

96 well plate position	Pri.SpotNo	Volume Ratio	Accession #	Protein ID	species	Score	Score MSMS	Pri. Area	Pri.Volume	Pri.PeakHeight	Pri.Slope	Pri.EqRadius	Pri.Xcoord
A1	549	-2.66	68475393	putative cobalamin-independent methionine synthase	Candida albicans SC5314	129	22	607	3.58E+05	1333	0.15	13.9	1141
D1	556	-1.69	68475393	putative cobalamin-independent methionine synthase	Candida albicans SC5314	155	54	1889	2.56E+06	3970	0.2	24.5	1255
E1	567	-1.36	68475393	putative cobalamin-independent methionine synthase	Candida albicans SC5314	203	117	1849	3.74E+06	5453	0.19	24.3	1298
F1	588	-1.01	68475393	putative cobalamin-independent methionine synthase	Candida albicans SC5314	232	112	1656	5.71E+06	9586	0.17	23	1356
G1	599	1.42	68475393	putative cobalamin-independent methionine synthase	Candida albicans SC5314	386	231	1866	8.99E+06	14236	0.14	24.4	1406
A2	698	1.37	68478032	putative protein disulfide isomerase	Candida albicans SC5314	79	22	472	6.99E+05	3279	0.22	12.3	489
C2	841	3.23	68480983	pyruvate decarboxylase	Candida albicans SC5314	331	208	905	5.45E+05	1096	0.14	17	1059
D2	842	3.44	68480983	pyruvate decarboxylase	Candida albicans SC5314	268	173	1305	1.43E+06	2074	0.07	20.4	1121
F2	863	2.43	68480983	pyruvate decarboxylase	Candida albicans SC5314	143	67	1781	2.12E+06	2273	0.09	23.8	1262
H2	866	2.58	68480983	pyruvate decarboxylase	Candida albicans SC5314	143	39	475	2.69E+05	979	0.12	12.3	698
A3	870	1.91	68480983	pyruvate decarboxylase	Candida albicans SC5314	95	41	1013	4.41E+05	945	0.28	18	746
C3	872	2.69	68480983	pyruvate decarboxylase	Candida albicans SC5314	340	188	1548	1.84E+06	2003	0.06	22.2	1175
D3	877	2.96	68480983	pyruvate decarboxylase	Candida albicans SC5314	335	182	873	1.05E+06	2272	0.07	16.7	1236
E3	882	2.64	68480983	pyruvate decarboxylase	Candida albicans SC5314	247	155	728	1.02E+06	2555	0.06	15.2	1155
F3	884	1.07	56199748 68486010	60kDa chaperonin and heat shock protein 60	Candida albicans SC5314	89	26	1396	2.22E+06	5783	0.16	21.1	887

G3	892	1.3	68486010	heat shock protein 60	Candida albicans SC5314	130	25	1125	2.71E+06	8959	0.22	18.9	920
H3	894	3.32	68480983	pyruvate decarboxylase	Candida albicans SC5314	340	216	654	8.96E+05	2629	0.09	14.4	1218
A4	904	2.79	68480983	pyruvate decarboxylase	Candida albicans SC5314	329	220	654	5.02E+05	1396	0.1	14.4	1076
B4	910	3.05	68480983	pyruvate decarboxylase	Candida albicans SC5314	485	300	436	4.87E+05	2324	0.2	11.8	1120
C4	911	2.73	68480983	pyruvate decarboxylase	Candida albicans SC5314	393	234	959	2.02E+06	3575	0.07	17.5	1139
D4	914	3.22	68480983	pyruvate decarboxylase	Candida albicans SC5314	406	266	1082	1.91E+06	3257	0.09	18.6	1202
E4	950	1.64	68481416	tentative match to aldehyde dehydrogenase	Candida albicans SC5314	73	24	1102	8.66E+05	1833	0.12	18.7	1443
F4	1207	1.9	68485502	mitochondrial F1F0 ATPase subunit beta	Candida albicans SC5314	186	83	1491	1.84E+06	4902	0.22	21.8	724
A5	1385	-1.5	68499516	hypothetical protein CaO19.395- (appears to be related to enolase)	Candida albicans SC5314	191	105	1632	1.22E+07	17340	0.12	22.8	1252
B5	1444	-2.53	68499516	hypothetical protein CaO19.395- (appears to be related to enolase)	Candida albicans SC5314	407	251	917	1.04E+06	1718	0.08	17.1	1213
C5	1470	-2.36	68467815	hypothetical protein CaO19.11480- appears to be the same as or highly related to alcohol dehydrogeanse	Candida albicans SC5314	116	44	1152	1.04E+06	1792	0.09	19.1	937
D5	1489	1.58		keratin contaminant				891	5.40E+05	1785	0.57	16.8	677
E5	1492	-2.22	68468132 68467815	hypothetical protein CaO19_3997 and the highly related hypothetical protein CaO19.11480- also appears to be the same as or highly related to alcohol dehydrogeanse	Candida albicans SC5314	98	28	1772	2.13E+06	2257	0.1	23.7	1041
F5	1495	-2.04	68468132 68467815	hypothetical protein CaO19_3997 and the highly related hypothetical protein CaO19.11480- also appears to be the same as or highly related to alcohol dehydrogeanse	Candida albicans SC5314	483	309	2275	3.72E+06	3633	0.1	26.9	1164

G5	1504	-1.47	68468132 68467815	hypothetical protein CaO19_3997 and the highly related hypothetical protein CaO19.11480- also appears to be the same as or highly related to alcohol dehydrogeanse Candida albicans	Candida albicans SC5314	129	24	1367	5.67E+06	7732	0.07	20.9	1280
H5	1510	1.51	68468132 68467815 576627	hypothetical protein CaO19_3997 and the highly related hypothetical protein CaO19.11480- also appears to be the same as or highly related to alcohol dehydrogeanse Candida albicans	Candida albicans SC5314	498	362	1954	2.57E+07	31848	0.19	24.9	1584
A6	1580	-1.76	68482001	putative cytosilic ribosomal protein L4	Candida albicans SC5314	112	43	888	3.41E+05	978	0.15	16.8	707
B6	1581	-1.73	68484035	putative mitochondrial ketol-acid reducoisomerase	Candida albicans SC5314	212	121	2465	2.89E+06	3165	0.12	28	979
C6	1588	-1.5	68484035	putative mitochondrial ketol-acid reducoisomerase	Candida albicans SC5314	481	347	2121	6.78E+06	11454	0.12	26	1053
F6	1596	1.67	68468132 68467815 576627	hypothetical protein CaO19_3997 and the hihgly related hypothetical protein CaO19.11480- also appears to be the same as or highly related to alcohol dehydrogeanse Candida albicans	Candida albicans SC5314	301	171	1313	1.99E+06	3730	0.14	20.4	1575
B7	1680	-1.73	68466416	fructose-bisphosphate aldolase	Candida albicans SC5314	138	26	2101	2.49E+07	29140	0.14	25.9	1703
E7	1686	-2.53	68466416	tentative match to fructose-bisphosphate aldolase	Candida albicans SC5314	74	no MSMS	832	4.62E+06	10568	0.1	16.3	1588
G7	1691	-3.97		keratin contaminant				1251	1.69E+06	2752	0.07	20	1496
A8	1697	-2.17	68466416	tentative match to fructose-bisphosphate aldolase	Candida albicans SC5314	70	no MSMS	877	3.90E+06	7949	0.07	16.7	1610
B8	1758	1.84	68472462	tentative match to glyceraldehyde-3-phosphate dehydrogenase	Candida albicans SC5314	70	20	452	3.17E+05	1257	0.13	12	348
C8	1798	-2.34	68466416	fructose-bisphosphate aldolase	Candida albicans SC5314	539	377	1476	1.78E+06	1993	0.12	21.7	1763
H8	2143	1.26	68470024	phosphoglycerate mutase	Candida albicans SC5314	134	30	1344	1.90E+06	3758	0.12	20.7	552
A9	2149	-1.18	68470024	phosphoglycerate mutase	Candida albicans SC5314	142	45	1660	1.50E+06	2132	0.11	23	485

B9	2151	1.83	68470024	phosphoglycerate mutase	Candida albicans SC5314	92	13	1182	1.51E+06	3169	0.11	19.4	620
D9	2190	-2.06	68470024	phosphoglycerate mutase	Candida albicans SC5314	117	24	1859	4.96E+06	7283	0.11	24.3	1595
			7270988	triosephosphate isomerase [Candida albicans] - and the same/highly realted hyothetical protein CaO19_14037 [Candida albicans SC5314]	Candida albicans SC5314	199	125	1921	1.00E+07	13560	0.14	24.7	1466
E9	2208	-1.44	68470024	phosphoglycerate mutase	Candida albicans SC5314	148	58						
A10	2277	2.38	68476166	hypothetical protein CaO19_10778	Candida albicans SC5314	109	63	1632	7.63E+05	1899	0.15	22.8	193
C10	2293	1.42	68479826	putative thioredoxin peroxidase	Candida albicans SC5314	148	92	639	4.31E+05	995	0.13	14.3	815
D10	2300	-2.26	68479826	putative thioredoxin peroxidase	Candida albicans SC5314	103	57	615	7.15E+05	3284	0.17	14	812

Pri.Ycoord	Sec.SpotNo	Sec.Area	Sec.Volume	Sec.PeakHeight	Sec.Slope	Sec.EqRadius	Sec.Xcoord	Sec.Ycoord	Abundance	Pick	Status	Exclude
263	549	607	127953	361	0.1	13.9	1141	263	DECREASED	Yes	Confirmed	Included
260	556	1889	1445892	1750	0.14	24.5	1255	260	DECREASED	Yes	Confirmed	Included
262	567	1849	2628577	3237	0.17	24.3	1298	262	SIMILAR	Yes	Confirmed	Included
266	588	1656	5369412	8685	0.17	23	1356	266	SIMILAR	Yes	Confirmed	Included
269	599	1866	12179662	21577	0.16	24.4	1406	269	SIMILAR	Yes	Confirmed	Included
326	698	472	913597	4082	0.21	12.3	489	326	SIMILAR	Yes	Confirmed	Included
388	841	905	1677982	3494	0.09	17	1059	388	INCREASED	Yes	Confirmed	Included
382	842	1305	4671474	7597	0.08	20.4	1121	382	INCREASED	Yes	Confirmed	Included
386	863	1781	4912654	5586	0.07	23.8	1262	386	INCREASED	Yes	Confirmed	Included
392	866	475	661591	2446	0.14	12.3	698	392	INCREASED	Yes	Confirmed	Included
390	870	1013	803306	1375	0.36	18	746	390	INCREASED	Yes	Confirmed	Included
386	872	1548	4721901	4909	0.05	22.2	1175	386	INCREASED	Yes	Confirmed	Included
389	877	873	2953007	6305	0.09	16.7	1236	389	INCREASED	Yes	Confirmed	Included
389	882	728	2571864	6129	0.05	15.2	1155	389	INCREASED	Yes	Confirmed	Included
395	884	1396	2258900	5708	0.15	21.1	887	395	SIMILAR	Yes	Confirmed	Included

398	892	1125	3348280	11942	0.24	18.9	920	398	SIMILAR	Yes	Confirmed	Included
391	894	654	2834722	7867	0.1	14.4	1218	391	INCREASED	Yes	Confirmed	Included
395	904	654	1336090	3386	0.07	14.4	1076	395	INCREASED	Yes	Confirmed	Included
403	910	436	1417126	6397	0.17	11.8	1120	403	INCREASED	Yes	Confirmed	Included
394	911	959	5244502	9338	0.07	17.5	1139	394	INCREASED	Yes	Confirmed	Included
394	914	1082	5853533	10547	0.08	18.6	1202	394	INCREASED	Yes	Confirmed	Included
420	950	1102	1356077	2797	0.13	18.7	1443	420	INCREASED	Yes	Unconfirmed	Excluded
535	1207	1491	3332029	7571	0.22	21.8	724	535	INCREASED	Yes	Confirmed	Included
601	1385	1632	7718409	12837	0.12	22.8	1252	601	DECREASED	Yes	Confirmed	Included
643	1444	917	392944	638	0.08	17.1	1213	643	DECREASED	Yes	Confirmed	Included
647	1470	1152	422102	796	0.11	19.1	937	647	DECREASED	Yes	Confirmed	Included
655	1489	891	811304	3116	0.32	16.8	677	655	INCREASED	Yes	Confirmed	Excluded
657	1492	1772	916962	816	0.09	23.7	1041	657	DECREASED	Yes	Confirmed	Included
655	1495	2275	1733427	1657	0.13	26.9	1164	655	DECREASED	Yes	Confirmed	Included

657	1504	1367	3679328	5617	0.07	20.9	1280	657	SIMILAR	Yes	Confirmed	Included
658	1510	1954	37032008	46758	0.24	24.9	1584	658	INCREASED	Yes	Confirmed	Included
694	1580	888	184334	531	0.13	16.8	707	694	DECREASED	Yes	Unconfirmed	Excluded
693	1581	2465	1593830	1512	0.12	28	979	693	DECREASED	Yes	Confirmed	Included
695	1588	2121	4295459	7524	0.12	26	1053	695	DECREASED	Yes	Confirmed	Included
697	1596	1313	3169515	6689	0.19	20.4	1575	697	INCREASED	Yes	Confirmed	Included
750	1680	2101	13732764	18355	0.13	25.9	1703	750	DECREASED	Yes	Confirmed	Included
757	1686	832	1737376	3777	0.09	16.3	1588	757	DECREASED	Yes	Confirmed	Included
754	1691	1251	406471	751	0.11	20	1496	754	DECREASED	Yes	Confirmed	Included
758	1697	877	1715163	3579	0.08	16.7	1610	758	DECREASED	Yes	Confirmed	Included
784	1758	452	556551	2261	0.15	12	348	784	INCREASED	Yes	Confirmed	Included
795	1798	1476	725395	671	0.15	21.7	1763	795	DECREASED	Yes	Confirmed	Included
1057	2143	1344	2287347	4748	0.12	20.7	552	1057	SIMILAR	Yes	Confirmed	Included
1054	2149	1660	1208593	1863	0.1	23	485	1054	SIMILAR	Yes	Confirmed	Included

1062	2151	1182	2629926	5541	0.14	19.4	620	1062	INCREASED	Yes	Confirmed	Included
1074	2190	1859	2296686	2888	0.08	24.3	1595	1074	DECREASED	Yes	Confirmed	Included
1079	2208	1921	6635551	8876	0.09	24.7	1466	1079	SIMILAR	Yes	Confirmed	Included
1180	2277	1632	1733025	4318	0.14	22.8	193	1180	INCREASED	Yes	Confirmed	Included
1210	2293	639	581497	2644	0.18	14.3	815	1210	SIMILAR	Yes	Confirmed	Included
1223	2300	615	301316	554	0.11	14	812	1223	DECREASED	Yes	Confirmed	Included