

This document contains the BLAST alignments for both sets of sequence data (one in which there is a mutation in ADE1 but not in ADE2, and one in which there is a mutation in ADE2 but not in ade1).

ADE1 BLASTN

>YAR015W ADE1 SGDID:S000000070 Chr I from 169370-170290, [Verified ORF](#), "N-succinyl-5-aminoimidazole-4-carboxamide ribotide (SAICAR) synthetase, required for 'de novo' purine nucleotide biosynthesis; red pigment accumulates in mutant cells deprived of adenine" [\[Retrieve Sequence / ORF Map / Genome Browser / SGD Locus page \]](#)

Length = 921

Score = 324.3 bits (2121), Expect = 6.3e-92, P = 6.3e-92, Identities = 425/426 (99%), Frame = +1 / +1

```
Query: 1   CGTAAAAACAGGTACTGTGCATGGTTTGAAACAACCTCAAGGACTTAAAGAATCTCAAGA 60
          |||
Sbjct: 399 CGTAAAAACAGGTACTGTGCATGGTTTGAAACAACCTCAAGGACTTAAAGAATCTCAAGA 458

Query: 61  GTTCCCAGAACCAATCTTCACCCCATCGACCAAGGCTGAACAAGGTGAACATGACGAAAA 120
          |||
Sbjct: 459 GTTCCCAGAACCAATCTTCACCCCATCGACCAAGGCTGAACAAGGTGAACATGACGAAAA 518

Query: 121 CATCTCTCCTGCCAGGCCGCTGAGCTGGTGGGTGAAGATTTGTCACGTAGAGTGGCAGA 180
          |||
Sbjct: 519 CATCTCTCCTGCCAGGCCGCTGAGCTGGTGGGTGAAGATTTGTCACGTAGAGTGGCAGA 578
```

Query: 181 ACTGGCTGTAAAACGTACTCCAAGTGCAAAGATTATGCTAAGGAGAAGGGCATCATCAT 240
|||||
Sbjct: 579 ACTGGCTGTAAAACGTACTCCAAGTGCAAAGATTATGCTAAGGAGAAGGGCATCATCAT 638

Query: 241 CGCAGACACTAAATTCGAATTCGGTATTGACGAAAAGACCAATGAAATTATTCTAGTGGA 300
|||||
Sbjct: 639 CGCAGACACTAAATTCGAATTCGGTATTGACGAAAAGACCAATGAAATTATTCTAGTGGA 698

Query: 301 CGAGGTGCTAACGCCAGACTCCTCTAGATTCTGGAACGGTGCCTCTTATAAGGTAGGAGA 360
|||||
Sbjct: 699 CGAGGTGCTAACGCCAGACTCCTCTAGATTCTGGAACGGTGCCTCTTATAAGGTAGGAGA 758

Query: 361 ATCCCAAGATTCTTACGATAAGCAATTTTAAAGAGACTGGCCTACTGCTAATAAGTTGAA 420
|||||
Sbjct: 759 ATCCCAAGATTCTTACGATAAGCAATTTTAAAGAGACTGGCCTACTGCTAATAAGTTGAA 818

Query: 421 CGGTGT 426
|||||
Sbjct: 819 CGGTGT 824

ADE1 BLASTP

>YAR015W ADE1 SGDID:S000000070 Chr I from 169370-170290, Verified ORF, "N-succinyl-5-aminoimidazole-4-carboxamide ribotide (SAICAR) synthetase, required for 'de novo' purine nucleotide biosynthesis; red pigment accumulates in mutant cells deprived of adenine" [Retrieve Sequence / ORF Map / Genome Browser / SGD Locus page]

Length = 307

Score = 259.9 bits (724), Expect = 2.6e-73, P = 2.6e-73 Identities = 140/141 (99%), Positives = 140/141 (99%)

Query: 1 VKTGTVHGLKQPQGLKESQEFPEPIFTPSTKAEQGEHDENISPAQAAELVGEDLSRRVAE 60
VKTGTVHGLKQPQGLKESQEFPEPIFTPSTKAEQGEHDENISPAQAAELVGEDLSRRVAE
Sbjct: 134 VKTGTVHGLKQPQGLKESQEFPEPIFTPSTKAEQGEHDENISPAQAAELVGEDLSRRVAE 193

Query: 61 LAVKLYSKCKDYAKEKGIIIADTKFEFGIDEKTNEIILVDEVLTPDSSRFWNGASYKVGE 120
LAVKLYSKCKDYAKEKGIIIADTKFEFGIDEKTNEIILVDEVLTPDSSRFWNGASYKVGE
Sbjct: 194 LAVKLYSKCKDYAKEKGIIIADTKFEFGIDEKTNEIILVDEVLTPDSSRFWNGASYKVGE 253

Query: 121 SQDSYDKQFLRDWPTANKLNG 141
SQDSYDKQFLRDW TANKLNG
Sbjct: 254 SQDSYDKQFLRDWLTANKLNG 274

ADE1 HUMAN HOMOLOG

>gi|119220559|ref|NP_001072993.1| UniGene infoGene info phosphoribosylaminoimidazole carboxylase,
phosphoribosylaminoimidazole succinocarboxamide synthetase isoform 1 [Homo sapiens]
Length=432

GENE ID: 10606 PAICS | phosphoribosylaminoimidazole carboxylase,
phosphoribosylaminoimidazole succinocarboxamide synthetase [Homo sapiens]
(Over 10 PubMed links)

Score = 57.8 bits (138), Expect = 4e-08
Identities = 57/257 (22%), Positives = 106/257 (41%), Gaps = 41/257 (15%)

```
Query 18  GKVRDIYEV--DAGTLLFVATDRISAYDVIMENSIPEKGILLTKLSEFWFKFLSNDVRNH 75
          GK +++YE+   G +L + D+I+A +   +N + K + K++ F+ L V ++
Sbjct 16  GKTKEVYELLDSPGKVLVLSQKDQITAGNAARKNHLEGKAAISNKITSCIFQLLQEAVTSY 75

Query 76  LVDIAPGKTIFDYLPAPKLEPKYKTQLEDRSLLVHKKHKLIPLEVIVRGYITGSAAWKEYVK 135
          + + + + + + + + ++IP+E + R TGS
Sbjct 76  -----KSNRIKTAFTRKCGETAFAIAPQCEMPIEWVCRRIATGSF----- 115

Query 136 TGTVHGLKQPQGLKESQEFPEP----IFTPSTKAEQGEHDENISPAQ---AAELVGEDLS 188
          LK+ G+KE +F P F + +E + A+ A L+G+
Sbjct 116 -----LKRNPGVKEGYKFYPPKVELFFKDDANNDPQWSEEQLIAAKFCFAGLLIGQTEV 169

Query 189 RRVAELAVKLYSKCKDYAKEKGI IADTKFEFGIDEKTNEI I LVDEVLTPDSSRFWNGAS 248
          ++ ++ + + + D K EFG+D T EI+L D V+ DS R W
Sbjct 170 DIMSHATQAI FEILEKSWLPQNCTLVDMKIEFGVDVTTKEIVLAD-VIDNDSWRLWPS-- 226

Query 249 YKVGESQDSYDKQFLRD 265
          G+ DKQ RD
Sbjct 227 ---GDRSQKDKQSYRD 240
```

ADE2 BLASTN

>**YOR128C** ADE2 SGDID:S000005654 Chr XV from 566192-564477, reverse complement, [Verified ORF](#),
"Phosphoribosylaminoimidazole carboxylase, catalyzes a step in the 'de novo' purine nucleotide biosynthetic pathway; red pigment accumulates in mutant cells deprived of adenine" [\[Retrieve Sequence / ORF Map / Genome Browser / SGD Locus page \]](#)

Length = 1,716

Score = 424.7 bits (2790), Expect = 2.0e-122, P = 2.0e-122 Identities = 558/558 (100%), Frame = +1 / +1

```
Query: 1   TTTACCCCTTCTCCAGAAACAATCAGATTGATACAAGACAAATATATTCAAAAAGAGCATT 60
          |||
Sbjct: 278 TTTACCCCTTCTCCAGAAACAATCAGATTGATACAAGACAAATATATTCAAAAAGAGCATT 337

Query: 61  TAATCAAAAATGGTATAGCAGTTACCCAAAGTGTTCCCTGTGGAACAAGCCAGTGAGACGT 120
          |||
Sbjct: 338 TAATCAAAAATGGTATAGCAGTTACCCAAAGTGTTCCCTGTGGAACAAGCCAGTGAGACGT 397

Query: 121 CCCTATTGAATGTTGGAAGAGATTTGGGTTTTCCATTCGTCTTGAAGTCGAGGACTTTGG 180
          |||
Sbjct: 398 CCCTATTGAATGTTGGAAGAGATTTGGGTTTTCCATTCGTCTTGAAGTCGAGGACTTTGG 457

Query: 181 CATACGATGGAAGAGGTAACCTTCGTTGTAAAGAATAAGGAAATGATTCCGGAAGCTTTGG 240
          |||
Sbjct: 458 CATACGATGGAAGAGGTAACCTTCGTTGTAAAGAATAAGGAAATGATTCCGGAAGCTTTGG 517
```

Query: 241 AAGTACTGAAGGATCGTCCTTTGTACGCCGAAAAATGGGCACCATTTACTAAAGAATTAG 300
|||||

Sbjct: 518 AAGTACTGAAGGATCGTCCTTTGTACGCCGAAAAATGGGCACCATTTACTAAAGAATTAG 577

Query: 301 CAGTCATGATTGTGAGATCTGTTAACGGTTTAGTGTTTTCTTACCCAATTGTAGAGACTA 360
|||||

Sbjct: 578 CAGTCATGATTGTGAGATCTGTTAACGGTTTAGTGTTTTCTTACCCAATTGTAGAGACTA 637

Query: 361 TCCACAAGGACAATATTTGTGACTTATGTTATGCGCCTGCTAGAGTTCCGGACTCCGTTC 420
|||||

Sbjct: 638 TCCACAAGGACAATATTTGTGACTTATGTTATGCGCCTGCTAGAGTTCCGGACTCCGTTC 697

Query: 421 AACTTAAGGCGAAGTTGTTGGCAGAAAATGCAATCAAATCTTTTCCCGTTGTGGTATAT 480
|||||

Sbjct: 698 AACTTAAGGCGAAGTTGTTGGCAGAAAATGCAATCAAATCTTTTCCCGTTGTGGTATAT 757

Query: 481 TTGGTGTGAAATGTTCTATTTAGAAACAGGGGAATTGCTTATTAACGAAATGCCCCAA 540
|||||

Sbjct: 758 TTGGTGTGAAATGTTCTATTTAGAAACAGGGGAATTGCTTATTAACGAAATGCCCCAA 817

Query: 541 GGCCTCACAACCTCTGGAC 558
|||||

Sbjct: 818 GGCCTCACAACCTCTGGAC 835

ADE2 BLASTP

>YOR128C ADE2 SGDID:S000005654 Chr XV from 566192-564477, reverse complement, [Verified ORF](#), "Phosphoribosylaminoimidazole carboxylase, catalyzes a step in the 'de novo' purine nucleotide biosynthetic pathway; red pigment accumulates in mutant cells deprived of adenine" [\[Retrieve Sequence / ORF Map / Genome Browser / SGD Locus page \]](#)

Length = 572

Score = 341.2 bits (955), Expect = 8.5e-98, P = 8.5e-98 Identities = 185/185 (100%), Positives = 185/185 (100%)

Query: 1 YPSPETIRLIQDKYIQKEHLIKNGIAVTQSVPEQASETSLLNVGRDLGFPFVLKSRTLA 60
YPSPETIRLIQDKYIQKEHLIKNGIAVTQSVPEQASETSLLNVGRDLGFPFVLKSRTLA
Sbjct: 94 YPSPETIRLIQDKYIQKEHLIKNGIAVTQSVPEQASETSLLNVGRDLGFPFVLKSRTLA 153

Query: 61 YDGRGNFVVKNKEMIPeALEVLKDRPLYAEKWAPFTKELAVMIVRSVNGLVFSYPIVETI 120
YDGRGNFVVKNKEMIPeALEVLKDRPLYAEKWAPFTKELAVMIVRSVNGLVFSYPIVETI
Sbjct: 154 YDGRGNFVVKNKEMIPeALEVLKDRPLYAEKWAPFTKELAVMIVRSVNGLVFSYPIVETI 213

Query: 121 HKDNICDLCYAPARVPDSVQLKAKLLAENAIKSFPGCGIFGVEMFYLETGELLINEIAPR 180
HKDNICDLCYAPARVPDSVQLKAKLLAENAIKSFPGCGIFGVEMFYLETGELLINEIAPR
Sbjct: 214 HKDNICDLCYAPARVPDSVQLKAKLLAENAIKSFPGCGIFGVEMFYLETGELLINEIAPR 273

Query: 181 PHNSG 185
PHNSG
Sbjct: 274 PHNSG 278

ADE2 Human Homolog

>gi|119625894|gb|EAX05489.1| Gene info phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase, isoform CRA_a [Homo sapiens]
Length=451

GENE ID: 10606 PAICS | phosphoribosylaminoimidazole carboxylase,
phosphoribosylaminoimidazole succinocarboxamide synthetase [Homo sapiens]
(Over 10 PubMed links)

Score = 47.4 bits (111), Expect = 1e-04
Identities = 39/143 (27%), Positives = 66/143 (46%), Gaps = 4/143 (2%)

```
Query 405 VGIIMGSDSDLPVMSAACAVLKDFGVPPFEVTIVSAHRTPHRMSAYAISASKRGIKTI-IA 463
          V ++MGS SDL +FG+P E+ + SAH+ P GI T+ +A
Sbjct 294 VVVLMSGSTSDLGHCEKIKKACGNFGIPCELRV TSAHKGPDETLRIKA EYEGDGIPTVFVA 353

Query 464 GAGGAAHLPGMVAAMTPLPVIGVPVKGSCLDGVDSLHSIVQMPRGVPVATVAINNSTNAA 523
          AG + L +++ T PVI P GV + S +++P G+ +TV + +A
Sbjct 354 VAGRSNGLGPVMSGNTAYPVISCPPLTPDW-GVQDVWSSRLRPSGLGCSTVL--SPEGSA 410

Query 524 LLAVRLLGAYDSSYTTKMEQFLL 546
          A ++ G + +K+ +L
Sbjct 411 QFAAQIFGLSNHLVWVSKLRASIL 433
```


ADE1 BLASTN

>YAR015W ADE1 SGDID:S000000070 Chr I from 169370-170290,
Verified ORF, "N-succinyl-5-aminoimidazole-4-carboxamide ribotide (SAICAR) synthetase,
required for 'de novo' purine nucleotide biosynthesis; red pigment accumulates in mutant cells
deprived of adenine"
[Retrieve Sequence / ORF Map / Genome Browser / SGD Locus page]

Length = 921
Score = 405.9 bits (2665), Expect = 1.7e-116, P = 1.7e-116
Identities = 533/533 (100%), Frame = +1 / +1

```
Query: 12  ATGTCAATTACGAAGACTGAACTGGACGGTATATTGCCATTGGTGGCCAGAGGTAAAGTT 71
          |||
Sbjct: 1   ATGTCAATTACGAAGACTGAACTGGACGGTATATTGCCATTGGTGGCCAGAGGTAAAGTT 60

Query: 72  AGAGACATATATGAGGTAGACGCTGGTACGTTGCTGTTTGTGCTACGGATCGTATCTCT 131
          |||
Sbjct: 61  AGAGACATATATGAGGTAGACGCTGGTACGTTGCTGTTTGTGCTACGGATCGTATCTCT 120

Query: 132 GCATATGACGTTATTATGGAAAACAGCATTCCGAAAAGGGGATCCTATTGACCAAACG 191
          |||
Sbjct: 121 GCATATGACGTTATTATGGAAAACAGCATTCCGAAAAGGGGATCCTATTGACCAAACG 180

Query: 192 TCAGAGTTCTGGTTCAAGTTCCTGTCCAACGATGTTTCGTAATCATTTGGTCGACATCGCC 251
          |||
Sbjct: 181 TCAGAGTTCTGGTTCAAGTTCCTGTCCAACGATGTTTCGTAATCATTTGGTCGACATCGCC 240

Query: 252 CCAGGTAAGACTATTTTCGATTATCTACCTGCAAAATTGAGCGAACCAAAGTACAAAACG 311
          |||
Sbjct: 241 CCAGGTAAGACTATTTTCGATTATCTACCTGCAAAATTGAGCGAACCAAAGTACAAAACG 300

Query: 312 CAACTAGAAGACCGCTCTCTATTGGTTCACAAACATAAACTAATTCCATTGGAAGTAATT 371
          |||
Sbjct: 301 CAACTAGAAGACCGCTCTCTATTGGTTCACAAACATAAACTAATTCCATTGGAAGTAATT 360

Query: 372 GTCAGAGGCTACATCACCGGATCTGCTTGGAAAGAGTACGTAAAAACAGGTACTGTGCAT 431
          |||
Sbjct: 361 GTCAGAGGCTACATCACCGGATCTGCTTGGAAAGAGTACGTAAAAACAGGTACTGTGCAT 420
```

Query: 432 GGTTTGAAACAACCTCAAGGACTTAAAGAATCTCAAGAGTTCCCAGAACCAATCTTCACC 491
|||
Sbjct: 421 GGTTTGAAACAACCTCAAGGACTTAAAGAATCTCAAGAGTTCCCAGAACCAATCTTCACC 480

Query: 492 CCATCGACCAAGGCTGAACAAGGTGAACATGACGAAAACATCTCTCCTGCCCA 544
|||
Sbjct: 481 CCATCGACCAAGGCTGAACAAGGTGAACATGACGAAAACATCTCTCCTGCCCA 533

ADE1 BLASTP

>YAR015W ADE1 SGDID:S000000070 Chr I from 169370-170290,
Verified ORF, "N-succinyl-5-aminoimidazole-4-carboxamide ribotide (SAICAR) synthetase,
required for 'de novo' purine nucleotide biosynthesis; red pigment accumulates in mutant cells
deprived of adenine"

[Retrieve Sequence / ORF Map / Genome Browser / SGD Locus page]

Length = 307

Score = 326.5 bits (913), Expect = 2.4e-93, P = 2.4e-93
Identities = 177/177 (100%), Positives = 177/177 (100%)

Query: 4 MSITKTELDGILPLVARGKVRDIYEVDAGTLLFVATDRISAYDVIMENSIPEKGILLTKL 63
MSITKTELDGILPLVARGKVRDIYEVDAGTLLFVATDRISAYDVIMENSIPEKGILLTKL
Sbjct: 1 MSITKTELDGILPLVARGKVRDIYEVDAGTLLFVATDRISAYDVIMENSIPEKGILLTKL 60

Query: 64 SEFWFKFLSNDVRNHLVDIAPGKTIFDYLPKLSPEPKYKTQLEDRSLLVHKHKLIPILEVI 123
SEFWFKFLSNDVRNHLVDIAPGKTIFDYLPKLSPEPKYKTQLEDRSLLVHKHKLIPILEVI
Sbjct: 61 SEFWFKFLSNDVRNHLVDIAPGKTIFDYLPKLSPEPKYKTQLEDRSLLVHKHKLIPILEVI 120

Query: 124 VRGYITGSAWKEYVKTGTVHGLKQPQGLKESQEFPEPIFTPSTKAEQGEHDENISPA 180
VRGYITGSAWKEYVKTGTVHGLKQPQGLKESQEFPEPIFTPSTKAEQGEHDENISPA
Sbjct: 121 VRGYITGSAWKEYVKTGTVHGLKQPQGLKESQEFPEPIFTPSTKAEQGEHDENISPA 177

ADE1 Human homolog

>gi|119220559|ref|NP_001072993.1| UniGene infoGene info phosphoribosylaminoimidazole
carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase isoform 1 [Homo
sapiens]
Length=432

GENE ID: 10606 PAICS | phosphoribosylaminoimidazole carboxylase,
phosphoribosylaminoimidazole succinocarboxamide synthetase [Homo sapiens]
(Over 10 PubMed links)

Score = 57.8 bits (138), Expect = 4e-08
Identities = 57/257 (22%), Positives = 106/257 (41%), Gaps = 41/257 (15%)

```
Query 18  GKVRDIYEV--DAGTLLFVATDRISAYDVIMENSIPEKGILLTKLSEFWFKFLSNDVRNH 75
          GK +++YE+   G +L  + D+I+A +   +N + K  + K++  F+ L  V ++
Sbjct 16  GKTKEVYELLDSPGKVLLQSKDQITAGNAARKNHLEGKAAISNKITSCIFQLLQEAVTSY 75

Query 76  LVDIAPGKTIFDYLPACLSEPKYKTQLEDRLVHKKHKLIPLEVIVRGYITGSWKEYVK 135
          +   +   +   +   +   +   +   +   +   +   +   +   +   +   +
Sbjct 76  -----KSNRIKTAFTTRKCGETAFAIAPQCEMPIEWVCRRIATGSF----- 115

Query 136 TGTVHGLKQPQGLKESQEFPEP----IFTPSTKAEQGEHDENISPAQ---AAELVGEDLS 188
          LK+  G+KE  +F  P   F   +   +E +  A+  A  L+G+
Sbjct 116  -----LKRNPGVKEGYKFYPPKVELFFKDDANNDPQWSEEQLIAAKFCFAGLLIGQTEV 169

Query 189 RRVAELAVKLYSKCKDYAKEKGIIIADTKFEFGIDEKTNEIILVDEVLTPDSSRFWNGAS 248
          ++   ++   +   +   +  D K  EFG+D  T  EI+L  D  V+  DS  R  W
Sbjct 170 DIMSHATQAI FEILEKSWLPQNCTLVDMKIEFGVDVTTKEIVLAD-VIDNDSWRLWPS-- 226

Query 249 YKVGESQDSYDKQFLRD 265
          G+   DKQ  RD
Sbjct 227 ---GDRSQQKDKQSYRD 240
```

ADE2 edited sequence file BLASTN:

>YOR128C ADE2 SGDID:S000005654 Chr XV from 566192-564477, reverse complement,
Verified ORF, "Phosphoribosylaminoimidazole carboxylase, catalyzes a step in the 'de novo'
purine nucleotide biosynthetic pathway; red pigment accumulates in mutant cells deprived of
adenine"

[Retrieve Sequence / ORF Map / Genome Browser / SGD Locus page]

Length = 1,716

Score = 467.6 bits (3076), Expect = 2.5e-135, P = 2.5e-135
Identities = 616/617 (99%), Frame = +1 / +1

```
Query: 1   GTTGAGGCAGCAAACAGGCTCAACATTAAGACGGTAATACTAGATGCTGAAAATTCTCCT 60
          |||
Sbjct: 55   GTTGAGGCAGCAAACAGGCTCAACATTAAGACGGTAATACTAGATGCTGAAAATTCTCCT 114

Query: 61   GCCAAACAAATAAGCAACTCCAATGACCACGTTAATGGCTCCTTTTCCAATCCTCTTGAT 120
          |||
Sbjct: 115  GCCAAACAAATAAGCAACTCCAATGACCACGTTAATGGCTCCTTTTCCAATCCTCTTGAT 174

Query: 121  ATCGAAAACACTAGCTTAAAAATGTGATGTGCTAACGATTGAGATTGAGCATGTTGATGTT 180
          |||
Sbjct: 175  ATCGAAAACACTAGCTGAAAAATGTGATGTGCTAACGATTGAGATTGAGCATGTTGATGTT 234

Query: 181  CCTACACTAAAGAATCTTCAAGTAAAAACATCCCAAATTAATAATTTACCCTTCTCCAGAA 240
          |||
Sbjct: 235  CCTACACTAAAGAATCTTCAAGTAAAAACATCCCAAATTAATAATTTACCCTTCTCCAGAA 294

Query: 241  ACAATCAGATTGATACAAGACAAATATATTCAAAAAGAGCATTTAATCAAAAATGGTATA 300
          |||
Sbjct: 295  ACAATCAGATTGATACAAGACAAATATATTCAAAAAGAGCATTTAATCAAAAATGGTATA 354

Query: 301  GCAGTTACCCAAAGTGTTCCTGTGGAACAAGCCAGTGAGACGTCCTATTGAATGTTGGA 360
          |||
Sbjct: 355  GCAGTTACCCAAAGTGTTCCTGTGGAACAAGCCAGTGAGACGTCCTATTGAATGTTGGA 414
Query: 361  AGAGATTTGGGTTTTCATTTCGTCCTGAAGTCGAGGACTTTGGCATACGATGGAAGAGGT 420
          |||
Sbjct: 415  AGAGATTTGGGTTTTCATTTCGTCCTGAAGTCGAGGACTTTGGCATACGATGGAAGAGGT 474
```

Query: 421 AACTTCGTTGTAAAGAATAAGGAAATGATTCCGGAAGCTTTGGAAGTACTGAAGGATCGT 480
|||
Sbjct: 475 AACTTCGTTGTAAAGAATAAGGAAATGATTCCGGAAGCTTTGGAAGTACTGAAGGATCGT 534

Query: 481 CCTTTGTACGCCGAAAAATGGGCACCATTTACTAAAGAATTAGCAGTCATGATTGTGAGA 540
|||
Sbjct: 535 CCTTTGTACGCCGAAAAATGGGCACCATTTACTAAAGAATTAGCAGTCATGATTGTGAGA 594

Query: 541 TCTGTTAACGGTTTAGTGTTTTCTTACCCAATTGTAGAGACTATCCACAAGGACAATATT 600
|||
Sbjct: 595 TCTGTTAACGGTTTAGTGTTTTCTTACCCAATTGTAGAGACTATCCACAAGGACAATATT 654

Query: 601 TGTGACTTATGTTATGC 617
|||
Sbjct: 655 TGTGACTTATGTTATGC 671

Ade2 protein, edited sequence file BLASTP

>YOR128C ADE2 SGDID:S000005654 Chr XV from 566192-564477, reverse complement,
Verified ORF, "Phosphoribosylaminoimidazole carboxylase, catalyzes a step in the 'de novo'
purine nucleotide biosynthetic pathway; red pigment accumulates in mutant cells deprived of
adenine"

[Retrieve Sequence / ORF Map / Genome Browser / SGD Locus page]

Length = 572

Score = 374.3 bits (1049), Expect = 9.3e-108, P = 9.3e-108
Identities = 204/205 (99%), Positives = 205/205 (100%)

Query: 1 VEAANRLNIKTVILDAENSPAKQISNSNDHVNGSFSNPLDIEKLAZKCDVLTIEIEHVDV 60
VEAANRLNIKTVILDAENSPAKQISNSNDHVNGSFSNPLDIEKLA+KCDVLTIEIEHVDV
Sbjct: 19 VEAANRLNIKTVILDAENSPAKQISNSNDHVNGSFSNPLDIEKLAEKCDVLTIEIEHVDV 78

Query: 61 PTLKNLQVKHPKPKLIYSPETIRLIQDKYIQKEHLIKNGIAVTQSVVVEQASETSLLNVG 120
PTLKNLQVKHPKPKLIYSPETIRLIQDKYIQKEHLIKNGIAVTQSVVVEQASETSLLNVG
Sbjct: 79 PTLKNLQVKHPKPKLIYSPETIRLIQDKYIQKEHLIKNGIAVTQSVVVEQASETSLLNVG 138

Query: 121 RDLGFPFVLKSRTLAYDGRGNFVVKNKEMIPAEVLKDRPLYAEKWAPFTKELAVMIVR 180
RDLGFPFVLKSRTLAYDGRGNFVVKNKEMIPAEVLKDRPLYAEKWAPFTKELAVMIVR
Sbjct: 139 RDLGFPFVLKSRTLAYDGRGNFVVKNKEMIPAEVLKDRPLYAEKWAPFTKELAVMIVR 198

Query: 181 SVNGLVFSYPIVETIHKDNICDLCY 205
SVNGLVFSYPIVETIHKDNICDLCY
Sbjct: 199 SVNGLVFSYPIVETIHKDNICDLCY 223

ADE2 Human homolog

>gi|119625894|gb|EAX05489.1| Gene info phosphoribosylaminoimidazole carboxylase,
phosphoribosylaminoimidazole
succinocarboxamide synthetase, isoform CRA_a [Homo
sapiens]
Length=451

GENE ID: 10606 PAICS | phosphoribosylaminoimidazole carboxylase,
phosphoribosylaminoimidazole succinocarboxamide synthetase [Homo sapiens]
(Over 10 PubMed links)

Score = 47.4 bits (111), Expect = 1e-04

Identities = 39/143 (27%), Positives = 66/143 (46%), Gaps = 4/143 (2%)

Query	405	VGIIMGSDSDLPVMSAACAVLKDFGVPFEVTIVSAHRTPHRMSAYAISASKRGIKTI-IA	463
		V ++MGS SDL +FG+P E+ + SAH+ P GI T+ +A	
Sbjct	294	VVVLMSGSTSDLGHCEKIKKACGNFGIPCELRVTSAHKGPDETLRIKAHEYEGDGIPTVFVA	353
Query	464	GAGGAAHLPGMVAAMTPLPVIGVPVKGSCLDGVDSLHSIVQMPRGVPVATVAINNSTNAA	523
		AG + L +++ T PVI P GV + S +++P G+ +TV + +A	
Sbjct	354	VAGRSNGLGPVMSGNTAYPVISCPPLTPDW-GVQDVWSSLRLPSGLGCSTVL--SPEGSA	410
Query	524	LLAVRLLGAYDSSYTTKMEQFLL	546
		A ++ G + +K+ +L	
Sbjct	411	QFAAQIFGLSNHLVWSKLRASIL	433