

Analysis of the NCBI standard entries  
Datapx program - Version V2.1 - Spring 2002  
Programmed by A. Galat - Protein Profile

Sliding frame = 9

Number of used codes 496

Database used CYP.dab.2010

1# 165( 165& 1 165) CSHUA 7.8 ( 7.8) 37.6 ( 37.6) 18.0 ( 18012.5)  
> peptidylprolyl isomerase (EC 5.2.1.8) A - human.

2# 164( 164& 1 164) NP\_839944 9.6 ( 9.6) 34.1 ( 34.1) 18.2 ( 18181.8)  
> cyclophilin-LC; cyclophilin homolog overexpressed in liver cancer;

3# 165( 165& 1 165) NP\_115861 6.6 ( 6.6) 27.3 ( 27.3) 18.6 ( 18627.3)  
> peptidylprolyl isomerase-like protein 3 isoform PPIL3a [Homo]

4# 161( 161& 1 161) NP\_570981 6.3 ( 6.3) 27.3 ( 27.3) 18.2 ( 18154.6)  
> peptidylprolyl isomerase-like protein 3 isoform PPIL3b [Homo]

5# 166( 166& 1 166) NP\_057143 8.2 ( 8.2) 33.7 ( 33.7) 18.2 ( 18236.9)  
> peptidylprolyl isomerase-like 1 [Homo sapiens].

6# 183( 208& 26 208) CSHUB 9.7 ( 9.8) 38.3 ( 42.3) 20.3 ( 22742.4)  
> peptidylprolyl isomerase (EC 5.2.1.8) B precursor [validated] -

7# 172( 301& 130 301) S66681 8.4 ( 5.3) 32.0 ( 33.2) 18.9 ( 33430.9)  
> peptidylprolyl isomerase (EC 5.2.1.8) A - human.

8# 181( 3224&30443224) A57545 6.7 ( 5.8) 35.9 ( 25.7) 19.9 (358220.6)  
> nucleoporin Nup358 - human

9# 173( 207& 36 208) A41581 9.3 ( 9.8) 35.8 ( 39.1) 18.5 ( 22040.3)  
> peptidylprolyl isomerase (EC 5.2.1.8) 3 precursor - human.

10# 181( 212& 28 208) A54204 9.4 ( 8.7) 48.1 ( 52.8) 19.6 ( 22763.3)  
> peptidylprolyl isomerase (EC 5.2.1.8) C precursor - human.

11# 176( 520& 271 446) S64705 8.6 ( 9.0) 22.7 ( 22.5) 20.0 ( 58823.6)  
> cyclophilin-like protein CyP-60 - human.

12# 170( 645& 476 645) D38552 6.8 ( 6.7) 30.0 ( 32.7) 18.9 ( 73443.9)  
> Human mRNA for KIAA0073 gene, partial cds

13# 165( 492& 1 165) NP\_624311 5.0 ( 5.6) 33.9 ( 20.9) 18.7 ( 57225.3)  
> peptidylprolyl isomerase-like 4 [Homo sapiens].

14# 177( 177& 1 177) G2708309 8.1 ( 8.1) 44.1 ( 44.1) 19.2 ( 19208.2)  
> U-snRNP-associated cyclophilin - Homo sapiens (human)

15# 187( 370& 6 192) A45981 6.8 ( 6.8) 38.0 ( 31.6) 20.4 ( 40763.7)  
> peptidylprolyl isomerase (EC 5.2.1.8) CyP-40 - human.

16# 184( 754& 1 184) U40763 8.4 (10.7) 34.8 ( 8.5) 20.5 ( 88618.4)  
> CARS-Cyp - Homo sapiens

17# 188( 1403& 51 238) A47328 8.3 (10.3) 37.2 ( 13.3) 20.7 (157712.2)  
> natural killer cell tumor-recognition protein - human.

18# 195( 205& 25 219) XP\_531396 8.5 ( 6.1) 38.5 ( 45.9) 21.4 ( 22517.7)  
> PREDICTED: similar to peptidylprolyl isomerase A isoform 1;

19# 175( 175& 1 175) XP\_525294 9.2 ( 9.2) 31.4 ( 31.4) 19.2 ( 19236.0)  
> PREDICTED: similar to peptidylprolyl isomerase A isoform 1;

20# 157( 157& 1 157) XP\_523512 8.5 ( 8.5) 28.0 ( 28.0) 17.0 ( 16976.4)  
> PREDICTED: similar to peptidylprolyl isomerase A isoform 1;

21# 211( 319& 40 250) XP\_507866 7.0 ( 8.4) 50.2 ( 48.3) 22.3 ( 33195.2)  
> PREDICTED: similar to Peptidyl-prolyl cis-trans isomerase,

22# 164( 164& 1 164) XP\_517783 5.9 ( 5.9) 42.1 ( 42.1) 17.8 ( 17772.2)  
> PREDICTED: similar to TRIM5/cyclophilin A fusion protein [Pan

23# 141( 141& 1 141) XP\_517773 9.8 ( 9.8) 34.0 ( 34.0) 15.5 ( 15462.0)  
> PREDICTED: similar to cyclophilin-LC; cyclophilin homolog

24# 180( 180& 1 180) XP\_526904 8.3 ( 8.3) 40.6 ( 40.6) 19.7 ( 19723.7)  
> PREDICTED: similar to peptidylprolyl isomerase A isoform 1;

25# 180( 229& 50 229) XP\_516556 9.3 ( 8.4) 49.4 ( 40.2) 19.5 ( 25176.3)  
> PREDICTED: similar to TRIM5/cyclophilin A fusion protein [Pan

26# 179( 179& 1 179) XP\_526001 8.3 ( 8.3) 34.1 ( 34.1) 19.7 ( 19675.6)  
> PREDICTED: similar to cyclophilin A [Pan troglodytes].

27# 175( 234& 60 234) XP\_516021 7.7 ( 9.7) 30.9 ( 28.6) 19.6 ( 26441.3)  
> PREDICTED: similar to peptidylprolyl isomerase-like protein 3

28# 205( 205& 1 205) XP\_515886 8.1 ( 8.1) 31.2 ( 31.2) 22.9 ( 22893.0)  
> PREDICTED: similar to peptidyl-prolyl isomerase G (cyclophilin G);

29# 143( 143& 1 143) XP\_525218 8.4 ( 8.4) 26.6 ( 26.6) 15.7 ( 15702.7)  
> PREDICTED: similar to cyclophilin-LC; cyclophilin homolog

30# 196( 196& 1 196) XP\_507684 9.2 ( 9.2) 39.3 ( 39.3) 21.3 ( 21324.4)  
> PREDICTED: similar to peptidylprolyl isomerase A isoform 1;

31# 193( 193& 1 193) XP\_524688 8.4 ( 8.4) 47.2 ( 47.2) 21.0 ( 20989.3)  
> PREDICTED: similar to peptidyl prolyl isomerase H; cyclophilin H;

32# 166( 314& 149 314) XP\_513346 9.0 ( 5.8) 29.5 ( 30.9) 18.3 ( 34964.5)  
> PREDICTED: similar to peptidylprolyl isomerase E isoform 2;

33# 173( 202& 30 202) XP\_524598 6.8 ( 7.2) 34.1 ( 38.1) 18.6 ( 21649.4)  
> PREDICTED: similar to TRIM5/cyclophilin A fusion protein [Pan

34# 166( 812& 280 445) XP\_515004 8.8 ( 8.7) 33.7 ( 33.5) 18.4 ( 88298.3)  
> PREDICTED: similar to peptidylprolyl isomerase-like 2 isoform a;

35# 140( 259& 120 259) XP\_523437 10.1 (10.0) 33.6 ( 32.4) 15.0 ( 27651.6)  
> PREDICTED: similar to peptidylprolyl isomerase A isoform 1;

36# 159( 159& 1 159) XP\_520485 6.8 ( 6.8) 42.1 ( 42.1) 17.1 ( 17072.4)  
> PREDICTED: similar to TRIM5/cyclophilin A fusion protein [Pan

37# 169( 218& 50 218) XP\_519076 7.8 ( 8.4) 39.1 ( 35.3) 18.4 ( 23646.9)  
> PREDICTED: similar to peptidylprolyl isomerase A isoform 1;

38# 158( 158& 1 158) XP\_527705 5.8 ( 5.8) 30.4 ( 30.4) 18.0 ( 17978.1)  
> PREDICTED: similar to peptidylprolyl isomerase A isoform 1;

39# 166( 770& 200 365) XP\_527529 9.6 ( 9.3) 27.7 ( 20.3) 18.0 ( 87449.5)  
> PREDICTED: similar to peptidylprolyl isomerase-like 4;

40# 156( 302& 228 383) XP\_518678 7.5 ( 9.0) 25.6 ( 29.1) 17.3 ( 34243.0)  
> PREDICTED: similar to peptidylprolyl isomerase (cyclophilin)-like 6

41# 164( 164& 1 164) CSMSA 8.0 ( 8.0) 31.7 ( 31.7) 18.0 ( 17971.4)  
> peptidylprolyl isomerase A - mouse

42# 177( 206& 30 206) NP\_598845 8.7 ( 9.5) 35.6 ( 40.3) 18.7 ( 21737.0)  
> peptidylprolyl isomerase F [Mus musculus].

43# 166( 166& 1 166) AAH58369 8.2 ( 8.2) 33.1 ( 33.1) 18.2 ( 18236.9)  
> Peptidylprolyl isomerase-like 1 [Mus musculus].

44# 184( 216& 34 217) A56861 9.9 (10.0) 38.0 ( 41.7) 20.3 ( 23713.5)  
> peptidylprolyl isomerase CyP-S1 precursor - mouse

45# 185( 212& 28 212) A40047 6.6 ( 7.3) 48.6 ( 52.4) 20.2 ( 22794.2)  
> peptidylprolyl isomerase (cyclophilin C) - mouse

46# 192( 1466& 11 202) NKCR\_MOUSE 8.8 (10.5) 35.9 ( 10.0) 21.3 (164745.2)  
> NK-tumor recognition (natural-killer cells cyclophilin-related protein)

47# 161( 161& 1 161) AAH61645 6.3 ( 6.3) 27.3 ( 27.3) 18.1 ( 18127.6)  
> Ppil3 protein [Mus musculus].

48# 161( 521& 290 450) BAC41068 6.1 ( 8.4) 24.8 ( 21.9) 18.1 ( 59064.8)  
> unnamed protein product [Mus musculus].

49# 201( 370& 10 210) BAC34686 5.3 ( 7.2) 32.3 ( 29.7) 21.9 ( 40742.7)

> unnamed protein product [Mus musculus].

50# 200( 460& 1 200) BAB30711 4.4 ( 5.1) 28.5 ( 22.2) 22.6 ( 53188.8)

> unnamed protein product [Mus musculus].

51# 188( 188& 1 188) BAB25645 8.1 ( 8.1) 45.7 ( 45.7) 20.5 ( 20463.8)

> unnamed protein product [Mus musculus].

52# 177( 177& 1 177) BAB23880 8.1 ( 8.1) 44.1 ( 44.1) 19.2 ( 19208.2)

> unnamed protein product [Mus musculus].

53# 174( 3053&28803053) NF00527760 5.9 ( 5.8) 38.5 ( 24.8) 19.2 (341092.6)

> Ran-binding protein 2 [Mus musculus]

54# 177( 646& 470 646) NF01138503 6.5 ( 6.6) 31.1 ( 33.0) 19.7 ( 73430.9)

> Mus musculus 0 day neonate skin cDNA, RIKEN full-length enriched lib

55# 162( 301& 140 301) NF00510830 7.7 ( 5.3) 34.0 ( 33.2) 17.9 ( 33449.0)

> Peptidyl-prolyl cis-trans isomerase E (EC 5.2.1.8) (PPIase E) (Rotam

56# 166( 166& 1 166) NF00510932 8.2 ( 8.2) 33.1 ( 33.1) 18.2 ( 18236.9)

> Peptidyl-prolyl cis-trans isomerase like 1 (EC 5.2.1.8) (PPIase) (Ro

57# 164( 164& 1 164) NF01595779 5.8 ( 5.8) 28.0 ( 28.0) 18.1 ( 18133.7)

> similar to Peptidyl-prolyl cis-trans isomerase A (PPIase) (Rotamase)

58# 164( 164& 1 164) NF02014914 6.2 ( 6.2) 27.4 ( 27.4) 18.0 ( 18014.3)

> similar to Peptidyl-prolyl cis-trans isomerase A (PPIase) (Rotamase)

59# 180( 180& 1 180) NF01930249 10.1 (10.1) 25.6 ( 25.6) 19.8 ( 19841.8)

> similar to Peptidyl-prolyl cis-trans isomerase A (PPIase) (Rotamase)

60# 165( 165& 1 165) NF01929278 7.2 ( 7.2) 32.1 ( 32.1) 18.1 ( 18145.6)

> similar to Peptidyl-prolyl cis-trans isomerase A (PPIase) (Rotamase)

61# 164( 164& 1 164) NF00523006 8.4 ( 8.4) 31.7 ( 31.7) 18.0 ( 17984.4)

> Mus musculus ES cells cDNA, RIKEN full-length enriched library, clon

62# 167( 167& 1 167) NF00508381 8.0 ( 8.0) 32.9 ( 32.9) 18.3 ( 18313.8)

> Mus musculus 11 days embryo whole body cDNA, RIKEN full-length enric

63# 161( 161& 1 161) NF01215170 6.3 ( 6.3) 27.3 ( 27.3) 18.2 ( 18189.6)

> CYP10L [Mus musculus]

64# 164( 164& 1 164) CSRTA 8.2 ( 8.2) 35.4 ( 35.4) 17.9 ( 17874.4)

> peptidylprolyl isomerase A - rat

65# 161( 161& 1 161) NP\_783638 6.3 ( 6.3) 27.3 ( 27.3) 18.1 ( 18113.5)

> peptidylprolyl isomerase (cyclophilin)-like 3 [Rattus norvegicus].

66# 180( 370& 1 180) NF01612782 7.3 ( 6.5) 35.6 ( 32.2) 19.5 ( 40710.7)

> similar to peptidylprolyl isomerase D (cyclophilin D) [Rattus norveg

67# 172( 311& 140 311) NF01612825 8.4 ( 5.4) 29.1 ( 33.8) 19.0 ( 34395.1)  
> similar to peptidylprolyl isomerase E (cyclophilin E) [Rattus norvegicus]

68# 201( 621& 130 330) NF01607941 5.7 ( 8.2) 32.8 ( 34.5) 21.7 ( 68896.2)  
> similar to peptidylprolyl isomerase D (cyclophilin D) [Rattus norvegicus]

69# 199( 199& 1 199) NF01607846 6.4 ( 6.4) 38.7 ( 38.7) 21.6 ( 21574.5)  
> similar to Peptidyl-prolyl cis-trans isomerase A (PPIase) (Rotamase)

70# 188( 212& 25 212) NF01609144 6.6 ( 8.5) 48.4 ( 52.4) 20.6 ( 23009.5)  
> Peptidylprolyl isomerase C [Rattus norvegicus]

71# 162( 162& 1 162) NF01608897 8.7 ( 8.7) 35.8 ( 35.8) 17.4 ( 17352.9)  
> similar to Peptidyl-prolyl cis-trans isomerase A (PPIase) (Rotamase)

72# 172( 206& 35 206) NP\_758443 9.3 ( 9.5) 36.0 ( 39.8) 18.3 ( 21810.0)  
> peptidylprolyl isomerase F (cyclophilin F) [Rattus norvegicus].

73# 216( 216& 1 216) AAH61971 9.9 ( 9.9) 41.2 ( 41.2) 23.8 ( 23802.6)  
> Ppib protein [Rattus norvegicus].

74# 188( 752& 1 188) G2828710 8.4 (10.7) 34.0 ( 8.5) 21.0 ( 88072.5)  
> matrin cyclophilin - Rattus norvegicus

75# 165( 165& 1 165) B38388 8.4 ( 8.4) 40.6 ( 40.6) 17.9 ( 17907.4)  
> peptidylprolyl isomerase (EC 5.2.1.8) (cyclophilin) cyp-1 - fruit

76# 169( 653& 1 169) AF132148 4.8 (10.3) 48.5 ( 19.4) 18.6 ( 75470.4)  
> Drosophila melanogaster clone GH01073 unknown mRNA

77# 154( 517& 279 432) NP\_611113 7.2 ( 8.1) 20.8 ( 22.4) 17.1 ( 58959.1)  
> CG7747-PA [Drosophila melanogaster].

78# 177( 205& 19 195) NP\_611695 9.4 ( 9.3) 32.2 ( 40.0) 19.3 ( 22199.3)  
> CG2852-PA, isoform A [Drosophila melanogaster].

79# 168( 168& 1 168) NP\_610590 7.1 ( 7.1) 39.3 ( 39.3) 18.7 ( 18721.3)  
> CG11777 gene product [Drosophila melanogaster].

80# 164( 164& 1 164) NP\_648697 8.2 ( 8.2) 33.5 ( 33.5) 17.8 ( 17771.2)  
> CG7768-PB, isoform B [Drosophila melanogaster].

81# 170( 502& 1 170) NP\_648508 6.2 ( 6.2) 30.6 ( 17.1) 19.1 ( 56610.3)  
> CG10907-PA [Drosophila melanogaster].

82# 189( 383& 1 189) NP\_648338 5.0 ( 7.5) 39.2 ( 27.4) 20.7 ( 43115.7)  
> CG8336-PA, isoform A [Drosophila melanogaster].

83# 173( 237& 18 190) NP\_476656 6.6 ( 6.7) 41.0 ( 49.8) 18.9 ( 26351.3)  
> CG3966-PA [Drosophila melanogaster].

84# 169( 176& 8 176) NP\_523874 7.5 ( 6.7) 33.1 ( 31.8) 18.8 ( 19525.2)  
> CG13892-PA [Drosophila melanogaster].

85# 172( 300& 129 300) NP\_523773 9.0 ( 5.7) 32.6 ( 29.7) 19.0 ( 33276.4)  
> CG4886-PA [Drosophila melanogaster].

86# 183( 183& 1 183) NP\_610224 7.0 ( 7.0) 45.4 ( 45.4) 20.2 ( 20182.1)  
> CG17266-PA [Drosophila melanogaster].

87# 188( 970& 1 188) NP\_733246 8.9 (11.1) 40.4 ( 10.7) 20.6 (112795.7)  
> CG1866-PA [Drosophila melanogaster].

88# 157( 637& 481 637) NP\_611935 9.3 ( 6.7) 31.2 ( 33.6) 17.7 ( 71761.7)  
> CG3511-PA [Drosophila melanogaster].

89# 200( 377& 1 200) EAA03569 4.7 ( 6.1) 32.5 ( 26.0) 21.8 ( 42936.2)  
> ENSANGP00000013567 [Anopheles gambiae str. PEST].

90# 202( 202& 1 202) EAA03948 9.3 ( 9.3) 34.2 ( 34.2) 21.8 ( 21815.8)  
> ENSANGP00000011257 [Anopheles gambiae str. PEST].

91# 184( 184& 1 184) EAA04625 7.6 ( 7.6) 45.7 ( 45.7) 20.4 ( 20435.7)  
> ENSANGP00000018327 [Anopheles gambiae str. PEST].

92# 164( 164& 1 164) EAA06299 8.6 ( 8.6) 34.8 ( 34.8) 18.0 ( 18004.5)  
> ENSANGP00000020778 [Anopheles gambiae str. PEST].

93# 180( 519& 1 180) EAA08127 8.6 (10.3) 36.7 ( 17.0) 19.8 ( 58606.6)  
> ENSANGP00000010906 [Anopheles gambiae str. PEST].

94# 161( 530& 270 430) EAA09839 9.4 ( 8.7) 25.5 ( 23.8) 18.1 ( 59716.8)  
> ENSANGP00000016027 [Anopheles gambiae str. PEST].

95# 183( 632& 450 632) EAA10133 7.3 ( 6.4) 25.7 ( 32.4) 20.5 ( 71854.0)  
> ENSANGP00000014257 [Anopheles gambiae str. PEST].

96# 168( 168& 1 168) EAL39647 5.1 ( 5.1) 37.5 ( 37.5) 18.8 ( 18779.3)  
> ENSANGP00000027110 [Anopheles gambiae str. PEST].

97# 161( 161& 1 161) EAA13913 5.8 ( 5.8) 31.1 ( 31.1) 18.0 ( 17977.3)  
> ENSANGP00000023432 [Anopheles gambiae str. PEST].

98# 191( 253& 10 200) EAA13914 5.2 ( 5.4) 45.5 ( 49.0) 20.9 ( 28129.3)  
> ENSANGP00000011942 [Anopheles gambiae str. PEST].

99# 186( 305& 120 305) EAA14200 8.6 ( 5.6) 36.6 ( 33.1) 20.3 ( 33487.8)  
> ENSANGP00000015053 [Anopheles gambiae str. PEST].

100# 167( 496& 330 496) EAA01474 7.7 ( 6.7) 45.5 ( 50.2) 18.4 ( 54540.2)  
> ENSANGP00000018314 [Anopheles gambiae str. PEST].

101# 173( 592& 420 592) XP\_321072 8.3 ( 7.0) 48.0 ( 52.0) 18.7 ( 63774.3)

> ENSANGP00000018314 [Anopheles gambiae].

102# 212( 212& 1 212) XP\_320182 9.5 ( 9.5) 31.6 ( 31.6) 23.5 ( 23531.8)  
> ENSANGP00000011602 [Anopheles gambiae].

103# 173( 257& 18 190) XP\_319131 5.9 ( 5.4) 39.9 ( 48.6) 19.0 ( 28584.8)  
> ENSANGP00000011942 [Anopheles gambiae].

104# 155( 155& 1 155) XP\_311949 6.5 ( 6.5) 36.8 ( 36.8) 16.8 ( 16824.1)  
> ENSANGP00000024687 [Anopheles gambiae].

105# 188( 307& 120 307) CAI11739 5.7 ( 5.9) 33.5 ( 35.2) 20.8 ( 34403.1)  
> novel cyclophilin protein [Danio rerio].

106# 164( 164& 1 164) AAQ91263 8.4 ( 8.4) 36.0 ( 36.0) 17.5 ( 17487.9)  
> peptidylprolyl isomerase A [Danio rerio].

107# 189( 189& 1 189) NP\_001004626 8.4 ( 8.4) 48.7 ( 48.7) 20.5 ( 20465.6)  
> peptidylprolyl isomerase F (cyclophilin F) [Danio rerio].

108# 210( 371& 1 210) NP\_001002065 4.9 ( 5.7) 34.8 ( 27.2) 22.8 ( 41282.0)  
> zgc:86711 [Danio rerio].

109# 181( 181& 1 181) NP\_957499 7.6 ( 7.6) 49.2 ( 49.2) 19.8 ( 19766.9)  
> similar to peptidyl prolyl isomerase H (cyclophilin H) [Danio

110# 177( 177& 1 177) AAQ94596 7.9 ( 7.9) 44.6 ( 44.6) 19.3 ( 19341.4)  
> peptidyl prolyl isomerase H [Danio rerio].

111# 196( 216& 21 216) NP\_998184 9.4 ( 9.7) 29.1 ( 32.9) 21.6 ( 23928.7)  
> zgc:73214 [Danio rerio].

112# 161( 161& 1 161) NP\_001002146 6.7 ( 6.7) 34.2 ( 34.2) 17.9 ( 17914.5)  
> zgc:86715 [Danio rerio].

113# 164( 164& 1 164) AAQ91264 8.7 ( 8.7) 40.9 ( 40.9) 17.4 ( 17400.8)  
> 2-peptidylprolyl isomerase A [Danio rerio].

114# 183( 183& 1 183) AAH59458 9.4 ( 9.4) 37.2 ( 37.2) 19.4 ( 19370.0)  
> Unknown (protein for IMAGE:4199657) [Danio rerio].

115# 201( 454& 10 210) AAH56814 4.4 ( 5.8) 24.9 ( 23.1) 22.6 ( 52854.4)  
> Unknown (protein for MGC:63746) [Danio rerio].

116# 184( 184& 1 184) AAH62863 9.5 ( 9.5) 38.6 ( 38.6) 19.5 ( 19472.2)  
> Unknown (protein for IMAGE:7002384) [Danio rerio].

117# 195( 687& 1 195) NP\_998629 9.4 (10.9) 34.9 ( 10.0) 21.6 ( 79984.3)  
> peptidyl-prolyl isomerase G (cyclophilin G) [Danio rerio].

118# 179( 486& 210 388) NP\_957285 9.5 ( 9.1) 22.3 ( 19.8) 19.7 ( 54669.7)  
> similar to peptidylprolyl isomerase (cyclophilin)-like 2 [Danio

119# 171( 171& 1 171) NP\_506749 8.6 ( 8.6) 36.3 ( 36.3) 18.4 ( 18401.0)  
> CYcloPhilin family CYP-7 (18.4 kD) (cyp-7) [Caenorhabditis]

120# 173( 192& 20 192) NP\_506561 6.2 ( 7.8) 37.6 ( 38.5) 18.6 ( 20710.6)  
> Peptidyl-prolyl cis-trans isomerase cyclophilin family member 1

121# 178( 517& 340 517) NP\_504522 8.6 ( 6.6) 39.9 ( 23.8) 19.6 ( 57706.7)  
> CYcloPhilin family CYP-17 (cyp-17) [Caenorhabditis elegans].

122# 173( 173& 1 173) NP\_506751 8.9 ( 8.9) 39.9 ( 39.9) 18.6 ( 18550.2)  
> Peptidyl-prolyl cis-trans isomerase cyclophilin family member 3

123# 177( 309& 1 177) NP\_497745 8.8 ( 9.9) 36.7 ( 21.7) 19.8 ( 35796.3)  
> Peptidyl-prolyl cis-trans isomerase cyclophilin family member 9

124# 172( 172& 1 172) NP\_499828 8.1 ( 8.1) 37.2 ( 37.2) 18.5 ( 18535.3)  
> Peptidyl-prolyl cis-trans isomerase cyclophilin family member 2

125# 176( 201& 20 195) NP\_497257 5.3 ( 5.6) 37.5 ( 40.8) 19.3 ( 21863.9)  
> Peptidyl-prolyl cis-trans isomerase cyclophilin family member 6

126# 175( 466& 5 179) NP\_509506 7.7 (10.3) 36.0 ( 15.2) 19.4 ( 53565.4)  
> CYcloPhilin family CYP-8 (53.6 kD) (cyp-8) [Caenorhabditis]

127# 166( 331& 135 300) NP\_503034 8.2 ( 5.6) 39.2 ( 33.8) 18.3 ( 36423.5)  
> CYcloPhilin family CYP-13 (36.4 kD) (cyp-13) [Caenorhabditis]

128# 169( 169& 1 169) NP\_501118 8.5 ( 8.5) 35.5 ( 35.5) 18.5 ( 18524.1)  
> CYcloPhilin family CYP-12 (cyp-12) [Caenorhabditis elegans].

129# 178( 222& 1 178) NP\_496562 7.2 ( 7.2) 29.2 ( 24.8) 20.0 ( 25229.6)  
> CYcloPhilin family CYP-16 (cyp-16) [Caenorhabditis elegans].

130# 173( 183& 11 183) NP\_495855 7.1 ( 6.1) 44.5 ( 42.1) 18.9 ( 20193.2)  
> Peptidyl-prolyl cis-trans isomerase cyclophilin family member 11

131# 167( 523& 272 438) NP\_496337 8.8 ( 9.2) 36.5 ( 29.1) 18.8 ( 58534.0)  
> Masculinisation Of Germline 6, sex determining protein, CYcloPhilin

132# 147( 147& 1 147) NP\_495417 5.2 ( 5.2) 23.8 ( 23.8) 16.5 ( 16483.6)  
> CYcloPhilin family CYP-10 (cyp-10) [Caenorhabditis elegans].

133# 164( 629& 466 629) NP\_493378 6.6 ( 6.4) 33.5 ( 34.2) 18.2 ( 70844.8)  
> cyclophilin [Caenorhabditis elegans]

134# 172( 381& 1 172) NP\_492343 4.8 ( 5.4) 22.7 ( 19.4) 19.8 ( 44422.9)  
> CYcloPhilin family CYP-14 (cyp-14) [Caenorhabditis elegans].

135# 180( 204& 20 199) NP\_493624 9.3 ( 9.5) 37.8 ( 40.2) 19.6 ( 21927.3)  
> Peptidyl-prolyl cis-trans isomerase cyclophilin family member 5



136# 172( 172& 1 172) T06073 7.8 ( 7.8) 38.4 ( 38.4) 18.4 ( 18372.9)  
> peptidylprolyl isomerase (EC 5.2.1.8) ROC1 - Arabidopsis thaliana.

137# 170( 506& 1 170) NP\_175776 5.9 ( 5.8) 26.5 ( 19.0) 19.1 ( 58829.2)  
> cyclophilin-RNA interacting protein, putative; protein id:

138# 181( 228& 48 228) NP\_567029 6.6 ( 6.6) 40.3 ( 44.7) 19.4 ( 24506.2)  
> cyclophilin-like protein; protein id: At3g55920.1, supported by

139# 168( 595& 331 498) NP\_201554 7.3 ( 8.2) 33.9 ( 32.3) 18.5 ( 65023.7)  
> peptidylprolyl isomerase (cyclophilin)-like; protein id:

140# 170( 204& 35 204) NP\_200679 9.0 ( 9.5) 39.4 ( 41.2) 18.3 ( 21961.3)  
> cyclophilin ROC7; protein id: At5g58710.1, supported by cDNA:

141# 175( 199& 25 199) NP\_181407 8.4 ( 8.1) 41.1 ( 41.2) 19.3 ( 21491.8)  
> peptidyl-prolyl cis-trans isomerase, putative / cyclophilin,

142# 176( 176& 1 176) NP\_191166 7.8 ( 7.8) 37.5 ( 37.5) 18.9 ( 18920.6)  
> peptidylprolyl isomerase; protein id: At3g56070.1, supported by cDNA: gi\_18

143# 166( 166& 1 166) NP\_171696 8.8 ( 8.8) 35.5 ( 35.5) 18.2 ( 18158.8)  
> hypothetical protein; protein id: At1g01940.1 [Arabidopsis thaliana]

144# 188( 224& 37 224) NP\_195222 6.4 ( 6.4) 38.3 ( 42.9) 20.4 ( 24594.2)  
> cyclophilin - like protein; protein id: At4g34960.1 [Arabidopsis

145# 172( 172& 1 172) NP\_195213 8.9 ( 8.9) 41.3 ( 41.3) 18.4 ( 18378.1)  
> peptidylprolyl isomerase (cyclophilin); protein id: At4g34870.1,

146# 171( 259& 89 259) NP\_196816 7.9 ( 9.7) 42.1 ( 38.6) 18.7 ( 28306.2)  
> peptidyl-prolyl isomerase protein; protein id: At5g13120.1, supported by CD

147# 175( 232& 1 175) NP\_188932 4.6 ( 4.7) 34.9 ( 35.8) 19.4 ( 26045.0)  
> cyclophilin, putative; protein id: At3g22920.1 [Arabidopsis

148# 171( 260& 90 260) NP\_191762 7.8 ( 8.7) 43.3 ( 43.5) 18.7 ( 28208.3)  
> peptidylprolyl isomerase - ROC4 - Arabidopsis thaliana

149# 162( 631& 470 631) NP\_190046 6.8 ( 6.2) 30.2 ( 34.2) 18.3 ( 70984.0)  
> putative protein; protein id: At3g44600.1, supported by cDNA: gi\_17065153 [

150# 182( 201& 20 201) NP\_180557 9.3 ( 9.5) 37.4 ( 42.3) 19.6 ( 21533.8)  
> cyclophilin; protein id: At2g29960.1, supported by cDNA: 19211.,

151# 164( 164& 1 164) NP\_181157 8.7 ( 8.7) 31.1 ( 31.1) 18.2 ( 18232.7)  
> cyclophilin-like protein; protein id: At2g36130.1, supported by

152# 173( 173& 1 173) NP\_179251 8.6 ( 8.6) 36.4 ( 36.4) 18.5 ( 18492.0)  
> cytosolic cyclophilin (ROC3); protein id: At2g16600.1, supported by

153# 174( 174& 1 174) NP\_179709 8.2 ( 8.2) 42.0 ( 42.0) 18.5 ( 18464.1)

> cyclophilin (CYP2); protein id: At2g21130.1, supported by cDNA:

154# 170( 361& 1 170) AAK02067 6.2 ( 5.5) 34.1 ( 27.4) 18.7 ( 40607.1)  
> cyclophilin-40 [Arabidopsis thaliana].

155# 162( 461& 300 461) P82869 4.4 ( 8.3) 40.7 ( 42.3) 17.4 ( 49965.1)  
> Peptidyl-prolyl cis-trans isomerase TLP38, chloroplast precursor

156# 162( 857& 1 162) T05352 9.4 (12.4) 35.8 ( 12.1) 17.9 ( 96855.4)  
> hypothetical protein F8B4.120 - Arabidopsis thaliana.

157# 176( 570& 1 176) T49181 8.9 (11.4) 41.5 ( 13.2) 18.7 ( 63540.5)  
> cyclophylin-like protein - Arabidopsis thaliana.

158# 171( 510& 1 171) T05314 5.9 ( 7.9) 40.9 ( 29.0) 18.9 ( 57118.8)  
> hypothetical protein F26P21.180 - Arabidopsis thaliana.

159# 162( 162& 1 162) CSZPA 8.9 ( 8.9) 40.7 ( 40.7) 17.4 ( 17401.9)  
> peptidylprolyl isomerase (EC 5.2.1.8) A - fission yeast

160# 170( 155& 1 170) E313994 6.3 ( 6.3) 42.9 ( 40.0) 18.4 ( 16864.3)  
> unknown - Schizosaccharomyces pombe (fission yeast)

161# 183( 201& 20 202) E1335804 5.5 ( 5.5) 28.4 ( 32.8) 20.0 ( 22156.0)  
> peptidyl-prolyl isomerase b precursor - Schizosaccharomyces pombe

162# 173( 173& 1 173) E1331567 5.5 ( 5.5) 43.9 ( 43.9) 18.9 ( 18905.6)  
> u-snrnp-associated cyclophilin - Schizosaccharomyces pombe

163# 180( 356& 1 180) S62327 6.1 ( 8.0) 31.7 ( 26.4) 20.1 ( 40161.6)  
> probable 40 kd peptidyl-prolyl cis-trans isomerase - fission yeast

164# 178( 471& 216 393) S62590 9.3 ( 9.2) 25.3 ( 22.1) 20.3 ( 53573.6)  
> hypothetical protein SPAC21E11.05c - fission yeast

165# 165( 610& 447 611) E1294518 5.4 ( 5.5) 30.3 ( 30.8) 18.4 ( 69048.3)  
> peptidyl prolyl cis/trans isomerase - Schizosaccharomyces pombe

166# 180( 432& 1 180) T39728 4.6 ( 5.5) 35.0 ( 27.5) 20.3 ( 50776.6)  
> probable PPIase with RNA binding region - (Schizosaccharomyces pombe)

167# 172( 463& 9 180) E1263915 5.7 ( 8.7) 38.4 ( 22.2) 19.2 ( 52174.3)  
> peptidyl-prolyl cis-trans isomerase - Schizosaccharomyces pombe

168# 162( 162& 1 162) CSBY 7.3 ( 7.3) 37.7 ( 37.7) 17.4 ( 17390.7)  
> peptidylprolyl isomerase, cytosolic - Saccharomyces cerevisiae

169# 174( 182& 10 183) S30507 8.7 ( 9.1) 32.2 ( 31.9) 18.9 ( 19918.8)  
> peptidylprolyl isomerase 3 precursor - Saccharomyces cerevisiae

170# 176( 205& 31 206) S12324 7.4 ( 5.7) 33.5 ( 38.5) 19.5 ( 22768.9)  
> peptidylprolyl isomerase 2 - Saccharomyces cerevisiae

171# 200( 393& 1 200) S57050 5.5 ( 5.1) 28.5 ( 24.4) 22.2 ( 45134.0)  
> hypothetical protein YJR032w CPR7 - *Saccharomyces cerevisiae*

172# 178( 371& 1 178) S48567 5.5 ( 5.8) 33.1 ( 28.3) 19.9 ( 42072.1)  
> hypothetical protein YLR216c - *Saccharomyces cerevisiae*

173# 194( 318& 47 240) CSBYC3 5.1 ( 6.5) 40.7 ( 38.1) 22.0 ( 35780.0)  
> peptidylprolyl isomerase SCC3 - *Saccharomyces cerevisiae*

174# 174( 308& 51 224) S63359 4.8 ( 6.6) 35.6 ( 34.1) 19.2 ( 34946.1)  
> probable membrane protein YNR028w - CPR8 (*Saccharomyces cerevisiae*)

175# 178( 225& 29 206) S38324 6.0 ( 5.3) 36.0 ( 36.0) 20.0 ( 25326.8)  
> peptidylprolyl isomerase D precursor - *Saccharomyces cerevisiae*

176# 177( 177& 1 177) TcCyP19 8.4 ( 8.4) 41.2 ( 41.2) 18.8 ( 18781.3)  
> *T.cruzi* from Argentina

177# 179( 179& 1 179) TcCyP20 5.9 ( 5.9) 38.0 ( 38.0) 19.8 ( 19805.5)  
> *T.cruzi* from Argentina

178# 194( 194& 1 194) TcCyP21.1 9.5 ( 9.5) 44.3 ( 44.3) 21.1 ( 21102.4)  
> *T.cruzi* from Argentina

179# 196( 196& 1 196) TcCyP21.3 9.2 ( 9.2) 29.1 ( 29.1) 21.4 ( 21374.4)  
> *T.cruzi* from Argentina

180# 205( 224& 20 224) TcCyP24.3 8.7 ( 8.9) 38.0 ( 43.3) 22.0 ( 24161.6)  
> *T.cruzi* from Argentina

181# 231( 231& 1 231) TcCyP26 8.1 ( 8.1) 43.3 ( 43.3) 25.6 ( 25647.5)  
> *T.cruzi* from Argentina

182# 210( 258& 1 210) TcCyP28 10.0 (10.2) 28.1 ( 23.3) 22.9 ( 28444.6)  
> *T.cruzi* from Argentina

183# 216( 265& 50 265) TcCyP30 7.2 ( 8.1) 40.7 ( 43.0) 23.7 ( 29664.2)  
> *T.cruzi* from Argentina

184# 209( 308& 100 308) TcCyP35.1 5.3 ( 5.7) 42.6 ( 40.9) 23.3 ( 34992.7)  
> *T.cruzi* from Argentina

185# 196( 325& 55 250) TcCyP35.3 7.0 ( 5.6) 34.7 ( 33.5) 21.7 ( 35298.5)  
> *T.cruzi* from Argentina

186# 175( 354& 1 175) TcCyP40 6.6 ( 5.6) 40.0 ( 34.7) 18.9 ( 38381.6)  
> *T.cruzi* from Argentina

187# 196( 995& 800 995) TcCyP110 5.1 ( 5.3) 54.1 ( 48.3) 21.6 (110007.6)  
> *T.cruzi* from Argentina

188# 164( 164& 1 164) AAT44353 8.6 ( 8.6) 36.6 ( 36.6) 17.5 ( 17538.0)  
> cyclophilin [Crassostrea gigas].

189# 172( 172& 1 172) EAL37431 7.0 ( 7.0) 46.5 ( 46.5) 18.5 ( 18544.3)  
> 20k cyclophilin [Cryptosporidium hominis].

190# 169( 169& 1 169) EAL37232 6.3 ( 6.3) 36.1 ( 36.1) 18.9 ( 18862.5)  
> cyclophilin-like protein [Cryptosporidium hominis].

191# 210( 210& 1 210) EAL37110 7.4 ( 7.4) 40.0 ( 40.0) 22.9 ( 22925.2)  
> cyclophilin Ta cyp [Cryptosporidium hominis].

192# 180( 302& 1 180) EAL36265 5.5 ( 4.7) 36.7 ( 35.1) 20.6 ( 34538.6)  
> cyclophilin-RNA interacting protein [Cryptosporidium hominis].

193# 189( 189& 1 189) EAL35294 7.6 ( 7.6) 37.0 ( 37.0) 21.2 ( 21241.4)  
> cyclophilin [Cryptosporidium hominis].

194# 177( 177& 1 177) U68268 7.3 ( 7.3) 37.3 ( 37.3) 18.8 ( 18803.2)  
> cyclophilin A - Trypanosoma congolense

195# 177( 177& 1 177) U68269 7.8 ( 7.8) 39.5 ( 39.5) 18.7 ( 18715.1)  
> cyclophilin A - Trypanosoma vivax

196# 189( 196& 8 196) AAQ15626 9.2 ( 9.4) 27.0 ( 28.6) 20.3 ( 21165.1)  
> cyclophilin, putative [Trypanosoma brucei].

197# 177( 177& 1 177) AAB07896 8.1 ( 8.1) 39.0 ( 39.0) 18.8 ( 18763.3)  
> cyclophilin A [Trypanosoma brucei brucei].

198# 174( 188& 15 188) AAK14937 8.7 ( 9.6) 36.2 ( 35.1) 19.0 ( 20711.5)  
> cyclophilin 1 [Theileria parva].

199# 182( 185& 4 185) CAC18541 6.5 ( 6.5) 39.6 ( 40.5) 19.8 ( 20121.2)  
> putative U-snrRNP-associated cyclophilin [Echinococcus

200# 162( 162& 1 162) A45000 6.1 ( 6.1) 36.4 ( 36.4) 17.2 ( 17223.5)  
> cyclophilin - tapeworm (Echinococcus granulosus) (fragment)

201# 169( 169& 1 169) Q9Y0F5 6.3 ( 6.3) 34.3 ( 34.3) 18.9 ( 18864.5)  
> Cyclophilin - Cryptosporidium parvum

202# 171( 171& 1 171) U47811 8.9 ( 8.9) 36.8 ( 36.8) 18.6 ( 18616.2)  
> cyclophilin Bmcyp-2 - Brugia malayi

203# 172( 172& 1 172) U50388 9.5 ( 9.5) 35.5 ( 35.5) 19.2 ( 19153.1)  
> cyclophilin A - Schistosoma mansoni

204# 161( 161& 1 161) L46884 8.1 ( 8.1) 34.2 ( 34.2) 17.7 ( 17671.1)  
> cyclophilin - Schistosoma mansoni

205# 170( 179& 11 180) M93420 9.7 ( 8.6) 30.6 ( 28.5) 19.0 ( 20049.9)

> cyclophilin - *Schistosoma japonicum*

206# 190( 213& 25 214) U50389 9.2 ( 8.2) 38.9 ( 44.1) 20.8 ( 23237.7)  
> cyclophilin B - *Schistosoma japonicum*

207# 190( 213& 25 214) G992633 9.5 ( 8.8) 38.4 ( 42.7) 20.8 ( 23293.9)  
> cyclophilin B - *Schistosoma mansoni*

208# 175( 273& 100 274) E323073 9.4 ( 6.0) 35.4 ( 27.8) 19.5 ( 30905.0)  
> *Schistosoma mansoni* cyclophylin-like protein trans-spliced mRNA

209# 183( 366& 155 337) S52758 5.7 ( 8.1) 38.3 ( 41.0) 20.2 ( 39971.3)  
> adenosine kinase (EC 2.7.1.20) - *Leishmania donovani*

210# 177( 177& 1 177) E1203753 7.8 ( 7.8) 28.2 ( 28.2) 18.8 ( 18823.4)  
> cyclophilin - *Leishmania major*

211# 192( 192& 1 192) CAB58290 6.6 ( 6.6) 60.9 ( 60.9) 20.4 ( 20356.3)  
> possible cyclophilin.

212# 165( 295& 21 185) CAB58298 10.1 (10.4) 36.4 ( 27.1) 17.7 ( 31496.9)  
> cyclophilin.

213# 180( 354& 1 180) AAF69736 6.1 ( 5.5) 38.3 ( 28.0) 19.4 ( 38420.4)  
> 354 PPIase (cyclophilin) D [*Leishmania major*].

214# 169( 187& 20 188) AAD46565 6.2 ( 6.2) 45.0 ( 49.7) 18.5 ( 20429.5)  
> Cyclophilin - *Leishmania donovani*

215# 171( 179& 10 180) A53522 6.1 ( 6.1) 36.3 ( 39.1) 18.6 ( 19638.4)  
> 18.5k cyclophilin precursor - *Toxoplasma gondii*

216# 180( 440& 1 180) NP\_702112 7.8 ( 6.6) 31.7 ( 14.5) 21.0 ( 51884.9)  
> cyclophilin, putative [*Plasmodium falciparum* 3D7].

217# 173( 280& 58 230) NP\_701512 6.6 ( 9.7) 48.0 ( 38.6) 19.5 ( 32336.5)  
> cyclophilin [*Plasmodium falciparum* 3D7].

218# 180( 226& 1 180) NP\_701389 9.5 ( 8.4) 36.7 ( 31.4) 20.9 ( 26429.4)  
> cyclophilin, putative [*Plasmodium falciparum* 3D7].

219# 167( 167& 1 167) NP\_701030 5.9 ( 5.9) 31.7 ( 31.7) 18.6 ( 18588.0)  
> cyclophilin, putative [*Plasmodium falciparum* 3D7].

220# 240( 677& 1 240) NF01067443 9.6 ( 9.6) 25.8 ( 12.4) 28.4 ( 80923.0)  
> Hypothetical protein PF08\_0128 [*Plasmodium falciparum*]

221# 217( 217& 1 217) NF01067965 6.3 ( 6.3) 38.7 ( 38.7) 24.9 ( 24892.4)  
> Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8) [*Plasmodium falcipa*

222# 178( 747& 570 747) NF01065889 7.8 ( 7.0) 36.0 ( 33.7) 20.2 ( 87040.3)  
> Cyclophilin, putative (EC 5.2.1.8) [*Plasmodium falciparum*]

223# 170( 170& 1 170) NF00926916 8.1 ( 8.1) 37.1 ( 37.1) 18.9 ( 18860.5)  
> Cyclophilin [Plasmodium falciparum]

224# 195( 195& 1 195) S52760 7.4 ( 7.4) 45.1 ( 45.1) 21.7 ( 21731.2)  
> peptidylprolyl isomerase (EC 5.2.1.8) precursor - malaria parasite

225# 183( 210& 29 211) U10322 7.1 ( 6.1) 43.7 ( 40.0) 20.9 ( 24049.4)  
> cyclophilin - Plasmodium falciparum (malaria parasite P. falciparum)

226# 171( 171& 1 171) CAB39039 8.1 ( 8.1) 36.8 ( 36.8) 19.0 ( 18952.6)  
> cyclophilin [Plasmodium falciparum].

227# 180( 204& 25 204) CAD51648 7.2 ( 5.3) 34.4 ( 30.9) 20.4 ( 23199.2)  
> cyclophilin, putative [Plasmodium falciparum 3D7].

228# 170( 170& 1 170) NF01497907 8.4 ( 8.4) 38.2 ( 38.2) 18.8 ( 18832.5)  
> Peptidyl-prolyl cis-trans isomerase, cyclophilin-type [Plasmodium yo

229# 176( 765& 590 765) NF01497552 7.8 ( 6.9) 36.4 ( 30.8) 20.0 ( 88434.4)  
> Hypothetical protein [Plasmodium yoelii]

230# 192( 192& 1 192) NF01497379 9.4 ( 9.4) 47.9 ( 47.9) 21.2 ( 21208.6)  
> Peptidyl-prolyl cis-trans isomerase, cyclophilin-type [Plasmodium yo

231# 210( 210& 1 210) NF01497199 5.4 ( 5.4) 37.1 ( 37.1) 23.9 ( 23909.3)  
> Cyclophilin [Plasmodium yoelii]

232# 200( 621& 1 200) NF01496968 9.8 ( 9.4) 29.0 ( 14.0) 23.6 ( 74002.7)  
> Drosophila melanogaster CG12343 gene product, putative [Plasmodium y

233# 163( 285& 58 220) NF01495390 6.5 ( 9.6) 45.4 ( 37.5) 18.5 ( 32765.9)  
> Peptidyl-prolyl cis-trans isomerase, cyclophilin-type, putative [Pla

234# 202( 202& 1 202) NF01495324 5.4 ( 5.4) 33.2 ( 33.2) 22.7 ( 22715.6)  
> Cyclophilin-like protein [Plasmodium yoelii]

235# 157( 157& 1 157) NF01493974 9.0 ( 9.0) 25.5 ( 25.5) 18.4 ( 18390.0)  
> Cyclophilin-related [Plasmodium yoelii]

236# 200( 354& 1 200) NF01493918 7.0 ( 4.5) 39.5 ( 28.0) 23.2 ( 41146.5)  
> Peptidyl-prolyl cis-trans isomerase, cyclophilin-type, putative [Pla

237# 162( 162& 1 162) E316521 9.4 ( 9.4) 34.6 ( 34.6) 17.7 ( 17704.2)  
> peptidylprolyl isomerase - Paramecium primaurelia

238# 165( 695& 1 165) CAC35733 5.8 ( 9.5) 33.3 ( 16.0) 18.8 ( 82646.6)  
> cyclophilin-RNA interacting protein [Paramecium tetraurelia].

239# 171( 171& 1 171) U47812 8.2 ( 8.2) 35.1 ( 35.1) 18.5 ( 18525.1)  
> cyclophilin Ovcyp-2 - Onchocerca volvulus

240# 171( 171& 1 171) U47813 8.6 ( 8.6) 38.0 ( 38.0) 18.5 ( 18542.1)  
> cyclophilin Dicyp-2 - *Dirofilaria immitis*

241# 167( 167& 1 167) G2624966 8.7 ( 8.7) 37.7 ( 37.7) 18.1 ( 18139.0)  
> cyclophilin - *Entamoeba histolytica*

242# 180( 526& 266 445) E1317902 7.8 ( 8.4) 30.0 ( 27.6) 20.0 ( 59564.1)  
> cyclophilin 4 - *Brugia malayi*

243# 180( 526& 266 445) E1319851 6.5 ( 8.5) 30.0 ( 28.3) 20.2 ( 59762.5)  
> *O. volvulus* cyclophilin 4 - *Onchocerca volvulus*

244# 180( 527& 266 445) G3057040 8.2 ( 8.1) 27.8 ( 26.2) 20.1 ( 59577.1)  
> cyclophilin Dicyp-3 - *Dirofilaria immitis*

245# 165( 165& 1 165) AAB81959 7.8 ( 7.8) 37.6 ( 37.6) 18.0 ( 18012.5)  
> Cyclophilin - baboon - *Papio hamadryas*

246# 165( 165& 1 165) AF023860 7.8 ( 7.8) 37.6 ( 37.6) 18.0 ( 18012.5)  
> Cyclophilin - African green monkey - *Chlorocebus aethiops*

247# 165( 165& 1 165) AAB81961 7.8 ( 7.8) 37.6 ( 37.6) 18.0 ( 18012.5)  
> Cyclophilin - rhesus monkey - *Macaca mulatta*

248# 164( 164& 1 164) AAF22215 7.2 ( 7.2) 38.4 ( 38.4) 17.8 ( 17837.3)  
> cyclophilin 18 [*Oryctolagus cuniculus*].

249# 156( 156& 1 156) AF243140\_1 8.3 ( 8.3) 34.0 ( 34.0) 16.9 ( 16933.3)  
> 156 - cyclophilin A [*Canis familiaris*].

250# 158( 158& 1 158) AF252388 8.0 ( 8.0) 36.7 ( 36.7) 16.8 ( 16811.0)  
> Cyclophilin from *Macaca mulatta*

251# 163( 163& 1 163) CSBOAB 8.2 ( 8.2) 36.8 ( 36.8) 17.7 ( 17738.2)  
> peptidylprolyl isomerase A - bovine

252# 167( 167& 1 167) NF01922219 5.2 ( 5.2) 39.5 ( 39.5) 18.1 ( 18059.4)  
> Peptidyl-prolyl cis-trans isomerase [*Euplotes vannus*]

253# 164( 164& 1 164) NF01725587 8.6 ( 8.6) 32.9 ( 32.9) 17.7 ( 17713.2)  
> Cyclophilin A [*Chlamys farreri*]

254# 198( 198& 1 198) NF01897292 4.8 ( 4.8) 31.3 ( 31.3) 22.7 ( 22665.4)  
> Peptidyl-prolyl cis-trans isomerase [*Oikopleura dioica*]

255# 164( 164& 1 164) CSHYAC 8.4 ( 8.4) 32.3 ( 32.3) 17.9 ( 17899.3)  
> peptidylprolyl isomerase A - Chinese hamster

256# 165( 165& 1 165) NF00071027 7.8 ( 7.8) 37.6 ( 37.6) 18.0 ( 18012.5)  
> cyclophilin A [*Papio hamadryas*]

257# 161( 572& 340 500) NF01951405 8.8 ( 9.4) 21.1 ( 25.3) 18.2 ( 64075.1)

> PREDICTED: similar to peptidylprolyl isomerase-like 2 isoform a; cyc

258# 164( 164& 1 164) NF01059378 7.8 ( 7.8) 37.2 ( 37.2) 17.9 ( 17881.3)  
> Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPIase) (Rotamas

259# 171( 171& 1 171) NF01105745 7.8 ( 7.8) 36.8 ( 36.8) 18.3 ( 18319.9)  
> Peptidylprolyl isomerase [*Phytophthora infestans*]

260# 164( 164& 1 164) NF00495096 8.4 ( 8.4) 32.3 ( 32.3) 17.9 ( 17899.3)  
> Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPIase) (Rotamas

261# 173( 173& 1 173) NF01053198 8.6 ( 8.6) 42.2 ( 42.2) 18.3 ( 18295.8)  
> Peptidylprolyl isomerase (Cyclophilin) (EC 5.2.1.8) [*Betula pendula*]

262# 163( 163& 1 163) CSPGA 8.2 ( 8.2) 36.8 ( 36.8) 17.7 ( 17738.2)  
> peptidylprolyl isomerase A - pig

263# 161( 161& 1 161) NF01950932 6.3 ( 6.3) 28.0 ( 28.0) 18.1 ( 18051.6)  
> Hypothetical protein [*Gallus gallus*]

264# 220( 341& 1 220) NF01951326 4.9 ( 5.5) 33.2 ( 31.1) 23.9 ( 37271.4)  
> PREDICTED: similar to cyclophilin [*Gallus gallus*]

265# 172( 172& 1 172) NF00909389 8.6 ( 8.6) 39.5 ( 39.5) 18.2 ( 18178.7)  
> Cyclophilin [*Glycine max*]

266# 172( 172& 1 172) NF01286555 8.9 ( 8.9) 42.4 ( 42.4) 18.2 ( 18241.8)  
> Cyclophilin [*Populus tremuloides*]

267# 173( 173& 1 173) NF01737225 8.6 ( 8.6) 41.6 ( 41.6) 18.4 ( 18384.1)  
> Cyclophilin [*Thellungiella halophila*]

268# 190( 322& 1 190) NF01590839 5.3 ( 6.1) 30.0 ( 32.3) 20.7 ( 35197.3)  
> Peptidyl-prolyl cis-trans isomerase [*Treponema denticola*]

269# 168( 168& 1 168) AAH51602 6.2 ( 6.2) 33.3 ( 33.3) 18.3 ( 18278.6)  
> LOC398596 protein [*Xenopus laevis*].

270# 164( 164& 1 164) AAT69672 9.0 ( 9.0) 37.8 ( 37.8) 17.7 ( 17720.3)  
> cyclophilin A [*Xenopus laevis*].

271# 184( 193& 10 193) AAH54186 8.7 ( 9.1) 42.9 ( 45.6) 19.9 ( 20909.2)  
> LOC398630 protein [*Xenopus laevis*].

272# 187( 216& 30 216) AAH54168 9.5 ( 9.7) 33.2 ( 38.4) 20.7 ( 23859.7)  
> Ppib-prov protein [*Xenopus laevis*].

273# 221( 521& 260 480) NF01208049 8.8 ( 8.9) 19.0 ( 22.3) 25.2 ( 59229.1)  
> MGC53046 protein [*Xenopus laevis*]

274# 226( 226& 1 226) NF01844632 8.0 ( 8.0) 30.5 ( 30.5) 25.0 ( 25034.9)  
> LOC443580 protein (Fragment) [*Xenopus laevis*]



275# 200( 477& 1 200) NF01844615 6.6 ( 5.0) 29.5 ( 15.7) 22.5 ( 54874.9)  
> MGC84139 protein [Xenopus laevis]

276# 166( 166& 1 166) NF01915773 6.4 ( 6.4) 33.7 ( 33.7) 18.3 ( 18253.7)  
> MGC79515 protein [Xenopus tropicalis]

277# 161( 161& 1 161) NF01915657 6.7 ( 6.7) 29.2 ( 29.2) 18.0 ( 18034.6)  
> MGC89451 protein [Xenopus tropicalis]

278# 210( 370& 1 210) NF01557564 5.1 ( 5.8) 31.9 ( 27.6) 22.9 ( 41035.5)  
> Hypothetical protein MGC75854 [Xenopus tropicalis]

279# 164( 164& 1 164) AAH41536 8.4 ( 8.4) 37.8 ( 37.8) 17.9 ( 17912.5)  
> Cyp-7-prov protein [Xenopus laevis].

280# 185( 752& 1 185) AAH85963 8.6 (10.7) 34.6 ( 8.5) 20.6 ( 88324.8)  
> Unknown (protein for MGC:97908) [Xenopus laevis].

281# 177( 177& 1 177) AAH64250 8.1 ( 8.1) 42.9 ( 42.9) 19.2 ( 19192.2)  
> Hypothetical protein MGC76244 [Xenopus tropicalis].

282# 200( 370& 1 200) AAH61335 5.7 ( 5.8) 33.5 ( 27.6) 21.8 ( 41035.5)  
> Hypothetical protein MGC75854 [Xenopus tropicalis].

283# 164( 164& 1 164) AAH59741 8.7 ( 8.7) 39.0 ( 39.0) 17.8 ( 17798.5)  
> Hypothetical protein MGC75715 [Xenopus tropicalis].

284# 186( 736& 10 195) AAH67931 8.3 (10.8) 32.3 ( 9.0) 20.7 ( 85639.4)  
> Unknown (protein for MGC:69461) [Xenopus tropicalis].

285# 181( 521& 270 450) AAH44993 8.6 ( 8.9) 19.3 ( 22.3) 20.6 ( 59229.1)  
> MGC53046 protein [Xenopus laevis].

286# 184( 207& 25 208) A40516 9.8 ( 9.9) 38.0 ( 42.0) 20.2 ( 22412.9)  
> peptidylprolyl isomerase (S-cyclophilin) precursor - chicken

287# 184( 208& 26 209) CYPB\_BOVIN 9.7 ( 9.7) 35.3 ( 39.9) 20.2 ( 22701.3)  
> Peptidyl-prolyl cis-trans isomerase b precursor

288# 160( 160& 1 160) AAR19276 8.9 ( 8.9) 38.1 ( 38.1) 17.1 ( 17145.5)  
> venom gland cyclophilin [Bitis gabonica].

289# 192( 370& 6 197) A46579 6.3 ( 6.1) 37.5 ( 30.3) 20.9 ( 40620.4)  
> estrogen receptor-binding cyclophilin - bovine

290# 180( 371& 1 180) AAV40687 5.9 ( 5.7) 38.9 ( 29.1) 19.3 ( 40735.0)  
> 40 kDa cyclophilin [Amanita muscaria].

291# 164( 164& 1 164) NF01637248 9.8 ( 9.8) 39.6 ( 39.6) 17.6 ( 17614.9)  
> putative cyclophilin [Pleurotus ostreatus] [Pleurotus pulmonarius]

292# 174( 252& 80 253) CYPR\_BOVIN 6.1 ( 7.1) 37.4 ( 33.7) 19.3 ( 28345.4)  
> retina-specific cyclophilin - Bos taurus

293# 182( 234& 20 201) CYPR\_CALVI 5.4 ( 6.0) 34.6 ( 47.4) 20.3 ( 26380.5)  
> PPIase from Calliphora vicina, rhodopsin specific isozyme precursor

294# 181( 507& 265 445) E1317906 6.6 ( 8.3) 31.5 ( 26.8) 20.4 ( 56989.1)  
> CB-CYP-4 - Caenorhabditis briggsae

295# 157( 157& 1 157) AAB87888 8.9 ( 8.9) 41.4 ( 41.4) 17.1 ( 17118.6)  
> cyclophilin 1 [Drosophila pseudoobscura].

296# 157( 157& 1 157) AAB87889 8.9 ( 8.9) 40.1 ( 40.1) 17.1 ( 17107.6)  
> cyclophilin 1 [Drosophila subobscura].

297# 164( 164& 1 164) Q9XZZ5 9.5 ( 9.5) 35.4 ( 35.4) 17.6 ( 17599.1)  
> CYPA - Lumbricus rubellus (Humus earthworm)

298# 164( 164& 1 164) S63995 9.2 ( 9.2) 31.7 ( 31.7) 17.9 ( 17935.4)  
> peptidylprolyl isomerase - German cockroach (Blattella germanica)

299# 164( 164& 1 164) G1703696 8.6 ( 8.6) 38.4 ( 38.4) 17.7 ( 17678.2)  
> Cyclophilin A from the sea urchin Hemicentrotus pulcherrimus

300# 143( 143& 1 143) U36797 6.3 ( 6.3) 31.5 ( 31.5) 15.4 ( 15398.3)  
> cyclophilin-A - Hirudo medicinalis (medicinal leech)

301# 164( 172& 1 164) AF017738 7.1 ( 9.4) 37.2 ( 35.5) 18.5 ( 19544.5)  
> Onchocerca volvulus cyclophilin-5 (Ovcyp5) mRNA, partial cds

302# 188( 843& 1 188) L37292 9.9 (10.7) 39.4 ( 13.4) 20.9 ( 97817.8)  
> peptidylprolyl isomerase - Brugia malayi

303# 151( 151& 1 151) AAS01736 8.0 ( 8.0) 46.4 ( 46.4) 16.1 ( 16068.4)  
> putative cyclophilin [Populus alba x Populus tremula].

304# 197( 197& 1 197) AAO61985 9.4 ( 9.4) 66.5 ( 66.5) 23.0 ( 22964.2)  
> cyclophilin D [Aster yellows phytoplasma].

305# 173( 173& 1 173) CAC80550 8.9 ( 8.9) 44.5 ( 44.5) 18.2 ( 18153.8)  
> cyclophilin [Ricinus communis].

306# 172( 172& 1 172) AAO63777 8.9 ( 8.9) 42.4 ( 42.4) 18.2 ( 18241.8)  
> cyclophilin [Populus tremuloides].

307# 179( 348& 170 348) B53522 8.0 ( 8.5) 34.1 ( 40.5) 19.7 ( 38124.9)  
> 20k cyclophilin - Toxoplasma gondii (fragment)

308# 194( 223& 27 220) E280557 6.2 ( 6.2) 49.0 ( 51.1) 21.4 ( 24368.2)  
> L. rubellus mRNA for cyclophilin

309# 189( 213& 1 189) U70827 9.8 (10.3) 41.8 ( 37.1) 21.0 ( 23586.2)

> *Onchocerca volvulus* cyclophilin (Ovcyp-1) mRNA, partial cds

310# 188( 188& 1 188) U70884 9.7 ( 9.7) 38.8 ( 38.8) 21.0 ( 20983.3)  
> *Dirofilaria immitis* cyclophilin 1 mRNA, partial cds

311# 182( 196& 15 196) U55771 7.4 ( 8.4) 39.6 ( 42.9) 19.9 ( 21607.9)  
> cyclophilin homolog Ta cyp - *Theileria annulata*

312# 197( 220& 25 221) D1024669 9.7 ( 9.6) 36.0 ( 40.9) 21.7 ( 24197.9)  
> cyclophilin G - *Tachypleus tridentatus*

313# 171( 179& 10 180) 227879 8.6 ( 8.6) 39.8 ( 37.4) 18.2 ( 19007.7)  
> cyclophilin.

314# 178( 197& 20 197) AAD48910 9.5 ( 9.7) 31.5 ( 36.0) 19.3 ( 21398.7)  
> cyclophilin B.

315# 186( 201& 16 201) AAO51811 7.1 ( 7.1) 36.6 ( 35.3) 20.5 ( 21998.0)  
> similar to *Homo sapiens* (Human). U-snRNP-associated cyclophilin (EC

316# 160( 160& 1 160) AAF76472 8.4 ( 8.4) 33.1 ( 33.1) 17.5 ( 17503.0)  
> Contains similarity to cyclophilin E from *Dictyostelium discoideum*

317# 172( 233& 61 232) AAP80861 9.7 (10.0) 40.7 ( 43.3) 18.4 ( 24791.5)  
> cyclophilin [*Triticum aestivum*].

318# 180( 204& 25 204) AAP73848 8.2 ( 8.1) 37.8 ( 40.7) 19.8 ( 21790.0)  
> putative cyclophilin [*Oryza sativa* (japonica cultivar-group)].

319# 164( 164& 1 164) BAB62329 8.7 ( 8.7) 32.3 ( 32.3) 18.1 ( 18083.6)  
> cyclophilin [*Oryza sativa* (japonica cultivar-group)].

320# 181( 181& 1 181) AAL75728 9.4 ( 9.4) 39.8 ( 39.8) 18.9 ( 18920.5)  
> Putative cyclophilin [*Oryza sativa*].

321# 172( 172& 1 172) S48017 8.4 ( 8.4) 41.3 ( 41.3) 18.4 ( 18361.1)  
> peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice.

322# 179( 179& 1 179) S48018 7.7 ( 7.7) 36.9 ( 36.9) 19.2 ( 19198.8)  
> peptidylprolyl isomerase (EC 5.2.1.8) Cyp1 - rice.

323# 181( 220& 40 220) BAD53622 9.7 (10.1) 38.1 ( 40.0) 19.3 ( 23492.2)  
> putative cyclophilin [*Oryza sativa* (japonica cultivar-group)].

324# 186( 225& 40 225) BAD53621 9.7 (10.1) 37.1 ( 41.3) 19.9 ( 24067.9)  
> putative cyclophilin [*Oryza sativa* (japonica cultivar-group)].

325# 189( 208& 20 208) BAD53620 9.4 ( 9.4) 40.2 ( 43.3) 20.0 ( 22111.5)  
> putative cyclophilin [*Oryza sativa* (japonica cultivar-group)].

326# 211( 327& 110 320) XP\_507188 7.0 ( 7.3) 40.3 ( 39.1) 23.1 ( 35887.9)  
> PREDICTED OSJNBb0075018.114 gene product [*Oryza sativa* (japonica

327# 174( 423& 250 423) XP\_483750 6.2 ( 7.7) 31.0 ( 28.8) 19.6 ( 48177.0)  
> putative cyclophilin (70.8 kD) (cyp-15) [Oryza sativa (japonica

328# 181( 503& 40 220) XP\_483749 6.4 ( 6.1) 39.8 ( 33.2) 20.3 ( 56069.0)  
> putative cyclophilin (70.8 kD) (cyp-15) [Oryza sativa (japonica

329# 186( 426& 236 421) XP\_482125 4.0 ( 4.7) 37.6 ( 36.4) 20.5 ( 46482.0)  
> putative Peptidyl-prolyl cis-trans isomerase, chloroplast precursor

330# 193( 432& 240 432) XP\_478742 4.5 ( 5.2) 41.5 ( 46.1) 20.6 ( 46090.9)  
> putative peptidyl-prolylcis-trans isomerase protein [Oryza sativa

331# 196( 465& 270 465) XP\_478741 4.5 ( 5.5) 40.8 ( 48.4) 21.0 ( 49787.2)  
> putative peptidyl-prolylcis-trans isomerase protein [Oryza sativa

332# 169( 169& 1 169) NP\_385690 5.1 ( 5.1) 25.4 ( 25.4) 18.6 ( 18639.1)  
> PUTATIVE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PROTEIN

333# 190( 190& 1 190) NP\_385689 4.5 ( 4.5) 40.0 ( 40.0) 20.1 ( 20055.7)  
> PUTATIVE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A SIGNAL PEPTIDE

334# 174( 174& 1 174) NP\_349373 4.5 ( 4.5) 32.2 ( 32.2) 19.4 ( 19418.8)  
> Peptidyl-prolyl cis-transisomerase, cyclophilin family [Clostridium

335# 200( 548& 1 200) BAD45990 5.7 ( 5.9) 39.5 ( 23.4) 22.5 ( 63174.3)  
> putative multidomain cyclophilin type peptidyl-prolyl cis-trans

336# 180( 564& 1 180) BAD45991 4.6 ( 5.6) 22.8 ( 15.6) 20.3 ( 64975.5)  
> peptidylprolyl isomerase-like [Oryza sativa (japonica

337# 170( 304& 81 250) NP\_908419 7.3 ( 9.4) 61.2 ( 55.6) 17.4 ( 31411.3)  
> P0439B06.15 [Oryza sativa (japonica cultivar-group)].

338# 186( 1089& 245 430) NP\_919903 9.9 ( 8.4) 26.3 ( 33.7) 21.7 (124775.6)  
> putative TNP2-like transposable element [Oryza sativa (japonica

339# 200( 396& 1 200) BAD35839 5.3 ( 5.6) 44.5 ( 33.8) 21.1 ( 43249.7)  
> putative cyclophilin-40 [Oryza sativa (japonica cultivar-group)].

340# 172( 172& 1 172) AAU87301 8.4 ( 8.4) 40.7 ( 40.7) 18.2 ( 18198.7)  
> cyclophilin [Pinus halepensis].

341# 208( 208& 1 208) CAG90469 5.8 ( 5.8) 37.0 ( 37.0) 23.0 ( 22954.1)  
> unnamed protein product [Debaryomyces hansenii CBS767].

342# 162( 162& 1 162) CAG88330 8.2 ( 8.2) 34.0 ( 34.0) 17.6 ( 17596.8)  
> unnamed protein product [Debaryomyces hansenii CBS767].

343# 180( 331& 1 180) CAG88054 4.9 ( 5.1) 41.7 ( 40.2) 20.5 ( 37707.0)  
> unnamed protein product [Debaryomyces hansenii CBS767].

344# 167( 636& 470 636) CAG86818 5.8 ( 5.7) 31.1 ( 31.9) 18.6 ( 71946.7)  
> unnamed protein product [Debaryomyces hansenii CBS767].

345# 164( 164& 1 164) NF01109982 8.6 ( 8.6) 36.0 ( 36.0) 17.5 ( 17531.0)  
> Cyclophilin A [Cordyceps bassiana]

346# 213( 213& 1 213) NF00686348 7.9 ( 7.9) 23.0 ( 23.0) 23.8 ( 23785.0)  
> Peptidyl prolyl cis-trans isomerase [Zymomonas mobilis]

347# 154( 154& 1 154) NF00686217 6.0 ( 6.0) 18.2 ( 18.2) 17.1 ( 17132.2)  
> Peptidyl prolyl cis trans isomerase (Fragment) [Zymomonas mobilis]

348# 174( 174& 1 174) NF02138644 7.8 ( 7.8) 35.6 ( 35.6) 18.9 ( 18873.5)  
> Cyclophilin 1 [Codonopsis lanceolata]

349# 226( 226& 1 226) NF00926921 5.8 ( 5.8) 31.9 ( 31.9) 24.8 ( 24764.2)  
> Cyclophilin [Arthroderma benhamiae]

350# 172( 172& 1 172) NF00909931 8.6 ( 8.6) 40.7 ( 40.7) 18.2 ( 18206.8)  
> CYP1 [Vigna radiata]

351# 161( 300& 140 300) NF00956595 8.2 ( 5.5) 27.3 ( 30.7) 17.9 ( 33367.9)  
> Cyclophilin [Takifugu rubripes]

352# 173( 173& 1 173) NF02035209 5.0 ( 5.0) 38.2 ( 38.2) 18.2 ( 18197.4)  
> Cyclophilin [Hyacinthus orientalis]

353# 182( 182& 1 182) NF01329591 10.2 (10.2) 42.9 ( 42.9) 19.8 ( 19828.0)  
> Rotamase [Pseudomonas citronellolis]

354# 190( 190& 1 190) CAG86678 6.7 ( 6.7) 20.0 ( 20.0) 21.5 ( 21504.0)  
> unnamed protein product [Debaryomyces hansenii CBS767].

355# 180( 285& 41 220) CAG86274 9.6 ( 7.9) 32.2 ( 40.0) 20.4 ( 32650.5)  
> unnamed protein product [Debaryomyces hansenii CBS767].

356# 180( 327& 1 180) CAG85447 8.9 ( 6.7) 35.6 ( 22.3) 20.5 ( 37319.3)  
> unnamed protein product [Debaryomyces hansenii CBS767].

357# 186( 186& 1 186) CAG85287 8.0 ( 8.0) 33.9 ( 33.9) 20.4 ( 20373.1)  
> unnamed protein product [Debaryomyces hansenii CBS767].

358# 200( 370& 1 200) CAG84900 4.9 ( 5.3) 29.0 ( 28.1) 22.1 ( 40748.0)  
> unnamed protein product [Debaryomyces hansenii CBS767].

359# 190( 385& 1 190) CAG84822 5.1 ( 5.1) 31.1 ( 29.1) 21.1 ( 43947.1)  
> unnamed protein product [Debaryomyces hansenii CBS767].

360# 169( 169& 1 169) CAG84723 6.5 ( 6.5) 39.6 ( 39.6) 18.8 ( 18803.5)  
> unnamed protein product [Debaryomyces hansenii CBS767].

361# 191( 228& 15 205) CAG79895 5.2 ( 5.4) 32.5 ( 33.3) 20.9 ( 24946.3)

> unnamed protein product [*Yarrowia lipolytica* CLIB99].

362# 151( 479& 250 400) CAG78939 8.6 ( 8.6) 23.2 ( 21.5) 16.7 ( 52765.7)  
> unnamed protein product [*Yarrowia lipolytica* CLIB99].

363# 190( 367& 1 190) CAG82238 5.1 ( 5.6) 35.3 ( 30.5) 20.6 ( 40061.3)  
> unnamed protein product [*Yarrowia lipolytica* CLIB99].

364# 163( 163& 1 163) CAG81980 7.3 ( 7.3) 32.5 ( 32.5) 17.7 ( 17734.0)  
> unnamed protein product [*Yarrowia lipolytica* CLIB99].

365# 176( 176& 1 176) CAG81971 9.1 ( 9.1) 32.4 ( 32.4) 19.3 ( 19270.7)  
> unnamed protein product [*Yarrowia lipolytica* CLIB99].

366# 171( 171& 1 171) CAG81844 5.8 ( 5.8) 36.3 ( 36.3) 19.1 ( 19109.7)  
> unnamed protein product [*Yarrowia lipolytica* CLIB99].

367# 200( 356& 1 200) CAG84141 8.7 ( 5.0) 34.5 ( 22.5) 22.1 ( 39665.4)  
> unnamed protein product [*Yarrowia lipolytica* CLIB99].

368# 190( 385& 1 190) CAG84091 4.9 ( 5.3) 43.2 ( 30.1) 20.4 ( 42637.2)  
> unnamed protein product [*Yarrowia lipolytica* CLIB99].

369# 200( 338& 1 200) CAG83821 6.4 (10.3) 36.0 ( 21.6) 22.8 ( 39408.9)  
> unnamed protein product [*Yarrowia lipolytica* CLIB99].

370# 189( 189& 1 189) CAG76968 9.8 ( 9.8) 46.6 ( 46.6) 20.3 ( 20285.1)  
> peptidyl-prolyl cis-trans isomerase A [*Erwinia carotovora* subsp.

371# 200( 387& 1 200) CAG62671 4.8 ( 5.2) 38.5 ( 28.9) 22.2 ( 44246.0)  
> unnamed protein product [*Candida glabrata* CBS138].

372# 164( 164& 1 164) CAG76052 5.3 ( 5.3) 37.2 ( 37.2) 18.1 ( 18092.3)  
> peptidyl-prolyl cis-trans isomerase B [*Erwinia carotovora* subsp.

373# 183( 183& 1 183) CAG59915 9.0 ( 9.0) 28.4 ( 28.4) 20.2 ( 20196.2)  
> unnamed protein product [*Candida glabrata* CBS138].

374# 162( 162& 1 162) CAG58658 7.2 ( 7.2) 34.6 ( 34.6) 17.4 ( 17391.7)  
> unnamed protein product [*Candida glabrata* CBS138].

375# 162( 162& 1 162) G3777556 7.8 ( 7.8) 37.7 ( 37.7) 17.3 ( 17253.6)  
> cyclophilin - *Griffithsia japonica*

376# 160( 160& 1 160) AAF65770 9.1 ( 9.1) 43.1 ( 43.1) 16.8 ( 16775.2)  
> cyclophilin [*Euphorbia esula*].

377# 171( 171& 1 171) BAA25755 9.0 ( 9.0) 37.4 ( 37.4) 18.1 ( 18065.6)  
> vCYP [*Vicia faba*].

378# 171( 171& 1 171) CSTO 8.7 ( 8.7) 43.3 ( 43.3) 17.9 ( 17926.6)  
> peptidylprolyl isomerase - tomato

379# 171( 171& 1 171) CSRP 8.4 ( 8.4) 33.3 ( 33.3) 18.5 ( 18500.2)  
> peptidylprolyl isomerase - rape

380# 172( 172& 1 172) CSZM 8.9 ( 8.9) 42.4 ( 42.4) 18.3 ( 18349.1)  
> peptidylprolyl isomerase - maize

381# 150( 150& 1 150) CYPH\_ALLCE 8.2 ( 8.2) 37.3 ( 37.3) 16.0 ( 16033.3)  
> cyclophilin - *Allium cepa* (onion)

382# 155( 155& 1 155) AAG01536 7.2 ( 7.2) 47.1 ( 47.1) 16.4 ( 16415.9)  
> locus AF291180 - cyclophilin - *Capsicum annuum* - plant.

383# 172( 172& 1 172) AAB51386 8.7 ( 8.7) 44.8 ( 44.8) 18.0 ( 18047.8)  
> Cyclophilin - Commerson's wild potato - *Solanum commersonii*

384# 172( 172& 1 172) S54833 8.2 ( 8.2) 41.3 ( 41.3) 18.2 ( 18159.7)  
> peptidylprolyl isomerase Cyp - kidney bean

385# 172( 172& 1 172) X85185 8.2 ( 8.2) 37.8 ( 37.8) 18.3 ( 18284.8)  
> cyclophilin - *Catharanthus roseus* (Madagascar periwinkle)

386# 172( 172& 1 172) Y08273 8.2 ( 8.2) 47.7 ( 47.7) 18.1 ( 18054.8)  
> cyclophilin - *Digitalis lanata*

387# 172( 172& 1 172) Y08320 8.2 ( 8.2) 44.8 ( 44.8) 18.1 ( 18127.9)  
> cyclophylin - *Digitalis lanata*

388# 172( 172& 1 172) E1226445 8.6 ( 8.6) 39.0 ( 39.0) 18.3 ( 18286.8)  
> cytosolic form of cyclophilin - *Lupinus luteus* (yellow lupine)

389# 170( 248& 80 249) L32095 5.8 ( 8.5) 41.8 ( 40.7) 18.2 ( 26547.1)  
> cyclophilin - *Vicia faba*

390# 181( 189& 10 190) CAA10766 8.4 ( 8.1) 42.0 ( 42.9) 20.0 ( 20649.9)  
> Cyclophilin - *Pseudotsuga menziesii* (Douglas fir)

391# 162( 162& 1 162) AAF69796 9.1 ( 9.1) 34.6 ( 34.6) 17.6 ( 17565.7)  
> cyclophilin A [*Filobasidiella neoformans* var. *neoformans*] - 162 AA.

392# 162( 162& 1 162) AAF69795 9.1 ( 9.1) 35.2 ( 35.2) 17.4 ( 17440.6)  
> cyclophilin A [*Filobasidiella neoformans* var. *neoformans*] - 162 AA.

393# 185( 223& 40 224) CSNCM 9.1 ( 9.6) 28.1 ( 33.2) 20.0 ( 24064.3)  
> peptidylprolyl isomerase precursor, mitochondrial - *Neurospora crassa*

394# 190( 494& 1 190) NF01287451 4.8 ( 5.7) 37.9 ( 25.5) 20.7 ( 56499.9)  
> Hypothetical protein B8G12.450 [*Neurospora crassa*]

395# 167( 167& 1 167) NF01527836 7.4 ( 7.4) 35.3 ( 35.3) 18.4 ( 18405.1)  
> Probable peptidylprolyl isomerase (Cyclophilin)-like protein [*Neuros*

396# 153( 153& 1 153) NF01488902 9.1 ( 9.1) 30.7 ( 30.7) 16.8 ( 16808.2)  
> Hypothetical protein (Probable cyclophilin E) [Neurospora crassa]

397# 200( 375& 1 200) NF00648058 6.0 ( 5.8) 36.5 ( 32.0) 21.5 ( 40570.8)  
> 41 kDa peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8) (PPIase) (Ro

398# 191( 282& 30 220) NF01487278 5.8 ( 7.7) 23.6 ( 33.0) 20.8 ( 30347.8)  
> Hypothetical protein [Neurospora crassa]

399# 173( 632& 460 632) NF01486260 9.0 ( 7.1) 26.6 ( 31.2) 19.3 ( 70602.4)  
> Hypothetical protein [Neurospora crassa]

400# 207( 207& 1 207) NF00904102 9.2 ( 9.2) 31.4 ( 31.4) 22.6 ( 22557.0)  
> Probable cyclophilin [Neurospora crassa]

401# 190( 803& 1 190) NF01484914 4.8 ( 9.0) 37.9 ( 27.4) 20.7 ( 90762.9)  
> Hypothetical protein [Neurospora crassa]

402# 182( 182& 1 182) NF01484255 7.1 ( 7.1) 40.7 ( 40.7) 19.7 ( 19733.6)  
> Hypothetical protein (Probable U-snRNP-associated cyclophilin) [Neur

403# 220( 541& 1 220) NF01483993 5.7 ( 8.4) 29.5 ( 19.2) 24.3 ( 60295.9)  
> Hypothetical protein (Related to peptidylprolyl isomerase (Cyclophil

404# 172( 172& 1 172) NF01533203 8.6 ( 8.6) 43.6 ( 43.6) 18.2 ( 18245.8)  
> Cyclophilin [Kandelia candel]

405# 181( 597& 320 500) NF01483647 10.0 ( 9.1) 26.0 ( 24.0) 20.5 ( 65800.9)  
> Hypothetical protein [Neurospora crassa]

406# 184( 227& 45 228) S71849 7.4 ( 9.7) 27.2 ( 32.6) 19.9 ( 24589.9)  
> peptidylprolyl isomerase A precursor, mitochondrial - CsA fungi

407# 184( 203& 17 200) U17900 9.1 ( 9.0) 37.5 ( 41.9) 19.9 ( 21969.1)  
> cyclophilin B precursor - the anaerobic fungus Orpinomyces sp. strain PC-2

408# 162( 162& 1 162) NF00873669 8.9 ( 8.9) 40.7 ( 40.7) 17.2 ( 17212.7)  
> Allergen [Malassezia sympodialis]

409# 162( 162& 1 162) NF01527595 8.0 ( 8.0) 38.9 ( 38.9) 17.2 ( 17243.6)  
> Cyclophilin [Malassezia pachydermatis]

410# 184( 223& 40 223) NF01539217 7.3 ( 9.5) 32.6 ( 33.2) 19.9 ( 24225.4)  
> Putative mitochondrial cyclophilin 1 [Botryotinia fuckeliana]

411# 186( 226& 20 205) D1035365 6.1 ( 5.8) 28.5 ( 31.9) 20.5 ( 24764.2)  
> cyclophilin - Trichophyton mentagrophytes

412# 165( 165& 1 165) YP\_116397 5.1 ( 5.1) 38.8 ( 38.8) 17.6 ( 17554.7)  
> putative peptidyl-prolyl cis-trans isomerase [Nocardia farcinica

413# 177( 292& 116 292) YP\_119877 3.9 ( 4.9) 36.2 ( 32.5) 18.3 ( 30326.0)



> putative peptidyl-prolyl cis-trans isomerase [*Nocardia farcinica*]

414# 187( 200& 14 200) CAD25897 5.9 ( 6.1) 34.2 ( 38.5) 21.1 ( 22558.7)  
> PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (CYCLOPHILIN) [*Encephalitozoon*]

415# 172( 172& 1 172) CAD26352 6.7 ( 6.7) 27.3 ( 27.3) 19.0 ( 19046.6)  
> PEPTIDYL-PROLYL CIS-TRANS ISOMERASE [*Encephalitozoon cuniculi*]

416# 186( 214& 20 205) AAD17998 6.5 ( 7.8) 24.7 ( 30.4) 20.3 ( 23406.6)  
> cyclophilin B; CYPB [*Emericella nidulans*].

417# 172( 172& 1 172) G2959712 7.7 ( 7.7) 35.5 ( 35.5) 18.4 ( 18427.9)  
> cyclophilin 1 - *Chlamydomonas reinhardtii*

418# 180( 180& 1 180) CSNCC 8.7 ( 8.7) 26.1 ( 26.1) 19.5 ( 19523.1)  
> peptidylprolyl isomerase, cytosolic - *Neurospora crassa*

419# 178( 178& 1 178) AJ006689 9.1 ( 9.1) 31.5 ( 31.5) 19.6 ( 19554.0)  
> *Aspergillus fumigatus* mRNA for rAsp f 11 allergen

420# 152( 152& 1 152) AAF28343 9.5 ( 9.5) 28.9 ( 28.9) 16.9 ( 16925.3)  
> cyclophilin E.

421# 174( 174& 1 174) AAD50375 8.6 ( 8.6) 37.9 ( 37.9) 19.0 ( 19015.6)  
> cyclophilin D.

422# 145( 145& 1 145) AAK21908 9.0 ( 9.0) 37.9 ( 37.9) 15.3 ( 15303.4)  
> cyclophilin [*Vaucheria litorea*].

423# 176( 215& 40 215) AAG13968 9.6 (10.3) 33.0 ( 33.5) 19.2 ( 23552.9)  
> cyclophilin [*Magnaporthe grisea*].

424# 165( 165& 1 165) BAB58884 9.1 ( 9.1) 34.5 ( 34.5) 17.8 ( 17845.2)  
> cyclophilin [*Magnaporthe grisea*].

425# 162( 162& 1 162) E1363908 8.9 ( 8.9) 40.7 ( 40.7) 17.2 ( 17212.7)  
> cyclophilin allergen - *Malassezia furfur*(fungi-Exobasidiomycetidae)

426# 174( 174& 1 174) AAD16142 9.1 ( 9.1) 35.1 ( 35.1) 18.9 ( 18873.4)  
> Cyclophilin - *Aspergillus niger*

427# 163( 163& 1 163) G1764137 8.4 ( 8.4) 28.2 ( 28.2) 18.0 ( 17992.5)  
> PIG28 - *Uromyces fabae*

428# 180( 180& 1 180) Z32674 9.8 ( 9.8) 30.6 ( 30.6) 18.8 ( 18757.1)  
> cyclophilin - *Tolyposcladium niveum*

429# 179( 179& 1 179) JT0686 6.4 ( 6.4) 29.6 ( 29.6) 19.4 ( 19375.7)  
> peptidylprolyl isomerase a, cytosolic - fungus (*Fusarium sporotrich*)

430# 162( 162& 1 162) CSMC 8.2 ( 8.2) 37.7 ( 37.7) 17.6 ( 17575.0)  
> peptidylprolyl isomerase - yeast (*Candida albicans*)

431# 162( 162& 1 162) NP\_986490 8.0 ( 8.0) 38.9 ( 38.9) 17.4 ( 17412.9)  
> AGL177Cp [Eremothecium gossypii].

432# 188( 188& 1 188) NP\_985014 8.7 ( 8.7) 35.1 ( 35.1) 20.3 ( 20295.0)  
> AER156Cp [Eremothecium gossypii].

433# 190( 383& 1 190) NP\_984799 5.0 ( 5.2) 37.4 ( 29.5) 20.6 ( 42800.6)  
> AEL062Cp [Eremothecium gossypii].

434# 190( 369& 1 190) NP\_984183 5.3 ( 5.6) 37.9 ( 38.5) 20.6 ( 39990.3)  
> ADR087Cp [Eremothecium gossypii].

435# 230( 309& 21 250) NP\_982586 5.6 ( 8.8) 29.1 ( 38.5) 25.8 ( 34317.4)  
> AAR045Cp [Eremothecium gossypii].

436# 203( 203& 1 203) NP\_982486 4.8 ( 4.8) 49.3 ( 49.3) 21.8 ( 21765.6)  
> AAL056Cp [Eremothecium gossypii].

437# 201( 201& 1 201) AAT09096 9.7 ( 9.7) 33.3 ( 33.3) 21.7 ( 21676.8)  
> cyclophilin [Bigelowiella natans].

438# 194( 194& 1 194) YP\_014938 4.4 ( 4.4) 33.0 ( 33.0) 21.4 ( 21434.3)  
> peptidyl-prolyl cis-trans isomerase, cyclophilin-type [Listeria

439# 171( 171& 1 171) NP\_951950 6.2 ( 6.2) 43.3 ( 43.3) 18.8 ( 18801.4)  
> peptidyl-prolyl cis-trans isomerase, cyclophilin-type [Geobacter

440# 181( 181& 1 181) NP\_935388 5.1 ( 5.1) 37.6 ( 37.6) 19.8 ( 19802.7)  
> Peptidyl-prolyl cis-trans isomerase [Vibrio vulnificus YJ016].

441# 181( 181& 1 181) NP\_907765 9.5 ( 9.5) 41.4 ( 41.4) 20.2 ( 20185.2)  
> CYCLOPHILIN-TYPE PEPTIDYL-PROLYL ISOMERASE [Wolinella succinogenes

442# 187( 522& 300 486) BAC91249 9.5 ( 5.8) 16.6 ( 26.2) 21.2 ( 58429.5)  
> gl13308 [Gloeobacter violaceus PCC 7421].

443# 189( 246& 58 246) BAC90551 9.8 ( 9.7) 38.6 ( 46.3) 20.0 ( 25591.7)  
> peptidyl-prolyl cis-trans isomerase [Gloeobacter violaceus PCC

444# 194( 283& 90 283) BAC89441 9.4 ( 9.8) 38.7 ( 43.8) 20.9 ( 30471.1)  
> glr1500 [Gloeobacter violaceus PCC 7421].

445# 199( 243& 45 243) BAC88914 7.8 ( 9.2) 42.7 ( 44.0) 20.7 ( 25131.3)  
> peptidyl-prolyl cis-trans isomerase [Gloeobacter violaceus PCC

446# 195( 234& 10 204) AAV50868 7.2 ( 8.9) 34.9 ( 30.8) 22.0 ( 26538.9)  
> peptidylprolyl isomerase [Mimivirus].

447# 196( 196& 1 196) AAV82698 5.0 ( 5.0) 35.7 ( 35.7) 22.0 ( 21980.9)  
> Peptidyl-prolyl cis-trans isomerase (rotamase), cyclophilin family

448# 165( 165& 1 165) AAV81872 4.6 ( 4.6) 34.5 ( 34.5) 18.2 ( 18155.3)  
 > Peptidyl-prolyl cis-trans isomerase (rotamase), cyclophilin family

449# 199( 267& 64 262) NP\_736022 9.6 ( 9.7) 33.7 ( 31.8) 21.7 ( 29344.6)  
 > hypothetical protein gbs1586 [Streptococcus agalactiae NEM316].

450# 177( 466& 270 446) NP\_734780 4.5 ( 4.9) 34.5 ( 36.3) 19.3 ( 51902.9)  
 > hypothetical protein gbs0311 [Streptococcus agalactiae NEM316].

451# 145( 145& 1 145) YP\_085398 5.3 ( 5.3) 26.2 ( 26.2) 15.8 ( 15773.8)  
 > peptidyl-prolyl cis-trans isomerase B [Bacillus cereus ZK].

452# 181( 323& 90 270) NP\_643098 4.9 ( 5.9) 29.3 ( 36.5) 19.6 ( 35139.9)  
 > peptidyl-prolyl cis-trans isomerase [Xanthomonas axonopodis pv.

453# 164( 164& 1 164) NP\_641352 5.1 ( 5.1) 39.6 ( 39.6) 17.5 ( 17456.6)  
 > peptidyl-prolyl cis-trans isomerase [Xanthomonas axonopodis pv.

454# 179( 368& 190 368) BAB76758 4.3 ( 5.0) 39.1 ( 35.9) 19.5 ( 40493.4)  
 > alr5059 [Nostoc sp. PCC 7120].

455# 180( 180& 1 180) YP\_129479 5.4 ( 5.4) 41.1 ( 41.1) 19.9 ( 19874.7)  
 > putative peptidyl-prolyl cis-trans isomerase B [Photobacterium

456# 165( 165& 1 165) YP\_129310 4.6 ( 4.6) 36.4 ( 36.4) 18.2 ( 18231.5)  
 > putative peptidyl-prolyl cis-trans isomerase B [Photobacterium

457# 183( 183& 1 183) YP\_129032 8.5 ( 8.5) 39.9 ( 39.9) 20.3 ( 20306.2)  
 > putative peptidyl-prolyl cis-trans isomerase A [Photobacterium

458# 171( 279& 30 200) YP\_101389 9.5 ( 6.7) 22.2 ( 29.0) 19.3 ( 31329.8)  
 > cyclophilin-type peptidyl-prolyl cis-trans isomerase [Bacteroides

459# 185( 185& 1 185) YP\_087816 9.7 ( 9.7) 36.2 ( 36.2) 20.6 ( 20609.5)  
 > PpiB protein [Mannheimia succiniciproducens MBEL55E].

460# 183( 183& 1 183) YP\_087815 6.1 ( 6.1) 27.3 ( 27.3) 20.5 ( 20536.3)  
 > PpiB protein [Mannheimia succiniciproducens MBEL55E].

461# 203( 203& 1 203) YP\_076496 4.5 ( 4.5) 33.5 ( 33.5) 21.9 ( 21943.6)  
 > peptidyl-prolyl cis-trans isomerase, cyclophilin-type

462# 148( 148& 1 148) AAT91289 9.7 ( 9.7) 31.1 ( 31.1) 15.9 ( 15871.9)  
 > putative cyclophilin [Paxillus involutus].

463# 149( 149& 1 149) AAT91260 9.9 ( 9.9) 31.5 ( 31.5) 16.0 ( 15985.1)  
 > putative cyclophilin [Paxillus filamentosus].

464# 207( 207& 1 207) NP\_868477 7.8 ( 7.8) 43.0 ( 43.0) 21.7 ( 21730.7)  
 > peptidylprolyl isomerase [Rhodopirellula baltica SH 1].

465# 143( 143& 1 143) NP\_867717 4.8 ( 4.8) 24.5 ( 24.5) 15.9 ( 15946.8)

> peptidylprolyl isomerase [Pirellula sp. 1].

466# 176( 1541& 235 410) NP\_867158 4.0 ( 3.8) 33.0 ( 45.3) 19.3 (159790.0)  
> probable cyclophilin type peptidylprolyl isomerase [Pirellula sp.

467# 171( 511& 310 480) NP\_865515 4.9 ( 5.2) 42.1 ( 30.7) 18.6 ( 57308.9)  
> peptidyl-prolyl cis-trans isomerase cyp2 [Pirellula sp. 1].

468# 164( 164& 1 164) NP\_992233 5.4 ( 5.4) 32.3 ( 32.3) 18.2 ( 18151.4)  
> peptidyl-prolyl cis-trans isomerase B [Yersinia pestis biovar

469# 199( 199& 1 199) NP\_991569 9.3 ( 9.3) 44.2 ( 44.2) 21.7 ( 21663.8)  
> peptidyl-prolyl cis-trans isomerase A [Yersinia pestis biovar

470# 189( 189& 1 189) NP\_280624 4.0 ( 4.0) 29.1 ( 29.1) 20.5 ( 20458.1)  
> PpiA [Halobacterium salinarum NRC-1].

471# 190( 324& 135 324) BAC18575 3.6 ( 4.3) 31.1 ( 27.5) 19.9 ( 34695.3)  
> putative peptidylprolyl isomerase [Corynebacterium efficiens

472# 202( 202& 1 202) BAC16839 5.0 ( 5.0) 40.6 ( 40.6) 21.8 ( 21829.5)  
> putative peptidylprolyl isomerase [Corynebacterium efficiens

473# 170( 170& 1 170) BAB82272 5.1 ( 5.1) 32.9 ( 32.9) 18.9 ( 18888.7)  
> peptidyl-prolyl cis-trans isomerase B [Clostridium perfringens str.

474# 169( 169& 1 169) BAB99042 3.7 ( 3.7) 32.5 ( 32.5) 17.5 ( 17506.1)  
> Peptidyl-prolyl cis-trans isomerase (rotamase) - cyclophilin family

475# 187( 187& 1 187) BAB97427 4.5 ( 4.5) 42.8 ( 42.8) 19.8 ( 19830.1)  
> Peptidyl-prolyl cis-trans isomerase (rotamase) - cyclophilin family

476# 203( 392& 190 392) BAC08372 4.5 ( 5.3) 40.4 ( 40.6) 22.4 ( 43449.1)  
> peptidyl-prolyl cis-trans isomerase [Thermosynechococcus elongatus

477# 184( 243& 60 243) BAC07690 5.1 ( 6.1) 37.5 ( 45.3) 19.9 ( 26003.7)  
> peptidyl-prolyl cis-trans isomerase [Thermosynechococcus elongatus

478# 189( 189& 1 189) YP\_072215 9.0 ( 9.0) 45.5 ( 45.5) 20.5 ( 20526.5)  
> peptidyl-prolyl cis-trans isomerase A [Yersinia pseudotuberculosis

479# 164( 164& 1 164) YP\_069574 5.4 ( 5.4) 32.3 ( 32.3) 18.2 ( 18151.4)  
> peptidyl-prolyl cis-trans isomerase B [Yersinia pseudotuberculosis

480# 164( 164& 1 164) NP\_778719 5.6 ( 5.6) 42.7 ( 42.7) 17.7 ( 17744.1)  
> peptidyl-prolyl cis-trans isomerase [Xylella fastidiosa Temecula1].

481# 169( 169& 1 169) NP\_245881 6.3 ( 6.3) 28.4 ( 28.4) 18.7 ( 18731.2)  
> PpiB [Pasteurella multocida subsp. multocida str. Pm70].

482# 183( 183& 1 183) NP\_245880 8.5 ( 8.5) 39.3 ( 39.3) 20.1 ( 20067.1)  
> hypothetical protein PM0943 [Pasteurella multocida subsp. multocida

483# 189( 189& 1 189) NP\_354667 9.6 ( 9.6) 47.1 ( 47.1) 19.9 ( 19881.9)  
> AGR\_C\_3090p [*Agrobacterium tumefaciens* str. C58].

484# 169( 169& 1 169) NP\_354666 5.3 ( 5.3) 36.7 ( 36.7) 18.4 ( 18420.0)  
> AGR\_C\_3088p [*Agrobacterium tumefaciens* str. C58].

485# 164( 164& 1 164) NP\_298502 6.7 ( 6.7) 43.9 ( 43.9) 17.8 ( 17788.2)  
> peptidyl-prolyl cis-trans isomerase [*Xylella fastidiosa* 9a5c].

486# 164( 164& 1 164) AAN39296 8.6 ( 8.6) 36.0 ( 36.0) 17.5 ( 17531.0)  
> cyclophilin A [*Beauveria bassiana*].

487# 164( 164& 1 164) AAQ24380 9.2 ( 9.2) 40.9 ( 40.9) 17.4 ( 17391.9)  
> cyclophilin A; rotamase [*Branchiostoma belcheri tsingtaunese*].

488# 150( 150& 1 150) ZP\_00353225 5.0 ( 5.0) 37.3 ( 37.3) 16.1 ( 16097.9)  
> COG0652: Peptidyl-prolyl cis-trans isomerase (rotamase) -

489# 167( 167& 1 167) ZP\_00244808 6.3 ( 6.3) 31.7 ( 31.7) 18.1 ( 18086.3)  
> COG0652: Peptidyl-prolyl cis-trans isomerase (rotamase) -

490# 188( 188& 1 188) ZP\_00244807 9.8 ( 9.8) 44.7 ( 44.7) 20.1 ( 20104.1)  
> COG0652: Peptidyl-prolyl cis-trans isomerase (rotamase) -

491# 150( 150& 1 150) ZP\_00358245 7.9 ( 7.9) 30.7 ( 30.7) 16.6 ( 16552.8)  
> COG0652: Peptidyl-prolyl cis-trans isomerase (rotamase) -

492# 163( 163& 1 163) ZP\_00350273 5.0 ( 5.0) 35.6 ( 35.6) 17.9 ( 17931.2)  
> COG0652: Peptidyl-prolyl cis-trans isomerase (rotamase) -

493# 169( 169& 1 169) ZP\_00129494 4.5 ( 4.5) 43.8 ( 43.8) 18.4 ( 18399.9)  
> COG0652: Peptidyl-prolyl cis-trans isomerase (rotamase) -

494# 157( 157& 1 157) ZP\_00130259 5.2 ( 5.2) 35.7 ( 35.7) 17.3 ( 17303.6)  
> COG0652: Peptidyl-prolyl cis-trans isomerase (rotamase) -

495# 187( 187& 1 187) ZP\_00136576 8.5 ( 8.5) 53.5 ( 53.5) 20.2 ( 20164.3)  
> COG0652: Peptidyl-prolyl cis-trans isomerase (rotamase) -

496# 151( 151& 1 151) NF01760157 5.9 ( 5.9) 32.5 ( 32.5) 16.7 ( 16736.9)  
> Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8) [*Picrophilus torrid*

Average pI = 7.4639  
Average HI = 36.0569  
Maximal pI = 10.1853  
Minimal pI = 3.5908  
Maximal HI = 66.4975  
Minimal HI = 16.5775

Sequences 245 246 have similar data  
Sequences 246 247 have similar data

-> Datapx: ((( Job finished )))