How To: Download all the reference sequences for a set of proteins (e.g., all *aac(6')-lb* sequences)

NCBI Pathogen Detection

https://www.ncbi.nlm.nih.gov/pathogens



U.S. National Library of Medicine National Center for Biotechnology Information How do I download all the reference sequences for a set of proteins? (e.g., all *aac(6')-lb* sequences)

- Use <u>MicroBIGG-E</u>
- Use filters or search to select gene family "aac(6')-lb*"
- Download table containing protein accessions
- Use Batch Entrez to download proteins



https://www.ncbi.nlm.nih.gov/pathogens

Pathogen Detection **BETA**

To assist the National Database of Antibiotic Resistant Organisms (NDARO), NCBI Pathogen Detection identifies the antimicrobial resistance, stress response, and virulence genes found in bacterial genomic sequences. This enables scientists to track the spread of resistance genes and to understand the relationships between antimicrobial resistance and virulence.

NCBI Pathogen Detection integrates bacterial pathogen genomic sequences originating in food, environmental sources, and patients. It quickly clusters and identifies related sequences to uncover potential food contamination sources, helping public health scientists investigate foodborne disease outbreaks.

There has been a change to the *Isolation type / epi_type* attribute that affects *min-same/min-diff* computation. Now where an isolate has no information to support the setting *environmental/other* the Browser will no longer default to that value but instead present as *NULL*. This means that the *min-same/min-diff* values for this isolate will present as *n/a*, and other *min-same/min-diff* values for isolates clustered with this isolate may change. Please see the <u>Help</u> text for more details.

Learn More About FAQ **Browser Factsheet** Antimicrobial Resistance Factsheet Antimicrobial Resistance Contributors Help Data Resour 1. Click Reference **Gene Catalog Isolates Browser** Microbial Browse Genomic Elements (Mi G-E) **Reference Gene Catalog** NEW Reference HMM Catalog

<u>Health</u> > <u>Pathogen Detection</u> > Reference Gene Catalog

Search			2. Click Filters show filte		,	
db version: 2021-08-11.1 Changelog					<u>_</u>	
						Filters 4
Available filters C	4	Search aac(6')-Ib		C	×	
Filter	gene	gene family		Count		
allele	e family	aac(6')-Ib				
gene family	ily	aac(6')-Ib-cr		10		4 Enter "acc(6') Ib" and coloct
product name		aac(6')-Ib11		2		4. Enter "aac(6')-lb" and select
scope		aac(3)-Ib/aac(6')-Ib"		1		the gene families of interest
3. Select gene family to show the gene family filter subclass curated refseq start whitelisted taxa blacklisted taxa genbank strand orientation genbank cds start pubmed reference		 aac(6')-30/aac(6')-Ib aac(6')-1b' ant(3'')-Ij/aac(6')-Ib catB8/aac(6')-Ib' 		1 1 1 1 1		
synonyms	~	Total unique values: 8				
Page 1 of 4 🕨 💦 Records	s per l	Page 20 🔽 🔲 Choos	e columns 🛛 📩 Download			

_ Search - gene_fa	amily:aac(6')-Ib*		5. Alternatively, use the search term "gene_family" to find the aac(6')-Ib family			×	
lb versio	on: 2021-08-11.1	Changelog	members				
					Filters		
14 4	Page 1 of 4	► N @	Records per Page 20 💉 🖸 Choose columns 🛃 Download				
#	allele	gene family	product name	scope	type	subtype	cla
1		aac(6')-Ib	AAC(6')-Ib family aminoglycoside 6'-N-acetyltransferase	core	AMR	AMR	A
2		aac(6')-Ib	AAC(6')-Ib family aminoglycoside 6'-N-acetyltransferase	core	AMR	AMR	A
3		aac(6')-Ib	AAC(6')-Ib family aminoglycoside 6'-N-acetyltransferase	core	AMR	AMR	A
4		aac(6')-Ib	AAC(6')-Ib family aminoglycoside 6'-N-acetyltransferase	core	AMR	AMR	A
5		aac(6')-Ib	AAC(6')-Ib family aminoglycoside 6'-N-acetyltransferase	core	AMR	AMR	A
6		aac(6')-Ib	AAC(6')-Ib family aminoglycoside 6'-N-acetyltransferase	core	AMR	AMR	A
7		aac(6')-Ib	AAC(6')-Ib family aminoglycoside 6'-N-acetyltransferase	core	AMR	AMR	A
8		aac(6')-Ib	AAC(6')-Ib family aminoglycoside 6'-N-acetyltransferase	core	AMR	AMR	A
9		aac(6')-Ib	AAC(6')-Ib family aminoglycoside 6'-N-acetyltransferase	core	AMR	AMR	AN
10		aac(6')-Ib	AAC(6')-Ib family aminoglycoside 6'-N-acetyltransferase	core	AMR	AMR	AN
11		aac(6')-Ib	AAC(6')-Ib family aminoglycoside 6'-N-acetyltransferase	core	AMR	AMR	AN
12		aac(6')-Ib	AAC(6')-Ib family aminoglycoside 6'-N-acetyltransferase	core	AMR	AMR	AN
13		aac(6')-Ib	AAC(6')-Ib family aminoglycoside 6'-N-acetyltransferase	core	AMR	AMR	A
14		aac(6')-Ib	AAC(6')-Ib family aminoglycoside 6'-N-acetyltransferase	core	AMR	AMR	AN
15		aac(6')-Ib	AAC(6')-Ib family aminoglycoside 6'-N-acetyltransferase	core	AMR	AMR	AN
16		aac(6')-Ib	AAC(6')-Ib family aminoglycoside 6'-N-acetyltransferase	core	AMR	AMR	AN
17		aac(6')-Ib	AAC(6')-Ib family aminoglycoside 6'-N-acetyltransferase	core	AMR	AMR	AM

1	-	
L	•	
L	,	
•	-	

_				

db version: 2021-08-11.1 Changelog

Search

Available	filters C	4	Search	aac(6')-Ib		C	×
Filter		gene family	gei	ne family	Co	ount	
allele	2	fam	🔽 aa	c(6')-Ib	55	5	
🔽 gene	family	γli	🔽 aa	c(6')-Ib-cr	10)	
prod	uct name		📝 aa	c(6')-Ib11	2		
scop	e		aa	c(3)-Ib/aac(6')-Ib''	1		
type			aa	c(6')-30/aac(6')-Ib'	1		
subt			📝 aa	c(6')-Ib'	1		
class			ant	t(3")-Ij/aac(6')-Ib	1		
subc			Cat	:B8/aac(6')-Ib'	1		
	Select Download to download table						
pubr	ned reference						
syno	nyms		Total ur	ique v. s: 8			
	Page 1 of 4 🕨 🔰 🍣 Rec	ords per P	age 20	Choose columns	Download		1

#	allele	gene family	product name	scope	type	subtype	class
1		aac(6')-Ib	AAC(6')-Ib family aminoglycoside 6'-N-acetyltransferase	core	AMR	AMR	AMI
2		aac(6')-Ib	AAC(6')-Ib family aminoglycoside 6'-N-acetyltransferase	core	AMR	AMR	AMIN

Fi	Iter	S	Λ
	itei	2	

	ilable filters	(C		Search	aac(6')-I	b			3	X			
	Filter			gene	gen	ne family			C	Count				
	allele				🚺 aac	:(6')-Ib			5	55				
7	gene family			Vii	🔽 aac	:(6')-Ib-cr			1	.0				
	product name			[🔽 aac	:(6')-Ib11			2	2				
	scope				aac	:(3)-Ib/aad	c(6')-Ib''		1	-				
	type			[aac	:(6')-30/aa	ac(6')-Ib'		1					
	subtype				🔽 aac	:(6')-Ib'			1					
	class				ant	(3'')-Ij/aa	c(6')-Ib		1					
	subclass			[cat	B8/aac(6')	-Ib'		1					
	curated refseq start													
	whitelisted taxa													
	blacklisted taxa													
_														
	genbank strand orientation													
	genbank strand orientation													
	ge	ad to												
	ge ge 7. Click Downlo		0											
	^{ge} 7. Click Downlo		o		Total un	ique value	es: 8							
	^{ge} ^{ge} ^{ge} ^{7.} Click Downlo ^{pu} download tal		0		Total un	ique value	es: 8							
	^{ge} ^{ge} ^{ge} ^{7.} Click Downlo ^{pu} download tal		•		Total un	ique value	es: 8							
	^{ge} ^{ge} ^{ge} ^{7.} Click Downlo ^{pu} download tal	ble	D Records			ique value	es: 8	ns 🛃 Dow	nload					
	ge ge pu syi	ble		per Pag	ge 20			ns 🛃 Dow	nload		×	type	subtype	clas
	ge ge pu syl Page 1 of 4	ble R mily	Records	per Pag t name	ge 20		Downlos					type AMR	subtype AMR	
	ge ge pu syi syi Page 1 of 4 allele gene far aac(6')-1	ble 2 R mily Ib	Records produc AAC(6'	per Pag t name)-Ib far	ge 20 e mily amin	noglycos	Shoose colum		nload -delimited	(.tsv)	×			AM
	ge ge pu syl Syl Page 1 of 4 M allele gene far	ble R mily Ib Ib	Records produc AAC(6' AAC(6'	per Pag t name)-Ib far)-Ib far	ge 20 e mily amin		Downlos	Tab		(.tsv)		AMR	AMR	AM AM
	ge 7. Click Download tal ge 7. Click Download tal ge 1 of 4 Page 1 of 4 allele gene far aac(6')-1 aac(6')-1 aac(6')-1 aac(6')-1	ble i and the second s	Records produc AAC(6' AAC(6'	per Pag tt name)-Ib far)-Ib far)-Ib far	ge 20 e mily amin mily amin mily amin	noglycos	Download Type:	Tab	-delimited	(.tsv)		AMR AMR	AMR AMR	AM AM
	ge ge pu syi Page 1 of 4 allele gene far aac(6')-1 aac(6')-1	ble Ring Ring Ring Ring Ring Ring Ring Ring	Records produc AAC(6' AAC(6' AAC(6' AAC(6'	per Pag t name)-Ib far)-Ib far)-Ib far)-Ib far	ge 20 e mily amin mily amin mily amin mily amin	noglycos noglycos noglycos	Download Type:	Tab refge	-delimited	(.tsv) Can	~	AMR AMR AMR	AMR AMR AMR	Clas AM AM AM AM

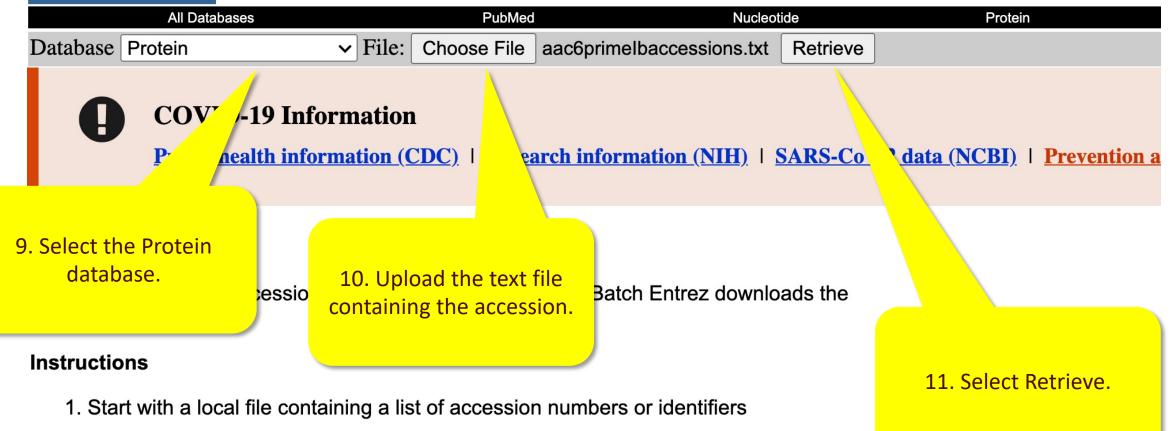
WP_071846254.1
WP_065187201.1
WP_063840283.1
WP_063978482.1
WP_063840319.1
WP_071846332.1
WP_101516660.1
WP_085844237.1
WP_085843736.1
WP_063612062.1
WP_071846208.1
WP_071846209.1
WP_071846373.1
WD 071946241 1

gene family	product namescope	type	subtype	class	subclass	refseq protein	refse
aac(6')-Ib	AAC(6')-Ib fai core	AMR	AMR	AMINOGLYC	AMIKACIN/G	WP_071846254.1	NG_C
aac(6')-Ib	AAC(6')-Ib fai core	AMR	AMR	AMINOGLYC	AMIKACIN/G	WP_065187201.1	NG_C
aac(6')-Ib	AAC(6')-Ib fai core	AMR	AMR	AMINOGLYC	AMIKACIN/K	WP_063840283.1	NG_C
aac(6')-Ib	AAC(6')-Ib fai core	AMR	AMR	AMINOGLYC	AMIKACIN/K	WP_063978482.1	NG_0
aac(6')-Ib	AAC(6')-Ib fai core	AMR	AMR	AMINOGLYC	AMIKACIN/K	WP_063840319.1	NG_0
aac(6')-Ib	AAC(6')-Ib fai core	AMR	AMR	AMINOGLYC	AMIKACIN/K	WP_071846332.1	NG_0
aac(6')-Ib	AAC(6')-Ib fai core	AMR	AMR	AMINOGLYC	AMIKACIN/K	WP_101516660.1	NG_0
aac(6')-Ib	AAC(6')-Ib fai core	AMR	AMR	AMINOGLYC	AMIKACIN/K	WP_085844237.1	NG_(
aac(6')-Ib	AAC(6')-Ib fai core	AMR	AMR	AMINOGLYC	AMIKACIN/K	WP_085843736.1	NG_0
aac(6')-Ib	AAC(6')-Ib fai core	AMR	AMR	AMINOGLYC	AMIKACIN/K	WP_063612062.1	NG_0
aac(6')-Ib	AAC(6')-Ib fai core	AMR	AMR	AMINOGLYC	AMIKACIN/K	WP_071846208.1	NG_0
aac(6')-Ib	AAC(6')-Ib fai core	AMR	AMR	AMINOGLYC	AMIKACIN/K	WP_071846209.1	NG_0
aac(6')-Ib	AAC(6')-Ib fai core	AMR	AMR	AMINOGLYC	AMIKACIN/K	WP_071846373.1	NG_0
aac(6')-Ib	AAC(6')-Ib fai core	AMR	AMR	AMINOGLYC	AMIKACIN/K	WP_071846241.1	NG_(
aac(6')-Ib	AAC(6')-Ib fai core	AMR	AMR	AMINOGLYC	AMIKACIN/K	WP_064765190.1	NG_0
aac(6')-Ib	AAC(6')-Ib fai core	AMR	AMR	AMINOGLYC	AMIKACIN/K	WP_071593230.1	NG_(
aac(6')-Ib	AAC(6')-Ib fai core	AMR	AMR	AMINOGLYC	AMIKACIN/K	WP_063840280.1	NG_0
aac(6')-Ib	AAC(6')-Ib fai core	AMR	AMR	AMINOGLYC	AMIKACIN/K	WP_069067473.1	NG_0
aac(6')-Ib	AAC(6')-Ib fai core	AMR	AMR	AMINOGLYC	AMIKACIN/K	WP_063840281.1	NG_0
aac(6')-Ib	AAC(6')-Ib fai core	AMR	AMR	AMINOGLYC	AMIKACIN/K	WP_159287722.1	NG_0
aac(6')-Ib	AAC(6')-Ib fai core	AMR	AMR	AMINOGLYC	AMIKACIN/K	WP_113613509.1	NG_0
aac(6')-Ib	AAC(6')-Ib fai core	AMR	AMR	AMINOGLYC	AMIKACIN/K	WP_123085936.1	NG_0
aac(6')-Ib	AAC(6')-Ib fai core	AMR	AMR	AMINOGLYC	AMIKACIN/K	WP_079452738.1	NG_0
aac(6')-Ib	AAC(6')-Ib fai core	AMR	AMR	AMINOGLYC	AMIKACIN/K	WP_132629969.1	NG_0
aac(6')-Ib	AAC(6')-Ib fai core	AMR	AMR	AMINOGLYC	AMIKACIN/K	WP 117046752.1	NG (

8. Place the protein accessions into a single column text file, with one accession per row. Then go to Batch Entrez

S NCBI

Batch Entrez

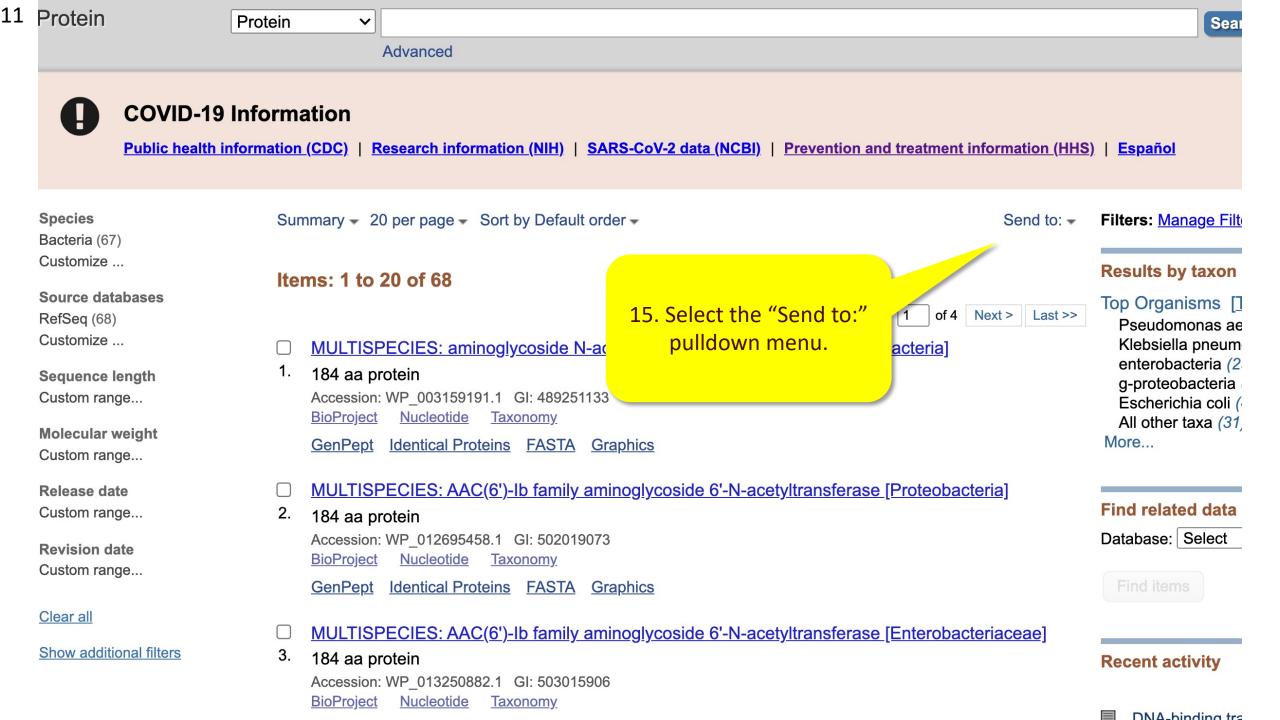


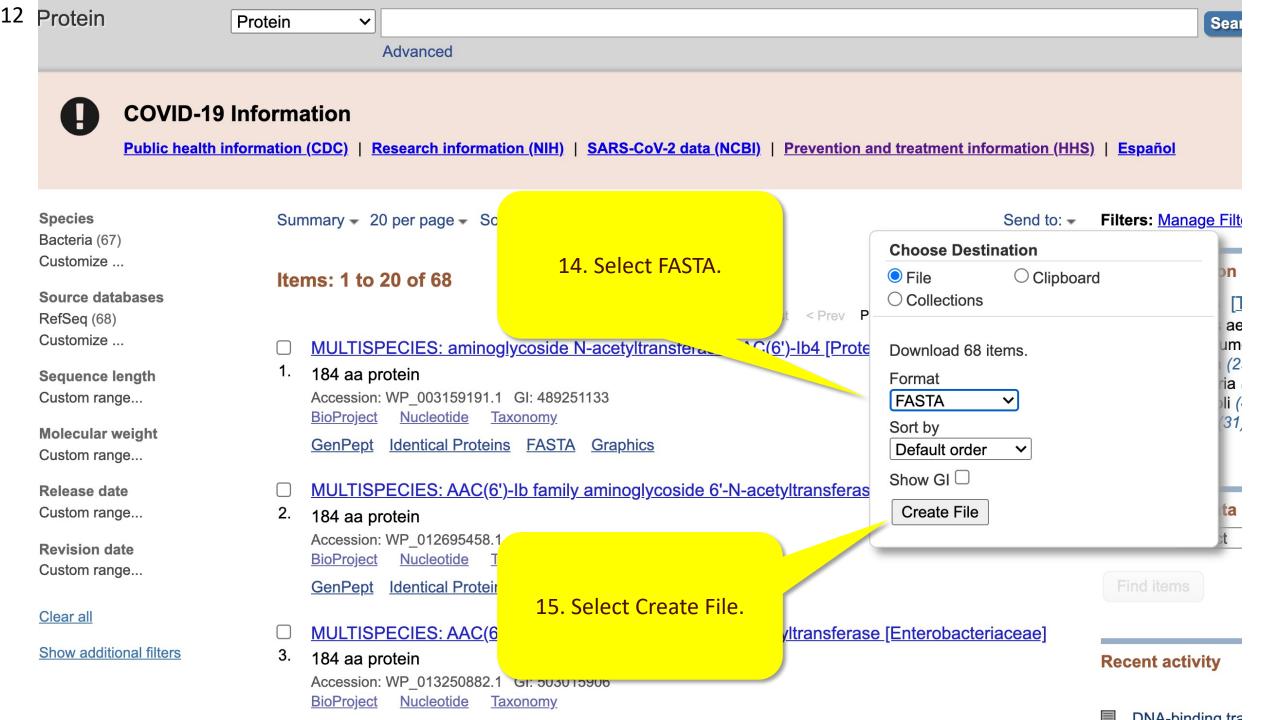
- 2. Select the database corresponding to the type of accession numbers or identifiers in your input file
- 3. Use the Browse or Choose File... button to select the input file
- 4. Press the Retrieve button to see a list of document summaries
- 5. Select a format in which to display the data for viewing, and/or saving
- 6. Select 'Send to file' to save the file.

10

Received lines: 68 Rejected lines: 0 Removed duplicates: 0 Passed to Entrez: 68 <u>Retrieve records for 68 UID(s)</u>

12. Select Retrieve.





More information

- For full help documentation of the Reference Gene Catalog see: https://www.ncbi.nlm.nih.gov/pathogens/pathogens_help/#reference-gene-catalog
- For details about filters see: https://www.ncbi.nlm.nih.gov/pathogens/pathogens_help/#refgene-filters
- For details about the table downloads see: https://www.ncbi.nlm.nih.gov/pathogens/pathogens_help/#refgene-access-download

Questions and further help: email pd-help@ncbi.nlm.nih.gov

