

Web resources for the Carbohydrate Chemist

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Stockholm University

roland@organ.su.se

SugaBase/CarbBank

<http://www.boc.chem.uu.nl/sugabase/databases.html>

Residue: C6 Sugar alpha D Man

Add
Add ?
Build
Remove
Unlink
Clear

Free Position: 2
Absolute: D D
M-Sub: Anhydro 2 3

Deoxy	Keto	Double bond
Anomeric: alpha	Ring: pyranose	
Substituent: NAc	Acid: Uronic	

CarbBank results

Query Results

Your query with the structure:

α -D-Manp-(1-6)- α -D-Manp

resulted in 459 hit(s)

Only the first 5 out of 459 hits are displayed!

Use 'Back' button to return to form

***** Hit 1 *****

CC: CCSD:4023

AU: Gunnarsson A; Svensson B; Nilsson B; Svensson S

TI: Structural studies on the O-glycosidically linked carbohydrate chains of glucoamylase G1 from *Aspergillus niger*

CT: Eur J Biochem (1984) 145: 463-467

FC: 19957e6c

BS: (GS) *Aspergillus niger*

AG: Threonine

SB: van Kuik A

DA: 06-02-1991

MT: O-linked glycoprotein

PM: glucoamylase G1

SI: CBank:4618

structure:

α -D-Manp-(1-6)- α -D-Manp-(1-3)-Ser

=====end of record

***** Hit 2 *****

CC: CCSD:8320

AU: Zopf DA; Tsai CM; Ginsburg V

TI: Antibodies against oligosaccharides

CT: ACS Symp Ser (1979) 88: 90-101

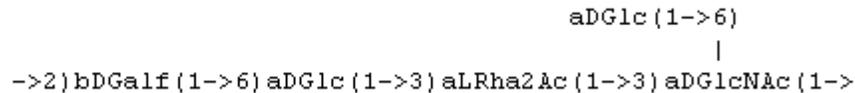
E. coli O-antigens

<http://www.casper.organ.su.se/ECODAB/>

ID	Serogroup	Serotype	Strain
<u>53</u>	O1A1		
			->3) aLRha (1->3) aLRha (1->3) bLRha (1->4) bDGlcNAc (1-> bDManNAc (1->2)
<u>82</u>	O1A		
			->3) aLRha (1->3) aLRha (1->3) bLRha (1->4) bDGlcNAc (1-> bDManNAc (1->2)
<u>54</u>	O1B	O1B:K1	A198
			->3) aLRha (1->2) aLRha (1->2) aDGal (1->3) bDGlcNAc (1-> bDManNAc (1->2)

Information about O-antigens

Structure



Structure

¹³C-NMR

107.2	87.5	76.8	83.4	71.4	64.2
98.1	72.1	74.1	70.2	71.4	66.7
99.7	69.7	74.5	71.7	69.9	17.7
96.5	54.0	80.8	69.6	72.6	67.4
99.3	72.7	74.3	70.8	73.1	61.8

NMR-data

Conditions Solvent: D2O; Temp.: 30C
Reference acetone=31.45ppm
Comment [1]

wzx (flippase)

TrEMBL entry [P37746](#)

Sequence

```
MNTNKLRLRRNVIYLAVVQGSNYLLPLLPFVYLVRTLGPENPGIPGFCQATMLYMIMPVE  
YGFNLTATQSIAKAADS KDKVTSIPWAVIPSKIVLIVITLIPLTSMTLLVPEYKHAVII  
WSPVPALVGNLIYPIWLPQCKEKMKWLTLSILSRLAIIPLTFIVNTKSDIAIAGPIQS  
SANTLVAGIIALAIVVHEGWIGKVTLSLHNVRRLADGFRVFI STSAISLYSTGIVII LGP  
ISGPTSVGNPNAANTIRNALQGLNPI TQAIYFRISSTLVINRVKGVILIKKSLTCLSLI  
GGAPSLIILLGASILVKISIGPCYDNAVIVLMIISPLPFLISLSNVYGIQVMLTRNYKKE  
PSKILIAAGLLSLLLIPPLTTLFKEIGAAITLLATECLVTSIMLMFVRNKKLLVC
```

Genetic information

References [1] J. Bacteriol. 176 (1994) 4144-4156 [[PubMed 7517391](#)]

Links to PubMed

CASPER

<http://www.casper.org.se/casper>

 **CASPER** 

Home Research Analysis ECDB **CASPER** Ke3690

Welcome *Help* *Simulate* *Determine Sequence*

Title
Source

Residue	Linkage position					
	1	2	3	4	5	6
<input type="text" value="D-Glcp"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>				
<input type="text" value="none"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
<input type="text" value="none"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
<input type="text" value="none"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
<input type="text" value="none"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
<input type="text" value="none"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
<input type="text" value="none"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>

Chemical shifts ^{13}C ^1H

Correct by subtracting ppm

Number of shifts - Required: Actual:

Minimum number of coupling constants of different magnitudes

	small	medium	large
$^3J_{\text{HH}}$	<input type="text" value="0"/> (<2 Hz)	<input type="text" value="0"/> (2-7 Hz)	<input type="text" value="0"/> (>7 Hz)
$^1J_{\text{CH}}$	<input type="text" value="0"/> (<169 Hz)		<input type="text" value="0"/> (>169 Hz)

As MIME

CASPER

Simulated structure

->6)aDGlcⁱ(1->

->6)aDGlc ⁱ (1->	98.90	72.39	74.32	70.66	71.28	66.90	
	4.97	3.59	3.74	3.54	3.90	3.98	3.77

Assignment of ¹³C resonances

	Experimental	Simulated	Exp-Sim	Assignment
	99.00	98.90	0.10	aDGlc ⁱ - 1
	74.50	74.32	0.18	aDGlc ⁱ - 3
	72.50	72.39	0.11	aDGlc ⁱ - 2
	71.30	71.28	0.02	aDGlc ⁱ - 5
	70.70	70.66	0.04	aDGlc ⁱ - 4
	66.70	66.90	-0.20	aDGlc ⁱ - 6

Error=0.65 ppm (0.11/shift), Systematic error=0.04 ppm, RMS error=0.13 ppm

Experimental structure

->6)aDGlcⁱ(1->

->6)aDGlc ⁱ (1->	99.00	72.50	74.50	70.70	71.30	66.70	
	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.

JCAMP-format

GlyTorsion

<http://www.glycosciences.de/tools/glytorsion/>

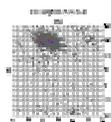
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GlyTorsion: Analysis of Carbohydrate Torsion Angles found in the Protein Data Bank (PDB)



Introduction

Such as protein conformation can be described by the backbone torsion angles, a carbohydrate structure is mainly characterised by its linkage torsions. With the aid of **pdb2linucs**, a dataset of carbohydrate torsion angles was derived from from carbohydrate structures found in the PDB.

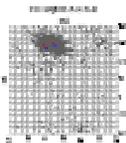
This weekly updated dataset contains, besides linkage torsions, also ring torsions, omega torsions, N-acetyl group torsions and sidechain torsions of Asn residues involved in Glycan bonds. It can be queried by *GlyTorsion*.

The same data is used by **carp** to generate PDB-derived plot backgrounds.

Contact: [Thomas Lütteke](#)

[References](#)

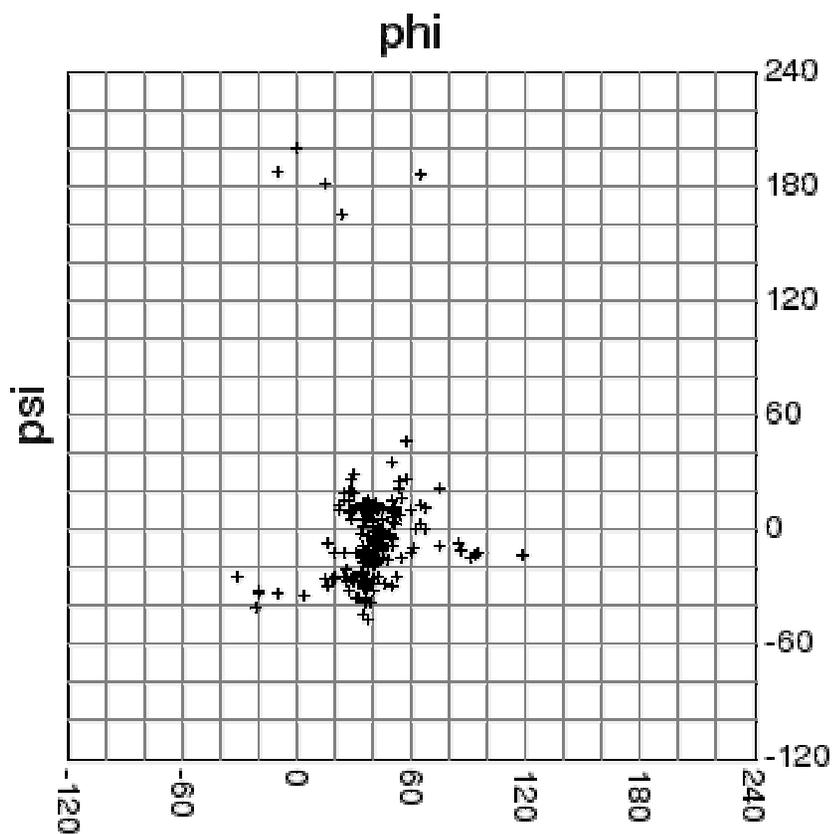
- [General Settings](#)
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- [Ring / Omega Torsion Analysis](#)
- [NAc Torsion Analysis](#)
- [ASN Torsion Analysis](#)



GlyTorsion Analysis Results

Linkage Torsion Analysis: β -D-Glcp-(1-4)- α -D-Glcp

Torsions analysed: 194



Glyco3D

<http://www.cermav.cnrs.fr/glyco3d/index.php>



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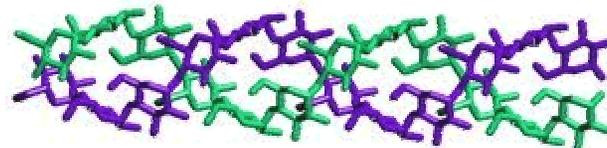
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GLYCO3D

A site for glycosciences



BP 53 - 38041 Grenoble Cedex 9 - France

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tél : 33 (0)4 76 03 76 03 - fax : 33 (0)4 76 54 72 03

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Cellulose



SUMMARY

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Chemical structure of the cellulose macromolecule
Crystallinity and polymorphism of cellulose
Crystalline structures of native celluloses
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Crystallines microfibrils of native cellulose
Microfibril organization
Conclusions
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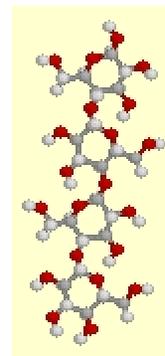


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STRUCTURE AND MORPHOLOGY OF CELLULOSE

Serge Pérez



William Mackie

Recommended viewing is full-screen 800x600 resolution or better !!

Monographs @ CERMAV

Modeling Polysaccharides: Present Status & Challenges

Serge Pérez¹, Milou Kouwijzer¹,
Karim Mazeau¹ & Søren Balling Engelsen²

¹Centre de Recherches sur les Macromolécules, CNRS,
BP 53, F-38041 Grenoble cedex 09, France

associated with Université Joseph Fourier, Grenoble, France

²The Royal Veterinary and Agricultural University, Food Technology,
Rolighedsvej 30, DK-1958 Frederiksberg C, Denmark

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[The ordered state of polysaccharides](#) [Conclusions](#) [References](#)

Introduction

Carbohydrates constitute one of the most abundant types of biomolecules occurring widely in all living matter. They function as structural or protective materials and as an energy storage. In addition, carbohydrates perform a much broader biological role [1]. For example, they appear to be essential in the process of infection by certain pathogenic

Glycan Binding Proteins

www.functionalglycomics.org/glycomics/molecule/jsp/gbpMolecule-home.jsp

Glycan Binding Proteins

The Glycan Binding Proteins (GBP) Molecule Page interface provides an integrated presentation of information from public databases and the Scientific Cores of the Consortium. The data from the Consortium is integrated with a given GBP molecule page via search interfaces that search for all the publicly accessible data pertaining to that GBP. There are a few fields colored in cyan that will be filled in by experts and will become available as they are completed. Please click on any of the families and subfamilies of GBPs below to obtain access to the individual molecule pages. [How To Navigate](#)

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- [Proteoglycan core proteins \(Group 1\)](#)
 - [Type II membrane receptors \(Group 2\)](#)
 - [Collectins \(Group 3\)](#)
 - [Selectins \(Group 4\)](#)
- [C-Type lectins\[110\]](#)

Glycan Binding Proteins

www.functionalglycomics.org/glycomics/molecule/jsp/gbpMolecule-home.jsp



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General

Reference

Genome

Proteome

Glycome

Biology

Neurocan (Human)

CFG ID	cbp_hum_Ctlect_213
GBP Name	Neurocan
Category	C-Type Lectin Family
Sub-Family	1-Proteoglycan
Other Names	Neurocan core protein [Precursor], Chondroitin sulfate proteoglycan 3
Species	Human
Summary	
Date Updated	05/24/2004
Email	glycomics-web@mit.edu

Glycosciences.de

<http://www.glycosciences.de>

GLYCO-SCIENCES.DE

dkfz.

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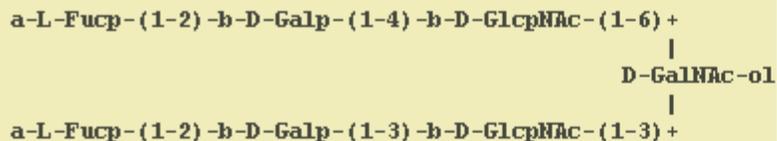
Click [here](#) to reset input.

with 3D-Co-ordinates (Sweet2) | with NMR data | max # residues | min # residues

with PDB entries | min. resolution | all chains | all methods

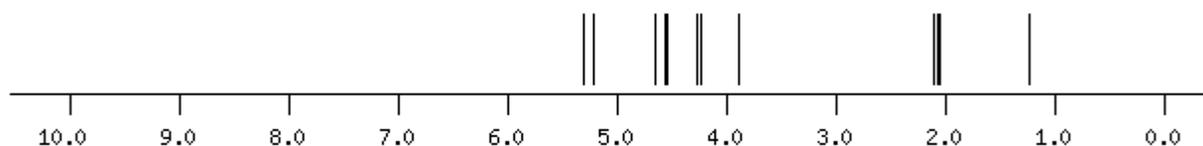
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Structure for LinucsID 8955



SugaBase - NMR-data

NMR ProtonChemical Shift Info for LinucsID 8955



MHZ	500						
Temperature	300						
Solvent	D2O						
Residue	Linkage	Proton	PPM	JFrom	JTo	Hz	Note
D-GalNAc-ol		H-2	4.26			0	
D-GalNAc-ol		H-5	4.22			0	
D-GalNAc-ol		NAc	2.042			0	
β -D-GlcpNAc	6	H-1	4.551			0	
β -D-GlcpNAc	6	NAc	2.065			0	
β -D-Galp	4,6	H-1	4.535			0	
β -D-Galp	4,6	H-4	3.89			0	
α -L-Fucp	2,4,6	H-1	5.304			0	
α -L-Fucp	2,4,6	H-5	4.224			0	

SweetDB – Bibliographic information (from CarbBank)

Found 2 References for **LinucsID 8955**

Primary structure of neutral oligosaccharides derived from respiratory mucus glycoproteins of a patient suffering from bronchiectasis, determined by combination of 500-MHz ¹H-NMR spectroscopy and quantitative sugar analysis 2. Structure of 19 oligosaccha

Breg J; van Halbeek H; Vliegenthart JFG; Klein A; Lamblin G; Roussel P
Published 1988 in Eur J Biochem, 171: 643-654

Reference contains 1 structure.

Structures

PubMed



subito



Separation of mucin oligosaccharide-alditols by high performance liquid chromatography on alkylamine-bonded silica columns. Effects of structural parameters

Klein A; Carnoy C; Lo-Guidice JM; Lamblin G; Roussel P
Published 1992 in Carbohydr Res, 236: 9-16

Reference contains 42 structures.

Structures

PubMed



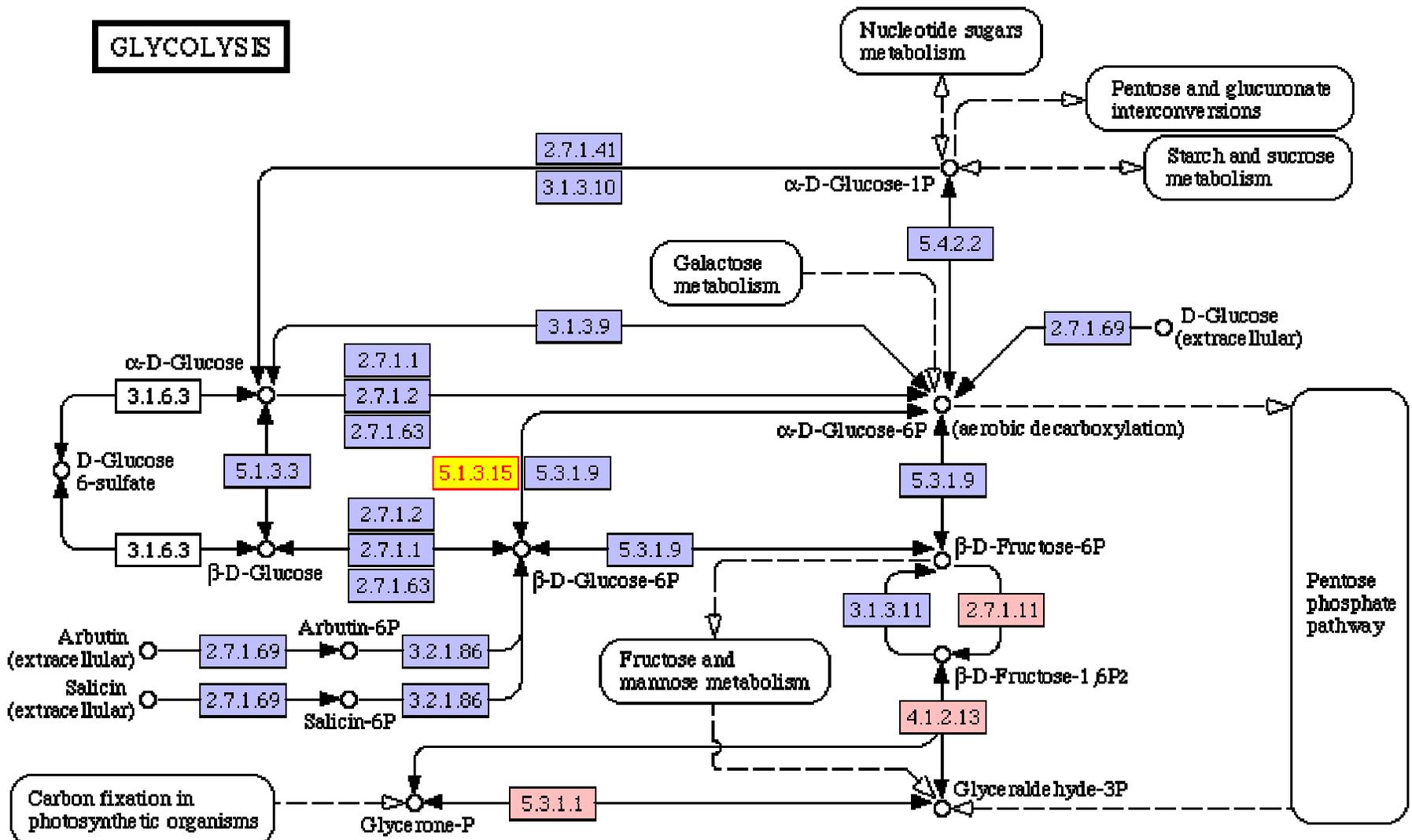
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KEGG - Kyoto Encyclopedia of Genes and Genomes

<http://www.genome.jp/kegg/>



Bacterial Polysaccharide Gene Database

<http://www.microbio.usyd.edu.au/BPGD/default.htm>

ECOLI EPS ECA gene cluster

This record was created on 14 May 1996 and released on 19 December 1996.

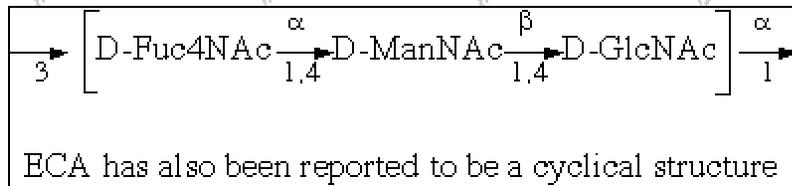
Biological source

Escherichia coli, strain K-12

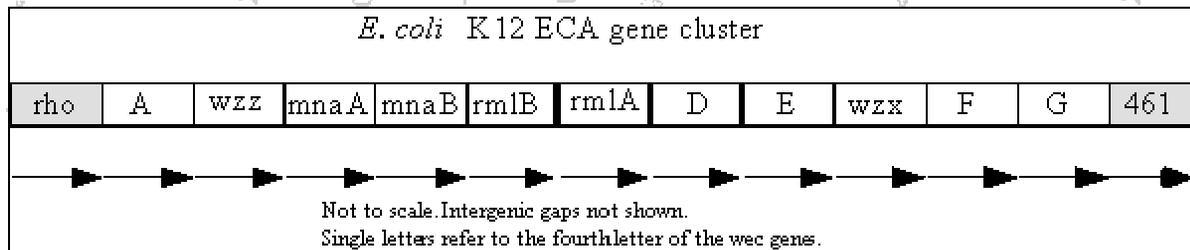
Description of polysaccharide

EPS: enterobacterial common antigen

Polysaccharide structure



Genetic map



IUPAC nomenclature

<http://www.chem.qmul.ac.uk/iupac>



INTERNATIONAL UNION OF PURE AND APPLIED CHEMISTRY

Recommendations on Organic & Biochemical Nomenclature, Symbols & Terminology etc.

<http://www.chem.qmul.ac.uk/iupac/>

World Wide Web material prepared by G. P. Moss

[Department of Chemistry, Queen Mary University of London,](#)

Mile End Road, London, E1 4NS, UK

g.p.moss@qmul.ac.uk

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Structural analysis

<http://www.casper.organ.su.se/sop/>



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Ke3690

Structural analysis of carbohydrates

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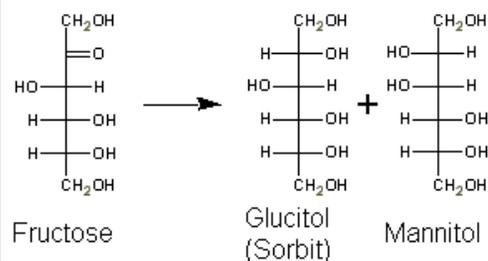
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Sugar analysis using alditol acetates

Introduction

The hydrolysis of glycosides and polysaccharides to reducing sugars and the concomitant conversion to alditol acetates (borohydride reduction and acetylation) is a standard method to analyse polysaccharides containing aldoses, ketoses, deoxyaldoses, and acetamidohexoses and other related sugars. Sugars that cannot be observed with this analysis are uronic acids, ulosonic acids (*e.g.* Kdo), 4-aminosugars, or charged species like phosphorylated sugars which may arise in a hydrolysate. The acids are not observed because the sodium salt of the acid that is formed on addition of NaBH_4 is not volatile. Of special concern is the difference in rate of hydrolysis between sugars. Thus, uronic acids are seldom completely hydrolysed and the sugar that the uronic acid is linked to is underrepresented. 2-Acetamidohexoses undergo partial *N*-deacetylation and the resulting 2-aminosugars are not hydrolysed at all and both the 2-aminosugar and the sugar to which it is linked are underrepresented. Normally, yields of 60-80% are obtained. 4-acetamido sugars are hydrolysed to pyrrole derivatives which are polymerised and such sugars are therefore not observed. Methanolysis is however possible with 4-acetamido sugars.

Note that all ketoses on reduction are expected to yield approximately equal amounts of both the *R*- and the *S*-isomer, which may or may not separate on GLC analysis. Thus, fructose gives an equimolar mixture of glucitol and mannitol.



Contemporary Carbohydrate Chemistry

<http://web.uct.ac.za/depts/cem/ccc/index.htm>

"CONTEMPORARY CARBOHYDRATE CHEMISTRY" by A M Stephen

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In mid-2003, the Chemistry Department of the University of Cape Town approved the placing of "Contemporary Carbohydrate Chemistry" on their server. Under the direction of Professor Georges R Delpierre (GRD TRAINING CORPORATION, P.O. Box 37838, Vallyland, 7978, South Africa), whose guidance and assistance have been invaluable and deeply appreciated, this work has been completed.

We are grateful for the invaluable help of the librarians of the University of Cape Town, the financial input of the J Murray Hofmeyr Charitable Trust, and the co-operation of Professor A L Rodgers (Head of the Department of Chemistry) and Mr Klaus Achleitner, (Webmaster). The advice and encouragement given by Professor Stephen G Wilkinson (Hull) is greatly valued, and I thank Helen Stephen most sincerely for much of the typing and her patience.

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Essentials of Glycobiology

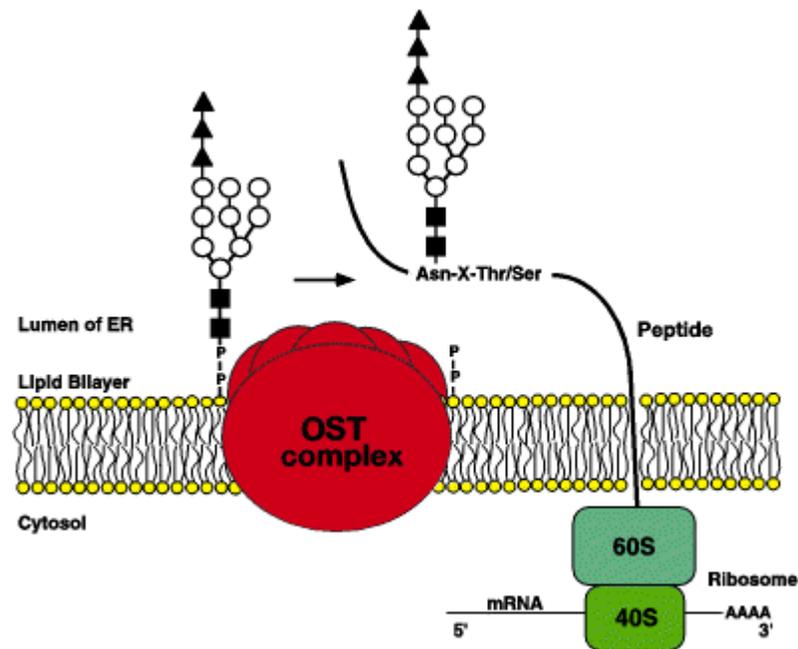
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Hudson Freeze, Gerald Hart, Jamey Marth



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