

读书报告

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KOMODO -- the Known Media Database

A platform for recommending microbial media

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Overview: KOMODO & GROWREC

Introduction

Culturing microorganisms is a classic microbiology challenge. Most microorganisms in nature still cannot be cultured (~99% by some estimates). Best-practices for culturing new organisms have been developed, and are embedded in guides such as Bergey's Manual of Systematic Bacteriology. However, even with these best practices, the typical procedure for culturing a new microorganism still requires a great deal of experience and trial and error.

In recent years, some culturing efforts, particularly for difficult-to-culture organisms, have begun to include genome and pathway analysis, as well as high-throughput technologies for determining microbial nutrient needs. Metagenomic sequencing technology, meanwhile, is now enabling the amassment of huge quantities of data about currently nonculturable organisms. Integrating all of these areas will require fresh approaches to rapidly bring new organisms into culture.

To this end, we provide here a large catalogue of lab media that have been manually developed to date, and tools to explore what insight these known media can give into

KOMODO(Known Media Database) 主页截图



ARTICLE

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OPEN

Harnessing the landscape of microbial culture media to predict new organism-media pairings

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2015年10月发表在NC上的微生物培养基预测文章 (IF: 12.353)



意义：

目前环境中的微生物绝大多数（90%~99%）是不可培养的，因对不同微生物培养条件(尤其是培养基配方)的不了解，阻碍了微生物的分离培养。

随着高通量测序技术的发展，目前有大量文章是在做基于16S rDNA的微生物非培养（免培养）多样性，但拿不到菌种使得目标微生物的应用和机理研究成为空中楼阁。



意义：

这个网站可有依据的预测目标微生物的培养基配方，因此可将基于16S rDNA的微生物多样性数据与目标菌株的分离培养有机衔接起来，大大加速从生态研究到微生物资源挖掘的进程，研究思路如下图。

基于16S rDNA的微生物多样性研究

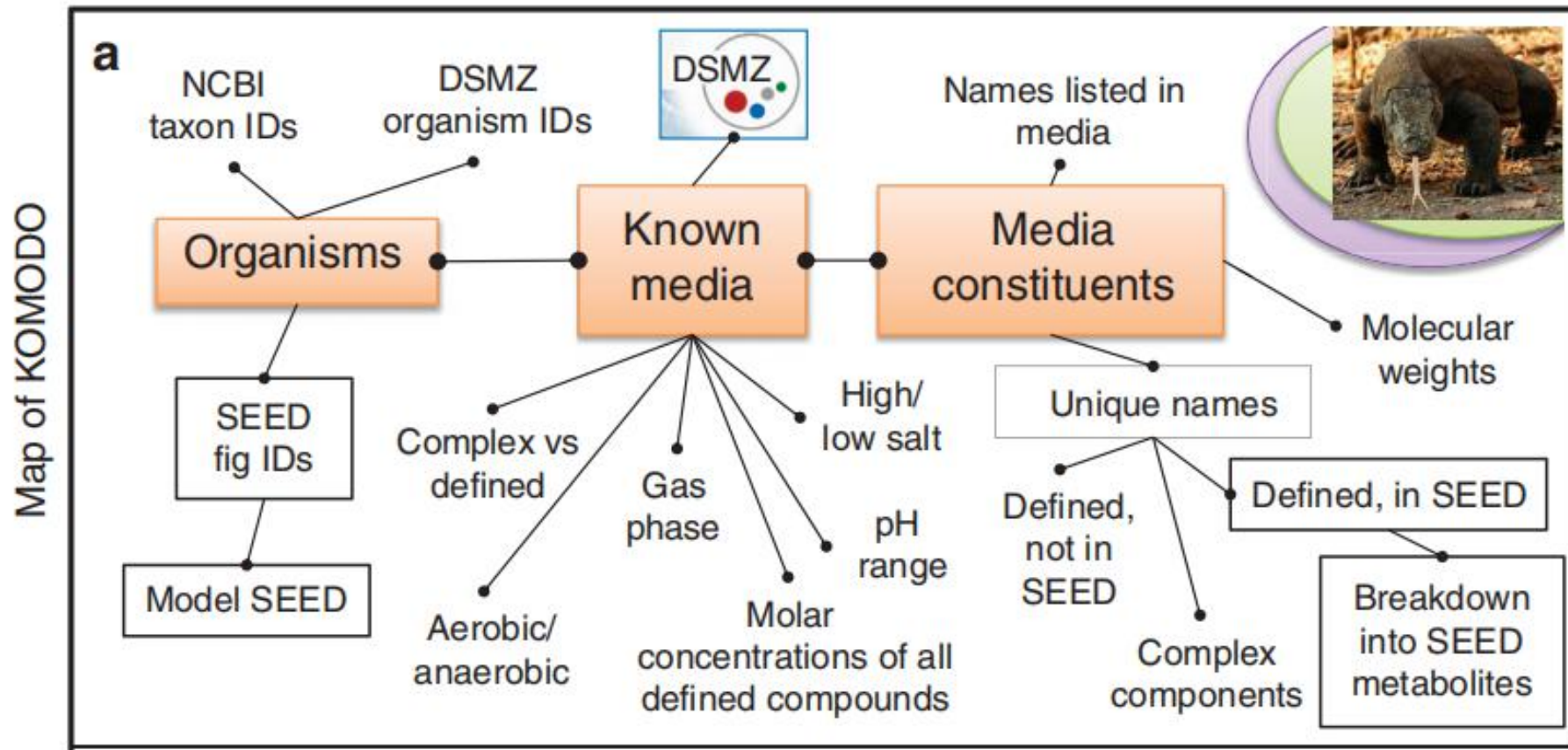
KOMODO预测目标
微生物培养基配方

目标微生物的选择性分离筛选

目标微生物的应用或功能机理研究

工作原理:

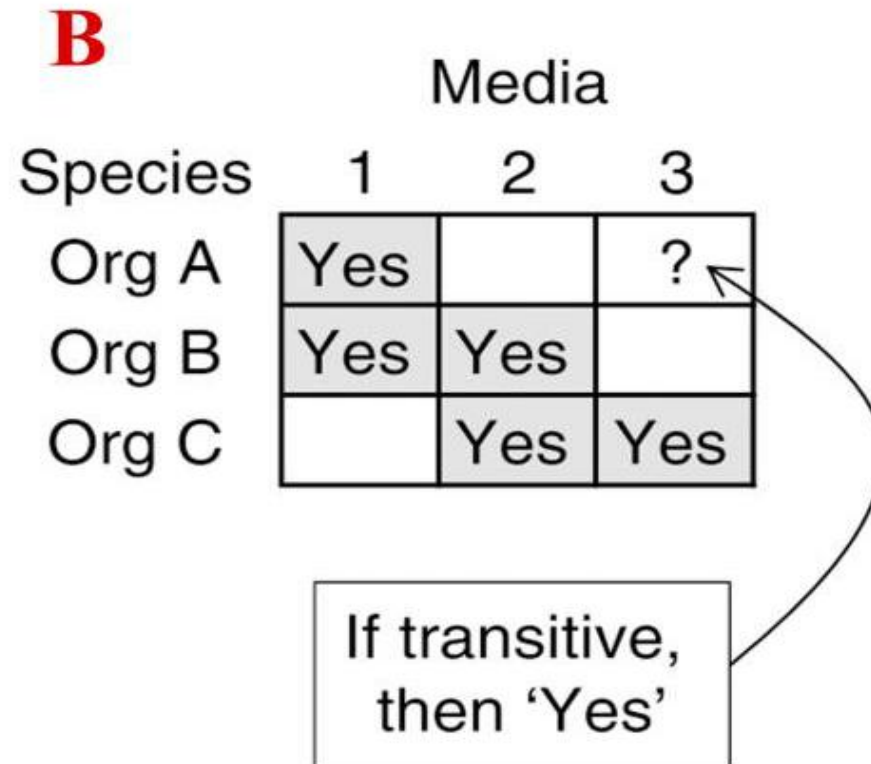
- 1、该网站结合了NCBI的微生物分类和微生物培养基数据库(DSMZ)等。



工作原理：

2、传递预测模式(Transitive prediction schema)：

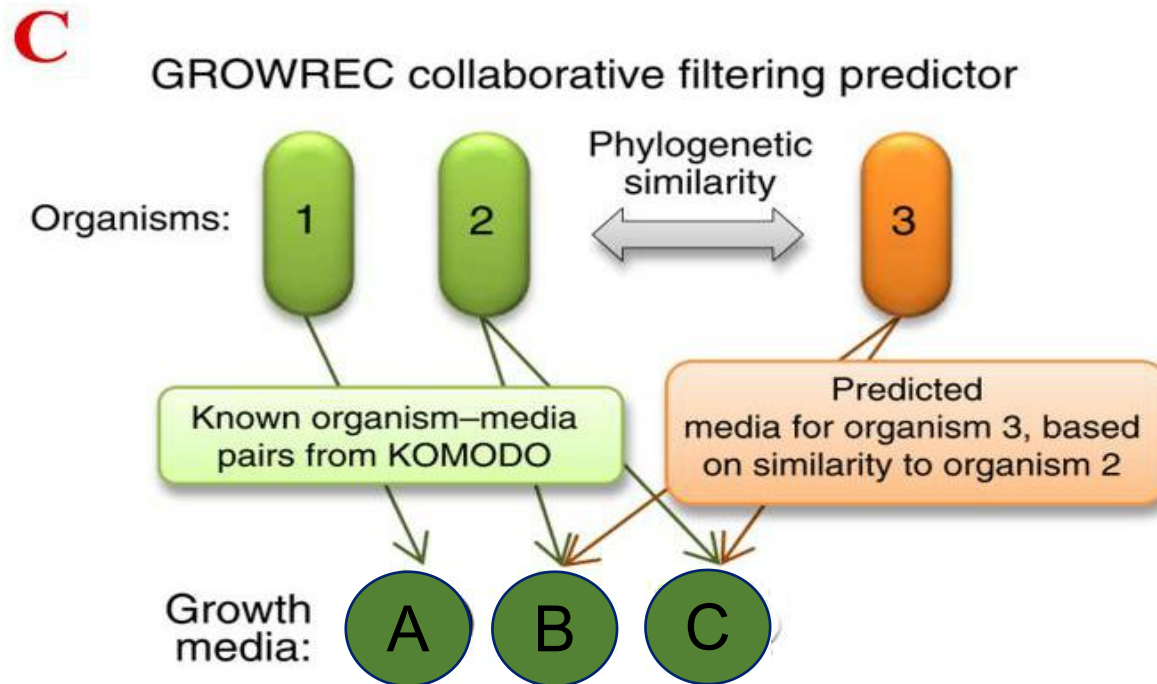
即若微生物A和B均可利用培养基1、微生物B和C可利用培养基2，微生物C可利用培养基3，那么依次传递推理，微生物A应该也可以利用培养基3。

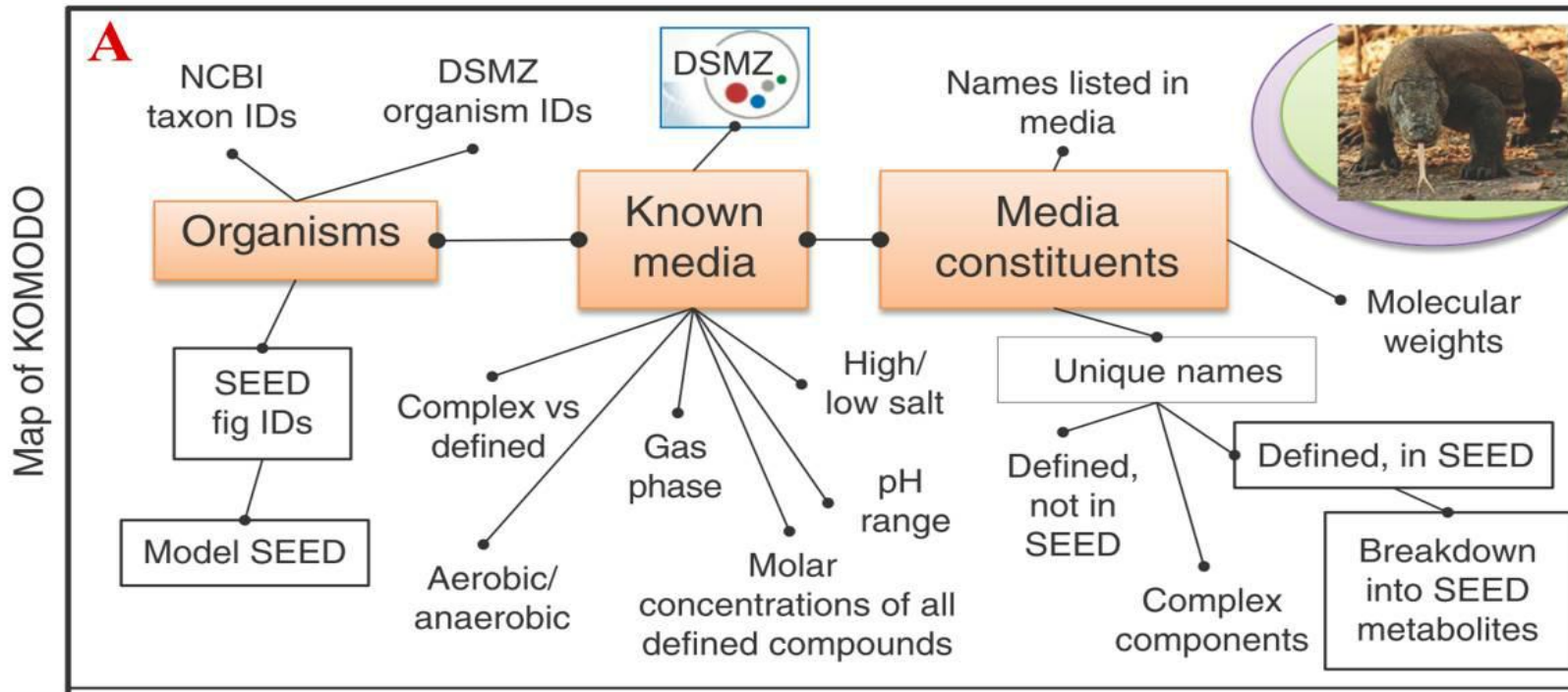


工作原理：

3、共同筛选预测(collaborative filtering predictor)：

即根据16S rDNA的系统进化相似性，根据已知培养基的物种来推断其相似性高的近缘物种的培养基。



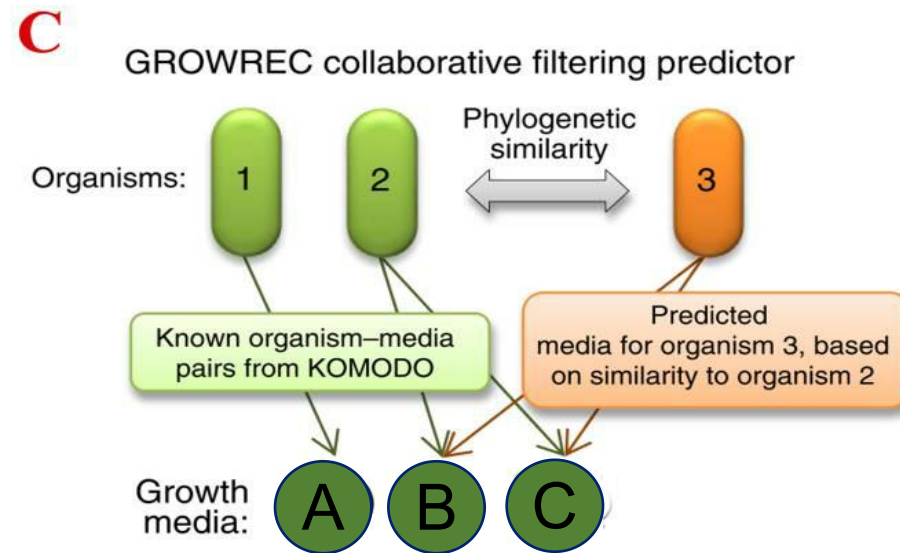


B

Media

Species	1	2	3
Org A	Yes		?
Org B	Yes	Yes	
Org C		Yes	Yes

If transitive, then 'Yes'



网站用法：

打开链接

(<http://delta-tomcat-vm.cs.tau.ac.il:40678/komodo/growrec.htm>) 进入KOMODO页面



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GROWREC: a media recommendation platform for microbes

Here we provide GROWREC, a tool that allows users to upload a 16S rDNA sequence or a NCBI taxon ID for any organism, and get predictions of likely lab media that the organism can grow on (from the known catalogue from DSMZ). The tool is based on collaborative filtering, an algorithm that is popularly employed by Amazon.com, Inc., to recommend products to consumers, based on products known to have been purchased by other consumers with similar past buying habits. Similarly, given an input 'test' organism for which we aim to predict growth media, we first select a set of organisms from within KOMODO that are phylogenetically close to the 'test' organism (which is not required to be in KOMODO); next, we integrate the known medium preferences of those organisms into a 'collaborative score' indicating the likelihood that the test organism will grow on a given medium. Please see the Overview page for more details.

Please note: If you upload a 16S rDNA sequence for prediction by GROWREC, we perform a BLAST search to look for the closest species that are in our database, in order to do analysis. If you upload an NCBI taxon ID, then you will get the results of GROWREC exactly as they are described in the source paper (Oberhardt & Zarecki et al.).

Phylogenetic distance

网站用法:

打开链接

(<http://delta-tomco>)

GROWREC M

Please enter information for
recommendation.
pressing the "Submit" will calcul

This operation may take a few

Is organism Aerobic (Ye

Does Organism gro

Maximal phyloge

NCBI taxon ID (

16S data (optional par

Blast 'Identities' Low Limit %

submit

Is organism A

(Yes|No)

况填写

填Yes或

Blast 'Identities' Low Limit % 表

示与你16S序列相似的最低限

是多少, 默认85%, 可根据实

际情况适当提高。

下面的16S data (optional parameter -

can be replaced by NCBI Taxon ID):两

者只能输入一个, 建议最好直接在

16S data右边的框里输入FASTA格式的

可。

COMODO页面

85.0

网站用法:

打开链接

(<http://delta-tomcat-vm.cs.tau.ac.il:40678/komodo/growrec.htm>) 进入KOMODO页面

GROWREC media recommendation system

Please enter information on the organism for which you want media recommendation.

pressing the "Submit" will calculate the recommended media entries.

This operation may take a few minutes

Is organism Aerobic (Yes|No|Unknown):

Does Organism grow in Salty Media (Yes|No|Unknown):

Maximal phylogenetic distance (range:0.0 - 1.0, default:0.04):

NCBI taxon ID (optional parameter - can be replaced by 16S data):

16S data (optional parameter - can be replaced by NCBI Taxon ID):

```
>gb|CP003466.1|:4098191-4099719 Alcanivorax dieselolei B5, complete genome
AGGTGATCCAGCCGAGGTTCCCTACGGTACCTTGTTACGACTTCACCCAGTCATGAACCACACCGT
GGTAATCGTCCCTCCGAAGGTTAGACTAACTACTTCTGGTGCAATCCACTCCCATGGTGTGACGGGCGGT
GTGTACAAGGCCCGGGAACGTATTCACCGCGGCATTCTGATCCGCGATTACTAGCGATTCCGACTTCATG
GAGTCGAGTTGCAGACTCCAATCCGACTACGATTGGCTTTGAGAGATTAGCTCCGCCTCGCGACTTCGC
AACCCCTCTGTACCAACCATTGTAGCACGTGTGTAGCCCAGGCCGTAAGGGCCATGATGACTTGACGTCGT
CCCCACCTTCTCCGGTTTGTACCGGCAGTCTCCCTAGAGTTCCACCCGAAGTGTGGCAACTAAGGA
CAAGGGTTGCGCTCGTTACGGGACTTAACCCAACATCTCAGGACAGGAGCTGACGACAGCCATGCAGCAC
CTGTCACTGCGTCCCGAAGGCACCAATCTATCTCTAGAAAAGTTCGAGGATGTCAAGGCCTGGTA^CTT
TCTTCGGTTGCATCGAATTAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCATTG
```

Blast 'Identities' Low Limit %

网站用法:



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GROWREC results

GROWREC input parameters

aerobic: Yes
salty environment: Yes
phylogenetic distance: 0.04
NCBI Taxon ID: NONE

16S Data:

```
>gb|CP003466.1|:4098191-4099719AlcanivoraxdieseloleiB5, completegenome  
AGGTGATCCAGCCGAGGTTCCCCTACGGCTACCTTGITAGACTTCACCCCAGTCATGAACCACACCGT  
GGTAATCGTCCCTCCCGAAGGTTAGACTAACTACTTCTGGTGCAATCCACTCCCATGGTGTGACGGGCGGT  
GTGTACAAGGCCCGGGAACGTATTCACCGCGGCATTCTGATCCGGGATTACTAGCGATTCCGACTTCATG  
GAGTCGAGTTGCAGACTCCAATCCGACTACGATTGGCTTTGAGAGATTAGCTCCGCCTCGCGACTTCGC  
AACCCCTCTGTACCAACCATTGTAGCACGTGTGTAGCCCAGGCCGTAAGGGCCATGATGACTTGACGTCGT  
CCCCACCTTCCTCCGGTTTGTACCGGCAGTCTCCCTAGAGTTCCCACCCGAAGTCTGGCAACTAAGGA  
CAAGGGTTGGCTCGTTACGGGACTTAACCCAACATCTCAGCACAGGCTGACGACAGCCATGCAGCAC  
CTGTCACTGCGTTCCCGAAGGCACCAATCTATCTAGAAAAGTTCGCAGGATGTCAAGGCCTGGTAAGGT  
TCTTCGCGTTGCATCGAATTAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCATTTGAGTT
```

Blast Identities low limit: 85.0

网站用法:

Media recommendations

fields explanation:

Name	Description
media_id	the id of the media as found in the DSMZ database.
media_name	the name of the media as found in the DSMZ database.
recommendation_score	the collaborative filtering algorithm score for this media - the higher the value the better is the recommendation.
link to media page	a link to the DSMZ media page, containing detailed instruction on how to build the media.

media_id	media_name	recommendation_score	link to media page
514	BACTO MARINE BROTH (DIFCO 2216)	82.04556603773584	http://www.dsmz.de/microorg
123	MARINE AGAR	18.232348008385742	http://www.dsmz.de/microorg
1176	HALOVIBRIO medium	9.116174004192871	http://www.dsmz.de/microorg
514b.6	For strains DSM 23437, DSM 23508, DSM23509, DSM 21076, DSM 26132	9.116174004192871	http://www.dsmz.de/microorg

网站会根据你填写的信息给出推荐的不同培养基，如上图例子中给出了四种培养基，点击培养基对应的链接可以直接下载PDF版的培养基配方，如下图PDF版推荐培养基示例：

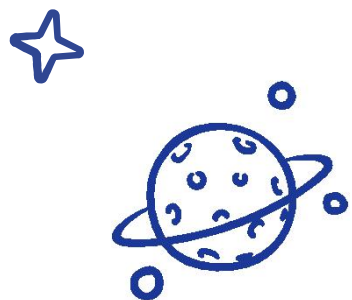


514. BACTO MARINE BROTH (DIFCO 2216)

Bacto peptone	5.00	g
Bacto yeast extract	1.00	g
Fe(III) citrate	0.10	g
NaCl	19.45	g
MgCl ₂ (anhydrous)	5.90	g
Na ₂ SO ₄	3.24	g
CaCl ₂	1.80	g
KCl	0.55	g
NaHCO ₃	0.16	g
KBr	0.08	g
SrCl ₂	34.00	mg
H ₃ BO ₃	22.00	mg
Na-silicate	4.00	mg
NaF	2.40	mg
(NH ₄)NO ₃	1.60	mg
Na ₂ HPO ₄	8.00	mg
Distilled water	1000.00	ml

Final pH should be 7.6 ± 0.2 at 25°C. If using the complete medium from Difco add 37.40 g to 1 litre water.

For [DSM 11879](#) and [DSM 16960](#) add to the medium after autoclaving 100 μ g Na₂SiO₃ · x H₂O from a stock solution sterilized by filtration. Check medium pH after autoclaving and adjust if necessary.



Thank You

敬请各位老师同学批评指正
