Title: GATA-type transcription factors play a vital role in radiation sensitivity of *Cryptococcus neoformans* by regulating the gene expression of specific amino acid permeases

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The GATA binding sites of *AAP4* and *AAP5* genes in *Cryptococcus neoformans*:

AAP4 gene (Genbank access number XM_012191441) spans H99 chromosome 1 (Genbank access number CP003820) from 1533591- 1536730. There are 4 GATA binding sites within 2 kb DNA sequence upstream of *AAP4* gene as highlighted.

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>gi|405117359|gb|CP003820.1|:1531591-1533591 Cryptococcus neoformans var.
grubii H99 chromosome 1, complete sequence
TTTCTATGCCCATCTACAGCACCTTGTTGTTCAGAATACGGGTACTGTGGAACAGATGGCTACTGTCTGG
GAGGTTGTGAGCCACTGTGTAAGCCAACTATAGCTATCTATGGGTGGTGATGTAGCTGACAGGATGCAGA
CTCCCACGAAGTCACTTCATGCCGGCCAGATCCTATCTGTACTTCCTTCAAGACAGACTTCACTGACCTT
AGCAGGGTTCAACAGAATGTATCTCTGTACGACGGTAATGCCACAGCGTACGATTGGGTTGGTGAGTACG
ATGGAAAATGTCTGCTCCAGGCTGTGCTAAAACCTGTCAGTTAACACGGGATCCCTGATCGCTTCATCCG
ATAATGATGGAGCTCGTCTCATCCTAACCCAGAATAACACTGGTTCCAAAATATCTAGTACCCGTTACCT
CCATTACGGAACTATCGACTTTACTTTGCAGACGTCAAAATGGGCCGGTGTGGTGACAGCAGCAATCACA
ATGTCCGACGTCAAGGATGAAATAGATTGGGAATGGCCTGGGGCTAATACCGATACGGTGCAGACAAACT
ATTGGTTCTTGGGTATTGCAAACTGTAAGCAGCAAGTGCCGAGATAATTAGCTGATAATAGACTCGGCGA
CGGAGGGTGCTTCCAGCTCGGTGTCTTCTGATACGGCTGCCCACTTTCACACCTACACTGTAAATATTAA
TGGAGTGACGTAGCGTTCGACTGACCCAATGACAGATTGACTGGCAAGAGAGTTACATCAGTTGGAGTAT
TGACGGGTTACTTGTTCGTACAGTCAGGAAGACAGATACCATTTCTGAAGACGGGACACAGTAGTAAGCA
AGCCTCTCACTCATCTCATAACATAGCAGTACAGAACAAAGGCTTGTAGATCTGACGTTTCTGCAGTAAA
TTCCCCTCCACTCCATCTCGTGTTCAAATCTCCATTTGGCCCGCTGGCACAGACGGCAATGCTCAGGGCA
CTATCGATTGGGCGGGTGGCTACATCGATTGGACAGATAATGACTACCTGTCCAAGGGGTATTTCTGGAA
CACCATCAAGAGTGTCAATATCAGCTGCGCATATGACACTGCTTCTTCTGGGGCGACAGGCTGGGCTTAC
TCTGGAAATGATACATCGGGGATACCGGTGAGTCCAACAATCTCATTTTCTTTTCCCTATTACTCCCTCT
CGTTCAACCGAGGCGACGACGAACAAGGAAAGTTAACGAGAGATGTTGACGTTTTATCATTTATCTCAGA
TTGTGACCACTACCAATGCGTCAACTCTGATCTCCGCCGGAAGGAAGAGAATTGTAGGAGTCGAGATCAA
TAGTCGAGGGATGGGTGGAGTGGGTCTGCTTATCATCAGTGGCTTTACATTGCTCGGAGGCGTAGCTCTC
ATCTAATCTTCTATGTCCGATGGTAACTGTACAGTGTTGAAAATTACGTATCTTTGCCATCGGTCGATGG
CGTTTGATTCAAAATAGATATGATATGAGATTTACCAAATTAGATCAATATGGGCCATTCATACTTATTA
ACCTGCTGGACGCTCGGAAAAAAGCATACGCATATTATGAATGACGGAGAAGAGGAGGCGAGCAATATAC
TTATATAAGTATAGTATGCCGTACATAGTGCATCAATCACCTTTACAGCCTCCCCACTCTTTCCCCCCAT
TCATAAAATGGTGAGCACACCATGTAAAATCATTAATTTCATTGTTTAGTTCGATAGTGATTTTGCTCTA
AATGTTCAATGATCTAATAGCAGTAATGAGTGCACGTAATATCTCAGTCTGATATCAGGGTTCAGCAGCT
GTGTAGCTGGCAGCCAAATGGGGCCAACAAGTTCCGCATGGGTAATGGTGACGGGTGACGGTGAATGAGC
GAAGCGGCATCATTTGTTCTCATTCTAGTCAGCGAAAATGACAAATGTCAGAAGCTAGAAGATGTATAAA
AAATACAAGTCACATTACTGAAAACTCACGAAGCTCCATTG
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AAP5 gene (Genbank access number XM_012191669) spans H99 chromosome 1 (Genbank access number CP003820) from 1424618-1422185 (Note the **minus** strand). There are 8 GATA binding sites within 2 kb DNA sequence upstream of *AAP5* gene as highlighted.

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>gi|405117359|gb|CP003820.1|:1420185-1422185 Cryptococcus neoformans var.
grubii H99 chromosome 1, complete sequence
AGATAACAGTTTTCATGACTGGCACAAAAGCAGACTCAACCGCCTACTTCATTCTCAGCACGGTTCCAGA
ATGTCTGTAATGAGCTCACAGAAATTTCAGTAACTGCTGGCCAAGCACGTAGCATATCTTGAAATTCACC
AAAGAAATGTTCTCTGTAGATATGCCGCGGGCAGACACAAATAGTATCAATATCAGACCCAGGGCCGTGA
ACACCGAGACTATGTACTAAGTTAGCCATTGAACTCGATATATCGAATTTACCCACCGATAAGAACCTGA
AGTATAGATTCGTCCACCAGCCTCTGAAGCTATTTTTTCTGACATGCCGAGTTTTATTGATACATCATGA
ACAAATTTAGCAACCAGCTGGGCGATATTTGAAAGCAATCGTTCTCTGCATCCAAATAAGCCTTCATCTT
CGCTTTTCCAGCTCAACGCAACATACCGAACCTTCCTTTCTTGATCAGATTCGAATTGATTCAGGGCCAC
AAGGTCCGCCATCAAAGCTTCACTAGACTTGATATCATTGGGCTTTGGAGGATCAGTCGTAATGGGAGGT
GTAACACCCAAGAACTTGACAGGCGGGTTACTGTTGTTCACTATCGTTAGTCTACACCAGGAATTGCCGC
TTCCAGACGGAATGACCAGCAATAGCACGCACGAAGTCATTGGTGTTTTCTGACAGATAGGAAGAACAAC
TCGGGGCTTGGAGTAAGACAGTCGAAATGAAGTTCGGTAATCGCAAGAGCCCAGTCGTGAAATAATTTGG
TATTCGGTGCTCAAATTCTTTGCAGCTACGTCAATTAGGTGCTGTACATCAATTGCTGATTCTTGATTAT
GAAGAAATGTAGAGATCAAGAAGCAACTAGAGATACGATACGTAAAGCACAAAGAACACCTTAGACGCTG
TTGTATCCTCGGTGGCAGTCGGAGTTATCCGCTGTGGCACTAATAATATGCAGCCGTGCTGGAGTCTCCT
CACCAGAGGAAAGGAGGCAAAACAATAGTTGTTCGTACCTTTTTAAGCATGATCCATTATACAAATTTGA
CGCCACTTATGTGTACGTGAGGGCCCGTTGTCCCTAGCGGACATCCACAGAGCTTTTTCTGCGCTCGTCC
TCTCTCTCACCCTCCACGAAGACTGACGGGGCCCGCCACCCGGCAACTAATAATAAAAGAAGCGCTCACC
GTACGCGCAGTAGAATTATCGTCACCCTTGTGCTCCCTTTTACCTGTAAGCCAAGCGGATCGCCCTTTGA
GCTAATTCTGGAGATTTATGATAAGCTCCTAGGAAAGAGGAAATGAGCAACGCGTTGATGCGAGGAGTAA
AAGCCGATGAGGACGAAGAAGAGAGGTGCGCCGAGCCGGATGTGTTGTTGTGAGGTTTGGGGAAGGTGCG
AATTCCCCGACTAAACAACATTCATCACTGCGGCCCAGCGGCAAGCTTCCATCGTTTACAATCCATTAAT
ACGTGACTATATATTTCTAAAACATAAGAGTTACTTTTACTAAAAACTGTTCTACTCCCAACCTAATCTA
ATCTTCCCTATCTTCATTCTTCGTCCATCTCTTCATTTCTTCCTGTTTTCTCTTACAATCCGACTTCCGT
TTGAGACGACCAGGAATTTAAATCAATCCCTCCCCCCACGGAAACAATAAGAAGCGGCGCTGGCCATGTG
AGCCCTGCTGCCCTCTTCTGCAGCGACCTGAGACACCAGCGTAGGACAAGGTCGCAGGATGACTTCCCCG
ATTCTCGCTTGTTGGCCGTAGTGTGGAGCGGGAGTTGTGCTGATGGACAGAGTTGTAAGACATTAGGTCA
ATGGACTTGTCGTAAGTGCGATGGTTCCACTGCGCAATATCATAATTGGCATCTCACTAGGCCCATTACT
AGGATGCATAGGTATATCTCATTCTGTGGACGCACGCCCATTTTGGGCCTCCTCCGATTAAGATACCTCA
TTAACCGACGCAGGCTCCTGAGTTTGGGTGCTTCGCGCTGC
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