BV-BRC Test Report

D8. Sequences Data Tab

Item to test	Sequences Data Tab
URL	https://www.bv-brc.org/view/Taxonomy/194#view_tab=sequences
Prerequisites	None
References	https://www.bv-brc.org/docs/quick_references/organisms_taxon/sequences.html
Tester(s)	Rebecca Wattam, Ron Kenyon
Test date	6-Jan-2022 (original – passed), 9-May-2022 (follow-up-passed)
Test result	Passed (minor issue reported)

Overview

- Test the Sequences Tab with example bacterial data.
- Verify appropriate genomes
- Test FASTA and Genome Browser action buttons.

Test Results

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- Test results were verified by examination of returned data via inspection and filters.
 - All operations performed as expected, with exception of FASTA action button.
 - Issue: Received RequestError error, when downloading FASTA sequence.
 - \circ $\;$ Resolution: The bug was fixed. The download is now working as expected.

Campylobacter:

Ov	verview I	Phylogen	y Taxonomy	Genomes A	AMR Phenotypes	Sequences	Proteins	Protein Structures	Specialty Genes	Domains and Motifs	Epitopes	Path
oow		YWORDS			ADV Search							HIDE
ea	uence Typ	e Q	Sequence Stat		nosome	오 Plasmid	Q					
icat hro ont las	tig (105) ffold (289) mosome (7 ig (540607 mid (123) fold (12138	16305))	complete (58)	megap pCC17 pCC22 pCC22 pCC22 pCC22 pCC42	olasmid pCL2100 (1) 78 (20) 228-1 (1) 228-2 (1) 228-3 (1)		(1 (1) 2 (1) (1) (1) 1 (1) 2 (1)]				
	Genome I	D Gen	ome Name	nCH4	Accession	Sequence Ty		/pe Descrip	tion	GC Content %	Length (b	op)
	195.2005	Cam	pylobacter coli strai	n FSIS1607083	195.2005.con.0095	contig		NODE_9	5_length_160_cov_38.9518	36.88	160	
	195.989	Cam	pylobacter coli strai	n W17A	FAYR01000021	contig		Campylol	bacter coli genome assemb	bly W17/ 32.3	322	
	199.799	Cam	pylobacter concisus	strain AAUH-120	D PPAK01000007	contig		PPAK010	00007.1	41.11	433	
	32022.589	Cam	pylobacter jejuni sul	bsp. jejuni strain (CF PHYZ01000035	contig		PHYZ010	000035.1	29.22	1030	
	195.1736	Cam	pylobacter coli strai	n FSIS1605612	195.1736.con.0053	contig		NODE_5	3_length_308_cov_47.225	108 32.47	308	
	195.1861	Cam	pylobacter coli strai	n FSIS1606302	195.1861.con.0098	contig		NODE_9	8_length_80_cov_49.0000	26.25	80	
	195.2202	Cam	pylobacter coli strai	n FSIS1606590	195.2202.con.0013	contig		NODE_1	3_length_32898_cov_25.16	68672 30.45	32898	
	197.11583	Cam	pylobacter jejuni str	ain RM3414	NFQU01000321	contig		NFQU010	000321.1	30.46	1773	
	197.11646	Cam	pylobacter jejuni str	ain isolate_C9	NFPP01000121	contig		NFPP010	000121.1	29.07	17323	
	195.1625	Cam	pylobacter coli strai	n FSIS11814805	ROKN01000076	contig		ROKN01	000076.1	27.7	1686	
	195.2435	Cam	pylobacter coli strai	n MON334	VAED01000077	contig		VAED010	000077.1	26.67	6401	
	197.15104	Cam	pylobacter jejuni str	ain SO-92	PQYF01000050	contig		PQYF010	000050.1	30.17	242	
	197.15236	Cam	pylobacter jejuni str	ain NCTC12851	LR134507	contig		LR13450	7.1	30.5	1634561	
	197.15627	Cam	pylobacter jejuni str	ain FSIS1606223	197.15627.con.0035	contig		NODE_3	5_length_483_cov_1.1966	29 35.4	483	
	197.4822	Cam	pylobacter jejuni str	ain OXC6588	CUUG01000139	contig		Campylol	bacter jejuni genome asser	nbly 721 31.24	573	
	199.763				JC POYN01000019	contig		POYN010		37.7	6531	
	32022.885	Cam	pylobacter jejuni sul	bsp. jejuni strain (CIT JAAQQA010000025	contig		JAAQQA	010000025.1	29.97	13924	
	889253.3	Cam	pylobacter jejuni sul	bsp. jejuni 2008-9	88 AIOS01000191	chromosome		Campylol	pacter jejuni subsp. jejuni 2	008-988 34	400	
	197.16019	Cam	pylobacter jejuni str	ain FSIS1605884	197.16019.con.0023	contig		NODE_2	3_length_944_cov_98.9363	353 30.72	944	
	197.20570		pylobacter jejuni str			2 contig		CAJGWV	01000002.1	30.62	31956	
	197.15609	Cam	pylobacter jejuni str	ain FSIS1606151	197.15609.con.0027	contig		NODE_2	7_length_5388_cov_40.834	4683 27.15	5388	
	197.15782		pylobacter jejuni str			-			B_length_132_cov_3.2000		132	
	1333529.4		pylobacter fetus sub			chromosome			pacter fetus subsp. venerea		257	
	593452.3				A NZ_ACLG01000303	chromosome			bacter fetus subsp. venerea		1121	
	1031542.14		pylobacter volucris						010000180.1	23.23	848	
	1440038.3		pylobacter jejuni CV		JAKD01000223	contig			pacter jejuni CVM 41902 co		2010	
٦ ۲	2040653.3		pylobacter sp. BCW		NXHW01000456	contig			000456.1	31.16	491	

Keyword: Campylobacter

Overview	Phylogeny Tax	onomy Gen	omes	AMR Phenotypes	Sequences	Proteins Pro	tein Structures	Specialty Genes	Domains and I	Motifs Epito	pes Path
+					amoxicillin	Resi	stant				-
OWNLOAD	KEYWORDS			ADV Search		RESISTANT_PH	ENOTYPE 🗙				HIDE
ublic Q	Antibiotic		۹	Resistant Phenoty	/pe	ice	Q Laboratory	Typing Method 〇			
ue (24)	amoxicillin (24) amikacin (1) ampicillin (5) beta-lactam (5333) cefepime (1) cefotaxime (14) ceftriaxone (6) cefuroxime (85) chloramphenicol (21 ciprofloxacin (3) cilindamycin (154)	(33)		Resistant (24) Intermediate (24) Susceptible (270)	Labora	tory Method (24)) MIC (4)				
Genor	co-trimoxazole (20) ne Name	An	tibiotic	Resistant Phenotype	Measurement Sign	Measurement Value	Measurement Units		Computational Ev	vidence	Pubmed
Strento	coccus pneumoniae GA5	8581 am	oxicillin	Resistant	=	8	Onits	Method		aboratory Method	
	coccus pneumoniae GA		oxicillin	Resistant	-	8				aboratory Method	
	coccus pneumoniae EU-		oxicillin	Resistant	-	8				aboratory Method	
	coccus pneumoniae GA4		oxicillin	Resistant	-	8				aboratory Method	
	coccus pneumoniae GA4		oxicillin	Resistant	-	8				aboratory Method	
	coccus pneumoniae strai		oxicillin	Resistant	-	8	mg/L	MIC		aboratory Method	
	coccus pneumoniae GA1		oxicillin	Resistant	=	2	iiig/L	MIC		aboratory Method	
_	coccus pneumoniae GA		oxicillin	Resistant	-	8				aboratory Method	
	coccus pneumoniae GA4		oxicillin	Resistant	-	8				aboratory Method	
	coccus pneumoniae GA4		oxicillin	Resistant	=	8				aboratory Method	
	coccus pneumoniae GA4		oxicillin	Resistant	=	8				aboratory Method	
	coccus pneumoniae GA4		oxicillin	Resistant	>	8				aboratory Method	
	coccus pneumoniae GA4		oxicillin	Resistant	=	8				aboratory Method	
	coccus pneumoniae P31		oxicillin	Resistant		•				aboratory Method	
	coccus pneumoniae P31		oxicillin	Resistant						aboratory Method	
	coccus pneumoniae GA4		oxicillin	Resistant	=	4				aboratory Method	
	coccus pneumoniae GA1		oxicillin	Resistant	=	8				aboratory Method	
_	coccus pneumoniae GA4		oxicillin	Resistant	=	8				aboratory Method	
	coccus pneumoniae P31		oxicillin	Resistant						aboratory Method	
_	coccus pneumoniae strai		oxicillin	Resistant	==	8	mg/L	MIC		aboratory Method	
Strepto			oxicillin	Resistant	=	8	-			aboratory Method	
	coccus pneumoniae GA5	am am									
Strepto	coccus pneumoniae GA5		oxicillin	Resistant	==	8	mg/L	MIC	La	aboratory Method	
Strepto		n 100 am				8	mg/L mg/L	MIC		aboratory Method aboratory Method	

1 - 24 of 24 results

FASTA Action Button:

	195.1861	Campylobacter coli strain FSIS1606302	195.1861.con.0098	contig	NODE_98_length_80_cov_49.000000	26.25
	195.2202	Campylobacter coli strain FSIS1606590	195.2202.con.0013	contig	NODE_13_length_32898_cov_25.168672	30.45
~	197.11583	Campylobacter jejuni strain RM3414	NFQU01000321	contig	NFQU01000321.1	30.46
] 197.11646	Campylobacter jejuni strain isolate_C9	NFPP01000121	contig	NFPP01000121.1	29.07
	105 1005		DOI/0104000070		DOI/01040000704	07.7

Result: Received RequestError error, logged into GitHub

There was an error retrieving the requested data: RequestError: Unable to load https://patricbrc.org/api/genome_feature/ status: 400

Genome Browser:

Browse File View					Specialty Genes	Domains and Motifs	Protein Families	i aanayo	oubbystems	
BIOWSE THE VIEW	Help									GD Share
100 200	300 400	500	600	700 800	900 1,000	1,100 1 <mark>,</mark> 200	1,300 1,40	00 1,500	1,600	1,700
		$\leftrightarrow \rightarrow ($		D OFQU01000	321 VFQU01000	321:5871186 (601 Go	A 💷			
						1,000				
Reference Sequence										
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DATRIC Appetation										
PATRIC Annotation										
		Reference Sequence	Ceference Sequence		← → Q Q Q Q NFQU01000 Reference Sequence	← → Q Q Q Q (NFQU01000321 - NFQU01000321 - NFQU0100000000000000000000000000000000000	← → Q Q Q Q Q NFQU01000321 - NFQU01000321:5871186 (601] Go Reference Sequence	← → Q Q Q Q Q NFQU01000321 - NFQU01000321.587.1186 (6011 Go 2 III) Reference Sequence		

Escherichia:

0\	verview	Phylogeny	Taxonomy	Genomes Al	WR Phenotypes	Sequences	Proteins P	rotein Structures	Specialty Ger	es Domains a	and Motifs E	pitopes	Pat
	L [- 4								1
DOW		EYWORDS			ADV Searc	h						н	IDE
Pub	olic Q	Antibiotic			Q Resistant P	henotype	C Evider	nce	<u>م</u> Laborator	y Typing Metho	d		
rue	(92068)	amoxicillin, amoxicillin amoxicillin ampicillin (ampicillin-s ampicillin/s augmentin	(2625) clavulanic acid (clavulanic acid (clavulanic_aci _clavulanic_ac 7160) sulbactam (4) ulbactam (259	4 (4141) d (2) id (1092)		a (1769) ible (6) (100) 7637) (63822) -dose dependen	t (4)	itory Method (9043	Etest (392/ Kirby-Baue MIC (8958 MIC:broth N206 card Vitek2 (36) agar dilutic agar-dilutic agar-dilutic	D) er disk diffusion () microdilution (36 on the Vitek 2 (1) n (10795) n (16 µg/m (184 n (16 µg/m) (3) 10364)) 68)		
	Genome	Name		Antibiotic	Resistant Phenotype	Measurement Sign	Measuremen Value	t Measurement Units	Lab typing Method	Computational Method	Evidence	Pubmed	• •
	Escherichi	ia coli strain 247	42_1#285	trimethoprim	Resistant				broth dilution		Laboratory Metho	c 3055056	4
	Escherichi	ia coli O23:H16	strain ECO0238	ceftazidime	Susceptible						Laboratory Metho	c 2872057	В
	Escherichi	ia coli strain 409		amoxicillin/clavul	a Intermediate	==	16/8	mg/L	MIC		Laboratory Metho	c	
	Escherichi	ia coli CVM N34	054PS	sulfisoxazole		>	256	mg/L	broth microdilution		Laboratory Metho	c 2614241	D
	Escherichi	ia coli strain G4	00792	gentamicin	Susceptible						Laboratory Metho	c 3012749	5
		ia coli CVM N36		tetracycline		<=	4	mg/L	broth microdilution		Laboratory Metho	c 2614241	0
		ia coli strain 198		tetracycline	Susceptible	<=	1	mg/L	MIC		Laboratory Metho		
		ia coli strain UR	-	ciprofloxacin	Susceptible	<=	0.25	mg/L	MIC		Laboratory Metho		
		ia coli O6:H1 str		tigecycline	Susceptible						Laboratory Metho	c 2872057	В
		ia coli strain PB		cefuroxime	Resistant				N206 card on the \		Laboratory Metho		
		ia coli strain AM	-	ampicillin	Resistant						Laboratory Metho		
		ia coli strain AM	-	amoxicillin			256	mg/L	agar_dilution		Laboratory Metho		
		ia coli strain 7-1		cefoxitin	Resistant				disk diffusion		Laboratory Metho		
		ia coli O18:H5 s		ceftazidime	Susceptible				agar dilution		Laboratory Metho		В
		ia coli strain MU	-	tigecycline	Susceptible	<	0.5	mg/L	MIC		Laboratory Metho		
		ia coli strain AM	-	amoxicillin			4	mg/L	agar_dilution		Laboratory Metho		
		ia coli strain 509		colistin	Susceptible				disk diffusion		Laboratory Metho		
		ia coli strain N44		aztreonam			8	mg/L	broth microdilution		Laboratory Metho	c 3014869	В
		ia coli strain UR	-	aztreonam	Resistant	>=	64	mg/L	MIC		Laborate Maria	0070057	0
		ia coli O4:H1 str ia coli O6:H1 str		cefuroxime	Susceptible				eger dilution		Laboratory Metho		
		ia coli O6:H1 str ia coli strain G0		gentamicin	Susceptible		4	ma/l	agar dilution		Laboratory Metho		
		ia coli strain GU		meropenem	Sussentible		4	mg/L	MIC		Laboratory Metho		
		ia coli 01:H7 str ia coli 075:H5 s			Susceptible				agar dilution				
		ia coli 075:H5 s ia coli strain UR		ciprofloxacin	Susceptible Resistant	>=	16	mg/L	agar dilution		Laboratory Metho		
		ia coli strain UR	-	ceftiofur	Susceptible	-	10	mg/c	Kirby-Bauer disk d		Laboratory Metho		4
		ia coli strain EC	_	ampicillin	Resistant				N206 card on the		Laboratory Metho		
		ia coli strain PB		kanamycin	1 Colotani	<=	8	mg/L	broth microdilution		Laboratory Metho		

Laboratory Typing Method: Etest

Over	rview Phyloger	ny Taxonomy	Genomes AN	IR Phenotypes	Sequences	Proteins Pr	otein Structure	s Specialty Ge	enes Domains	and Motifs E	oitopes	Pat
				-		Etest						r
DOWNL	OAD KEYWORDS			ADV Searc	h LABORATORY_	TYPING_METHOD :	×				н	DE
ublic	Antibiot	ic	<u>م</u>	Resistant Phe	enotype 🤍 Ev	vidence	Q Lab	oratory Typing M	lethod		٩	1
ue (3	aztreona cefotaxir ceftazidii cefuroxir ciproflox gentamid	m (104) ne (259) me (460) ne (335) acin (459) cin (460) em (456)	60)	Intermediate (Resistant (254 Susceptible (3		boratory Methoc	Disk Kirby MIC MIC N20 Vitel agar	t (3920) Diffusion (5) y-Bauer disk diffu (8958) broth microdilutio 5 card on the Vite (2 (36) dilution (10795) -dilution (16 µg/m	on (36) ek 2 (10364)			
G	enome Name		Antibiotic	Resistant Phenotype	Measurement Sign	Measurement Value	Measurement Units	Lab typing Method	Computational Method	Evidence	Pubmed	
ΓE	scherichia coli 8c13f	e74-7bb8-11e9-a8d3	- ampicillin	Susceptible				Etest		Laboratory Metho		
E	scherichia coli 8c13f	e74-7bb8-11e9-a8d3	- ceftazidime	Susceptible				Etest		Laboratory Metho		
E	scherichia coli 8c13f	e74-7bb8-11e9-a8d3	- cefuroxime	Susceptible				Etest		Laboratory Metho		
E	scherichia coli 8c13f	e74-7bb8-11e9-a8d3	- ciprofloxacin	Susceptible				Etest		Laboratory Metho		
E	scherichia coli 8c13f	e74-7bb8-11e9-a8d3-	- gentamicin	Susceptible				Etest		Laboratory Metho		
E	scherichia coli 8c13f	e74-7bb8-11e9-a8d3	- meropenem	Susceptible				Etest		Laboratory Metho		
E	scherichia coli 8c13f	e74-7bb8-11e9-a8d3	- piperacillin_tazob	a Susceptible				Etest		Laboratory Metho	-	
E	scherichia coli 8c13f	e74-7bb8-11e9-a8d3	- trimethoprim_sulp	I Susceptible				Etest		Laboratory Metho		
E	scherichia coli 7ef17	73a-7bb8-11e9-a8d3	- ampicillin	Susceptible				Etest		Laboratory Metho	-	
E	scherichia coli 7ef17	73a-7bb8-11e9-a8d3	- ceftazidime	Susceptible				Etest		Laboratory Metho		
E	scherichia coli 7ef17	73a-7bb8-11e9-a8d3	- cefuroxime	Susceptible				Etest		Laboratory Metho		
E	scherichia coli 7ef17	73a-7bb8-11e9-a8d3	- ciprofloxacin	Susceptible				Etest		Laboratory Metho		
E	scherichia coli 7ef17	73a-7bb8-11e9-a8d3	- gentamicin	Susceptible				Etest		Laboratory Metho		
E	scherichia coli 7ef17	73a-7bb8-11e9-a8d3	- meropenem	Susceptible				Etest		Laboratory Metho		
E	scherichia coli 7ef17	73a-7bb8-11e9-a8d3	- piperacillin tazob	a Susceptible				Etest		Laboratory Metho		
_		73a-7bb8-11e9-a8d3						Etest		Laboratory Metho		
ТЕ	scherichia coli 7f9cb	3fc-7bb8-11e9-a8d3-	6 ampicillin	Resistant				Etest		Laboratory Metho		
ТЕ	scherichia coli 7f9cb	3fc-7bb8-11e9-a8d3-	6 ceftazidime	Susceptible				Etest		Laboratory Metho		
ЭЕ	scherichia coli 7f9cb	3fc-7bb8-11e9-a8d3-	6 cefuroxime	Susceptible				Etest		Laboratory Metho		
E	scherichia coli 7f9cb	3fc-7bb8-11e9-a8d3-	6 ciprofloxacin	Susceptible				Etest		Laboratory Metho		
_] Е	scherichia coli 7f9cb	3fc-7bb8-11e9-a8d3-	6 gentamicin	Susceptible				Etest		Laboratory Metho		
_		3fc-7bb8-11e9-a8d3-	•	Susceptible				Etest		Laboratory Metho		
_		3fc-7bb8-11e9-a8d3-						Etest		Laboratory Metho		
_		3fc-7bb8-11e9-a8d3-						Etest		Laboratory Metho		
_		15a-7bb8-11e9-a8d3		Resistant				Etest		Laboratory Metho		
_		e15a-7bb8-11e9-a8d3		Susceptible				Etest		Laboratory Metho		
_		e15a-7bb8-11e9-a8d3		Susceptible				Etest		Laboratory Metho		
_		15a-7bb8-11e9-a8d3		Susceptible				Etest		Laboratory Metho		

Acinetobacter:

Overview	Phylogeny	Taxonomy	Genomes A	MR Phenotypes	Sequences	Proteins I	Protein Structures	Specialty Gene	es Domains	and Motifs	Epitopes	Pa
	KEYWORDS			ADV Searc	:h						F	HIDE
ublic ⁽	그 Antibiotic	:	c	Resistant Phe	enotype 🔍	Evidence	۹	Laboratory Typi	ng Method	م	Compu	tatic
ue (39894)	amoxicillin amoxicillin amoxicillin ampicillin (ampicillin-	(1) /clavulanate (1 /clavulanic acid (869) sulbactam (5) sulbactam (50) cin (12) n (908) cicilin (1) em (8957) 782)	d (55)	undefined (148 Intermediate (1 Non-susceptibl Not defined (14 Resistant (226 Susceptible (12	1933) le (7) 43) 28)	Computational M Computational P Laboratory Meth	rediction (3295)	BD-Phoenix (680 Computational Pi Etest (170) Kirby Bauer disk Kirby-Bauer disk MIC (22161) ab_biodisk (154) agar dilution (26) disc diffusion on I disk diffusion (50 forest_pharmace glaxosmith_kline, oxoid (375)	diffusion (260) diffusion (1092 diffusion (1232 Müller-Hinton II 6) uticals (25) _pharmaceutica) Agar (140) als (25)	AdaBoc AdaBoc	
Genom	e Name	7001	Antibiotic	Resistant Phenotype	Measureme Sign	nt Measuremer Value	nt Measurement Units	Lab typing	Computational Method		Pubme	d
Acinetob	acter baumannii	strain MRSN7336	6 ceftriaxone	Resistant	>	32	mg/L	MIC		Laboratory Meth	noc	
Acinetob	acter baumannii	strain CCF39	piperacillin	Resistant	>=	128	µg/mL			Laboratory Meth	100	
Acinetob	acter baumannii	strain MRSN7249	e trimethoprim/sul	far Susceptible	==	2/38	mg/L	MIC		Laboratory Meth	100	
Acinetob	acter baumannii	strain MRSN1037	7' ceftriaxone	Resistant	>	32	mg/L	MIC		Laboratory Meth	100	
Acinetob	acter baumannii	strain MRSN7658	8 ceftazidime	Resistant	>	16	mg/L	MIC		Laboratory Meth	noc	
Acinetob	acter baumannii	strain MRSN7213	3 levofloxacin	Susceptible	<=	2	mg/L	MIC				
Acinetob	acter baumannii	strain AB_363	carbapenem	Susceptible					AdaBoost Classifie	Computational I	Vle	
Acinetob	acter baumannii	strain ABCRPUT	H imipenem	Resistant	=	64	mg/L	agar dilution		Laboratory Meth	100	
Acinetob	acter baumannii	strain MRSN7388	8 tobramycin	Susceptible	==	4	mg/L	MIC		Laboratory Meth	100	
Acinetob	acter baumannii	strain MRSN3207	7€ ampicillin/sulbad	ta Susceptible	<=	8/4	mg/L	MIC				
Acinetob	acter baumannii	strain MRSN7731	1 ceftriaxone	Susceptible	==	8	mg/L	MIC		Laboratory Meth	noc	
Acinetob	acter baumannii	strain MRSN7629	9 imipenem	Susceptible	<=	1	mg/L	MIC		Laboratory Meth	юс	
Acinetob	acter baumannii	strain MRSN7305	5 cefotaxime	Resistant	>	32	mg/L	MIC		Laboratory Meth	юс	
Acinetob	acter baumannii	strain MRSN7706	6 cefoxitin	Resistant	>=	64	mg/L	MIC		Laboratory Meth	юс	
Acinetob	acter baumannii	strain MRSN7355	5 gentamicin	Resistant	>	8	mg/L	MIC		Laboratory Meth	noc	
Acinetob	acter baumannii	strain MRSN1179	0 carbapenem	Resistant					AdaBoost Classifie	Computational I	Vle	
Acinetob	acter baumannii	strain MRSN3152	2: amikacin	Susceptible	<=	16	mg/L	MIC				
Acinetob	acter baumannii	strain MRSN7220	0 ceftriaxone	Resistant	>	32	mg/L	MIC		Laboratory Meth	noc	
Acinetob	acter baumannii	strain MRSN7548	8 ceftazidime	Resistant	>	16	mg/L	MIC		Laboratory Meth	noc	
Acinetob	acter baumannii	strain MRSN7393	3 carbapenem	Susceptible					AdaBoost Classifie	Computational I	Me	
	acter baumannii	strain MRSN2999	95 tetracycline	Susceptible	<=	4	mg/L	MIC				
Acinetob	aatar haumannii	strain BL12	carbapenem	Resistant					AdaBoost Classifie	Computational I	Me	
_	acter baumannin											
Acinetob		strain MRSN7139	e imipenem	Susceptible	==	2	mg/L	MIC		Laboratory Meth	noc	

Antibiotic action button: Tobramycin (Overview display)

	Acinetobacter baumannii strain AB_363	carbapenem	Susceptible					AdaBoost Classifie	Computational Me
	Acinetobacter baumannii strain ABCRPUTH	imipenem	Resistant	=	64	mg/L	agar dilution		Laboratory Methoc
	Acinetobacter baumannii strain MRSN7388	tobramycin	Susceptible	==	4	mg/L	MIC		Laboratory Methoc
	Acinetobacter baumannii strain MRSN32076	ampicillin/sulbacta	Susceptible	<=	8/4	mg/L	MIC		
\square	Asiatishasia basancii shala MDON7794		Oursestible		0		140		1

Antibiotic View AMR Phenotypes AMR Genes AMR Regions Overview Antibiotic Name tobramycin Description PubChem CID 36294 CAS ID 32986-56-4 C18H37N5O9 Molecular Formula Molecular Weight 467.52 a/mol InChl Key NLVFBUXFDBBNBW-PBSUHMDJSA-N ATC Classification Antiinfectives for systemic use Antibacterials for systemic use Aminoglycoside antibacterials Other aminoglycosides

Tobramycin Sensory organs

Antiinfectives Antibiotics

Ophthalmologicals

Tobramycin

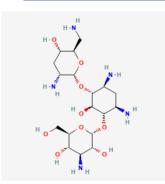
An aminoglycoside, broad-spectrum antibiotic produced by Streptomyces tenebrarius. It is effective against gramnegative bacteria, especially the pseudomonas species. It is a 10% component of the antibiotic complex, nebramycin, produced by the same species. [PubChem]

FDA Pharmacology Summary: Tobramycin is an Aminoglycoside Antibacterial. The chemical classification of tobramycin is Aminoglycosides.

LiverTox Summary: Tobramycin is a parenterally administered, broad spectrum aminoglycoside antibiotic that is widely used in the treatment of moderate to severe bacterial infections due to sensitive organisms. Despite its wide use, tobramycin has rarely been linked to instances of clinically apparent liver injury.

Metabolite Description: Tobramycin is only found in individuals that have used or taken this drug. It is an aminoglycoside, broad-spectrum antibiotic produced by Streptomyces tenebrarius. It is effective against gramnegative bacteria, especially the pseudomonas species. It is a 10% component of the antibiotic complex, nebramycin, produced by the same species. [PubChem]Tobramycin binds irreversibly to one of two aminoglycoside binding sites on the 30 S ribosomal subunit, inhibiting bacterial protein synthesis. Tobramycin may also destabilize bacterial memebrane by binding to 16 S 16 S r-RNA. An active transport mechanism for aminoglycoside uptake is necessary in the bacteria in order to attain a significant intracellular concentration of tobramycin.

2D Structure



Pharmacology: Tobramycin Base is an aminoglycoside antibiotic derived from Streptomyces tenebrarius with bacteriostatic activity. Following active transport into the cell, tobramycin binds irreversibly to a specific aminoglycoside receptor on the bacterial 30S ribosomal subunit and interferes with the initiation complex between messenger RNA and the 30S subunit, thereby inhibiting initiation of protein synthesis, consequently leading to bacterial cell death. In addition, tobramycin induces misreading of the mRNA template causing incorrect amino acids to be incorporated into the growing polypeptide chain, consequently interfering with protein elongation.

An aminoglycoside, broad-spectrum antibiotic produced by Streptomyces tenebrarius. It is effective against gramnegative bacteria, especially the PSEUDOMONAS species. It is a 10% component of the antibiotic complex, NEBRAMYCIN, produced by the same species.

Mechanism Of Action

(AMINOGLYCOSIDES/ INHIBIT PROTEIN BIOSYNTHESIS & DECR FIDELITY OF TRANSLATION OF GENETIC CODE. /AMINOGLYCOSIDES/

Aminoglycosides are usually bacterial in action. Although the exact mechanism of action has not been fully elucidated, the drugs appear to inhibit protein synthesis in susceptible bacteria by irreversibly binding to 30S ribosomal subunits. /Aminoglycosides/

Tobramycin binds irreversibly to one of two aminoglycoside binding sites on the 30 S ribosomal subunit, inhibiting bacterial protein synthesis. Tobramycin may also destabilize bacterial memebrane by binding to 16 S 16 S r-RNA. An active transport mechanism for aminoglycoside uptake is necessary in the bacteria in order to attain a significant intracellular concentration of tobramycin.

Pharmacology

Overview	AMR Phenotypes AMR	Genes AM	R Regions							
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OWNLOAD	KEYWORDS		ADV Sea	arch						HIDE
ublic (୍ Antibiotic ୍ ୧ ନ	esistant Phe	notype Q Evid	lence	۹	Laboratory Typin	a Method		Q Comp	utational N
ue (26229)		ndefined (669		nputational Method		Agar dilution (10)				oost Classif
	lı N F	ntermediate (6 lonsusceptible Resistant (124 susceptible (12	594) Com e (2) Labo 21)	iputational Predict	ion (6439) 095)	BD Phoenix ad E-t Computational Pre Etest (16) MIC (5402) MIC, broth microdi Microscan NEG 38 N206 card on the VITEK 2 (64)	diction (109) lution (23) g panel (11)			bost Classif
Genom	e Name	Antibiotic	Resistant Phenotype	Measurement Sign	Measuremer Value	nt Measurement Units	Lab typing Method	Computational Method	Evidence	Pubmed
Klebsiell	a pneumoniae strain EuSCAPE_R	C tobramycin	Resistant					AdaBoost Classifie	Computational Me	
Klebsiell	a pneumoniae strain SRRSH8	tobramycin	Susceptible					AdaBoost Classifie	Computational Me	
Klebsiell	a pneumoniae KPN1261ec	tobramycin	Resistant	>	8	mg/L	MIC		Laboratory Method	28512093,2
Klebsiell	a pneumoniae strain EuSCAPE_T	R tobramycin	Susceptible					AdaBoost Classifie	Computational Me	
Pseudon	nonas aeruginosa strain F2045	tobramycin			256	mg/L	MIC		Laboratory Method	32048461
Acinetob	acter baumannii strain MRSN738	8 tobramycin	Susceptible	==	4	mg/L	MIC		Laboratory Method	
Klebsiell	a pneumoniae KPN1102ec	tobramycin	Resistant					AdaBoost Classifie	Computational Me	
Klebsiell	a pneumoniae strain EuSCAPE_G	F tobramycin	Resistant					AdaBoost Classifie	Computational Me	
Klebsiell	a pneumoniae KPN238ec	tobramycin	Susceptible					AdaBoost Classifie	Computational Me	
Klebsiell	a pneumoniae strain EuSCAPE_I	f' tobramycin	Resistant					AdaBoost Classifie	Computational Me	
Klebsiell	a pneumoniae KPN377ec	tobramycin	Resistant					AdaBoost Classifie	Computational Me	
Klebsiell	a pneumoniae KPN1713ec	tobramycin	Resistant	>	8	mg/L	MIC		Laboratory Method	28512093,2
Pseudon	nonas aeruginosa strain PAER_4	tobramycin			8	mg/L	thermofisher_scier		Laboratory Method	31530672
Klebsiell	a pneumoniae strain NR0390	tobramycin	Resistant					AdaBoost Classifie	Computational Me	
Klebsiell	a pneumoniae strain Kpngiani713	24 tobramycin	Susceptible					AdaBoost Classifie	Computational Me	
Klebsiell	a pneumoniae subsp. pneumoniae	tobramycin	Susceptible					AdaBoost Classifie	Computational Me	
Klebsiell	a pneumoniae strain EuSCAPE_G	F tobramycin	Resistant					AdaBoost Classifie	Computational Me	
Klebsiell	a pneumoniae subsp. pneumoniae	e tobramycin		>	8	mg/L	MIC		Laboratory Method	24639510
Klebsiell	a pneumoniae subsp. pneumoniae	tobramycin	Resistant					AdaBoost Classifie	Computational Me	
Pseudon	nonas aeruginosa strain ESP039	tobramycin			2	mg/L	MIC		Laboratory Method	32048461
Klebsiell	a pneumoniae KPN1877ec	tobramycin	Resistant					AdaBoost Classifie	Computational Me	
Escheric	hia coli O11:H18 strain ECO0037	tobramycin	Susceptible						Laboratory Method	28720578
Klebsiell	a pneumoniae strain Kpngiani713	28 tobramycin	Resistant					AdaBoost Classifie	Computational Me	
Pseudon	nonas aeruginosa strain PSAE143	9 tobramycin			2	mg/L	MIC		Laboratory Method	32048461
Acinetob	acter baumannii strain MRSN741	7 tobramycin	Susceptible	==	2	mg/L	MIC		Laboratory Method	
Klebsiell	a pneumoniae strain EuSCAPE_I	r(tobramycin	Susceptible					AdaBoost Classifie	Computational Me	
Klebsiell	a pneumoniae strain KPM_76	tobramycin	Resistant					AdaBoost Classifie	Computational Me	
Klebsiell	a pneumoniae strain RHBSTW-00	0 tobramycin	Resistant					AdaBoost Classifie	Computational Me	

Antibiotic action button: Tobramycin (AMR Phenotypes display)

Antibiotic action button: Tobramycin (AMR Genes display)

Ov	erview AMR Phenotypes AMR	Genes Al	IR Regions							
				4						T
DOW	NLOAD KEYWORDS		A	DV Search						HIDE
Publ	ic Q Antibiotic Q R	esistant Ph	enotype 오	Evidence	۹ ۱	Laboratory Typin	g Method		Q Com	putational M
rue	in N R	ndefined (66 termediate onsusceptit esistant (12 usceptible ((694) ble (2) 421)	Computational Metho Computational Predic Laboratory Method (8	tion (6439) E (095) (E I I I I I I I I I I I I I I I I I I	Agar dilution (10) BD Phoenix ad E-t Computational Pre Etest (16) MIC (5402) MIC, broth microdi Microscan NEG 38 N206 card on the ¹ VITEK 2 (64)	diction (109) lution (23) 8 panel (11)		11	3oost Classifi∉ 3oost Classifi∉
	Genome Name	Antibiotic	Resistar Phenoty		Measurement Value	t Measurement Units	Lab typing Method	Computational Method	Evidence	Pubmed
	Klebsiella pneumoniae strain EuSCAPE_R	tobramycin	Resistant					AdaBoost Classifie	Computational N	e
	Klebsiella pneumoniae strain SRRSH8	tobramycin	Susceptib	le				AdaBoost Classifie	Computational N	e
	Klebsiella pneumoniae KPN1261ec	tobramycin	Resistant	>	8	mg/L	MIC		Laboratory Methe	oc 28512093,287
	Klebsiella pneumoniae strain EuSCAPE_TI	tobramycin	Susceptib	le				AdaBoost Classifie	Computational N	e
	Pseudomonas aeruginosa strain F2045	tobramycin			256	mg/L	MIC		Laboratory Methe	oc 32048461
	Acinetobacter baumannii strain MRSN7388	tobramycin	Susceptib	le ==	4	mg/L	MIC		Laboratory Methe	DC
	Klebsiella pneumoniae KPN1102ec	tobramycin	Resistant					AdaBoost Classifie	Computational N	e
	Klebsiella pneumoniae strain EuSCAPE_G	F tobramycin	Resistant					AdaBoost Classifie	Computational N	e
	Klebsiella pneumoniae KPN238ec	tobramycin	Susceptib	le				AdaBoost Classifie	Computational N	e
	Klebsiella pneumoniae strain EuSCAPE_IT	1 tobramycin	Resistant					AdaBoost Classifie	Computational N	e
	Klebsiella pneumoniae KPN377ec	tobramycin	Resistant					AdaBoost Classifie	Computational N	e
	Klebsiella pneumoniae KPN1713ec	tobramycin	Resistant	>	8	mg/L	MIC		Laboratory Methe	
	Pseudomonas aeruginosa strain PAER_4	tobramycin			8	mg/L	thermofisher_scier		Laboratory Meth	
	Klebsiella pneumoniae strain NR0390	tobramycin	Resistant					AdaBoost Classifie		
	Klebsiella pneumoniae strain Kpngiani7132		Susceptib					AdaBoost Classifie		
	Klebsiella pneumoniae subsp. pneumoniae		Susceptib	le				AdaBoost Classifie		
	Klebsiella pneumoniae strain EuSCAPE_G		Resistant	>				AdaBoost Classifie		
4	Klebsiella pneumoniae subsp. pneumoniae Klebsiella pneumoniae subsp. pneumoniae		Resistant	>	8	mg/L	MIC	AdaBoost Classifie	Laboratory Meth	
	Pseudomonas aeruginosa strain ESP039	tobramycin	Resistant		2	mg/L	MIC	Adaboost Classille	Laboratory Meth	
	Klebsiella pneumoniae KPN1877ec	tobramycin	Resistant		2	mg/L	MIC	AdaBoost Classifie	,	
	Escherichia coli O11:H18 strain ECO0037		Susceptib					Adaboost olassint	Laboratory Meth	
	Klebsiella pneumoniae strain Kpngiani7132		Resistant					AdaBoost Classifie		
	Pseudomonas aeruginosa strain PSAE143				2	mg/L	MIC		Laboratory Meth	
	Acinetobacter baumannii strain MRSN7417		Susceptib	le ==	2	mg/L	MIC		Laboratory Meth	
	Klebsiella pneumoniae strain EuSCAPE_IT		Susceptib			-		AdaBoost Classifie		
	Klebsiella pneumoniae strain KPM_76	tobramycin	Resistant					AdaBoost Classifie		
	-								Computational N	

Ov	verview	AMR Phenoty	pes AMR Genes	AMR Regions						
	L.				-					T
DOW		EYWORDS		A	DV Search					FILTERS
	Evidence	e Source	BRC ID	RefSeq Locus Tag	Source ID	Gene	Product	Pubmed	Identity	E-value
	BLAT	CARD	fig 573.43776.peg.49		ACL36604.1	AAC(6')-Ib	6'-N-acetyltransferase		100	1e-114
	BLAT	CARD	fig 573.15292.peg.33	8	AAA26550.1		hypothetical protein		100	2e-37
	BLAT	CARD	fig 287.2438.peg.790		AAA26550.1		hypothetical protein		100	5e-40
	BLAT	CARD	fig 133448.27.peg.55	5(AAA26550.1	AAC(6')-Ib	hypothetical protein		100	2e-37
	BLAT	CARD	fig 1733.8031.peg.47	r(AAA26550.1	AAC(6')-Ib	6'-N-acetyltransferase		98	3e-34
	BLAT	CARD	fig 587.278.peg.241		AAA26550.1	AAC(6')-Ib	hypothetical protein		100	3e-22
	BLAT	CARD	fig 72407.98.peg.681		AAA26550.1		hypothetical protein		100	3e-45
	BLAT	CARD	fig 573.46545.peg.59):	AAA26550.1	AAC(6')-Ib	6'-N-acetyltransferase		100	2e-18
	BLAT	CARD	fig 550.1213.peg.220	CIG53_27825	AAA26550.1		hypothetical protein		100	2e-14
	BLAT	CARD	fig 57706.121.peg.38	5(AAA26550.1	AAC(6')-Ib	hypothetical protein		100	6e-07
	BLAT	CARD	fig 573.24143.peg.59	0:	AAA26550.1	AAC(6')-Ib	6'-N-acetyltransferase		100	2e-18
	BLASTP	ARDB	fig 573.13023.peg.58	5(ABC54722		hypothetical protein		96	0.0000000
	BLAT	CARD	fig 573.17846.peg.58	5	AAA26550.1	AAC(6')-Ib	hypothetical protein		95	2e-47
	BLAT	CARD	fig 573.35466.peg.30	r	AAA26550.1	AAC(6')-Ib	6'-N-acetyltransferase		100	4e-11
	BLAT	CARD	fig 573.24422.peg.53	51	AAA26550.1	AAC(6')-Ib	6'-N-acetyltransferase		100	2e-18
	BLASTP	ARDB	fig 573.13398.peg.56	5t	P20092		hypothetical protein		96	0.0000000
	BLAT	CARD	fig 1733.8879.peg.45	5	AAA26550.1	AAC(6')-Ib	hypothetical protein		81	5e-02
	BLAT	CARD	fig 573.1438.peg.574	H.	ACL36604.1		Aminoglycoside N(6')-acetyltransferase (EC 2.3.1.82) =		100	1e-114
	BLAT	CARD	fig 573.1468.peg.583	5	ACL36604.1		Aminoglycoside N(6')-acetyltransferase (EC 2.3.1.82) =		100	1e-102
	BLAT	CARD	fig 573.1474.peg.562	2	ACL36604.1		Aminoglycoside N(6')-acetyltransferase (EC 2.3.1.82) =		100	1e-114
	BLAT	CARD	fig 573.1454.peg.585	51	ACL36604.1		Aminoglycoside N(6')-acetyltransferase (EC 2.3.1.82) =		100	1e-114
	BLAT	CARD	fig 573.1467.peg.586	5.	ACL36604.1		Aminoglycoside N(6')-acetyltransferase (EC 2.3.1.82) =		100	1e-113
	BLAT	CARD	fig 573.1384.peg.559		ACL36604.1		Aminoglycoside N(6')-acetyltransferase (EC 2.3.1.82) =		100	1e-114
	BLAT	CARD	fig 573.1381.peg.557	с.	ACL36604.1		Aminoglycoside N(6')-acetyltransferase (EC 2.3.1.82) =		100	1e-114
	BLAT	CARD	fig 573.1438.peg.434		ACL36604.1		Aminoglycoside N(6')-acetyltransferase (EC 2.3.1.82) =		100	8e-36
	BLAT	CARD	fig 573.1468.peg.551	1	ACL36604.1		Aminoglycoside N(6')-acetyltransferase (EC 2.3.1.82) =		100	2e-54
	BLAT	CARD	fig 1733.9038.peg.45	5	AAA26550.1	AAC(6')-Ib	6'-N-acetyltransferase		98	2e-46
	BLAT	CARD	fig 573.1389.peg.536	6	ACL36604.1		Aminoglycoside N(6')-acetyltransferase (EC 2.3.1.82) =		99	1e-113
	BLAT	CARD	fig 573.1414.peg.576	č.	ACL36604.1		Aminoglycoside N(6')-acetyltransferase (EC 2.3.1.82) =		100	1e-114
	BLAT	CARD	fig 573.1403.peg.586	<u>.</u>	ACL36604.1		Aminoglycoside N(6')-acetyltransferase (EC 2.3.1.82) =		100	1e-114
	BLAT	CARD	fig 1733.9012.peg.50)(AAA26550.1	AAC(6')-Ib	6'-N-acetyltransferase		98	6e-35
	BLAT	CARD	fig 573.1420.peg.558	8.	ACL36604.1		Aminoglycoside N(6')-acetyltransferase (EC 2.3.1.82) =		100	4e-91
	BLAT	CARD	fig 573.1424.peg.576	ò	ACL36604.1		Aminoglycoside N(6')-acetyltransferase (EC 2.3.1.82) =		100	1e-114
	BLAT	CARD	fig 573.1437.peg.565	5	ACL36604.1		Aminoglycoside N(6')-acetyltransferase (EC 2.3.1.82) =		99	1e-113
	BLAT	CARD	fig 573.1469.peg.583	9	ACL36604.1		Aminoglycoside N(6')-acetyltransferase (EC 2.3.1.82) =		100	1e-113
	BLAT	CARD	fig 573.44634.peg.75	LVA95_28960	AAA26550.1	AAC(6')-Ib	6'-N-acetyltransferase		100	2e-37
	BLAT	CARD	fig 573.1427.peg.591	(ACL36604.1		Aminoglycoside N(6')-acetyltransferase (EC 2.3.1.82) =		100	1e-114

Antibiotic action button: Tobramycin (AMR Genes display)

0	verview	AMR Phenotypes	AMR Genes	AMR	Regions								
	•					-							T
00	WNLOAD	KEYWORDS				ADV Search FILTERS							
	Genome ID	Genome Name	Acces	sion	Feature Type	BRC ID	RefSeq Locus Tag	Start	End	Strand	Length (NA)	Gene Symbol	Product
	573.15849	Klebsiella pneumoniae	AF479	774	classifier_pr	fig 573.15849.0		6288	6302	+	15		Tobramycin resistance predicted regi
	573.15849	Klebsiella pneumoniae	AF479	774	classifier_pr	fig 573.15849.0	:	11161	11180	+	20		Tobramycin resistance predicted regi
]	573.27727	Klebsiella pneumoniae	CABH	KH01000	classifier_pr	fig 573.27727.0	:	311936	311950	+	15		Tobramycin resistance predicted regi
	573.27727	Klebsiella pneumoniae	CABH	KH01000	classifier_pr	fig 573.27727.0	:	1745373	1745387	+	15		Tobramycin resistance predicted regi
	573.27727	Klebsiella pneumoniae	CABH	KH01000	classifier_pr	fig 573.27727.0	:	1749837	1749851	+	15		Tobramycin resistance predicted regi
	573.27727	Klebsiella pneumoniae	CABH	KH01000	classifier_pr	fig 573.27727.0		4390054	4390068	+	15		Tobramycin resistance predicted regi
]	573.27727	Klebsiella pneumoniae	CABH	KH01000	classifier_pr	fig 573.27727.0		78494	78508	+	15		Tobramycin resistance predicted regi
	573.27727	Klebsiella pneumoniae	CABH	KH01000	classifier_pr	fig 573.27727.0	2	154228	154242	+	15		Tobramycin resistance predicted regi
	573.27729	Klebsiella pneumoniae	CABH	KI010000	classifier_pr	fig 573.27729.0	si	195694	195708	+	15		Tobramycin resistance predicted regi
]	573.27729	Klebsiella pneumoniae	CABH	KI010000	classifier_pr	fig 573.27729.0	si i	3980	3994	+	15		Tobramycin resistance predicted reg
	573.27729	Klebsiella pneumoniae	CABH	KI010000	classifier_pr	fig 573.27729.0	si i	7393	7407	+	15		Tobramycin resistance predicted reg
]	573.27729	Klebsiella pneumoniae	CABH	KI010000	classifier_pr	fig 573.27729.0	:l	2392291	2392305	+	15		Tobramycin resistance predicted reg
]	573.27729	Klebsiella pneumoniae	CABH	KI010000	classifier_pr	fig 573.27729.0	:	2396744	2396758	+	15		Tobramycin resistance predicted reg
]	573.27729	Klebsiella pneumoniae	CABH	KI010000	classifier_pr	fig 573.27729.0	:l	4651	4665	+	15		Tobramycin resistance predicted reg
]	573.27729	Klebsiella pneumoniae	CABH	KI010000	classifier_pr	fig 573.27729.0	:	8071	8085	+	15		Tobramycin resistance predicted reg
)	573.27729	Klebsiella pneumoniae				fig 573.27729.0		11491	11505	+	15		Tobramycin resistance predicted reg
)	573.27729	Klebsiella pneumoniae	CABH	KI010000	classifier_pr	fig 573.27729.0	:I	20116	20130	+	15		Tobramycin resistance predicted reg
]	573.27729	Klebsiella pneumoniae	CABH	KI010000	classifier_pr	fig 573.27729.0	:l	21450	21464	+	15		Tobramycin resistance predicted reg
]	573.27729	Klebsiella pneumoniae				fig 573.27729.0		22070	22084	+	15		Tobramycin resistance predicted reg
ן	573.27729	Klebsiella pneumoniae				fig 573.27729.0		62806	62820	+	15		Tobramycin resistance predicted reg
ר	573.27729	Klebsiella pneumoniae				fig 573.27729.0		66226	66240	+	15		Tobramycin resistance predicted reg
ר	573.27729	Klebsiella pneumoniae				fig 573.27729.0		69643	69657	+	15		Tobramycin resistance predicted reg
ר	573.27729	Klebsiella pneumoniae				fig 573.27729.0		73053	73067	+	15		Tobramycin resistance predicted reg
ר	573.27724	Klebsiella pneumoniae				fig 573.27724.c		1736	1750	+	15		Tobramycin resistance predicted reg
ר	573.27724	Klebsiella pneumoniae				fig 573.27724.c		173161	173175	+	15		Tobramycin resistance predicted reg
ר	573.27724	Klebsiella pneumoniae				fig 573.27724.c		522612	522626	+	15		Tobramycin resistance predicted reg
ר	573.27724	Klebsiella pneumoniae				fig 573.27724.0		3250210	3250224	+	15		Tobramycin resistance predicted reg
ר	573.27724	Klebsiella pneumoniae				fig 573.27724.0		3254663	3254677	+	15		Tobramycin resistance predicted reg
ר	573.27724	Klebsiella pneumoniae				fig 573.27724.0		79537	79556	+	20		Tobramycin resistance predicted reg
ר	573.27724	Klebsiella pneumoniae				fig 573.27724.0		82765	82779	+	15		Tobramycin resistance predicted reg
ר	573.27725	Klebsiella pneumoniae				fig 573.27724.0		1604	1618	+	15		Tobramycin resistance predicted reg
ר	573.27725	Klebsiella pneumoniae				fig 573.27725.c		15578	15597	+	20		Tobramycin resistance predicted reg
ר ר	573.27725	Klebsiella pneumoniae				fig 573.27725.0		26418	26432	+	15		Tobramycin resistance predicted reg
ר	573.27725	Klebsiella pneumoniae				fig 573.27725.0		26418	26432	+	15		Tobramycin resistance predicted reg
ר	573.27725	Klebsiella pneumoniae						28372		+			
L						fig 573.27725.0			28386	+	15		Tobramycin resistance predicted reg
	573.27725	Klebsiella pneumoniae				fig 573.27725.0		220390	220404		15		Tobramycin resistance predicted reg
J	573.27725	Klebsiella pneumoniae	CABH	KKU1000	classifier_pr	fig 573.27725.0	2	148	162	+	15		Tobramycin resistance predicted reg

Antibiotic action button: Tobramycin (AMR Regions display)