff=11.100

Q ss\_pred chHHHHHhhCCc--EEEEEECCEEEEEEEEEeC----CEEEEEEECHHHCCCC--HHHHHHHHHHHcccc---CeeEEEE

Q Phabba\_Draft 15 FEPFDTMWSNGI--MARHAHDDRPVGHLHWHPD----GEIDSITVHPDLQRRG--IGTAMLKHAQDNPHI---YESSYPV 83 (219)

Q Consensus 15 ~~~l~~~~~~~~--~~v~~~~~~liG~~~~~~~----~~i~~l~V~p~~R~~G--ig~~Ll~~~~~~~~~---~~i~l~v 83 (219)

.+.+...+.... ++++..++++||++.+... .++..++|+|++|++| +|+.|++.+++.+.. ..+.+.+

T Consensus 59 ~~~~~~~~~~~~~~~~v~~~~~~ivG~~~~~~~~~~~~~i~~~~v~~~~rg~G~~i~~~l~~~~~~~~~~~g~~~i~~~~ 138 (181)

T 2Q7B\_A 59 IFQIENYYQNRKGQFWIALENEKVVGSIALLRIDDKTAVLKKFFTYPKYRGNPVRLGRKLFERFMLFARASKFTRIVLDT 138 (181)

T ss\_dssp GGCHHHHTGGGTCEEEEEEETTEEEEEEEEEECSSSEEEEEEEEECGGGSSTTTCHHHHHHHHHHHHHHHTTCCEEEEEE

T ss\_pred HHHHHHHhhcCCceEEEEEECCEEEEEEEEEEcCCCEEEEEEEEECHHHCCCCchHHHHHHHHHHHHHHHCCCCEEEEEC

Q ss\_pred EcCCcccccccccchhHHHHHcCCCEEeeeeec

Q Phabba\_Draft 84 RHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADD 116 (219)

Q Consensus 84 ~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~ 116 (219)

...|. .+.++|+++||+..+....

T Consensus 139 ~~~n~---------~~~~~~~~~Gf~~~~~~~~ 162 (181)

T 2Q7B\_A 139 PEKEK---------RSHFFYENQGFKQITRDEL 162 (181)

T ss\_dssp ETTCH---------HHHHHHHTTTCEEECTTTC

T ss\_pred ccccH---------HHHHHHHHCCCEEcccccc

No 219

>d2jlmb1 d.108.1.0 (B:7-182) automated matches {Acinetobacter baylyi [TaxId: 202950]}

Probab=98.32 E-value=2.2e-07 Score=72.15 Aligned\_cols=92 Identities=12% Similarity=0.060 Sum\_probs=0.0 Template\_Neff=12.300

Q ss\_pred chHHHHHhhCCc-EEEEEE-CCEEEEEEEEEeC--------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEE

Q Phabba\_Draft 15 FEPFDTMWSNGI-MARHAH-DDRPVGHLHWHPD--------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSY 81 (219)

Q Consensus 15 ~~~l~~~~~~~~-~~v~~~-~~~liG~~~~~~~--------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l 81 (219)

..++........ ++++.. ++++||++.+... ..+..+.|+|++|++|++..|++.+++.++. ..+.+

T Consensus 44 ~~~~~~~~~~~~~~~~~~~~~~~ivG~~~~~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~~g~~~~~~ 123 (176)

T d2jlmb1 44 AAWFATKRQNNFPIIGAVNEVGQLLGFASWGSFRAFPAYKYTVEHSVYIHKDYRGLGLSKHLMNELIKRAVESEVHVMVG 123 (176)

T ss\_dssp HHHHHHHHHHTCCEEEEEETTCCEEEEEEEEESSCSGGGTTEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHTTCCEEEE

T ss\_pred HHHHHHhcccCCcEEEEEccCCeEEEEEEEeecccCCccceEEEEEEEECHhhCCCCHHHHHHHHHHHHHHHCCCCEEEE

Q ss\_pred EEEcCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 82 PVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 82 ~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

.+...|. .+.++|+++||+..+...

T Consensus 124 ~~~~~n~---------~~~~~~~~~Gf~~~~~~~ 148 (176)

T d2jlmb1 124 CIDATNV---------ASIQLHQKLGFIHSGTIQ 148 (176)

T ss\_dssp EEETTCH---------HHHHHHHHTTCEEEEEEE

T ss\_pred EeeCCCH---------HHHHHHHHcCCEEEEEEe

No 220

>1VKC\_B putative acetyl transferase; structural genomics, acetyl transferase, Pyrococcus; HET: IOD; 1.89A {Pyrococcus furiosus} SCOP: d.108.1.1

Probab=98.31 E-value=2.6e-07 Score=71.57 Aligned\_cols=91 Identities=20% Similarity=0.178 Sum\_probs=0.0 Template\_Neff=11.500

Q ss\_pred chHHHHHhhCCc--EEEEEE-CCEEEEEEEEEeC---------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---Cee

Q Phabba\_Draft 15 FEPFDTMWSNGI--MARHAH-DDRPVGHLHWHPD---------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YES 79 (219)

Q Consensus 15 ~~~l~~~~~~~~--~~v~~~-~~~liG~~~~~~~---------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i 79 (219)

.+.+......+. ++++.+ +|++||++.+... ..+..+.|+|++|++|+|+.|++.+++.+.. ..+

T Consensus 49 ~~~~~~~~~~~~~~~~v~~~~~~~ivG~~~~~~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~i 128 (158)

T 1VKC\_B 49 EELFESLLSQGEHKFFVALNERSELLGHVWICITLDTVDYVKIAYIYDIEVVKWARGLGIGSALLRKAEEWAKERGAKKI 128 (158)

T ss\_dssp HHHHHHHHHSSEEEEEEEECTTCCEEEEEEEEEEECTTTCSEEEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHTTCSCE

T ss\_pred HHHHHHHHhcCCcEEEEEEeCCCcEEEEEEEEEecCccCCceEEEEEEEEECHHHCCCCHHHHHHHHHHHHHHHCCCcEE

Q ss\_pred EEEEEcCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 80 SYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 80 ~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

.+.+...|. +.++|+++||+..+...

T Consensus 129 ~~~~~~~n~----------~~~~~~~~Gf~~~~~~~ 154 (158)

T 1VKC\_B 129 VLRVEIDNP----------AVKWYEERGYKARALIM 154 (158)

T ss\_dssp EECCCTTCT----------HHHHHHHTTCCCCCCCC

T ss\_pred EEEEEeCCH----------HHHHHHHCCCEEEEeee

No 221

>d2zxva\_ d.108.1.0 (A:) automated matches {Thermus thermophilus HB8 [TaxId: 300852]}

Probab=98.31 E-value=1.9e-07 Score=73.11 Aligned\_cols=91 Identities=5% Similarity=-0.068 Sum\_probs=0.0 Template\_Neff=12.400

Q ss\_pred chHHHHHhhCCc--EEEEEECCEEEEEEEEEeC------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc----CeeEEE

Q Phabba\_Draft 15 FEPFDTMWSNGI--MARHAHDDRPVGHLHWHPD------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI----YESSYP 82 (219)

Q Consensus 15 ~~~l~~~~~~~~--~~v~~~~~~liG~~~~~~~------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~----~~i~l~ 82 (219)

...+........ ++++..++++||++.+... ..+. +.|+|++|++|+|+.|++.+++.+.+ ..+.+.

T Consensus 51 ~~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~i~-~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~~i~~~ 129 (188)

T d2zxva\_ 51 RAHLEGLLGEPGRVNWAILFGKEVAGRISVIAPEPEHAKLELG-TMLFKPFWGSPANKEAKYLLLRHAFEVLRAERVQFK 129 (188)

T ss\_dssp HHHHHHHHTSTTCEEEEEECSSSEEEEEEEEEEETTTTEEEEE-EEECGGGTTSHHHHHHHHHHHHCCCCCSCCSEEEEE

T ss\_pred HHHHHHHhcCCCceEEEEEeCCeEEEEEEEEcCChhHheeEEE-EEechhhcCChhHHHHHHHHHHHHhHccCCcEEEEE

Q ss\_pred EEcCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 83 VRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 83 v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

+...|. .+.++|+++||+..+...

T Consensus 130 ~~~~n~---------~~~~~~~~~Gf~~~~~~~ 153 (188)

T d2zxva\_ 130 VDLRNE---------RSQRALEALGAVREGVLR 153 (188)

T ss\_dssp EESSCH---------HHHHHHHHHTCEEEEEEE

T ss\_pred EeCCCH---------HHHHHHHHcCCeEEEEeE

No 222

>3R95\_A MccE protein; Microcin C7, Acetyltransferase, Self immunity; HET: ACO; 1.6A {Escherichia coli}

Probab=98.31 E-value=2.3e-07 Score=72.48 Aligned\_cols=92 Identities=8% Similarity=-0.042 Sum\_probs=0.0 Template\_Neff=12.500

Q ss\_pred chHHHHHh-----hCCcEEEEEECCEEEEEEEEEeC-----CEEEEEEECHHHCCCCHHHHHHHHHHHcccc----CeeE

Q Phabba\_Draft 15 FEPFDTMW-----SNGIMARHAHDDRPVGHLHWHPD-----GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI----YESS 80 (219)

Q Consensus 15 ~~~l~~~~-----~~~~~~v~~~~~~liG~~~~~~~-----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~----~~i~ 80 (219)

...+.... ....++++..++++||++.+... .....+.|+|++|++|+|+.|++.+++.+.. ..+.

T Consensus 63 ~~~~~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~~v~~~~r~~G~~~~l~~~~~~~~~~~~~~~~i~ 142 (188)

T 3R95\_A 63 VSFIEQSMIDNQNEKALILFIKYKTKIAGVVSFNIIDHANKTAYIGYWLGANFQGKGIVTNAINKLIQEYGDSGVIKRFV 142 (188)

T ss\_dssp HHHHHHHHHHHHTTSCEEEEEEETTEEEEEEEEEEEETTTTEEEEEEEECGGGTTSSHHHHHHHHHHHHHHTTTSCSEEE

T ss\_pred HHHHHHHHHHccCCceEEEEEEeCCEEEEEEEEEEeeCCCCEEEEEEEECHhHcCCCHHHHHHHHHHHHHHHcCCccEEE

Q ss\_pred EEEEcCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 81 YPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 81 l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

+.+...|. .+.++|+++||+..+...

T Consensus 143 ~~~~~~n~---------~~~~~~~~~Gf~~~~~~~ 168 (188)

T 3R95\_A 143 IKCIVDNK---------KSNATALRCGFTLEGVLQ 168 (188)

T ss\_dssp EEEETTCH---------HHHHHHHHTTCEEEEEEE

T ss\_pred EEEEeCCH---------HHHHHHHHcCCEEEEEEe

No 223

>3R9F\_A MccE protein; Microcin C7, Acetyltransferase, Self immunity; HET: COA, GSU; 1.2A {Escherichia coli}

Probab=98.31 E-value=2.3e-07 Score=72.48 Aligned\_cols=92 Identities=8% Similarity=-0.042 Sum\_probs=0.0 Template\_Neff=12.500

Q ss\_pred chHHHHHh-----hCCcEEEEEECCEEEEEEEEEeC-----CEEEEEEECHHHCCCCHHHHHHHHHHHcccc----CeeE

Q Phabba\_Draft 15 FEPFDTMW-----SNGIMARHAHDDRPVGHLHWHPD-----GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI----YESS 80 (219)

Q Consensus 15 ~~~l~~~~-----~~~~~~v~~~~~~liG~~~~~~~-----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~----~~i~ 80 (219)

...+.... ....++++..++++||++.+... .....+.|+|++|++|+|+.|++.+++.+.. ..+.

T Consensus 63 ~~~~~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~~v~~~~r~~G~~~~l~~~~~~~~~~~~~~~~i~ 142 (188)

T 3R9F\_A 63 VSFIEQSMIDNQNEKALILFIKYKTKIAGVVSFNIIDHANKTAYIGYWLGANFQGKGIVTNAINKLIQEYGDSGVIKRFV 142 (188)

T ss\_dssp HHHHHHHHHHHHTTSCEEEEEEETTEEEEEEEEEEEETTTTEEEEEEEECGGGTTSSHHHHHHHHHHHHHHTTTSCSEEE

T ss\_pred HHHHHHHHHHccCCceEEEEEEeCCEEEEEEEEEEeeCCCCEEEEEEEECHhHcCCCHHHHHHHHHHHHHHHcCCccEEE

Q ss\_pred EEEEcCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 81 YPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 81 l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

+.+...|. .+.++|+++||+..+...

T Consensus 143 ~~~~~~n~---------~~~~~~~~~Gf~~~~~~~ 168 (188)

T 3R9F\_A 143 IKCIVDNK---------KSNATALRCGFTLEGVLQ 168 (188)

T ss\_dssp EEEETTCH---------HHHHHHHHTTCEEEEEEE

T ss\_pred EEEEeCCH---------HHHHHHHHcCCEEEEEEe

No 224

>5K04\_B Uncharacterized protein, Peptide alpha-N-acetyltransferase; N-terminal acetyltransferase complex, TRANSFERASE; HET: MES, COA; 2.4A {Candida albicans (strain WO-1)}

Probab=98.31 E-value=2.3e-07 Score=72.00 Aligned\_cols=91 Identities=10% Similarity=0.082 Sum\_probs=0.0 Template\_Neff=12.000

Q ss\_pred chHHHHHhhCCc-EEEEEE--CCEEEEEEEEEeC---------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---Cee

Q Phabba\_Draft 15 FEPFDTMWSNGI-MARHAH--DDRPVGHLHWHPD---------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YES 79 (219)

Q Consensus 15 ~~~l~~~~~~~~-~~v~~~--~~~liG~~~~~~~---------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i 79 (219)

............ .+++.. ++++||++.+... .++..++|+|++|++|+|++|++.+++.+.. ..+

T Consensus 30 ~~~~~~~~~~~~~~~~~~~~~~~~ivG~~~~~~~~~~~~~~~~~~i~~~~v~~~~r~~G~~~~l~~~~~~~~~~~~~~~i 109 (170)

T 5K04\_B 30 SFYSQYLIEWPQLFYKSVETPNGQASGYMMAKTEGQLSKKEWHTHITAVTVLDQYRRIGLASKLCLELENLTQVKDTLFI 109 (170)

T ss\_dssp HHHHHHHHHCGGGEEEEEETTTTEEEEEEEEEEEEEC-CCEEEEEEEEEEECGGGCSSSHHHHHHHHGGGSHHHHTSSEE

T ss\_pred HHHHHHhhhcCccEEEEEeCCCCeEEEEEEEEEcCCCCCCeeEEEEEEEEECHHHCCCCHHHHHHHHHHHHHHhcCCcEE

Q ss\_pred EEEEEcCCcccccccccchhHHHHHcCCCEEeeee

Q Phabba\_Draft 80 SYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKA 114 (219)

Q Consensus 80 ~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~ 114 (219)

.+.+...|. .+.++|+++||+..+..

T Consensus 110 ~~~~~~~n~---------~~~~~~~k~Gf~~~~~~ 135 (170)

T 5K04\_B 110 DLFVKVTNT---------LGRILYEKLGYSVFRRV 135 (170)

T ss\_dssp EEEEETTCH---------HHHHHHHHTTCEEEEEE

T ss\_pred EEEEecCCH---------HHHHHHHHcCcEEEehh

No 225

>d4jxqa\_ d.108.1.0 (A:) automated matches {Sinorhizobium meliloti [TaxId: 266834]}

Probab=98.31 E-value=2.1e-07 Score=72.99 Aligned\_cols=91 Identities=20% Similarity=0.076 Sum\_probs=0.0 Template\_Neff=12.200

Q ss\_pred hHHHHHhhCCcEEEEEEC--CEEEEEEEEEeC--------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEE

Q Phabba\_Draft 16 EPFDTMWSNGIMARHAHD--DRPVGHLHWHPD--------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYP 82 (219)

Q Consensus 16 ~~l~~~~~~~~~~v~~~~--~~liG~~~~~~~--------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~ 82 (219)

..+.....+...+++..+ +++||++.+... ..+..++|+|++|++|+|+.|++.+++.++. ..+.+.

T Consensus 43 ~~~~~~~~~~~~~~~~~~~~~~ivG~~~~~~~~~~~~~~~~~~~~~~v~~~~r~~G~~~~l~~~~~~~~~~~g~~~i~~~ 122 (185)

T d4jxqa\_ 43 LRFSTITGNGYPYVVALDERGAVIGYAYASAFRNRTAYRFLVEDSIYLSPEARGKGIGKALLSELVGRCTALGFRQMIAV 122 (185)

T ss\_dssp HHHHHHHHTTCCEEEEECTTSCEEEEEEEEESSCSGGGTTEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHHTCCEEEEE

T ss\_pred HHHHhhhCCCceEEEEECCCCCEEEEEEEEecccCccccEEEEEEEEeCHHHCCCCHHHHHHHHHHHHHHHcCCCeEEEE

Q ss\_pred EEcCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 83 VRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 83 v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

+...|. .+.++|+++||+..+...

T Consensus 123 ~~~~n~---------~~~~~~~~~Gf~~~~~~~ 146 (185)

T d4jxqa\_ 123 IGGAHP---------SSIALHRALGFELQGLMK 146 (185)

T ss\_dssp EETTCH---------HHHHHHHHTTCEEEEEEE

T ss\_pred eecCCH---------HHHHHHHHcCCEEEEEEE

No 226

>3GY9\_A GCN5-related N-acetyltransferase; YP\_001815201.1, putative acetyltransferase, Structural Genomics; HET: COA, GOL, SO4; 1.52A {Exiguobacterium sibiricum 255-15}

Probab=98.30 E-value=1.8e-07 Score=70.41 Aligned\_cols=86 Identities=22% Similarity=0.279 Sum\_probs=0.0 Template\_Neff=12.500

Q ss\_pred hCCcEEEEEE-CCEEEEEEEEEeC------CEEEEEEECHHHCCCCHHHHHHHHHHHccccCeeEEEEEcCCcccccccc

Q Phabba\_Draft 23 SNGIMARHAH-DDRPVGHLHWHPD------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHIYESSYPVRHSSHFSAAGRA 95 (219)

Q Consensus 23 ~~~~~~v~~~-~~~liG~~~~~~~------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~~~i~l~v~~~n~~~~~~~~ 95 (219)

....++++.. +|++||++.+... ..+..+.|+|++||+|+|+.|+..+++.+.+....+.+. |.

T Consensus 47 ~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~i~~~~v~~~~rg~G~~~~l~~~~~~~~~~~~~~~~~~--n~------- 117 (150)

T 3GY9\_A 47 DGEAMFVALSTTNQVLACGGYMKQSGQARTGRIRHVYVLPEARSHGIGTALLEKIMSEAFLTYDRLVLY--SE------- 117 (150)

T ss\_dssp TTCEEEEEECTTCCEEEEEEEEECTTSTTEEEEEEEEECGGGTTSSHHHHHHHHHHHHHTTTCSEEEEC--CS-------

T ss\_pred cCcEEEEEEecCCeEEEEEEEEeccCCCCeEEEEEEEECHHHccCCHHHHHHHHHHHHHhhcCCEEEEE--cC-------

Q ss\_pred cchhHHHHHcCCCEEeeeeecccc

Q Phabba\_Draft 96 WAQSDPDYHDPGDQNVTKADDDVS 119 (219)

Q Consensus 96 ~~~~~~~y~r~Gf~~~~~~~~~~~ 119 (219)

.+.++|+++||+..+.......

T Consensus 118 --~~~~~~~~~Gf~~~~~~~~~~~ 139 (150)

T 3GY9\_A 118 --QADPFYQGLGFQLVSGEKITHT 139 (150)

T ss\_dssp --SCHHHHHHTTCEECCCSSCSEE

T ss\_pred --CcHHHHHhcCcEEecCCceecC

No 227

>4FD7\_B Putative uncharacterized protein (E.C.2.3.1.87); Gnat, CoA binding, transferase; HET: IOD, EDO, SO4; 1.8A {Aedes aegypti}

Probab=98.30 E-value=1.4e-07 Score=77.55 Aligned\_cols=92 Identities=16% Similarity=0.090 Sum\_probs=0.0 Template\_Neff=11.800

Q ss\_pred chHHHHHhhCCcEEEEEE--CCEEEEEEEEE----------------------------------------eCCEEEEEE

Q Phabba\_Draft 15 FEPFDTMWSNGIMARHAH--DDRPVGHLHWH----------------------------------------PDGEIDSIT 52 (219)

Q Consensus 15 ~~~l~~~~~~~~~~v~~~--~~~liG~~~~~----------------------------------------~~~~i~~l~ 52 (219)

...+...+.....+++.+ ++++||++.+. ...++..++

T Consensus 75 ~~~~~~~~~~~~~~v~~~~~~~~ivG~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~i~~l~ 154 (238)

T 4FD7\_B 75 VALWKAMLPDRMSLVCFREGSDEIVGVNILDVASRSDKDNAQFNSAIFQAIYDTIEYVSHQANIFDRYNVDHYLNAMGLS 154 (238)

T ss\_dssp HHHHHHHGGGSCCEEEEETTCCSEEEEEEEEEEETTCCCCCCCSCHHHHHHHHHHHHHHHHTTHHHHHTCSEEEEEEEEE

T ss\_pred HHHHHHHCcCCcEEEEEECCCCCEEEEEEEEecCCCCCCchhhcCHHHHHHHHHHHHHHHhhcHHHhcCCccEEEEEEEE

Q ss\_pred ECHHHCCCCHHHHHHHHHHHcccc--CeeEEEEEcCCcccccccccchhHHHHHcCCCEEeeeeec

Q Phabba\_Draft 53 VHPDLQRRGIGTAMLKHAQDNPHI--YESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADD 116 (219)

Q Consensus 53 V~p~~R~~Gig~~Ll~~~~~~~~~--~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~ 116 (219)

|+|++||+|||+.|++.+++.+++ ..+.+.+..++. +.++|+++||+..+....

T Consensus 155 v~p~~rg~Gig~~L~~~~~~~a~~~g~~~~~~~~~~~~----------~~~~y~k~Gf~~~~~~~~ 210 (238)

T 4FD7\_B 155 VDPKYRGRGIATEILRARIPLCRAVGLKLSATCFTGPN----------SQTAATRVGFQEDFTITY 210 (238)

T ss\_dssp ECGGGCSSSHHHHHHHTHHHHHHHHTCCEEEEEECSHH----------HHHHHHHHTCEEEEEEEH

T ss\_pred eCHHHCCCcHHHHHHHHHHHHHHHhCCCEEEEEecCHH----------HHHHHHHcCCEEEEEEEh

No 228

>3FBU\_B Acetyltransferase, GNAT family; acetyltransferase (GNAT family),Bacillus anthracis, structural; HET: COA; 1.8A {Bacillus anthracis str. Sterne}

Probab=98.30 E-value=1.5e-07 Score=73.16 Aligned\_cols=84 Identities=10% Similarity=0.012 Sum\_probs=0.0 Template\_Neff=11.800

Q ss\_pred hCCcEEEEEECCEEEEEEEEEeC----CEEEEEEECHHHCCCCHHHHHHHHHHHcccc----CeeEEEEEcCCccccccc

Q Phabba\_Draft 23 SNGIMARHAHDDRPVGHLHWHPD----GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI----YESSYPVRHSSHFSAAGR 94 (219)

Q Consensus 23 ~~~~~~v~~~~~~liG~~~~~~~----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~----~~i~l~v~~~n~~~~~~~ 94 (219)

....++++..++++||++.+... .....+.|+|++|++|+|++|++.+++.+.+ ..+.+.+...|.

T Consensus 56 ~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~v~~~~r~~G~g~~ll~~~~~~~~~~~~~~~~~~~~~~~n~------ 129 (168)

T 3FBU\_B 56 AKNFPVILIGENILVGHIVFHKYFGEHTYEIGWVFNPKYFNKGYASEAAQATLKYGFKEMKLHRIIATCQPENT------ 129 (168)

T ss\_dssp CCEEEEEETTTTEEEEEEEEEEEETTTEEEEEEEECGGGGGGCHHHHHHHHHHHCCCCCSCCSEEEEEECTTCH------

T ss\_pred hhcccEEEEeCCeEEEEEEEEeecCCceEEEEEEECHHHCCCCHHHHHHHHHHHHHHHHcCCCEEEEEecCCCH------

Q ss\_pred ccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 95 AWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 95 ~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

.+.++|+++||+..+...

T Consensus 130 ---~a~~~~~~~Gf~~~~~~~ 147 (168)

T 3FBU\_B 130 ---PSYRVMEKIGMRREGYFK 147 (168)

T ss\_dssp ---HHHHHHHHTTCEEEEEEE

T ss\_pred ---HHHHHHHHhCCEEEEEee

No 229

>d1bo4b\_ d.108.1.1 (B:) Aminoglycoside 3-N-acetyltransferase {Serratia marcescens [TaxId: 615]}

Probab=98.30 E-value=2.7e-07 Score=67.41 Aligned\_cols=87 Identities=14% Similarity=0.097 Sum\_probs=0.0 Template\_Neff=13.000

Q ss\_pred CCCCchHHHHHhhCCc--EEEEEECCEEEEEEEEEeC---------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---

Q Phabba\_Draft 11 PPLKFEPFDTMWSNGI--MARHAHDDRPVGHLHWHPD---------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI--- 76 (219)

Q Consensus 11 ~~~~~~~l~~~~~~~~--~~v~~~~~~liG~~~~~~~---------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~--- 76 (219)

.....+.+......+. ++++..+|++||++.+... ..+..+.|+|++||+|+|++|++.+++.++.

T Consensus 36 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~~~~~~v~~~~rg~G~~~~l~~~~~~~~~~~~~ 115 (136)

T d1bo4b\_ 36 HQPDSDYLGNLLRSKTFIALAAFDQEAVVGALAAYVLPKFEQPRSEIYIYDLAVSGEHRRQGIATALINLLKHEANALGA 115 (136)

T ss\_dssp SCCCHHHHHHHHHCSSEEEEEEEETTEEEEEEEEEEEECSSSSCEEEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHHTC

T ss\_pred CCCChHHHHHHhhCCCEEEEEEEcCCcEEEEEEEEEcCcCCCCccEEEEEEEEECHHHccCCHHHHHHHHHHHHHHHcCC

Q ss\_pred CeeEEEEEcCCcccccccccchhHHHHHcC

Q Phabba\_Draft 77 YESSYPVRHSSHFSAAGRAWAQSDPDYHDP 106 (219)

Q Consensus 77 ~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~ 106 (219)

..+.+.+...|. .+.++|+|+

T Consensus 116 ~~~~~~~~~~n~---------~~~~~~~k~ 136 (136)

T d1bo4b\_ 116 YVIYVQADYGDD---------PAVALYTKL 136 (136)

T ss\_dssp CEEEEECCCSCC---------SSEEEEEC-

T ss\_pred cEEEEEEeeCCh---------HHHHHHhhC

No 230

>d1z9ua\_ d.108.1.0 (A:) automated matches {Salmonella typhimurium [TaxId: 99287]}

Probab=98.30 E-value=2.8e-07 Score=71.89 Aligned\_cols=91 Identities=10% Similarity=-0.065 Sum\_probs=0.0 Template\_Neff=12.000

Q ss\_pred chHHHHHh-----hCCcEEEEEECCEEEEEEEEEeC-----CEEEEEEECHHHCCCCHHHHHHHHHHHcccc----CeeE

Q Phabba\_Draft 15 FEPFDTMW-----SNGIMARHAHDDRPVGHLHWHPD-----GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI----YESS 80 (219)

Q Consensus 15 ~~~l~~~~-----~~~~~~v~~~~~~liG~~~~~~~-----~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~----~~i~ 80 (219)

...+.... ....++++.+++++||++.+... .....+.|+|++||+|+|++|++.+.+.+.+ ..+.

T Consensus 50 ~~~~~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~i~~~v~~~~rg~G~~~~l~~~~~~~~~~~~~~~~~~ 129 (175)

T d1z9ua\_ 50 RKHVQGNILLHQRGYAKMYLIFCQNEMAGVLSFNAIEPINKAAYIGYWLDESFQGQGIMSQSLQALMTHYARRGDIRRFV 129 (175)

T ss\_dssp HHHHHHHHHHHHHTSCEEEEEEETTEEEEEEEEEEEETTTTEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHTTSCCEEE

T ss\_pred HHHHHHHHHHhhcCceEEEEEEECCEEEEEEEEEEeeccccEEEEEEEeCHHHCCCCHHHHHHHHHHHHHHHcCCccEEE

Q ss\_pred EEEEcCCcccccccccchhHHHHHcCCCEEeeee

Q Phabba\_Draft 81 YPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKA 114 (219)

Q Consensus 81 l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~ 114 (219)

+.+...|. .+.++|+++||+..+..

T Consensus 130 ~~~~~~n~---------~~~~~~~~~Gf~~~~~~ 154 (175)

T d1z9ua\_ 130 IKCRVDNQ---------ASNAVARRNHFTLEGCM 154 (175)

T ss\_dssp EEEETTCH---------HHHHHHHHTTCEEEEEE

T ss\_pred EEEEcCCH---------HHHHHHHHCCCEEEEEE

No 231

>5K18\_B Uncharacterized protein, Peptide alpha-N-acetyltransferase, CHY; N-terminal acetyltransferase complex, TRANSFERASE-TRANSFERASE INHIBITOR; HET: COA; 2.73A {Candida albicans (strain WO-1)}

Probab=98.29 E-value=3e-07 Score=73.57 Aligned\_cols=95 Identities=9% Similarity=0.056 Sum\_probs=0.0 Template\_Neff=11.300

Q ss\_pred chHHHHHhhCCc-EEEEEE--CCEEEEEEEEEeC---------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---Cee

Q Phabba\_Draft 15 FEPFDTMWSNGI-MARHAH--DDRPVGHLHWHPD---------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YES 79 (219)

Q Consensus 15 ~~~l~~~~~~~~-~~v~~~--~~~liG~~~~~~~---------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i 79 (219)

............ .+++.. ++++||++.+... .++..+.|+|++||+|+|+.|+..+++.+.. ..+

T Consensus 30 ~~~~~~~~~~~~~~~~~~~~~~~~ivG~~~~~~~~~~~~~~~~~~i~~~~v~~~~rg~Gig~~l~~~~~~~~~~~~~~~i 109 (188)

T 5K18\_B 30 SFYSQYLIEWPQLFYKSVETPNGQASGYMMAKTEGQLSKKEWHTHITAVTVLDQYRRIGLASKLCLELENLTQVKDTLFI 109 (188)

T ss\_dssp HHHHHHHHHCGGGEEEEECSSSCCEEEEEEEEEECCTTTTCCEEEEEEEEECGGGTTSSHHHHHHHHHHHSHHHHTSSEE

T ss\_pred HHHHHHHHHCCCcEEEEEeCCCCCEEEEEEEEEcCCcccCceEEEEEEEEECHHHcCCCHHHHHHHHHHHHhhccCCeEE

Q ss\_pred EEEEEcCCcccccccccchhHHHHHcCCCEEeeeeeccc

Q Phabba\_Draft 80 SYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKADDDV 118 (219)

Q Consensus 80 ~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~~ 118 (219)

.+.+...|. .+.++|+++||+..+.....+

T Consensus 110 ~~~~~~~n~---------~~~~~~~k~Gf~~~~~~~~~~ 139 (188)

T 5K18\_B 110 DLFVKVTNT---------LGRILYEKLGYSVFRRVVGYY 139 (188)

T ss\_dssp EEEEETTCH---------HHHHHHHHHTCEEEEEETTTT

T ss\_pred EEEEEecCH---------HHHHHHHHcCCEEEEEEeccc

No 232

>2REE\_A CurA (E.C.2.3.1.38, 4.1.1.9); GNAT, CURACIN, S-ACETYLTRANSFERASE, DECARBOXYLASE, POLYKETIDE; HET: SO4, GOL; 1.95A {Lyngbya majuscula}

Probab=98.29 E-value=4.1e-07 Score=74.34 Aligned\_cols=99 Identities=11% Similarity=-0.021 Sum\_probs=0.0 Template\_Neff=11.700

Q ss\_pred CCCCchHHHHHhhC--CcEEEEEECCEEEEEEEEEeCC------------------------EEEEEEECHHHCCCCHHH

Q Phabba\_Draft 11 PPLKFEPFDTMWSN--GIMARHAHDDRPVGHLHWHPDG------------------------EIDSITVHPDLQRRGIGT 64 (219)

Q Consensus 11 ~~~~~~~l~~~~~~--~~~~v~~~~~~liG~~~~~~~~------------------------~i~~l~V~p~~R~~Gig~ 64 (219)

..+..+.+...+.. ..++++.+++++||++.+.... ++..++|+|++||+|||+

T Consensus 38 ~~~~~~~~~~~~~~~~~~~~v~~~~~~ivG~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~i~~l~v~p~~rg~Gig~ 117 (224)

T 2REE\_A 38 LQVDNEEIYRRIFKIPQGQFILELEDKIVGAIYSQRIDNPQLLDNKTCTQVPLLHTESGVVVQLLAVNILPELQNQGLGD 117 (224)

T ss\_dssp TCCCHHHHHHHHHHCGGGCEEEEESSCEEEEEEEEEESCGGGGTTCCTTTGGGGCCTTCSEEEEEEEEECGGGCSSSHHH

T ss\_pred cCCCHHHHHHHHHhCCCcEEEEEECCEEEEEEEEEEcCCcccCCCCchhhcccccCCCCcEEEEEEEEeCHHHcCCCHHH

Q ss\_pred HHHHHHHHcccc----CeeEEEEEcC-----------------------CcccccccccchhHHHHHcCCCEEeeeeecc

Q Phabba\_Draft 65 AMLKHAQDNPHI----YESSYPVRHS-----------------------SHFSAAGRAWAQSDPDYHDPGDQNVTKADDD 117 (219)

Q Consensus 65 ~Ll~~~~~~~~~----~~i~l~v~~~-----------------------n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~ 117 (219)

.|++.+++.+.. ..+.+.+... |. .+.+||+++||+..+.....

T Consensus 118 ~ll~~~~~~~~~~~g~~~i~~~~~~~n~~~~~~~~~~~~~~~~~~~~~~n~---------~~~~~y~k~Gf~~~~~~~~~ 188 (224)

T 2REE\_A 118 RLLEFMLQYCAQISGVEKVVAVTLCRNYPDYSPMPMAEYIHQKNESGLLVD---------PLLRFHQIHGAKIEKLLPGY 188 (224)

T ss\_dssp HHHHHHHHHHTTSTTCCEEEEEECCSSGGGTTTSCHHHHTTCBCTTSCBSS---------HHHHHHHHTTCEEEEEETTS

T ss\_pred HHHHHHHHHHHHhhCCCEEEEEEeCCCCcccCCCCHHHHHHHhcccCCCCC---------HHHHHHHHcCcEEeEecCCC

Q ss\_pred c

Q Phabba\_Draft 118 V 118 (219)

Q Consensus 118 ~ 118 (219)

+

T Consensus 189 ~ 189 (224)

T 2REE\_A 189 R 189 (224)

T ss\_dssp C

T ss\_pred C

No 233

>2REF\_B CurA (E.C.2.3.1.38, 4.1.1.9); GNAT, CURACIN, S-ACETYLTRANSFERASE, DECARBOXYLASE, POLYKETIDE; HET: ACO; 2.75A {Lyngbya majuscula}

Probab=98.29 E-value=4.1e-07 Score=74.34 Aligned\_cols=99 Identities=11% Similarity=-0.021 Sum\_probs=0.0 Template\_Neff=11.700

Q ss\_pred CCCCchHHHHHhhC--CcEEEEEECCEEEEEEEEEeCC------------------------EEEEEEECHHHCCCCHHH

Q Phabba\_Draft 11 PPLKFEPFDTMWSN--GIMARHAHDDRPVGHLHWHPDG------------------------EIDSITVHPDLQRRGIGT 64 (219)

Q Consensus 11 ~~~~~~~l~~~~~~--~~~~v~~~~~~liG~~~~~~~~------------------------~i~~l~V~p~~R~~Gig~ 64 (219)

..+..+.+...+.. ..++++.+++++||++.+.... ++..++|+|++||+|||+

T Consensus 38 ~~~~~~~~~~~~~~~~~~~~v~~~~~~ivG~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~i~~l~v~p~~rg~Gig~ 117 (224)

T 2REF\_B 38 LQVDNEEIYRRIFKIPQGQFILELEDKIVGAIYSQRIDNPQLLDNKTCTQVPLLHTESGVVVQLLAVNILPELQNQGLGD 117 (224)

T ss\_dssp GCCCHHHHHHHHHHCGGGCEEEEETTEEEEEEEEEEESCGGGGTTCCTTSSGGGCCTTCSEEEEEEEEECGGGCSSSHHH

T ss\_pred cCCCHHHHHHHHHhCCCcEEEEEECCEEEEEEEEEEcCCcccCCCCchhhcccccCCCCcEEEEEEEEeCHHHcCCCHHH

Q ss\_pred HHHHHHHHcccc----CeeEEEEEcC-----------------------CcccccccccchhHHHHHcCCCEEeeeeecc

Q Phabba\_Draft 65 AMLKHAQDNPHI----YESSYPVRHS-----------------------SHFSAAGRAWAQSDPDYHDPGDQNVTKADDD 117 (219)

Q Consensus 65 ~Ll~~~~~~~~~----~~i~l~v~~~-----------------------n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~~~ 117 (219)

.|++.+++.+.. ..+.+.+... |. .+.+||+++||+..+.....

T Consensus 118 ~ll~~~~~~~~~~~g~~~i~~~~~~~n~~~~~~~~~~~~~~~~~~~~~~n~---------~~~~~y~k~Gf~~~~~~~~~ 188 (224)

T 2REF\_B 118 RLLEFMLQYCAQISGVEKVVAVTLCRNYPDYSPMPMAEYIHQKNESGLLVD---------PLLRFHQIHGAKIEKLLPGY 188 (224)

T ss\_dssp HHHHHHHHHHHTSTTCCEEEEEECCSSGGGGTTSCHHHHTTCBCTTSCBSS---------HHHHHHHTTTCEEEEEETTS

T ss\_pred HHHHHHHHHHHHhhCCCEEEEEEeCCCCcccCCCCHHHHHHHhcccCCCCC---------HHHHHHHHcCcEEeEecCCC

Q ss\_pred c

Q Phabba\_Draft 118 V 118 (219)

Q Consensus 118 ~ 118 (219)

+

T Consensus 189 ~ 189 (224)

T 2REF\_B 189 R 189 (224)

T ss\_dssp C

T ss\_pred C

No 234

>2B5G\_A Diamine acetyltransferase 1 (E.C.2.3.1.57); Structural Genomics, PSI, Protein Structure; HET: SO4; 1.7A {Homo sapiens} SCOP: d.108.1.1

Probab=98.29 E-value=1e-07 Score=74.22 Aligned\_cols=78 Identities=17% Similarity=0.152 Sum\_probs=0.0 Template\_Neff=11.900

Q ss\_pred EEEEEE--------CCEEEEEEEEEeC--------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEEEcCC

Q Phabba\_Draft 27 MARHAH--------DDRPVGHLHWHPD--------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPVRHSS 87 (219)

Q Consensus 27 ~~v~~~--------~~~liG~~~~~~~--------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v~~~n 87 (219)

++++.. ++++||++.+... .++..++|+|++|++|+|+.|+..+++.+.. ..+.+.+...|

T Consensus 54 ~~v~~~~~~~~~~~~~~ivG~~~~~~~~~~~~~~~~~i~~~~v~~~~r~~G~~~~l~~~~~~~~~~~g~~~i~~~~~~~n 133 (171)

T 2B5G\_A 54 CLVAEVPKEHWTPEGHSIVGFAMYYFTYDPWIGKLLYLEDFFVMSDYRGFGIGSEILKNLSQVAMRCRCSSMHFLVAEWN 133 (171)

T ss\_dssp EEEEECCGGGCCTTCCCEEEEEEEEEEEETTTEEEEEEEEEEECGGGCSSSHHHHHHHHHHHHHHHHTCSEEEEEEETTC

T ss\_pred EEEEEcCcccCCCCCCeEEEEEEEEeccCccccceEEeEEEEECcccCCCCHHHHHHHHHHHHHHHCCCCEEEEEEecCC

Q ss\_pred cccccccccchhHHHHHcCCCEEeee

Q Phabba\_Draft 88 HFSAAGRAWAQSDPDYHDPGDQNVTK 113 (219)

Q Consensus 88 ~~~~~~~~~~~~~~~y~r~Gf~~~~~ 113 (219)

. .+.++|+++||+..+.

T Consensus 134 ~---------~~~~~~~~~Gf~~~~~ 150 (171)

T 2B5G\_A 134 E---------PSINFYKRRGASDLSS 150 (171)

T ss\_dssp H---------HHHHHHHTTTCEEHHH

T ss\_pred h---------hHHHHHHhCCCeecCc

No 235

>3I3G\_B N-acetyltransferase; TRANSFERASE, Trypanosoma brucei, malaria, structural; 1.86A {Trypanosoma brucei}

Probab=98.29 E-value=1.4e-07 Score=72.67 Aligned\_cols=80 Identities=21% Similarity=0.267 Sum\_probs=0.0 Template\_Neff=12.000

Q ss\_pred EEEEEECCEEEEEEEEEeC----------CEEEEEEECHHHCCCCHHHHHHHHHHHccccCeeEEEEEcCCccccccccc

Q Phabba\_Draft 27 MARHAHDDRPVGHLHWHPD----------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHIYESSYPVRHSSHFSAAGRAW 96 (219)

Q Consensus 27 ~~v~~~~~~liG~~~~~~~----------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~~~i~l~v~~~n~~~~~~~~~ 96 (219)

+++...+|++||++.+... ..+..++|+|++|++|+|+.|++.+++.+....+...+...|.

T Consensus 68 ~~~~~~~~~ivG~~~~~~~~~~~~~~~~~~~i~~~~v~p~~r~~G~~~~l~~~~~~~~~~~g~~~~~~~~n~-------- 139 (161)

T 3I3G\_B 68 VFCHQPTGRIVGSASLMIQPKFTRGGRAVGHIEDVVVDPSYRGAGLGKALIMDLCEISRSKGCYKVILDSSE-------- 139 (161)

T ss\_dssp EEEETTTTEEEEEEEEEEECCSSGGGCCEEEEEEEEECGGGTTTTHHHHHHHHHHHHHHHTTCSEEEEEECT--------

T ss\_pred EEEeCCCCcEEEEEEEEEccchhcCCCcEEEEEEEEECHHHCCCCHHHHHHHHHHHHHHhCCceEEEEeCCc--------

Q ss\_pred chhHHHHHcCCCEEeeeee

Q Phabba\_Draft 97 AQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 97 ~~~~~~y~r~Gf~~~~~~~ 115 (219)

.+.++|+++||+..+...

T Consensus 140 -~~~~~~~k~Gf~~~~~~~ 157 (161)

T 3I3G\_B 140 -KSLPFYEKLGFRAHERQM 157 (161)

T ss\_dssp -TTHHHHHHTTCEEEEEEE

T ss\_pred -chHHHHHHhCceeeecee

No 236

>3FB3\_B N-acetyltransferase; trypanosoma, malaria, structural genomics, Structural; 2.35A {Trypanosoma brucei}

Probab=98.29 E-value=1.4e-07 Score=72.67 Aligned\_cols=80 Identities=21% Similarity=0.267 Sum\_probs=0.0 Template\_Neff=12.000

Q ss\_pred EEEEEECCEEEEEEEEEeC----------CEEEEEEECHHHCCCCHHHHHHHHHHHccccCeeEEEEEcCCccccccccc

Q Phabba\_Draft 27 MARHAHDDRPVGHLHWHPD----------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHIYESSYPVRHSSHFSAAGRAW 96 (219)

Q Consensus 27 ~~v~~~~~~liG~~~~~~~----------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~~~i~l~v~~~n~~~~~~~~~ 96 (219)

+++...+|++||++.+... ..+..++|+|++|++|+|+.|++.+++.+....+...+...|.

T Consensus 68 ~~~~~~~~~ivG~~~~~~~~~~~~~~~~~~~i~~~~v~p~~r~~G~~~~l~~~~~~~~~~~g~~~~~~~~n~-------- 139 (161)

T 3FB3\_B 68 VFCHQPTGRIVGSASLMIQPKFTRGGRAVGHIEDVVVDPSYRGAGLGKALIMDLCEISRSKGCYKVILDSSE-------- 139 (161)

T ss\_dssp EEEETTTCCEEEEEEEEEECCSSGGGCCEEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHTTCSEEEEEECS--------

T ss\_pred EEEeCCCCcEEEEEEEEEccchhcCCCcEEEEEEEEECHHHCCCCHHHHHHHHHHHHHHhCCceEEEEeCCc--------

Q ss\_pred chhHHHHHcCCCEEeeeee

Q Phabba\_Draft 97 AQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 97 ~~~~~~y~r~Gf~~~~~~~ 115 (219)

.+.++|+++||+..+...

T Consensus 140 -~~~~~~~k~Gf~~~~~~~ 157 (161)

T 3FB3\_B 140 -KSLPFYEKLGFRAHERQM 157 (161)

T ss\_dssp -TTHHHHHHTTCEEEEEEE

T ss\_pred -chHHHHHHhCceeeecee

No 237

>1QSO\_C HISTONE ACETYLTRANSFERASE HPA2 (E.C.2.3.1.48); TETRAMER, HISTONE ACETYLTRANSFERASE, TRANSFERASE; 2.9A {Saccharomyces cerevisiae} SCOP: d.108.1.1

Probab=98.29 E-value=1.5e-07 Score=70.43 Aligned\_cols=80 Identities=14% Similarity=0.202 Sum\_probs=0.0 Template\_Neff=12.700

Q ss\_pred EEEEEE--CCEEEEEEEEEe---------CCEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEEEcCCccccc

Q Phabba\_Draft 27 MARHAH--DDRPVGHLHWHP---------DGEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPVRHSSHFSAA 92 (219)

Q Consensus 27 ~~v~~~--~~~liG~~~~~~---------~~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v~~~n~~~~~ 92 (219)

++++.+ ++++||++.+.. ...+..++|+|++|++|+++.|++.+++.++. ..+.+.+...|.

T Consensus 51 ~~~~~~~~~~~ivG~~~~~~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~i~~~~~~~n~---- 126 (149)

T 1QSO\_C 51 AAVAVESSSEKIIGMINFFNHMTTWDFKDKIYINDLYVDENSRVKGAGGKLIQFVYDEADKLGTPSVYWCTDESNH---- 126 (149)

T ss\_dssp EEEEECTTTCCEEEEEEEEEECCTTCSSCEEEEEEEEECTTTCCCCCHHHHHHHHHHHHHHTTCCCEEEEEETTCH----

T ss\_pred EEEEEeCCCCcEEEEEEEEEcCCcccccceEEEEEEEECHHHCCCCHHHHHHHHHHHHHHHhCCCEEEEEecCCCH----

Q ss\_pred ccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 93 GRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 93 ~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

.+.++|+++||+..+...

T Consensus 127 -----~~~~~~~~~Gf~~~~~~~ 144 (149)

T 1QSO\_C 127 -----RAQLLYVKVGYKAPKILY 144 (149)

T ss\_dssp -----HHHHHHHHHEEEEEEEEE

T ss\_pred -----HHHHHHHHcCCccceEEe

No 238

>d1qsoa\_ d.108.1.1 (A:) Histone acetyltransferase HPA2 {Baker's yeast (Saccharomyces cerevisiae) [TaxId: 4932]}

Probab=98.29 E-value=1.5e-07 Score=70.43 Aligned\_cols=80 Identities=14% Similarity=0.202 Sum\_probs=0.0 Template\_Neff=12.700

Q ss\_pred EEEEEE--CCEEEEEEEEEe---------CCEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEEEcCCccccc

Q Phabba\_Draft 27 MARHAH--DDRPVGHLHWHP---------DGEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPVRHSSHFSAA 92 (219)

Q Consensus 27 ~~v~~~--~~~liG~~~~~~---------~~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v~~~n~~~~~ 92 (219)

++++.+ ++++||++.+.. ...+..++|+|++|++|+++.|++.+++.++. ..+.+.+...|.

T Consensus 51 ~~~~~~~~~~~ivG~~~~~~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~i~~~~~~~n~---- 126 (149)

T d1qsoa\_ 51 AAVAVESSSEKIIGMINFFNHMTTWDFKDKIYINDLYVDENSRVKGAGGKLIQFVYDEADKLGTPSVYWCTDESNH---- 126 (149)

T ss\_dssp EEEEECTTTCCEEEEEEEEEECCSSCSSCEEEEEEEEECSTTCSSSTTHHHHHHHHHHHHHHTCCCEEEEEETTCH----

T ss\_pred EEEEEeCCCCcEEEEEEEEEcCCcccccceEEEEEEEECHHHCCCCHHHHHHHHHHHHHHHhCCCEEEEEecCCCH----

Q ss\_pred ccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 93 GRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 93 ~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

.+.++|+++||+..+...

T Consensus 127 -----~~~~~~~~~Gf~~~~~~~ 144 (149)

T d1qsoa\_ 127 -----RAQLLYVKVGYKAPKILY 144 (149)

T ss\_dssp -----HHHHHHHHHEEECSEEEE

T ss\_pred -----HHHHHHHHcCCccceEEe

No 239

>3IGR\_B Ribosomal-protein-S5-alanine N-acetyltransferase (E.C.2.3.1.128); Ribosomal-protein, alanine, acetyltransferase, vibrio, fischeri; 2.0A {Vibrio fischeri}

Probab=98.28 E-value=1.7e-07 Score=73.48 Aligned\_cols=80 Identities=10% Similarity=0.028 Sum\_probs=0.0 Template\_Neff=12.200

Q ss\_pred EEEEEE--CCEEEEEEEEE------eCCEEEEEEECHHHCCCCHHHHHHHHHHHcc-cc---CeeEEEEEcCCccccccc

Q Phabba\_Draft 27 MARHAH--DDRPVGHLHWH------PDGEIDSITVHPDLQRRGIGTAMLKHAQDNP-HI---YESSYPVRHSSHFSAAGR 94 (219)

Q Consensus 27 ~~v~~~--~~~liG~~~~~------~~~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~-~~---~~i~l~v~~~n~~~~~~~ 94 (219)

++++.. ++++||++.+. ....+..++|+|++|++|+|+.|++.+++.+ .. ..+.+.+...|.

T Consensus 69 ~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~~~~~~~~~~~~~~~~~n~------ 142 (184)

T 3IGR\_B 69 YFVVVDKNEHKIIGTVSYSNITRFPFHAGHVGYSLDSEYQGKGIMRRAVNVTIDWMFKAQNLHRIMAAYIPRNE------ 142 (184)

T ss\_dssp EEEEEETTTTEEEEEEEEEEEECTTTCEEEEEEEECTTSTTSSHHHHHHHHHHHHHHHTTCCSEEEEEECTTCH------

T ss\_pred EEEEEECCCCcEEEEEEEEeCCCCCCeeEEEEEEeCHHHcCCcHHHHHHHHHHHHHHHhCCccEEEEEEcCCCH------

Q ss\_pred ccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 95 AWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 95 ~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

.+.++|+++||+..+...

T Consensus 143 ---~~~~~~~~~Gf~~~~~~~ 160 (184)

T 3IGR\_B 143 ---KSAKVLAALGFVKEGEAK 160 (184)

T ss\_dssp ---HHHHHHHHTTCEEEEEEE

T ss\_pred ---HHHHHHHHcCCeEEEEEE

No 240

>5NNR\_E N-terminal acetyltransferase-like protein, Naa10, HypK; N-acetylation, NATs, Naa15, Naa10, HypK; HET: MSE, FME; 3.1A {Chaetomium thermophilum}

Probab=98.28 E-value=3.3e-07 Score=74.83 Aligned\_cols=90 Identities=18% Similarity=0.072 Sum\_probs=0.0 Template\_Neff=10.300

Q ss\_pred hHHHHHhhCCc-EEEEEE----------CCEEEEEEEEEeCC---------EEEEEEECHHHCCCCHHHHHHHHHH-Hcc

Q Phabba\_Draft 16 EPFDTMWSNGI-MARHAH----------DDRPVGHLHWHPDG---------EIDSITVHPDLQRRGIGTAMLKHAQ-DNP 74 (219)

Q Consensus 16 ~~l~~~~~~~~-~~v~~~----------~~~liG~~~~~~~~---------~i~~l~V~p~~R~~Gig~~Ll~~~~-~~~ 74 (219)

..+........ ++++.. ++++||++.+.... ++..++|+|++||+|+|++|++.++ ..+

T Consensus 30 ~~~~~~~~~~~~~~v~~~~~~~~~~~~~~~~ivG~~~~~~~~~~~~~~~~~~i~~i~v~p~~rg~G~g~~l~~~~~~~~~ 109 (195)

T 5NNR\_E 30 YYLYHALSWPQLSFVAVDVSRPAKSPYDYPKIVGYVLAKMEEEPADGVPHGHITSLSVMRTHRRLGIAEKLMRQSQLAMV 109 (195)

T ss\_dssp HHHHHHHHCTTSCEEEECTTCCCSSTTCCCCEEEEEEEEECSSCSSSCCCEEEEEEEECGGGTTSSHHHHHHHHHHHHHH

T ss\_pred HHHHHhccCCCeEEEEEeCCCCCCCCCCCCCEEEEEEEEEecCCCCCCCEEEEEEEEECHHHCCCCHHHHHHHHHHHHHH

Q ss\_pred cc---CeeEEEEEcCCcccccccccchhHHHHH-cCCCEEeeee

Q Phabba\_Draft 75 HI---YESSYPVRHSSHFSAAGRAWAQSDPDYH-DPGDQNVTKA 114 (219)

Q Consensus 75 ~~---~~i~l~v~~~n~~~~~~~~~~~~~~~y~-r~Gf~~~~~~ 114 (219)

.. ..+.+.+...|. .+.++|+ ++||+..+..

T Consensus 110 ~~~g~~~i~~~~~~~N~---------~~~~~~~~k~GF~~~~~~ 144 (195)

T 5NNR\_E 110 ETYNAHYVSLHVRVSNK---------AAIHLYRDTLGFKTEKVE 144 (195)

T ss\_dssp HHHCCSEEEEEEETTCH---------HHHHCCCCCTCCEEEEEE

T ss\_pred HhcCCCEEEEEEEeCCH---------HHHHHHHHcCCCEEEEEE

No 241

>5NNP\_B N-terminal acetyltransferase-like protein, Naa10, HypK; N-acetylation, NATs, Naa15, Naa10, HypK; HET: FME, PO4, GOL, CMC; 2.602A {Chaetomium thermophilum (strain DSM 1495 / CBS 144.50 / IMI 039719)}

Probab=98.28 E-value=3.3e-07 Score=74.83 Aligned\_cols=90 Identities=18% Similarity=0.072 Sum\_probs=0.0 Template\_Neff=10.300

Q ss\_pred hHHHHHhhCCc-EEEEEE----------CCEEEEEEEEEeCC---------EEEEEEECHHHCCCCHHHHHHHHHH-Hcc

Q Phabba\_Draft 16 EPFDTMWSNGI-MARHAH----------DDRPVGHLHWHPDG---------EIDSITVHPDLQRRGIGTAMLKHAQ-DNP 74 (219)

Q Consensus 16 ~~l~~~~~~~~-~~v~~~----------~~~liG~~~~~~~~---------~i~~l~V~p~~R~~Gig~~Ll~~~~-~~~ 74 (219)

..+........ ++++.. ++++||++.+.... ++..++|+|++||+|+|++|++.++ ..+

T Consensus 30 ~~~~~~~~~~~~~~v~~~~~~~~~~~~~~~~ivG~~~~~~~~~~~~~~~~~~i~~i~v~p~~rg~G~g~~l~~~~~~~~~ 109 (195)

T 5NNP\_B 30 YYLYHALSWPQLSFVAVDVSRPAKSPYDYPKIVGYVLAKMEEEPADGVPHGHITSLSVMRTHRRLGIAEKLMRQSQLAMV 109 (195)

T ss\_dssp HHHHHHHHCTTSCEEEEETTSCCSSTTCCCEEEEEEEEEECSSCSSSCCEEEEEEEEECGGGTTSSHHHHHHHHHHHHHH

T ss\_pred HHHHHhccCCCeEEEEEeCCCCCCCCCCCCCEEEEEEEEEecCCCCCCCEEEEEEEEECHHHCCCCHHHHHHHHHHHHHH

Q ss\_pred cc---CeeEEEEEcCCcccccccccchhHHHHH-cCCCEEeeee

Q Phabba\_Draft 75 HI---YESSYPVRHSSHFSAAGRAWAQSDPDYH-DPGDQNVTKA 114 (219)

Q Consensus 75 ~~---~~i~l~v~~~n~~~~~~~~~~~~~~~y~-r~Gf~~~~~~ 114 (219)

.. ..+.+.+...|. .+.++|+ ++||+..+..

T Consensus 110 ~~~g~~~i~~~~~~~N~---------~~~~~~~~k~GF~~~~~~ 144 (195)

T 5NNP\_B 110 ETYNAHYVSLHVRVSNK---------AAIHLYRDTLGFKTEKVE 144 (195)

T ss\_dssp HHHCCSEEEEEEETTCH---------HHHHCCCCCTCCEEEEEE

T ss\_pred HhcCCCEEEEEEEeCCH---------HHHHHHHHcCCCEEEEEE

No 242

>5ISV\_A Ornithine aminotransferase, mitochondrial (E.C.2.6.1.13); RimI, AcCoA, GNAT, Structural Genomics; 1.35A {Escherichia coli O157:H7}

Probab=98.28 E-value=2.1e-07 Score=72.41 Aligned\_cols=80 Identities=23% Similarity=0.227 Sum\_probs=0.0 Template\_Neff=11.600

Q ss\_pred EEEEEECCEEEEEEEEEeC---CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEEEcCCcccccccccchhH

Q Phabba\_Draft 27 MARHAHDDRPVGHLHWHPD---GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPVRHSSHFSAAGRAWAQSD 100 (219)

Q Consensus 27 ~~v~~~~~~liG~~~~~~~---~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v~~~n~~~~~~~~~~~~~ 100 (219)

++++..++++||++.+... ..+..++|+|++|++|+|+.|++.+++.+.. ..+.+.+...|. .+.

T Consensus 42 ~~~~~~~~~ivG~~~~~~~~~~~~~~~~~v~~~~r~~G~~~~l~~~~~~~~~~~g~~~i~~~~~~~n~---------~~~ 112 (165)

T 5ISV\_A 42 NFQLTQNGKMAAFAITQVVLDEATLFNIAVDPDYQRQGLGRALLEHLIDELEKRGVATLWLEVRASNA---------AAI 112 (165)

T ss\_dssp CEEEEETTEEEEEEEEEEETTEEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHTTCCEEEEEEETTCH---------HHH

T ss\_pred EEEEEECCeEEEEEEEEEeCCeEEEEEEEECHHHcCCCHHHHHHHHHHHHHHHcCCCEEEEEEEcCCH---------HHH

Q ss\_pred HHHHcCCCEEeeeee

Q Phabba\_Draft 101 PDYHDPGDQNVTKAD 115 (219)

Q Consensus 101 ~~y~r~Gf~~~~~~~ 115 (219)

++|+++||+..+...

T Consensus 113 ~~~~k~Gf~~~~~~~ 127 (165)

T 5ISV\_A 113 ALYESLGFNEATIRR 127 (165)

T ss\_dssp HHHHHTTCEEEEEEE

T ss\_pred HHHHHcCCeEeEeec

No 243

>4U9V\_B NatD; Acetyltransferase, GNAT fold, N-terminal acetylation; HET: ACO; 1.78A {Homo sapiens}

Probab=98.28 E-value=2.4e-07 Score=73.71 Aligned\_cols=98 Identities=11% Similarity=0.042 Sum\_probs=0.0 Template\_Neff=12.000

Q ss\_pred CCCchHHHHHhhCCc--EEEEEEC-CEEEEEEEEEeC-------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---Ce

Q Phabba\_Draft 12 PLKFEPFDTMWSNGI--MARHAHD-DRPVGHLHWHPD-------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YE 78 (219)

Q Consensus 12 ~~~~~~l~~~~~~~~--~~v~~~~-~~liG~~~~~~~-------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~ 78 (219)

++..+.+...+.... ++++..+ +++||++.+... .++..++|+|++|++|+|+.|++.+++.+.+ ..

T Consensus 68 ~~~~~~~~~~~~~~~~~~~~~~~~~~~ivG~~~~~~~~~~~~~~~~i~~~~v~~~~r~~Gig~~l~~~~~~~~~~~~~~~ 147 (197)

T 4U9V\_B 68 GWKDREKREEMTDDRAWYLIAWENSSVPVAFSHFRFDVECGDEVLYCYEVQLESKVRRKGLGKFLIQILQLMANSTQMKK 147 (197)

T ss\_dssp CCCHHHHHHHHHCTTCEEEEEEETTTEEEEEEEEEEEEETTEEEEEEEEEEECGGGCSSSHHHHHHHHHHHHHHHTTCSE

T ss\_pred CCChHHHHHHhhcCCCeEEEEECCCCCeeEEEEEEEecCCCCcEEEEEEEEECHHHhcCCHHHHHHHHHHHHHHhcCCCE

Q ss\_pred eEEEEEcCCcccccccccchhHHHHH-cCCCEEeeeeeccc

Q Phabba\_Draft 79 SSYPVRHSSHFSAAGRAWAQSDPDYH-DPGDQNVTKADDDV 118 (219)

Q Consensus 79 i~l~v~~~n~~~~~~~~~~~~~~~y~-r~Gf~~~~~~~~~~ 118 (219)

+.+.+...|. .+.++|+ ++||+..+......

T Consensus 148 i~~~~~~~n~---------~~~~~~~~~~Gf~~~~~~~~~~ 179 (197)

T 4U9V\_B 148 VMLTVFKHNH---------GAYQFFREALQFEIDDSSPSMS 179 (197)

T ss\_dssp EEEEEETTCH---------HHHHCCCCCSCCEECTTSCCTT

T ss\_pred EEEEEeccCH---------HHHHHhhhhcCCEEceeCCccc

No 244

>1GHE\_B ACETYLTRANSFERASE (E.C.2.3.1.-); Acyl Coenzyme A complex, TRANSFERASE; HET: ACO; 1.55A {Pseudomonas syringae pv. tabaci} SCOP: d.108.1.1

Probab=98.28 E-value=2.4e-07 Score=71.55 Aligned\_cols=89 Identities=15% Similarity=0.169 Sum\_probs=0.0 Template\_Neff=12.600

Q ss\_pred hHHHHHhhCCc--EEEEEECCEEEEEEEEEeC--------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEE

Q Phabba\_Draft 16 EPFDTMWSNGI--MARHAHDDRPVGHLHWHPD--------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYP 82 (219)

Q Consensus 16 ~~l~~~~~~~~--~~v~~~~~~liG~~~~~~~--------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~ 82 (219)

+.+......+. ++++..++++||++.+... .++..+.|+|++|++|+|+.|++.+++.+.. ..+.+.

T Consensus 51 ~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~i~~~~v~~~~r~~g~~~~l~~~~~~~~~~~g~~~~~~~ 130 (177)

T 1GHE\_B 51 DGLKADIAAGSLLLWVVAEDDNVLASAQLSLCQKPNGLNRAEVQKLMVLPSARGRGLGRQLMDEVEQVAVKHKRGLLHLD 130 (177)

T ss\_dssp HHHHHHHHTTSEEEEEEEETTEEEEEEEEEECCSTTCTTEEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHTTCCEEEEE

T ss\_pred HHHHHHHHcCCEEEEEEeeCCeEEEEEEEEeecCCCCCceEEEEEEEECHHHCCCCHHHHHHHHHHHHHHHCCCcEEEEE

Q ss\_pred EEcCCcccccccccchhHHHHHcCCCEEeeee

Q Phabba\_Draft 83 VRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKA 114 (219)

Q Consensus 83 v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~ 114 (219)

+...|. +.++|+++||+..+..

T Consensus 131 ~~~~n~----------~~~~~~k~Gf~~~~~~ 152 (177)

T 1GHE\_B 131 TEAGSV----------AEAFYSALAYTRVGEL 152 (177)

T ss\_dssp EETTSH----------HHHHHHHTTCEEEEEE

T ss\_pred cCCCcH----------HHHHHHHcCCEEeccC

No 245

>1GHE\_A ACETYLTRANSFERASE (E.C.2.3.1.-); Acyl Coenzyme A complex, TRANSFERASE; HET: ACO; 1.55A {Pseudomonas syringae pv. tabaci} SCOP: d.108.1.1

Probab=98.28 E-value=2.4e-07 Score=71.55 Aligned\_cols=89 Identities=15% Similarity=0.169 Sum\_probs=0.0 Template\_Neff=12.600

Q ss\_pred hHHHHHhhCCc--EEEEEECCEEEEEEEEEeC--------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEE

Q Phabba\_Draft 16 EPFDTMWSNGI--MARHAHDDRPVGHLHWHPD--------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYP 82 (219)

Q Consensus 16 ~~l~~~~~~~~--~~v~~~~~~liG~~~~~~~--------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~ 82 (219)

+.+......+. ++++..++++||++.+... .++..+.|+|++|++|+|+.|++.+++.+.. ..+.+.

T Consensus 51 ~~~~~~~~~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~i~~~~v~~~~r~~g~~~~l~~~~~~~~~~~g~~~~~~~ 130 (177)

T 1GHE\_A 51 DGLKADIAAGSLLLWVVAEDDNVLASAQLSLCQKPNGLNRAEVQKLMVLPSARGRGLGRQLMDEVEQVAVKHKRGLLHLD 130 (177)

T ss\_dssp HTTHHHHHHTSEEEEEEEETTEEEEEEEEEECCSTTCTTEEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHTTCCEEEEE

T ss\_pred HHHHHHHHcCCEEEEEEeeCCeEEEEEEEEeecCCCCCceEEEEEEEECHHHCCCCHHHHHHHHHHHHHHHCCCcEEEEE

Q ss\_pred EEcCCcccccccccchhHHHHHcCCCEEeeee

Q Phabba\_Draft 83 VRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKA 114 (219)

Q Consensus 83 v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~ 114 (219)

+...|. +.++|+++||+..+..

T Consensus 131 ~~~~n~----------~~~~~~k~Gf~~~~~~ 152 (177)

T 1GHE\_A 131 TEAGSV----------AEAFYSALAYTRVGEL 152 (177)

T ss\_dssp EETTSH----------HHHHHHHTTCEEEEEE

T ss\_pred cCCCcH----------HHHHHHHcCCEEeccC

No 246

>2B4B\_B Diamine acetyltransferase 1 (E.C.2.3.1.57); Structural Genomics, PSI, Protein Structure; HET: B33, COA; 2.0A {Homo sapiens} SCOP: d.108.1.1

Probab=98.28 E-value=1.4e-07 Score=73.21 Aligned\_cols=84 Identities=15% Similarity=0.114 Sum\_probs=0.0 Template\_Neff=12.100

Q ss\_pred hCCcEEEEEE--------CCEEEEEEEEE--------eCCEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEE

Q Phabba\_Draft 23 SNGIMARHAH--------DDRPVGHLHWH--------PDGEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPV 83 (219)

Q Consensus 23 ~~~~~~v~~~--------~~~liG~~~~~--------~~~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v 83 (219)

....++++.. ++++||++.+. ...++..++|+|++|++|+|+.|+..+++.++. ..+.+.+

T Consensus 50 ~~~~~~v~~~~~~~~~~~~~~~vG~~~~~~~~~~~~~~~~~i~~~~v~~~~r~~gi~~~l~~~~~~~~~~~g~~~i~~~~ 129 (171)

T 2B4B\_B 50 PFYHCLVAEVPKEHWTPEGHSIVGFAMYYFTYDPWIGKLLYLEDFFVMSDYRGFGIGSEILKNLSQVAMRCRCSSMHFLV 129 (171)

T ss\_dssp CSCEEEEEECCGGGCCTTCCSEEEEEEEEEEEETTTEEEEEEEEEEECGGGCSSSHHHHHHHHHHHHHHHTTCSEEEEEE

T ss\_pred CceEEEEEEcCcccCCCCCCceEEEEEEEeeccCCccceEeEEEEEEChhhcCCCHHHHHHHHHHHHHHHcCCCeeEEEE

Q ss\_pred EcCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 84 RHSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 84 ~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

...|. .+.++|+++||+..+...

T Consensus 130 ~~~n~---------~~~~~~~~~Gf~~~~~~~ 152 (171)

T 2B4B\_B 130 AEWNE---------PSINFYKRRGASDLSSEE 152 (171)

T ss\_dssp ETTCH---------HHHHHHHTTTCEEHHHHH

T ss\_pred ecCCh---------hHHHHHHHcCCeeecccc

No 247

>4JXQ\_A Acetyltransferase (E.C.2.3.1.-); Structural Genomics, PSI-Biology, New York; HET: FLC, 2PE, EDO; 1.15A {Sinorhizobium meliloti}

Probab=98.27 E-value=3.1e-07 Score=72.11 Aligned\_cols=91 Identities=20% Similarity=0.088 Sum\_probs=0.0 Template\_Neff=12.200

Q ss\_pred hHHHHHhhCCcEEEEEEC--CEEEEEEEEEeCC--------EEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEE

Q Phabba\_Draft 16 EPFDTMWSNGIMARHAHD--DRPVGHLHWHPDG--------EIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYP 82 (219)

Q Consensus 16 ~~l~~~~~~~~~~v~~~~--~~liG~~~~~~~~--------~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~ 82 (219)

..+.........+++..+ +++||++.+.... .+..++|+|++|++|+|+.|++.+++.++. ..+.+.

T Consensus 44 ~~~~~~~~~~~~~~~~~~~~~~ivG~~~~~~~~~~~~~~~~~~~~~~v~~~~r~~G~~~~l~~~~~~~~~~~g~~~~~~~ 123 (186)

T 4JXQ\_A 44 LRFSTITGNGYPYVVALDERGAVIGYAYASAFRNRTAYRFLVEDSIYLSPEARGKGIGKALLSELVGRCTALGFRQMIAV 123 (186)

T ss\_dssp HHHHHHHHTTCCEEEEECTTSCEEEEEEEEESSCSGGGTTEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHHTCCEEEEE

T ss\_pred HHHHhHhCCCeEEEEEECCCCCEEEEEEEEecCCccccceEEEEEEEECHHHcCCCHHHHHHHHHHHHHHHcCCCEEEEE

Q ss\_pred EEcCCcccccccccchhHHHHHcCCCEEeeeee

Q Phabba\_Draft 83 VRHSSHFSAAGRAWAQSDPDYHDPGDQNVTKAD 115 (219)

Q Consensus 83 v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~~~ 115 (219)

+...|. .+.++|+++||+..+...

T Consensus 124 ~~~~n~---------~~~~~~~~~Gf~~~~~~~ 147 (186)

T 4JXQ\_A 124 IGGAHP---------SSIALHRALGFELQGLMK 147 (186)

T ss\_dssp EETTCH---------HHHHHHHHTTCEEEEEEE

T ss\_pred ecCCCH---------HHHHHHHHcCCEEEeeee

No 248

>2G3A\_A acetyltransferase; acetyltransferase, structural genomics, PSI, Protein; 1.9A {Agrobacterium tumefaciens str. C58} SCOP: d.108.1.1

Probab=98.27 E-value=2.2e-07 Score=71.17 Aligned\_cols=91 Identities=14% Similarity=0.106 Sum\_probs=0.0 Template\_Neff=11.700

Q ss\_pred EEEEEECCEEEEEEEEEeC---CEEEEEEECHHHCCCCHHHHHHHHHHHcccc-CeeEEEEEcCCcccccccccchhHHH

Q Phabba\_Draft 27 MARHAHDDRPVGHLHWHPD---GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI-YESSYPVRHSSHFSAAGRAWAQSDPD 102 (219)

Q Consensus 27 ~~v~~~~~~liG~~~~~~~---~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~-~~i~l~v~~~n~~~~~~~~~~~~~~~ 102 (219)

+++...+|++||++.+... ..+..++|+|++||+|+|..|++.+++.+.+ ....+.+...|. .+.++

T Consensus 54 ~~~~~~~~~~vG~~~~~~~~~~~~i~~~~v~~~~rg~Gi~~~l~~~~~~~~~~~g~~~i~~~~~n~---------~~~~~ 124 (152)

T 2G3A\_A 54 ITIRNDDNSVTGGLVGHTARGWLYVQLLFVPEAMRGQGIAPKLLAMAEEEARKRGCMGAYIDTMNP---------DALRT 124 (152)

T ss\_dssp EEEECTTCCEEEEEEEEEETTEEEEEEEECCGGGCSSSHHHHHHHHHHHHHHHTTCCEEEEEESCH---------HHHHH

T ss\_pred EEEECCCCCEEEEEEEEecCCeEEEEEEEcCHHHCCCChHHHHHHHHHHHHHHCCCCEEEEEcCCH---------HHHHH

Q ss\_pred HHcCCCEEeeeeeccccccceEEe

Q Phabba\_Draft 103 YHDPGDQNVTKADDDVSNWGYTAM 126 (219)

Q Consensus 103 y~r~Gf~~~~~~~~~~~~~~~~~~ 126 (219)

|+++||+..+.......+.....+

T Consensus 125 ~~~~Gf~~~~~~~~~~~~~~~~~~ 148 (152)

T 2G3A\_A 125 YERYGFTKIGSLGPLSSGQSITWL 148 (152)

T ss\_dssp HHHHTCEEEEEECCCTTSCCEEEE

T ss\_pred HHHcCcEEEEEecCCCCcceEEEE

No 249

>PF13673.6 ; Acetyltransf\_10 ; Acetyltransferase (GNAT) domain

Probab=98.27 E-value=4.1e-07 Score=67.14 Aligned\_cols=90 Identities=20% Similarity=0.280 Sum\_probs=0.0 Template\_Neff=12.000

Q ss\_pred CCchHHHHHhhCCc--EEEEEECCEEEEEEEEEeCCEEEEEEECHHHCCCCHHHHHHHHHHHcccc---CeeEEEEEcCC

Q Phabba\_Draft 13 LKFEPFDTMWSNGI--MARHAHDDRPVGHLHWHPDGEIDSITVHPDLQRRGIGTAMLKHAQDNPHI---YESSYPVRHSS 87 (219)

Q Consensus 13 ~~~~~l~~~~~~~~--~~v~~~~~~liG~~~~~~~~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~---~~i~l~v~~~n 87 (219)

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T Consensus 17 ~~~~~~~~~~~~~~~~~~~~~~~~~~vg~~~~~~~~~~~~~~v~~~~r~~g~~~~l~~~~~~~~-~~~~~~~~~~~~~~~ 95 (127)

T R5CYJ1\_9FIRM/2 17 ISYDSFREMFERQEVTIFGAFEGVQICGMIAVTNSGHISLFFVRKAFQRHGIGRMLYLAAVAFA-AREVHTSKITVNAAP 95 (127)

T ss\_pred cCHHHHHHHHhcCCeEEEEEeeCCEEEEEEEEEcCceEEEEEeCHHHhcCCHHHHHHHHHHHHH-HhcCCeEEEEEeCCc

Q ss\_pred cccccccccchhHHHHHcCCCEEeee

Q Phabba\_Draft 88 HFSAAGRAWAQSDPDYHDPGDQNVTK 113 (219)

Q Consensus 88 ~~~~~~~~~~~~~~~y~r~Gf~~~~~ 113 (219)

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T Consensus 96 ~----------~~~~~~~~Gf~~~~~ 111 (127)

T R5CYJ1\_9FIRM/2 96 Q----------AVETYEHLGMHKVTE 111 (127)

T ss\_pred h----------HHHHHHhCCCEECCc

No 250

>4UA3\_B NatD (Naa40p); Acetyltransferase, GNAT fold, N-terminal acetylation; HET: COA, MSE; 1.85A {Schizosaccharomyces pombe}

Probab=98.26 E-value=3.4e-07 Score=72.50 Aligned\_cols=95 Identities=16% Similarity=0.035 Sum\_probs=0.0 Template\_Neff=12.100

Q ss\_pred CCCCCchHHHHHhhCCc-EEEEEE--CCEEEEEEEEEeC-------CEEEEEEECHHHCCCCHHHHHHHHHHHcccc---

Q Phabba\_Draft 10 LPPLKFEPFDTMWSNGI-MARHAH--DDRPVGHLHWHPD-------GEIDSITVHPDLQRRGIGTAMLKHAQDNPHI--- 76 (219)

Q Consensus 10 ~~~~~~~~l~~~~~~~~-~~v~~~--~~~liG~~~~~~~-------~~i~~l~V~p~~R~~Gig~~Ll~~~~~~~~~--- 76 (219)

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T Consensus 59 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ivG~~~~~~~~~~~~~~~~~~~~~v~~~~r~~G~~~~l~~~~~~~~~~~~~ 138 (194)

T 4UA3\_B 59 FGWDDSEKLKEMEMEKLEYICIFEKTSKKLVGFLSFEDTVEAGLTCLYIYEIQLDEHIRGRNVGKWLLKNASILAYRRNL 138 (194)

T ss\_dssp TCCCHHHHHHHHTCTTCEEEEEEETTTCCEEEEEEEEEEEETTEEEEEEEEEEECGGGTTSSHHHHHHHHHHHHHHHTTC

T ss\_pred cCCCchHHHHHHhhcCCeEEEEEEcCCCcEEEEEEEEEeccCCceEEEEEEEEECHHHCCCCHHHHHHHHHHHHHHHCCC

Q ss\_pred CeeEEEEEcCCcccccccccchhHHHHHcCCCEEeee

Q Phabba\_Draft 77 YESSYPVRHSSHFSAAGRAWAQSDPDYHDPGDQNVTK 113 (219)

Q Consensus 77 ~~i~l~v~~~n~~~~~~~~~~~~~~~y~r~Gf~~~~~ 113 (219)

..+.+.+...|. .+.++|+++||+..+.

T Consensus 139 ~~i~~~~~~~n~---------~~~~~~~~~Gf~~~~~ 166 (194)

T 4UA3\_B 139 KYIFLTVFSANL---------NALNFYHHFDFVPHES 166 (194)

T ss\_dssp CEEEEEEETTCH---------HHHHHHHHTTCEECTT

T ss\_pred cEEEEEEecCCH---------HHHHHHHhCCCEECCC