

Report of ssn-clustering run 2206101141

Metadata

CD-HIT threshold: 99%

Length filter: min 320, max 600

Expansion threshold: e-value 1e-15

SSN threshold: score 110

Info

Total number of proteins in network: 6176

Number of singletons: 46

Number of nodes in clusters: 6130

Number of clusters: 205

[File with accessions in each cluster](#)

Number of different taxonomical ranks before and after expansion:

	kingdom	phylum	class	order	family	genus	species
before	1	2	2	4	5	10	15
after	1	42	52	95	200	610	2359

Navigation

[8\(548\)](#) [3\(478\)](#) [32\(270\)](#) [15\(258\)](#) [9\(240\)](#) [11\(152\)](#) [6\(139\)](#) [29\(136\)](#) [23\(134\)](#) [50\(129\)](#) [33\(129\)](#) [39\(119\)](#) [2\(107\)](#) [46\(91\)](#) [1\(89\)](#) [44\(83\)](#) [37\(82\)](#) [67\(71\)](#) [27\(67\)](#) [68\(66\)](#) [12\(66\)](#) [56\(59\)](#) [36\(59\)](#) [21\(58\)](#) [75\(51\)](#) [17\(48\)](#) [22\(46\)](#) [58\(45\)](#) [57\(43\)](#) [31\(43\)](#) [79\(42\)](#) [53\(41\)](#) [48\(41\)](#) [13\(40\)](#) [63\(39\)](#) [84\(37\)](#) [43\(37\)](#) [94\(36\)](#) [65\(36\)](#) [171\(36\)](#) [66\(35\)](#) [4\(34\)](#) [93\(33\)](#) [59\(33\)](#) [73\(29\)](#) [72\(29\)](#) [54\(28\)](#) [41\(26\)](#) [28\(25\)](#) [98\(24\)](#) [25\(24\)](#) [69\(23\)](#) [81\(22\)](#) [40\(22\)](#) [24\(22\)](#) [91\(21\)](#) [89\(21\)](#) [80\(21\)](#) [123\(21\)](#) [101\(21\)](#) [62\(20\)](#) [126\(20\)](#) [77\(19\)](#) [145\(19\)](#) [86\(18\)](#) [158\(18\)](#) [144\(18\)](#) [141\(18\)](#) [116\(18\)](#) [113\(18\)](#) [99\(17\)](#) [95\(17\)](#) [42\(17\)](#) [177\(17\)](#) [162\(17\)](#) [140\(17\)](#) [61\(16\)](#) [51\(16\)](#) [38\(16\)](#) [157\(16\)](#) [14\(16\)](#) [139\(16\)](#) [138\(16\)](#) [129\(16\)](#) [125\(16\)](#) [104\(16\)](#) [96\(15\)](#) [88\(15\)](#) [70\(15\)](#) [26\(15\)](#) [164\(15\)](#) [130\(15\)](#) [110\(15\)](#) [55\(14\)](#) [30\(14\)](#) [19\(14\)](#) [154\(14\)](#) [121\(14\)](#) [120\(14\)](#) [115\(14\)](#) [60\(13\)](#) [47\(13\)](#) [45\(13\)](#) [173\(13\)](#) [20\(12\)](#) [180\(12\)](#) [124\(12\)](#) [102\(12\)](#) [198\(11\)](#) [163\(11\)](#) [149\(11\)](#) [147\(11\)](#) [76\(10\)](#) [5\(10\)](#) [49\(10\)](#) [35\(10\)](#) [34\(10\)](#) [174\(10\)](#) [153\(10\)](#) [150\(10\)](#) [112\(10\)](#) [105\(10\)](#) [85\(9\)](#) [190\(9\)](#) [179\(9\)](#) [168\(9\)](#) [161\(9\)](#) [155\(9\)](#) [146\(9\)](#) [119\(9\)](#) [97\(8\)](#) [78\(8\)](#) [71\(8\)](#) [166\(8\)](#) [152\(8\)](#) [148\(8\)](#) [135\(8\)](#) [128\(8\)](#) [127\(8\)](#) [114\(8\)](#) [7\(7\)](#) [199\(7\)](#) [186\(7\)](#) [181\(7\)](#) [18\(7\)](#) [176\(7\)](#) [170\(7\)](#) [169\(7\)](#) [160\(7\)](#) [143\(7\)](#) [133\(7\)](#) [132\(7\)](#) [111\(7\)](#) [10\(7\)](#) [16\(6\)](#) [156\(6\)](#) [142\(6\)](#) [136\(6\)](#) [118\(6\)](#) [106\(6\)](#) [103\(6\)](#) [74\(5\)](#) [64\(5\)](#) [202\(5\)](#) [137\(5\)](#) [100\(5\)](#) [92\(4\)](#) [87\(4\)](#) [204\(4\)](#) [200\(4\)](#) [192\(4\)](#) [191\(4\)](#) [184\(4\)](#) [159\(4\)](#) [131\(4\)](#) [108\(4\)](#) [107\(4\)](#) [90\(3\)](#) [203\(3\)](#) [201\(3\)](#) [196\(3\)](#) [195\(3\)](#) [194\(3\)](#) [183\(3\)](#) [167\(3\)](#) [165\(3\)](#) [134\(3\)](#) [122\(3\)](#) [117\(3\)](#) [109\(3\)](#) [83\(2\)](#) [82\(2\)](#) [52\(2\)](#) [205\(2\)](#) [197\(2\)](#) [193\(2\)](#) [189\(2\)](#) [188\(2\)](#) [187\(2\)](#) [185\(2\)](#) [182\(2\)](#) [178\(2\)](#) [175\(2\)](#) [172\(2\)](#) [151\(2\)](#)

Clusters

Cluster 8

Total number of members in cluster: 548

Average length of proteins in cluster: 448.2

Conserved (non-aliphatic) residues:

Y 160 (98.4%) Y 275 (100.0%) Y 295 (97.8%) Y 331 (98.5%) R 338 (100.0%) R 382 (100.0%) Y 383 (99.8%) D 415 (97.4%) S 418 (99.1%) N 473 (98.9%) T 479 (99.8%) S 506 (97.8%) T 508 (99.5%) S 512 (97.8%) D 538 (99.5%) R 578 (99.6%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
AAC45844.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O8	1
ACF61556.1	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	ssp. enterica sv. Newport	1
ACF69242.1	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Heidelberg	1
WP_000055605.1	Enterobacterales	Enterobacteriaceae	Salmonella	nan	ssp. enterica sv. Kentucky O8 98/39	1
ACF89798.1	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Schwarzengrund	1
ACH73921.1	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Dublin	1
ACH50550.1	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Agona	1
CAS11643.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O127	1
CAR10598.2	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O81	1
BAI33073.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O103	1
ADT77417.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O6	1

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

[Logoplot](#)

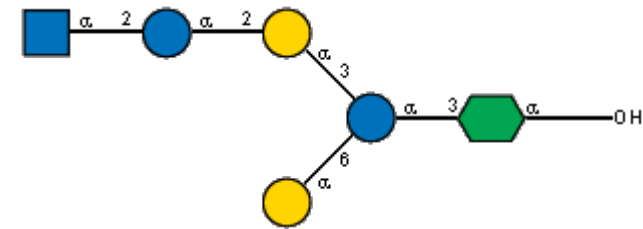
[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

Sugars for blast hits:

CAB3270026.1 Salmonella enterica Typhimurium:



CSDB record ID: 911

Alphafold models:

[ACH50550.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (491)	Enterobacteriaceae (235)	Enterobacter (60)
		Escherichia (35)
		Salmonella (23)
		Citrobacter (22)
		Klebsiella (13)
		Cronobacter (11)
		Kosakonia (8)
		Cedecea (7)
		Buttiauxella (6)
		Kluyvera (4)
		Raoultella (4)
		Leclercia (4)
		Pseudocitrobacter (3)
		Pluralibacter (3)
		Lelliottia (3)
		Trabulsiella (2)
		Phytobacter (2)
		Atlantibacter (2)
		Franconibacter (2)
		Mangrovibacter (2)
		Candidatus Symbiopectobacterium (2)
		Yokenella (1)
		Scandinavium (1)
		Tenebrionibacter (1)
		Siccibacter (1)
		Shigella (1)
		Plesiomonas (1)
	Yersiniaceae (70)	Serratia (32)
		Yersinia (19)
		Rahnella (9)
		Rouxiella (4)
		Chimaeribacter (2)
		Candidatus Fukatsuia (1)

order (count)	family (count)	genus (count)
Pasteurellales (42)	Morganellaceae (65)	Ewingella (1)
		Nissabacter (1)
		Xenorhabdus (20)
		Proteus (13)
		Providencia (12)
		Photorhabdus (10)
		Morganella (5)
		Arsenophonus (4)
		Moellerella (1)
	Pectobacteriaceae (54)	Dickeya (21)
		Pectobacterium (19)
		Brenneria (6)
		Lonsdalea (5)
		Affinibrenneria (1)
		Samsonia (1)
		Musicola (1)
	Erwiniaceae (52)	Pantoea (25)
		Erwinia (16)
		nan (6)
		Tatumella (4)
		Mixta (3)
		Izhakiella (2)
		Phaseolibacter (1)
	Hafniaceae (9)	Hafnia (4)
		Edwardsiella (3)
		Enterobacillus (1)
	Budviciaceae (3)	Obesumbacterium (1)
		Jinshanibacter (1)
		Pragia (1)
	Bruguierivoracaceae (2)	Budvicia (1)
	Pasteurellaceae (42)	Sodalis (2)
		Glaesserella (13)
		Actinobacillus (8)
		Mannheimia (7)
		Haemophilus (3)
		Ursidibacter (2)
		Bibersteinia (2)
		Lonepinella (1)
		Nicoletella (1)
		Muribacter (1)
		Otariodibacter (1)
		Paraburkholderia (3)
Burkholderiales (5)	Burkholderiaceae (5)	Mycoavidus (2)
Vibrionales (3)	Vibrionaceae (3)	Vibrio (2)
		Aliivibrio (1)
Pseudomonadales (2)	Pseudomonadaceae (2)	Pseudomonas (2)

order (count)	family (count)	genus (count)
Flavobacteriales (1)	nan (2)	nan (6)
Alteromonadales (1)	Pseudoalteromonadaceae (1)	Flocculibacter (1)
Moraxellales (1)	Moraxellaceae (1)	Acinetobacter (1)
Xanthomonadales (1)	Rhodanobacteraceae (1)	Dyella (1)
nan (1)	nan (2)	nan (6)

[top](#)

Cluster 3

Total number of members in cluster: 478

Average length of proteins in cluster: 398.0

Conserved (non-aliphatic) residues:

R 824 (98.3%) R 1156 (100.0%) D 1224 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
CAI33309.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	13	0
CAI33441.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	16A	0
CAI34080.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	29	0
CAI34348.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	35F	0
CAI34286.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	35A	0
CAI34310.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	35B	0
CAI34328.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	35C	0
CAI34369.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	36	0
CAI34519.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	42	0
CAI34657.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	47F	0

[MSA fasta](#)

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[Fasta of members](#)

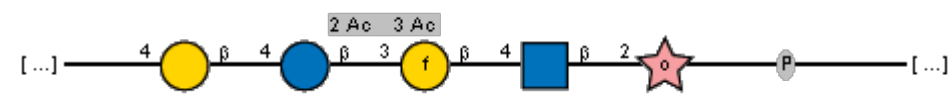
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

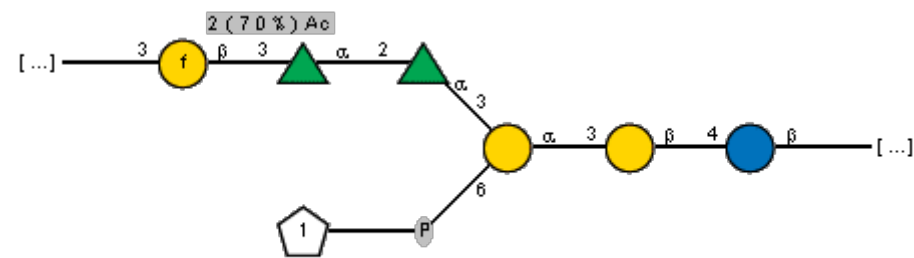
Sugars in cluster:

CAI33309.1 Streptococcus pneumoniae 13:



CSDB record ID: 7061

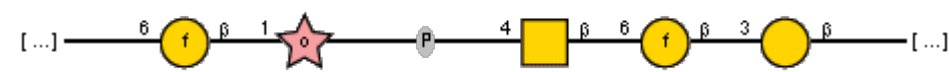
CAI33441.1 Streptococcus pneumoniae 16A:



1 = Gro

CSDB record ID: 1490

CAI34080.1 Streptococcus pneumoniae 29:



CSDB record ID: 1227

CAI34348.1 Streptococcus pneumoniae 35F:



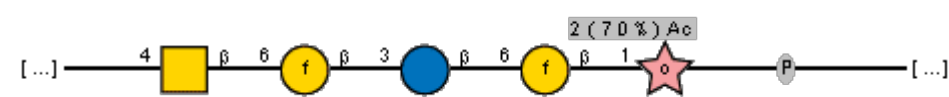
CSDB record ID: 7095

CAI34286.1 Streptococcus pneumoniae 35A:



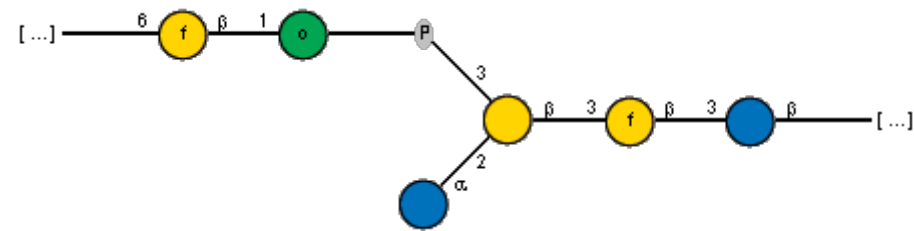
CSDB record ID: 1611

CAI34310.1 Streptococcus pneumoniae 35B:



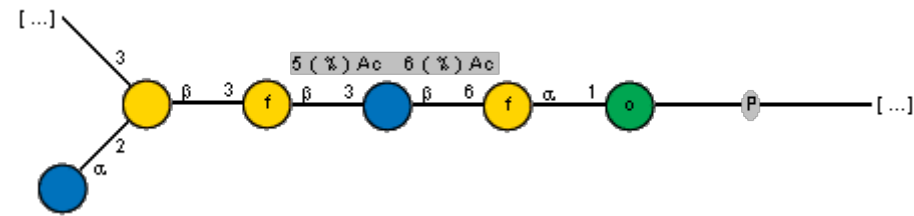
CSDB record ID: 1609

CAI34328.1 Streptococcus pneumoniae 35C:



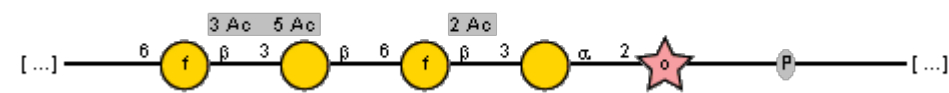
CSDB record ID: 7097

CAI34519.1 Streptococcus pneumoniae 42:



CSDB record ID: 25003

CAI34657.1 Streptococcus pneumoniae 47F:



CSDB record ID: 25005

Sugars for blast hits:

Alphafold models:

[CAI33309.1](#)

[CAI34369.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Lactobacillales (301)	Lactobacillaceae (170)	Limosilactobacillus (67)
		Lactiplantibacillus (31)
		Ligilactobacillus (18)
		Lactobacillus (15)
		Loigolactobacillus (9)
		Pediococcus (8)
		Liquorilactobacillus (6)
		Levilactobacillus (3)
		Lacticaseibacillus (3)
		Companilactobacillus (3)
		Latilactobacillus (2)
		Paucilactobacillus (2)
		Fructilactobacillus (1)
		Streptococcaceae (129)
		Streptococcus (129)

order (count)	family (count)	genus (count)
	Enterococcaceae (1)	Bavariicoccus (1)
Eubacteriales (138)	Lachnospiraceae (87)	nan (19)
		Coprococcus (9)
		Blautia (6)
		Mediterraneibacter (3)
		Oribacterium (3)
		Lachnoclostridium (2)
		Enterocloster (2)
		Dorea (2)
		Bilifactor (2)
		Lacrimispora (1)
		Muricomes (1)
		Luxibacter (1)
		Bariatricus (1)
		Kineothrix (1)
		Butyrivibrio (1)
		Anaerostipes (1)
		Faecalicatena (1)
		Fusicatenibacter (1)
		Lachnospira (1)
		Parasporobacterium (1)
		Roseburia (1)
		Eisenbergiella (1)
	Clostridiaceae (13)	Clostridium (9)
	Eubacteriaceae (13)	Eubacterium (7)
		Pseudoramibacter (6)
	Oscillospiraceae (12)	Ruminococcus (4)
		Pseudoflavonifractor (1)
Pasteurellales (10)	Pasteurellaceae (10)	Haemophilus (7)
		Gallibacterium (2)
		Rodentibacter (1)
nan (6)	nan (10)	Sedimentibacter (1)
Coriobacteriales (5)	Atopobiaceae (3)	nan (19)
		Atopobium (1)
	Coriobacteriaceae (2)	Collinsella (1)
Bacteroidales (4)	nan (10)	nan (19)
	Bacteroidaceae (3)	Phocaeicola (2)
		Bacteroides (1)
Erysipelotrichales (4)	Coprobacillaceae (2)	Eggerthia (1)
		Sharpea (1)
	Erysipelotrichaceae (2)	Solobacterium (2)
Bacillales (3)	nan (10)	Gemella (3)
Bifidobacteriales (2)	Bifidobacteriaceae (2)	Bifidobacterium (2)
Selenomonadales (1)	Selenomonadaceae (1)	Anaerovibrio (1)
Enterobacterales (1)	Enterobacteriaceae (1)	Citrobacter (1)
Eggerthellales (1)	Eggerthellaceae (1)	Berryella (1)

order (count)	family (count)	genus (count)
Actinomycetales (1)	Actinomycetaceae (1)	nan (19)
Veillonellales (1)	Veillonellaceae (1)	Dialister (1)

[top](#)

Cluster 32

Total number of members in cluster: 270

Average length of proteins in cluster: 348.9

Conserved (non-aliphatic) residues:

D 199 (99.6%) Y 205 (97.8%) R 351 (100.0%) H 393 (100.0%) R 664 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
AHB32462.1	Moraxellales	Moraxellaceae	Acinetobacter	Acinetobacter baumannii	O17	0
AFV46136.1	Enterobacterales	Yersiniaceae	Yersinia	Yersinia similis	O:12	0
BAQ01024.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O51	0
ADC54967.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O75	0
BAQ00622.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O10	0
AQU71752.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O1	0
AFW04820.1	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	O11	0
AFW04883.1	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	O57	0
ABX51892.1	Enterobacterales	Enterobacteriaceae	Cronobacter	Cronobacter sakazakii	O2	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

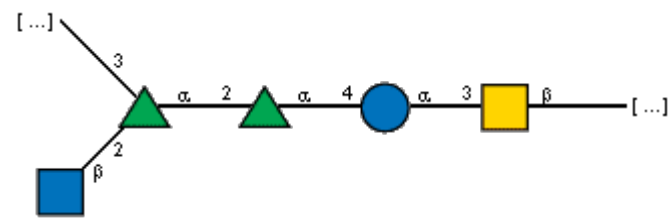
[Logoplot](#)

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[Hits in cluster](#)

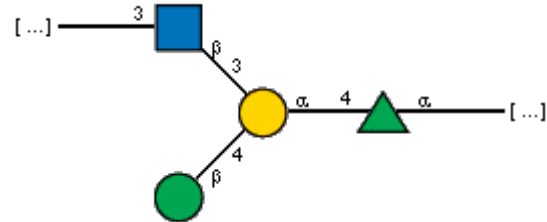
Sugars in cluster:

BAQ01024.1 Escherichia coli O51:



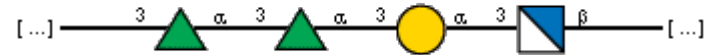
CSDB record ID: 1558

ADC54967.1 Escherichia coli O75:



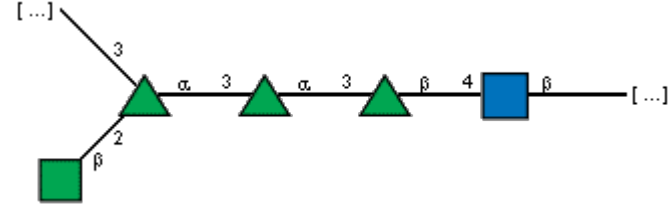
CSDB record ID: 619

BAQ00622.1 Escherichia coli O10:



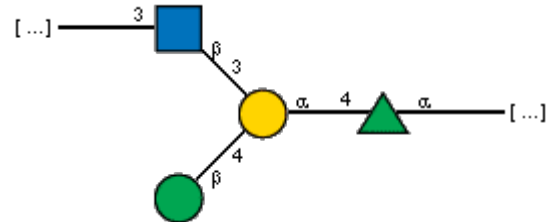
CSDB record ID: 1512

AQU71752.1 Escherichia coli O1:



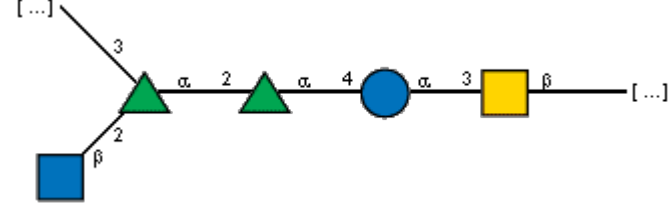
CSDB record ID: 7222

AFW04820.1 Salmonella enterica O11:

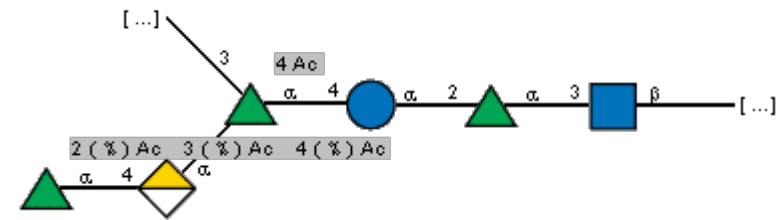


CSDB record ID: 2600

AFW04883.1 Salmonella enterica O57:



CSDB record ID: 701



CSDB record ID: 27572

Sugars for blast hits:

Alphafold models:

[ADC54967.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Bacteroidales (97)	Prevotellaceae (40)	Prevotella (37)
		Pseudoprevotella (1)
		Paraprevotella (1)
		Prevotellamassilia (1)
	Bacteroidaceae (33)	Bacteroides (11)
		Phocaeicola (1)
		Alistipes (7)
Enterobacterales (84)	Paludibacteraceae (4)	nan (9)
	Muribaculaceae (1)	nan (9)
	Tannerellaceae (1)	Parabacteroides (1)
		Escherichia (25)
	Enterobacteriaceae (68)	Salmonella (14)
		Klebsiella (10)
		Enterobacter (8)
		Cronobacter (3)
		Citrobacter (3)
		Lelliottia (1)
		Cedecea (1)
		Jejubacter (1)
		Pseudocitrobacter (1)
		Yersinia (2)
	Yersiniaceae (6)	Rahnella (2)
		Ewingella (1)
		Serratia (1)
	Morganellaceae (5)	Providencia (3)
		Xenorhabdus (1)
		Proteus (1)
	Pectobacteriaceae (3)	Pectobacterium (2)
		Dickeya (1)
	Budviciaceae (1)	nan (9)

order (count)	family (count)	genus (count)
	Erwiniaceae (1)	Pantoea (1)
Flavobacteriales (24)	Weeksellaceae (15)	Chryseobacterium (11)
		Epilithonimonas (3)
		Kaistella (1)
	Flavobacteriaceae (9)	Flavobacterium (6)
		Maribacter (1)
		Cellulophaga (1)
Burkholderiales (11)	Oxalobacteraceae (5)	Janthinobacterium (5)
	Comamonadaceae (3)	Comamonas (2)
		Acidovorax (1)
	Burkholderiaceae (2)	Ralstonia (1)
		Cupriavidus (1)
nan (9)	nan (22)	nan (9)
Sphingobacteriales (8)	Sphingobacteriaceae (8)	Pedobacter (6)
		Arcticibacter (1)
		Mucilaginibacter (1)
Moraxellales (5)	Moraxellaceae (5)	Acinetobacter (5)
Chitinophagales (5)	Chitinophagaceae (5)	nan (9)
		Chitinophaga (2)
		Ferruginibacter (1)
Vibrionales (4)	Vibrionaceae (4)	Vibrio (3)
		Photobacterium (1)
Pseudomonadales (4)	Pseudomonadaceae (3)	Pseudomonas (3)
	Marinobacteraceae (1)	Marinobacter (1)
Lactobacillales (3)	Enterococcaceae (2)	Enterococcus (2)
	Carnobacteriaceae (1)	Marinilactibacillus (1)
Alteromonadales (3)	Pseudoalteromonadaceae (1)	Pseudoalteromonas (1)
	Moritellaceae (1)	Moritella (1)
	Colwelliaceae (1)	Colwellia (1)
Campylobacterales (3)	Arcobacteraceae (1)	Aliarcobacter (1)
	Thiovulaceae (1)	Sulfurimonas (1)
Aeromonadales (3)	Aeromonadaceae (3)	Aeromonas (3)
Cytophagales (2)	Spirosomaceae (1)	Dyadobacter (1)
	Cyclobacteriaceae (1)	Algoriphagus (1)
Rickettsiales (1)	nan (22)	nan (9)
Selenomonadales (1)	Sporomusaceae (1)	Pelosinus (1)
Neisseriales (1)	Chromobacteriaceae (1)	Iodobacter (1)
Aquificales (1)	Aquificaceae (1)	Hydrogenobacter (1)
Desulfuromonadales (1)	Geobacteraceae (1)	Geotalea (1)

[top](#)

Cluster 15

Total number of members in cluster: 258

Average length of proteins in cluster: 430.3

Conserved (non-aliphatic) residues:

Y 503 (99.2%) R 506 (100.0%) Y 533 (99.2%) K 582 (97.3%) R 709 (100.0%) N 814 (99.2%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
CDF66396.1	Enterobacterales	Yersiniaceae	Yersinia	Yersinia similis	O:9	0
BAQ00780.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O30	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

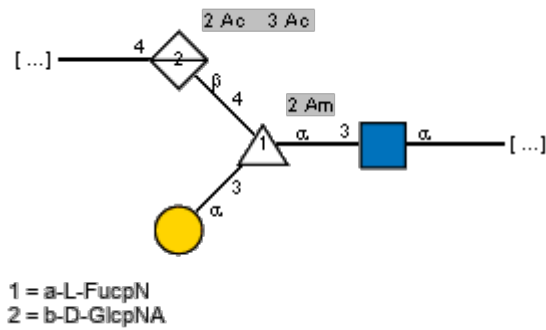
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[Phylogenetic tree](#)

[Hits in cluster](#)

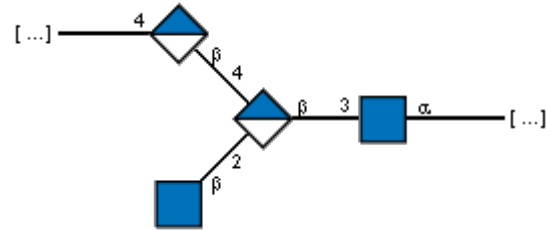
Sugars in cluster:

CDF66396.1 Yersinia pseudotuberculosis O:9:



CSDB record ID: 12130

BAQ00780.1 Escherichia coli O30:



CSDB record ID: 1539

Sugars for blast hits:

Alphafold models:

[CDF66396.1](#)

Taxonomy:

order (count)	family (count)	genus (count)	
Bacillales (79)	Listeriaceae (49)	Listeria (49)	
	Bacillaceae (21)	Bacillus (12)	
		Peribacillus (4)	
		Halobacillus (1)	
		Neobacillus (1)	
		Virgibacillus (1)	
		Rossellomorea (1)	
		Aneurinibacillus (3)	
		Cohnella (1)	
		Staphylococcus (2)	
Jeotgalicoccus (1)			
Bacteroidales (33)	Paenibacillaceae (4)	Paenisporosarcina (1)	
	Planococcaceae (2)	Planomicrobium (1)	
		Prevotellaceae (14)	Prevotella (13)
	Bacteroidaceae (6)	Bacteroides (6)	
	Odoribacteraceae (2)	Butyricimonas (2)	
	Porphyromonadaceae (2)	Sanguibacteroides (2)	
	Flavobacteriales (28)	Flavobacteriaceae (17)	Muricauda (3)
			Flavobacterium (2)
			Maribacter (2)
			Myroides (1)
Galbibacter (1)			
Cellulophaga (1)			
Winogradskyella (1)			
Pseudozobellia (1)			
Zobellia (1)			
Pareuzebyella (1)			
Zeaxanthinibacter (1)			
Aquimarina (1)			
Polaribacter (1)			
Chryseobacterium (5)			
Elizabethkingia (1)			
nan (2)			
nan (2)			
Ramlibacter (2)			
Rhodoferax (2)			
Limnohabitans (1)			
Pandoraea (2)			
Achromobacter (2)			
Janthinobacterium (1)			
Hyphomicrobiales (11)	Mesorhizobium (7)		
	Hoeflea (1)		
	Nitrobacter (1)		
	Afipia (1)		
	nan (2)		
	Burkholderiales (11)	Burkholderiaceae (3)	nan (2)
			Alcaligenaceae (2)
			Oxalobacteraceae (1)
		Phyllobacteriaceae (8)	
	Bradyrhizobiaceae (2)		
Rhizobiaceae (1)			

order (count)	family (count)	genus (count)
Eubacteriales (11)	Clostridiaceae (4)	Caminicella (1)
		Clostridium (1)
		Alkaliphilus (1)
	Lachnospiraceae (2)	Paraclostridium (1)
		nan (2)
	Oscillospiraceae (2)	Lachnoclostridium (1)
Sphingomonadales (9)	Sphingomonadaceae (7)	Ruminiclostridium (1)
		Hydrogenoanaerobacterium (1)
		Anaerobranca (1)
	Erythrobacteraceae (1)	Fusibacter (1)
		Citromicrobium (2)
		Sphingomonas (2)
Vibrionales (9)	Sphingosinicellaceae (1)	Sphingopyxis (2)
		Sphingobium (1)
		Alteriqipengyuania (1)
	Vibrionaceae (9)	Sphingosinicella (1)
		Vibrio (8)
		Aliivibrio (1)
Enterobacterales (8)	Enterobacteriaceae (4)	Escherichia (4)
		Xenorhabdus (2)
		Proteus (1)
	Morganellaceae (3)	Yersinia (1)
		Yersiniaceae (1)
Lactobacillales (8)	Enterococcaceae (6)	Enterococcus (6)
		Carnobacterium (1)
		Ligilactobacillus (1)
	Carnobacteriaceae (1)	
Pseudomonadales (6)	Lactobacillaceae (1)	
	Pseudomonadaceae (5)	Pseudomonas (5)
		Marinobacter (1)
Moraxellales (5)	Marinobacteraceae (1)	Acinetobacter (5)
	Moraxellaceae (5)	Marinomonas (1)
		Oceanospirillum (1)
Oceanospirillales (3)	Oceanospirillaceae (2)	Halomonas (1)
		Idiomarina (1)
		Pseudoalteromonas (1)
	Halomonadaceae (1)	Alteromonas (1)
Alteromonadales (3)	Idiomarinaceae (1)	Aliarcobacter (2)
		Campylobacter (1)
		Microbacterium (1)
	Pseudoalteromonadaceae (1)	Citricoccus (1)
		Sphaerospermopsis (1)
		Calothrix (1)
Campylobacterales (3)	Alteromonadaceae (1)	Marinifilum (1)
		Pseudonocardia (1)
	Arcobacteraceae (2)	Lignipirellula (1)
		Rubinisphaera (1)
		Actinoplanes (1)
Micrococcales (2)	Campylobacteraceae (1)	Tepidimicrobium (1)
	Microbacteriaceae (1)	
Nostocales (2)	Micrococcaceae (1)	
	Aphanizomenonaceae (1)	
Marinilabiales (1)	Calotrichaceae (1)	
	Marinifilaceae (1)	
Pseudonocardiales (1)	Pseudonocardiaceae (1)	
	Pirellulaceae (1)	
Pirellulales (1)	Planctomycetaceae (1)	
	Micromonosporaceae (1)	
Planctomycetales (1)	Tissierellaceae (1)	
	Tissierellaceae (1)	
Micromonosporales (1)	Tissierellaceae (1)	
	Tissierellaceae (1)	
Tissierellales (1)	Tissierellaceae (1)	
	Tissierellaceae (1)	

order (count)	family (count)	genus (count)
Sphingobacteriales (1)	Sphingobacteriaceae (1)	Solitalea (1)
Propionibacteriales (1)	Actinopolymorphaceae (1)	Actinopolymorpha (1)
Elusimicrobiales (1)	Elusimicrobiaceae (1)	nan (2)
Nitrosomonadales (1)	Nitrosomonadaceae (1)	Nitrosomonas (1)
Rhodobacterales (1)	Roseobacteraceae (1)	Roseovarius (1)
Chromatiales (1)	Ectothiorhodospiraceae (1)	Thioalkalivibrio (1)
Dictyoglomales (1)	Dictyoglomaceae (1)	Dictyoglomus (1)
Eggerthellales (1)	Eggerthellaceae (1)	Adlercreutzia (1)

[top](#)

Cluster 9

Total number of members in cluster: 240

Average length of proteins in cluster: 353.5

Conserved (non-aliphatic) residues:

R 234 (99.6%) D 240 (99.6%) Y 244 (99.6%) R 417 (99.2%) Q 418 (100.0%) H 459 (99.6%) Y 578 (97.5%) R 627 (97.9%) D 710 (97.9%) R 711 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
AHB32215.1	Moraxellales	Moraxellaceae	Acinetobacter	Acinetobacter baumannii	O1	0
AHB32861.1	Moraxellales	Moraxellaceae	Acinetobacter	Acinetobacter baumannii	O25	0
AHB32799.1	Moraxellales	Moraxellaceae	Acinetobacter	Acinetobacter baumannii	O26	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

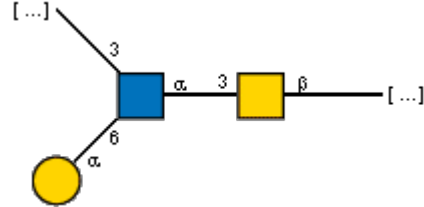
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

AHB32215.1 Acinetobacter baumannii O1:



Sugars for blast hits:

Alphafold models:

[AHB32215.1](#)

[AHB32861.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Sphingomonadales (49)	Sphingomonadaceae (44)	Sphingomonas (34)
		Novosphingobium (5)
		nan (2)
		Allosphingosinicella (1)
		Novosphingopyxis (1)
		Sphingorhabdus (1)
		Pontixanthobacter (3)
		Sphingosinicella (2)
		nan (2)
		Acinetobacter (21)
nan (26)	Erythrobacteraceae (3)	
	Sphingosinicellaceae (2)	
Moraxellales (21)	nan (2)	
	Moraxellaceae (21)	
Hyphomicrobiales (17)	Methylocystaceae (6)	Methylosinus (3)
		Methylocystis (3)
		Mesorhizobium (2)
		Tianweitania (1)
		Pseudaminobacter (1)
		Hoeflea (1)
		Devosia (2)
		Aurantimonas (1)
		Aureimonas (1)
		nan (2)
Campylobacterales (15)	Rhizobiaceae (1)	
	Hyphomicrobiaceae (1)	Rhodomicrobium (1)
	Campylobacteraceae (9)	Campylobacter (8)
		Sulfurovum (4)
	Sulfurovaceae (4)	
	Thiovulaceae (1)	Sulfurimonas (1)
Vibrionales (14)	Arcobacteraceae (1)	Poseidonibacter (1)
	Vibrionaceae (14)	Vibrio (11)
		Photobacterium (3)
		Alcanivorax (6)
Oceanospirillales (10)	Alcanivoracaceae (6)	
	Halomonadaceae (3)	Halomonas (3)
	Oceanospirillaceae (1)	Marinobacterium (1)
Xanthomonadales (8)	Xanthomonadaceae (6)	Luteimonas (5)
		Pseudoxanthomonas (1)
		Rhodanobacter (1)
		Dokdonella (1)
Rhodobacterales (7)	Rhodobacteraceae (4)	Thioclava (2)
		Rhodovulum (1)

order (count)	family (count)	genus (count)
	Roseobacteraceae (3)	Maritimibacter (1)
		Sulfitobacter (1)
		Jannaschia (1)
Burkholderiales (7)	Comamonadaceae (3)	Polaromonas (1)
		Ramlibacter (1)
		Diaphorobacter (1)
Enterobacterales (6)	Burkholderiaceae (3)	Polynucleobacter (3)
	Morganellaceae (5)	Proteus (3)
		Photorhabdus (1)
Pseudomonadales (6)	Xenorhabdus (1)	
	Enterobacteriaceae (1)	Enterobacter (1)
	Marinobacteraceae (5)	Marinobacter (5)
Flavobacteriales (4)	Pseudomonadaceae (1)	Pseudomonas (1)
	Flavobacteriaceae (1)	Capnocytophaga (1)
	Crocinitomicaceae (1)	nan (2)
Chromatiales (4)	Weeksellaceae (1)	Chryseobacterium (1)
	Ectothiorhodospiraceae (2)	Alkalilimnicola (1)
		Spiribacter (1)
Synechococcales (4)	Chromatiaceae (2)	Candidatus Thiosymbion (2)
	Synechococcaceae (3)	Synechococcus (3)
	Prochlorococcaceae (1)	Prochlorococcus (1)
Pasteurellales (3)	Pasteurellaceae (3)	Actinobacillus (3)
Aeromonadales (3)	Aeromonadaceae (3)	Aeromonas (3)
Pseudanabaenales (3)	Thermosynechococcaceae (3)	Thermosynechococcus (3)
Thermotogales (3)	Thermotogaceae (2)	Pseudothermotoga (1)
		Thermotoga (1)
		Fervidobacterium (1)
Thermotichales (2)	Thermotichaceae (2)	Thermotichus (2)
Nitrosomonadales (2)	nan (2)	nan (2)
	Methylophilaceae (1)	nan (2)
	Salinisphaeraceae (2)	Salinisphaera (2)
Cellvibrionales (2)	Halieaceae (2)	Haliea (2)
Caulobacterales (2)	Caulobacteraceae (2)	Caulobacter (1)
		Brevundimonas (1)
		Desulfuromonas (2)
Desulfuromonadales (2)	Desulfuromonadaceae (2)	Desulfuromonas (2)
Nevskiales (2)	Sinobacteraceae (2)	Fontimonas (1)
		Flagellatimonas (1)
		Candidatus Electrothrix (1)
Desulfobacterales (2)	Desulfobulbaceae (1)	Desulfopila (1)
	Desulfocapsaceae (1)	Methylovulum (1)
	Methylococcales (2)	Methylococcaceae (2)
Pirellulales (2)	Pirellulaceae (2)	Rhodopirellula (2)
Hydrogenophilales (1)	Hydrogenophilaceae (1)	Tepidiphilus (1)
Neisseriales (1)	Chromobacteriaceae (1)	Chromobacterium (1)
Rhodocyclales (1)	Azonexaceae (1)	Dechloromonas (1)
Bacteroidales (1)	Lentimicrobiaceae (1)	nan (2)

order (count)	family (count)	genus (count)
Mariprofundales (1)	Mariprofundaceae (1)	Mariprofundus (1)
Leptospirales (1)	Leptospiraceae (1)	nan (2)
Acidiferrobacterales (1)	Acidiferrobacteraceae (1)	nan (2)
Desulfurellales (1)	Desulfurellaceae (1)	Hippea (1)
Pelagibacterales (1)	Pelagibacteraceae (1)	nan (2)
Rickettsiales (1)	nan (2)	nan (2)

[top](#)

Cluster 11

Total number of members in cluster: 152

Average length of proteins in cluster: 412.2

Conserved (non-aliphatic) residues:

R 593 (100.0%) Y 633 (98.0%) D 664 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
CAI34150.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	32F	0
CAI34124.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	32A	0
CAI34680.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	48	0

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[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

CAI34150.1 Streptococcus pneumoniae 32F:

order (count)	family (count)	genus (count)
Eubacteriales (66)	Lachnospiraceae (27)	nan (6)
		Blautia (4)
		Coprococcus (2)
		Anaerostipes (2)
		Mediterraneibacter (2)
		Lachnospira (1)
		Oribacterium (1)
		Oliverpabstia (1)
		Lachnotalea (1)
		Anaerobutyricum (1)
		Butyrivibrio (1)
		Lacrimispora (1)
	Clostridiaceae (20)	Clostridium (19)
		Paraclostridium (1)
	Oscillospiraceae (9)	nan (6)
Ruminococcus (2)		

order (count)	family (count)	genus (count)
		Ruminiclostridium (2)
		Faecalibacterium (1)
		Drancourtella (1)
	Eubacteriaceae (6)	Eubacterium (6)
	nan (5)	nan (6)
	Peptostreptococcaceae (1)	Romboutsia (1)
Lactobacillales (38)	Lactobacillaceae (18)	Lactobacillus (7)
		Leuconostoc (2)
		Levilactobacillus (2)
		Lactiplantibacillus (2)
		Loigolactobacillus (1)
		Weissella (1)
		Ligilactobacillus (1)
		Limosilactobacillus (1)
	Enterococcaceae (10)	Enterococcus (10)
	Streptococcaceae (9)	Streptococcus (8)
		Lactococcus (1)
	Carnobacteriaceae (1)	Carnobacterium (1)
Bacillales (20)	Listeriaceae (15)	Listeria (15)
	Bacillaceae (5)	Priestia (4)
		Bacillus (1)
Coriobacteriales (9)	Coriobacteriaceae (9)	Collinsella (9)
Erysipelotrichales (5)	Erysipelotrichaceae (5)	Erysipelatoclostridium (2)
		Lactimicrobium (1)
		Amedibacillus (1)
		Candidatus Stoquefichus (1)
Eggerthellales (4)	Eggerthellaceae (4)	Gordonibacter (1)
		Slackia (1)
		Eggerthella (1)
		Adlercreutzia (1)
Bacteroidales (3)	Bacteroidaceae (2)	Bacteroides (1)
		Phocaeicola (1)
	Muribaculaceae (1)	Duncaniella (1)
nan (3)	nan (5)	nan (6)
Fibrobacterales (1)	Fibrobacteraceae (1)	Fibrobacter (1)
Bifidobacteriales (1)	Bifidobacteriaceae (1)	Bifidobacterium (1)
Aeromonadales (1)	Succinivibrionaceae (1)	nan (6)
Tissierellales (1)	Peptoniphilaceae (1)	Anaerococcus (1)

[top](#)

Cluster 6

Total number of members in cluster: 139

Average length of proteins in cluster: 443.5

Conserved (non-aliphatic) residues:

R 401 (100.0%) Y 510 (100.0%) N 608 (100.0%) D 619 (97.1%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
CAI32823.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	6A	0
CAI32843.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	6B	0
CAI33700.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	19F	0
CAI33631.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	19A	0
CAI34269.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	34	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

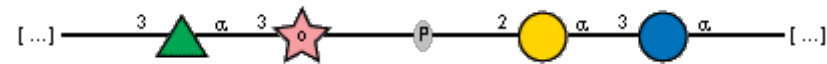
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[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

CAI32823.1 Streptococcus pneumoniae 6A:



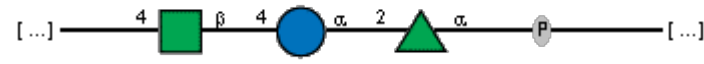
CSDB record ID: 1087

CAI32843.1 Streptococcus pneumoniae 6B:



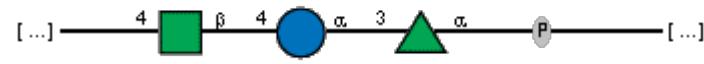
CSDB record ID: 937

CAI33700.1 Streptococcus pneumoniae 19F:



CSDB record ID: 739

CAI33631.1 Streptococcus pneumoniae 19A:



CSDB record ID: 740

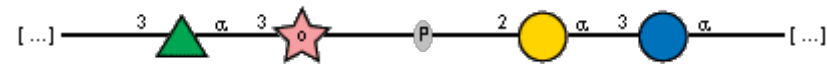
CAI34269.1 Streptococcus pneumoniae 34:



CSDB record ID: 7043

Sugars for blast hits:

AAL82786.1 Streptococcus pneumoniae 6A:



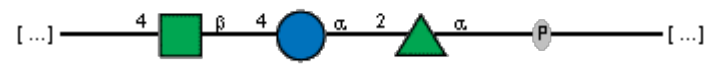
CSDB record ID: 1087

VJK41440.1 Streptococcus pneumoniae 6C:



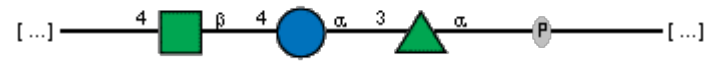
CSDB record ID: 3661

VNC99741.1 Streptococcus pneumoniae 19F, VSB76654.1 Streptococcus pneumoniae 19F, CMX58981.1 Streptococcus pneumoniae 19F:



CSDB record ID: 739

VOS41126.1 Streptococcus pneumoniae 19A:



CSDB record ID: 740

VMG48693.1 Streptococcus pneumoniae 34:



CSDB record ID: 7043

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Lactobacillales (67)	Streptococcaceae (35)	Streptococcus (35)
	Lactobacillaceae (19)	Lactobacillus (5)
		Limosilactobacillus (3)
		Liquorilactobacillus (2)
		Lactiplantibacillus (2)

order (count)	family (count)	genus (count)
Eubacteriales (41)	nan (11)	Leuconostoc (1)
		Levilactobacillus (1)
		Ligilactobacillus (1)
		Companilactobacillus (1)
		Lacticaseibacillus (1)
		Latilactobacillus (1)
		Lentilactobacillus (1)
		nan (2)
	Enterococcaceae (11)	Enterococcus (11)
	Carnobacteriaceae (1)	Carnobacterium (1)
	Lachnospiraceae (20)	Blautia (5)
		Butyrivibrio (2)
		Coprococcus (2)
		Anaerostipes (1)
		Enterocloster (1)
		Lachnoclostridium (1)
		Roseburia (1)
		Oribacterium (1)
		Sellimonas (1)
		Epulopiscium (1)
	Oscillospiraceae (9)	Faecalibacterium (4)
		nan (2)
		Drancourtella (1)
	Clostridiaceae (6)	Clostridium (4)
		Massilioclostridium (1)
	Eubacteriaceae (2)	Youngiibacter (1)
		Eubacterium (2)
	Xylanivirgaceae (1)	Xylanivirga (1)
	Christensenellaceae (1)	Christensenella (1)
nan (10)	nan (11)	Candidatus Avigastranaerophilus (1)
Pasteurellales (5)	Pasteurellaceae (5)	Haemophilus (2)
		Actinobacillus (1)
		Mannheimia (1)
		Pasteurella (1)
Coriobacteriales (4)	Coriobacteriaceae (3)	nan (2)
		Collinsella (2)
	Atopobiaceae (1)	Olsenella (1)
Bifidobacteriales (3)	Bifidobacteriaceae (3)	Bifidobacterium (3)
Erysipelotrichales (3)	Erysipelotrichaceae (2)	Massilimicrobiota (1)
		Absiella (1)
Bacillales (2)	Coprobacillaceae (1)	Sharpea (1)
	Bacillaceae (1)	Bacillus (1)
	Paenibacillaceae (1)	Paenibacillus (1)
Synergistales (1)	Synergistaceae (1)	Cloacibacillus (1)
Fusobacteriales (1)	Fusobacteriaceae (1)	Fusobacterium (1)
Methanobacteriales (1)	Methanobacteriaceae (1)	Methanobrevibacter (1)

order (count)

Anaerolineales (1)

family (count)

Anaerolineaceae (1)

genus (count)

nan (2)

[top](#)

Cluster 29

Total number of members in cluster: 136

Average length of proteins in cluster: 394.0

Conserved (non-aliphatic) residues:

R 292 (98.5%) R 364 (99.3%) Y 423 (97.8%) Y 425 (100.0%) N 432 (98.5%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
AHB32411.1	Moraxellales	Moraxellaceae	Acinetobacter	Acinetobacter baumannii	O10	0
AFC91458.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O45	0
AFC91419.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O45	0
AAX07747.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O45	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

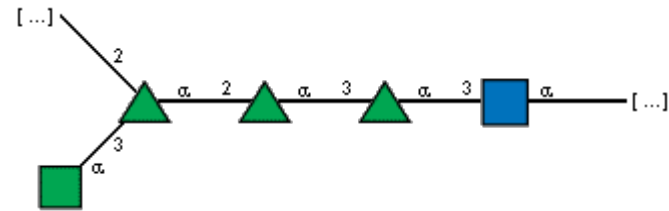
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

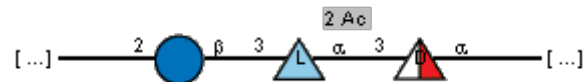
Sugars in cluster:

AHB32411.1 Acinetobacter baumannii O10:



CSDB record ID: 27746

AFC91458.1 Escherichia coli O45, AFC91419.1 Escherichia coli O45, AAX07747.1 Escherichia coli O45:



CSDB record ID: 1552

Sugars for blast hits:

AlphaFold models:

[AHB32411.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (25)	Enterobacteriaceae (19)	Escherichia (7)
		Klebsiella (5)
		Enterobacter (5)
		Raoultella (1)
		Kosakonia (1)
	Pectobacteriaceae (4)	Pectobacterium (3)
	Yersiniaceae (2)	Brenneria (1)
		Rahnella (1)
Sphingobacteriales (16)	Sphingobacteriaceae (16)	Serratia (1)
		Pedobacter (9)
		Mucilaginibacter (6)
Lactobacillales (14)	Lactobacillaceae (9)	Latilactobacillus (3)
		Lacticaseibacillus (2)
		Lactobacillus (1)
		Lactiplantibacillus (1)
		Lapidilactobacillus (1)
		Ligilactobacillus (1)
	Carnobacteriaceae (4)	Carnobacterium (3)
		Isobaculum (1)
Bacteroidales (12)	Streptococcaceae (1)	Streptococcus (1)
	Bacteroidaceae (8)	Bacteroides (7)
		Phocaeicola (1)
	Muribaculaceae (2)	nan (3)
	Prevotellaceae (1)	Prevotella (1)
Eubacteriales (9)	Clostridiaceae (6)	Clostridium (6)
	Peptostreptococcaceae (1)	Romboutsia (1)
	Eubacteriaceae (1)	nan (3)
Burkholderiales (8)	Burkholderiaceae (8)	Ralstonia (8)
Pseudomonadales (8)	Pseudomonadaceae (8)	Pseudomonas (8)
Bacillales (7)	Bacillaceae (6)	Bacillus (4)
		Rossellomorea (1)
Flavobacteriales (6)	Sporolactobacillaceae (1)	Sporolactobacillus (1)
	Flavobacteriaceae (6)	Flavobacterium (5)
		Maribacter (1)
Moraxellales (5)	Moraxellaceae (5)	Acinetobacter (5)
Cytophagales (5)	Cytophagaceae (2)	Spirosoma (2)
	Spirosomaceae (2)	Fibrella (2)
	Reichenbachiellaceae (1)	Reichenbachiella (1)
Vibrionales (4)	Vibrionaceae (4)	Vibrio (3)
		Photobacterium (1)

order (count)	family (count)	genus (count)
nan (2)	nan (1)	nan (3)
Chitinophagales (2)	Chitinophagaceae (2)	Ilyomonas (1)
Aeromonadales (2)	Aeromonadaceae (2)	Aeromonas (2)
Sphingomonadales (2)	Sphingomonadaceae (2)	Sphingomonas (2)
Rhodospirillales (2)	Rhodospirillaceae (2)	Inquilinus (2)
Methanotrichales (1)	Methanotrichaceae (1)	Methanothrix (1)
Nostocales (1)	Calotrichaceae (1)	Calothrix (1)
Chlorobiales (1)	Chlorobiaceae (1)	nan (3)
Rickettsiales (1)	nan (1)	nan (3)
Spirochaetales (1)	Treponemataceae (1)	Treponema (1)
Acidobacteriales (1)	Acidobacteriaceae (1)	Granulicella (1)
Salinisphaerales (1)	Salinisphaeraceae (1)	Salinisphaera (1)

[top](#)

Cluster 23

Total number of members in cluster: 134

Average length of proteins in cluster: 356.2

Conserved (non-aliphatic) residues:

R 163 (99.3%) D 170 (100.0%) Y 175 (100.0%) R 298 (100.0%) H 336 (100.0%) R 561 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
AHB32715.1	Moraxellales	Moraxellaceae	Acinetobacter	Acinetobacter baumannii	O23	0
AHB32637.1	Moraxellales	Moraxellaceae	Acinetobacter	Acinetobacter baumannii	O23	0
CAI33718.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	20	0

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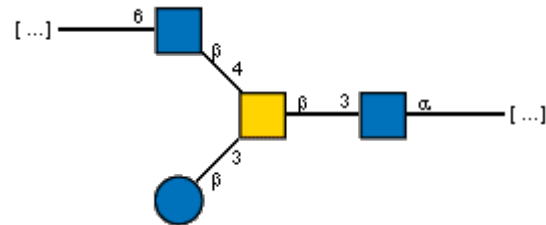
[Logoplot](#)

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[Hits in cluster](#)

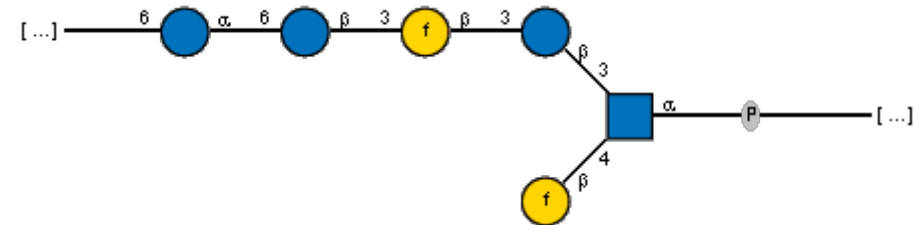
Sugars in cluster:

AHB32715.1 Acinetobacter baumannii O23, AHB32637.1 Acinetobacter baumannii O23:



CSDB record ID: 563

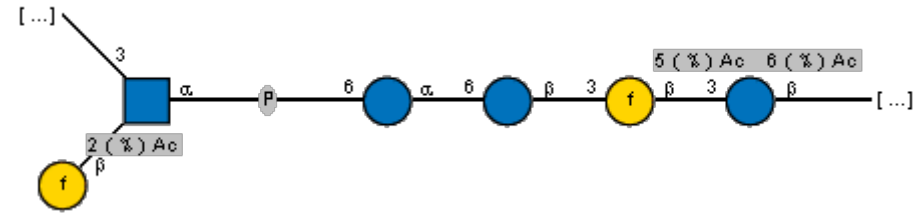
CAI33718.1 *Streptococcus pneumoniae* 20:



CSDB record ID: 1928

Sugars for blast hits:

VLD07009.1 *Streptococcus pneumoniae* 20A:



CSDB record ID: 7079

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Moraxellales (39)	Moraxellaceae (39)	Acinetobacter (23)
		Psychrobacter (13)
		Moraxella (2)
Lactobacillales (29)	Lactobacillaceae (19)	Lactiplantibacillus (7)
		Pediococcus (6)
		Loigolactobacillus (1)
		Lactobacillus (1)
		Weissella (1)
		Companilactobacillus (1)
		Latilactobacillus (1)
		Leuconostoc (1)
	Streptococcaceae (5)	Streptococcus (5)
	Enterococcaceae (5)	Enterococcus (5)
Eubacteriales (18)	Lachnospiraceae (9)	nan (5)
		Eisenbergiella (1)

order (count)	family (count)	genus (count)
	Clostridiaceae (5)	Clostridium (5)
	Oscillospiraceae (3)	Ruminiclostridium (1)
		Ruminococcus (1)
		Faecalibacterium (1)
Enterobacterales (13)	Enterobacteriaceae (10)	Klebsiella (7)
		Raoultella (2)
		Escherichia (1)
	Erwiniaceae (2)	Pantoea (1)
		Erwinia (1)
	Hafniaceae (1)	Edwardsiella (1)
Flavobacteriales (6)	Flavobacteriaceae (6)	Flavobacterium (3)
		Lutibacter (1)
		Robertkochia (1)
nan (6)	nan (2)	Candidatus Coprosoma (1)
Bacillales (5)	Bacillaceae (3)	Bacillus (2)
		Halobacillus (1)
	nan (2)	Exiguobacterium (1)
	Sporolactobacillaceae (1)	Sporolactobacillus (1)
Bacteroidales (3)	Bacteroidaceae (2)	Bacteroides (2)
	Tannerellaceae (1)	Parabacteroides (1)
Alteromonadales (3)	Colwelliaceae (1)	Thalassotalea (1)
	Shewanellaceae (1)	Shewanella (1)
	Pseudoalteromonadaceae (1)	Pseudoalteromonas (1)
Fibrobacterales (2)	Fibrobacteraceae (2)	Fibrobacter (2)
Xanthomonadales (2)	Xanthomonadaceae (2)	Lysobacter (1)
		Stenotrophomonas (1)
Vibrionales (2)	Vibrionaceae (2)	Vibrio (2)
Pseudomonadales (1)	Marinobacteraceae (1)	Marinobacter (1)
Sphingomonadales (1)	Erythrobacteraceae (1)	Alteriqipengyuania (1)
Oceanospirillales (1)	Halomonadaceae (1)	Halomonas (1)
Chromatiales (1)	Chromatiaceae (1)	Rheinheimera (1)
Erysipelotrichales (1)	Coprobacillaceae (1)	Coprobacillus (1)
Coriobacteriales (1)	nan (2)	nan (5)

[top](#)

Cluster 50

Total number of members in cluster: 129

Average length of proteins in cluster: 452.7

Conserved (non-aliphatic) residues:

R 250 (97.7%) K 324 (100.0%) R 402 (100.0%) K 516 (98.4%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common
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AAT77177.1	Enterobacterales	Enterobacteriaceae	Escherichia coli	Escherichia coli	O114	0
AFN02899.1	Enterobacterales	Enterobacteriaceae	Escherichia coli	Escherichia coli	O180	0
BAQ00569.1	Enterobacterales	Enterobacteriaceae	Escherichia coli	Escherichia coli	O5	0

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[Fasta of members](#)

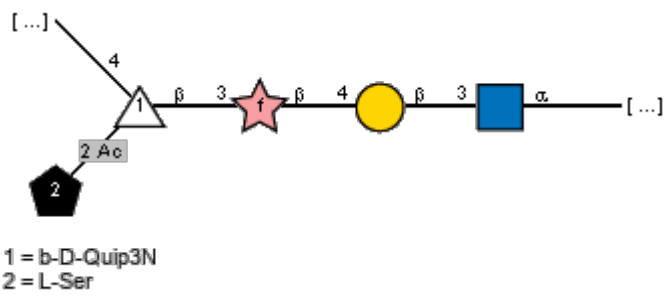
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

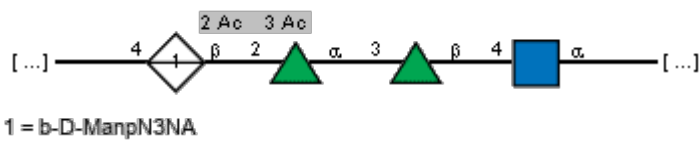
Sugars in cluster:

AAT77177.1 Escherichia coli O114:



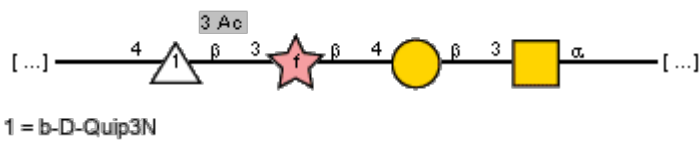
CSDB record ID: 1854

AFN02899.1 Escherichia coli O180:



CSDB record ID: 704

BAQ00569.1 Escherichia coli O5:



CSDB record ID: 3191

Sugars for blast hits:

Alphafold models:

[AAT77177.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Bacillales (53)	Bacillaceae (49)	Bacillus (14)
		Geobacillus (11)
		Cytobacillus (7)
		nan (5)
		Psychrobacillus (4)
		Anoxybacillus (2)
		Metabacillus (2)
		Fictibacillus (2)
		Alkalihalobacillus (1)
		Siminovitchia (1)
		Lederbergia (1)
		Thermoactinomycetaceae (3)
		Risungbinella (1)
		Hazenella (1)
Shimazuella (1)		
Eubacteriales (26)	Planococcaceae (1)	
	Clostridiaceae (20)	Chryseomicrobium (1)
		Clostridium (18)
		nan (5)
	Hathewayia (1)	
	Lachnospiraceae (2)	
nan (5)		
Mediterraneibacter (1)		
Oscillospiraceae (2)		
Ruminococcus (1)		
Eubacteriaceae (1)		
Eubacterium (1)		
Enterobacterales (12)	Enterobacteriaceae (10)	Escherichia (5)
		Shigella (1)
		Citrobacter (1)
		Klebsiella (1)
		Salmonella (1)
		Enterobacter (1)
		Budviciaceae (1)
		Pragia (1)
		Morganellaceae (1)
		Providencia (1)
nan (7)	nan (4)	nan (5)
Moraxellales (6)	Moraxellaceae (6)	Acinetobacter (6)
Bacteroidales (6)	Bacteroidaceae (3)	Bacteroides (3)
	Rikenellaceae (1)	Acetobacteroides (1)
Flavobacteriales (3)	Odoribacteraceae (1)	Odoribacter (1)
	Flavobacteriaceae (2)	Tenacibaculum (2)
	Crocinitomicaceae (1)	Crocinitomix (1)
Chitinophagales (3)	nan (4)	nan (5)
	Chitinophagaceae (1)	Chitinophaga (1)
Tissierellales (3)	Peptoniphilaceae (3)	Anaerococcus (2)
		Miniphocaeibacter (1)
Vibrionales (2)	Vibrionaceae (2)	Vibrio (2)
Campylobacterales (2)	Arcobacteraceae (2)	Aliarcobacter (2)
Cytophagales (2)	Cyclobacteriaceae (2)	Cecembia (1)
		Echinicola (1)

order (count)	family (count)	genus (count)
Thiotrichales (1)	Thiotrichaceae (1)	Thiothrix (1)
Alteromonadales (1)	Alteromonadaceae (1)	Paraglaciecola (1)
Silvanigrellales (1)	nan (4)	nan (5)
Synergistales (1)	Synergistaceae (1)	Acetomicrobium (1)

[top](#)

Cluster 33

Total number of members in cluster: 129

Average length of proteins in cluster: 395.6

Conserved (non-aliphatic) residues:

D 33 (99.2%) R 42 (100.0%) Y 118 (100.0%) K 120 (98.4%) Q 159 (99.2%) S 199 (99.2%) E 200 (100.0%) Q 204 (99.2%) Y 206 (100.0%) R 207 (100.0%) T 212 (98.4%) S 220 (99.2%) R 261 (100.0%) S 270 (98.4%) Y 274 (98.4%) Y 283 (98.4%) H 310 (99.2%) E 313 (100.0%) N 317 (98.4%) S 345 (99.2%) Q 361 (97.7%) D 366 (99.2%) Y 369 (100.0%) Y 380 (98.4%) Y 381 (100.0%) D 385 (99.2%) S 386 (99.2%) R 390 (99.2%) Q 391 (98.4%) Y 394 (99.2%) Y 399 (98.4%) S 430 (98.4%) K 441 (98.4%) D 443 (99.2%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
BAQ00795.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O33	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

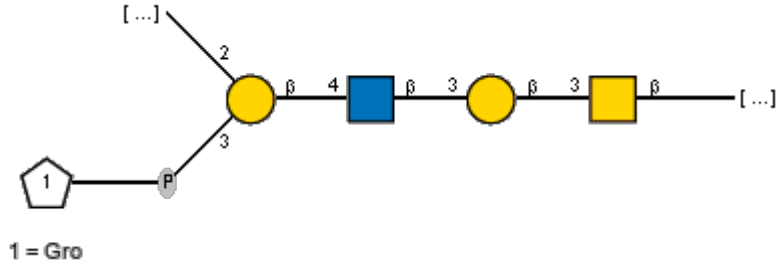
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

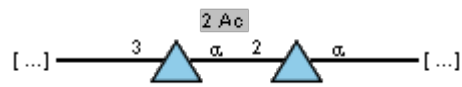
Sugars in cluster:

BAQ00795.1 Escherichia coli O33:



CSDB record ID: 1401

Sugars for blast hits:



CSDB record ID: 27705

AlphaFold models:

[BAQ00795.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Pasteurellales (122)	Pasteurellaceae (122)	Haemophilus (35)
		Aggregatibacter (20)
		Pasteurella (18)
		Rodentibacter (13)
		Mannheimia (9)
		Actinobacillus (8)
		Glaesserella (4)
		Ursidibacter (3)
		Muribacter (2)
		Avibacterium (2)
		Bibersteinia (2)
		Frederiksenia (1)
		nan (1)
		Bisgaardia (1)
		Basfia (1)
Nicoletella (1)		
Lonepinella (1)		
Enterobacterales (4)	Enterobacteriaceae (2)	Escherichia (2)
	Morganellaceae (2)	Providencia (2)
Aeromonadales (2)	Aeromonadaceae (2)	Aeromonas (2)
Vibrionales (1)	Vibrionaceae (1)	Photobacterium (1)

[top](#)

Cluster 39

Total number of members in cluster: 119

Average length of proteins in cluster: 423.2

Conserved (non-aliphatic) residues:

R 501 (97.5%) N 502 (100.0%) E 508 (100.0%) S 685 (98.3%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
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protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
CAI34254.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	33F	0
CAI34177.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	33A	0
CAI34198.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	33B	0
CAI34217.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	33C	0
CAI34236.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	33D	0

[MSA fasta](#)

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[Fasta of members](#)

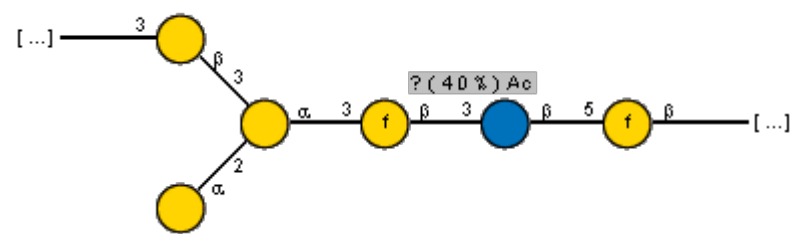
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

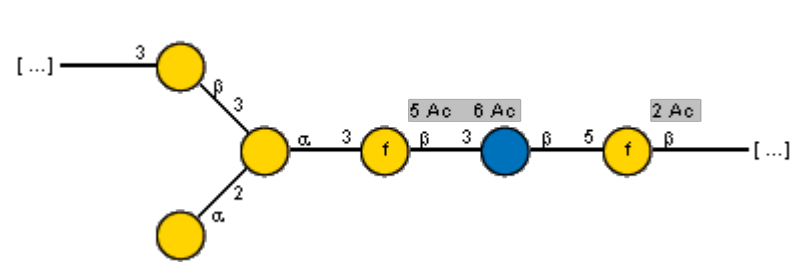
Sugars in cluster:

CAI34254.1 Streptococcus pneumoniae 33F:



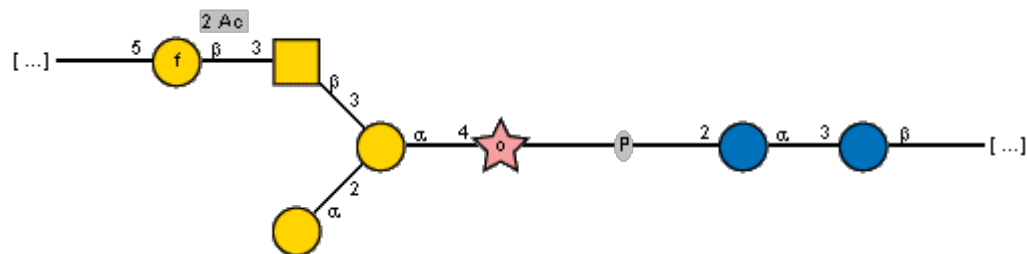
CSDB record ID: 1965

CAI34177.1 Streptococcus pneumoniae 33A:



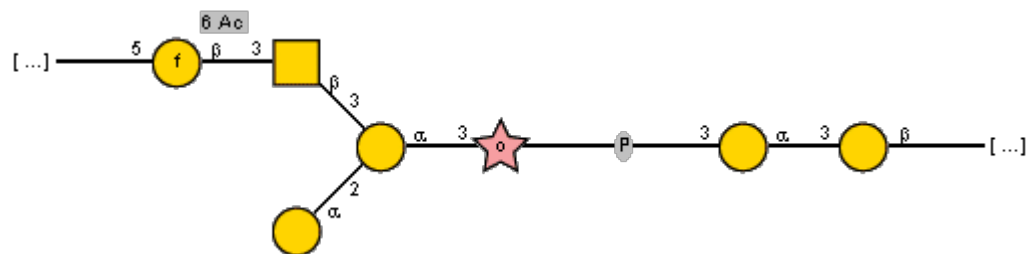
CSDB record ID: 7091

CAI34198.1 Streptococcus pneumoniae 33B:



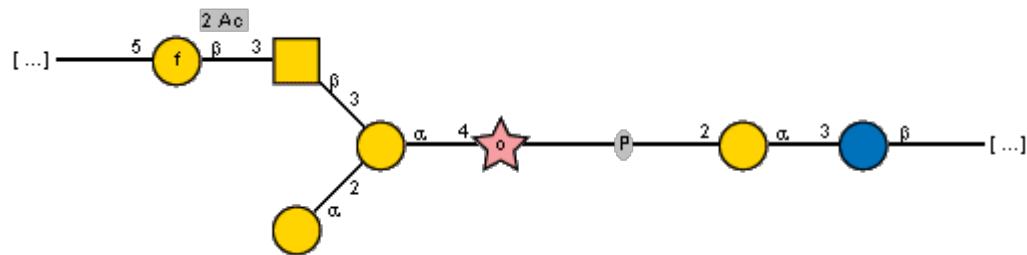
CSDB record ID: 7092

CAI34217.1 *Streptococcus pneumoniae* 33C:



CSDB record ID: 7093

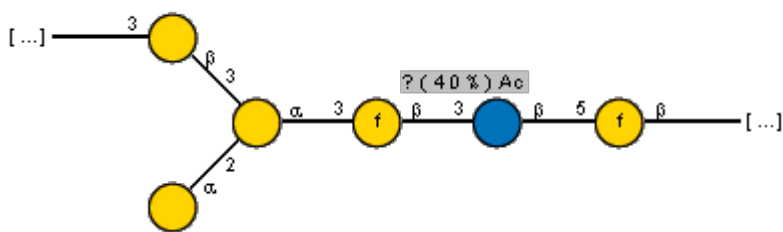
CAI34236.1 *Streptococcus pneumoniae* 33D:



CSDB record ID: 7094

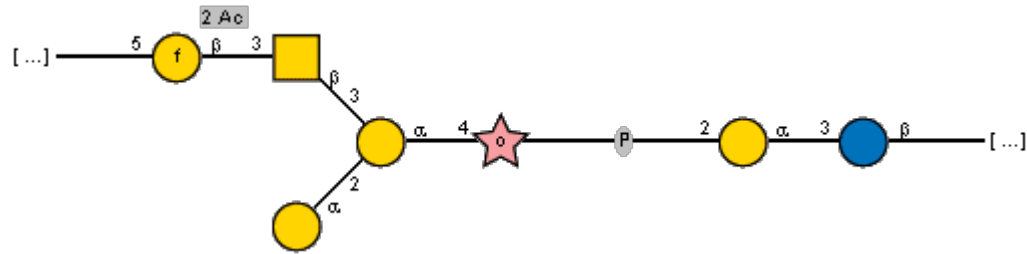
Sugars for blast hits:

VQJ42306.1 *Streptococcus pneumoniae* 33F:



CSDB record ID: 1965

VIU37569.1 *Streptococcus pneumoniae* 33D:



Alphafold models:

- [CAI34254.1](#)
- [CAI34198.1](#)
- [CAI34217.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Lactobacillales (60)	Lactobacillaceae (39)	Lactobacillus (11)
		Pediococcus (5)
		Levilactobacillus (5)
		Lactiplantibacillus (4)
		Limosilactobacillus (2)
		Leuconostoc (2)
		Companilactobacillus (2)
		Lacticaseibacillus (2)
		Ligilactobacillus (2)
		Latilactobacillus (1)
		Weissella (1)
		Liquorilactobacillus (1)
		Secundilactobacillus (1)
	Streptococcaceae (18)	Streptococcus (18)
Eubacteriales (37)	Enterococcaceae (3)	Enterococcus (3)
	Lachnospiraceae (19)	Mediterraneibacter (3)
		Enterocloster (3)
		Blautia (2)
		Cuneatibacter (1)
		Roseburia (1)
		Butyrivibrio (1)
		Pseudobutyrvibrio (1)
	nan (16)	nan (18)
	Clostridiaceae (10)	Clostridium (10)
	Oscillospiraceae (5)	nan (18)
		Ruminococcus (1)
nan (14)	nan (16)	nan (18)
Pasteurellales (3)	Pasteurellaceae (3)	Haemophilus (2)
Bacteroidales (3)	Bacteroidaceae (3)	nan (18)
		Phocaeicola (2)
Coriobacteriales (2)	Coriobacteriaceae (1)	Collinsella (1)
	Atopobiaceae (1)	nan (18)

[top](#)

Cluster 2

Total number of members in cluster: 107

Average length of proteins in cluster: 411.8

Conserved (non-aliphatic) residues:

Q 243 (98.1%) R 291 (100.0%) R 356 (100.0%) S 480 (100.0%) D 537 (100.0%) R 542 (98.1%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
AHB32563.2	Moraxellales	Moraxellaceae	Acinetobacter	Acinetobacter baumannii	O3	0
ACA24764.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O143	0
BAQ02088.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O187	0
ACA24754.1	Enterobacterales	Enterobacteriaceae	Shigella	Shigella boydii	8	0
AFW04847.1	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	O59	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

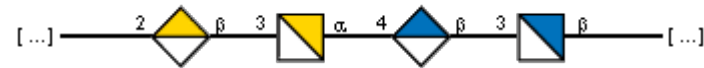
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

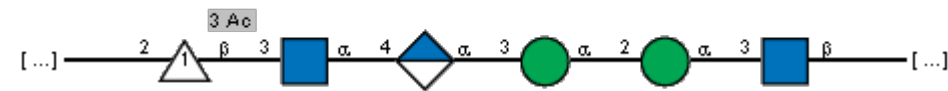
Sugars in cluster:

ACA24764.1 Escherichia coli O143, ACA24754.1 Shigella boydii 8:



CSDB record ID: 1885

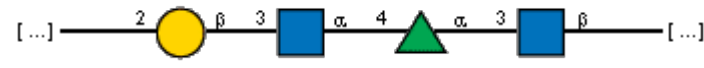
BAQ02088.1 Escherichia coli O187:



1 = b-D-Fucp3N

CSDB record ID: 1934

AFW04847.1 Salmonella enterica O59:



CSDB record ID: 3362

Sugars for blast hits:

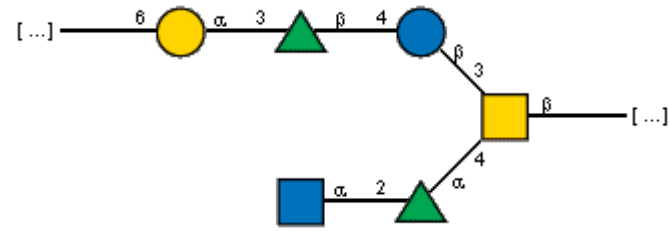
Alphafold models:

[BAQ02088.1](#)

[ACA24754.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Moraxellales (21)	Moraxellaceae (21)	Acinetobacter (21)
Enterobacterales (21)	Enterobacteriaceae (12)	Escherichia (6)
		Shigella (3)
		Salmonella (1)
		Citrobacter (1)
		Buttiauxella (1)
	Morganellaceae (6)	Providencia (3)
		Proteus (2)
		Photorhabdus (1)
	Erwiniaceae (1)	Mixta (1)
	Hafniaceae (1)	Obesumbacterium (1)
	Pectobacteriaceae (1)	Pectobacterium (1)
Bacteroidales (18)	Bacteroidaceae (8)	Bacteroides (7)
		nan (2)
	nan (2)	nan (2)
	Tannerellaceae (2)	Parabacteroides (2)
	Rikenellaceae (2)	nan (2)
		Alistipes (1)
	Prevotellaceae (1)	Prevotella (1)
	Odoribacteraceae (1)	Odoribacter (1)
	Muribaculaceae (1)	nan (2)
Pasteurellales (10)	Pasteurellaceae (10)	Gallibacterium (9)
		Glaesserella (1)
Vibrionales (10)	Vibrionaceae (10)	Vibrio (9)
		Photobacterium (1)
Aeromonadales (5)	Aeromonadaceae (5)	Aeromonas (5)
Alteromonadales (5)	Shewanellaceae (3)	Shewanella (3)
	Colwelliaceae (1)	Colwellia (1)
	Pseudoalteromonadaceae (1)	Pseudoalteromonas (1)
Flavobacteriales (4)	Weeksellaceae (2)	Elizabethkingia (2)
	Flavobacteriaceae (2)	Polaribacter (1)
		Tenacibaculum (1)
Sphingobacteriales (4)	Sphingobacteriaceae (4)	Parapedobacter (2)
		Pseudopedobacter (1)
		Sphingobacterium (1)
nan (2)	nan (2)	Gallaecimonas (1)
Spirochaetales (1)	Treponemataceae (1)	Treponema (1)
Synergistales (1)	Synergistaceae (1)	Dethiosulfovibrio (1)
Lactobacillales (1)	Lactobacillaceae (1)	Ligilactobacillus (1)
Eubacteriales (1)	Clostridiaceae (1)	Clostridium (1)



CSDB record ID: 2624

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Eubacteriales (44)	Lachnospiraceae (17)	nan (19)
		Butyrivibrio (5)
		Blautia (2)
		Dorea (1)
		Faecalicatena (1)
		Anaerostipes (1)
	Oscillospiraceae (16)	nan (19)
		Ruminococcus (4)
		Faecalibacterium (3)
	nan (14)	nan (19)
Lactobacillales (17)	Clostridiaceae (5)	nan (19)
		Clostridium (4)
	Eubacteriaceae (4)	Eubacterium (4)
	Streptococcaceae (12)	Streptococcus (10)
		Lactococcus (2)
	Enterococcaceae (2)	Enterococcus (2)
	Lactobacillaceae (2)	Limosilactobacillus (2)
nan (13)	Carnobacteriaceae (1)	Trichococcus (1)
	nan (14)	nan (19)
Coriobacteriales (5)	Atopobiaceae (4)	Olsenella (2)
		Atopobium (1)
		Parafannyhessea (1)
	Coriobacteriaceae (1)	Collinsella (1)
Erysipelotrichales (4)	Erysipelotrichaceae (3)	Amedibacillus (1)
		Faecalicoccus (1)
	Turicibacteraceae (1)	Turicibacter (1)
Bacillales (3)	Bacillaceae (2)	Bacillus (2)
	Planococcaceae (1)	Ureibacillus (1)
Eggerthellales (2)	Eggerthellaceae (2)	Adlercreutzia (1)
		Eggerthella (1)
Tissierellales (1)	Peptoniphilaceae (1)	Anaerococcus (1)
Fibrobacterales (1)	Fibrobacteraceae (1)	Fibrobacter (1)
Bifidobacteriales (1)	Bifidobacteriaceae (1)	Bifidobacterium (1)

Cluster 1

Total number of members in cluster: 89

Average length of proteins in cluster: 427.7

Conserved (non-aliphatic) residues:

Q 78 (100.0%) R 249 (100.0%) R 295 (100.0%) E 364 (97.8%) Q 399 (98.9%) K 406 (100.0%) T 462 (97.8%) H 519 (98.9%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
WP_097449287.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O57	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

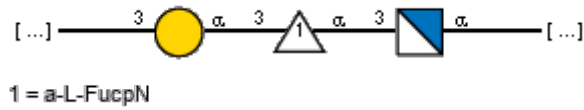
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

WP_097449287.1 Escherichia coli O57:



CSDB record ID: 699

Sugars for blast hits:

Alphafold models:

[WP_097449287.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Hyphomicrobiales (61)	Rhizobiaceae (23)	Rhizobium (10)
		Agrobacterium (8)
		Shinella (3)
		Neorhizobium (1)
	Brucellaceae (21)	Brucella (14)

order (count)	family (count)	genus (count)
		Ochrobactrum (6)
	Phyllobacteriaceae (8)	Phyllobacterium (4)
		Mesorhizobium (3)
		Aquamicrobium (1)
	Methylocystaceae (4)	Methylopila (3)
		Hansschlegelia (1)
	Chelatococcaceae (2)	Chelatococcus (2)
	Kaistiaceae (1)	Kaistia (1)
	Afifellaceae (1)	Afifella (1)
nan (6)	nan (1)	nan (1)
Pseudanabaenales (3)	Leptolyngbyaceae (3)	Leptolyngbya (2)
		nan (1)
Chromatiales (2)	Chromatiaceae (2)	Halochromatium (1)
		Thiohalocapsa (1)
Burkholderiales (2)	Alcaligenaceae (1)	nan (1)
	Comamonadaceae (1)	Kinneretia (1)
Verrucomicrobiales (2)	Verrucomicrobiaceae (2)	Phragmitibacter (1)
		Prostheco bacter (1)
Enterobacterales (1)	Enterobacteriaceae (1)	Escherichia (1)
Sphingomonadales (1)	Erythrobacteraceae (1)	Altererythrobacter (1)
Nostocales (1)	Nostocaceae (1)	Richelia (1)
Corynebacteriales (1)	Mycobacteriaceae (1)	Mycobacterium (1)
Chroococcidiopsidales (1)	Chroococcidiopsidaceae (1)	Chroococcidiopsis (1)
Rhodospirillales (1)	nan (1)	nan (1)
Kiritimatiellales (1)	Pontiellaceae (1)	nan (1)
Bryobacterales (1)	Bryobacteraceae (1)	nan (1)
Vibrionales (1)	Vibrionaceae (1)	Vibrio (1)
Pirellulales (1)	nan (1)	nan (1)
Bacteroidales (1)	Tannerellaceae (1)	Parabacteroides (1)
Hyphomonadales (1)	Hyphomonadaceae (1)	Henriciella (1)
Synechococcales (1)	Coelosphaeriaceae (1)	Snowella (1)

[top](#)

Cluster 44

Total number of members in cluster: 83

Average length of proteins in cluster: 448.1

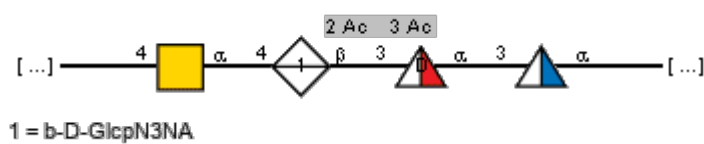
Conserved (non-aliphatic) residues:

Y 264 (100.0%) R 345 (100.0%) R 421 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
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protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
AHB32510.1	Moraxellales	Moraxellaceae	Acinetobacter	Acinetobacter nosocomialis	O11	0
AHB32490.1	Moraxellales	Moraxellaceae	Acinetobacter	Acinetobacter baumannii	O15	0
ABF01010.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O28ac	0
ACK44379.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O42	0
BAQ02048.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O185	0
AAM27546.1	Pseudomonadales	Pseudomonadaceae	Pseudomonas	Pseudomonas aeruginosa	O1	0



CSDB record ID: 6636

Sugars for blast hits:

Alphafold models:

[AHB32490.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (28)	Enterobacteriaceae (17)	Escherichia (15)
		Citrobacter (1)
		Enterobacter (1)
	Morganellaceae (6)	Morganella (3)
		Providencia (2)
		Proteus (1)
	Hafniaceae (3)	Edwardsiella (3)
Moraxellales (19)	Budviciaceae (1)	Limnobaculum (1)
	Yersiniaceae (1)	Yersinia (1)
	Moraxellaceae (19)	Acinetobacter (18)
		Psychrobacter (1)
Pseudomonadales (11)	Pseudomonadaceae (11)	Pseudomonas (11)
Bacteroidales (9)	Paludibacteraceae (3)	nan (1)
	Tannerellaceae (3)	Parabacteroides (3)
	Bacteroidaceae (2)	Bacteroides (2)
	nan (1)	nan (1)
Vibrionales (6)	Vibrionaceae (6)	Photobacterium (3)
		Vibrio (3)
Neisseriales (2)	Neisseriaceae (2)	Vitreoscilla (1)
		Conchiformibius (1)
Burkholderiales (2)	Burkholderiaceae (2)	Caballeronia (1)
		Burkholderia (1)
Alteromonadales (2)	Pseudoalteromonadaceae (1)	Pseudoalteromonas (1)
	Shewanellaceae (1)	Shewanella (1)
Oceanospirillales (1)	Halomonadaceae (1)	Zymobacter (1)
Cytophagales (1)	Cytophagaceae (1)	Siphonobacter (1)
Hyphomicrobiales (1)	Devosiaceae (1)	Devosia (1)
Aeromonadales (1)	Aeromonadaceae (1)	Aeromonas (1)

[top](#)

Cluster 37

Total number of members in cluster: 82

Average length of proteins in cluster: 403.3

Conserved (non-aliphatic) residues:

E 271 (100.0%) S 273 (98.8%) Y 377 (98.8%) R 381 (100.0%) N 393 (100.0%) N 457 (98.8%) D 460 (100.0%) K 467 (98.8%) E 471 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
ADI43263.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O25	0
ADR74237.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O109	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

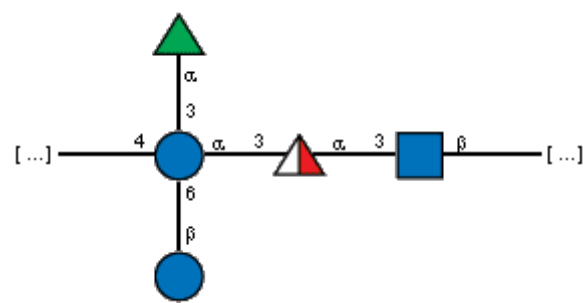
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

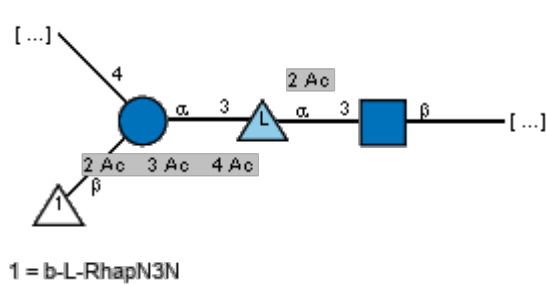
Sugars in cluster:

ADI43263.1 Escherichia coli O25:



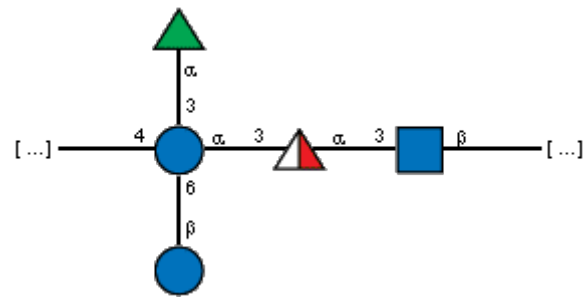
CSDB record ID: 12694

ADR74237.1 Escherichia coli O109:



CSDB record ID: 1848

Sugars for blast hits:



CSDB record ID: 12694

Alphafold models:

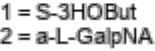
[ADI43263.1](#)

[ADR74237.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (50)	Enterobacteriaceae (40)	Escherichia (17)
		Klebsiella (11)
		Citrobacter (4)
		Enterobacter (4)
		Leclercia (2)
		Salmonella (2)
	Pectobacteriaceae (8)	Dickeya (8)
	Erwiniaceae (1)	Erwinia (1)
	Morganellaceae (1)	Proteus (1)
Sphingomonadales (8)	Sphingomonadaceae (7)	Sphingomonas (7)
	Sphingosiniceae (1)	Polymorphobacter (1)
Vibrionales (4)	Vibrionaceae (4)	Vibrio (3)
		Photobacterium (1)
Burkholderiales (3)	nan (2)	Rhizobacter (1)
	Comamonadaceae (1)	Comamonas (1)
	Burkholderiaceae (1)	Polynucleobacter (1)
Alteromonadales (3)	Shewanellaceae (2)	Shewanella (2)
	Colwelliaceae (1)	Colwellia (1)
Flavobacteriales (2)	Weeksellaceae (1)	Chryseobacterium (1)
Pseudomonadales (2)	Pseudomonadaceae (2)	Pseudomonas (2)
Oceanospirillales (2)	Halomonadaceae (2)	Halomonas (2)
Kordiimonadales (1)	Kordiimonadaceae (1)	nan (2)
Rhodobacterales (1)	Rhodobacteraceae (1)	nan (2)
Campylobacterales (1)	Thiovulaceae (1)	Sulfurimonas (1)
Nitrosomonadales (1)	Thiobacillaceae (1)	Thiobacillus (1)
Cytophagales (1)	Cyclobacteriaceae (1)	Algoriphagus (1)
Rhodocyclales (1)	Zoogloeaceae (1)	Zoogloea (1)
Methylococcales (1)	Methylococcaceae (1)	Methyloprofundus (1)
Aeromonadales (1)	Aeromonadaceae (1)	Aeromonas (1)

AAM27766.1 *Pseudomonas aeruginosa* O3:

AAM27615.1 *Pseudomonas aeruginosa* O13:AAM27645.1 *Pseudomonas aeruginosa* O15:

Sugars for blast hits:

Alphafold models:

AAM27615.1

Taxonomy:

order (count)	family (count)	genus (count)
Pseudomonadales (23)	Pseudomonadaceae (22)	Pseudomonas (22)
	Marinobacteraceae (1)	Marinobacter (1)
nan (6)	nan (5)	nan (2)
	Dissulfurirhabdaceae (1)	Dissulfurirhabdus (1)
Vibrionales (5)	Vibrionaceae (5)	Vibrio (4)
		Photobacterium (1)
Lactobacillales (4)	Enterococcaceae (3)	Enterococcus (2)
		Vagococcus (1)
	Carnobacteriaceae (1)	Desemzia (1)
Enterobacterales (3)	Enterobacteriaceae (3)	Escherichia (3)
Bacteroidales (3)	Bacteroidaceae (2)	Bacteroides (2)
	Tannerellaceae (1)	Parabacteroides (1)
Bacillales (3)	Bacillaceae (3)	Bacillus (2)
		Gracilibacillus (1)
Micrococcales (3)	Microbacteriaceae (2)	Salinibacterium (1)
		Cryobacterium (1)

order (count)	family (count)	genus (count)
	Intrasporangiaceae (1)	Tetrasphaera (1)
Deinococcales (3)	Deinococcaceae (3)	Deinococcus (3)
Campylobacterales (2)	nan (5)	nan (2)
	Campylobacteraceae (1)	nan (2)
Alteromonadales (2)	Shewanellaceae (2)	Parashewanella (1)
		Shewanella (1)
Eubacteriales (2)	Clostridiaceae (1)	Alkaliphilus (1)
	Syntrophomonadaceae (1)	nan (2)
Chitinophagales (2)	Chitinophagaceae (2)	Chitinophaga (2)
Flavobacteriales (2)	Flavobacteriaceae (2)	Flavobacterium (1)
		Winogradskyella (1)
Burkholderiales (1)	Comamonadaceae (1)	Variovorax (1)
Deferribacterales (1)	nan (5)	nan (2)
Thermoanaerobacterales (1)	Thermoanaerobacterales Family III. Incertae Sedis (1)	Thermoanaerobacterium (1)
Oceanospirillales (1)	Halomonadaceae (1)	Halomonas (1)
Chitinivibrionales (1)	nan (5)	nan (2)
Sphingobacteriales (1)	Sphingobacteriaceae (1)	Pedobacter (1)
Neisseriales (1)	Chromobacteriaceae (1)	Deefgea (1)
Eggerthellales (1)	Eggerthellaceae (1)	Adlercreutzia (1)

[top](#)

Cluster 27

Total number of members in cluster: 67

Average length of proteins in cluster: 396.9

Conserved (non-aliphatic) residues:

R 189 (100.0%) K 255 (97.0%) R 301 (97.0%) Y 326 (100.0%) N 393 (100.0%) D 404 (100.0%) Y 441 (97.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
ADC54950.1	Enterobacteriales	Enterobacteriaceae	Escherichia	Escherichia coli	O18	0
BAQ00669.1	Enterobacteriales	Enterobacteriaceae	Escherichia	Escherichia coli	O18ab	0
BAQ01732.1	Enterobacteriales	Enterobacteriaceae	Escherichia	Escherichia coli	O142	0
BAQ00687.1	Enterobacteriales	Enterobacteriaceae	Escherichia	Escherichia coli	O18ac	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

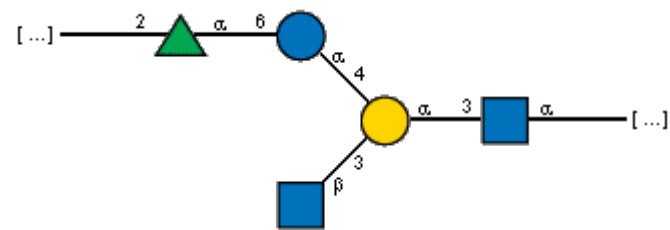
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

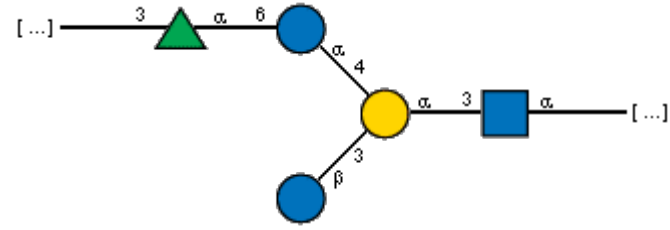
Sugars in cluster:

ADC54950.1 Escherichia coli O18:



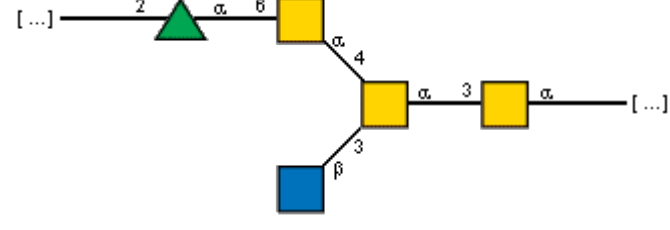
CSDB record ID: 20645

BAQ00669.1 Escherichia coli O18ab:



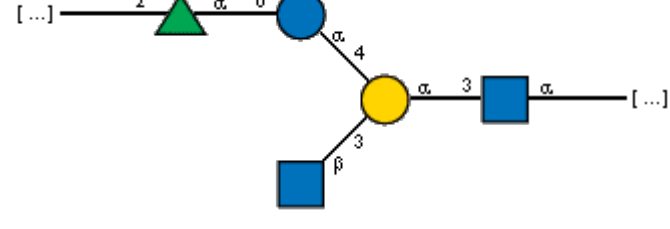
CSDB record ID: 1524

BAQ01732.1 Escherichia coli O142:



CSDB record ID: 1884

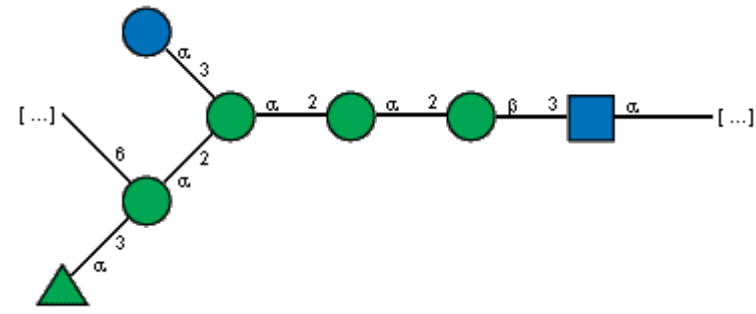
BAQ00687.1 Escherichia coli O18ac:



CSDB record ID: 1521

Sugars for blast hits:

ARD51912.1 Escherichia coli O68:



CSDB record ID: 1574

AlphaFold models:

[ADC54950.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Bacteroidales (32)	Prevotellaceae (25)	Prevotella (18)
		Alloprevotella (5)
		Paraprevotella (1)
Enterobacterales (14)	Paludibacteraceae (5)	nan (9)
	Enterobacteriaceae (13)	Escherichia (11)
		Leclercia (1)
		Salmonella (1)
Moraxellales (5)	Morganellaceae (1)	Morganella (1)
	Moraxellaceae (5)	Acinetobacter (5)
Flavobacteriales (5)	Weeksellaceae (3)	Elizabethkingia (2)
		Chryseobacterium (1)
	Flavobacteriaceae (2)	Capnocytophaga (1)
		Flavobacterium (1)
nan (5)	nan (7)	nan (9)
Vibrionales (4)	Vibrionaceae (4)	Photobacterium (3)
		Aliivibrio (1)
Pseudomonadales (1)	Pseudomonadaceae (1)	Pseudomonas (1)
Thermoanaerobacterales (1)	Thermoanaerobacteraceae (1)	nan (9)

[top](#)

Cluster 68

Total number of members in cluster: 66

Average length of proteins in cluster: 402.1

Conserved (non-aliphatic) residues:

D 220 (100.0%) S 252 (100.0%) R 256 (100.0%) K 321 (100.0%) R 325 (100.0%) R 401 (100.0%) Q 403 (98.5%)

Seeds in cluster:

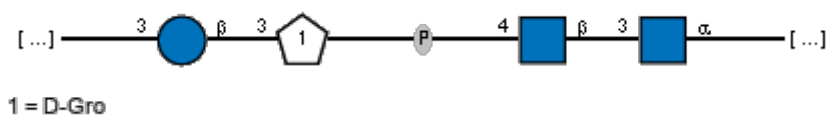
protein_accession	order	family	genus	species	serotype	Enterobacterial common
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BAQ00758.1	Enterobacterales Enterobacteriaceae Escherichia coli	O28ab	0
BAQ00879.1	Enterobacterales Enterobacteriaceae Escherichia coli	O39	0
ABG81806.1	Enterobacterales Enterobacteriaceae Escherichia coli	O123	0
BAQ02068.1	Enterobacterales Enterobacteriaceae Escherichia coli	O186	0
AAD44158.1	Enterobacterales Enterobacteriaceae Escherichia coli	O7	0
BAH24292.1	Enterobacterales Enterobacteriaceae Escherichia coli	O7	0
AFC91472.1	Enterobacterales Enterobacteriaceae Escherichia coli	O121	0
AFC91514.1	Enterobacterales Enterobacteriaceae Escherichia coli	O121	0
AAO39700.1	Enterobacterales Enterobacteriaceae Escherichia coli	O121	0
AFC91570.1	Enterobacterales Enterobacteriaceae Escherichia coli	O121	0
AJR19430.1	Enterobacterales Enterobacteriaceae Escherichia coli	O186	0
BAQ02224.1	Enterobacterales Enterobacteriaceae Escherichia coli	O123	0
AAR97964.1	Enterobacterales Enterobacteriaceae Shigella dysenteriae	7	0

- [MSA fasta](#)
- [Malign view](#)
- [Fasta of members](#)
- [Logoplot](#)
- [Phylogenetic tree](#)
- [Hits in cluster](#)

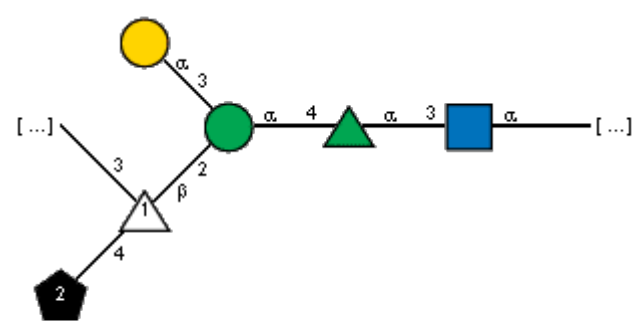
Sugars in cluster:

BAQ00758.1 Escherichia coli O28ab:



CSDB record ID: 736

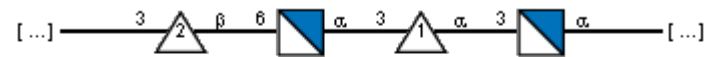
BAQ00879.1 Escherichia coli O39:



1 = b-D-Quip4N
2 = R-3HOBuT

CSDB record ID: 1383

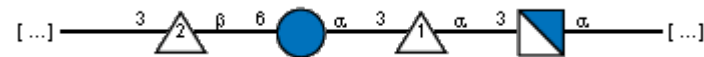
ABG81806.1 Escherichia coli O123, BAQ02224.1 Escherichia coli O123:



1 = a-L-QuipN
2 = b-D-Quip4N

CSDB record ID: 697

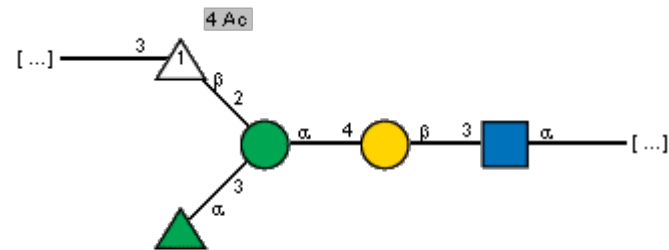
BAQ02068.1 Escherichia coli O186, AJR19430.1 Escherichia coli O186:



1 = a-L-QuipN
2 = b-D-Quip4N

CSDB record ID: 1933

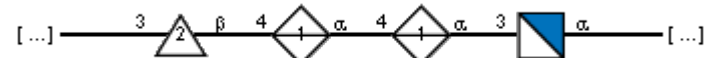
AAD44158.1 Escherichia coli O7, BAH24292.1 Escherichia coli O7:



1 = b-D-Quip4N

CSDB record ID: 1385

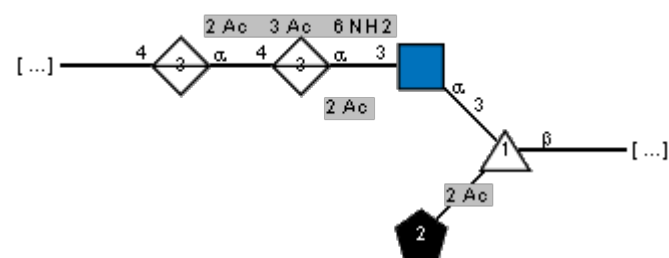
AFC91472.1 Escherichia coli O121, AFC91514.1 Escherichia coli O121, AAO39700.1 Escherichia coli O121, AFC91570.1 Escherichia coli O121:



1 = a-D-GalpNA
2 = b-D-Quip4N

CSDB record ID: 1861

AAR97964.1 Shigella dysenteriae 7:



1 = b-D-Quip4N
 2 = Gly
 3 = a-D-GalpNA

CSDB record ID: 108660

Sugars for blast hits:

Alphafold models:

[ABG81806.1](#)

[AFC91472.1](#)

[BAQ02224.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (37)	Enterobacteriaceae (30)	Escherichia (19)
		Salmonella (5)
		Citrobacter (2)
		Enterobacter (2)
		Shigella (1)
		Kluyvera (1)
		Providencia (2)
		Proteus (2)
		Photorhabdus (2)
		Hafnia (1)
Aeromonadales (6)	Aeromonadaceae (6)	Aeromonas (6)
		Massilia (1)
Burkholderiales (5)	Oxalobacteraceae (2)	Noviherbaspirillum (1)
		Polynucleobacter (1)
		Pandoraea (1)
		Pelomonas (1)
		Vibrio (5)
Vibrionales (5)	Vibrionaceae (5)	Acinetobacter (5)
Pseudomonadales (2)	Pseudomonadaceae (2)	Aquitalea (1)
Neisseriales (1)	Chromobacteriaceae (1)	Shewanella (1)
Alteromonadales (1)	Shewanellaceae (1)	Propionivibrio (1)
Rhodocyclales (1)	Rhodocyclaceae (1)	nan (1)
Nitrosomonadales (1)	Methylophilaceae (1)	Methylostenobacterium (1)
Oceanospirillales (1)	Oceanospirillaceae (1)	Marinobacterium (1)

Cluster 12

Total number of members in cluster: 66

Average length of proteins in cluster: 369.6

Conserved (non-aliphatic) residues:

R 188 (100.0%) K 218 (100.0%) D 226 (100.0%) S 227 (100.0%) N 228 (100.0%) S 281 (100.0%) R 282 (98.5%) D 367 (100.0%) S 369 (100.0%) K 373 (98.5%) H 414 (100.0%) E 423 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
AHB32538.1	Moraxellales	Moraxellaceae	Acinetobacter	Acinetobacter nosocomialis	O2	0
BAQ00846.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O37	0
BAQ00975.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O48	0
ACD37014.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O112ac	0
ACD37157.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O130	0
BAQ01494.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O102	0
AFS33314.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O102	0
ACD37006.1	Enterobacterales	Enterobacteriaceae	Shigella	Shigella dysenteriae	2	0
AFW04741.1	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	O21	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

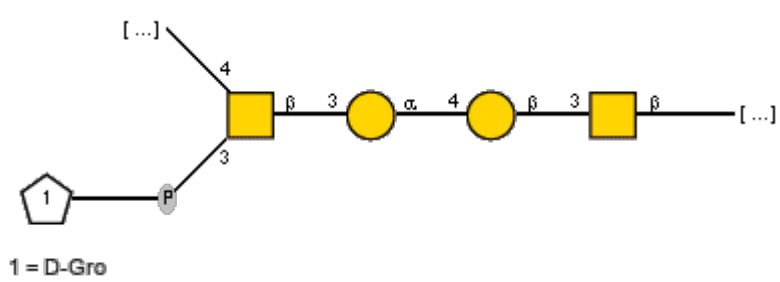
[Logoplot](#)

[Phylogenetic tree](#)

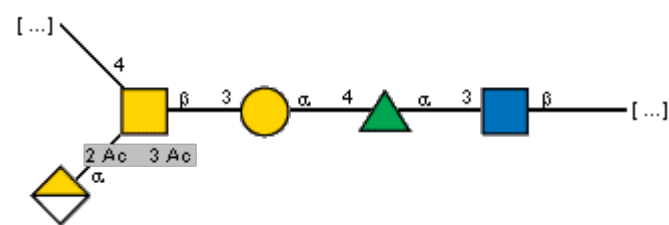
[Hits in cluster](#)

Sugars in cluster:

BAQ00846.1 Escherichia coli O37:

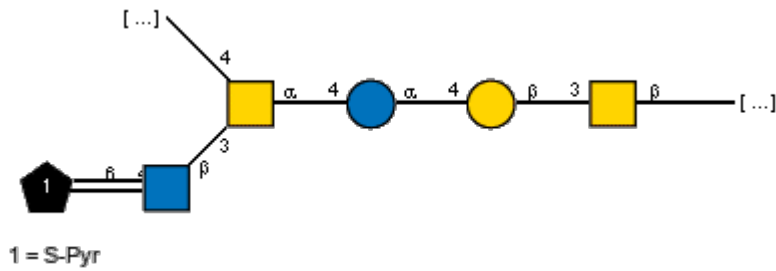


BAQ00975.1 Escherichia coli O48:



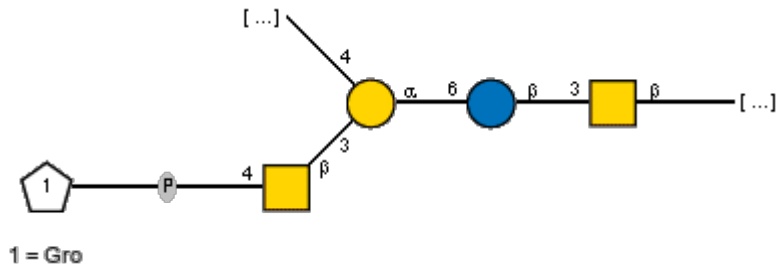
CSDB record ID: 1555

ACD37014.1 Escherichia coli O112ac:



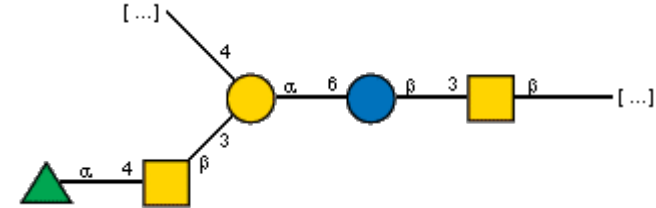
CSDB record ID: 1852

ACD37157.1 Escherichia coli O130:



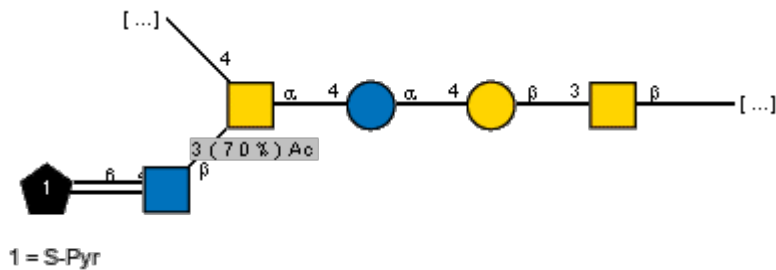
CSDB record ID: 1871

BAQ01494.1 Escherichia coli O102, AFS33314.1 Escherichia coli O102:



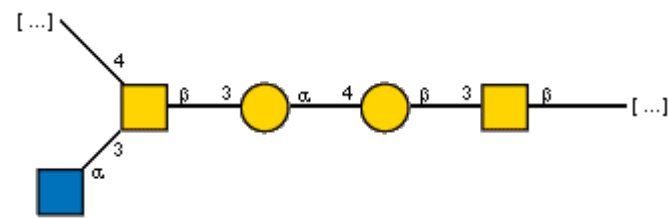
CSDB record ID: 1841

ACD37006.1 Shigella dysenteriae 2:



CSDB record ID: 1869

AFW04741.1 Salmonella enterica O21:



CSDB record ID: 30351

Sugars for blast hits:

Alphafold models:

[AHB32538.1](#)

[ACD37014.1](#)

[ACD37157.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (35)	Enterobacteriaceae (31)	Escherichia (22)
		Salmonella (4)
		Citrobacter (2)
		Enterobacter (2)
		Shigella (1)
	Morganellaceae (3)	Proteus (1)
		Providencia (1)
		Xenorhabdus (1)
	Hafniaceae (1)	Edwardsiella (1)
	Moraxellales (9)	Moraxellaceae (9)
Vibrionales (8)	Vibrionaceae (8)	Vibrio (5)
		Photobacterium (2)
		Aliivibrio (1)
Eubacteriales (5)	Peptostreptococcaceae (2)	Paeniclostridium (2)
	Clostridiaceae (1)	Paraclostridium (1)
	Oscillospiraceae (1)	Pseudobacteroides (1)
	Lachnospiraceae (1)	Schaedlerella (1)
nan (3)	nan (3)	nan (3)
Bacillales (2)	Bacillaceae (2)	Bacillus (2)
Campylobacterales (1)	Arcobacteraceae (1)	Aliarcobacter (1)
Cytophagales (1)	Marivirgaceae (1)	Marivirga (1)
Spirochaetales (1)	Treponemataceae (1)	Rectinema (1)
Aeromonadales (1)	Aeromonadaceae (1)	Aeromonas (1)

[top](#)

Cluster 56

Total number of members in cluster: 59

Average length of proteins in cluster: 359.0

Conserved (non-aliphatic) residues:

R 65 (100.0%) D 71 (100.0%) Y 75 (100.0%) E 101 (100.0%) R 168 (100.0%) H 214 (100.0%) Y 288 (100.0%) R 371 (100.0%) Y 443 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
ADQ37335.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O118	0
ACA24821.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O152	0
ADN43894.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O173	0
ADQ37322.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O151	0
ACA24811.1	Enterobacterales	Enterobacteriaceae	Shigella	Shigella dysenteriae	12	0
AFW04867.1	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	O47	0

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[Fasta of members](#)

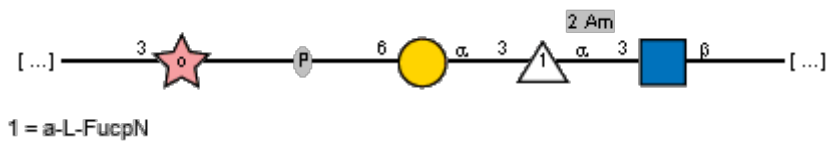
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

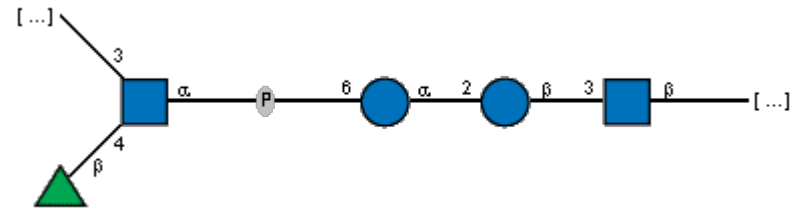
Sugars in cluster:

ADQ37335.1 Escherichia coli O118:



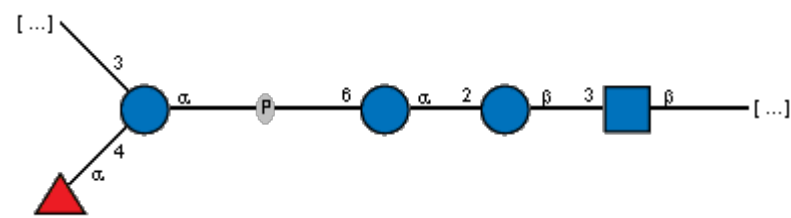
CSDB record ID: 1858

ACA24821.1 Escherichia coli O152, ACA24811.1 Shigella dysenteriae 12:



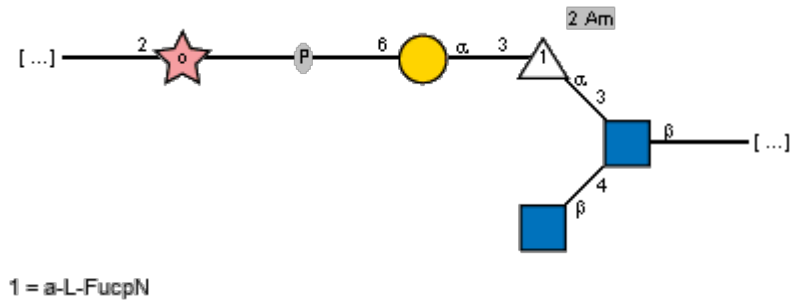
CSDB record ID: 1893

ADN43894.1 Escherichia coli O173:



CSDB record ID: 3159

ADQ37322.1 Escherichia coli O151:



CSDB record ID: 1892

Sugars for blast hits:

Alphafold models:

[ACA24821.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (36)	Enterobacteriaceae (23)	Escherichia (11)
		Salmonella (7)
		Citrobacter (2)
		Shigella (1)
		nan (1)
		Buttiauxella (1)
	Morganellaceae (10)	Morganella (4)
		Providencia (3)
		Proteus (3)
		Pantoea (2)
Bacteroidales (8)	Erwiniaceae (2)	Hafnia (1)
	Bacteroidaceae (5)	Bacteroides (5)
		Parabacteroides (3)
Spirochaetales (5)	Treponemataceae (4)	Treponema (4)
	Spirochaetaceae (1)	nan (1)
Pasteurellales (2)	Pasteurellaceae (2)	Haemophilus (1)
		Spirabiiibacterium (1)
Aeromonadales (2)	Aeromonadaceae (2)	Aeromonas (2)
nan (2)	nan (2)	Wohlfahrtiimonas (2)
Pseudomonadales (1)	Pseudomonadaceae (1)	Thiopseudomonas (1)
Oceanospirillales (1)	Oceanospirillaceae (1)	Venatorbacter (1)

order (count)	family (count)	genus (count)
Campylobacterales (1)	Campylobacteraceae (1)	Campylobacter (1)
Flavobacteriales (1)	Flavobacteriaceae (1)	Flavobacterium (1)

[top](#)

Cluster 36

Total number of members in cluster: 59

Average length of proteins in cluster: 357.0

Conserved (non-aliphatic) residues:

Q 75 (100.0%) D 81 (100.0%) Y 82 (100.0%) Y 85 (100.0%) E 106 (100.0%) N 178 (98.3%) R 181 (100.0%) H 216 (100.0%) Y 292 (100.0%) K 314 (100.0%) R 380 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
AHB32283.1	Moraxellales	Moraxellaceae	Acinetobacter	Acinetobacter baumannii	O21	0
ACH97162.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O21	0

MSA fasta

Malign view

Fasta of members

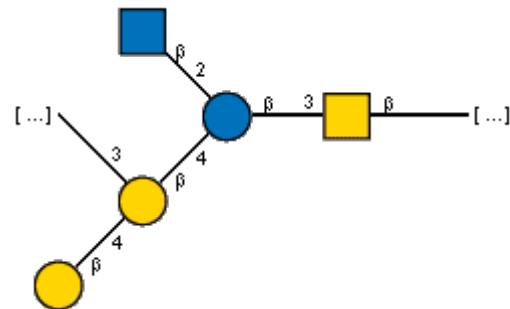
Logoplot

Phylogenetic tree

Hits in cluster

Sugars in cluster:

ACH97162.1 Escherichia coli O21:



CSDb record ID: 1529

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (15)	Morganellaceae (8)	Providencia (4)
		Photorhabdus (1)
		Morganella (1)
		Xenorhabdus (1)
		Proteus (1)
	Enterobacteriaceae (7)	Salmonella (3)
		Escherichia (2)
		Citrobacter (1)
Vibrionales (15)	Vibrionaceae (15)	Vibrio (13)
		Photobacterium (1)
		Enterovibrio (1)
Moraxellales (8)	Moraxellaceae (8)	Acinetobacter (8)
Bacteroidales (7)	Bacteroidaceae (4)	Bacteroides (4)
	Tannerellaceae (1)	Parabacteroides (1)
	Muribaculaceae (1)	nan (1)
	nan (1)	nan (1)
Alteromonadales (7)	Pseudoalteromonadaceae (3)	Pseudoalteromonas (3)
	Shewanellaceae (2)	Shewanella (2)
	Moritellaceae (1)	Moritella (1)
	Idiomarinaceae (1)	Idiomarina (1)
Flavobacteriales (3)	Flavobacteriaceae (2)	Tenacibaculum (2)
	Weeksellaceae (1)	Empedobacter (1)
Aeromonadales (3)	Aeromonadaceae (3)	Aeromonas (3)
Campylobacterales (1)	Arcobacteraceae (1)	Arcobacter (1)

[top](#)

Cluster 21

Total number of members in cluster: 58

Average length of proteins in cluster: 374.2

Conserved (non-aliphatic) residues:

Q 170 (100.0%) D 185 (100.0%) R 198 (100.0%) R 212 (100.0%) E 219 (100.0%) S 262 (100.0%) R 313 (100.0%) D 322 (100.0%) S 324 (100.0%) K 328 (100.0%) D 366 (100.0%) K 413 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
BAQ00994.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O49	0
ADC54974.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O85	0

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
BAQ01917.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O175	0
CAN87666.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O45	0
AFW04828.1	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	O44	0
AFW04837.1	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	O53	0

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[Fasta of members](#)

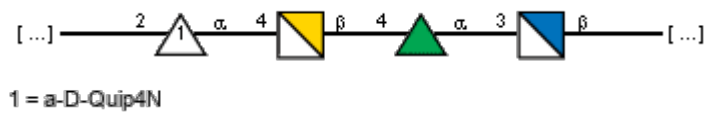
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

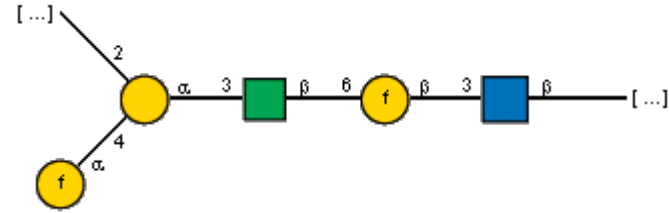
Sugars in cluster:

BAQ00994.1 Escherichia coli O49:



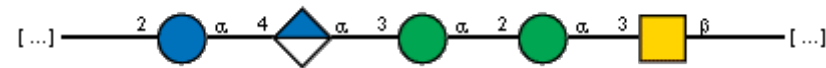
CSDB record ID: 1556

ADC54974.1 Escherichia coli O85:



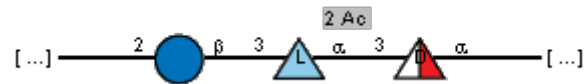
CSDB record ID: 1591

BAQ01917.1 Escherichia coli O175:

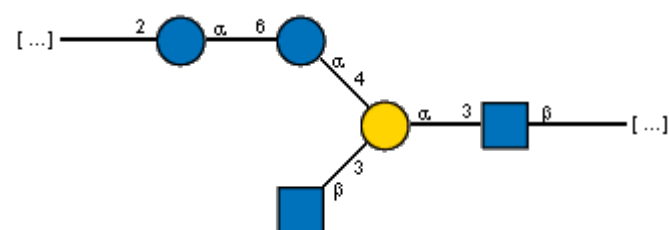


CSDB record ID: 1917

CAN87666.1 Escherichia coli O45:



CSDB record ID: 1552

AFW04828.1 *Salmonella enterica* O44:

CSDb record ID: 3367

AFW04837.1 *Salmonella enterica* O53:

CSDb record ID: 26312

Sugars for blast hits:

Alphafold models:

BAQ00994.1

BAQ01917.1

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (46)	Enterobacteriaceae (37)	Escherichia (16)
		Salmonella (15)
		Citrobacter (3)
		Buttiauxella (1)
		Plesiomonas (1)
		Shigella (1)
	Morganellaceae (8)	Providencia (4)
		Proteus (4)
	Hafniaceae (1)	Hafnia (1)
Moraxellales (5)	Moraxellaceae (5)	Acinetobacter (5)
Vibrionales (5)	Vibrionaceae (5)	Vibrio (4)
		Photobacterium (1)
Aeromonadales (1)	Aeromonadaceae (1)	Aeromonas (1)
nan (1)	nan (1)	Wohlfahrtiimonas (1)

[top](#)

Cluster 75

Total number of members in cluster: 51

Average length of proteins in cluster: 400.1

Conserved (non-aliphatic) residues:

S 57 (100.0%) R 84 (98.0%) S 101 (100.0%) D 114 (100.0%) E 146 (100.0%) R 221 (100.0%) Q 222 (100.0%) H 255 (100.0%) K 320 (100.0%) R 399 (100.0%)

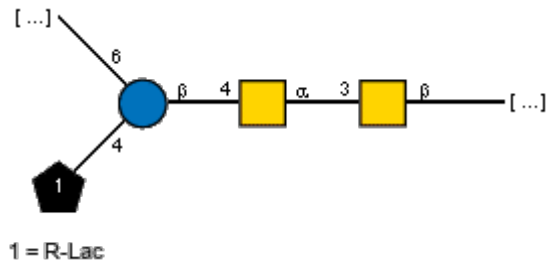
Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
AHB32687.1	Moraxellales	Moraxellaceae	Acinetobacter	Acinetobacter baumannii	O14	0
BAQ01743.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O144	0
ABI55342.1	Enterobacterales	Enterobacteriaceae	Shigella	Shigella boydii	17	0

- [MSA fasta](#)
- [Malign view](#)
- [Fasta of members](#)
- [Logoplot](#)
- [Phylogenetic tree](#)
- [Hits in cluster](#)

Sugars in cluster:

ABI55342.1 Shigella boydii 17:



CSDB record ID: 714

Sugars for blast hits:

Alphafold models:

- [AHB32687.1](#)
- [BAQ01743.1](#)
- [ABI55342.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (42)	Enterobacteriaceae (24)	Klebsiella (14)
		Escherichia (3)
		Raoultella (3)
		Citrobacter (3)

order (count)	family (count)	genus (count)
		Shigella (1)
	Yersiniaceae (17)	Serratia (17)
	Morganellaceae (1)	Proteus (1)
Vibrionales (4)	Vibrionaceae (4)	Vibrio (4)
Moraxellales (2)	Moraxellaceae (2)	Acinetobacter (2)
Flavobacteriales (2)	Flavobacteriaceae (2)	Capnocytophaga (2)
Campylobacterales (1)	Campylobacteraceae (1)	Campylobacter (1)

[top](#)

Cluster 17

Total number of members in cluster: 48

Average length of proteins in cluster: 368.2

Conserved (non-aliphatic) residues:

D 86 (100.0%) Y 90 (97.9%) E 195 (97.9%) R 337 (100.0%) E 373 (100.0%) N 439 (100.0%) R 445 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
AAN23041.1	Enterobacterales	Yersiniaceae	Yersinia	Yersinia pseudotuberculosis	O:1A	0
AAN23078.1	Enterobacterales	Yersiniaceae	Yersinia	Yersinia pseudotuberculosis	O:2a	0
AAN23057.1	Enterobacterales	Yersiniaceae	Yersinia	Yersinia pseudotuberculosis	O:4b	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

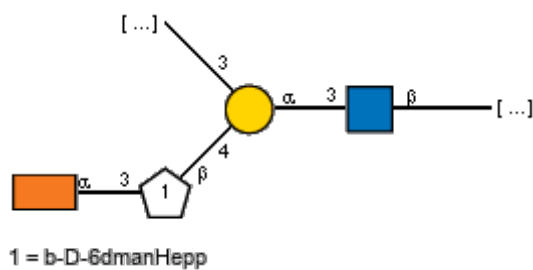
[Logoplot](#)

[Phylogenetic tree](#)

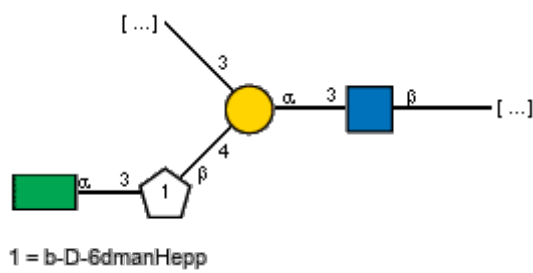
[Hits in cluster](#)

Sugars in cluster:

AAN23078.1 Yersinia pseudotuberculosis O:2a:



AAN23057.1 Yersinia pseudotuberculosis O:4b:



CSDB record ID: 12136

Sugars for blast hits:

Alphafold models:

[AAN23041.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (15)	Yersiniaceae (13)	Yersinia (12)
		Rahnella (1)
	Budviciaceae (2)	Pragia (1)
		Budvicia (1)
Xanthomonadales (9)	Xanthomonadaceae (8)	Lysobacter (4)
		Luteimonas (3)
		Vulcaniibacterium (1)
		Dyella (1)
Alteromonadales (4)	Pseudoalteromonadaceae (4)	Pseudoalteromonas (3)
		Psychrosphaera (1)
Burkholderiales (4)	Burkholderiaceae (2)	Polynucleobacter (2)
	Oxalobacteraceae (1)	Herbaspirillum (1)
	Alcaligenaceae (1)	Pusillimonas (ex Stolz et al. 2005) (1)
Vibrionales (4)	Vibrionaceae (4)	Vibrio (4)
Legionellales (3)	Legionellaceae (3)	Legionella (3)
Bacteroidales (2)	Bacteroidaceae (2)	Bacteroides (2)
Campylobacterales (2)	Arcobacteraceae (1)	Aliarcobacter (1)
		nan (1)
Spirulinales (1)	Spirulinaceae (1)	Spirulina (1)
Cytophagales (1)	Cytophagaceae (1)	Siphonobacter (1)
Marinilabiales (1)	Marinifilaceae (1)	Ancylomarina (1)
Nostocales (1)	Tolypothrichaceae (1)	Tolypothrix (1)
Sphingobacteriales (1)	Sphingobacteriaceae (1)	Mucilagininibacter (1)

[top](#)

Cluster 22

Total number of members in cluster: 46

Average length of proteins in cluster: 408.4

Conserved (non-aliphatic) residues:

R 160 (100.0%) Y 163 (100.0%) T 166 (100.0%) R 167 (100.0%) S 177 (97.8%) K 216 (97.8%) Y 304 (100.0%) D 306 (100.0%) R 309 (97.8%) N 310 (97.8%) E 331 (100.0%) R 340 (100.0%) K 346 (100.0%) D 381 (100.0%) E 440 (97.8%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
WP_000905563.1	Enterobacterales	Enterobacteriaceae	Salmonella	nan	Typhi	0
AAO68867.1	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Typhi	0
AAV77445.1	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Paratyphi A	0
ACF69726.1	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Heidelberg	0
CAR59582.1	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Paratyphi A	0
ACH74809.1	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Dublin	0
CAR37642.1	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Gallinarum bv. Pullorum 11	0
AAL20257.1	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	O4 (B) Typhimurium	0

[MSA fasta](#)

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[Fasta of members](#)

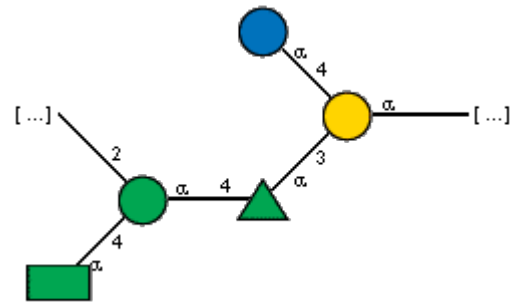
[Logoplot](#)

[Phylogenetic tree](#)

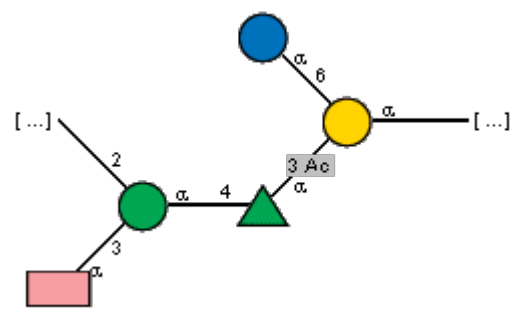
[Hits in cluster](#)

Sugars in cluster:

WP_000905563.1 Salmonella enterica Typhi, AAO68867.1 Salmonella enterica Typhi:

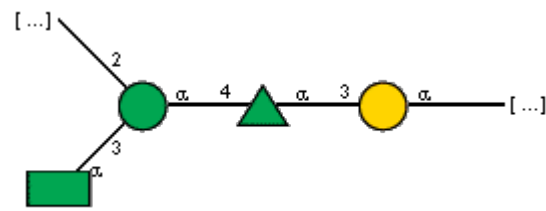


AAV77445.1 Salmonella enterica Paratyphi A, CAR59582.1 Salmonella enterica Paratyphi A:



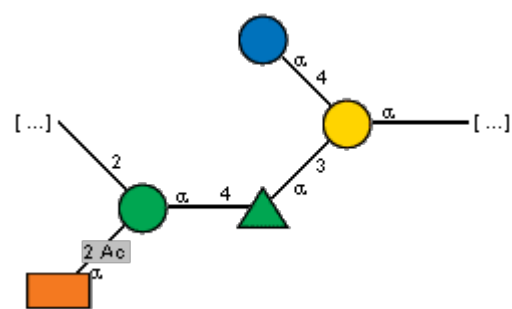
CSDB record ID: 7418

CAR37642.1 Salmonella enterica Gallinarum bv. Pullorum 11:



CSDB record ID: 30403

AAL20257.1 Salmonella enterica O4 (B) Typhimurium:



CSDB record ID: 30397

Sugars for blast hits:

Alphafold models:

[WP_000905563.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (30)	Enterobacteriaceae (29)	Salmonella (23)
		Citrobacter (5)
		Raoultella (1)
		Pectobacterium (1)
Acidobacteriales (4)	Acidobacteriaceae (4)	Edaphobacter (1)
		Acidobacterium (1)
		Terriglobus (1)
		Bryocella (1)
		nan (4)
nan (4)	nan (4)	nan (4)

order (count)	family (count)	genus (count)
Sphingomonadales (3)	Sphingomonadaceae (3)	Sphingomonas (3)
Burkholderiales (3)	Oxalobacteraceae (3)	Massilia (1)
		Duganella (1)
		Janthinobacterium (1)
Planctomycetales (1)	Planctomycetaceae (1)	nan (4)
Desulfuromonadales (1)	Geobacteraceae (1)	Geobacter (1)

[top](#)

Cluster 58

Total number of members in cluster: 45

Average length of proteins in cluster: 410.4

Conserved (non-aliphatic) residues:

D 82 (100.0%) D 109 (100.0%) R 191 (100.0%) H 228 (100.0%) S 230 (97.8%) Y 287 (100.0%) R 371 (100.0%) R 436 (97.8%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
ADI43271.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O27	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

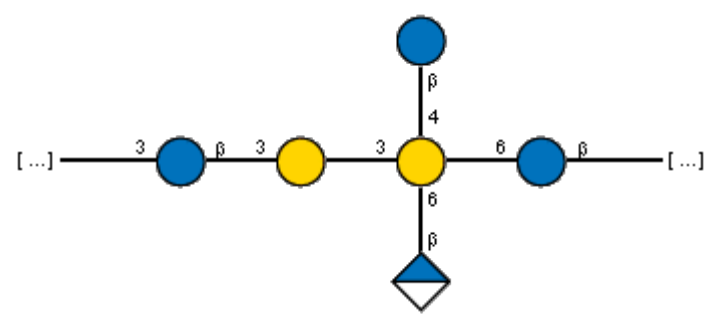
ADI43271.1 Escherichia coli O27:



CSDB record ID: 1535

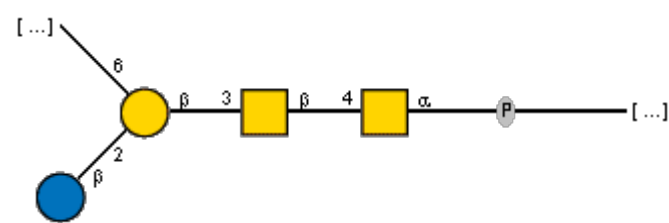
Sugars for blast hits:

CZQ24278.1 Klebsiella pneumoniae K27:



CSDB record ID: 6079

AXY99682.1 *Proteus vulgaris* O34:



CSDB record ID: 20104

Alphafold models:

[ADI43271.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (45)	Enterobacteriaceae (25)	Klebsiella (17)
		Escherichia (6)
		Raoultella (2)
	Yersiniaceae (13)	Serratia (11)
		Gibbsiella (1)
		Rouxiella (1)
	Erwiniaceae (6)	Tatumella (2)
		Pantoea (2)
		Erwinia (1)
		Rosenbergiella (1)
	Morganellaceae (1)	Proteus (1)

[top](#)

Cluster 57

Total number of members in cluster: 43

Average length of proteins in cluster: 379.6

Conserved (non-aliphatic) residues:

Y 31 (100.0%) R 85 (100.0%) D 92 (100.0%) Y 96 (100.0%) N 203 (100.0%) Q 207 (100.0%) H 249 (100.0%) R 485 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
CAI34008.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	27	0

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[Malign view](#)

[Fasta of members](#)

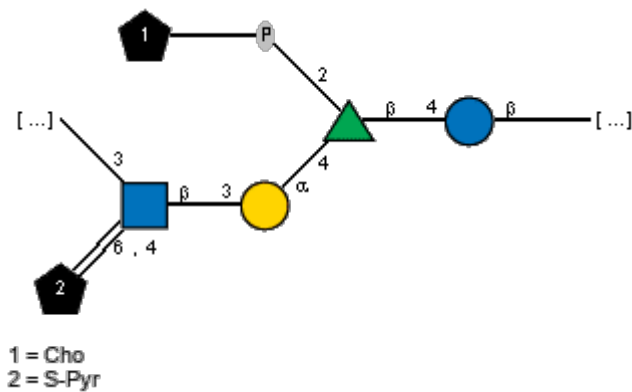
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

CAI34008.1 Streptococcus pneumoniae 27:



CSDB record ID: 7085

Sugars for blast hits:

Alphafold models:

[CAI34008.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Eubacteriales (21)	Lachnospiraceae (8)	Blautia (3)
		nan (2)
		Anaerostipes (1)
		Enterocloster (1)
		Fusicatenibacter (1)
		Coproccoccus (1)
	Oscillospiraceae (7)	Faecalibacterium (5)
		Ruminococcus (2)
	Clostridiaceae (5)	Clostridium (4)
		Candidatus Dwaynia (1)
	Peptococcaceae (1)	Desulfosporosinus (1)

order (count)	family (count)	genus (count)
Lactobacillales (12)	Lactobacillaceae (8)	Lactobacillus (5)
		Limosilactobacillus (2)
		Ligilactobacillus (1)
	Streptococcaceae (3)	Streptococcus (3)
	Carnobacteriaceae (1)	Granulicatella (1)
nan (2)	nan (2)	nan (2)
Eggerthellales (2)	Eggerthellaceae (2)	Eggerthella (2)
Fibrobacterales (1)	Fibrobacteraceae (1)	Fibrobacter (1)
Anaerolineales (1)	Anaerolineaceae (1)	Flexilinea (1)
Pasteurellales (1)	Pasteurellaceae (1)	Actinobacillus (1)
Synergistales (1)	Synergistaceae (1)	nan (2)
Bacteroidales (1)	Bacteroidaceae (1)	Bacteroides (1)
Coriobacteriales (1)	Coriobacteriaceae (1)	Collinsella (1)

[top](#)

Cluster 31

Total number of members in cluster: 43

Average length of proteins in cluster: 376.9

Conserved (non-aliphatic) residues:

D 160 (100.0%) R 162 (97.7%) R 166 (100.0%) T 168 (97.7%) N 175 (100.0%) S 228 (100.0%) R 229 (100.0%) T 230 (100.0%) Q 283 (100.0%) R 307 (100.0%) Y 332 (97.7%) D 336 (100.0%) Y 344 (97.7%) E 386 (97.7%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
BAQ00957.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O46	0
BAQ01812.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O160	0
BAQ01687.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O134	0

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[Malign view](#)

[Fasta of members](#)

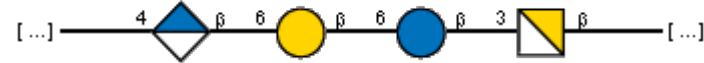
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

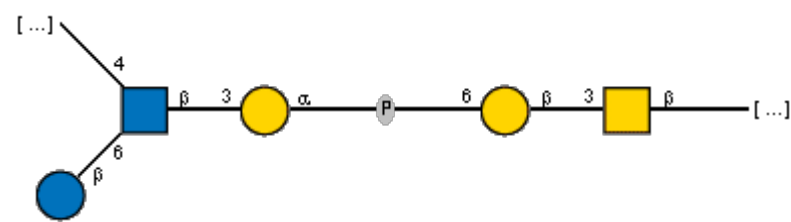
Sugars in cluster:

BAQ00957.1 Escherichia coli O46:



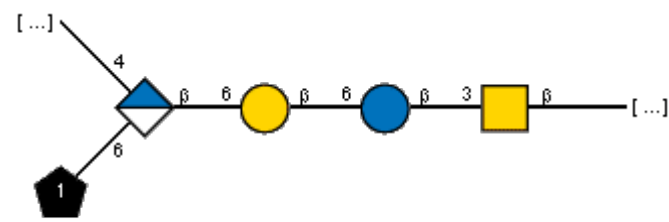
CSDB record ID: 1554

BAQ01812.1 Escherichia coli O160:



CSDB record ID: 1901

BAQ01687.1 Escherichia coli O134:



1 = L-Thr

CSDB record ID: 1876

Sugars for blast hits:

Alphafold models:

[BAQ00957.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (42)	Yersiniaceae (25)	Serratia (24)
		Chania (1)
	Enterobacteriaceae (13)	Escherichia (9)
		Klebsiella (2)
		Enterobacter (1)
		Pluralibacter (1)
		Proteus (2)
	Morganellaceae (2)	Tatumella (1)
	Erwiniaceae (1)	Hafnia (1)
	Hafniaceae (1)	
Aeromonadales (1)	Aeromonadaceae (1)	Aeromonas (1)

[top](#)

Cluster 79

Total number of members in cluster: 42

Average length of proteins in cluster: 429.9

Conserved (non-aliphatic) residues:

R 264 (97.6%) N 449 (100.0%) D 461 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
CAI33798.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	22F	0
CAI33774.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	22A	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

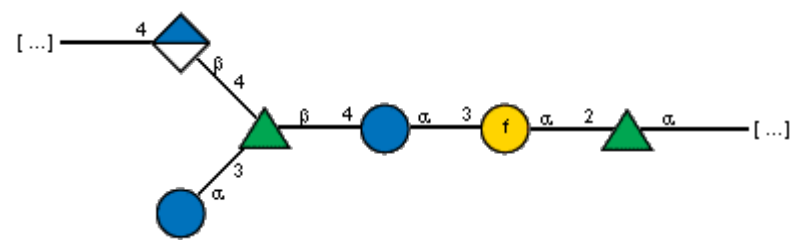
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[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

CAI33798.1 Streptococcus pneumoniae 22F:



CSDB record ID: 625

Sugars for blast hits:

Alphafold models:

[CAI33798.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Lactobacillales (20)	Streptococcaceae (14)	Streptococcus (11)
		Lactococcus (3)
	Lactobacillaceae (5)	Lactiplantibacillus (1)
		Liquorilactobacillus (1)
		Leuconostoc (1)
		Limosilactobacillus (1)
		Lactobacillus (1)
	Enterococcaceae (1)	Enterococcus (1)

order (count)	family (count)	genus (count)
Eubacteriales (14)	Clostridiaceae (3)	Clostridium (3)
	Lachnospiraceae (3)	Blautia (1)
		Oribacterium (1)
		Dorea (1)
	Oscillospiraceae (3)	Faecalibacterium (2)
	nan (2)	nan (3)
Bacillales (3)	Peptococcaceae (1)	Desulfosporosinus (1)
	Bacillaceae (3)	Allobacillus (1)
		Halobacillus (1)
		Bacillus (1)
Bifidobacteriales (3)	Bifidobacteriaceae (3)	Bifidobacterium (3)
Coriobacteriales (1)	Coriobacteriaceae (1)	Collinsella (1)
Bacteroidales (1)	nan (2)	nan (3)

[top](#)

Cluster 53

Total number of members in cluster: 41

Average length of proteins in cluster: 441.7

Conserved (non-aliphatic) residues:

Y 104 (97.6%) R 194 (100.0%) R 207 (97.6%) K 263 (100.0%) R 346 (100.0%) H 425 (100.0%) D 427 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
ACD75796.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O63	0

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[Fasta of members](#)

[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

ACD75796.1 Escherichia coli O63:

order (count)	family (count)	genus (count)
Enterobacterales (18)	Enterobacteriaceae (12)	Escherichia (8)
		Enterobacter (2)
		Citrobacter (1)
		Cedecea (1)
	Morganellaceae (4)	Proteus (2)
		Providencia (1)
		Morganella (1)
	Erwiniaceae (2)	Erwinia (2)
Pseudomonadales (10)	Pseudomonadaceae (10)	Pseudomonas (10)
Vibrionales (5)	Vibrionaceae (5)	Vibrio (5)
Burkholderiales (2)	Burkholderiaceae (1)	nan (1)
	Comamonadaceae (1)	Schlegelella (1)
Sphingomonadales (2)	Sphingomonadaceae (2)	Sphingomonas (2)
Moraxellales (1)	Moraxellaceae (1)	Acinetobacter (1)
Fusobacteriales (1)	Fusobacteriaceae (1)	nan (1)
Campylobacterales (1)	Arcobacteraceae (1)	Aliarcobacter (1)
Pasteurellales (1)	Pasteurellaceae (1)	Mannheimia (1)

Cluster 48

Total number of members in cluster: 41

Average length of proteins in cluster: 405.1

Conserved (non-aliphatic) residues:

Y 279 (97.6%) R 310 (100.0%) E 317 (100.0%) T 323 (97.6%) S 357 (97.6%) S 359 (100.0%) R 460 (97.6%) N 473 (97.6%) R 474 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
AAK60458.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O91	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

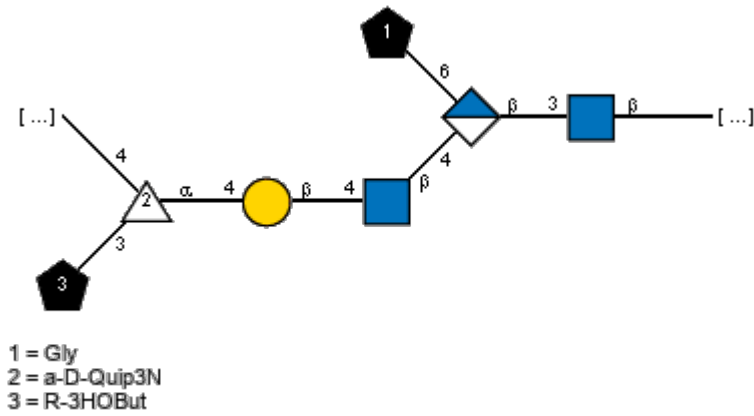
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[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

AAK60458.1 Escherichia coli O91:



CSDB record ID: 895

Sugars for blast hits:

Alphafold models:

[AAK60458.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Bacillales (12)	Bacillaceae (12)	Bacillus (12)
Enterobacterales (11)	Enterobacteriaceae (10)	Escherichia (9)
		Citrobacter (1)
	Hafniaceae (1)	Hafnia (1)
Eubacteriales (4)	Clostridiaceae (1)	Clostridium (1)
	Lachnospiraceae (1)	Lachnoclostridium (1)
	Eubacteriaceae (1)	Acetobacterium (1)
	Desulfallaceae (1)	Sporotomaculum (1)
Vibrionales (4)	Vibrionaceae (4)	Vibrio (4)
Pseudomonadales (3)	Pseudomonadaceae (3)	Pseudomonas (3)
Bacteroidales (2)	Bacteroidaceae (2)	Bacteroides (2)
nan (1)	nan (1)	nan (1)
Legionellales (1)	Legionellaceae (1)	Legionella (1)
Burkholderiales (1)	Burkholderiaceae (1)	Ralstonia (1)
Hydrogenophilales (1)	nan (1)	nan (1)
Bifidobacteriales (1)	Bifidobacteriaceae (1)	Aeriscardovia (1)

[top](#)

Cluster 13

Total number of members in cluster: 40

Average length of proteins in cluster: 432.2

Conserved (non-aliphatic) residues:

Y 76 (100.0%) R 79 (100.0%) Q 176 (100.0%) K 179 (100.0%) Y 183 (100.0%) S 190 (100.0%) H 194 (100.0%) R 213 (100.0%) S 216 (100.0%) S 246 (97.5%) R 253 (100.0%) K 255 (100.0%) S 297 (100.0%) S 300 (100.0%) R 303 (100.0%) E 304 (100.0%) Y 313 (100.0%) D 319 (100.0%) S 320 (97.5%) Q 356 (100.0%) S 390 (100.0%) S 391 (100.0%) S 392 (100.0%) E 396 (100.0%) Y 413 (97.5%) R 449 (97.5%) E 451 (97.5%) K 461 (97.5%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
AKA20935.1	Enterobacterales	Yersiniaceae	Yersinia	Yersinia pseudotuberculosis	O:2c	0
AKA20966.1	Enterobacterales	Yersiniaceae	Yersinia	Yersinia pseudotuberculosis	O:4a	0
AKL88154.1	Enterobacterales	Yersiniaceae	Yersinia	Yersinia pseudotuberculosis	O:8	0
AAY23739.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O77	0
AAY23733.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O73	0
AAY23745.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O106	0
BAQ01935.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O176	0
BAQ02177.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O77	0
BAQ02105.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O17	0
BAQ00945.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O44	0

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[Malign view](#)

[Fasta of members](#)

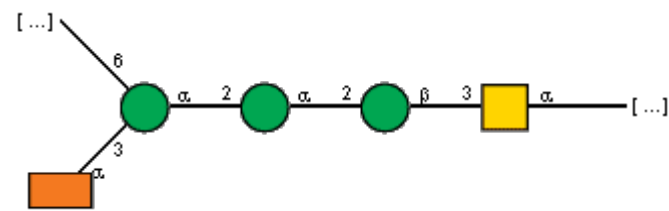
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

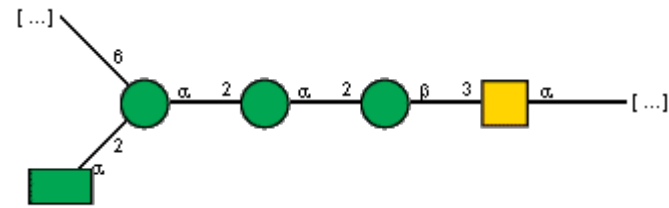
Sugars in cluster:

AKA20935.1 *Yersinia pseudotuberculosis* O:2c:



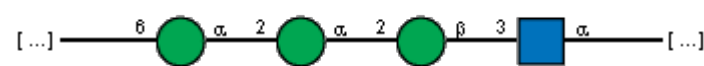
CSDB record ID: 12128

AKA20966.1 *Yersinia pseudotuberculosis* O:4a:



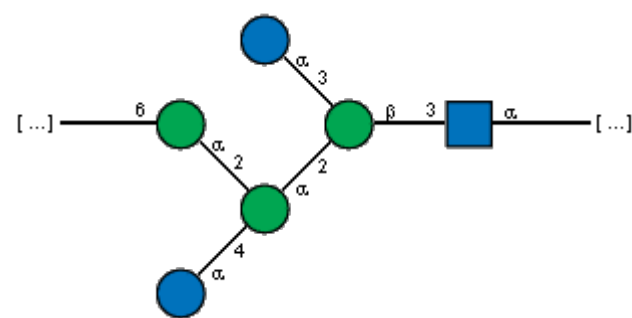
CSDB record ID: 12129

AAY23739.1 *Escherichia coli* O77, BAQ02177.1 *Escherichia coli* O77:



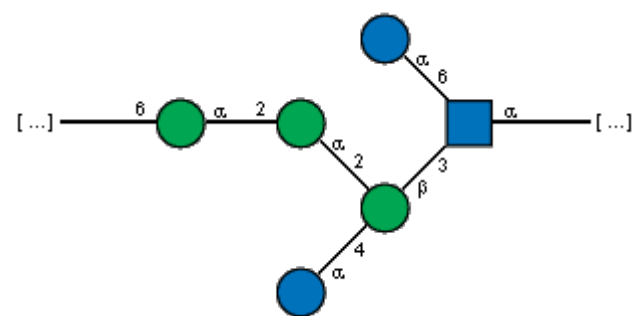
CSDB record ID: 1583

AAY23733.1 *Escherichia coli* O73:



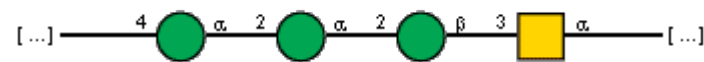
CSDB record ID: 1578

AAY23745.1 *Escherichia coli* O106:



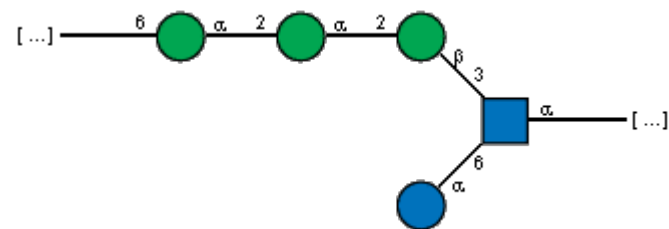
CSDB record ID: 1845

BAQ01935.1 *Escherichia coli* O176:



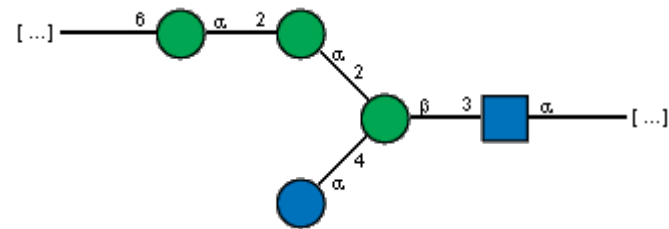
CSDB record ID: 1918

BAQ02105.1 *Escherichia coli* O17:



CSDB record ID: 1520

BAQ00945.1 *Escherichia coli* O44:



CSDB record ID: 1551

Sugars for blast hits:

Alphafold models:

[AKA20935.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (37)	Enterobacteriaceae (31)	Escherichia (13)
		Salmonella (10)
		Enterobacter (6)
		Citrobacter (2)
	Yersiniaceae (6)	Yersinia (5)
		Serratia (1)

order (count)	family (count)	genus (count)
Pseudomonadales (18)	Pseudomonadaceae (18)	Pseudomonas (18)
Burkholderiales (7)	Oxalobacteraceae (3)	Undibacterium (1)
		Janthinobacterium (1)
		Massilia (1)
	nan (2)	Paucibacter (1)
	Burkholderiaceae (2)	Pandoraea (1)
		Paucimonas (1)
Vibrionales (5)	Vibrionaceae (5)	Vibrio (5)
Enterobacterales (3)	Enterobacteriaceae (2)	Salmonella (2)
	Yersiniaceae (1)	Yersinia (1)
nan (1)	nan (2)	nan (2)
Thiotrichales (1)	Fastidiosibacteraceae (1)	Cysteiniphilum (1)
Pirellulales (1)	Pirellulaceae (1)	Roseimaritima (1)
Aeromonadales (1)	Aeromonadaceae (1)	Aeromonas (1)
Eubacteriales (1)	Eubacteriales Family XII. Incertae Sedis (1)	Fusibacter (1)
Moraxellales (1)	Moraxellaceae (1)	Acinetobacter (1)

[top](#)

Cluster 84

Total number of members in cluster: 37

Average length of proteins in cluster: 447.0

Conserved (non-aliphatic) residues:

K 257 (100.0%) R 311 (100.0%) Y 371 (100.0%) N 483 (100.0%) T 486 (97.3%) R 489 (100.0%) D 494 (100.0%) S 546 (97.3%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
AAM27560.1	Pseudomonadales	Pseudomonadaceae	Pseudomonas	Pseudomonas aeruginosa	O10	0
AAM27711.1	Pseudomonadales	Pseudomonadaceae	Pseudomonas	Pseudomonas aeruginosa	O19	0

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[Malign view](#)

[Fasta of members](#)

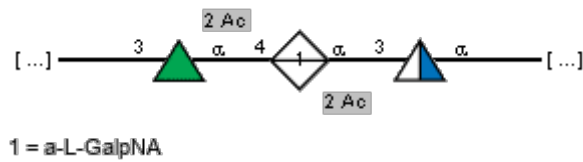
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

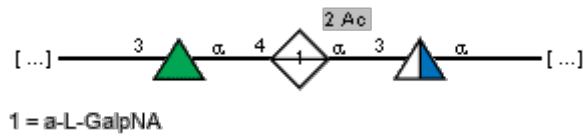
Sugars in cluster:

AAM27560.1 *Pseudomonas aeruginosa* O10:



CSDB record ID: 11180

AAM27711.1 *Pseudomonas aeruginosa* O19:



CSDB record ID: 11026

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Pseudomonadales (20)	Pseudomonadaceae (18)	Pseudomonas (18)
	Marinobacteraceae (1)	Marinobacter (1)
Burkholderiales (7)	Burkholderiaceae (4)	nan (3)
		Cupriavidus (2)
		Pandoraea (1)
	Oxalobacteraceae (2)	Collimonas (2)
	Comamonadaceae (1)	Limnohabitans (1)
nan (2)	nan (3)	nan (3)
Sphingomonadales (2)	Sphingomonadaceae (2)	Sphingomonas (2)
Rhodocyclales (1)	Rhodocyclaceae (1)	Aromatoleum (1)
Alteromonadales (1)	Shewanellaceae (1)	Shewanella (1)
Sphingobacteriales (1)	Sphingobacteriaceae (1)	Pedobacter (1)
Enterobacterales (1)	Enterobacteriaceae (1)	Plesiomonas (1)
Aeromonadales (1)	Aeromonadaceae (1)	Aeromonas (1)
Hyphomicrobiales (1)	Stappiaceae (1)	Pannonibacter (1)

[top](#)

Cluster 43

Total number of members in cluster: 37

Average length of proteins in cluster: 395.6

Conserved (non-aliphatic) residues:

N 160 (100.0%) S 247 (97.3%) R 343 (100.0%) H 399 (100.0%) E 455 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
CAI33515.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	17F	0
CAI33491.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	17A	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

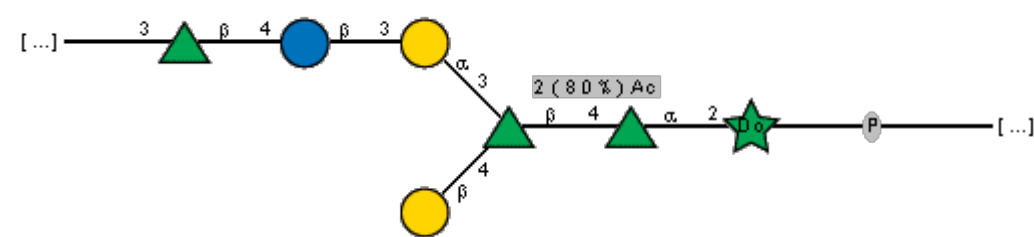
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

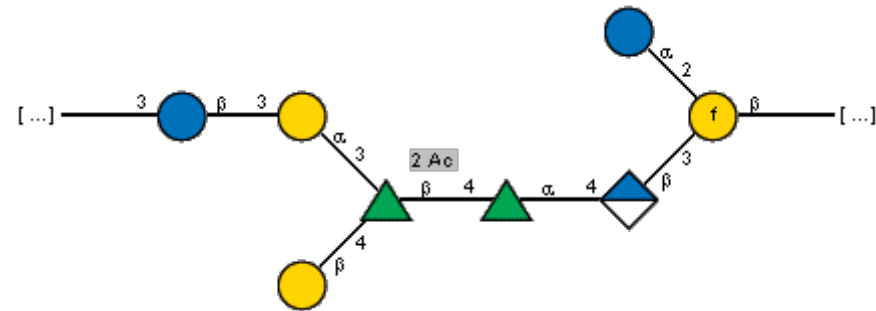
Sugars in cluster:

CAI33515.1 Streptococcus pneumoniae 17F:



CSDB record ID: 815

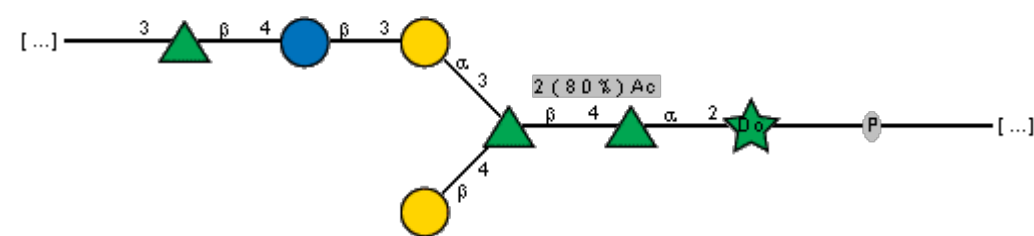
CAI33491.1 Streptococcus pneumoniae 17A:



CSDB record ID: 7070

Sugars for blast hits:

VIQ20135.1 Streptococcus pneumoniae 17F:



Alphafold models:

[CAI33491.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Eubacteriales (16)	Clostridiaceae (6)	nan (4)
		Clostridium (4)
		Hungatella (1)
	Oscillospiraceae (5)	Ruminococcus (4)
	Eubacteriaceae (3)	Eubacterium (3)
Lactobacillales (13)	Lachnospiraceae (2)	Blautia (1)
		Candidatus Pullilachnospira (1)
	Streptococcaceae (12)	Streptococcus (11)
		Lactococcus (1)
	Aerococcaceae (1)	Abiotrophia (1)
nan (3)	nan (3)	nan (4)
Bifidobacteriales (3)	Bifidobacteriaceae (3)	Bifidobacterium (3)
Erysipelotrichales (1)	Erysipelotrichaceae (1)	Faecalitalea (1)
Bacillales (1)	Bacillaceae (1)	Alkalihalobacillus (1)

[top](#)

Cluster 94

Total number of members in cluster: 36

Average length of proteins in cluster: 432.9

Conserved (non-aliphatic) residues:

D 52 (97.2%) K 243 (97.2%) R 326 (100.0%) D 332 (100.0%) N 408 (100.0%) R 410 (100.0%) D 470 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
AIG62684.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O20	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (11)	Enterobacteriaceae (8)	Escherichia (5)
		Enterobacter (2)
		Lelliottia (1)
	Hafniaceae (1)	Edwardsiella (1)
	Erwiniaceae (1)	Erwinia (1)
Bacteroidales (7)	Morganellaceae (1)	Providencia (1)
	Bacteroidaceae (6)	Bacteroides (4)
		Mediterranea (2)
	Paludibacteraceae (1)	Paludibacter (1)
	Flavobacteriaceae (6)	Flavobacterium (6)
Chitinophagales (2)	Chitinophagaceae (2)	Chitinophaga (2)
Vibrionales (2)	Vibrionaceae (2)	Vibrio (2)
nan (1)	nan (1)	nan (1)
Cytophagales (1)	Spirosomaceae (1)	Dyadobacter (1)
Pseudomonadales (1)	Marinobacteraceae (1)	Marinobacter (1)
Sphingobacteriales (1)	Sphingobacteriaceae (1)	Pedobacter (1)
Eubacteriales (1)	Clostridiaceae (1)	Clostridium (1)
Thermodesulfovibrionales (1)	Thermodesulfovibrionaceae (1)	Thermodesulfovibrio (1)
Spirochaetales (1)	Spirochaetaceae (1)	nan (1)
Burkholderiales (1)	Burkholderiaceae (1)	nan (1)

[top](#)

Cluster 65

Total number of members in cluster: 36

Average length of proteins in cluster: 387.6

Conserved (non-aliphatic) residues:

R 190 (100.0%) D 201 (100.0%) Y 203 (97.2%) N 218 (97.2%) N 257 (100.0%) R 353 (97.2%) Q 356 (100.0%) Y 395 (100.0%) E 397 (100.0%) Q 399 (100.0%) Y 402 (97.2%) Q 406 (100.0%) Y 440 (100.0%) N 447 (100.0%) Y 449 (100.0%) D 452 (97.2%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
ABE98437.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O146	0
ABI98986.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O147	0

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
ABU80601.1	Enterobacterales	Enterobacteriaceae	Shigella	Shigella flexneri	6	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

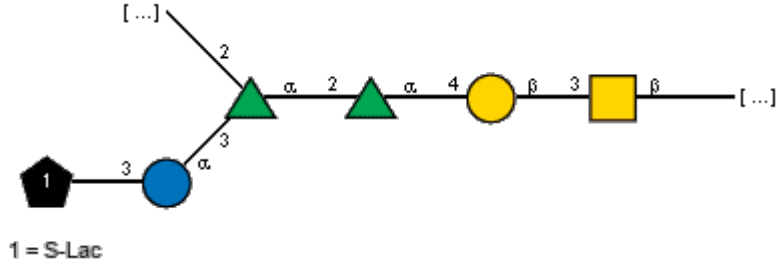
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

ABE98437.1 Escherichia coli O146:



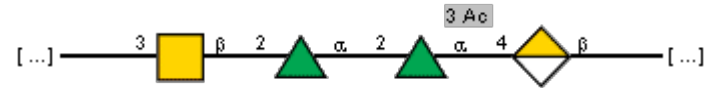
CSDB record ID: 1887

ABI98986.1 Escherichia coli O147:



CSDB record ID: 1624

ABU80601.1 Shigella flexneri 6:



CSDB record ID: 188

Sugars for blast hits:

Alphafold models:

[ABI98986.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (10)	Enterobacteriaceae (9)	Escherichia (6)
		Shigella (3)
	Pectobacteriaceae (1)	Pectobacterium (1)

order (count)	family (count)	genus (count)
Vibrionales (5)	Vibrionaceae (5)	Vibrio (5)
Eubacteriales (5)	Lachnospiraceae (3)	Pseudobutyrvibrio (1)
		Schaedlerella (1)
	Oscillospiraceae (2)	Ruminococcus (1)
Bacteroidales (3)	Odoribacteraceae (2)	Butyricimonas (2)
	Bacteroidaceae (1)	Bacteroides (1)
Moraxellales (3)	Moraxellaceae (3)	Acinetobacter (3)
Bacillales (2)	Bacillaceae (2)	Bacillus (2)
Burkholderiales (2)	nan (2)	Rhizobacter (1)
Campylobacterales (1)	Arcobacteraceae (1)	Aliarcobacter (1)
Cytophagales (1)	Cyclobacteriaceae (1)	Litoribacter (1)
Selenomonadales (1)	Selenomonadaceae (1)	Propionispira (1)
Neisseriales (1)	Chromobacteriaceae (1)	Aquitalea (1)
Spirochaetales (1)	Treponemataceae (1)	Treponema (1)
Erysipelotrichales (1)	Erysipelotrichaceae (1)	nan (3)

[top](#)

Cluster 171

Total number of members in cluster: 36

Average length of proteins in cluster: 363.1

Conserved (non-aliphatic) residues:

R 60 (100.0%) D 66 (100.0%) Y 67 (100.0%) Y 70 (97.2%) R 184 (97.2%) Q 185 (100.0%) H 219 (100.0%) R 360 (97.2%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
BAQ02116.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O54	0
AAK64372.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O104	0

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[Malign view](#)

[Fasta of members](#)

[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

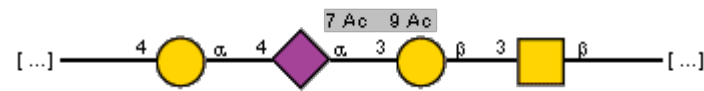
Sugars in cluster:

BAQ02116.1 Escherichia coli O54:



CSDB record ID: 1561

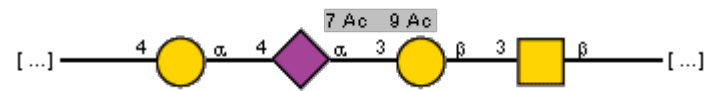
AAK64372.1 Escherichia coli O104:



CSDB record ID: 1843

Sugars for blast hits:

EGR73751.1 Escherichia coli O104:



CSDB record ID: 1843

Alphafold models:

[AAK64372.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (19)	Enterobacteriaceae (15)	Escherichia (10)
		Enterobacter (5)
	Morganellaceae (3)	Proteus (2)
		Providencia (1)
Bacteroidales (9)	Hafniaceae (1)	Hafnia (1)
	Bacteroidaceae (3)	Bacteroides (3)
	Odoribacteraceae (2)	Butyricimonas (1)
		Odoribacter (1)
	Tannerellaceae (2)	Parabacteroides (2)
	Prevotellaceae (1)	Prevotella (1)
Vibrionales (3)	nan (1)	nan (1)
	Vibrionaceae (3)	Photobacterium (1)
		Vibrio (1)
		Aliivibrio (1)
Flavobacteriales (3)	Flavobacteriaceae (3)	Polaribacter (1)
		Tenacibaculum (1)
		Paucihalobacter (1)
Aeromonadales (1)	Aeromonadaceae (1)	Aeromonas (1)
Lactobacillales (1)	Enterococcaceae (1)	Enterococcus (1)

[top](#)

Sugars for blast hits:

Alphafold models:

[AHB32438.2](#)

Taxonomy:

order (count)	family (count)	genus (count)
Moraxellales (11)	Moraxellaceae (11)	Acinetobacter (9)
		Psychrobacter (2)
Oceanospirillales (6)	Halomonadaceae (6)	Kushneria (4)
		Halomonas (1)
		Cobetia (1)
Pasteurellales (4)	Pasteurellaceae (4)	Glaesserella (3)
		Mannheimia (1)
Vibrionales (4)	Vibrionaceae (4)	Vibrio (4)
Alteromonadales (4)	Idiomarinaceae (2)	Aliidiomarina (1)
		Idiomarina (1)
	Shewanellaceae (1)	Shewanella (1)
Enterobacterales (2)	Enterobacteriaceae (2)	Buttiauxella (2)
Hyphomicrobiales (1)	nan (1)	nan (2)
Chromatiales (1)	Chromatiaceae (1)	Rheinheimera (1)
Flavobacteriales (1)	Flavobacteriaceae (1)	Capnocytophaga (1)
nan (1)	nan (1)	Ignatzschineria (1)

[top](#)

Cluster 4

Total number of members in cluster: 34

Average length of proteins in cluster: 403.9

Conserved (non-aliphatic) residues:

R 204 (97.1%) E 244 (100.0%) Y 282 (97.1%) K 289 (100.0%) R 293 (100.0%) R 316 (100.0%) E 349 (100.0%) Y 397 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
CAB63298.1	Enterobacterales	Yersiniaceae	Yersinia	Yersinia pseudotuberculosis	O:1B	0
AKA20948.1	Enterobacterales	Yersiniaceae	Yersinia	Yersinia pseudotuberculosis	O:3	0
ACV52983.1	Enterobacterales	Yersiniaceae	Yersinia	Yersinia pseudotuberculosis	O:11	0
ACV53000.1	Enterobacterales	Yersiniaceae	Yersinia	Yersinia pseudotuberculosis	O:14	0
BAQ01843.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O163	0

[MSA fasta](#)

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[Fasta of members](#)

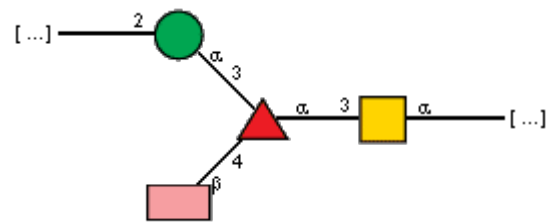
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

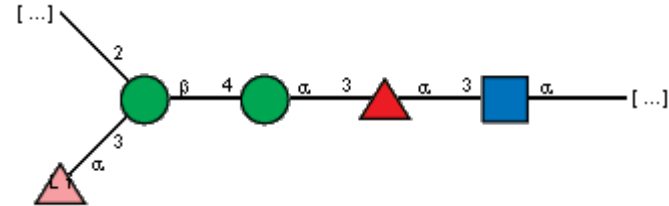
Sugars in cluster:

AKA20948.1 *Yersinia pseudotuberculosis* O:3:



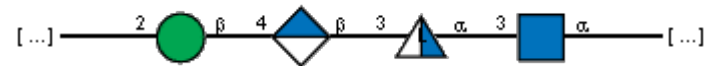
CSDB record ID: 12133

ACV52983.1 *Yersinia pseudotuberculosis* O:11:



CSDB record ID: 12124

BAQ01843.1 *Escherichia coli* O163:



CSDB record ID: 1905

Sugars for blast hits:

AlphaFold models:

[CAB63298.1](#)

[BAQ01843.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (23)	Enterobacteriaceae (14)	Escherichia (6)
		Salmonella (5)
		Enterobacter (3)

order (count)	family (count)	genus (count)
	Yersiniaceae (8)	Yersinia (8)
	Morganellaceae (1)	Xenorhabdus (1)
Vibrionales (3)	Vibrionaceae (3)	Vibrio (2)
		Photobacterium (1)
nan (2)	nan (2)	nan (2)
Spirochaetales (2)	Treponemataceae (2)	Treponema (2)
Bacteroidales (2)	Bacteroidaceae (2)	Bacteroides (2)
Neisseriales (1)	Chromobacteriaceae (1)	Chromobacterium (1)
Eubacteriales (1)	Eubacteriaceae (1)	Eubacterium (1)

[top](#)

Cluster 93

Total number of members in cluster: 33

Average length of proteins in cluster: 344.3

Conserved (non-aliphatic) residues:

Y 78 (100.0%) Y 134 (100.0%) Q 144 (100.0%) Q 147 (100.0%) R 149 (100.0%) Q 150 (100.0%) H 189 (100.0%) Y 258 (100.0%) R 327 (100.0%) E 336 (100.0%) Y 384 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
AHB32666.1	Moraxellales	Moraxellaceae	Acinetobacter	Acinetobacter nosocomialis	O4	0
AHB32888.2	Moraxellales	Moraxellaceae	Acinetobacter	Acinetobacter baumannii	O7	0
AHB32334.1	Moraxellales	Moraxellaceae	Acinetobacter	Acinetobacter baumannii	O18	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

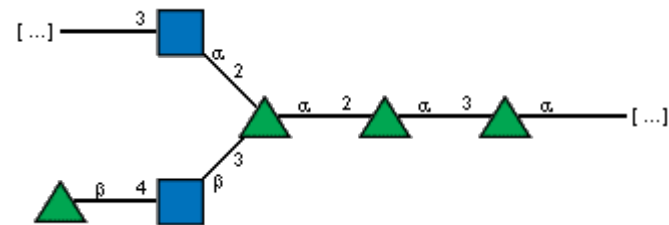
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

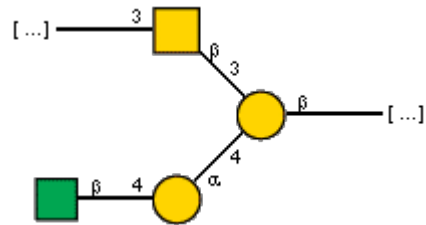
Sugars in cluster:

AHB32888.2 Acinetobacter baumannii O7:



CSDB record ID: 495

AHB32334.1 *Acinetobacter baumannii* O18:



CSDB record ID: 483

Sugars for blast hits:

AlphaFold models:

[AHB32666.1](#)

[AHB32888.2](#)

[AHB32334.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Moraxellales (22)	Moraxellaceae (22)	Acinetobacter (22)
Flavobacteriales (5)	Flavobacteriaceae (5)	Capnocytophaga (5)
Vibrionales (1)	Vibrionaceae (1)	Vibrio (1)
Aeromonadales (1)	Aeromonadaceae (1)	Aeromonas (1)
Alteromonadales (1)	Pseudoalteromonadaceae (1)	Pseudoalteromonas (1)
nan (1)	nan (1)	Wohlfahrtiimonas (1)
Burkholderiales (1)	nan (1)	Rhizobacter (1)
Enterobacterales (1)	Pectobacteriaceae (1)	Pectobacterium (1)

[top](#)

Cluster 59

Total number of members in cluster: 33

Average length of proteins in cluster: 382.3

Conserved (non-aliphatic) residues:

R 61 (100.0%) D 118 (100.0%) R 197 (100.0%) K 206 (100.0%) R 248 (100.0%) R 334 (100.0%) K 378 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
ACD37165.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O13	0
ACD37173.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O135	0
ACD37181.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O129	0
BAQ02259.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O13/O129/O135	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

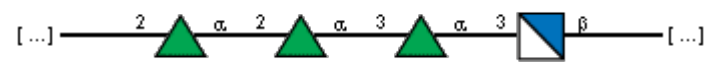
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

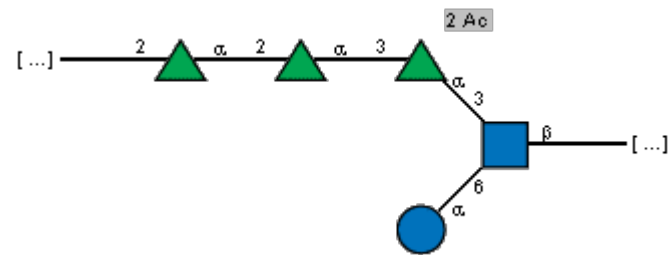
Sugars in cluster:

ACD37165.1 Escherichia coli O13:



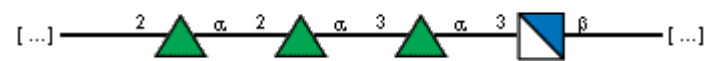
CSDB record ID: 1515

ACD37173.1 Escherichia coli O135:



CSDB record ID: 1877

ACD37181.1 Escherichia coli O129:



CSDB record ID: 1870

Sugars for blast hits:

Alphafold models:

[ACD37165.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (19)	Enterobacteriaceae (18)	Escherichia (8)
		Shigella (5)
		nan (3)
		Citrobacter (1)
		Buttiauxella (1)
Moraxellales (4)	Erwiniaceae (1)	Pantoea (1)
	Moraxellaceae (4)	Acinetobacter (4)
	nan (3)	nan (3)
Burkholderiales (2)	Burkholderiaceae (2)	Cupriavidus (1)
		Ralstonia (1)
Flavobacteriales (2)	Flavobacteriaceae (2)	Flavobacterium (2)
Vibrionales (1)	Vibrionaceae (1)	Photobacterium (1)
Alteromonadales (1)	Ferrimonadaceae (1)	Ferrimonas (1)
Nitrosomonadales (1)	Methylophilaceae (1)	Methyлотenera (1)

[top](#)

Cluster 73

Total number of members in cluster: 29

Average length of proteins in cluster: 413.9

Conserved (non-aliphatic) residues:

Y 165 (100.0%) R 210 (100.0%) Y 267 (100.0%) R 269 (100.0%) S 371 (100.0%) T 415 (100.0%) D 416 (100.0%) R 421 (100.0%) E 483 (100.0%) K 485 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
ACD37046.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O167	0
ACD37037.1	Enterobacterales	Enterobacteriaceae	Shigella	Shigella boydii	3	0

[MSA fasta](#)

[Malign view](#)

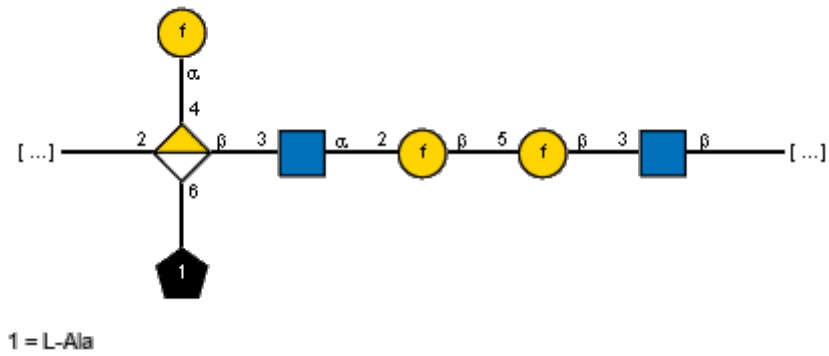
[Fasta of members](#)

[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:



CSDB record ID: 1909

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Eubacteriales (7)	Lachnospiraceae (5)	Butyrivibrio (1)
	Clostridiaceae (1)	Clostridium (1)
	Oscillospiraceae (1)	Ruminococcus (1)
nan (6)	nan (7)	nan (12)
Enterobacterales (4)	Enterobacteriaceae (4)	Escherichia (2)
		Shigella (2)
Erysipelotrichales (3)	Erysipelotrichaceae (3)	Faecalibacillus (1)
		Erysipelatoclostridium (1)
Lactobacillales (3)	Carnobacteriaceae (2)	Marinilactibacillus (1)
	Enterococcaceae (1)	Carnobacterium (1)
		Enterococcus (1)
Bacteroidales (3)	Bacteroidaceae (2)	Bacteroides (2)
Selenomonadales (2)	Selenomonadaceae (2)	Selenomonas (2)
Spirochaetales (1)	Treponemataceae (1)	Treponema (1)

[top](#)

Cluster 72

Total number of members in cluster: 29

Average length of proteins in cluster: 431.8

Conserved (non-aliphatic) residues:

R 187 (100.0%) R 188 (100.0%) Y 203 (100.0%) S 206 (100.0%) D 300 (100.0%) R 304 (100.0%) R 305 (100.0%) Y 329 (100.0%) D 331 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen
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AAA97573.1	Pseudomonadales Pseudomonadaceae Pseudomonas	Pseudomonas aeruginosa	O5	0
AAC45857.1	Pseudomonadales Pseudomonadaceae Pseudomonas	Pseudomonas aeruginosa	O5	0
AAM27728.1	Pseudomonadales Pseudomonadaceae Pseudomonas	Pseudomonas aeruginosa	O2	0
AAM27801.1	Pseudomonadales Pseudomonadaceae Pseudomonas	Pseudomonas aeruginosa	O5	0
AAM27662.1	Pseudomonadales Pseudomonadaceae Pseudomonas	Pseudomonas aeruginosa	O16	0
AAM27693.1	Pseudomonadales Pseudomonadaceae Pseudomonas	Pseudomonas aeruginosa	O18	0
AAM27748.1	Pseudomonadales Pseudomonadaceae Pseudomonas	Pseudomonas aeruginosa	O20	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

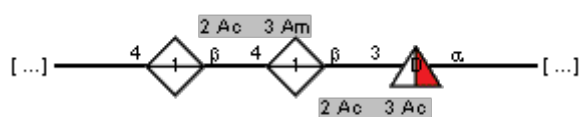
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

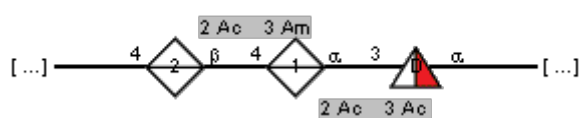
AAA97573.1 Pseudomonas aeruginosa O5, AAC45857.1 Pseudomonas aeruginosa O5, AAM27801.1 Pseudomonas aeruginosa O5:



1 = α -D-ManpN3NA

CSDB record ID: 1672

AAM27728.1 Pseudomonas aeruginosa O2:

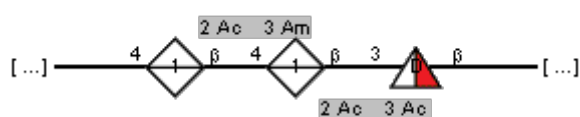


1 = α -L-GalpN3NA

2 = α -D-ManpN3NA

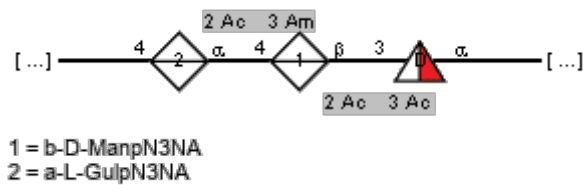
CSDB record ID: 6565

AAM27662.1 Pseudomonas aeruginosa O16:



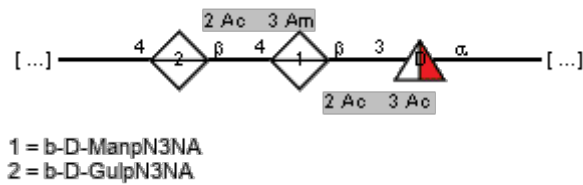
1 = α -D-ManpN3NA

AAM27693.1 *Pseudomonas aeruginosa* O18:



CSDB record ID: 7836

AAM27748.1 *Pseudomonas aeruginosa* O20:



CSDB record ID: 6655

Sugars for blast hits:

Alphafold models:

[AAA97573.1](#)

[AAC45857.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Pseudomonadales (25)	Pseudomonadaceae (25)	Pseudomonas (25)
Vibrionales (2)	Vibrionaceae (2)	Vibrio (2)
Oceanospirillales (1)	Oceanospirillaceae (1)	Nitrocola (1)
Burkholderiales (1)	Alcaligenaceae (1)	Bordetella (1)

[top](#)

Cluster 54

Total number of members in cluster: 28

Average length of proteins in cluster: 384.1

Conserved (non-aliphatic) residues:

Y 197 (100.0%) S 211 (100.0%) R 272 (100.0%) S 350 (100.0%) R 352 (100.0%) H 384 (100.0%) N 385 (100.0%) D 389 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
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Cluster 41

Total number of members in cluster: 26

Average length of proteins in cluster: 416.3

Conserved (non-aliphatic) residues:

D 159 (100.0%) Y 163 (100.0%) Y 164 (100.0%) N 166 (100.0%) E 188 (100.0%) N 195 (100.0%) K 256 (100.0%) R 265 (100.0%) Q 266 (100.0%) H 296 (100.0%) K 355 (100.0%) R 435 (100.0%) Y 502 (100.0%) R 518 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
BAQ01584.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O120	0
BAQ01641.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O131	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

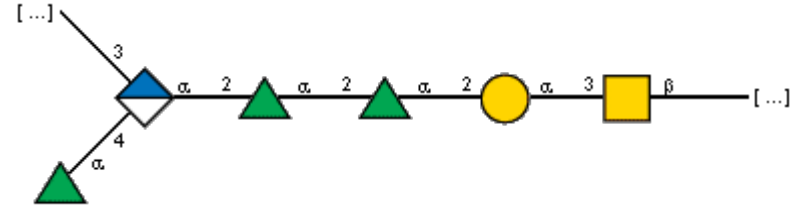
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

BAQ01584.1 Escherichia coli O120:



CSDB record ID: 1860

BAQ01641.1 Escherichia coli O131:



CSDB record ID: 1873

Sugars for blast hits:

Alphafold models:

[BAQ01641.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Vibrionales (13)	Vibrionaceae (13)	Vibrio (10)
		Photobacterium (2)
		Enterovibrio (1)
Enterobacterales (7)	Enterobacteriaceae (6)	Escherichia (6)
	Morganellaceae (1)	Proteus (1)
Alteromonadales (4)	Pseudoalteromonadaceae (3)	Pseudoalteromonas (3)
	Shewanellaceae (1)	Shewanella (1)
nan (1)	nan (1)	Gallaecimonas (1)
Aeromonadales (1)	Aeromonadaceae (1)	Aeromonas (1)

[top](#)

Cluster 28

Total number of members in cluster: 25

Average length of proteins in cluster: 381.6

Conserved (non-aliphatic) residues:

Y 43 (100.0%) N 45 (100.0%) D 48 (100.0%) Y 52 (100.0%) E 69 (100.0%) N 113 (100.0%) E 132 (100.0%) Q 133 (100.0%) R 135 (100.0%) Q 136 (100.0%) H 171 (100.0%) K 226 (100.0%) Y 230 (100.0%) R 296 (100.0%) S 350 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
ABK27355.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O103	0
ABK27354.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O103	0
ABK27351.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O103	0
BAI31288.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O103	0
ABK27350.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O103	0
ABK27321.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O103	0
ABK27352.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O103	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

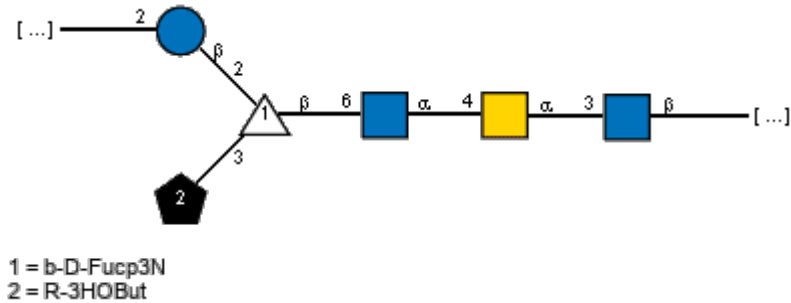
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

ABK27355.1 Escherichia coli O103, ABK27354.1 Escherichia coli O103, ABK27351.1 Escherichia coli O103, BAI31288.1 Escherichia coli O103, ABK27350.1 Escherichia coli O103, ABK27321.1 Escherichia coli O103, ABK27352.1 Escherichia coli O103:



CSDB record ID: 1842

Sugars for blast hits:

AlphaFold models:

[ABK27355.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (23)	Enterobacteriaceae (18)	Escherichia (13)
		Citrobacter (2)
		Cronobacter (1)
		Leclercia (1)
		Salmonella (1)
		Yersinia (2)
	Morganellaceae (1)	Morganella (1)
	Pectobacteriaceae (1)	Pectobacterium (1)
	Hafniaceae (1)	Hafnia (1)
	Oxalobacteraceae (1)	Glaciimonas (1)
Burkholderiales (1)	Pseudomonadaceae (1)	Pseudomonas (1)

[top](#)

Cluster 98

Total number of members in cluster: 24

Average length of proteins in cluster: 409.8

Conserved (non-aliphatic) residues:

R 53 (100.0%) D 60 (100.0%) D 61 (100.0%) H 65 (100.0%) Y 96 (100.0%) Y 98 (100.0%) Y 109 (100.0%) S 118 (100.0%) S 121 (100.0%) Y 129 (100.0%) N 167 (100.0%) R 169 (100.0%) S 173 (100.0%) R 176 (100.0%) Y 208

(100.0%) H 215 (100.0%) R 225 (100.0%) K 272 (100.0%) Y 276 (100.0%) Y 331 (100.0%) R 348 (100.0%) N 402 (100.0%) D 414 (100.0%) N 424 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
CAI33105.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	10F	0
CAI33048.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	10A	0
CAI34733.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	10B	0
CAI33084.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	10C	0
CAI34436.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	39	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

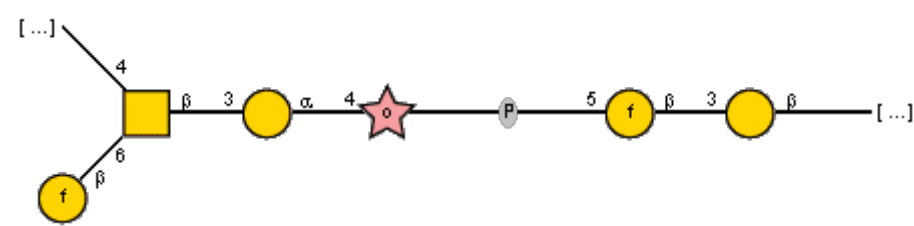
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

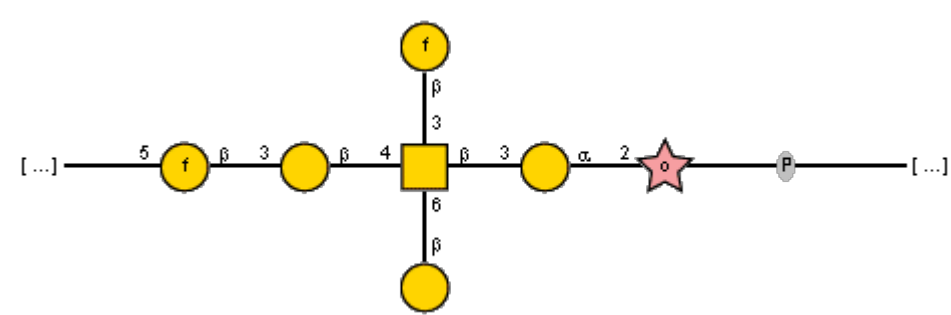
Sugars in cluster:

CAI33105.1 Streptococcus pneumoniae 10F:



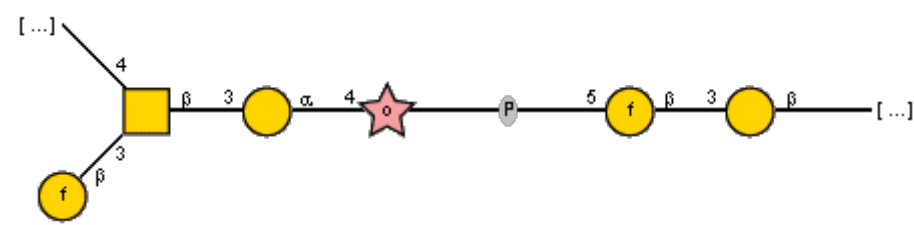
CSDB record ID: 7049

CAI33048.1 Streptococcus pneumoniae 10A:



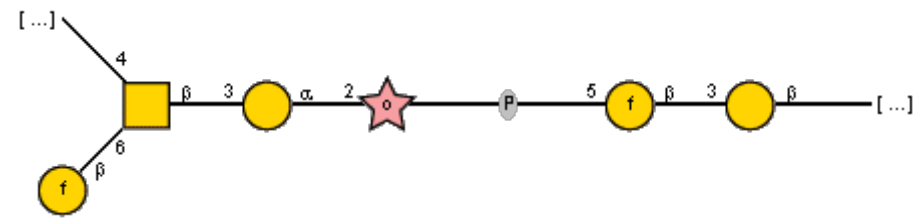
CSDB record ID: 1953

CAI34733.1 Streptococcus pneumoniae 10B:



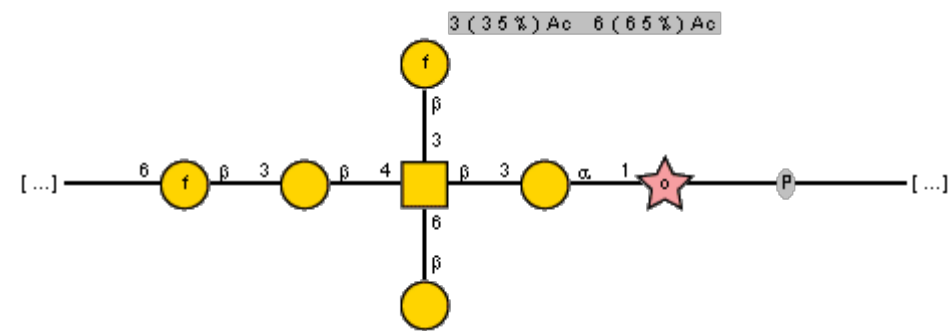
CSDB record ID: 7051

CAI33084.1 *Streptococcus pneumoniae* 10C:



CSDB record ID: 7052

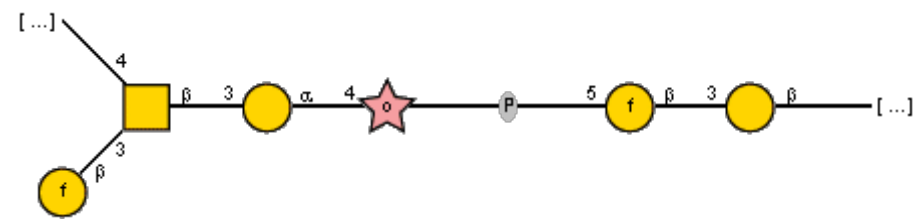
CAI34436.1 *Streptococcus pneumoniae* 39:



CSDB record ID: 3663

Sugars for blast hits:

CIV98579.1 *Streptococcus pneumoniae* 10B:



CSDB record ID: 7051

Alphafold models:

[CAI33105.1](#)

[CAI33084.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Lactobacillales (20)	Streptococcaceae (20)	Streptococcus (20)

order (count)	family (count)	genus (count)
Bacillales (3)	nan (3)	Gemella (3)
Pasteurellales (1)	Pasteurellaceae (1)	Haemophilus (1)

[top](#)

Cluster 25

Total number of members in cluster: 24

Average length of proteins in cluster: 399.5

Conserved (non-aliphatic) residues:

N 194 (100.0%) R 302 (100.0%) Y 336 (100.0%) R 341 (100.0%) K 360 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
CAI33862.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	23F	0
CAI33840.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	23B	0

[MSA fasta](#)

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[Fasta of members](#)

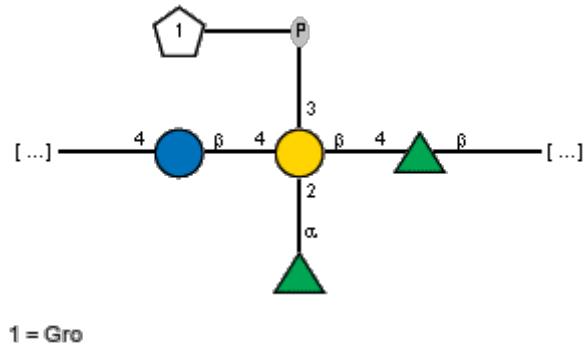
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

CAI33862.1 Streptococcus pneumoniae 23F:



CSDB record ID: 1964

CAI33840.1 Streptococcus pneumoniae 23B:

order (count)	family (count)	genus (count)
Lactobacillales (16)	Streptococcaceae (12)	Streptococcus (12)
	Lactobacillaceae (4)	Ligilactobacillus (2)
		Limosilactobacillus (1)
		Liquorilactobacillus (1)
Eubacteriales (5)	Lachnospiraceae (3)	Acetatifactor (1)
		Blautia (1)
		Oribacterium (1)
		Clostridiaceae (1)
Bacteroidales (2)	Bacteroidaceae (2)	nan (2)

order (count)	family (count)	genus (count)
		Phocaeicola (1)
nan (1)	nan (2)	nan (2)

[top](#)

Cluster 69

Total number of members in cluster: 23

Average length of proteins in cluster: 398.1

Conserved (non-aliphatic) residues:

R 206 (100.0%) R 229 (100.0%) D 235 (100.0%) E 236 (100.0%) T 272 (100.0%) S 274 (100.0%) R 342 (100.0%) R 358 (100.0%) Q 454 (100.0%) R 455 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
BAQ01793.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O156	0
BAQ01878.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O170	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

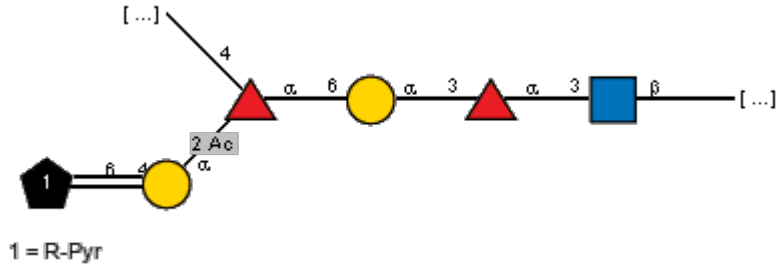
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

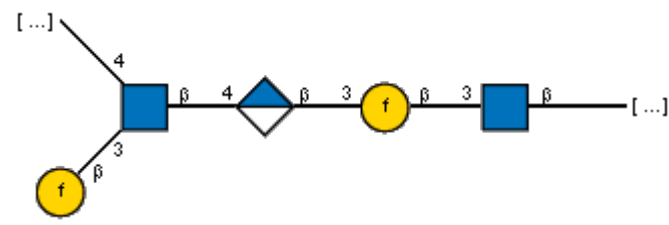
Sugars in cluster:

BAQ01793.1 Escherichia coli O156:



CSDB record ID: 1897

BAQ01878.1 Escherichia coli O170:



CSDB record ID: 1407

Sugars for blast hits:

Alphafold models:

[BAQ01793.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (8)	Enterobacteriaceae (5)	Escherichia (4)
		nan (1)
	Morganellaceae (3)	Photorhabdus (2)
		Providencia (1)
Vibrionales (4)	Vibrionaceae (4)	Vibrio (4)
Aeromonadales (3)	Aeromonadaceae (3)	Aeromonas (3)
Spirochaetales (2)	Treponemataceae (1)	Treponema (1)
	Spirochaetaceae (1)	Alkalispirochaeta (1)
Chlorobiales (1)	Chlorobiaceae (1)	Chlorobium (1)
Pseudomonadales (1)	Marinobacteraceae (1)	Marinobacter (1)
Burkholderiales (1)	Oxalobacteraceae (1)	Oxalicibacterium (1)
Alteromonadales (1)	Alteromonadaceae (1)	Paraglaciecola (1)
Synechococcales (1)	Synechococcaceae (1)	Vulcanococcus (1)
Hyphomicrobiales (1)	Amorphaceae (1)	Acuticoccus (1)

[top](#)

Cluster 81

Total number of members in cluster: 22

Average length of proteins in cluster: 396.3

Conserved (non-aliphatic) residues:

R 64 (100.0%) Q 117 (100.0%) D 175 (100.0%) Y 188 (100.0%) Y 192 (100.0%) Y 203 (100.0%) R 208 (100.0%) D 215 (100.0%) Y 221 (100.0%) T 260 (100.0%) R 261 (100.0%) Y 308 (100.0%) R 315 (100.0%) D 318 (100.0%) S 319 (100.0%) S 323 (100.0%) S 326 (100.0%) R 330 (100.0%) S 337 (100.0%) Q 353 (100.0%) R 365 (100.0%) N 367 (100.0%) T 368 (100.0%) D 369 (100.0%) N 370 (100.0%) E 378 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
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protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
CAA43912.1	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Muenchen	0
WP_001529369.1	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	ssp. enterica sv. Kentucky O8 98/39	0
WP_000936592.1	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	ssp. enterica sv. Newport	0
WP_000936591.1	Enterobacterales	Enterobacteriaceae	Salmonella	nan	Hadar	0
ACF64132.1	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	ssp. enterica sv. Newport	0
WP_000936589.1	Enterobacterales	Enterobacteriaceae	Salmonella	nan	ssp. enterica sv. Kentucky O8 98/39	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

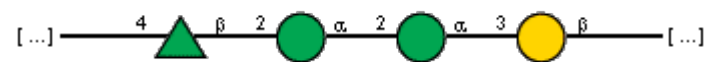
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

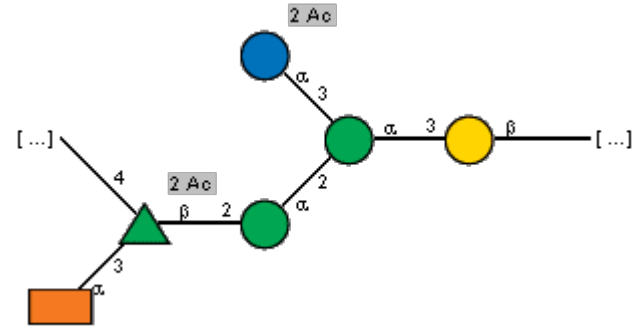
Sugars in cluster:

WP_001529369.1 Salmonella enterica ssp. enterica sv. Kentucky O8 98/39, WP_000936589.1 Salmonella enterica ssp. enterica sv. Kentucky O8 98/39:



CSDB record ID: 27410

WP_000936592.1 Salmonella enterica ssp. enterica sv. Newport, ACF64132.1 Salmonella enterica ssp. enterica sv. Newport:



CSDB record ID: 28331

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (21)	Enterobacteriaceae (21)	Salmonella (15)
		Enterobacter (3)
		Kosakonia (2)
		Citrobacter (1)
Burkholderiales (1)	nan (1)	nan (1)

[top](#)

Cluster 40

Total number of members in cluster: 22

Average length of proteins in cluster: 394.2

Conserved (non-aliphatic) residues:

Q 160 (100.0%) Y 170 (100.0%) D 172 (100.0%) R 183 (100.0%) R 199 (100.0%) T 201 (100.0%) E 206 (100.0%) S 208 (100.0%) R 322 (100.0%) N 379 (100.0%) D 380 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
BAQ01533.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O110	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

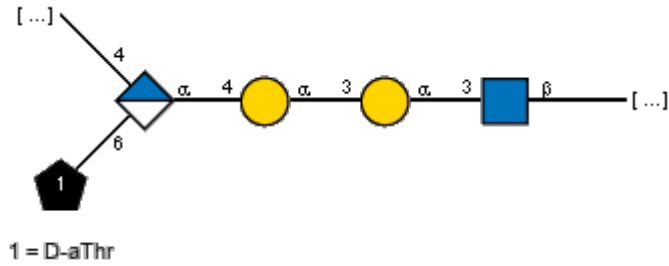
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

BAQ01533.1 Escherichia coli O110:



CSDB record ID: 1849

Sugars for blast hits:

Alphafold models:

[BAQ01533.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Vibrionales (10)	Vibrionaceae (10)	Photobacterium (6) Vibrio (4)
Enterobacterales (9)	Enterobacteriaceae (5) Morganellaceae (2) Yersiniaceae (1) Erwiniaceae (1)	Escherichia (5) Proteus (2) Chania (1) Mixta (1)
Oceanospirillales (1)	Endozoicomonadaceae (1)	Kistimonas (1)
Chitinophagales (1)	Chitinophagaceae (1)	Arachidicoccus (1)
Pseudomonadales (1)	Marinobacteraceae (1)	Marinobacter (1)

[top](#)

Cluster 24

Total number of members in cluster: 22

Average length of proteins in cluster: 368.3

Conserved (non-aliphatic) residues:

Y 56 (100.0%) D 57 (100.0%) Y 61 (100.0%) E 80 (100.0%) Y 113 (100.0%) E 140 (100.0%) R 143 (100.0%) Q 144 (100.0%) H 177 (100.0%) K 242 (100.0%) R 311 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
ABI98976.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O141	0
WP_046788607.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O141ab	0
WP_000456161.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O141ac	0

[MSA fasta](#)

[Malign view](#)

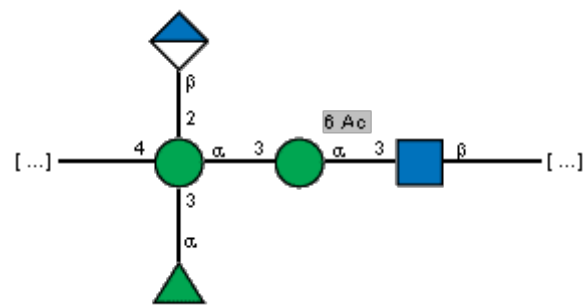
[Fasta of members](#)

[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:



CSDB record ID: 1883

Sugars for blast hits:

AlphaFold models:

[ABI98976.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (20)	Enterobacteriaceae (20)	Klebsiella (10)
		Escherichia (8)
		Enterobacter (1)
		Citrobacter (1)
Aeromonadales (2)	Aeromonadaceae (2)	Aeromonas (2)

[top](#)

Cluster 91

Total number of members in cluster: 21

Average length of proteins in cluster: 427.1

Conserved (non-aliphatic) residues:

Q 240 (100.0%) K 241 (100.0%) R 306 (100.0%) Q 311 (100.0%) N 369 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
CBN82200.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O70	0
ADI77033.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O71	0

[MSA fasta](#)

[Malign view](#)

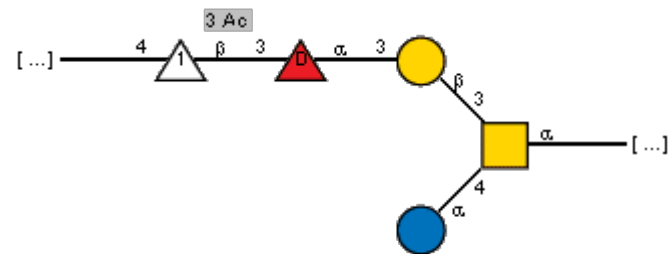
[Fasta of members](#)

Logoplot

Phylogenetic tree

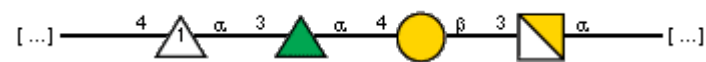
Hits in cluster

Sugars in cluster:

CBN82200.1 *Escherichia coli* O70:

1 = b-D-Quip3N

CSDB record ID: 1576

ADI77033.1 *Escherichia coli* O71:

1 = a-D-Quip3N

CSDB record ID: 1577

Sugars for blast hits:

Alphafold models:

CBN82200.1

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (13)	Enterobacteriaceae (13)	Escherichia (6)
		Enterobacter (2)
		Citrobacter (2)
		Leclercia (1)
		Salmonella (1)
		Lelliottia (1)
Alteromonadales (4)	Pseudoalteromonadaceae (2)	Pseudoalteromonas (2)
	Shewanellaceae (1)	Shewanella (1)
	Ferrimonadaceae (1)	Paraferriomonas (1)
Burkholderiales (3)	Comamonadaceae (2)	Comamonas (1)
		Polaromonas (1)
	Burkholderiaceae (1)	Ralstonia (1)
Aeromonadales (1)	Aeromonadaceae (1)	Aeromonas (1)

[top](#)

Cluster 89

Total number of members in cluster: 21

Average length of proteins in cluster: 394.2

Conserved (non-aliphatic) residues:

R 229 (100.0%) R 284 (100.0%) R 356 (100.0%) S 359 (100.0%) R 363 (100.0%) S 398 (100.0%) H 399 (100.0%) Y 407 (100.0%) D 460 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
CAI33324.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	14	0
CAI33366.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	15B	0
CAI33389.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	15C	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

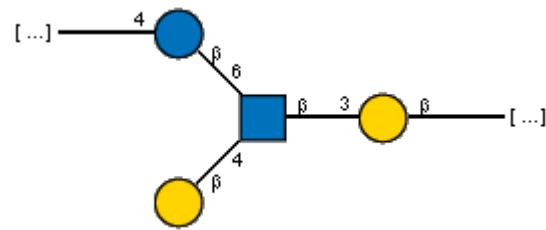
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

CAI33324.1 Streptococcus pneumoniae 14:



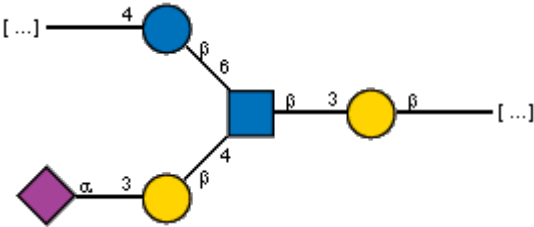
CSDB record ID: 5348

CAI33366.1 Streptococcus pneumoniae 15B:

CAI33389.1 *Streptococcus pneumoniae* 15C:

Sugars for blast hits:

AAL57082.1 *Streptococcus agalactiae* III:



Alphafold models:

CAI33324.1

CAI33366.1

Taxonomy:

order (count)	family (count)	genus (count)
Lactobacillales (15)	Streptococcaceae (14)	Streptococcus (14)
	Lactobacillaceae (1)	Lactiplantibacillus (1)
Bacillales (3)	Planococcaceae (2)	Ureibacillus (1)
		Planomicrobium (1)
	Bacillaceae (1)	Peribacillus (1)
Pasteurellales (1)	Pasteurellaceae (1)	Rodentibacter (1)
nan (1)	nan (1)	nan (1)

order (count) family (count) genus (count)

Coriobacteriales (1) Coriobacteriaceae (1) Collinsella (1)

[top](#)

Cluster 80

Total number of members in cluster: 21

Average length of proteins in cluster: 396.0

Conserved (non-aliphatic) residues:

Y 30 (100.0%) Y 37 (100.0%) Y 73 (100.0%) Y 115 (100.0%) Y 118 (100.0%) T 124 (100.0%) Y 126 (100.0%) N 136 (100.0%) D 140 (100.0%) S 144 (100.0%) S 182 (100.0%) Q 186 (100.0%) R 188 (100.0%) R 189 (100.0%) E 190 (100.0%) S 201 (100.0%) Y 233 (100.0%) R 235 (100.0%) S 237 (100.0%) T 240 (100.0%) S 241 (100.0%) E 256 (100.0%) T 257 (100.0%) H 258 (100.0%) N 266 (100.0%) E 267 (100.0%) H 271 (100.0%) K 304 (100.0%) E 314 (100.0%) Y 318 (100.0%) D 320 (100.0%) K 321 (100.0%) T 328 (100.0%) H 332 (100.0%) Y 354 (100.0%) R 378 (100.0%) K 379 (100.0%) D 380 (100.0%) Y 383 (100.0%) K 386 (100.0%) Y 387 (100.0%) S 389 (100.0%) Y 402 (100.0%) K 408 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
CAA43077.1	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	O3,10 (E1) Anatum	0
AAB48190.1	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	ssp. enterica sv. Strasbourg	0
WP_000231472.1	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Weltevreden	0
AGS07316.1	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	O1,3,19 (E4) Senftenberg	0
AGS07327.1	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	O3,10 (E1) Anatum	0
AGS07363.1	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	ssp. enterica sv. Strasbourg	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

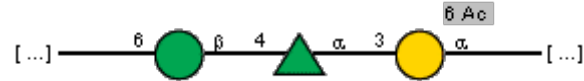
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

CAA43077.1 Salmonella enterica O3,10 (E1) Anatum, AGS07327.1 Salmonella enterica O3,10 (E1) Anatum:



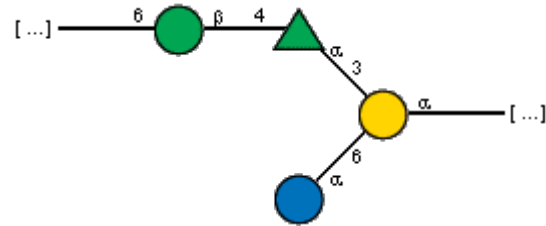
CSDB record ID: 30407

AAB48190.1 *Salmonella enterica* ssp. *enterica* sv. *Strasbourg*, AGS07363.1 *Salmonella enterica* ssp. *enterica* sv. *Strasbourg*:



CSDB record ID: 30404

AGS07316.1 *Salmonella enterica* O1,3,19 (E4) *Senftenberg*:



CSDB record ID: 30411

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (21)	Enterobacteriaceae (20)	Salmonella (14)
		Klebsiella (4)
		Citrobacter (2)
	Yersiniaceae (1)	Serratia (1)

[top](#)

Cluster 123

Total number of members in cluster: 21

Average length of proteins in cluster: 465.9

Conserved (non-aliphatic) residues:

R 277 (100.0%) R 330 (100.0%) E 361 (100.0%) R 488 (100.0%) R 496 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
CAI32772.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	4	0

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[Malign view](#)

[Fasta of members](#)

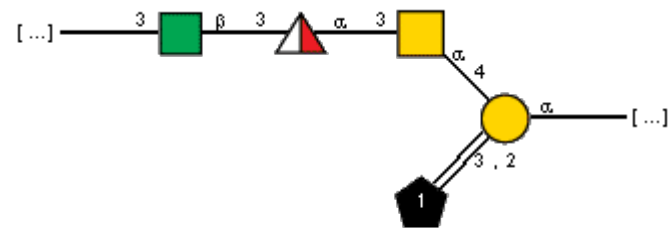
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

CAI32772.1 Streptococcus pneumoniae 4:



1 = Pyr

CSDB record ID: 805

Sugars for blast hits:

Alphafold models:

[CAI32772.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Lactobacillales (9)	Streptococcaceae (8)	Streptococcus (8)
	Lactobacillaceae (1)	Lactiplantibacillus (1)
Bacillales (4)	Bacillaceae (2)	Priestia (1)
		Cytobacillus (1)
	Paenibacillaceae (1)	Chengkuizengella (1)
Eubacteriales (4)	Lachnospiraceae (2)	nan (2)
		Eisenbergiella (1)
	Eubacteriaceae (1)	Eubacterium (1)
	Clostridiaceae (1)	Natronincola (1)
nan (2)	nan (3)	nan (2)
Erysipelotrichales (1)	Erysipelotrichaceae (1)	Amedibacterium (1)
Acholeplasmatales (1)	Acholeplasmataceae (1)	nan (2)

[top](#)

Cluster 101

Total number of members in cluster: 21

Average length of proteins in cluster: 372.5

Conserved (non-aliphatic) residues:

Total number of members in cluster: 20

Average length of proteins in cluster: 421.1

Conserved (non-aliphatic) residues:

D 189 (100.0%) R 193 (100.0%) E 200 (100.0%) S 202 (100.0%) S 237 (100.0%) K 240 (100.0%) T 307 (100.0%) T 310 (100.0%) R 311 (100.0%) E 362 (100.0%) Y 366 (100.0%) K 381 (100.0%) D 382 (100.0%) S 385 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
BAQ01317.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O88	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

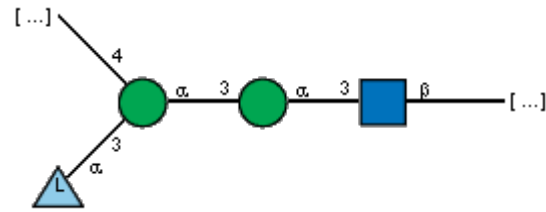
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

BAQ01317.1 Escherichia coli O88:



CSDB record ID: 1595

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (19)	Enterobacteriaceae (19)	Escherichia (9)
		Enterobacter (6)
		nan (2)
		Lelliottia (1)
		Cedecea (1)
Aeromonadales (1)	Aeromonadaceae (1)	Aeromonas (1)

[top](#)

Cluster 126

Total number of members in cluster: 20

Average length of proteins in cluster: 346.6

Conserved (non-aliphatic) residues:

D 76 (100.0%) K 101 (100.0%) D 102 (100.0%) S 130 (100.0%) Q 166 (100.0%) R 168 (100.0%) H 202 (100.0%) R 266 (100.0%) Y 270 (100.0%) D 340 (100.0%) R 345 (100.0%) D 354 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
ACV67289.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O35	0
AFW04785.1	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	O62	0

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[Malign view](#)

[Fasta of members](#)

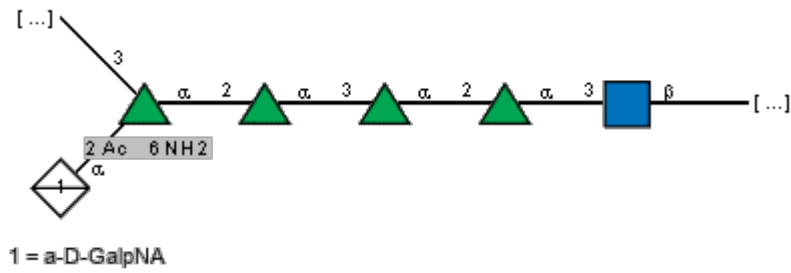
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

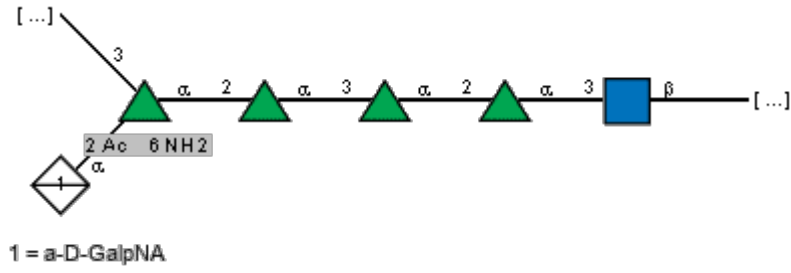
Sugars in cluster:

ACV67289.1 Escherichia coli O35:



CSDB record ID: 1542

AFW04785.1 Salmonella enterica O62:



CSDB record ID: 3359

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (12)	Enterobacteriaceae (7)	Escherichia (3)
		Salmonella (3)
		Leclercia (1)
	Erwiniaceae (4)	Pantoea (3)
		Tatumella (1)
	Pectobacteriaceae (1)	Pectobacterium (1)
Pseudomonadales (6)	Pseudomonadaceae (6)	Pseudomonas (6)
Vibrionales (1)	Vibrionaceae (1)	Vibrio (1)
Alteromonadales (1)	Pseudoalteromonadaceae (1)	Pseudoalteromonas (1)

[top](#)

Cluster 77

Total number of members in cluster: 19

Average length of proteins in cluster: 387.7

Conserved (non-aliphatic) residues:

R 156 (100.0%) N 160 (100.0%) Y 161 (100.0%) Y 173 (100.0%) Y 175 (100.0%) Y 226 (100.0%) T 231 (100.0%) K 233 (100.0%) K 235 (100.0%) R 247 (100.0%) S 254 (100.0%) S 272 (100.0%) K 278 (100.0%) Y 297 (100.0%) N 301 (100.0%) D 306 (100.0%) T 338 (100.0%) N 339 (100.0%) T 342 (100.0%) Y 345 (100.0%) H 367 (100.0%) Q 396 (100.0%) Y 402 (100.0%) Y 407 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
BAQ01675.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O133	0
ACD37126.1	Enterobacterales	Enterobacteriaceae	Shigella	Shigella boydii	2	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

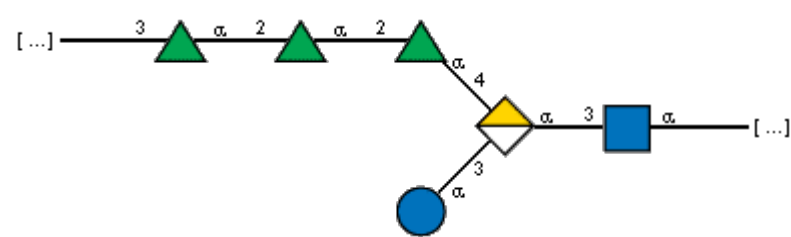
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

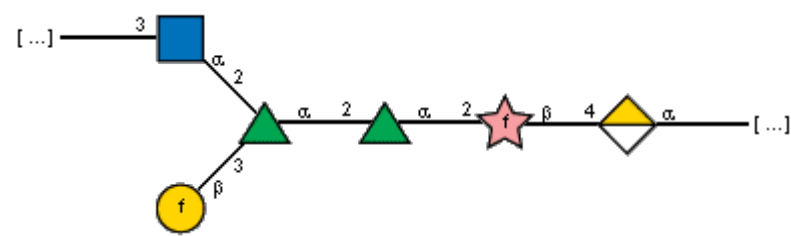
Sugars in cluster:

BAQ01675.1 Escherichia coli O133:



CSDB record ID: 1875

ACD37126.1 Shigella boydii 2:



CSDB record ID: 3982

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (19)	Enterobacteriaceae (18)	Enterobacter (8)
		Escherichia (6)
		Shigella (2)
		Superficieibacter (2)
	Hafniaceae (1)	Hafnia (1)

[top](#)

Cluster 145

Total number of members in cluster: 19

Average length of proteins in cluster: 392.7

Conserved (non-aliphatic) residues:

D 43 (100.0%) Y 47 (100.0%) Y 51 (100.0%) E 67 (100.0%) N 93 (100.0%) Y 123 (100.0%) E 125 (100.0%) R 128 (100.0%) Q 129 (100.0%) S 134 (100.0%) H 162 (100.0%) K 220 (100.0%) Y 224 (100.0%) Y 230 (100.0%) D 243 (100.0%) R 295 (100.0%) Y 299 (100.0%) Q 341 (100.0%) R 344 (100.0%) K 380 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
AAT85653.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O4	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

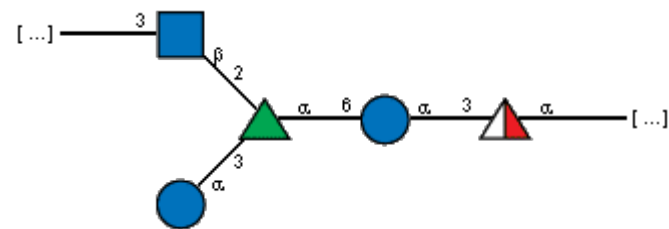
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[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

AAT85653.1 Escherichia coli O4:



CSDB record ID: 10216

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (15)	Enterobacteriaceae (11)	Enterobacter (6)
		Escherichia (5)
	Erwiniaceae (4)	Pantoea (4)
Moraxellales (2)	Moraxellaceae (2)	Acinetobacter (2)
Burkholderiales (2)	Burkholderiaceae (1)	Ralstonia (1)
	Comamonadaceae (1)	Comamonas (1)

[top](#)

Cluster 86

Total number of members in cluster: 18

Average length of proteins in cluster: 404.2

Conserved (non-aliphatic) residues:

S 59 (100.0%) D 90 (100.0%) E 93 (100.0%) Y 94 (100.0%) Y 98 (100.0%) R 113 (100.0%) E 119 (100.0%) N 136 (100.0%) Y 183 (100.0%) R 186 (100.0%) S 190 (100.0%) H 219 (100.0%) S 221 (100.0%) R 351 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
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protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
BAQ00858.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O38	0
WP_016238111.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O81	0
ACA24776.1	Enterobacterales	Enterobacteriaceae	Shigella	Shigella dysenteriae	8	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

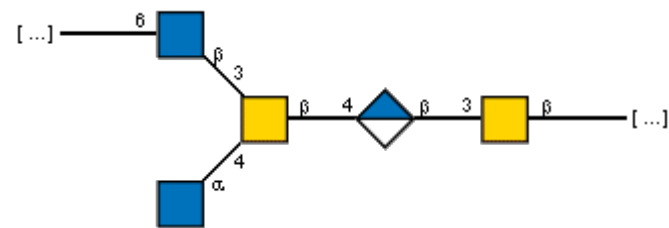
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

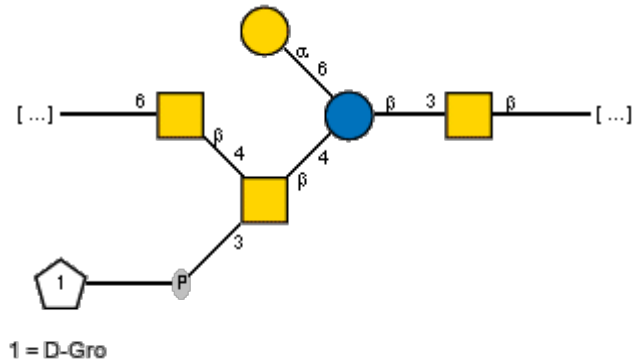
Sugars in cluster:

BAQ00858.1 Escherichia coli O38:



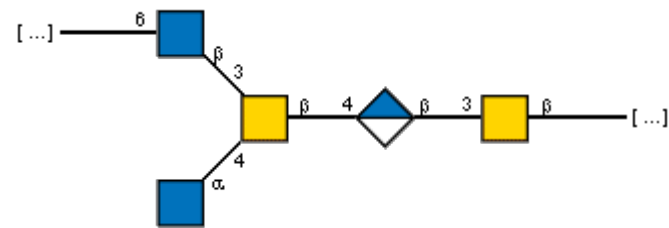
CSDB record ID: 1545

WP_016238111.1 Escherichia coli O81:



CSDB record ID: 1587

ACA24776.1 Shigella dysenteriae 8:



Sugars for blast hits:

Alphafold models:

[WP_016238111.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (15)	Enterobacteriaceae (13)	Escherichia (7)
		Citrobacter (3)
		Enterobacter (2)
		Shigella (1)
	Erwiniaceae (2)	Pantoea (1)
Vibrionales (3)	Vibrionaceae (3)	Erwinia (1)
		Photobacterium (3)

[top](#)

Cluster 158

Total number of members in cluster: 18

Average length of proteins in cluster: 476.8

Conserved (non-aliphatic) residues:

R 300 (100.0%) T 301 (100.0%) R 362 (100.0%) Y 424 (100.0%) D 438 (100.0%) E 483 (100.0%) N 487 (100.0%) Y 523 (100.0%) R 537 (100.0%) R 538 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
CAI33983.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	25F	0
CAI33966.2	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	25A	0
CAI34407.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	38	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Lactobacillales (10)	Streptococcaceae (8)	Streptococcus (8)
	Enterococcaceae (1)	Enterococcus (1)
	Lactobacillaceae (1)	Limosilactobacillus (1)
Erysipelotrichales (5)	Erysipelotrichaceae (5)	Solobacterium (5)
Eubacteriales (3)	Oscillospiraceae (1)	Ruminococcus (1)
	Lachnospiraceae (1)	Dorea (1)
	Clostridiaceae (1)	Clostridium (1)

[top](#)

Cluster 144

Total number of members in cluster: 18

Average length of proteins in cluster: 329.0

Conserved (non-aliphatic) residues:

D 99 (100.0%) Y 103 (100.0%) E 132 (100.0%) Y 191 (100.0%) E 200 (100.0%) K 203 (100.0%) H 236 (100.0%) Q 238 (100.0%) K 311 (100.0%) Y 315 (100.0%) R 369 (100.0%) Y 399 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
AHB32242.2	Moraxellales	Moraxellaceae	Acinetobacter	Acinetobacter baumannii	O5	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

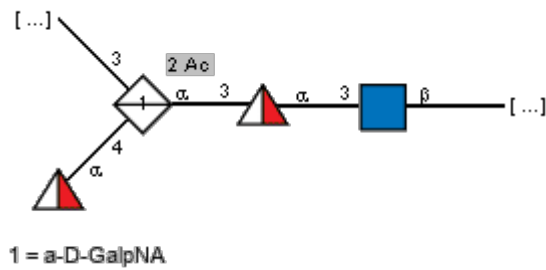
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

AHB32242.2 Acinetobacter baumannii O5:



CSDB record ID: 487

Sugars for blast hits:

Alphafold models:

[AHB32242.2](#)

Taxonomy:

order (count)	family (count)	genus (count)
Moraxellales (5)	Moraxellaceae (5)	Acinetobacter (5)
Sphingomonadales (4)	Erythrobacteraceae (3)	Altererythrobacter (1)
		Erythrobacter (1)
		Qipengyuania (1)
	Sphingomonadaceae (1)	Sphingobium (1)
Rhodobacterales (3)	Rhodobacteraceae (2)	nan (1)
		Haematobacter (1)
	Roseobacteraceae (1)	Roseobacter (1)
Pseudomonadales (2)	Pseudomonadaceae (2)	Pseudomonas (2)
Burkholderiales (1)	Alcaligenaceae (1)	Pigmentiphaga (1)
Aeromonadales (1)	Aeromonadaceae (1)	Aeromonas (1)
Alteromonadales (1)	Pseudoalteromonadaceae (1)	Pseudoalteromonas (1)
Hyphomicrobiales (1)	Devosiaceae (1)	Devosia (1)

[top](#)

Cluster 141

Total number of members in cluster: 18

Average length of proteins in cluster: 421.3

Conserved (non-aliphatic) residues:

E 215 (100.0%) K 264 (100.0%) R 265 (100.0%) R 339 (100.0%) H 387 (100.0%) D 443 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
CAI33610.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	18F	0
CAI33537.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	18A	0

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
CAI33561.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	18B	0
CAI33585.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	18C	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

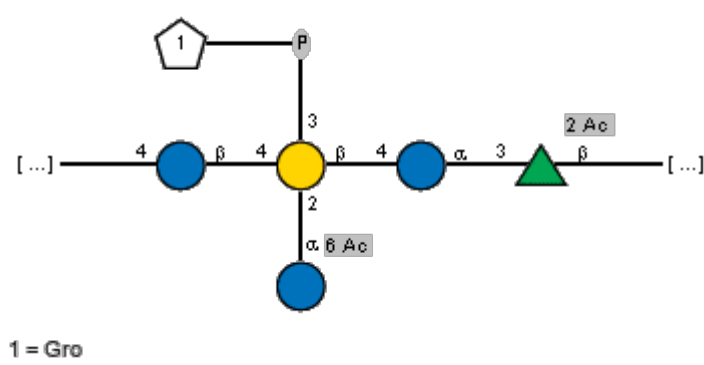
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

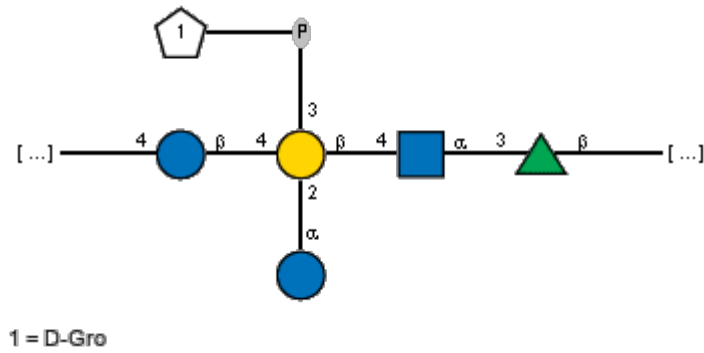
Sugars in cluster:

CAI33610.1 Streptococcus pneumoniae 18F:



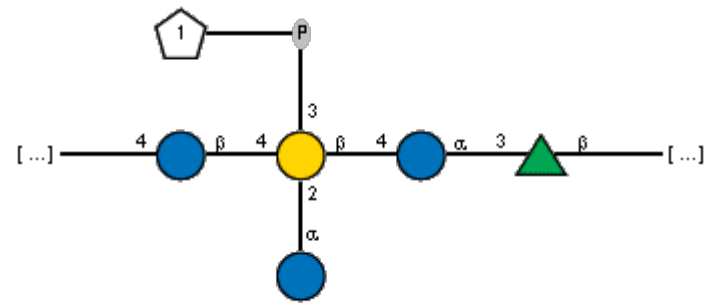
CSDB record ID: 7071

CAI33537.1 Streptococcus pneumoniae 18A:



CSDB record ID: 7074

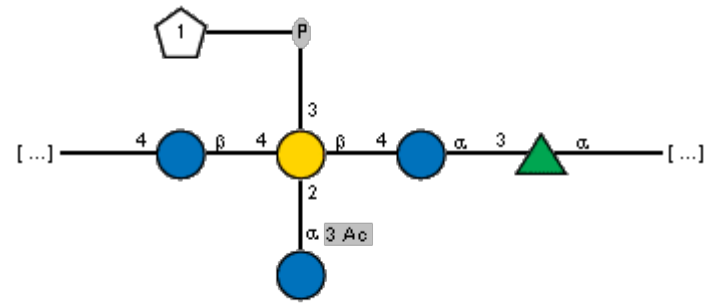
CAI33561.1 Streptococcus pneumoniae 18B:



1 = D-Glc

CSDB record ID: 846

CAI33585.1 *Streptococcus pneumoniae* 18C:

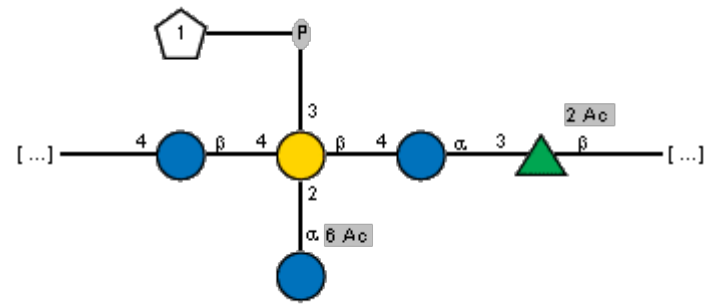


1 = D-Glc

CSDB record ID: 939

Sugars for blast hits:

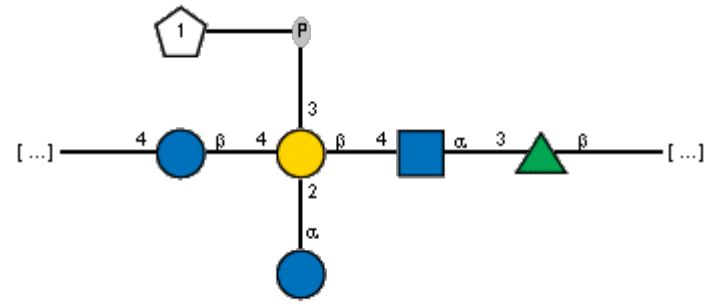
VOG14504.1 *Streptococcus pneumoniae* 18F:



1 = Glc

CSDB record ID: 7071

VQM63531.1 *Streptococcus pneumoniae* 18A:



1 = D-Glc

CSDB record ID: 7074

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Lactobacillales (11)	Streptococcaceae (11)	Streptococcus (11)
Eubacteriales (4)	Eubacteriaceae (2)	Eubacterium (2)
	Lachnospiraceae (1)	Coproccoccus (1)
	nan (1)	nan (1)
Erysipelotrichales (1)	Erysipelotrichaceae (1)	nan (1)
Bacteroidales (1)	Tannerellaceae (1)	nan (1)
Coriobacteriales (1)	Coriobacteriaceae (1)	Collinsella (1)

[top](#)

Cluster 116

Total number of members in cluster: 18

Average length of proteins in cluster: 381.6

Conserved (non-aliphatic) residues:

Q 123 (100.0%) N 130 (100.0%) Y 135 (100.0%) Y 165 (100.0%) K 201 (100.0%) Q 203 (100.0%) S 204 (100.0%) K 224 (100.0%) T 239 (100.0%) R 240 (100.0%) R 243 (100.0%) N 244 (100.0%) Y 264 (100.0%) S 267 (100.0%) N 271 (100.0%) Y 274 (100.0%) D 282 (100.0%) Y 285 (100.0%) Q 293 (100.0%) K 294 (100.0%) S 299 (100.0%) D 307 (100.0%) T 309 (100.0%) S 310 (100.0%) S 321 (100.0%) Y 329 (100.0%) Q 338 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
BAQ01361.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O90	0
CAS09721.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O127	0
AAR90892.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O127	0

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[Malign view](#)

[Fasta of members](#)

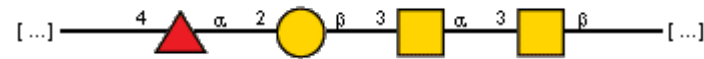
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

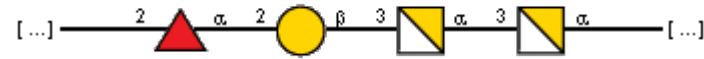
Sugars in cluster:

BAQ01361.1 Escherichia coli O90:



CSDB record ID: 1596

CAS09721.1 Escherichia coli O127, AAR90892.1 Escherichia coli O127:



CSDB record ID: 1866

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (17)	Enterobacteriaceae (17)	Salmonella (8)
		Escherichia (6)
		Citrobacter (2)
		nan (1)
Aeromonadales (1)	Aeromonadaceae (1)	Aeromonas (1)

[top](#)

Cluster 113

Total number of members in cluster: 18

Average length of proteins in cluster: 326.7

Conserved (non-aliphatic) residues:

D 56 (100.0%) S 57 (100.0%) Y 60 (100.0%) Q 63 (100.0%) K 85 (100.0%) E 87 (100.0%) N 112 (100.0%) N 117 (100.0%) Y 149 (100.0%) N 154 (100.0%) Y 157 (100.0%) R 160 (100.0%) H 191 (100.0%) S 242 (100.0%) R 264 (100.0%) S 301 (100.0%) N 307 (100.0%) Q 309 (100.0%) R 313 (100.0%) S 346 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
AEP25500.1	Enterobacterales	Yersiniaceae	Yersinia	Yersinia pseudotuberculosis	O:6	0
WP_000482333.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O55	0
BAG11898.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O55	0
AAV34523.1	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	50	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

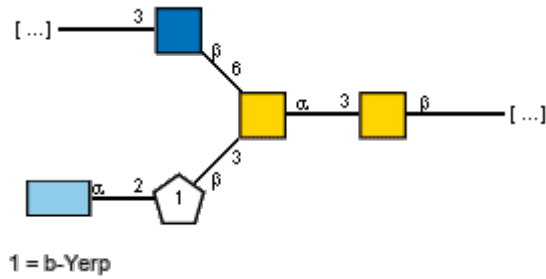
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

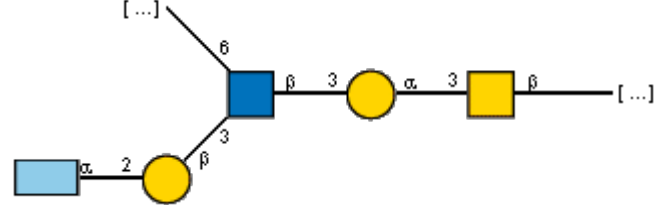
Sugars in cluster:

AEP25500.1 *Yersinia pseudotuberculosis* O:6:



CSDB record ID: 12139

WP_000482333.1 *Escherichia coli* O55, BAG11898.1 *Escherichia coli* O55:



CSDB record ID: 1562

Sugars for blast hits:

Alphafold models:

[BAG11898.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (17)	Enterobacteriaceae (13)	<i>Escherichia</i> (6)
		<i>Salmonella</i> (5)
		<i>Citrobacter</i> (2)
	Yersiniaceae (3)	<i>Yersinia</i> (3)
	Pectobacteriaceae (1)	<i>Pectobacterium</i> (1)
Neisseriales (1)	Chromobacteriaceae (1)	<i>Chromobacterium</i> (1)

[top](#)

Cluster 99

Total number of members in cluster: 17

Average length of proteins in cluster: 327.3

Conserved (non-aliphatic) residues:

D 79 (100.0%) Y 80 (100.0%) Y 83 (100.0%) E 99 (100.0%) K 131 (100.0%) Y 157 (100.0%) Q 169 (100.0%) R 171 (100.0%) H 203 (100.0%) Y 249 (100.0%) S 262 (100.0%) K 264 (100.0%) R 319 (100.0%) D 322 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
AHB32832.1	Moraxellales	Moraxellaceae	Acinetobacter	Acinetobacter baumannii	O19	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Moraxellales (8)	Moraxellaceae (8)	Acinetobacter (8)
Burkholderiales (6)	Burkholderiaceae (6)	Ralstonia (6)
Pseudomonadales (3)	Pseudomonadaceae (3)	Pseudomonas (3)

[top](#)

Cluster 95

Total number of members in cluster: 17

Average length of proteins in cluster: 411.9

Conserved (non-aliphatic) residues:

S 132 (100.0%) E 136 (100.0%) H 146 (100.0%) K 186 (100.0%) Q 187 (100.0%) K 189 (100.0%) Y 235 (100.0%) K 238 (100.0%) H 260 (100.0%) Y 264 (100.0%) S 267 (100.0%) S 273 (100.0%) Y 275 (100.0%) N 298 (100.0%) N 329 (100.0%) T 336 (100.0%) Y 349 (100.0%) S 378 (100.0%) S 383 (100.0%) Y 387 (100.0%) Y 388 (100.0%) Y 389 (100.0%) E 396 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
ABX51880.1	Enterobacterales	Enterobacteriaceae	Cronobacter	Cronobacter sakazakii	O1	0

MSA fasta

Malign view

Fasta of members

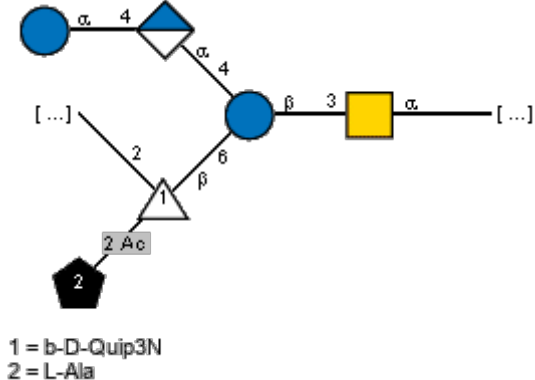
Logoplot

Phylogenetic tree

Hits in cluster

Sugars in cluster:

ABX51880.1 Cronobacter sakazakii O1:



CSDB record ID: 27329

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (17)	Enterobacteriaceae (15)	Cronobacter (6)
		Enterobacter (6)
		Escherichia (3)
	Erwiniaceae (2)	Pantoea (2)

[top](#)

Cluster 42

Total number of members in cluster: 17

Average length of proteins in cluster: 408.1

Conserved (non-aliphatic) residues:

H 150 (100.0%) R 199 (100.0%) T 251 (100.0%) R 252 (100.0%) R 327 (100.0%) Q 330 (100.0%) R 357 (100.0%) Y
365 (100.0%) E 366 (100.0%) S 368 (100.0%) K 375 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
AAY28257.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O177	0
AAM27782.1	Pseudomonadales	Pseudomonadaceae	Pseudomonas	Pseudomonas aeruginosa	O4	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

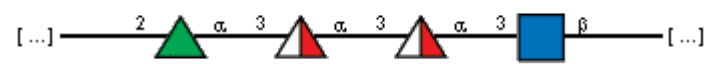
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

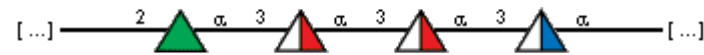
Sugars in cluster:

AAY28257.1 Escherichia coli O177:



CSDB record ID: 1919

AAM27782.1 Pseudomonas aeruginosa O4:



CSDB record ID: 24033

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Pseudomonadales (10)	Pseudomonadaceae (10)	Pseudomonas (10)
Burkholderiales (4)	Burkholderiaceae (2)	Polynucleobacter (1)
		Paraburkholderia (1)
	Comamonadaceae (1)	Comamonas (1)
	nan (1)	nan (1)
Enterobacterales (3)	Enterobacteriaceae (3)	Escherichia (2)
		Kosakonia (1)

[top](#)

Cluster 177

Total number of members in cluster: 17

Average length of proteins in cluster: 398.7

Conserved (non-aliphatic) residues:

S 130 (100.0%) R 146 (100.0%) Q 194 (100.0%) R 209 (100.0%) R 214 (100.0%) S 217 (100.0%) S 221 (100.0%) T 223 (100.0%) R 252 (100.0%) Q 268 (100.0%) K 269 (100.0%) N 274 (100.0%) R 384 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
AAD45264.1	Pseudomonadales	Pseudomonadaceae	Pseudomonas	Pseudomonas aeruginosa	O11	0
AAM27574.1	Pseudomonadales	Pseudomonadaceae	Pseudomonas	Pseudomonas aeruginosa	O11	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

AAD45264.1 Pseudomonas aeruginosa O11, AAM27574.1 Pseudomonas aeruginosa O11:



CSDB record ID: 10219

Sugars for blast hits:

Alphafold models:

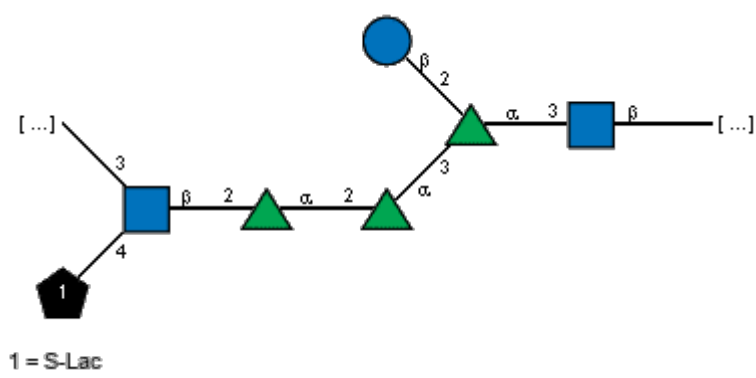
[AAD45264.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Pseudomonadales (14)	Pseudomonadaceae (14)	Pseudomonas (14)
Burkholderiales (1)	Oxalobacteraceae (1)	Janthinobacterium (1)
Bacillales (1)	Bacillaceae (1)	Oceanobacillus (1)
Desulfobacterales (1)	Desulfobacteraceae (1)	Desulfobotulus (1)

[top](#)

ACA24792.1 *Shigella dysenteriae* 13:



CSDB record ID: 1891

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (15)	Enterobacteriaceae (14)	Escherichia (9)
		Enterobacter (4)
		Shigella (1)
		Hafnia (1)
Vibrionales (2)	Hafniaceae (1)	Photobacterium (1)
	Vibrionaceae (2)	Vibrio (1)

[top](#)

Cluster 140

Total number of members in cluster: 17

Average length of proteins in cluster: 482.9

Conserved (non-aliphatic) residues:

Q 149 (100.0%) N 150 (100.0%) R 249 (100.0%) E 293 (100.0%) R 344 (100.0%) R 345 (100.0%) D 352 (100.0%) S 396 (100.0%) K 397 (100.0%) S 446 (100.0%) H 450 (100.0%) E 493 (100.0%) E 556 (100.0%) S 560 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
CAI33817.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	23A	0

[MSA fasta](#)

[Malign view](#)

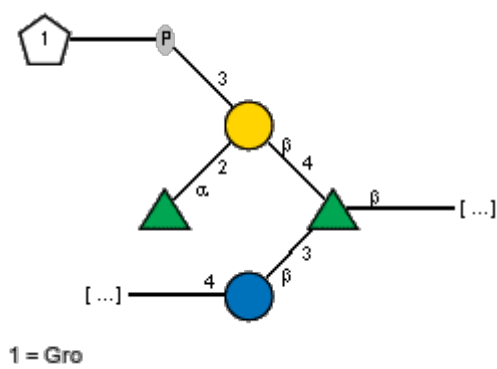
[Fasta of members](#)

[Logoplot](#)

[Phylogenetic tree](#)

Sugars in cluster:

CAI33817.1 Streptococcus pneumoniae 23A:



CSDB record ID: 7084

Sugars for blast hits:

Alphafold models:

[CAI33817.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Micrococcales (9)	Micrococcaceae (5)	Arthrobacter (4)
		Pseudarthrobacter (1)
	Microbacteriaceae (3)	Curtobacterium (1)
		Frondihabitans (1)
		Microbacterium (1)
Lactobacillales (3)	Streptococcaceae (3)	Demequina (1)
		Streptococcus (3)
Eubacteriales (2)	Lachnospiraceae (1)	nan (1)
	Eubacteriaceae (1)	Eubacterium (1)
Nitrosomonadales (1)	Methylophilaceae (1)	Methylobacillus (1)
Bacillales (1)	Bacillaceae (1)	Mesobacillus (1)
nan (1)	nan (1)	nan (1)

[top](#)

Cluster 61

Total number of members in cluster: 16

Average length of proteins in cluster: 381.9

Conserved (non-aliphatic) residues:

D 85 (100.0%) R 103 (100.0%) S 111 (100.0%) Q 141 (100.0%) K 156 (100.0%) N 171 (100.0%) N 177 (100.0%) R 181 (100.0%) N 190 (100.0%) Q 219 (100.0%) N 222 (100.0%) S 223 (100.0%) N 224 (100.0%) E 283 (100.0%) T 292 (100.0%) D 332 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
AAV74543.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O15	0

- [MSA fasta](#)
- [Malign view](#)
- [Fasta of members](#)
- [Logoplot](#)
- [Phylogenetic tree](#)
- [Hits in cluster](#)

Sugars in cluster:

AAV74543.1 Escherichia coli O15:



CSDB record ID: 1516

Sugars for blast hits:

AlphaFold models:

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (8)	Enterobacteriaceae (8)	Escherichia (5) nan (1) Citrobacter (1) Salmonella (1)
Vibrionales (3)	Vibrionaceae (3)	Vibrio (3)
Pasteurellales (1)	Pasteurellaceae (1)	Glaesserella (1)
Thiotrichales (1)	Thiotrichaceae (1)	nan (1)
Pseudomonadales (1)	Marinobacteraceae (1)	Marinobacter (1)
Oceanospirillales (1)	Oceanospirillaceae (1)	Marinomonas (1)
Chromatiales (1)	Ectothiorhodospiraceae (1)	Arhodomonas (1)

[top](#)

Cluster 51

Total number of members in cluster: 16

Average length of proteins in cluster: 439.1

Conserved (non-aliphatic) residues:

Y 103 (100.0%) K 218 (100.0%) E 280 (100.0%) R 281 (100.0%) K 325 (100.0%) N 359 (100.0%) Y 471 (100.0%) R 483 (100.0%) K 495 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
CAI32705.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	1	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

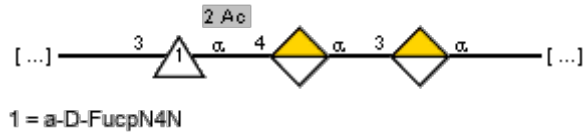
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

CAI32705.1 Streptococcus pneumoniae 1:



CSDB record ID: 31499

Sugars for blast hits:

Alphafold models:

[CAI32705.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Bacillales (4)	Bacillaceae (2)	Bacillus (1)
		Salicibibacter (1)
	Staphylococcaceae (1)	Salinicoccus (1)
	Planococcaceae (1)	Sporosarcina (1)
Erysipelotrichales (4)	Erysipelotrichaceae (4)	Holdemania (2)
		Holdemanella (1)
		Erysipelothrix (1)
Lactobacillales (2)	Streptococcaceae (2)	Streptococcus (2)
nan (2)	nan (2)	nan (2)
Eubacteriales (1)	Clostridiaceae (1)	Clostridium (1)
Eggerthellales (1)	Eggerthellaceae (1)	Adlercreutzia (1)
Bacteroidales (1)	Bacteroidaceae (1)	Bacteroides (1)
Vibrionales (1)	Vibrionaceae (1)	Vibrio (1)

Cluster 38

Total number of members in cluster: 16

Average length of proteins in cluster: 409.1

Conserved (non-aliphatic) residues:

S 28 (100.0%) Q 231 (100.0%) S 234 (100.0%) Y 235 (100.0%) R 288 (100.0%) R 354 (100.0%) R 373 (100.0%) H 406 (100.0%) S 462 (100.0%) Y 465 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
CAI33278.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	12F	0
CAI33226.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	12A	0
CAI33252.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	12B	0
CAI34753.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	44	0
CAI34613.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	46	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

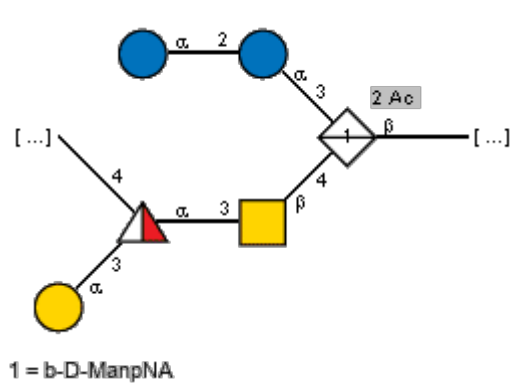
[Logoplot](#)

[Phylogenetic tree](#)

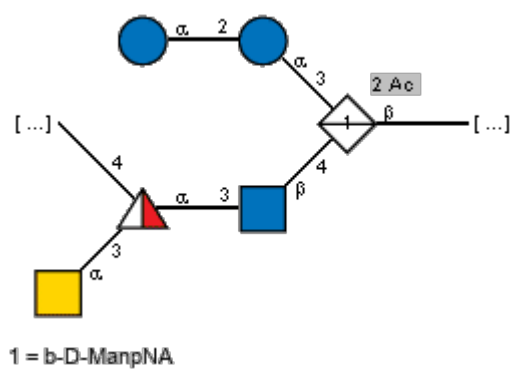
[Hits in cluster](#)

Sugars in cluster:

CAI33278.1 Streptococcus pneumoniae 12F:



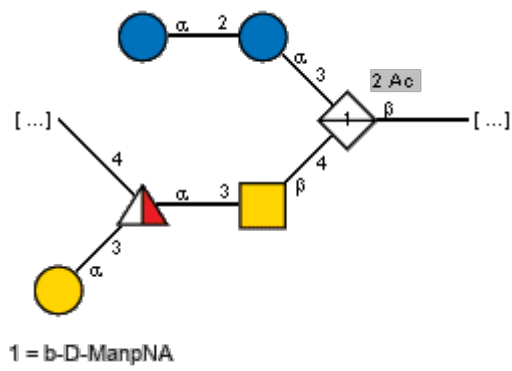
CAI33226.1 Streptococcus pneumoniae 12A:



CSDB record ID: 7060

Sugars for blast hits:

VPT20589.1 Streptococcus pneumoniae 12F:



CSDB record ID: 1955

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Lactobacillales (9)	Streptococcaceae (9)	Streptococcus (9)
Bacteroidales (3)	Tannerellaceae (1)	Parabacteroides (1)
	Bacteroidaceae (1)	Bacteroides (1)
	Prevotellaceae (1)	nan (1)
Bacillales (3)	Bacillaceae (2)	Sutcliffiella (1)
		Cerasibacillus (1)
	Planococcaceae (1)	Planococcus (1)
Eubacteriales (1)	nan (1)	nan (1)

[top](#)

Cluster 157

Total number of members in cluster: 16

Average length of proteins in cluster: 408.2

Conserved (non-aliphatic) residues:

D 52 (100.0%) K 73 (100.0%) N 185 (100.0%) Y 198 (100.0%) N 219 (100.0%) S 222 (100.0%) T 263 (100.0%) K 264 (100.0%) R 332 (100.0%) S 348 (100.0%) R 350 (100.0%) E 388 (100.0%) D 390 (100.0%) D 393 (100.0%) H 454 (100.0%)

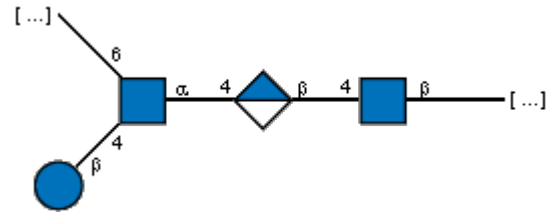
Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
ADN43858.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O137	0

- [MSA fasta](#)
- [Malign view](#)
- [Fasta of members](#)
- [Logoplot](#)
- [Phylogenetic tree](#)
- [Hits in cluster](#)

Sugars in cluster:

ADN43858.1 Escherichia coli O137:



CSDB record ID: 1879

Sugars for blast hits:

Alphafold models:

[ADN43858.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Vibrionales (6)	Vibrionaceae (6)	Vibrio (6)
Alteromonadales (5)	Alteromonadaceae (4)	Aliagarivorans (1) Planctobacterium (1) nan (1) Bowmanella (1)
	Colwelliaceae (1)	Thalassotalea (1)
Enterobacterales (3)	Enterobacteriaceae (3)	Escherichia (2) Citrobacter (1)
Bacteroidales (2)	Bacteroidaceae (2)	Bacteroides (2)

Cluster 14

Total number of members in cluster: 16

Average length of proteins in cluster: 392.2

Conserved (non-aliphatic) residues:

Q 127 (100.0%) H 194 (100.0%) Q 196 (100.0%) R 308 (100.0%) Y 353 (100.0%) H 355 (100.0%) Q 360 (100.0%) D 364 (100.0%) S 411 (100.0%) Y 415 (100.0%) Y 417 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
CAI33207.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	11F	0
CAI33128.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	11A	0
CAI33149.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	11B	0
CAI33169.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	11C	0
CAI33188.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	11D	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

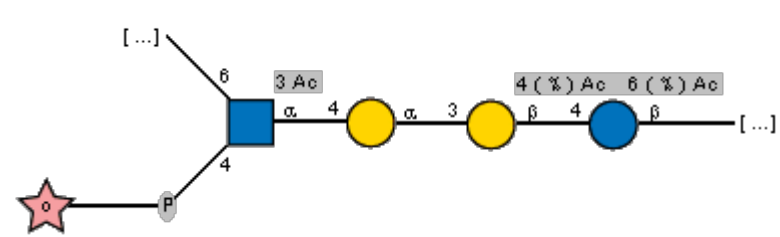
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

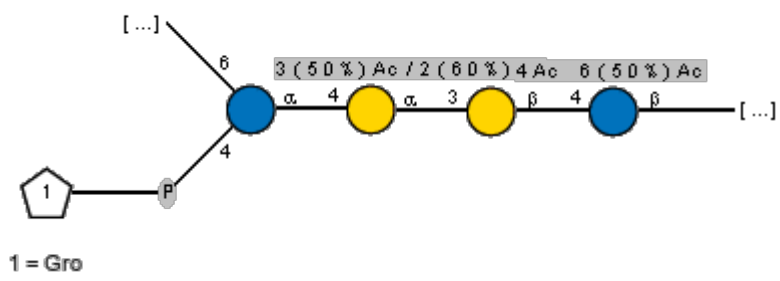
Sugars in cluster:

CAI33207.1 Streptococcus pneumoniae 11F:



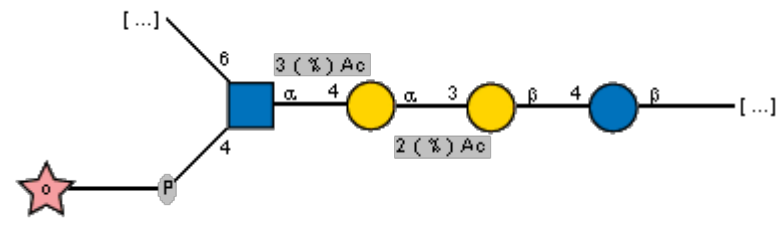
CSDB record ID: 7053

CAI33128.1 Streptococcus pneumoniae 11A:



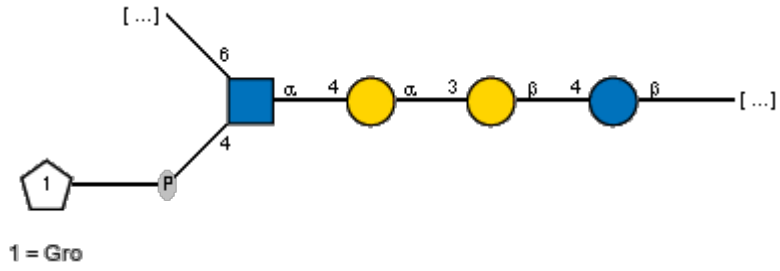
CSDB record ID: 1493

CAI33149.1 *Streptococcus pneumoniae* 11B:



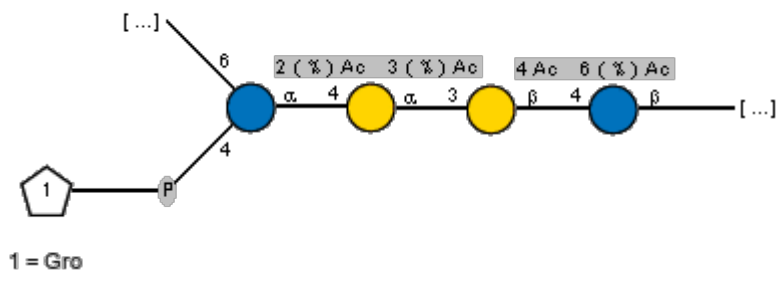
CSDB record ID: 7054

CAI33169.1 *Streptococcus pneumoniae* 11C:



CSDB record ID: 31003

CAI33188.1 *Streptococcus pneumoniae* 11D:



CSDB record ID: 7056

Sugars for blast hits:

Alphafold models:

[CAI33149.1](#)

Taxonomy:

order (count) family (count) genus (count)

order (count)	family (count)	genus (count)
Lactobacillales (9)	Streptococcaceae (8)	Streptococcus (8)
	Lactobacillaceae (1)	Ligilactobacillus (1)
Eubacteriales (4)	Clostridiaceae (2)	Clostridium (2)
	Eubacteriaceae (1)	Eubacterium (1)
nan (1)	nan (2)	nan (2)
Bacillales (1)	Paenibacillaceae (1)	Gorillibacterium (1)
Coriobacteriales (1)	Coriobacteriaceae (1)	Collinsella (1)

[top](#)

Cluster 139

Total number of members in cluster: 16

Average length of proteins in cluster: 414.9

Conserved (non-aliphatic) residues:

R 195 (100.0%) R 201 (100.0%) R 246 (100.0%) R 323 (100.0%) Y 330 (100.0%) D 369 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
CAI33652.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	19B	0
CAI33675.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	19C	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

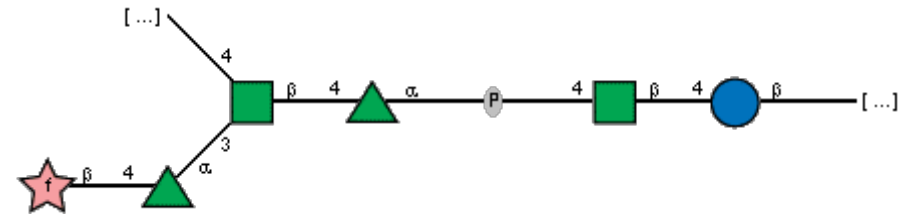
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

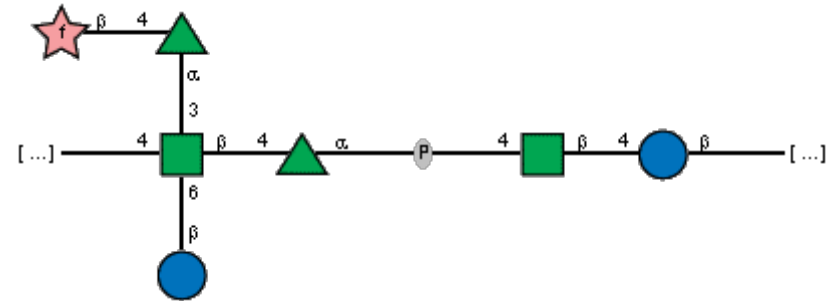
Sugars in cluster:

CAI33652.1 Streptococcus pneumoniae 19B:



CSDB record ID: 2254

CAI33675.1 Streptococcus pneumoniae 19C:



CSDB record ID: 2255

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Lactobacillales (11)	Streptococcaceae (9)	Streptococcus (9)
	Lactobacillaceae (2)	Limosilactobacillus (2)
Eubacteriales (3)	Lachnospiraceae (2)	Butyrivibrio (1)
		Enterocloster (1)
	Clostridiaceae (1)	Clostridium (1)
nan (2)	nan (2)	nan (1)

[top](#)

Cluster 138

Total number of members in cluster: 16

Average length of proteins in cluster: 436.0

Conserved (non-aliphatic) residues:

R 173 (100.0%) Q 216 (100.0%) Q 263 (100.0%) T 268 (100.0%) N 273 (100.0%) S 321 (100.0%) S 424 (100.0%) E 473 (100.0%) E 552 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
CAI33466.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	16F	0

[MSA fasta](#)

[Malign view](#)

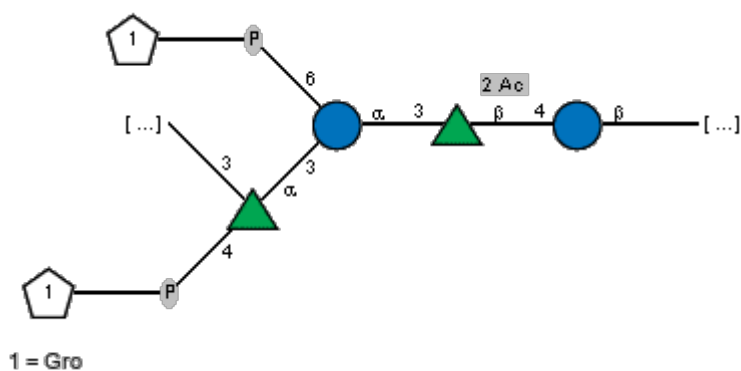
[Fasta of members](#)

[Logoplot](#)

[Phylogenetic tree](#)

Sugars in cluster:

CAI33466.1 Streptococcus pneumoniae 16F:



CSDB record ID: 1062

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Eubacteriales (8)	Lachnospiraceae (4)	nan (1)
		Coprococcus (1)
	Oscillospiraceae (2)	nan (1)
	nan (1)	nan (1)
	Clostridiaceae (1)	nan (1)
Lactobacillales (5)	Streptococcaceae (2)	Streptococcus (2)
	Enterococcaceae (2)	Enterococcus (2)
	Carnobacteriaceae (1)	Trichococcus (1)
Bacillales (3)	Bacillaceae (3)	Anoxybacillus (1)
		Anaerobacillus (1)
		Bacillus (1)

[top](#)

Cluster 129

Total number of members in cluster: 16

Average length of proteins in cluster: 399.3

Conserved (non-aliphatic) residues:

S 63 (100.0%) D 75 (100.0%) Y 79 (100.0%) E 94 (100.0%) E 98 (100.0%) Q 122 (100.0%) N 127 (100.0%) Q 157 (100.0%) R 164 (100.0%) Q 165 (100.0%) H 200 (100.0%) D 257 (100.0%) R 258 (100.0%) K 259 (100.0%) S 280 (100.0%) H 287 (100.0%) Y 318 (100.0%) R 333 (100.0%) K 359 (100.0%) R 379 (100.0%) N 384 (100.0%) D 385 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
BAQ01716.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O140	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

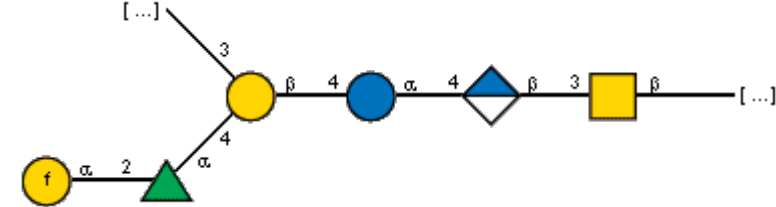
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

BAQ01716.1 Escherichia coli O140:



CSDB record ID: 1882

Sugars for blast hits:

Alphafold models:

[BAQ01716.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (15)	Enterobacteriaceae (14)	Escherichia (4)
		Enterobacter (4)
		Cronobacter (4)
		Siccibacter (2)
	Hafniaceae (1)	Hafnia (1)
Vibrionales (1)	Vibrionaceae (1)	Vibrio (1)

[top](#)

Cluster 125

Total number of members in cluster: 16

Average length of proteins in cluster: 415.1

Conserved (non-aliphatic) residues:

R 180 (100.0%) Y 183 (100.0%) K 242 (100.0%) Y 306 (100.0%) D 308 (100.0%) R 343 (100.0%) K 349 (100.0%) Y 353 (100.0%) D 384 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
BAQ00830.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O36	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

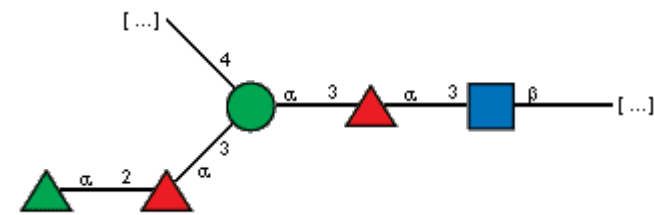
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

BAQ00830.1 Escherichia coli O36:



CSDB record ID: 1543

Sugars for blast hits:

Alphafold models:

[BAQ00830.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (5)	Enterobacteriaceae (5)	Escherichia (4) Yokenella (1)
Bacteroidales (3)	Bacteroidaceae (2) Tannerellaceae (1)	Bacteroides (2) Parabacteroides (1)
Pseudomonadales (2)	Pseudomonadaceae (2)	Pseudomonas (2)
Burkholderiales (1)	nan (1)	Paucibacter (1)
Flavobacteriales (1)	Flavobacteriaceae (1)	Flavobacterium (1)
Alteromonadales (1)	Colwelliaceae (1)	Colwellia (1)
Chthonomonadales (1)	Chthonomonadaceae (1)	Chthonomonas (1)
Rhodospirillales (1)	Azospirillaceae (1)	Niveispirillum (1)
nan (1)	nan (1)	nan (1)

[top](#)

Cluster 104

Total number of members in cluster: 16

Average length of proteins in cluster: 453.4

Conserved (non-aliphatic) residues:

S 37 (100.0%) Y 39 (100.0%) T 45 (100.0%) N 56 (100.0%) K 57 (100.0%) T 59 (100.0%) S 60 (100.0%) S 63 (100.0%) S 68 (100.0%) S 69 (100.0%) R 76 (100.0%) S 80 (100.0%) D 86 (100.0%) R 88 (100.0%) D 91 (100.0%) Y 97 (100.0%) N 106 (100.0%) Y 107 (100.0%) Y 113 (100.0%) Y 116 (100.0%) N 125 (100.0%) K 160 (100.0%) S 170 (100.0%) N 171 (100.0%) S 172 (100.0%) Y 173 (100.0%) Y 177 (100.0%) Y 187 (100.0%) S 191 (100.0%) Y 195 (100.0%) R 209 (100.0%) S 225 (100.0%) K 228 (100.0%) S 230 (100.0%) R 231 (100.0%) E 233 (100.0%) T 236 (100.0%) T 240 (100.0%) Y 245 (100.0%) N 247 (100.0%) N 253 (100.0%) S 271 (100.0%) E 272 (100.0%) S 275 (100.0%) R 278 (100.0%) S 282 (100.0%) N 291 (100.0%) Y 298 (100.0%) S 303 (100.0%) Y 304 (100.0%) Q 309 (100.0%) S 310 (100.0%) Q 328 (100.0%) T 332 (100.0%) S 335 (100.0%) S 347 (100.0%) Y 348 (100.0%) S 349 (100.0%) S 353 (100.0%) T 355 (100.0%) N 357 (100.0%) Y 361 (100.0%) S 370 (100.0%) Y 371 (100.0%) E 374 (100.0%) S 375 (100.0%) N 396 (100.0%) E 399 (100.0%) T 402 (100.0%) Y 409 (100.0%) Y 412 (100.0%) S 414 (100.0%) R 424 (100.0%) E 425 (100.0%) Y 429 (100.0%) K 436 (100.0%) Y 447 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
CAD19991.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O6	0
WP_000864940.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O6	0
ADT75640.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O6	0
AFW04706.1	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	O40	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

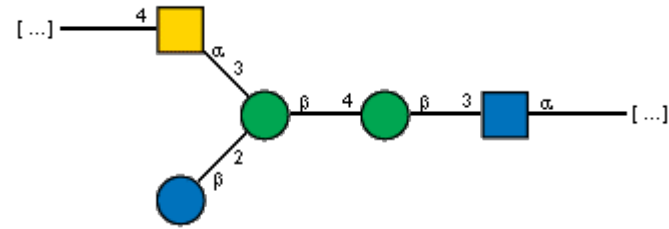
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

CAD19991.1 Escherichia coli O6, WP_000864940.1 Escherichia coli O6, ADT75640.1 Escherichia coli O6:



Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (16)	Enterobacteriaceae (16)	Salmonella (6)
		Escherichia (5)
		Citrobacter (5)

[top](#)

Cluster 96

Total number of members in cluster: 15

Average length of proteins in cluster: 402.9

Conserved (non-aliphatic) residues:

Y 56 (100.0%) D 60 (100.0%) R 63 (100.0%) H 64 (100.0%) K 104 (100.0%) S 115 (100.0%) Y 116 (100.0%) S 163 (100.0%) R 166 (100.0%) Y 176 (100.0%) H 206 (100.0%) S 208 (100.0%) Y 272 (100.0%) Y 276 (100.0%) D 278 (100.0%) S 344 (100.0%) S 346 (100.0%) R 352 (100.0%) S 375 (100.0%) S 408 (100.0%) Y 414 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
ADV17650.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O11	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

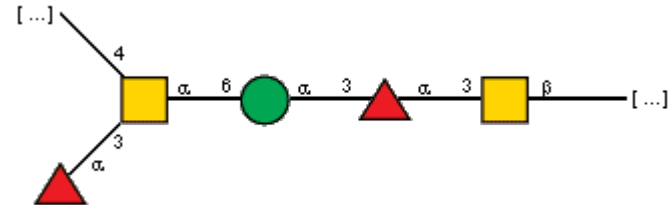
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

ADV17650.1 Escherichia coli O11:



Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (7)	Enterobacteriaceae (7)	Salmonella (5)
		Escherichia (2)
Pasteurellales (5)	Pasteurellaceae (5)	Haemophilus (5)
Aeromonadales (2)	Aeromonadaceae (2)	Aeromonas (2)
Vibrionales (1)	Vibrionaceae (1)	Vibrio (1)

[top](#)

Cluster 88

Total number of members in cluster: 15

Average length of proteins in cluster: 395.7

Conserved (non-aliphatic) residues:

D 76 (100.0%) D 102 (100.0%) Y 131 (100.0%) R 174 (100.0%) H 211 (100.0%) S 213 (100.0%) Y 292 (100.0%) R 374 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
ACD37086.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O112ab	0
BAQ01999.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O181	0
ACD37078.1	Enterobacterales	Enterobacteriaceae	Shigella	Shigella boydii	15	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

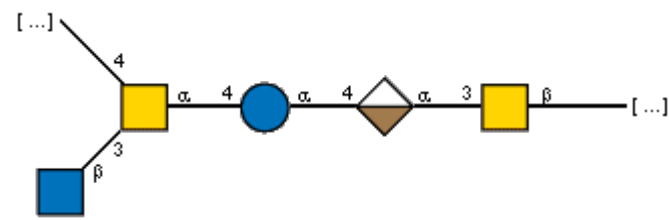
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

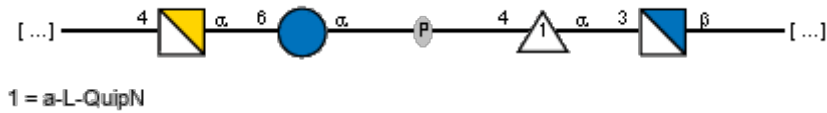
Sugars in cluster:

ACD37086.1 Escherichia coli O112ab:



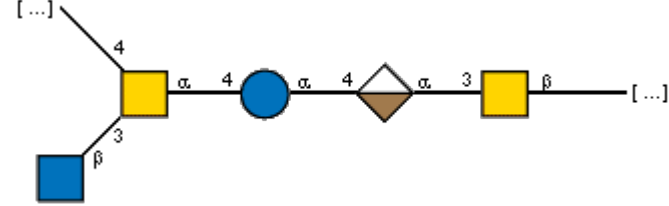
CSDB record ID: 705

BAQ01999.1 Escherichia coli O181:



CSDB record ID: 1923

ACD37078.1 Shigella boydii 15:



CSDB record ID: 1851

Sugars for blast hits:

Alphafold models:

[ACD37078.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (11)	Enterobacteriaceae (9)	Escherichia (8)
		Shigella (1)
	Morganellaceae (2)	Proteus (1)
		Providencia (1)
Vibrionales (3)	Vibrionaceae (3)	Vibrio (3)
nan (1)	nan (1)	nan (1)

[top](#)

Cluster 70

Total number of members in cluster: 15

Average length of proteins in cluster: 451.6

Conserved (non-aliphatic) residues:

S 105 (100.0%) R 113 (100.0%) S 205 (100.0%) K 241 (100.0%) R 277 (100.0%) Y 279 (100.0%) Y 283 (100.0%) R 320 (100.0%) Q 342 (100.0%) E 347 (100.0%) D 380 (100.0%) R 383 (100.0%) S 396 (100.0%) E 400 (100.0%) Y 403

(100.0%) N 456 (100.0%) Y 459 (100.0%) R 462 (100.0%) S 463 (100.0%) K 471 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
AAO37717.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O86	0
AFW04802.1	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	O43	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

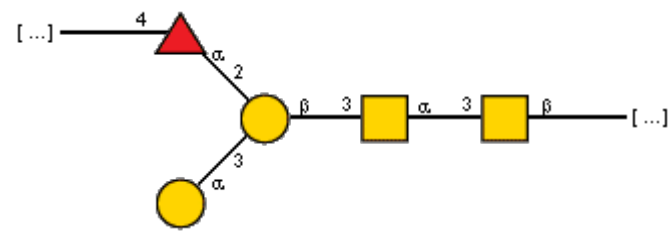
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

AAO37717.1 Escherichia coli O86:



CSDB record ID: 1439

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (6)	Enterobacteriaceae (6)	Escherichia (3) Salmonella (3)
Pseudomonadales (6)	Pseudomonadaceae (5)	Pseudomonas (5)
	Marinobacteraceae (1)	Marinobacter (1)
nan (1)	nan (1)	nan (1)
Vibrionales (1)	Vibrionaceae (1)	Vibrio (1)
Oceanospirillales (1)	Halomonadaceae (1)	Halomonas (1)

[top](#)

Average length of proteins in cluster: 340.1

Conserved (non-aliphatic) residues:

S 41 (100.0%) N 42 (100.0%) D 43 (100.0%) Y 47 (100.0%) D 49 (100.0%) E 64 (100.0%) S 92 (100.0%) K 96
(100.0%) Y 117 (100.0%) S 120 (100.0%) H 125 (100.0%) E 126 (100.0%) T 128 (100.0%) Q 129 (100.0%) R 131
(100.0%) H 165 (100.0%) Y 166 (100.0%) S 167 (100.0%) N 214 (100.0%) Y 220 (100.0%) N 223 (100.0%) S 224
(100.0%) S 234 (100.0%) T 236 (100.0%) S 294 (100.0%) S 296 (100.0%) S 300 (100.0%) R 302 (100.0%) Y 304
(100.0%) E 305 (100.0%) S 308 (100.0%) R 343 (100.0%) S 354 (100.0%) H 356 (100.0%) R 357 (100.0%) N 365
(100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
AQU71717.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O1	0
AQU71739.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O1	0
AFW04812.1	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	O42	0

MSA fasta

Malign view

Fasta of members

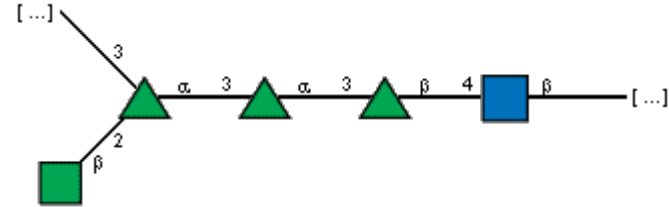
Logoplot

Phylogenetic tree

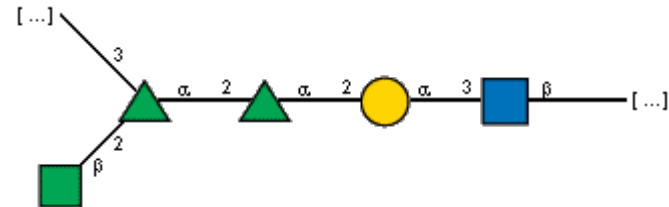
Hits in cluster

Sugars in cluster:

AQU71717.1 *Escherichia coli* O1, AQU71739.1 *Escherichia coli* O1:



CSDB record ID: 7222

AFW04812.1 *Salmonella enterica* O42:

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (14)	Enterobacteriaceae (13)	Salmonella (7)
		Escherichia (5)
		Enterobacter (1)
	Morganellaceae (1)	Proteus (1)
Aeromonadales (1)	Aeromonadaceae (1)	Aeromonas (1)

[top](#)

Cluster 164

Total number of members in cluster: 15

Average length of proteins in cluster: 396.9

Conserved (non-aliphatic) residues:

Q 41 (100.0%) Y 177 (100.0%) Y 179 (100.0%) K 182 (100.0%) N 183 (100.0%) S 184 (100.0%) R 234 (100.0%) S 312 (100.0%) R 314 (100.0%) E 400 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
CAI32797.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	5	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

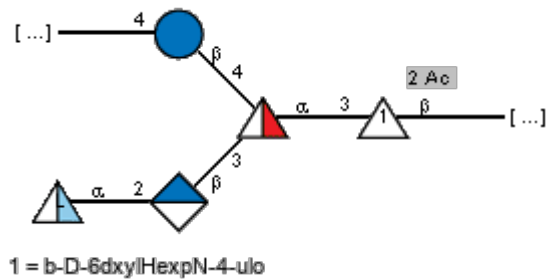
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

CAI32797.1 Streptococcus pneumoniae 5:



CSDB record ID: 1947

Sugars for blast hits:

Alphafold models:

[CAI32797.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Eubacteriales (5)	Lachnospiraceae (5)	Blautia (2)
		Parasporobacterium (1)
		Mediterraneibacter (1)
		Lachnoclostridium (1)
nan (4)	nan (4)	Candidatus Gallimonas (1)
Lactobacillales (3)	Streptococcaceae (3)	Streptococcus (3)
Bacillales (1)	Planococcaceae (1)	Planococcus (1)
Erysipelotrichales (1)	Erysipelotrichaceae (1)	Absicoccus (1)
Bacteroidales (1)	Prevotellaceae (1)	Prevotella (1)

[top](#)

Cluster 130

Total number of members in cluster: 15

Average length of proteins in cluster: 395.5

Conserved (non-aliphatic) residues:

S 30 (100.0%) Y 33 (100.0%) Y 34 (100.0%) K 54 (100.0%) K 57 (100.0%) Y 58 (100.0%) S 65 (100.0%) E 154 (100.0%) Y 165 (100.0%) T 169 (100.0%) R 173 (100.0%) S 174 (100.0%) S 176 (100.0%) N 180 (100.0%) N 183 (100.0%) Y 187 (100.0%) S 220 (100.0%) S 222 (100.0%) R 223 (100.0%) T 224 (100.0%) Y 271 (100.0%) R 284 (100.0%) R 294 (100.0%) D 306 (100.0%) D 313 (100.0%) Y 327 (100.0%) N 332 (100.0%) Y 378 (100.0%) S 391 (100.0%) N 395 (100.0%) Q 396 (100.0%) S 401 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
AHG15281.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O145	0
AFD18613.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O145	0

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
AAX58762.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O145	0
AFW04668.1	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	O48	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

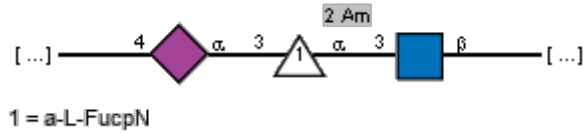
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

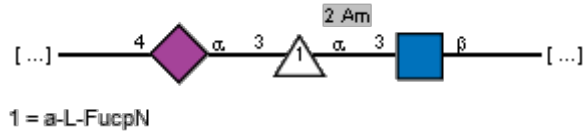
AHG15281.1 Escherichia coli O145, AFD18613.1 Escherichia coli O145, AAX58762.1 Escherichia coli O145:



CSDB record ID: 1886

Sugars for blast hits:

GEF03964.1 Escherichia coli O145:



CSDB record ID: 1886

Alphafold models:

[AFW04668.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (14)	Enterobacteriaceae (13)	Salmonella (8)
		Escherichia (5)
	Morganellaceae (1)	Photorhabdus (1)
Pseudomonadales (1)	Pseudomonadaceae (1)	Pseudomonas (1)

[top](#)

Total number of members in cluster: 15

Average length of proteins in cluster: 438.1

Conserved (non-aliphatic) residues:

S 60 (100.0%) S 101 (100.0%) K 126 (100.0%) H 186 (100.0%) R 197 (100.0%) R 199 (100.0%) E 204 (100.0%) S 206 (100.0%) S 245 (100.0%) K 246 (100.0%) D 299 (100.0%) S 305 (100.0%) T 308 (100.0%) R 309 (100.0%) Y 329 (100.0%) E 363 (100.0%) K 377 (100.0%) K 416 (100.0%) Y 440 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
ACA24882.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O58	0
ACA24868.1	Enterobacterales	Enterobacteriaceae	Shigella	Shigella dysenteriae	5	0

MSA fasta

Malign view

Fasta of members

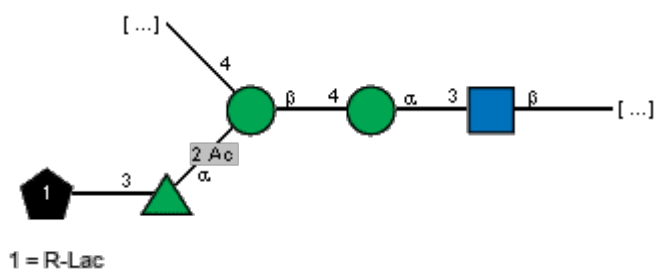
Logoplot

Phylogenetic tree

Hits in cluster

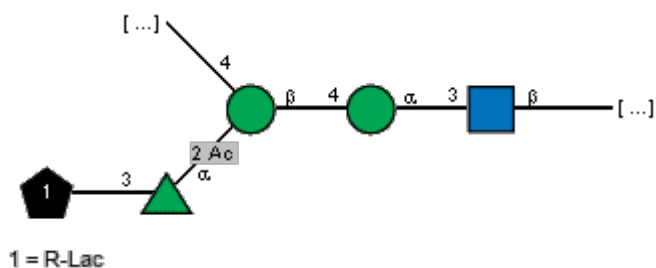
Sugars in cluster:

ACA24882.1 Escherichia coli O58:



CSDb record ID: 108653

ACA24868.1 *Shigella dysenteriae* 5:



CSDb record ID: 1565

Sugars for blast hits:

Alphafold models:

[ACA24882.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (12)	Enterobacteriaceae (12)	Escherichia (3)
		Enterobacter (3)
		Citrobacter (2)
		Leclercia (2)
		Shigella (1)
		Klebsiella (1)
Vibrionales (1)	Vibrionaceae (1)	Vibrio (1)
Aquificales (1)	Hydrogenothermaceae (1)	Sulfurihydrogenibium (1)
nan (1)	nan (1)	nan (1)

[top](#)

Cluster 55

Total number of members in cluster: 14

Average length of proteins in cluster: 383.7

Conserved (non-aliphatic) residues:

Y 8 (100.0%) D 22 (100.0%) R 52 (100.0%) Y 53 (100.0%) D 58 (100.0%) Y 62 (100.0%) E 77 (100.0%) E 137 (100.0%) R 140 (100.0%) Q 141 (100.0%) H 174 (100.0%) S 176 (100.0%) K 235 (100.0%) Y 239 (100.0%) K 256 (100.0%) T 306 (100.0%) R 310 (100.0%) Y 314 (100.0%) Y 359 (100.0%) Y 367 (100.0%) N 369 (100.0%) R 386 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
ACA24852.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O29	0
ACA24840.1	Enterobacterales	Enterobacteriaceae	Shigella	Shigella dysenteriae	11	0

[MSA fasta](#)

[Malign view](#)

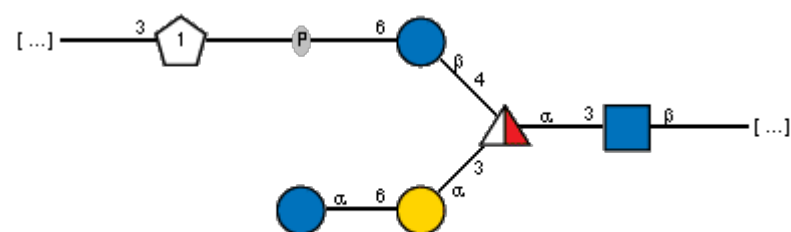
[Fasta of members](#)

[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

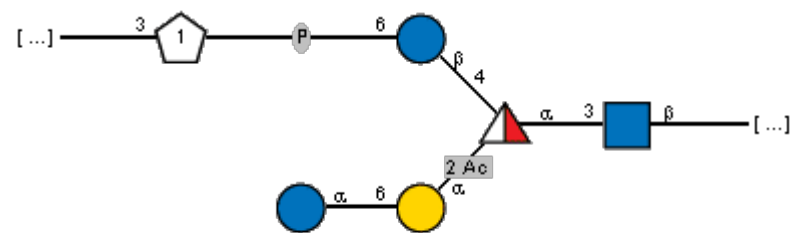
Sugars in cluster:

ACA24852.1 *Escherichia coli* O29:

1 = D-Gro

CSDb record ID: 1538

ACA24840.1 *Shigella dysenteriae* 11:



1 = D-Gro

CSDb record ID: 1932

Sugars for blast hits:

Alphafold models:

ACA24852.1

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (14)	Enterobacteriaceae (6)	Escherichia (2)
		Cronobacter (2)
		Shigella (1)
		Enterobacter (1)
	Morganellaceae (4)	Arsenophonus (2)
		Proteus (2)
	Hafniaceae (2)	Hafnia (1)
		Obesumbacterium (1)
	Erwiniaceae (1)	Pantoea (1)
	Yersiniaceae (1)	Yersinia (1)

[top](#)

Cluster 30

Total number of members in cluster: 14

Average length of proteins in cluster: 350.3

Conserved (non-aliphatic) residues:

D 56 (100.0%) T 57 (100.0%) Y 60 (100.0%) N 89 (100.0%) S 133 (100.0%) E 138 (100.0%) T 141 (100.0%) N 142 (100.0%) R 145 (100.0%) Q 146 (100.0%) S 149 (100.0%) H 179 (100.0%) Y 235 (100.0%) R 246 (100.0%) Y 297 (100.0%) R 301 (100.0%) Y 304 (100.0%) N 339 (100.0%) S 350 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
ABI98966.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O149	0
AAV41072.1	Enterobacterales	Enterobacteriaceae	Shigella	Shigella boydii	O1	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

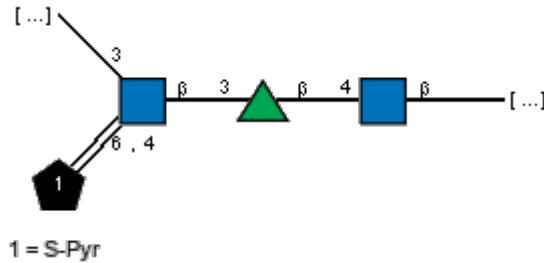
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

ABI98966.1 Escherichia coli O149:



CSDB record ID: 1890

Sugars for blast hits:

Alphafold models:

[ABI98966.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (7)	Enterobacteriaceae (7)	Enterobacter (3) Escherichia (2) Shigella (1) Buttiauxella (1)
Burkholderiales (5)	Burkholderiaceae (5)	Cupriavidus (3) Ralstonia (2)
Vibrionales (2)	Vibrionaceae (2)	Vibrio (2)

Cluster 19

Total number of members in cluster: 14

Average length of proteins in cluster: 380.4

Conserved (non-aliphatic) residues:

K 53 (100.0%) K 59 (100.0%) D 64 (100.0%) Q 74 (100.0%) T 83 (100.0%) Y 99 (100.0%) K 103 (100.0%) Q 128 (100.0%) Q 132 (100.0%) D 140 (100.0%) D 147 (100.0%) R 149 (100.0%) Y 151 (100.0%) R 155 (100.0%) K 156 (100.0%) N 157 (100.0%) T 160 (100.0%) Y 162 (100.0%) Y 173 (100.0%) S 203 (100.0%) T 205 (100.0%) Y 229 (100.0%) S 270 (100.0%) R 272 (100.0%) N 286 (100.0%) T 301 (100.0%) N 302 (100.0%) H 310 (100.0%) N 311 (100.0%) D 315 (100.0%) R 319 (100.0%) K 339 (100.0%) Y 357 (100.0%) E 361 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
CAI32973.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	9A	0
CAI32993.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	9L	0
CAI33011.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	9N	0
CAI33029.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	9V	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

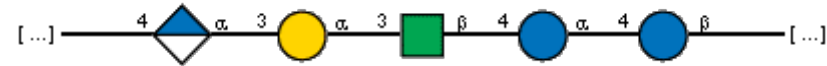
[Logoplot](#)

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[Hits in cluster](#)

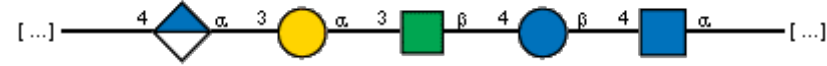
Sugars in cluster:

CAI32973.1 Streptococcus pneumoniae 9A:



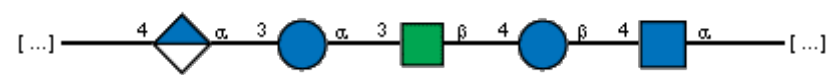
CSDB record ID: 112112

CAI32993.1 Streptococcus pneumoniae 9L:



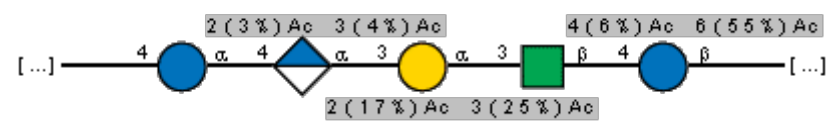
CSDB record ID: 7046

CAI33011.1 Streptococcus pneumoniae 9N:



CSDB record ID: 7415

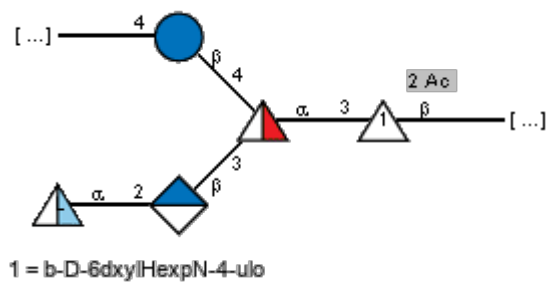
CAI33029.1 Streptococcus pneumoniae 9V:



CSDB record ID: 320

Sugars for blast hits:

CZE39046.1 Streptococcus pneumoniae 5:



CSDB record ID: 1947

Alphafold models:

[CAI33029.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Lactobacillales (14)	Streptococcaceae (13)	Streptococcus (13)
	Aerococcaceae (1)	Globicatella (1)

[top](#)

Cluster 154

Total number of members in cluster: 14

Average length of proteins in cluster: 395.8

Conserved (non-aliphatic) residues:

D 52 (100.0%) Y 217 (100.0%) K 219 (100.0%) S 252 (100.0%) R 332 (100.0%) E 373 (100.0%) D 375 (100.0%) H 376 (100.0%) R 381 (100.0%) N 427 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
BAQ01456.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O100	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

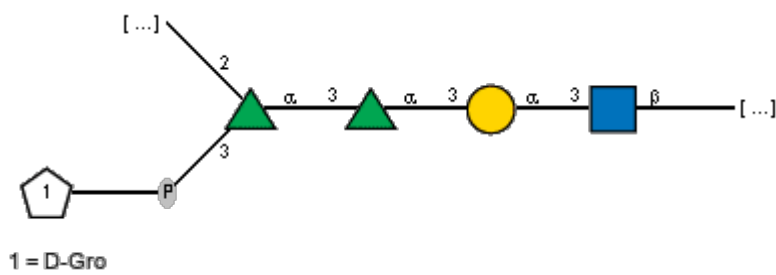
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[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

BAQ01456.1 Escherichia coli O100:



CSDB record ID: 1838

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (4)	Enterobacteriaceae (4)	Escherichia (2) Enterobacter (2)
Aeromonadales (2)	Aeromonadaceae (2)	Aeromonas (2)
Desulfuromonadales (2)	Geobacteraceae (2)	Geobacter (2)
Bacteroidales (2)	Odoribacteraceae (2)	Odoribacter (2)
Burkholderiales (2)	Oxalobacteraceae (1)	Janthinobacterium (1)
	Comamonadaceae (1)	Polaromonas (1)
Rhodothermales (1)	Salisaetaceae (1)	Salisaeta (1)
Xanthomonadales (1)	nan (1)	nan (1)

[top](#)

Cluster 121

Total number of members in cluster: 14

Average length of proteins in cluster: 489.3

Conserved (non-aliphatic) residues:

S 59 (100.0%) R 93 (100.0%) R 312 (100.0%) K 384 (100.0%) S 402 (100.0%) R 406 (100.0%) E 409 (100.0%) N 412 (100.0%) H 467 (100.0%) Y 485 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
BAQ01386.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O93	0
ACA24912.1	Enterobacterales	Enterobacteriaceae	Shigella	Shigella dysenteriae	10	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

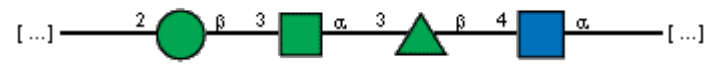
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[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

ACA24912.1 Shigella dysenteriae 10:



CSDB record ID: 23812

Sugars for blast hits:

Alphafold models:

[BAQ01386.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (9)	Enterobacteriaceae (9)	Escherichia (4)
		Enterobacter (4)
		Shigella (1)
nan (2)	nan (2)	nan (2)
Eubacteriales (1)	Eubacteriaceae (1)	nan (2)
Bacteroidales (1)	Bacteroidaceae (1)	Bacteroides (1)
Vibrionales (1)	Vibrionaceae (1)	Photobacterium (1)

[top](#)

Total number of members in cluster: 14

Average length of proteins in cluster: 391.1

Conserved (non-aliphatic) residues:

S 33 (100.0%) S 66 (100.0%) K 95 (100.0%) S 108 (100.0%) K 109 (100.0%) Y 118 (100.0%) Y 121 (100.0%) D 124 (100.0%) S 136 (100.0%) S 140 (100.0%) E 141 (100.0%) S 170 (100.0%) N 172 (100.0%) H 175 (100.0%) T 177 (100.0%) R 178 (100.0%) T 181 (100.0%) Y 191 (100.0%) K 203 (100.0%) R 226 (100.0%) S 227 (100.0%) S 246 (100.0%) Y 250 (100.0%) E 251 (100.0%) S 252 (100.0%) Q 256 (100.0%) S 258 (100.0%) D 281 (100.0%) T 286 (100.0%) K 295 (100.0%) S 309 (100.0%) S 315 (100.0%) Y 317 (100.0%) Y 323 (100.0%) Y 332 (100.0%) Y 359 (100.0%) Y 361 (100.0%) D 365 (100.0%) R 369 (100.0%) R 372 (100.0%) D 373 (100.0%) K 380 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
AAC38177.1	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	1,9,12,46,27:c:z39	0
AAL91079.1	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Schleissheim	0
AAL91080.1	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Vellore	0
AAL91081.1	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	II 4,12,27:i:z35	0
AAL91082.1	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Sloterdijk	0
WP_237703389.1	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Schwarzengrund	0
ACF92750.1	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Schwarzengrund	0
AGS07346.1	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	D3	0

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[Fasta of members](#)

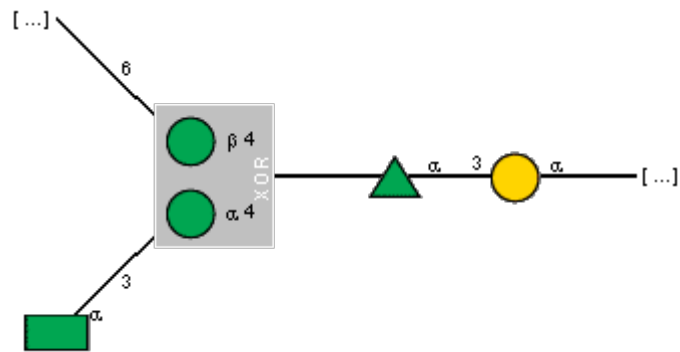
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[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

AGS07346.1 Salmonella enterica D3:



CSDB record ID: 30907

Sugars for blast hits:

Alphafold models:

[AAC38177.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (13)	Enterobacteriaceae (13)	Salmonella (11)
		Citrobacter (2)
Gloeobacterales (1)	Gloeobacteraceae (1)	Anthocerotibacter (1)

[top](#)

Cluster 115

Total number of members in cluster: 14

Average length of proteins in cluster: 412.3

Conserved (non-aliphatic) residues:

E 209 (100.0%) S 352 (100.0%) E 429 (100.0%) R 486 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
ACD36996.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O168	0
ACD36984.1	Enterobacterales	Enterobacteriaceae	Shigella	Shigella dysenteriae	4	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

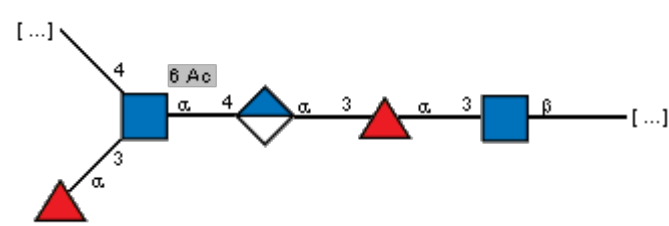
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

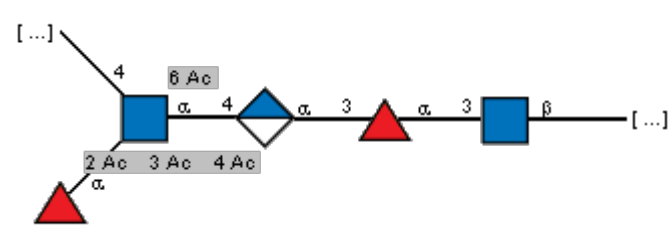
Sugars in cluster:

ACD36996.1 Escherichia coli O168:



CSDB record ID: 1910

ACD36984.1 Shigella dysenteriae 4:



CSDB record ID: 1937

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (4)	Enterobacteriaceae (4)	Escherichia (2) Shigella (2)
nan (3)	nan (3)	nan (2)
Pseudomonadales (1)	Pseudomonadaceae (1)	Pseudomonas (1)
Bacillales (1)	Bacillaceae (1)	Bacillus (1)
Vibrionales (1)	Vibrionaceae (1)	Vibrio (1)
Bacteroidales (1)	Bacteroidaceae (1)	Bacteroides (1)
Sphingobacteriales (1)	Sphingobacteriaceae (1)	Mucilaginibacter (1)
Eubacteriales (1)	Lachnospiraceae (1)	Mediterraneibacter (1)
Flavobacteriales (1)	Flavobacteriaceae (1)	nan (2)

[top](#)

Cluster 60

Total number of members in cluster: 13

Average length of proteins in cluster: 416.8

Conserved (non-aliphatic) residues:

H 26 (100.0%) H 114 (100.0%) Y 140 (100.0%) R 143 (100.0%) E 150 (100.0%) N 159 (100.0%) Y 160 (100.0%) R 202 (100.0%) Y 216 (100.0%) K 248 (100.0%) Y 271 (100.0%) Q 274 (100.0%) Y 282 (100.0%) H 315 (100.0%) N 329 (100.0%) Y 331 (100.0%) S 332 (100.0%) S 336 (100.0%) Y 353 (100.0%) S 385 (100.0%) S 388 (100.0%) D 389 (100.0%) K 400 (100.0%)

Seeds in cluster:

protein_accession order family genus species serotype Enterobacterial common antigen Wzy

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Pseudomonadales (11)	Pseudomonadaceae (11)	Pseudomonas (11)
Burkholderiales (1)	Comamonadaceae (1)	Variovorax (1)
nan (1)	nan (1)	nan (1)

[top](#)

Cluster 47

Total number of members in cluster: 13

Average length of proteins in cluster: 416.1

Conserved (non-aliphatic) residues:

Q 112 (100.0%) R 122 (100.0%) Q 166 (100.0%) R 192 (100.0%) R 240 (100.0%) R 317 (100.0%) D 367 (100.0%) N 368 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
CAI32889.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	7B	0
CAI32910.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	7C	0

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
CAI34454.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	40	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

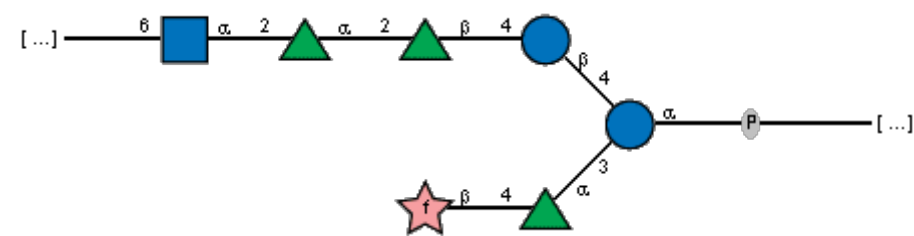
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

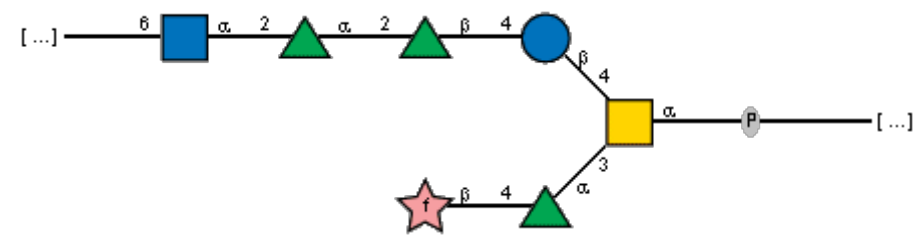
Sugars in cluster:

CAI32889.1 Streptococcus pneumoniae 7B:



CSDB record ID: 7041

CAI32910.1 Streptococcus pneumoniae 7C:



CSDB record ID: 7042

Sugars for blast hits:

Alphafold models:

[CAI34454.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Lactobacillales (5)	Streptococcaceae (5)	Streptococcus (5)
Eubacteriales (4)	Clostridiaceae (4)	Clostridium (4)
Bifidobacteriales (3)	Bifidobacteriaceae (3)	Bifidobacterium (3)
Coriobacteriales (1)	Atopobiaceae (1)	Olsenella (1)

Cluster 45

Total number of members in cluster: 13

Average length of proteins in cluster: 391.5

Conserved (non-aliphatic) residues:

Y 15 (100.0%) Q 18 (100.0%) D 25 (100.0%) R 27 (100.0%) Q 44 (100.0%) Q 62 (100.0%) T 82 (100.0%) E 84 (100.0%) K 93 (100.0%) E 94 (100.0%) D 100 (100.0%) D 102 (100.0%) K 107 (100.0%) N 114 (100.0%) Y 117 (100.0%) R 119 (100.0%) Y 120 (100.0%) K 122 (100.0%) Y 123 (100.0%) N 126 (100.0%) K 140 (100.0%) Y 150 (100.0%) T 153 (100.0%) Y 159 (100.0%) R 160 (100.0%) S 161 (100.0%) E 162 (100.0%) Q 169 (100.0%) Y 170 (100.0%) Y 205 (100.0%) S 207 (100.0%) Q 210 (100.0%) N 215 (100.0%) N 220 (100.0%) R 223 (100.0%) N 226 (100.0%) R 227 (100.0%) T 229 (100.0%) E 231 (100.0%) Q 232 (100.0%) E 234 (100.0%) Y 238 (100.0%) E 242 (100.0%) S 243 (100.0%) D 247 (100.0%) T 251 (100.0%) E 253 (100.0%) K 256 (100.0%) E 257 (100.0%) N 263 (100.0%) R 264 (100.0%) K 269 (100.0%) Y 275 (100.0%) E 277 (100.0%) R 278 (100.0%) H 280 (100.0%) K 281 (100.0%) D 286 (100.0%) N 290 (100.0%) S 293 (100.0%) T 295 (100.0%) T 296 (100.0%) E 300 (100.0%) T 330 (100.0%) Y 339 (100.0%) S 340 (100.0%) Q 348 (100.0%) Y 349 (100.0%) N 354 (100.0%) S 356 (100.0%) H 377 (100.0%) D 378 (100.0%) K 381 (100.0%) R 382 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
EKI39969.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O157	0
BAK68980.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O157	0
EKK44895.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O157	0
BAK69191.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O157	0
BAK69033.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O157	0
AAC32340.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O157	0
EKI95922.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O157	0
AAV34494.1	Enterobacterales	Enterobacteriaceae	Citrobacter	Citrobacter freundii	90	0

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[Malign view](#)

[Fasta of members](#)

[Logoplot](#)

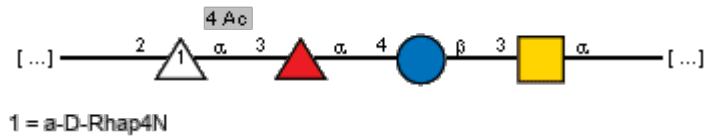
[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

EKI39969.1 Escherichia coli O157, BAK68980.1 Escherichia coli O157, EKK44895.1 Escherichia coli O157,

BAK69191.1 Escherichia coli O157, BAK69033.1 Escherichia coli O157, AAC32340.1 Escherichia coli O157, EKI95922.1 Escherichia coli O157:



CSDB record ID: 695

Sugars for blast hits:

Alphafold models:

[AAC32340.1](#)

[EKI95922.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (13)	Enterobacteriaceae (13)	Escherichia (11)
		Citrobacter (1)
		Salmonella (1)

[top](#)

Cluster 173

Total number of members in cluster: 13

Average length of proteins in cluster: 405.0

Conserved (non-aliphatic) residues:

R 75 (100.0%) Y 93 (100.0%) E 138 (100.0%) S 148 (100.0%) R 149 (100.0%) D 152 (100.0%) N 155 (100.0%) T 166 (100.0%) Y 169 (100.0%) Y 170 (100.0%) N 171 (100.0%) E 172 (100.0%) N 173 (100.0%) D 174 (100.0%) S 212 (100.0%) K 213 (100.0%) Y 222 (100.0%) K 232 (100.0%) R 277 (100.0%) D 295 (100.0%) S 297 (100.0%) E 300 (100.0%) R 301 (100.0%) Y 305 (100.0%) Y 329 (100.0%) E 330 (100.0%) R 340 (100.0%) H 345 (100.0%) N 346 (100.0%) E 350 (100.0%) T 353 (100.0%) Y 360 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
BAQ00736.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O22	0
ACD37058.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O32	0
BAQ01277.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O83	0
ACD37051.1	Enterobacterales	Enterobacteriaceae	Shigella	Shigella boydii	14	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

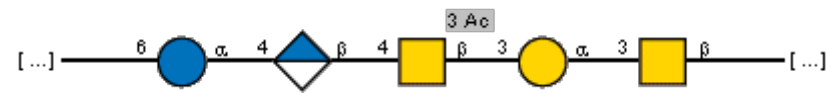
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

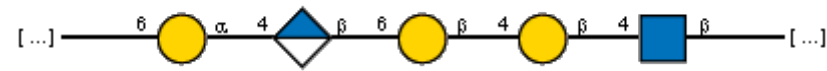
Sugars in cluster:

BAQ00736.1 *Escherichia coli* O22:



CSDB record ID: 1530

ACD37058.1 *Escherichia coli* O32:



CSDB record ID: 1540

BAQ01277.1 *Escherichia coli* O83:



CSDB record ID: 1589

ACD37051.1 *Shigella boydii* 14:



CSDB record ID: 3977

Sugars for blast hits:

Alphafold models:

[BAQ00736.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (13)	Enterobacteriaceae (12)	Escherichia (9)
		Enterobacter (2)
		Shigella (1)
	Hafniaceae (1)	Hafnia (1)

[top](#)

Total number of members in cluster: 12

Average length of proteins in cluster: 407.6

Conserved (non-aliphatic) residues:

N 150 (100.0%) R 180 (100.0%) D 187 (100.0%) Y 221 (100.0%) R 229 (100.0%) R 296 (100.0%) D 343 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
CAI33745.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	21	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Lactobacillales (11)	Lactobacillaceae (9)	Lactobacillus (7)
		Limosilactobacillus (2)
	Streptococcaceae (2)	Streptococcus (2)
Eubacteriales (1)	Lachnospiraceae (1)	nan (1)

[top](#)

Cluster 180

Total number of members in cluster: 12

Average length of proteins in cluster: 366.5

Conserved (non-aliphatic) residues:

K 25 (100.0%) S 39 (100.0%) R 42 (100.0%) Y 43 (100.0%) D 48 (100.0%) S 51 (100.0%) Y 52 (100.0%) Y 55 (100.0%) Y 66 (100.0%) N 84 (100.0%) Q 86 (100.0%) Y 92 (100.0%) Y 101 (100.0%) Y 128 (100.0%) S 129 (100.0%) N 137 (100.0%) Q 138 (100.0%) R 140 (100.0%) S 144 (100.0%) Y 150 (100.0%) H 172 (100.0%) S 173 (100.0%) Y 227 (100.0%) S 230 (100.0%) E 240 (100.0%) Y 243 (100.0%) S 284 (100.0%) D 286 (100.0%) R 292 (100.0%) D 295 (100.0%) K 298 (100.0%) K 318 (100.0%) N 341 (100.0%) S 346 (100.0%) N 347 (100.0%) Y 359 (100.0%) Y 361

(100.0%) N 364 (100.0%)

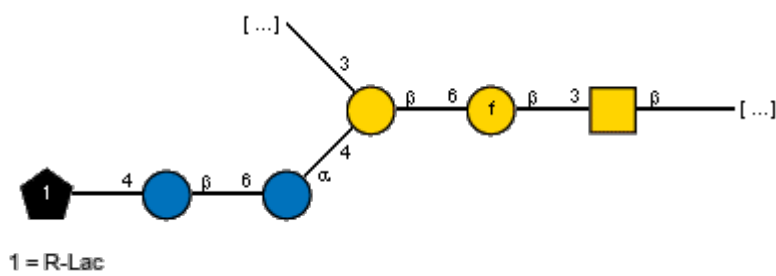
Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
ACD37138.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O124	0
ACD37146.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O164	0
ACD37105.1	Enterobacterales	Enterobacteriaceae	Shigella	Shigella dysenteriae	3	0

- [MSA fasta](#)
- [Malign view](#)
- [Fasta of members](#)
- [Logoplot](#)
- [Phylogenetic tree](#)
- [Hits in cluster](#)

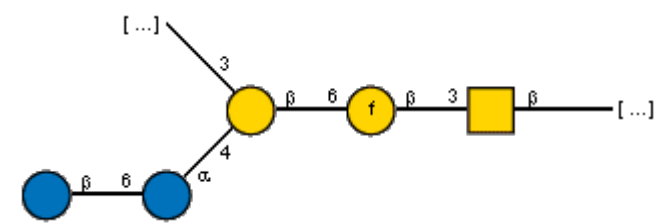
Sugars in cluster:

ACD37138.1 Escherichia coli O124:



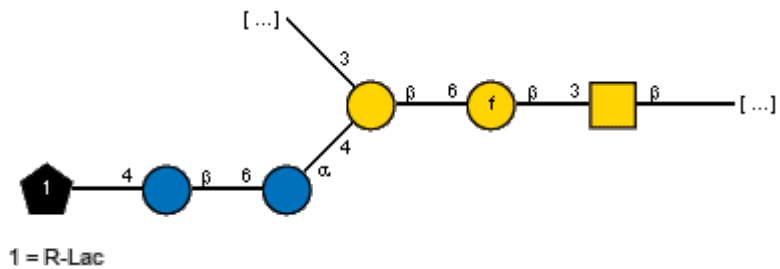
CSDB record ID: 1863

ACD37146.1 Escherichia coli O164:



CSDB record ID: 1906

ACD37105.1 Shigella dysenteriae 3:



CSDB record ID: 718

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (11)	Enterobacteriaceae (9)	Escherichia (7)
		Shigella (1)
		Citrobacter (1)
		Pectobacterium (2)
Vibrionales (1)	Vibrionaceae (1)	Photobacterium (1)

[top](#)

Cluster 124

Total number of members in cluster: 12

Average length of proteins in cluster: 370.7

Conserved (non-aliphatic) residues:

R 24 (100.0%) D 28 (100.0%) K 48 (100.0%) D 98 (100.0%) R 99 (100.0%) Y 111 (100.0%) R 112 (100.0%) Y 117 (100.0%) R 119 (100.0%) Y 120 (100.0%) Y 126 (100.0%) R 171 (100.0%) N 178 (100.0%) S 216 (100.0%) T 218 (100.0%) S 220 (100.0%) Y 270 (100.0%) Y 272 (100.0%) S 275 (100.0%) N 278 (100.0%) R 279 (100.0%) D 309 (100.0%) N 310 (100.0%) S 317 (100.0%) Y 329 (100.0%) Q 350 (100.0%) Y 361 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
BAQ01960.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O179	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

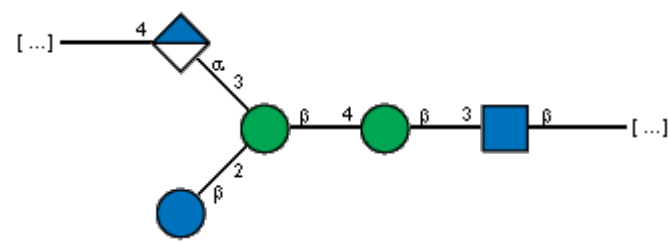
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

BAQ01960.1 Escherichia coli O179:



CSDB record ID: 1921

Sugars for blast hits:

Alphafold models:

[BAQ01960.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (7)	Enterobacteriaceae (7)	Escherichia (4)
		Enterobacter (3)
Vibrionales (5)	Vibrionaceae (5)	Vibrio (4)
		Aliivibrio (1)

[top](#)

Cluster 102

Total number of members in cluster: 12

Average length of proteins in cluster: 410.8

Conserved (non-aliphatic) residues:

R 183 (100.0%) S 238 (100.0%) R 239 (100.0%) T 240 (100.0%) K 305 (100.0%) E 312 (100.0%) R 331 (100.0%) E 334 (100.0%) H 386 (100.0%) N 387 (100.0%) Y 389 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
CAI34057.2	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	28F	0
CAI34032.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	28A	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Lactobacillales (11)	Streptococcaceae (5)	Streptococcus (5)
	Enterococcaceae (3)	Enterococcus (3)
	Lactobacillaceae (3)	Leuconostoc (2)
		Oenococcus (1)
Eubacteriales (1)	Peptostreptococcaceae (1)	Paeniclostridium (1)

[top](#)

Cluster 198

Total number of members in cluster: 11

Average length of proteins in cluster: 345.0

Conserved (non-aliphatic) residues:

Y 3 (100.0%) S 10 (100.0%) N 13 (100.0%) R 19 (100.0%) T 21 (100.0%) S 33 (100.0%) Y 37 (100.0%) N 38 (100.0%) D 42 (100.0%) N 45 (100.0%) Y 46 (100.0%) Y 50 (100.0%) D 55 (100.0%) E 61 (100.0%) Y 78 (100.0%) S 83 (100.0%) S 86 (100.0%) T 89 (100.0%) Y 93 (100.0%) Y 94 (100.0%) R 98 (100.0%) Y 113 (100.0%) Y 118 (100.0%) Y 120 (100.0%) E 122 (100.0%) H 123 (100.0%) N 125 (100.0%) R 128 (100.0%) Q 129 (100.0%) Y 138 (100.0%) S 139 (100.0%) K 141 (100.0%) Y 151 (100.0%) S 159 (100.0%) H 162 (100.0%) Y 172 (100.0%) R 176 (100.0%) K 181 (100.0%) Y 184 (100.0%) Y 185 (100.0%) D 199 (100.0%) S 207 (100.0%) K 213 (100.0%) D 216 (100.0%) R 220 (100.0%) Y 221 (100.0%) S 225 (100.0%) D 230 (100.0%) S 233 (100.0%) K 234 (100.0%) K 235 (100.0%) S 236 (100.0%) S 241 (100.0%) K 242 (100.0%) Y 244 (100.0%) R 264 (100.0%) D 265 (100.0%) N 270 (100.0%) S 282 (100.0%) Q 284 (100.0%) D 286 (100.0%) R 290 (100.0%) S 293 (100.0%) E 296 (100.0%) S 298 (100.0%) Y 303 (100.0%) N 311 (100.0%) Y 342 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
AAO37701.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O128ab	0
WP_024244058.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O128ac	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

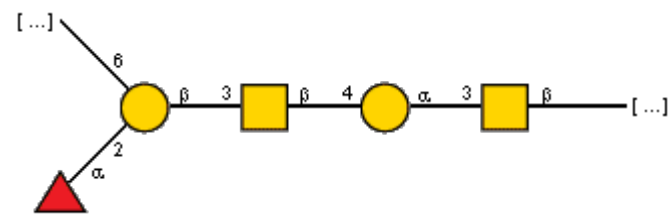
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[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

AAO37701.1 Escherichia coli O128ab, WP_024244058.1 Escherichia coli O128ac:



CSDB record ID: 1867

Sugars for blast hits:

Alphafold models:

[WP_024244058.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (11)	Enterobacteriaceae (11)	Escherichia (8)
		Citrobacter (3)

[top](#)

Cluster 163

Total number of members in cluster: 11

Average length of proteins in cluster: 343.3

Conserved (non-aliphatic) residues:

Y 29 (100.0%) S 76 (100.0%) N 82 (100.0%) D 85 (100.0%) K 86 (100.0%) S 88 (100.0%) Y 89 (100.0%) S 100 (100.0%) D 101 (100.0%) N 107 (100.0%) T 108 (100.0%) D 110 (100.0%) S 111 (100.0%) Y 114 (100.0%) Y 115 (100.0%) Q 135 (100.0%) N 136 (100.0%) K 149 (100.0%) H 164 (100.0%) S 170 (100.0%) R 172 (100.0%) H 174 (100.0%) H 203 (100.0%) K 248 (100.0%) Y 252 (100.0%) Y 259 (100.0%) K 296 (100.0%) S 306 (100.0%) R 317 (100.0%) D 323 (100.0%) R 355 (100.0%) K 358 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
ABE98419.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O126	0
ADN43845.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O126	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

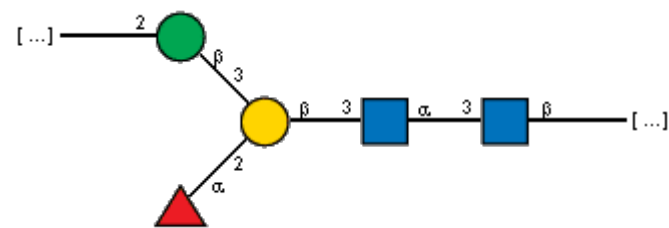
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

ABE98419.1 Escherichia coli O126, ADN43845.1 Escherichia coli O126:



CSDB record ID: 1865

Sugars for blast hits:

Alphafold models:

[ABE98419.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (10)	Enterobacteriaceae (4)	Escherichia (4)
	Yersiniaceae (4)	Yersinia (4)
	Morganellaceae (2)	Photorhabdus (2)
Vibrionales (1)	Vibrionaceae (1)	Photobacterium (1)

[top](#)

Cluster 149

Total number of members in cluster: 11

Average length of proteins in cluster: 382.5

Conserved (non-aliphatic) residues:

Y 73 (100.0%) E 74 (100.0%) N 124 (100.0%) S 126 (100.0%) R 147 (100.0%) Q 148 (100.0%) H 181 (100.0%) S 183 (100.0%) K 238 (100.0%) D 259 (100.0%) H 294 (100.0%) Q 304 (100.0%) R 305 (100.0%) Y 357 (100.0%) D 396 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common
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Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
ADB02825.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O119	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

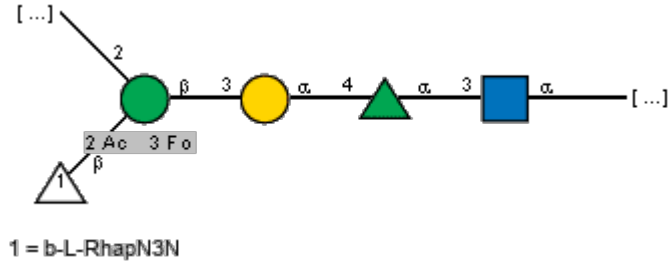
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

ADB02825.1 Escherichia coli O119:



CSDB record ID: 1859

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Bacteroidales (3)	Tannerellaceae (2)	Parabacteroides (2)
	Dysgonomonadaceae (1)	Dysgonomonas (1)
Flavobacteriales (3)	Flavobacteriaceae (3)	Capnocytophaga (3)
Enterobacterales (2)	Enterobacteriaceae (2)	Escherichia (2)
Vibrionales (1)	Vibrionaceae (1)	Vibrio (1)
Neisseriales (1)	Chromobacteriaceae (1)	Chromobacterium (1)
Sphingomonadales (1)	Erythrobacteraceae (1)	Porphyrobacter (1)

[top](#)

Cluster 76

Total number of members in cluster: 10

Average length of proteins in cluster: 359.4

Conserved (non-aliphatic) residues:

Y 11 (100.0%) S 48 (100.0%) R 50 (100.0%) D 55 (100.0%) R 56 (100.0%) D 57 (100.0%) Y 61 (100.0%) S 81 (100.0%) Q 86 (100.0%) E 87 (100.0%) K 95 (100.0%) R 108 (100.0%) Y 139 (100.0%) R 147 (100.0%) D 148 (100.0%) T 150 (100.0%) Q 151 (100.0%) R 153 (100.0%) S 164 (100.0%) S 176 (100.0%) H 187 (100.0%) N 188 (100.0%) Q 242 (100.0%) T 244 (100.0%) R 245 (100.0%) Y 246 (100.0%) T 257 (100.0%) Y 286 (100.0%) K 287 (100.0%) Y 290 (100.0%) Q 313 (100.0%) T 318 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
ADC54957.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O166	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

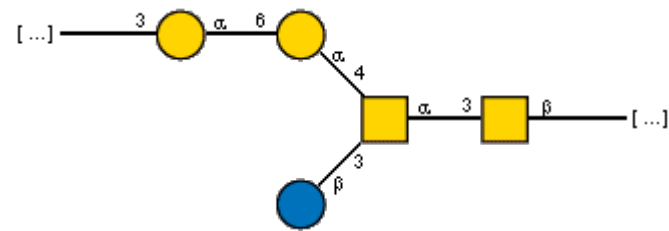
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

ADC54957.1 Escherichia coli O166:



CSDB record ID: 1908

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Vibrionales (6)	Vibrionaceae (6)	Photobacterium (6)
Enterobacterales (4)	Enterobacteriaceae (4)	Escherichia (3)
		Citrobacter (1)

[top](#)

Cluster 5

Total number of members in cluster: 10

Average length of proteins in cluster: 375.2

Conserved (non-aliphatic) residues:

Y 3 (100.0%) R 44 (100.0%) H 46 (100.0%) T 47 (100.0%) D 50 (100.0%) E 52 (100.0%) Y 54 (100.0%) D 55 (100.0%) Y 56 (100.0%) N 73 (100.0%) Y 77 (100.0%) E 78 (100.0%) T 103 (100.0%) S 110 (100.0%) Y 114 (100.0%) Y 127 (100.0%) Y 130 (100.0%) Y 132 (100.0%) H 134 (100.0%) N 135 (100.0%) S 137 (100.0%) R 140 (100.0%) Q 141 (100.0%) Y 150 (100.0%) S 151 (100.0%) R 153 (100.0%) H 174 (100.0%) S 176 (100.0%) S 206 (100.0%) S 216 (100.0%) S 226 (100.0%) Y 235 (100.0%) N 238 (100.0%) S 242 (100.0%) Y 243 (100.0%) K 244 (100.0%) S 248 (100.0%) K 250 (100.0%) Y 251 (100.0%) E 253 (100.0%) Y 293 (100.0%) S 294 (100.0%) N 297 (100.0%) D 298 (100.0%) S 300 (100.0%) Y 303 (100.0%) E 304 (100.0%) R 305 (100.0%) E 311 (100.0%) S 313 (100.0%) R 345 (100.0%) Y 346 (100.0%) R 358 (100.0%) E 362 (100.0%) H 365 (100.0%) E 367 (100.0%) R 368 (100.0%) E 370 (100.0%) N 371 (100.0%) Y 372 (100.0%) S 374 (100.0%) R 383 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
ACV67297.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O78	0
AFW04684.1	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	O65	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

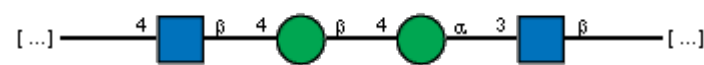
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

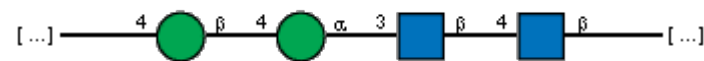
Sugars in cluster:

ACV67297.1 Escherichia coli O78:



CSDB record ID: 1584

AFW04684.1 Salmonella enterica O65:



CSDB record ID: 30392

Sugars for blast hits:

Alphafold models:

[ACV67297.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (7)	Enterobacteriaceae (7)	Escherichia (3)
		Salmonella (2)
		Citrobacter (2)
Vibrionales (3)	Vibrionaceae (3)	Vibrio (2)
		Photobacterium (1)

[top](#)

Cluster 49

Total number of members in cluster: 10

Average length of proteins in cluster: 410.4

Conserved (non-aliphatic) residues:

D 26 (100.0%) D 141 (100.0%) K 143 (100.0%) S 206 (100.0%) R 207 (100.0%) R 256 (100.0%) Y 280 (100.0%) Y 282 (100.0%) N 289 (100.0%) N 291 (100.0%) N 338 (100.0%) D 349 (100.0%) Y 370 (100.0%) K 389 (100.0%) N 398 (100.0%) Y 399 (100.0%) Y 410 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
AHB32586.1	Moraxellales	Moraxellaceae	Acinetobacter	Acinetobacter baumannii	O24	0
BAQ01516.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O108	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

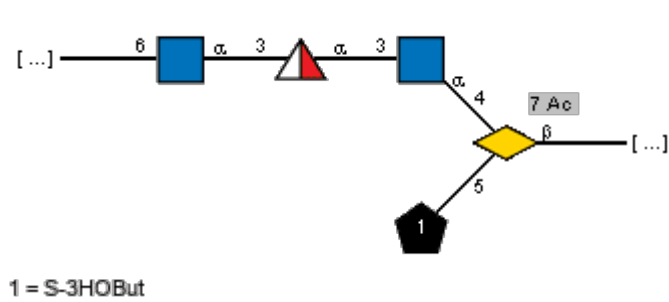
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

AHB32586.1 Acinetobacter baumannii O24:



BAQ01516.1 Escherichia coli O108:



CSDB record ID: 25389

Sugars for blast hits:

Alphafold models:

[BAQ01516.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (6)	Enterobacteriaceae (4)	Escherichia (2)
		Cedecea (1)
		nan (1)
	Morganellaceae (2)	Providencia (2)
Moraxellales (1)	Moraxellaceae (1)	Acinetobacter (1)
Alteromonadales (1)	nan (1)	Motilimonas (1)
Bacteroidales (1)	Rikenellaceae (1)	Alistipes (1)
nan (1)	nan (1)	nan (1)

[top](#)

Cluster 35

Total number of members in cluster: 10

Average length of proteins in cluster: 341.5

Conserved (non-aliphatic) residues:

N 8 (100.0%) R 46 (100.0%) D 52 (100.0%) Y 56 (100.0%) Y 59 (100.0%) Y 70 (100.0%) Y 74 (100.0%) N 78 (100.0%) K 82 (100.0%) S 95 (100.0%) Q 103 (100.0%) Y 108 (100.0%) Y 122 (100.0%) S 125 (100.0%) D 130 (100.0%) R 135 (100.0%) S 137 (100.0%) H 169 (100.0%) E 170 (100.0%) N 213 (100.0%) N 219 (100.0%) N 221 (100.0%) Y 225 (100.0%) S 233 (100.0%) E 261 (100.0%) Y 265 (100.0%) S 279 (100.0%) Y 280 (100.0%) R 287 (100.0%) E 290 (100.0%) Y 296 (100.0%) Y 323 (100.0%) R 327 (100.0%) N 329 (100.0%) D 336 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
BAQ00746.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O23	0
AFW04888.1	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	O51	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

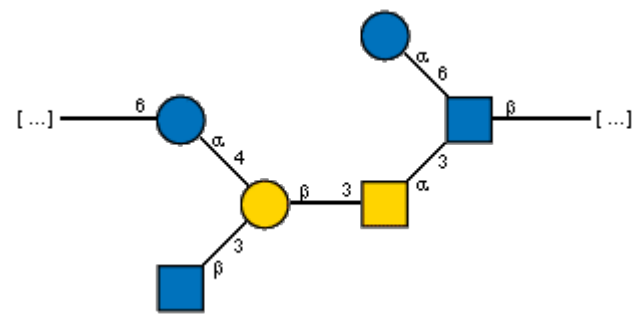
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

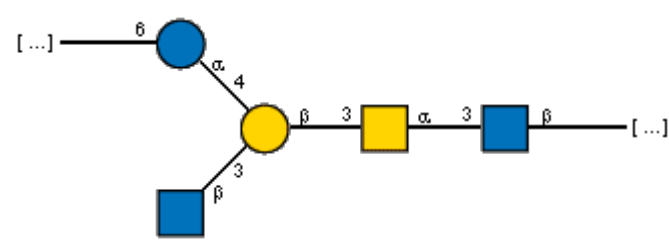
Sugars in cluster:

BAQ00746.1 *Escherichia coli* O23:



CSDB record ID: 20006

AFW04888.1 *Salmonella enterica* O51:



CSDB record ID: 3366

Sugars for blast hits:

Alphafold models:

[BAQ00746.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (10)	Enterobacteriaceae (10)	<i>Escherichia</i> (4)
		<i>Salmonella</i> (3)
		<i>Citrobacter</i> (3)

[top](#)

Cluster 34

Total number of members in cluster: 10

Average length of proteins in cluster: 389.4

Conserved (non-aliphatic) residues:

N 76 (100.0%) Y 119 (100.0%) D 152 (100.0%) H 153 (100.0%) Y 159 (100.0%) Y 167 (100.0%) R 183 (100.0%) E 190 (100.0%) T 193 (100.0%) Y 197 (100.0%) R 221 (100.0%) S 232 (100.0%) S 234 (100.0%) K 253 (100.0%) Y 289 (100.0%) R 290 (100.0%) D 294 (100.0%) R 297 (100.0%) N 302 (100.0%) R 304 (100.0%) K 343 (100.0%) Q 346 (100.0%) R 347 (100.0%) Q 388 (100.0%) E 390 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
BAQ01238.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O80	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

BAQ01238.1 Escherichia coli O80:



CSDB record ID: 1452

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Vibrionales (6)	Vibrionaceae (6)	Photobacterium (4) Vibrio (2)
Enterobacterales (3)	Enterobacteriaceae (3)	Escherichia (3)
Aeromonadales (1)	Aeromonadaceae (1)	Aeromonas (1)

[top](#)

Cluster 174

Total number of members in cluster: 10

Average length of proteins in cluster: 346.7

Conserved (non-aliphatic) residues:

R 55 (100.0%) D 63 (100.0%) Y 67 (100.0%) S 117 (100.0%) Q 152 (100.0%) R 154 (100.0%) Q 155 (100.0%) H 188 (100.0%) S 218 (100.0%) K 247 (100.0%) Y 251 (100.0%) S 263 (100.0%) Y 269 (100.0%) K 282 (100.0%) N 306

(100.0%) N 310 (100.0%) S 311 (100.0%) R 317 (100.0%) T 319 (100.0%) Y 320 (100.0%)

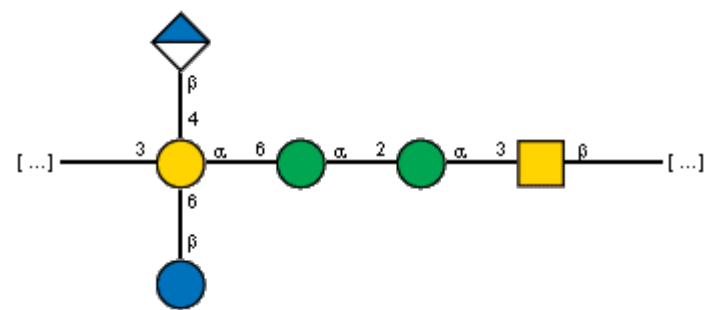
Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
BAQ01860.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O169	0
BAL03056.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O183	0
AAL27339.1	Enterobacterales	Enterobacteriaceae	Shigella	Shigella boydii	6	0

- [MSA fasta](#)
- [Malign view](#)
- [Fasta of members](#)
- [Logoplot](#)
- [Phylogenetic tree](#)
- [Hits in cluster](#)

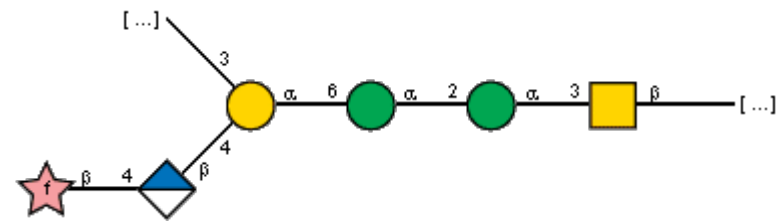
Sugars in cluster:

BAQ01860.1 Escherichia coli O169:



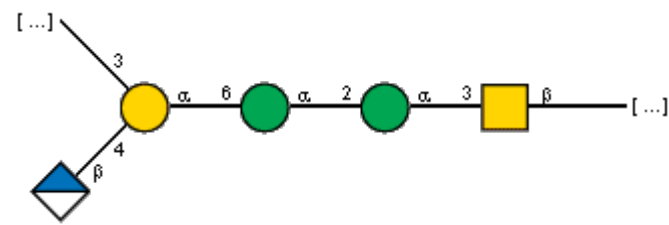
CSDB record ID: 1911

BAL03056.1 Escherichia coli O183:



CSDB record ID: 1925

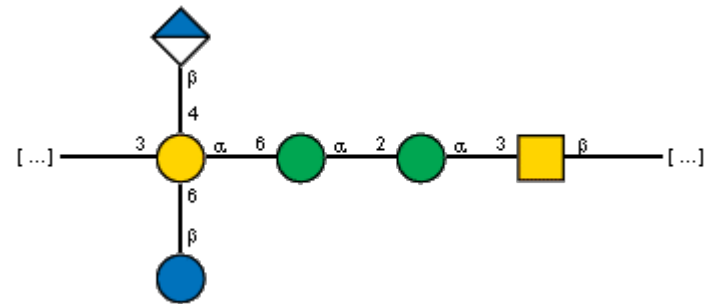
AAL27339.1 Shigella boydii 6:



CSDB record ID: 712

Sugars for blast hits:

AIG62720.1 Escherichia coli O169:



CSDB record ID: 1911

Alphafold models:

[BAQ01860.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (6)	Enterobacteriaceae (6)	Escherichia (5)
		Shigella (1)
Flavobacteriales (3)	Flavobacteriaceae (3)	Maribacter (2)
		Zobellia (1)
Vibrionales (1)	Vibrionaceae (1)	Vibrio (1)

[top](#)

Cluster 153

Total number of members in cluster: 10

Average length of proteins in cluster: 383.4

Conserved (non-aliphatic) residues:

S 51 (100.0%) N 54 (100.0%) D 57 (100.0%) Y 59 (100.0%) Y 61 (100.0%) Y 89 (100.0%) N 115 (100.0%) R 143 (100.0%) E 145 (100.0%) S 147 (100.0%) T 148 (100.0%) R 150 (100.0%) Q 151 (100.0%) H 186 (100.0%) S 188 (100.0%) Y 315 (100.0%) R 326 (100.0%) Y 329 (100.0%) Y 330 (100.0%) R 370 (100.0%) R 375 (100.0%) Y 381 (100.0%) R 397 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common
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BAQ01293.1

Enterobacterales Enterobacteriaceae Escherichia coli

Escherichia coli

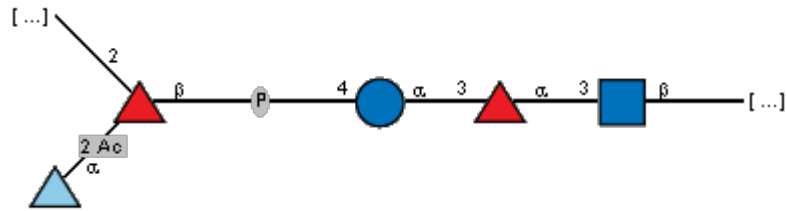
O84

0

- [MSA fasta](#)
- [Malign view](#)
- [Fasta of members](#)
- [Logoplot](#)
- [Phylogenetic tree](#)
- [Hits in cluster](#)

Sugars in cluster:

BAQ01293.1 Escherichia coli O84:



CSDb record ID: 1590

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (6)	Enterobacteriaceae (6)	Escherichia (4)
		Enterobacter (1)
		Cedecea (1)
Vibrionales (4)	Vibrionaceae (4)	Vibrio (3)
		Photobacterium (1)

[top](#)

Cluster 150

Total number of members in cluster: 10

Average length of proteins in cluster: 389.2

Conserved (non-aliphatic) residues:

D 21 (100.0%) T 43 (100.0%) D 45 (100.0%) T 55 (100.0%) Y 115 (100.0%) R 119 (100.0%) Y 123 (100.0%) S 128 (100.0%) Y 153 (100.0%) T 200 (100.0%) K 202 (100.0%) Q 203 (100.0%) S 211 (100.0%) R 244 (100.0%) Y 258 (100.0%) Y 262 (100.0%) S 265 (100.0%) Q 271 (100.0%) E 272 (100.0%) Y 274 (100.0%) S 284 (100.0%) H 307 (100.0%) T 317 (100.0%) N 318 (100.0%) Y 320 (100.0%) S 324 (100.0%) Y 326 (100.0%) H 341 (100.0%) Y 362

(100.0%) H 375 (100.0%) E 376 (100.0%) S 383 (100.0%) Q 387 (100.0%) S 396 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
BAQ00653.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O16	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

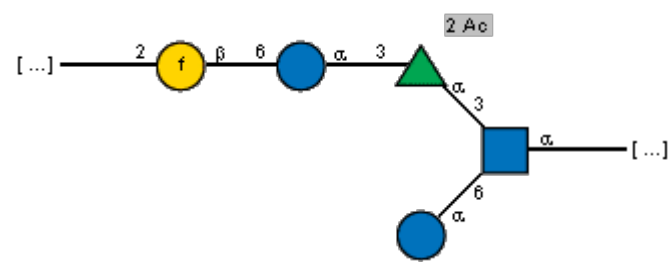
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

BAQ00653.1 Escherichia coli O16:



CSDB record ID: 1517

Sugars for blast hits:

Alphafold models:

[BAQ00653.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (10)	Enterobacteriaceae (9)	Enterobacter (6)
		Escherichia (3)
	Budviciaceae (1)	Jinshanibacter (1)

[top](#)

Cluster 112

Total number of members in cluster: 10

Average length of proteins in cluster: 378.9

Conserved (non-aliphatic) residues:

K 30 (100.0%) D 32 (100.0%) R 97 (100.0%) Q 100 (100.0%) K 162 (100.0%) D 163 (100.0%) H 176 (100.0%) N 178 (100.0%) K 220 (100.0%) R 281 (100.0%) Y 285 (100.0%) Y 299 (100.0%) H 319 (100.0%) N 320 (100.0%) S 324 (100.0%) E 328 (100.0%) N 373 (100.0%) Y 376 (100.0%) Y 378 (100.0%) K 379 (100.0%) H 381 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
BAQ01207.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O74	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

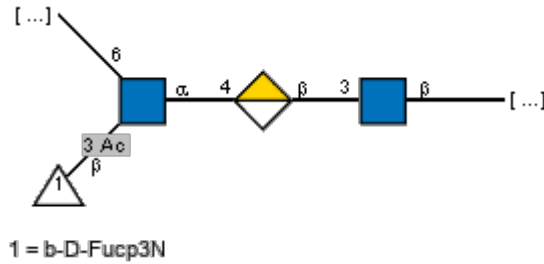
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[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

BAQ01207.1 Escherichia coli O74:



CSDB record ID: 1580

Sugars for blast hits:

Alphafold models:

[BAQ01207.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (5)	Enterobacteriaceae (3)	Escherichia (3)
	Yersiniaceae (1)	Yersinia (1)
	Erwiniaceae (1)	Pantoea (1)
Pseudomonadales (4)	Pseudomonadaceae (4)	Pseudomonas (4)
Vibrionales (1)	Vibrionaceae (1)	Vibrio (1)

[top](#)

Total number of members in cluster: 10

Average length of proteins in cluster: 437.4

Conserved (non-aliphatic) residues:

S 127 (100.0%) R 146 (100.0%) E 236 (100.0%) K 284 (100.0%) R 285 (100.0%) Y 332 (100.0%) R 355 (100.0%) Y 359 (100.0%) H 407 (100.0%) T 462 (100.0%) N 464 (100.0%)

Seeds in cluster:

protein_accession order family genus species serotype Enterobacterial common antigen Wzy

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Eubacteriales (10)	Oscillospiraceae (4)	Faecalibacterium (3)
		nan (1)
	Lachnospiraceae (3)	Eisenbergiella (2)
	Clostridiaceae (1)	Clostridium (1)
	Christensenellaceae (1)	nan (1)
	nan (1)	nan (1)

[top](#)

Cluster 85

Total number of members in cluster: 9

Average length of proteins in cluster: 425.1

Conserved (non-aliphatic) residues:

Y 100 (100.0%) N 184 (100.0%) Q 187 (100.0%) R 196 (100.0%) S 203 (100.0%) K 229 (100.0%) N 246 (100.0%) R 247 (100.0%) N 248 (100.0%) K 315 (100.0%) T 318 (100.0%) R 322 (100.0%) Q 346 (100.0%) D 358 (100.0%) N 359 (100.0%) N 425 (100.0%) N 426 (100.0%) E 430 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
ABZ79721.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O53	0
ABB65530.1	Enterobacterales	Enterobacteriaceae	Shigella	Shigella boydii	4	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

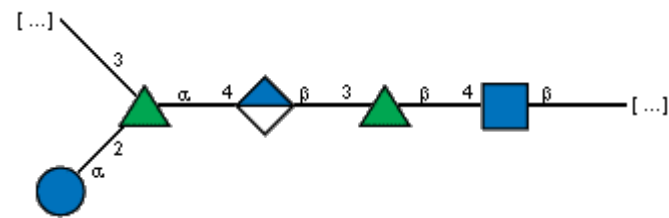
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

ABZ79721.1 Escherichia coli O53, ABB65530.1 Shigella boydii 4:



CSDB record ID: 1560

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (7)	Enterobacteriaceae (7)	Escherichia (4)
		Shigella (1)
		Enterobacter (1)
		Kosakonia (1)
Alteromonadales (2)	Pseudoalteromonadaceae (1)	Pseudoalteromonas (1)
	Shewanellaceae (1)	Shewanella (1)

[top](#)

Cluster 190

Total number of members in cluster: 9

Average length of proteins in cluster: 350.2

Conserved (non-aliphatic) residues:

E 10 (100.0%) K 68 (100.0%) S 98 (100.0%) K 110 (100.0%) S 112 (100.0%) K 140 (100.0%) D 152 (100.0%) Q 155 (100.0%) R 162 (100.0%) Q 164 (100.0%) Y 196 (100.0%) T 218 (100.0%) S 220 (100.0%) N 221 (100.0%) E 223 (100.0%) R 224 (100.0%) Y 229 (100.0%) D 237 (100.0%) Y 255 (100.0%) K 256 (100.0%) Y 259 (100.0%) N 267 (100.0%) D 268 (100.0%) H 270 (100.0%) Q 320 (100.0%) R 335 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
ADX97403.1	Enterobacterales	Yersiniaceae	Yersinia	Yersinia pseudotuberculosis	O:10	0
AFE83402.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O111	0
WP_001300154.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O111	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

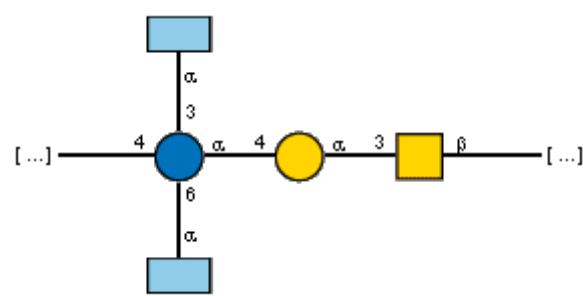
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

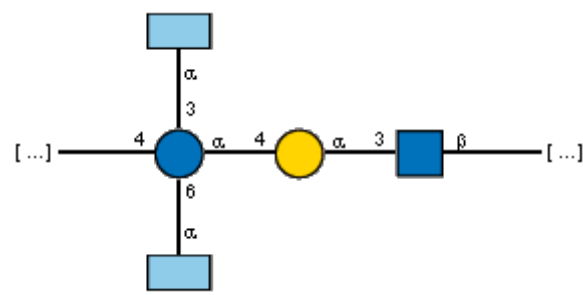
Sugars in cluster:

ADX97403.1 Yersinia pseudotuberculosis O:10:



CSDB record ID: 12137

AFE83402.1 Escherichia coli O111, WP_001300154.1 Escherichia coli O111:



CSDB record ID: 616

Sugars for blast hits:

Alphafold models:

[ADX97403.1](#)

[WP_001300154.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (9)	Enterobacteriaceae (7)	Escherichia (4)
		Salmonella (2)
		Citrobacter (1)
	Yersiniaceae (1)	Yersinia (1)
	Erwiniaceae (1)	Pantoea (1)

[top](#)

Cluster 179

Total number of members in cluster: 9

Average length of proteins in cluster: 446.2

Conserved (non-aliphatic) residues:

E 8 (100.0%) Y 11 (100.0%) S 41 (100.0%) Y 43 (100.0%) S 44 (100.0%) S 46 (100.0%) R 51 (100.0%) Q 52 (100.0%) D 53 (100.0%) Y 58 (100.0%) Y 61 (100.0%) N 63 (100.0%) N 68 (100.0%) N 71 (100.0%) Y 73 (100.0%) K 74 (100.0%) S 79 (100.0%) D 82 (100.0%) N 92 (100.0%) Y 118 (100.0%) S 121 (100.0%) E 129 (100.0%) D 131 (100.0%) K 141 (100.0%) Y 145 (100.0%) Y 150 (100.0%) Y 176 (100.0%) Y 191 (100.0%) T 192 (100.0%) K 195 (100.0%) Y 196 (100.0%) N 199 (100.0%) Y 200 (100.0%) D 204 (100.0%) Q 205 (100.0%) T 206 (100.0%) D 207 (100.0%) Q 208 (100.0%) K 230 (100.0%) S 243 (100.0%) K 246 (100.0%) Y 250 (100.0%) S 251 (100.0%) S 282 (100.0%) S 286 (100.0%) D 295 (100.0%) S 297 (100.0%) Y 299 (100.0%) R 301 (100.0%) Y 302 (100.0%) Q 304 (100.0%) Q 307 (100.0%) N 311 (100.0%) Y 312 (100.0%) K 327 (100.0%) Y 329 (100.0%) D 339 (100.0%) Y 343 (100.0%) E 347 (100.0%) Q 357 (100.0%) Y 360 (100.0%) K 365 (100.0%) N 366 (100.0%) Y 406 (100.0%) D 414 (100.0%) K 421 (100.0%) T 422 (100.0%) Y 429 (100.0%) Y 431 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
BAQ02031.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O184	0
AFW04696.1	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	O39	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

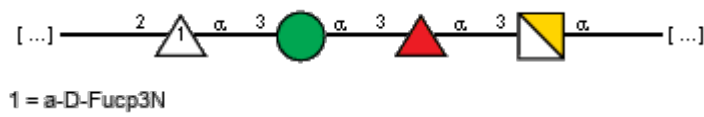
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

BAQ02031.1 Escherichia coli O184:



CSDB record ID: 1926

Sugars for blast hits:

Alphafold models:

[BAQ02031.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (9)	Enterobacteriaceae (8)	Escherichia (3)
		Salmonella (3)
		Enterobacter (1)
		Citrobacter (1)
	Morganellaceae (1)	Photorhabdus (1)

[top](#)

Cluster 168

Total number of members in cluster: 9

Average length of proteins in cluster: 441.2

Conserved (non-aliphatic) residues:

Q 9 (100.0%) Q 24 (100.0%) Q 27 (100.0%) R 33 (100.0%) E 39 (100.0%) N 47 (100.0%) Q 57 (100.0%) D 58 (100.0%) S 62 (100.0%) S 63 (100.0%) Y 64 (100.0%) Q 69 (100.0%) Q 76 (100.0%) S 77 (100.0%) T 78 (100.0%) N 83 (100.0%) T 90 (100.0%) Y 105 (100.0%) S 118 (100.0%) N 120 (100.0%) S 128 (100.0%) Q 129 (100.0%) Y 130 (100.0%) Q 131 (100.0%) H 133 (100.0%) K 136 (100.0%) K 138 (100.0%) E 147 (100.0%) K 151 (100.0%) N 179 (100.0%) Y 212 (100.0%) Q 216 (100.0%) S 219 (100.0%) Q 220 (100.0%) N 223 (100.0%) Q 224 (100.0%) R 226 (100.0%) T 227 (100.0%) Q 228 (100.0%) D 230 (100.0%) K 236 (100.0%) Y 246 (100.0%) S 247 (100.0%) K 250 (100.0%) Q 255 (100.0%) K 258 (100.0%) N 265 (100.0%) R 266 (100.0%) R 271 (100.0%) E 274 (100.0%) Q 276 (100.0%) S 297 (100.0%) Y 316 (100.0%) R 337 (100.0%) T 343 (100.0%) Q 348 (100.0%) N 350 (100.0%) T 353 (100.0%) E 356 (100.0%) N 360 (100.0%) S 388 (100.0%) Q 391 (100.0%) S 395 (100.0%) Y 414 (100.0%)

Seeds in cluster:

protein_accession order family genus species serotype Enterobacterial common antigen Wzy

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (9)	Enterobacteriaceae (6)	Klebsiella (6)
	Pectobacteriaceae (1)	Acerihabitans (1)
	Bruguierivoracaceae (1)	Sodalis (1)
	Yersiniaceae (1)	Serratia (1)

[top](#)

Cluster 161

Total number of members in cluster: 9

Average length of proteins in cluster: 358.8

Conserved (non-aliphatic) residues:

Y 3 (100.0%) R 45 (100.0%) T 50 (100.0%) D 51 (100.0%) Y 55 (100.0%) E 77 (100.0%) N 84 (100.0%) Y 94 (100.0%) K 109 (100.0%) D 134 (100.0%) R 139 (100.0%) Q 140 (100.0%) H 175 (100.0%) R 323 (100.0%) Y 360 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
AFW04860.1	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	O60	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

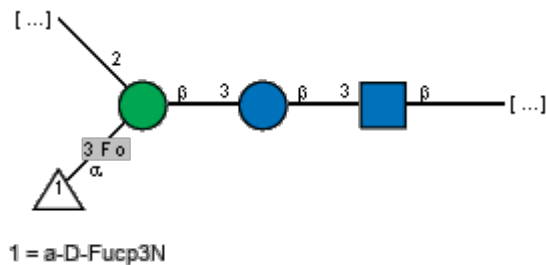
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

AFW04860.1 Salmonella enterica O60:



CSDB record ID: 3360

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (7)	Enterobacteriaceae (7)	Escherichia (4)
		Salmonella (3)
Chitinophagales (1)	Chitinophagaceae (1)	Chitinophaga (1)
Selenomonadales (1)	Selenomonadaceae (1)	Selenomonas (1)

[top](#)

Cluster 155

Total number of members in cluster: 9

Average length of proteins in cluster: 403.6

Conserved (non-aliphatic) residues:

Q 153 (100.0%) D 162 (100.0%) N 165 (100.0%) Y 173 (100.0%) S 186 (100.0%) E 218 (100.0%) K 220 (100.0%) N 272 (100.0%) Y 285 (100.0%) R 300 (100.0%) N 302 (100.0%) Y 334 (100.0%) K 338 (100.0%) N 393 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
CAI33412.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	15F	0
CAI33343.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	15A	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

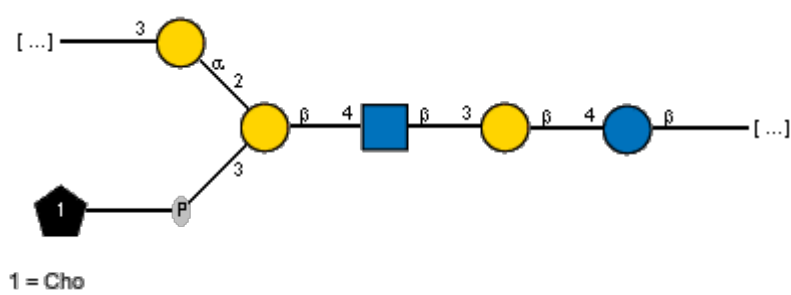
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

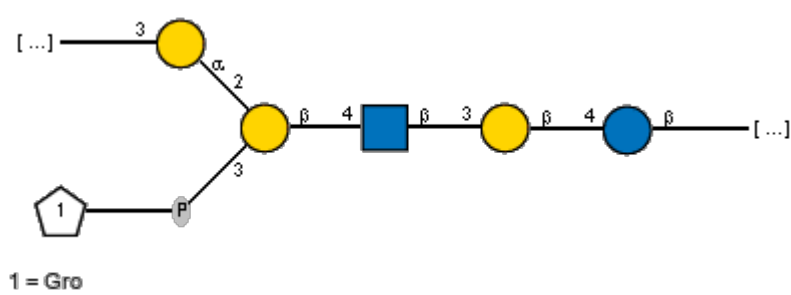
Sugars in cluster:

CAI33412.1 *Streptococcus pneumoniae* 15F:



CSDB record ID: 2972

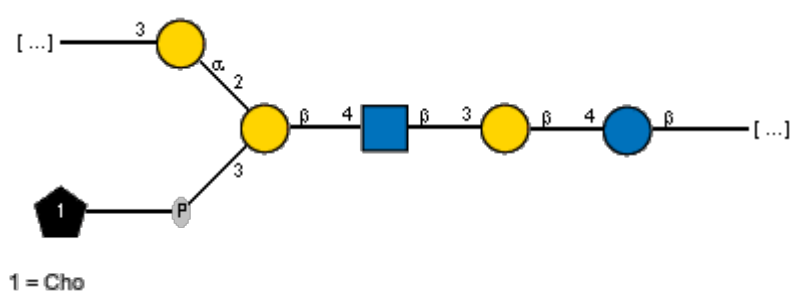
CAI33343.1 *Streptococcus pneumoniae* 15A:



CSDB record ID: 2973

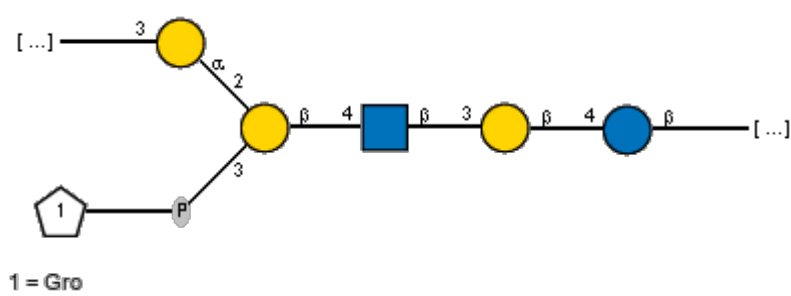
Sugars for blast hits:

VQD68897.1 *Streptococcus pneumoniae* 15F:



CSDB record ID: 2972

VSN79485.1 *Streptococcus pneumoniae* 15A:



CSDB record ID: 2973

Alphafold models:

[CAI33412.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Lactobacillales (4)	Streptococcaceae (4)	Streptococcus (4)
Eubacteriales (3)	Lachnospiraceae (2)	nan (1)
		Roseburia (1)
	Oscillospiraceae (1)	nan (1)
Bacillales (1)	Staphylococcaceae (1)	Staphylococcus (1)
Erysipelotrichales (1)	Erysipelotrichaceae (1)	Amedibacterium (1)

[top](#)

Cluster 146

Total number of members in cluster: 9

Average length of proteins in cluster: 379.3

Conserved (non-aliphatic) residues:

Y 10 (100.0%) E 23 (100.0%) H 26 (100.0%) H 31 (100.0%) E 47 (100.0%) Y 50 (100.0%) Y 55 (100.0%) N 61 (100.0%) K 78 (100.0%) Y 104 (100.0%) N 118 (100.0%) S 120 (100.0%) R 123 (100.0%) Y 125 (100.0%) D 129 (100.0%) D 130 (100.0%) N 133 (100.0%) R 139 (100.0%) S 144 (100.0%) S 147 (100.0%) S 148 (100.0%) S 162 (100.0%) K 176 (100.0%) Y 182 (100.0%) T 190 (100.0%) S 197 (100.0%) K 198 (100.0%) R 217 (100.0%) Y 218 (100.0%) Y 228 (100.0%) Y 229 (100.0%) Y 231 (100.0%) N 232 (100.0%) Y 233 (100.0%) S 235 (100.0%) Q 243 (100.0%) S 256 (100.0%) R 258 (100.0%) N 259 (100.0%) Y 261 (100.0%) Q 277 (100.0%) N 287 (100.0%) Y 289 (100.0%) Y 291 (100.0%) R 293 (100.0%) Y 295 (100.0%) D 298 (100.0%) Y 301 (100.0%) S 303 (100.0%) S 314 (100.0%) R 316 (100.0%) Y 318 (100.0%) K 321 (100.0%) Y 328 (100.0%) Y 329 (100.0%) Y 332 (100.0%) Y 337 (100.0%) Q 342 (100.0%) D 346 (100.0%) Q 347 (100.0%) Y 348 (100.0%) T 350 (100.0%) N 354 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
BAQ00705.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O19	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (9)	Enterobacteriaceae (9)	Enterobacter (4)
		Escherichia (2)
		Citrobacter (2)
		nan (1)

[top](#)

Cluster 119

Total number of members in cluster: 9

Average length of proteins in cluster: 360.8

Conserved (non-aliphatic) residues:

K 27 (100.0%) N 90 (100.0%) Y 119 (100.0%) D 144 (100.0%) R 146 (100.0%) Y 147 (100.0%) N 157 (100.0%) N 159 (100.0%) S 160 (100.0%) Q 163 (100.0%) Y 203 (100.0%) S 261 (100.0%) R 263 (100.0%) D 298 (100.0%) S 300 (100.0%) Y 345 (100.0%) E 349 (100.0%) N 350 (100.0%) N 358 (100.0%) Y 362 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
BAQ01266.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O82	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

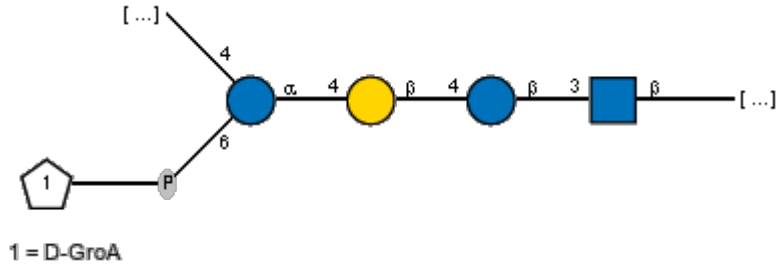
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

BAQ01266.1 Escherichia coli O82:



CSDB record ID: 1588

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (8)	Enterobacteriaceae (6)	Escherichia (4)
		Citrobacter (2)
	Hafniaceae (2)	Hafnia (1)
Moraxellales (1)	Moraxellaceae (1)	Obesumbacterium (1)
		Acinetobacter (1)

[top](#)

Cluster 97

Total number of members in cluster: 8

Average length of proteins in cluster: 362.2

Conserved (non-aliphatic) residues:

S 2 (100.0%) Y 6 (100.0%) N 12 (100.0%) N 18 (100.0%) S 29 (100.0%) Y 37 (100.0%) N 40 (100.0%) R 42 (100.0%) S 46 (100.0%) D 47 (100.0%) Y 51 (100.0%) R 52 (100.0%) R 54 (100.0%) Y 55 (100.0%) S 61 (100.0%) D 66 (100.0%) Y 69 (100.0%) D 74 (100.0%) S 77 (100.0%) H 78 (100.0%) S 82 (100.0%) Q 84 (100.0%) S 94 (100.0%) S 95 (100.0%) Y 99 (100.0%) K 103 (100.0%) K 104 (100.0%) N 108 (100.0%) Y 109 (100.0%) N 110 (100.0%) S 117 (100.0%) Y 120 (100.0%) Y 123 (100.0%) E 126 (100.0%) R 129 (100.0%) S 135 (100.0%) Y 142 (100.0%) R 149 (100.0%) H 163 (100.0%) S 165 (100.0%) Y 176 (100.0%) K 179 (100.0%) K 183 (100.0%) S 192 (100.0%) N 199 (100.0%) N 204 (100.0%) S 206 (100.0%) S 207 (100.0%) Y 208 (100.0%) S 219 (100.0%) K 223 (100.0%) R 225 (100.0%) Y 229 (100.0%) T 230 (100.0%) S 233 (100.0%) T 234 (100.0%) R 235 (100.0%) Y 241 (100.0%) Y 244 (100.0%) N 248 (100.0%) K 257 (100.0%) N 264 (100.0%) Y 277 (100.0%) Q 278 (100.0%) R 298 (100.0%) Y 299 (100.0%) T 303 (100.0%) N 307 (100.0%) S 321 (100.0%) K 324 (100.0%) T 339 (100.0%) E 347 (100.0%) N 348 (100.0%) Y 353 (100.0%) E 354 (100.0%) N 359 (100.0%) N 362 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
CAI34587.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	45	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

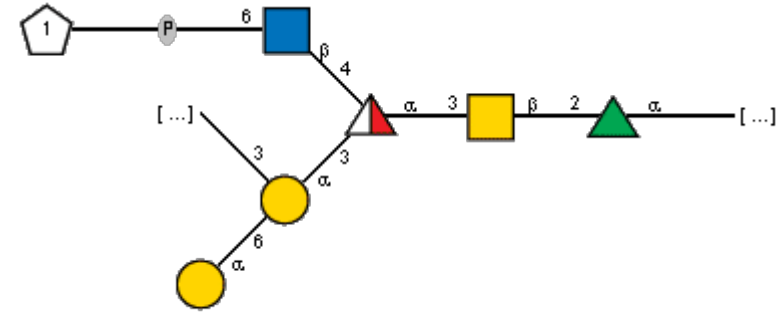
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

CAI34587.1 Streptococcus pneumoniae 45:



1 = Gro

CSDB record ID: 25004

Sugars for blast hits:

Alphafold models:

[CAI34587.1](#)

Taxonomy:

order (count) family (count) genus (count)
 Lactobacillales (8) Streptococcaceae (8) Streptococcus (8)

[top](#)

Cluster 78

Total number of members in cluster: 8

Average length of proteins in cluster: 386.0

Conserved (non-aliphatic) residues:

K 30 (100.0%) N 168 (100.0%) N 176 (100.0%) T 210 (100.0%) R 211 (100.0%) T 212 (100.0%) R 278 (100.0%) D 306 (100.0%) T 316 (100.0%) D 318 (100.0%) Y 321 (100.0%) Y 361 (100.0%) T 364 (100.0%) E 365 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
CAI32957.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	8	0

[MSA fasta](#)

[Malign view](#)

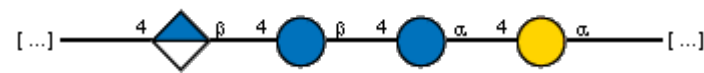
[Fasta of members](#)

[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:



CSDB record ID: 938

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Lactobacillales (3)	Streptococcaceae (3)	Streptococcus (2)
		Lactococcus (1)
Eubacteriales (3)	Lachnospiraceae (3)	Coprococcus (2)
		Anaerocolumna (1)
nan (1)	nan (1)	nan (1)
Bifidobacteriales (1)	Bifidobacteriaceae (1)	Bifidobacterium (1)

[top](#)

Cluster 71

Total number of members in cluster: 8

Average length of proteins in cluster: 416.1

Conserved (non-aliphatic) residues:

Y 52 (100.0%) D 55 (100.0%) Y 129 (100.0%) R 196 (100.0%) R 201 (100.0%) K 251 (100.0%) T 252 (100.0%) R 253 (100.0%) Y 258 (100.0%) D 311 (100.0%) R 317 (100.0%) Y 324 (100.0%) Y 364 (100.0%) Y 365 (100.0%) S 367 (100.0%) D 368 (100.0%) N 404 (100.0%) D 434 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
CAI33941.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	24F	0
CAI33890.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	24A	0
CAI33915.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	24B	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Lactobacillales (6)	Streptococcaceae (5)	Streptococcus (5)
	Lactobacillaceae (1)	Lactobacillus (1)
Eubacteriales (1)	Lachnospiraceae (1)	nan (1)
Eggerthellales (1)	Eggerthellaceae (1)	nan (1)

[top](#)

Cluster 166

Total number of members in cluster: 8

Average length of proteins in cluster: 415.0

Conserved (non-aliphatic) residues:

H 36 (100.0%) Q 76 (100.0%) S 98 (100.0%) R 101 (100.0%) E 146 (100.0%) K 167 (100.0%) Y 182 (100.0%) Y 183 (100.0%) Q 225 (100.0%) S 226 (100.0%) K 227 (100.0%) T 287 (100.0%) R 304 (100.0%) E 333 (100.0%) R 342 (100.0%) Y 343 (100.0%) Q 396 (100.0%) S 398 (100.0%) E 403 (100.0%) K 406 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
BAQ01419.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O96	0

[MSA fasta](#)

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[Fasta of members](#)

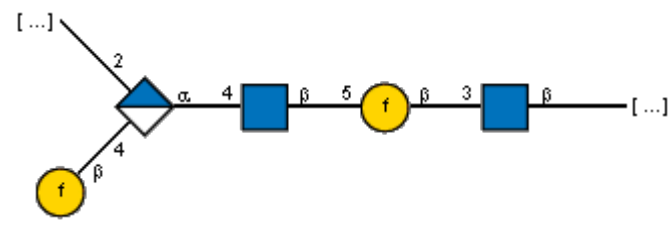
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[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

BAQ01419.1 Escherichia coli O96:



CSDB record ID: 1600

Sugars for blast hits:

Alphafold models:

[BAQ01419.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (4)	Enterobacteriaceae (4)	Escherichia (4)
Vibrionales (2)	Vibrionaceae (2)	Vibrio (2)
Alteromonadales (2)	Pseudoalteromonadaceae (1)	Pseudoalteromonas (1)
	Shewanellaceae (1)	Shewanella (1)

[top](#)

Cluster 152

Total number of members in cluster: 8

Average length of proteins in cluster: 363.5

Conserved (non-aliphatic) residues:

K 71 (100.0%) S 73 (100.0%) S 77 (100.0%) T 84 (100.0%) R 90 (100.0%) S 98 (100.0%) N 100 (100.0%) Y 104 (100.0%) Y 105 (100.0%) N 110 (100.0%) K 132 (100.0%) S 150 (100.0%) R 151 (100.0%) S 164 (100.0%) Q 193 (100.0%) R 195 (100.0%) T 196 (100.0%) R 205 (100.0%) N 209 (100.0%) Y 213 (100.0%) S 235 (100.0%) Y 238 (100.0%) Y 241 (100.0%) S 244 (100.0%) N 254 (100.0%) D 258 (100.0%) Y 263 (100.0%) S 271 (100.0%) Y 274 (100.0%) N 280 (100.0%) Y 283 (100.0%) D 292 (100.0%) Y 301 (100.0%) R 326 (100.0%) S 335 (100.0%) R 340 (100.0%) D 341 (100.0%) E 345 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
ACA24739.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O79	0
AAL27327.1	Enterobacterales	Enterobacteriaceae	Shigella	Shigella boydii	5	0

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[Malign view](#)

[Fasta of members](#)

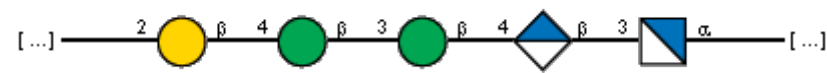
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

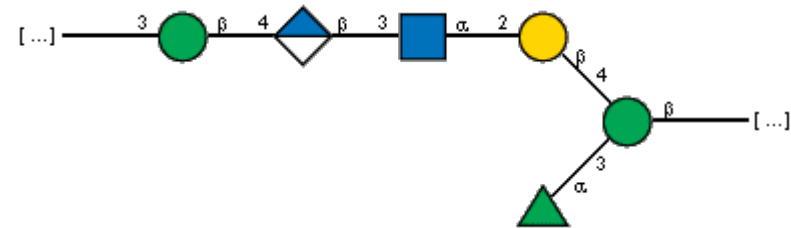
Sugars in cluster:

ACA24739.1 Escherichia coli O79:



CSDB record ID: 1585

AAL27327.1 Shigella boydii 5:



CSDB record ID: 1422

Sugars for blast hits:

AlphaFold models:

[ACA24739.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (7)	Enterobacteriaceae (6)	Escherichia (3)
		Enterobacter (2)
		Shigella (1)
	Erwiniaceae (1)	Erwinia (1)
Alteromonadales (1)	Pseudoalteromonadaceae (1)	Pseudoalteromonas (1)

[top](#)

Cluster 148

Total number of members in cluster: 8

Average length of proteins in cluster: 445.9

Conserved (non-aliphatic) residues:

D 41 (100.0%) D 73 (100.0%) Y 83 (100.0%) S 87 (100.0%) R 127 (100.0%) S 165 (100.0%) S 176 (100.0%) R 185 (100.0%) E 187 (100.0%) K 200 (100.0%) Y 201 (100.0%) Y 206 (100.0%) Y 237 (100.0%) S 246 (100.0%) R 247 (100.0%) R 248 (100.0%) E 249 (100.0%) R 293 (100.0%) N 307 (100.0%) E 311 (100.0%) S 317 (100.0%) T 318 (100.0%) Y 321 (100.0%) S 335 (100.0%) Q 338 (100.0%) N 342 (100.0%) K 346 (100.0%) K 353 (100.0%) Y 376 (100.0%) T 379 (100.0%) T 382 (100.0%) E 383 (100.0%) N 387 (100.0%) S 404 (100.0%) E 408 (100.0%) Q 424 (100.0%) N 427 (100.0%) Q 429 (100.0%) R 430 (100.0%) S 435 (100.0%) E 439 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
BAQ01598.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O125ac	0
WP_038349068.1	Enterobacterales	Enterobacteriaceae	nan	nan	O125ab	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (4)	Enterobacteriaceae (4)	Escherichia (3) nan (1)
Pseudomonadales (3)	Pseudomonadaceae (3)	Pseudomonas (3)
Rhodocyclales (1)	Zoogloeaceae (1)	Thauera (1)

[top](#)

Cluster 135

Total number of members in cluster: 8

Average length of proteins in cluster: 393.9

Conserved (non-aliphatic) residues:

E 134 (100.0%) N 140 (100.0%) N 158 (100.0%) Y 165 (100.0%) S 168 (100.0%) S 169 (100.0%) H 173 (100.0%) Y 174 (100.0%) T 175 (100.0%) Y 176 (100.0%) Y 179 (100.0%) N 195 (100.0%) Q 214 (100.0%) R 216 (100.0%) R 275 (100.0%) D 286 (100.0%) S 288 (100.0%) Q 291 (100.0%) R 292 (100.0%) T 295 (100.0%) N 298 (100.0%) Y 327 (100.0%) S 328 (100.0%) T 335 (100.0%) D 337 (100.0%) S 338 (100.0%) T 341 (100.0%) D 395 (100.0%) N 399 (100.0%) Y 407 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
CAI32727.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus	2	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

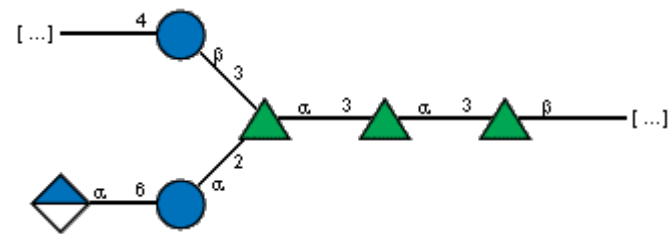
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

CAI32727.1 Streptococcus pneumoniae 2:



CSDB record ID: 1944

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Lactobacillales (8)	Streptococcaceae (8)	Streptococcus (8)

[top](#)

Cluster 128

Total number of members in cluster: 8

Average length of proteins in cluster: 365.4

Conserved (non-aliphatic) residues:

S 15 (100.0%) E 18 (100.0%) Y 47 (100.0%) D 52 (100.0%) Y 56 (100.0%) E 71 (100.0%) K 96 (100.0%) T 119 (100.0%) N 130 (100.0%) D 131 (100.0%) R 134 (100.0%) Q 135 (100.0%) H 166 (100.0%) K 227 (100.0%) Y 231 (100.0%) N 239 (100.0%) Y 241 (100.0%) R 246 (100.0%) E 287 (100.0%) Q 298 (100.0%) R 299 (100.0%) Y 303 (100.0%) N 314 (100.0%) Y 352 (100.0%) N 357 (100.0%) N 369 (100.0%)

Seeds in cluster:

BAQ00634.1

Enterobacterales Enterobacteriaceae Escherichia coli

Escherichia coli

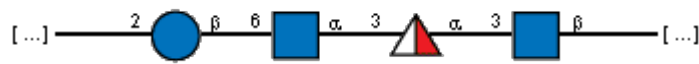
O12

0

- [MSA fasta](#)
- [Malign view](#)
- [Fasta of members](#)
- [Logoplot](#)
- [Phylogenetic tree](#)
- [Hits in cluster](#)

Sugars in cluster:

BAQ00634.1 Escherichia coli O12:



CSDB record ID: 1514

Sugars for blast hits:

AXY99336.1 Proteus vulgaris O2:



CSDB record ID: 3058

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (6)	Morganellaceae (4)	Proteus (4)
	Enterobacteriaceae (2)	Escherichia (2)
Moraxellales (2)	Moraxellaceae (2)	Psychrobacter (2)

[top](#)

Cluster 127

Total number of members in cluster: 8

Average length of proteins in cluster: 381.4

Conserved (non-aliphatic) residues:

Y 44 (100.0%) E 51 (100.0%) Y 53 (100.0%) Y 123 (100.0%) R 144 (100.0%) D 146 (100.0%) K 149 (100.0%) N 201 (100.0%) K 202 (100.0%) Y 238 (100.0%) Y 254 (100.0%) S 258 (100.0%) R 262 (100.0%) Q 267 (100.0%) K 293 (100.0%) Y 301 (100.0%) S 304 (100.0%) S 307 (100.0%) E 315 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
ADJ19217.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O61	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

ADJ19217.1 Escherichia coli O61:



CSDB record ID: 1568

Sugars for blast hits:

Alphafold models:

[ADJ19217.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (5)	Enterobacteriaceae (4)	Escherichia (3)
		Citrobacter (1)
	Morganellaceae (1)	Morganella (1)
Vibrionales (2)	Vibrionaceae (2)	Photobacterium (1)
		Vibrio (1)
Aeromonadales (1)	Aeromonadaceae (1)	Aeromonas (1)

[top](#)

Cluster 114

Total number of members in cluster: 8

Average length of proteins in cluster: 394.4

Conserved (non-aliphatic) residues:

S 89 (100.0%) R 144 (100.0%) R 153 (100.0%) T 155 (100.0%) E 160 (100.0%) S 162 (100.0%) H 163 (100.0%) Y 164 (100.0%) T 195 (100.0%) S 197 (100.0%) S 199 (100.0%) K 250 (100.0%) S 267 (100.0%) R 271 (100.0%) S 274 (100.0%) Y 310 (100.0%) Y 311 (100.0%) N 314 (100.0%) N 325 (100.0%) S 333 (100.0%) S 368 (100.0%) Y 373 (100.0%)

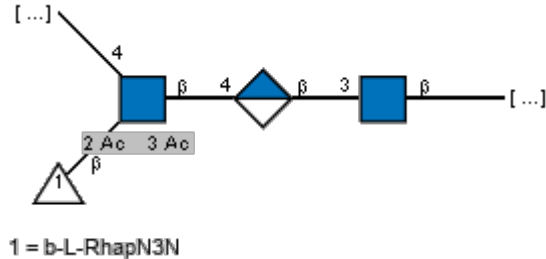
Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
BAQ02015.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O182	0

- [MSA fasta](#)
- [Malign view](#)
- [Fasta of members](#)
- [Logoplot](#)
- [Phylogenetic tree](#)
- [Hits in cluster](#)

Sugars in cluster:

BAQ02015.1 Escherichia coli O182:



CSDB record ID: 1924

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (6)	Enterobacteriaceae (6)	Escherichia (4)
		Trabulsiella (1)
		Enterobacter (1)
Vibrionales (2)	Vibrionaceae (2)	Vibrio (2)

[top](#)

Cluster 7

Total number of members in cluster: 7

Average length of proteins in cluster: 321.1

Conserved (non-aliphatic) residues:

K 8 (100.0%) K 11 (100.0%) Y 18 (100.0%) Q 35 (100.0%) S 40 (100.0%) R 41 (100.0%) D 42 (100.0%) Y 43

(100.0%) N 45 (100.0%) Y 46 (100.0%) Q 48 (100.0%) S 51 (100.0%) E 54 (100.0%) E 60 (100.0%) Y 63 (100.0%) R 64 (100.0%) T 70 (100.0%) S 84 (100.0%) K 88 (100.0%) Y 95 (100.0%) N 98 (100.0%) S 100 (100.0%) Y 108 (100.0%) Y 109 (100.0%) D 118 (100.0%) Y 119 (100.0%) T 120 (100.0%) Q 121 (100.0%) R 123 (100.0%) N 124 (100.0%) S 129 (100.0%) S 134 (100.0%) Y 136 (100.0%) Y 137 (100.0%) Y 147 (100.0%) S 149 (100.0%) T 156 (100.0%) H 157 (100.0%) S 159 (100.0%) Y 167 (100.0%) Y 171 (100.0%) S 172 (100.0%) R 176 (100.0%) Y 180 (100.0%) S 184 (100.0%) S 192 (100.0%) E 197 (100.0%) R 203 (100.0%) Q 209 (100.0%) K 210 (100.0%) N 213 (100.0%) N 218 (100.0%) N 221 (100.0%) S 222 (100.0%) S 224 (100.0%) T 226 (100.0%) S 234 (100.0%) S 237 (100.0%) E 242 (100.0%) R 247 (100.0%) Y 252 (100.0%) Q 256 (100.0%) Y 257 (100.0%) S 264 (100.0%) R 271 (100.0%) E 274 (100.0%) Y 276 (100.0%) Q 289 (100.0%) Y 294 (100.0%) K 300 (100.0%) Y 306 (100.0%) T 308 (100.0%) Y 309 (100.0%) Y 310 (100.0%) Y 311 (100.0%) H 312 (100.0%) N 319 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
ACD75809.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O2	0
BAQ01012.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O50	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

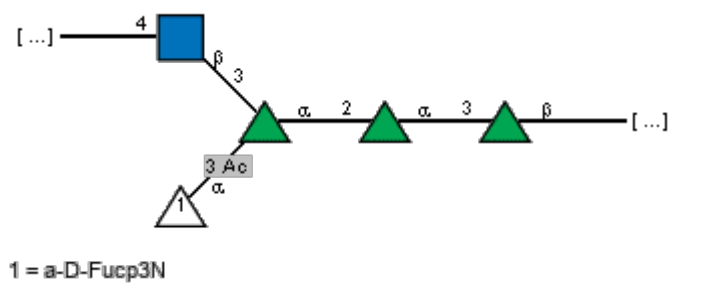
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[Phylogenetic tree](#)

[Hits in cluster](#)

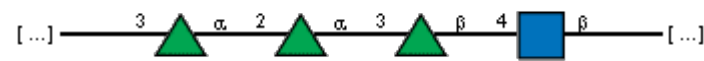
Sugars in cluster:

ACD75809.1 Escherichia coli O2:



CSDB record ID: 108685

BAQ01012.1 Escherichia coli O50:



CSDB record ID: 1557

Sugars for blast hits:

AlphaFold models:

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (7)	Enterobacteriaceae (7)	Escherichia (5)
		Enterobacter (2)

[top](#)

Cluster 199

Total number of members in cluster: 7

Average length of proteins in cluster: 385.4

Conserved (non-aliphatic) residues:

T 22 (100.0%) S 28 (100.0%) N 95 (100.0%) N 100 (100.0%) K 101 (100.0%) Y 107 (100.0%) R 108 (100.0%) D 113 (100.0%) S 115 (100.0%) R 116 (100.0%) N 118 (100.0%) Y 129 (100.0%) Y 131 (100.0%) Y 132 (100.0%) Y 164 (100.0%) D 165 (100.0%) S 170 (100.0%) R 171 (100.0%) T 172 (100.0%) Y 175 (100.0%) Y 176 (100.0%) K 193 (100.0%) S 206 (100.0%) S 210 (100.0%) R 213 (100.0%) N 229 (100.0%) Y 230 (100.0%) H 231 (100.0%) D 239 (100.0%) N 241 (100.0%) Y 250 (100.0%) S 257 (100.0%) Y 261 (100.0%) N 262 (100.0%) D 269 (100.0%) N 277 (100.0%) R 280 (100.0%) N 284 (100.0%) Y 287 (100.0%) Y 297 (100.0%) Y 300 (100.0%) N 301 (100.0%) Y 303 (100.0%) Y 304 (100.0%) T 305 (100.0%) Y 311 (100.0%) D 313 (100.0%) S 340 (100.0%) E 356 (100.0%) S 357 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
AJE24464.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O153	0
AFW04790.1	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	O52	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

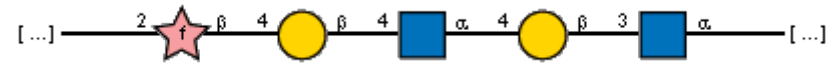
Sugars in cluster:

AJE24464.1 Escherichia coli O153:



CSDB record ID: 1894

AFW04790.1 Salmonella enterica O52:



CSDB record ID: 3364

Sugars for blast hits:

Alphafold models:

[AJE24464.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (7)	Enterobacteriaceae (5)	Citrobacter (2)
		Escherichia (1)
		Salmonella (1)
		nan (1)
	Morganellaceae (2)	Proteus (1)
		Xenorhabdus (1)

[top](#)

Cluster 186

Total number of members in cluster: 7

Average length of proteins in cluster: 411.4

Conserved (non-aliphatic) residues:

R 56 (100.0%) Y 64 (100.0%) N 133 (100.0%) D 181 (100.0%) N 183 (100.0%) N 189 (100.0%) N 191 (100.0%) T 193 (100.0%) S 239 (100.0%) R 240 (100.0%) R 304 (100.0%) D 328 (100.0%) R 331 (100.0%) T 350 (100.0%) Y 357 (100.0%) H 378 (100.0%) N 379 (100.0%) Y 381 (100.0%) S 383 (100.0%) Y 384 (100.0%) N 435 (100.0%) E 436 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
AAZ91245.1	Enterobacterales	Enterobacteriaceae	Shigella	Shigella sonnei	nan	0

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[Malign view](#)

[Fasta of members](#)

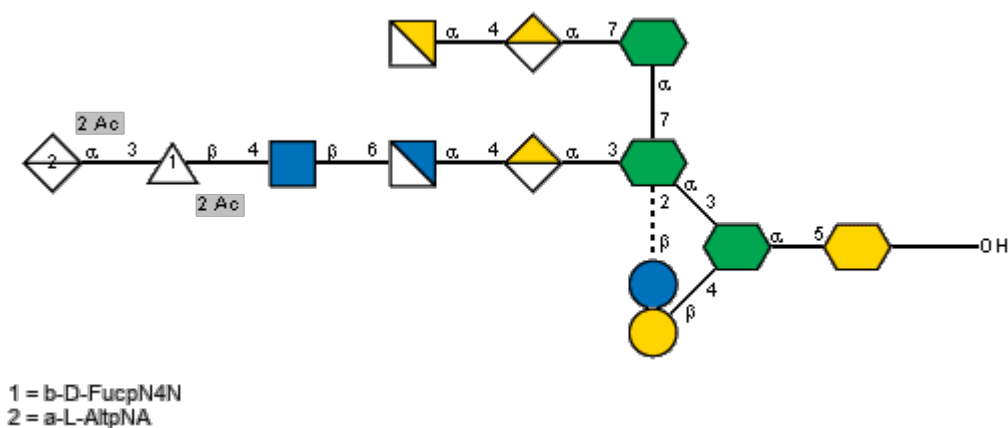
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

Sugars for blast hits:

AAG17411.1 *Plesiomonas shigelloides* O17:

CSDB record ID: 22678

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (4)	Enterobacteriaceae (4)	Shigella (3)
		Plesiomonas (1)
Desulfobacterales (1)	nan (1)	nan (1)
Burkholderiales (1)	Alcaligenaceae (1)	Candidimonas (1)
Pirellulales (1)	Pirellulaceae (1)	Rosistilla (1)

[top](#)

Cluster 181

Total number of members in cluster: 7

Average length of proteins in cluster: 405.9

Conserved (non-aliphatic) residues:

Y 16 (100.0%) K 145 (100.0%) Y 157 (100.0%) R 177 (100.0%) K 199 (100.0%) N 204 (100.0%) R 260 (100.0%) D 266 (100.0%) T 268 (100.0%) Y 277 (100.0%) Y 289 (100.0%) D 292 (100.0%) S 296 (100.0%) Y 299 (100.0%) Y 317 (100.0%) N 324 (100.0%) D 325 (100.0%) S 326 (100.0%) N 329 (100.0%) Y 330 (100.0%) K 339 (100.0%) D 357 (100.0%) Y 380 (100.0%) Q 388 (100.0%) T 392 (100.0%) R 399 (100.0%) Y 401 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
AKA20981.1	Enterobacterales	Yersiniaceae	Yersinia	Yersinia pseudotuberculosis	O:5a	0
AKA20999.1	Enterobacterales	Yersiniaceae	Yersinia	Yersinia pseudotuberculosis	O:5b	0
CAX18360.1	Enterobacterales	Yersiniaceae	Yersinia	Yersinia pseudotuberculosis	O:15	0

genus (count)

order (count)	family (count)	genus (count)
Enterobacterales (4)	Yersiniaceae (4)	Yersinia (4)
Pseudomonadales (2)	Pseudomonadaceae (2)	Pseudomonas (2)
Vibrionales (1)	Vibrionaceae (1)	Vibrio (1)

[top](#)

Cluster 18

Total number of members in cluster: 7

Average length of proteins in cluster: 378.0

Conserved (non-aliphatic) residues:

S 5 (100.0%) Y 26 (100.0%) N 29 (100.0%) S 31 (100.0%) K 33 (100.0%) Y 36 (100.0%) K 37 (100.0%) N 42 (100.0%) K 63 (100.0%) S 91 (100.0%) R 100 (100.0%) S 103 (100.0%) Y 145 (100.0%) D 147 (100.0%) N 152 (100.0%) H 153 (100.0%) N 155 (100.0%) T 157 (100.0%) N 195 (100.0%) S 201 (100.0%) R 202 (100.0%) K 226 (100.0%) S 243 (100.0%) Y 254 (100.0%) K 258 (100.0%) D 269 (100.0%) S 270 (100.0%) R 271 (100.0%) Y 272 (100.0%) Y 275 (100.0%) Y 291 (100.0%) N 293 (100.0%) Y 294 (100.0%) E 300 (100.0%) Y 302 (100.0%) H 304 (100.0%) N 305 (100.0%) E 309 (100.0%) N 313 (100.0%) S 314 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
AAY28249.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O174	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

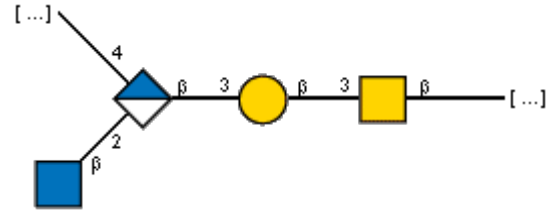
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

AAY28249.1 Escherichia coli O174:



CSDB record ID: 30040

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (7)	Enterobacteriaceae (6)	Escherichia (4)
		Enterobacter (2)
	Morganellaceae (1)	Proteus (1)

[top](#)

Cluster 176

Total number of members in cluster: 7

Average length of proteins in cluster: 395.9

Conserved (non-aliphatic) residues:

D 26 (100.0%) T 28 (100.0%) T 32 (100.0%) N 34 (100.0%) S 35 (100.0%) Q 38 (100.0%) T 41 (100.0%) K 59 (100.0%) H 78 (100.0%) E 80 (100.0%) Y 83 (100.0%) H 84 (100.0%) Y 85 (100.0%) K 91 (100.0%) T 92 (100.0%) N 98 (100.0%) Y 109 (100.0%) Q 126 (100.0%) S 129 (100.0%) Y 133 (100.0%) S 134 (100.0%) Q 139 (100.0%) R 142 (100.0%) S 147 (100.0%) R 149 (100.0%) H 152 (100.0%) N 156 (100.0%) S 160 (100.0%) Y 163 (100.0%) R 164 (100.0%) D 165 (100.0%) T 167 (100.0%) S 169 (100.0%) N 170 (100.0%) Q 171 (100.0%) Y 173 (100.0%) S 174 (100.0%) Y 176 (100.0%) H 189 (100.0%) S 198 (100.0%) Y 201 (100.0%) N 218 (100.0%) R 220 (100.0%) S 221 (100.0%) Y 229 (100.0%) Y 232 (100.0%) Y 244 (100.0%) S 268 (100.0%) E 276 (100.0%) Q 277 (100.0%) K 278 (100.0%) D 285 (100.0%) S 286 (100.0%) D 289 (100.0%) N 293 (100.0%) H 294 (100.0%) T 302 (100.0%) Y 309 (100.0%) S 320 (100.0%) D 321 (100.0%) Y 325 (100.0%) R 326 (100.0%) Q 327 (100.0%) Y 339 (100.0%) S 342 (100.0%) R 348 (100.0%) N 367 (100.0%) K 369 (100.0%) Q 370 (100.0%) E 371 (100.0%) N 374 (100.0%) N 375 (100.0%) Y 380 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
ACD37117.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O40	0
ACD37111.1	Enterobacterales	Enterobacteriaceae	Shigella	Shigella dysenteriae	9	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

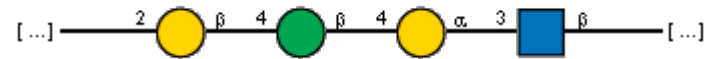
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

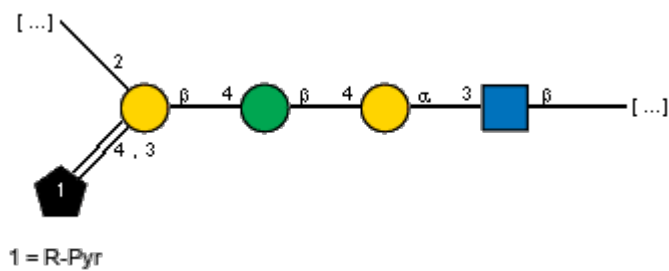
Sugars in cluster:

ACD37117.1 Escherichia coli O40:



CSDB record ID: 1547

ACD37111.1 *Shigella dysenteriae* 9:



CSDB record ID: 713

Sugars for blast hits:

Alphafold models:

[ACD37111.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (6)	Enterobacteriaceae (6)	Escherichia (3)
		Shigella (2)
		Citrobacter (1)
Aeromonadales (1)	Aeromonadaceae (1)	Aeromonas (1)

[top](#)

Cluster 170

Total number of members in cluster: 7

Average length of proteins in cluster: 410.9

Conserved (non-aliphatic) residues:

K 6 (100.0%) Y 8 (100.0%) T 20 (100.0%) S 23 (100.0%) Y 31 (100.0%) D 64 (100.0%) S 86 (100.0%) Y 87 (100.0%)
T 88 (100.0%) E 89 (100.0%) D 90 (100.0%) R 92 (100.0%) S 95 (100.0%) R 98 (100.0%) Y 99 (100.0%) Y 100
(100.0%) S 107 (100.0%) Y 111 (100.0%) K 115 (100.0%) Y 128 (100.0%) Y 134 (100.0%) T 141 (100.0%) K 151
(100.0%) D 153 (100.0%) S 155 (100.0%) D 159 (100.0%) S 161 (100.0%) Y 166 (100.0%) Q 167 (100.0%) S 170
(100.0%) D 171 (100.0%) S 172 (100.0%) S 187 (100.0%) K 188 (100.0%) T 198 (100.0%) N 206 (100.0%) R 208
(100.0%) S 209 (100.0%) D 252 (100.0%) E 261 (100.0%) N 264 (100.0%) S 265 (100.0%) R 266 (100.0%) Y 268
(100.0%) N 269 (100.0%) S 272 (100.0%) N 274 (100.0%) D 277 (100.0%) D 278 (100.0%) S 280 (100.0%) R 284
(100.0%) K 286 (100.0%) H 290 (100.0%) S 291 (100.0%) S 293 (100.0%) H 298 (100.0%) S 306 (100.0%) Q 307
(100.0%) D 313 (100.0%) R 318 (100.0%) Y 322 (100.0%) T 323 (100.0%) H 324 (100.0%) N 325 (100.0%) Y 329
(100.0%) D 331 (100.0%) Q 332 (100.0%) Y 350 (100.0%) N 351 (100.0%) N 352 (100.0%) K 356 (100.0%) D 362
(100.0%) S 372 (100.0%) Q 373 (100.0%) Q 374 (100.0%) K 378 (100.0%) S 379 (100.0%) T 381 (100.0%) Y 382
(100.0%) Y 384 (100.0%) E 393 (100.0%) K 396 (100.0%) K 400 (100.0%) N 402 (100.0%) Y 403 (100.0%) N 404
(100.0%) K 407 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
BAQ01218.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O76	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

BAQ01218.1 Escherichia coli O76:



CSDB record ID: 1582

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (7)	Enterobacteriaceae (7)	Escherichia (3)
		Citrobacter (2)
		Enterobacter (1)
		Cedecea (1)

[top](#)

Cluster 169

Total number of members in cluster: 7

Average length of proteins in cluster: 351.1

Conserved (non-aliphatic) residues:

Y 3 (100.0%) D 24 (100.0%) R 42 (100.0%) D 48 (100.0%) Y 52 (100.0%) S 88 (100.0%) K 104 (100.0%) K 109 (100.0%) T 110 (100.0%) T 125 (100.0%) R 129 (100.0%) Q 130 (100.0%) Y 150 (100.0%) H 161 (100.0%) S 163 (100.0%) K 177 (100.0%) S 179 (100.0%) Y 223 (100.0%) Y 227 (100.0%) S 232 (100.0%) Y 238 (100.0%) N 264 (100.0%) Y 266 (100.0%) K 277 (100.0%) D 278 (100.0%) N 279 (100.0%) N 284 (100.0%) R 285 (100.0%) T 290 (100.0%) N 291 (100.0%) K 311 (100.0%) Y 321 (100.0%) Y 326 (100.0%) K 328 (100.0%) T 332 (100.0%) R 335 (100.0%) Y 342 (100.0%) Y 345 (100.0%) N 352 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
ABB29906.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O24	0
ABB29916.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O56	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

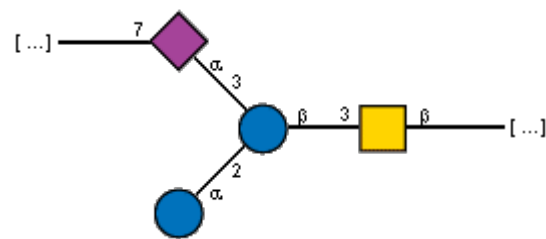
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

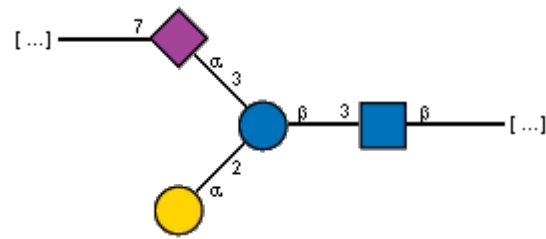
Sugars in cluster:

ABB29906.1 Escherichia coli O24:



CSDB record ID: 8411

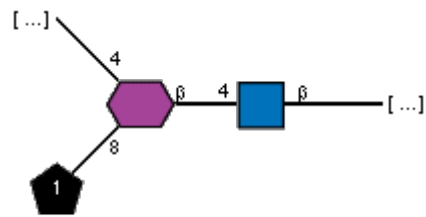
ABB29916.1 Escherichia coli O56:



CSDB record ID: 8382

Sugars for blast hits:

AXL96526.1 Providencia alcalifaciens O38:



1 = L-Ala

CSDB record ID: 27606

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (5)	Enterobacteriaceae (4)	Escherichia (4)
	Morganellaceae (1)	Providencia (1)
Vibrionales (2)	Vibrionaceae (2)	Vibrio (2)

[top](#)

Cluster 160

Total number of members in cluster: 7

Average length of proteins in cluster: 394.0

Conserved (non-aliphatic) residues:

N 14 (100.0%) S 33 (100.0%) S 38 (100.0%) D 55 (100.0%) Y 60 (100.0%) N 81 (100.0%) K 89 (100.0%) K 98 (100.0%) E 99 (100.0%) T 106 (100.0%) Y 110 (100.0%) S 146 (100.0%) N 149 (100.0%) R 152 (100.0%) S 153 (100.0%) H 186 (100.0%) S 187 (100.0%) K 214 (100.0%) S 241 (100.0%) Y 245 (100.0%) Y 255 (100.0%) S 310 (100.0%) S 320 (100.0%) R 322 (100.0%) Y 323 (100.0%) Q 324 (100.0%) Y 369 (100.0%) R 372 (100.0%) Y 373 (100.0%) S 378 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
AAD50486.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O113	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

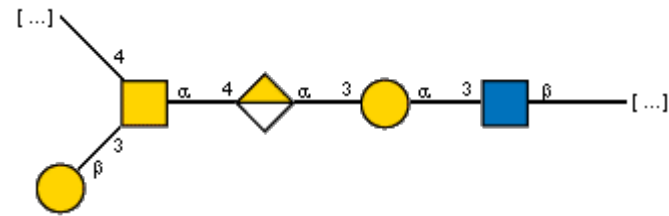
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

AAD50486.1 Escherichia coli O113:



Sugars for blast hits:

AlphaFold models:

[AAD50486.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (6)	Enterobacteriaceae (6)	Escherichia (4)
		Enterobacter (2)
Vibrionales (1)	Vibrionaceae (1)	Vibrio (1)

[top](#)

Cluster 143

Total number of members in cluster: 7

Average length of proteins in cluster: 343.6

Conserved (non-aliphatic) residues:

N 44 (100.0%) R 45 (100.0%) N 47 (100.0%) D 49 (100.0%) Y 50 (100.0%) Y 53 (100.0%) E 65 (100.0%) Y 68 (100.0%) K 76 (100.0%) K 106 (100.0%) Y 115 (100.0%) D 123 (100.0%) Q 126 (100.0%) R 128 (100.0%) N 129 (100.0%) H 162 (100.0%) Y 168 (100.0%) Y 221 (100.0%) D 241 (100.0%) K 261 (100.0%) E 286 (100.0%) R 289 (100.0%) R 292 (100.0%) N 293 (100.0%) K 298 (100.0%) Y 299 (100.0%) Y 335 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
AAN60459.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O26	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

AAN60459.1 Escherichia coli O26:



CSDB record ID: 1534

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (4)	Enterobacteriaceae (3)	Escherichia (3)
	Budviciaceae (1)	nan (1)
Eubacteriales (2)	Clostridiaceae (2)	Clostridium (2)
Bacillales (1)	Bacillaceae (1)	Bacillus (1)

[top](#)

Cluster 133

Total number of members in cluster: 7

Average length of proteins in cluster: 344.4

Conserved (non-aliphatic) residues:

N 9 (100.0%) N 30 (100.0%) S 38 (100.0%) Y 53 (100.0%) D 55 (100.0%) Y 59 (100.0%) Y 63 (100.0%) E 73 (100.0%) T 102 (100.0%) T 129 (100.0%) S 131 (100.0%) Y 134 (100.0%) E 138 (100.0%) R 141 (100.0%) K 166 (100.0%) Y 168 (100.0%) H 178 (100.0%) Y 179 (100.0%) S 180 (100.0%) K 230 (100.0%) Y 234 (100.0%) T 238 (100.0%) S 241 (100.0%) T 243 (100.0%) R 247 (100.0%) Y 267 (100.0%) Y 271 (100.0%) Y 274 (100.0%) D 285 (100.0%) E 286 (100.0%) R 289 (100.0%) R 290 (100.0%) K 311 (100.0%) Y 326 (100.0%) Y 334 (100.0%) Y 338 (100.0%) Y 343 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
AHB32311.1	Moraxellales	Moraxellaceae	Acinetobacter	Acinetobacter baumannii	O8	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Moraxellales (6)	Moraxellaceae (6)	Acinetobacter (6)

order (count) family (count) genus (count)
Vibrionales (1) Vibrionaceae (1) Vibrio (1)

[top](#)

Cluster 132

Total number of members in cluster: 7

Average length of proteins in cluster: 387.4

Conserved (non-aliphatic) residues:

Y 20 (100.0%) Y 24 (100.0%) K 38 (100.0%) R 39 (100.0%) Y 40 (100.0%) S 72 (100.0%) Y 94 (100.0%) D 101 (100.0%) S 111 (100.0%) S 113 (100.0%) D 115 (100.0%) Y 127 (100.0%) K 129 (100.0%) Y 140 (100.0%) D 147 (100.0%) R 152 (100.0%) R 159 (100.0%) H 160 (100.0%) S 161 (100.0%) Y 162 (100.0%) H 166 (100.0%) N 168 (100.0%) S 169 (100.0%) D 180 (100.0%) S 182 (100.0%) K 186 (100.0%) T 208 (100.0%) D 209 (100.0%) S 210 (100.0%) R 211 (100.0%) T 212 (100.0%) N 269 (100.0%) R 275 (100.0%) H 280 (100.0%) Y 282 (100.0%) R 293 (100.0%) N 302 (100.0%) Y 312 (100.0%) D 314 (100.0%) R 318 (100.0%) Q 319 (100.0%) Q 334 (100.0%) H 344 (100.0%) E 358 (100.0%) Y 360 (100.0%) N 373 (100.0%) Y 374 (100.0%)

Seeds in cluster:

protein_accession order family genus species serotype Enterobacterial common antigen Wzy

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count) family (count) genus (count)
Lactobacillales (7) Streptococcaceae (7) Streptococcus (7)

[top](#)

Cluster 111

Total number of members in cluster: 7

Average length of proteins in cluster: 418.7

Conserved (non-aliphatic) residues:

Q 21 (100.0%) Y 32 (100.0%) S 35 (100.0%) N 147 (100.0%) T 168 (100.0%) R 174 (100.0%) E 178 (100.0%) S 184 (100.0%) K 219 (100.0%) R 220 (100.0%) T 221 (100.0%) S 299 (100.0%) R 303 (100.0%) N 318 (100.0%) N 326 (100.0%) D 351 (100.0%) N 352 (100.0%) Y 354 (100.0%) D 360 (100.0%) D 414 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
CAI34099.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	31	0
CAI34498.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	41F	0
CAI34475.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	41A	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

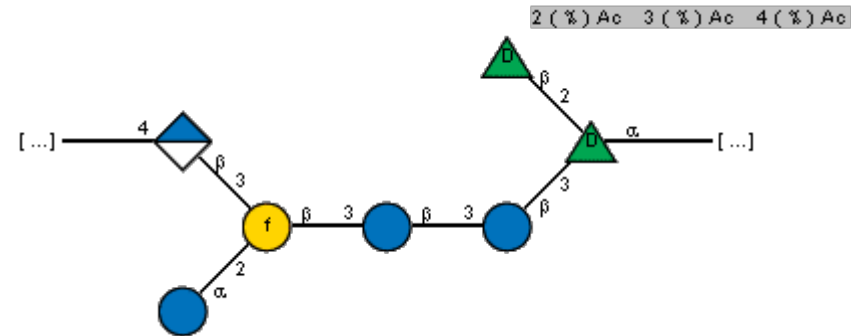
Sugars in cluster:

CAI34099.1 Streptococcus pneumoniae 31:



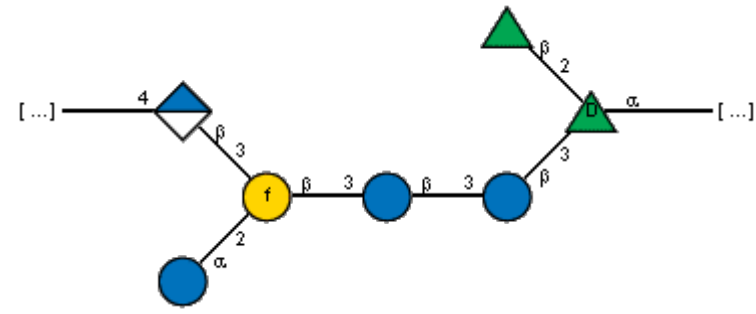
CSDB record ID: 7087

CAI34498.1 Streptococcus pneumoniae 41F:



CSDB record ID: 25001

CAI34475.1 Streptococcus pneumoniae 41A:



CSDB record ID: 25002

Sugars for blast hits:

Alphafold models:

[CAI34475.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Lactobacillales (7)	Streptococcaceae (6)	Streptococcus (6)
	Lactobacillaceae (1)	Lactobacillus (1)

[top](#)

Cluster 10

Total number of members in cluster: 7

Average length of proteins in cluster: 376.9

Conserved (non-aliphatic) residues:

Y 44 (100.0%) D 49 (100.0%) Y 53 (100.0%) R 131 (100.0%) Q 132 (100.0%) H 165 (100.0%) S 167 (100.0%) Y 232 (100.0%) R 248 (100.0%) Y 293 (100.0%) E 294 (100.0%) R 306 (100.0%) Y 342 (100.0%) Y 361 (100.0%) Y 364 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
AAM27879.1	Pseudomonadales	Pseudomonadaceae	Pseudomonas	Pseudomonas aeruginosa	O9	0

[MSA fasta](#)

[Malign view](#)

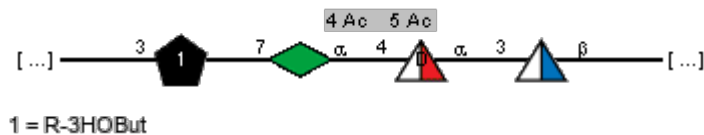
[Fasta of members](#)

[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

AAM27879.1 *Pseudomonas aeruginosa* O9:

CSDB record ID: 24037

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Pseudomonadales (5)	Pseudomonadaceae (5)	Pseudomonas (5)
nan (1)	nan (1)	Wohlfahrtiimonas (1)
Enterobacterales (1)	Enterobacteriaceae (1)	Pseudocitrobacter (1)

[top](#)

Cluster 16

Total number of members in cluster: 6

Average length of proteins in cluster: 387.5

Conserved (non-aliphatic) residues:

K 34 (100.0%) T 42 (100.0%) S 56 (100.0%) S 70 (100.0%) K 106 (100.0%) E 109 (100.0%) N 116 (100.0%) S 127 (100.0%) K 132 (100.0%) R 134 (100.0%) S 140 (100.0%) H 148 (100.0%) Y 150 (100.0%) Y 157 (100.0%) N 166 (100.0%) E 167 (100.0%) N 168 (100.0%) N 171 (100.0%) S 178 (100.0%) R 179 (100.0%) N 180 (100.0%) S 183 (100.0%) Y 198 (100.0%) K 203 (100.0%) Y 205 (100.0%) S 207 (100.0%) S 216 (100.0%) R 222 (100.0%) S 223 (100.0%) S 228 (100.0%) Y 237 (100.0%) K 239 (100.0%) K 242 (100.0%) K 247 (100.0%) T 284 (100.0%) N 285 (100.0%) S 288 (100.0%) D 291 (100.0%) T 292 (100.0%) R 294 (100.0%) Y 301 (100.0%) N 304 (100.0%) D 306 (100.0%) S 319 (100.0%) N 328 (100.0%) H 330 (100.0%) N 331 (100.0%) S 332 (100.0%) Q 337 (100.0%) R 339 (100.0%) Y 353 (100.0%) R 375 (100.0%) D 379 (100.0%) D 388 (100.0%) N 401 (100.0%) N 402 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
BAQ01894.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O171	0

MSA fasta

Malign view

Fasta of members

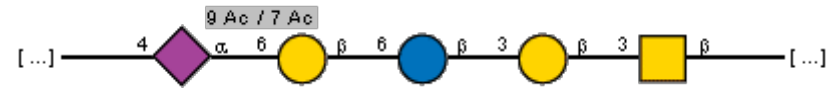
Logoplot

Phylogenetic tree

[Hits in cluster](#)

Sugars in cluster:

BAQ01894.1 Escherichia coli O171:



CSDB record ID: 1913

Sugars for blast hits:

Alphafold models:

[BAQ01894.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (6)	Enterobacteriaceae (4)	Escherichia (4)
	Hafniaceae (2)	Hafnia (2)

[top](#)

Cluster 156

Total number of members in cluster: 6

Average length of proteins in cluster: 386.3

Conserved (non-aliphatic) residues:

Y 10 (100.0%) Y 12 (100.0%) D 32 (100.0%) R 34 (100.0%) Y 36 (100.0%) Y 38 (100.0%) K 64 (100.0%) T 95 (100.0%) K 121 (100.0%) N 123 (100.0%) Q 155 (100.0%) S 157 (100.0%) Q 159 (100.0%) Y 205 (100.0%) R 208 (100.0%) R 212 (100.0%) R 228 (100.0%) S 230 (100.0%) S 233 (100.0%) S 234 (100.0%) S 250 (100.0%) S 272 (100.0%) S 274 (100.0%) N 278 (100.0%) Y 288 (100.0%) S 331 (100.0%) N 354 (100.0%) R 377 (100.0%) Y 386 (100.0%) S 391 (100.0%) D 393 (100.0%) E 396 (100.0%) S 398 (100.0%) Q 402 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
AAZ20761.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O66	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

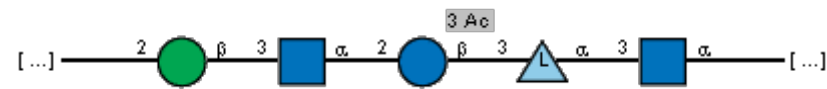
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

AAZ20761.1 Escherichia coli O66:



CSDB record ID: 1573

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (4)	Enterobacteriaceae (4)	Enterobacter (3)
		Escherichia (1)
Aeromonadales (1)	Aeromonadaceae (1)	Aeromonas (1)
Vibrionales (1)	Vibrionaceae (1)	Photobacterium (1)

[top](#)

Cluster 142

Total number of members in cluster: 6

Average length of proteins in cluster: 469.2

Conserved (non-aliphatic) residues:

E 31 (100.0%) S 70 (100.0%) Y 73 (100.0%) Y 76 (100.0%) Y 82 (100.0%) Y 83 (100.0%) K 92 (100.0%) K 132 (100.0%) S 142 (100.0%) Y 168 (100.0%) Q 188 (100.0%) H 192 (100.0%) Y 204 (100.0%) Y 207 (100.0%) Y 208 (100.0%) S 243 (100.0%) R 246 (100.0%) T 248 (100.0%) R 269 (100.0%) Y 287 (100.0%) R 290 (100.0%) S 293 (100.0%) N 294 (100.0%) D 301 (100.0%) N 318 (100.0%) D 321 (100.0%) Q 323 (100.0%) Q 324 (100.0%) T 331 (100.0%) Y 343 (100.0%) D 345 (100.0%) N 349 (100.0%) S 361 (100.0%) Y 370 (100.0%) S 375 (100.0%) T 379 (100.0%) E 385 (100.0%) Y 387 (100.0%) N 389 (100.0%) Y 424 (100.0%) S 425 (100.0%) Y 435 (100.0%) K 437 (100.0%) D 439 (100.0%) S 440 (100.0%) T 441 (100.0%) N 445 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
AHB32357.1	Moraxellales	Moraxellaceae	Acinetobacter	Acinetobacter baumannii	O27	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Moraxellales (4)	Moraxellaceae (4)	Acinetobacter (4)
Alteromonadales (1)	Pseudoalteromonadaceae (1)	Pseudoalteromonas (1)
Aeromonadales (1)	Aeromonadaceae (1)	Aeromonas (1)

[top](#)

Cluster 136

Total number of members in cluster: 6

Average length of proteins in cluster: 406.5

Conserved (non-aliphatic) residues:

K 7 (100.0%) K 8 (100.0%) Y 9 (100.0%) S 13 (100.0%) Q 23 (100.0%) S 26 (100.0%) H 32 (100.0%) E 38 (100.0%) T 47 (100.0%) S 56 (100.0%) D 57 (100.0%) S 60 (100.0%) S 61 (100.0%) K 68 (100.0%) N 82 (100.0%) S 86 (100.0%) Y 124 (100.0%) Y 126 (100.0%) R 128 (100.0%) N 136 (100.0%) E 142 (100.0%) S 145 (100.0%) K 146 (100.0%) S 174 (100.0%) Y 175 (100.0%) R 178 (100.0%) Y 192 (100.0%) Y 212 (100.0%) N 215 (100.0%) Q 216 (100.0%) S 219 (100.0%) Q 220 (100.0%) N 223 (100.0%) Y 224 (100.0%) D 230 (100.0%) S 235 (100.0%) E 241 (100.0%) Y 246 (100.0%) K 250 (100.0%) D 251 (100.0%) T 253 (100.0%) K 255 (100.0%) S 257 (100.0%) S 261 (100.0%) K 266 (100.0%) S 270 (100.0%) R 314 (100.0%) R 335 (100.0%) N 339 (100.0%) Q 346 (100.0%) T 351 (100.0%) E 354 (100.0%) N 358 (100.0%) S 361 (100.0%) Y 393 (100.0%) S 396 (100.0%) Y 399 (100.0%) K 406 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
ABI34565.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O22	0

[MSA fasta](#)

[Malign view](#)

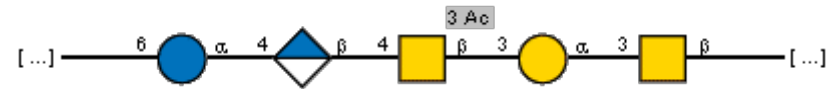
[Fasta of members](#)

[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:



CSDB record ID: 1530

Sugars for blast hits:

AlphaFold models:

[ABI34565.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (6)	Enterobacteriaceae (4)	Escherichia (3)
		Enterobacter (1)
	Hafniaceae (2)	Hafnia (2)

[top](#)

Cluster 118

Total number of members in cluster: 6

Average length of proteins in cluster: 388.5

Conserved (non-aliphatic) residues:

K 10 (100.0%) E 19 (100.0%) Y 25 (100.0%) E 31 (100.0%) D 35 (100.0%) Y 36 (100.0%) K 79 (100.0%) N 87 (100.0%) Y 97 (100.0%) T 104 (100.0%) K 108 (100.0%) D 123 (100.0%) K 124 (100.0%) K 134 (100.0%) N 136 (100.0%) Y 142 (100.0%) K 149 (100.0%) Y 153 (100.0%) Y 154 (100.0%) E 164 (100.0%) R 167 (100.0%) E 180 (100.0%) N 205 (100.0%) Y 208 (100.0%) N 209 (100.0%) K 211 (100.0%) R 215 (100.0%) Y 220 (100.0%) Y 222 (100.0%) R 235 (100.0%) S 237 (100.0%) S 240 (100.0%) N 241 (100.0%) E 267 (100.0%) E 270 (100.0%) T 273 (100.0%) S 277 (100.0%) E 283 (100.0%) K 284 (100.0%) E 287 (100.0%) K 290 (100.0%) S 302 (100.0%) S 307 (100.0%) S 329 (100.0%) Q 346 (100.0%) Y 359 (100.0%) Q 360 (100.0%) N 368 (100.0%) Y 369 (100.0%) Y 376 (100.0%) K 389 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
AAT28922.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O172	0
AAR24270.1	Enterobacterales	Enterobacteriaceae	Shigella	Shigella boydii	13	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

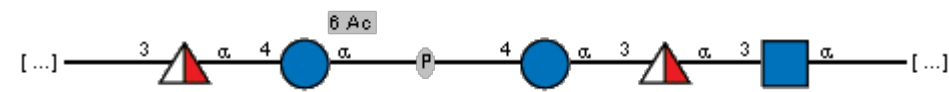
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

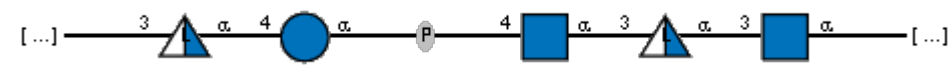
Sugars in cluster:

AAT28922.1 Escherichia coli O172:



CSDB record ID: 1914

AAR24270.1 Shigella boydii 13:



CSDB record ID: 1405

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (6)	Enterobacteriaceae (4)	Escherichia (3)
		Shigella (1)
	Morganellaceae (2)	Morganella (1)
		Proteus (1)

[top](#)

Cluster 106

Total number of members in cluster: 6

Average length of proteins in cluster: 435.3

Conserved (non-aliphatic) residues:

Y 63 (100.0%) Y 70 (100.0%) Q 75 (100.0%) S 78 (100.0%) E 83 (100.0%) E 91 (100.0%) N 140 (100.0%) Y 161 (100.0%) N 171 (100.0%) R 172 (100.0%) Y 175 (100.0%) Y 202 (100.0%) K 208 (100.0%) E 227 (100.0%) K 228 (100.0%) Y 237 (100.0%) Y 243 (100.0%) S 270 (100.0%) N 274 (100.0%) Y 275 (100.0%) E 279 (100.0%) R 289 (100.0%) Q 293 (100.0%) Q 295 (100.0%) Y 299 (100.0%) N 302 (100.0%) S 336 (100.0%) Y 345 (100.0%) T 353 (100.0%) S 354 (100.0%) Y 363 (100.0%) S 389 (100.0%) S 401 (100.0%) K 424 (100.0%) Y 428 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
ADN43883.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O165	0

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
ACD37072.1	Enterobacterales	Enterobacteriaceae	Shigella	Shigella boydii	7	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

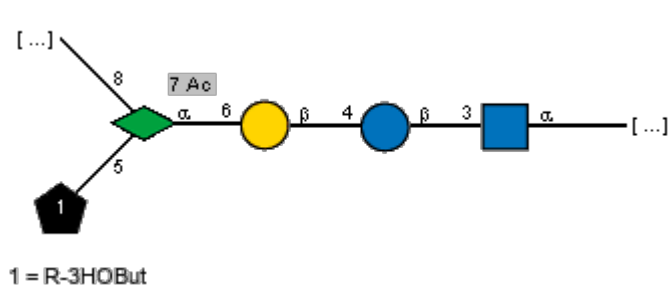
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

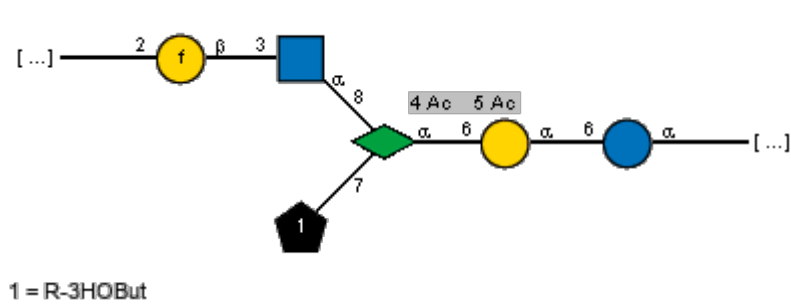
Sugars in cluster:

ADN43883.1 Escherichia coli O165:



CSDB record ID: 1907

ACD37072.1 Shigella boydii 7:



CSDB record ID: 3984

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (6)	Enterobacteriaceae (6)	Escherichia (5)
		Shigella (1)

Cluster 103

Total number of members in cluster: 6

Average length of proteins in cluster: 449.0

Conserved (non-aliphatic) residues:

R 7 (100.0%) Y 8 (100.0%) Y 21 (100.0%) H 29 (100.0%) K 54 (100.0%) N 69 (100.0%) E 81 (100.0%) H 121 (100.0%) R 156 (100.0%) K 162 (100.0%) Y 201 (100.0%) Q 204 (100.0%) T 218 (100.0%) S 229 (100.0%) E 236 (100.0%) R 237 (100.0%) H 239 (100.0%) K 242 (100.0%) Y 271 (100.0%) N 278 (100.0%) S 280 (100.0%) S 282 (100.0%) K 340 (100.0%) R 354 (100.0%) Y 362 (100.0%) Y 366 (100.0%) Y 372 (100.0%) S 375 (100.0%) R 378 (100.0%) Q 396 (100.0%) D 448 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
ADI59429.1		Enterobacterales	Yersiniaceae	Yersinia pseudotuberculosis	O:1c	0
ADI59445.1		Enterobacterales	Yersiniaceae	Yersinia pseudotuberculosis	O:2b	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

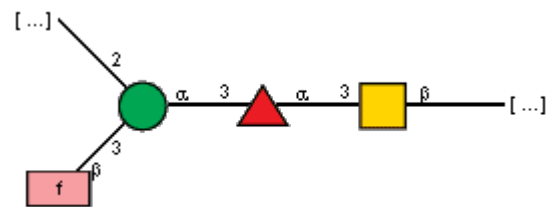
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

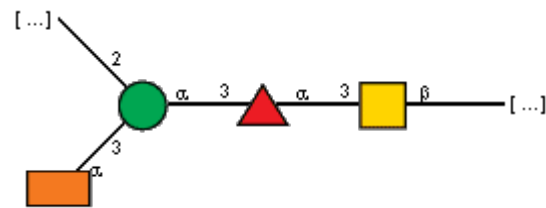
Sugars in cluster:

ADI59429.1 Yersinia pseudotuberculosis O:1c:



CSDB record ID: 12131

ADI59445.1 Yersinia pseudotuberculosis O:2b:



CSDB record ID: 12132

Sugars for blast hits:

Alphafold models:

[ADI59429.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (4)	Yersiniaceae (4)	Yersinia (4)
Nostocales (1)	Aphanizomenonaceae (1)	Aphanizomenon (1)
Oceanospirillales (1)	Endozoicomonadaceae (1)	Endozoicomonas (1)

[top](#)

Cluster 74

Total number of members in cluster: 5

Average length of proteins in cluster: 342.2

Conserved (non-aliphatic) residues:

Y 2 (100.0%) K 22 (100.0%) Y 23 (100.0%) S 38 (100.0%) D 45 (100.0%) D 47 (100.0%) Y 48 (100.0%) N 50 (100.0%) Y 51 (100.0%) Y 54 (100.0%) S 60 (100.0%) S 64 (100.0%) R 66 (100.0%) D 72 (100.0%) N 76 (100.0%) T 86 (100.0%) Y 92 (100.0%) K 99 (100.0%) K 105 (100.0%) Y 117 (100.0%) Y 123 (100.0%) H 125 (100.0%) D 126 (100.0%) T 128 (100.0%) Q 129 (100.0%) R 131 (100.0%) Y 144 (100.0%) Y 145 (100.0%) Y 147 (100.0%) K 152 (100.0%) S 162 (100.0%) H 166 (100.0%) S 168 (100.0%) S 194 (100.0%) S 216 (100.0%) D 218 (100.0%) Y 222 (100.0%) Y 223 (100.0%) D 228 (100.0%) Q 230 (100.0%) K 233 (100.0%) N 242 (100.0%) K 268 (100.0%) S 273 (100.0%) Q 274 (100.0%) R 289 (100.0%) S 291 (100.0%) Q 292 (100.0%) S 297 (100.0%) S 306 (100.0%) Y 320 (100.0%) S 321 (100.0%) Y 338 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
ACA24829.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O105	0
AAS98031.1	Enterobacterales	Enterobacteriaceae	Shigella	Shigella boydii	11	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

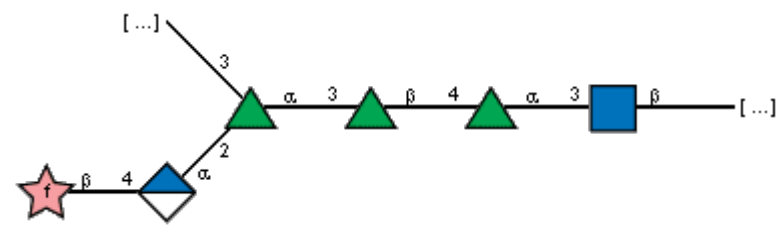
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

ACA24829.1 Escherichia coli O105, AAS98031.1 Shigella boydii 11:



CSDB record ID: 1844

Sugars for blast hits:

Alphafold models:

[AAS98031.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (5)	Enterobacteriaceae (4)	Escherichia (3)
		Shigella (1)
	Hafniaceae (1)	Hafnia (1)

[top](#)

Cluster 64

Total number of members in cluster: 5

Average length of proteins in cluster: 415.8

Conserved (non-aliphatic) residues:

N 105 (100.0%) E 109 (100.0%) S 113 (100.0%) R 116 (100.0%) Y 120 (100.0%) N 171 (100.0%) R 175 (100.0%) S 232 (100.0%) R 233 (100.0%) K 256 (100.0%) N 277 (100.0%) T 278 (100.0%) R 283 (100.0%) D 296 (100.0%) S 298 (100.0%) T 299 (100.0%) R 302 (100.0%) N 328 (100.0%) H 343 (100.0%) N 344 (100.0%) E 352 (100.0%) N 418 (100.0%) Y 421 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
BAQ01702.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O136	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

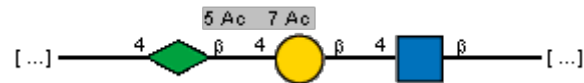
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

BAQ01702.1 Escherichia coli O136:



CSDB record ID: 1878

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (2)	Enterobacteriaceae (2)	Escherichia (1)
		nan (1)
Vibrionales (1)	Vibrionaceae (1)	Vibrio (1)
Deferribacterales (1)	Deferribacteraceae (1)	Geovibrio (1)
Flavobacteriales (1)	Flavobacteriaceae (1)	Cellulophaga (1)

[top](#)

Cluster 202

Total number of members in cluster: 5

Average length of proteins in cluster: 355.2

Conserved (non-aliphatic) residues:

S 9 (100.0%) K 49 (100.0%) D 60 (100.0%) E 61 (100.0%) Y 64 (100.0%) N 66 (100.0%) Y 77 (100.0%) N 94 (100.0%) Y 135 (100.0%) K 142 (100.0%) E 143 (100.0%) S 146 (100.0%) R 176 (100.0%) E 178 (100.0%) K 195 (100.0%) N 196 (100.0%) Y 201 (100.0%) K 224 (100.0%) S 229 (100.0%) R 231 (100.0%) D 240 (100.0%) S 257 (100.0%) N 267 (100.0%) S 270 (100.0%) N 289 (100.0%) T 323 (100.0%) H 324 (100.0%) S 325 (100.0%) Y 327 (100.0%) R 328 (100.0%) Y 329 (100.0%) N 331 (100.0%) N 359 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
ADN43838.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O115	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

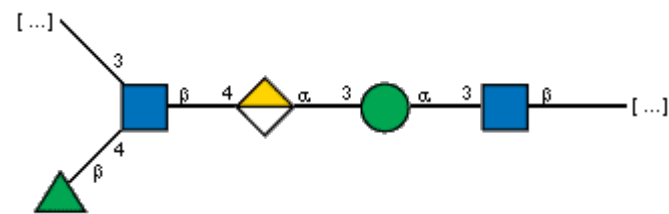
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

ADN43838.1 Escherichia coli O115:



CSDB record ID: 1855

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (5)	Enterobacteriaceae (3)	Escherichia (3)
	Erwiniaceae (1)	Erwinia (1)
	Morganellaceae (1)	Providencia (1)

[top](#)

Cluster 137

Total number of members in cluster: 5

Average length of proteins in cluster: 324.4

Conserved (non-aliphatic) residues:

R 133 (100.0%) Q 134 (100.0%) H 165 (100.0%) S 166 (100.0%) Y 211 (100.0%) R 215 (100.0%) Q 216 (100.0%) Y 220 (100.0%) Y 243 (100.0%) Y 270 (100.0%) R 280 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
AHB32614.2	Moraxellales	Moraxellaceae	Acinetobacter	Acinetobacter baumannii	O20	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count) family (count) genus (count)

Moraxellales (5) Moraxellaceae (5) Acinetobacter (4)

Psychrobacter (1)

[top](#)

Cluster 100

Total number of members in cluster: 5

Average length of proteins in cluster: 386.4

Conserved (non-aliphatic) residues:

N 95 (100.0%) S 121 (100.0%) Q 124 (100.0%) S 170 (100.0%) Q 173 (100.0%) R 181 (100.0%) N 188 (100.0%) Q 190 (100.0%) S 209 (100.0%) T 232 (100.0%) S 234 (100.0%) R 303 (100.0%) S 309 (100.0%) N 333 (100.0%) S 341 (100.0%) Y 342 (100.0%) Q 378 (100.0%) S 381 (100.0%) Y 382 (100.0%) Y 383 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
WP_074526664.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O188	0
ABD19779.1	Enterobacterales	Enterobacteriaceae	Shigella	Shigella boydii	16	0

MSA fasta

Malign view

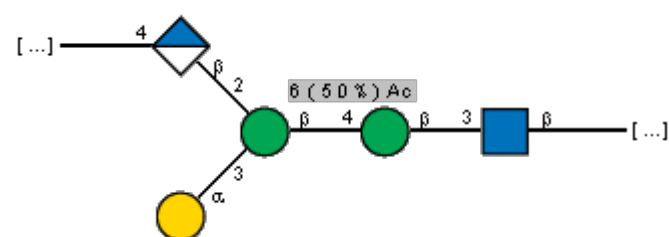
Fasta of members

Logoplot

Phylogenetic tree

Hits in cluster

Sugars in cluster:

ABD19779.1 *Shigella boydii* 16:

Sugars for blast hits:

Alphafold models:

[WP_074526664.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (3)	Enterobacteriaceae (3)	Escherichia (2)
		Shigella (1)
Vibrionales (2)	Vibrionaceae (2)	Aliivibrio (1)
		Vibrio (1)

[top](#)

Cluster 92

Total number of members in cluster: 4

Average length of proteins in cluster: 399.5

Conserved (non-aliphatic) residues:

N 16 (100.0%) S 28 (100.0%) S 46 (100.0%) N 54 (100.0%) Y 65 (100.0%) Y 67 (100.0%) Y 71 (100.0%) N 77 (100.0%) R 78 (100.0%) E 79 (100.0%) Y 80 (100.0%) E 86 (100.0%) D 90 (100.0%) D 91 (100.0%) T 92 (100.0%) R 94 (100.0%) Y 95 (100.0%) D 116 (100.0%) S 119 (100.0%) E 121 (100.0%) R 125 (100.0%) N 139 (100.0%) Q 145 (100.0%) S 161 (100.0%) R 163 (100.0%) S 177 (100.0%) Y 178 (100.0%) T 179 (100.0%) Y 182 (100.0%) T 183 (100.0%) H 186 (100.0%) R 189 (100.0%) Q 190 (100.0%) S 195 (100.0%) Y 200 (100.0%) R 209 (100.0%) S 219 (100.0%) H 220 (100.0%) E 231 (100.0%) S 242 (100.0%) Y 257 (100.0%) K 266 (100.0%) Y 270 (100.0%) N 275 (100.0%) N 277 (100.0%) Y 278 (100.0%) K 282 (100.0%) Y 286 (100.0%) K 299 (100.0%) Y 322 (100.0%) D 332 (100.0%) N 335 (100.0%) R 336 (100.0%) Y 337 (100.0%) S 342 (100.0%) R 355 (100.0%) K 370 (100.0%) D 379 (100.0%) N 381 (100.0%) Y 383 (100.0%) N 395 (100.0%) D 398 (100.0%) Y 403 (100.0%) R 406 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
BAQ00893.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O41	0

[MSA fasta](#)

[Malign view](#)

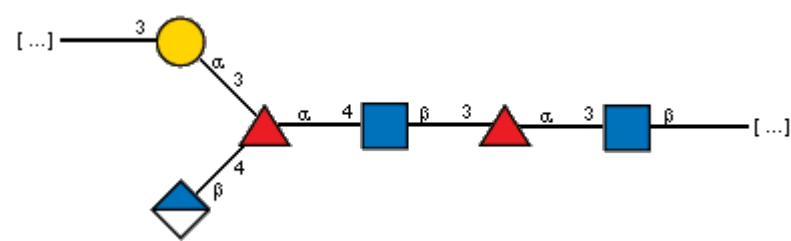
[Fasta of members](#)

[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:



CSDB record ID: 1548

Sugars for blast hits:

Alphafold models:

[BAQ00893.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (3)	Enterobacteriaceae (3)	Escherichia (3)
Aeromonadales (1)	Aeromonadaceae (1)	Aeromonas (1)

[top](#)

Cluster 87

Total number of members in cluster: 4

Average length of proteins in cluster: 429.2

Conserved (non-aliphatic) residues:

Y 28 (100.0%) N 36 (100.0%) Y 38 (100.0%) Y 41 (100.0%) D 47 (100.0%) R 71 (100.0%) S 73 (100.0%) N 161 (100.0%) S 165 (100.0%) Y 174 (100.0%) R 176 (100.0%) R 177 (100.0%) E 179 (100.0%) R 181 (100.0%) S 188 (100.0%) Y 192 (100.0%) N 199 (100.0%) Y 230 (100.0%) K 235 (100.0%) R 253 (100.0%) E 278 (100.0%) S 285 (100.0%) D 289 (100.0%) Y 290 (100.0%) R 293 (100.0%) R 294 (100.0%) E 337 (100.0%) N 346 (100.0%) N 348 (100.0%) N 350 (100.0%) Y 364 (100.0%) T 367 (100.0%) D 379 (100.0%) Y 382 (100.0%) Y 397 (100.0%) E 403 (100.0%) Q 404 (100.0%) T 408 (100.0%) S 412 (100.0%) S 413 (100.0%)

Seeds in cluster:

protein_accession order family genus species serotype Enterobacterial common antigen Wzy

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (2)	Enterobacteriaceae (2)	Plesiomonas (2)
Pseudomonadales (1)	Pseudomonadaceae (1)	Pseudomonas (1)
Burkholderiales (1)	Alcaligenaceae (1)	Corticimicrobacter (1)

[top](#)

Cluster 204

Total number of members in cluster: 4

Average length of proteins in cluster: 370.2

Conserved (non-aliphatic) residues:

S 22 (100.0%) K 27 (100.0%) S 75 (100.0%) N 79 (100.0%) D 83 (100.0%) D 109 (100.0%) T 120 (100.0%) N 128 (100.0%) N 143 (100.0%) N 145 (100.0%) S 146 (100.0%) Y 151 (100.0%) S 158 (100.0%) Y 167 (100.0%) T 189 (100.0%) S 192 (100.0%) N 193 (100.0%) S 194 (100.0%) R 195 (100.0%) S 200 (100.0%) K 220 (100.0%) K 221 (100.0%) D 253 (100.0%) K 258 (100.0%) K 262 (100.0%) R 273 (100.0%) N 283 (100.0%) R 291 (100.0%) D 300 (100.0%) H 304 (100.0%) T 306 (100.0%) S 309 (100.0%) Q 313 (100.0%) S 318 (100.0%) Y 342 (100.0%) S 352 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
AHB32386.1	Moraxellales	Moraxellaceae	Acinetobacter	Acinetobacter baumannii	O13	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

Sugars for blast hits:

Alphafold models:

[AHB32386.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Moraxellales (3)	Moraxellaceae (3)	Acinetobacter (3)
Rhodocyclales (1)	Rhodocyclaceae (1)	Aromatoleum (1)

[top](#)

Cluster 200

Total number of members in cluster: 4

Average length of proteins in cluster: 440.0

Conserved (non-aliphatic) residues:

N 2 (100.0%) N 8 (100.0%) Y 19 (100.0%) K 24 (100.0%) S 25 (100.0%) K 26 (100.0%) K 27 (100.0%) R 30 (100.0%) Y 35 (100.0%) E 44 (100.0%) S 45 (100.0%) H 46 (100.0%) T 52 (100.0%) T 53 (100.0%) S 54 (100.0%) N 56 (100.0%) T 59 (100.0%) S 60 (100.0%) E 61 (100.0%) N 65 (100.0%) E 67 (100.0%) D 69 (100.0%) Y 70 (100.0%) N 71 (100.0%) T 72 (100.0%) K 73 (100.0%) T 74 (100.0%) E 75 (100.0%) T 78 (100.0%) S 79 (100.0%) N 81 (100.0%) S 91 (100.0%) S 96 (100.0%) T 97 (100.0%) T 99 (100.0%) Y 100 (100.0%) K 101 (100.0%) S 102 (100.0%) S 103 (100.0%) S 104 (100.0%) Y 105 (100.0%) D 106 (100.0%) T 108 (100.0%) E 110 (100.0%) N 111 (100.0%) K 112 (100.0%) S 113 (100.0%) R 116 (100.0%) S 118 (100.0%) S 124 (100.0%) Y 132 (100.0%) S 141 (100.0%) S 142 (100.0%) N 143 (100.0%) Y 146 (100.0%) S 147 (100.0%) Y 149 (100.0%) N 151 (100.0%) N 153 (100.0%) K 154 (100.0%) S 156 (100.0%) Y 159 (100.0%) D 162 (100.0%) T 167 (100.0%) Y 169 (100.0%) S 170 (100.0%) S 174 (100.0%) K 176 (100.0%) N 177 (100.0%) K 178 (100.0%) K 179 (100.0%) K 180 (100.0%) Y 192 (100.0%) T 197 (100.0%) R 198 (100.0%) E 200 (100.0%) K 204 (100.0%) Y 211 (100.0%) Y 212 (100.0%) S 216 (100.0%) K 217 (100.0%) N 218 (100.0%) H 220 (100.0%) K 221 (100.0%) Y 222 (100.0%) R 224 (100.0%) K 226 (100.0%) N 227 (100.0%) S 232 (100.0%) S 241 (100.0%) Q 243 (100.0%) Y 244 (100.0%) S 245 (100.0%) S 247 (100.0%) R 249 (100.0%) D 250 (100.0%) N 251 (100.0%) E 253 (100.0%) S 256 (100.0%) N 257 (100.0%) T 260 (100.0%) T 261 (100.0%) K 264 (100.0%) Q 265 (100.0%) Q 266 (100.0%) S 269 (100.0%) N 271 (100.0%) K 278 (100.0%) D 279 (100.0%) K 280 (100.0%) N 281 (100.0%) N 282 (100.0%) S 283 (100.0%) S 286 (100.0%) E 287 (100.0%) S 288 (100.0%) S 292 (100.0%) Y 295 (100.0%) D 296 (100.0%) S 297 (100.0%) S 300 (100.0%) N 303 (100.0%) S 304 (100.0%) Q 309 (100.0%) S 310 (100.0%) N 311 (100.0%) N 313 (100.0%) S 314 (100.0%) E 316 (100.0%) E 319 (100.0%) N 320 (100.0%) S 321 (100.0%) S 323 (100.0%) S 325 (100.0%) H 326 (100.0%) K 327 (100.0%) S 329 (100.0%) Y 330 (100.0%) E 332 (100.0%) D 333 (100.0%) S 335 (100.0%) Y 337 (100.0%) Y 341 (100.0%) E 350 (100.0%) Y 352 (100.0%) Y 357 (100.0%) T 367 (100.0%) Y 368 (100.0%) S 372 (100.0%) E 375 (100.0%) K 376 (100.0%) K 379 (100.0%) K 380 (100.0%) S 381 (100.0%) N 384 (100.0%) T 392 (100.0%) K 394 (100.0%) Y 397 (100.0%) S 398 (100.0%) R 400 (100.0%) E 402 (100.0%) S 405 (100.0%) S 408 (100.0%) D 410 (100.0%) R 411 (100.0%) T 420 (100.0%) S 422 (100.0%) Y 423 (100.0%) K 424 (100.0%) T 429 (100.0%) S 430 (100.0%) N 431 (100.0%) K 432 (100.0%) K 433 (100.0%) S 435 (100.0%) K 437 (100.0%) N 438 (100.0%) E 439 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
ACH97132.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O107	0
ACH97143.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O117	0
ABE98413.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O117	0

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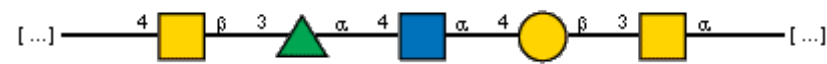
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

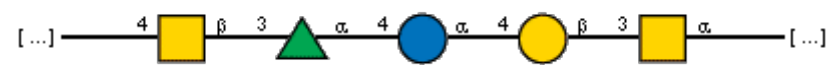
Sugars in cluster:

ACH97132.1 Escherichia coli O107:



CSDB record ID: 1846

ACH97143.1 Escherichia coli O117, ABE98413.1 Escherichia coli O117:



CSDB record ID: 1857

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (4)	Enterobacteriaceae (4)	Escherichia (4)

[top](#)

Cluster 192

Total number of members in cluster: 4

Average length of proteins in cluster: 362.8

Conserved (non-aliphatic) residues:

K 1 (100.0%) Y 6 (100.0%) N 7 (100.0%) N 11 (100.0%) S 15 (100.0%) Y 21 (100.0%) K 24 (100.0%) N 27 (100.0%) H 49 (100.0%) Y 53 (100.0%) N 56 (100.0%) K 59 (100.0%) Y 90 (100.0%) N 97 (100.0%) K 102 (100.0%) H 104 (100.0%) R 131 (100.0%) R 137 (100.0%) H 144 (100.0%) N 146 (100.0%) S 147 (100.0%) Y 153 (100.0%) T 156 (100.0%) R 167 (100.0%) K 169 (100.0%) Y 173 (100.0%) N 180 (100.0%) D 188 (100.0%) S 189 (100.0%) R 190 (100.0%) T 191 (100.0%) S 192 (100.0%) S 196 (100.0%) D 207 (100.0%) S 228 (100.0%) E 240 (100.0%) N 249 (100.0%) K 250 (100.0%) T 253 (100.0%) N 254 (100.0%) R 255 (100.0%) S 258 (100.0%) E 265 (100.0%) Y 266 (100.0%) D 289 (100.0%) S 290 (100.0%) Y 292 (100.0%) R 314 (100.0%) K 316 (100.0%) E 324 (100.0%) S 330 (100.0%) S 334 (100.0%) E 338 (100.0%) S 339 (100.0%) Y 340 (100.0%) D 353 (100.0%) R 358 (100.0%) K 359 (100.0%) E 360 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
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protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
CAI34544.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	43	0
CAI34641.1	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus pneumoniae	47A	0

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[Malign view](#)

[Fasta of members](#)

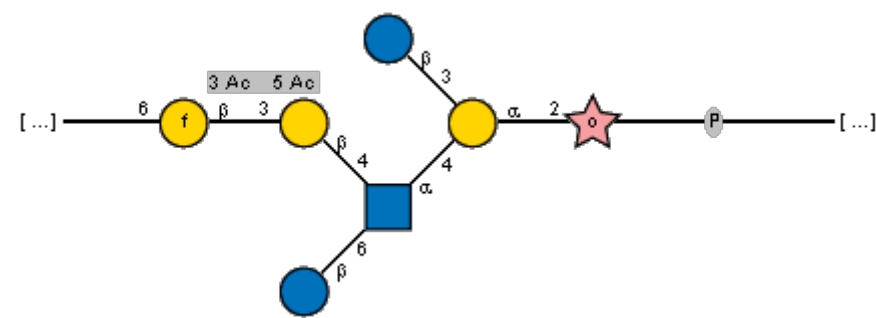
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[Hits in cluster](#)

Sugars in cluster:

CAI34641.1 Streptococcus pneumoniae 47A:



CSDB record ID: 25006

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Lactobacillales (4)	Streptococcaceae (4)	Streptococcus (4)

[top](#)

Cluster 191

Total number of members in cluster: 4

Average length of proteins in cluster: 403.5

Conserved (non-aliphatic) residues:

H 17 (100.0%) Y 26 (100.0%) K 33 (100.0%) R 37 (100.0%) K 38 (100.0%) K 39 (100.0%) T 41 (100.0%) H 42 (100.0%) T 45 (100.0%) S 52 (100.0%) S 56 (100.0%) Y 59 (100.0%) H 62 (100.0%) T 64 (100.0%) Y 68 (100.0%) E 69 (100.0%) S 71 (100.0%) Y 72 (100.0%) E 73 (100.0%) S 74 (100.0%) Y 75 (100.0%) Y 78 (100.0%) N 82 (100.0%)

S 84 (100.0%) T 92 (100.0%) D 93 (100.0%) R 97 (100.0%) R 98 (100.0%) N 99 (100.0%) K 101 (100.0%) N 102 (100.0%) Q 105 (100.0%) N 109 (100.0%) K 117 (100.0%) T 122 (100.0%) Y 126 (100.0%) Y 131 (100.0%) E 133 (100.0%) K 135 (100.0%) H 136 (100.0%) T 138 (100.0%) D 140 (100.0%) K 146 (100.0%) R 149 (100.0%) R 151 (100.0%) E 152 (100.0%) R 153 (100.0%) E 156 (100.0%) E 157 (100.0%) Q 158 (100.0%) Y 160 (100.0%) S 161 (100.0%) T 162 (100.0%) T 164 (100.0%) N 165 (100.0%) N 166 (100.0%) S 171 (100.0%) S 172 (100.0%) Y 177 (100.0%) T 179 (100.0%) S 183 (100.0%) K 185 (100.0%) K 186 (100.0%) N 188 (100.0%) Y 190 (100.0%) Y 191 (100.0%) Y 192 (100.0%) T 195 (100.0%) Y 202 (100.0%) N 203 (100.0%) T 206 (100.0%) T 208 (100.0%) R 209 (100.0%) S 216 (100.0%) Y 223 (100.0%) N 226 (100.0%) T 227 (100.0%) N 228 (100.0%) K 229 (100.0%) S 234 (100.0%) K 235 (100.0%) S 240 (100.0%) T 244 (100.0%) K 258 (100.0%) D 259 (100.0%) E 262 (100.0%) R 263 (100.0%) D 264 (100.0%) E 265 (100.0%) S 266 (100.0%) N 270 (100.0%) N 272 (100.0%) K 273 (100.0%) D 276 (100.0%) N 277 (100.0%) Y 278 (100.0%) S 280 (100.0%) Y 281 (100.0%) T 282 (100.0%) Q 284 (100.0%) D 290 (100.0%) Y 292 (100.0%) R 296 (100.0%) E 297 (100.0%) K 298 (100.0%) T 300 (100.0%) N 302 (100.0%) D 304 (100.0%) S 307 (100.0%) S 309 (100.0%) E 311 (100.0%) N 314 (100.0%) K 315 (100.0%) T 317 (100.0%) S 319 (100.0%) N 320 (100.0%) S 326 (100.0%) K 327 (100.0%) S 329 (100.0%) E 330 (100.0%) S 332 (100.0%) H 333 (100.0%) K 336 (100.0%) K 338 (100.0%) D 339 (100.0%) N 341 (100.0%) T 344 (100.0%) Y 346 (100.0%) Y 350 (100.0%) Y 353 (100.0%)

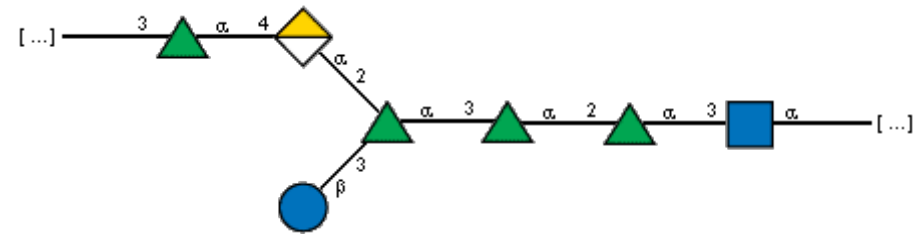
Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
AAZ85718.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O139	0

- [MSA fasta](#)
- [Malign view](#)
- [Fasta of members](#)
- [Logoplot](#)
- [Phylogenetic tree](#)
- [Hits in cluster](#)

Sugars in cluster:

AAZ85718.1 Escherichia coli O139:



CSDB record ID: 1881

Sugars for blast hits:

Alphafold models:

[AAZ85718.1](#)

Taxonomy:

order (count) family (count) genus (count)

Enterobacterales (4) Enterobacteriaceae (4) Escherichia (4)

[top](#)

Cluster 184

Total number of members in cluster: 4

Average length of proteins in cluster: 333.2

Conserved (non-aliphatic) residues:

N 7 (100.0%) S 20 (100.0%) K 26 (100.0%) D 28 (100.0%) Y 29 (100.0%) D 33 (100.0%) Y 37 (100.0%) T 38 (100.0%) Y 41 (100.0%) D 42 (100.0%) T 44 (100.0%) Y 45 (100.0%) E 47 (100.0%) E 52 (100.0%) Y 57 (100.0%) T 59 (100.0%) H 63 (100.0%) Y 64 (100.0%) Y 69 (100.0%) K 84 (100.0%) R 89 (100.0%) K 90 (100.0%) S 95 (100.0%) Y 96 (100.0%) Y 104 (100.0%) Y 108 (100.0%) H 112 (100.0%) T 115 (100.0%) Q 116 (100.0%) R 118 (100.0%) Y 127 (100.0%) Y 131 (100.0%) Y 133 (100.0%) H 153 (100.0%) Y 154 (100.0%) S 155 (100.0%) Y 168 (100.0%) R 169 (100.0%) Y 188 (100.0%) Y 195 (100.0%) N 198 (100.0%) E 199 (100.0%) K 200 (100.0%) Y 204 (100.0%) Y 206 (100.0%) S 207 (100.0%) S 209 (100.0%) S 211 (100.0%) N 222 (100.0%) N 224 (100.0%) S 239 (100.0%) R 240 (100.0%) K 243 (100.0%) E 248 (100.0%) K 253 (100.0%) Y 254 (100.0%) Q 256 (100.0%) S 258 (100.0%) Y 277 (100.0%) R 278 (100.0%) E 281 (100.0%) R 284 (100.0%) Y 287 (100.0%) K 299 (100.0%) N 300 (100.0%) S 315 (100.0%) T 322 (100.0%) R 324 (100.0%) S 327 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
ADC54929.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O1	0

[MSA fasta](#)

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[Fasta of members](#)

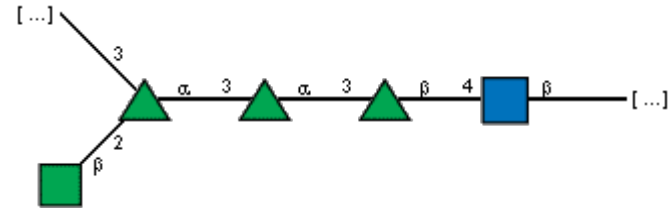
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[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

ADC54929.1 Escherichia coli O1:



CSDB record ID: 7222

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (4)	Enterobacteriaceae (4)	Escherichia (3)
		Citrobacter (1)

[top](#)

Cluster 159

Total number of members in cluster: 4

Average length of proteins in cluster: 319.8

Conserved (non-aliphatic) residues:

Y 33 (100.0%) S 35 (100.0%) D 44 (100.0%) T 45 (100.0%) Y 48 (100.0%) N 51 (100.0%) D 58 (100.0%) Y 62 (100.0%) E 65 (100.0%) N 107 (100.0%) N 125 (100.0%) R 131 (100.0%) Q 132 (100.0%) Y 133 (100.0%) K 151 (100.0%) S 156 (100.0%) S 163 (100.0%) S 166 (100.0%) H 167 (100.0%) R 231 (100.0%) K 232 (100.0%) Y 236 (100.0%) S 262 (100.0%) S 288 (100.0%) N 297 (100.0%) R 303 (100.0%) S 312 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
AFW04735.1	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	O63	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (2)	Enterobacteriaceae (2)	Salmonella (2)
Aeromonadales (2)	Aeromonadaceae (2)	Tolumonas (1)
		Aeromonas (1)

[top](#)

Cluster 131

Total number of members in cluster: 4

Average length of proteins in cluster: 380.0

Conserved (non-aliphatic) residues:

T 1 (100.0%) Y 2 (100.0%) T 4 (100.0%) K 16 (100.0%) R 17 (100.0%) T 19 (100.0%) S 21 (100.0%) Q 22 (100.0%) S 23 (100.0%) K 24 (100.0%) K 25 (100.0%) N 26 (100.0%) N 32 (100.0%) Y 42 (100.0%) N 45 (100.0%) E 46 (100.0%) Q 47 (100.0%) Y 48 (100.0%) S 53 (100.0%) T 55 (100.0%) T 56 (100.0%) S 68 (100.0%) T 70 (100.0%) Y 71 (100.0%) R 76 (100.0%) S 77 (100.0%) R 79 (100.0%) S 83 (100.0%) T 86 (100.0%) E 90 (100.0%) S 91 (100.0%) K 92 (100.0%) Y 93 (100.0%) Y 95 (100.0%) N 102 (100.0%) S 105 (100.0%) Y 114 (100.0%) N 115 (100.0%) N 116 (100.0%) H 117 (100.0%) S 119 (100.0%) K 121 (100.0%) R 124 (100.0%) E 125 (100.0%) D 129 (100.0%) S 131 (100.0%) S 133 (100.0%) S 140 (100.0%) S 144 (100.0%) Y 149 (100.0%) R 152 (100.0%) H 153 (100.0%) E 154 (100.0%) N 155 (100.0%) K 156 (100.0%) K 157 (100.0%) N 158 (100.0%) Y 159 (100.0%) Y 161 (100.0%) T 164 (100.0%) S 167 (100.0%) S 174 (100.0%) T 175 (100.0%) S 176 (100.0%) K 177 (100.0%) Y 186 (100.0%) N 191 (100.0%) S 192 (100.0%) Y 193 (100.0%) S 195 (100.0%) K 196 (100.0%) K 197 (100.0%) K 198 (100.0%) Y 202 (100.0%) S 213 (100.0%) S 214 (100.0%) K 219 (100.0%) S 221 (100.0%) S 222 (100.0%) D 223 (100.0%) E 225 (100.0%) K 227 (100.0%) S 230 (100.0%) D 234 (100.0%) T 235 (100.0%) R 237 (100.0%) Y 239 (100.0%) S 242 (100.0%) N 248 (100.0%) Y 250 (100.0%) E 252 (100.0%) K 253 (100.0%) N 254 (100.0%) T 256 (100.0%) E 259 (100.0%) N 260 (100.0%) Y 264 (100.0%) K 267 (100.0%) E 268 (100.0%) T 272 (100.0%) T 273 (100.0%) K 274 (100.0%) K 278 (100.0%) T 279 (100.0%) D 280 (100.0%) N 286 (100.0%) D 291 (100.0%) T 292 (100.0%) N 293 (100.0%) Y 295 (100.0%) T 296 (100.0%) Y 302 (100.0%) Q 303 (100.0%) S 304 (100.0%) Y 308 (100.0%) Y 320 (100.0%) Y 321 (100.0%) S 326 (100.0%) R 328 (100.0%) Q 329 (100.0%) N 330 (100.0%) Y 336 (100.0%) Q 337 (100.0%) T 338 (100.0%) Q 350 (100.0%) E 351 (100.0%) H 352 (100.0%) Y 353 (100.0%) S 356 (100.0%) K 358 (100.0%) H 360 (100.0%) Y 363 (100.0%) R 373 (100.0%) K 374 (100.0%) E 377 (100.0%) Y 378 (100.0%) E 379 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
ABA42232.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O148	0
WP_000220864.1	Enterobacterales	Enterobacteriaceae	Shigella	Shigella dysenteriae	O148	0

[MSA fasta](#)

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[Fasta of members](#)

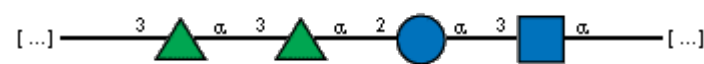
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

ABA42232.1 Escherichia coli O148:



Sugars for blast hits:

Alphafold models:

[ABA42232.1](#)

[WP_000220864.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (4)	Enterobacteriaceae (4)	Escherichia (3)
		Shigella (1)

[top](#)

Cluster 108

Total number of members in cluster: 4

Average length of proteins in cluster: 402.8

Conserved (non-aliphatic) residues:

K 3 (100.0%) Y 114 (100.0%) K 118 (100.0%) S 122 (100.0%) Y 125 (100.0%) R 134 (100.0%) Y 151 (100.0%) S 154 (100.0%) D 194 (100.0%) R 200 (100.0%) N 225 (100.0%) N 240 (100.0%) R 243 (100.0%) R 246 (100.0%) S 255 (100.0%) Y 278 (100.0%) Y 280 (100.0%) S 283 (100.0%) S 284 (100.0%) N 313 (100.0%) R 324 (100.0%) N 339 (100.0%) D 346 (100.0%) Y 348 (100.0%) Y 404 (100.0%) N 405 (100.0%) S 408 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
AAL27351.1	Enterobacterales	Enterobacteriaceae	Shigella	Shigella boydii	9	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

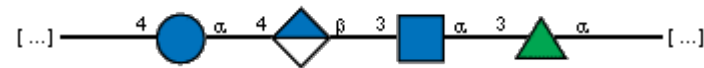
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

AAL27351.1 Shigella boydii 9:



Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (2)	Enterobacteriaceae (2)	Shigella (1)
		Escherichia (1)
Vibrionales (1)	Vibrionaceae (1)	Vibrio (1)
Chitinophagales (1)	Chitinophagaceae (1)	Chitinophaga (1)

[top](#)

Cluster 107

Total number of members in cluster: 4

Average length of proteins in cluster: 375.0

Conserved (non-aliphatic) residues:

S 25 (100.0%) S 40 (100.0%) N 42 (100.0%) Y 43 (100.0%) N 45 (100.0%) Y 47 (100.0%) D 48 (100.0%) N 51 (100.0%) Y 52 (100.0%) N 55 (100.0%) Q 57 (100.0%) Y 61 (100.0%) K 69 (100.0%) Y 70 (100.0%) Y 74 (100.0%) Y 79 (100.0%) S 82 (100.0%) Y 88 (100.0%) H 89 (100.0%) S 96 (100.0%) N 99 (100.0%) T 100 (100.0%) Y 101 (100.0%) N 110 (100.0%) N 113 (100.0%) S 123 (100.0%) Y 125 (100.0%) Y 130 (100.0%) S 131 (100.0%) E 132 (100.0%) T 133 (100.0%) R 135 (100.0%) Q 136 (100.0%) S 141 (100.0%) H 169 (100.0%) S 171 (100.0%) N 214 (100.0%) R 216 (100.0%) Y 220 (100.0%) N 232 (100.0%) Q 237 (100.0%) S 239 (100.0%) S 276 (100.0%) K 286 (100.0%) Q 290 (100.0%) Y 291 (100.0%) E 293 (100.0%) S 296 (100.0%) R 297 (100.0%) N 299 (100.0%) Y 300 (100.0%) Y 301 (100.0%) Y 309 (100.0%) N 321 (100.0%) K 322 (100.0%) Y 335 (100.0%) R 339 (100.0%) S 343 (100.0%) K 346 (100.0%) E 349 (100.0%) Y 350 (100.0%) Y 354 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
ACA24901.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O87	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

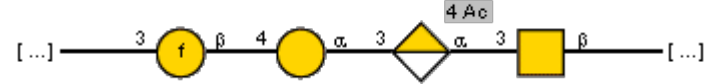
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

ACA24901.1 Escherichia coli O87:



CSDB record ID: 1594

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (4)	Enterobacteriaceae (3)	Escherichia (3)
	Budviciaceae (1)	Budvicia (1)

[top](#)

Cluster 90

Total number of members in cluster: 3

Average length of proteins in cluster: 417.0

Conserved (non-aliphatic) residues:

S 126 (100.0%) N 134 (100.0%) R 141 (100.0%) Y 142 (100.0%) Q 153 (100.0%) Y 160 (100.0%) K 177 (100.0%) R 179 (100.0%) S 185 (100.0%) T 195 (100.0%) K 199 (100.0%) S 249 (100.0%) R 253 (100.0%) K 268 (100.0%) H 276 (100.0%) D 281 (100.0%) T 301 (100.0%) N 336 (100.0%) T 339 (100.0%) R 342 (100.0%) E 346 (100.0%) D 347 (100.0%) Y 391 (100.0%) S 395 (100.0%) S 399 (100.0%) Y 403 (100.0%) S 405 (100.0%)

Seeds in cluster:

protein_accession order family genus species serotype Enterobacterial common antigen Wzy

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
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order (count)	family (count)	genus (count)
Flavobacteriales (1)	nan (1)	nan (1)
Bacillales (1)	nan (1)	Exiguobacterium (1)
Bacteroidales (1)	Bacteroidaceae (1)	Bacteroides (1)

[top](#)

Cluster 203

Total number of members in cluster: 3

Average length of proteins in cluster: 423.0

Conserved (non-aliphatic) residues:

Y 2 (100.0%) T 4 (100.0%) S 16 (100.0%) K 19 (100.0%) K 20 (100.0%) S 21 (100.0%) N 22 (100.0%) S 25 (100.0%) S 27 (100.0%) T 36 (100.0%) T 37 (100.0%) S 41 (100.0%) S 46 (100.0%) Y 49 (100.0%) T 50 (100.0%) S 52 (100.0%) Y 54 (100.0%) S 55 (100.0%) Y 58 (100.0%) T 63 (100.0%) T 64 (100.0%) S 65 (100.0%) S 67 (100.0%) S 70 (100.0%) E 74 (100.0%) Q 75 (100.0%) N 77 (100.0%) K 79 (100.0%) S 80 (100.0%) K 81 (100.0%) S 83 (100.0%) N 85 (100.0%) S 88 (100.0%) N 90 (100.0%) S 92 (100.0%) Y 94 (100.0%) Y 95 (100.0%) T 101 (100.0%) D 110 (100.0%) E 111 (100.0%) N 114 (100.0%) K 115 (100.0%) N 121 (100.0%) Y 125 (100.0%) E 127 (100.0%) Y 128 (100.0%) Y 129 (100.0%) R 130 (100.0%) S 133 (100.0%) T 134 (100.0%) S 135 (100.0%) E 137 (100.0%) D 138 (100.0%) K 141 (100.0%) D 142 (100.0%) S 143 (100.0%) N 145 (100.0%) Y 146 (100.0%) R 149 (100.0%) N 150 (100.0%) D 152 (100.0%) S 159 (100.0%) Y 164 (100.0%) S 167 (100.0%) T 168 (100.0%) R 169 (100.0%) R 170 (100.0%) S 172 (100.0%) S 173 (100.0%) K 176 (100.0%) T 178 (100.0%) S 186 (100.0%) T 188 (100.0%) S 193 (100.0%) R 196 (100.0%) S 197 (100.0%) R 201 (100.0%) R 215 (100.0%) R 217 (100.0%) K 219 (100.0%) S 226 (100.0%) Y 232 (100.0%) Y 241 (100.0%) S 243 (100.0%) Y 246 (100.0%) S 247 (100.0%) S 248 (100.0%) S 250 (100.0%) E 251 (100.0%) S 252 (100.0%) Y 255 (100.0%) S 259 (100.0%) R 262 (100.0%) Y 263 (100.0%) S 265 (100.0%) Y 268 (100.0%) Y 269 (100.0%) T 270 (100.0%) D 272 (100.0%) S 273 (100.0%) Y 274 (100.0%) K 278 (100.0%) D 280 (100.0%) R 284 (100.0%) D 289 (100.0%) S 290 (100.0%) K 294 (100.0%) D 296 (100.0%) T 297 (100.0%) T 298 (100.0%) T 300 (100.0%) K 307 (100.0%) Y 312 (100.0%) N 315 (100.0%) H 316 (100.0%) E 318 (100.0%) Q 321 (100.0%) E 326 (100.0%) N 327 (100.0%) S 330 (100.0%) N 331 (100.0%) Y 333 (100.0%) T 334 (100.0%) S 341 (100.0%) N 342 (100.0%) Y 350 (100.0%) S 352 (100.0%) S 360 (100.0%) Y 362 (100.0%) K 363 (100.0%) K 366 (100.0%) S 367 (100.0%) R 369 (100.0%) Y 376 (100.0%) S 377 (100.0%) S 387 (100.0%) S 389 (100.0%) E 390 (100.0%) Y 391 (100.0%) Q 395 (100.0%) R 401 (100.0%) Y 406 (100.0%) K 411 (100.0%) S 413 (100.0%) H 415 (100.0%) K 416 (100.0%) N 417 (100.0%) K 418 (100.0%) E 420 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
BAQ01137.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O65	0

[MSA fasta](#)

[Malign view](#)

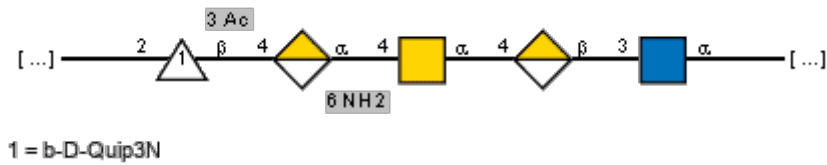
[Fasta of members](#)

[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:



CSDB record ID: 1572

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (3)	Enterobacteriaceae (3)	Escherichia (3)

[top](#)

Cluster 201

Total number of members in cluster: 3

Average length of proteins in cluster: 404.7

Conserved (non-aliphatic) residues:

S 4 (100.0%) S 20 (100.0%) R 27 (100.0%) S 29 (100.0%) T 77 (100.0%) H 91 (100.0%) S 104 (100.0%) N 143 (100.0%) N 161 (100.0%) K 181 (100.0%) N 198 (100.0%) D 199 (100.0%) K 201 (100.0%) R 223 (100.0%) D 282 (100.0%) S 286 (100.0%) R 290 (100.0%) Y 296 (100.0%) S 304 (100.0%) N 313 (100.0%) T 314 (100.0%) Y 323 (100.0%) S 328 (100.0%) S 331 (100.0%) H 333 (100.0%) N 334 (100.0%) Q 338 (100.0%) S 364 (100.0%) K 368 (100.0%) S 385 (100.0%) S 389 (100.0%) S 394 (100.0%) N 395 (100.0%) Y 396 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
ADJ19203.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O161	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

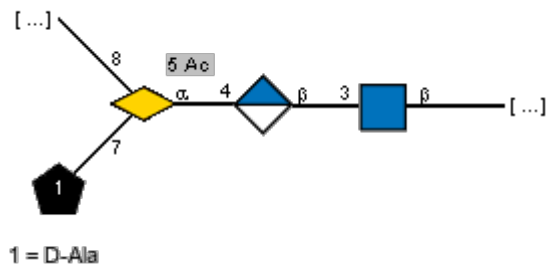
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

ADJ19203.1 Escherichia coli O161:



CSDB record ID: 1902

Sugars for blast hits:

Alphafold models:

[ADJ19203.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (2)	Enterobacteriaceae (2)	Escherichia (2)
Oceanospirillales (1)	Halomonadaceae (1)	Halomonas (1)

[top](#)

Cluster 196

Total number of members in cluster: 3

Average length of proteins in cluster: 437.0

Conserved (non-aliphatic) residues:

S 13 (100.0%) Y 14 (100.0%) H 17 (100.0%) S 19 (100.0%) N 23 (100.0%) Y 30 (100.0%) K 40 (100.0%) K 41 (100.0%) E 42 (100.0%) S 49 (100.0%) S 54 (100.0%) T 57 (100.0%) T 58 (100.0%) S 61 (100.0%) E 66 (100.0%) T 67 (100.0%) E 73 (100.0%) E 76 (100.0%) S 78 (100.0%) T 79 (100.0%) N 81 (100.0%) T 84 (100.0%) N 87 (100.0%) S 89 (100.0%) T 94 (100.0%) S 99 (100.0%) N 100 (100.0%) N 106 (100.0%) R 108 (100.0%) N 114 (100.0%) T 115 (100.0%) S 116 (100.0%) N 120 (100.0%) E 124 (100.0%) Y 127 (100.0%) T 135 (100.0%) K 144 (100.0%) D 150 (100.0%) Y 151 (100.0%) Q 153 (100.0%) D 154 (100.0%) R 155 (100.0%) Y 157 (100.0%) Y 158 (100.0%) N 160 (100.0%) N 161 (100.0%) S 165 (100.0%) N 168 (100.0%) R 171 (100.0%) E 175 (100.0%) Q 176 (100.0%) S 177 (100.0%) Y 185 (100.0%) K 187 (100.0%) K 189 (100.0%) K 191 (100.0%) S 203 (100.0%) Q 204 (100.0%) E 209 (100.0%) K 210 (100.0%) T 212 (100.0%) Q 216 (100.0%) S 229 (100.0%) N 230 (100.0%) S 234 (100.0%) K 235 (100.0%) K 236 (100.0%) S 239 (100.0%) S 247 (100.0%) T 259 (100.0%) S 260 (100.0%) Y 261 (100.0%) S 263 (100.0%) S 265 (100.0%) D 267 (100.0%) S 268 (100.0%) E 273 (100.0%) S 274 (100.0%) K 276 (100.0%) T 277 (100.0%) R 278 (100.0%) Q 282 (100.0%) S 283 (100.0%) Q 284 (100.0%) T 290 (100.0%) S 295 (100.0%) S 301 (100.0%) N 306 (100.0%) E 315 (100.0%) N 316 (100.0%) T 317 (100.0%) S 320 (100.0%) Y 321 (100.0%) Q 329 (100.0%) N 333 (100.0%) Y 335 (100.0%) Q 336 (100.0%) E 337 (100.0%) T 343 (100.0%) N 349 (100.0%) T 377 (100.0%) Y 379 (100.0%) T 380 (100.0%) R 382 (100.0%) N 383 (100.0%) K 384 (100.0%) D 385 (100.0%) Y 386 (100.0%) K 394 (100.0%) N 397 (100.0%) Q 401 (100.0%) R 407 (100.0%) Y 409 (100.0%) E 413 (100.0%) K 415 (100.0%) H 430 (100.0%) S 431 (100.0%) K 432 (100.0%) R 434 (100.0%) N 439 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial	common antigen	Wzy
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[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

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[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (3)	Enterobacteriaceae (3)	Enterobacter (3)

[top](#)

Cluster 195

Total number of members in cluster: 3

Average length of proteins in cluster: 383.7

Conserved (non-aliphatic) residues:

Y 2 (100.0%) S 8 (100.0%) S 15 (100.0%) S 18 (100.0%) T 19 (100.0%) T 22 (100.0%) S 24 (100.0%) S 27 (100.0%) N 32 (100.0%) Y 34 (100.0%) Y 36 (100.0%) K 38 (100.0%) S 40 (100.0%) T 41 (100.0%) S 42 (100.0%) R 47 (100.0%) S 56 (100.0%) S 66 (100.0%) Y 69 (100.0%) H 70 (100.0%) D 71 (100.0%) S 74 (100.0%) K 75 (100.0%) T 76 (100.0%) N 78 (100.0%) Y 79 (100.0%) Y 83 (100.0%) S 88 (100.0%) S 94 (100.0%) S 97 (100.0%) Y 98 (100.0%) T 99 (100.0%) K 100 (100.0%) D 103 (100.0%) K 105 (100.0%) K 106 (100.0%) N 108 (100.0%) K 109 (100.0%) T 111 (100.0%) Y 113 (100.0%) E 125 (100.0%) Y 126 (100.0%) Y 127 (100.0%) Y 128 (100.0%) T 131 (100.0%) N 132 (100.0%) N 133 (100.0%) Y 135 (100.0%) S 137 (100.0%) R 141 (100.0%) E 143 (100.0%) R 144 (100.0%) D 146 (100.0%) Y 147 (100.0%) S 149 (100.0%) N 150 (100.0%) S 151 (100.0%) S 153 (100.0%) Y 156 (100.0%) R 157 (100.0%) R 159 (100.0%) T 162 (100.0%) Y 163 (100.0%) E 164 (100.0%) S 165 (100.0%) S 166 (100.0%) S 167 (100.0%) S 174 (100.0%) Y 176 (100.0%) K 190 (100.0%) N 191 (100.0%) S 198 (100.0%) H 202 (100.0%) S 207 (100.0%) S 208 (100.0%) T 209 (100.0%) Q 210 (100.0%) Q 221 (100.0%) S 224 (100.0%) S 225 (100.0%) N 226 (100.0%) S 229 (100.0%) R 230 (100.0%) K 231 (100.0%) K 233 (100.0%) S 248 (100.0%) H 249 (100.0%) E 250 (100.0%) N 256 (100.0%) Y 257 (100.0%) S 259 (100.0%) N 260 (100.0%) K 261 (100.0%) D 263 (100.0%) T 267 (100.0%) N 269 (100.0%) S 271 (100.0%) N 272 (100.0%) S 274 (100.0%) S 276 (100.0%) E 277 (100.0%) R 278 (100.0%) N 279 (100.0%) K 280 (100.0%) N 287 (100.0%) E 291 (100.0%) N 292 (100.0%) S 301 (100.0%) Y 303 (100.0%) N 304 (100.0%) Y 305 (100.0%) D 307 (100.0%) T 308 (100.0%) N 312 (100.0%) H 314 (100.0%) Q 316 (100.0%) T 317 (100.0%) Q 319 (100.0%) Q 320 (100.0%) Y 326 (100.0%) T 331 (100.0%) Y 335 (100.0%) K 341 (100.0%) Q 342 (100.0%) Y 343 (100.0%) T 344 (100.0%) E 346 (100.0%) K 348 (100.0%) T 354 (100.0%) T 357 (100.0%) S 361 (100.0%) S 363 (100.0%) D 366 (100.0%) S 367 (100.0%) N 368 (100.0%) Y 370 (100.0%) Y 373 (100.0%) K 379 (100.0%) S 380 (100.0%) N 381 (100.0%) E 382 (100.0%) R 383 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
ADN43871.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia	O158	0

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
				coli		

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

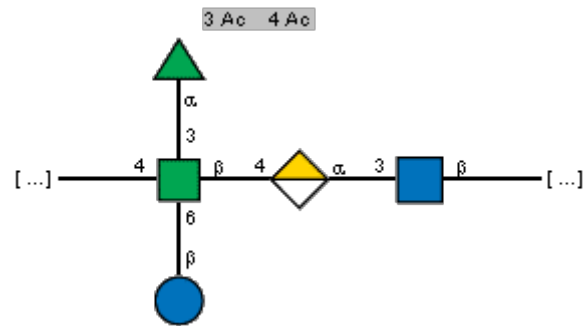
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

ADN43871.1 Escherichia coli O158:



CSDB record ID: 1287

Sugars for blast hits:

Alphafold models:

[ADN43871.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (3)	Enterobacteriaceae (3)	Escherichia (3)

[top](#)

Cluster 194

Total number of members in cluster: 3

Average length of proteins in cluster: 374.3

Conserved (non-aliphatic) residues:

K 28 (100.0%) Y 29 (100.0%) E 70 (100.0%) Y 81 (100.0%) S 115 (100.0%) N 127 (100.0%) Y 140 (100.0%) R 141 (100.0%) R 150 (100.0%) N 157 (100.0%) N 159 (100.0%) S 160 (100.0%) Y 172 (100.0%) R 176 (100.0%) N 181 (100.0%) D 184 (100.0%) Y 196 (100.0%) S 201 (100.0%) R 202 (100.0%) T 203 (100.0%) K 234 (100.0%) N 258 (100.0%) R 264 (100.0%) Y 271 (100.0%) D 288 (100.0%) D 297 (100.0%) S 299 (100.0%) Y 300 (100.0%) K 328

(100.0%) Y 344 (100.0%) E 348 (100.0%) N 349 (100.0%) N 357 (100.0%) T 359 (100.0%)

Seeds in cluster:

protein_accession order family genus species serotype Enterobacterial common antigen Wzy

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Eubacteriales (2)	Peptostreptococcaceae (2)	Peptacetobacter (1)
		Clostridioides (1)
Enterobacterales (1)	Morganellaceae (1)	Providencia (1)

[top](#)

Cluster 183

Total number of members in cluster: 3

Average length of proteins in cluster: 399.0

Conserved (non-aliphatic) residues:

H 1 (100.0%) R 5 (100.0%) T 6 (100.0%) T 7 (100.0%) S 8 (100.0%) T 15 (100.0%) N 27 (100.0%) K 29 (100.0%) E 31 (100.0%) S 39 (100.0%) R 45 (100.0%) N 47 (100.0%) Q 48 (100.0%) K 54 (100.0%) S 57 (100.0%) S 62 (100.0%) Y 63 (100.0%) Y 66 (100.0%) T 72 (100.0%) S 76 (100.0%) T 78 (100.0%) D 80 (100.0%) S 83 (100.0%) R 85 (100.0%) N 86 (100.0%) Y 89 (100.0%) K 93 (100.0%) K 107 (100.0%) K 108 (100.0%) T 109 (100.0%) Q 110 (100.0%) T 111 (100.0%) Y 114 (100.0%) D 115 (100.0%) N 117 (100.0%) R 118 (100.0%) D 127 (100.0%) S 128 (100.0%) K 131 (100.0%) E 134 (100.0%) S 139 (100.0%) S 142 (100.0%) N 146 (100.0%) S 149 (100.0%) D 151 (100.0%) D 152 (100.0%) K 155 (100.0%) D 156 (100.0%) T 157 (100.0%) R 161 (100.0%) N 162 (100.0%) R 166 (100.0%) S 169 (100.0%) Y 171 (100.0%) D 172 (100.0%) Y 173 (100.0%) S 174 (100.0%) T 178 (100.0%) D 184 (100.0%) S 186 (100.0%) R 188 (100.0%) S 189 (100.0%) R 190 (100.0%) K 191 (100.0%) K 192 (100.0%) N 194 (100.0%) Y 198 (100.0%) S 204 (100.0%) S 207 (100.0%) S 208 (100.0%) R 210 (100.0%) T 211 (100.0%) T 220 (100.0%) Y 223 (100.0%) Y 225 (100.0%) R 226 (100.0%) Y 227 (100.0%) K 230 (100.0%) S 234 (100.0%) Y 244 (100.0%) S 246 (100.0%) H 249 (100.0%) S 250 (100.0%) N 251 (100.0%) E 252 (100.0%) H 255 (100.0%) N 256 (100.0%) Q 257 (100.0%) Q 258 (100.0%) S 260 (100.0%) E 264 (100.0%) N 268 (100.0%) N 271 (100.0%) N 273 (100.0%) E 275 (100.0%) T 276 (100.0%) E 277 (100.0%) S 278 (100.0%) T 279 (100.0%) D 280 (100.0%) D 281 (100.0%) E 284 (100.0%) N 285 (100.0%) H 286 (100.0%) D 291 (100.0%) N 292 (100.0%) Y 296 (100.0%) Q 301 (100.0%) Y 302 (100.0%) D 304 (100.0%) S 308 (100.0%) T 309 (100.0%) R 311 (100.0%) S 313 (100.0%) D 314 (100.0%) S 315

(100.0%) Y 317 (100.0%) Y 323 (100.0%) S 336 (100.0%) S 338 (100.0%) Y 339 (100.0%) Y 342 (100.0%) Y 344 (100.0%) K 346 (100.0%) S 347 (100.0%) Q 348 (100.0%) D 349 (100.0%) K 350 (100.0%) K 351 (100.0%) S 353 (100.0%) T 359 (100.0%) K 366 (100.0%) Y 371 (100.0%) S 372 (100.0%) D 373 (100.0%) Y 374 (100.0%) N 375 (100.0%) S 381 (100.0%) S 387 (100.0%) Y 389 (100.0%) K 393 (100.0%) K 395 (100.0%) E 396 (100.0%) N 397 (100.0%) E 398 (100.0%)

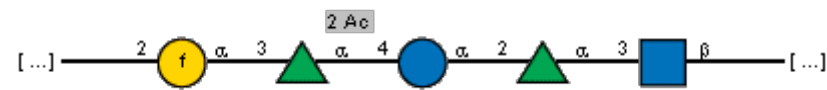
Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
BAQ01659.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O132	0

- [MSA fasta](#)
- [Align view](#)
- [Fasta of members](#)
- [Logoplot](#)
- [Phylogenetic tree](#)
- [Hits in cluster](#)

Sugars in cluster:

BAQ01659.1 Escherichia coli O132:



CSDB record ID: 1874

Sugars for blast hits:

Alphafold models:

[BAQ01659.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (3)	Enterobacteriaceae (3)	Escherichia (3)

[top](#)

Cluster 167

Total number of members in cluster: 3

Average length of proteins in cluster: 353.3

Conserved (non-aliphatic) residues:

K 7 (100.0%) S 23 (100.0%) T 38 (100.0%) Y 40 (100.0%) D 41 (100.0%) E 42 (100.0%) R 44 (100.0%) Y 45 (100.0%)

T 49 (100.0%) D 55 (100.0%) K 57 (100.0%) Y 59 (100.0%) Y 63 (100.0%) T 64 (100.0%) E 66 (100.0%) N 67 (100.0%) Y 69 (100.0%) N 70 (100.0%) Y 71 (100.0%) Q 73 (100.0%) S 74 (100.0%) H 76 (100.0%) H 79 (100.0%) Y 80 (100.0%) R 87 (100.0%) Y 88 (100.0%) N 91 (100.0%) D 92 (100.0%) S 93 (100.0%) Y 100 (100.0%) Q 101 (100.0%) Y 105 (100.0%) E 119 (100.0%) Y 120 (100.0%) Y 138 (100.0%) S 147 (100.0%) R 150 (100.0%) D 151 (100.0%) Y 165 (100.0%) K 166 (100.0%) N 168 (100.0%) S 181 (100.0%) Y 183 (100.0%) R 184 (100.0%) N 186 (100.0%) Y 194 (100.0%) D 198 (100.0%) Q 199 (100.0%) Y 211 (100.0%) S 215 (100.0%) D 223 (100.0%) R 236 (100.0%) E 248 (100.0%) S 255 (100.0%) D 262 (100.0%) Y 268 (100.0%) R 270 (100.0%) S 276 (100.0%) Y 312 (100.0%) Y 316 (100.0%) E 319 (100.0%) R 325 (100.0%) Q 326 (100.0%) S 328 (100.0%) Y 335 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
AHB32267.1	Moraxellales	Moraxellaceae	Acinetobacter	Acinetobacter baumannii	O6	0

- [MSA fasta](#)
- [Malign view](#)
- [Fasta of members](#)
- [Logoplot](#)
- [Phylogenetic tree](#)
- [Hits in cluster](#)

Sugars in cluster:

Sugars for blast hits:

Alphafold models:

[AHB32267.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Moraxellales (3)	Moraxellaceae (3)	Acinetobacter (3)

[top](#)

Cluster 165

Total number of members in cluster: 3

Average length of proteins in cluster: 366.3

Conserved (non-aliphatic) residues:

S 15 (100.0%) T 30 (100.0%) N 51 (100.0%) D 56 (100.0%) Y 60 (100.0%) S 67 (100.0%) H 83 (100.0%) T 84 (100.0%) E 85 (100.0%) Q 92 (100.0%) S 101 (100.0%) T 103 (100.0%) S 113 (100.0%) R 117 (100.0%) Y 118 (100.0%) Y 121 (100.0%) D 130 (100.0%) H 141 (100.0%) E 142 (100.0%) R 145 (100.0%) K 146 (100.0%) D 147 (100.0%) Q 150 (100.0%) R 152 (100.0%) N 153 (100.0%) S 157 (100.0%) Y 162 (100.0%) S 163 (100.0%) R 172 (100.0%) Q 186 (100.0%) T 188 (100.0%) R 199 (100.0%) S 203 (100.0%) Y 206 (100.0%) K 227 (100.0%) N 245 (100.0%) Y 246 (100.0%) Y 248 (100.0%) E 251 (100.0%) S 253 (100.0%) K 254 (100.0%) S 257 (100.0%) N 260

(100.0%) K 265 (100.0%) Q 266 (100.0%) D 283 (100.0%) K 285 (100.0%) Q 291 (100.0%) Y 293 (100.0%) T 297 (100.0%) Y 299 (100.0%) Y 300 (100.0%) R 304 (100.0%) D 305 (100.0%) E 307 (100.0%) R 312 (100.0%) S 315 (100.0%) Y 318 (100.0%) E 321 (100.0%) K 334 (100.0%) N 335 (100.0%) K 339 (100.0%) K 340 (100.0%) Y 347 (100.0%) N 354 (100.0%) T 357 (100.0%)

Seeds in cluster:

protein_accession order family genus species serotype Enterobacterial common antigen Wzy

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Spirochaetales (3)	Treponemataceae (3)	Treponema (3)

[top](#)

Cluster 134

Total number of members in cluster: 3

Average length of proteins in cluster: 390.0

Conserved (non-aliphatic) residues:

T 1 (100.0%) K 4 (100.0%) K 5 (100.0%) K 6 (100.0%) Q 7 (100.0%) N 9 (100.0%) N 12 (100.0%) R 15 (100.0%) R 16 (100.0%) S 18 (100.0%) S 28 (100.0%) S 30 (100.0%) N 32 (100.0%) Y 33 (100.0%) Y 38 (100.0%) E 40 (100.0%) K 42 (100.0%) D 59 (100.0%) R 61 (100.0%) K 62 (100.0%) K 65 (100.0%) T 66 (100.0%) Y 67 (100.0%) S 68 (100.0%) S 69 (100.0%) Y 76 (100.0%) T 82 (100.0%) S 83 (100.0%) S 86 (100.0%) Y 87 (100.0%) Y 90 (100.0%) N 92 (100.0%) N 94 (100.0%) Y 97 (100.0%) S 99 (100.0%) S 101 (100.0%) K 105 (100.0%) S 115 (100.0%) K 117 (100.0%) D 118 (100.0%) D 120 (100.0%) K 126 (100.0%) N 130 (100.0%) S 139 (100.0%) E 143 (100.0%) Y 146 (100.0%) N 149 (100.0%) T 154 (100.0%) N 155 (100.0%) S 156 (100.0%) E 158 (100.0%) Q 160 (100.0%) T 161 (100.0%) Y 162 (100.0%) Y 164 (100.0%) H 165 (100.0%) S 168 (100.0%) Y 169 (100.0%) T 174 (100.0%) S 176 (100.0%) D 178 (100.0%) Y 180 (100.0%) K 183 (100.0%) R 186 (100.0%) N 187 (100.0%) Q 188 (100.0%) S 189 (100.0%) Q 192 (100.0%) E 193 (100.0%) Y 200 (100.0%) T 204 (100.0%) S 209 (100.0%) Q 212 (100.0%) K 213 (100.0%) Y 215 (100.0%) S 216 (100.0%) K 217 (100.0%) N 218 (100.0%) H 219 (100.0%) Y 224 (100.0%) T 230 (100.0%) S 233 (100.0%) T 234 (100.0%) S 236 (100.0%) T 238 (100.0%) S 243 (100.0%) S 247 (100.0%) Y 249 (100.0%) R 252 (100.0%) N 257 (100.0%) S 258 (100.0%) S 261 (100.0%) S 264 (100.0%) S 266 (100.0%) T 269 (100.0%) Y 270 (100.0%) S 274 (100.0%) D 275 (100.0%) N 276 (100.0%) Y 278 (100.0%) N 280 (100.0%) K 281 (100.0%) S 284 (100.0%) D 286 (100.0%) E 287 (100.0%) R 288 (100.0%) Y 290 (100.0%) N 294 (100.0%) N 297

(100.0%) Y 300 (100.0%) S 301 (100.0%) N 302 (100.0%) Y 312 (100.0%) E 313 (100.0%) S 314 (100.0%) E 315 (100.0%) D 321 (100.0%) K 323 (100.0%) N 325 (100.0%) N 326 (100.0%) E 330 (100.0%) Y 334 (100.0%) S 335 (100.0%) N 339 (100.0%) Y 343 (100.0%) Y 349 (100.0%) R 352 (100.0%) K 353 (100.0%) Y 355 (100.0%) K 358 (100.0%) K 360 (100.0%) Y 361 (100.0%) Y 367 (100.0%) T 370 (100.0%) T 371 (100.0%) S 376 (100.0%)

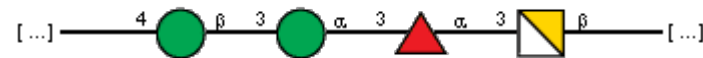
Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
BAQ00927.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O43	0

- [MSA fasta](#)
- [Malign view](#)
- [Fasta of members](#)
- [Logoplot](#)
- [Phylogenetic tree](#)
- [Hits in cluster](#)

Sugars in cluster:

BAQ00927.1 Escherichia coli O43:



CSDB record ID: 1381

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (3)	Enterobacteriaceae (3)	Escherichia (3)

[top](#)

Cluster 122

Total number of members in cluster: 3

Average length of proteins in cluster: 368.0

Conserved (non-aliphatic) residues:

Y 2 (100.0%) T 4 (100.0%) N 5 (100.0%) Y 10 (100.0%) Q 11 (100.0%) T 15 (100.0%) S 22 (100.0%) S 23 (100.0%) S 26 (100.0%) E 31 (100.0%) Y 32 (100.0%) T 33 (100.0%) S 43 (100.0%) T 45 (100.0%) Y 47 (100.0%) T 50 (100.0%) K 51 (100.0%) R 52 (100.0%) N 54 (100.0%) S 55 (100.0%) K 57 (100.0%) Y 58 (100.0%) Q 60 (100.0%) S 62 (100.0%) S 67 (100.0%) K 68 (100.0%) Q 72 (100.0%) N 82 (100.0%) S 84 (100.0%) E 85 (100.0%) T 91 (100.0%) H 92 (100.0%) H 95 (100.0%) Q 96 (100.0%) Y 99 (100.0%) D 102 (100.0%) R 103 (100.0%) K 112 (100.0%) Y 120

(100.0%) T 123 (100.0%) T 128 (100.0%) K 129 (100.0%) N 130 (100.0%) Y 131 (100.0%) S 134 (100.0%) R 135 (100.0%) S 144 (100.0%) T 148 (100.0%) S 150 (100.0%) R 151 (100.0%) T 154 (100.0%) Y 161 (100.0%) T 165 (100.0%) R 173 (100.0%) K 175 (100.0%) S 186 (100.0%) Y 192 (100.0%) Y 193 (100.0%) R 194 (100.0%) E 195 (100.0%) N 198 (100.0%) S 200 (100.0%) D 203 (100.0%) Y 204 (100.0%) S 210 (100.0%) S 211 (100.0%) N 213 (100.0%) E 214 (100.0%) S 219 (100.0%) N 221 (100.0%) S 223 (100.0%) N 224 (100.0%) Q 226 (100.0%) S 230 (100.0%) N 231 (100.0%) T 234 (100.0%) Q 235 (100.0%) D 238 (100.0%) K 244 (100.0%) S 245 (100.0%) D 246 (100.0%) R 248 (100.0%) T 251 (100.0%) T 254 (100.0%) E 255 (100.0%) S 258 (100.0%) S 262 (100.0%) E 263 (100.0%) K 264 (100.0%) Y 266 (100.0%) S 269 (100.0%) S 270 (100.0%) S 271 (100.0%) E 275 (100.0%) S 276 (100.0%) K 277 (100.0%) N 282 (100.0%) Y 287 (100.0%) S 293 (100.0%) N 295 (100.0%) S 296 (100.0%) S 300 (100.0%) R 304 (100.0%) S 305 (100.0%) S 307 (100.0%) R 308 (100.0%) S 310 (100.0%) H 311 (100.0%) S 316 (100.0%) Y 323 (100.0%) S 324 (100.0%) R 326 (100.0%) T 327 (100.0%) E 328 (100.0%) Y 331 (100.0%) Y 333 (100.0%) K 338 (100.0%) Y 342 (100.0%) N 350 (100.0%) Q 351 (100.0%) K 355 (100.0%) S 356 (100.0%) S 357 (100.0%)

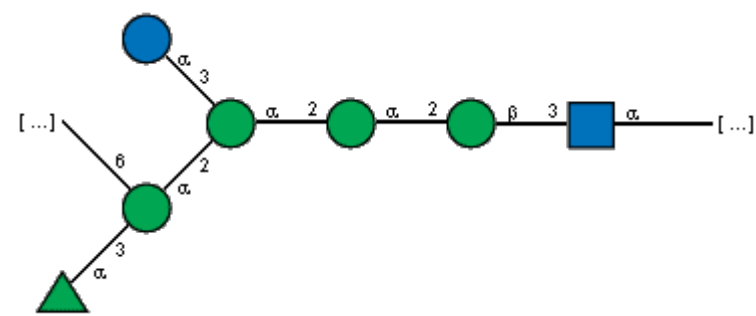
Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
BAQ01155.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O68	0

- [MSA fasta](#)
- [Malign view](#)
- [Fasta of members](#)
- [Logoplot](#)
- [Phylogenetic tree](#)
- [Hits in cluster](#)

Sugars in cluster:

BAQ01155.1 Escherichia coli O68:



CSDB record ID: 1574

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (3)	Enterobacteriaceae (3)	Escherichia (2)

order (count)	family (count)	genus (count)
		nan (1)

[top](#)

Cluster 117

Total number of members in cluster: 3

Average length of proteins in cluster: 454.3

Conserved (non-aliphatic) residues:

Y 30 (100.0%) Y 40 (100.0%) Q 41 (100.0%) D 42 (100.0%) N 47 (100.0%) E 51 (100.0%) R 54 (100.0%) S 55 (100.0%) E 68 (100.0%) K 74 (100.0%) K 76 (100.0%) Q 85 (100.0%) K 86 (100.0%) Y 87 (100.0%) Y 94 (100.0%) Y 102 (100.0%) Y 112 (100.0%) E 117 (100.0%) K 122 (100.0%) K 125 (100.0%) Y 129 (100.0%) R 138 (100.0%) H 139 (100.0%) S 145 (100.0%) K 148 (100.0%) E 171 (100.0%) N 177 (100.0%) H 183 (100.0%) S 184 (100.0%) Y 189 (100.0%) R 191 (100.0%) R 193 (100.0%) T 196 (100.0%) E 198 (100.0%) S 199 (100.0%) S 200 (100.0%) T 202 (100.0%) Y 209 (100.0%) S 210 (100.0%) Y 215 (100.0%) N 222 (100.0%) Y 240 (100.0%) T 244 (100.0%) S 246 (100.0%) K 247 (100.0%) R 269 (100.0%) K 273 (100.0%) N 274 (100.0%) S 298 (100.0%) S 299 (100.0%) D 303 (100.0%) E 305 (100.0%) Y 307 (100.0%) T 308 (100.0%) S 309 (100.0%) T 312 (100.0%) R 313 (100.0%) T 333 (100.0%) Y 336 (100.0%) S 362 (100.0%) N 365 (100.0%) E 368 (100.0%) K 377 (100.0%) K 382 (100.0%) S 383 (100.0%) K 405 (100.0%) K 412 (100.0%) S 427 (100.0%) E 435 (100.0%) K 437 (100.0%) Y 438 (100.0%) E 439 (100.0%)

Seeds in cluster:

protein_accession order family genus species serotype Enterobacterial common antigen Wzy

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Bacillales (3)	Paenibacillaceae (2)	Paenibacillus (2)
	Bacillaceae (1)	Bacillus (1)

[top](#)

Cluster 109

Total number of members in cluster: 3

Average length of proteins in cluster: 365.7

Conserved (non-aliphatic) residues:

N 5 (100.0%) Q 22 (100.0%) Y 24 (100.0%) K 26 (100.0%) S 31 (100.0%) D 32 (100.0%) Q 36 (100.0%) Y 41 (100.0%) S 54 (100.0%) S 67 (100.0%) Y 71 (100.0%) N 76 (100.0%) K 81 (100.0%) D 93 (100.0%) D 129 (100.0%) R 136 (100.0%) T 138 (100.0%) D 142 (100.0%) N 143 (100.0%) N 145 (100.0%) K 146 (100.0%) Y 150 (100.0%) K 165 (100.0%) Y 183 (100.0%) T 188 (100.0%) T 192 (100.0%) Y 207 (100.0%) S 240 (100.0%) Y 247 (100.0%) H 248 (100.0%) N 254 (100.0%) R 260 (100.0%) Y 263 (100.0%) Y 265 (100.0%) D 290 (100.0%) N 291 (100.0%) S 292 (100.0%) N 325 (100.0%) S 327 (100.0%) Y 339 (100.0%) E 343 (100.0%) T 344 (100.0%) E 348 (100.0%) N 352 (100.0%) T 354 (100.0%) Y 361 (100.0%) R 363 (100.0%) N 366 (100.0%) E 369 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
AIG62747.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O178	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

AIG62747.1 Escherichia coli O178:



CSDB record ID: 1920

Sugars for blast hits:

Alphafold models:

[AIG62747.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (2)	Enterobacteriaceae (2)	Escherichia (2)
Vibrionales (1)	Vibrionaceae (1)	Aliivibrio (1)

[top](#)

Cluster 83

Total number of members in cluster: 2

Average length of proteins in cluster: 373.5

Conserved (non-aliphatic) residues:

N 2 (100.0%) Y 3 (100.0%) K 5 (100.0%) N 11 (100.0%) H 13 (100.0%) S 21 (100.0%) S 22 (100.0%) Y 24 (100.0%) K 27 (100.0%) T 29 (100.0%) Q 30 (100.0%) S 32 (100.0%) Y 35 (100.0%) S 38 (100.0%) Q 48 (100.0%) S 51 (100.0%) R 53 (100.0%) K 54 (100.0%) S 56 (100.0%) S 61 (100.0%) Y 70 (100.0%) S 71 (100.0%) Q 72 (100.0%) Q 75 (100.0%) N 78 (100.0%) Y 79 (100.0%) N 80 (100.0%) S 81 (100.0%) S 83 (100.0%) T 84 (100.0%) Y 85 (100.0%) N 87 (100.0%) S 89 (100.0%) R 102 (100.0%) Y 105 (100.0%) D 106 (100.0%) Y 107 (100.0%) D 108 (100.0%) N 112 (100.0%) S 113 (100.0%) K 115 (100.0%) Y 117 (100.0%) D 128 (100.0%) S 129 (100.0%) Y 131 (100.0%) R 132 (100.0%) N 135 (100.0%) T 137 (100.0%) S 140 (100.0%) K 142 (100.0%) E 145 (100.0%) N 149 (100.0%) S 150 (100.0%) S 151 (100.0%) E 152 (100.0%) Y 156 (100.0%) Y 158 (100.0%) K 159 (100.0%) D 167 (100.0%) S 168 (100.0%) N 169 (100.0%) T 170 (100.0%) T 171 (100.0%) T 177 (100.0%) Y 183 (100.0%) Y 184 (100.0%) K 187 (100.0%) H 189 (100.0%) K 192 (100.0%) T 194 (100.0%) S 195 (100.0%) T 201 (100.0%) S 206 (100.0%) S 209 (100.0%) R 210 (100.0%) S 211 (100.0%) S 215 (100.0%) T 219 (100.0%) Y 227 (100.0%) K 228 (100.0%) R 230 (100.0%) S 237 (100.0%) S 249 (100.0%) N 251 (100.0%) S 253 (100.0%) D 254 (100.0%) S 256 (100.0%) D 258 (100.0%) S 259 (100.0%) K 260 (100.0%) Y 262 (100.0%) S 265 (100.0%) K 266 (100.0%) D 268 (100.0%) E 269 (100.0%) Y 270 (100.0%) T 272 (100.0%) S 273 (100.0%) S 275 (100.0%) S 278 (100.0%) D 286 (100.0%) S 288 (100.0%) S 289 (100.0%) D 293 (100.0%) N 294 (100.0%) Y 296 (100.0%) H 298 (100.0%) Y 301 (100.0%) T 303 (100.0%) E 307 (100.0%) S 308 (100.0%) Y 316 (100.0%) S 318 (100.0%) S 322 (100.0%) Y 326 (100.0%) T 327 (100.0%) N 328 (100.0%) K 330 (100.0%) S 342 (100.0%) S 344 (100.0%) Y 345 (100.0%) Y 348 (100.0%) Y 362 (100.0%) N 363 (100.0%) Y 367 (100.0%) E 368 (100.0%)

Seeds in cluster:

protein_accession order family genus species serotype Enterobacterial common antigen Wzy

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count) family (count) genus (count)
Vibrionales (2) Vibrionaceae (2) Vibrio (2)

[top](#)

Cluster 82

Total number of members in cluster: 2

Average length of proteins in cluster: 415.0

Conserved (non-aliphatic) residues:

D 4 (100.0%) R 70 (100.0%) R 108 (100.0%) Y 122 (100.0%) T 123 (100.0%) D 128 (100.0%) H 132 (100.0%) T 135 (100.0%) Q 150 (100.0%) S 163 (100.0%) R 165 (100.0%) R 170 (100.0%) S 173 (100.0%) S 177 (100.0%) T 179 (100.0%) S 184 (100.0%) Y 188 (100.0%) S 214 (100.0%) N 216 (100.0%) K 217 (100.0%) N 222 (100.0%) R 235 (100.0%) K 240 (100.0%) R 265 (100.0%) S 272 (100.0%) N 284 (100.0%) Y 285 (100.0%) D 286 (100.0%) E 291 (100.0%) S 292 (100.0%) R 296 (100.0%) N 304 (100.0%) E 306 (100.0%) S 309 (100.0%) S 313 (100.0%) Y 317 (100.0%) S 327 (100.0%) T 328 (100.0%) H 342 (100.0%) N 343 (100.0%) Q 344 (100.0%) E 347 (100.0%) T 350 (100.0%) R 370 (100.0%) N 396 (100.0%) S 397 (100.0%) N 401 (100.0%) T 403 (100.0%) Y 405 (100.0%) Q 406 (100.0%) S 408 (100.0%) S 411 (100.0%) E 428 (100.0%) R 433 (100.0%) R 438 (100.0%)

Seeds in cluster:

protein_accession order family genus species serotype Enterobacterial common antigen Wzy

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Micrococcales (2)	Microbacteriaceae (2)	Cryobacterium (2)

[top](#)

Cluster 52

Total number of members in cluster: 2

Average length of proteins in cluster: 340.0

Conserved (non-aliphatic) residues:

T 1 (100.0%) N 2 (100.0%) T 3 (100.0%) N 4 (100.0%) Y 5 (100.0%) Y 7 (100.0%) N 8 (100.0%) E 9 (100.0%) R 13 (100.0%) S 21 (100.0%) T 25 (100.0%) S 27 (100.0%) T 28 (100.0%) K 30 (100.0%) E 32 (100.0%) D 35 (100.0%) H 36 (100.0%) D 37 (100.0%) Y 38 (100.0%) K 39 (100.0%) Q 40 (100.0%) Y 41 (100.0%) Y 43 (100.0%) E 46 (100.0%) Y 48 (100.0%) K 49 (100.0%) N 50 (100.0%) S 51 (100.0%) D 53 (100.0%) Y 58 (100.0%) E 59 (100.0%) E 61 (100.0%) Y 66 (100.0%) S 68 (100.0%) R 69 (100.0%) N 72 (100.0%) N 75 (100.0%) Y 85 (100.0%) T 86 (100.0%) K

93 (100.0%) K 98 (100.0%) R 99 (100.0%) T 101 (100.0%) K 102 (100.0%) K 103 (100.0%) T 104 (100.0%) S 105 (100.0%) Q 106 (100.0%) Y 114 (100.0%) S 115 (100.0%) Y 119 (100.0%) H 122 (100.0%) E 123 (100.0%) T 125 (100.0%) Q 126 (100.0%) R 128 (100.0%) S 130 (100.0%) S 140 (100.0%) Q 142 (100.0%) K 143 (100.0%) N 144 (100.0%) K 145 (100.0%) T 155 (100.0%) S 158 (100.0%) H 159 (100.0%) Y 160 (100.0%) S 161 (100.0%) S 165 (100.0%) S 170 (100.0%) R 173 (100.0%) Y 174 (100.0%) N 176 (100.0%) D 177 (100.0%) K 178 (100.0%) R 181 (100.0%) T 182 (100.0%) Q 183 (100.0%) Y 202 (100.0%) S 204 (100.0%) R 205 (100.0%) Q 206 (100.0%) T 207 (100.0%) K 209 (100.0%) Y 210 (100.0%) D 211 (100.0%) T 213 (100.0%) N 214 (100.0%) Y 218 (100.0%) Y 220 (100.0%) H 223 (100.0%) Y 225 (100.0%) S 226 (100.0%) S 232 (100.0%) Y 235 (100.0%) R 237 (100.0%) R 238 (100.0%) Y 239 (100.0%) K 241 (100.0%) N 242 (100.0%) H 243 (100.0%) Y 245 (100.0%) Y 246 (100.0%) Q 247 (100.0%) Y 250 (100.0%) Y 256 (100.0%) Y 257 (100.0%) S 262 (100.0%) Q 267 (100.0%) S 268 (100.0%) Q 269 (100.0%) R 274 (100.0%) E 277 (100.0%) N 291 (100.0%) S 292 (100.0%) S 293 (100.0%) K 295 (100.0%) S 296 (100.0%) S 297 (100.0%) K 300 (100.0%) T 309 (100.0%) Y 313 (100.0%) E 314 (100.0%) H 315 (100.0%) E 320 (100.0%) N 324 (100.0%) D 326 (100.0%) H 329 (100.0%) N 330 (100.0%) S 331 (100.0%) S 333 (100.0%) K 334 (100.0%) D 336 (100.0%) T 337 (100.0%) Q 339 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
BAQ00812.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O34	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (2)	Enterobacteriaceae (2)	Escherichia (2)

[top](#)

Cluster 205

Total number of members in cluster: 2

Average length of proteins in cluster: 335.0

Conserved (non-aliphatic) residues:

N 5 (100.0%) S 7 (100.0%) Y 8 (100.0%) K 10 (100.0%) K 12 (100.0%) K 13 (100.0%) E 16 (100.0%) Y 17 (100.0%) Y 18 (100.0%) S 31 (100.0%) R 34 (100.0%) D 41 (100.0%) Y 42 (100.0%) Y 45 (100.0%) E 47 (100.0%) T 50

(100.0%) R 56 (100.0%) D 57 (100.0%) S 58 (100.0%) E 60 (100.0%) Y 63 (100.0%) R 64 (100.0%) R 67 (100.0%) N 70 (100.0%) D 71 (100.0%) D 75 (100.0%) H 77 (100.0%) Y 82 (100.0%) S 85 (100.0%) T 88 (100.0%) S 91 (100.0%) K 93 (100.0%) S 99 (100.0%) S 101 (100.0%) S 102 (100.0%) H 103 (100.0%) N 105 (100.0%) Y 111 (100.0%) S 114 (100.0%) H 119 (100.0%) E 120 (100.0%) Y 121 (100.0%) T 122 (100.0%) Q 123 (100.0%) R 125 (100.0%) S 136 (100.0%) K 138 (100.0%) D 139 (100.0%) E 142 (100.0%) N 143 (100.0%) R 144 (100.0%) K 151 (100.0%) T 156 (100.0%) H 159 (100.0%) Y 160 (100.0%) S 161 (100.0%) Y 171 (100.0%) T 172 (100.0%) R 173 (100.0%) R 176 (100.0%) S 177 (100.0%) K 179 (100.0%) T 185 (100.0%) S 192 (100.0%) E 197 (100.0%) S 200 (100.0%) T 203 (100.0%) K 204 (100.0%) Y 205 (100.0%) Y 207 (100.0%) Q 210 (100.0%) D 211 (100.0%) N 216 (100.0%) K 217 (100.0%) S 218 (100.0%) E 221 (100.0%) S 222 (100.0%) D 223 (100.0%) S 226 (100.0%) N 229 (100.0%) K 231 (100.0%) Y 232 (100.0%) T 234 (100.0%) S 243 (100.0%) T 244 (100.0%) K 247 (100.0%) K 248 (100.0%) E 249 (100.0%) D 250 (100.0%) S 251 (100.0%) N 253 (100.0%) T 255 (100.0%) Y 257 (100.0%) K 258 (100.0%) S 261 (100.0%) Y 267 (100.0%) Y 268 (100.0%) Y 269 (100.0%) Q 274 (100.0%) S 279 (100.0%) R 281 (100.0%) E 284 (100.0%) Y 286 (100.0%) S 287 (100.0%) Y 290 (100.0%) N 296 (100.0%) Y 299 (100.0%) N 300 (100.0%) K 301 (100.0%) D 302 (100.0%) Y 303 (100.0%) T 305 (100.0%) K 307 (100.0%) Y 310 (100.0%) S 316 (100.0%) T 320 (100.0%) Y 323 (100.0%) Y 325 (100.0%) K 329 (100.0%) T 330 (100.0%) T 332 (100.0%)

Seeds in cluster:

protein_accession order family genus species serotype Enterobacterial common antigen Wzy

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Bacteroidales (2)	Bacteroidaceae (2)	Bacteroides (2)

[top](#)

Cluster 197

Total number of members in cluster: 2

Average length of proteins in cluster: 429.0

Conserved (non-aliphatic) residues:

Y 2 (100.0%) T 10 (100.0%) T 13 (100.0%) D 15 (100.0%) R 20 (100.0%) S 21 (100.0%) K 24 (100.0%) S 26 (100.0%) S 32 (100.0%) S 36 (100.0%) S 37 (100.0%) Y 41 (100.0%) N 43 (100.0%) Y 44 (100.0%) R 45 (100.0%) Q 46 (100.0%) D 48 (100.0%) S 52 (100.0%) T 53 (100.0%) K 54 (100.0%) Y 58 (100.0%) S 61 (100.0%) S 65 (100.0%) R 74 (100.0%) R 78 (100.0%) K 79 (100.0%) K 80 (100.0%) D 81 (100.0%) K 82 (100.0%) N 83 (100.0%) Y 84 (100.0%)

E 85 (100.0%) K 89 (100.0%) E 90 (100.0%) D 92 (100.0%) N 94 (100.0%) T 95 (100.0%) H 96 (100.0%) S 98 (100.0%) T 105 (100.0%) Y 112 (100.0%) S 116 (100.0%) K 118 (100.0%) D 119 (100.0%) Q 121 (100.0%) S 123 (100.0%) N 125 (100.0%) N 128 (100.0%) S 131 (100.0%) Q 132 (100.0%) Y 134 (100.0%) Y 135 (100.0%) K 136 (100.0%) N 137 (100.0%) Q 139 (100.0%) H 140 (100.0%) N 141 (100.0%) S 143 (100.0%) N 144 (100.0%) S 145 (100.0%) N 149 (100.0%) Q 150 (100.0%) E 153 (100.0%) T 156 (100.0%) Y 160 (100.0%) S 162 (100.0%) Q 165 (100.0%) S 168 (100.0%) R 170 (100.0%) Y 171 (100.0%) K 174 (100.0%) D 175 (100.0%) R 176 (100.0%) N 177 (100.0%) R 178 (100.0%) Q 179 (100.0%) T 180 (100.0%) N 182 (100.0%) Y 183 (100.0%) N 185 (100.0%) T 188 (100.0%) S 196 (100.0%) T 197 (100.0%) D 198 (100.0%) R 199 (100.0%) N 200 (100.0%) R 204 (100.0%) Y 208 (100.0%) Y 217 (100.0%) T 218 (100.0%) K 219 (100.0%) S 220 (100.0%) N 221 (100.0%) Q 222 (100.0%) S 224 (100.0%) K 226 (100.0%) S 227 (100.0%) N 229 (100.0%) K 231 (100.0%) R 234 (100.0%) K 235 (100.0%) S 236 (100.0%) Y 248 (100.0%) Y 249 (100.0%) K 252 (100.0%) K 254 (100.0%) N 255 (100.0%) Y 256 (100.0%) T 257 (100.0%) S 258 (100.0%) D 259 (100.0%) Q 261 (100.0%) R 262 (100.0%) Y 267 (100.0%) S 270 (100.0%) Y 273 (100.0%) N 274 (100.0%) N 276 (100.0%) N 280 (100.0%) K 281 (100.0%) T 285 (100.0%) N 286 (100.0%) K 288 (100.0%) Y 289 (100.0%) S 292 (100.0%) T 293 (100.0%) R 295 (100.0%) T 296 (100.0%) S 298 (100.0%) D 299 (100.0%) T 300 (100.0%) T 303 (100.0%) N 308 (100.0%) T 309 (100.0%) T 313 (100.0%) T 314 (100.0%) S 315 (100.0%) S 318 (100.0%) E 319 (100.0%) Q 324 (100.0%) S 325 (100.0%) S 326 (100.0%) T 327 (100.0%) Y 331 (100.0%) S 333 (100.0%) N 334 (100.0%) Y 336 (100.0%) S 337 (100.0%) R 340 (100.0%) E 344 (100.0%) D 345 (100.0%) Y 348 (100.0%) Y 354 (100.0%) E 363 (100.0%) Y 366 (100.0%) E 367 (100.0%) R 370 (100.0%) R 371 (100.0%) K 372 (100.0%) Y 374 (100.0%) S 375 (100.0%) Y 381 (100.0%) S 382 (100.0%) Y 383 (100.0%) S 384 (100.0%) Y 386 (100.0%) Y 390 (100.0%) E 394 (100.0%) E 395 (100.0%) Q 396 (100.0%) R 399 (100.0%) R 400 (100.0%) H 402 (100.0%) T 405 (100.0%) Y 407 (100.0%) E 408 (100.0%) S 410 (100.0%) Y 416 (100.0%) Q 421 (100.0%) R 422 (100.0%) K 423 (100.0%) R 425 (100.0%) K 427 (100.0%)

Seeds in cluster:

protein_accession order family genus species serotype Enterobacterial common antigen Wzy

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Lactobacillales (2)	Streptococcaceae (2)	Streptococcus (2)

[top](#)

Cluster 193

Total number of members in cluster: 2

Average length of proteins in cluster: 393.5

Conserved (non-aliphatic) residues:

D 2 (100.0%) Y 3 (100.0%) R 26 (100.0%) S 28 (100.0%) S 43 (100.0%) R 46 (100.0%) Y 47 (100.0%) Y 48 (100.0%)
D 52 (100.0%) E 54 (100.0%) Y 56 (100.0%) Q 57 (100.0%) Y 60 (100.0%) Y 64 (100.0%) S 66 (100.0%) N 74
(100.0%) Y 78 (100.0%) R 79 (100.0%) R 86 (100.0%) S 89 (100.0%) S 91 (100.0%) S 107 (100.0%) S 111 (100.0%) K
117 (100.0%) Y 130 (100.0%) Y 133 (100.0%) E 134 (100.0%) Y 135 (100.0%) Q 142 (100.0%) R 143 (100.0%) Q 144
(100.0%) H 148 (100.0%) N 164 (100.0%) K 166 (100.0%) T 179 (100.0%) H 181 (100.0%) S 183 (100.0%) Y 191
(100.0%) S 198 (100.0%) S 216 (100.0%) S 222 (100.0%) N 225 (100.0%) K 251 (100.0%) Y 254 (100.0%) Y 255
(100.0%) Y 258 (100.0%) K 263 (100.0%) S 267 (100.0%) R 269 (100.0%) Y 270 (100.0%) E 272 (100.0%) Y 273
(100.0%) S 289 (100.0%) K 292 (100.0%) Y 295 (100.0%) Y 305 (100.0%) H 310 (100.0%) S 318 (100.0%) Q 324
(100.0%) R 326 (100.0%) E 328 (100.0%) Y 330 (100.0%) H 335 (100.0%) S 340 (100.0%) K 349 (100.0%) S 361
(100.0%) K 367 (100.0%) Y 368 (100.0%) R 370 (100.0%) S 374 (100.0%) Y 377 (100.0%) D 381 (100.0%) S 382
(100.0%) H 383 (100.0%) Y 384 (100.0%) Q 385 (100.0%) R 386 (100.0%) Y 390 (100.0%)

Seeds in cluster:

protein_accession order family genus species serotype Enterobacterial common antigen Wzy

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Vibrionales (2)	Vibrionaceae (2)	Photobacterium (1)
		Vibrio (1)

[top](#)

Cluster 189

Total number of members in cluster: 2

Average length of proteins in cluster: 452.5

Conserved (non-aliphatic) residues:

T 46 (100.0%) Y 48 (100.0%) T 56 (100.0%) S 62 (100.0%) R 64 (100.0%) K 68 (100.0%) N 69 (100.0%) R 71
(100.0%) E 72 (100.0%) T 73 (100.0%) T 76 (100.0%) E 77 (100.0%) D 80 (100.0%) R 84 (100.0%) T 85 (100.0%) R
89 (100.0%) T 90 (100.0%) R 94 (100.0%) T 95 (100.0%) R 99 (100.0%) T 103 (100.0%) S 107 (100.0%) S 109
(100.0%) R 110 (100.0%) R 112 (100.0%) R 114 (100.0%) S 115 (100.0%) T 122 (100.0%) R 123 (100.0%) T 124
(100.0%) S 126 (100.0%) S 127 (100.0%) T 128 (100.0%) R 129 (100.0%) Y 130 (100.0%) R 131 (100.0%) R 133

(100.0%) S 134 (100.0%) T 140 (100.0%) E 141 (100.0%) E 142 (100.0%) E 143 (100.0%) T 144 (100.0%) R 146 (100.0%) R 149 (100.0%) R 150 (100.0%) T 152 (100.0%) D 155 (100.0%) T 160 (100.0%) S 166 (100.0%) R 169 (100.0%) Y 170 (100.0%) D 171 (100.0%) T 174 (100.0%) D 175 (100.0%) Y 176 (100.0%) T 178 (100.0%) Y 179 (100.0%) E 180 (100.0%) N 184 (100.0%) N 187 (100.0%) D 189 (100.0%) D 190 (100.0%) D 194 (100.0%) E 197 (100.0%) S 198 (100.0%) T 199 (100.0%) Q 200 (100.0%) E 201 (100.0%) Y 204 (100.0%) T 205 (100.0%) K 212 (100.0%) T 213 (100.0%) T 215 (100.0%) E 216 (100.0%) D 217 (100.0%) K 219 (100.0%) T 229 (100.0%) Y 234 (100.0%) K 238 (100.0%) R 239 (100.0%) S 241 (100.0%) D 243 (100.0%) E 255 (100.0%) Y 256 (100.0%) T 257 (100.0%) S 258 (100.0%) S 259 (100.0%) N 261 (100.0%) R 264 (100.0%) Q 265 (100.0%) Y 266 (100.0%) T 277 (100.0%) Y 278 (100.0%) R 281 (100.0%) K 282 (100.0%) N 283 (100.0%) S 295 (100.0%) H 297 (100.0%) T 299 (100.0%) R 311 (100.0%) R 312 (100.0%) R 314 (100.0%) T 316 (100.0%) Q 318 (100.0%) T 319 (100.0%) T 320 (100.0%) R 335 (100.0%) S 342 (100.0%) E 345 (100.0%) N 348 (100.0%) R 350 (100.0%) Y 351 (100.0%) D 353 (100.0%) Y 354 (100.0%) D 356 (100.0%) S 357 (100.0%) Q 359 (100.0%) T 360 (100.0%) S 364 (100.0%) Y 365 (100.0%) S 367 (100.0%) Y 371 (100.0%) S 383 (100.0%) R 384 (100.0%) K 385 (100.0%) T 389 (100.0%) R 390 (100.0%) E 392 (100.0%) S 393 (100.0%) Q 394 (100.0%) T 410 (100.0%) Q 411 (100.0%) S 416 (100.0%) R 417 (100.0%) S 419 (100.0%) Y 421 (100.0%) N 432 (100.0%) R 433 (100.0%) K 436 (100.0%) Q 438 (100.0%) D 439 (100.0%) R 440 (100.0%) T 441 (100.0%) T 444 (100.0%) Y 454 (100.0%) Y 455 (100.0%) Q 460 (100.0%) N 461 (100.0%) Y 462 (100.0%) E 464 (100.0%) Y 468 (100.0%) R 469 (100.0%) T 470 (100.0%) Y 471 (100.0%) Q 474 (100.0%)

Seeds in cluster:

protein_accession order family genus species serotype Enterobacterial common antigen Wzy

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Micrococcales (2)	Dermabacteraceae (2)	Brachybacterium (2)

[top](#)

Cluster 188

Total number of members in cluster: 2

Average length of proteins in cluster: 337.5

Conserved (non-aliphatic) residues:

Y 2 (100.0%) S 41 (100.0%) D 43 (100.0%) N 46 (100.0%) Y 47 (100.0%) N 49 (100.0%) Y 51 (100.0%) Y 52

(100.0%) E 61 (100.0%) S 64 (100.0%) S 81 (100.0%) K 93 (100.0%) S 105 (100.0%) Y 111 (100.0%) K 114 (100.0%) D 120 (100.0%) T 122 (100.0%) Q 123 (100.0%) R 125 (100.0%) Y 151 (100.0%) H 159 (100.0%) S 161 (100.0%) K 174 (100.0%) N 177 (100.0%) S 192 (100.0%) K 197 (100.0%) H 208 (100.0%) N 212 (100.0%) Y 213 (100.0%) Y 216 (100.0%) N 226 (100.0%) N 235 (100.0%) K 246 (100.0%) D 251 (100.0%) N 255 (100.0%) K 259 (100.0%) Y 261 (100.0%) S 264 (100.0%) S 267 (100.0%) Y 269 (100.0%) S 278 (100.0%) R 280 (100.0%) S 282 (100.0%) E 283 (100.0%) Y 288 (100.0%) Q 289 (100.0%) Q 304 (100.0%) R 305 (100.0%) S 316 (100.0%) Q 319 (100.0%) Y 321 (100.0%) T 323 (100.0%) Y 324 (100.0%) N 325 (100.0%) Y 333 (100.0%)

Seeds in cluster:

protein_accession order family genus species serotype Enterobacterial common antigen Wzy

- [MSA fasta](#)
- [Malign view](#)
- [Fasta of members](#)
- [Logoplot](#)
- [Phylogenetic tree](#)
- [Hits in cluster](#)

Sugars in cluster:

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (2)	Erwiniaceae (1)	Erwinia (1)
	Enterobacteriaceae (1)	Escherichia (1)

[top](#)

Cluster 187

Total number of members in cluster: 2

Average length of proteins in cluster: 362.0

Conserved (non-aliphatic) residues:

Y 3 (100.0%) Y 19 (100.0%) N 20 (100.0%) Y 24 (100.0%) N 28 (100.0%) R 39 (100.0%) D 46 (100.0%) T 47 (100.0%) Y 50 (100.0%) N 58 (100.0%) N 65 (100.0%) N 68 (100.0%) Q 76 (100.0%) R 77 (100.0%) E 79 (100.0%) T 80 (100.0%) N 86 (100.0%) K 87 (100.0%) Y 90 (100.0%) S 93 (100.0%) N 95 (100.0%) Q 97 (100.0%) E 99 (100.0%) T 103 (100.0%) T 109 (100.0%) Y 122 (100.0%) N 137 (100.0%) S 138 (100.0%) N 140 (100.0%) R 143 (100.0%) Q 144 (100.0%) S 145 (100.0%) K 162 (100.0%) H 177 (100.0%) T 179 (100.0%) Y 187 (100.0%) S 190 (100.0%) N 195 (100.0%) E 214 (100.0%) K 215 (100.0%) S 221 (100.0%) S 224 (100.0%) T 225 (100.0%) E 226 (100.0%) S 231 (100.0%) N 237 (100.0%) N 244 (100.0%) Y 261 (100.0%) D 271 (100.0%) K 272 (100.0%) K 278 (100.0%) S 280 (100.0%) Y 282 (100.0%) S 294 (100.0%) K 296 (100.0%) S 298 (100.0%) Q 299 (100.0%) R 302 (100.0%) Y 306 (100.0%) E 311 (100.0%) N 324 (100.0%) K 328 (100.0%) Y 342 (100.0%) Q 347 (100.0%) R 350 (100.0%) E 352 (100.0%) S 354 (100.0%) Y 359 (100.0%)

Seeds in cluster:

protein_accession order family genus species serotype Enterobacterial common antigen Wzy

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Lactobacillales (2)	Lactobacillaceae (2)	Limosilactobacillus (2)

[top](#)

Cluster 185

Total number of members in cluster: 2

Average length of proteins in cluster: 361.0

Conserved (non-aliphatic) residues:

S 4 (100.0%) T 5 (100.0%) Y 10 (100.0%) S 16 (100.0%) K 23 (100.0%) E 24 (100.0%) R 27 (100.0%) N 29 (100.0%) K 31 (100.0%) Y 32 (100.0%) Y 34 (100.0%) D 37 (100.0%) Y 39 (100.0%) Y 41 (100.0%) S 46 (100.0%) Y 50 (100.0%) T 54 (100.0%) R 55 (100.0%) D 56 (100.0%) S 59 (100.0%) D 60 (100.0%) S 61 (100.0%) D 62 (100.0%) T 63 (100.0%) E 64 (100.0%) R 65 (100.0%) Y 66 (100.0%) S 68 (100.0%) E 71 (100.0%) Y 72 (100.0%) Y 73 (100.0%) R 74 (100.0%) N 76 (100.0%) Y 79 (100.0%) D 82 (100.0%) K 83 (100.0%) N 84 (100.0%) Y 85 (100.0%) Y 90 (100.0%) T 91 (100.0%) Y 92 (100.0%) Y 94 (100.0%) S 95 (100.0%) Y 97 (100.0%) D 99 (100.0%) Y 101 (100.0%) Y 102 (100.0%) Y 104 (100.0%) T 111 (100.0%) Y 114 (100.0%) S 115 (100.0%) Y 116 (100.0%) K 118 (100.0%) K 121 (100.0%) K 124 (100.0%) Y 125 (100.0%) Y 128 (100.0%) S 129 (100.0%) S 131 (100.0%) T 137 (100.0%) Q 143 (100.0%) S 145 (100.0%) S 147 (100.0%) K 150 (100.0%) Q 151 (100.0%) S 156 (100.0%) H 164 (100.0%) Q 167 (100.0%) T 168 (100.0%) K 169 (100.0%) Y 170 (100.0%) K 171 (100.0%) Q 172 (100.0%) S 177 (100.0%) S 181 (100.0%) S 182 (100.0%) H 184 (100.0%) T 186 (100.0%) T 189 (100.0%) S 194 (100.0%) Y 198 (100.0%) R 200 (100.0%) K 201 (100.0%) E 202 (100.0%) R 203 (100.0%) S 205 (100.0%) N 207 (100.0%) S 216 (100.0%) S 220 (100.0%) S 222 (100.0%) N 225 (100.0%) S 226 (100.0%) Y 227 (100.0%) S 230 (100.0%) Y 235 (100.0%) D 236 (100.0%) E 240 (100.0%) S 241 (100.0%) K 242 (100.0%) N 244 (100.0%) Y 246 (100.0%) E 248 (100.0%) S 249 (100.0%) T 250 (100.0%) N 251 (100.0%) N 252 (100.0%) T 254 (100.0%) R 257 (100.0%) D 259 (100.0%) S 264 (100.0%) N 274 (100.0%) R 275 (100.0%) T 276 (100.0%) K 280 (100.0%) D 281 (100.0%) R 282 (100.0%) Y 283 (100.0%) K 285 (100.0%) S 290 (100.0%) Y 291 (100.0%) Y 293 (100.0%) N 295 (100.0%) S 296 (100.0%) Y 298 (100.0%) N 299 (100.0%) S 302 (100.0%) S 307 (100.0%) D 308 (100.0%) R 309 (100.0%) Y 313 (100.0%) S 314 (100.0%) S 318 (100.0%) S 325 (100.0%) K 328 (100.0%) R 330 (100.0%) S 331 (100.0%) S 332 (100.0%) Y 334 (100.0%) S 337 (100.0%) S 338 (100.0%) N 345 (100.0%) Y 351 (100.0%) Y 352 (100.0%) N 353 (100.0%) S 354

(100.0%) K 360 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
ACH97152.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O3	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

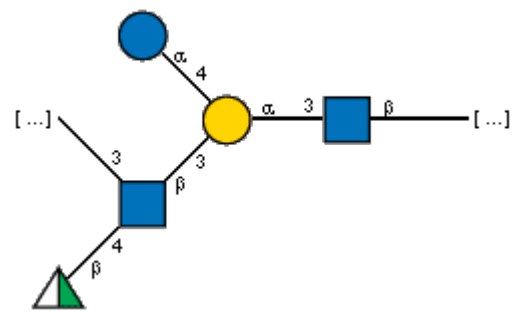
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

ACH97152.1 Escherichia coli O3:



CSDB record ID: 1501

Sugars for blast hits:

AlphaFold models:

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (2)	Enterobacteriaceae (2)	Escherichia (2)

[top](#)

Cluster 182

Total number of members in cluster: 2

Average length of proteins in cluster: 339.0

Conserved (non-aliphatic) residues:

K 4 (100.0%) S 5 (100.0%) R 6 (100.0%) Y 22 (100.0%) K 23 (100.0%) E 25 (100.0%) N 27 (100.0%) Y 28 (100.0%) T

30 (100.0%) D 32 (100.0%) E 33 (100.0%) Y 36 (100.0%) S 39 (100.0%) D 40 (100.0%) S 41 (100.0%) T 44 (100.0%) D 45 (100.0%) T 47 (100.0%) S 50 (100.0%) R 51 (100.0%) Y 52 (100.0%) K 53 (100.0%) Y 57 (100.0%) R 60 (100.0%) Y 63 (100.0%) E 64 (100.0%) Y 65 (100.0%) E 67 (100.0%) Y 68 (100.0%) S 70 (100.0%) N 75 (100.0%) T 77 (100.0%) N 84 (100.0%) K 85 (100.0%) S 87 (100.0%) K 88 (100.0%) S 89 (100.0%) S 90 (100.0%) N 91 (100.0%) N 92 (100.0%) N 93 (100.0%) D 94 (100.0%) N 96 (100.0%) Y 97 (100.0%) Y 100 (100.0%) S 106 (100.0%) Y 110 (100.0%) S 112 (100.0%) R 116 (100.0%) D 117 (100.0%) Y 119 (100.0%) Y 129 (100.0%) R 131 (100.0%) R 132 (100.0%) K 134 (100.0%) H 135 (100.0%) K 136 (100.0%) Q 140 (100.0%) K 151 (100.0%) E 153 (100.0%) S 165 (100.0%) R 166 (100.0%) K 168 (100.0%) S 170 (100.0%) Y 176 (100.0%) T 184 (100.0%) H 190 (100.0%) N 191 (100.0%) Q 192 (100.0%) T 193 (100.0%) Y 198 (100.0%) N 200 (100.0%) T 201 (100.0%) E 203 (100.0%) R 204 (100.0%) E 206 (100.0%) T 208 (100.0%) S 211 (100.0%) E 212 (100.0%) Y 213 (100.0%) N 214 (100.0%) T 215 (100.0%) Q 221 (100.0%) Q 222 (100.0%) E 224 (100.0%) T 226 (100.0%) N 229 (100.0%) N 233 (100.0%) S 237 (100.0%) Y 238 (100.0%) N 240 (100.0%) S 243 (100.0%) S 248 (100.0%) S 251 (100.0%) N 252 (100.0%) T 253 (100.0%) N 255 (100.0%) N 258 (100.0%) T 262 (100.0%) D 264 (100.0%) S 265 (100.0%) N 280 (100.0%) T 281 (100.0%) K 282 (100.0%) K 283 (100.0%) Y 284 (100.0%) Y 285 (100.0%) S 286 (100.0%) D 287 (100.0%) D 288 (100.0%) Y 290 (100.0%) R 291 (100.0%) S 293 (100.0%) S 300 (100.0%) Y 303 (100.0%) Y 305 (100.0%) T 309 (100.0%) T 312 (100.0%) S 313 (100.0%) R 315 (100.0%) H 317 (100.0%) H 319 (100.0%)

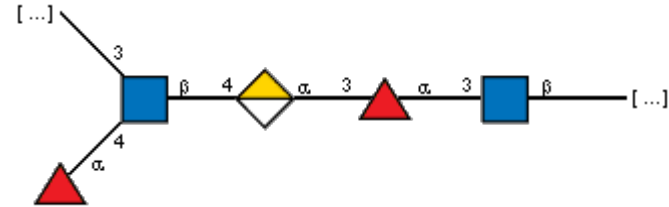
Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
ACA24890.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O159	0

- [MSA fasta](#)
- [Malign view](#)
- [Fasta of members](#)
- [Logoplot](#)
- [Phylogenetic tree](#)
- [Hits in cluster](#)

Sugars in cluster:

ACA24890.1 Escherichia coli O159:



CSDB record ID: 1900

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (2)	Enterobacteriaceae (2)	Escherichia (2)

Cluster 178

Total number of members in cluster: 2

Average length of proteins in cluster: 409.0

Conserved (non-aliphatic) residues:

D 1 (100.0%) S 2 (100.0%) N 4 (100.0%) R 5 (100.0%) S 6 (100.0%) S 7 (100.0%) K 9 (100.0%) K 12 (100.0%) S 13 (100.0%) N 14 (100.0%) S 18 (100.0%) Y 23 (100.0%) T 24 (100.0%) T 26 (100.0%) Y 28 (100.0%) D 31 (100.0%) D 36 (100.0%) N 37 (100.0%) K 40 (100.0%) N 44 (100.0%) T 45 (100.0%) S 46 (100.0%) K 52 (100.0%) S 59 (100.0%) T 64 (100.0%) Y 66 (100.0%) T 67 (100.0%) K 69 (100.0%) S 71 (100.0%) R 72 (100.0%) E 74 (100.0%) Y 84 (100.0%) S 86 (100.0%) S 87 (100.0%) T 92 (100.0%) S 93 (100.0%) D 94 (100.0%) Y 96 (100.0%) E 97 (100.0%) Y 100 (100.0%) S 103 (100.0%) N 104 (100.0%) Y 105 (100.0%) Y 108 (100.0%) Y 112 (100.0%) T 115 (100.0%) K 116 (100.0%) Y 118 (100.0%) E 120 (100.0%) K 121 (100.0%) Y 122 (100.0%) Y 124 (100.0%) Y 125 (100.0%) K 126 (100.0%) T 128 (100.0%) K 129 (100.0%) S 130 (100.0%) T 132 (100.0%) S 135 (100.0%) S 142 (100.0%) Y 144 (100.0%) D 146 (100.0%) Y 150 (100.0%) E 151 (100.0%) R 152 (100.0%) R 156 (100.0%) S 157 (100.0%) E 158 (100.0%) T 162 (100.0%) Y 163 (100.0%) S 166 (100.0%) Q 167 (100.0%) S 169 (100.0%) R 171 (100.0%) K 172 (100.0%) S 176 (100.0%) S 177 (100.0%) N 178 (100.0%) N 180 (100.0%) T 184 (100.0%) E 192 (100.0%) Y 193 (100.0%) Y 195 (100.0%) Y 198 (100.0%) N 199 (100.0%) R 200 (100.0%) H 202 (100.0%) T 203 (100.0%) K 204 (100.0%) T 205 (100.0%) T 206 (100.0%) T 220 (100.0%) S 222 (100.0%) K 223 (100.0%) T 224 (100.0%) S 229 (100.0%) T 236 (100.0%) T 238 (100.0%) K 239 (100.0%) S 241 (100.0%) R 244 (100.0%) Q 245 (100.0%) K 246 (100.0%) S 247 (100.0%) T 248 (100.0%) S 254 (100.0%) S 256 (100.0%) T 264 (100.0%) D 268 (100.0%) Y 269 (100.0%) Y 271 (100.0%) E 272 (100.0%) S 275 (100.0%) S 276 (100.0%) R 277 (100.0%) S 280 (100.0%) N 282 (100.0%) D 285 (100.0%) S 286 (100.0%) S 287 (100.0%) R 289 (100.0%) Y 290 (100.0%) E 291 (100.0%) Y 293 (100.0%) D 298 (100.0%) K 299 (100.0%) N 301 (100.0%) Q 302 (100.0%) N 303 (100.0%) T 308 (100.0%) D 311 (100.0%) R 313 (100.0%) E 314 (100.0%) D 315 (100.0%) Y 316 (100.0%) S 317 (100.0%) Q 318 (100.0%) Y 319 (100.0%) R 325 (100.0%) S 327 (100.0%) D 328 (100.0%) S 329 (100.0%) Y 331 (100.0%) N 333 (100.0%) S 337 (100.0%) S 338 (100.0%) T 347 (100.0%) T 349 (100.0%) T 356 (100.0%) K 359 (100.0%) K 360 (100.0%) D 361 (100.0%) R 362 (100.0%) R 364 (100.0%) S 372 (100.0%) E 378 (100.0%) D 379 (100.0%) Y 380 (100.0%) R 383 (100.0%) S 386 (100.0%) S 392 (100.0%) T 394 (100.0%) Y 396 (100.0%) S 399 (100.0%) T 400 (100.0%) N 401 (100.0%) K 403 (100.0%) N 406 (100.0%) T 407 (100.0%) K 408 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
BAQ01114.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O64	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

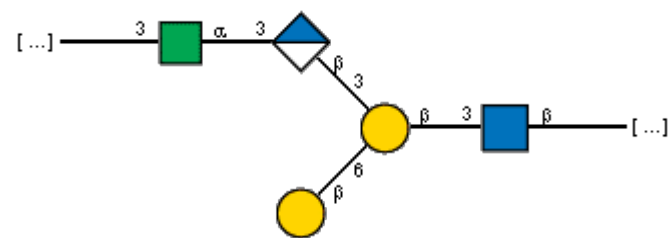
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

BAQ01114.1 Escherichia coli O64:



CSDB record ID: 1571

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (2)	Enterobacteriaceae (2)	Escherichia (2)

[top](#)

Cluster 175

Total number of members in cluster: 2

Average length of proteins in cluster: 358.0

Conserved (non-aliphatic) residues:

S 42 (100.0%) N 68 (100.0%) Y 76 (100.0%) S 92 (100.0%) D 99 (100.0%) D 153 (100.0%) N 156 (100.0%) S 163 (100.0%) R 164 (100.0%) N 165 (100.0%) S 168 (100.0%) Y 178 (100.0%) K 187 (100.0%) S 200 (100.0%) R 207 (100.0%) S 213 (100.0%) Y 225 (100.0%) T 235 (100.0%) S 243 (100.0%) N 256 (100.0%) R 265 (100.0%) Y 272 (100.0%) S 275 (100.0%) N 301 (100.0%) H 303 (100.0%) N 304 (100.0%) H 310 (100.0%) S 331 (100.0%) K 336 (100.0%) R 350 (100.0%) Y 351 (100.0%) D 354 (100.0%) D 363 (100.0%) K 390 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial	common antigen	Wzy
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[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
Moraxellales (1)	Moraxellaceae (1)	Acinetobacter (1)
Aeromonadales (1)	Aeromonadaceae (1)	Aeromonas (1)

[top](#)

Cluster 172

Total number of members in cluster: 2

Average length of proteins in cluster: 443.0

Conserved (non-aliphatic) residues:

N 1 (100.0%) K 6 (100.0%) S 25 (100.0%) Y 34 (100.0%) Y 36 (100.0%) T 37 (100.0%) K 46 (100.0%) D 51 (100.0%) R 53 (100.0%) Y 63 (100.0%) T 65 (100.0%) R 70 (100.0%) N 78 (100.0%) D 82 (100.0%) E 83 (100.0%) S 89 (100.0%) R 91 (100.0%) Q 93 (100.0%) S 104 (100.0%) N 105 (100.0%) R 112 (100.0%) Q 113 (100.0%) S 129 (100.0%) E 130 (100.0%) R 131 (100.0%) S 151 (100.0%) S 155 (100.0%) K 156 (100.0%) R 157 (100.0%) E 158 (100.0%) D 161 (100.0%) K 167 (100.0%) S 170 (100.0%) D 171 (100.0%) T 178 (100.0%) R 184 (100.0%) R 187 (100.0%) D 195 (100.0%) Y 201 (100.0%) Y 208 (100.0%) T 212 (100.0%) E 214 (100.0%) R 215 (100.0%) D 216 (100.0%) K 220 (100.0%) Y 229 (100.0%) D 231 (100.0%) R 233 (100.0%) S 255 (100.0%) Q 256 (100.0%) Y 257 (100.0%) K 259 (100.0%) S 264 (100.0%) D 270 (100.0%) R 271 (100.0%) D 275 (100.0%) Y 279 (100.0%) S 280 (100.0%) E 281 (100.0%) S 284 (100.0%) S 286 (100.0%) R 287 (100.0%) N 288 (100.0%) Y 290 (100.0%) S 291 (100.0%) Q 299 (100.0%) S 302 (100.0%) S 306 (100.0%) D 307 (100.0%) R 310 (100.0%) T 315 (100.0%) Q 324 (100.0%) S 325 (100.0%) R 332 (100.0%) R 335 (100.0%) E 337 (100.0%) T 343 (100.0%) S 344 (100.0%) T 349 (100.0%) Y 355 (100.0%) Y 370 (100.0%) Y 378 (100.0%) N 379 (100.0%) R 381 (100.0%) R 383 (100.0%) S 384 (100.0%) Y 386 (100.0%) Y 388 (100.0%) Y 391 (100.0%) Y 400 (100.0%) R 403 (100.0%) D 405 (100.0%) N 408 (100.0%) S 411 (100.0%) K 415 (100.0%) S 417 (100.0%) H 428 (100.0%) R 432 (100.0%) R 433 (100.0%)

Seeds in cluster:

protein_accession order family genus species serotype Enterobacterial common antigen Wzy

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

Sugars for blast hits:

Alphafold models:

Taxonomy:

order (count)	family (count)	genus (count)
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order (count) family (count) genus (count)

Pseudomonadales (2) Pseudomonadaceae (2) Pseudomonas (2)

[top](#)

Cluster 151

Total number of members in cluster: 2

Average length of proteins in cluster: 346.0

Conserved (non-aliphatic) residues:

E 1 (100.0%) H 2 (100.0%) N 4 (100.0%) R 5 (100.0%) Y 7 (100.0%) N 10 (100.0%) T 11 (100.0%) T 12 (100.0%) N 15 (100.0%) S 30 (100.0%) S 31 (100.0%) Y 34 (100.0%) K 35 (100.0%) D 37 (100.0%) S 38 (100.0%) S 39 (100.0%) S 40 (100.0%) S 46 (100.0%) T 47 (100.0%) S 52 (100.0%) S 57 (100.0%) S 61 (100.0%) S 62 (100.0%) K 63 (100.0%) Y 64 (100.0%) Y 65 (100.0%) N 67 (100.0%) T 68 (100.0%) S 69 (100.0%) N 70 (100.0%) S 72 (100.0%) K 74 (100.0%) S 75 (100.0%) Y 80 (100.0%) T 81 (100.0%) T 82 (100.0%) T 83 (100.0%) S 89 (100.0%) S 90 (100.0%) S 91 (100.0%) E 93 (100.0%) Y 94 (100.0%) K 96 (100.0%) H 104 (100.0%) Y 107 (100.0%) E 109 (100.0%) Y 112 (100.0%) H 116 (100.0%) H 117 (100.0%) S 119 (100.0%) S 122 (100.0%) T 128 (100.0%) N 130 (100.0%) S 131 (100.0%) K 133 (100.0%) N 134 (100.0%) R 135 (100.0%) N 148 (100.0%) N 154 (100.0%) R 155 (100.0%) D 156 (100.0%) T 161 (100.0%) K 172 (100.0%) R 173 (100.0%) K 174 (100.0%) S 176 (100.0%) K 178 (100.0%) S 185 (100.0%) E 196 (100.0%) Y 197 (100.0%) R 198 (100.0%) S 199 (100.0%) H 204 (100.0%) T 205 (100.0%) D 207 (100.0%) S 211 (100.0%) N 213 (100.0%) Y 214 (100.0%) E 215 (100.0%) K 216 (100.0%) T 220 (100.0%) Y 227 (100.0%) T 229 (100.0%) S 230 (100.0%) S 231 (100.0%) S 232 (100.0%) N 234 (100.0%) Y 236 (100.0%) Y 237 (100.0%) N 238 (100.0%) K 240 (100.0%) T 241 (100.0%) N 245 (100.0%) Y 247 (100.0%) S 249 (100.0%) N 250 (100.0%) N 252 (100.0%) E 256 (100.0%) Y 258 (100.0%) Y 259 (100.0%) S 261 (100.0%) S 262 (100.0%) D 265 (100.0%) S 266 (100.0%) Y 277 (100.0%) S 283 (100.0%) R 285 (100.0%) H 286 (100.0%) Y 287 (100.0%) T 290 (100.0%) K 291 (100.0%) K 292 (100.0%) T 293 (100.0%) S 294 (100.0%) E 295 (100.0%) T 297 (100.0%) Y 301 (100.0%) Y 303 (100.0%) Y 306 (100.0%) Q 307 (100.0%) Y 309 (100.0%) T 310 (100.0%) K 316 (100.0%) N 319 (100.0%) T 320 (100.0%) H 321 (100.0%) T 322 (100.0%) Q 333 (100.0%) N 336 (100.0%) K 341 (100.0%) K 342 (100.0%) R 343 (100.0%) R 344 (100.0%) S 345 (100.0%)

Seeds in cluster:

protein_accession	order	family	genus	species	serotype	Enterobacterial common antigen Wzy
BAQ01780.1	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	O154	0

[MSA fasta](#)

[Malign view](#)

[Fasta of members](#)

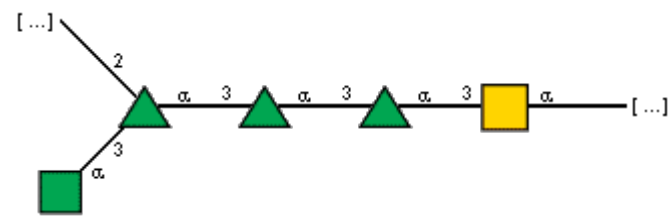
[Logoplot](#)

[Phylogenetic tree](#)

[Hits in cluster](#)

Sugars in cluster:

BAQ01780.1 Escherichia coli O154:



CSDB record ID: 696

Sugars for blast hits:

Alphafold models:

[BAQ01780.1](#)

Taxonomy:

order (count)	family (count)	genus (count)
Enterobacterales (2)	Enterobacteriaceae (2)	Escherichia (2)

[top](#)