

**Supplementary Table S3.** Protein peptide table with BLAST (Basic Local Alignment Search Tool) of Forty-two differentially expressed proteins in *Orbicella faveolata*

<b>Spot 1.</b>	<b>Heat shock protein sp H16.2</b>	<b>KJD18266.1</b>	<b>PEPTIDE SEQUENCES:</b>			<b>mslyhyfrpaqrs</b>
	Description	<u>Max score</u>	<u>Total score</u>	<u>E value</u>	<u>Ident</u>	Accession
Select seq gb AAL29201.1 AF3:	<a href="#">nuclear receptor AmNR8 [Acropora millepora]</a>	21.4	72.5	52	100%	<a href="#">AAL29201.1</a>
Select seq gb KJD18728.1	<a href="#">oxaloacetate decarboxylase subunit beta [Halomonas meridiar]</a>	22.3	115	29	71%	<a href="#">KJD18728.1</a>
Select seq gb ADI50284.1	<a href="#">galaxin-like 1 [Acropora millepora]</a>	22.3	167	29	70%	<a href="#">ADI50284.1</a>
Select seq gb AAC47388.1	<a href="#">Ub52 [Acropora millepora]</a>	23.1	72.3	14	69%	<a href="#">AAC47388.1</a>
Select seq gb KJD18996.1	<a href="#">2,3,4,5-tetrahydropyridine-2,6-carboxylate N-succinyltransfera</a>	21.4	109	51	67%	<a href="#">KJD18996.1</a>
Select seq dbj BAQ19091.1	<a href="#">activin 1 protein [Acropora digitifera]</a>	21.8	139	38	65%	<a href="#">BAQ19091.1</a>
Select seq gb KJD20155.1	<a href="#">glucosamine--fructose-6-phosphate aminotransferase [Halomc</a>	21	176	71	58%	<a href="#">KJD20155.1</a>
Select seq gb KJD20155.1	<a href="#">glucosamine--fructose-6-phosphate aminotransferase [Halomc</a>	21	176	71	58%	<a href="#">KJD20155.1</a>
Select seq gb KJD17909.1	<a href="#">NADH oxidase [Halomonas meridiana]</a>	21.4	81.9	51	56%	<a href="#">KJD17909.1</a>
Select seq gb KJD18811.1	<a href="#">1-deoxy-D-xylulose-5-phosphate synthase [Halomonas meridia</a>	22.7	182	21	53%	<a href="#">KJD18811.1</a>
Select seq gb KJD18969.1	<a href="#">3-octaprenyl-4-hydroxybenzoate carboxy-lyase [Halomonas m</a>	20.6	96.5	95	53%	<a href="#">KJD18969.1</a>
Select seq gb KJD18969.1	<a href="#">3-octaprenyl-4-hydroxybenzoate carboxy-lyase [Halomonas m</a>	20.6	96.5	95	53%	<a href="#">KJD18969.1</a>
Select seq gb KJD20261.1	<a href="#">amino acid transporter [Halomonas meridiana]</a>	22.3	73.6	28	47%	<a href="#">KJD20261.1</a>
Select seq gb KJD18273.1	<a href="#">deoxyguanosinetriphosphate triphosphohydrolase [Halomona:</a>	20.6	110	94	43%	<a href="#">KJD18273.1</a>
Select seq gb KJD18273.1	<a href="#">deoxyguanosinetriphosphate triphosphohydrolase [Halomona:</a>	20.6	110	94	43%	<a href="#">KJD18273.1</a>
Select seq gb KJD18560.1	<a href="#">ABC transporter substrate-binding protein [Halomonas meridi</a>	22.3	105	28	42%	<a href="#">KJD18560.1</a>
Select seq dbj BAQ19137.1	<a href="#">mothers against decapentaplegic 6/7 [Acropora digitifera]</a>	21.4	117	52	41%	<a href="#">BAQ19137.1</a>
Select seq gb ADG44979.1	<a href="#">hypothetical protein [Acropora millepora]</a>	22.3	101	27	38%	<a href="#">ADG44979.1</a>
Select seq gb AET09723.1	<a href="#">hypothetical protein C002-G4 [Acropora millepora]</a>	22.3	116	27	38%	<a href="#">AET09723.1</a>
Select seq gb KJD18266.1	<a href="#">heat-shock protein Hsp</a>	32	47.9	0.027	33%	<a href="#">KJD18266.1</a>
<b>Spot 2.</b>	<b>Heat shock transcription factor</b>	<b>ACH53605.1</b>	<b>PEPTIDE SEQUENCES:</b>			<b>ssnihsnvpaflv</b>
	Description	<u>Max Score</u>	<u>Total Score</u>	<u>E value</u>	<u>Per. Ident</u>	Accession
Select seq gb ACH53605.1	<a href="#">heat shock transcription factor [Acropora millepora]</a>	258	258	5.00E-85	100%	<a href="#">ACH53605.1</a>
Select seq gb KJD20828.1	<a href="#">terminase [Halomonas meridiana]</a>	26.9	38.2	0.46	100%	<a href="#">KJD20828.1</a>
Select seq gb KJD20631.1	<a href="#">DNA gyrase subunit A [Halomonas meridiana]</a>	22.3	154	14	100%	<a href="#">KJD20631.1</a>
Select seq gb KJD18236.1	<a href="#">ubiquinone biosynthesis protein UbiB [Halomonas meridiana]</a>	21	119	34	100%	<a href="#">KJD18236.1</a>
Select seq gb KJD18616.1	<a href="#">hypothetical protein VE30_12345 [Halomonas meridiana]</a>	19.7	56.6	78	100%	<a href="#">KJD18616.1</a>
Select seq gb KJD19941.1	<a href="#">30S ribosomal protein S7 [Halomonas meridiana]</a>	19.7	28.8	79	100%	<a href="#">KJD19941.1</a>
Select seq gb KJD18057.1	<a href="#">transposase [Halomonas meridiana]</a>	19.7	78.7	83	100%	<a href="#">KJD18057.1</a>
Select seq gb KJD18339.1	<a href="#">transposase [Halomonas meridiana]</a>	19.7	69.6	83	100%	<a href="#">KJD18339.1</a>
Select seq gb KJD19082.1	<a href="#">exonuclease I [Halomonas meridiana]</a>	19.7	136	84	100%	<a href="#">KJD19082.1</a>
Select seq gb KJD19612.1	<a href="#">diguanylate cyclase [Halomonas meridiana]</a>	19.7	173	84	100%	<a href="#">KJD19612.1</a>
Select seq gb KJD19048.1	<a href="#">hypothetical protein VE30_10100 [Halomonas meridiana]</a>	19.3	32.2	110	100%	<a href="#">KJD19048.1</a>
Select seq gb KJD18847.1	<a href="#">endonuclease [Halomonas meridiana]</a>	19.3	64.7	111	100%	<a href="#">KJD18847.1</a>

Select seq gb|KJD20370.1| [DL-methionine transporter ATP-binding subunit \[Halomonas m](#) 18.9 67.5 151 100% [KJD20370.1](#)

**Spot 3.** **Heat shock protein 70 A1-like [Orbicella faveolata]** **XP\_020619238.1** **PEPTIDE SEQUENCES:** **dakrligrkfdpd**

	Description	Max Score	Total Score	E value	Per. Ident	Accession
	<a href="#">heat shock protein 70 A1-like [Orbicella faveolata]</a>	1304	1304	0	100.00%	<a href="#">XP_020619238.1</a>
Select seq ref XP_027037242.1	<a href="#">heat shock protein 70 A1-like [Pocillopora damicornis]</a>	1106	1106	0	82.78%	<a href="#">XP_027037242.1</a>
Select seq gb RMX51493.1	<a href="#">hypothetical protein pdam_00014847 [Pocillopora damicornis]</a>	1106	1106	0	82.78%	<a href="#">RMX51493.1</a>
Select seq gb AKC91104.1	<a href="#">heat shock protein 70 [Stylophora pistillata]</a>	1008	1008	0	77.48%	<a href="#">AKC91104.1</a>
Select seq ref XP_022779048.1	<a href="#">heat shock protein 70 B2-like [Stylophora pistillata]</a>	1006	1006	0	77.32%	<a href="#">XP_022779048.1</a>
Select seq gb AOF40010.1	<a href="#">heat shock protein 70 [Stylophora pistillata]</a>	1005	1005	0	77.94%	<a href="#">AOF40010.1</a>
Select seq gb PFX32589.1	<a href="#">Heat shock protein 70 B2 [Stylophora pistillata]</a>	1002	1002	0	78.63%	<a href="#">PFX32589.1</a>
Select seq ref XP_015748938.1	<a href="#">PREDICTED: heat shock 70 kDa protein 1-like isoform X2 [Acropora digitifera]</a>	1001	1001	0	74.53%	<a href="#">XP_015748938.1</a>
Select seq ref XP_027039067.1	<a href="#">heat shock 70 kDa protein 1-like [Pocillopora damicornis]</a>	998	998	0	76.46%	<a href="#">XP_027039067.1</a>
Select seq ref XP_015748936.1	<a href="#">PREDICTED: heat shock 70 kDa protein 1-like isoform X1 [Acropora digitifera]</a>	998	998	0	75.20%	<a href="#">XP_015748936.1</a>
Select seq gb AMX23290.1	<a href="#">heat shock protein 70 [Pocillopora damicornis]</a>	998	998	0	76.31%	<a href="#">AMX23290.1</a>
Select seq dbj BAD89541.1	<a href="#">heat shock protein 70 [Pocillopora damicornis]</a>	996	996	0	76.31%	<a href="#">BAD89541.1</a>
Select seq ref XP_015774165.1	<a href="#">PREDICTED: galanin receptor type 2-like [Acropora digitifera]</a>	94	94	2.00E-20	28.32%	<a href="#">XP_015774165.1</a>
Select seq ref XP_015775064.1	<a href="#">PREDICTED: G-protein coupled receptor 161-like [Acropora digitifera]</a>	90.5	90.5	2.00E-19	28.08%	<a href="#">XP_015775064.1</a>
Select seq ref XP_015774818.1	<a href="#">PREDICTED: probable G-protein coupled receptor No9 [Acropora digitifera]</a>	123	123	1.00E-30	28.08%	<a href="#">XP_015774818.1</a>
Select seq ref XP_015756285.1	<a href="#">PREDICTED: histamine H1 receptor-like isoform X1 [Acropora digitifera]</a>	82.4	82.4	5.00E-17	27.62%	<a href="#">XP_015756285.1</a>
Select seq ref XP_015764657.1	<a href="#">PREDICTED: melanopsin-like [Acropora digitifera]</a>	103	103	5.00E-24	27.54%	<a href="#">XP_015764657.1</a>

**Spot 4.** **Heat shock protein 90** **XP\_020618369.1** **PEPTIDE SEQUENCES:** **stkelkielipnr**

	Description	Max Score	Total Score	E value	Per. Ident	Accession
Select seq ref XP_020618369.1	<a href="#">heat shock protein HSP 90-beta-like [Orbicella faveolata]</a>	1497	1497	0	100.00%	<a href="#">XP_020618369.1</a>
Select seq ref XP_015763591.1	<a href="#">PREDICTED: heat shock protein HSP 90-alpha-like [Acropora digitifera]</a>	1203	1203	0	92.22%	<a href="#">XP_015763591.1</a>
Select seq dbj BBA20361.1	<a href="#">heat shock protein 90 [Acropora tenuis]</a>	1236	2473	0	91.84%	<a href="#">BBA20361.1</a>
Select seq ref XP_029211734.1	<a href="#">heat shock protein HSP 90-alpha-like [Acropora millepora]</a>	1233	1233	0	91.70%	<a href="#">XP_029211734.1</a>
Select seq ref XP_022803600.1	<a href="#">heat shock protein HSP 90-beta-like [Stylophora pistillata]</a>	1259	1259	0	91.16%	<a href="#">XP_022803600.1</a>
Select seq ref XP_027044932.1	<a href="#">heat shock protein HSP 90-beta-like [Pocillopora damicornis]</a>	1252	1252	0	90.07%	<a href="#">XP_027044932.1</a>
Select seq ref XP_020896728.1	<a href="#">heat shock protein HSP 90-alpha [Exaiptasia pallida]</a>	1104	1104	0	82.31%	<a href="#">XP_020896728.1</a>
Select seq ref XP_001640689.1	<a href="#">predicted protein [Nematostella vectensis]</a>	1144	1144	0	81.25%	<a href="#">XP_001640689.1</a>
Select seq ref XP_028677486.1	<a href="#">heat shock protein HSP 90-alpha [Erpetoichthys calabaricus]</a>	1092	1092	0	80.03%	<a href="#">XP_028677486.1</a>
Select seq gb EEC18473.1	<a href="#">Hsp90 protein, putative [Ixodes scapularis]</a>	1123	1123	0	80.03%	<a href="#">EEC18473.1</a>
Select seq ref XP_029834818.1	<a href="#">heat shock protein HSP 90-alpha [Ixodes scapularis]</a>	1122	1122	0	80.03%	<a href="#">XP_029834818.1</a>

## Appendix A.3 (continued)

Spot 5.	Endoplasmin-like [ <i>Orbicella faveolata</i> ]	XP_020606735.1	PEPTIDE SEQUENCES:	aqmkelreka		
	Description	Max Score	Total Score	E value	Per. Ident	Accession
Select seq ref XP_020606735.1	<a href="#">endoplasmin-like [<i>Orbicella faveolata</i>]</a>	514	514	0	100.00%	<a href="#">XP_020606735.1</a>
Select seq ref XP_020606732.1	<a href="#">endoplasmin-like isoform X1 [<i>Orbicella faveolata</i>]</a>	514	514	2.00E-175	100.00%	<a href="#">XP_020606732.1</a>
Select seq gb RMX38721.1	<a href="#">hypothetical protein pdam_00012456 [<i>Pocillopora damicornis</i>]</a>	442	885	4.00E-147	95.28%	<a href="#">RMX38721.1</a>
Select seq ref XP_027052700.1	<a href="#">endoplasmin-like [<i>Pocillopora damicornis</i>]</a>	440	440	1.00E-146	95.26%	<a href="#">XP_027052700.1</a>
Select seq ref XP_022802311.1	<a href="#">endoplasmin-like [<i>Stylophora pistillata</i>]</a>	438	438	1.00E-145	94.86%	<a href="#">XP_022802311.1</a>
Select seq ref XP_029205156.1	<a href="#">endoplasmin-like [<i>Acropora millepora</i>]</a>	431	431	6.00E-143	88.14%	<a href="#">XP_029205156.1</a>
Select seq ref XP_020907283.1	<a href="#">endoplasmin [<i>Exaiptasia pallida</i>]</a>	430	430	2.00E-142	86.22%	<a href="#">XP_020907283.1</a>
Select seq ref XP_001637407.1	<a href="#">predicted protein [<i>Nematostella vectensis</i>]</a>	412	412	7.00E-136	81.82%	<a href="#">XP_001637407.1</a>
Select seq ref XP_028407863.1	<a href="#">LOW QUALITY PROTEIN: endoplasmin-like [<i>Dendronephthya gi</i>]</a>	409	409	2.00E-134	79.38%	<a href="#">XP_028407863.1</a>
Select seq gb KFM57735.1	<a href="#">Endoplasmin [<i>Stegodyphus mimosarum</i>]</a>	389	389	2.00E-127	76.10%	<a href="#">KFM57735.1</a>

Spot 6.	Cytochrome b [ <i>Montastraea faveolata</i> ]	Q762T3	PEPTIDE SEQUENCES:	gytvdflypypvse		
	Description	Total Score	E value	Per. Ident	Accession	
Select seq dbj BAD11494.0	<a href="#">cytochrome b [<i>Orbicella annularis</i>]</a>	748	100%	0	100.00%	<a href="#">YP_271926.1</a>
Select seq dbj BAD11494.1	<a href="#">cytochrome b [<i>Echinopora pacificus</i>]</a>	746	100%	0	99.21%	<a href="#">BAD11494.1</a>
Select seq dbj BAD11495.1	<a href="#">cytochrome b [<i>Echinopora pacificus</i>]</a>	746	100%	0	98.94%	<a href="#">BAD11495.1</a>
Select seq dbj BAD11488.1	<a href="#">cytochrome b [<i>Cyphastrea serailia</i>]</a>	744	100%	0	98.68%	<a href="#">BAD11488.1</a>
Select seq gb AEL17177.1	<a href="#">cytochrome b [<i>Favia pallida</i>]</a>	743	100%	0	99.21%	<a href="#">AEL17177.1</a>
Select seq dbj BAD11490.1	<a href="#">cytochrome b [<i>Cyphastrea chalcidicum</i>]</a>	743	100%	0	98.15%	<a href="#">BAD11490.1</a>
Select seq ref YP_007317708.1	<a href="#">cytochrome b [<i>Platygyra carnosa</i>]</a>	742	100%	0	98.94%	<a href="#">YP_007317708.1</a>
Select seq dbj BAD11497.1	<a href="#">cytochrome b [<i>Favia stelligera</i>]</a>	742	100%	0	99.21%	<a href="#">BAD11497.1</a>
Select seq ref YP_009378909.1	<a href="#">cytochrome b [<i>Favites pentagona</i>]</a>	741	100%	0	98.68%	<a href="#">YP_009378909.1</a>
Select seq dbj BAD11501.1	<a href="#">cytochrome b [<i>Favites halicora</i>]</a>	741	100%	0	98.68%	<a href="#">BAD11501.1</a>

Spot 7.	Cytochrome oxidase subunit I [ <i>Montastraea faveolata</i> ]	AHA90940.1	PEPTIDE SEQUENCES:	sfwllppalfill		
	Description	Total Score	Query	E value	Per. Ident	Accession
Select seq gb AHA90940.1	<a href="#">cytochrome oxidase subunit I [<i>Orbicella faveolata</i>]</a>	245	100%	7.00E-82	100.00%	<a href="#">AHA90940.1</a>
Select seq gb AHA90942.1	<a href="#">cytochrome oxidase subunit I [<i>Orbicella faveolata</i>]</a>	245	100%	5.00E-81	99.20%	<a href="#">AHA90942.1</a>
Select seq gb AHA90943.1	<a href="#">cytochrome oxidase subunit I [<i>Orbicella faveolata</i>]</a>	243	100%	6.00E-81	99.20%	<a href="#">AHA90943.1</a>
Select seq gb AHA90945.1	<a href="#">cytochrome oxidase subunit I [<i>Orbicella faveolata</i>]</a>	244	100%	6.00E-81	99.20%	<a href="#">AHA90945.1</a>
Select seq gb AHA90941.1	<a href="#">cytochrome oxidase subunit I [<i>Orbicella faveolata</i>]</a>	244	100%	8.00E-81	99.20%	<a href="#">AHA90941.1</a>
Select seq gb AFP73387.1	<a href="#">cytochrome oxidase subunit I [<i>Pseudodiploria strigosa</i>]</a>	243	100%	4.00E-80	97.60%	<a href="#">AFP73387.1</a>
Select seq gb AAS17027.1	<a href="#">cytochrome oxidase subunit I [<i>Orbicella annularis</i>]</a>	244	100%	4.00E-80	99.20%	<a href="#">AAS17027.1</a>
Select seq gb ACJ09533.1	<a href="#">cytochrome oxidase subunit I [<i>Platygyra pini</i>]</a>	242	100%	6.00E-80	98.40%	<a href="#">ACJ09533.1</a>

Select seq gb|ABY85346.1| [cytochrome oxidase subunit I \[Favites cf. valenciennesi DH-201\]](#) 243 100% 6.00E-80 98.40% [ABY85346.1](#)

### Appendix A.3 (continued)

Select seq gb|ABY85297.1| [cytochrome oxidase subunit I \[Favia danae\]](#) 486 100% 9.00E-80 98.40% [ABY85297.1](#)

Select seq dbj|BAD11414.1| [cytochrome oxidase I \[Orbicella annularis\]](#) 243 100% 9.00E-80 99.20% [BAD11414.1](#)

#### Spot 8.

#### Cytochrome P450 74A

#### ACD42778.1

#### PEPTIDE SEQUENCES:

#### sdvieilklavna

	Description	Total Score	Query	E value	Per. Ident	Accession
Select seq gb ACD42778.1	<a href="#">cytochrome P450 74A [Acropora palmata]</a>	904	904	0	100.00%	<a href="#">ACD42778.1</a>
Select seq ref XP_015765607.1	<a href="#">PREDICTED: allene oxide synthase, chloroplastic-like isoform X:</a>	872	872	0	96.06%	<a href="#">XP_015765607.1</a>
Select seq ref XP_029184931.1	<a href="#">allene oxide synthase, chloroplastic-like isoform X1 [Acropora i</a>	867	867	0	96.06%	<a href="#">XP_029184931.1</a>
Select seq ref XP_015765609.1	<a href="#">PREDICTED: allene oxide synthase, chloroplastic-like isoform X:</a>	855	855	0	94.90%	<a href="#">XP_015765609.1</a>
Select seq ref XP_029184932.1	<a href="#">allene oxide synthase, chloroplastic-like isoform X2 [Acropora i</a>	850	850	0	94.90%	<a href="#">XP_029184932.1</a>
Select seq ref XP_020613338.1	<a href="#">allene oxide synthase-like [Orbicella faveolata]</a>	644	644	0	67.44%	<a href="#">XP_020613338.1</a>
Select seq ref XP_027060358.1	<a href="#">allene oxide synthase-like isoform X1 [Pocillopora damicornis]</a>	634	634	0	66.90%	<a href="#">XP_027060358.1</a>
Select seq ref XP_027060359.1	<a href="#">allene oxide synthase-like isoform X2 [Pocillopora damicornis]</a>	632	632	0	66.90%	<a href="#">XP_027060359.1</a>
Select seq ref XP_022797645.1	<a href="#">allene oxide synthase-like isoform X2 [Stylophora pistillata]</a>	622	622	0	65.59%	<a href="#">XP_022797645.1</a>
Select seq gb PFX21200.1	<a href="#">Allene oxide synthase [Stylophora pistillata]</a>	619	873	0	65.59%	<a href="#">PFX21200.1</a>

#### Spot 9.

#### Activin 1

#### BAQ19091.1

#### PEPTIDE SEQUENCES:

#### rcpscndsakene

	Description	Max Score	Total Score	E value	Per. Ident	Accession
Select seq ref XP_029198106.0	<a href="#">PREDICTED: growth/differentiation factor 8-like [Acropora digi</a>	885	885	100%	100.00%	<a href="#">XP_015761587.1</a>
Select seq ref XP_029198106.1	<a href="#">growth/differentiation factor 8-like [Acropora millepora]</a>	861	861	0	97.17%	<a href="#">XP_029198106.1</a>
Select seq ref XP_015761586.1	<a href="#">PREDICTED: growth/differentiation factor 8-like [Acropora digi</a>	478	478	4.00E-164	57.64%	<a href="#">XP_015761586.1</a>
Select seq ref XP_029198105.1	<a href="#">growth/differentiation factor 8-like [Acropora millepora]</a>	476	476	2.00E-163	57.64%	<a href="#">XP_029198105.1</a>
Select seq ref XP_020629122.1	<a href="#">inhibin beta B chain-like isoform X3 [Orbicella faveolata]</a>	286	286	7.00E-89	42.08%	<a href="#">XP_020629122.1</a>
Select seq ref XP_020629118.1	<a href="#">inhibin beta B chain-like isoform X2 [Orbicella faveolata]</a>	286	286	8.00E-89	42.08%	<a href="#">XP_020629118.1</a>
Select seq ref XP_020629111.1	<a href="#">inhibin beta B chain-like isoform X1 [Orbicella faveolata]</a>	286	286	1.00E-88	41.86%	<a href="#">XP_020629111.1</a>
Select seq ref XP_027045428.1	<a href="#">inhibin beta B chain-like [Pocillopora damicornis]</a>	263	263	9.00E-80	37.50%	<a href="#">XP_027045428.1</a>
Select seq ref XP_022785216.1	<a href="#">inhibin beta B chain-like [Stylophora pistillata]</a>	258	258	9.00E-78	37.18%	<a href="#">XP_022785216.1</a>
Select seq ref XP_019632507.1	<a href="#">PREDICTED: growth/differentiation factor 8-like [Branchiostom</a>	147	147	5.00E-36	30.59%	<a href="#">XP_019632507.1</a>
Select seq gb ABF61781.1	<a href="#">activin [Nematostella vectensis]</a>	144	144	5.00E-35	27.11%	<a href="#">ABF61781.1</a>

#### Spot 10.

#### NADH-ubiquinone oxidoreductase chain 1

#### Q4G6D2

#### PEPTIDE SEQUENCES:

#### aqmkelreka

	Description	Max Score	Total Score	E value	Per. Ident	Accession
Select seq gb ATC69366.1	<a href="#">NADH dehydrogenase subunit 1 [Acropora pruinosa]</a>	468	468	8.00E-168	74.69%	<a href="#">ATC69366.1</a>
Select seq gb YP_008815375.1	<a href="#">NADH dehydrogenase subunit 1 [Acropora humilis]</a>	469	469	9.00E-168	74.69%	<a href="#">YP_008815375.1</a>
Select seq gb ATC69390.1	<a href="#">NADH dehydrogenase subunit 1 [Acropora nana]</a>	468	468	9.00E-168	74.69%	<a href="#">ATC69390.1</a>
Select seq gb ABD17707.1	<a href="#">NADH dehydrogenase subunit 1 [Acropora acuminata]</a>	70.5	70.5	8.00E-16	74.47%	<a href="#">ABD17707.1</a>
Select seq ref NP_612817.1	<a href="#">NADH dehydrogenase subunit 1 [Acropora tenuis]</a>	467	467	6.00E-167	74.38%	<a href="#">NP_612817.1</a>

Select seq gb ABD17695.1	<a href="#">NADH dehydrogenase subunit 1 [Acropora acuminata]</a>	211	211	5.00E-69	72.86%	<a href="#">ABD17695.1</a>
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### Appendix A.3 (continued)

<b>Spot 11.</b>	<b>Thioredoxin reductase [A. millepora]</b>	<b>AFI99106.2</b>	<b>PEPTIDE SEQUENCES:</b>			<b>spigttwlggt</b>
	Description	<u>Total Score</u>	<u>Query</u>	<u>E value</u>	Per. Ident	Accession
Select seq gb AFI99106.2	<a href="#">thioredoxin reductase [Acropora millepora]</a>	1227	1227	0	100.00%	<a href="#">AFI99106.2</a>
Select seq ref XP_029185498.1	<a href="#">thioredoxin reductase 1, cytoplasmic-like isoform X3 [Acropora millepora]</a>	1221	1221	0	99.83%	<a href="#">XP_029185498.1</a>
Select seq ref XP_029185497.1	<a href="#">thioredoxin reductase 1, cytoplasmic-like isoform X2 [Acropora millepora]</a>	1221	1221	0	99.83%	<a href="#">XP_029185497.1</a>
Select seq ref XP_029185496.1	<a href="#">thioredoxin reductase 1, cytoplasmic-like isoform X1 [Acropora millepora]</a>	1220	1220	0	99.83%	<a href="#">XP_029185496.1</a>
Select seq ref XP_029185499.1	<a href="#">thioredoxin reductase 1, cytoplasmic-like isoform X4 [Acropora millepora]</a>	1155	1155	0	99.82%	<a href="#">XP_029185499.1</a>
Select seq ref XP_020605984.1	<a href="#">thioredoxin reductase 1, cytoplasmic-like isoform X1 [Orbicella annularis]</a>	1053	1053	0	83.25%	<a href="#">XP_020605984.1</a>
Select seq ref XP_020605985.1	<a href="#">thioredoxin reductase 1, cytoplasmic-like isoform X2 [Orbicella annularis]</a>	1051	1051	0	83.25%	<a href="#">XP_020605985.1</a>
Select seq ref XP_001630291.1	<a href="#">predicted protein [Nematostella vectensis]</a>	895	895	0	70.71%	<a href="#">XP_001630291.1</a>
Select seq ref XP_015763837.1	<a href="#">PREDICTED: thioredoxin reductase 3-like isoform X2 [Acropora millepora]</a>	790	790	0	99.21%	<a href="#">XP_015763837.1</a>
Select seq ref XP_015763830.1	<a href="#">PREDICTED: thioredoxin reductase 3-like isoform X1 [Acropora millepora]</a>	790	790	0	99.21%	<a href="#">XP_015763830.1</a>
Select seq gb RXM93140.1	<a href="#">Thioredoxin reductase 3 [Acipenser ruthenus]</a>	783	783	0	65.31%	<a href="#">RXM93140.1</a>

<b>Spot 12.</b>	<b>Apextrin</b>	<b>ADT3F5</b>	<b>PEPTIDE SEQUENCES:</b>			<b>mfvilgvll</b>
	Description	<u>Total Score</u>	<u>Query</u>	<u>E value</u>	Per. Ident	Accession
Select seq gb ABK63971.2	<a href="#">apextrin [Acropora millepora]</a>	35.4	35.4	2.00E-06	100%	<a href="#">ABK63971.2</a>
Select seq gb KJD18891.1	<a href="#">sulfite oxidase [Halomonas meridiana]</a>	24	24	0.011	78%	<a href="#">KJD18891.1</a>
Select seq gb KJD20797.1	<a href="#">ABC transporter permease [Halomonas meridiana]</a>	21	21	0.095	100%	<a href="#">KJD20797.1</a>
Select seq gb KJD18783.1	<a href="#">cytochrome B [Halomonas meridiana]</a>	21	45.6	0.096	70%	<a href="#">KJD18783.1</a>
Select seq gb KJD19402.1	<a href="#">C4-dicarboxylate ABC transporter permease [Halomonas meridiana]</a>	21	21	0.096	100%	<a href="#">KJD19402.1</a>
Select seq gb KJD18161.1	<a href="#">hypothetical protein VE30_14675 [Halomonas meridiana]</a>	21	49	0.096	100%	<a href="#">KJD18161.1</a>
Select seq gb ABY74499.1	<a href="#">integrin beta 2 [Acropora millepora]</a>	21	21	0.096	100%	<a href="#">ABY74499.1</a>
Select seq gb KJD18722.1	<a href="#">cytochrome C biogenesis protein CcmC [Halomonas meridiana]</a>	20.6	20.6	0.13	70%	<a href="#">KJD18722.1</a>
Select seq gb KJD19494.1	<a href="#">cell division protein FtsQ [Halomonas meridiana]</a>	20.6	20.6	0.13	100%	<a href="#">KJD19494.1</a>
Select seq gb KJD19467.1	<a href="#">NADH dehydrogenase [Halomonas meridiana]</a>	20.6	38.2	0.13	100%	<a href="#">KJD19467.1</a>

<b>Spot 13.</b>	<b>ATP synthase</b>	<b>YP_271955</b>	<b>PEPTIDE SEQUENCES:</b>			<b>fflvlnifglc</b>
	Description	<u>Total Score</u>	<u>Query</u>	<u>E value</u>	Per. Ident	Accession
Select seq ref YP_009428246.0	<a href="#">ATP synthase F0 subunit 6 [Orbicella annularis]</a>	436	100%	100.00%		<a href="#">YP_271929.1</a>
Select seq ref YP_009428246.1	<a href="#">ATP synthase F0 subunit 6 [Favites abdita]</a>	431	3.00E-152	99.11%		<a href="#">YP_009428246.1</a>
Select seq ref YP_009679161.1	<a href="#">ATP synthase subunit 6 [Dipsastraea rotumana]</a>	430	6.00E-152	98.67%		<a href="#">YP_009679161.1</a>
Select seq ref YP_009654478.1	<a href="#">ATP synthase F0 subunit 6 [Hydnophora exesa]</a>	859	1.00E-151	98.22%		<a href="#">YP_009654478.1</a>
Select seq ref YP_654359.1	<a href="#">ATP synthase F0 subunit 6 [Mussa angulosa]</a>	429	3.00E-151	97.78%		<a href="#">YP_654359.1</a>

Select seq ref YP_007317711.1	<a href="#">ATP synthase F0 subunit 6 [Platygyra carnosa]</a>	427	7.00E-151	97.78%	<a href="#">YP_007317711.1</a>
Select seq ref YP_009547093.1	<a href="#">ATP synthase F0 subunit 6 [Echinophyllia aspera]</a>	427	1.00E-150	96.89%	<a href="#">YP_009547093.1</a>

### Appendix A.3 (continued)

Select seq ref YP_009378912.1	<a href="#">ATP synthase F0 subunit 6 [Favites pentagona]</a>	427	1.00E-150	97.33%	<a href="#">YP_009378912.1</a>
Select seq ref YP_654346.1	<a href="#">ATP synthase F0 subunit 6 [Colpophyllia natans]</a>	427	1.00E-150	97.78%	<a href="#">YP_654346.1</a>

<b>Spot 14.</b>	<b>ATP synthase subunit 8</b>	<b>Q8SJB2</b>	<b>PEPTIDE SEQUENCES:</b>		<b>tqyrwtllvl</b>
	Description	<u>Total Score</u>	<u>Query Cover</u>	<u>E value</u>	Per. Ident Accession
Select seq ref NP_612827.1	<a href="#">ATP synthase F0 subunit 8 [Acropora tenuis]</a>	146	146	5.00E-48	100.00% <a href="#">NP_612827.1</a>
Select seq ref XP_015780370.1	<a href="#">PREDICTED: adenosine receptor A3-like [Acropora digitifera]</a>	25.4	25.4	3.8	50.00% <a href="#">XP_015780370.1</a>
Select seq ref XP_015768528.1	<a href="#">PREDICTED: fibronectin-like [Acropora digitifera]</a>	24.6	24.6	7.5	44.00% <a href="#">XP_015768528.1</a>

<b>Spot 15.</b>	<b>ATPase subunit 6, (ATP synthase subunit 6)</b>	<b>Q9TBW1</b>	<b>PEPTIDE SEQUENCES:</b>		<b>fmpsgaplgf</b>
	Description	<u>Total Score</u>	<u>Query</u>	<u>E value</u>	Per. Ident Accession
Select seq ref NP_612821.1	<a href="#">ATP synthase F0 subunit 6 [Acropora tenuis]</a>	448	896	1.00E-158	100.00% <a href="#">NP_612821.1</a>
Select seq ref YP_009029625.1	<a href="#">ATP synthase F0 subunit 6 [Isopora palifera]</a>	446	446	6.00E-158	99.57% <a href="#">YP_009029625.1</a>
Select seq ref YP_009472225.1	<a href="#">ATP synthase F0 subunit 6 [Montipora aequituberculata]</a>	444	444	4.00E-157	98.71% <a href="#">YP_009472225.1</a>
Select seq ref YP_214919.1	<a href="#">ATP synthase F0 subunit 6 [Anacropora matthai]</a>	442	442	3.00E-156	98.28% <a href="#">YP_214919.1</a>
Select seq gb AHY04480.1	<a href="#">ATP synthase F0 subunit 6 [Alveopora sp. MFL-2014]</a>	439	439	5.00E-155	98.28% <a href="#">AHY04480.1</a>
Select seq ref YP_009029612.1	<a href="#">ATP synthase F0 subunit 6 [Astreopora explanata]</a>	437	437	3.00E-154	97.41% <a href="#">YP_009029612.1</a>
Select seq ref YP_009545481.1	<a href="#">ATP synthase F0 subunit 6 [Alveopora japonica]</a>	431	431	3.00E-152	96.98% <a href="#">YP_009545481.1</a>
Select seq ref YP_004581257.1	<a href="#">ATP synthase F0 subunit 6 [Fungiacyathus stephanus]</a>	415	830	1.00E-145	90.95% <a href="#">YP_004581257.1</a>
Select seq ref YP_009159301.1	<a href="#">ATP synthase F0 subunit 6 [Dendrophyllia arbuscula]</a>	414	414	2.00E-145	91.38% <a href="#">YP_009159301.1</a>
Select seq ref YP_009122416.1	<a href="#">ATP synthase F0 subunit 6 [Pseudosiderastrea tayami]</a>	413	413	5.00E-145	94.83% <a href="#">YP_009122416.1</a>
Select seq dbj BAA85613.1	<a href="#">ATPase 6 [Isopora brueggemanni]</a>	412	412	8.00E-145	100.00% <a href="#">BAA85613.1</a>

<b>Spot 16.</b>	<b>Toll-like receptor 2</b>	<b>XP_020617122</b>	<b>PEPTIDE SEQUENCES:</b>		<b>qwcnfelqqaiyqhl</b>
	Description	<u>Total Score</u>	<u>Query</u>	<u>E value</u>	Per. Ident Accession
Select seq ref XP_020617122.1	<a href="#">toll-like receptor 2 isoform X4 [Orbicella faveolata]</a>	438	100%	1.00E-155	100.00% <a href="#">XP_020617122.1</a>
Select seq ref XP_020617118.1	<a href="#">toll-like receptor 2 isoform X1 [Orbicella faveolata]</a>	431	100%	3.00E-152	94.64% <a href="#">XP_020617118.1</a>
Select seq ref XP_020617121.1	<a href="#">toll-like receptor 2 isoform X3 [Orbicella faveolata]</a>	429	100%	9.00E-152	94.62% <a href="#">XP_020617121.1</a>
Select seq ref XP_020630889.1	<a href="#">uncharacterized protein LOC110067885 isoform X3 [Orbicella faveolata]</a>	187	84%	6.00E-54	53.01% <a href="#">XP_020630889.1</a>
Select seq ref XP_020630888.1	<a href="#">uncharacterized protein LOC110067885 isoform X2 [Orbicella faveolata]</a>	187	84%	9.00E-54	53.01% <a href="#">XP_020630888.1</a>
Select seq ref XP_020630887.1	<a href="#">uncharacterized protein LOC110067885 isoform X1 [Orbicella faveolata]</a>	187	84%	2.00E-53	53.01% <a href="#">XP_020630887.1</a>
Select seq ref XP_015769651.1	<a href="#">PREDICTED: toll-like receptor 4 isoform X2 [Acropora digitifera]</a>	157	91%	3.00E-43	41.62% <a href="#">XP_015769651.1</a>
Select seq ref XP_015769650.1	<a href="#">PREDICTED: uncharacterized protein LOC107348148 isoform X1 [Acropora digitifera]</a>	157	84%	4.00E-43	42.78% <a href="#">XP_015769650.1</a>

Select seq ref XP_027036966.1	<a href="#">uncharacterized protein LOC113665468 [Pocillopora damicornis]</a>	155	93%	3.00E-41	39.90%	<a href="#">XP_027036966.1</a>
Select seq gb RMX51749.1	<a href="#">hypothetical protein pdam_00011740 [Pocillopora damicornis]</a>	249	93%	2.00E-39	41.21%	<a href="#">RMX51749.1</a>

### Appendix A.3 (continued)

<b>Spot 17.</b>	<b>Mini-collagen</b>	<b>AAM74869.1</b>	<b>PEPTIDE SEQUENCES:</b>			<b>ekreaspcgyg</b>
	Description	<u>Total Score</u>	<u>Query</u>	<u>E value</u>	Per. Ident	Accession
Select seq gb AAM74852.1	<a href="#">mini-collagen [Acropora cervicornis]</a>	94	94	100%	5.00E-24	<a href="#">AAM74852.1</a>
Select seq gb AAM74869.1	<a href="#">mini-collagen [Acropora palmata]</a>	93.6	93.6	100%	7.00E-24	<a href="#">AAM74869.1</a>
Select seq gb AAM74878.1	<a href="#">mini-collagen [Acropora palmata]</a>	91.3	91.3	100%	5.00E-23	<a href="#">AAM74878.1</a>
Select seq ref XP_015771910.1	<a href="#">PREDICTED: putative cuticle collagen 155 [Acropora digitifera]</a>	94.4	94.4	100%	9.00E-23	<a href="#">XP_015771910.1</a>
Select seq dbj BAA06407.1	<a href="#">mini-collagen [Acropora donei]</a>	92.8	92.8	100%	3.00E-22	<a href="#">BAA06407.1</a>
Select seq ref XP_029208364.1	<a href="#">basic proline-rich protein-like [Acropora millepora]</a>	92.8	92.8	100%	3.00E-22	<a href="#">XP_029208364.1</a>
Select seq ref XP_022804287.1	<a href="#">cuticle collagen 34-like [Stylophora pistillata]</a>	53.1	53.1	60%	6.00E-07	<a href="#">XP_022804287.1</a>
Select seq ref XP_028415759.1	<a href="#">cuticle collagen 1-like [Dendronephthya gigantea]</a>	40.8	40.8	48%	0.017	<a href="#">XP_028415759.1</a>
Select seq gb AAM74851.1	<a href="#">mini-collagen [Acropora nasuta]</a>	38.9	38.9	60%	0.032	<a href="#">AAM74851.1</a>
Select seq ref XP_001641074.1	<a href="#">predicted protein [Nematostella vectensis]</a>	39.7	39.7	53%	0.04	<a href="#">XP_001641074.1</a>
Select seq ref XP_020625137.1	<a href="#">cuticle collagen 14-like [Orbicella faveolata]</a>	40	40	55%	0.066	<a href="#">XP_020625137.1</a>

### Appendix A.3 (continued)

<b>Spot 18.</b>	<b>2-acylglycerol O-acyltransferase 1-like [Orbicella faveolata]</b>	<b>XP_020602679.1</b>	<b>PEPTIDE SEQUENCES:</b>			<b>grrsnfvrrlv</b>
	Description	<u>Total Score</u>	<u>Query</u>	<u>E value</u>	Per. Ident	Accession
Select seq ref XP_020602679.1	<a href="#">2-acylglycerol O-acyltransferase 1-like [Orbicella faveolata]</a>	688	100%	0	100.00%	<a href="#">XP_020602679.1</a>
Select seq ref XP_029187260.1	<a href="#">2-acylglycerol O-acyltransferase 1-like [Acropora millepora]</a>	1264	99%	0	89.29%	<a href="#">XP_029187260.1</a>
Select seq ref XP_022791455.1	<a href="#">2-acylglycerol O-acyltransferase 1-like [Stylophora pistillata]</a>	625	100%	0	88.43%	<a href="#">XP_022791455.1</a>
Select seq ref XP_027048695.1	<a href="#">2-acylglycerol O-acyltransferase 1-like [Pocillopora damicornis]</a>	619	99%	0	88.10%	<a href="#">XP_027048695.1</a>
Select seq ref XP_015752089.1	<a href="#">PREDICTED: 2-acylglycerol O-acyltransferase 1-like [Acropora d</a>	611	99%	0	88.69%	<a href="#">XP_015752089.1</a>
Select seq ref XP_028401261.1	<a href="#">2-acylglycerol O-acyltransferase 2-A-like [Dendronephthya giga</a>	541	99%	0	75.45%	<a href="#">XP_028401261.1</a>
Select seq ref XP_001630435.1	<a href="#">predicted protein [Nematostella vectensis]</a>	541	99%	0	76.79%	<a href="#">XP_001630435.1</a>
Select seq ref XP_020902957.1	<a href="#">2-acylglycerol O-acyltransferase 1 [Exaiptasia pallida]</a>	535	99%	0	73.51%	<a href="#">XP_020902957.1</a>
Select seq ref XP_008591845.1	<a href="#">PREDICTED: 2-acylglycerol O-acyltransferase 1 [Galeopterus va</a>	392	98%	2.00E-133	56.33%	<a href="#">XP_008591845.1</a>
Select seq ref XP_017390802.1	<a href="#">PREDICTED: 2-acylglycerol O-acyltransferase 1 isoform X1 [Ceb</a>	391	98%	6.00E-133	56.93%	<a href="#">XP_017390802.1</a>
Select seq ref XP_027046098.1	<a href="#">2-acylglycerol O-acyltransferase 2-like [Pocillopora damicornis]</a>	391	99%	6.00E-133	55.22%	<a href="#">XP_027046098.1</a>
Select seq ref XP_002749878.1	<a href="#">PREDICTED: 2-acylglycerol O-acyltransferase 1 [Callithrix jacchu</a>	391	98%	9.00E-133	56.93%	<a href="#">XP_002749878.1</a>
Select seq ref XP_003925530.1	<a href="#">PREDICTED: 2-acylglycerol O-acyltransferase 1 [Saimiri bolivien</a>	390	98%	2.00E-132	56.63%	<a href="#">XP_003925530.1</a>

Spot 19.	Integrin beta	Description	XP_020602679.1 PEPTIDE SEQUENCES: grrsnfvrrlr				
			Total Score	Query	E value	Per. Ident	Accession
Select seq gb AAB66910.1	<a href="#">integrin subunit betaCn1 [Acropora millepora]</a>		1630	1630	0	100.00%	<a href="#">AAB66910.1</a>
Select seq ref XP_015755972.1	<a href="#">PREDICTED: integrin beta-1-like [Acropora digitifera]</a>		1094	1094	0	73.96%	<a href="#">XP_015755972.1</a>
Select seq ref XP_015762689.1	<a href="#">PREDICTED: uncharacterized protein LOC107341737 isoform X</a>		30	30	6.1	66.67%	<a href="#">XP_015762689.1</a>

### Appendix A.3 (continued)

Select seq ref XP_015762690.1	<a href="#">PREDICTED: uncharacterized protein LOC107341738 isoform X</a>		30	30	6.3	66.67%	<a href="#">XP_015762690.1</a>
Select seq ref XP_015762686.1	<a href="#">PREDICTED: uncharacterized protein LOC107341736 [Acropora</a>		30	30	6.9	66.67%	<a href="#">XP_015762686.1</a>
Select seq ref XP_015765150.1	<a href="#">PREDICTED: versican core protein-like isoform X1 [Acropora di</a>		30	30	6.7	51.52%	<a href="#">XP_015765150.1</a>
Select seq ref XP_015775330.1	<a href="#">PREDICTED: uncharacterized protein LOC107353528 [Acropora</a>		29.6	29.6	6.4	50.00%	<a href="#">XP_015775330.1</a>
Select seq ref XP_015755165.1	<a href="#">PREDICTED: ALK tyrosine kinase receptor-like [Acropora digitif</a>		29.6	29.6	9.8	46.67%	<a href="#">XP_015755165.1</a>
Select seq ref XP_015759479.1	<a href="#">PREDICTED: attractin-like protein 1 [Acropora digitifera]</a>		32.7	32.7	1	46.15%	<a href="#">XP_015759479.1</a>
Select seq gb ARA71555.1	<a href="#">MAM and LDL-receptor domain-containing protein [Acropora c</a>		32.3	32.3	2	41.94%	<a href="#">ARA71555.1</a>

Spot 20.	Actin	Description	ABY40470.1 PEPTIDE SEQUENCES: mkcdvdirkdlyant				
			Max Score	Total Score	E value	Per. Ident	Accession
Select seq gb ABY40470.1	<a href="#">actin [Acropora millepora]</a>		323	323	1.00E-115	100.00%	<a href="#">ABY40470.1</a>
Select seq ref XP_015762563.1	<a href="#">PREDICTED: actin, cytoplasmic-like [Acropora digitifera]</a>		324	324	1.00E-112	100.00%	<a href="#">XP_015762563.1</a>
Select seq ref XP_015751952.1	<a href="#">PREDICTED: actin-15B [Acropora digitifera]</a>		309	309	1.00E-106	94.19%	<a href="#">XP_015751952.1</a>
Select seq ref XP_015753791.1	<a href="#">PREDICTED: actin, cytoplasmic [Acropora digitifera]</a>		306	306	8.00E-106	93.55%	<a href="#">XP_015753791.1</a>
Select seq ref XP_015753792.1	<a href="#">PREDICTED: actin-3 [Acropora digitifera]</a>		301	301	8.00E-104	92.26%	<a href="#">XP_015753792.1</a>
Select seq ref XP_015768232.1	<a href="#">PREDICTED: uncharacterized protein LOC107346890 [Acropora</a>		306	497	5.00E-101	92.90%	<a href="#">XP_015768232.1</a>
Select seq gb AEX31637.1	<a href="#">beta-actin [Acropora pruinosa]</a>		157	157	6.00E-51	96.05%	<a href="#">AEX31637.1</a>
Select seq ref XP_015748011.1	<a href="#">PREDICTED: alpha-centractin [Acropora digitifera]</a>		162	162	3.00E-50	49.68%	<a href="#">XP_015748011.1</a>
Select seq ref XP_015764694.1	<a href="#">PREDICTED: LOW QUALITY PROTEIN: actin-related protein 2-lik</a>		139	139	2.00E-40	41.77%	<a href="#">XP_015764694.1</a>
Select seq ref XP_015763253.1	<a href="#">PREDICTED: actin-like [Acropora digitifera]</a>		114	114	1.00E-31	39.10%	<a href="#">XP_015763253.1</a>
Select seq ref XP_015768231.1	<a href="#">PREDICTED: actin, alpha skeletal muscle-like [Acropora digitife</a>		102	102	6.00E-29	52.81%	<a href="#">XP_015768231.1</a>
Select seq ref XP_015757596.1	<a href="#">PREDICTED: actin-like protein 6A [Acropora digitifera]</a>		108	108	1.00E-28	40.80%	<a href="#">XP_015757596.1</a>
Select seq ref XP_015762522.1	<a href="#">PREDICTED: actin [Acropora digitifera]</a>		100	100	2.00E-26	72.86%	<a href="#">XP_015762522.1</a>
Select seq ref XP_015762037.1	<a href="#">PREDICTED: actin-related protein 6-like [Acropora digitifera]</a>		80.5	80.5	2.00E-19	27.54%	<a href="#">XP_015762037.1</a>
Select seq ref XP_015748134.1	<a href="#">PREDICTED: actin-related protein 6-like [Acropora digitifera]</a>		79	79	7.00E-18	26.44%	<a href="#">XP_015748134.1</a>
Select seq ref XP_015765936.1	<a href="#">PREDICTED: actin-related protein 5-like [Acropora digitifera]</a>		65.1	65.1	6.00E-13	30.21%	<a href="#">XP_015765936.1</a>
Select seq ref XP_015765935.1	<a href="#">PREDICTED: actin-related protein 5-like [Acropora digitifera]</a>		62	62	7.00E-12	36.00%	<a href="#">XP_015765935.1</a>
Select seq ref XP_015757125.1	<a href="#">PREDICTED: actin-related protein 3-like [Acropora digitifera]</a>		30.8	30.8	0.33	31.91%	<a href="#">XP_015757125.1</a>
Select seq ref XP_015779499.1	<a href="#">PREDICTED: dynein heavy chain domain-containing protein 1-li</a>		27.3	27.3	6.2	36.59%	<a href="#">XP_015779499.1</a>

<b>Spot 21.</b>	<b>Beta-tubulin</b>		<b>AHZ61618.1</b>	<b>PEPTIDE SEQUENCES:</b>		<b>natlsvhqlventdet</b>
	Description		<u>Total Score</u>	<u>Query</u>	<u>Per. Ident</u>	Accession
Select seq gb AHZ61578.1	<a href="#">beta-tubulin [Acropora cervicornis]</a>		163	163	1.00E-54	100.00% <a href="#">AHZ61578.1</a>
Select seq ref XP_015747460.1	<a href="#">PREDICTED: tubulin beta-4B chain isoform X4 [Acropora digitifera]</a>		169	169	2.00E-52	100.00% <a href="#">XP_015747460.1</a>
Select seq ref XP_015747441.1	<a href="#">PREDICTED: tubulin beta-4B chain isoform X1 [Acropora digitifera]</a>		169	169	2.00E-52	100.00% <a href="#">XP_015747441.1</a>
Select seq ref XP_015761439.1	<a href="#">PREDICTED: tubulin beta chain-like [Acropora digitifera]</a>		161	161	5.00E-50	94.94% <a href="#">XP_015761439.1</a>
Select seq ref XP_015768684.1	<a href="#">PREDICTED: tubulin alpha-1 chain [Acropora digitifera]</a>		75.1	75.1	1.00E-17	42.86% <a href="#">XP_015768684.1</a>

### Appendix A.3 (continued)

Select seq ref XP_015773084.1	<a href="#">PREDICTED: tubulin alpha-3 chain [Acropora digitifera]</a>		72.8	72.8	5.00E-17	38.96% <a href="#">XP_015773084.1</a>
Select seq ref XP_015771897.1	<a href="#">PREDICTED: tubulin alpha chain-like [Acropora digitifera]</a>		73.2	73.2	6.00E-17	40.26% <a href="#">XP_015771897.1</a>
Select seq ref XP_015747471.1	<a href="#">PREDICTED: LOW QUALITY PROTEIN: tubulin alpha-8 chain-like</a>		72.4	72.4	1.00E-16	38.96% <a href="#">XP_015747471.1</a>
Select seq ref XP_015770470.1	<a href="#">PREDICTED: tubulin gamma-1 chain isoform X1 [Acropora digitifera]</a>		60.1	60.1	3.00E-12	37.18% <a href="#">XP_015770470.1</a>
Select seq ref XP_015770471.1	<a href="#">PREDICTED: tubulin gamma-1 chain isoform X2 [Acropora digitifera]</a>		60.1	60.1	3.00E-12	37.18% <a href="#">XP_015770471.1</a>
Select seq ref XP_015757049.1	<a href="#">PREDICTED: tubulin beta chain-like [Acropora digitifera]</a>		50.8	50.8	6.00E-09	57.14% <a href="#">XP_015757049.1</a>
Select seq ref XP_015757384.1	<a href="#">PREDICTED: tubulin epsilon chain-like [Acropora digitifera]</a>		45.4	45.4	5.00E-07	38.81% <a href="#">XP_015757384.1</a>

<b>Spot 22.</b>	<b>Gelsolin</b>		<b>XP_012559373.1</b>	<b>PEPTIDE SEQUENCES:</b>		<b>eeelkydvhfwige</b>
	Description		<u>Max Score</u>	<u>Total Score</u>	<u>E value</u>	<u>Per. Ident</u> Accession
Select seq ref XP_015766322.1	<a href="#">PREDICTED: gelsolin-like protein 1 [Acropora digitifera]</a>		294	294	2.00E-99	60.34% <a href="#">XP_015766322.1</a>
Select seq ref XP_015766340.1	<a href="#">PREDICTED: gelsolin-like protein 1 [Acropora digitifera]</a>		153	153	1.00E-45	51.95% <a href="#">XP_015766340.1</a>
Select seq ref XP_015766323.1	<a href="#">PREDICTED: gelsolin-like protein 1 [Acropora digitifera]</a>		350	350	9.00E-120	49.86% <a href="#">XP_015766323.1</a>
Select seq ref XP_015765697.1	<a href="#">PREDICTED: advillin-like [Acropora digitifera]</a>		204	318	5.00E-60	40.00% <a href="#">XP_015765697.1</a>
Select seq ref XP_015766301.1	<a href="#">PREDICTED: gelsolin-like protein 1 [Acropora digitifera]</a>		127	127	1.00E-34	33.74% <a href="#">XP_015766301.1</a>
Select seq ref XP_015752858.1	<a href="#">PREDICTED: protein flightless-1 homolog [Acropora digitifera]</a>		103	103	4.00E-24	26.16% <a href="#">XP_015752858.1</a>
Select seq ref XP_015776614.1	<a href="#">PREDICTED: supervillin-like [Acropora digitifera]</a>		33.5	33.5	0.29	24.72% <a href="#">XP_015776614.1</a>
Select seq ref XP_015750047.1	<a href="#">PREDICTED: supervillin-like [Acropora digitifera]</a>		35	35	0.08	20.51% <a href="#">XP_015750047.1</a>

<b>Spot 23.</b>	<b>Myosin</b>		<b>XP_001637809.1</b>	<b>PEPTIDE SEQUENCES:</b>		<b>sgagktestkfiicq</b>
	Description		<u>Max Score</u>	<u>Total Score</u>	<u>E value</u>	<u>Per. Ident</u> Accession
Select seq ref XP_015769762.1	<a href="#">PREDICTED: unconventional myosin-VIIa-like [Acropora digitifera]</a>		758	758	0	68.12% <a href="#">XP_015769762.1</a>
Select seq ref XP_015769761.1	<a href="#">PREDICTED: myosin-1-like [Acropora digitifera]</a>		77.8	77.8	2.00E-17	50.00% <a href="#">XP_015769761.1</a>
Select seq ref XP_015779248.1	<a href="#">PREDICTED: LOW QUALITY PROTEIN: unconventional myosin-X</a>		164	278	8.00E-43	48.50% <a href="#">XP_015779248.1</a>
Select seq ref XP_015756084.1	<a href="#">PREDICTED: unconventional myosin-VI-like [Acropora digitifera]</a>		174	283	4.00E-46	45.45% <a href="#">XP_015756084.1</a>
Select seq ref XP_015761879.1	<a href="#">PREDICTED: myosin-VIIa-like [Acropora digitifera]</a>		236	347	4.00E-67	44.04% <a href="#">XP_015761879.1</a>
Select seq ref XP_015766505.1	<a href="#">PREDICTED: unconventional myosin-XV-like [Acropora digitifera]</a>		407	407	4.00E-126	42.34% <a href="#">XP_015766505.1</a>
Select seq ref XP_015749129.1	<a href="#">PREDICTED: unconventional myosin-VIIa-like [Acropora digitifera]</a>		200	200	2.00E-60	41.18% <a href="#">XP_015749129.1</a>
Select seq ref XP_015752126.1	<a href="#">PREDICTED: unconventional myosin-Ib-like [Acropora digitifera]</a>		352	352	5.00E-109	39.46% <a href="#">XP_015752126.1</a>
Select seq ref XP_015758662.1	<a href="#">PREDICTED: unconventional myosin-Ie-like isoform X2 [Acropora digitifera]</a>		340	340	4.00E-105	39.25% <a href="#">XP_015758662.1</a>

Select seq ref XP_015758661.1	<a href="#">PREDICTED: unconventional myosin-le-like isoform X1 [Acropora digitifera]</a>	339	339	9.00E-103	39.18%	<a href="#">XP_015758661.1</a>
Select seq ref XP_015758734.1	<a href="#">PREDICTED: myosin-1B-like [Acropora digitifera]</a>	340	340	5.00E-109	38.31%	<a href="#">XP_015758734.1</a>
Select seq ref XP_015759619.1	<a href="#">PREDICTED: unconventional myosin-VIIa-like [Acropora digitifera]</a>	358	358	7.00E-113	38.17%	<a href="#">XP_015759619.1</a>
Select seq ref XP_015779047.1	<a href="#">PREDICTED: unconventional myosin-1d-like [Acropora digitifera]</a>	326	326	1.00E-100	37.50%	<a href="#">XP_015779047.1</a>
Select seq ref XP_015768410.1	<a href="#">PREDICTED: unconventional myosin-Vb-like [Acropora digitifera]</a>	321	321	2.00E-96	37.08%	<a href="#">XP_015768410.1</a>
Select seq ref XP_015774550.1	<a href="#">PREDICTED: myosin heavy chain, striated muscle-like [Acropora digitifera]</a>	327	327	3.00E-98	36.84%	<a href="#">XP_015774550.1</a>
Select seq ref XP_015752855.1	<a href="#">PREDICTED: myosin-10-like [Acropora digitifera]</a>	321	321	2.00E-96	36.63%	<a href="#">XP_015752855.1</a>
Select seq ref XP_015760291.1	<a href="#">PREDICTED: unconventional myosin-XVIIIa-like [Acropora digitifera]</a>	90.1	131	1.00E-18	36.42%	<a href="#">XP_015760291.1</a>
Select seq ref XP_015778219.1	<a href="#">PREDICTED: myosin-9-like [Acropora digitifera]</a>	187	187	4.00E-51	36.36%	<a href="#">XP_015778219.1</a>

### Appendix A.3 (continued)

Select seq ref XP_015757748.1	<a href="#">PREDICTED: unconventional myosin-XIX-like [Acropora digitifera]</a>	297	297	4.00E-90	35.70%	<a href="#">XP_015757748.1</a>
Select seq ref XP_015761283.1	<a href="#">PREDICTED: myosin-IIIa-like [Acropora digitifera]</a>	233	297	2.00E-66	35.68%	<a href="#">XP_015761283.1</a>
Select seq ref XP_015769070.1	<a href="#">PREDICTED: unconventional myosin-1f-like [Acropora digitifera]</a>	293	293	4.00E-90	35.61%	<a href="#">XP_015769070.1</a>
Select seq ref XP_015749603.1	<a href="#">PREDICTED: unconventional myosin-le-like [Acropora digitifera]</a>	40	40	0.002	32.35%	<a href="#">XP_015749603.1</a>
Select seq ref XP_015753714.1	<a href="#">PREDICTED: unconventional myosin-X-like [Acropora digitifera]</a>	157	157	4.00E-41	28.42%	<a href="#">XP_015753714.1</a>

#### Spot 24.

#### GFP-like fluorescent chromoprotein cFP484 [Orbicella]

#### XP\_020605513.1

#### PEPTIDE SEQUENCES:

#### yprdiadyfkqsf

Description	Total Score	Query	E value	Per. Ident	Accession
Select seq ref XP_020605513.1 <a href="#">GFP-like fluorescent chromoprotein cFP484 [Orbicella faveolata]</a>	467	100%	1.00E-166	100.00%	<a href="#">XP_020605513.1</a>
Select seq gb ACD13193.1  <a href="#">green fluorescent GFP-like protein [Favites abdita]</a>	420	100%	5.00E-148	87.95%	<a href="#">ACD13193.1</a>
Select seq gb ABS87212.1  <a href="#">green fluorescent protein [Montastraea cavernosa]</a>	837	100%	3.00E-147	88.11%	<a href="#">ABS87212.1</a>
Select seq gb ABB17968.1  <a href="#">green fluorescent GFP-like protein [Echinophyllia echinata]</a>	417	100%	6.00E-147	87.50%	<a href="#">ABB17968.1</a>
Select seq gb AAO61601.1  <a href="#">green fluorescent protein [Montastraea cavernosa]</a>	417	100%	7.00E-147	87.67%	<a href="#">AAO61601.1</a>
Select seq gb AAO64989.1  <a href="#">green fluorescent protein R4 [synthetic construct]</a>	417	100%	1.00E-146	88.11%	<a href="#">AAO64989.1</a>
Select seq gb AAK83923.1  <a href="#">green fluorescent protein [Orbicella faveolata]</a>	417	100%	1.00E-146	88.11%	<a href="#">AAK83923.1</a>
Select seq gb AAO64994.1  <a href="#">green fluorescent protein G4 [synthetic construct]</a>	417	100%	1.00E-146	88.11%	<a href="#">AAO64994.1</a>
Select seq gb AAU04449.1  <a href="#">green fluorescent protein G1 [Orbicella faveolata]</a>	416	100%	3.00E-146	87.67%	<a href="#">AAU04449.1</a>
Select seq gb AAO43180.1  <a href="#">green fluorescent protein [Monster GFP vector pHMGFP]</a>	414	99%	1.00E-145	87.61%	<a href="#">AAO43180.1</a>
Select seq gb AAV66356.1  <a href="#">'Red/Green ancestor' ancestral fluorescent protein variant C05</a>	414	100%	3.00E-145	87.05%	<a href="#">AAV66356.1</a>

#### Spot 25.

#### GPI inositol-deacylase-like [Orbicella faveolata]

#### XP\_020615720.1

#### PEPTIDE SEQUENCES:

#### lygegyadrskgrlrgsp

Description	Total Score	Query	E value	Per. Ident	Accession
Select seq ref XP_020615720.1 <a href="#">GPI inositol-deacylase-like [Orbicella faveolata]</a>	1811	100%	0	100.00%	<a href="#">XP_020615720.1</a>
Select seq ref XP_020616369.1 <a href="#">GPI inositol-deacylase-like [Orbicella faveolata]</a>	1797	100%	0	98.98%	<a href="#">XP_020616369.1</a>
Select seq ref XP_027038149.1 <a href="#">GPI inositol-deacylase-like [Pocillopora damicornis]</a>	1229	99%	0	68.71%	<a href="#">XP_027038149.1</a>
Select seq ref XP_022805945.1 <a href="#">GPI inositol-deacylase-like isoform X1 [Stylophora pistillata]</a>	1207	100%	0	67.27%	<a href="#">XP_022805945.1</a>
Select seq ref XP_015778864.1 <a href="#">PREDICTED: GPI inositol-deacylase-like [Acropora digitifera]</a>	1193	100%	0	64.07%	<a href="#">XP_015778864.1</a>
Select seq gb RMX50689.1  <a href="#">hypothetical protein pdam_00013226 [Pocillopora damicornis]</a>	1169	94%	0	68.62%	<a href="#">RMX50689.1</a>

Select seq gb PFX15813.1	<a href="#">GPI inositol-deacylase [Stylophora pistillata]</a>	1093	88%	0	69.12%	<a href="#">PFX15813.1</a>
Select seq ref XP_022805946.1	<a href="#">GPI inositol-deacylase-like isoform X2 [Stylophora pistillata]</a>	959	81%	0	64.69%	<a href="#">XP_022805946.1</a>
Select seq ref XP_020907447.1	<a href="#">GPI inositol-deacylase [Exaiptasia pallida]</a>	818	99%	0	45.02%	<a href="#">XP_020907447.1</a>
Select seq ref XP_001637866.1	<a href="#">predicted protein [Nematostella vectensis]</a>	602	64%	0	51.40%	<a href="#">XP_001637866.1</a>
Select seq ref XP_002600834.1	<a href="#">hypothetical protein BRAFLDRAFT_279100 [Branchiostoma flo]</a>	498	96%	6.00E-159	33.98%	<a href="#">XP_002600834.1</a>

<b>Spot 26.</b>	<b>Green fluorescent protein</b>	<b>ABC68475.1</b>	<b>PEPTIDE SEQUENCES:</b>			<b>dlkvvdggplpf</b>
	Description	<u>Total Score</u>	<u>Query</u> Cover	<u>E value</u>	<u>Per. Ident</u>	Accession
Select seq gb ABC68475.1	<a href="#">green fluorescent protein [Orbicella faveolata]</a>	469	100%	7.00E-171	100.00%	<a href="#">ABC68475.1</a>
Select seq ref XP_020605513.1	<a href="#">GFP-like fluorescent chromoprotein cFP484 [Orbicella faveolat</a>	399	100%	3.00E-143	84.89%	<a href="#">XP_020605513.1</a>

### Appendix A.3 (continued)

Select seq ref XP_020605512.1	<a href="#">GFP-like fluorescent chromoprotein cFP484 [Orbicella faveolat</a>	397	100%	2.00E-142	83.84%	<a href="#">XP_020605512.1</a>
Select seq gb AAU04449.1	<a href="#">green fluorescent protein G1 [Orbicella faveolata]</a>	397	100%	3.00E-142	84.21%	<a href="#">AAU04449.1</a>
Select seq gb AAK83923.1	<a href="#">green fluorescent protein [Orbicella faveolata]</a>	394	100%	3.00E-141	83.77%	<a href="#">AAK83923.1</a>
Select seq ref XP_020623141.1	<a href="#">GFP-like fluorescent chromoprotein cFP484 [Orbicella faveolat</a>	394	100%	3.00E-141	82.53%	<a href="#">XP_020623141.1</a>
Select seq ref XP_020605521.1	<a href="#">GFP-like fluorescent chromoprotein cFP484 isoform X1 [Orbice</a>	387	100%	2.00E-138	81.22%	<a href="#">XP_020605521.1</a>
Select seq ref XP_020630220.1	<a href="#">GFP-like fluorescent chromoprotein cFP484 [Orbicella faveolat</a>	340	95%	3.00E-120	77.21%	<a href="#">XP_020630220.1</a>
Select seq ref XP_020630140.1	<a href="#">GFP-like fluorescent chromoprotein cFP484 [Orbicella faveolat</a>	307	99%	7.00E-107	65.64%	<a href="#">XP_020630140.1</a>
Select seq ref XP_020627712.1	<a href="#">GFP-like fluorescent chromoprotein cFP484 [Orbicella faveolat</a>	291	80%	3.00E-101	75.96%	<a href="#">XP_020627712.1</a>
Select seq ref XP_020630143.1	<a href="#">GFP-like fluorescent chromoprotein cFP484 [Orbicella faveolat</a>	580	96%	3.00E-100	63.47%	<a href="#">XP_020630143.1</a>
Select seq ref XP_020630180.1	<a href="#">GFP-like fluorescent chromoprotein cFP484 [Orbicella faveolat</a>	275	76%	5.00E-95	73.91%	<a href="#">XP_020630180.1</a>

<b>Spot 27.</b>	<b>Pax C</b>	<b>B6DC09</b>	<b>PEPTIDE SEQUENCES:</b>			<b>kshypdvatreela</b>
	Description	<u>Total score</u>	<u>E value</u>	<u>Ident</u>	<u>Accession</u>	
<a href="#">paired box protein Pax-3-B-like</a>	75.5	100%	2.00E-18	92.50%	<a href="#">XP_020628638.1</a>	
Select seq ref XP_020630062.1	<a href="#">paired box protein Pax-3-B-like [Orbicella faveolata]</a>	63.5	97%	3.00E-14	71.79%	<a href="#">XP_020630062.1</a>
Select seq ref XP_020631883.1	<a href="#">retinal homeobox protein Rx-B-like [Orbicella faveolata]</a>	62	95%	5.00E-14	76.32%	<a href="#">XP_020631883.1</a>
Select seq ref XP_020603228.1	<a href="#">paired box protein Pax-6-like isoform X1 [Orbicella faveolata]</a>	62.8	97%	6.00E-14	66.67%	<a href="#">XP_020603228.1</a>
Select seq ref XP_020629450.1	<a href="#">aristaless-related homeobox protein-like [Orbicella faveolata]</a>	62.4	95%	8.00E-14	73.68%	<a href="#">XP_020629450.1</a>
Select seq ref XP_020632255.1	<a href="#">homeobox protein goosecoid-like [Orbicella faveolata]</a>	59.3	97%	4.00E-13	66.67%	<a href="#">XP_020632255.1</a>
Select seq ref XP_020630078.1	<a href="#">paired box protein Pax-3-like [Orbicella faveolata]</a>	58.2	97%	2.00E-12	64.10%	<a href="#">XP_020630078.1</a>
Select seq ref XP_020611047.1	<a href="#">homeobox protein unc-4 homolog [Orbicella faveolata]</a>	58.2	100%	2.00E-12	65.00%	<a href="#">XP_020611047.1</a>
Select seq ref XP_020625918.1	<a href="#">paired box protein Pax-3-B-like [Orbicella faveolata]</a>	57.8	100%	4.00E-12	62.50%	<a href="#">XP_020625918.1</a>
Select seq ref XP_020620522.1	<a href="#">ALX homeobox protein 1-like [Orbicella faveolata]</a>	57.4	95%	5.00E-12	65.79%	<a href="#">XP_020620522.1</a>
Select seq ref XP_020628711.1	<a href="#">diencephalon/mesencephalon homeobox protein 1-A-like [Ork</a>	56.6	97%	6.00E-12	56.41%	<a href="#">XP_020628711.1</a>
Select seq ref XP_020628665.1	<a href="#">paired mesoderm homeobox protein 2-like [Orbicella faveolat</a>	56.2	97%	6.00E-12	58.97%	<a href="#">XP_020628665.1</a>

<b>Spot 28.</b>	<b>BMP2/4, partial [Orbicella faveolata]</b>	<b>AH621804</b>	<b>PEPTIDE SEQUENCES:</b>			<b>vappgykafy</b>
	Description	<u>Total Score</u>	<u>Query</u>	<u>E value</u>	<u>Per. Ident</u>	Accession

Select seq gb AHZ61804.1	<a href="#">BMP2/4 [Orbicella faveolata]</a>	99	100%	3.00E-26	100.00%	<a href="#">AHZ61804.1</a>
Select seq gb AHZ61802.1	<a href="#">BMP2/4 [Astrea curta]</a>	97.4	100%	1.00E-25	97.83%	<a href="#">AHZ61802.1</a>
Select seq gb AHZ61765.1	<a href="#">BMP2/4 [Dichocoenia stokesii]</a>	97.4	100%	1.00E-25	97.83%	<a href="#">AHZ61765.1</a>
Select seq gb AHZ61740.1	<a href="#">BMP2/4 [Acanthastrea echinata]</a>	96.7	100%	2.00E-25	95.65%	<a href="#">AHZ61740.1</a>
Select seq gb AHZ61789.1	<a href="#">BMP2/4 [Isophyllia sinuosa]</a>	95.9	100%	4.00E-25	95.65%	<a href="#">AHZ61789.1</a>
Select seq gb AHZ61761.1	<a href="#">BMP2/4 [Dendrogyra cylindrus]</a>	95.5	100%	6.00E-25	95.65%	<a href="#">AHZ61761.1</a>
Select seq gb AHZ61769.1	<a href="#">BMP2/4 [Dichocoenia stokesii]</a>	95.5	100%	7.00E-25	95.65%	<a href="#">AHZ61769.1</a>
Select seq gb AHZ61773.1	<a href="#">BMP2/4 [Pseudodiploria strigosa]</a>	95.1	100%	8.00E-25	93.48%	<a href="#">AHZ61773.1</a>
Select seq gb AHZ61757.1	<a href="#">BMP2/4 [Coscinaraea monile]</a>	95.1	100%	8.00E-25	95.65%	<a href="#">AHZ61757.1</a>
Select seq gb AHZ61794.1	<a href="#">BMP2/4 [Lobophyllia hemprichii]</a>	95.1	100%	9.00E-25	93.48%	<a href="#">AHZ61794.1</a>

### Appendix A.3 (continued)

Select seq gb AHZ61815.1	<a href="#">BMP2/4 [Sandalolitha robusta]</a>	94	100%	2.00E-24	93.48%	<a href="#">AHZ61815.1</a>
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#### Spot 29.

#### Caspase 8

	Description	ADG23096.1	PEPTIDE SEQUENCES:			Accession
		Max Score	Total Score	E value	Per. Ident	
Select seq gb ADG23096.1	<a href="#">caspase 8 [Acropora palmata]</a>	944	944	0	100.00%	<a href="#">ADG23096.1</a>
Select seq ref XP_015756325.1	<a href="#">PREDICTED: caspase-10-like [Acropora digitifera]</a>	619	712	0	92.84%	<a href="#">XP_015756325.1</a>
Select seq gb AJG36593.1	<a href="#">caspase 8 [Acropora millepora]</a>	616	848	0	92.54%	<a href="#">AJG36593.1</a>
Select seq gb AJG36591.1	<a href="#">caspase 8 [Acropora millepora]</a>	615	848	0	92.54%	<a href="#">AJG36591.1</a>
Select seq ref XP_015756331.1	<a href="#">PREDICTED: caspase-3-like [Acropora digitifera]</a>	416	644	5.00E-143	86.83%	<a href="#">XP_015756331.1</a>
Select seq ref XP_015758750.1	<a href="#">PREDICTED: LOW QUALITY PROTEIN: dynein heavy chain 2, axc</a>	29.6	29.6	6.3	55.56%	<a href="#">XP_015758750.1</a>
Select seq ref XP_015780003.1	<a href="#">PREDICTED: volume-regulated anion channel subunit LRRC8A-I</a>	71.2	71.2	6.00E-13	45.12%	<a href="#">XP_015780003.1</a>
Select seq ref XP_015780009.1	<a href="#">PREDICTED: volume-regulated anion channel subunit LRRC8A-I</a>	72	72	4.00E-13	44.74%	<a href="#">XP_015780009.1</a>
Select seq ref XP_015768208.1	<a href="#">PREDICTED: caspase-3-like [Acropora digitifera]</a>	39.3	39.3	0.005	42.37%	<a href="#">XP_015768208.1</a>
Select seq ref XP_015766400.1	<a href="#">PREDICTED: caspase-3-like [Acropora digitifera]</a>	89.4	89.4	3.00E-19	36.69%	<a href="#">XP_015766400.1</a>
Select seq ref XP_015774399.1	<a href="#">PREDICTED: uncharacterized protein LOC107352599 [Acropora</a>	57.4	57.4	1.00E-08	36.59%	<a href="#">XP_015774399.1</a>
Select seq ref XP_015770993.1	<a href="#">PREDICTED: uncharacterized protein LOC107349364 isoform X</a>	60.5	60.5	1.00E-09	34.78%	<a href="#">XP_015770993.1</a>
Select seq ref XP_015770992.1	<a href="#">PREDICTED: uncharacterized protein LOC107349364 isoform X</a>	60.5	60.5	1.00E-09	34.78%	<a href="#">XP_015770992.1</a>

#### Spot 30.

#### Ectonucleoside triphosphate diphosphohydrolase 1

	Description	XP_015779265	PEPTIDE SEQUENCES:			Accession
		Max Score	Total Score	E value	Per. Ident	
Select seq ref XP_015779265.1	<a href="#">PREDICTED: ectonucleoside triphosphate diphosphohydrolase</a>	596	596	0	100.00%	<a href="#">XP_015779265.1</a>
Select seq ref XP_015756595.1	<a href="#">PREDICTED: nucleoside-triphosphatase ntp-1-like [Acropora di]</a>	111	111	5.00E-29	33.90%	<a href="#">XP_015756595.1</a>
Select seq ref XP_015756628.1	<a href="#">PREDICTED: ectonucleoside triphosphate diphosphohydrolase</a>	94	94	1.00E-21	32.33%	<a href="#">XP_015756628.1</a>
Select seq ref XP_015768859.1	<a href="#">PREDICTED: ectonucleoside triphosphate diphosphohydrolase</a>	93.2	93.2	1.00E-21	33.90%	<a href="#">XP_015768859.1</a>
Select seq ref XP_015768456.1	<a href="#">PREDICTED: ectonucleoside triphosphate diphosphohydrolase</a>	84	84	1.00E-18	33.68%	<a href="#">XP_015768456.1</a>

#### Spot 31.

#### Carbonic anhydrase 5A, mitochondrial-like [Orbicella

	Description	XP_020613891.1	PEPTIDE SEQUENCES:			Accession
		Total Score	Query	E value	Per. Ident	

Select seq ref XP_020613615.1	<a href="#">carbonic anhydrase 2-like [Orbicella faveolata]</a>	229	86%	2.00E-74	92.50%	<a href="#">XP_020613615.1</a>
Select seq ref XP_022803955.1	<a href="#">carbonic anhydrase 1-like [Stylophora pistillata]</a>	171	71%	1.00E-49	79.59%	<a href="#">XP_022803955.1</a>
Select seq ref XP_027050584.1	<a href="#">carbonic anhydrase 1-like [Pocillopora damicornis]</a>	169	71%	6.00E-49	77.55%	<a href="#">XP_027050584.1</a>
Select seq ref XP_029205258.1	<a href="#">uncharacterized protein LOC114969126 [Acropora millepora]</a>	161	78%	3.00E-43	66.97%	<a href="#">XP_029205258.1</a>
Select seq ref XP_015770689.1	<a href="#">PREDICTED: uncharacterized protein LOC107349103 [Acropora]</a>	160	78%	5.00E-43	66.06%	<a href="#">XP_015770689.1</a>
Select seq ref XP_020901977.1	<a href="#">carbonic anhydrase 7 [Exaiptasia pallida]</a>	141	72%	1.00E-38	62.00%	<a href="#">XP_020901977.1</a>
Select seq gb ANJ59782.1	<a href="#">alpha carbonic anhydrase 6 [Exaiptasia pallida]</a>	140	72%	2.00E-38	62.00%	<a href="#">ANJ59782.1</a>
Select seq ref XP_001632501.1	<a href="#">predicted protein [Nematostella vectensis]</a>	131	69%	3.00E-35	60.82%	<a href="#">XP_001632501.1</a>
Select seq gb ODN05569.1	<a href="#">Carbonic anhydrase 2 [Orchesella cincta]</a>	101	65%	3.00E-23	51.65%	<a href="#">ODN05569.1</a>
Select seq ref XP_020600771.1	<a href="#">carbonic anhydrase-like isoform X2 [Orbicella faveolata]</a>	100	67%	2.00E-22	48.39%	<a href="#">XP_020600771.1</a>
Select seq ref XP_020600769.1	<a href="#">carbonic anhydrase-like isoform X1 [Orbicella faveolata]</a>	100	67%	5.00E-22	48.39%	<a href="#">XP_020600769.1</a>
Select seq gb PRD34444.1	<a href="#">Ca13 [Trichonephila clavipes]</a>	91.7	74%	1.00E-20	45.63%	<a href="#">PRD34444.1</a>

### Appendix A.3 (continued)

<b>Spot 32.</b>	<b>Calmodullin</b>	<b>ACY07618.1</b>	<b>PEPTIDE SEQUENCES:</b>			<b>vmrncgesltnae</b>
	Description	<u>Max score</u>	<u>Total score</u>	<u>E value</u>	<u>Ident</u>	Accession
Select seq gb ACY07618.1	<a href="#">calmodulin-like protein [Acropora millepora]</a>	16.8	25.9	26	67%	<a href="#">ACY07618.1</a>
Select seq dbj BAQ19096.1	<a href="#">paired box B protein [Acropora digitifera]</a>	15.9	15.9	54	100%	<a href="#">BAQ19096.1</a>
Select seq gb AAF64460.1 AF2	<a href="#">transcription factor PaxB [Acropora millepora]</a>	15.9	15.9	54	100%	<a href="#">AAF64460.1</a>
Select seq sp B3EWZ3.1 CADN	<a href="#">RecName: Full=Coadhesin</a>	15.9	47.7	54	100%	<a href="#">B3EWZ3.1</a>
Select seq sp B3EWZ5.1 MLRP	<a href="#">RecName: Full=MAM and LDL-receptor class A domain-contain</a>	15.9	31.8	54	100%	<a href="#">B3EWZ5.1</a>
Select seq sp B3EWZ6.1 MLRP	<a href="#">RecName: Full=MAM and LDL-receptor class A domain-contain</a>	15.9	25.9	54	100%	<a href="#">B3EWZ6.1</a>
Select seq gb KJD18916.1	<a href="#">hypothetical protein VE30_10855 [Halomonas meridiana]</a>	15.5	15.5	79	67%	<a href="#">KJD18916.1</a>
Select seq gb AFI99104.1	<a href="#">56kDa selenium binding protein [Acropora millepora]</a>	15.5	15.5	79	80%	<a href="#">AFI99104.1</a>
Select seq sp B3EWY9.1 MLP_	<a href="#">RecName: Full=Mucin-like protein</a>	15.5	29.7	79	71%	<a href="#">B3EWY9.1</a>
Select seq gb AET09738.1	<a href="#">hypothetical protein p4_37 [Acropora millepora]</a>	15.1	15.1	116	100%	<a href="#">AET09738.1</a>
Select seq gb ADG44981.1	<a href="#">hypothetical protein [Acropora millepora]</a>	15.1	15.1	116	100%	<a href="#">ADG44981.1</a>
Select seq gb KJD20578.1	<a href="#">spermidine/putrescine ABC transporter substrate-binding prot</a>	15.1	15.1	116	100%	<a href="#">KJD20578.1</a>
Select seq dbj BAQ19100.1	<a href="#">orthodenticle homeobox A protein [Acropora digitifera]</a>	13.4	13.4	531	80%	<a href="#">BAQ19100.1</a>
Select seq gb ABK41270.1	<a href="#">orthodenticle A [Acropora millepora]</a>	13.4	13.4	531	80%	<a href="#">ABK41270.1</a>
Select seq sp B8RJM0.1 USOM	<a href="#">RecName: Full=Uncharacterized skeletal organic matrix proteir</a>	12.5	12.5	1128	60%	<a href="#">B8RJM0.1</a>
<b>Spot 33.</b>	<b>Scleractinian cysteine-rich protein [Montastraea faveolata]</b>	<b>B2ZG38</b>	<b>PEPTIDE SEQUENCES:</b>			<b>aakfhlcIII</b>
	Description	<u>Total Score</u>	<u>Query</u>	<u>E value</u>	<u>Per. Ident</u>	Accession
Select seq sp B2ZG38.1	<a href="#">RecName: Full=Small cysteine-rich protein 8; Short=Mfav-SCRi</a>	153	100%	6.00E-47	100.00%	<a href="#">B2ZG38.1</a>
Select seq sp COH693.1	<a href="#">RecName: Full=Small cysteine-rich protein 1 1; Short=Mcap-SC</a>	51.2	97%	1.00E-06	36.25%	<a href="#">COH693.1</a>
Select seq sp COH694.1	<a href="#">RecName: Full=Small cysteine-rich protein 1 2; Short=Mcap-SC</a>	50.8	97%	2.00E-06	36.25%	<a href="#">COH694.1</a>
Select seq ref XP_020613205.1	<a href="#">small cysteine-rich protein 8-like [Orbicella faveolata]</a>	48.1	98%	3.00E-05	53.57%	<a href="#">XP_020613205.1</a>

Select seq ref XP_015765734.1	<a href="#">PREDICTED: small cysteine-rich protein 1 2-like isoform X1 [Acr</a>	40.8	89%	0.026	32.00%	<a href="#">XP_015765734.1</a>
Select seq ref XP_020631985.1	<a href="#">small cysteine-rich protein 6 [Orbicella faveolata]</a>	37	63%	0.59	48.00%	<a href="#">XP_020631985.1</a>
Select seq ref XP_020610104.1	<a href="#">small cysteine-rich protein 6-like [Orbicella faveolata]</a>	36.6	87%	0.64	42.86%	<a href="#">XP_020610104.1</a>
Select seq ref XP_020610088.1	<a href="#">small cysteine-rich protein 6-like [Orbicella faveolata]</a>	36.6	63%	1.3	46.00%	<a href="#">XP_020610088.1</a>
Select seq ref WP_126197983.1	<a href="#">oligopeptide ABC transporter ATP-binding protein OppD [Serra</a>	37.4	44%	1.3	51.52%	<a href="#">WP_126197983.1</a>
Select seq ref NP_536705.3	<a href="#">mucin-4 precursor [Mus musculus]</a>	37.4	51%	1.3	38.64%	<a href="#">NP_536705.3</a>
Select seq ref WP_126199601.1	<a href="#">oligopeptide ABC transporter ATP-binding protein OppD [Serra</a>	37.4	44%	1.4	51.52%	<a href="#">WP_126199601.1</a>
Select seq ref XP_021041269.1	<a href="#">mucin-4 [Mus caroli]</a>	37.4	51%	1.7	38.64%	<a href="#">XP_021041269.1</a>
Select seq ref WP_079656102.1	<a href="#">dipeptide ABC transporter ATP-binding protein [Serratia marce</a>	37	44%	1.9	51.52%	<a href="#">WP_079656102.1</a>

### Appendix A.3 (continued)

<b>Spot 34.</b>	<b>DnaJ homolog subfamily C member 5-like [Orbicella</b>	<b>XP_020605856.1</b>	<b>PEPTIDE SEQUENCES:</b>	<b>malkhhpdkn</b>	
	Description	<u>Total Score</u>	<u>Query</u>	<u>E value</u>	<u>Per. Ident</u> <u>Accession</u>
Select seq ref XP_020605856.1	<a href="#">dnaJ homolog subfamily C member 5-like [Orbicella faveolata]</a>	153	100%	7.00E-51	100.00% <a href="#">XP_020605856.1</a>
Select seq ref XP_020629051.1	<a href="#">dnaJ homolog subfamily B member 2-like [Orbicella faveolata]</a>	56.2	63%	3.00E-11	57.45% <a href="#">XP_020629051.1</a>
Select seq ref XP_020614854.1	<a href="#">dnaJ homolog subfamily A member 2-like [Orbicella faveolata]</a>	55.8	65%	6.00E-11	53.19% <a href="#">XP_020614854.1</a>
Select seq ref XP_020626187.1	<a href="#">dnaJ homolog subfamily B member 11-like [Orbicella faveolata]</a>	55.5	75%	1.00E-10	44.44% <a href="#">XP_020626187.1</a>
Select seq ref XP_020622054.1	<a href="#">dnaJ protein homolog 1-like [Orbicella faveolata]</a>	53.9	86%	3.00E-10	45.16% <a href="#">XP_020622054.1</a>
Select seq ref XP_020606156.1	<a href="#">dnaJ homolog subfamily B member 6-like [Orbicella faveolata]</a>	53.1	59%	4.00E-10	56.82% <a href="#">XP_020606156.1</a>
Select seq ref XP_020622055.1	<a href="#">dnaJ homolog subfamily B member 1-like [Orbicella faveolata]</a>	53.5	73%	4.00E-10	49.06% <a href="#">XP_020622055.1</a>
Select seq ref XP_020618047.1	<a href="#">dnaJ homolog subfamily A member 1-like [Orbicella faveolata]</a>	52.8	65%	7.00E-10	51.06% <a href="#">XP_020618047.1</a>

<b>Spot 35.</b>	<b>Alpha i G protein</b>	<b>AFZ78088.1</b>	<b>PEPTIDE SEQUENCES:</b>	<b>caqyrqvvv</b>	
	Description	<u>Max Score</u>	<u>Total Score</u>	<u>E value</u>	<u>Per. Ident</u> <u>Accession</u>
Select seq gb AFZ78088.1	<a href="#">alpha i G protein [Acropora palmata]</a>	741	741	0	100.00% <a href="#">AFZ78088.1</a>
Select seq ref XP_015777008.1	<a href="#">PREDICTED: guanine nucleotide-binding protein G(o) subunit a</a>	496	496	1.00E-177	66.95% <a href="#">XP_015777008.1</a>
Select seq ref XP_015780306.1	<a href="#">PREDICTED: guanine nucleotide-binding protein G(q) subunit a</a>	328	328	2.00E-111	49.15% <a href="#">XP_015780306.1</a>
Select seq ref XP_015772099.1	<a href="#">PREDICTED: guanine nucleotide-binding protein subunit alpha-</a>	298	298	3.00E-99	42.49% <a href="#">XP_015772099.1</a>
Select seq gb AFZ78087.1	<a href="#">alpha c G protein [Acropora palmata]</a>	269	269	7.00E-88	38.59% <a href="#">AFZ78087.1</a>
Select seq ref XP_015764888.1	<a href="#">PREDICTED: guanine nucleotide-binding protein G(i) subunit al</a>	207	207	2.00E-67	100.00% <a href="#">XP_015764888.1</a>
Select seq ref XP_015770327.1	<a href="#">PREDICTED: guanine nucleotide-binding protein G(s) subunit al</a>	213	213	6.00E-66	36.71% <a href="#">XP_015770327.1</a>
Select seq ref XP_015768491.1	<a href="#">PREDICTED: guanine nucleotide-binding protein G(t) subunit al</a>	88.2	88.2	8.00E-21	34.90% <a href="#">XP_015768491.1</a>
Select seq ref XP_015779045.1	<a href="#">PREDICTED: ADP-ribosylation factor 1 isoform X2 [Acropora dig</a>	50.1	50.1	3.00E-07	29.00% <a href="#">XP_015779045.1</a>
Select seq ref XP_015779044.1	<a href="#">PREDICTED: ADP-ribosylation factor 1 isoform X1 [Acropora dig</a>	48.5	48.5	1.00E-06	29.00% <a href="#">XP_015779044.1</a>
Select seq ref XP_020632509.1	<a href="#">dnaJ homolog subfamily B member 13-like [Orbicella faveolata]</a>	51.6	65%	2.00E-09	53.19% <a href="#">XP_020632509.1</a>

Select seq ref XP_020609046.1	<a href="#">dnaJ homolog subfamily B member 9-like [Orbicella faveolata]</a>	47.4	65%	6.00E-08	44.68%	<a href="#">XP_020609046.1</a>
Select seq ref XP_020625391.1	<a href="#">dnaJ homolog subfamily B member 14-like [Orbicella faveolata]</a>	46.2	59%	2.00E-07	48.84%	<a href="#">XP_020625391.1</a>
Select seq ref XP_020603256.1	<a href="#">dnaJ homolog subfamily C member 21-like [Orbicella faveolata]</a>	45.4	58%	3.00E-07	51.16%	<a href="#">XP_020603256.1</a>
Select seq ref XP_020618202.1	<a href="#">dnaJ homolog subfamily C member 17-like [Orbicella faveolata]</a>	44.7	54%	6.00E-07	51.28%	<a href="#">XP_020618202.1</a>
Select seq ref XP_020617012.1	<a href="#">dnaJ homolog subfamily C member 11-like [Orbicella faveolata]</a>	44.3	65%	9.00E-07	42.00%	<a href="#">XP_020617012.1</a>

**Spot 36. Small cysteine-rich protein 6 C1KIZ5 PEPTIDE SEQUENCES: iilgaltvqg avsg**

	Description	Max Score	Total Score	E value	Per. Ident	Accession
Select seq ref XP_020631985.1	<a href="#">small cysteine-rich protein 6 [Orbicella faveolata]</a>	169	169	2.00E-53	100.00%	<a href="#">XP_020631985.1</a>
Select seq ref XP_020610088.1	<a href="#">small cysteine-rich protein 6-like [Orbicella faveolata]</a>	129	129	7.00E-37	76.54%	<a href="#">XP_020610088.1</a>
Select seq ref XP_020610104.1	<a href="#">small cysteine-rich protein 6-like [Orbicella faveolata]</a>	86.7	86.7	2.00E-20	61.54%	<a href="#">XP_020610104.1</a>
Select seq sp C1KIZ3.1	<a href="#">RecName: Full=Small cysteine-rich protein 4; Short=Mfav-SCRI</a>	84.3	84.3	2.00E-19	63.29%	<a href="#">C1KIZ3.1</a>
Select seq ref XP_022817917.1	<a href="#">uncharacterized protein LOC111350529 [Spodoptera litura]</a>	39.7	39.7	0.27	37.04%	<a href="#">XP_022817917.1</a>

**Appendix A.3 (continued)**

**Spot 37. Zinc finger protein 768-like [Orbicella faveolata] XP\_020615964.1 PEPTIDE SEQUENCES: gytvdflypypvse**

	Description	Max Score	Total Score	E value	Per. Ident	Accession
Select seq gb AHA90941.1	<a href="#">cytochrome oxidase subunit I [Orbicella faveolata]</a>	245	245	100%	100.00%	<a href="#">AHA90940.1</a>
Select seq gb AHA90942.1	<a href="#">cytochrome oxidase subunit I [Orbicella faveolata]</a>	245	245	5.00E-81	99.20%	<a href="#">AHA90942.1</a>
Select seq gb AHA90943.1	<a href="#">cytochrome oxidase subunit I [Orbicella faveolata]</a>	243	243	6.00E-81	99.20%	<a href="#">AHA90943.1</a>
Select seq gb AHA90945.1	<a href="#">cytochrome oxidase subunit I [Orbicella faveolata]</a>	244	244	6.00E-81	99.20%	<a href="#">AHA90945.1</a>
Select seq gb AHA90941.1	<a href="#">cytochrome oxidase subunit I [Orbicella faveolata]</a>	244	244	8.00E-81	99.20%	<a href="#">AHA90941.1</a>
Select seq gb AFP73387.1	<a href="#">cytochrome oxidase subunit I [Pseudodiploria strigosa]</a>	243	243	4.00E-80	97.60%	<a href="#">AFP73387.1</a>
Select seq gb AAS17027.1	<a href="#">cytochrome oxidase subunit I [Orbicella annularis]</a>	244	244	4.00E-80	99.20%	<a href="#">AAS17027.1</a>
Select seq gb ACJ09533.1	<a href="#">cytochrome oxidase subunit I [Platygyra pini]</a>	242	242	6.00E-80	98.40%	<a href="#">ACJ09533.1</a>
Select seq gb ABY85346.1	<a href="#">cytochrome oxidase subunit I [Favites cf. valenciennesi DH-201]</a>	243	243	6.00E-80	98.40%	<a href="#">ABY85346.1</a>
Select seq gb ABY85345.1	<a href="#">cytochrome oxidase subunit I [Favites cf. valenciennesi DH-201]</a>	243	243	7.00E-80	98.40%	<a href="#">ABY85345.1</a>
Select seq dbj BAD11414.1	<a href="#">cytochrome oxidase I [Orbicella annularis]</a>	243	243	9.00E-80	99.20%	<a href="#">BAD11414.1</a>
Select seq gb ABY85307.1	<a href="#">cytochrome oxidase subunit I [Dipsastraea matthaii]</a>	242	242	1.00E-79	98.40%	<a href="#">ABY85307.1</a>

**Spot 38. Alpha q G protein AFZ78090 PEPTIDE SEQUENCES: ndegmkecyd**

	Description	Max Score	Total Score	E value	Per. Ident	Accession
Select seq gb AFZ78090.1	<a href="#">alpha q G protein [Acropora palmata]</a>	736	736	0	100.00%	<a href="#">AFZ78090.1</a>
Select seq ref XP_015780306.1	<a href="#">PREDICTED: guanine nucleotide-binding protein G(q) subunit a</a>	733	733	0	99.43%	<a href="#">XP_015780306.1</a>
Select seq ref XP_015777008.1	<a href="#">PREDICTED: guanine nucleotide-binding protein G(o) subunit a</a>	333	333	4.00E-113	49.72%	<a href="#">XP_015777008.1</a>
Select seq gb AFZ78089.1	<a href="#">alpha o G protein [Acropora palmata]</a>	329	329	9.00E-112	49.44%	<a href="#">AFZ78089.1</a>
Select seq gb AFZ78088.1	<a href="#">alpha i G protein [Acropora palmata]</a>	329	329	1.00E-111	49.15%	<a href="#">AFZ78088.1</a>

Select seq ref XP_015772099.1	<a href="#">PREDICTED: guanine nucleotide-binding protein subunit alpha-</a>	348	348	2.00E-119	49.15%	<a href="#">XP_015772099.1</a>
Select seq ref XP_015764888.1	<a href="#">PREDICTED: guanine nucleotide-binding protein G(i) subunit al</a>	81.3	81.3	7.00E-19	43.16%	<a href="#">XP_015764888.1</a>
Select seq ref XP_015770327.1	<a href="#">PREDICTED: guanine nucleotide-binding protein G(s) subunit al</a>	233	233	2.00E-73	37.47%	<a href="#">XP_015770327.1</a>
Select seq gb AFZ78087.1	<a href="#">alpha c G protein [Acropora palmata]</a>	226	226	2.00E-71	35.40%	<a href="#">AFZ78087.1</a>
Select seq ref XP_015768491.1	<a href="#">PREDICTED: guanine nucleotide-binding protein G(t) subunit al</a>	71.2	71.2	9.00E-15	29.58%	<a href="#">XP_015768491.1</a>
Select seq ref XP_015759852.1	<a href="#">PREDICTED: ADP-ribosylation factor 3-like [Acropora digitifera]</a>	46.2	46.2	8.00E-06	27.84%	<a href="#">XP_015759852.1</a>
Select seq ref XP_015779044.1	<a href="#">PREDICTED: ADP-ribosylation factor 1 isoform X1 [Acropora dig</a>	41.6	41.6	2.00E-04	26.60%	<a href="#">XP_015779044.1</a>
Select seq ref XP_015779045.1	<a href="#">PREDICTED: ADP-ribosylation factor 1 isoform X2 [Acropora dig</a>	40	40	7.00E-04	26.60%	<a href="#">XP_015779045.1</a>

**Spot 39.** **Alpha carbonic anhydrase** **AHZ61699.1** **PEPTIDE SEQUENCES:** **nisggllsqfraa**

Description	Max Score	Total Score	E value	Per. Ident	Accession
Select seq ref XP_015757476.1	25.4	25.4	8.9	88.89%	<a href="#">XP_015757476.1</a>
Select seq ref XP_015757475.1	25.4	25.4	9.9	72.73%	<a href="#">XP_015757475.1</a>
Select seq gb AHZ61629.1	155	155	1.00E-50	71.00%	<a href="#">AHZ61629.1</a>

**Appendix A.3 (continued)**

Select seq gb AHZ61634.1	<a href="#">alpha carbonic anhydrase [Acropora tenuis]</a>	145	145	4.00E-47	67.33%	<a href="#">AHZ61634.1</a>
Select seq ref XP_015774933.1	<a href="#">PREDICTED: carbonic anhydrase 1-like isoform X1 [Acropora di]</a>	67	67	5.00E-15	46.43%	<a href="#">XP_015774933.1</a>
Select seq ref XP_015761724.1	<a href="#">PREDICTED: putative carbonic anhydrase [Acropora digitifera]</a>	40.8	40.8	3.00E-05	46.15%	<a href="#">XP_015761724.1</a>
Select seq ref XP_015760670.1	<a href="#">PREDICTED: low-density lipoprotein receptor-related protein 4</a>	27.7	27.7	1.8	42.42%	<a href="#">XP_015760670.1</a>
Select seq gb ACJ64663.1	<a href="#">hypothetical protein A030-E11 [Acropora millepora]</a>	85.5	85.5	1.00E-21	41.67%	<a href="#">ACJ64663.1</a>
Select seq ref XP_015771455.1	<a href="#">PREDICTED: carbonic anhydrase 2-like [Acropora digitifera]</a>	85.5	85.5	1.00E-21	41.67%	<a href="#">XP_015771455.1</a>
Select seq ref XP_015771376.1	<a href="#">PREDICTED: carbonic anhydrase 12-like [Acropora digitifera]</a>	71.2	129	8.00E-16	41.10%	<a href="#">XP_015771376.1</a>
Select seq ref XP_015759239.1	<a href="#">PREDICTED: putative carbonic anhydrase-like protein 2 [Acrop</a>	65.9	65.9	5.00E-14	41.10%	<a href="#">XP_015759239.1</a>
Select seq ref XP_015759705.1	<a href="#">PREDICTED: carbonic anhydrase 2-like [Acropora digitifera]</a>	77.4	77.4	3.00E-18	38.24%	<a href="#">XP_015759705.1</a>
Select seq ref XP_015774481.1	<a href="#">PREDICTED: putative carbonic anhydrase [Acropora digitifera]</a>	45.8	45.8	5.00E-07	36.36%	<a href="#">XP_015774481.1</a>
Select seq gb ACJ64662.1	<a href="#">hypothetical protein C007-E7 [Acropora millepora]</a>	69.7	69.7	2.00E-15	35.64%	<a href="#">ACJ64662.1</a>
Select seq ref XP_015750571.1	<a href="#">PREDICTED: putative carbonic anhydrase [Acropora digitifera]</a>	47	47	2.00E-07	34.33%	<a href="#">XP_015750571.1</a>
Select seq ref XP_015770689.1	<a href="#">PREDICTED: uncharacterized protein LOC107349103 [Acropora</a>	69.7	69.7	3.00E-15	30.93%	<a href="#">XP_015770689.1</a>

**Spot 40.** **alpha carbonic anhydrase [Montastraea faveolata]** **XP\_020628594.1** **PEPTIDE SEQUENCES:** **kdyrdlkiaf**

Description	Total Score	Query	E value	Per. Ident	Accession
Select seq ref XP_020628594.1	863	863	100%	0	<a href="#">XP_020628594.1</a>
Select seq ref XP_020628593.1	332	332	47%	9.00E-109	<a href="#">XP_020628593.1</a>
Select seq ref XP_027055172.1	211	374	50%	8.00E-60	<a href="#">XP_027055172.1</a>
Select seq gb RMX36692.1	213	400	50%	1.00E-59	<a href="#">RMX36692.1</a>
Select seq gb ANJ59776.1	204	409	49%	3.00E-59	<a href="#">ANJ59776.1</a>
Select seq ref XP_022801331.1	192	192	49%	1.00E-54	<a href="#">XP_022801331.1</a>
Select seq gb PFX18799.1	192	192	49%	2.00E-54	<a href="#">PFX18799.1</a>
Select seq ref XP_027050353.1	188	188	40%	2.00E-54	<a href="#">XP_027050353.1</a>

Select seq ref XP_022799897.1	<a href="#">N66 matrix protein-like [Stylophora pistillata]</a>	180	242	45%	1.00E-48	<a href="#">XP_022799897.1</a>
Select seq ref XP_022801327.1	<a href="#">carbonic anhydrase 2-like [Stylophora pistillata]</a>	171	171	35%	3.00E-47	<a href="#">XP_022801327.1</a>
Select seq ref XP_022801328.1	<a href="#">carbonic anhydrase 2-like [Stylophora pistillata]</a>	169	169	35%	2.00E-46	<a href="#">XP_022801328.1</a>
Select seq gb PFX19740.1	<a href="#">Carbonic anhydrase 2 [Stylophora pistillata]</a>	181	461	50%	7.00E-46	<a href="#">PFX19740.1</a>

<b>Spot 41.</b>	<b>Galaxin</b>	<b>Description</b>	<b>D9IQ16.1</b>	<b>PEPTIDE SEQUENCES:</b>		<b>nveprvgaspmc</b>	
			<b>Total Score</b>	<b>Querv</b>	<b>E value</b>	<b>Per. Ident</b>	<b>Accession</b>
Select seq sp D9IQ16.1		<a href="#">RecName: Full=Galaxin; Flags: Precursor [Acropora millepora]</a>	681	100%	0	100.00%	<a href="#">D9IQ16.1</a>
Select seq ref XP_029187982.1		<a href="#">galaxin [Acropora millepora]</a>	676	100%	0	99.41%	<a href="#">XP_029187982.1</a>
Select seq ref XP_015751001.1		<a href="#">PREDICTED: galaxin [Acropora digitifera]</a>	674	100%	0	98.82%	<a href="#">XP_015751001.1</a>
Select seq gb ARA71553.1		<a href="#">galaxin [Acropora digitifera]</a>	668	100%	0	97.93%	<a href="#">ARA71553.1</a>
Select seq gb ART34494.1		<a href="#">galaxin [Galaxea astreata]</a>	387	97%	3.00E-131	58.88%	<a href="#">ART34494.1</a>
Select seq pir JC7958		<a href="#">galaxin precursor - reef coral [Galaxea fascicularis]</a>	387	97%	6.00E-131	58.58%	<a href="#">JC7958</a>
Select seq gb ABV24967.1		<a href="#">galaxin [Montipora capitata]</a>	647	87%	4.00E-55	67.91%	<a href="#">ABV24967.1</a>
Select seq gb PFX30452.1		<a href="#">Usherin [Stylophora pistillata]</a>	1044	85%	6.00E-51	39.56%	<a href="#">PFX30452.1</a>

### Appendix A.3 (continued)

Select seq ref XP_022782678.1	<a href="#">galaxin-like [Stylophora pistillata]</a>	1038	85%	4.00E-50	38.79%	<a href="#">XP_022782678.1</a>
Select seq ref XP_015761791.1	<a href="#">PREDICTED: galaxin-like [Acropora digitifera]</a>	472	83%	7.00E-47	35.56%	<a href="#">XP_015761791.1</a>
Select seq gb RMX54379.1	<a href="#">hypothetical protein pdam_00021390 [Pocillopora damicornis]</a>	722	86%	8.00E-44	34.34%	<a href="#">RMX54379.1</a>
Select seq ref XP_027050600.1	<a href="#">galaxin-like [Pocillopora damicornis]</a>	718	82%	2.00E-43	36.61%	<a href="#">XP_027050600.1</a>
Select seq gb ELU11211.1	<a href="#">hypothetical protein CAPTEDRAFT_64481 [Capitella teleta]</a>	152	80%	4.00E-40	36.33%	<a href="#">ELU11211.1</a>

<b>Spot 42.</b>	<b>Procollagen</b>	<b>Description</b>	<b>XP_020604034</b>	<b>PEPTIDE SEQUENCES:</b>		<b>dhnedntsailq</b>	
			<b>Total Score</b>	<b>Query</b>	<b>E value</b>	<b>Per. Ident</b>	<b>Accession</b>
Select seq ref XP_020604034.1		<a href="#">procollagen galactosyltransferase 1-like [Orbicella faveolata]</a>	1239	100%	0	100.00%	<a href="#">XP_020604034.1</a>
Select seq ref XP_027048049.1		<a href="#">procollagen galactosyltransferase 1-like [Pocillopora damicornis]</a>	1081	100%	0	86.36%	<a href="#">XP_027048049.1</a>
Select seq ref XP_015757920.1		<a href="#">PREDICTED: procollagen galactosyltransferase 1-like [Acropora]</a>	989	100%	0	80.98%	<a href="#">XP_015757920.1</a>
Select seq ref XP_029214257.1		<a href="#">procollagen galactosyltransferase 1-like [Acropora millepora]</a>	988	100%	0	80.98%	<a href="#">XP_029214257.1</a>
Select seq ref XP_022783764.1		<a href="#">procollagen galactosyltransferase 1-like [Stylophora pistillata]</a>	955	98%	0	79.05%	<a href="#">XP_022783764.1</a>
Select seq ref XP_001635452.1		<a href="#">predicted protein [Nematostella vectensis]</a>	1499	91%	0	63.92%	<a href="#">XP_001635452.1</a>
Select seq gb PFX29736.1		<a href="#">Procollagen galactosyltransferase 1 [Stylophora pistillata]</a>	884	85%	0	80.83%	<a href="#">PFX29736.1</a>
Select seq ref XP_028394615.1		<a href="#">procollagen galactosyltransferase 1-like [Dendronephthya giga]</a>	586	100%	0	48.24%	<a href="#">XP_028394615.1</a>
Select seq ref XP_027404007.1		<a href="#">procollagen galactosyltransferase 1 [Bos indicus x Bos taurus]</a>	576	90%	0	51.49%	<a href="#">XP_027404007.1</a>
Select seq ref NP_001092425.1		<a href="#">procollagen galactosyltransferase 1 precursor [Bos taurus]</a>	576	90%	0	51.49%	<a href="#">NP_001092425.1</a>
Select seq ref XP_006057968.1		<a href="#">LOW QUALITY PROTEIN: procollagen galactosyltransferase 1 [Bos taurus]</a>	575	90%	0	51.49%	<a href="#">XP_006057968.1</a>
Select seq ref XP_025313769.1		<a href="#">procollagen galactosyltransferase 1 [Canis lupus dingo]</a>	575	90%	0	51.30%	<a href="#">XP_025313769.1</a>
Select seq ref XP_023989967.1		<a href="#">procollagen galactosyltransferase 1 [Physeter catodon]</a>	574	90%	0	50.93%	<a href="#">XP_023989967.1</a>
Select seq gb OWK12026.1		<a href="#">COLGALT1 [Cervus elaphus hippelaphus]</a>	574	92%	0	50.64%	<a href="#">OWK12026.1</a>