

## LAMPIRAN

- Hak Cipta Dilindungi Undang-undang
1. Dilarang mengutip sebagian atau seluruh karya tulis ini tanpa mencantumkan dan menyebutkan sumber :
    - a. Pengutipan hanya untuk kepentingan pendidikan, penelitian, penulisan karya ilmiah, penyusunan laporan, penulisan kritik atau tinjauan suatu masalah
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## Lampiran 1 Dokumentasi sampel penelitian



Ikan tuna beku



Ikan tongkol beku



Ikan cakalang beku



Tuna Loin



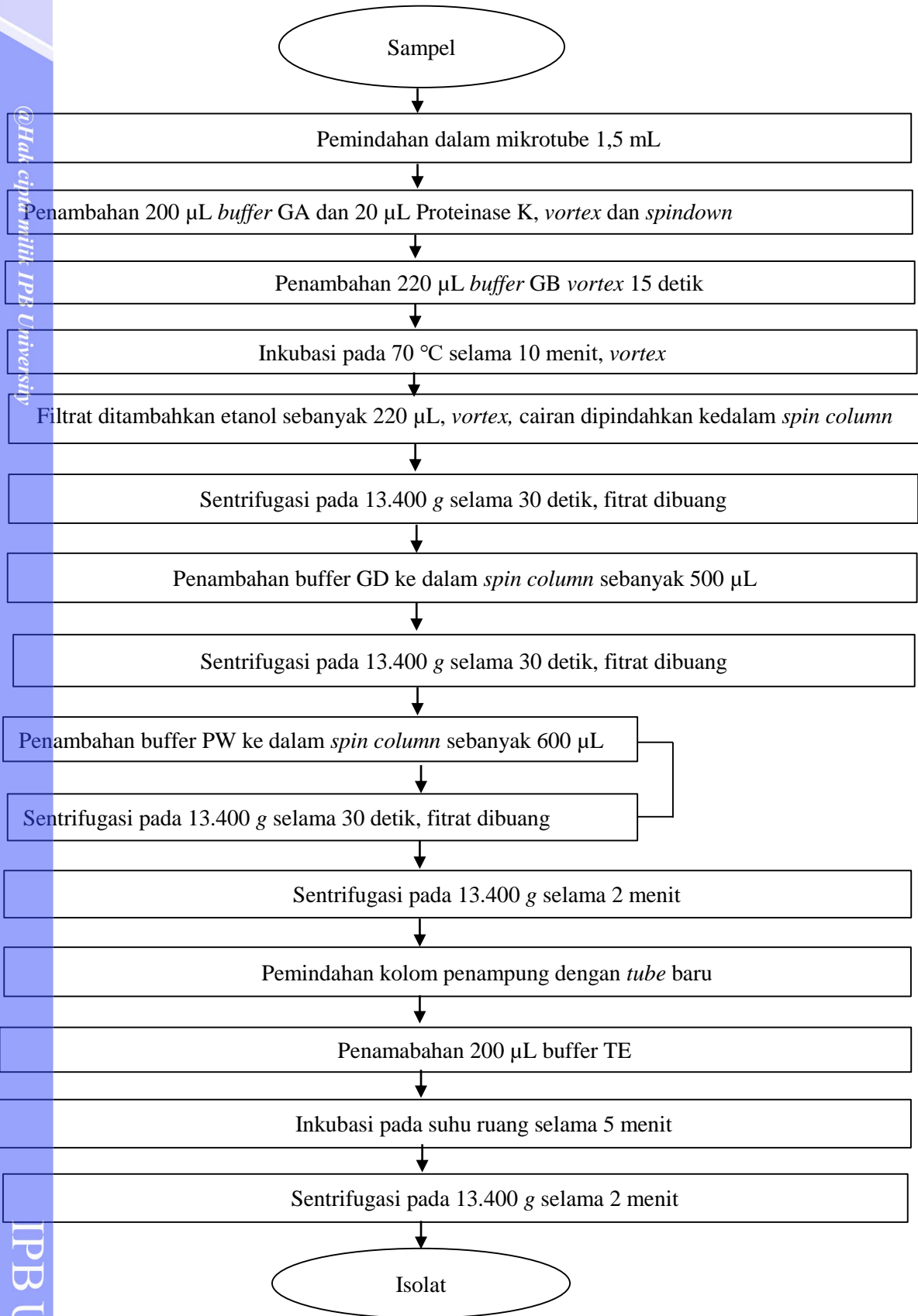
Pindang potong



Pindang bumbu kuning



Lampiran 2 Isolasi DNA menggunakan KIT TianAmp



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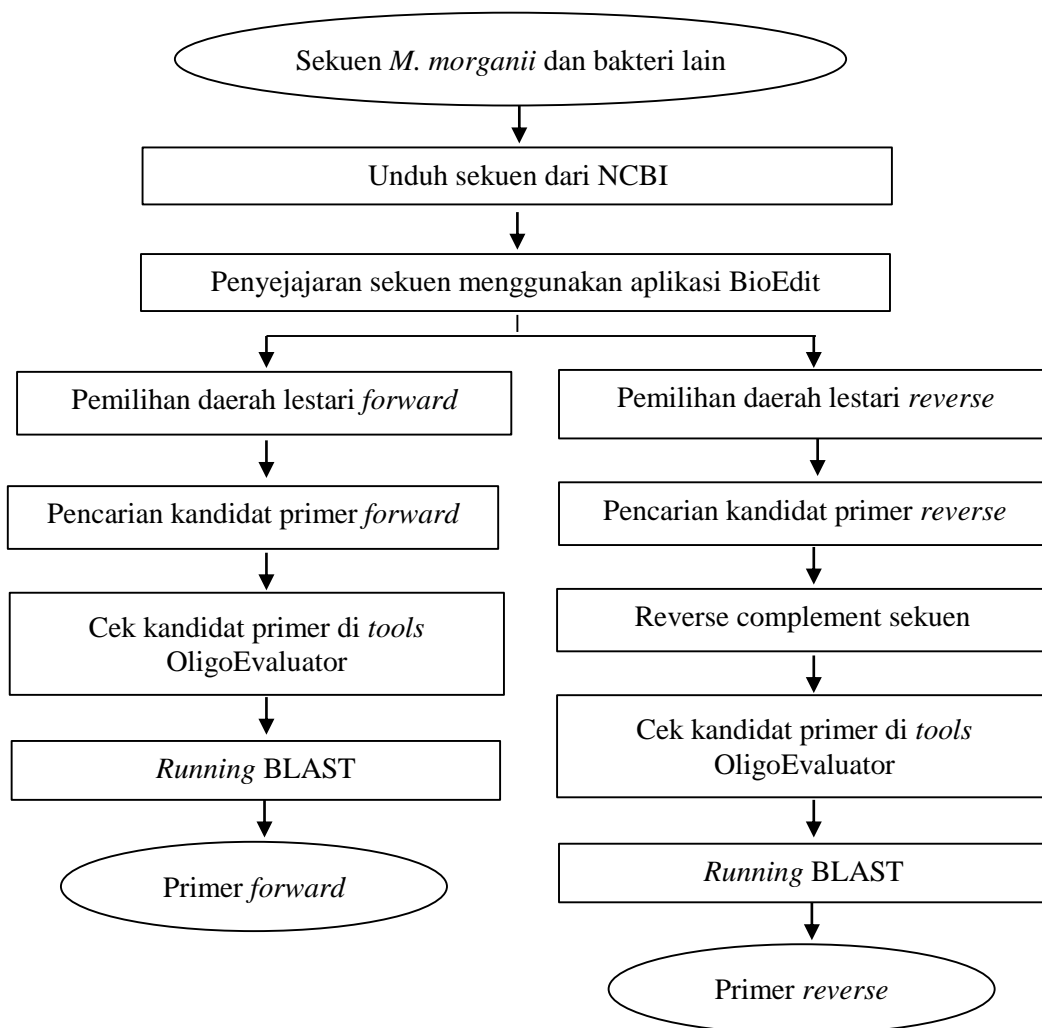
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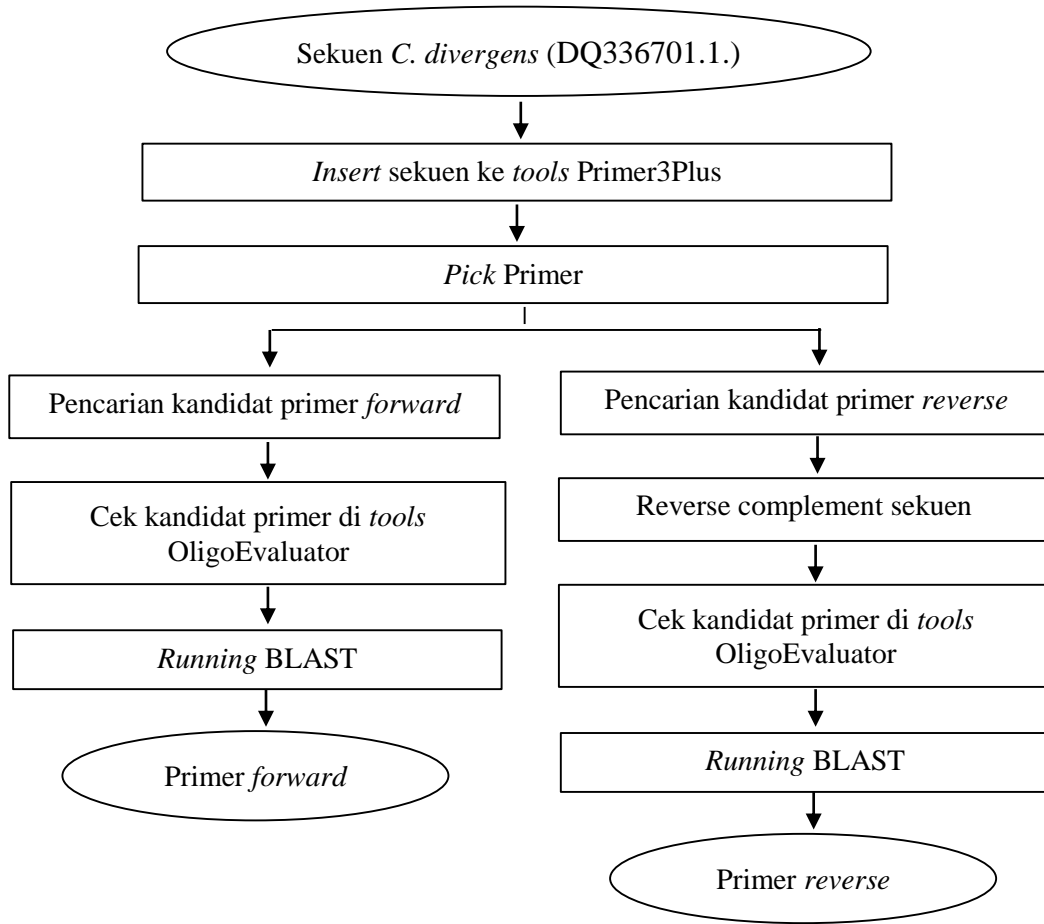
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Lampiran 3 Langkah desain primer spesifik *M. morganii*

### Lampiran 4 Langkah desain primer spesifik *C. divergens*



## Lampiran 5. Screenshot hasil BLAST spesies bakteri

Bakteri daging ikan kontrol positif gen *ldc*

Sequences producing significant alignments						
Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
<input checked="" type="checkbox"/> Citrobacter sp. LUTT5 chromosome, complete genome	270	270	44%	6e-68	83.50%	CP047806.1
<input checked="" type="checkbox"/> Citrobacter freundii strain E51 chromosome, complete genome	270	270	44%	6e-68	83.50%	CP042534.1
<input checked="" type="checkbox"/> Citrobacter freundii strain E11 chromosome, complete genome	270	270	44%	6e-68	83.50%	CP042524.1
<input checked="" type="checkbox"/> Citrobacter sp. CF971 chromosome, complete genome	270	270	44%	6e-68	83.50%	CP041051.1
<input checked="" type="checkbox"/> Citrobacter freundii strain 18-1, complete genome	270	270	44%	6e-68	83.50%	CP022273.1
<input checked="" type="checkbox"/> Citrobacter freundii strain ZY198 chromosome, complete genome	265	265	44%	3e-66	83.17%	CP055247.1
<input checked="" type="checkbox"/> Citrobacter freundii strain Cit8 chromosome, complete genome	265	265	44%	3e-66	83.17%	CP048416.1
<input checked="" type="checkbox"/> Citrobacter freundii strain E33 chromosome, complete genome	265	265	44%	3e-66	83.17%	CP042517.1
<input checked="" type="checkbox"/> Citrobacter freundii strain C50 chromosome, complete genome	265	265	44%	3e-66	83.17%	CP042478.1
<input checked="" type="checkbox"/> Citrobacter freundii strain R47 chromosome R47, complete sequence	265	265	44%	3e-66	83.17%	CP040998.1
<input checked="" type="checkbox"/> Citrobacter freundii strain FDAARGOS_549 chromosome, complete genome	265	265	44%	3e-66	83.17%	CP033744.1
<input checked="" type="checkbox"/> Citrobacter freundii strain UMH16 chromosome, complete genome	265	265	44%	3e-66	83.17%	CP024677.1
<input checked="" type="checkbox"/> Citrobacter freundii strain UMH14 chromosome, complete genome	265	265	44%	3e-66	83.17%	CP024680.1
<input checked="" type="checkbox"/> Citrobacter freundii strain AR_0116 chromosome, complete genome	265	265	44%	3e-66	83.17%	CP024680.1
<input checked="" type="checkbox"/> Citrobacter freundii complex so, CFNIH4 chromosome, complete genome	265	265	44%	3e-66	83.17%	CP024680.1

Bakteri kontrol positif hasil *enrichment lactose broth* gen *ldc*

Sequences producing significant alignments						
Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
<input checked="" type="checkbox"/> Hafnia paralvei strain FDAARGOS_158 chromosome, complete genome	712	712	95%	0.0	87.87%	CP014031.2
<input checked="" type="checkbox"/> Enterobacteriaceae bacterium bta3-1, complete genome	656	656	95%	0.0	86.23%	CP004083.1
<input checked="" type="checkbox"/> Obesumbacterium proteus strain DSM 2777, complete genome	377	694	95%	3e-100	77.89%	CP014608.1
<input checked="" type="checkbox"/> Klebsiella pneumoniae DNA, complete genome, strain: YH43	353	463	96%	6e-93	77.12%	AP014950.1
<input checked="" type="checkbox"/> Klebsiella aerogenes strain Y1 chromosome, complete genome	348	348	96%	3e-91	76.96%	CP045870.1
<input checked="" type="checkbox"/> Klebsiella aerogenes strain Y3 chromosome, complete genome	348	348	96%	3e-91	76.96%	CP045869.1
<input checked="" type="checkbox"/> Klebsiella aerogenes strain Y6 chromosome, complete genome	348	348	96%	3e-91	76.96%	CP045868.1
<input checked="" type="checkbox"/> Klebsiella aerogenes strain LU2 chromosome, complete genome	348	348	96%	3e-91	76.96%	CP035466.1
<input checked="" type="checkbox"/> Klebsiella aerogenes strain 4928STDY7071344 genome assembly, chromosome:1	348	348	96%	3e-91	76.96%	LR607333.1
<input checked="" type="checkbox"/> Klebsiella pneumoniae strain KPN1344 chromosome	348	348	96%	3e-91	77.00%	CP033801.1
<input checked="" type="checkbox"/> Klebsiella quasivariicola strain KPN1705 chromosome, complete genome	348	447	96%	3e-91	76.92%	CP022823.1
<input checked="" type="checkbox"/> Klebsiella varicicola strain 118 chromosome, complete genome	342	452	96%	1e-89	76.80%	CP048379.1
<input checked="" type="checkbox"/> Klebsiella aerogenes strain C9 chromosome, complete genome	342	342	96%	1e-89	76.80%	CP042530.1
<input checked="" type="checkbox"/> Klebsiella quasipneumoniae strain A708 chromosome, complete genome	342	342	96%	1e-89	76.84%	CP026368.1
<input checked="" type="checkbox"/> Klebsiella aerogenes strain KA_P10_L5_03_19 chromosome, complete genome	342	342	96%	1e-89	76.80%	CP044214.1
<input checked="" type="checkbox"/> Klebsiella pneumoniae strain T4 chromosome	342	342	96%	1e-89	76.80%	CP034540.1
<input checked="" type="checkbox"/> Klebsiella quasipneumoniae subsp. quasipneumoniae strain A708 chromosome, complete genome	342	342	96%	1e-89	76.84%	CP026368.1
<input checked="" type="checkbox"/> Klebsiella aerogenes strain FDAARGOS_263 chromosome, complete genome	342	342	96%	1e-89	76.80%	CP042530.1



## Bakteri kontrol positif hasil enrichment marine broth gen *ldc*

Sequences producing significant alignments

Download Manage Columns Show 100

select all 100 sequences selected

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
<a href="#">Enterobacter cloacae strain E3442 chromosome, complete genome</a>	390	390	76%	3e-104	85.45%	CP033466.1
<a href="#">Enterobacter hormaechei strain 388 chromosome, complete genome</a>	390	390	76%	3e-104	85.45%	CP021167.1
<a href="#">Enterobacter hormaechei strain 234 chromosome, complete genome</a>	390	390	76%	3e-104	85.45%	CP021162.1
<a href="#">Enterobacter hormaechei strain CEant1 chromosome</a>	390	390	76%	3e-104	85.45%	CP058553.1
<a href="#">Klebsiella aerogenes strain RHBSTW-00938 chromosome</a>	374	374	95%	3e-99	81.36%	CP055904.1
<a href="#">Escherichia coli strain EcPF5 chromosome, complete genome</a>	368	368	97%	2e-97	80.87%	CP054236.1
<a href="#">Escherichia coli strain EcPF7 chromosome, complete genome</a>	368	368	97%	2e-97	80.87%	CP054232.1
<a href="#">Escherichia coli strain EcPF14 chromosome, complete genome</a>	368	368	97%	2e-97	80.87%	CP054230.1
<a href="#">Escherichia coli strain EcPF18 chromosome, complete genome</a>	368	368	97%	2e-97	80.87%	CP054219.1
<a href="#">Escherichia coli strain SCU-487 chromosome, complete genome</a>	368	368	97%	2e-97	80.87%	CP054454.1
<a href="#">Escherichia coli strain SCU-121 chromosome, complete genome</a>	368	368	97%	2e-97	80.87%	CP054328.1
<a href="#">Escherichia coli strain SCU-479 chromosome, complete genome</a>	368	368	97%	2e-97	80.87%	CP054317.1
<a href="#">Escherichia coli strain SCU-182 chromosome, complete genome</a>	368	368	97%	2e-97	80.87%	CP054372.1
<a href="#">Escherichia coli strain SCU-101 chromosome, complete genome</a>	368	368	97%	2e-97	80.87%	CP048920.1
<a href="#">Escherichia coli strain ATCC 25922 chromosome, complete genome</a>	368	368	97%	2e-97	80.87%	CP037449.1
<a href="#">Escherichia coli strain SCU-124 chromosome, complete genome</a>	368	368	97%	2e-97	80.87%	CP051706.1
<a href="#">Escherichia coli strain SCU-112 chromosome, complete genome</a>	368	368	97%	2e-97	80.87%	CP051725.1
<a href="#">Klebsiella aerogenes strain 18-2341 chromosome, complete genome</a>	368	368	95%	2e-97	81.10%	CP049600.1
<a href="#">Escherichia coli strain EC28 chromosome, complete genome</a>	368	368	97%	2e-97	80.87%	CP049101.1
<a href="#">Escherichia coli strain 9 plasmid p009_C, complete sequence</a>	368	368	97%	2e-97	80.87%	CP048307.1
<a href="#">Escherichia coli E302 DNA, complete genome</a>	368	368	97%	2e-97	80.87%	AP022362.1
<a href="#">Escherichia coli E138 DNA, complete genome</a>	368	368	97%	2e-97	80.87%	AP022351.1

## Bakteri kontrol positif hasil enrichment marine broth gen *tdc*

Sequences producing significant alignments

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select all 83 sequences selected

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
<a href="#">Enterococcus faecalis strain 111540047-1 chromosome, complete genome</a>	784	784	95%	0.0	97.82%	CP046111.1
<a href="#">Enterococcus faecalis strain 111540027-2 chromosome, complete genome</a>	784	784	95%	0.0	97.82%	CP046112.1
<a href="#">Enterococcus faecalis strain 092160007-3 chromosome, complete genome</a>	784	784	95%	0.0	97.82%	CP046113.1
<a href="#">Enterococcus faecalis strain 4928STDY7387719 genome assembly, chromosome: 1</a>	784	784	95%	0.0	97.82%	LR607365.1
<a href="#">Enterococcus faecalis strain 4928STDY7071765 genome assembly, chromosome: 1</a>	784	784	95%	0.0	97.82%	LR607359.1
<a href="#">Enterococcus faecalis strain 4928STDY7071766 genome assembly, chromosome: 1</a>	784	784	95%	0.0	97.82%	LR607356.1
<a href="#">Enterococcus faecalis strain 4928STDY7387674 genome assembly, chromosome: 1</a>	784	784	95%	0.0	97.82%	LR607354.1
<a href="#">Enterococcus faecalis strain 4928STDY7071355 genome assembly, chromosome: 1</a>	784	784	95%	0.0	97.82%	LR607334.1
<a href="#">Enterococcus faecalis strain DM01 chromosome, complete genome</a>	784	784	95%	0.0	97.82%	CP041344.1
<a href="#">Enterococcus faecalis strain FDAARGOS_611 chromosome, complete genome</a>	784	784	95%	0.0	97.82%	CP041012.1
<a href="#">Enterococcus faecalis strain NCTC8732 genome assembly, chromosome: 1</a>	784	784	95%	0.0	97.82%	LR594051.1
<a href="#">Enterococcus faecalis strain 110 chromosome</a>	784	784	95%	0.0	97.82%	CP039752.1
<a href="#">Enterococcus faecalis strain NCTC8745 genome assembly, chromosome: 1</a>	784	784	95%	0.0	97.82%	LR134312.1
<a href="#">Enterococcus faecalis strain H25 chromosome, complete genome</a>	784	784	95%	0.0	97.82%	CP029612.1
<a href="#">Enterococcus faecalis KUB3007 DNA, complete genome</a>	784	784	95%	0.0	97.82%	AP018543.1
<a href="#">Enterococcus faecalis KUB3006 DNA, complete genome</a>	784	784	95%	0.0	97.82%	AP018538.1
<a href="#">Enterococcus faecalis strain FDAARGOS_324 chromosome, complete genome</a>	784	784	95%	0.0	97.82%	CP039752.1

## Bakteri daging ikan kontrol positif gen *hdc*

Sequences producing significant alignments

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select all 85 sequences selected

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
<a href="#">Morganella morganii subsp. morganii strain 171229813 chromosome, complete genome</a>	941	941	99%	0.0	99.05%	CP043955.1
<a href="#">Morganella morganii strain MP63 chromosome, complete genome</a>	941	941	99%	0.0	99.05%	CP048806.1
<a href="#">Morganella morganii strain NCTC235 genome assembly, chromosome: 1</a>	941	941	99%	0.0	99.05%	LR133904.1
<a href="#">Morganella morganii strain KC-TI-01 chromosome, complete genome</a>	941	941	99%	0.0	99.05%	CP025933.1
<a href="#">Morganella morganii strain JIANGXI chromosome, complete genome</a>	941	941	99%	0.0	99.05%	CP039377.1
<a href="#">Morganella morganii strain ATCC 25830 histidine decarboxylase (hdc) gene, partial cds</a>	941	941	99%	0.0	99.05%	FJ469558.1
<a href="#">Morganella morganii hdc gene for histidine decarboxylase, complete cds, strain: JCM 1672</a>	941	941	99%	0.0	99.05%	AB259280.1
<a href="#">Morganella morganii strain DG56-16 chromosome, complete genome</a>	935	935	99%	0.0	98.85%	CP032295.1
<a href="#">Uncultured Morganella clone MM1 histidine decarboxylase (hdc) gene, partial cds</a>	935	935	99%	0.0	98.85%	KY352311.1
<a href="#">Morganella morganii strain FDAARGOS_365 chromosome, complete genome</a>	935	935	99%	0.0	98.85%	CP023505.1
<a href="#">Morganella morganii strain BO255 histidine decarboxylase (hdc) gene, partial cds</a>	935	935	99%	0.0	98.85%	FJ469561.1
<a href="#">Morganella morganii strain U6/1 Hdc (hdc) gene, partial cds</a>	935	935	99%	0.0	99.04%	DQ360919.1
<a href="#">Morganella morganii hdc gene for histidine decarboxylase, partial cds, strain:jcm1672</a>	935	935	99%	0.0	98.85%	AB083200.1
<a href="#">Morganella morganii strain HPP309 histidine decarboxylase (hdc) gene, partial cds</a>	929	929	99%	0.0	98.66%	FJ469563.1
<a href="#">Morganella morganii strain M04090 Hdc (hdc) gene, partial cds</a>	929	929	99%	0.0	98.85%	DQ360932.1
<a href="#">Morganella morganii strain N18-00103 chromosome, complete genome</a>	924	924	99%	0.0	98.47%	CP048275.1
<a href="#">Morganella morganii subsp. morganii strain ATCC 25830 chromosome, complete genome</a>	924	924	99%	0.0	98.47%	CP039752.1

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### Bakteri kontrol positif hasil *enrichment lactose broth gen hdc*

Sequences producing significant alignments

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select all 78 sequences selected

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
Morganella morganii subsp. morganii strain 171229813 chromosome, complete genome	401	401	62%	2e-107	85.75%	CP043955.1
Morganella morganii strain MP63 chromosome, complete genome	401	401	62%	2e-107	85.75%	CP048806.1
Morganella morganii strain N18-00103 chromosome, complete genome	401	401	60%	2e-107	85.97%	CP048275.1
Morganella morganii subsp. morganii strain ATCC 25630 chromosome, complete genome	401	401	60%	2e-107	85.97%	CP034944.1
Morganella morganii strain NCTC235 genome assembly, chromosome:1	401	401	62%	2e-107	85.75%	LR133904.1
Morganella morganii strain L241 chromosome, complete genome	401	401	60%	2e-107	85.97%	CP033056.1
Morganella morganii strain DG56-16 chromosome, complete genome	401	401	62%	2e-107	85.75%	CP032295.1
Morganella morganii strain NCTC12028 genome assembly, chromosome:1	401	401	60%	2e-107	85.97%	LS483498.1
Morganella morganii strain KC-TI-01 chromosome, complete genome	401	401	62%	2e-107	85.75%	CP025933.1
Uncultured Morganella clone MM1 histidine decarboxylase (hdc) gene, partial cds	401	401	62%	2e-107	85.75%	KY352311.1
Morganella morganii strain FDAARGOS_365 chromosome, complete genome	401	401	62%	2e-107	85.79%	CP023505.1
Morganella morganii subsp. morganii KT, complete genome	401	401	60%	2e-107	85.97%	CP004345.1
Morganella morganii strain Jlangxi chromosome, complete genome	401	401	62%	2e-107	85.75%	CP039377.1
Morganella morganii strain HPP309 histidine decarboxylase (hdc) gene, partial cds	401	401	62%	2e-107	85.79%	FJ469563.1
Morganella morganii strain BO255 histidine decarboxylase (hdc) gene, partial cds	401	401	62%	2e-107	85.75%	FJ469561.1
Morganella morganii strain ATCC 25830 histidine decarboxylase (hdc) gene, partial cds	401	401	62%	2e-107	85.75%	FJ469562.1
Morganella morganii strain M04090 Hdc (hdc) gene, partial cds	401	401	62%	2e-107	85.75%	CP004345.1

### Bakteri kontrol positif hasil *enrichment marine broth gen hdc*

Sequences producing significant alignments

Download Manage Columns Show 100

select all 74 sequences selected

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
Enterobacter aerogenes strain DI-269 histidine decarboxylase gene, complete cds	760	760	97%	0.0	93.26%	KP728798.1
Klebsiella aerogenes strain HNHF1 chromosome, complete genome	754	754	97%	0.0	93.06%	CP047669.1
Klebsiella aerogenes strain Y1 chromosome, complete genome	754	754	97%	0.0	93.06%	CP045870.1
Klebsiella aerogenes strain Y3 chromosome, complete genome	754	754	97%	0.0	93.06%	CP045869.1
Klebsiella aerogenes strain Y6 chromosome, complete genome	754	754	97%	0.0	93.06%	CP045868.1
Klebsiella aerogenes strain C9 chromosome, complete genome	754	754	97%	0.0	93.06%	CP042530.1
Klebsiella aerogenes strain AR_0007 chromosome, complete genome	754	754	97%	0.0	93.06%	CP024883.1
Klebsiella aerogenes strain AR_0018 chromosome, complete genome	754	754	97%	0.0	93.06%	CP024880.1
Enterobacter aerogenes strain ATCC 29007 histidine decarboxylase gene, complete cds	754	754	97%	0.0	93.06%	KP728797.1
Klebsiella aerogenes strain FDAARGOS_641 chromosome, complete genome	749	749	97%	0.0	92.87%	CP044083.1
Klebsiella aerogenes strain Ka37751 chromosome, complete genome	749	749	97%	0.0	92.87%	CP041925.1
Klebsiella aerogenes strain NCTC10006 genome assembly, plasmid:2	749	749	97%	0.0	92.87%	LR134122.1
Klebsiella aerogenes strain NCTC9735 genome assembly, chromosome:1	749	749	97%	0.0	92.87%	LR134475.1
Klebsiella aerogenes strain FDAARGOS_363 chromosome, complete genome	749	749	97%	0.0	92.87%	CP023963.1
Enterobacter aerogenes KCTC 2190, complete genome	749	749	97%	0.0	92.87%	CP002824.1
Enterobacter aerogenes strain ATCC 13048 histidine decarboxylase (hdc) gene, partial cds	749	749	97%	0.0	92.87%	FJ469563.1
Enterobacter aerogenes pyridoxal phosphate-dependent histidine decarboxylase (hdc) gene, complete cds	749	749	97%	0.0	92.87%	CP002824.1

### Bakteri tuna beku hasil *enrichment media marine broth gen ldc*

Sequences producing significant alignments

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select all 100 sequences selected

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
Enterobacter cloacae strain RHBSTW-00473 chromosome, complete genome	1435	1435	98%	0.0	91.03%	CP056474.1
Enterobacter roggenkampii strain RHBSTW-00925 chromosome, complete genome	1435	1435	98%	0.0	91.03%	CP056129.1
Enterobacter roggenkampii strain KQ-01 chromosome, complete genome	1430	1430	98%	0.0	90.93%	CP056837.1
Enterobacter cloacae complex sp. 35734 chromosome 1, complete sequence	1417	1417	98%	0.0	90.74%	CP012162.1
Enterobacter roggenkampii strain DSM 16690 chromosome, complete genome	1413	1413	98%	0.0	90.66%	CP017184.1
Enterobacter roggenkampii strain FDAARGOS_523 chromosome, complete genome	1411	1411	98%	0.0	90.65%	CP033800.1
Enterobacter roggenkampii strain ECV546 chromosome, complete genome	1411	1411	98%	0.0	90.65%	CP032916.1
Enterobacter roggenkampii strain RHBSTW-00695 chromosome, complete genome	1406	1406	98%	0.0	90.56%	CP056168.1
Enterobacter cloacae strain 339389L chromosome	1402	1402	98%	0.0	90.48%	CP026536.1
Enterobacter cloacae strain RHBSTW-00399 chromosome, complete genome	1402	1402	98%	0.0	90.48%	CP056560.1
Enterobacter roggenkampii strain RHBSTW-00309 chromosome, complete genome	1402	1402	98%	0.0	90.48%	CP056737.1
Enterobacter roggenkampii strain BP10374 chromosome, complete genome	1397	1397	98%	0.0	90.39%	CP038471.1
Enterobacter roggenkampii strain T04SK10 chromosome, complete genome	1397	1397	98%	0.0	90.39%	CP022148.1
Enterobacter roggenkampii strain R11 chromosome, complete genome	1397	1397	98%	0.0	90.39%	CP056837.1



## Bakteri pindang bumbu kuning hasil *enrichment* media *marine broth* gen *ldc*

Sequences producing significant alignments		Download	Manage Columns	Show	100	
select all 100 sequences selected		GenBank	Graphics	Distance tree of results		
Description	Max Score	Total Score	Query Cover	E value	Per Ident	Accession
<input checked="" type="checkbox"/> Enterobacter hormaechei strain 20710 chromosome .complete genome	1604	1604	98%	0.0	94.02%	CP030076.1
<input checked="" type="checkbox"/> Enterobacter hormaechei strain E70 chromosome .complete genome	1592	1592	97%	0.0	93.98%	CP046271.1
<input checked="" type="checkbox"/> Enterobacter hormaechei strain AUH-ENM30 chromosome	1592	1592	96%	0.0	93.83%	CP045611.1
<input checked="" type="checkbox"/> Enterobacter hormaechei strain C15 chromosome .complete genome	1592	1592	97%	0.0	93.98%	CP042488.1
<input checked="" type="checkbox"/> Enterobacter cloacae strain 174 chromosome .complete genome	1592	1592	97%	0.0	93.98%	CP020528.1
<input checked="" type="checkbox"/> Enterobacter hormaechei strain WCHEH020038 chromosome .complete genome	1592	1592	97%	0.0	93.98%	CP031726.1
<input checked="" type="checkbox"/> Enterobacter sp. CRENT-193 chromosome .complete genome	1592	1592	98%	0.0	93.83%	CP024812.1
<input checked="" type="checkbox"/> Enterobacter hormaechei subsp. xiangfangensis strain 34399 chromosome .complete genome	1592	1592	97%	0.0	93.98%	CP010384.1
<input checked="" type="checkbox"/> Enterobacter xiangfangensis strain LMG27195 .complete genome	1581	1581	97%	0.0	93.79%	CP017183.1
<input checked="" type="checkbox"/> Enterobacter hormaechei strain Y2152 chromosome .complete genome	1576	1576	97%	0.0	93.70%	CP049192.1
<input checked="" type="checkbox"/> Enterobacter hormaechei strain Y323 chromosome .complete genome	1576	1576	98%	0.0	93.55%	CP049188.1
<input checked="" type="checkbox"/> Enterobacter cloacae strain E3442 chromosome .complete genome	1576	1576	98%	0.0	93.55%	CP033466.1
<input checked="" type="checkbox"/> Enterobacter hormaechei strain EGYMCRVIM chromosome .complete genome	1570	1570	97%	0.0	93.60%	CP053190.1
<input checked="" type="checkbox"/> Enterobacter hormaechei subsp. xiangfangensis strain WCHEX045001 chromosome .complete genome	1570	1570	98%	0.0	93.46%	CP043382.1
<input checked="" type="checkbox"/> Enterobacter hormaechei strain WCHEH090011 chromosome .complete genome	1570	1570	98%	0.0	93.48%	CP026310.1
<input checked="" type="checkbox"/> Enterobacter hormaechei subsp. xiangfangensis strain UM_CRE-14 chromosome	1570	1570	97%	0.0	93.60%	CP023430.1
<input checked="" type="checkbox"/> Enterobacter hormaechei subsp. xiangfangensis strain OSUJVMCKPC4.2 chromosome .complete genome	1570	1570	98%	0.0	93.46%	CP029246.1
<input checked="" type="checkbox"/> Enterobacter hormaechei subsp. xiangfangensis strain OSUJVMCKPC4.1 chromosome .complete genome	1570	1570	98%	0.0	93.46%	CP029246.1

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## Bakteri pindang potong hasil *enrichment* media *marine broth* gen *ldc*

Description	Max Score	Total Score	Query Cover	E value	Per Ident	Accession
<input checked="" type="checkbox"/> Enterobacter hormaechei strain 20710 chromosome .complete genome	1604	1604	98%	0.0	94.02%	CP030076.1
<input checked="" type="checkbox"/> Enterobacter hormaechei strain E70 chromosome .complete genome	1592	1592	97%	0.0	93.98%	CP046271.1
<input checked="" type="checkbox"/> Enterobacter hormaechei strain AUH-ENM30 chromosome	1592	1592	96%	0.0	93.83%	CP045611.1
<input checked="" type="checkbox"/> Enterobacter hormaechei strain C15 chromosome .complete genome	1592	1592	97%	0.0	93.98%	CP042488.1
<input checked="" type="checkbox"/> Enterobacter cloacae strain 174 chromosome .complete genome	1592	1592	97%	0.0	93.98%	CP020528.1
<input checked="" type="checkbox"/> Enterobacter hormaechei strain WCHEH020038 chromosome .complete genome	1592	1592	97%	0.0	93.98%	CP031726.1
<input type="checkbox"/> Enterobacter sp. CRENT-193 chromosome .complete genome	1592	1592	98%	0.0	93.83%	CP024812.1
<input type="checkbox"/> Enterobacter hormaechei subsp. xiangfangensis strain 34399 chromosome .complete genome	1592	1592	97%	0.0	93.98%	CP010384.1
<input type="checkbox"/> Enterobacter xiangfangensis strain LMG27195 .complete genome	1581	1581	97%	0.0	93.79%	CP017183.1
<input type="checkbox"/> Enterobacter hormaechei strain Y2152 chromosome .complete genome	1576	1576	97%	0.0	93.70%	CP049192.1
<input type="checkbox"/> Enterobacter hormaechei strain Y323 chromosome .complete genome	1576	1576	98%	0.0	93.55%	CP049188.1
<input type="checkbox"/> Enterobacter cloacae strain E3442 chromosome .complete genome	1576	1576	98%	0.0	93.55%	CP033466.1
<input type="checkbox"/> Enterobacter hormaechei strain EGYMCRVIM chromosome .complete genome	1570	1570	97%	0.0	93.60%	CP053190.1
<input type="checkbox"/> Enterobacter hormaechei subsp. xiangfangensis strain WCHEX045001 chromosome .complete genome	1570	1570	98%	0.0	93.46%	CP043382.1
<input type="checkbox"/> Enterobacter hormaechei strain WCHEH090011 chromosome .complete genome	1570	1570	98%	0.0	93.48%	CP026310.1
<input type="checkbox"/> Enterobacter hormaechei subsp. xiangfangensis strain UM_CRE-14 chromosome	1570	1570	97%	0.0	93.60%	CP023430.1
<input type="checkbox"/> Enterobacter hormaechei subsp. xiangfangensis strain OSUJVMCKPC4.2 chromosome .complete genome	1570	1570	98%	0.0	93.46%	CP029246.1

## Bakteri ikan tuna beku hasil *enrichment* media *marine broth* gen *tdc*

Sequences producing significant alignments		Download	New Select columns	Show	100			
select all 86 sequences selected		GenBank	Graphics	Distance tree of results				
Description	Common Name	Max Score	Total Score	Query Cover	E value	Per Ident	Acc Len	Accession
<input checked="" type="checkbox"/> Enterococcus faecalis strain 092160007-3 chromosome .complete genome	Enterococcus f...	499	499	94%	3e-137	99.64%	2675479	CP046113.1
<input checked="" type="checkbox"/> Enterococcus faecalis strain TH4125 chromosome .complete genome	Enterococcus f...	499	499	94%	3e-137	99.64%	2993403	CP051005.1
<input checked="" type="checkbox"/> Enterococcus faecalis strain ES-1 chromosome .complete genome	Enterococcus f...	499	499	94%	3e-137	99.64%	2833478	CP049775.1
<input checked="" type="checkbox"/> Enterococcus faecalis strain JY32 chromosome .complete genome	Enterococcus f...	499	499	94%	3e-137	99.64%	2933718	CP045045.1
<input checked="" type="checkbox"/> Enterococcus faecalis strain L14 chromosome	Enterococcus f...	499	499	94%	3e-137	99.64%	2814099	CP043724.1
<input checked="" type="checkbox"/> Enterococcus faecalis strain BFFF11 chromosome .complete genome	Enterococcus f...	499	499	94%	3e-137	99.64%	3067042	CP045918.1
<input checked="" type="checkbox"/> Enterococcus faecalis strain L15 chromosome .complete genome	Enterococcus f...	499	499	94%	3e-137	99.64%	2846134	CP042213.1
<input checked="" type="checkbox"/> Enterococcus faecalis EnGen0107 strain B594 chromosome .complete genome	Enterococcus f...	499	499	94%	3e-137	99.64%	3152103	CP041738.1
<input checked="" type="checkbox"/> Enterococcus faecalis strain 4928STDY7387896 genome assembly chromosome.1	Enterococcus f...	499	499	94%	3e-137	99.64%	3093718	LR607378.1
<input checked="" type="checkbox"/> Enterococcus faecalis strain 4928STDY7387888 genome assembly chromosome.1	Enterococcus f...	499	499	94%	3e-137	99.64%	2870977	LR607378.1
<input checked="" type="checkbox"/> Enterococcus faecalis strain 4928STDY7387713 genome assembly chromosome.1	Enterococcus f...	499	499	94%	3e-137	99.64%	3396661	LR607361.1
<input checked="" type="checkbox"/> Enterococcus faecalis strain 4928STDY7071325 genome assembly chromosome.1	Enterococcus f...	499	499	94%	3e-137	99.64%	3380441	LR607329.1
<input checked="" type="checkbox"/> Enterococcus faecalis strain DM01 chromosome .complete genome	Enterococcus f...	499	499	94%	3e-137	99.64%	2785968	CP041344.1
<input checked="" type="checkbox"/> Enterococcus faecalis strain VE14089 chromosome .complete genome	Enterococcus f...	499	499	94%	3e-137	99.64%	3238854	CP039296.1
<input checked="" type="checkbox"/> Enterococcus faecalis strain VE18379 chromosome .complete genome	Enterococcus f...	499	499	94%	3e-137	99.64%	3218315	CP039548.1
<input checked="" type="checkbox"/> Enterococcus faecalis strain VE18395 chromosome .complete genome	Enterococcus f...	499	499	94%	3e-137	99.64%	3201501	CP039549.1
<input checked="" type="checkbox"/> Enterococcus faecalis strain HA-1 chromosome .complete genome	Enterococcus f...	499	499	94%	3e-137	99.64%	2881081	CP040898.1
<input checked="" type="checkbox"/> Enterococcus faecalis strain C54 chromosome .complete genome	Enterococcus f...	499	499	94%	3e-137	99.64%	2813589	CP030045.1
<input checked="" type="checkbox"/> Enterococcus faecalis strain C25 chromosome .complete genome	Enterococcus f...	499	499	94%	3e-137	99.64%	2825273	CP030042.1
<input checked="" type="checkbox"/> Enterococcus faecalis strain FC chromosome .complete genome	Enterococcus f...	499	499	94%	3e-137	99.64%	2934454	CP028835.1

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Hak Cipta Dilindungi Undang-undang  
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## Bakteri pandang potong hasil *enrichment* media *marine broth* gen *tdc*

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
<input checked="" type="checkbox"/> <a href="#">Enterococcus faecalis strain 092160007-3 chromosome .complete genome</a>	1249	1249	97%	0.0	95.29%	<a href="#">CP046113.1</a>
<input checked="" type="checkbox"/> <a href="#">Enterococcus faecalis strain DM01 chromosome .complete genome</a>	1249	1249	97%	0.0	95.29%	<a href="#">CP041344.1</a>
<input checked="" type="checkbox"/> <a href="#">Enterococcus faecalis strain NCTC8745 genome assembly .chromosome_1</a>	1249	1249	97%	0.0	95.29%	<a href="#">LR134312.1</a>
<input checked="" type="checkbox"/> <a href="#">Enterococcus faecalis KUB3007 DNA .complete genome</a>	1249	1249	97%	0.0	95.29%	<a href="#">AP018543.1</a>
<input checked="" type="checkbox"/> <a href="#">Enterococcus faecalis KUB3006 DNA .complete genome</a>	1249	1249	97%	0.0	95.29%	<a href="#">AP018538.1</a>
<input checked="" type="checkbox"/> <a href="#">Enterococcus faecalis strain serialis .complete genome</a>	1249	1249	97%	0.0	95.29%	<a href="#">CP015883.1</a>
<input checked="" type="checkbox"/> <a href="#">Enterococcus faecalis strain DD14 .genome</a>	1249	1249	97%	0.0	95.29%	<a href="#">CP021161.1</a>
<input checked="" type="checkbox"/> <a href="#">Enterococcus faecalis strain 111540047-1 chromosome .complete genome</a>	1243	1243	97%	0.0	95.16%	<a href="#">CP046111.1</a>
<input checked="" type="checkbox"/> <a href="#">Enterococcus faecalis strain 111540027-2 chromosome .complete genome</a>	1243	1243	97%	0.0	95.16%	<a href="#">CP046112.1</a>
<input checked="" type="checkbox"/> <a href="#">Enterococcus faecalis strain ES-1 chromosome .complete genome</a>	1243	1243	97%	0.0	95.16%	<a href="#">CP049775.1</a>
<input checked="" type="checkbox"/> <a href="#">Enterococcus faecalis EnGen0107 strain B594 chromosome .complete genome</a>	1243	1243	97%	0.0	95.16%	<a href="#">CP041738.1</a>
<input checked="" type="checkbox"/> <a href="#">Enterococcus faecalis strain 4928STDY7387886 genome assembly .chromosome_1</a>	1243	1243	97%	0.0	95.16%	<a href="#">LR607378.1</a>
<input checked="" type="checkbox"/> <a href="#">Enterococcus faecalis strain 4928STDY7387888 genome assembly .chromosome_1</a>	1243	1243	97%	0.0	95.16%	<a href="#">LR607376.1</a>
<input checked="" type="checkbox"/> <a href="#">Enterococcus faecalis strain 4928STDY7387719 genome assembly .chromosome_1</a>	1243	1243	97%	0.0	95.16%	<a href="#">LR607365.1</a>
<input checked="" type="checkbox"/> <a href="#">Enterococcus faecalis strain 4928STDY7071765 genome assembly .chromosome_1</a>	1243	1243	97%	0.0	95.16%	<a href="#">LR607359.1</a>
<input checked="" type="checkbox"/> <a href="#">Enterococcus faecalis strain 4928STDY7071766 genome assembly .chromosome_1</a>	1243	1243	97%	0.0	95.16%	<a href="#">LR607356.1</a>
<input checked="" type="checkbox"/> <a href="#">Enterococcus faecalis strain 4928STDY7387674 genome assembly .chromosome_1</a>	1243	1243	97%	0.0	95.16%	<a href="#">LR607354.1</a>
<input checked="" type="checkbox"/> <a href="#">Enterococcus faecalis strain 4928STDY7071355 genome assembly .chromosome_1</a>	1243	1243	97%	0.0	95.16%	<a href="#">LR607334.1</a>

## Bakteri pandang bumbu kuning hasil *enrichment* media *marine broth* gen *tdc*

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
<input checked="" type="checkbox"/> <a href="#">Enterococcus faecalis strain 111540047-1 chromosome .complete genome</a>	929	1169	94%	0.0	93.06%	<a href="#">CP046111.1</a>
<input checked="" type="checkbox"/> <a href="#">Enterococcus faecalis strain 111540027-2 chromosome .complete genome</a>	929	1169	94%	0.0	93.06%	<a href="#">CP046112.1</a>
<input checked="" type="checkbox"/> <a href="#">Enterococcus faecalis strain 092160007-3 chromosome .complete genome</a>	929	1169	94%	0.0	93.06%	<a href="#">CP046113.1</a>
<input checked="" type="checkbox"/> <a href="#">Enterococcus faecalis strain ES-1 chromosome .complete genome</a>	929	1174	94%	0.0	93.06%	<a href="#">CP049775.1</a>
<input checked="" type="checkbox"/> <a href="#">Enterococcus faecalis EnGen0107 strain B594 chromosome .complete genome</a>	929	1174	94%	0.0	93.06%	<a href="#">CP041738.1</a>
<input checked="" type="checkbox"/> <a href="#">Enterococcus faecalis strain 4928STDY7387888 genome assembly .chromosome_1</a>	929	1174	94%	0.0	93.06%	<a href="#">LR607376.1</a>
<input checked="" type="checkbox"/> <a href="#">Enterococcus faecalis strain 4928STDY7387718 genome assembly .chromosome_1</a>	929	1174	94%	0.0	93.06%	<a href="#">LR607371.1</a>
<input checked="" type="checkbox"/> <a href="#">Enterococcus faecalis strain 4928STDY7387719 genome assembly .chromosome_1</a>	929	1169	94%	0.0	93.06%	<a href="#">LR607365.1</a>
<input checked="" type="checkbox"/> <a href="#">Enterococcus faecalis strain 4928STDY7071765 genome assembly .chromosome_1</a>	929	1169	94%	0.0	93.06%	<a href="#">LR607359.1</a>
<input checked="" type="checkbox"/> <a href="#">Enterococcus faecalis strain 4928STDY7071766 genome assembly .chromosome_1</a>	929	1169	94%	0.0	93.06%	<a href="#">LR607356.1</a>
<input checked="" type="checkbox"/> <a href="#">Enterococcus faecalis strain 4928STDY7387674 genome assembly .chromosome_1</a>	929	1169	94%	0.0	93.06%	<a href="#">LR607354.1</a>
<input checked="" type="checkbox"/> <a href="#">Enterococcus faecalis strain 4928STDY7071355 genome assembly .chromosome_1</a>	929	1169	94%	0.0	93.06%	<a href="#">LR607334.1</a>
<input checked="" type="checkbox"/> <a href="#">Enterococcus faecalis strain DM01 chromosome .complete genome</a>	929	1169	94%	0.0	93.06%	<a href="#">CP041344.1</a>
<input checked="" type="checkbox"/> <a href="#">Enterococcus faecalis strain VE14089 chromosome .complete genome</a>	929	1174	94%	0.0	93.06%	<a href="#">CP038296.1</a>
<input checked="" type="checkbox"/> <a href="#">Enterococcus faecalis strain VE18379 chromosome .complete genome</a>	929	1174	94%	0.0	93.06%	<a href="#">CP039548.1</a>
<input checked="" type="checkbox"/> <a href="#">Enterococcus faecalis strain VE18395 chromosome .complete genome</a>	929	1174	94%	0.0	93.06%	<a href="#">CP039549.1</a>
<input checked="" type="checkbox"/> <a href="#">Enterococcus faecalis strain FDAARGOS_611 chromosome .complete genome</a>	929	1169	94%	0.0	93.06%	<a href="#">CP041012.1</a>
<input checked="" type="checkbox"/> <a href="#">Enterococcus faecalis strain C54 chromosome .complete genome</a>	929	1174	94%	0.0	93.06%	<a href="#">CP030045.1</a>
<input checked="" type="checkbox"/> <a href="#">Enterococcus faecalis strain NCTC8732 genome assembly .chromosome_1</a>	929	1169	94%	0.0	93.06%	<a href="#">LR594051.1</a>

## Bakteri tuna beku hasil *enrichment* media *marine broth* gen *hdc*

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
<input checked="" type="checkbox"/> <a href="#">Acinetobacter baumannii strain D015 genomic sequence</a>	686	686	96%	0.0	90.72%	<a href="#">KJ1768338.1</a>
<input checked="" type="checkbox"/> <a href="#">Acinetobacter baumannii ATCC 17978 chromosome .complete genome</a>	680	680	96%	0.0	90.55%	<a href="#">CP053098.1</a>
<input checked="" type="checkbox"/> <a href="#">Acinetobacter baumannii strain 7835 chromosome .complete genome</a>	680	680	99%	0.0	90.00%	<a href="#">CP033243.1</a>
<input checked="" type="checkbox"/> <a href="#">Acinetobacter baumannii strain AB043 chromosome .complete genome</a>	680	680	96%	0.0	90.55%	<a href="#">CP043910.1</a>
<input checked="" type="checkbox"/> <a href="#">Acinetobacter baumannii ATCC 17978 substr. Lab-WT chromosome</a>	680	680	96%	0.0	90.55%	<a href="#">CP039028.2</a>
<input checked="" type="checkbox"/> <a href="#">Acinetobacter baumannii ATCC 17978 substr. PMR.HIGH chromosome .complete genome</a>	680	680	96%	0.0	90.55%	<a href="#">CP039025.2</a>
<input type="checkbox"/> <a href="#">Acinetobacter baumannii ATCC 17978 substr. PMR.Low chromosome</a>	680	680	96%	0.0	90.55%	<a href="#">CP039023.2</a>
<input type="checkbox"/> <a href="#">Acinetobacter baumannii strain TG29392 chromosome .complete genome</a>	680	680	99%	0.0	90.02%	<a href="#">CP039930.1</a>
<input type="checkbox"/> <a href="#">Acinetobacter baumannii strain TG31302 chromosome .complete genome</a>	680	680	99%	0.0	90.02%	<a href="#">CP039343.1</a>
<input type="checkbox"/> <a href="#">Acinetobacter baumannii strain TG31986 chromosome .complete genome</a>	680	680	99%	0.0	90.02%	<a href="#">CP039341.1</a>
<input type="checkbox"/> <a href="#">Acinetobacter baumannii strain MRSN15313 chromosome .complete genome</a>	680	680	99%	0.0	90.00%	<a href="#">CP033869.1</a>
<input type="checkbox"/> <a href="#">Acinetobacter baumannii strain 9102 chromosome .complete genome</a>	680	680	99%	0.0	90.00%	<a href="#">CP023029.1</a>
<input type="checkbox"/> <a href="#">Acinetobacter baumannii strain 9201 chromosome .complete genome</a>	680	680	96%	0.0	90.53%	<a href="#">CP023020.1</a>
<input type="checkbox"/> <a href="#">Acinetobacter baumannii strain A52 chromosome .complete genome</a>	680	680	99%	0.0	90.02%	<a href="#">CP034092.1</a>
<input type="checkbox"/> <a href="#">Acinetobacter baumannii strain 810CP chromosome .complete genome</a>	680	680	99%	0.0	90.00%	<a href="#">CP026338.1</a>
<input type="checkbox"/> <a href="#">Acinetobacter baumannii strain ABNIH28 chromosome .complete genome</a>	680	680	96%	0.0	90.53%	<a href="#">CP026125.1</a>
<input type="checkbox"/> <a href="#">Acinetobacter baumannii strain 11510 chromosome</a>	680	680	99%	0.0	90.00%	<a href="#">CP018861.2</a>
<input type="checkbox"/> <a href="#">Acinetobacter baumannii strain AB042 .complete genome</a>	680	680	96%	0.0	90.55%	<a href="#">CP019034.1</a>
<input type="checkbox"/> <a href="#">Acinetobacter baumannii strain ATCC 17978 .complete genome</a>	680	680	96%	0.0	90.55%	<a href="#">CP018664.1</a>
<input type="checkbox"/> <a href="#">Acinetobacter baumannii strain AF-401 .complete genome</a>	680	680	99%	0.0	90.00%	<a href="#">CP018254.1</a>
<input type="checkbox"/> <a href="#">Acinetobacter baumannii strain PR07 .genome</a>	680	680	96%	0.0	90.00%	<a href="#">CP012035.1</a>

## Bakteri pindang bumbu kuning hasil *enrichment* media *marine broth* gen *hdc*

Sequences producing significant alignments							Download	Manage Columns	Show
select all 41 sequences selected							GenBank	Graphics	Distance tree of results
Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession			
<a href="#">Morganella morganii strain BO255 histidine decarboxylase (hdc) gene, partial cds</a>	662	662	82%	0.0	93.20%	FJ469561.1			
<a href="#">Morganella morganii strain ATCC 25830 histidine decarboxylase (hdc) gene, partial cds</a>	654	654	81%	0.0	92.97%	FJ469558.1			
<a href="#">Morganella morganii subsp. morganii strain 171229813 chromosome, complete genome</a>	651	651	82%	0.0	92.76%	CP043955.1			
<a href="#">Morganella morganii strain MP63 chromosome, complete genome</a>	651	651	82%	0.0	92.76%	CP048806.1			
<a href="#">Morganella morganii strain NCTC235 genome assembly, chromosome_1</a>	651	651	82%	0.0	92.76%	LR133904.1			
<a href="#">Morganella morganii strain DG56-16 chromosome, complete genome</a>	651	651	82%	0.0	92.76%	CP032295.1			
<a href="#">Morganella morganii strain KC-TL-01 chromosome, complete genome</a>	651	651	82%	0.0	92.76%	CP025933.1			
<a href="#">Morganella morganii strain Jiangxi chromosome, complete genome</a>	651	651	82%	0.0	92.76%	CP039377.1			
<a href="#">Morganella morganii hdc gene for histidine decarboxylase, complete cds, strain JCM 1672</a>	651	651	82%	0.0	92.76%	AB259290.1			
<a href="#">Morganella morganii strain HPP309 histidine decarboxylase (hdc) gene, partial cds</a>	649	649	81%	0.0	92.75%	FJ469563.1			
<a href="#">Morganella morganii strain FDAARGOS_365 chromosome, complete genome</a>	645	645	82%	0.0	92.54%	CP023505.1			
<a href="#">Morganella morganii hdc gene for histidine decarboxylase, partial cds, strain jcm1672</a>	643	643	81%	3e-180	92.53%	AB083200.1			
<a href="#">Morganella morganii strain N18-00103 chromosome, complete genome</a>	640	640	82%	3e-179	92.32%	CP048275.1			
<a href="#">Morganella morganii subsp. morganii strain ATCC 25830 chromosome, complete genome</a>	640	640	82%	3e-179	92.32%	CP034944.1			
<a href="#">Morganella morganii strain L241 chromosome, complete genome</a>	640	640	82%	3e-179	92.32%	CP033056.1			
<a href="#">Morganella morganii strain NCTC12028 genome assembly, chromosome_1</a>	640	640	82%	3e-179	92.32%	LS483498.1			
<a href="#">Morganella morganii subsp. morganii KT, complete genome</a>	640	640	82%	3e-179	92.32%	CP004345.1			
<a href="#">Morganella morganii strain BO249 histidine decarboxylase (hdc) gene, partial cds</a>	638	638	81%	1e-178	92.31%	FJ469560.1			

## Bakteri pindang potong hasil *enrichment* media *marine broth* gen *hdc*

Sequences producing significant alignments							Download	Manage Columns	Show
select all 100 sequences selected							GenBank	Graphics	Distance tree of results
Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession			
<a href="#">Acinetobacter baumannii strain SP304 chromosome, complete genome</a>	737	737	90%	0.0	94.29%	CP040080.1			
<a href="#">Acinetobacter baumannii DNA, complete genome, strain WP4-W18-ESBL-11</a>	737	737	90%	0.0	94.29%	AF022077.1			
<a href="#">Acinetobacter baumannii strain VB82 chromosome, complete genome</a>	732	732	90%	0.0	94.08%	CP050385.1			
<a href="#">Acinetobacter baumannii strain AbCAN2 chromosome, complete genome</a>	732	732	90%	0.0	94.08%	CP045428.1			
<a href="#">Acinetobacter baumannii strain XL380 chromosome, complete genome</a>	732	732	90%	0.0	94.08%	CP046536.1			
<a href="#">Acinetobacter baumannii strain CAM180-1 chromosome, complete genome</a>	732	732	90%	0.0	94.08%	CP044356.1			
<a href="#">Acinetobacter baumannii strain P7774 chromosome, complete genome</a>	732	732	90%	0.0	94.08%	CP040259.1			
<a href="#">Acinetobacter baumannii strain UPAR1 chromosome, complete genome</a>	732	732	90%	0.0	94.08%	CP032215.1			
<a href="#">Acinetobacter baumannii strain EH chromosome, complete genome</a>	732	732	90%	0.0	94.08%	CP038258.1			
<a href="#">Acinetobacter baumannii strain EC chromosome, complete genome</a>	732	732	89%	0.0	94.25%	CP038262.1			
<a href="#">Acinetobacter baumannii strain AB046 chromosome</a>	732	732	90%	0.0	94.08%	CP037872.1			
<a href="#">Acinetobacter sp. FDAARGOS_493 chromosome, complete genome</a>	732	732	88%	0.0	94.59%	CP033858.1			
<a href="#">Acinetobacter baumannii strain DA33382 chromosome, complete genome</a>	732	732	90%	0.0	94.08%	CP030106.1			
<a href="#">Acinetobacter baumannii strain AR_0088 chromosome, complete genome</a>	732	732	90%	0.0	94.08%	CP027550.1			

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