About Search Families Download Top
Help! Blast Publications CBiB

Search results

Génolevures found 31 elements for “+(glucan homocitrate) +synthase” using a keyword search:

26	Genes or other elements that have or may have a translation product
76	Genes as above, including orthologs (to *S. cerevisiae* genes) predicted using Génolevures protein families
0	RNA genes or other elements that have or may have a transcription product only
0	Cis-active elements having neither translation nor transcription products
5	Protein families

Genes for “+(glucan homocitrate) +synthase”

1. CAGL0I10054g: similar to sp|P33336 Saccharomyces cerevisiae YGR143w SKN1 glucan synthase or sp|P32486 Saccharomyces cerevisiae YPR159w KRE6, start by similarity · score=1.00
2. CAGL0K04037g: tr|Q9P8N8 Candida glabrata 1, 3-beta-glucan synthase, identified start · score=1.00
3. DEHA0A07436g: similar to sp|Q04952 Saccharomyces cerevisiae YMR306w FKS3 1,3-beta-glucan synthase, start by similarity · score=1.00
4. DEHA0B14080g: similar to sp|P32486 Saccharomyces cerevisiae YPR159w KRE6 glucan synthase subunit, start by similarity · score=1.00
5. DEHA0B14201g: similar to CA5661|CaKRE6 Candida albicans CaKRE6 Glucan synthase subunit, hypothetical start · score=1.00
6. DEHA0B14223g: similar to CA5661|CaKRE6 Candida albicans CaKRE6 Glucan synthase subunit, hypothetical start · score=1.00
7. DEHA0C02112g: highly similar to tr|O13428 Candida albicans Beta-1, 3-glucan synthase catalytic subunit 1, start by similarity · score=1.00
8. DEHA0F09405g: highly similar to ca|CA2335|CaLYS21 Candida albicans CaLYS21 homocitrate synthase (by homology), start by similarity · score=1.00
9. KLLA0B05841g: highly similar to sp|P40989 Saccharomyces cerevisiae GR032w GSC2 1, 3-beta-D-glucan synthase subunit, start by similarity · score=1.00
10. KLLA0C08888g: similar to sp|O13423 Candida albicans Glucan synthase, start by similarity · score=1.00
11. KLLA0E03597g: similar to sp|P32486 Saccharomyces cerevisiae YPR159w KRE6 glucan synthase subunit, start by similarity · score=1.00
12. KLLA0E23782g: highly similar to sp|Q12122 Saccharomyces cerevisiae YDL131w LYS21 homocitrate synthase, start by similarity · score=1.00
13. KLLA0F05489g: highly similar to sp|Q12122 Saccharomyces cerevisiae YDL131w LYS21 homocitrate synthase, start by similarity · score=1.00
14. YALI0B20570g: weakly similar to sp|P38678 Neurospora crassa Glucan synthase-1 (EC 2.4.1.34), start by similarity · score=1.00
15. YALI0C01639g: pseudogene, similar to sp|Q06472 Saccharomyces cerevisiae Beta-glucan

synthesis-associated protein (Killer toxin-resistance protein 6) and sp|P33336 Saccharomyces cerevisiae YGR143w SKN1 glucan synthase subunit, frameshift · score=1.00

16. YALI0C14190g: similar to sp|P33336 Saccharomyces cerevisiae YGR143w SKN1 glucan synthase subunit P2.4.f2.1 and sp|P32486 Saccharomyces cerevisiae YPR159w KRE6 glucan synthase subunit P2.4.f2.1 associated protein, hypothetical start · score=1.00
17. YALI0E21021g: tr|Q9UVK9 Yarrowia lipolytica 1,3-beta-glucan synthase activity, identified start · score=1.00
18. YALI0F31075g: sp|Q12726 Yarrowia lipolytica Homocitrate synthase, identified start · score=1.00
19. YCR034w: FEN1, Fatty acid elongase, involved in sphingolipid biosynthesis; acts on fatty acids of up to 24 carbons in length; mutations have regulatory effects on 1,3-beta-glucan synthase, vacuolar ATPase, and the secretory pathway · score=1.00
20. YDL131w: LYS21, Homocitrate synthase isozyme, catalyzes the condensation of acetyl-CoA and alpha-ketoglutarate to form homocitrate, which is the first step in the lysine biosynthesis pathway; highly similar to the other isozyme, Lys20p · score=1.00
21. YDL182w: LYS20, Homocitrate synthase isozyme, catalyzes the condensation of acetyl-CoA and alpha-ketoglutarate to form homocitrate, which is the first step in the lysine biosynthesis pathway; highly similar to the other isozyme, Lys21p · score=1.00
22. YGR032w: GSC2, Catalytic subunit of 1,3-beta-glucan synthase, has similarity to an alternate catalytic subunit, Fks1p (Gsc1p); Rho1p encodes the regulatory subunit; involved in cell wall synthesis and maintenance · score=1.00
23. YLR342w: FKS1, Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling · score=1.00
24. YMR306w: FKS3, Protein of unknown function, has similarity to 1,3-beta-D-glucan synthase catalytic subunits Fks1p and Gsc2p · score=1.00
25. YPR159w: KRE6, Protein required for beta-1,6 glucan biosynthesis; putative beta-glucan synthase; appears functionally redundant with Skn1p · score=1.00
26. YPR165w: RHO1, GTP-binding protein of the rho subfamily of Ras-like proteins, involved in establishment of cell polarity; regulates protein kinase C (Pkc1p) and the cell wall synthesizing enzyme 1,3-beta-glucan synthase (Fks1p and Gsc2p) · score=1.00

Genes for “+(glucan homocitrate) +synthase”, including orthologs to *S. cerevisiae* genes for “+(glucan homocitrate) +synthase”

1. CAGL0F05269g: highly similar to sp|P19073 Saccharomyces cerevisiae YLR229c CDC42, start by similarity · score=1
2. CAGL0G01034g: highly similar to sp|P40989 Saccharomyces cerevisiae YGR032w GSC2 or sp|P38631 Saccharomyces cerevisiae YLR342w FKS1, start by similarity · score=1
3. CAGL0G04851g: highly similar to sp|P40319 Saccharomyces cerevisiae YLR372w SUR4 sterol isomerase, fatty acid elongase, hypothetical start · score=1
4. CAGL0G05764g: similar to sp|P53879 Saccharomyces cerevisiae YNL180c RHO5, start by similarity · score=1
5. CAGL0G08558g: highly similar to sp|Q00245 Saccharomyces cerevisiae YIL118w RHO3, start by similarity · score=1
6. CAGL0I08459g: highly similar to sp|P06780 Saccharomyces cerevisiae YPR165w RHO1, start by similarity · score=1
7. CAGL0I10054g: similar to sp|P33336 Saccharomyces cerevisiae YGR143w SKN1 glucan synthase or sp|P32486 Saccharomyces cerevisiae YPR159w KRE6, start by similarity · score=1
8. CAGL0J05632g: highly similar to sp|P06781 Saccharomyces cerevisiae YNL090w RHO2, start by similarity · score=1

9. CAGL0J06402g: highly similar to sp|Q12122 Saccharomyces cerevisiae YDL131w LYS21 or sp|P48570 Saccharomyces cerevisiae YDL182w LYS20, hypothetical start · score=1
10. CAGL0J09240g: highly similar to sp|Q12122 Saccharomyces cerevisiae YDL131w LYS21 or sp|P48570 Saccharomyces cerevisiae YDL182w LYS20, start by similarity · score=1
11. CAGL0J11242g: similar to sp|P53879 Saccharomyces cerevisiae YNL180c RHO5, start by similarity · score=1
12. CAGL0K00583g: highly similar to sp|P25358 Saccharomyces cerevisiae YCR034w V-SNARE bypass mutant, hypothetical start · score=1
13. CAGL0K04037g: tr|Q9P8N8 Candida glabrata 1, 3-beta-glucan synthase, identified start · score=1
14. CAGL0K08316g: some similarities with sp|Q00246 Saccharomyces cerevisiae YKR055w RHO4 GTP-binding protein, hypothetical start · score=1
15. CAGL0L08184g: highly similar to sp|P25358 Saccharomyces cerevisiae YCR034w GNS1, start by similarity · score=1
16. CAGL0M13827g: similar to sp|Q04952 Saccharomyces cerevisiae YMR306w FKS3, hypothetical start · score=1
17. DEHA0A07436g: similar to sp|Q04952 Saccharomyces cerevisiae YMR306w FKS3 1,3-beta-glucan synthase, start by similarity · score=1
18. DEHA0B11792g: highly similar to sp|P06780 Saccharomyces cerevisiae YPR165w RHO1 GTP-binding protein of the rho subfamily of ras-like proteins, start by similarity · score=1
19. DEHA0B14080g: similar to sp|P32486 Saccharomyces cerevisiae YPR159w KRE6 glucan synthase subunit, start by similarity · score=1
20. DEHA0B14102g: similar to sp|P87023 Candida albicans Beta-glucan synthesis-associated protein KRE6, hypothetical start · score=1
21. DEHA0B14201g: similar to CA5661|CaKRE6 Candida albicans CaKRE6 Glucan synthase subunit, hypothetical start · score=1
22. DEHA0B14223g: similar to CA5661|CaKRE6 Candida albicans CaKRE6 Glucan synthase subunit, hypothetical start · score=1
23. DEHA0C02112g: highly similar to tr|O13428 Candida albicans Beta-1, 3-glucan synthase catalytic subunit 1, start by similarity · score=1
24. DEHA0C07293g: similar to sp|Q00245 Saccharomyces cerevisiae YIL118w RHO3, hypothetical start · score=1
25. DEHA0C09031g: similar to sp|P06781 Saccharomyces cerevisiae YNL090w RHO2, start by similarity · score=1
26. DEHA0D14498g: highly similar to CA0261|CaLYS22 Candida albicans CaLYS22, start by similarity · score=1
27. DEHA0D16555g: similar to CA2933|IPF11512 Candida albicans IPF11512, hypothetical start · score=1
28. DEHA0F04004g: highly similar to CA3005|CaCC43 Candida albicans CaCC43 Cell Division Control-like (by homology), start by similarity · score=1
29. DEHA0F09405g: highly similar to ca|CA2335|CaLYS21 Candida albicans CaLYS21 homocitrate synthase (by homology), start by similarity · score=1
30. DEHA0G06116g: similar to sp|P40319 Saccharomyces cerevisiae Elongation of fatty acids protein 3 (SUR4 protein) (SRE1 protein) (V-SNARE bypass mutant gene 1 protein), hypothetical start · score=1
31. DEHA0G10912g: highly similar to CA3497|CaFEN11 Candida albicans CaFEN11 Fatty acid elongase required for sphingolipid formation (by homology), hypothetical start · score=1
32. DEHA0G14751g: weakly similar to CA6143|IPF1873 Candida albicans IPF1873, start by similarity · score=1
33. DEHA0G15037g: highly similar to CA3879|CaCDC42 Candida albicans CaCDC42 Cell Division Control, start by similarity · score=1
34. KLLA0A04213g: highly similar to sp|P19073 Saccharomyces cerevisiae YLR229c CDC42 GTP-

binding protein of RAS superfamily, start by similarity · score=1

35. KLLA0A05643g: similar to sp|Q00246 Saccharomyces cerevisiae YKR055w RHO4 GTP-binding protein of the rho family, hypothetical start · score=1
36. KLLA0B05841g: highly similar to sp|P40989 Saccharomyces cerevisiae GR032w GSC2 1, 3-beta-D-glucan synthase subunit, start by similarity · score=1
37. KLLA0B07777g: similar to sp|P40319 Saccharomyces cerevisiae YLR372w SUR4 sterol isomerase, fatty acid elongase, start by similarity · score=1
38. KLLA0B10626g: gi|22858698|gb|AAN05733.1 Kluyveromyces lactis RHO1, start by similarity · score=1
39. KLLA0C03542g: similar to sp|P25358 Saccharomyces cerevisiae YCR034w GNS1 fatty acid elongase required for sphingolipid formation, start by similarity · score=1
40. KLLA0C08888g: similar to sp|O13423 Candida albicans Glucan synthase, start by similarity · score=1
41. KLLA0C13816g: highly similar to sp|P06781 Saccharomyces cerevisiae YNL090w RHO2 GTP-binding protein of the RHO subfamily of RAS-like proteins, start by similarity · score=1
42. KLLA0C14069g: similar to sp|Q04952 Saccharomyces cerevisiae YMR306w FKS3, start by similarity · score=1
43. KLLA0D08327g: similar to sp|P53879 Saccharomyces cerevisiae YNL180c RHO5, start by similarity · score=1
44. KLLA0E03597g: similar to sp|P32486 Saccharomyces cerevisiae YPR159w KRE6 glucan synthase subunit, start by similarity · score=1
45. KLLA0E23782g: highly similar to sp|Q12122 Saccharomyces cerevisiae YDL131w LYS21 homocitrate synthase, start by similarity · score=1
46. KLLA0F03443g: highly similar to sp|Q9HF51 Ashbya gossypii Rho3, start by similarity · score=1
47. KLLA0F05489g: highly similar to sp|Q12122 Saccharomyces cerevisiae YDL131w LYS21 homocitrate synthase, start by similarity · score=1
48. YALI0B13662g: similar to tr|Q96WY0 Emericella nidulans Rho3 GTPase, hypothetical start · score=1
49. YALI0B15752g: tr|Q9P8U2 Yarrowia lipolytica CDC42 GTP-binding protein of RAS superfamily, identified start · score=1
50. YALI0B20196g: similar to sp|P25358 Saccharomyces cerevisiae YCR034w GNS1 fatty acid elongase required for sphingolipid formation, hypothetical start · score=1
51. YALI0C01411g: similar to tr|Q9UVK9 Yarrowia lipolytica Fks1p, hypothetical start · score=1
52. YALI0C01639g: pseudogene, similar to sp|Q06472 Saccharomyces cerevisiae Beta-glucan synthesis-associated protein (Killer toxin-resistance protein 6) and sp|P33336 Saccharomyces cerevisiae YGR143w SKN1 glucan synthase subunit, frameshift · score=1
53. YALI0C13530g: similar to sp|P06781 Saccharomyces cerevisiae YNL090w RHO2 GTP-binding protein of the RHO subfamily of RAS-like proteins, hypothetical start · score=1
54. YALI0C14190g: similar to sp|P33336 Saccharomyces cerevisiae YGR143w SKN1 glucan synthase subunit P2.4.f2.1 and sp|P32486 Saccharomyces cerevisiae YPR159w KRE6 glucan synthase subunit P2.4.f2.1 associated protein, hypothetical start · score=1
55. YALI0D01045g: tr|Q9HGU7 Yarrowia lipolytica GTP-binding protein Rho1, GTP-binding protein of the rho subfamily of ras-like proteins, identified start · score=1
56. YALI0E21021g: tr|Q9UVK9 Yarrowia lipolytica 1,3-beta-glucan synthase activity, identified start · score=1
57. YALI0E23001g: tr|Q9HGU7 Yarrowia lipolytica GTP-binding protein, identified start · score=1
58. YALI0F06754g: similar to ca|CA6061|IPF8302 Candida albicans hypothetical start · score=1
59. YALI0F17270g: similar to sp|Q00245 Saccharomyces cerevisiae YIL118w RHO3 GTP-binding protein of the rho family, hypothetical start · score=1
60. YALI0F31075g: sp|Q12726 Yarrowia lipolytica Homocitrate synthase, identified start · score=1
61. YCR034w: FEN1, Fatty acid elongase, involved in sphingolipid biosynthesis; acts on fatty acids of

up to 24 carbons in length; mutations have regulatory effects on 1,3-beta-glucan synthase, vacuolar ATPase, and the secretory pathway · score=1.00

62. YDL131w: LYS21, Homocitrate synthase isozyme, catalyzes the condensation of acetyl-CoA and alpha-ketoglutarate to form homocitrate, which is the first step in the lysine biosynthesis pathway; highly similar to the other isozyme, Lys20p · score=1.00
63. YDL182w: LYS20, Homocitrate synthase isozyme, catalyzes the condensation of acetyl-CoA and alpha-ketoglutarate to form homocitrate, which is the first step in the lysine biosynthesis pathway; highly similar to the other isozyme, Lys21p · score=1.00
64. YGR032w: GSC2, Catalytic subunit of 1,3-beta-glucan synthase, has similarity to an alternate catalytic subunit, Fks1p (Gsc1p); Rho1p encodes the regulatory subunit; involved in cell wall synthesis and maintenance · score=1.00
65. YGR143w: SKN1, Protein involved in sphingolipid biosynthesis; type II membrane protein with similarity to Kre6p · score=1
66. YIL118w: RHO3, Non-essential small GTPase of the Rho/Rac subfamily of Ras-like proteins involved in the establishment of cell polarity; GTPase activity positively regulated by the GTPase activating protein (GAP) Rgd1p · score=1
67. YJL196c: ELO1, Elongase I, medium-chain acyl elongase, catalyzes carboxy-terminal elongation of unsaturated C12-C16 fatty acyl-CoAs to C16-C18 fatty acids · score=1
68. YKR055w: RHO4, Non-essential small GTPase of the Rho/Rac subfamily of Ras-like proteins, likely to be involved in the establishment of cell polarity · score=1
69. YLR229c: CDC42, Small rho-like GTPase, essential for establishment and maintenance of cell polarity; mutants have defects in the organization of actin and septins · score=1
70. YLR342w: FKS1, Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling · score=1.00
71. YLR372w: SUR4, Elongase, involved in fatty acid and sphingolipid biosynthesis; synthesizes very long chain 20-26-carbon fatty acids from C18-CoA primers; involved in regulation of sphingolipid biosynthesis · score=1
72. YMR306w: FKS3, Protein of unknown function, has similarity to 1,3-beta-D-glucan synthase catalytic subunits Fks1p and Gsc2p · score=1.00
73. YNL090w: RHO2, Non-essential small GTPase of the Rho/Rac subfamily of Ras-like proteins, involved in the establishment of cell polarity and in microtubule assembly · score=1
74. YNL180c: RHO5, Non-essential small GTPase of the Rho/Rac subfamily of Ras-like proteins, likely involved in protein kinase C (Pkc1p)-dependent signal transduction pathway that controls cell integrity · score=1
75. YPR159w: KRE6, Protein required for beta-1,6 glucan biosynthesis; putative beta-glucan synthase; appears functionally redundant with Skn1p · score=1.00
76. YPR165w: RHO1, GTP-binding protein of the rho subfamily of Ras-like proteins, involved in establishment of cell polarity; regulates protein kinase C (Pkc1p) and the cell wall synthesizing enzyme 1,3-beta-glucan synthase (Fks1p and Gsc2p) · score=1.00

RNA genes for “+(glucan homocitrate) +synthase”

none found

Cis-active elements for “+(glucan homocitrate) +synthase”

none found

Protein families for “+(glucan homocitrate) +synthase”

1. GLC.36: 32-member family, sckdy (6 7 6 7 6)
2. GLR.15: 13-member family, sckdy (2 1 1 6 3)
3. GLR.23: 13-member family, sckdy (3 3 3 2 2)
4. GLR.3247: 13-member family, sckdy (3 3 2 3 2)
5. GLR.48: 9-member family, sckdy (2 2 2 2 1)

Center for Bioinformatics · Bordeaux
mail Webmaster@cbi.labri.fr

URL: http://cbi.labri.fr/Genolevures/concordance
Update: Monday, 1 August 2005