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BLAT--the BLAST-like alignment tool

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#	Paper	IF	Citations
2323	Selected General References for Genome Databases and Browsers. 284-287		
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2305 Question 1 How does one find a gene of interest and determine that gene's structure? Once the gene has been located on the map, how does one easily examine other genes in that same region?. **2002**, 32, 9-17

2304 Question 2 How can sequence-tagged sites within a DNA sequence be identified?. **2002**, 32, 18-20

2303 Question 3 During a positional cloning project aimed at finding a human disease gene, linkage data have been obtained suggesting that the gene of interest lies between two sequence-tagged site markers. How can all the known and predicted candidate genes in this interval be identified? What

2302 Question 4 A user wishes to find all the single nucleotide polymorphisms that lie between two sequence-tagged sites. Do any of these single nucleotide polymorphisms fall within the coding region of a gene? Where can any additional information about the function of these genes be

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2298 Question 9 Are there ways to customize displays and designate preferences? Can tracks or features be added to displays by users on the basis of their own research?. **2002**, 32, 53-56

2297 Question 10 For a given protein, how can one determine whether it contains any functional domains of interest? What other proteins contain the same functional domains as this protein? How can one determine whether there is a similarity to other proteins, not only at the sequence level,

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