

**Standard BLASTP output for comparing Pub1 to the yeast proteome (from the NCBI blast server**

<https://blast.ncbi.nlm.nih.gov/Blast.cgi>; the lines for Pab1 are highlighted in yellow)

Select for downloading or viewing reports	Description	Max Score	Total Score	Query Coverage	E value	Per. Ident	Accession
Select seq ref NP_014382.1	<a href="#">Pub1p [Saccharomyces cerevisiae S288C]</a>	931	931	100 %	0.0	100.0 %	<a href="#">NP_014382.1</a>
Select seq ref NP_011954.1	<a href="#">Nam8p [Saccharomyces cerevisiae S288C]</a>	108	108	75 %	4e-26	29.65 %	<a href="#">NP_011954.1</a>
Select seq ref NP_009771.3	<a href="#">Ngr1p [Saccharomyces cerevisiae S288C]</a>	97.1	97.1	66 %	6e-22	27.67 %	<a href="#">NP_009771.3</a>
Select seq pdb 6R5K D	<a href="#">Chain D, Polyadenylate-binding protein, cytoplasmic and nuclear [Saccharomyces cerevisiae S288C]</a>	90.1	173	41 %	1e-19	26.60 %	<a href="#">6R5K_D</a>
Select seq ref NP_011092.1	<a href="#">polyadenylate-binding protein [Saccharomyces cerevisiae S288C]</a>	90.1	173	41 %	1e-19	26.60 %	<a href="#">NP_011092.1</a>
Select seq ref NP_011675.1	<a href="#">Nsr1p [Saccharomyces cerevisiae S288C]</a>	82.4	149	38 %	2e-17	26.09 %	<a href="#">NP_011675.1</a>
Select seq ref NP_014518.1	<a href="#">Hrp1p [Saccharomyces cerevisiae S288C]</a>	65.5	110	36 %	6e-12	26.04 %	<a href="#">NP_014518.1</a>
Select seq ref NP_116678.1	<a href="#">Pes4p [Saccharomyces cerevisiae S288C]</a>	58.5	58.5	20 %	1e-09	34.74 %	<a href="#">NP_116678.1</a>
Select seq ref NP_011879.1	<a href="#">Mip6p [Saccharomyces cerevisiae S288C]</a>	55.1	55.1	24 %	1e-08	30.28 %	<a href="#">NP_011879.1</a>

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**Standard BLASTP output for comparing Nam8 to the yeast proteome (as above)**

Select seq ref NP_011954.1	<a href="#">Nam8p [Saccharomyces cerevisiae S288C]</a>	106 7	106 7	100 %	0.0	100.0 0%	<a href="#">NP_0119 54.1</a>
Select seq ref NP_009771.3	<a href="#">Ngr1p [Saccharomyces cerevisiae S288C]</a>	189	189	67 %	2e- 53	30.28 %	<a href="#">NP_0097 71.3</a>
Select seq ref NP_014382.1	<a href="#">Pub1p [Saccharomyces cerevisiae S288C]</a>	78. 6	78. 6	35 %	4e- 16	34.03 %	<a href="#">NP_0143 82.1</a>
Select seq pdb 6R5K D	<a href="#">Chain D, Polyadenylate-binding protein, cytoplasmic and nuclear [Saccharomyces cerevisiae S288C]</a>	66. 6	66. 6	69 %	4e- 12	21.38 %	<a href="#">6R5K_D</a>
Select seq ref NP_011092.1	<a href="#">polyadenylate-binding protein [Saccharomyces cerevisiae S288C]</a>	66. 6	66. 6	69 %	5e- 12	21.38 %	<a href="#">NP_0110 92.1</a>
Select seq ref NP_014964.1	<a href="#">U2 snRNP complex subunit HSH49 [Saccharomyces cerevisiae S288C]</a>	53. 5	84. 3	63 %	1e- 08	23.81 %	<a href="#">NP_0149 64.1</a>
Select seq pdb 5LSB A	<a href="#">Chain A, Protein Hsh49 [Saccharomyces cerevisiae S288C]</a>	53. 1	85. 9	65 %	2e- 08	23.81 %	<a href="#">5LSB_A</a>
Select seq ref NP_014518.1	<a href="#">Hrp1p [Saccharomyces cerevisiae S288C]</a>	46. 2	130	24 %	1e- 05	38.89 %	<a href="#">NP_0145 18.1</a>
Select seq ref NP_011471.1	<a href="#">Rna15p [Saccharomyces cerevisiae S288C]</a>	40. 8	40. 8	14 %	4e- 04	29.87 %	<a href="#">NP_0114 71.1</a>

**Standard BLASTP output for comparing Ngr1 to the yeast proteome (as above)**

<u>Description</u>	<u>Max Score</u>	<u>Total Score</u>	<u>Query Cover</u>	<u>E value</u>	<u>Per. Ident</u>	<u>Accession</u>
Select seq ref NP_009771.3	<a href="#">Ngr1p [Saccharomyces cerevisiae S288C]</a>	1385	1385	100%	0.0	100.00% <a href="#">NP_009771.3</a>
Select seq ref NP_011954.1	<a href="#">Nam8p [Saccharomyces cerevisiae S288C]</a>	194	194	62%	1e-54	31.15% <a href="#">NP_011954.1</a>
Select seq ref NP_014382.1	<a href="#">Pub1p [Saccharomyces cerevisiae S288C]</a>	70.5	70.5	21%	3e-13	35.17% <a href="#">NP_014382.1</a>
Select seq ref NP_011092.1	<a href="#">polyadenylate-binding protein [Saccharomyces cerevisiae S288C]</a>	55.8	55.8	13%	1e-08	33.33% <a href="#">NP_011092.1</a>
Select seq pdb 6R5K D	<a href="#">Chain D, Polyadenylate-binding protein, cytoplasmic and nuclear [Saccharomyces cerevisiae S288C]</a>	55.8	55.8	13%	2e-08	33.33% <a href="#">6R5K_D</a>
Select seq ref NP_014518.1	<a href="#">Hrp1p [Saccharomyces cerevisiae S288C]</a>	44.7	44.7	11%	4e-05	30.49% <a href="#">NP_014518.1</a>
Select seq ref NP_014148.1	<a href="#">Nrd1 complex RNA-binding subunit [Saccharomyces cerevisiae S288C]</a>	43.9	43.9	10%	7e-05	32.86% <a href="#">NP_014148.1</a>
Select seq ref NP_011766.3	<a href="#">Rie1p [Saccharomyces cerevisiae S288C]</a>	40.0	40.0	10%	0.001	30.26% <a href="#">NP_011766.3</a>
Select seq ref NP_009819.1	<a href="#">Rgd1p [Saccharomyces cerevisiae S288C]</a>	28.1	28.1	11%	7.0	28.57% <a href="#">NP_009819.1</a>