

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

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

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:** **dakrligrkfdpdp**

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

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

Appendix A.3 (continued)

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

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

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

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	cytochrome P450 74A [Acropora palmata]	904	904	0	100.00%	ACD42778.1
Select seq ref XP_015765607.1	PREDICTED: allene oxide synthase, chloroplastic-like isoform X:	872	872	0	96.06%	XP_015765607.1
Select seq ref XP_029184931.1	allene oxide synthase, chloroplastic-like isoform X1 [Acropora i	867	867	0	96.06%	XP_029184931.1
Select seq ref XP_015765609.1	PREDICTED: allene oxide synthase, chloroplastic-like isoform X:	855	855	0	94.90%	XP_015765609.1
Select seq ref XP_029184932.1	allene oxide synthase, chloroplastic-like isoform X2 [Acropora i	850	850	0	94.90%	XP_029184932.1
Select seq ref XP_020613338.1	allene oxide synthase-like [Orbicella faveolata]	644	644	0	67.44%	XP_020613338.1
Select seq ref XP_027060358.1	allene oxide synthase-like isoform X1 [Pocillopora damicornis]	634	634	0	66.90%	XP_027060358.1
Select seq ref XP_027060359.1	allene oxide synthase-like isoform X2 [Pocillopora damicornis]	632	632	0	66.90%	XP_027060359.1
Select seq ref XP_022797645.1	allene oxide synthase-like isoform X2 [Stylophora pistillata]	622	622	0	65.59%	XP_022797645.1
Select seq gb PFX21200.1	Allene oxide synthase [Stylophora pistillata]	619	873	0	65.59%	PFX21200.1

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

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	NADH dehydrogenase subunit 1 [Acropora pruinosa]	468	468	8.00E-168	74.69%	ATC69366.1
Select seq ref YP_008815375.1	NADH dehydrogenase subunit 1 [Acropora humilis]	469	469	9.00E-168	74.69%	YP_008815375.1
Select seq gb ATC69390.1	NADH dehydrogenase subunit 1 [Acropora nana]	468	468	9.00E-168	74.69%	ATC69390.1
Select seq gb ABD17707.1	NADH dehydrogenase subunit 1 [Acropora acuminata]	70.5	70.5	8.00E-16	74.47%	ABD17707.1
Select seq ref NP_612817.1	NADH dehydrogenase subunit 1 [Acropora tenuis]	467	467	6.00E-167	74.38%	NP_612817.1

Select seq gb ABD17695.1	NADH dehydrogenase subunit 1 [Acropora acuminata]	211	211	5.00E-69	72.86%	ABD17695.1
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Appendix A.3 (continued)

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

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

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

Select seq ref YP_007317711.1	ATP synthase F0 subunit 6 [Platygyra carnosa]	427	7.00E-151	97.78%	YP_007317711.1
Select seq ref YP_009547093.1	ATP synthase F0 subunit 6 [Echinophyllia aspera]	427	1.00E-150	96.89%	YP_009547093.1

Appendix A.3 (continued)

Select seq ref YP_009378912.1	ATP synthase F0 subunit 6 [Favites pentagona]	427	1.00E-150	97.33%	YP_009378912.1
Select seq ref YP_654346.1	ATP synthase F0 subunit 6 [Colpophyllia natans]	427	1.00E-150	97.78%	YP_654346.1

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

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

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

Select seq ref XP_027036966.1	uncharacterized protein LOC113665468 [Pocillopora damicornis]	155	93%	3.00E-41	39.90%	XP_027036966.1
Select seq gb RMX51749.1	hypothetical protein pdam_00011740 [Pocillopora damicornis]	249	93%	2.00E-39	41.21%	RMX51749.1

Appendix A.3 (continued)

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

Appendix A.3 (continued)

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

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

Appendix A.3 (continued)

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

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

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

Appendix A.3 (continued)

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

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

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

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

Appendix A.3 (continued)

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

Spot 24.		GFP-like fluorescent chromoprotein cFP484 [Orbicella faveolata]		XP_020605513.1	PEPTIDE SEQUENCES:		yprdiadyfkqsf
		Description	Total Score	Query	E value	Per. Ident	Accession
Select seq ref XP_020605513.1		GFP-like fluorescent chromoprotein cFP484 [Orbicella faveolata]	467	100%	1.00E-166	100.00%	XP_020605513.1
Select seq gb ACD13193.1		green fluorescent GFP-like protein [Favites abdita]	420	100%	5.00E-148	87.95%	ACD13193.1
Select seq gb ABS87212.1		green fluorescent protein [Montastraea cavernosa]	837	100%	3.00E-147	88.11%	ABS87212.1
Select seq gb ABB17968.1		green fluorescent GFP-like protein [Echinophyllia echinata]	417	100%	6.00E-147	87.50%	ABB17968.1
Select seq gb AAO61601.1		green fluorescent protein [Montastraea cavernosa]	417	100%	7.00E-147	87.67%	AAO61601.1
Select seq gb AAO64989.1		green fluorescent protein R4 [synthetic construct]	417	100%	1.00E-146	88.11%	AAO64989.1
Select seq gb AAK83923.1		green fluorescent protein [Orbicella faveolata]	417	100%	1.00E-146	88.11%	AAK83923.1
Select seq gb AAO64994.1		green fluorescent protein G4 [synthetic construct]	417	100%	1.00E-146	88.11%	AAO64994.1
Select seq gb AAU04449.1		green fluorescent protein G1 [Orbicella faveolata]	416	100%	3.00E-146	87.67%	AAU04449.1
Select seq gb AAO43180.1		green fluorescent protein [Monster GFP vector pHMGFP]	414	99%	1.00E-145	87.61%	AAO43180.1
Select seq gb AAV66356.1		'Red/Green ancestor' ancestral fluorescent protein variant C05	414	100%	3.00E-145	87.05%	AAV66356.1

Spot 25.		GPI inositol-deacylase-like [Orbicella faveolata]		XP_020615720.1	PEPTIDE SEQUENCES:		lygegyadrskgrlrlsgip
		Description	Total Score	Query	E value	Per. Ident	Accession
Select seq ref XP_020615720.1		GPI inositol-deacylase-like [Orbicella faveolata]	1811	100%	0	100.00%	XP_020615720.1
Select seq ref XP_020616369.1		GPI inositol-deacylase-like [Orbicella faveolata]	1797	100%	0	98.98%	XP_020616369.1
Select seq ref XP_027038149.1		GPI inositol-deacylase-like [Pocillopora damicornis]	1229	99%	0	68.71%	XP_027038149.1
Select seq ref XP_022805945.1		GPI inositol-deacylase-like isoform X1 [Stylophora pistillata]	1207	100%	0	67.27%	XP_022805945.1
Select seq ref XP_015778864.1		PREDICTED: GPI inositol-deacylase-like [Acropora digitifera]	1193	100%	0	64.07%	XP_015778864.1
Select seq gb RMX50689.1		hypothetical protein pdam_00013226 [Pocillopora damicornis]	1169	94%	0	68.62%	RMX50689.1

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

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

Appendix A.3 (continued)

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

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

Spot 28.	BMP2/4, partial [<i>Orbicella faveolata</i>]	AHZ61804	PEPTIDE SEQUENCES:		vappgykafy	
	Description	Total Score	Query	E value	Per. Ident	Accession

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

Appendix A.3 (continued)

Select seq gb AHZ61815.1	BMP2/4 [Sandalolitha robusta]	94	100%	2.00E-24	93.48%	AHZ61815.1
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Spot 29.	Caspase 8	ADG23096.1	PEPTIDE SEQUENCES:		adlpygieeriqn	
	Description	Max Score	Total Score	E value	Per. Ident	Accession
Select seq gb ADG23096.1	caspase 8 [Acropora palmata]	944	944	0	100.00%	ADG23096.1
Select seq ref XP_015756325.1	PREDICTED: caspase-10-like [Acropora digitifera]	619	712	0	92.84%	XP_015756325.1
Select seq gb AJG36593.1	caspase 8 [Acropora millepora]	616	848	0	92.54%	AJG36593.1
Select seq gb AJG36591.1	caspase 8 [Acropora millepora]	615	848	0	92.54%	AJG36591.1
Select seq ref XP_015756331.1	PREDICTED: caspase-3-like [Acropora digitifera]	416	644	5.00E-143	86.83%	XP_015756331.1
Select seq ref XP_015758750.1	PREDICTED: LOW QUALITY PROTEIN: dynein heavy chain 2, axc	29.6	29.6	6.3	55.56%	XP_015758750.1
Select seq ref XP_015780003.1	PREDICTED: volume-regulated anion channel subunit LRRC8A-I	71.2	71.2	6.00E-13	45.12%	XP_015780003.1
Select seq ref XP_015780009.1	PREDICTED: volume-regulated anion channel subunit LRRC8A-I	72	72	4.00E-13	44.74%	XP_015780009.1
Select seq ref XP_015768208.1	PREDICTED: caspase-3-like [Acropora digitifera]	39.3	39.3	0.005	42.37%	XP_015768208.1
Select seq ref XP_015766400.1	PREDICTED: caspase-3-like [Acropora digitifera]	89.4	89.4	3.00E-19	36.69%	XP_015766400.1
Select seq ref XP_015774399.1	PREDICTED: uncharacterized protein LOC107352599 [Acropora	57.4	57.4	1.00E-08	36.59%	XP_015774399.1
Select seq ref XP_015770993.1	PREDICTED: uncharacterized protein LOC107349364 isoform X	60.5	60.5	1.00E-09	34.78%	XP_015770993.1
Select seq ref XP_015770992.1	PREDICTED: uncharacterized protein LOC107349364 isoform X	60.5	60.5	1.00E-09	34.78%	XP_015770992.1

Spot 30.	Ectonucleoside triphosphate diphosphohydrolase 1		XP_015779265	PEPTIDE SEQUENCES:		gdiikgtalvkqi	
	Description		Max Score	Total Score	E value	Per. Ident	Accession
	Select seq ref XP_015779265.1	PREDICTED: ectonucleoside triphosphate diphosphohydrolase	596	596	0	100.00%	XP_015779265.1
	Select seq ref XP_015756595.1	PREDICTED: nucleoside-triphosphatase ntp-1-like [Acropora di	111	111	5.00E-29	33.90%	XP_015756595.1
	Select seq ref XP_015756628.1	PREDICTED: ectonucleoside triphosphate diphosphohydrolase	94	94	1.00E-21	32.33%	XP_015756628.1
	Select seq ref XP_015768859.1	PREDICTED: ectonucleoside triphosphate diphosphohydrolase	93.2	93.2	1.00E-21	33.90%	XP_015768859.1
	Select seq ref XP_015768456.1	PREDICTED: ectonucleoside triphosphate diphosphohydrolase	84	84	1.00E-18	33.68%	XP_015768456.1

Spot 31.	Carbonic anhydrase 5A, mitochondrial-like [Orbicella	XP_020613891.1	PEPTIDE SEQUENCES:	laqflktvrhl		
	Description	Total Score	Query	E value	Per. Ident	Accession

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

Appendix A.3 (continued)

Spot 32.		Calmodullin	ACY07618.1	PEPTIDE SEQUENCES:			vmrncgesltnae
	Description		<u>Max score</u>	<u>Total score</u>	<u>E value</u>	<u>Ident</u>	Accession
Select seq gb ACY07618.1	calmodulin-like protein [Acropora millepora]		16.8	25.9	26	67%	ACY07618.1
Select seq dbj BAQ19096.1	paired box B protein [Acropora digitifera]		15.9	15.9	54	100%	BAQ19096.1
Select seq gb AAF64460.1 AF2	transcription factor PaxB [Acropora millepora]		15.9	15.9	54	100%	AAF64460.1
Select seq sp B3EWZ3.1 CADN	RecName: Full=Coadhesin		15.9	47.7	54	100%	B3EWZ3.1
Select seq sp B3EWZ5.1 MLRP	RecName: Full=MAM and LDL-receptor class A domain-contain		15.9	31.8	54	100%	B3EWZ5.1
Select seq sp B3EWZ6.1 MLRP	RecName: Full=MAM and LDL-receptor class A domain-contain		15.9	25.9	54	100%	B3EWZ6.1
Select seq gb KJD18916.1	hypothetical protein VE30_10855 [Halomonas meridiana]		15.5	15.5	79	67%	KJD18916.1
Select seq gb AFI99104.1	56kDa selenium binding protein [Acropora millepora]		15.5	15.5	79	80%	AFI99104.1
Select seq sp B3EWY9.1 MLP_	RecName: Full=Mucin-like protein		15.5	29.7	79	71%	B3EWY9.1
Select seq gb AET09738.1	hypothetical protein p4_37 [Acropora millepora]		15.1	15.1	116	100%	AET09738.1
Select seq gb ADG44981.1	hypothetical protein [Acropora millepora]		15.1	15.1	116	100%	ADG44981.1
Select seq gb KJD20578.1	spermidine/putrescine ABC transporter substrate-binding prot		15.1	15.1	116	100%	KJD20578.1
Select seq dbj BAQ19100.1	orthodenticle homeobox A protein [Acropora digitifera]		13.4	13.4	531	80%	BAQ19100.1
Select seq gb ABK41270.1	orthodenticle A [Acropora millepora]		13.4	13.4	531	80%	ABK41270.1
Select seq sp B8RJM0.1 USOM	RecName: Full=Uncharacterized skeletal organic matrix proteir		12.5	12.5	1128	60%	B8RJM0.1

Spot 33.		Scleractinian cysteine-rich protein [Montastraea faveolata]	B2ZG38	PEPTIDE SEQUENCES:			aakfhlcIII
	Description		<u>Total Score</u>	<u>Query</u>	<u>E value</u>	<u>Per. Ident</u>	Accession
Select seq sp B2ZG38.1	RecName: Full=Small cysteine-rich protein 8; Short=Mfav-SCRi		153	100%	6.00E-47	100.00%	B2ZG38.1
Select seq sp COH693.1	RecName: Full=Small cysteine-rich protein 1 1; Short=Mcap-SC		51.2	97%	1.00E-06	36.25%	COH693.1
Select seq sp COH694.1	RecName: Full=Small cysteine-rich protein 1 2; Short=Mcap-SC		50.8	97%	2.00E-06	36.25%	COH694.1
Select seq ref XP_020613205.1	small cysteine-rich protein 8-like [Orbicella faveolata]		48.1	98%	3.00E-05	53.57%	XP_020613205.1

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

Appendix A.3 (continued)

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

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

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

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	small cysteine-rich protein 6 [Orbicella faveolata]	169	169	2.00E-53	100.00%	XP_020631985.1
Select seq ref XP_020610088.1	small cysteine-rich protein 6-like [Orbicella faveolata]	129	129	7.00E-37	76.54%	XP_020610088.1
Select seq ref XP_020610104.1	small cysteine-rich protein 6-like [Orbicella faveolata]	86.7	86.7	2.00E-20	61.54%	XP_020610104.1
Select seq sp C1KIZ3.1	RecName: Full=Small cysteine-rich protein 4; Short=Mfav-SCRi	84.3	84.3	2.00E-19	63.29%	C1KIZ3.1
Select seq ref XP_022817917.1	uncharacterized protein LOC111350529 [Spodoptera litura]	39.7	39.7	0.27	37.04%	XP_022817917.1

Appendix A.3 (continued)

Spot 37. **Zinc finger protein 768-like [Orbicella faveolata]** **XP_020615964.1** **PEPTIDE SEQUENCES:** **gytvdfllpypvse**

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

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	alpha q G protein [Acropora palmata]	736	736	0	100.00%	AFZ78090.1
Select seq ref XP_015780306.1	PREDICTED: guanine nucleotide-binding protein G(q) subunit a	733	733	0	99.43%	XP_015780306.1
Select seq ref XP_015777008.1	PREDICTED: guanine nucleotide-binding protein G(o) subunit a	333	333	4.00E-113	49.72%	XP_015777008.1
Select seq gb AFZ78089.1	alpha o G protein [Acropora palmata]	329	329	9.00E-112	49.44%	AFZ78089.1
Select seq gb AFZ78088.1	alpha i G protein [Acropora palmata]	329	329	1.00E-111	49.15%	AFZ78088.1

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

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

	Description	Max Score	Total Score	E value	Per. Ident	Accession
Select seq ref XP_015757476.1	PREDICTED: pancreatic secretory granule membrane major gly	25.4	25.4	8.9	88.89%	XP_015757476.1
Select seq ref XP_015757475.1	PREDICTED: multiple epidermal growth factor-like domains prc	25.4	25.4	9.9	72.73%	XP_015757475.1
Select seq gb AHZ61629.1	alpha carbonic anhydrase [Acropora cervicornis]	155	155	1.00E-50	71.00%	AHZ61629.1

Appendix A.3 (continued)

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

Spot 40. **alpha carbonic anhydrase [Montastraea faveolata]** **XP_020628594.1** **PEPTIDE SEQUENCES:** **kdyrdlkiaf**

	Description	Total Score	Querv	E value	Per. Ident	Accession
Select seq ref XP_020628594.1	uncharacterized protein LOC110065766 [Orbicella faveolata]	863	863	100%	0	XP_020628594.1
Select seq ref XP_020628593.1	carbonic anhydrase 2-like [Orbicella faveolata]	332	332	47%	9.00E-109	XP_020628593.1
Select seq ref XP_027055172.1	carbonic anhydrase-related protein 10-like [Pocillopora damicc	211	374	50%	8.00E-60	XP_027055172.1
Select seq gb RMX36692.1	hypothetical protein pdam_00015839 [Pocillopora damicornis]	213	400	50%	1.00E-59	RMX36692.1
Select seq gb ANJ59776.1	alpha carbonic anhydrase 16 [Stylophora pistillata]	204	409	49%	3.00E-59	ANJ59776.1
Select seq ref XP_022801331.1	carbonic anhydrase 2-like [Stylophora pistillata]	192	192	49%	1.00E-54	XP_022801331.1
Select seq gb PFX18799.1	Carbonic anhydrase 2 [Stylophora pistillata]	192	192	49%	2.00E-54	PFX18799.1
Select seq ref XP_027050353.1	carbonic anhydrase 2-like [Pocillopora damicornis]	188	188	40%	2.00E-54	XP_027050353.1

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

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

Appendix A.3 (continued)

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

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