

**A** Query Length=534

	Score	E
Sequences producing significant alignments:	(Bits)	Value
YER069W ARG5,6 SGDID:S000000871, Chr V from 295410-298001, Genome...	132	4e-33
YJL071W ARG2 SGDID:S000003607, Chr X from 306132-307856, Genome R...	47.8	3e-06

## B NAGS vs. ARG5/6

Aligned Length = 540    Gapped Segments = 7    Total Mismatches (including gaps) = 430  
Identities = 110 (20.6%)    Similarities = 94 (17.6%)

[illegible]

### C NAGS vs. ARG2

Aligned Length = 579   Gapped Segments = 13   Total Mismatches (including gaps) = 493  
Identities = 86 (15.0%)   Similarities = 88 (15.3%)

[illegible]

**Supplementary Figure S2.** Alignment of human NAGS with yeast *ARG2* and *ARG5/6*.

A, The results of a BLASTP search of SGD database using the human NAGS as query sequence. B, C, ClustalW alignments of human NAGS with yeast *ARG5/6* and *ARG2*, respectively. Similarities and conservative substitutions are shown by asterisks and dots, respectively.