

Group	Sub-group	Description	Redundancy	MW	Evalue	LTQx 1	LTQx 2	LTQx 3	LTQx 4	LTQx 5	LTQx 6	LTQx 7	Type
1	1.01	YHR174W ENO2 'Enolase II, a pl	-	46.8	-515.44476	134.0	146.0	148.0	146.0	172.0	166.0	168.0	Spectra
1	1.02	YGR254W ENO1 'Enolase I, a ph	-	46.7	-408.2716	100.0	109.0	105.0	110.0	120.0	117.0	122.0	Spectra
2	2.01	YGR192C TDH3 'Glyceraldehyde	-	35.6	-443.95404	101.0	112.0	111.0	117.0	121.0	124.0	122.0	Spectra
2	2.02	YJR009C TDH2 'Glyceraldehyde	-	35.7	-372.37628	95.0	101.0	105.0	115.0	109.0	98.0	99.0	Spectra
2	2.03	YJL052W TDH1 'Glyceraldehyde	-	35.6	-297.6118	68.0	79.0	78.0	85.0	71.0	84.0	83.0	Spectra
3	3.01	YAL038W CDC19 'Pyruvate kina	-	54.4	-380.46527	80.0	91.0	92.0	89.0	98.0	93.0	90.0	Spectra
3	3.02	YBL087C RPL23A 'Protein comp	2*	14.4	-46.771473	5.0	8.0	3.0	4.0	6.0	3.0	4.0	Spectra
3	3.03	YOR347C PYK2 'Pyruvate kinase	-	55.1	-22.56686	4.0	5.0	7.0	3.0	5.0	4.0	5.0	Spectra
4	4.01	YCR012W PGK1 '3-phosphoglyci	-	44.6	-330.4942	79.0	90.0	85.0	77.0	82.0	91.0	90.0	Spectra
5	5.01	YLR044C PDC1 'Major of three p	-	61.4	-382.53018	69.0	71.0	75.0	69.0	69.0	79.0	70.0	Spectra
5	5.02	YLR134W PDC5 'Minor isoform c	-	61.8	-234.60945	30.0	32.0	39.0	31.0	36.0	38.0	33.0	Spectra
5	5.03	YGR087C PDC6 'Minor isoform c	-	61.4	-115.29745	21.0	23.0	28.0	23.0	29.0	27.0	27.0	Spectra
6	6.01	YKL060C FBA1 'Fructose 1,6-bis	-	39.5	-386.50046	76.0	74.0	78.0	80.0	80.0	76.0	77.0	Spectra
7	7.01	YDR385W EFT2 'Elongation fact	2*	93.1	-399.65784	50.0	48.0	51.0	49.0	49.0	48.0	50.0	Spectra
7	7.02	YLR048W RPS0B 'Protein compo	-	27.9	-67.70055	8.0	9.0	8.0	9.0	8.0	7.0	7.0	Spectra
8	8.01	YER091C MET6 'Cobalamin-inde	-	85.7	-368.73746	54.0	52.0	50.0	47.0	46.0	57.0	43.0	Spectra
9	9.01	YOL086C ADH1 'Alcohol dehydro	-	36.7	-210.06001	48.0	46.0	47.0	56.0	55.0	50.0	59.0	Spectra
9	9.02	YMR303C ADH2 'Glucose-repres	-	36.6	-87.34199	17.0	20.0	21.0	29.0	29.0	29.0	28.0	Spectra
9	9.03	YMR083W ADH3 'Mitochondrial	-	40.3	-74.741035	9.0	9.0	5.0	9.0	7.0	6.0	6.0	Spectra
9	9.04	YBR145W ADH5 'Alcohol dehydi	-	37.5	-25.602282	5.0	4.0	3.0	6.0	6.0	5.0	3.0	Spectra
10	10.01	YLL024C SSA2 'ATP binding prot	-	69.3	-327.67297	41.0	33.0	38.0	31.0	38.0	41.0	35.0	Spectra
10	10.02	YAL005C SSA1 'ATPase involved	-	69.5	-305.5065	33.0	28.0	33.0	29.0	32.0	37.0	29.0	Spectra
10	10.03	YER103W SSA4 'Heat shock pro	-	69.5	-111.07699	12.0	12.0	14.0	12.0	16.0	15.0	12.0	Spectra
10	10.04	YJL034W KAR2 'ATPase involvec	-	74.3	-115.55334	10.0	13.0	12.0	9.0	8.0	11.0	12.0	Spectra
11	11.01	YBR118W TEF2 'Translational el	2*	49.9	-175.64958	42.0	37.0	39.0	44.0	44.0	42.0	40.0	Spectra
12	12.01	YDR050C TPI1 'Triose phosphate	-	26.7	-150.63466	34.0	38.0	39.0	46.0	42.0	42.0	42.0	Spectra
13	13.01	YHR183W GND1 '6-phosphogluc	-	53.4	-261.45218	35.0	33.0	35.0	33.0	37.0	34.0	33.0	Spectra
14	14.01	YDL185W TFP1 'Subunit A of the	-	118.4	-293.85382	31.0	34.0	38.0	32.0	30.0	34.0	27.0	Spectra
15	15.01	YLR355C ILV5 'Acetohydroxyaci	-	44.3	-209.51605	26.0	25.0	28.0	29.0	31.0	27.0	29.0	Spectra
16	16.01	YOR375C GDH1 'NADP(+)-depe	-	49.4	-240.86363	26.0	23.0	26.0	27.0	24.0	23.0	25.0	Spectra