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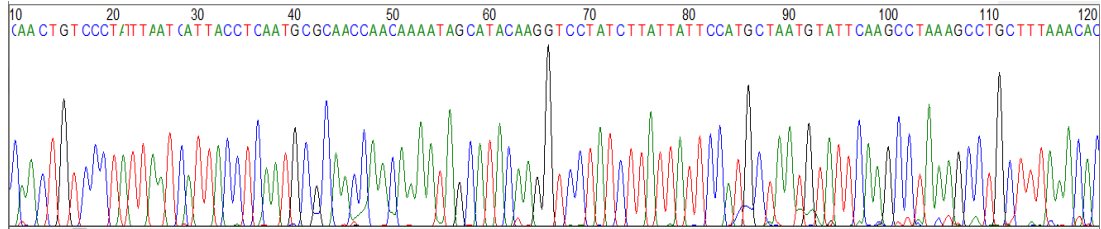
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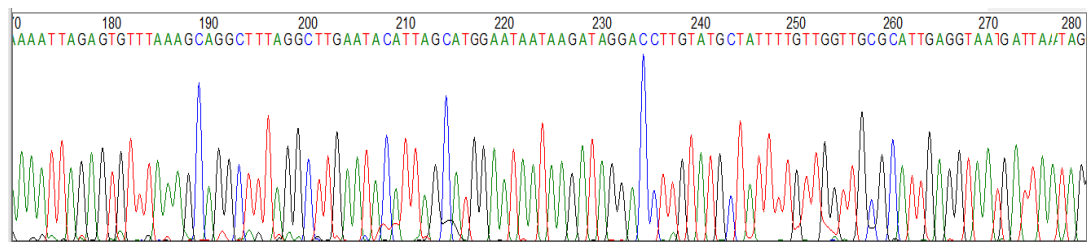
LAMPIRAN

Lampiran 1. Kromotogram hasil edit alignment

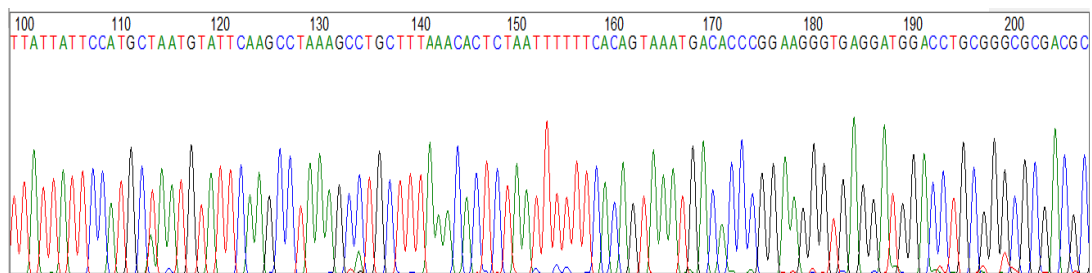
1. P.I *Prorocentrum lima*



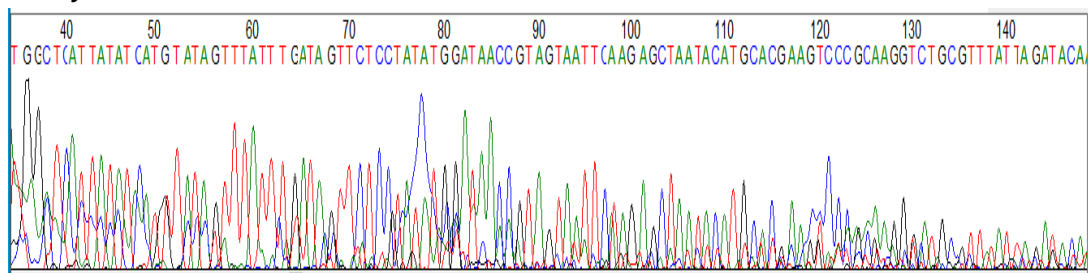
2. P.II *Alexandrium affine*



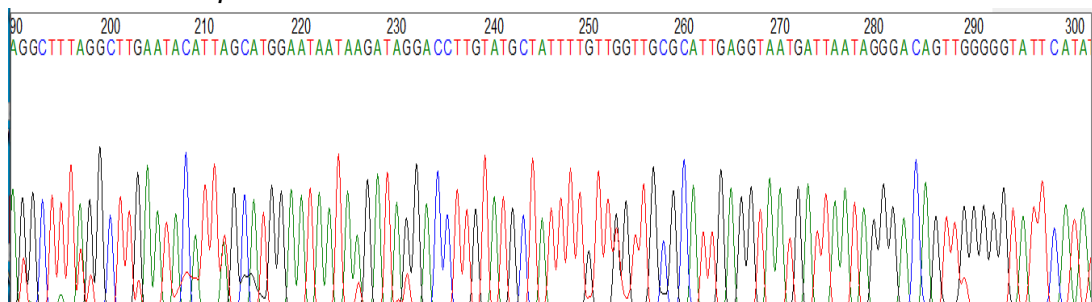
3. P.III *Alexandrium affine*



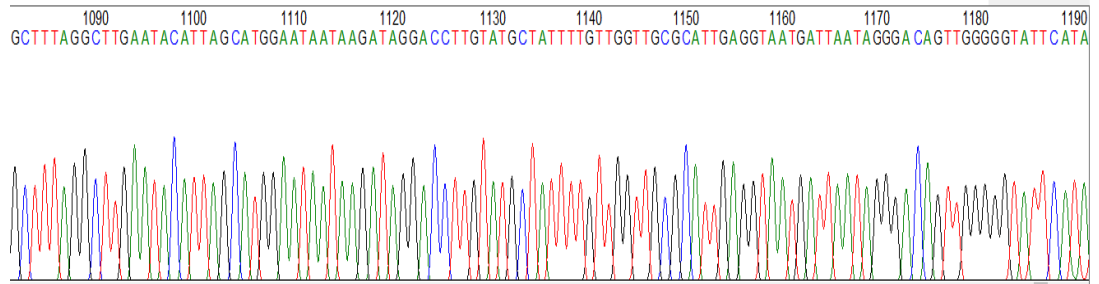
4. K.I *Gyrodinium aureolum*



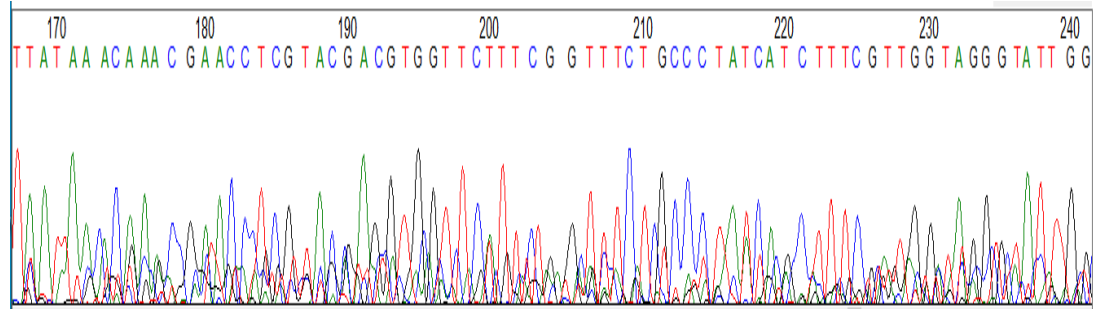
5. K.II *Durinskia capensis*



6. C.II *Exuviaella pusilla*



7. C.IV *Peridinium foliaceum*



Lampiran 2. Hasil alignment pada NCBI

1. P.I *Prorocentrum lima*

Sequences producing significant alignments										Download	Select columns	Show	100	
<input checked="" type="checkbox"/> select all 100 sequences selected										GenBank	Graphics	Distance tree of results	MSA Viewer	
	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession					
<input checked="" type="checkbox"/>	Prorocentrum lima 18S ribosomal RNA gene, partial sequence	Prorocentrum lima	2684	3254	97%	0.0	100.00%	1761	EF025381.1					
<input checked="" type="checkbox"/>	Uncultured Amoebophrya clone F small subunit ribosomal RNA gene, partial sequence	uncultured Amoe...	1700	2042	94%	0.0	88.14%	1731	AY829526.1					
<input checked="" type="checkbox"/>	Uncultured Amoebophrya clone E small subunit ribosomal RNA gene, partial sequence	uncultured Amoe...	1700	1930	94%	0.0	88.07%	1740	AY829525.1					
<input checked="" type="checkbox"/>	Uncultured dinoflagellate clone ML1 dino18S-14 18S small subunit ribosomal RNA gene, partial sequence	uncultured dinof...	1472	1690	80%	0.0	88.62%	1510	GU647174.1					
<input checked="" type="checkbox"/>	Azadinium cuneatum strain 3D6 isolate 13_023 small subunit ribosomal RNA gene, partial sequence	Azadinium cune...	1461	1730	95%	0.0	85.08%	1794	KJ481822.1					
<input checked="" type="checkbox"/>	Takayama cf. pulchellum 18S ribosomal RNA gene, complete sequence	Takayama cf. pu...	1456	1743	96%	0.0	84.98%	1799	AY800130.1					
<input checked="" type="checkbox"/>	Amphidoma languida isolate IFR13-025 small subunit ribosomal RNA gene, partial sequence	Amphidoma lang...	1454	1730	96%	0.0	84.88%	1799	KR362880.1					
<input checked="" type="checkbox"/>	Amphidoma languida strain AND-A0920 small subunit ribosomal RNA gene, partial sequence	Amphidoma lang...	1450	1725	96%	0.0	84.86%	1784	KX671042.1					
<input checked="" type="checkbox"/>	Azadinium dexteroporum isolate IFR13-318 small subunit ribosomal RNA gene, partial sequence	Azadinium dexte...	1450	1723	95%	0.0	84.95%	1795	KR362889.1					
<input checked="" type="checkbox"/>	Gyrodinium galatheanum strain CCCM 555 small subunit ribosomal RNA gene, complete sequence	Karlodinium ven...	1448	1688	93%	0.0	85.02%	1755	AF274262.1					
<input checked="" type="checkbox"/>	Amphidoma languida isolate IFR13-283 small subunit ribosomal RNA gene, partial sequence	Amphidoma lang...	1447	1727	96%	0.0	84.82%	1798	KR362881.1					
<input checked="" type="checkbox"/>	Psammodesma pacifica small subunit ribosomal RNA gene, partial sequence	Psammodesma paci...	1447	1447	79%	0.0	84.96%	1647	JN873311.1					
<input checked="" type="checkbox"/>	Karlodinium veneficum 18S ribosomal RNA gene, partial sequence: internal transcribed spacer 1, 5.8S ribosom...	Karlodinium ven...	1445	1723	95%	0.0	84.85%	3183	KU314867.1					
<input checked="" type="checkbox"/>	Karlodinium veneficum strain Kv-LYG5 small subunit ribosomal RNA gene, partial sequence	Karlodinium ven...	1445	1723	95%	0.0	84.85%	1800	OK093377.1					
<input checked="" type="checkbox"/>	Azadinium cuneatum strain 3D6 isolate 13_279 small subunit ribosomal RNA gene, partial sequence	Azadinium cune...	1445	1701	94%	0.0	84.99%	1771	KJ481819.1					
<input checked="" type="checkbox"/>	Karlodinium micrum isolate NEPC734 18S small subunit ribosomal RNA gene, partial sequence	Karlodinium ven...	1445	1721	95%	0.0	84.85%	1794	EF492506.1					
<input checked="" type="checkbox"/>	Karlodinium micrum partial 18S rRNA gene, strain KMKS 0701	Karlodinium ven...	1445	1723	95%	0.0	84.85%	1802	AM494500.1					
<input checked="" type="checkbox"/>	Karlodinium micrum small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene...	Karlodinium ven...	1445	1728	95%	0.0	84.85%	3348	AY245692.1					
<input checked="" type="checkbox"/>	Gymnodinium galatheanum small subunit ribosomal RNA gene, complete sequence	Karlodinium ven...	1445	1728	95%	0.0	84.85%	1789	AF272046.1					
<input checked="" type="checkbox"/>	Gymnodinium galatheanum small subunit ribosomal RNA gene, complete sequence	Karlodinium ven...	1445	1728	95%	0.0	84.85%	1789	AF272045.1					

Prorocentrum lima 18S ribosomal RNA gene, partial sequence

Sequence ID: [EF025381.1](#) Length: 1761 Number of Matches: 2

Range 1: 309 to 1761 [GenBank](#) [Graphics](#) [Next Match](#) [Print](#)

Score	Expect	Identical	Gaps	Strand
2684 bits(1453)	0.0	1453/1453(100%)	0/1453(0%)	Plus/Plus
Query 358	TTGCACGTATCAAGTGTAGCAGCGCTGC	GGCCACGACATCTAAGGGCATCACAGACCTGT		417
Sbjct 309	TTGCACGTATCAAGTGTAGCAGCGCTGC	GGCCACGACATCTAAGGGCATCACAGACCTGT		368
Query 418	TATTGCCCAAACTTCCTTAGACTTGC	GGCTAAAGTCCCCTAAGAAGTTCACCCCGATG		477
Sbjct 369	TATTGCCCAAACTTCCTTAGACTTGC	GGCTAAAGTCCCCTAAGAAGTTCACCCCGATG		428
Query 478	TTGATCAAGGCAACTATTTAGCAGGTT	AAGGTC TCGTTCGTAAACGGAAATTAACAGACA		537
Sbjct 429	TTGATCAAGGCAACTATTTAGCAGGTT	AAGGTC TCGTTCGTAAACGGAAATTAACAGACA		488
Query 538	AATCACTCCACCAACTAAGAACGGGCA	TGCACCCACCCATAGAAATCAAGAAAGACTC		597
Sbjct 489	AATCACTCCACCAACTAAGAACGGGCA	TGCACCCACCCATAGAAATCAAGAAAGACTC		548
Query 598	TCAATCTGTCAATCCCTAGCTATGTC	TGGACCTGGTAAGT TTTCCCGTGTGAGTCAAAT		657
Sbjct 549	TCAATCTGTCAATCCCTAGCTATGTC	TGGACCTGGTAAGT TTTCCCGTGTGAGTCAAAT		608
Query 658	AAGCCGACAGGCTCCACTCCTGGTGG	TGCCCTCCGTCAA TCC TTAAG TTTGAGCTTTG		717
Sbjct 609	AAGCCGACAGGCTCCACTCCTGGTGG	TGCCCTCCGTCAA TCC TTAAG TTTGAGCTTTG		668
Query 718	CGACCAATCTCCCCCAGAACCCAAAGAC	TTGATTTCTCATATGGTTCCGACAGGGTTA		777
Sbjct 669	CGACCAATCTCCCCCAGAACCCAAAGAC	TTGATTTCTCATATGGTTCCGACAGGGTTA		728
Query 778	AAATGTCGACCC TCCGATCCCAAGTC	GGTATAG TTTATGGTAAAGACTACGACGGTATCT		837
Sbjct 729	AAATGTCGACCC TCCGATCCCAAGTC	GGTATAG TTTATGGTAAAGACTACGACGGTATCT		788
Query 838	GATCGTCTTTGATCCCCCTAAC TTC	GTCTTGA TTAATGAAAAACATCCCTGGCAAAATGCT		897
Sbjct 789	GATCGTCTTTGATCCCCCTAAC TTC	GTCTTGA TTAATGAAAAACATCCCTGGCAAAATGCT		848
Query 898	TTGCGATAGTTCGCTCTTAATAAAAT	CCAGSAA TTTCACTCTGACAAATAAATACGAAAT		957
Sbjct 849	TTGCGATAGTTCGCTCTTAATAAAAT	CCAGSAA TTTCACTCTGACAAATAAATACGAAAT		908
Query 958	GCCCCCAACTGTCCCTATTAATCAT	TACTCTGTACTCAAACCAACGAAATAGTCCAGAGTC		1017
Sbjct 909	GCCCCCAACTGTCCCTATTAATCAT	TACTCTGTACTCAAACCAACGAAATAGTCCAGAGTC		968
Query 1018	CTATTTCCATTATCCATGCTGGAGT	ATCCAAGCGATGGCTGCC TGGAGCACTCTAA TTT		1077
Sbjct 969	CTATTTCCATTATCCATGCTGGAGT	ATCCAAGCGATGGCTGCC TGGAGCACTCTAA TTT		1028
Query 1078	GTTCACAGTAAAATGTAGGTTCCAC	GCACC GACCACTGAAGACCGTACATACGATCCCC		1137
Sbjct 1029	GTTCACAGTAAAATGTAGGTTCCAC	GCACC GACCACTGAAGACCGTACATACGATCCCC		1088
Query 1138	TACGGATGACCAAGGCGACGAGCCGAC	GAA TGCCTGAAACGCGACCGGCAGAAAATCAA		1197
Sbjct 1089	TACGGATGACCAAGGCGACGAGCCGAC	GAA TGCCTGAAACGCGACCGGCAGAAAATCAA		1148
Query 1198	CTACGAGCTTTTAACTGCACCAACT	TTAATATACGCTATTTGGAGCTGGAATTACCGCGG		1257
Sbjct 1149	CTACGAGCTTTTAACTGCACCAACT	TTAATATACGCTATTTGGAGCTGGAATTACCGCGG		1208
Query 1258	CTGCTGGCACCAGACTTGCCTCCAA	TGTTCTTCGATAAGTGGTTTAAATTTGTTCTCAT		1317
Sbjct 1209	CTGCTGGCACCAGACTTGCCTCCAA	TGTTCTTCGATAAGTGGTTTAAATTTGTTCTCAT		1268
Query 1318	TGCAATCTCGCAGACCCCGSAGGGT	CCCGAGTTGTTATTCTTTGTCACTGCC TCCCTGAA		1377
Sbjct 1269	TGCAATCTCGCAGACCCCGSAGGGT	CCCGAGTTGTTATTCTTTGTCACTGCC TCCCTGAA		1328

2. P.II *Alexandrium affine*

Descriptions		Graphic Summary	Alignments	Taxonomy				
Sequences producing significant alignments								
<input checked="" type="checkbox"/> select all 100 sequences selected		Download Select columns Show 100						
		GenBank	Graphics	Distance tree of results MSA Viewer				
Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/> Alexandrium affine isolate AACQ-1 18S ribosomal RNA gene, partial sequence	Alexandrium affine	1280	1459	92%	0.0	100.00%	799	JQ638932.1
<input checked="" type="checkbox"/> Dinophyta sp. HG204 nucleomorph gene for small subunit rRNA, partial sequence	Dinophyta sp. H...	699	904	90%	0.0	86.76%	1525	LC192340.1
<input checked="" type="checkbox"/> Durinskia capensis nucleomorph gene for small subunit rRNA, partial sequence, strain_Kommetjia-2A	Durinskia capensis	695	900	90%	0.0	86.60%	1486	LC192342.1
<input checked="" type="checkbox"/> Durinskia baltica nucleomorph gene for small subunit rRNA, partial sequence, strain_CS-38	Durinskia baltica	689	895	90%	0.0	86.47%	1561	LC192343.1
<input checked="" type="checkbox"/> Dinophyta sp. HG180 nucleomorph gene for small subunit rRNA, partial sequence	Dinophyta sp. H...	676	882	90%	0.0	86.20%	1466	LC192339.1
<input checked="" type="checkbox"/> Durinskia cf. baltica HG171 nucleomorph gene for small subunit rRNA, partial sequence	Durinskia cf. balti...	662	739	73%	0.0	87.27%	874	LC192341.1
<input checked="" type="checkbox"/> Uncultured dinoflagellate clone HL2SCM10.11 18S ribosomal RNA gene, partial sequence	uncultured dinofl...	640	711	74%	0.0	86.33%	1711	LC488424.1
<input checked="" type="checkbox"/> Peridiniopsis niei strain Donghu 18S ribosomal RNA gene, partial sequence	Unruhdimium niei	630	707	74%	5e-180	85.95%	1340	JX141779.1
<input checked="" type="checkbox"/> Azadinium perforatum strain AZA-2H small subunit ribosomal RNA gene, partial sequence	Azadinium perfor...	593	665	74%	7e-169	84.98%	1599	MK883043.1
<input checked="" type="checkbox"/> Azadinium perforatum strain AZA-2E small subunit ribosomal RNA gene, partial sequence	Azadinium perfor...	593	665	74%	7e-169	84.98%	1731	MK883042.1
<input checked="" type="checkbox"/> Azadinium perforatum strain AZA-2C small subunit ribosomal RNA gene, partial sequence	Azadinium perfor...	593	665	74%	7e-169	84.98%	1734	MK883041.1
<input checked="" type="checkbox"/> Heterocapsa rotundata isolate BH56_144 small subunit ribosomal RNA gene, partial sequence	Heterocapsa rot...	593	665	74%	7e-169	85.01%	1694	KY980285.1
<input checked="" type="checkbox"/> Durinskia kwazulunatensis gene for 18S ribosomal RNA, partial sequence	Durinskia kwazul...	593	665	74%	7e-169	84.98%	1777	LC054929.1
<input checked="" type="checkbox"/> Durinskia kwazulunatensis gene for 18S ribosomal RNA, partial sequence	Durinskia kwazul...	593	665	74%	7e-169	84.98%	1785	LC054928.1
<input checked="" type="checkbox"/> Durinskia kwazulunatensis gene for 18S ribosomal RNA, partial sequence	Durinskia kwazul...	593	665	74%	7e-169	84.98%	1774	LC054927.1

Alexandrium affine isolate AACQ-1 18S ribosomal RNA gene, partial sequence

Sequence ID: [JQ638932.1](#) Length: 799 Number of Matches: 2

Range 1: 107 to 799 [GenBank](#) [Graphics](#)

[Next Match](#) [Previo](#)

Score	Expect	Identities	Gaps	Strand
1280 bits(693)	0.0	693/693(100%)	0/693(0%)	Plus/Plus
Query 158	ACCC TGACTTCTGGAAAGGGTGACTTATTAGATGGAAACCAATGCGGGGCAACCCGGAT	217		
Sbjct 107	ACCC TGACTTCTGGAAAGGGTGACTTATTAGATGGAAACCAATGCGGGGCAACCCGGAT	166		
Query 218	ACTGGTGATT CATAATAATTTTCGGATCGATCGTAGGATCGATGCATCATTCAAGTTTCT	277		
Sbjct 167	ACTGGTGATT CATAATAATTTTCGGATCGATCGTAGGATCGATGCATCATTCAAGTTTCT	226		
Query 278	GCCC TATCAGCTTTGGATGGTAGGGTATGGCC TACCATGGCATT AACGGGTAACGGAGA	337		
Sbjct 227	GCCC TATCAGCTTTGGATGGTAGGGTATGGCC TACCATGGCATT AACGGGTAACGGAGA	286		
Query 338	ATTAGGGTTCGATTCGGAGAGGGAGCCTGAGAAATGGCTACCACATCCAAGGAAGGCAG	397		
Sbjct 287	ATTAGGGTTCGATTCGGAGAGGGAGCCTGAGAAATGGCTACCACATCCAAGGAAGGCAG	346		
Query 398	CAGGCGCGTAAATACCCAATCCTGACACAGGGAGGTAGTGACAATAAATAACAATGTCG	457		
Sbjct 347	CAGGCGCGTAAATACCCAATCCTGACACAGGGAGGTAGTGACAATAAATAACAATGTCG	406		
Query 458	GGCTTTTCTAAGTCTGACAATTGGAATGAGAACAATTTAAATCCCTTATCGAGGATCAAT	517		
Sbjct 407	GGCTTTTCTAAGTCTGACAATTGGAATGAGAACAATTTAAATCCCTTATCGAGGATCAAT	466		
Query 518	TGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATCCAGCTCCAATAGCGTATACTAAA	577		
Sbjct 467	TGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATCCAGCTCCAATAGCGTATACTAAA	526		
Query 578	GTTGTTGCAGTAAAAAGCTCGTAGTTGAAATTTCTGGTCTCGAGACGCGGCCAGCCTCAA	637		
Sbjct 527	GTTGTTGCAGTAAAAAGCTCGTAGTTGAAATTTCTGGTCTCGAGACGCGGCCAGCCTCAA	586		
Query 638	GGGGCGATGCTGTGGATCGGGACCATCCTCGAGGAGAACATATCTGTCAATTGAGTTGATG	697		
Sbjct 587	GGGGCGATGCTGTGGATCGGGACCATCCTCGAGGAGAACATATCTGTCAATTGAGTTGATG	646		
Query 698	GGTATGGGACCTCGTCATTTACTGTGAGCAAAAAAGAGTGTTCAAAGCAAGCTTACGCC	757		
Sbjct 647	GGTATGGGACCTCGTCATTTACTGTGAGCAAAAAAGAGTGTTCAAAGCAAGCTTACGCC	706		
Query 758	GTTGAATACATTAGCATGGCAATAAAGATAGGACCTTGGTCTATTTTGTGGTTATAC	817		
Sbjct 707	GTTGAATACATTAGCATGGCAATAAAGATAGGACCTTGGTCTATTTTGTGGTTATAC	766		
Query 818	TCCGAGGGAATGATTAATAGGGACAGTTGGGGG	850		
Sbjct 767	TCCGAGGGAATGATTAATAGGGACAGTTGGGGG	799		

3. P.III *Alexandrium affine*

Sequences producing significant alignments										Download	Select columns	Show	100
<input checked="" type="checkbox"/> select all 100 sequences selected										GenBank	Graphics	Distance tree of results	MSA Viewer
	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession				
<input checked="" type="checkbox"/>	Alexandrium affine isolate AACQ-1 18S ribosomal RNA gene, partial sequence	Alexandrium affine	1463	1463	91%	0.0	100.00%	799	JQ638932.1				
<input checked="" type="checkbox"/>	Dinophyta sp. HG204 nucleomorph gene for small subunit rRNA, partial sequence	Dinophyta sp. H...	797	797	91%	0.0	85.22%	1525	LC192340.1				
<input checked="" type="checkbox"/>	Duninskia capensis nucleomorph gene for small subunit rRNA, partial sequence, strain: Kommetje 2-A	Duninskia capensis	793	793	91%	0.0	85.09%	1486	LC192342.1				
<input checked="" type="checkbox"/>	Duninskia ballica nucleomorph gene for small subunit rRNA, partial sequence, strain: CS-38	Duninskia ballica	787	787	91%	0.0	84.99%	1561	LC192343.1				
<input checked="" type="checkbox"/>	Dinophyta sp. HG180 nucleomorph gene for small subunit rRNA, partial sequence	Dinophyta sp. H...	774	774	91%	0.0	84.78%	1466	LC192339.1				
<input checked="" type="checkbox"/>	Uncultured dinoflagellate clone HL2SCM10.11 18S ribosomal RNA gene, partial sequence	uncultured dinof...	747	747	91%	0.0	84.01%	1711	KC488424.1				
<input checked="" type="checkbox"/>	Uncultured dinoflagellate clone PROSOPE E5-25m.86 18S ribosomal RNA gene, partial sequence	uncultured dinof...	725	725	91%	0.0	83.54%	1689	EU793378.1				
<input checked="" type="checkbox"/>	Uncultured dinoflagellate clone PROSOPE CM-5m.204 18S ribosomal RNA gene, partial sequence	uncultured dinof...	725	725	91%	0.0	83.52%	924	EU793087.1				
<input checked="" type="checkbox"/>	Pentapansodinium lytherenicum clone 7909 18S ribosomal RNA gene, partial sequence	Pentapansodini...	719	719	91%	0.0	83.42%	1777	JF791053.1				
<input checked="" type="checkbox"/>	Pentapansodinium lytherenicum clone 3920 18S ribosomal RNA gene, partial sequence	Pentapansodini...	719	719	91%	0.0	83.39%	1777	JF791029.1				
<input checked="" type="checkbox"/>	Uncultured dinoflagellate clone PROSOPE CD-15m.145 18S ribosomal RNA gene, partial sequence	uncultured dinof...	719	719	91%	0.0	83.42%	925	EU793006.1				
<input checked="" type="checkbox"/>	Uncultured dinoflagellate clone HL5SCM10.93 18S ribosomal RNA gene, partial sequence	uncultured dinof...	702	702	91%	0.0	83.03%	1696	KC488446.1				
<input checked="" type="checkbox"/>	Uncultured dinoflagellate clone HL5SCM10.23 18S ribosomal RNA gene, partial sequence	uncultured dinof...	702	702	91%	0.0	83.05%	1703	KC488441.1				
<input checked="" type="checkbox"/>	Uncultured dinoflagellate clone PROSOPE CM-110m.78 18S ribosomal RNA gene, partial sequence	uncultured dinof...	702	702	91%	0.0	83.03%	917	EU793022.1				
<input checked="" type="checkbox"/>	Heterocapsa rotunda isolate BH56 144 small subunit ribosomal RNA gene, partial sequence	Heterocapsa rot...	699	699	90%	0.0	83.00%	1694	KY980285.1				
<input checked="" type="checkbox"/>	Heterocapsa rotunda isolate BH65 152 small subunit ribosomal RNA gene, partial sequence	Heterocapsa rot...	697	697	91%	0.0	82.92%	1695	KY980406.1				
<input checked="" type="checkbox"/>	Heterocapsa rotunda isolate BH56 213 small subunit ribosomal RNA gene, partial sequence	Heterocapsa rot...	697	697	91%	0.0	82.92%	1695	KY980322.1				
<input checked="" type="checkbox"/>	Gymnodinium sp. small subunit ribosomal RNA gene, complete sequence	Gymnodinium sp.	697	697	91%	0.0	82.92%	1755	AF274260.1				
<input checked="" type="checkbox"/>	Heterocapsa rotunda isolate NY13S 148 small subunit ribosomal RNA gene, partial sequence	Heterocapsa rot...	695	695	91%	0.0	82.90%	1692	KY980024.1				

Alexandrium affine isolate AACQ-1 18S ribosomal RNA gene, partial sequence

Sequence ID: [JQ638932.1](#) Length: 799 Number of Matches: 1

Range 1: 8 to 799 [GenBank](#) [Graphics](#)

[Next Match](#) [Previous](#)

Score	Expect	Identities	Gaps	Strand
1463 bits(792)	0.0	792/792(100%)	0/792(0%)	Plus/Plus
Query 74	CGTGAAAC TGC GAATGGCTCA TTATATCAGT TATAGT TATTATTTGATGGGCATTGCTACTT	133		
Sbjct 8	CGTGAAAC TGC GAATGGCTCA TTATATCAGT TATAGT TATTATTTGATGGGCATTGCTACTT	67		
Query 134	GGATAACCGTAGTAATTC TAGAGC TAATACATGCATAAAAACCC T GACTTCTGGAAAGGGT	193		
Sbjct 68	GGATAACCGTAGTAATTC TAGAGC TAATACATGCATAAAAACCC T GACTTCTGGAAAGGGT	127		
Query 194	GTACTTATAGATGGAAACCAATGCGGGGCAACCCGGATCTGGTGATTCATAATAATTT	253		
Sbjct 128	GTACTTATAGATGGAAACCAATGCGGGGCAACCCGGATCTGGTGATTCATAATAATTT	187		
Query 254	TCGGATCGATCGTAGGATCGATGCATCATTCAAGTTTCTGCCCTATCAGCTTTGGATGGT	313		
Sbjct 188	TCGGATCGATCGTAGGATCGATGCATCATTCAAGTTTCTGCCCTATCAGCTTTGGATGGT	247		
Query 314	AGGGTATTGGCC TACCATGGCATT AACGGGT AACGGAGAATTAGGGTTCGATTCGGGAGA	373		
Sbjct 248	AGGGTATTGGCC TACCATGGCATT AACGGGT AACGGAGAATTAGGGTTCGATTCGGGAGA	387		
Query 374	GGGAGCC TGGAAATGGCTACCAATCC AAGGAAAGGCAGCAGGC GCGTAAATACCCAAT	433		
Sbjct 388	GGGAGCC TGGAAATGGCTACCAATCC AAGGAAAGGCAGCAGGC GCGTAAATACCCAAT	367		
Query 434	CCTGACACAGGGAGGTAGTGACAA TAAATAACAATGT CBBGC TTTCTAAGTCTGACAAAT	493		
Sbjct 368	CCTGACACAGGGAGGTAGTGACAA TAAATAACAATGT CBBGC TTTCTAAGTCTGACAAAT	427		
Query 494	TGSAATGAGAACAA TTAATCCC T TATCGAGGATCAAT TGGAGGGCAAGCTCTGGTGCCA	553		
Sbjct 428	TGSAATGAGAACAA TTAATCCC T TATCGAGGATCAAT TGGAGGGCAAGCTCTGGTGCCA	487		
Query 554	GCAGCCGCGGTAATTC CAGCTCCAATAGCGTATACTAAAGTTGTTGCAGT TAAAAAGCTC	613		
Sbjct 488	GCAGCCGCGGTAATTC CAGCTCCAATAGCGTATACTAAAGTTGTTGCAGT TAAAAAGCTC	547		
Query 614	GTAGTTGAA TTTCTGGTCTCGAGACGCGGCCAGCTCAAGGGGGGATGCTGTGGATCGGG	673		
Sbjct 548	GTAGTTGAA TTTCTGGTCTCGAGACGCGGCCAGCTCAAGGGGGGATGCTGTGGATCGGG	687		
Query 674	ACCATCCTCGAGGAGAACATATCTGT CATTGAGT TGA TGGGATGGGACCTCTGTCATTT	733		
Sbjct 688	ACCATCCTCGAGGAGAACATATCTGT CATTGAGT TGA TGGGATGGGACCTCTGTCATTT	667		
Query 734	ACTGTGAGCAAAAAAGAGTGT TCAAAGCAAGCTTACGCCGTTGAATACAT TAGCATGGCA	793		
Sbjct 668	ACTGTGAGCAAAAAAGAGTGT TCAAAGCAAGCTTACGCCGTTGAATACAT TAGCATGGCA	727		
Query 794	ATAATAAGATAGGACCTTGGTCTATTTTGT TGGT TATACTCCGAGGGGAATGATTAATAGG	853		
Sbjct 728	ATAATAAGATAGGACCTTGGTCTATTTTGT TGGT TATACTCCGAGGGGAATGATTAATAGG	787		
Query 854	GACAGTTGGGGG 865			
Sbjct 788	GACAGTTGGGGG 799			

4. *K.1 Gyrodinium aureolum*

Sequences producing significant alignments		Download	Select columns	Show	100			
select all 100 sequences selected		GenBank	Graphics	Distance tree of results	MSA Viewer			
Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
Gyrodinium aureolum 18S ribosomal RNA gene, partial sequence	Gyrodinium au...	698	956	85%	0.0	99.80%	530	DQ887503.1
Durinskia caensis nucleomorph gene for small subunit rRNA, partial sequence, strain: Kommetjie 2-A	Durinskia caensis	569	569	80%	8e-162	88.21%	1486	LC192342.1
Alexandrium affine isolate AACQ-1 18S ribosomal RNA gene, partial sequence	Alexandrium affine	568	568	80%	3e-161	87.96%	799	JQ638932.1
Peridinium foliaceum isolate Xmm11S5 18S ribosomal RNA gene, partial sequence	Peridinium foliac...	560	560	80%	5e-159	87.78%	1706	KU561157.1
Durinskia baltica nucleomorph gene for small subunit rRNA, partial sequence, strain: CS-38	Durinskia baltica	558	558	80%	2e-158	87.78%	1561	LC192343.1
Dinophyta sp. HG204 nucleomorph gene for small subunit rRNA, partial sequence	Dinophyta sp. H...	558	558	80%	2e-158	87.78%	1525	LC192340.1
Dinophyta sp. HG180 nucleomorph gene for small subunit rRNA, partial sequence	Dinophyta sp. H...	547	547	80%	4e-155	87.37%	1466	LC192339.1
Uncultured dinoflagellate clone HL2SCM10.11 18S ribosomal RNA gene, partial sequence	uncultured dinofi...	525	525	80%	2e-148	86.15%	1711	KC488424.1
Uncultured dinoflagellate clone CCA32 18S small subunit ribosomal RNA gene, partial sequence	uncultured dinofi...	518	518	80%	3e-146	85.86%	1821	AY176990.1
Uncultured dinoflagellate clone PROSOPE E5-25m.36 18S ribosomal RNA gene, partial sequence	uncultured dinofi...	514	514	80%	4e-145	85.77%	1689	EU793378.1
Uncultured Peridinium partial 18S rRNA gene, isolate DGGE band 47	uncultured Peridi...	512	512	74%	1e-144	87.53%	450	AM084306.1
Uncultured dinoflagellate clone PROSOPE E5-25m.37 18S ribosomal RNA gene, partial sequence	uncultured dinofi...	508	508	80%	2e-143	85.54%	720	EU793363.1
Uncultured dinoflagellate clone PROSOPE CD-15m.145 18S ribosomal RNA gene, partial sequence	uncultured dinofi...	508	508	80%	2e-143	85.51%	925	EU793005.1
Uncultured dinoflagellate clone OL1 18S ribosomal RNA gene, partial sequence	uncultured dinofi...	507	507	80%	6e-143	85.54%	1789	GX485147.1
Prorocentrum minimum 18S ribosomal RNA gene, partial sequence	Prorocentrum mj...	507	507	80%	6e-143	85.63%	1790	EF017804.1
Uncultured Paulsenella isolate LT82 M23 18S ribosomal RNA gene, partial sequence	uncultured Pauls...	497	497	80%	4e-140	85.19%	1649	KC487605.1
Uncultured dinoflagellate clone HL4SF04.63 18S ribosomal RNA gene, partial sequence	uncultured dinofi...	492	492	80%	2e-138	84.96%	1696	KC488436.1
Pentapichardium tyrrenicum clone 7909 18S ribosomal RNA gene, partial sequence	Pentapichardini...	492	492	80%	2e-138	84.98%	1777	JF791053.1
Uncultured dinoflagellate clone PROSOPE CM-5m.204 18S ribosomal RNA gene, partial sequence	uncultured dinofi...	492	492	80%	2e-138	84.96%	924	EU793087.1
Uncultured Gymnodinium clone Pink_G05 18S ribosomal RNA gene, partial sequence	uncultured Gymn...	490	490	80%	6e-138	84.96%	787	GQ483805.1
Gyrodinium flavescens strain LIMS-PS-2721 small subunit ribosomal RNA gene, partial sequence	Torquentidium fla...	488	488	80%	8e-137	84.79%	1684	MK733283.1
Torquentidium convolutum strain LIMS-PS-2394 small subunit ribosomal RNA gene, partial sequence	Torquentidium co...	488	488	80%	8e-137	84.79%	1719	MF948365.1

Gyrodinium aureolum 18S ribosomal RNA gene, partial sequence

Sequence ID: [DQ887503.1](#) Length: 530 Number of Matches: 2

Range 1: 43 to 530 [GenBank](#) [Graphics](#)

[Next Match](#)

Score	Expect	Identities	Gaps	Strand
896 bits(485)	0.0	487/488(99%)	0/488(0%)	Plus/Plus
Query 120	GCAAATGGCTCATTATATCAGTTATAGTTTATTTGATAGTCACCTACTACTTGGATAACC	179		
Sbjct 43	GCGAATGGCTCATTATATCAGTTATAGTTTATTTGATAGTCACCTACTACTTGGATAACC	102		
Query 180	GTAGTAATTCAGAGCTAATACATGCATCAACTCCCAACTGCTTGGACGGGATGTATTTA	239		
Sbjct 103	GTAGTAATTCAGAGCTAATACATGCATCAACTCCCAACTGCTTGGACGGGATGTATTTA	162		
Query 240	TTAGATGGAACCAATACCGAGTTTTCTCGGTTTTTGTGGTGAATCATAGTAACGTGCG	299		
Sbjct 163	TTAGATGGAACCAATACCGAGTTTTCTCGGTTTTTGTGGTGAATCATAGTAACGTGCG	222		
Query 300	AATCGACTTGCATCAGCGGTCGATGGTTTCATTCAAGTTTCTGCCCTATCAGCTTCGGATG	359		
Sbjct 223	AATCGACTTGCATCAGCGGTCGATGGTTTCATTCAAGTTTCTGCCCTATCAGCTTCGGATG	282		
Query 360	GTAGGGTATTGGCTACCATGGCTTTAACGGGTAACGGAGAATTGGGGTTCGATTCGGGA	419		
Sbjct 283	GTAGGGTATTGGCTACCATGGCTTTAACGGGTAACGGAGAATTGGGGTTCGATTCGGGA	342		
Query 420	GAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGTAAATTACCCA	479		
Sbjct 343	GAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGTAAATTACCCA	402		
Query 480	ATCCTGACATAGGGAGGTAGTGACAATAAATAACAATGCTAGGCTTTTAAAGTCCGGCAA	539		
Sbjct 403	ATCCTGACATAGGGAGGTAGTGACAATAAATAACAATGCTAGGCTTTTAAAGTCCGGCAA	462		
Query 540	TTGGAATGAGAACAATTTAAATCCCTTATCGAGGAACCATGGAGGGCAAGTCTGGTGCC	599		
Sbjct 463	TTGGAATGAGAACAATTTAAATCCCTTATCGAGGAACCATGGAGGGCAAGTCTGGTGCC	522		
Query 600	AGCAGCCA 607			
Sbjct 523	AGCAGCCA 530			

5. K.II *Durinskia capensis*

Sequences producing significant alignments		Download	Select columns	Show	100				
select all 100 sequences selected		GenBank	Graphics	Distance tree of results	MSA Viewer				
	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	Durinskia capensis nucleomorph gene for small subunit rRNA, partial sequence, strain: Kommetjie 2-A	Durinskia capensis	1844	2514	78%	0.0	100.00%	1486	LC192342.1
<input checked="" type="checkbox"/>	Durinskia baltica nucleomorph gene for small subunit rRNA, partial sequence, strain: CS-38	Durinskia baltica	1757	2411	78%	0.0	98.40%	1561	LC192343.1
<input checked="" type="checkbox"/>	Dinophyta sp. HG204 nucleomorph gene for small subunit rRNA, partial sequence	Dinophyta sp. H...	1744	2398	78%	0.0	98.20%	1525	LC192340.1
<input checked="" type="checkbox"/>	Peridinium foliaceum isolate Xmm11S5 18S ribosomal RNA gene, partial sequence	Peridinium foliac...	1652	2206	75%	0.0	96.51%	1706	KJ581157.1
<input checked="" type="checkbox"/>	Dinophyta sp. HG180 nucleomorph gene for small subunit rRNA, partial sequence	Dinophyta sp. H...	1611	2259	78%	0.0	95.90%	1486	LC192339.1
<input checked="" type="checkbox"/>	Peridiniopsis niei strain Donghu 18S ribosomal RNA gene, partial sequence	Unrubidium niei	1360	1539	65%	0.0	91.30%	1340	JX141779.1
<input checked="" type="checkbox"/>	Durinskia cf. baltica HG171 nucleomorph gene for small subunit rRNA, partial sequence	Durinskia cf. balt...	1160	1300	41%	0.0	98.77%	874	LC192341.1
<input checked="" type="checkbox"/>	Torquentidium convolutum strain LIMS-PS-2394 small subunit ribosomal RNA gene, partial sequence	Torquentidium co...	1064	1064	56%	0.0	86.45%	1719	MF948385.1
<input checked="" type="checkbox"/>	Cochlodinium helix strain LIMS-PS-2554 small subunit ribosomal RNA gene, partial sequence	Pselodinium helix	1064	1064	56%	0.0	86.44%	1676	MH465611.1
<input checked="" type="checkbox"/>	Kinithra sigma clone GYM32 small subunit ribosomal RNA gene, partial sequence	Kinithra sigma	1061	1137	59%	0.0	86.35%	1800	MW874846.1
<input checked="" type="checkbox"/>	Prorocentrum triestinum isolate NY13S_196 small subunit ribosomal RNA gene, partial sequence	Prorocentrum tri...	1059	1059	56%	0.0	86.30%	1689	KY980052.1
<input checked="" type="checkbox"/>	Kinithra sigma clone GYM20 small subunit ribosomal RNA gene, partial sequence	Kinithra sigma	1059	1136	59%	0.0	86.34%	1799	MW874842.1
<input checked="" type="checkbox"/>	Kinithra sigma clone GYM04 small subunit ribosomal RNA gene, partial sequence	Kinithra sigma	1055	1132	59%	0.0	86.25%	1800	MW874836.1
<input checked="" type="checkbox"/>	Dactyloidium arachnoides LUD75 genes for 18S rRNA, ITS1, 5.8S rRNA, ITS2, 28S rRNA, partial and complete...	Dactyloidium ar...	1053	1227	63%	0.0	86.28%	3430	LC485280.1
<input checked="" type="checkbox"/>	Dactyloidium arachnoides LMD2 genes for 18S rRNA, ITS1, 5.8S rRNA, ITS2, 28S rRNA, partial and complete...	Dactyloidium ar...	1053	1231	63%	0.0	86.28%	3926	LC485279.1
<input checked="" type="checkbox"/>	Uncultured marine dinoflagellate isolate ZBA-68 small subunit ribosomal RNA gene, partial sequence	uncultured marin...	1053	1053	56%	0.0	86.24%	1538	MZ620902.1
<input checked="" type="checkbox"/>	Kinithra sigma clone GYM27 small subunit ribosomal RNA gene, partial sequence	Kinithra sigma	1053	1130	59%	0.0	86.24%	1799	MW874844.1
<input checked="" type="checkbox"/>	Kinithra sigma clone GYM07 small subunit ribosomal RNA gene, partial sequence	Kinithra sigma	1053	1130	59%	0.0	86.24%	1799	MW874837.1
<input checked="" type="checkbox"/>	Kofoidinium cf. pavillardii isolate FG540 18S ribosomal RNA gene, partial sequence	Kofoidinium cf. p...	1050	1050	55%	0.0	86.57%	1208	GU355680.1
<input checked="" type="checkbox"/>	Prorocentrum sp. strain RCC8872 small subunit ribosomal RNA gene, partial sequence	Prorocentrum sp.	1048	1048	56%	0.0	86.14%	1676	MN824022.1
<input checked="" type="checkbox"/>	Prorocentrum sp. strain RCC8871 small subunit ribosomal RNA gene, partial sequence	Prorocentrum sp.	1048	1048	56%	0.0	86.14%	1670	MN824021.1
<input checked="" type="checkbox"/>	Prorocentrum sp. strain RCC8872 small subunit ribosomal RNA gene, partial sequence	Prorocentrum sp.	1048	1048	56%	0.0	86.14%	1677	ON427000.1

Durinskia capensis nucleomorph gene for small subunit rRNA, partial sequence, strain: Kommetjie 2-A
 Sequence ID: [LC192342.1](#) Length: 1486 Number of Matches: 6

Range 1: 474 to 1471 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
1844 bits(998)	0.0	998/998(100%)	0/998(0%)	Plus/Plus
Query 741	AATGAGAACAATTTAAACCCCTTATCGAGTATCAATTGGAGGGCAAGTCTGGTGCCAGCA			800
Sbjct 474	AATGAGAACAATTTAAACCCCTTATCGAGTATCAATTGGAGGGCAAGTCTGGTGCCAGCA			533
Query 801	GCCGCGGTAATCCAGCTCCAATAGCGTATATTAAGTTGTTGTCAGTTAAAAAGCTCGTA			860
Sbjct 534	GCCGCGGTAATCCAGCTCCAATAGCGTATATTAAGTTGTTGTCAGTTAAAAAGCTCGTA			593
Query 861	GTTGGATTGTGGCGTTCGCGTGCAGCCCGGCATTGTCGCCGGTGTGCTAGCGTCGCC			920
Sbjct 594	GTTGGATTGTGGCGTTCGCGTGCAGCCCGGCATTGTCGCCGGTGTGCTAGCGTCGCC			653
Query 921	ATCCTTGGGTGGATGCTGTGTGGCATTAAAGTTGTCGTGACAGGGGATGCCATCGTTACT			980
Sbjct 654	ATCCTTGGGTGGATGCTGTGTGGCATTAAAGTTGTCGTGACAGGGGATGCCATCGTTACT			713
Query 981	GTGAAAAAATAGAGTGTCAAAAGCAGGCTTACGCCGTTGAATATATTAGCATGGAATAA			1040
Sbjct 714	GTGAAAAAATAGAGTGTCAAAAGCAGGCTTACGCCGTTGAATATATTAGCATGGAATAA			773
Query 1041	TAAGATAGGACCTTGGTACTATTTTGGTTTGGCGACCAAGGTAATGATTAATAGGGA			1100
Sbjct 774	TAAGATAGGACCTTGGTACTATTTTGGTTTGGCGACCAAGGTAATGATTAATAGGGA			833
Query 1101	CAGTTGGGGTATTTCGATTCCATTGTCAGAGGTGAAATCTTGGATTTTGGAAAGACGA			1160
Sbjct 834	CAGTTGGGGTATTTCGATTCCATTGTCAGAGGTGAAATCTTGGATTTTGGAAAGACGA			893
Query 1161	ACTACTGCGAAAGCATTACCAAGGATGTTTTTCATTAAATCAAGAACGAAAGTTAGGGGAT			1220
Sbjct 894	ACTACTGCGAAAGCATTACCAAGGATGTTTTTCATTAAATCAAGAACGAAAGTTAGGGGAT			953
Query 1221	CGAAGATGATTAGATACCATCGTAGTCTTAACCATAAATATGCCCACAAAGGGATTGGCG			1280
Sbjct 954	CGAAGATGATTAGATACCATCGTAGTCTTAACCATAAATATGCCCACAAAGGGATTGGCG			1013
Query 1281	GAGTCTCGTTTTGTCTCCGTCAGCACCTTATGAGAAATCACAAAGCTTTGGGTTCCGGGG			1340
Sbjct 1014	GAGTCTCGTTTTGTCTCCGTCAGCACCTTATGAGAAATCACAAAGCTTTGGGTTCCGGGG			1073

6. C.II *Exuviaella pusilla*

Sequences producing significant alignments		Download	Select columns	Show	100			
select all 100 sequences selected		GenBank	Graphics	Distance tree of results	MSA Viewer			
Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/> Exuviaella pusilla strain LB1008 small subunit ribosomal RNA gene, partial sequence	Exuviaella pusilla	1445	3006	89%	0.0	100.00%	1722	DQ388459.1
<input checked="" type="checkbox"/> Uncultured marine dinoflagellate clone S1 18S ribosomal RNA gene, partial sequence	uncultured marin...	894	1525	72%	0.0	87.64%	1523	FJ914451.1
<input checked="" type="checkbox"/> Uncultured dinoflagellate clone HL2SCM10.11 18S ribosomal RNA gene, partial sequence	uncultured dinofl...	889	1518	72%	0.0	87.52%	1711	KC488424.1
<input checked="" type="checkbox"/> Karenia papilionacea strain CAWD01 18S ribosomal RNA gene, partial sequence	Karenia papilion...	870	1523	72%	0.0	87.13%	1741	HM067005.1
<input checked="" type="checkbox"/> Uncultured dinoflagellate clone HL2SF10.47 18S ribosomal RNA gene, partial sequence	uncultured dinofl...	867	1567	78%	0.0	87.01%	1690	KC488433.1
<input checked="" type="checkbox"/> Karenia bidigitata strain CAWD92 18S ribosomal RNA gene, partial sequence	Karenia bidigitata	865	1523	72%	0.0	87.01%	1741	HM067002.1
<input checked="" type="checkbox"/> Parvodinium umbonatum strain FACHB 329 small subunit ribosomal RNA gene, partial sequence	Parvodinium um...	865	1507	72%	0.0	87.01%	1740	GU001637.1
<input checked="" type="checkbox"/> Gymnodinium aureolum strain GrA01 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1...	Gymnodinium au...	865	1523	72%	0.0	87.01%	5897	DQ779991.1
<input checked="" type="checkbox"/> Parvodinium mixtum strain GeoM*754 small subunit ribosomal RNA gene, partial sequence; internal transcribed...	Parvodinium mix...	859	1518	72%	0.0	86.88%	3762	MG255426.2
<input checked="" type="checkbox"/> Uncultured Pfesteriaceae clone DD09.f.a small subunit ribosomal RNA gene, partial sequence	uncultured Pfest...	859	1602	81%	0.0	86.88%	1701	MK177614.1
<input checked="" type="checkbox"/> Achradina pulchra clone 3 18S ribosomal RNA gene, partial sequence	Achradina pulchra	859	1619	81%	0.0	86.86%	1704	MF543365.1
<input checked="" type="checkbox"/> Achradina pulchra clone 2 18S ribosomal RNA gene, partial sequence	Achradina pulchra	859	1619	81%	0.0	86.86%	1704	MF543364.1
<input checked="" type="checkbox"/> Achradina pulchra clone 1 18S ribosomal RNA gene, partial sequence	Achradina pulchra	859	1619	81%	0.0	86.86%	1704	MF543363.1
<input checked="" type="checkbox"/> Pyramodinium spinulosum gene for 18S ribosomal RNA gene, partial sequence, strain: HG289	Pyramodinium ...	859	1604	81%	0.0	86.86%	1726	LC209793.1
<input checked="" type="checkbox"/> Parvodinium sp. isolate Bucaco small subunit ribosomal RNA gene, partial sequence; internal transcribed space...	Parvodinium sp...	859	1518	72%	0.0	86.88%	3592	OM955144.1
<input checked="" type="checkbox"/> Parvodinium elpatiewskiy isolate lhavo small subunit ribosomal RNA gene, partial sequence; internal transcribe...	Parvodinium ele...	859	1518	72%	0.0	86.88%	3595	OM955145.1
<input checked="" type="checkbox"/> Stoeckeria sp. SSS09 genomic DNA containing 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA g...	Stoeckeria sp. S...	859	1523	72%	0.0	86.86%	3148	HG005132.1
<input checked="" type="checkbox"/> Parvodinium parvulum strain TIO879 small subunit ribosomal RNA gene, partial sequence	Parvodinium parv...	859	1518	72%	0.0	86.88%	1726	MT465326.1
<input checked="" type="checkbox"/> Brachidinium capitatum 18S ribosomal RNA gene, partial sequence	Brachidinium ca...	859	1523	72%	0.0	86.88%	1738	HM069908.1
<input checked="" type="checkbox"/> Stoeckeria sp. SSM90908 18S rRNA gene (partial), ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene (partial), s...	Stoeckeria sp. S...	859	1518	72%	0.0	86.86%	3172	FN557541.1
<input checked="" type="checkbox"/> Parvodinium inconsequum strain CCAP1140.3 small subunit ribosomal RNA gene, partial sequence	Parvodinium inc...	859	1518	72%	0.0	86.88%	1716	EF068247.1

Exuviaella pusilla strain LB1008 small subunit ribosomal RNA gene, partial sequence

Sequence ID: [DQ388459.1](#) Length: 1722 Number of Matches: 5

Range 1: 216 to 997 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
1445 bits(782)	0.0	782/782(100%)	0/782(0%)	Plus/Plus
Query 329	GATCGCATGGCTTCACGCCGGCGACAGATCATTCAAATTTCTGCCCCATCAGCTTTCGAC	388		
Sbjct 216	GATCGCATGGCTTCACGCCGGCGACAGATCATTCAAATTTCTGCCCCATCAGCTTTCGAC	275		
Query 389	GGTAGTGTAGTGGACTACCGTGGCATTAAACGGGTGACGGAGAAATAGGGTTCGATCCCGG	448		
Sbjct 276	GGTAGTGTAGTGGACTACCGTGGCATTAAACGGGTGACGGAGAAATAGGGTTCGATCCCGG	335		
Query 449	AGAGGGAGCCCTGAGAAACGGCTACACATCCAAAGGAAGGCAGCAGGCCGCAAAATACCC	588		
Sbjct 336	AGAGGGAGCCCTGAGAAACGGCTACACATCCAAAGGAAGGCAGCAGGCCGCAAAATACCC	395		
Query 589	AATCCTGACACAGGGAGGTAGTGACAAAGAAATAACAATACCGGGCTTTTTAGGTCTGGT	568		
Sbjct 396	AATCCTGACACAGGGAGGTAGTGACAAAGAAATAACAATACCGGGCTTTTTAGGTCTGGT	455		
Query 569	AATTGGAAATGAGTACAAATTTAAATCCCTTAAACGAGGATCCAATGGAGGGCAAGTCTGGT	628		
Sbjct 456	AATTGGAAATGAGTACAAATTTAAATCCCTTAAACGAGGATCCAATGGAGGGCAAGTCTGGT	515		
Query 629	CCAGCAGCCGCGGTAAATCCAGCTCCAATAGCGTATATTAAAGTTGTTGCAAGTAAAAAG	688		
Sbjct 516	CCAGCAGCCGCGGTAAATCCAGCTCCAATAGCGTATATTAAAGTTGTTGCAAGTAAAAAG	575		
Query 689	CTCGTAGTGGATTTCTGGTACGGTGCGCCCTGGTCCGCCCTTTATGGTGTGTGAGTACC	748		
Sbjct 576	CTCGTAGTGGATTTCTGGTACGGTGCGCCCTGGTCCGCCCTTTATGGTGTGTGAGTACC	635		
Query 749	GGCGCGCGCCCTGCCATCCTTCTGAGAGCCGCGCTACCTTCACTGGCCGGCGTGGCAA	888		
Sbjct 636	GGCGCGCGCCCTGCCATCCTTCTGAGAGCCGCGCTACCTTCACTGGCCGGCGTGGCAA	695		
Query 889	TCTGGATCGTTTACTTTTGAATAATAGAGTGTTCAGCAGGCATACTCGCTTTGAATA	868		
Sbjct 696	TCTGGATCGTTTACTTTTGAATAATAGAGTGTTCAGCAGGCATACTCGCTTTGAATA	755		
Query 869	CATTAGCATGGAATAAATAGATAGGACTTGGGTCTATTTGTTGGTTCTAGGACCGAA	928		
Sbjct 756	CATTAGCATGGAATAAATAGATAGGACTTGGGTCTATTTGTTGGTTCTAGGACCGAA	815		
Query 929	GTAATGATTGATAGGGAAGTTGGGGTGTAGTATTAGCGGCCAGAGGTGAAATCTT	988		
Sbjct 816	GTAATGATTGATAGGGAAGTTGGGGTGTAGTATTAGCGGCCAGAGGTGAAATCTT	875		
Query 989	GGATTCGCTAAAGACTAACTAATGCGAAAGCATTCACCAAGGATGTCCTTCTTAATCAAG	1048		
Sbjct 876	GGATTCGCTAAAGACTAACTAATGCGAAAGCATTCACCAAGGATGTCCTTCTTAATCAAG	935		
Query 1049	AACGAAAGTTGGGGGATCGAAGACGATCAGATACCGTCTAGTCTCAACCATAAACGATG	1108		
Sbjct 936	AACGAAAGTTGGGGGATCGAAGACGATCAGATACCGTCTAGTCTCAACCATAAACGATG	995		
Query 1109	CC 1110			
Sbjct 996	CC 997			

7. C.IV *Peridinium foliaceum*

Sequences producing significant alignments		Download	Select columns	Show	100			
<input checked="" type="checkbox"/> select all 100 sequences selected		GenBank	Graphics	Distance tree of results	MSA Viewer			
Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/> Peridinium foliaceum isolate Xmm11S5 18S ribosomal RNA gene, partial sequence	Peridinium foliac...	2966	3039	94%	0.0	99.57%	1706	KJ561157.1
<input checked="" type="checkbox"/> Durinskia baltica nucleomorph gene for small subunit rRNA, partial sequence, strain CS-38	Durinskia baltica	2562	2622	87%	0.0	97.42%	1561	LC192343.1
<input checked="" type="checkbox"/> Dinophyta sp. HG204 nucleomorph gene for small subunit rRNA, partial sequence	Dinophyta sp. H...	2505	2565	86%	0.0	97.36%	1525	LC192340.1
<input checked="" type="checkbox"/> Durinskia capensis nucleomorph gene for small subunit rRNA, partial sequence, strain Kommetjie 2-A	Durinskia capensis	2388	2449	84%	0.0	96.61%	1486	LC192342.1
<input checked="" type="checkbox"/> Dinophyta sp. HG180 nucleomorph gene for small subunit rRNA, partial sequence	Dinophyta sp. H...	2281	2341	83%	0.0	95.60%	1466	LC192339.1
<input checked="" type="checkbox"/> Peridiniopsis niei strain Donohu 18S ribosomal RNA gene, partial sequence	Unruhidium niei	1853	1853	75%	0.0	91.75%	1340	JX141779.1
<input checked="" type="checkbox"/> Uncultured marine dinoflagellate isolate ZBL-41 small subunit ribosomal RNA gene, partial sequence	uncultured marin...	1685	1685	83%	0.0	87.56%	1594	MZ620774.1
<input checked="" type="checkbox"/> Uncultured marine dinoflagellate isolate ZBO-57 small subunit ribosomal RNA gene, partial sequence	uncultured marin...	1587	1587	81%	0.0	86.81%	1589	MZ620974.1
<input checked="" type="checkbox"/> Prorocentrum micans strain BGERL21 small subunit ribosomal RNA gene, partial sequence	Prorocentrum mi...	1576	1576	90%	0.0	84.84%	1696	MW979841.1
<input checked="" type="checkbox"/> Prorocentrum micans strain BGERL20 small subunit ribosomal RNA gene, partial sequence	Prorocentrum mi...	1576	1576	90%	0.0	84.84%	1692	MW979840.1
<input checked="" type="checkbox"/> Prorocentrum mexicanum strain SKLMP_W062 small subunit ribosomal RNA gene, partial sequence	Prorocentrum m...	1570	1570	90%	0.0	84.79%	1709	MK547145.1
<input checked="" type="checkbox"/> Prorocentrum mexicanum strain SKLMP_W023 small subunit ribosomal RNA gene, partial sequence	Prorocentrum m...	1570	1570	90%	0.0	84.79%	1680	MK547144.1
<input checked="" type="checkbox"/> Prorocentrum mexicanum strain SKLMP_Ve105 small subunit ribosomal RNA gene, partial sequence	Prorocentrum m...	1570	1570	90%	0.0	84.79%	1696	MK547143.1
<input checked="" type="checkbox"/> Prorocentrum mexicanum strain SKLMP_Ve103 small subunit ribosomal RNA gene, partial sequence	Prorocentrum m...	1570	1570	90%	0.0	84.79%	1699	MK547142.1
<input checked="" type="checkbox"/> Prorocentrum mexicanum strain SKLMP_Ve076 small subunit ribosomal RNA gene, partial sequence	Prorocentrum m...	1570	1570	90%	0.0	84.79%	1712	MK547140.1
<input checked="" type="checkbox"/> Prorocentrum mexicanum strain SKLMP_Ve062 small subunit ribosomal RNA gene, partial sequence	Prorocentrum m...	1570	1570	90%	0.0	84.79%	1710	MK547139.1
<input checked="" type="checkbox"/> Prorocentrum koreanum strain SKLMP_W111 small subunit ribosomal RNA gene, partial sequence	Prorocentrum ko...	1570	1570	90%	0.0	84.79%	1710	MK547137.1
<input checked="" type="checkbox"/> Prorocentrum koreanum strain SKLMP_W090 small subunit ribosomal RNA gene, partial sequence	Prorocentrum ko...	1570	1570	90%	0.0	84.79%	1697	MK547136.1
<input checked="" type="checkbox"/> Prorocentrum koreanum strain SKLMP_W054 small subunit ribosomal RNA gene, partial sequence	Prorocentrum ko...	1570	1570	90%	0.0	84.79%	1682	MK547135.1
<input checked="" type="checkbox"/> Prorocentrum koreanum strain SKLMP_W050 small subunit ribosomal RNA gene, partial sequence	Prorocentrum ko...	1570	1570	90%	0.0	84.79%	1709	MK547134.1

Peridinium foliaceum isolate Xmm11S5 18S ribosomal RNA gene, partial sequence

Sequence ID: [KJ561157.1](#) Length: 1706 Number of Matches: 2

Range 1: 49 to 1672 [GenBank](#) [Graphics](#)

[Next Match](#) [Previous M](#)

Score	Expect	Identifiers	Gaps	Strand					
2966 bits(1606)	0.0	1624/1631(99%)	7/1631(0%)	Plus/Plus					
Query 136	ACTTTGAAAC	TGCGAACG	GCCCTCATT	AATTC	CGTCAGT	TATAGT	TTATTTG	GATAGTCC	195
Sbjct 49	ACTTTGAAAC	TGCGAACG	GCCCTCATT	AATA-----	TCAGT	TATAGT	TTATTTG	GATAGTCC	181
Query 196	CTTACTACT	TGGATAAC	CGTAGT	AATTC	TAGAGCT	TAACAT	GCCTCA	TACCCCTCT	255
Sbjct 182	CTTACTACT	TGGATAAC	CGTAGT	AATTC	TAGAGCT	TAACAT	GCCTCA	TACCCCTCT	161
Query 256	GGTAGTAT	TTAGATT	TGAACCA	CCCCCTC	GGGGT	GATGG	GATTCA	TAATAAGC	315
Sbjct 162	GGTAGTAT	TTAGATT	TGAACCA	CCCCCTC	GGGGT	GATGG	GATTCA	TAATAAGC	221
Query 316	TCGCGGAT	CGCATGG	CGTAAG	CCGCG	CGATG	GATCA	AGTTT	CGCCCTA	375
Sbjct 222	TCGCGGAT	CGCATGG	CGTAAG	CCGCG	CGATG	GATCA	AGTTT	CGCCCTA	281
Query 376	GGATGGT	AGGGTAT	TGGCCT	ACCATG	GCCTT	AACGG	GAACGG	GAATAG	435
Sbjct 282	GGATGGT	AGGGTAT	TGGCCT	ACCATG	GCCTT	AACGG	GAACGG	GAATAG	341
Query 436	CCGAGAG	GGGACCT	TGAGAC	CGGCT	TACCAC	ATCCA	AGGAAG	GCAGG	495
Sbjct 342	CCGAGAG	GGGACCT	TGAGAC	CGGCT	TACCAC	ATCCA	AGGAAG	GCAGG	401
Query 496	ACCCAAT	CCTGAC	ACAGG	AGGTAG	TGACAA	TAAATA	AACAAT	GCCGGG	555
Sbjct 482	ACCCAAT	CCTGAC	ACAGG	AGGTAG	TGACAA	TAAATA	AACAAT	GCCGGG	461
Query 556	TGGCAAT	TGSAAT	GAGAAC	AAATTA	AACCCCT	TATC	GAGT	ATCAAT	615
Sbjct 462	TGGCAAT	TGSAAT	GAGAAC	AAATTA	AACCCCT	TATC	GAGT	ATCAAT	521
Query 616	GGTGCC	CAGC	CGCGT	AAATTC	CAGC	TCCAAT	AGCGT	ATATAA	675
Sbjct 522	GGTGCC	CAGC	CGCGT	AAATTC	CAGC	TCCAAT	AGCGT	ATATAA	581
Query 676	AAAGCT	CGTAGT	TGGAT	TGTGG	CTGT	CGTGC	GGCCGT	GCACAT	735
Sbjct 582	AAAGCT	CGTAGT	TGGAT	TGTGG	CTGT	CGTGC	GGCCGT	GCACAT	641
Query 736	CGTGG	ACGCC	ATCCT	TGGG	TAGT	CTGT	GGCATT	AGGTTG	795
Sbjct 642	CGTGG	ACGCC	ATCCT	TGGG	TAGT	CTGT	GGCATT	AGGTTG	701
Query 796	CATCTTT	TACTGT	GAGAAA	TTAG	AGTGT	TCAA	AGGCT	TATGCC	855
Sbjct 782	CATCTTT	TACTGT	GAGAAA	TTAG	AGTGT	TCAA	AGGCT	TATGCC	761
Query 856	GCATG	GAATAA	TAGAT	AGGAC	TTGGT	TACT	ATTTGT	TGGTTG	915
Sbjct 762	GCATG	GAATAA	TAGAT	AGGAC	TTGGT	TACT	ATTTGT	TGGTTG	821
Query 916	ATTAAT	AGGAC	AGTGT	GGGGT	ATCGT	ATTC	ATG	CAGAGT	975
Sbjct 822	ATTAAT	AGGAC	AGTGT	GGGGT	ATCGT	ATTC	ATG	CAGAGT	881
Query 976	TTGGA	AGC	GAAC	TACT	GC	GAA	GCAT	TACCA	1035
Sbjct 882	TTGGA	AGC	GAAC	TACT	GC	GAA	GCAT	TACCA	941
Query 1036	AGTT	AGGG	GATC	GAAG	TGAT	TAG	TAC	CAAT	1095
Sbjct 942	AGTT	AGGG	GATC	GAAG	TGAT	TAG	TAC	CAAT	1001
Query 1096	AGGGAT	TGGCG	GAGTT	CGTTT	TG	CTCC	GT	CAGC	1155
Sbjct 1082	AGGGAT	TGGCG	GAGTT	CGTTT	TG	CTCC	GT	CAGC	1061

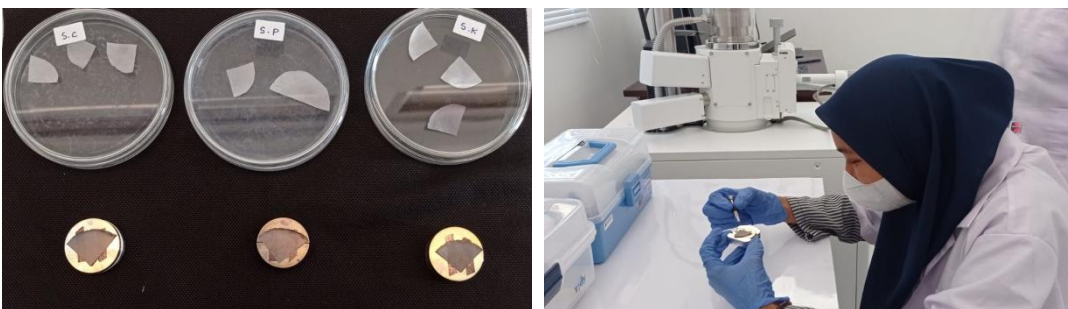
Lampiran 3. Dokumentasi Pengambilan Sampel Lapangan

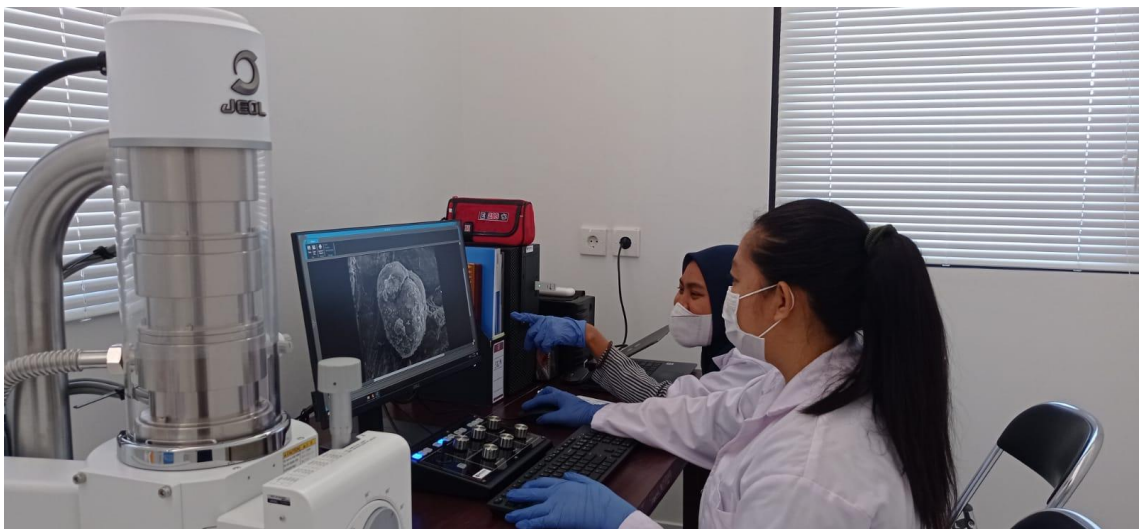
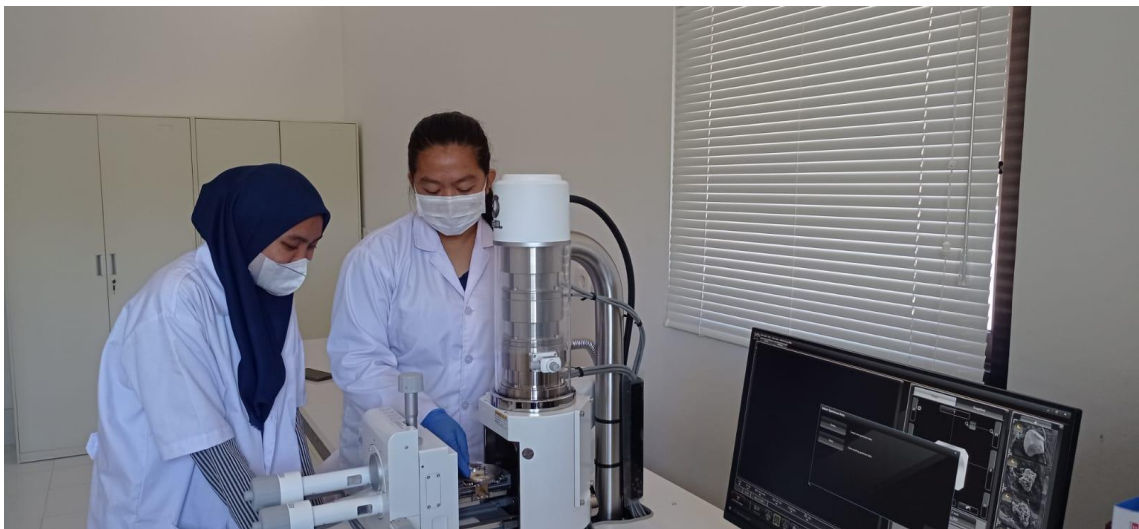


Lampiran 4. Pemisahan Kista Dinoflagellata dari Sedimen



Lampiran 5. Analisis Morfologi menggunakan Mikroskop Cahaya dan Mikroskop Elektron







Lampiran 6. Analisis Genetik Kista Dinoflagellata



