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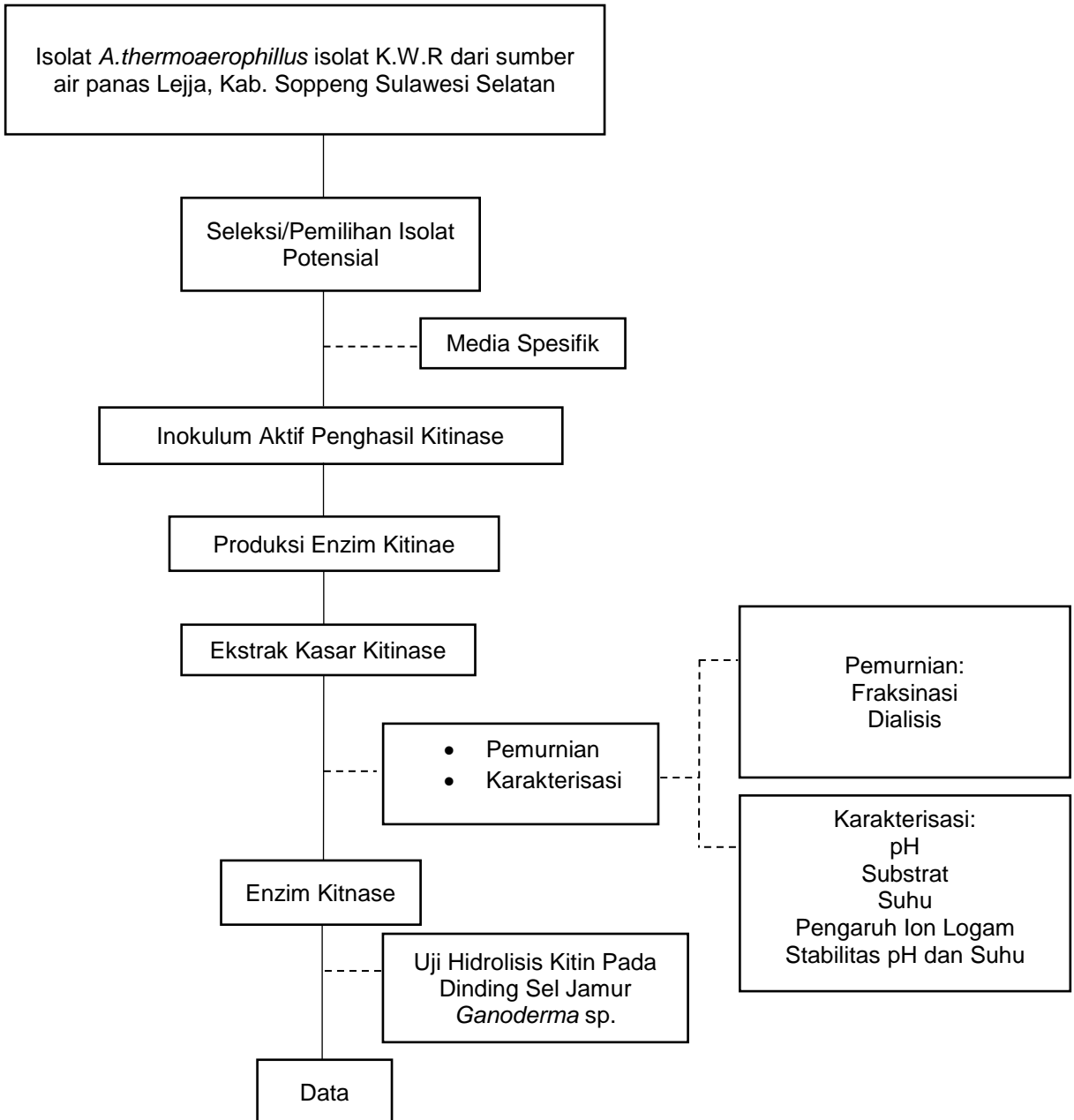
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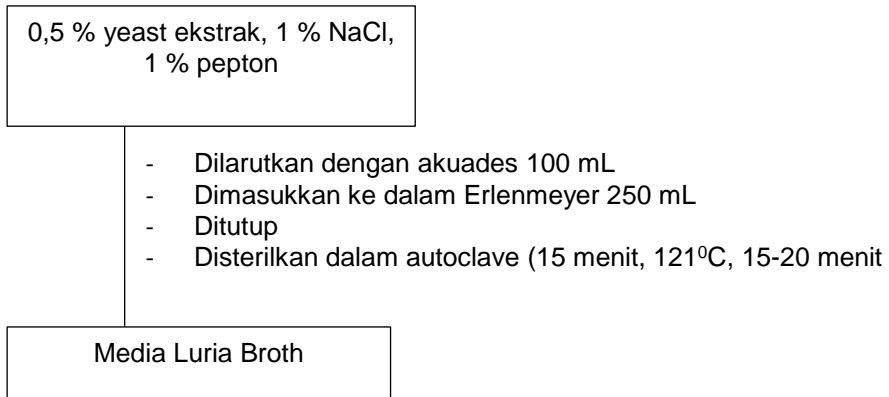
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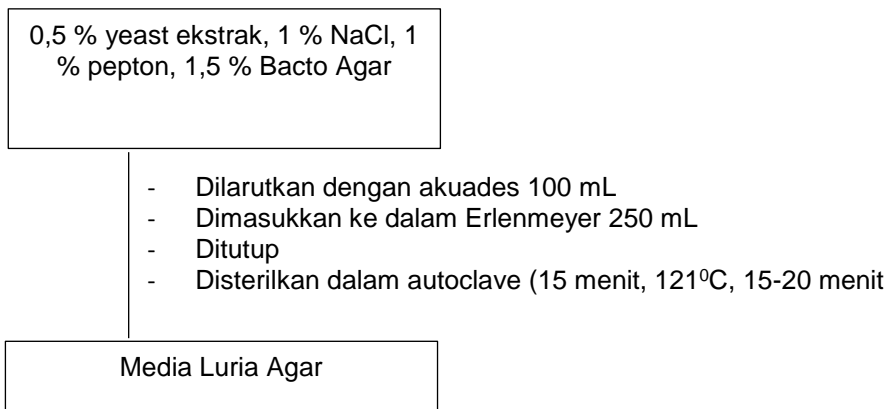
LAMPIRAN**Lampiran 1.** Diagram alir penelitian

Lampiran 2. Prosedur Kerja

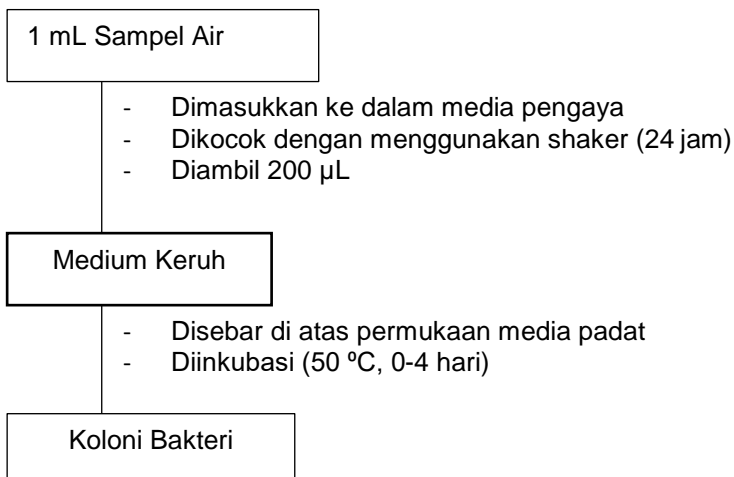
Pembuatan Medium Luria Broth



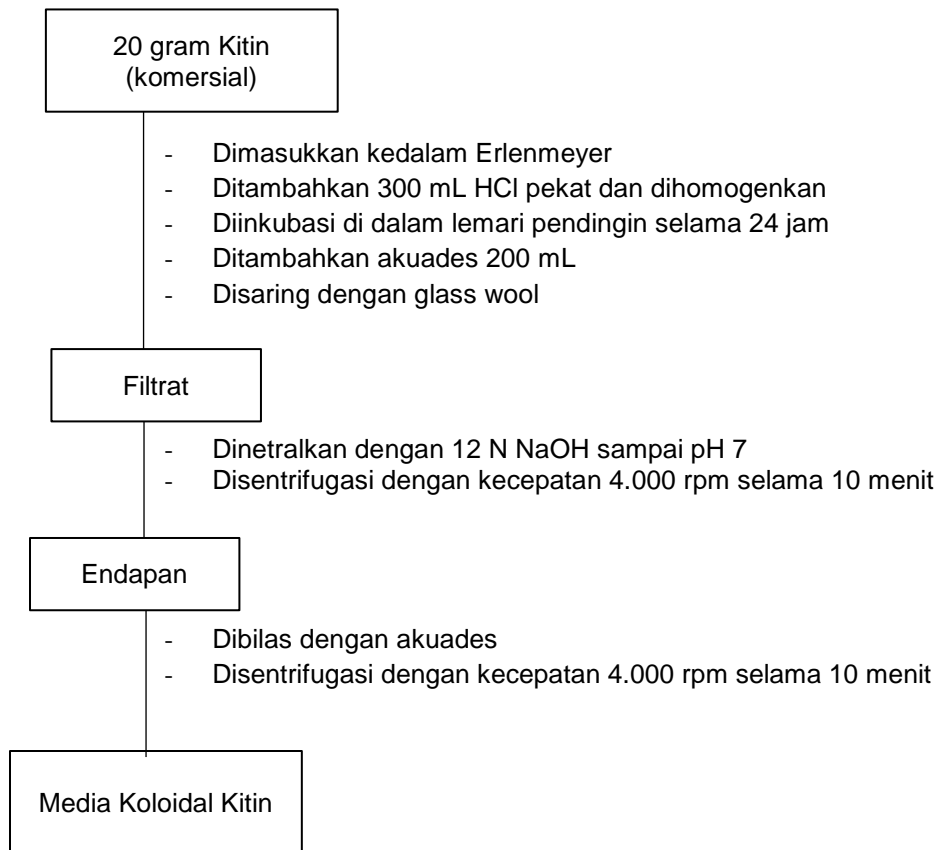
Pembuatan Media Luria Agar



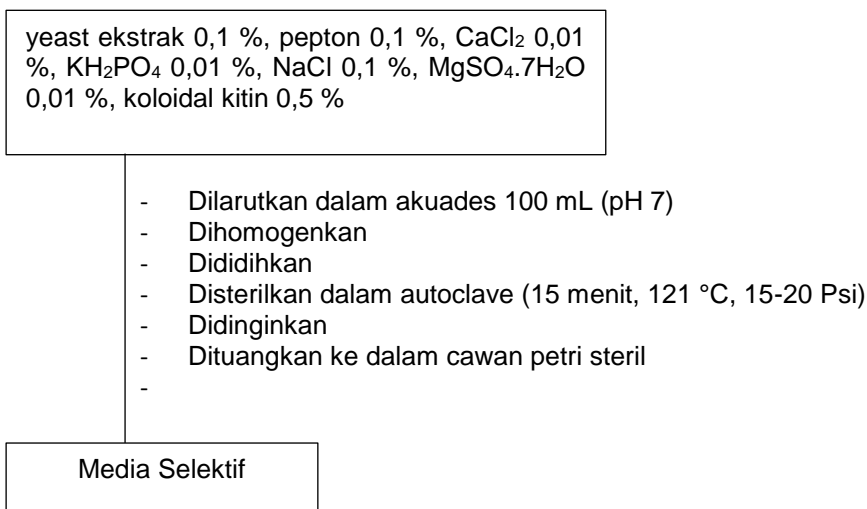
Isolasi Mikroba dari Sumber Air Panas



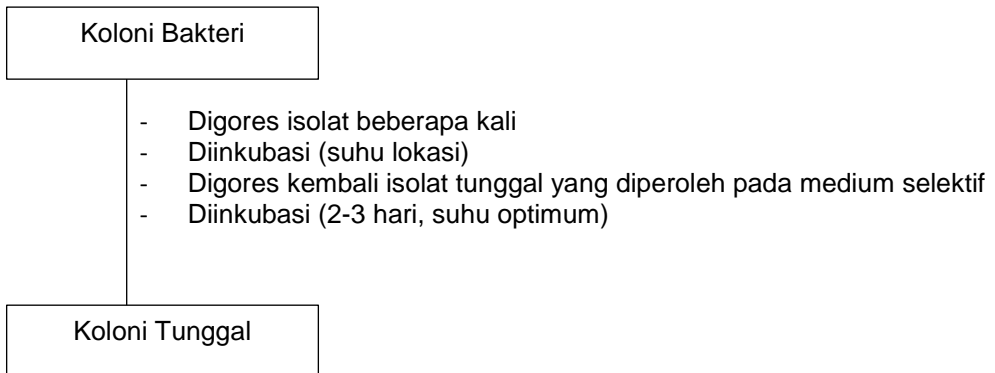
Pembuatan Substrat Koloidal Kitin



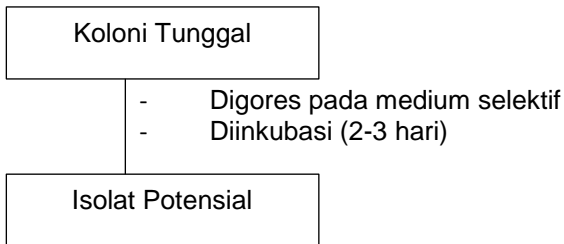
Pembuatan Media Selektif Kitinolitik



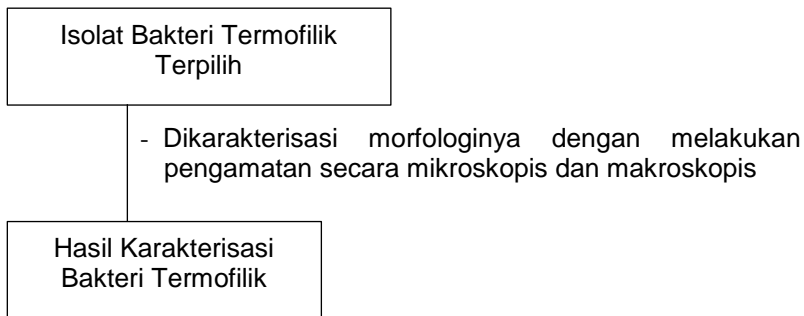
Pemurnian Bakteri



Pemilihan Isolat Potensial



Uji Morfologi Bakteri Penghasil Enzim Kitinase



Pembuatan dan Penyiapan Inokulum

yeast ekstrak 0,5 %, pepton 0,01 %, amonium sulfat, CaCl_2 0,01 %, KH_2PO_4 0,01 %, NaCl 0,1 %, $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$ 0,01 % dan koloidal kitin 0,5 %

- Dilarutkan dalam akuades 100 mL
- Dihomogenkan, dipanaskan, dituang ke dalam Erlenmeyer steril
- Diambil 2 hingga 3 ose bakteri yang telah tumbuh dengan baik
- Diinokulasikan ke dalam medium inokulum yang telah disiapkan
- Dikocok ke dalam shaker (40 °C, 180 rpm, 18-24 jam) untuk diinokulasikan lebih lanjut dalam medium produksi

Media Inokulum Aktif

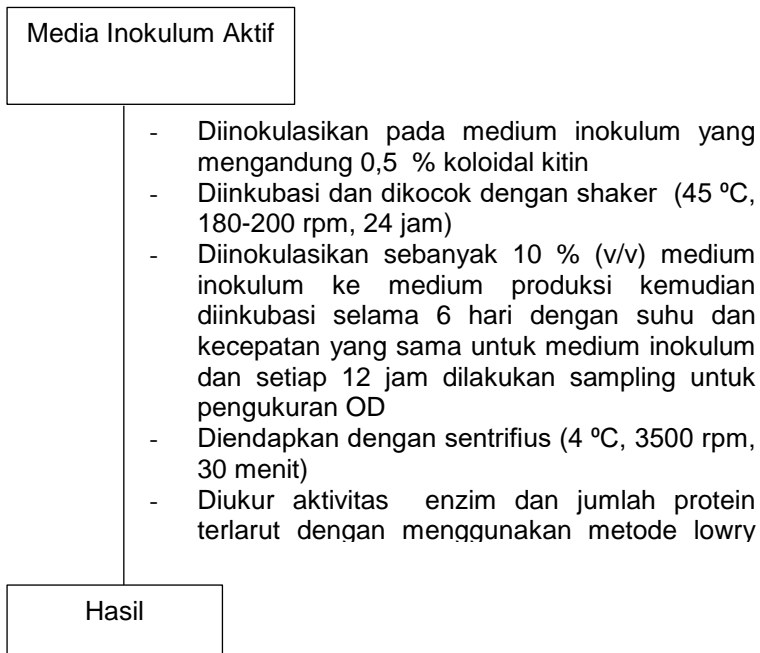
Pembuatan Medium Produksi

amonium sulfat 0,7 %, yeast ekstrak 0,05 %, bakto pepton 0,1 %, NaCl 0,1 %, KH_2PO_4 0,01 %, CaCl_2 0,01 %, $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$ 0,01 %, koloidal kitin 0,5 %

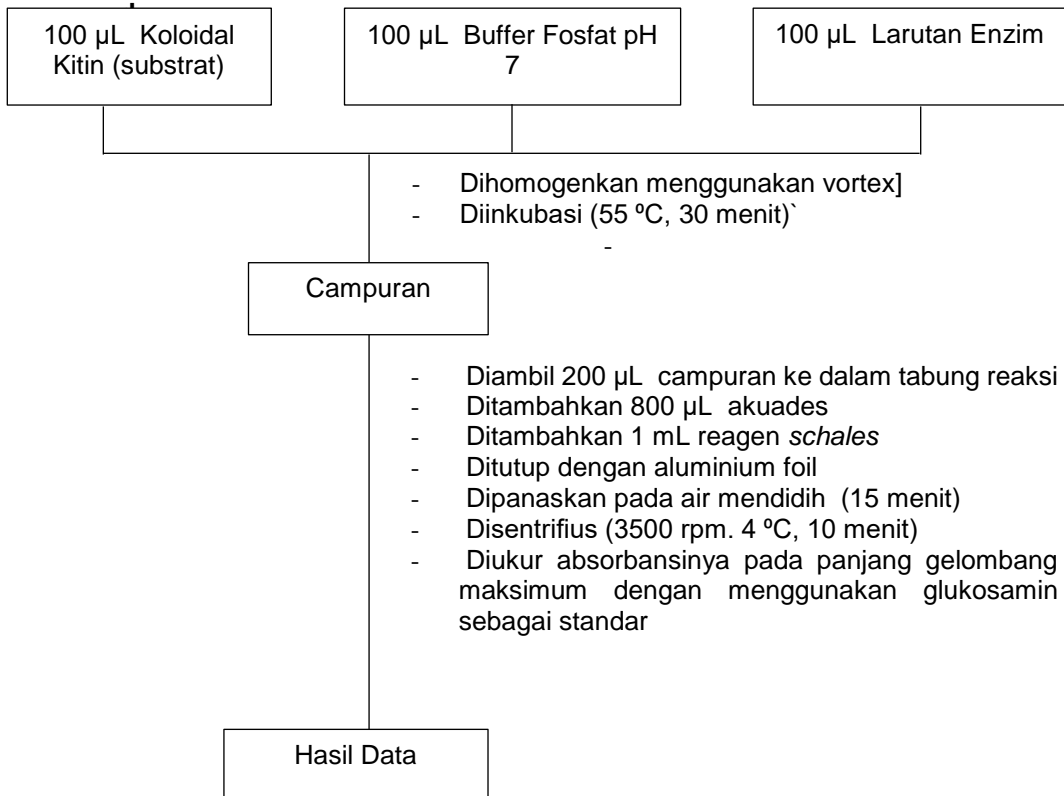
- Dilarutkan dengan akuades 500 mL
- Dihomogenkan
- Disterilkan dengan *autoclave*.

Medium Produksi

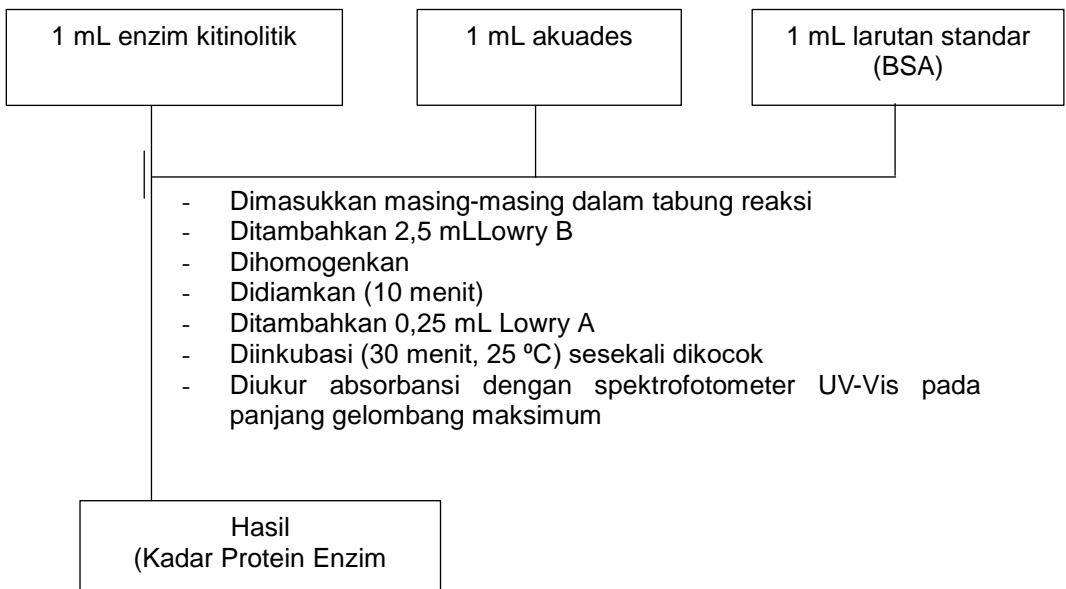
Produksi Ekstrak Kitinase



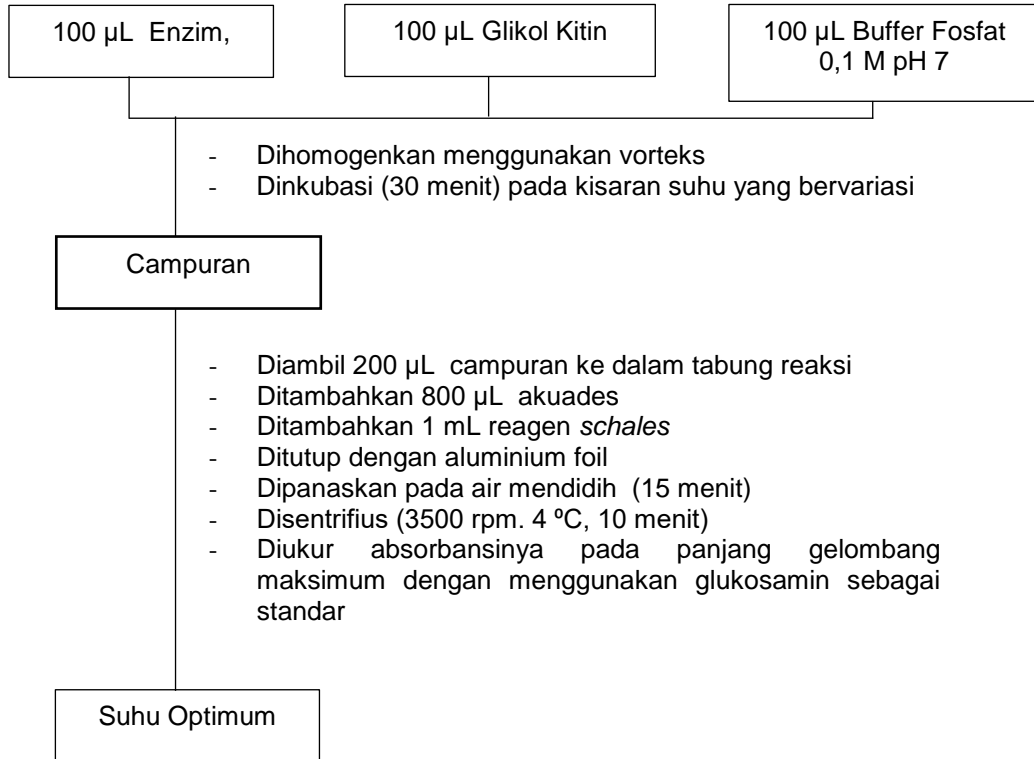
Pengukuran Aktivitas Enzim Kitinase (Natsir et al., 2014)



Penentuan Kadar Protein dengan Metode Lowry



Karakterisasi Enzim Kitinase dari Mikroba Termofil Penentuan Suhu Optimum



Lampiran 3. Tabel Fraksinasi Ammonium Sulfat

Konsentrasi awal dari amonium sulfat (% kejenuhan pada 0°C)	% Kejenuhan pada 0°C																
	20	25	30	35	40	45	50	55	60	65	70	75	80	85	90	95	100
	Penambahan amonium sulfat kristal (gram) untuk pada 1 liter larutan																
0	106	134	164	194	226	258	291	326	361	398	436	476	516	559	603	650	697
5	79	108	137	166	197	229	262	296	331	368	405	444	484	526	570	615	662
10	53	81	109	139	169	200	233	266	301	337	374	412	452	493	536	581	627
15	26	54	82	111	141	172	204	237	271	306	343	381	420	460	503	547	592
20	0	27	55	83	113	143	175	207	241	276	312	349	387	427	469	512	557
25		0	27	56	84	115	146	179	211	245	280	317	355	395	436	478	522
30			0	28	56	86	117	148	181	214	249	285	323	362	402	445	488
35				0	28	57	87	118	151	184	218	254	291	329	369	410	453
40					0	29	58	89	120	153	187	222	258	296	335	376	418
45						0	29	59	90	123	156	190	226	263	302	342	383
50							0	30	60	92	125	159	194	230	268	308	348
55								0	30	61	93	127	161	197	235	273	313
60									0	31	62	95	129	164	201	239	279
65										0	31	63	97	132	168	205	244
70											0	32	65	99	134	171	209
75												0	32	66	101	137	174
80													0	33	67	103	139
85														0	34	68	105
90															0	34	70

Lampiran 4. Data

Hubungan antara OD dan aktivitas kitinase

Waktu inkubasi (jam)	Absorbansi (660nm)	Aktivitas kitinase (U/mL)
0	0.065	0.002
12	0.097	0.003
24	0.252	0.018
36	0.435	0.090
48	0.452	0.167
60	0.427	0.049
72	0.327	0.031
84	0.300	0.015
96	0.261	0.009
108	0.189	0.003
120	0.021	0.001

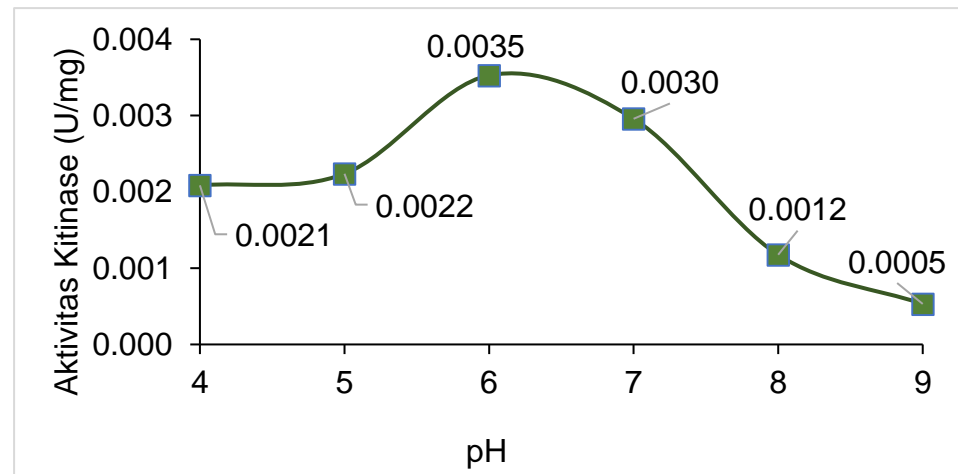
Hubungan antara kadar protein dan aktivitas spesifik

Waktu inkubasi (jam)	Kadar protein (mg/mL)	Aktivitas spesifik (U/mg)
0	0.357	0.006
12	0.406	0.008
24	0.629	0.029
36	0.748	0.121
48	0.937	0.178
60	1.282	0.038
72	1.251	0.025
84	0.885	0.017
96	0.866	0.010
108	0.677	0.005

Karakterisasi pH

Konsentrasi pH	Abs Sampel	Abs Kontrol	Konsentrasi N-Ac-Glu Sampel	Konsentrasi N-Ac-Glu Kontrol	xs-xk	1000/200	600/400	1/30.	1/221.21	aktivitas
4	0.356	0.411	8.5738	6.7282	1.8456	5.0000	1.5000	0.0333	0.0045	0.0021
5	0.326	0.385	9.5805	7.6007	1.9799	5.0000	1.5000	0.0333	0.0045	0.0022
6	0.322	0.415	9.7148	6.5940	3.1208	5.0000	1.5000	0.0333	0.0045	0.0035
7	0.312	0.39	10.0503	7.4329	2.6174	5.0000	1.5000	0.0333	0.0045	0.0030
8	0.348	0.379	8.8423	7.8020	1.0403	5.0000	1.5000	0.0333	0.0045	0.0012
9	0.357	0.371	8.5403	8.0705	0.4698	5.0000	1.5000	0.0333	0.0045	0.0005

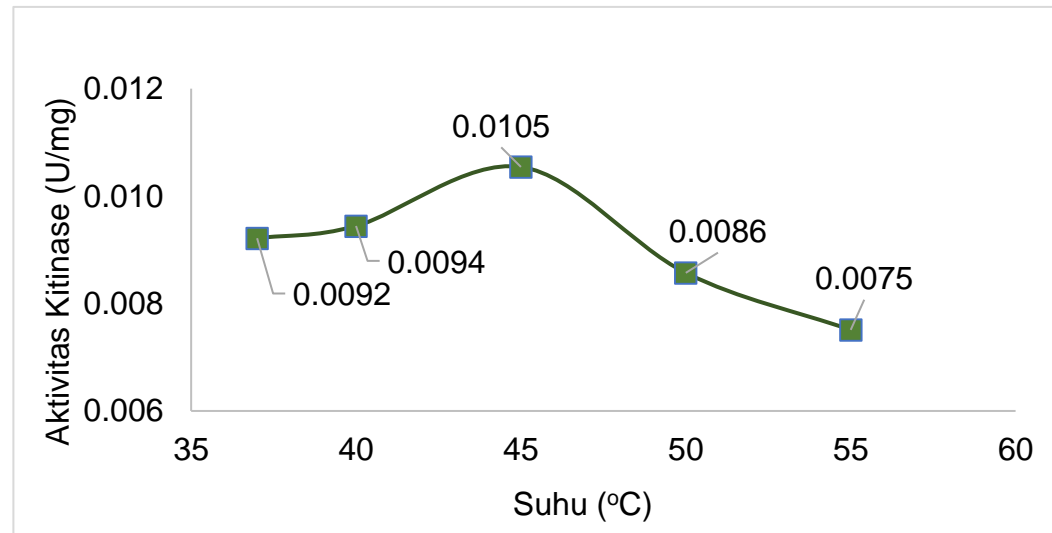
Konsentrasi pH	aktivitas
4	0.0021
5	0.0022
6	0.0035
7	0.0030
8	0.0012
9	0.0005



Karakterisasi suhu

Suhu	Abs Sampel	Abs Kontrol	Konsentrasi N-Ac-Glu Sampel	Konsentrasi N-Ac-Glu Kontrol	xs-xk	1000/200	600/400	1/30.	1/221.21	aktivitas
37	0.235	0.478	12.6342	4.4799	8.1544	5.0000	1.5000	0.0333	0.0045	0.0092
40	0.223	0.472	13.0369	4.6812	8.3557	5.0000	1.5000	0.0333	0.0045	0.0094
45	0.213	0.491	13.3725	4.0436	9.3289	5.0000	1.5000	0.0333	0.0045	0.0105
50	0.226	0.452	12.9362	5.3523	7.5839	5.0000	1.5000	0.0333	0.0045	0.0086
55	0.223	0.421	13.0369	6.3926	6.6443	5.0000	1.5000	0.0333	0.0045	0.0075

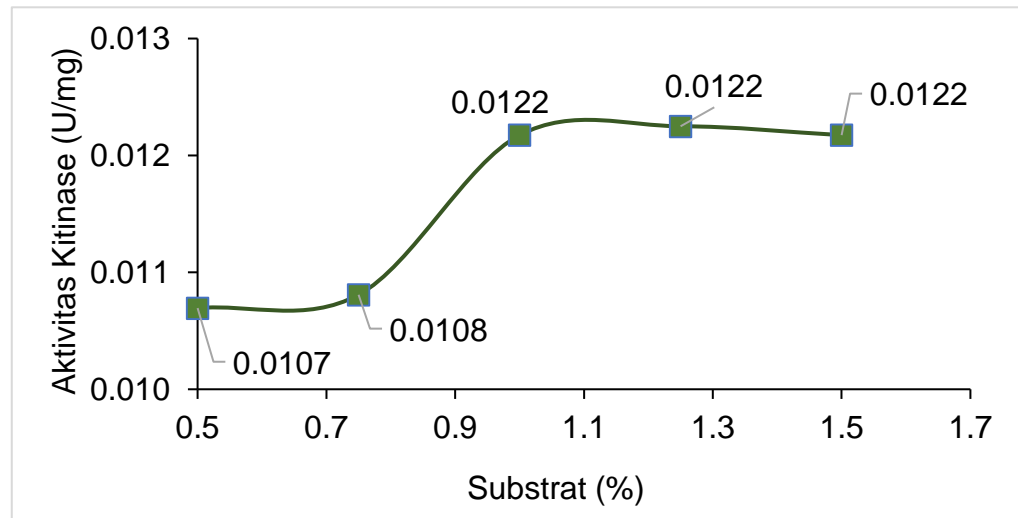
Suhu	aktivitas
37	0.0092
40	0.0094
45	0.0105
50	0.0086
55	0.0075



Penentuan substrat optimum

Konsentrasi Substrat (%)	Abs Sampel	Abs Kontrol	Konsentrasi N-Ac-Glu Sampel	Konsentrasi N-Ac-Glu Kontrol	xs-xk	1000/200	600/400	1/30.	1/221.21	aktivitas
0.5	0.239	0.521	12.5000	3.0369	9.4631	5.0000	1.5000	0.0333	0.0045	0.0107
0.75	0.242	0.527	12.3993	2.8356	9.5638	5.0000	1.5000	0.0333	0.0045	0.0108
1	0.262	0.583	11.7282	0.9564	10.7718	5.0000	1.5000	0.0333	0.0045	0.0122
1.25	0.244	0.567	12.3322	1.4933	10.8389	5.0000	1.5000	0.0333	0.0045	0.0122
1.5	0.233	0.554	12.7013	1.9295	10.7718	5.0000	1.5000	0.0333	0.0045	0.0122

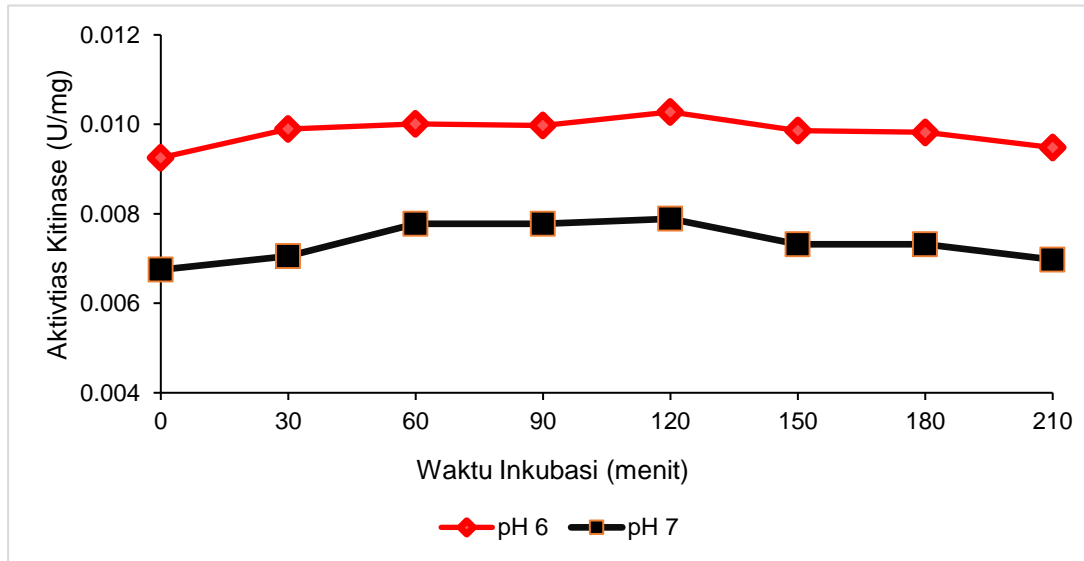
Konsentrasi Substrat (%)	aktivitas
0.5	0.0107
0.75	0.0108
1	0.0122
1.25	0.0122
1.5	0.0122



Stabilitas pH

Stabilitas kitinase pH 6										
Waktu inkubasi(menit)	Absorbansi Sampel	Absorbansi Kontrol	Konsentrasi N-Ac-Glu Sampel	Konsentrasi N-Ac-Glu Kontrol	xs-xk	1000/200	600/400	1/30.	1/221.21	aktivitas
0	0.311	0.555	10.0839	1.8960	8.1879	5.0000	1.5000	0.0333	0.0045	0.0093
30	0.324	0.585	9.6477	0.8893	8.7584	5.0000	1.5000	0.0333	0.0045	0.0099
60	0.323	0.587	9.6812	0.8221	8.8591	5.0000	1.5000	0.0333	0.0045	0.0100
90	0.328	0.591	9.5134	0.6879	8.8255	5.0000	1.5000	0.0333	0.0045	0.0100
120	0.346	0.617	8.9094	-0.1846	9.0940	5.0000	1.5000	0.0333	0.0045	0.0103
150	0.325	0.585	9.6141	0.8893	8.7248	5.0000	1.5000	0.0333	0.0045	0.0099
180	0.326	0.585	9.5805	0.8893	8.6913	5.0000	1.5000	0.0333	0.0045	0.0098
210	0.322	0.572	9.7148	1.3255	8.3893	5.0000	1.5000	0.0333	0.0045	0.0095
Stabilitas kitinase pH 7										
Waktu inkubasi(menit)	Absorbansi Sampel	Absorbansi Kontrol	Konsentrasi N-Ac-Glu Sampel	Konsentrasi N-Ac-Glu Kontrol	xs-xk	1000/200	600/400	1/30.	1/221.21	aktivitas
0	0.283	0.461	11.0235	5.0503	5.9732	5.0000	1.5000	0.0333	0.0045	0.0068
30	0.279	0.465	11.1577	4.9161	6.2416	5.0000	1.5000	0.0333	0.0045	0.0071
60	0.298	0.503	10.5201	3.6409	6.8792	5.0000	1.5000	0.0333	0.0045	0.0078
90	0.294	0.499	10.6544	3.7752	6.8792	5.0000	1.5000	0.0333	0.0045	0.0078
120	0.317	0.525	9.8826	2.9027	6.9799	5.0000	1.5000	0.0333	0.0045	0.0079
150	0.292	0.485	10.7215	4.2450	6.4765	5.0000	1.5000	0.0333	0.0045	0.0073
180	0.303	0.496	10.3523	3.8758	6.4765	5.0000	1.5000	0.0333	0.0045	0.0073
210	0.279	0.463	11.1577	4.9832	6.1745	5.0000	1.5000	0.0333	0.0045	0.0070

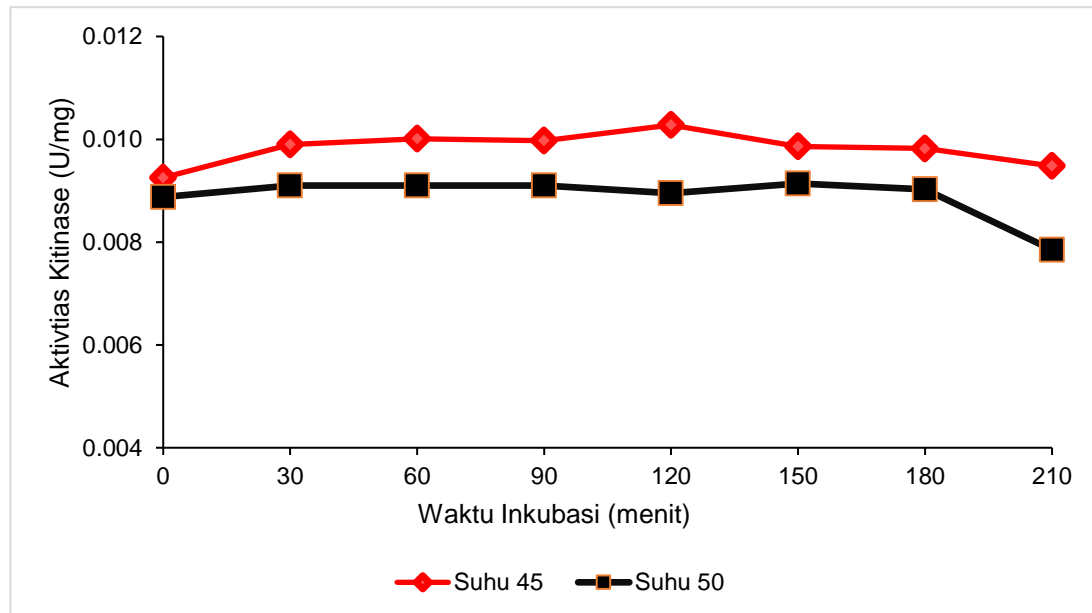
Waktu inkubasi(menit)	pH 6	pH 7
0	0.0093	0.0068
30	0.0099	0.0071
60	0.0100	0.0078
90	0.0100	0.0078
120	0.0103	0.0079
150	0.0099	0.0073
180	0.0098	0.0073
210	0.0095	0.0070



Stabilitas suhu

Suhu 45									
Absorbansi Sampel	Absorbansi Kontrol	Konsentrasi N-Ac-Glu Sampel	Konsentrasi N-Ac-Glu Kontrol	xs-xk	1000/200	600/400	1/30.	1/221.21	aktivitas
0.311	0.555	10.0839	1.8960	8.1879	5.0000	1.5000	0.0333	0.0045	0.0093
0.324	0.585	9.6477	0.8893	8.7584	5.0000	1.5000	0.0333	0.0045	0.0099
0.323	0.587	9.6812	0.8221	8.8591	5.0000	1.5000	0.0333	0.0045	0.0100
0.328	0.591	9.5134	0.6879	8.8255	5.0000	1.5000	0.0333	0.0045	0.0100
0.346	0.617	8.9094	-0.1846	9.0940	5.0000	1.5000	0.0333	0.0045	0.0103
0.325	0.585	9.6141	0.8893	8.7248	5.0000	1.5000	0.0333	0.0045	0.0099
0.326	0.585	9.5805	0.8893	8.6913	5.0000	1.5000	0.0333	0.0045	0.0098
0.322	0.572	9.7148	1.3255	8.3893	5.0000	1.5000	0.0333	0.0045	0.0095
Suhu 50									
Absorbansi Sampel	Absorbansi Kontrol	Konsentrasi N-Ac-Glu Sampel	Konsentrasi N-Ac-Glu Kontrol	xs-xk	1000/200	600/400	1/30.	1/221.21	aktivitas
0.321	0.555	9.7483	1.8960	7.8523	5.0000	1.5000	0.0333	0.0045	0.0089
0.324	0.564	9.6477	1.5940	8.0537	5.0000	1.5000	0.0333	0.0045	0.0091
0.324	0.564	9.6477	1.5940	8.0537	5.0000	1.5000	0.0333	0.0045	0.0091
0.326	0.566	9.5805	1.5268	8.0537	5.0000	1.5000	0.0333	0.0045	0.0091
0.322	0.558	9.7148	1.7953	7.9195	5.0000	1.5000	0.0333	0.0045	0.0090
0.327	0.568	9.5470	1.4597	8.0872	5.0000	1.5000	0.0333	0.0045	0.0091
0.33	0.568	9.4463	1.4597	7.9866	5.0000	1.5000	0.0333	0.0045	0.0090
0.355	0.562	8.6074	1.6611	6.9463	5.0000	1.5000	0.0333	0.0045	0.0079

Suhu 45	Suhu 50
0.0093	0.0089
0.0099	0.0091
0.0100	0.0091
0.0100	0.0091
0.0103	0.0090
0.0099	0.0091
0.0098	0.0090
0.0095	0.0079



Lampiran 5. *rRNA_typestrains/16S_ribosomal_RNA 16S ribosomal RNA (Bacteria and Archaea type strains)*

Job Title:4318396_K.W.R.4.1

Program: BLASTN

Query: 4318396_K.W.R ID: lcl|Query_152129(dna) Length: 702

Database: rRNA_typestrains/16S_ribosomal_RNA 16S ribosomal RNA (Bacteria and Archaea type strains)

Sequences producing significant alignments:

Description	Scientific Name	Common Name
Aneurinibacillus thermoaerophilus strain DSM 10154 16S ribosom...	Aneurinibaci...	NA
Aneurinibacillus thermoaerophilus strain L420-91 16S ribosomal...	Aneurinibaci...	NA
Aneurinibacillus sediminis strain 1-10M-8-7-50 16S ribosomal...	Aneurinibaci...	NA
Aneurinibacillus danicus strain DB4 16S ribosomal RNA, partial...	Aneurinibaci...	NA
Aneurinibacillus danicus strain NBRC 102444 16S ribosomal RNA,...	Aneurinibaci...	NA
Aneurinibacillus humi strain U33 16S ribosomal RNA, partial...	Aneurinibaci...	NA
Aneurinibacillus aneurinilyticus ATCC 12856 strain DSM 5562 16...	Aneurinibaci...	NA
Aneurinibacillus aneurinilyticus ATCC 12856 strain DSM 5562 16...	Aneurinibaci...	NA
Aneurinibacillus migulanus strain B0270 16S ribosomal RNA,...	Aneurinibaci...	NA
Aneurinibacillus aneurinilyticus strain Murayama 16S ribosomal...	Aneurinibaci...	NA

Taxid	Max Score	Total Score	Query cover	E Value	Per. Ident	Acc. Len	Accession
143495	1234	1234	99%	0.0	98.57	1491	NR_112216.1
143495	1229	1229	99%	0.0	98.43	1485	NR_029303.1
1776164	1099	1099	99%	0.0	95.26	1414	NR_157740.1
267746	1070	1070	97%	0.0	94.90	1417	NR_028657.1
267746	1066	1066	97%	0.0	94.75	1501	NR_114088.1
1515627	1066	1066	99%	0.0	94.40	1451	NR_169383.1
649747	1050	1050	96%	0.0	94.57	1489	NR_112215.1
649747	1050	1050	96%	0.0	94.57	1489	NR_112203.1
47500	1050	1050	96%	0.0	94.57	1483	NR_036799.1
1391	1050	1050	96%	0.0	94.57	1482	NR_036798.1

>Aneurinibacillus thermoaerophilus strain DSM 10154 16S ribosomal RNA, partial sequence

Sequence ID: NR_112216.1 Length: 1491

Range 1: 47 to 743

Score:1234 bits(668), Expect:0.0,

Identities:690/700(99%), Gaps:4/700(0%), Strand: Plus/Plus

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Query 4   GGA-TGCTTGGCCTTCCTGAGSTTAGCGSCGSAACCGSTGAGTAAACACGTAAGCGACCTGC 62
          ||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 47   GGAGTGCTT-GCATTCTGAGSTTAGCGSCGSAACCGSTGAGTAAACACGTAAGCGCAACCTGC 105

Query 63   CTGTACGACCCGGGATAAATCCGGGAAACCGGAGCTAATACCGGATAGGATGCCGAACCGC 122
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Sbjct 186   CTGTACGACCCGGGATAAATCCGGGAAACCGGAGCTAATACCGGATAGGATGCCGAACCGC 165

Query 123  ATGSTTCGGCATGSAAGGGCTTTGAGCCGCGTACAGATGGGCCTGCGGCGCATTAGCTG 182
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Sbjct 166   ATGSTTCGGCATGSAAGGGCTTTGAGCCGCGTACAGATGGGCCTGCGGCGCATTAGCTA 225

Query 183  GTTGGTGGGGTAACGGCCTACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACG 242
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Sbjct 226   GTTGGTGGGGTAACGGCCTACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGA-ACG 284

Query 243  GCCACACTGGGACTGAGACACGGCTCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTT 302
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Sbjct 344   CCGCAATGSAACGAAAGTCTGACGGAGCAACGCCGCGTGAGTGAGGSAAGGTCTTCGGATCG 403

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          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 464   GAGAAAGCCCGGCTAACTACGTGCCAGCAGCCGCGTAATACGTAGGGGGCAAGCGTTG 523

Query 483  TCCGSAATTATTGGGCGTAAAGCGCGCGCAGGCGGCTTCTTAAGTCAGGTGTGAAAGCCC 542
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 524   TCCGSAATTATTGGGCGTAAAGCGCGCGCAGGCGGCTTCTTAAGTCAGGTGTGAAAGCCC 583

Query 543  ACGSCTCAACCGTGGAGGGCCATCTGAAACTGGGGAGCTTGAGTGCAAGGATAGGAGAGCG 602
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 584   ACGSCTCAACCGTGGAGGGCCATCTGAAACTGGGGAGCTTGAGTGCAAGGATAGGAGAGCG 643

Query 603  GAATTCACGTGTAGCGGTGAAATGCGTAAAGATGTGAGGAAACACCAAGTGGCGAAGGCG 662
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 644   GAATTCACGTGTAGCGGTGAAATGCGTAAAGATGTGAGGAAACACCAAGTGGCGAAGGCG 703

Query 663  GCTCTCTGSCCTGTAACCTGACGCTGAGGCGGAAAGCGTG 702
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 704   GCTCTCTGSCCTGTAACCTGACGCTGAGGCGGAAAGCGTG 743

```

>Aneurinibacillus thermoaerophilus strain L420-91 16S ribosomal RNA, partial sequence

Sequence ID: NR_029303.1 Length: 1485

Range 1: 51 to 747

Score:1229 bits(665), Expect:0.0,

Identities:689/700(98%), Gaps:4/700(0%), Strand: Plus/Plus

```

Query 4   GGA-TGCTTGGCCTTCCTGAGGTTAGCGGCGGACGGGTGAGTAACACGTAAGCGACCTGC 62
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 51   GGAAGTGCTT-GCATTCTGAGGTTAGCGGCGGACGGGTGAGTAACACGTAAGCGAACCTGC 109

Query 63   CTGTACGACCCGGGATAACTCCGGGAAACCGGAGCTAATACCGGATAGSATGCCGAACCGC 122
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 110  CTGTACGACCCGGGATAACTCCGGGAAACCGGAGCTAATACCGGATAGSATGCCGAACCGC 169

Query 123  ATGGTTCGGCATGGAAGAGGCTTTGAGCCGCGTACAGATGGGCCTGCGGCGCATTAGCTG 182
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 170  ATGGTTCGGCATGGAAGAGGCTTTGAGCCGCGTACAGATGGGCCTGCGGCGCATTAGCTA 229

Query 183  GTTGGTGGGTAACGGCCTACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGATACG 242
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 230  GTTGGTGGGTAACGGCCTACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGA-ACG 288

Query 243  GCCCAGACTGGGACTGAGACACGGCTCCAGACTCCTACGGGAGGCGACGATAGGSAATCTT 302
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 289  GCCCAGACTGGGACTGAGACACGTC-CCAGACTCCTACGGGAGGCGACGATAGGSAATCTT 347

Query 303  CCGCAATGGACGAAAGTCTGACGGAACAACGCCGCGTGAGTGAGGAAGGTCTTCGGATCG 362
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 348  CCGCAATGGACGAAAGTCTGACGGAACAACGCCGCGTGAGTGAGGAAGGTCTTCGGATCG 407

Query 363  TAAAAGTCTGTTGTCAAGGAAAGAACCGCCGGGATGACCTCCCGGTCTGACGGTACCTGAC 422
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 408  TAAAAGTCTGTTGTCAAGGAAAGAACCGCCGGGATGACCTCCCGGTCTGACGGTACCTGAC 467

Query 423  GAGAAAGCCCCGGCTAACTACGTGCCAGCAGCCGCGTAATACGTAAGGGGCAAGCGTTG 482
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 468  GAGAAAGCCCCGGCTAACTACGTGCCAGCAGCCGCGTAATACGTAAGGGGCAAGCGTTG 527

Query 483  TCCGGAAATATTGGGCGTAAAGCGCGCGCAGGCGGCTTCTTAAAGTCAGGTGTGAAAGCCC 542
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 528  TCCGGAAATATTGGGCGTAAAGCGCGCGCAGGCGGCTTCTTAAAGTCAGGTGTGAAAGCCC 587

Query 543  ACGGCTCAACCGTGGAGGGCCATCTGAAACTGGGGAGCTTGAGTGCAAGGATAGGAGAGCG 602
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 588  ACGGCTCAACCGTGGAGGGCCATCTGAAACTGGGGAGCTTGAGTGCAAGGAGAGGAGAGCG 647

Query 603  GAATTCACGCTGAGCGGTGAAATGCGTAAAGATGTGGAGGAACACCAAGTGGCGAAAGGCG 662
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 648  GAATTCACGCTGAGCGGTGAAATGCGTAAAGATGTGGAGGAACACCAAGTGGCGAAAGGCG 707

Query 663  GCTCTCTGGCCTGTAAGTACGCTGAGGCGCGAAAGCGTG 702
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 708  GCTCTCTGGCCTGTAAGTACGCTGAGGCGCGAAAGCGTG 747

```

>Aneurinibacillus sediminis strain 1-10M-8-7-50 16S ribosomal RNA, partial sequence

Sequence ID: NR_157740.1 Length: 1414

Range 1: 25 to 716

Score:1099 bits(595), Expect:0.0,

Identities:663/696(95%), Gaps:4/696(0%), Strand: Plus/Plus

```

Query 7   TGCTTGGCCTTCTCGAGSTTAGCGGCGGACGGGTGAGTAACACGTAAGGCGACCTGCCTGT 66
          |||||  |||  | |||||||||||||||||||||||||||||||||||  |||||||
Sbjct 25   TGCTTGCACCTT-CGGAGSTTAGCGGCGGACGGGTGAGTAACACGTAAGGCAACCTGCCTGT 83

Query 67   ACGACCGGGATAAACTCCGGGAAACCGGAGCTAATACCGGATAGSATGCCGAAACCGCATGG 126
          |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Sbjct 84   ACGACCGGGATAAACTTCGGGAAACCGAAAGCTAATACCGSATACGATGGCAAAACCGCATGG 143

Query 127  TTCGGCATGGAAAAGGGCTTTGAGCCGCGTACAGATGGGCCTGCGGCGCATTAGCTGSTTG 186
          ||  | |||||||  ||  | ||||  | ||||  | ||||  | ||||  | ||||  | ||||
Sbjct 144  TTTGCCATGGAAA-GACCATGAGTCACGTACAGATGGGCCTGCGGCGCATTAGCTAGTTG 202

Query 187  GTGGGTAACGGCCTACCAAGGGGACGATGCGTAGCCGACCTGAGAGGGTGATACGGCCA 246
          ||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Sbjct 203  GTAGGTAACGGCCTACCAAGGGGACGATGCGTAGCCGACCTGAGAGGGTGAT-CGGCCA 261

Query 247  CACTGGGACTGAGACACGGCTCCAGACTCCTACGGGAGGCAAGCAGTAGGSAATCTTCCGC 306
          |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Sbjct 262  CACTGGGACTGAGACACGGC-CCAGACTCCTACGGGAGGCAAGCAGTAGGSAATCTTCCGC 320

Query 307  AATGSAAGAAAGTCTGACGGAGCAACGCGCGTGAAGTGAAGAAAGTCTTCGATCGTAAA 366
          |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Sbjct 321  AATGSAAGAAAGTCTGACGGAGCAACGCGCGTGAACGATGAAGGTTTTTCGATCGTAAA 380

Query 367  ACTCTGTTGTCAGGSAAGAAACCGCCGGATGACCTCCCGCTCTGACGTTACCTAAGCAGA 426
          |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Sbjct 381  GTTCTGTTGTTAGGSAAGAAACCGCCGGATGACCTCCCGCTCTGACGTTACCTAAGCAGA 440

Query 427  AAGCCCCGGCTAACTACGTGCCAGCAGCCGCGTAAACGTAAGGGGCAAGCGTTGTCCG 486
          |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Sbjct 441  AAGCCCCGGCTAACTACGTGCCAGCAGCCGCGTAAACGTAAGGGGCAAGCGTTGTCCG 500

Query 487  GAATTATTGGGCGTAAAGCGCGCGCAGGCGCTTCTTAAAGTCAAGTGTGAAAAGCCACGG 546
          |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Sbjct 501  GAATTATTGGGCGTAAAGCGCGCGCAGGCGCTTCTTAAAGTCAAGTGTGAAAAGCCACGG 560

Query 547  CTCAACCGTGGAGGGCCATCTGAAACTGGGAGCTTGAGTGCAAGGATAGSAGAGCGSAAT 606
          |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Sbjct 561  CTCAACCGTGGAGGGCCATCTGAAACTGGGAGCTTGAGTGCAAGGATAGSAGAGCGSAAT 620

Query 607  TCCACGTGTAGCGGTGAAATGCGTAAAGATGTGGAGSAACACCAAGTGGCGAAGGCGGCTC 666
          |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Sbjct 621  TCCACGTGTAGCGGTGAAATGCGTAAAGATGTGGAGSAACACCCCGTGGCGAAGGCGGCTC 680

Query 667  TCTGGCCTGTAAGTACGCTGAGGCGCGAAAAGCGTG 702
          |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Sbjct 681  TCTGGCCTGTAAGTACGCTGAGGCGCGAAAAGCGTG 716

```

>Aneurinibacillus danicus strain DB4 16S ribosomal RNA, partial sequence

Sequence ID: NR_028657.1 Length: 1417

Range 1: 60 to 742

Score:1070 bits(579), Expect:0.0,

Identities:651/686(95%), Gaps:3/686(0%), Strand: Plus/Plus

```
Query 17 TCCTGAGGTTAGCGGCGGACGGGTGAGTAACACGTAAGGCGACCTGCCTGTACGACCGGGA 76
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
sbjct 68 TCCTGCGGTCAGCGGCGGACGGGTGAGTAACACGTAAGGCAACCTGCCTGTACGACCGGGA 119

Query 77 TAACTCCGGGAAACCGGAGCTAATACCGGATAGSATGCCGAAACCGCATGGTTGCGCATGG 136
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
sbjct 128 TAACTCCGGGAAACCGGAGCTAATACCGGATAGSATTTTCAGACCGCATGGTTTGGAAATGG 179

Query 137 AAAGGGCTTTGAGCCGCGTACAGATGGGCCTGCGGCGCATTAGCTGGTTGGTGGGTAAC 196
      ||| | | ||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
sbjct 188 AAA-GACCTGTGTACGTACAGATGGGCCTGCGGCGCATTAGCTAGTTGGTGGGTAAC 238

Query 197 GGCCTACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGATACGGCCACACTGGGACT 256
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
sbjct 239 GGCCTACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGA-ACGGCCACACTGGGACT 297

Query 257 GAGACACGGCTCCAGACTCCTACGGGAGGCGAGTAGGGAATCTTCCGCAATGGAACGAA 316
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
sbjct 298 GAGACACGGC-CCAGACTCCTACGGGAGGCGAGTAGGGAATCTTCCGCAATGGAACGAA 356

Query 317 AGTCTGACGAGCAACGCCGCGTGAGTGAGGSAAGGTCTTCGGATCGTAAACTCTGTTGT 376
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
sbjct 357 AGTCTGACGAGCAACGCCGCGTGAAACGSAAGGTTTTCGGATCGTAAAGTTCTGTTGT 416

Query 377 CAGGSAAGAACCGCCGGGATGACCTCCCGGTCTGACGGTACCTGACGAGAAAGCCCCGGC 436
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
sbjct 417 TAGGSAAGAACCGCCGGGATAACCTCCCGGTCTGACGGTACCTAACGAGAAAGCCCCGGC 476

Query 437 TAACTACGTGCCAGCAGCCGCGTAATACGTAGGGGGCAAGCGTTGTCCGSAATTATTGG 496
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
sbjct 477 TAACTACGTGCCAGCAGCCGCGTAATACGTAGGGGGCAAGCGTTGTCCGSAATTATTGG 536

Query 497 GCGTAAAGCGCGCGCAGGCGGCTTCTTAAAGTCAGGTGTGAAAGCCACGGCTCAACCGTG 556
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
sbjct 537 GCGTAAAGCGCGCGCAGGCGGCTTCTTAAAGTCAGGTGTGAAAGCCACGGCTCAACCGTG 596

Query 557 GAGGGCCACTCTGAAACTGGGAGCTTGAGTGCAAGGATAGGAGAGCGGAATTCACAGTGTA 616
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
sbjct 597 GAGGGCCACTCTGAAACTGGGAGCTTGAGTGCAAGGAGAGGAGAGCGGAATTCACAGTGTA 656

Query 617 GCGGTGAAATGCGTAAAGATGTGSAGGAACACCAAGTGGCGAAAGGCGCTCTCTGGCCTGT 676
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
sbjct 657 GCGGTGAAATGCGTAAAGATGTGSAGGAACACCTGTGGCGAAAGGCGCTCTCTGGCCTGT 716

Query 677 AACTGACGCTGAGGCGCGAAAGCGTG 782
      ||||| ||||| ||||| |||||
sbjct 717 AACTGACGCTGAGGCGCGAAAGCGTG 742
```

>Aneurinibacillus danicus strain NBRC 102444 16S ribosomal RNA, partial sequence

Sequence ID: NR_114088.1 Length: 1501

Range 1: 62 to 744

Score:1066 bits(577), Expect:0.0,

Identities:650/686(95%), Gaps:3/686(0%), Strand: Plus/Plus

```

Query 17 TCCTGAGGTTAGCGGCGGACGGSTGAGTAACACGTAAGCGACCTGCCTGTACGACCGGSA 76
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 62 TCCTGCCGTCAGCGGCGGACGGSTGAGTAACACGTAAGCGAACCTGCCTGTACGACCGGSA 121

Query 77 TAACTCCGGGAAACCGGAGCTAATAACCGSATAGSATGCCGAACCGCATGTTCCGGCATGG 136
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 122 TAACTCCGGGAAACCGGAGCTAATAACCGSATAGSATTTTCAAGCCGATGTTTGGAAATGG 181

Query 137 AAAGGGCTTTGAGCCGCTACAGATGGGCTGCGGCGCATTAGCTGTTGGTGGGTAAC 196
      ||| | | || | | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 182 AAA-GACCCCTGTGTCACTACAGATGGGCTGCGGCGCATTAGCTAGTTGGTGGGTAAC 240

Query 197 GGCCTACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGATACGGCCACACTGGGACT 256
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 241 GGCCTACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGA-ACGGCCACACTGGGACT 299

Query 257 GAGACACGGCTCCAGACTCCTACGGGAGGCGAGTAGGSAATCTTCCGCAATGGACGAA 316
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 300 GAGACACGGC-CCAGACTCCTACGGGAGGCGAGTAGGSAATCTTCCGCAATGGACGAA 358

Query 317 AGTCTGACGAGCAACGCCGCTGAGTGAGGSAAGGTTCTCGSATCGTAAAACTCTGTTGT 376
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 359 AGTCTGACGAGCAACGCCGCTGAACGSAAGGTTCTCGSATCGTAAAGTTCTGTTGT 418

Query 377 CAGGSAAGAACCCGCCGGATGACCTCCCCTGCTGACGGTACCTGACGAGAAAGCCCCGGC 436
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 419 TAGGSAAGAACCCGCCGGATAACCTCCCCTGCTGACGGTACCTAACGAGAAAGCCCCGGC 478

Query 437 TAACTACGTGCCAGCAGCCGCGTAATAACGTAGGGGGCAAGCGTTGTCCGSAATTATTGG 496
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 479 TAACTACGTGCCAGCAGCCGCGTAATAACGTAGGGGGCAAGCGTTGTCCGSAATTATTGG 538

Query 497 GCGTAAAGCGCGCGCAGGCGCTTCTTAAGTCAAGGTGTGAAAGCCACGGCTCAACCGTG 556
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 539 GCGTAAAGCGCGCGCAGGCGCTTCTTAAGTCAAGGTGTGAAAGCCACGGCTCAACCGTG 598

Query 557 GAGGGCCATCTGAAACTGGGGAGCTTGAGTGCAAGSATAGGAGAGCGSAATCCACGTGTA 616
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 599 GAGGGCCACTTGAAACTGGGGAGCTTGAGTGCAAGSATAGGAGAGCGSAATCCACGTGTA 658

Query 617 GCGGTGAAATGCGTAAGATGTGSAAGSAACACCAAGTGGCGAAGGCGGCTCTCTGSCCTGT 676
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 659 GCGGTGAAATGCGTAGAGATGTGSAAGSAACACCAAGTGGCGAAGGCGGCTCTCTGSCCTGT 718

Query 677 AACTGACGCTGAGGCGGAAAGCGTG 702
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 719 AACTGACGCTGAGGCGGAAAGCGTG 744

```


>Aneurinibacillus humi strain U33 16S ribosomal RNA, partial sequence

Sequence ID: NR_169383.1 Length: 1451

Range 1: 54 to 745

Score:1066 bits(577), Expect:0.0,

Identities:657/696(94%), Gaps:4/696(0%), Strand: Plus/Plus

```

Query 7      TGCTTGGCCTTCCTGAGGTTAGCGGCGGACGGGTGAGTAACACGTAAGGCGACCTGCCTGT 66
          ||||| ||| | | |||||||||||||||||||||||||||||||||||||||
Sbjct 54      TGCTTGCACTT-CGSCGTTAGCGGCGGACGGGTGAGTAACACGTAAGGCGAACCTGCCTGT 112

Query 67     ACGACCGGGATAACTCCGGGAAACCGGAGCTAATACCGSATAGSATGCCGAACCGCATGG 126
          ||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct 113     ACGACTGGGATAACTCCGGGAAACCGAAGCTAATACCGSATAGSTTAACGAACCGCATGG 172

Query 127    TTCGGCATGGAAAAGGGCTTTGAGCCCGGTACAGATGGGCCTGCGGCGCATTAGCTGGTTG 186
          |||| | |||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Sbjct 173    TTCGTTAAAGAAA-GACCTTGCCTCACGTACAGATGGGCCTGCGGCGCATTAGCTAGTTG 231

Query 187    GTGGGGTAACGGGCTACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGATACGGCCA 246
          || ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct 232    GTAGGGTAACGGGCTACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAT-CGGCCA 290

Query 247    CACTGGGACTGAGACACGGCTCCAGACTCCTACGGGAGGSCAGCAGTAGGGAAATCTTCCGC 306
          ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct 291    CACTGGGACTGAGACACGGC-CCAGACTCCTACGGGAGGSCAGCAGTAGGGAAATCTTCCGC 349

Query 307    AATGSAACGAAAGTCTGACGGAGCAACGCCGCGTGAGTGAGGAAGGTCTTCGGATCGTAAA 366
          ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct 350    AATGSAACGAAAGTCTGACGGAGCAACGCCGCGTGAAACGATGAAAGSTTTTCGGATCGTAAA 409

Query 367    ACTCTGTTGTGACGGGAAGAACC GCCGGATGACCTCCCGGTCTGACGGTACCTGACGAGA 426
          ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct 410    GTTCTGTTGTTAGGGAAGAACC GCCGGATAACCTCCCGGTCTGACGGTACCTAACGAGA 469

Query 427    AAGCCCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCG 486
          ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct 470    AAGCCCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCG 529

Query 487    GAATTATTGGGCGTAAAGCGCGCGCAGGGCGCTTCTTAAGTCAGGTGTGAAAGCCCACGG 546
          ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct 530    GAATTATTGGGCGTAAAGCGCGCGCAGGGCGCTTCTTAAGTCAGGTGTGAAAGCCCACGG 589

Query 547    CTCAACCGTGGAGGGCCATCTGAAACTGGGGAGCTTGAGTGCAGSAATAGGAGAGCGGAAT 606
          ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct 590    CTCAACCGTGGAGGGCCATCTGAAACTGGGAAGCTTGAGTGCAGSAATAGGAGAGCGGAAT 649

Query 607    TCCACGTGTAGCGGTGAAATGCGTAAAGATGTGSAAGSAACACCAAGTGGCGAAGGCGGCTC 666
          ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct 650    TCCACGTGTAGCGGTGAAATGCGTAAAGATGTGSAAGSAACACCAAGTGGCGAAGGCGGCTC 709

Query 667    TCTGGCCTGTAAGTACGCTGAGGCGCGAAAGCGTG 702
          ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct 710    TCTGGCCTGTAAGTACGCTGAGGCGCGAAAGCGTG 745

```

>Aneurinibacillus aneurinilyticus ATCC 12856 strain DSM 5562 16S ribosomal RNA, partial sequence

Sequence ID: NR_112215.1 Length: 1489

Range 1: 66 to 743

Score:1050 bits(568), Expect:0.0,

Identities:645/682(95%), Gaps:6/682(0%), Strand: Plus/Plus

```

Query   23  GGTTAGCGGCGGACGGGTGAGTAACACGTAAGGCGACCTGCCTGTACGACCCGGATAAATC 82
      |||
Sbjct   66  GGTTAGCGGCGGACGGGTGAGTAACACGTAAGGCGAACCTGCCTGTACGACTGGGATAAATC 125

Query   83  CGGSAACCGGAGCTAATACCGGATA-GGATGCCGAACCGCATGGTTCGGCATG-GAAAG 140
      |||
Sbjct  126  CGGSAACCGGAGCTAATACCGGATACGTTTTTTCAGACCCGCATGG-TCTGAAAGAGAAAAG 184

Query  141  GGCTTTGAGCCCGGTACAGATGGGCTGCGGCGCATTAGCTGGTTGGTGGGTAACGGCC 200
      |||
Sbjct  185  ACCTTTG-GTCACTACAGATGGGCTGCGGCGCATTAGCTAGTTGGTGGGTAACGGCC 243

Query  201  TACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGTATCGGCCACACTGGGACTGAGA 260
      |||
Sbjct  244  TACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGTATCGGCCACACTGGGACTGAGA 302

Query  261  CACGGCTCCAGACTCCTACGGGAGGCGAGCAGTAGGGAACTCTCCGCAATGGACGAAAATC 320
      |||
Sbjct  303  CACGGC-CCAGACTCCTACGGGAGGCGAGCAGTAGGGAACTCTCCGCAATGGACGAAAATC 361

Query  321  TGACGGAGCAACGCCGCGTGAGTGAGGAAAGGTTCTCGGATCGTAAAACTCTGTTGTCAGG 380
      |||
Sbjct  362  TGACGGAGCAACGCCGCGTGAAAGATGAAAGGTTTTTCGGATCGTAAAGTCTGTTGTTAGG 421

Query  381  GAAGAACCGCCGGATGACCTCCCCTGCTGACGGTACCTGACGAGAAAAGCCCCGGCTAAC 440
      |||
Sbjct  422  GAAGAACCGCCGGATGACCTCCCCTGCTGACGGTACCTAACGAGAAAAGCCCCGGCTAAC 481

Query  441  TACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGSAATTATTGGGCGT 500
      |||
Sbjct  482  TACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGSAATTATTGGGCGT 541

Query  501  AAAGCGCGCGCAGGCGGCTTCTTAAGTCAAGTGTGAAAGCCACGGCTCAACCGTGSAGG 560
      |||
Sbjct  542  AAAGCGCGCGCAGGCGGCTTCTTAAGTCAAGTGTGAAAGCCACGGCTCAACCGTGSAGG 601

Query  561  GCCATCTGAAACTGGGAGCTTGAGTGCAAGGATAGGAGAGCGGAATCCACGTGTAGCGG 620
      |||
Sbjct  602  GCCACTTGAAACTGGGAGGCTTGAGTGCAAGGATAGGAGAGCGGAATCCACGTGTAGCGG 661

Query  621  TGAAATGCGTAAAGATGTGAGGAAACACCCAGTGGCGAAGGCGGCTCTCTGGCCTGTAAT 680
      |||
Sbjct  662  TGAAATGCGTAAAGATGTGAGGAAACACCCAGTGGCGAAGGCGGCTCTCTGGCCTGTAAT 721

Query  681  GACGCTGAGGCGGAAAAGCGTG 702
      |||
Sbjct  722  GACGCTGAGGCGGAAAAGCGTG 743

```

>Aneurinibacillus aneurinilyticus ATCC 12856 strain DSM 5562 16S ribosomal RNA, partial sequence

Sequence ID: NR_112203.1 Length: 1489

Range 1: 66 to 743

Score:1050 bits(568), Expect:0.0,

Identities:645/682(95%), Gaps:6/682(0%), Strand: Plus/Plus

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Query   23  GGTTAGCGGCGGACGGGTGAGTAACACGTAAGCGACCTGCCTGTACGACCGGGATAAAGTC 82
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Sbjct   66  GGTTAGCGGCGGACGGGTGAGTAACACGTAAGCGAACCTGCCTGTACGACTGGGATAAAGTC 125

Query   83  CGGGAAACCGGAGCTAATACCGGATA-GGATGCCGAACCGCATGGTTCGGCATG-GAAAG 140
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Sbjct  126  CGGGAAACCGGAGCTAATACCGGATACGTTTTTCAGACCGCATGG-TCTGAAAGAGAAAG 184

Query  141  GGCTTTGAGCCGCGTACAGATGGGCTGCGGCGCATTAGCTGGTGGTGGGGTAACGGCC 200
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Sbjct  185  ACCTTTG-GTCACGTACAGATGGGCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCC 243

Query  201  TACCAAAGCGCAGATGCGTAGCCGACCTGAGAGGGTGATACGGCCCACTGGGACTGAGA 260
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Sbjct  244  TACCAAAGCGCAGATGCGTAGCCGACCTGAGAGGGTGAT-CGGCCCACTGGGACTGAGA 302

Query  261  CACGGCTCCAGACTCCTACGGGAGGCAGCAAGTAGGSAATCTTCCGCAATGGACGAAAGTC 320
      |||
Sbjct  303  CACGGC-CCAGACTCCTACGGGAGGCAGCAAGTAGGSAATCTTCCGCAATGGACGAAAGTC 361

Query  321  TGACGGAGCAACGCCGCGTGAGTGAGGAAAGSTCTTCGGATCGTAAAGTCTGTTGTCAGG 380
      |||
Sbjct  362  TGACGGAGCAACGCCGCGTGAAACGATGAAAGSTTTTCGGATCGTAAAGTCTGTTGTTAGG 421

Query  381  GAAGAAACCGCCGGGATGACCTCCCGGTCTGACGGTACCTGACGAGAAAGCCCGGCTAAC 440
      |||
Sbjct  422  GAAGAAACCGCCGGGATGACCTCCCGGTCTGACGGTACCTAACGAGAAAGCCCGGCTAAC 481

Query  441  TACGTGCCAGCAGCCGCGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGGCGT 500
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Sbjct  482  TACGTGCCAGCAGCCGCGTAATACGTAGGGGGCAAGCGTTGTCCGGAATTATTGGGCGT 541

Query  501  AAAGCGCGCGCAGGGCGCTTCTTAAGTCAGGTGTGAAAGCCACGGCTCAACCGTGGAGG 560
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Sbjct  542  AAAGCGCGCGCAGGGCGCTTCTTAAGTCAGGTGTGAAAGCCACGGCTCAACCGTGGAGG 601

Query  561  GCCATCTGAAACTGGGAGCTTGAGTGCAAGATAGGAGAGCGGAATTCACGTGTAGCGG 620
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Sbjct  602  GCCACTTGAAACTGGGAGCTTGAGTGCAAGATAGGAGAGCGGAATTCACGTGTAGCGG 661

Query  621  TGAAATGCGTAAAGATGTGGAGGAACACCAAGTGCCGAAAGGCGGCTCTCTGGCCTGTAAGT 680
      |||
Sbjct  662  TGAAATGCGTAGAGATGTGGAGGAACACCCGTTGGCGAAAGGCGGCTCTCTGGCCTGTAAGT 721

Query  681  GACGCTGAGGCGCGAAAGCGTG 702
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Sbjct  722  GACGCTGAGGCGCGAAAGCGTG 743

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>Aneurinibacillus migulanus strain B0270 16S ribosomal RNA, partial sequence

Sequence ID: NR_036799.1 Length: 1483

Range 1: 70 to 747

Score:1050 bits(568), Expect:0.0,

Identities:645/682(95%), Gaps:6/682(0%), Strand: Plus/Plus

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Query 23  GSTTAGCGSCGSAACCGSTGAGTAACACGTAAGCGACCTGCCTGTACGACCCGGGATAACTC 82
          |||
Sbjct 70  GSTTAGCGSCGSAACCGSTGAGTAACACGTAAGCGAACCTGCCTGTACGACTGGGATAACTC 129

Query 83  CGGGAAACCGGAGCTAATACCGGATA--GGATGCCGAACCCGCATGGTTCGGCATG--GAAAG 140
          |||
Sbjct 130 CGGGAAACCGGAGCTAATACCGGATACTTCTTTCAGACCCGCATGG--TCTGAAAGAGAAAG 188

Query 141 GGCTTTGAGCCGCTACAGATGGSCCTGCGCGCATTAGCTGTTGGTGGGTAACGGCC 200
          |||
Sbjct 189 ACCTTTG--GTCACGTACAGATGGSCCTGCGCGCATTAGCTAGTTGGTGGGTAACGGCC 247

Query 201 TACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGATACGGCCACACTGGGACTGAGA 260
          |||
Sbjct 248 TACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAT--CGGCCACACTGGGACTGAGA 306

Query 261 CACGCTCCAGACTCCTACGGGAGGCAAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTC 320
          |||
Sbjct 307 CACGSC--CCAGACTCCTACGGGAGGCAAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTC 365

Query 321 TGACGGAGCAACGCCGCGTGAGTGAGGAAGSTCTTCGATCGTAAACTCTGTTGTCAGG 380
          |||
Sbjct 366 TGACGGAGCAACGCCGCGTGAACGATGAAGSTTTTCGATCGTAAAGTTCTGTTGTTAGG 425

Query 381 GAAAGAACCCCGGGATGACCTCCCGSTCTGACGCTACCTGACGAGAAAGCCCGGCTAAC 440
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Sbjct 426 GAAAGAACCCCGGGATGACCTCCCGSTCTGACGCTACCTAACGAGAAAGCCCGGCTAAC 485

Query 441 TACGTGCCAGCAGCCGCGTAATACGTAAGGGGCAAGCGTTGTCCGGAATTATTGGGCGT 500
          |||
Sbjct 486 TACGTGCCAGCAGCCGCGTAATACGTAAGGGGCAAGCGTTGTCCGGAATTATTGGGCGT 545

Query 501 AAAGCGCGCGCAGGCGGCTTCTTAAGTCAGGTGTGAAAGCCACGCTCAACCGTGSAGG 560
          |||
Sbjct 546 AAAGCGCGCGCAGGCGGCTTCTTAAGTCAGGTGTGAAAGCCACGCTCAACCGTGSAGG 605

Query 561 GCCATCTGAAACTGGGAGCTTGAGTGCAGGATAGGAGAGCGGAAATCCACGTGTAGCGG 620
          |||
Sbjct 606 GCCACTTGAAACTGGGAAAGCTTGAGTGCAGGAGAGGAGAGCGGAAATCCACGTGTAGCGG 665

Query 621 TGAAATGCGTAAAGATGTGGAGGAACACCAAGTGGCGAAGGCGGCTCTCTGGCCTGTAAC 680
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Sbjct 666 TGAAATGCGTAGAGATGTGGAGGAACACCCGAGGCGAAGGCGGCTCTCTGGCCTGTAAC 725

Query 681 GACGCTGAGGCGCGAAAGCGTG 702
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Sbjct 726 GACGCTGAGGCGCGAAAGCGTG 747

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>Aneurinibacillus aneurinilyticus strain Murayama 16S ribosomal RNA, partial sequence

Sequence ID: NR_036798.1 Length: 1482

Range 1: 70 to 747

Score:1050 bits(568), Expect:0.0,

Identities:645/682(95%), Gaps:6/682(0%), Strand: Plus/Plus

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          |||
sbjct 70  GGTTAGCGGCGGACGGSTGAGTAACACAGTAGGCGAACCTGCCTGTACGACTGGGATAACTC 129

Query 83  CGGGAAACCGGAGCTAATACCGSATA-GGATGCCGAACCGCATGGTTCCGGCATG-GAAAG 140
          |||
sbjct 130  CGGGAAACCGGAGCTAATACCGSATAACGTTTTCAGACCGCATGG-TCTGAAAGAGAAAG 188

Query 141  GGCTTTGAGCCGCGTACAGATGGGCCTGCGGCGCATTAGCTGGTTGGTGGGTAACGGCC 200
          |||
sbjct 189  ACCTTTG-GTCACGTACAGATGGGCCTGCGGCGCATTAGCTAGTTGGTGGGTAACGGCC 247

Query 201  TACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGATACGGCCACACTGGGACTGAGA 260
          |||
sbjct 248  TACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAT-CGGCCACACTGGGACTGAGA 306

Query 261  CACGGCTCCGACTCCTACGGGAGGCGAGTAGGGAATCTTCCGCAATGGACGAAAGTC 320
          |||
sbjct 307  CACGGC-CCAGACTCCTACGGGAGGCGAGTAGGGAATCTTCCGCAATGGACGAAAGTC 365

Query 321  TGACGAGCAACGCCCGGTGAGTGAGGSAAGGTCTTCGGATCGTAAAACTCTGTTGTCAGG 380
          |||
sbjct 366  TGACGAGCAACGCCCGGTGAACGATGAAGSTTTTCGGATCGTAAAGTCTCTGTTGTTAGG 425

Query 381  GAAGAACCGCCGGGATGACCTCCCAGTCTGACGGTACCTGACGAGAAAGCCCCGGCTAAC 440
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sbjct 426  GAAGAACCGCCGGGATGACCTCCCAGTCTGACGGTACCTAACGAGAAAGCCCCGGCTAAC 485

Query 441  TACGTGCCAGCAGCCCGGTAAACGTAAGGGGCAAGCGTTGTCCGSAATTATTGGGCGT 500
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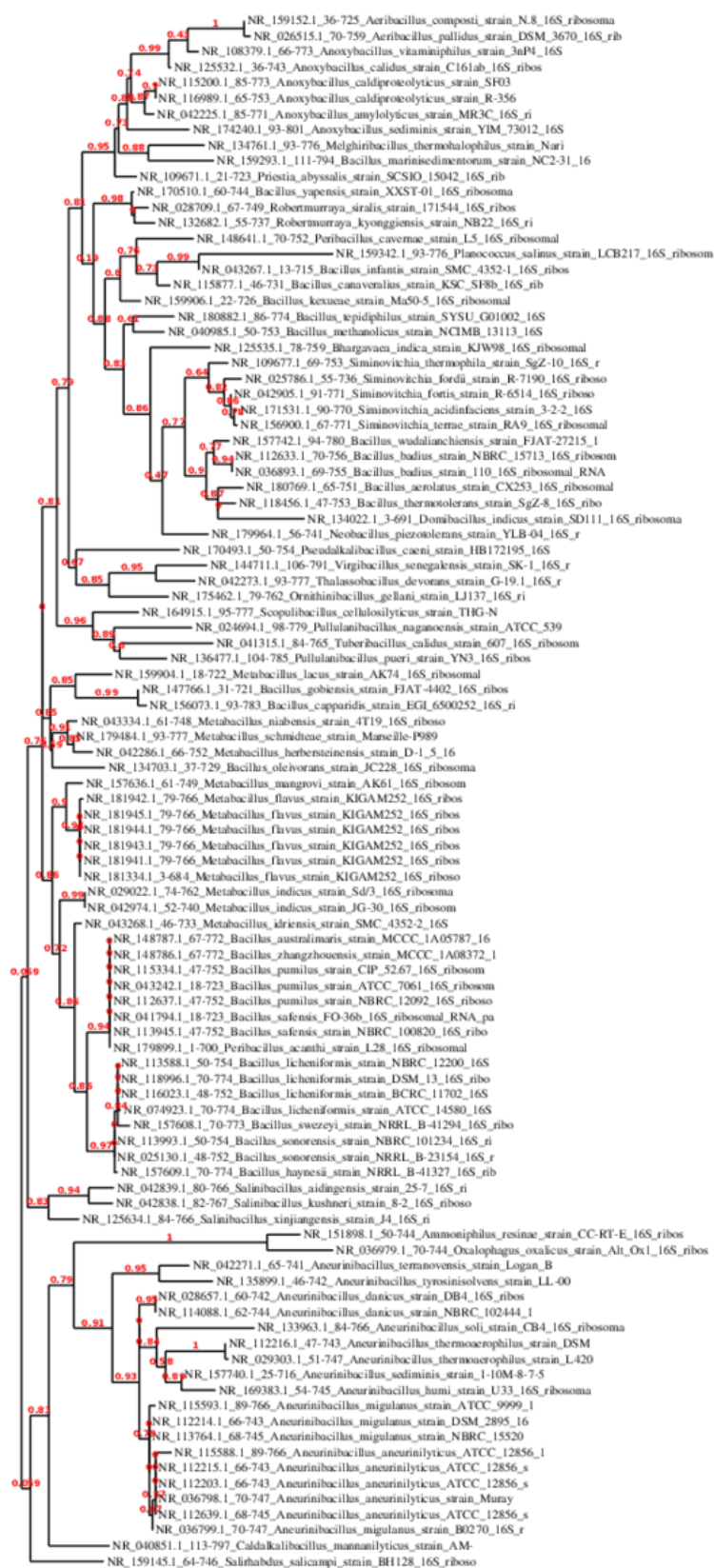
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sbjct 546  AAAGCGCGCGCAGGCGGCTTCTTAAGTCAGGTGTGAAAGCCCACGGCTCAACCGTGSAGG 605

Query 561  GCCATCTGAAACTGGGAGCTTGAGTGCAAGGATAGGAGAGCGGAATCCACGTGTAGCGG 620
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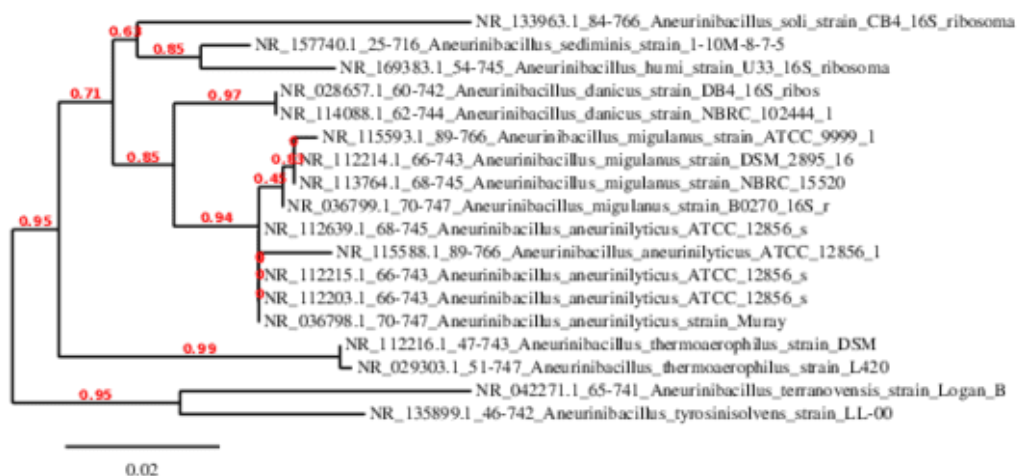
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sbjct 666  TGAAATGCGTAAAGATGTGSAGSAACACCCAGTGGCGAAGGCGGCTCTCTGGCCTGTAAC 725

Query 681  GACGCTGAGGCGCGAAAGCGTG 702
          |||
sbjct 726  GACGCTGAGGCGCGAAAGCGTG 747

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Pohon filogenetik kekerabatan bakteri hasil seq 16s RNA



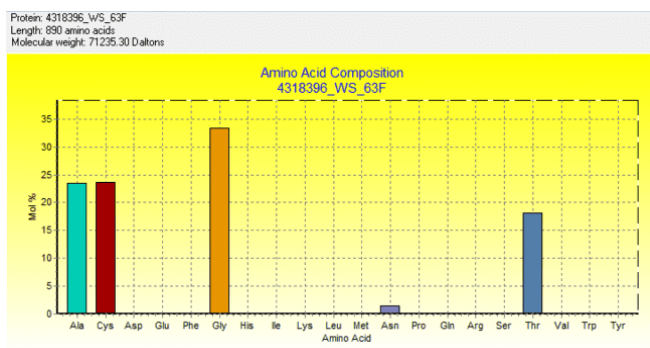
Protein Penyusun

Protein: Isolt Bakteri K.W.R-4.1

Length = 890 amino acids

Molecular Weight = 71235.30 Daltons

Amino Acid	Number	Mol%
Ala A	209	23.48
Cys C	210	23.60
Asp D	0	0.00
Glu E	0	0.00
Phe F	0	0.00
Gly G	297	33.37
His H	0	0.00
Ile I	0	0.00
Lys K	0	0.00
Leu L	0	0.00
Met M	0	0.00
Asn N	13	1.46
Pro P	0	0.00
Gln Q	0	0.00
Arg R	0	0.00
Ser S	0	0.00
Thr T	161	18.09
Val V	0	0.00
Trp W	0	0.00
Tyr Y	0	0.00



Nuclotide Composition

DNA molecule: 4318396_WS_63F

Length = 890 base pairs

Molecular Weight = 269976.00 Daltons, single stranded

Molecular Weight = 542232.00 Daltons, double stranded

G+C content = 56.97%

A+T content = 41.57%

Nucleotide	Number	Mol%
A	209	23.48
C	210	23.60
G	297	33.37
T	161	18.09
N	13	1.46

Lampiran 6. Dokumentasi penelitian

Proses pengambilan sampel dan penentuan kondisi lingkungan sampel



Proses pengambilan sampel



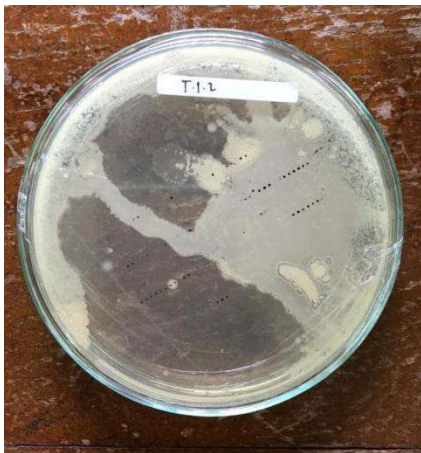
Pengukuran pH



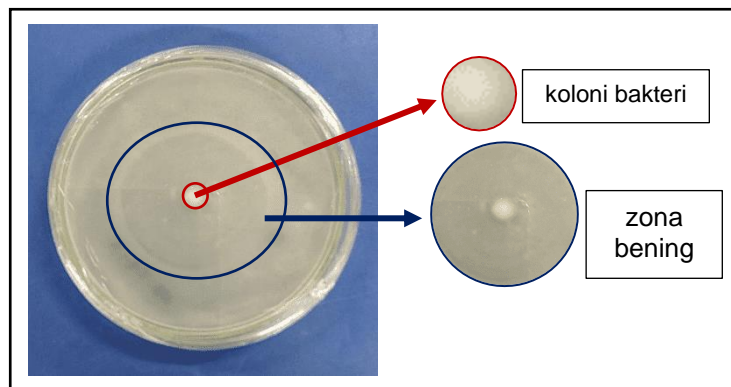
Pengukuran suhu



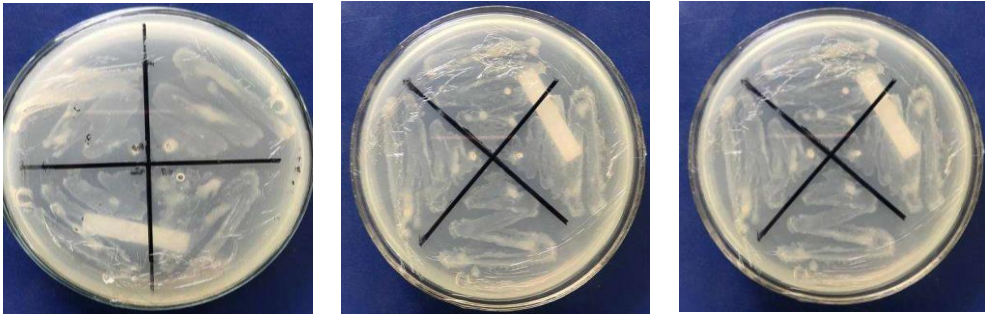
Proses pembuatan media



Isolasi bakteri



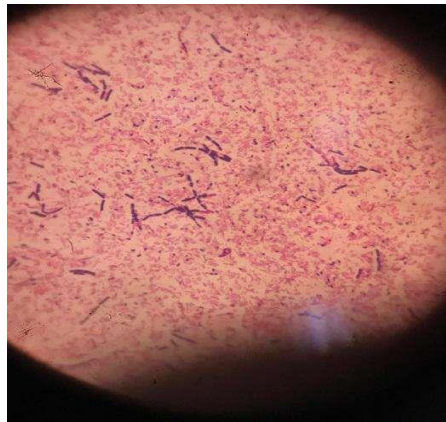
Hasil seleksi bakteri termofilik penghasil kitinase



Penyiapan produksi enzim kitinase (media selektif)



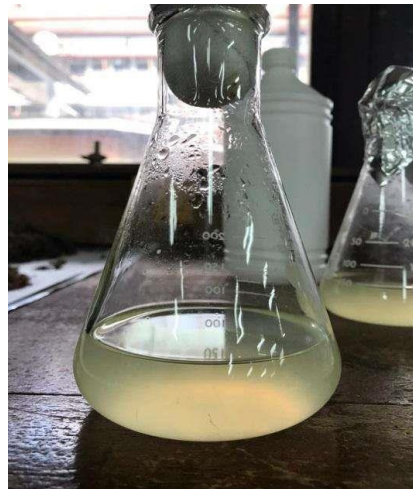
Uji biokimia isolate bakteri termofilik K.W.R 4-1



Pengamatan secara makroskopis



Penyiapan media inoculum



Inokulum aktif



Standar N-asetil glukosamin



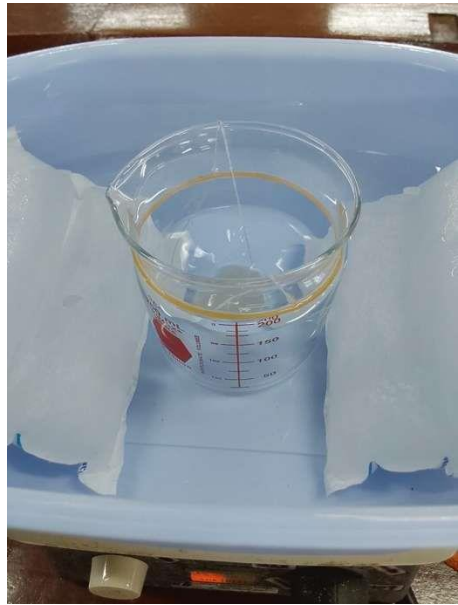
Pengukuran aktivitas kitinase



Pengukuran kadar protein



Karakterisasi enzim



Tahapan dialisis

