Meeting Notes with Farny 7/10/17

Community Outreach

- So many contacts are getting back to us! Exciting
- Lead assay
    - Document protocol as detailed as possible (i.e. how many seconds lead and gold should sit together before GSH is added)
    - Should be reproducible in someone else's hands/lab (i.e. collaboration with BU—so great! Helping us and them)

Social Media

- Important to tell other teams through social media where we are getting our products
- Share on wiki programing that allows her to post to Instagram, Facebook, and twitter at the same time
    - Judges like to see that we are helping other teams

Graphic Design

- Important updates to make it easier to understand our presentation (from comments from NEGEM)
- Jamboree banners
- Make a version of design with Pbr gene that has all three chromoproteins (different promotors for each): hopeful product
- Proof of principle version: contains GFP
    - Showing that we can get different amounts of GFP with our altered promotors
    - GOLD medal requirements

Collaborations

- Aachen: we will look into salt in water in US, they will look into whether lead in water is a problem there
    - Great to know where lead is a problem (not only in US, but globally)
- Way better than last year's collaborations ☺

Human Practices

- Boston public schools spends so much on bottled water
- Probiotic = prophylactic; biosensor? What if we need to test a lot of water for a low cost?
    - Maybe use biosensor in those public health emergency situations (lessens negative comments about having people growing bacteria in their own homes)
    - Form that people could submit their data so the city can map out where contamination is coming from
    - Options given at end of presentation: multiple implementations of our design
    - Showing that we asked for advice (from DEP), took that advice and changed how we see our project being implemented → integrated human practices

- Case Study
    - Part 1: use narrative to come up with educated guess about synthetic bio and then discuss
    - Part 2 and 3: more data based
    - Data analysis for students to do is always good → ask them to draw conclusions

Wiki Master

- Post information where the judges will be looking for it **** very important
- Great that we are working on this ahead of time ☺
- It is okay if notebooks are PDFs
- Supplemental data for week x bullet point under bullet point for week PDF
- Integrated human practices need to be very detailed on the page to explain how we asked for advice, took that advice, and integrated into our project

KEY to our project is reproducibility: we are basing everything on the fact that the work the team in Australia did is reproducible which is why we are working with the promotors first using GFP

Parts: compound part with various promotors and three chromoproteins; different versions of the lead promotor on their own; pbrR if it isn't already in the registry

- Look to see if pbr and pbrR parts are in the registry
- Always good to check in with medal requirements

Modeling

- Contact from iGEM measurement committee (Jake?)
- Phone call/skype with someone at iGEM HQ
- Prof Johnson: Dif. Eqs
- Reach out to a team that has won a modeling award
- Part:BBa_I721002 page: contains modeling?
    - Alignment needed to make sure that the promotor that exists in this part is the same

CONTINUED RESEARCH NEEDED ON PAST IGEM TEAMS! (see link on 7/10/17 benchling)

Culturelle: pure Lactobacillus rhamnosis GG?

- PCR small ribosomal binding site; additional small world identification stuff

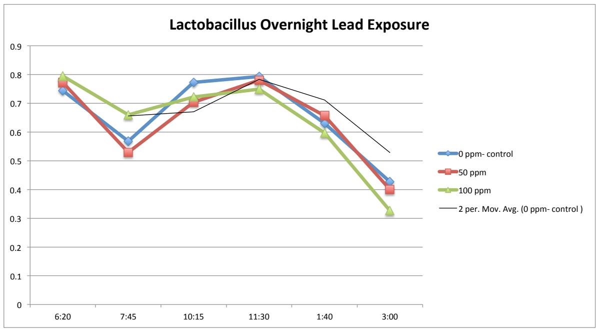
Lactobacillus: growth on lead plates instead of growth curves?

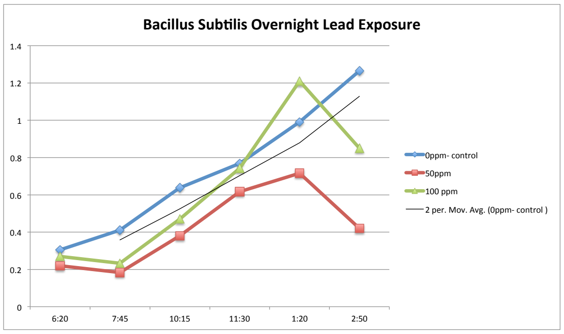
Thursday 1:30 pm: PBS NOVA

Lead Growth Curve Optimization Trial 1

Lactobacillus	Experiment 1	Overnight Lead Exposure	
Time	0 ppm- control	50 ppm	100 ppm
6:20	0.744	0.772	0.795 (1:10)
7:45	0.568	0.529	0.66 (1:10)
10:15	0.773	0.704	0.722 (1:10)
11:30	0.793	0.78	0.749 (1:10)
1:40	0.63	0.657	0.597 (1:10)
3:00	0.427	0.4	0.3265 (1:10)

B.subtilis			
Time	0ppm- contr	50ppm	100 ppm
6:20	0.305	0.22	0.27
7:45	0.411	0.183	0.233
10:15	0.638	0.38	0.47
11:30	0.768	0.617	0.743
1:20	0.991	0.716	1.21
2:50	1.265	0.42	0.85



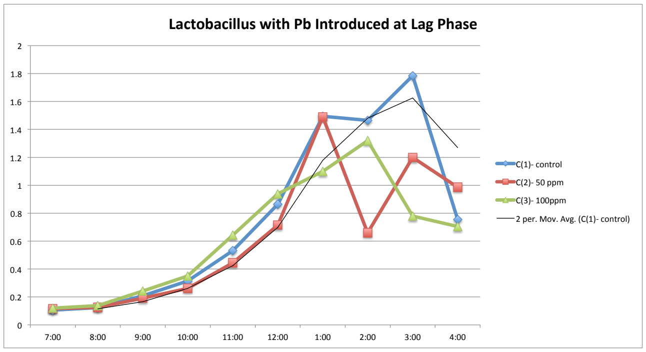


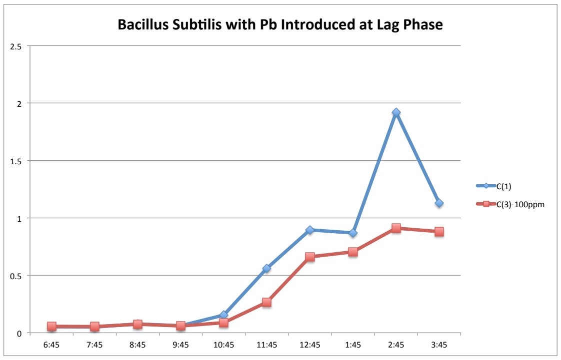
Parent culture - 1.038

Lactobacillus	Experiment 2	Added lead at lag phase	
Time	C(1)- control	C(2)- 50 ppm	C(3)- 100ppm
7:00	0.106	0.116	0.12
8:00	0.124	0.125	0.138
9:00	0.209	0.191	0.243
10:00	0.315	0.261	0.35
11:00	0.532	0.444	0.642
12:00	0.864	0.714	0.939
1:00	1.495	1.49	1.1
2:00	1.465	0.66	1.32
3:00	1.785	1.2	0.78
4:00	0.755	0.985	0.705

Parent culture- 0.230

B.subtilis		
Time	C(1)	C(3)-100ppm
6:45	0.051	0.056
7:45	0.049	0.053
8:45	0.076	0.074
9:45	0.062	0.059
10:45	0.154	0.088
11:45	0.56	0.266
12:45	0.896	0.661
1:45	0.87	0.705
2:45	1.92	0.91
3:45	1.13	0.88



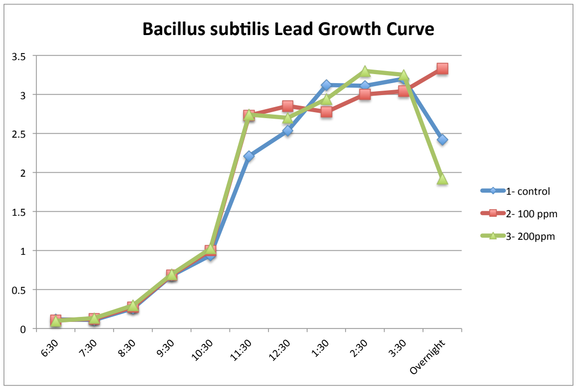


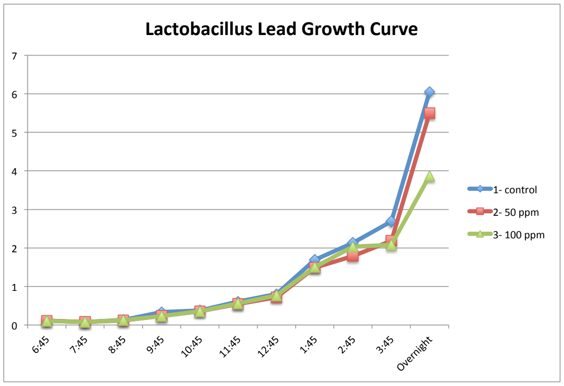
Lead Growth Curve Optimization Trial 2

(7/11/17)

Time	B.subtilis			
	1- control	2- 100 ppm	3- 200ppm	
6:30	0.118	0.106	0.099	Add Lead/H20
7:30	0.11	0.1225	0.133	
8:30	0.2585	0.274	0.296	
9:30	0.68	0.685	0.695	
10:30	0.939	1	1.023	
11:30	2.21	2.73	2.74	
12:30	2.535	2.85	2.7	
1:30	3.12	2.775	2.94	
2:30	3.11	3	3.3	
3:30	3.2	3.04	3.25	
Overnight	2.42	3.33	1.92	

Time	Lactobacillus			
	1- control	2- 50 ppm	3- 100 ppm	
6:45	0.11	0.11	0.105	Add lead/ h20
7:45	0.077	0.0745	0.078	
8:45	0.132	0.122	0.123	
9:45	0.3365	0.235	0.2305	
10:45	0.377	0.357	0.359	
11:45	0.6115	0.5445	0.5575	
12:45	0.807	0.722	0.77	
1:45	1.69	1.49	1.5	
2:45	2.13	1.79	2.03	
3:45	2.69	2.19	2.08	
Overnight	6.05	5.5	3.87	





LB (2)

1:30

0-No GSH 0 5000 2000 1500 1000

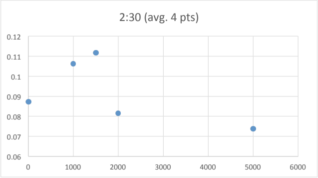
	1	2	3	4	5	6	7	8	9	10	11	12	
A	0.099	0.089	0.074	0.077	0.118	0.114							595
B	0.098	0.082	0.072	0.078	0.115	0.103							595
C	0.094	0.093	0.071	0.08	0.106	0.108							595
D	0.092	0.08	0.073	0.086	0.107	0.106							595
E													595
F													595
G													595
H													595

	0-No GSH	0	5000	2000	1500	1000
Avg. (3/4)	0.097	0.0836667	0.072	0.0783333	0.1093333	0.1056667
St. Dev.	0.0026458	0.0047258	0.001	0.0015275	0.0049329	0.0025166
Avg. (3/4)	0.09575	0.086	0.0725	0.08025	0.1115	0.10775
St. Dev.	0.003304	0.0060553	0.001291	0.0040311	0.0059161	0.0046458

2:30

	1	2	3	4	5	6	7	8	9	10	11	12	
A	0.099	0.088	0.073	0.079	0.12	0.114							595
B	0.099	0.083	0.074	0.079	0.113	0.102							595
C	0.094	0.096	0.073	0.081	0.106	0.106							595
D	0.092	0.082	0.075	0.087	0.108	0.103							595
E													595
F													595
G													595
H													595

	0-No GSH	0	5000	2000	1500	1000
Avg. (3/4)	0.0973333	0.0843333	0.074	0.0796667	0.109	0.1036667
St. Dev.	0.0028868	0.0032146	0.001	0.0011547	0.0036056	0.0020817
		0	5000	2000	1500	1000
Avg. (3/4)	0.096	0.08725	0.07375	0.0815	0.11175	0.10625
St. Dev.	0.003559	0.0063966	0.0009574	0.0037859	0.0062383	0.0054391



3:30

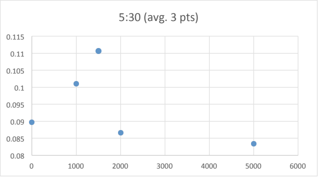
	1	2	3	4	5	6	7	8	9	10	11	12	
A	0.099	0.088	0.074	0.082	0.122	0.113							595
B	0.1	0.083	0.076	0.081	0.115	0.101							595
C	0.095	0.097	0.077	0.082	0.107	0.105							595
D	0.093	0.083	0.078	0.089	0.108	0.101							595
E													595
F													595
G													595
H													595

	0-No GSH	0	5000	2000	1500	1000
Avg. (3/4)	0.098	0.0846667	0.077	0.0816667	0.11	0.1023333
St. Dev.	0.0026458	0.0028868	0.001	0.0005774	0.0043589	0.0023094
Avg. (3/4)	0.09675	0.08775	0.07625	0.0835	0.113	0.105
St. Dev.	0.003304	0.0066018	0.0017078	0.0036968	0.0069761	0.0056569

4:30

	1	2	3	4	5	6	7	8	9	10	11	12	
A	0.1	0.089	0.076	0.076	0.122	0.112							595
B	0.1	0.084	0.079	0.079	0.115	0.101							595
C	0.096	0.099	0.081	0.081	0.107	0.104							595
D	0.094	0.086	0.081	0.081	0.108	0.1							595
E													595
F													595
G													595
H													595

	0-No GSH	0	5000	2000	1500	1000
Avg. (3/4)	0.0986667	0.0863333	0.0803333	0.0786667	0.11	0.1016667
St. Dev.	0.0023094	0.0025166	0.0011547	0.0025166	0.0043589	0.0020817
Avg. (3/4)	0.0975	0.0895	0.07925	0.07925	0.113	0.10425
St. Dev.	0.003	0.0066583	0.0023629	0.0023629	0.0069761	0.0054391



5:30

	1	2	3	4	5	6	7	8	9	10	11	12	
A	0.101	0.092	0.08	0.088	0.121	0.111							595
B	0.1	0.087	0.082	0.086	0.115	0.101							595
C	0.097	0.101	0.084	0.086	0.108	0.103							595
D	0.097	0.09	0.084	0.094	0.109	0.099							595
E													595
F													595
G													595
H													595

	0-No GSH	0	5000	2000	1500	1000
Avg. (3/4)	0.0993333	0.0896667	0.0833333	0.0866667	0.1106667	0.101
St. Dev.	0.0020817	0.0025166	0.0011547	0.0011547	0.0037859	0.002
Avg. (3/4)	0.09875	0.0925	0.0825	0.0885	0.11325	0.1035
St. Dev.	0.0020616	0.0060277	0.0019149	0.0037859	0.0060208	0.0052599

DIY Lead Assay Protocol

This is a preliminary protocol for the DIY lead assay developed by the 2017 WPI iGEM team. The assay described below is most accurate when detecting lead in Luria-Bertani (LB) Broth or De Man, Rogosa, Sharpe (MRS) Broth media at concentrations between 1000 and 5000 parts per billion (ppb).

Materials

- 96-well plate
- Lead-spiked LB Broth
- Lead-spiked MRS Broth
- 20 nm gold nanoparticles (AuNPs)
- GSH solution
- 595 nm Plate Reader

Protocol

Step	Action
Perform Measurements For a Standard Curve Note: a separate standard curve is needed for LB and MRS	1. Add 41.5 uL of lead-spiked media at a concentration of 5000 ppb into wells A1, B1, C1, and D1 (A1-D1) of a 96 well plate. 2. Add 34.6 uL of AuNPs to wells A1-D1 and start a timer. Use a multi-channel whenever possible to decrease the standard deviation of the samples. 3. For LB media, add 10 uL of GSH solution to wells A1-D1. For MRS media add 8 uL of GSH. The GSH should be added between 15 and 20 seconds after adding the AuNPs. 4. Measure the absorbance at 595 nm of wells A1-D1 at 1:30, 2:30, 3:30, 4:30, and 5:30 relative to when the AuNPs were added. Export data to an excel sheet between each time point for later analysis. 5. Repeat steps 1-4 with lead-spiked media at concentrations of 2000 ppb, 1500 ppb, and 1000 ppb into wells A2-D2, A3-D3, and A4-D4,

	respectively. 6. For the negative control, add 51.5 uL of dilute media into wells A5-D5. 7. Add 34.6 uL of AuNPs to wells A5-D5 and start a timer. 8. Measure the absorbance at 595 nm of wells A5-D5 at 1:30, 2:30, 3:30, 4:30, and 5:30 relative to when the AuNPs were added. Export data to an excel sheet between each time point for later analysis. 9. Dispose of the lead-spiked media and the contents of wells A1..D5 in a container designated for lead waste. Dispose of containers for lead-spiked media and plate in biohazard.
Data Analysis for Standard Curve	1. Transfer all data to one spreadsheet so that there is one table four rows by five columns from lowest to highest lead concentration for each time point for a total of five tables. Label the columns accordingly. 2. Copy and paste these labels to the right of the table. Below these labels, use the “=AVERAGE(..)” function to find the average of the four samples for each concentration. 3. Below the average values, use the “=STDEV.S(..)” function to find the standard deviation of the four samples for each of concentration. 4. Select the concentration labels and averages to make a scatter plot for each time point. Adjust the axes so that the minimum and maximum values are appropriately scaled. 5. Select the data points to add a linear trendline. Display the equation and R^2 value on the graph. 6. Use the standard deviation to create custom error bars. 7. If the R^2 value is below 0.95 or the standard deviation causes overlap

	between different concentrations, repeat measurements for the standard curve.
Perform Assay	1. Add 41.5 uL of the sample in four replicates into the 96 well plate. 2. Add 34.6 uL of 20 nm gold nanoparticles (AuNPs) to samples and start timer. 3. For LB media, add 10 uL of GSH solution to wells A1-D1. For MRS media add 8 uL of GSH. The GSH should be added between 15 and 20 seconds after adding the AuNPs. 4. Measure the absorbance at 595 nm, and at the time point with the lowest standard deviation dependent on the standard curve. Export data to Excel for analysis later. 5. Repeat steps 1-4 for any other unknown samples. 6. Dispose of the lead-spiked media and the contents of wells in a container designated for lead waste. Dispose of containers for lead-spiked media and plate in biohazard.
Data Analysis for Unknown Sample	1. Transfer all data to one spreadsheet so that there is one table that contains all samples and associated replicates. Label the columns accordingly. 2. Copy and paste these labels to the right of the table. Below these labels, use the “=AVERAGE(..)” function to find the average of the four replicates for each concentration. 3. Insert the calculated averages into the equation of the line from the standard curve. The averages will be the y-values and the equation will need to be solved for x, the lead concentration.

Recipes

For GSH solution

1. Add 110 uL of NaCL solution, 620 uL of phosphate buffer, 480 uL of L-glutathione solution, and 790 uL of deionized (D.I.) water to a 15 mL conical tube.
2. Vortex thoroughly for 5 seconds.
3. If not used entirely for the assay, store at 4°C.

For 1M NaCl solution

1. Tare a weigh boat.
2. Measure 11.86 g of NaCl into the weigh boat.
3. Transfer the measured NaCl into an autoclaved 250 mL bottle.
4. Add 200 mL of D.I. water to the 250 mL bottle. Shake thoroughly to mix.
5. Store at room temperature (25ºC).

For 50 mM phosphate buffer

1. Tare a weigh boat.
2. Measure 65.82 g of Sodium Phosphate Monobasic Monohydrate ($NaH_2PO_4•H_2O$) into the weigh boat.
3. Transfer the measured $NaH_2PO_4•H_2O$ into a 1 L graduated cylinder.
4. Tare a weigh boat.
5. Measure 93.1 g of Sodium Phosphate Dibasic Dihydrate ($Na_2HPO_4•2H_2O$) into the weigh boat.
6. Transfer the measured $Na_2HPO_4•2H_2O$ into the graduated cylinder.
7. Add 100 mL of D.I. water to the graduated cylinder.
8. Test pH with pH meter and adjust solution to a pH of 7 using 10 N NaOH.
9. Fill graduated cylinder to 1 L.
10. Add 1 mL of 1 L stock from steps 1-9 to 19 mL of D.I. water in a 50 mL conical tube.
11. Store at 4ºC.

For 100mM L-glutathione solution

1. Tare a weigh boat.
2. Measure 0.5 g of the L-glutathione powder reduced ≥ 98%* into the weigh boat.
3. Transfer the powder into a 25 mL beaker.
4. Add 16.3 mL of D.I. water to the beaker.
5. Make 1 mL aliquots to store in the freezer (-20ºC).

*Linear formula: $H_2NCH(CO_2H)CH_2CH_2CONHCH(CH_2SH)CONHCH_2CO_2H$
Left over powder should be stored in the 4°C.

For 500 ppm lead-spiked water stock

1. Tare a weigh boat.
2. Measure 250 g of lead nitrate [$Pb(NO_3)^2$].

3. Transfer the lead nitrate into an autoclaved 500 mL bottle.
4. Add 500 mL of D.I. water to the 500 mL bottle.
5. Store at room temperature (25ºC).

For lead-spiked LB broth

1. Using sterile technique, add 1 mL of autoclaved LB broth to a sterile 15 mL conical tube.
2. For the negative control, add 1 mL of D.I. water
3. Add 979.9 uL of D.I. water and 20.1 uL of 500ppm Pb stock solution for 5000ppb
4. Add 992.0 uL of D.I. water and 8.0 uL of 500ppm Pb stock solution for 2000ppb
5. Add 994.0 uL of D.I. water and 6.0 uL of 500ppm Pb stock solution for 1500ppb
6. Add 996.0 uL of D.I. water and 4.0 uL of 500ppm Pb stock solution for 1000ppb

For lead-spiked MRS broth

1. Using sterile technique, add 1 mL aliquots of autoclaved MRS broth to 5 sterile 15 mL conical tube.
2. For the negative control, add 1 mL of D.I. water
3. Add 979.4 uL of D.I. water and 20.6 uL of 500ppm Pb stock solution for 5000ppb
4. Add 991.8 uL of D.I. water and 8.2 uL of 500ppm Pb stock solution for 2000ppb
5. Add 993.8 uL of D.I. water and 6.2 uL of 500ppm Pb stock solution for 1500ppb
6. Add 995.9 uL of D.I. water and 4.1 uL of 500ppm Pb stock solution for 1000ppb

Massachusetts Department of Environmental Protection
Drinking Water Program
One Winter Street – Boston, MA 02108
617-292-5770 email: Program.Director-DWP@state.ma.us
Web: http://www.mass.gov/eea/agencies/massdep/water/drinking/

Fact Sheet – Assistance Program for Lead in School Drinking Water

Follow-up Steps for Schools and Early Education and Child Care Facilities Based on Lead and Copper Sampling Results above the Action Level

Steps you should take if lead or copper results are *above* the Action Level of 0.015 milligrams per liter (mg/L) for lead or 1.3 milligrams per liter (mg/L) for copper.

1. **Shut Off Problem Fixtures**
   Immediately shut off or disconnect any tap with sample results exceeding the applicable Action Level. Place a placard on the tap indicating that it has been shut off due to high lead or copper levels and will remain out of service until the problem has been corrected. Other interim measures may include:
    - Flush the piping system in your building every morning and especially after vacations.
    - Provide bottled water if necessary.
    - Use only cold water for food and beverage preparation.
2. **Contact the Local Public Water System (PWS) and the MassDEP Drinking Water Program**
   If the sampling was conducted by you or on your behalf, make your public water supplier aware of any results that exceed the applicable Action Level. You should also notify the MassDEP Drinking Water Program of any sampling result that exceeds the applicable Action Level. Notification should be sent to MassDEP Drinking Water Program at 617-292-5770 or Director-DWP@state.ma.us.

3. **Conduct Outreach to Staff and Parents**
   Provide staff, students, and parents with a letter informing them of the lab results and describing your plans to address any results over an Action Level. Sample letters are attached.

4. **Follow-up Sampling**
   Conduct follow-up sampling to determine if the source of the contamination is the fixture or the connecting plumbing. (See Fact Sheet – Assistance Program for Lead in School Drinking Water – Sampling for Lead and Copper).

5. **Permanent Measures**
   Permanently reduce or eliminate the sources of lead that originate in your building's plumbing. All measures must be conducted by a licensed plumber. Permanent measures to address long-term health concerns may include:

    - Shut off and remove or replace problem taps or components.
    - Check ground wires and eliminate any that may accelerate corrosion.
    - Check and replace all Lead Service lines. *Contact local PWS to check status of lead service line.*

- Replace lead pipes within the school or reconfigure plumbing to bypass sources of lead contamination.
- Install time-operated solenoid valves to automatically flush problem outlets.
- Use lead-free materials to repair or replace the facility's plumbing system.
- Use only cold water for food and beverage preparation.
- Clean aerators in accordance with regular maintenance schedule.

6. Report Actions Taken

Review the results for all schools and report any remedial actions taken through the online MassDEP Lead & Copper Reporting Tool.

- The Lead & Copper Reporting Tool is located at https://script.google.com/macros/s/AKfycbxP99K-Cd5B3ioE7nswn0peOEndcGrXwVk6zJcS5iHxzGO55B1k/exec
- Instructions for using the Reporting Tool can be found on the MassDEP website at http://www.mass.gov/eea/docs/dep/water/drinking/lcca-reporting-tool-guide.pdf

All sampling results reported by a Massachusetts certified laboratory to MassDEP electronic reporting system, eDEP, will be posted two weeks from the date the samples were reported to eDEP on the MassDEP website at http://www.mass.gov/eea/agencies/massdep/water/drinking/lead-and-copper-in-school-drinking-water-sampling-results.html

If your school’s lead and copper sampling results are not available through the Reporting Tool please contact the MassDEP Drinking Water Program via email at Program.Director-DWP@state.ma.us (Subject: LCCA Reporting Tool – Sampling Results).

It is important that you share your results and follow-up remedial actions with your school community and other interested stakeholders.

7. Seek Assistance from Others

Schools, school districts and early education and child care facilities should research opportunities for assistance from local officials including the public water supplier, Board of Health, Plumbing Inspector, and elected officials; as well as from certified water testing laboratories.

Modified from EPA’s "3T's for Reducing Lead in Drinking Water in Schools: Revised Technical Guidance"

Template for Lead Results over the Action Level

(NOTE: This is a sample letter to students, families, and staff from a school or early education or child care facility with laboratory results that exceed the Massachusetts Action Level for lead in drinking water. Delete or replace all items in red including this paragraph and add your school letterhead here.)

(***Insert date***)

To the Students, Families, and Staff of ***(insert school/early education or child care facility name)***:

During recent sampling for lead and copper, some water taps at our school had lead levels that exceed the Massachusetts Action Level for lead in drinking water at schools and early education and child care facilities. See sample results below. The Massachusetts Action Level for lead in drinking water is 0.015 milligrams per liter (also known as parts per million).

We would like to inform you about our plans to reduce potential exposure to lead in drinking water at our school. Lead is not believed to be in our water source but plumbing and fixtures in our buildings may contain lead, resulting in an increase in the lead content in tap water. Exposure to lead is a concern because lead is a toxic metal that has a range of adverse health effects.

Sampling Results		
Date Sample Collected	**Location**	**Lead result in mg/L**

The administration takes these results very seriously and is moving immediately to safeguard the health of the students, faculty and staff. The following information describes steps we are taking to address the issue of lead in the water.

To safeguard our students and other sensitive individuals (including woman who are pregnant or nursing), our school is working closely and cooperatively with MassDEP and taking actions as follows:

Only include applicable items

What we are doing:

1. While exceeding the Action Level does not require provision of alternative drinking water sources, beginning XXXX we will be /are providing bottled water and will be shutting down all bubblers.
2. We have removed from service all taps with lead levels over the Action Level.
3. We are implementing a public information process that will include distribution of outreach material to all students, parents, teachers, staff and local officials.
4. We have developed a sampling plan to conduct testing at outlets (faucets, water fountains, etc.) where students and staff get water for drinking, beverage preparation and cooking.
5. We are implementing a flushing and water usage plan to safeguard against lead exposure from drinking water in the school at outlets that are found to be above the MassDEP Action Level for lead. This includes the daily flushing of water fountains and/or faucets at sinks and the limitation of water consumption to cold-water faucets for food and beverage preparation.
6. We will undertake efforts to determine the cause of this lead Action Level exceedance and evaluate the adequacy of our existing corrosion control system. We will develop and put into place a corrective action plan as quickly as possible following additional testing and consultation.
7. Through periodic reports, we will keep you informed as to the progress of our efforts. These reports will serve to let you know what has been done and what is being done to safeguard against lead exposure from drinking water at our school(s)/child care facility(ies).
8. *Optional information can be included that announces an information display at the school on Lead in Drinking Water at Schools and/or an announcement about a workshop that will provide further information and will provide an opportunity for Q&A.*

A Reminder*:* The water system at the school is not unlike water systems found in other buildings. Older plumbing systems and fixtures, especially, can contain lead pipes or solder that can allow lead to enter tap water. If you have questions about lead in your home's water supply, and are using a private well, you can have your water tested. If you are receiving water from a public water system (i.e., if you pay a water bill) you can call your local water department for information or check the Consumer Confidence Report sent out by the public water supplier annually.

If you have any questions on this information please contact ___________ at _________.

Sincerely,

(Insert signature and title)

Modified from EPA’s "3T's for Reducing Lead in Drinking Water in Schools: Revised Technical Guidance"

Template for Copper Results over the Action Level

(NOTE: This is a sample letter to students, families, and staff from a school or early education or child care facility with laboratory results that exceed the Action Level for copper in drinking water. Delete or replace all items in red including this paragraph and add your school letterhead here.)

(*Insert date*)

To the Students, Families, and Staff of ***(insert school/early education or child care facility name)***:

During recent sampling for lead and copper, some water taps at our school had copper levels that exceed the Massachusetts and federal Action Level for copper in drinking water at schools and early education and child care facilities. See sample results below. The Action Level for copper in drinking water is 1.3 milligrams per liter (also known as parts per million).

We would like to inform you about our plans to reduce potential exposure to copper in drinking water at our school. Copper is not believed to be in our water source but plumbing and fixtures in our buildings may contain copper, resulting in an increase in the copper content in tap water.

Sampling Results

Date Sample Collected	**Location**	**Copper results in mg/L**

Copper is a necessary micronutrient and is needed in small “trace” amounts for good health but too much copper in the diet or in drinking water may cause adverse health effects. Some people who consume drinking water with copper in excess of the EPA action level may experience nausea, vomiting, diarrhea, and stomach cramps. However, most people are unlikely to experience health problems from exposure to modestly elevated copper levels in drinking water because the human body has a natural mechanism for maintaining the proper level of copper in it. People with Wilson's disease, children less than one year old, and individuals with liver disease cannot eliminate excess copper from their bodies as well and are more likely to experience negative health effects on the liver and kidney from short-term exposure to copper levels that exceed the EPA’s action level. See the MassDEP Fact Sheet on copper and your health at http://www.mass.gov/eea/docs/dep/water/drinking/alpha/a-thru-h/copperfs.pdf

The administration takes these results very seriously and is moving immediately to safeguard the health of the students, faculty and staff. The following information describes steps we are taking to address the issue of copper in the water.

To safeguard our students and other sensitive individuals (including woman who are pregnant or nursing), our school is working closely and cooperatively with MassDEP and others and taking actions as follows:

Only include applicable items

What we are doing:

1. While exceeding the Action Level does not require provision of alternative drinking water sources, beginning XXXX we will be /are providing bottled water and will be shutting down all bubblers.
2. We have removed from service all taps with copper levels over the Action Level.
3. We are implementing a public information process that will include distribution of outreach

7. Through periodic reports, we will keep you informed as to the progress of our efforts. These reports will serve to let you know what has been done and what is being done to safeguard against copper exposure from drinking water at our school(s)/child care facility (ies).
8. *Optional information can be included that announces an information display at the school on Copper in Drinking Water at Schools and/or an announcement about a workshop that will provide further information and will provide an opportunity for Q&A.*

***A Reminder**:* The water system at the school is not unlike water systems found in other buildings. Older plumbing systems and fixtures, especially, can contain lead pipes or solder that can allow lead to enter tap water. Plumbing systems also contain copper. If you have questions about lead or copper in your home's water supply, and are using a private well, you can have your water tested. If you are receiving water from a public water system (i.e., if you pay a water bill) you can call your local water department for information or check the Consumer Confidence Report sent out by the public water supplier annually.

If you have any questions on this information please contact ___________ at _________.

Sincerely,

(Insert signature and title)

Modified from EPA's "3T's for Reducing Lead in Drinking Water in Schools: Revised Technical Guidance

Template for Lead and Copper Results over the Action Levels

(NOTE: This is a sample letter to students, families, and staff from a school or early education or child care facility with laboratory results that exceed the Action Levels for lead and copper in drinking water. Delete or replace all items in red including this paragraph and add your school letterhead here.)

(***Insert date***)

To the Students, Families, and Staff of ***(insert school/early education or child care facility name)***:

During recent lead and copper sampling, some water taps at our school had lead and copper levels that exceed the Massachusetts Action Level for lead and the Massachusetts and federal Action Level for copper in drinking water at schools and early education and child care facilities. See sample results below. The Massachusetts Action Level for lead in drinking water is 0.015 milligrams per liter (also known as parts per million). The Massachusetts and federal Action Level for copper in drinking water is 1.3 milligrams per liter (also known as parts per million).

We would like to inform you about our plans to reduce potential exposure to lead and copper in drinking water at our school.

Lead is not believed to be in our water source but plumbing and fixtures in our buildings may contain lead, resulting in an increase in the lead content in tap water. Exposure to lead is a concern because lead is a toxic metal that has a range of adverse health effects.

Copper is also not believed to be in our water source but plumbing and fixtures in our buildings may contain copper, resulting in an increase in the copper content in tap water. The same mechanisms that cause plumbing to contribute lead to drinking water may also contribute copper.

Copper is a necessary micronutrient and is needed in small “trace” amounts for good health but too much copper in the diet or in drinking water may cause adverse health effects. Some people who consume drinking water with copper in excess of the EPA action level may experience nausea, vomiting, diarrhea, and stomach cramps. However, most people are unlikely to experience health problems from exposure to modestly elevated copper levels in drinking water because the human body has a natural mechanism for maintaining the proper level of copper in it. People with Wilson's disease, children less than one year old, and individuals with liver disease cannot eliminate excess copper from their bodies as well and are more likely to experience negative health effects on the liver and kidney from short-term exposure to copper levels that exceed the EPA’s action level. See the MassDEP Fact Sheet on copper and your health at http://www.mass.gov/eea/docs/dep/water/drinking/alpha/a-thru-h/copperfs.pdf

Sampling Results			
Date Sample Collected	**Location**	**Lead result in mg/L**	**Copper results in mg/L**

The administration takes these results very seriously and is moving immediately to safeguard the health of the students, faculty and staff. The following information describes steps we are taking to address the issue of lead and copper in the water.

To safeguard our students and other sensitive individuals (including woman who are pregnant or nursing),

5. We are implementing a flushing and water usage plan to safeguard against lead and copper exposure from drinking water in the school at outlets that are found to be above the Action Levels for lead and copper. This includes the daily flushing of water fountains and/or faucets at sinks and the limitation of water consumption to cold-water faucets for food and beverage preparation.
6. We will undertake efforts to determine the cause of this lead and copper Action Level exceedance and evaluate the adequacy of our existing corrosion control system. We will develop and put into place a corrective action plan as quickly as possible following additional testing and consultation.
7. Through periodic reports, we will keep you informed as to the progress of our efforts. These reports will serve to let you know what has been done and what is being done to safeguard against lead and copper exposure from drinking water at our school(s)/child care facility (ies).
8. *Optional information can be included that announces an information display at the school on Lead and Copper in Drinking Water at Schools and/or an announcement about a workshop that will provide further information and will provide an opportunity for Q&A.*

***A Reminder**:* The water system at the school is not unlike water systems found in other buildings. Older plumbing systems and fixtures, especially, can contain lead pipes or solder that can allow lead to enter tap water. Plumbing systems also contain copper. If you have questions about lead or copper in your home's water supply, and are using a private well, you can have your water tested. If you are receiving water from a public water system (i.e., if you pay a water bill) you can call your local water department for information or check the Consumer Confidence Report sent out by the public water supplier annually.

If you have any questions on this information please contact ___________ at _________.

Sincerely,

(Insert signature and title)

Modified from EPA's "3T's for Reducing Lead in Drinking Water in Schools: Revised Technical Guidance"

Template for Lead and Copper Results below Action Levels

(NOTE: This is a sample letter to students, families, and staff from a school or early education or child care facility with laboratory results that do not exceed the Action Levels for lead and copper in drinking water. Delete or replace all items in red including this paragraph and add your school letterhead here.)

(*Insert date*)

To the Students, Families, and Staff of ***(insert school/early education or child care facility name)***:

On ***insert date*** samples were collected from all taps and fixtures used for drinking, cooking and medical uses at ***insert school/early education or child care facility name***. Samples were taken at each tap or fixture for both a first draw sample with the water standing in the tap overnight as well as a flushed sample after the tap was run. For information on sample collection procedures for school samples please see: http://www.mass.gov/eea/agencies/massdep/water/drinking/how-to-collect-a-drinking-water-sample-for-lead-and-coppe.html

We are pleased to report that all samples taken from our taps and fixtures had lead and copper levels below the Massachusetts Action Levels for lead and copper in drinking water

The Massachusetts Action Level for lead in drinking water is 0.015 milligrams per liter (also known as parts per million). The Massachusetts Action Level for copper in drinking water is 1.3 milligrams per liter (also known as parts per million).

For MassDEP information on lead and copper in drinking water see:
Lead: http://www.mass.gov/eea/agencies/massdep/water/drinking/lead-in-drinking-water.html
Copper: http://www.mass.gov/eea/docs/dep/water/drinking/alpha/a-thru-h/copperfs.pdf
For Massachusetts Department of Public Health information on Lead and Copper see:
http://www.mass.gov/eohhs/gov/departments/dph/programs/environmental-health/exposure-topics/lead/child-health/sources-of-lead-besides-lead-paint.html.

A Reminder*:* The water system at the school is not unlike water systems found in other buildings. Older plumbing systems and fixtures, especially, can contain lead pipes or solder that can allow lead to enter tap water. Plumbing systems also contain copper. If you have questions about lead or copper in your home's water supply, and are using a private well, you can have your water tested. If you are receiving water from a public water system (i.e., if you pay a water bill) you can call your local water department for information or check the Consumer Confidence Report sent out by the public water supplier annually.

If you have any questions on this information please contact ___________ at _________.

Sincerely,

(Insert signature and title)

LB trial 2c

Control no GSH

1:30

	1	2	3	4	5	6	7	8	9	10	11	12	
A	0.064												596
B	0.067												596
C	0.065												596
D	0.066												596
E													596
F													596
G													596
H													596

2:30

	1	2	3	4	5	6	7	8	9	10	11	12	
A	0.064												596
B	0.067												596
C	0.065												596
D	0.067												596
E													596
F													596
G													596
H													596

3:30

	1	2	3	4	5	6	7	8	9	10	11	12	
A	0.064												596
B	0.067												596
C	0.065												596
D	0.067												596
E													596
F													596
G													596
H													596

4:30

	1	2	3	4	5	6	7	8	9	10	11	12	
A	0.064												596
B	0.067												596
C	0.065												596
D	0.067												596
E													596
F													596
G													596
H													596

5:30

	1	2	3	4	5	6	7	8	9	10	11	12	
A	0.064												596
B	0.067												596
C	0.065												596
D	0.067												596
E													596
F													596
G													596
H													596

Control with GSH

1:30

	1	2	3	4	5	6	7	8	9	10	11	12	
A		0.081											596
B		0.095											596
C		0.073											596
D		0.097											596
E													596
F													596
G													596
H													596

2:30

	1	2	3	4	5	6	7	8	9	10	11	12	
A		0.095											596
B		0.106											596
C		0.086											596
D		0.101											596
E													596
F													596
G													596
H													596

3:30

	1	2	3	4	5	6	7	8	9	10	11	12	
A		0.102											596
B		0.109											596
C		0.094											596
D		0.103											596
E													596
F													596
G													596
H													596

4:30

	1	2	3	4	5	6	7	8	9	10	11	12	
A		0.107											596
B		0.11											596
C		0.098											596
D		0.105											596
E													596
F													596
G													596
H													596

5:30

	1	2	3	4	5	6	7	8	9	10	11	12	
A		0.11											596
B		0.111											596
C		0.101											596
D		0.107											596
E													596
F													596
G													596
H													596

5,000ppb

1:30

	1	2	3	4	5	6	7	8	9	10	11	12	
A			0.088										596
B			0.107										596
C			0.101										596
D			0.099										596
E													596
F													596
G													596
H													596

2:30

	1	2	3	4	5	6	7	8	9	10	11	12	
A			0.1										596
B			0.115										596
C			0.114										596
D			0.111										596
E													596
F													596
G													596
H													596

3:30

	1	2	3	4	5	6	7	8	9	10	11	12	
A			0.107										596
B			0.117										596
C			0.114										596
D			0.114										596
E													596
F													596
G													596
H													596

4:30

	1	2	3	4	5	6	7	8	9	10	11	12	
A			0.112										596
B			0.117										596
C			0.112										596
D			0.112										596
E													596
F													596
G													596
H													596

5:30

	1	2	3	4	5	6	7	8	9	10	11	12	
A			0.115										596
B			0.116										596
C			0.11										596
D			0.11										596
E													596
F													596
G													596
H													596

2,000ppb

1:30

	1	2	3	4	5	6	7	8	9	10	11	12	
A				0.109									596
B				0.112									596
C				0.112									596
D				0.096									596
E													596
F													596
G													596
H													596

2:30

	1	2	3	4	5	6	7	8	9	10	11	12	
A				0.118									596
B				0.121									596
C				0.117									596
D				0.106									596
E													596
F													596
G													596
H													596

3:30

	1	2	3	4	5	6	7	8	9	10	11	12	
A				0.118									596
B				0.123									596
C				0.116									596
D				0.108									596
E													596
F													596
G													596
H													596

4:30

	1	2	3	4	5	6	7	8	9	10	11	12	
A				0.117									596
B				0.121									596
C				0.115									596
D				0.108									596
E													596
F													596
G													596
H													596

5:30

	1	2	3	4	5	6	7	8	9	10	11	12	
A				0.116									596
B				0.119									596
C				0.113									596
D				0.107									596
E													596
F													596
G													596
H													596

1,500ppb

1:30

	1	2	3	4	5	6	7	8	9	10	11	12	
A					0.088								596
B					0.102								596
C					0.1								596
D					0.101								596
E													596
F													596
G													596
H													596

2:30

	1	2	3	4	5	6	7	8	9	10	11	12	
A					0.099								596
B					0.116								596
C					0.113								596
D					0.113								596
E													596
F													596
G													596
H													596

3:30

	1	2	3	4	5	6	7	8	9	10	11	12	
A					0.106								596
B					0.116								596
C					0.113								596
D					0.115								596
E													596
F													596
G													596
H													596

4:30

	1	2	3	4	5	6	7	8	9	10	11	12	
A					0.108								596
B					0.115								596
C					0.111								596
D					0.114								596
E													596
F													596
G													596
H													596

5:30

	1	2	3	4	5	6	7	8	9	10	11	12	
A					0.108								596
B					0.113								596
C					0.109								596
D					0.112								596
E													596
F													596
G													596
H													596

1,000ppb

1:30

	1	2	3	4	5	6	7	8	9	10	11	12	
A						0.088							596
B						0.085							596
C						0.095							596
D						0.106							596
E													596
F													596
G													596
H													596

2:30

	1	2	3	4	5	6	7	8	9	10	11	12	
A						0.097							596
B						0.094							596
C						0.1							596
D						0.113							596
E													596
F													596
G													596
H													596

3:30

	1	2	3	4	5	6	7	8	9	10	11	12	
A						0.103							596
B						0.1							596
C						0.101							596
D						0.113							596
E													596
F													596
G													596
H													596

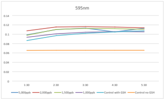
4:30

	1	2	3	4	5	6	7	8	9	10	11	12	
A						0.105							596
B						0.105							596
C						0.1							596
D						0.112							596
E													596
F													596
G													596
H													596

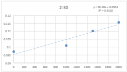
5:30

	1	2	3	4	5	6	7	8	9	10	11	12	
A						0.105							596
B						0.106							596
C						0.1							596
D						0.11							596
E													596
F													596
G													596
H													596

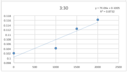
	5,000ppb	2,000ppb	1,500ppb	1,000ppb	Control with GSH	Control no GSH
1:30	0.09875	0.10725	0.09775	0.0935	0.0865	0.0655
2:30	0.11	0.1155	0.11025	0.101	0.097	0.06575
3:30	0.113	0.11625	0.1125	0.10425	0.102	0.06575
4:30	0.105	0.11525	0.112	0.1055	0.105	0.06575
5:30	0.11275	0.11375	0.1105	0.10525	0.10725	0.06575



5000	2000	1500	1000	0
0.11	0.1155	0.11025	0.101	0.097



5000	2000	1500	1000	0
0.113	0.11625	0.1125	0.10425	0.102



BLAST ® » blastn suite » RID-PEN7801Z014

BLAST Results

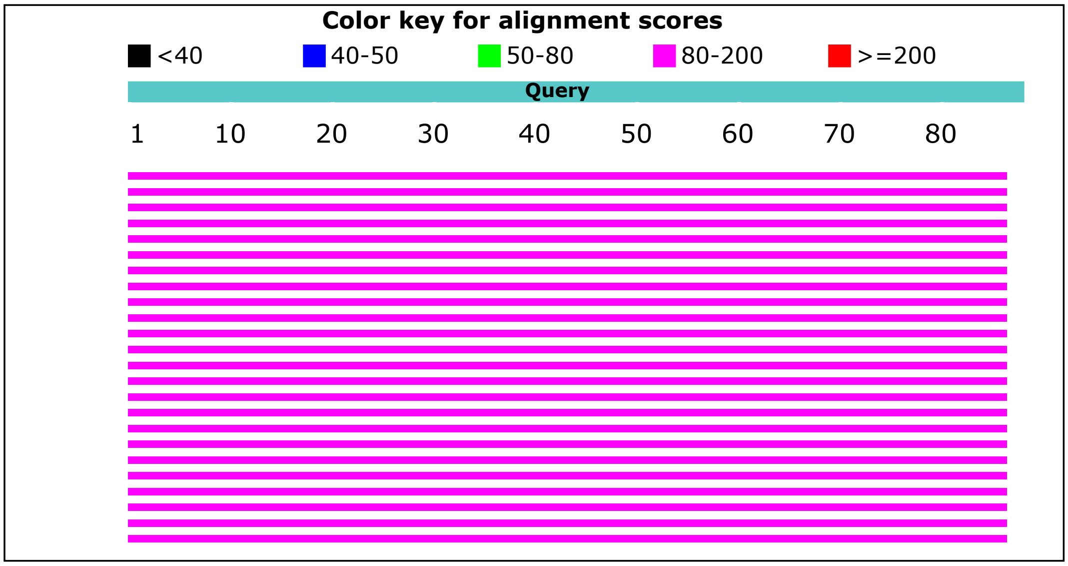
Australia pbrR Promotor Blast Result

Job title: Nucleotide Sequence (85 letters)

RID	PEN7801Z014 (Expires on 07-14 19:09 pm)		
Query ID	lcl|Query_110865	**Database Name**	nr
Description	None	**Description**	Nucleotide collection (nt)
Molecule type	nucleic acid	**Program**	BLASTN 2.6.1+
Query Length	85		

Graphic Summary

Distribution of the top 24 Blast Hits on 24 subject sequences



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Enterobacter asburiae strain AMA 497 plasmid pOXA436, complete sequence	158	158	100%	2e-35	100%	KY863418.1
Klebsiella pneumoniae subsp. pneumoniae strain RJA166 plasmid pRJA166b, complete sequence	158	158	100%	2e-35	100%	CP019049.1
Thauera chlorobenzoica strain 3CB1, complete genome	158	158	100%	2e-35	100%	CP018839.1
Klebsiella pneumoniae isolate Kp_Goe_154414 plasmid pKp_Goe_414-2, complete sequence	158	158	100%	2e-35	100%	CP018338.1
Salmonella enterica subsp. enterica serovar Typhimurium strain MU1 plasmid pIMP4-SEM1, complete sequence	158	158	100%	2e-35	100%	KX810825.1
Salmonella enterica subsp. enterica serovar Newport strain 0307-213, complete genome	158	158	100%	2e-35	100%	CP012599.1
Salmonella enterica subsp. enterica serovar Heidelberg strain 09-036813-1A plasmid p09-036813-1A_261, complete sequence	158	158	100%	2e-35	100%	CP016526.1
Obesumbacterium proteus strain DSM 2777, complete genome	158	158	100%	2e-35	100%	CP014608.1
Klebsiella pneumoniae subsp. pneumoniae strain RJF999 plasmid pRJF999, complete sequence	158	158	100%	2e-35	100%	CP014011.1
Klebsiella pneumoniae subsp. pneumoniae strain RJF293 plasmid pRJF293, complete sequence	158	158	100%	2e-35	100%	CP014009.1
Klebsiella pneumoniae subsp. pneumoniae strain H11 plasmid pH11, complete sequence	158	158	100%	2e-35	100%	CP013215.1
Kluyvera intermedia strain CAV1151 plasmid pCAV1151-296, complete sequence	158	158	100%	2e-35	100%	CP011601.1
Kluyvera intermedia strain CAV1151 plasmid pCAV1151-215, complete sequence	158	158	100%	2e-35	100%	CP011600.1
Enterobacter cloacae ECNIH3 plasmid pENT-8a4, complete sequence	158	158	100%	2e-35	100%	CP008899.1
Enterobacter cloacae ECNIH2 plasmid pKPC-272, complete sequence	158	158	100%	2e-35	100%	CP008825.1
Klebsiella pneumoniae KCTC 2242 plasmid pKCTC2242, complete sequence	158	158	100%	2e-35	100%	CP002911.1
Enterobacter cloacae plasmid pEC-IMPQ, complete sequence	158	158	100%	2e-35	100%	EU855788.1
Enterobacter cloacae plasmid pEC-IMP, complete sequence	158	158	100%	2e-35	100%	EU855787.1
Shewanella sp. ANA-3 plasmid 1, complete sequence	158	158	100%	2e-35	100%	CP000470.1
Shewanella frigidimarina NCIMB 400, complete genome	158	158	100%	2e-35	100%	CP000447.1
Klebsiella pneumoniae plasmid pLVPK, complete sequence	158	158	100%	2e-35	100%	AY378100.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Alcaligenes faecalis strain NCIB 8687 arsenite oxidation genes, partial sequence	158	158	100%	2e-35	100%	AY297781.1
Klebsiella pneumoniae subsp. pneumoniae NTUH-K2044 plasmid pK2044 DNA, complete genome	158	158	100%	2e-35	100%	AP006726.1
Klebsiella pneumoniae strain ED23 plasmid unamed, complete sequence	152	152	100%	1e-33	99%	CP016815.1

Alignments

Enterobacter asburiae strain AMA 497 plasmid pOXA436, complete sequence
Sequence ID: **KY863418.1** Length: 314137 Number of Matches: 1
Range 1: 98477 to 98561

Score	Expect	Identities	Gaps	Strand	Frame
158 bits(85)	2e-35()	85/85(100%)	0/85(0%)	Plus/Plus	

Features:

```
Query  1      GCATCAATCTCCAATTATCACTTGACTCTATAGTGACTATAGAGATTTTAATGGAGGCTG  60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  98477  GCATCAATCTCCAATTATCACTTGACTCTATAGTGACTATAGAGATTTTAATGGAGGCTG  98536

Query  61     AATAGAAGATTTTCAGGAGTTACTC  85
              |||||||||||||||||||||||||
Sbjct  98537  AATAGAAGATTTTCAGGAGTTACTC  98561
```

Klebsiella pneumoniae subsp. pneumoniae strain RJA166 plasmid pRJA166b, complete sequence
Sequence ID: **CP019049.1** Length: 228613 Number of Matches: 1
Range 1: 70480 to 70564

Score	Expect	Identities	Gaps	Strand	Frame
158 bits(85)	2e-35()	85/85(100%)	0/85(0%)	Plus/Minus	

Features:

```
Query  1      GCATCAATCTCCAATTATCACTTGACTCTATAGTGACTATAGAGATTTTAATGGAGGCTG  60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  70564  GCATCAATCTCCAATTATCACTTGACTCTATAGTGACTATAGAGATTTTAATGGAGGCTG  70505

Query  61     AATAGAAGATTTTCAGGAGTTACTC  85
              |||||||||||||||||||||||||
Sbjct  70504  AATAGAAGATTTTCAGGAGTTACTC  70480
```

Thauera chlorobenzoica strain 3CB1, complete genome
Sequence ID: **CP018839.1** Length: 3735506 Number of Matches: 1
Range 1: 3303782 to 3303866

Score	Expect	Identities	Gaps	Strand	Frame
158 bits(85)	2e-35()	85/85(100%)	0/85(0%)	Plus/Minus	

Features:

```
Query  1        GCATCAATCTCCAATTATCACTTGACTCTATAGTGACTATAGAGATTTTAATGGAGGCTG  60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3303866  GCATCAATCTCCAATTATCACTTGACTCTATAGTGACTATAGAGATTTTAATGGAGGCTG  3303807

Query  61       AATAGAAGATTTTCAGGAGTTACTC  85
                |||||||||||||||||||||||||
Sbjct  3303806  AATAGAAGATTTTCAGGAGTTACTC  3303782
```

Klebsiella pneumoniae isolate Kp_Goe_154414 plasmid pKp_Goe_414-2, complete sequence
Sequence ID: **CP018338.1** Length: 202175 Number of Matches: 1

Range 1: 79447 to 79531

Score	Expect	Identities	Gaps	Strand	Frame
158 bits(85)	2e-35()	85/85(100%)	0/85(0%)	Plus/Plus	

Features:

```
Query  1      GCATCAATCTCCAATTATCACTTGACTCTATAGTGACTATAGAGATTTTAATGGAGGCTG  60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  79447  GCATCAATCTCCAATTATCACTTGACTCTATAGTGACTATAGAGATTTTAATGGAGGCTG  79506

Query  61     AATAGAAGATTTTCAGGAGTTACTC  85
              |||||||||||||||||||||||||
Sbjct  79507  AATAGAAGATTTTCAGGAGTTACTC  79531
```

Salmonella enterica subsp. enterica serovar Typhimurium strain MU1 plasmid pIMP4-SEM1, complete sequence
Sequence ID: **KX810825.1** Length: 339962 Number of Matches: 1
Range 1: 228798 to 228882

Score	Expect	Identities	Gaps	Strand	Frame
158 bits(85)	2e-35()	85/85(100%)	0/85(0%)	Plus/Minus	

Features:

```
Query  1       GCATCAATCTCCAATTATCACTTGACTCTATAGTGACTATAGAGATTTTAATGGAGGCTG  60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  228882  GCATCAATCTCCAATTATCACTTGACTCTATAGTGACTATAGAGATTTTAATGGAGGCTG  228823

Query  61      AATAGAAGATTTTCAGGAGTTACTC  85
               |||||||||||||||||||||||||
Sbjct  228822  AATAGAAGATTTTCAGGAGTTACTC  228798
```

BLAST ® » blastn suite » RID-PEN5XPTC014

Australia pbrR Blast Result

BLAST Results

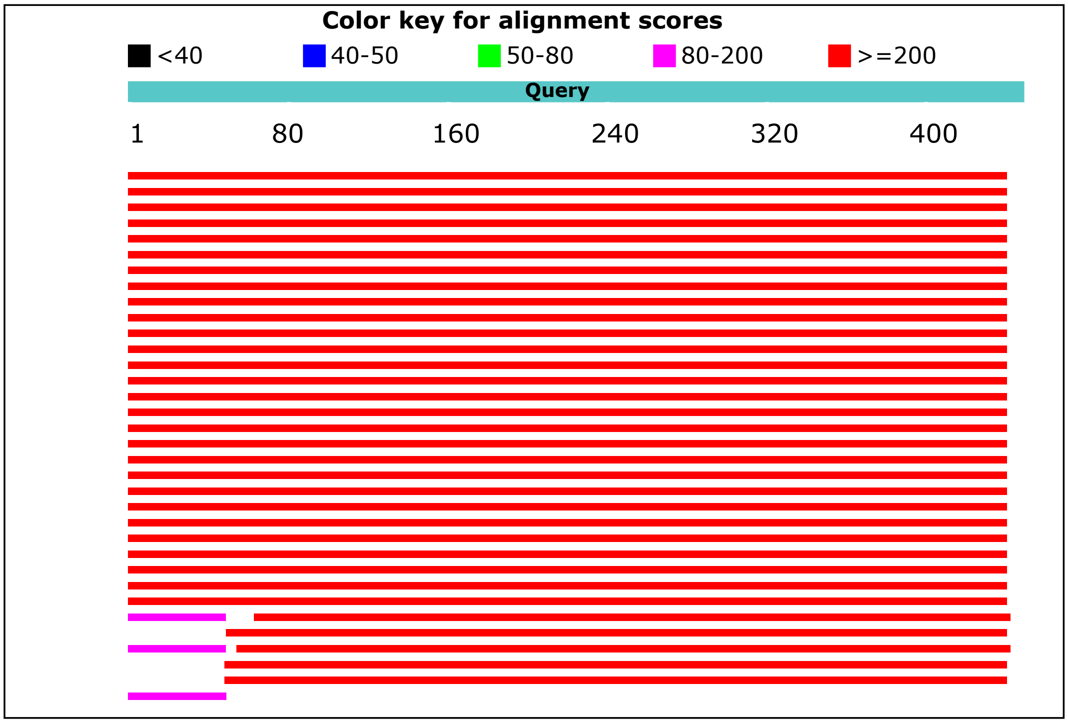
Job title: Nucleotide Sequence (435 letters)

RID PEN5XPTC014 (Expires on 07-14 19:08 pm)

Query ID	lcl|Query_181811	**Database Name**	nr
Description	None	**Description**	Nucleotide collection (nt)
Molecule type	nucleic acid	**Program**	BLASTN 2.6.1+
Query Length	435		

Graphic Summary

Distribution of the top 36 Blast Hits on 36 subject sequences



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Enterobacter asburiae strain AMA 497 plasmid pOXA436, complete sequence	804	804	100%	0.0	100%	KY863418.1
Klebsiella pneumoniae subsp. pneumoniae strain RJA166 plasmid pRJA166b, complete sequence	804	804	100%	0.0	100%	CP019049.1
Klebsiella pneumoniae isolate Kp_Goe_154414 plasmid pKp_Goe_414-2, complete sequence	804	804	100%	0.0	100%	CP018338.1
Salmonella enterica subsp. enterica serovar Typhimurium strain MU1 plasmid pIMP4-SEM1, complete sequence	804	804	100%	0.0	100%	KX810825.1
Salmonella enterica subsp. enterica serovar Newport strain 0307-213, complete genome	804	804	100%	0.0	100%	CP012599.1
Klebsiella pneumoniae strain ED23 plasmid unamed, complete sequence	804	804	100%	0.0	100%	CP016815.1
Salmonella enterica subsp. enterica serovar Heidelberg strain 09-036813-1A plasmid p09-036813-1A_261, complete sequence	804	804	100%	0.0	100%	CP016526.1
Klebsiella pneumoniae subsp. pneumoniae strain RJF999 plasmid pRJF999, complete sequence	804	804	100%	0.0	100%	CP014011.1
Klebsiella pneumoniae subsp. pneumoniae strain RJF293 plasmid pRJF293, complete sequence	804	804	100%	0.0	100%	CP014009.1
Klebsiella pneumoniae subsp. pneumoniae strain H11 plasmid pH11, complete sequence	804	804	100%	0.0	100%	CP013215.1
Kluyvera intermedia strain CAV1151 plasmid pCAV1151-296, complete sequence	804	804	100%	0.0	100%	CP011601.1
Enterobacter cloacae ECNIH3 plasmid pENT-8a4, complete sequence	804	804	100%	0.0	100%	CP008899.1
Enterobacter cloacae ECNIH2 plasmid pKPC-272, complete sequence	804	804	100%	0.0	100%	CP008825.1
Klebsiella pneumoniae KCTC 2242 plasmid pKCTC2242, complete sequence	804	804	100%	0.0	100%	CP002911.1
Enterobacter cloacae plasmid pEC-IMPQ, complete sequence	804	804	100%	0.0	100%	EU855788.1
Enterobacter cloacae plasmid pEC-IMP, complete sequence	804	804	100%	0.0	100%	EU855787.1
Klebsiella pneumoniae plasmid pLVPK, complete sequence	804	804	100%	0.0	100%	AY378100.1
Klebsiella pneumoniae subsp. pneumoniae NTUH-K2044 plasmid pK2044 DNA, complete genome	804	804	100%	0.0	100%	AP006726.1
Kluyvera intermedia strain CAV1151 plasmid pCAV1151-215, complete sequence	776	776	100%	0.0	99%	CP011600.1
Thauera chlorobenzoica strain 3CB1, complete genome	754	754	100%	0.0	98%	CP018839.1
Alcaligenes faecalis strain NCIB 8687 arsenite oxidation genes, partial sequence	754	754	100%	0.0	98%	AY297781.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Shewanella sp. ANA-3 plasmid 1, complete sequence	749	749	100%	0.0	98%	CP000470.1
Shewanella frigidimarina NCIMB 400, complete genome	749	749	100%	0.0	98%	CP000447.1
Obesumbacterium proteus strain DSM 2777, complete genome	743	743	100%	0.0	97%	CP014608.1
Candidatus Accumulibacter phosphatis clade IIA str. UW-1 plasmid pAph03, complete sequence	732	732	100%	0.0	97%	CP001718.1
Candidatus Accumulibacter phosphatis clade IIA str. UW-1 plasmid pAph02, complete sequence	732	732	100%	0.0	97%	CP001717.1
Candidatus Accumulibacter phosphatis clade IIA str. UW-1 plasmid pAph01, complete sequence	732	732	100%	0.0	97%	CP001716.1
Rugosibacter aromaticivorans strain Ca6, complete genome	726	726	100%	0.0	97%	CP010554.1
Sphingopyxis fribergensis strain Kp5.2 plasmid pSfKp5.2, complete sequence	375	375	85%	4e-100	85%	CP009123.1
Thiomonas sp. CB2 genome assembly ThiCB2, scaffold THICB2_Contig_87	320	320	88%	2e-83	82%	LK931666.1
Thiomonas intermedia K12 plasmid pTINT01, complete sequence	320	320	88%	2e-83	82%	CP002022.1
Alcanivorax pacificus W11-5, complete genome	278	278	88%	1e-70	80%	CP004387.1
Thioalkalivibrio sulfidophilus HL-EbGr7, complete genome	278	278	88%	1e-70	80%	CP001339.1
Sphingobium sp. TKS chromosome 1, complete sequence	87.9	87.9	10%	2e-13	100%	CP005083.1
Sphingobium sp. MI1205 plasmid pMI2, complete sequence	87.9	87.9	10%	2e-13	100%	CP005191.1
Alicycliphilus denitrificans BC plasmid pALIDE02, complete sequence	87.9	87.9	10%	2e-13	100%	CP002451.1

Alignments

Enterobacter asburiae strain AMA 497 plasmid pOXA436, complete sequence
Sequence ID: **KY863418.1** Length: 314137 Number of Matches: 1
Range 1: 98042 to 98476

Score	Expect	Identities	Gaps	Strand	Frame
804 bits(435)	0.0()	435/435(100%)	0/435(0%)	Plus/Plus	

Features:

```
Query  1      TTACCCAGATGTTTGACTGTTCGTGGCACTTTCACCATGGCAATTGCCCAACCCTTGCAA  60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  98042  TTACCCAGATGTTTGACTGTTCGTGGCACTTTCACCATGGCAATTGCCCAACCCTTGCAA  98101

Query  61     AATGCCGCACGCCTCTACAGATCGAGAGCCAGAACACTTCTCGCGCAAATCAACCAAGTG  120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  98102  AATGCCGCACGCCTCTACAGATCGAGAGCCAGAACACTTCTCGCGCAAATCAACCAAGTG  98161

Query  121    CCGTTTTAACTGCAACAGCGCGGACACACGCATTTCCACCTGTTGAATATGGGCCTCCAG  180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  98162  CCGTTTTAACTGCAACAGCGCGGACACACGCATTTCCACCTGTTGAATATGGGCCTCCAG  98221

Query  181    CAGCGTGATGACCTCCCCACAGTCCTGCATCGGGTTGTCTCGCAGACCCAGCAATGCGCG  240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  98222  CAGCGTGATGACCTCCCCACAGTCCTGCATCGGGTTGTCTCGCAGACCCAGCAATGCGCG  98281

Query  241    AATCTCGCTCAACGTCATGTCGAGCGAACGGCAATGACGGATGAATTGCAAGCGCTCAAT  300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  98282  AATCTCGCTCAACGTCATGTCGAGCGAACGGCAATGACGGATGAATTGCAAGCGCTCAAT  98341
```

```
Query  301    GTGCGCCTCACCGTACAACCGAAAGTTGCCACCGCTTCGCGCTGGCTTTGGCAGTAGCCC  360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  98342  GTGCGCCTCACCGTACAACCGAAAGTTGCCACCGCTTCGCGCTGGCTTTGGCAGTAGCCC  98401

Query  361    TTCCTTCTCGTAGTAGCGGATGGTCACGACCTCGCACCCAGAGCGCTTGGCGAGGTCGCC  420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  98402  TTCCTTCTCGTAGTAGCGGATGGTCACGACCTCGCACCCAGAGCGCTTGGCGAGGTCGCC  98461

Query  421    AATTCTGATTTCCAT  435
              |||||||||||||||
Sbjct  98462  AATTCTGATTTCCAT  98476
```

Klebsiella pneumoniae subsp. pneumoniae strain RJA166 plasmid pRJA166b, complete sequence
Sequence ID: **CP019049.1** Length: 228613 Number of Matches: 1
Range 1: 70565 to 70999

Score	Expect	Identities	Gaps	Strand	Frame
804 bits(435)	0.0()	435/435(100%)	0/435(0%)	Plus/Minus	

Features:

```
Query  1      TTACCCAGATGTTTGACTGTTCGTGGCACTTTCACCATGGCAATTGCCCAACCCTTGCAA  60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  70999  TTACCCAGATGTTTGACTGTTCGTGGCACTTTCACCATGGCAATTGCCCAACCCTTGCAA  70940

Query  61     AATGCCGCACGCCTCTACAGATCGAGAGCCAGAACACTTCTCGCGCAAATCAACCAAGTG  120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  70939  AATGCCGCACGCCTCTACAGATCGAGAGCCAGAACACTTCTCGCGCAAATCAACCAAGTG  70880

Query  121    CCGTTTTAACTGCAACAGCGCGGACACACGCATTTCCACCTGTTGAATATGGGCCTCCAG  180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  70879  CCGTTTTAACTGCAACAGCGCGGACACACGCATTTCCACCTGTTGAATATGGGCCTCCAG  70820

Query  181    CAGCGTGATGACCTCCCCACAGTCCTGCATCGGGTTGTCTCGCAGACCCAGCAATGCGCG  240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  70819  CAGCGTGATGACCTCCCCACAGTCCTGCATCGGGTTGTCTCGCAGACCCAGCAATGCGCG  70760

Query  241    AATCTCGCTCAACGTCATGTCGAGCGAACGGCAATGACGGATGAATTGCAAGCGCTCAAT  300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  70759  AATCTCGCTCAACGTCATGTCGAGCGAACGGCAATGACGGATGAATTGCAAGCGCTCAAT  70700

Query  301    GTGCGCCTCACCGTACAACCGAAAGTTGCCACCGCTTCGCGCTGGCTTTGGCAGTAGCCC  360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  70699  GTGCGCCTCACCGTACAACCGAAAGTTGCCACCGCTTCGCGCTGGCTTTGGCAGTAGCCC  70640

Query  361    TTCCTTCTCGTAGTAGCGGATGGTCACGACCTCGCACCCAGAGCGCTTGGCGAGGTCGCC  420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  70639  TTCCTTCTCGTAGTAGCGGATGGTCACGACCTCGCACCCAGAGCGCTTGGCGAGGTCGCC  70580

Query  421    AATTCTGATTTCCAT  435
              |||||||||||||||
Sbjct  70579  AATTCTGATTTCCAT  70565
```

Klebsiella pneumoniae isolate Kp_Goe_154414 plasmid pKp_Goe_414-2, complete sequence
Sequence ID: **CP018338.1** Length: 202175 Number of Matches: 1
Range 1: 79012 to 79446

Score	Expect	Identities	Gaps	Strand	Frame
804 bits(435)	0.0()	435/435(100%)	0/435(0%)	Plus/Plus	

Features:

```
Query  1      TTACCCAGATGTTTGACTGTTCGTGGCACTTTCACCATGGCAATTGCCCAACCCTTGCAA  60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  79012  TTACCCAGATGTTTGACTGTTCGTGGCACTTTCACCATGGCAATTGCCCAACCCTTGCAA  79071

Query  61     AATGCCGCACGCCTCTACAGATCGAGAGCCAGAACACTTCTCGCGCAAATCAACCAAGTG  120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  79072  AATGCCGCACGCCTCTACAGATCGAGAGCCAGAACACTTCTCGCGCAAATCAACCAAGTG  79131

Query  121    CCGTTTTAACTGCAACAGCGCGGACACACGCATTTCCACCTGTTGAATATGGGCCTCCAG  180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  79132  CCGTTTTAACTGCAACAGCGCGGACACACGCATTTCCACCTGTTGAATATGGGCCTCCAG  79191

Query  181    CAGCGTGATGACCTCCCCACAGTCCTGCATCGGGTTGTCTCGCAGACCCAGCAATGCGCG  240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  79192  CAGCGTGATGACCTCCCCACAGTCCTGCATCGGGTTGTCTCGCAGACCCAGCAATGCGCG  79251

Query  241    AATCTCGCTCAACGTCATGTCGAGCGAACGGCAATGACGGATGAATTGCAAGCGCTCAAT  300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  79252  AATCTCGCTCAACGTCATGTCGAGCGAACGGCAATGACGGATGAATTGCAAGCGCTCAAT  79311

Query  301    GTGCGCCTCACCGTACAACCGAAAGTTGCCACCGCTTCGCGCTGGCTTTGGCAGTAGCCC  360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  79312  GTGCGCCTCACCGTACAACCGAAAGTTGCCACCGCTTCGCGCTGGCTTTGGCAGTAGCCC  79371

Query  361    TTCCTTCTCGTAGTAGCGGATGGTCACGACCTCGCACCCAGAGCGCTTGGCGAGGTCGCC  420
```

```
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  79372  TTCCTTCTCGTAGTAGCGGATGGTCACGACCTCGCACCCAGAGCGCTTGGCGAGGTCGCC  79431

Query  421    AATTCTGATTTCCAT  435
              |||||||||||||||
Sbjct  79432  AATTCTGATTTCCAT  79446
```

Salmonella enterica subsp. enterica serovar Typhimurium strain MU1 plasmid pIMP4-SEM1, complete sequence
Sequence ID: **KX810825.1** Length: 339962 Number of Matches: 1
Range 1: 228883 to 229317

Score	**Expect**	**Identities**	**Gaps**	**Strand**	**Frame**
804 bits(435)	0.0()	435/435(100%)	0/435(0%)	Plus/Minus	

Features:

```
Query  1       TTACCCAGATGTTTGACTGTTCGTGGCACTTTCACCATGGCAATTGCCCAACCCTTGCAA  60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  229317  TTACCCAGATGTTTGACTGTTCGTGGCACTTTCACCATGGCAATTGCCCAACCCTTGCAA  229258

Query  61      AATGCCGCACGCCTCTACAGATCGAGAGCCAGAACACTTCTCGCGCAAATCAACCAAGTG  120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  229257  AATGCCGCACGCCTCTACAGATCGAGAGCCAGAACACTTCTCGCGCAAATCAACCAAGTG  229198

Query  121     CCGTTTTAACTGCAACAGCGCGGACACACGCATTTCCACCTGTTGAATATGGGCCTCCAG  180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  229197  CCGTTTTAACTGCAACAGCGCGGACACACGCATTTCCACCTGTTGAATATGGGCCTCCAG  229138

Query  181     CAGCGTGATGACCTCCCCACAGTCCTGCATCGGGTTGTCTCGCAGACCCAGCAATGCGCG  240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  229137  CAGCGTGATGACCTCCCCACAGTCCTGCATCGGGTTGTCTCGCAGACCCAGCAATGCGCG  229078

Query  241     AATCTCGCTCAACGTCATGTCGAGCGAACGGCAATGACGGATGAATTGCAAGCGCTCAAT  300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  229077  AATCTCGCTCAACGTCATGTCGAGCGAACGGCAATGACGGATGAATTGCAAGCGCTCAAT  229018

Query  301     GTGCGCCTCACCGTACAACCGAAAGTTGCCACCGCTTCGCGCTGGCTTTGGCAGTAGCCC  360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  229017  GTGCGCCTCACCGTACAACCGAAAGTTGCCACCGCTTCGCGCTGGCTTTGGCAGTAGCCC  228958

Query  361     TTCCTTCTCGTAGTAGCGGATGGTCACGACCTCGCACCCAGAGCGCTTGGCGAGGTCGCC  420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  228957  TTCCTTCTCGTAGTAGCGGATGGTCACGACCTCGCACCCAGAGCGCTTGGCGAGGTCGCC  228898

Query  421     AATTCTGATTTCCAT  435
               |||||||||||||||
Sbjct  228897  AATTCTGATTTCCAT  228883
```

Salmonella enterica subsp. enterica serovar Newport strain 0307-213, complete genome
Sequence ID: **CP012599.1** Length: 4512838 Number of Matches: 1
Range 1: 196906 to 197340

Score	**Expect**	**Identities**	**Gaps**	**Strand**	**Frame**
804 bits(435)	0.0()	435/435(100%)	0/435(0%)	Plus/Plus	

Features:

```
Query  1       TTACCCAGATGTTTGACTGTTCGTGGCACTTTCACCATGGCAATTGCCCAACCCTTGCAA  60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  196906  TTACCCAGATGTTTGACTGTTCGTGGCACTTTCACCATGGCAATTGCCCAACCCTTGCAA  196965

Query  61      AATGCCGCACGCCTCTACAGATCGAGAGCCAGAACACTTCTCGCGCAAATCAACCAAGTG  120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  196966  AATGCCGCACGCCTCTACAGATCGAGAGCCAGAACACTTCTCGCGCAAATCAACCAAGTG  197025

Query  121     CCGTTTTAACTGCAACAGCGCGGACACACGCATTTCCACCTGTTGAATATGGGCCTCCAG  180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  197026  CCGTTTTAACTGCAACAGCGCGGACACACGCATTTCCACCTGTTGAATATGGGCCTCCAG  197085

Query  181     CAGCGTGATGACCTCCCCACAGTCCTGCATCGGGTTGTCTCGCAGACCCAGCAATGCGCG  240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  197086  CAGCGTGATGACCTCCCCACAGTCCTGCATCGGGTTGTCTCGCAGACCCAGCAATGCGCG  197145

Query  241     AATCTCGCTCAACGTCATGTCGAGCGAACGGCAATGACGGATGAATTGCAAGCGCTCAAT  300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  197146  AATCTCGCTCAACGTCATGTCGAGCGAACGGCAATGACGGATGAATTGCAAGCGCTCAAT  197205

Query  301     GTGCGCCTCACCGTACAACCGAAAGTTGCCACCGCTTCGCGCTGGCTTTGGCAGTAGCCC  360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  197206  GTGCGCCTCACCGTACAACCGAAAGTTGCCACCGCTTCGCGCTGGCTTTGGCAGTAGCCC  197265

Query  361     TTCCTTCTCGTAGTAGCGGATGGTCACGACCTCGCACCCAGAGCGCTTGGCGAGGTCGCC  420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  197266  TTCCTTCTCGTAGTAGCGGATGGTCACGACCTCGCACCCAGAGCGCTTGGCGAGGTCGCC  197325

Query  421     AATTCTGATTTCCAT  435
               |||||||||||||||
```

```
Sbjct  197326  AATTCTGATTTCCAT  197340
```

BLAST ® » blastn suite » RID-PENYW28C014

BBa_I721001 Promotor

BLAST Results

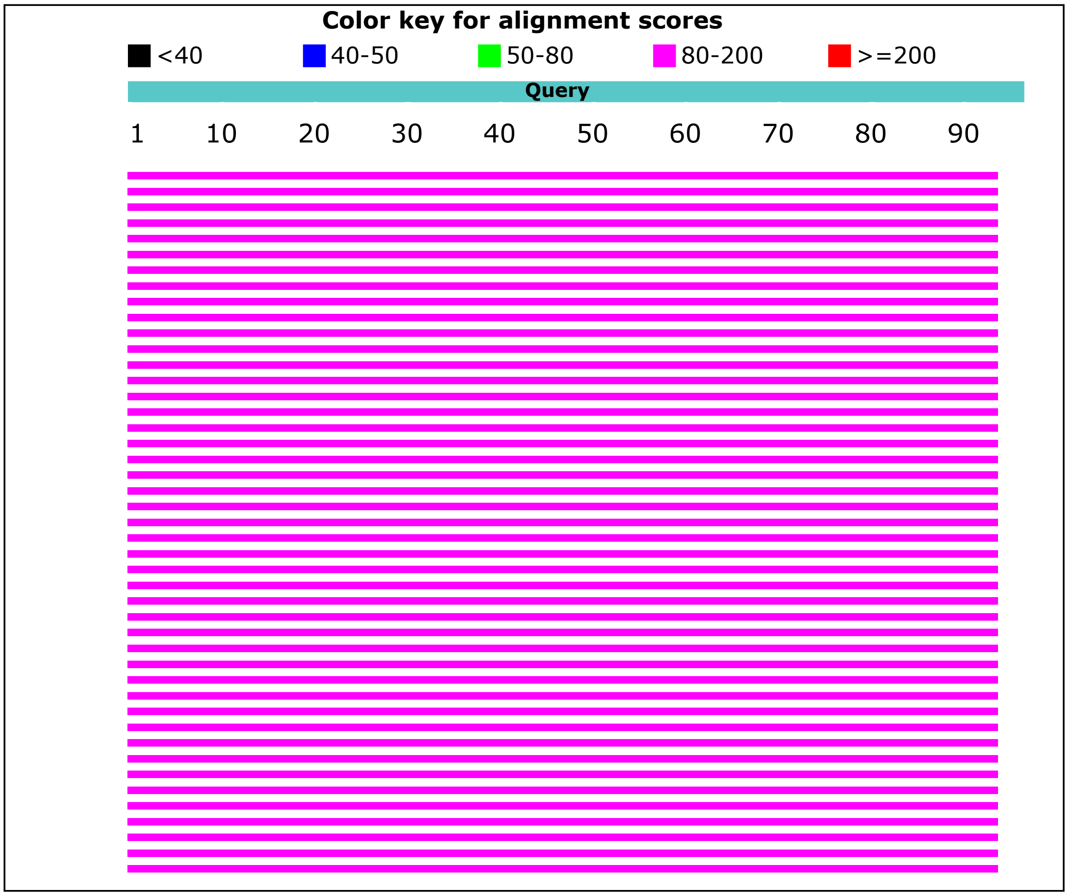
Job title: Nucleotide Sequence (94 letters)

RID PENYW28C014 (Expires on 07-14 19:22 pm)

Query ID	lcl|Query_44837	**Database Name**	nr
Description	None	**Description**	Nucleotide collection (nt)
Molecule type	nucleic acid	**Program**	BLASTN 2.6.1+
Query Length	94		

Graphic Summary

Distribution of the top 48 Blast Hits on 45 subject sequences



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Pseudomonas aeruginosa strain 1242, complete genome	172	172	98%	8e-40	100%	CP022002.1
Pseudomonas aeruginosa strain 1207, complete genome	172	345	98%	8e-40	100%	CP022001.1
Pseudomonas aeruginosa C-NN2 isolate early isolate NN2 (clone C) genome assembly, chromosome: I	172	172	98%	8e-40	100%	LT883143.1
Bordetella genomosp. 13 strain AU7206, complete genome	172	172	98%	8e-40	100%	CP021111.1
Pseudomonas aeruginosa strain W45909, complete genome	172	172	98%	8e-40	100%	CP008871.2
Pseudomonas aeruginosa strain T38079, complete genome	172	172	98%	8e-40	100%	CP008866.2
Pseudomonas aeruginosa strain S86968, complete genome	172	172	98%	8e-40	100%	CP008865.2
Pseudomonas aeruginosa strain W60856, complete genome	172	172	98%	8e-40	100%	CP008864.2
Pseudomonas aeruginosa strain RIVM-EMC2982, complete genome	172	172	98%	8e-40	100%	CP016955.1
Burkholderia cenocepacia strain VC1254 chromosome 1, complete sequence	172	172	98%	8e-40	100%	CP019678.1
Burkholderia cenocepacia strain VC2307 chromosome 1 sequence	172	172	98%	8e-40	100%	CP019666.1
Pseudomonas aeruginosa strain PAER4_119, complete genome	172	172	98%	8e-40	100%	CP013113.1
Pseudomonas rhodesiae strain BS2777 genome assembly, chromosome: I	172	172	98%	8e-40	100%	LT629801.1
Delftia tsuruhatensis strain CM13, complete genome	172	172	98%	8e-40	100%	CP017420.1
Pseudomonas aeruginosa strain FA-HZ1, complete genome	172	172	98%	8e-40	100%	CP017353.1
Ralstonia insidiosa strain ATCC 49129 chromosome 1, complete sequence	172	172	98%	8e-40	100%	CP016022.1
Pseudomonas aeruginosa strain BAMCPA07-48, complete genome	172	172	98%	8e-40	100%	CP015377.1
Pseudomonas aeruginosa strain ATCC 27853, complete genome	172	172	98%	8e-40	100%	CP015117.1
Burkholderia cenocepacia strain 895 chromosome 1, complete sequence	172	172	98%	8e-40	100%	CP015036.1
Pseudomonas aeruginosa strain F9670, complete genome	172	172	98%	8e-40	100%	CP008873.1
Pseudomonas aeruginosa strain F30658, complete genome	172	518	98%	8e-40	100%	CP008857.1
Burkholderia cenocepacia strain ST32 chromosome 1, complete sequence	172	172	98%	8e-40	100%	CP011917.1
Pseudomonas aeruginosa DNA, complete genome, strain: 8380	172	172	98%	8e-40	100%	AP014839.2
Pseudomonas aeruginosa strain S04 90 genome	172	172	98%	8e-40	100%	CP011369.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Pseudomonas aeruginosa strain Carb01 63, complete genome	172	172	98%	8e-40	100%	CP011317.1
Achromobacter xylosoxidans genome assembly NCTC10807, chromosome : 1	172	172	98%	8e-40	100%	LN831029.1
Pseudomonas aeruginosa strain FRD1, complete genome	172	172	98%	8e-40	100%	CP010555.1
Burkholderia cepacia strain DDS 7H-2 chromosome 1, complete sequence	172	172	98%	8e-40	100%	CP007787.1
Pseudomonas aeruginosa LESlike4 sequence	172	172	98%	8e-40	100%	CP006985.1
Pseudomonas aeruginosa LESlike1 sequence	172	172	98%	8e-40	100%	CP006984.1
Pseudomonas aeruginosa LESB65 sequence	172	172	98%	8e-40	100%	CP006983.1
Pseudomonas aeruginosa LES400 sequence	172	172	98%	8e-40	100%	CP006982.1
Pseudomonas aeruginosa LESlike7 sequence	172	172	98%	8e-40	100%	CP006981.1
Pseudomonas aeruginosa LESlike5 sequence	172	172	98%	8e-40	100%	CP006980.1
Pseudomonas aeruginosa PA38182, complete genome	172	172	98%	8e-40	100%	HG530068.1
Pseudomonas aeruginosa SCV20265, complete genome	172	172	98%	8e-40	100%	CP006931.1
Pseudomonas aeruginosa LES431, complete genome	172	172	98%	8e-40	100%	CP006937.1
Achromobacter xylosoxidans NH44784-1996 complete genome	172	172	98%	8e-40	100%	HE798385.1
Pseudomonas aeruginosa DK2, complete genome	172	172	98%	8e-40	100%	CP003149.1
Tistrella mobilis KA081020-065 plasmid pTM3, complete sequence	172	172	98%	8e-40	100%	CP003239.1
Stenotrophomonas maltophilia D457 complete genome	172	172	98%	8e-40	100%	HE798556.1
Pseudomonas aeruginosa LESB58 complete genome sequence	172	172	98%	8e-40	100%	FM209186.1
Parvibaculum lavamentivorans DS-1, complete genome	172	172	98%	8e-40	100%	CP000774.1
Cupriavidus metallidurans CH34, complete genome	172	172	98%	8e-40	100%	CP000352.1
Pseudomonas aeruginosa strain C genomic sequence, gene island PAGI-2(C)	172	172	98%	8e-40	100%	AF440523.1

Alignments

Pseudomonas aeruginosa strain 1242, complete genome

Sequence ID: **CP022002.1** Length: 7050510 Number of Matches: 1
Range 1: 4951456 to 4951548

Score	Expect	Identities	Gaps	Strand	Frame
172 bits(93)	8e-40()	93/93(100%)	0/93(0%)	Plus/Plus	

Features:
copper-translocating P-type ATPase

```
Query  1        GTTGCTTCCTATAAAAAACTTGACTCTATATCTACTAGAGGTTTTCTAATGATGGCATCC  60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Sbjct  4951456  GTTGCTTCCTATAAAAAACTTGACTCTATATCTACTAGAGGTTTTCTAATGATGGCATCC  4951515

Query  61       GGGGAAAACCTTGTCAATGAAGAGCGATCTATG  93
                |||||||||||||||||||||||||||||||||
Sbjct  4951516  GGGGAAAACCTTGTCAATGAAGAGCGATCTATG  4951548
```

Pseudomonas aeruginosa strain 1207, complete genome

Sequence ID: **CP022001.1** Length: 7411863 Number of Matches: 2
Range 1: 4537645 to 4537737

Score	Expect	Identities	Gaps	Strand	Frame
172 bits(93)	8e-40()	93/93(100%)	0/93(0%)	Plus/Plus	

Features:
copper-translocating P-type ATPase

```
Query  1        GTTGCTTCCTATAAAAAACTTGACTCTATATCTACTAGAGGTTTTCTAATGATGGCATCC  60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4537645  GTTGCTTCCTATAAAAAACTTGACTCTATATCTACTAGAGGTTTTCTAATGATGGCATCC  4537704

Query  61       GGGGAAAACCTTGTCAATGAAGAGCGATCTATG  93
                |||||||||||||||||||||||||||||||||
Sbjct  4537705  GGGGAAAACCTTGTCAATGAAGAGCGATCTATG  4537737
```

Range 2: 5285763 to 5285855

Score	Expect	Identities	Gaps	Strand	Frame
172 bits(93)	8e-40()	93/93(100%)	0/93(0%)	Plus/Plus	

Features:
copper-translocating P-type ATPase

```
Query  1        GTTGCTTCCTATAAAAAACTTGACTCTATATCTACTAGAGGTTTTCTAATGATGGCATCC  60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5285763  GTTGCTTCCTATAAAAAACTTGACTCTATATCTACTAGAGGTTTTCTAATGATGGCATCC  5285822

Query  61       GGGGAAAACCTTGTCAATGAAGAGCGATCTATG  93
                |||||||||||||||||||||||||||||||||
Sbjct  5285823  GGGGAAAACCTTGTCAATGAAGAGCGATCTATG  5285855
```

Pseudomonas aeruginosa C-NN2 isolate early isolate NN2 (clone C) genome assembly, chromosome: I

Sequence ID: **LT883143.1** Length: 6902967 Number of Matches: 1
Range 1: 2503098 to 2503190

Score	Expect	Identities	Gaps	Strand	Frame
172 bits(93)	8e-40()	93/93(100%)	0/93(0%)	Plus/Minus	

Features:
Lead, cadmium, zinc and mercury transporting ATPase; Copp...

```
Query  1        GTTGCTTCCTATAAAAAACTTGACTCTATATCTACTAGAGGTTTTCTAATGATGGCATCC  60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2503190  GTTGCTTCCTATAAAAAACTTGACTCTATATCTACTAGAGGTTTTCTAATGATGGCATCC  2503131

Query  61       GGGGAAAACCTTGTCAATGAAGAGCGATCTATG  93
                |||||||||||||||||||||||||||||||||
Sbjct  2503130  GGGGAAAACCTTGTCAATGAAGAGCGATCTATG  2503098
```

Bordetella genomosp. 13 strain AU7206, complete genome

Sequence ID: **CP021111.1** Length: 5380929 Number of Matches: 1
Range 1: 4154245 to 4154337

Score	Expect	Identities	Gaps	Strand	Frame
172 bits(93)	8e-40()	93/93(100%)	0/93(0%)	Plus/Minus	

Features:
copper-translocating P-type ATPase

```
Query  1        GTTGCTTCCTATAAAAAACTTGACTCTATATCTACTAGAGGTTTTCTAATGATGGCATCC  60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4154337  GTTGCTTCCTATAAAAAACTTGACTCTATATCTACTAGAGGTTTTCTAATGATGGCATCC  4154278

Query  61       GGGGAAAACCTTGTCAATGAAGAGCGATCTATG  93
                |||||||||||||||||||||||||||||||||
Sbjct  4154277  GGGGAAAACCTTGTCAATGAAGAGCGATCTATG  4154245
```

Pseudomonas aeruginosa strain W45909, complete genome

Sequence ID: **CP008871.2** Length: 6777566 Number of Matches: 1
Range 1: 2740844 to 2740936

Score	Expect	Identities	Gaps	Strand	Frame
172 bits(93)	8e-40()	93/93(100%)	0/93(0%)	Plus/Minus	

Features:
copper-translocating P-type ATPase

```
Query  1        GTTGCTTCCTATAAAAAACTTGACTCTATATCTACTAGAGGTTTTCTAATGATGGCATCC  60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2740936  GTTGCTTCCTATAAAAAACTTGACTCTATATCTACTAGAGGTTTTCTAATGATGGCATCC  2740877

Query  61       GGGGAAAACCTTGTCAATGAAGAGCGATCTATG  93
                |||||||||||||||||||||||||||||||||
Sbjct  2740876  GGGGAAAACCTTGTCAATGAAGAGCGATCTATG  2740844
```

BLAST ® » blastn suite » RID-PEN0N21C015

BBa_I721002 Lead binding protein part 3 Blast Result

BLAST Results

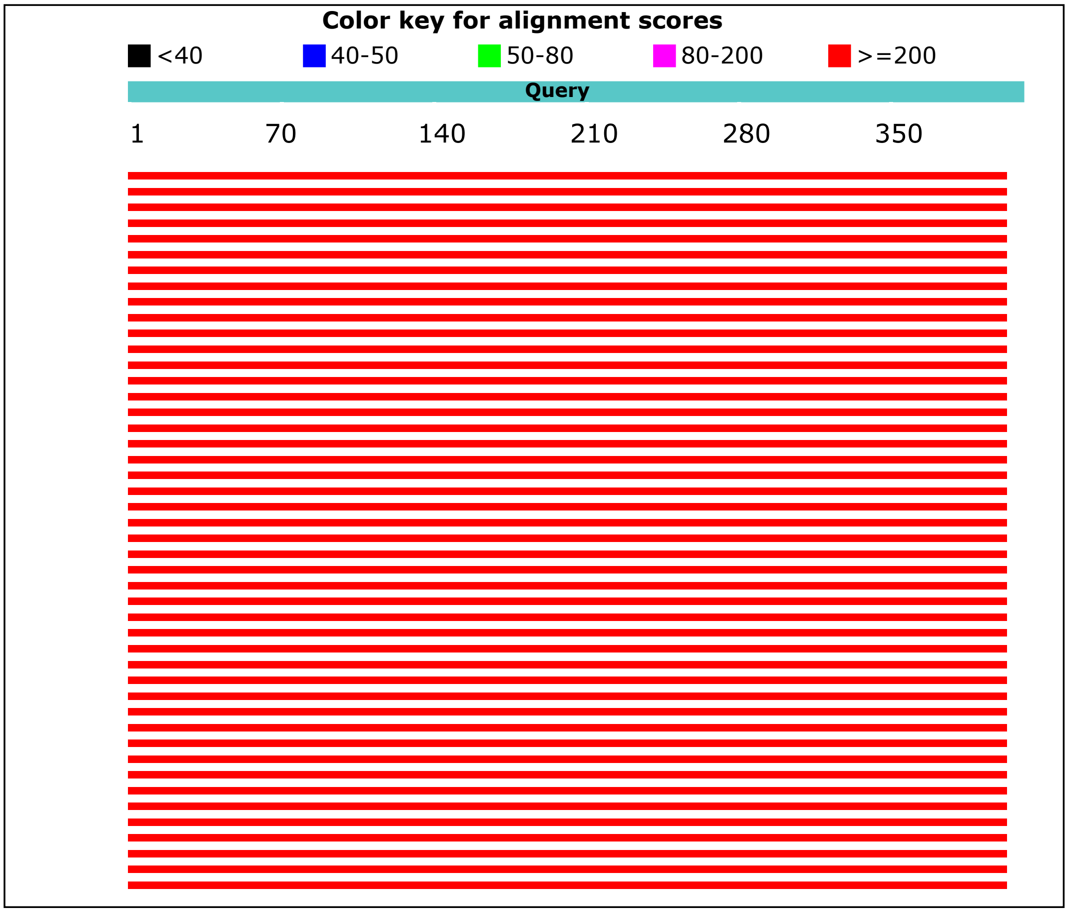
Job title: Nucleotide Sequence (399 letters)

RID PEN0N21C015 (Expires on 07-14 19:05 pm)

Query ID	lcl|Query_172571	**Database Name**	nr
Description	None	**Description**	Nucleotide collection (nt)
Molecule type	nucleic acid	**Program**	BLASTN 2.6.1+
Query Length	399		

Graphic Summary

Distribution of the top 49 Blast Hits on 46 subject sequences



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Pseudomonas aeruginosa strain 1242, complete genome	737	737	100%	0.0	100%	CP022002.1
Pseudomonas aeruginosa strain 1207, complete genome	737	1475	100%	0.0	100%	CP022001.1
Pseudomonas aeruginosa C-NN2 isolate early isolate NN2 (clone C) genome assembly, chromosome: I	737	737	100%	0.0	100%	LT883143.1
Bordetella genomosp. 13 strain AU7206, complete genome	737	737	100%	0.0	100%	CP021111.1
Pseudomonas aeruginosa strain W45909, complete genome	737	737	100%	0.0	100%	CP008871.2
Pseudomonas aeruginosa strain T38079, complete genome	737	737	100%	0.0	100%	CP008866.2
Pseudomonas aeruginosa strain S86968, complete genome	737	737	100%	0.0	100%	CP008865.2
Pseudomonas aeruginosa strain W60856, complete genome	737	737	100%	0.0	100%	CP008864.2
Pseudomonas aeruginosa strain RIVM-EMC2982, complete genome	737	737	100%	0.0	100%	CP016955.1
Burkholderia cenocepacia strain VC1254 chromosome 1, complete sequence	737	737	100%	0.0	100%	CP019678.1
Burkholderia cenocepacia strain VC2307 chromosome 1 sequence	737	737	100%	0.0	100%	CP019666.1
Pseudomonas aeruginosa strain PAER4_119, complete genome	737	737	100%	0.0	100%	CP013113.1
Pseudomonas rhodesiae strain BS2777 genome assembly, chromosome: I	737	737	100%	0.0	100%	LT629801.1
Delftia tsuruhatensis strain CM13, complete genome	737	737	100%	0.0	100%	CP017420.1
Pseudomonas aeruginosa strain FA-HZ1, complete genome	737	737	100%	0.0	100%	CP017353.1
Ralstonia insidiosa strain ATCC 49129 chromosome 1, complete sequence	737	737	100%	0.0	100%	CP016022.1
Pseudomonas aeruginosa strain BAMCPA07-48, complete genome	737	737	100%	0.0	100%	CP015377.1
Pseudomonas aeruginosa strain ATCC 27853, complete genome	737	737	100%	0.0	100%	CP015117.1
Burkholderia cenocepacia strain 895 chromosome 1, complete sequence	737	737	100%	0.0	100%	CP015036.1
Pseudomonas aeruginosa strain F9670, complete genome	737	737	100%	0.0	100%	CP008873.1
Pseudomonas aeruginosa strain F30658, complete genome	737	2213	100%	0.0	100%	CP008857.1
Burkholderia cenocepacia strain ST32 chromosome 1, complete sequence	737	737	100%	0.0	100%	CP011917.1
Pseudomonas aeruginosa DNA, complete genome, strain: 8380	737	737	100%	0.0	100%	AP014839.2
Pseudomonas aeruginosa strain S04 90 genome	737	737	100%	0.0	100%	CP011369.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Pseudomonas aeruginosa strain Carb01 63, complete genome	737	737	100%	0.0	100%	CP011317.1
Achromobacter xylosoxidans genome assembly NCTC10807, chromosome : 1	737	737	100%	0.0	100%	LN831029.1
Pseudomonas aeruginosa strain FRD1, complete genome	737	737	100%	0.0	100%	CP010555.1
Burkholderia cepacia strain DDS 7H-2 chromosome 1, complete sequence	737	737	100%	0.0	100%	CP007787.1
Pseudomonas aeruginosa LESlike4 sequence	737	737	100%	0.0	100%	CP006985.1
Pseudomonas aeruginosa PA38182, complete genome	737	737	100%	0.0	100%	HG530068.1
Pseudomonas aeruginosa SCV20265, complete genome	737	737	100%	0.0	100%	CP006931.1
Achromobacter xylosoxidans NH44784-1996 complete genome	737	737	100%	0.0	100%	HE798385.1
Pseudomonas aeruginosa DK2, complete genome	737	737	100%	0.0	100%	CP003149.1
Tistrella mobilis KA081020-065 plasmid pTM3, complete sequence	737	737	100%	0.0	100%	CP003239.1
Stenotrophomonas maltophilia D457 complete genome	737	737	100%	0.0	100%	HE798556.1
Parvibaculum lavamentivorans DS-1, complete genome	737	737	100%	0.0	100%	CP000774.1
Cupriavidus metallidurans CH34, complete genome	737	737	100%	0.0	100%	CP000352.1
Pseudomonas aeruginosa strain C genomic sequence, gene island PAGI-2(C)	737	737	100%	0.0	100%	AF440523.1
Pseudomonas aeruginosa LESlike1 sequence	732	732	100%	0.0	99%	CP006984.1
Pseudomonas aeruginosa LESB65 sequence	732	732	100%	0.0	99%	CP006983.1
Pseudomonas aeruginosa LES400 sequence	732	732	100%	0.0	99%	CP006982.1
Pseudomonas aeruginosa LESlike7 sequence	732	732	100%	0.0	99%	CP006981.1
Pseudomonas aeruginosa LESlike5 sequence	732	732	100%	0.0	99%	CP006980.1
Pseudomonas aeruginosa LES431, complete genome	732	732	100%	0.0	99%	CP006937.1
Pseudomonas aeruginosa LESB58 complete genome sequence	732	732	100%	0.0	99%	FM209186.1
Acidovorax ebreus TPSY, complete genome	494	494	100%	9e-136	89%	CP001392.1

Alignments

Pseudomonas aeruginosa strain 1242, complete genome

Sequence ID: **CP022002.1** Length: 7050510 Number of Matches: 1

Range 1: 4951056 to 4951454

Score	Expect	Identities	Gaps	Strand	Frame
737 bits(399)	0.0()	399/399(100%)	0/399(0%)	Plus/Minus	

Features:

Cd(II)/Pb(II)-responsive transcriptional regulator

```
Query  1        ATGATGCGGATCGGTGAACTGGGCAAGAAGGCAGATTGCTTGGTGCAGACCGTGCGCTTT  60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4951454  ATGATGCGGATCGGTGAACTGGGCAAGAAGGCAGATTGCTTGGTGCAGACCGTGCGCTTT  4951395

Query  61       TACGAGTCAGAAGGCTTGCTGCCCGAGCCTGCACGTAGCGAGGGCAACTTCAGGCTCTAT  120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4951394  TACGAGTCAGAAGGCTTGCTGCCCGAGCCTGCACGTAGCGAGGGCAACTTCAGGCTCTAT  4951335

Query  121      GACGAAGTCCATTTGCAGCGCTTGCTGTTCATCCGCCGCTGCCGGGCGAAGGACATGACG  180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4951334  GACGAAGTCCATTTGCAGCGCTTGCTGTTCATCCGCCGCTGCCGGGCGAAGGACATGACG  4951275

Query  181      CTGGATGAGATCCGTCAACTGCTGAACTTACGGATCGGCCAGAGTTGGGCTGCGGCGAG  240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4951274  CTGGATGAGATCCGTCAACTGCTGAACTTACGGATCGGCCAGAGTTGGGCTGCGGCGAG  4951215

Query  241      GTGAACGCGCTGGTCGACGCTCATATCGCGCAAGTGCGGACCAAGATGAAGGAATTGCGC  300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4951214  GTGAACGCGCTGGTCGACGCTCATATCGCGCAAGTGCGGACCAAGATGAAGGAATTGCGC  4951155

Query  301      GCCTTGGAGCGCGAGTTAATGGATCTGCGACGCTCCTGCGATAGCGCCCGAACCTCGCGC  360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4951154  GCCTTGGAGCGCGAGTTAATGGATCTGCGACGCTCCTGCGATAGCGCCCGAACCTCGCGC  4951095

Query  361      GAGTGCGGCATTCTCAACAGCTTGGCCGAGCCCGCCTGA  399
                |||||||||||||||||||||||||||||||||||||||
Sbjct  4951094  GAGTGCGGCATTCTCAACAGCTTGGCCGAGCCCGCCTGA  4951056
```

Pseudomonas aeruginosa strain 1207, complete genome
Sequence ID: **CP022001.1** Length: 7411863 Number of Matches: 2
Range 1: 4537245 to 4537643

Score	Expect	Identities	Gaps	Strand	Frame
737 bits(399)	0.0()	399/399(100%)	0/399(0%)	Plus/Minus	

Features:
Cd(II)/Pb(II)-responsive transcriptional regulator

```
Query  1        ATGATGCGGATCGGTGAACTGGGCAAGAAGGCAGATTGCTTGGTGCAGACCGTGCGCTTT  60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4537643  ATGATGCGGATCGGTGAACTGGGCAAGAAGGCAGATTGCTTGGTGCAGACCGTGCGCTTT  4537584

Query  61       TACGAGTCAGAAGGCTTGCTGCCCGAGCCTGCACGTAGCGAGGGCAACTTCAGGCTCTAT  120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4537583  TACGAGTCAGAAGGCTTGCTGCCCGAGCCTGCACGTAGCGAGGGCAACTTCAGGCTCTAT  4537524

Query  121      GACGAAGTCCATTTGCAGCGCTTGCTGTTCATCCGCCGCTGCCGGGCGAAGGACATGACG  180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4537523  GACGAAGTCCATTTGCAGCGCTTGCTGTTCATCCGCCGCTGCCGGGCGAAGGACATGACG  4537464

Query  181      CTGGATGAGATCCGTCAACTGCTGAACTTACGGATCGGCCAGAGTTGGGCTGCGGCGAG  240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4537463  CTGGATGAGATCCGTCAACTGCTGAACTTACGGATCGGCCAGAGTTGGGCTGCGGCGAG  4537404

Query  241      GTGAACGCGCTGGTCGACGCTCATATCGCGCAAGTGCGGACCAAGATGAAGGAATTGCGC  300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4537403  GTGAACGCGCTGGTCGACGCTCATATCGCGCAAGTGCGGACCAAGATGAAGGAATTGCGC  4537344

Query  301      GCCTTGGAGCGCGAGTTAATGGATCTGCGACGCTCCTGCGATAGCGCCCGAACCTCGCGC  360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4537343  GCCTTGGAGCGCGAGTTAATGGATCTGCGACGCTCCTGCGATAGCGCCCGAACCTCGCGC  4537284

Query  361      GAGTGCGGCATTCTCAACAGCTTGGCCGAGCCCGCCTGA  399
                |||||||||||||||||||||||||||||||||||||||
Sbjct  4537283  GAGTGCGGCATTCTCAACAGCTTGGCCGAGCCCGCCTGA  4537245
```

Range 2: 5285363 to 5285761

Score	Expect	Identities	Gaps	Strand	Frame
737 bits(399)	0.0()	399/399(100%)	0/399(0%)	Plus/Minus	

Features:
Cd(II)/Pb(II)-responsive transcriptional regulator

```
Query  1        ATGATGCGGATCGGTGAACTGGGCAAGAAGGCAGATTGCTTGGTGCAGACCGTGCGCTTT  60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5285761  ATGATGCGGATCGGTGAACTGGGCAAGAAGGCAGATTGCTTGGTGCAGACCGTGCGCTTT  5285702

Query  61       TACGAGTCAGAAGGCTTGCTGCCCGAGCCTGCACGTAGCGAGGGCAACTTCAGGCTCTAT  120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5285701  TACGAGTCAGAAGGCTTGCTGCCCGAGCCTGCACGTAGCGAGGGCAACTTCAGGCTCTAT  5285642

Query  121      GACGAAGTCCATTTGCAGCGCTTGCTGTTCATCCGCCGCTGCCGGGCGAAGGACATGACG  180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5285641  GACGAAGTCCATTTGCAGCGCTTGCTGTTCATCCGCCGCTGCCGGGCGAAGGACATGACG  5285582

Query  181      CTGGATGAGATCCGTCAACTGCTGAACTTACGGATCGGCCAGAGTTGGGCTGCGGCGAG  240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5285581  CTGGATGAGATCCGTCAACTGCTGAACTTACGGATCGGCCAGAGTTGGGCTGCGGCGAG  5285522
```

```
Query  241      GTGAACGCGCTGGTCGACGCTCATATCGCGCAAGTGCGGACCAAGATGAAGGAATTGCGC  300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5285521  GTGAACGCGCTGGTCGACGCTCATATCGCGCAAGTGCGGACCAAGATGAAGGAATTGCGC  5285462
Query  301      GCCTTGGAGCGCGAGTTAATGGATCTGCGACGCTCCTGCGATAGCGCCCGAACCTCGCGC  360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5285461  GCCTTGGAGCGCGAGTTAATGGATCTGCGACGCTCCTGCGATAGCGCCCGAACCTCGCGC  5285402
Query  361      GAGTGCGGCATTCTCAACAGCTTGGCCGAGCCCGCCTGA  399
                |||||||||||||||||||||||||||||||||||||||
Sbjct  5285401  GAGTGCGGCATTCTCAACAGCTTGGCCGAGCCCGCCTGA  5285363
```

Pseudomonas aeruginosa C-NN2 isolate early isolate NN2 (clone C) genome assembly, chromosome: I
Sequence ID: **LT883143.1** Length: 6902967 Number of Matches: 1
Range 1: 2503192 to 2503590

Score	Expect	Identities	Gaps	Strand	Frame
737 bits(399)	0.0()	399/399(100%)	0/399(0%)	Plus/Plus	

Features:
Transcriptional regulator, MerR family

```
Query  1        ATGATGCGGATCGGTGAACTGGGCAAGAAGGCAGATTGCTTGGTGCAGACCGTGCGCTTT  60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2503192  ATGATGCGGATCGGTGAACTGGGCAAGAAGGCAGATTGCTTGGTGCAGACCGTGCGCTTT  2503251
Query  61       TACGAGTCAGAAGGCTTGCTGCCCGAGCCTGCACGTAGCGAGGGCAACTTCAGGCTCTAT  120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2503252  TACGAGTCAGAAGGCTTGCTGCCCGAGCCTGCACGTAGCGAGGGCAACTTCAGGCTCTAT  2503311
Query  121      GACGAAGTCCATTTGCAGCGCTTGCTGTTCATCCGCCGCTGCCGGGCGAAGGACATGACG  180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2503312  GACGAAGTCCATTTGCAGCGCTTGCTGTTCATCCGCCGCTGCCGGGCGAAGGACATGACG  2503371
Query  181      CTGGATGAGATCCGTCAACTGCTGAACTTACGGGATCGGCCAGAGTTGGGCTGCGGCGAG  240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2503372  CTGGATGAGATCCGTCAACTGCTGAACTTACGGGATCGGCCAGAGTTGGGCTGCGGCGAG  2503431
Query  241      GTGAACGCGCTGGTCGACGCTCATATCGCGCAAGTGCGGACCAAGATGAAGGAATTGCGC  300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2503432  GTGAACGCGCTGGTCGACGCTCATATCGCGCAAGTGCGGACCAAGATGAAGGAATTGCGC  2503491
Query  301      GCCTTGGAGCGCGAGTTAATGGATCTGCGACGCTCCTGCGATAGCGCCCGAACCTCGCGC  360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2503492  GCCTTGGAGCGCGAGTTAATGGATCTGCGACGCTCCTGCGATAGCGCCCGAACCTCGCGC  2503551
Query  361      GAGTGCGGCATTCTCAACAGCTTGGCCGAGCCCGCCTGA  399
                |||||||||||||||||||||||||||||||||||||||
Sbjct  2503552  GAGTGCGGCATTCTCAACAGCTTGGCCGAGCCCGCCTGA  2503590
```

Bordetella genomosp. 13 strain AU7206, complete genome
Sequence ID: **CP021111.1** Length: 5380929 Number of Matches: 1
Range 1: 4154339 to 4154737

Score	Expect	Identities	Gaps	Strand	Frame
737 bits(399)	0.0()	399/399(100%)	0/399(0%)	Plus/Plus	

Features:
Cd(II)/Pb(II)-responsive transcriptional regulator

```
Query  1        ATGATGCGGATCGGTGAACTGGGCAAGAAGGCAGATTGCTTGGTGCAGACCGTGCGCTTT  60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4154339  ATGATGCGGATCGGTGAACTGGGCAAGAAGGCAGATTGCTTGGTGCAGACCGTGCGCTTT  4154398
Query  61       TACGAGTCAGAAGGCTTGCTGCCCGAGCCTGCACGTAGCGAGGGCAACTTCAGGCTCTAT  120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4154399  TACGAGTCAGAAGGCTTGCTGCCCGAGCCTGCACGTAGCGAGGGCAACTTCAGGCTCTAT  4154458
Query  121      GACGAAGTCCATTTGCAGCGCTTGCTGTTCATCCGCCGCTGCCGGGCGAAGGACATGACG  180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4154459  GACGAAGTCCATTTGCAGCGCTTGCTGTTCATCCGCCGCTGCCGGGCGAAGGACATGACG  4154518
Query  181      CTGGATGAGATCCGTCAACTGCTGAACTTACGGGATCGGCCAGAGTTGGGCTGCGGCGAG  240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4154519  CTGGATGAGATCCGTCAACTGCTGAACTTACGGGATCGGCCAGAGTTGGGCTGCGGCGAG  4154578
Query  241      GTGAACGCGCTGGTCGACGCTCATATCGCGCAAGTGCGGACCAAGATGAAGGAATTGCGC  300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4154579  GTGAACGCGCTGGTCGACGCTCATATCGCGCAAGTGCGGACCAAGATGAAGGAATTGCGC  4154638
Query  301      GCCTTGGAGCGCGAGTTAATGGATCTGCGACGCTCCTGCGATAGCGCCCGAACCTCGCGC  360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4154639  GCCTTGGAGCGCGAGTTAATGGATCTGCGACGCTCCTGCGATAGCGCCCGAACCTCGCGC  4154698
Query  361      GAGTGCGGCATTCTCAACAGCTTGGCCGAGCCCGCCTGA  399
                |||||||||||||||||||||||||||||||||||||||
Sbjct  4154699  GAGTGCGGCATTCTCAACAGCTTGGCCGAGCCCGCCTGA  4154737
```

Pseudomonas aeruginosa strain W45909, complete genome

Sequence ID: **CP008871.2** Length: 6777566 Number of Matches: 1
Range 1: 2740938 to 2741336

Score	Expect	Identities	Gaps	Strand	Frame
737 bits(399)	0.0()	399/399(100%)	0/399(0%)	Plus/Plus	

Features:
Cd(II)/Pb(II)-responsive transcriptional regulator

```
Query  1        ATGATGCGGATCGGTGAACTGGGCAAGAAGGCAGATTGCTTGGTGCAGACCGTGCGCTTT  60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2740938  ATGATGCGGATCGGTGAACTGGGCAAGAAGGCAGATTGCTTGGTGCAGACCGTGCGCTTT  2740997

Query  61       TACGAGTCAGAAGGCTTGCTGCCCGAGCCTGCACGTAGCGAGGGCAACTTCAGGCTCTAT  120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2740998  TACGAGTCAGAAGGCTTGCTGCCCGAGCCTGCACGTAGCGAGGGCAACTTCAGGCTCTAT  2741057

Query  121      GACGAAGTCCATTTGCAGCGCTTGCTGTTCATCCGCCGCTGCCGGGCGAAGGACATGACG  180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2741058  GACGAAGTCCATTTGCAGCGCTTGCTGTTCATCCGCCGCTGCCGGGCGAAGGACATGACG  2741117

Query  181      CTGGATGAGATCCGTCAACTGCTGAACTTACGGGATCGGCCAGAGTTGGGCTGCGGCGAG  240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2741118  CTGGATGAGATCCGTCAACTGCTGAACTTACGGGATCGGCCAGAGTTGGGCTGCGGCGAG  2741177

Query  241      GTGAACGCGCTGGTCGACGCTCATATCGCGCAAGTGCGGACCAAGATGAAGGAATTGCGC  300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2741178  GTGAACGCGCTGGTCGACGCTCATATCGCGCAAGTGCGGACCAAGATGAAGGAATTGCGC  2741237

Query  301      GCCTTGGAGCGCGAGTTAATGGATCTGCGACGCTCCTGCGATAGCGCCCGAACCTCGCGC  360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2741238  GCCTTGGAGCGCGAGTTAATGGATCTGCGACGCTCCTGCGATAGCGCCCGAACCTCGCGC  2741297

Query  361      GAGTGCGGCATTCTCAACAGCTTGGCCGAGCCCGCCTGA  399
                |||||||||||||||||||||||||||||||||||||||
Sbjct  2741298  GAGTGCGGCATTCTCAACAGCTTGGCCGAGCCCGCCTGA  2741336
```

BLAST ® » blastn suite » RID-PEN2DYH0015

BBa_I721003 Lead binding and promoter part 8 version B Blast Result

BLAST Results

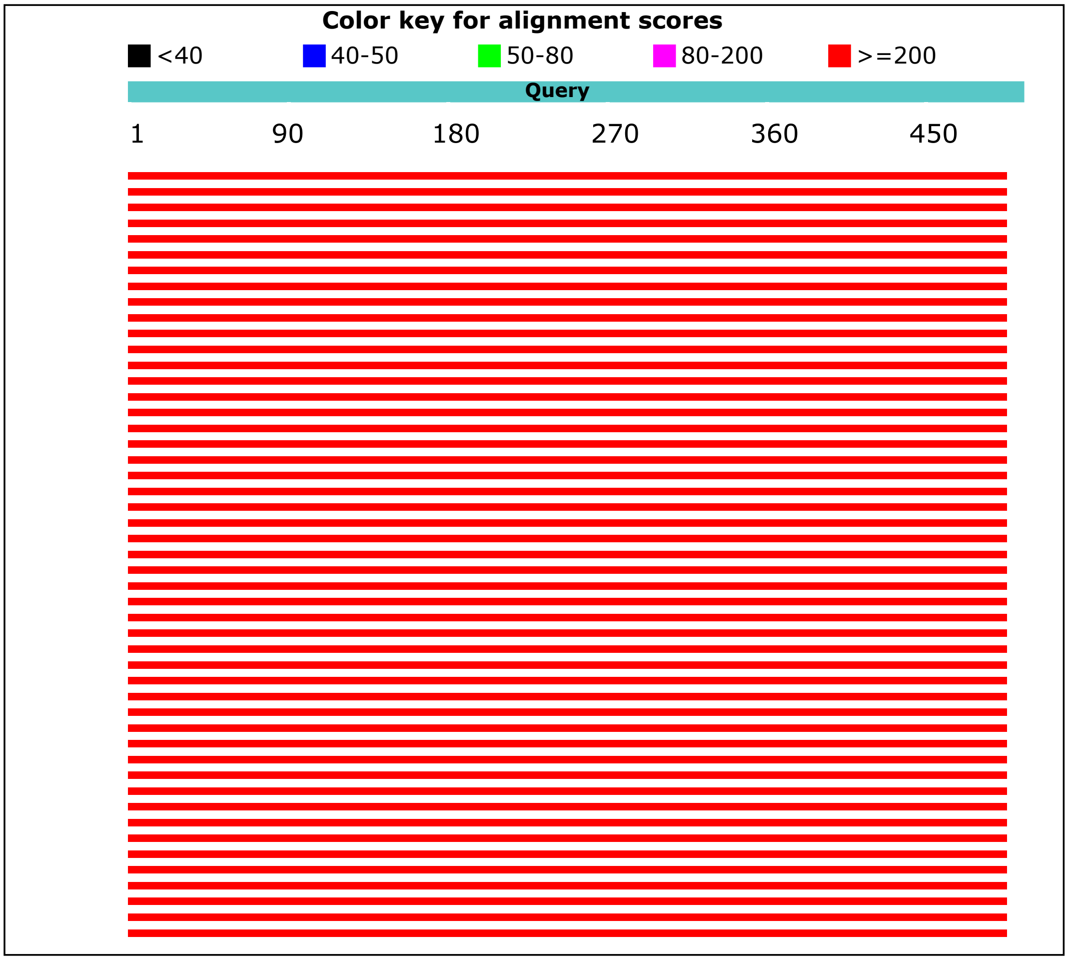
Job title: Nucleotide Sequence (493 letters)

RID PEN2DYH0015 (Expires on 07-14 19:06 pm)

Query ID	lcl|Query_182603	**Database Name**	nr
Description	None	**Description**	Nucleotide collection (nt)
Molecule type	nucleic acid	**Program**	BLASTN 2.6.1+
Query Length	493		

Graphic Summary

Distribution of the top 52 Blast Hits on 49 subject sequences



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Pseudomonas aeruginosa strain 1242, complete genome	911	911	100%	0.0	100%	CP022002.1
Pseudomonas aeruginosa strain 1207, complete genome	911	1823	100%	0.0	100%	CP022001.1
Pseudomonas aeruginosa C-NN2 isolate early isolate NN2 (clone C) genome assembly, chromosome: I	911	911	100%	0.0	100%	LT883143.1
Bordetella genomosp. 13 strain AU7206, complete genome	911	911	100%	0.0	100%	CP021111.1
Pseudomonas aeruginosa strain W45909, complete genome	911	911	100%	0.0	100%	CP008871.2
Pseudomonas aeruginosa strain T38079, complete genome	911	911	100%	0.0	100%	CP008866.2
Pseudomonas aeruginosa strain S86968, complete genome	911	911	100%	0.0	100%	CP008865.2
Pseudomonas aeruginosa strain W60856, complete genome	911	911	100%	0.0	100%	CP008864.2
Pseudomonas aeruginosa strain RIVM-EMC2982, complete genome	911	911	100%	0.0	100%	CP016955.1
Burkholderia cenocepacia strain VC1254 chromosome 1, complete sequence	911	911	100%	0.0	100%	CP019678.1
Burkholderia cenocepacia strain VC2307 chromosome 1 sequence	911	911	100%	0.0	100%	CP019666.1
Pseudomonas aeruginosa strain PAER4_119, complete genome	911	911	100%	0.0	100%	CP013113.1
Pseudomonas rhodesiae strain BS2777 genome assembly, chromosome: I	911	911	100%	0.0	100%	LT629801.1
Delftia tsuruhatensis strain CM13, complete genome	911	911	100%	0.0	100%	CP017420.1
Pseudomonas aeruginosa strain FA-HZ1, complete genome	911	911	100%	0.0	100%	CP017353.1
Ralstonia insidiosa strain ATCC 49129 chromosome 1, complete sequence	911	911	100%	0.0	100%	CP016022.1
Pseudomonas aeruginosa strain BAMCPA07-48, complete genome	911	911	100%	0.0	100%	CP015377.1
Pseudomonas aeruginosa strain ATCC 27853, complete genome	911	911	100%	0.0	100%	CP015117.1
Burkholderia cenocepacia strain 895 chromosome 1, complete sequence	911	911	100%	0.0	100%	CP015036.1
Pseudomonas aeruginosa strain F9670, complete genome	911	911	100%	0.0	100%	CP008873.1
Pseudomonas aeruginosa strain F30658, complete genome	911	2734	100%	0.0	100%	CP008857.1
Burkholderia cenocepacia strain ST32 chromosome 1, complete sequence	911	911	100%	0.0	100%	CP011917.1
Pseudomonas aeruginosa DNA, complete genome, strain: 8380	911	911	100%	0.0	100%	AP014839.2
Pseudomonas aeruginosa strain S04 90 genome	911	911	100%	0.0	100%	CP011369.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Pseudomonas aeruginosa strain Carb01 63, complete genome	911	911	100%	0.0	100%	CP011317.1
Achromobacter xylosoxidans genome assembly NCTC10807, chromosome : 1	911	911	100%	0.0	100%	LN831029.1
Pseudomonas aeruginosa strain FRD1, complete genome	911	911	100%	0.0	100%	CP010555.1
Burkholderia cepacia strain DDS 7H-2 chromosome 1, complete sequence	911	911	100%	0.0	100%	CP007787.1
Pseudomonas aeruginosa LESlike4 sequence	911	911	100%	0.0	100%	CP006985.1
Pseudomonas aeruginosa PA38182, complete genome	911	911	100%	0.0	100%	HG530068.1
Pseudomonas aeruginosa SCV20265, complete genome	911	911	100%	0.0	100%	CP006931.1
Achromobacter xylosoxidans NH44784-1996 complete genome	911	911	100%	0.0	100%	HE798385.1
Pseudomonas aeruginosa DK2, complete genome	911	911	100%	0.0	100%	CP003149.1
Tistrella mobilis KA081020-065 plasmid pTM3, complete sequence	911	911	100%	0.0	100%	CP003239.1
Stenotrophomonas maltophilia D457 complete genome	911	911	100%	0.0	100%	HE798556.1
Parvibaculum lavamentivorans DS-1, complete genome	911	911	100%	0.0	100%	CP000774.1
Cupriavidus metallidurans CH34, complete genome	911	911	100%	0.0	100%	CP000352.1
Pseudomonas aeruginosa strain C genomic sequence, gene island PAGI-2(C)	911	911	100%	0.0	100%	AF440523.1
Pseudomonas aeruginosa LESlike1 sequence	905	905	100%	0.0	99%	CP006984.1
Pseudomonas aeruginosa LESB65 sequence	905	905	100%	0.0	99%	CP006983.1
Pseudomonas aeruginosa LES400 sequence	905	905	100%	0.0	99%	CP006982.1
Pseudomonas aeruginosa LESlike7 sequence	905	905	100%	0.0	99%	CP006981.1
Pseudomonas aeruginosa LESlike5 sequence	905	905	100%	0.0	99%	CP006980.1
Pseudomonas aeruginosa LES431, complete genome	905	905	100%	0.0	99%	CP006937.1
Pseudomonas aeruginosa LESB58 complete genome sequence	905	905	100%	0.0	99%	FM209186.1
Acidovorax ebreus TPSY, complete genome	595	595	100%	3e-166	88%	CP001392.1
Cupriavidus necator strain NH9 plasmid pENH91, complete sequence	538	538	100%	5e-149	86%	CP017760.1
Achromobacter xylosoxidans A8 plasmid pA81, complete sequence	538	538	100%	5e-149	86%	CP002288.1
Achromobacter xylosoxidans plasmid pA81, strain A8	538	538	100%	5e-149	86%	AJ515144.2

Alignments

Pseudomonas aeruginosa strain 1242, complete genome

Sequence ID: **CP022002.1** Length: 7050510 Number of Matches: 1
Range 1: 4951056 to 4951548

Score	Expect	Identities	Gaps	Strand	Frame
911 bits(493)	0.0()	493/493(100%)	0/493(0%)	Plus/Plus	

Features:
Cd(II)/Pb(II)-responsive transcriptional regulatorcopper-translocating P-type ATPase

```
Query  1        TCAGGCGGGCTCGGCCAAGCTGTTGAGAATGCCGCACTCGCGCGAGGTTCGGGCGCTATC  60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4951056  TCAGGCGGGCTCGGCCAAGCTGTTGAGAATGCCGCACTCGCGCGAGGTTCGGGCGCTATC  4951115

Query  61       GCAGGAGCGTCGCAGATCCATTAACTCGCGCTCCAAGGCGCGCAATTCCTTCATCTTGGT  120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4951116  GCAGGAGCGTCGCAGATCCATTAACTCGCGCTCCAAGGCGCGCAATTCCTTCATCTTGGT  4951175

Query  121      CCGCACTTGCGCGATATGAGCGTCGACCAGCGCGTTCACCTCGCCGCAGCCCAACTCTGG  180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4951176  CCGCACTTGCGCGATATGAGCGTCGACCAGCGCGTTCACCTCGCCGCAGCCCAACTCTGG  4951235

Query  181      CCGATCCCGTAAGTTCAGCAGTTGACGGATCTCATCCAGCGTCATGTCCTTCGCCCGGCA  240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4951236  CCGATCCCGTAAGTTCAGCAGTTGACGGATCTCATCCAGCGTCATGTCCTTCGCCCGGCA  4951295

Query  241      GCGGCGGATGAACAGCAAGCGCTGCAAATGGACTTCGTCATAGAGCCTGAAGTTGCCCTC  300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4951296  GCGGCGGATGAACAGCAAGCGCTGCAAATGGACTTCGTCATAGAGCCTGAAGTTGCCCTC  4951355

Query  301      GCTACGTGCAGGCTCGGGCAGCAAGCCTTCTGACTCGTAAAAGCGCACGGTCTGCACCAA  360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4951356  GCTACGTGCAGGCTCGGGCAGCAAGCCTTCTGACTCGTAAAAGCGCACGGTCTGCACCAA  4951415

Query  361      GCAATCTGCCTTCTTGCCCAGTTCACCGATCCGCATCATGGTTGCTTCCTATAAAAAACT  420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4951416  GCAATCTGCCTTCTTGCCCAGTTCACCGATCCGCATCATGGTTGCTTCCTATAAAAAACT  4951475

Query  421      TGACTCTATATCTACTAGAGGTTTTCTAATGATGGCATCCGGGGAAAACCTTGTCAATGA  480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4951476  TGACTCTATATCTACTAGAGGTTTTCTAATGATGGCATCCGGGGAAAACCTTGTCAATGA  4951535

Query  481      AGAGCGATCTATG  493
                |||||||||||||
Sbjct  4951536  AGAGCGATCTATG  4951548
```

Pseudomonas aeruginosa strain 1207, complete genome
Sequence ID: **CP022001.1** Length: 7411863 Number of Matches: 2
Range 1: 4537245 to 4537737

Score	Expect	Identities	Gaps	Strand	Frame
911 bits(493)	0.0()	493/493(100%)	0/493(0%)	Plus/Plus	

Features:
Cd(II)/Pb(II)-responsive transcriptional regulatorcopper-translocating P-type ATPase

```
Query  1        TCAGGCGGGCTCGGCCAAGCTGTTGAGAATGCCGCACTCGCGCGAGGTTCGGGCGCTATC  60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4537245  TCAGGCGGGCTCGGCCAAGCTGTTGAGAATGCCGCACTCGCGCGAGGTTCGGGCGCTATC  4537304

Query  61       GCAGGAGCGTCGCAGATCCATTAACTCGCGCTCCAAGGCGCGCAATTCCTTCATCTTGGT  120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4537305  GCAGGAGCGTCGCAGATCCATTAACTCGCGCTCCAAGGCGCGCAATTCCTTCATCTTGGT  4537364

Query  121      CCGCACTTGCGCGATATGAGCGTCGACCAGCGCGTTCACCTCGCCGCAGCCCAACTCTGG  180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4537365  CCGCACTTGCGCGATATGAGCGTCGACCAGCGCGTTCACCTCGCCGCAGCCCAACTCTGG  4537424

Query  181      CCGATCCCGTAAGTTCAGCAGTTGACGGATCTCATCCAGCGTCATGTCCTTCGCCCGGCA  240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4537425  CCGATCCCGTAAGTTCAGCAGTTGACGGATCTCATCCAGCGTCATGTCCTTCGCCCGGCA  4537484

Query  241      GCGGCGGATGAACAGCAAGCGCTGCAAATGGACTTCGTCATAGAGCCTGAAGTTGCCCTC  300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4537485  GCGGCGGATGAACAGCAAGCGCTGCAAATGGACTTCGTCATAGAGCCTGAAGTTGCCCTC  4537544

Query  301      GCTACGTGCAGGCTCGGGCAGCAAGCCTTCTGACTCGTAAAAGCGCACGGTCTGCACCAA  360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4537545  GCTACGTGCAGGCTCGGGCAGCAAGCCTTCTGACTCGTAAAAGCGCACGGTCTGCACCAA  4537604

Query  361      GCAATCTGCCTTCTTGCCCAGTTCACCGATCCGCATCATGGTTGCTTCCTATAAAAAACT  420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4537605  GCAATCTGCCTTCTTGCCCAGTTCACCGATCCGCATCATGGTTGCTTCCTATAAAAAACT  4537664

Query  421      TGACTCTATATCTACTAGAGGTTTTCTAATGATGGCATCCGGGGAAAACCTTGTCAATGA  480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4537665  TGACTCTATATCTACTAGAGGTTTTCTAATGATGGCATCCGGGGAAAACCTTGTCAATGA  4537724

Query  481      AGAGCGATCTATG  493
                |||||||||||||
Sbjct  4537725  AGAGCGATCTATG  4537737
```

Range 2: 5285363 to 5285855

Score	Expect	Identities	Gaps	Strand	Frame
911 bits(493)	0.0()	493/493(100%)	0/493(0%)	Plus/Plus	

Features:
Cd(II)/Pb(II)-responsive transcriptional regulatorcopper-translocating P-type ATPase

```
Query  1        TCAGGCGGGCTCGGCCAAGCTGTTGAGAATGCCGCACTCGCGCGAGGTTCGGGCGCTATC  60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5285363  TCAGGCGGGCTCGGCCAAGCTGTTGAGAATGCCGCACTCGCGCGAGGTTCGGGCGCTATC  5285422

Query  61       GCAGGAGCGTCGCAGATCCATTAACTCGCGCTCCAAGGCGCGCAATTCCTTCATCTTGGT  120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5285423  GCAGGAGCGTCGCAGATCCATTAACTCGCGCTCCAAGGCGCGCAATTCCTTCATCTTGGT  5285482

Query  121      CCGCACTTGCGCGATATGAGCGTCGACCAGCGCGTTCACCTCGCCGCAGCCCAACTCTGG  180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5285483  CCGCACTTGCGCGATATGAGCGTCGACCAGCGCGTTCACCTCGCCGCAGCCCAACTCTGG  5285542

Query  181      CCGATCCCGTAAGTTCAGCAGTTGACGGATCTCATCCAGCGTCATGTCCTTCGCCCGGCA  240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5285543  CCGATCCCGTAAGTTCAGCAGTTGACGGATCTCATCCAGCGTCATGTCCTTCGCCCGGCA  5285602

Query  241      GCGGCGGATGAACAGCAAGCGCTGCAAATGGACTTCGTCATAGAGCCTGAAGTTGCCCTC  300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5285603  GCGGCGGATGAACAGCAAGCGCTGCAAATGGACTTCGTCATAGAGCCTGAAGTTGCCCTC  5285662

Query  301      GCTACGTGCAGGCTCGGGCAGCAAGCCTTCTGACTCGTAAAAGCGCACGGTCTGCACCAA  360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5285663  GCTACGTGCAGGCTCGGGCAGCAAGCCTTCTGACTCGTAAAAGCGCACGGTCTGCACCAA  5285722

Query  361      GCAATCTGCCTTCTTGCCCAGTTCACCGATCCGCATCATGGTTGCTTCCTATAAAAAACT  420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5285723  GCAATCTGCCTTCTTGCCCAGTTCACCGATCCGCATCATGGTTGCTTCCTATAAAAAACT  5285782

Query  421      TGACTCTATATCTACTAGAGGTTTTCTAATGATGGCATCCGGGGAAAACCTTGTCAATGA  480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5285783  TGACTCTATATCTACTAGAGGTTTTCTAATGATGGCATCCGGGGAAAACCTTGTCAATGA  5285842

Query  481      AGAGCGATCTATG  493
                |||||||||||||
Sbjct  5285843  AGAGCGATCTATG  5285855
```

Pseudomonas aeruginosa C-NN2 isolate early isolate NN2 (clone C) genome assembly, chromosome: I
Sequence ID: **LT883143.1** Length: 6902967 Number of Matches: 1
Range 1: 2503098 to 2503590

Score	Expect	Identities	Gaps	Strand	Frame
911 bits(493)	0.0()	493/493(100%)	0/493(0%)	Plus/Minus	

Features:
Lead, cadmium, zinc and mercury transporting ATPase; Copp...Transcriptional regulator, MerR family

```
Query  1        TCAGGCGGGCTCGGCCAAGCTGTTGAGAATGCCGCACTCGCGCGAGGTTCGGGCGCTATC  60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2503590  TCAGGCGGGCTCGGCCAAGCTGTTGAGAATGCCGCACTCGCGCGAGGTTCGGGCGCTATC  2503531

Query  61       GCAGGAGCGTCGCAGATCCATTAACTCGCGCTCCAAGGCGCGCAATTCCTTCATCTTGGT  120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2503530  GCAGGAGCGTCGCAGATCCATTAACTCGCGCTCCAAGGCGCGCAATTCCTTCATCTTGGT  2503471

Query  121      CCGCACTTGCGCGATATGAGCGTCGACCAGCGCGTTCACCTCGCCGCAGCCCAACTCTGG  180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2503470  CCGCACTTGCGCGATATGAGCGTCGACCAGCGCGTTCACCTCGCCGCAGCCCAACTCTGG  2503411

Query  181      CCGATCCCGTAAGTTCAGCAGTTGACGGATCTCATCCAGCGTCATGTCCTTCGCCCGGCA  240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2503410  CCGATCCCGTAAGTTCAGCAGTTGACGGATCTCATCCAGCGTCATGTCCTTCGCCCGGCA  2503351

Query  241      GCGGCGGATGAACAGCAAGCGCTGCAAATGGACTTCGTCATAGAGCCTGAAGTTGCCCTC  300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2503350  GCGGCGGATGAACAGCAAGCGCTGCAAATGGACTTCGTCATAGAGCCTGAAGTTGCCCTC  2503291

Query  301      GCTACGTGCAGGCTCGGGCAGCAAGCCTTCTGACTCGTAAAAGCGCACGGTCTGCACCAA  360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2503290  GCTACGTGCAGGCTCGGGCAGCAAGCCTTCTGACTCGTAAAAGCGCACGGTCTGCACCAA  2503231

Query  361      GCAATCTGCCTTCTTGCCCAGTTCACCGATCCGCATCATGGTTGCTTCCTATAAAAAACT  420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2503230  GCAATCTGCCTTCTTGCCCAGTTCACCGATCCGCATCATGGTTGCTTCCTATAAAAAACT  2503171

Query  421      TGACTCTATATCTACTAGAGGTTTTCTAATGATGGCATCCGGGGAAAACCTTGTCAATGA  480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2503170  TGACTCTATATCTACTAGAGGTTTTCTAATGATGGCATCCGGGGAAAACCTTGTCAATGA  2503111

Query  481      AGAGCGATCTATG  493
                |||||||||||||
Sbjct  2503110  AGAGCGATCTATG  2503098
```

Bordetella genomosp. 13 strain AU7206, complete genome

Sequence ID: **CP021111.1** Length: 5380929 Number of Matches: 1

Range 1: 4154245 to 4154737

Score	Expect	Identities	Gaps	Strand	Frame
911 bits(493)	0.0()	493/493(100%)	0/493(0%)	Plus/Minus	

Features:
copper-translocating P-type ATPaseCd(II)/Pb(II)-responsive transcriptional regulator

```
Query  1        TCAGGCGGGCTCGGCCAAGCTGTTGAGAATGCCGCACTCGCGCGAGGTTCGGGCGCTATC  60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4154737  TCAGGCGGGCTCGGCCAAGCTGTTGAGAATGCCGCACTCGCGCGAGGTTCGGGCGCTATC  4154678

Query  61       GCAGGAGCGTCGCAGATCCATTAACTCGCGCTCCAAGGCGCGCAATTCCTTCATCTTGGT  120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4154677  GCAGGAGCGTCGCAGATCCATTAACTCGCGCTCCAAGGCGCGCAATTCCTTCATCTTGGT  4154618

Query  121      CCGCACTTGCGCGATATGAGCGTCGACCAGCGCGTTCACCTCGCCGCAGCCCAACTCTGG  180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4154617  CCGCACTTGCGCGATATGAGCGTCGACCAGCGCGTTCACCTCGCCGCAGCCCAACTCTGG  4154558

Query  181      CCGATCCCGTAAGTTCAGCAGTTGACGGATCTCATCCAGCGTCATGTCCTTCGCCCGGCA  240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4154557  CCGATCCCGTAAGTTCAGCAGTTGACGGATCTCATCCAGCGTCATGTCCTTCGCCCGGCA  4154498

Query  241      GCGGCGGATGAACAGCAAGCGCTGCAAATGGACTTCGTCATAGAGCCTGAAGTTGCCCTC  300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4154497  GCGGCGGATGAACAGCAAGCGCTGCAAATGGACTTCGTCATAGAGCCTGAAGTTGCCCTC  4154438

Query  301      GCTACGTGCAGGCTCGGGCAGCAAGCCTTCTGACTCGTAAAAGCGCACGGTCTGCACCAA  360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4154437  GCTACGTGCAGGCTCGGGCAGCAAGCCTTCTGACTCGTAAAAGCGCACGGTCTGCACCAA  4154378

Query  361      GCAATCTGCCTTCTTGCCCAGTTCACCGATCCGCATCATGGTTGCTTCCTATAAAAAACT  420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4154377  GCAATCTGCCTTCTTGCCCAGTTCACCGATCCGCATCATGGTTGCTTCCTATAAAAAACT  4154318

Query  421      TGACTCTATATCTACTAGAGGTTTTCTAATGATGGCATCCGGGGAAAACCTTGTCAATGA  480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4154317  TGACTCTATATCTACTAGAGGTTTTCTAATGATGGCATCCGGGGAAAACCTTGTCAATGA  4154258

Query  481      AGAGCGATCTATG  493
                |||||||||||||
Sbjct  4154257  AGAGCGATCTATG  4154245
```

Pseudomonas aeruginosa strain W45909, complete genome

Sequence ID: **CP008871.2** Length: 6777566 Number of Matches: 1

Range 1: 2740844 to 2741336

Score	Expect	Identities	Gaps	Strand	Frame
911 bits(493)	0.0()	493/493(100%)	0/493(0%)	Plus/Minus	

Features:
copper-translocating P-type ATPaseCd(II)/Pb(II)-responsive transcriptional regulator

```
Query  1        TCAGGCGGGCTCGGCCAAGCTGTTGAGAATGCCGCACTCGCGCGAGGTTCGGGCGCTATC  60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2741336  TCAGGCGGGCTCGGCCAAGCTGTTGAGAATGCCGCACTCGCGCGAGGTTCGGGCGCTATC  2741277

Query  61       GCAGGAGCGTCGCAGATCCATTAACTCGCGCTCCAAGGCGCGCAATTCCTTCATCTTGGT  120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2741276  GCAGGAGCGTCGCAGATCCATTAACTCGCGCTCCAAGGCGCGCAATTCCTTCATCTTGGT  2741217

Query  121      CCGCACTTGCGCGATATGAGCGTCGACCAGCGCGTTCACCTCGCCGCAGCCCAACTCTGG  180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2741216  CCGCACTTGCGCGATATGAGCGTCGACCAGCGCGTTCACCTCGCCGCAGCCCAACTCTGG  2741157

Query  181      CCGATCCCGTAAGTTCAGCAGTTGACGGATCTCATCCAGCGTCATGTCCTTCGCCCGGCA  240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2741156  CCGATCCCGTAAGTTCAGCAGTTGACGGATCTCATCCAGCGTCATGTCCTTCGCCCGGCA  2741097

Query  241      GCGGCGGATGAACAGCAAGCGCTGCAAATGGACTTCGTCATAGAGCCTGAAGTTGCCCTC  300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2741096  GCGGCGGATGAACAGCAAGCGCTGCAAATGGACTTCGTCATAGAGCCTGAAGTTGCCCTC  2741037

Query  301      GCTACGTGCAGGCTCGGGCAGCAAGCCTTCTGACTCGTAAAAGCGCACGGTCTGCACCAA  360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2741036  GCTACGTGCAGGCTCGGGCAGCAAGCCTTCTGACTCGTAAAAGCGCACGGTCTGCACCAA  2740977

Query  361      GCAATCTGCCTTCTTGCCCAGTTCACCGATCCGCATCATGGTTGCTTCCTATAAAAAACT  420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2740976  GCAATCTGCCTTCTTGCCCAGTTCACCGATCCGCATCATGGTTGCTTCCTATAAAAAACT  2740917

Query  421      TGACTCTATATCTACTAGAGGTTTTCTAATGATGGCATCCGGGGAAAACCTTGTCAATGA  480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Sbjct  2740916  TGACTCTATATCTACTAGAGGTTTTCTAATGATGGCATCCGGGGAAAACCTTGTCAATGA  2740857

Query  481      AGAGCGATCTATG  493
                |||||||||||||
Sbjct  2740856  AGAGCGATCTATG  2740844
```

BLAST ® » blastn suite » RID-PEN48ZYE014

BBa_I721004 Lead binding protein and promoter part 11 version a Blast Result

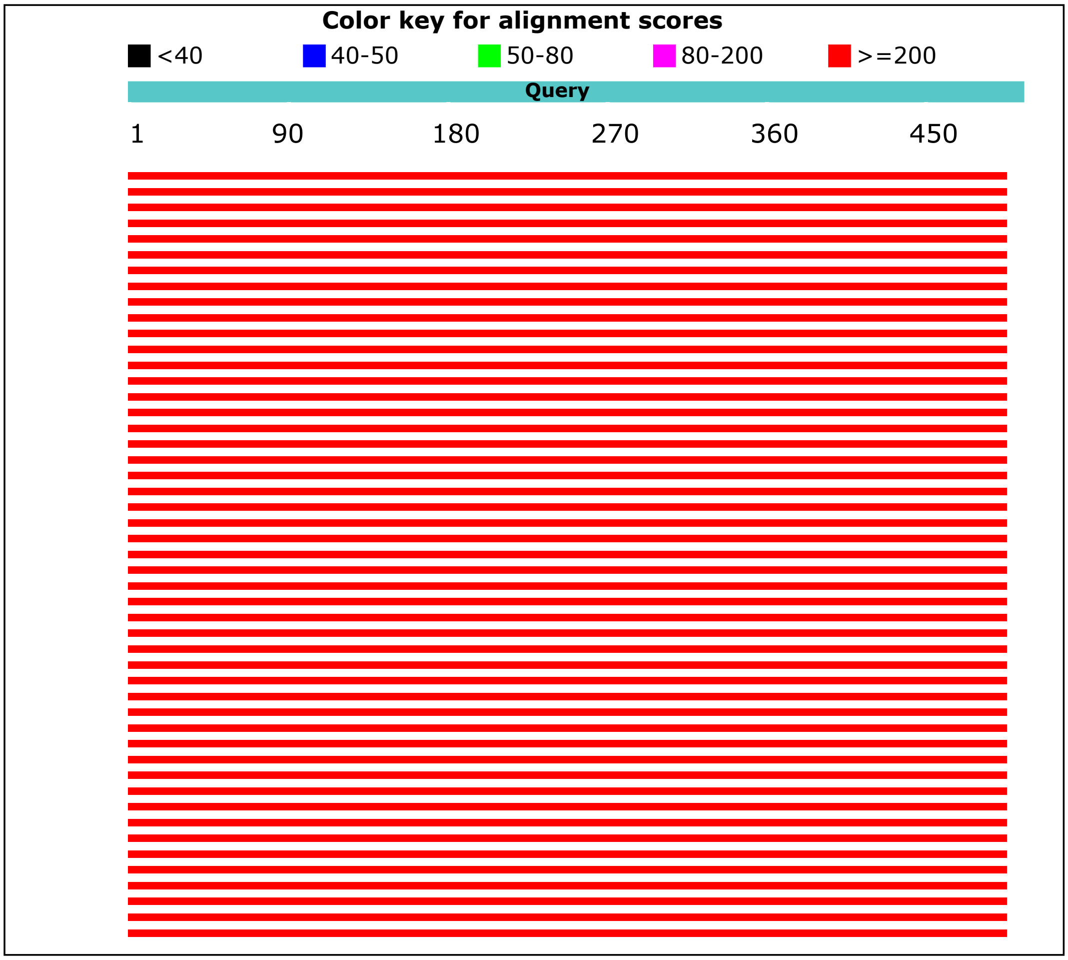
BLAST Results

Job title: Nucleotide Sequence (493 letters)

RID	PEN48ZYE014 (Expires on 07-14 19:07 pm)		
Query ID	lcl|Query_202163	**Database Name**	nr
Description	None	**Description**	Nucleotide collection (nt)
Molecule type	nucleic acid	**Program**	BLASTN 2.6.1+
Query Length	493		

Graphic Summary

Distribution of the top 52 Blast Hits on 49 subject sequences



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Pseudomonas aeruginosa strain 1242, complete genome	911	911	100%	0.0	100%	CP022002.1
Pseudomonas aeruginosa strain 1207, complete genome	911	1823	100%	0.0	100%	CP022001.1
Pseudomonas aeruginosa C-NN2 isolate early isolate NN2 (clone C) genome assembly, chromosome: I	911	911	100%	0.0	100%	LT883143.1
Bordetella genomosp. 13 strain AU7206, complete genome	911	911	100%	0.0	100%	CP021111.1
Pseudomonas aeruginosa strain W45909, complete genome	911	911	100%	0.0	100%	CP008871.2
Pseudomonas aeruginosa strain T38079, complete genome	911	911	100%	0.0	100%	CP008866.2
Pseudomonas aeruginosa strain S86968, complete genome	911	911	100%	0.0	100%	CP008865.2
Pseudomonas aeruginosa strain W60856, complete genome	911	911	100%	0.0	100%	CP008864.2
Pseudomonas aeruginosa strain RIVM-EMC2982, complete genome	911	911	100%	0.0	100%	CP016955.1
Burkholderia cenocepacia strain VC1254 chromosome 1, complete sequence	911	911	100%	0.0	100%	CP019678.1
Burkholderia cenocepacia strain VC2307 chromosome 1 sequence	911	911	100%	0.0	100%	CP019666.1
Pseudomonas aeruginosa strain PAER4_119, complete genome	911	911	100%	0.0	100%	CP013113.1
Pseudomonas rhodesiae strain BS2777 genome assembly, chromosome: I	911	911	100%	0.0	100%	LT629801.1
Delftia tsuruhatensis strain CM13, complete genome	911	911	100%	0.0	100%	CP017420.1
Pseudomonas aeruginosa strain FA-HZ1, complete genome	911	911	100%	0.0	100%	CP017353.1
Ralstonia insidiosa strain ATCC 49129 chromosome 1, complete sequence	911	911	100%	0.0	100%	CP016022.1
Pseudomonas aeruginosa strain BAMCPA07-48, complete genome	911	911	100%	0.0	100%	CP015377.1
Pseudomonas aeruginosa strain ATCC 27853, complete genome	911	911	100%	0.0	100%	CP015117.1
Burkholderia cenocepacia strain 895 chromosome 1, complete sequence	911	911	100%	0.0	100%	CP015036.1
Pseudomonas aeruginosa strain F9670, complete genome	911	911	100%	0.0	100%	CP008873.1
Pseudomonas aeruginosa strain F30658, complete genome	911	2734	100%	0.0	100%	CP008857.1
Burkholderia cenocepacia strain ST32 chromosome 1, complete sequence	911	911	100%	0.0	100%	CP011917.1
Pseudomonas aeruginosa DNA, complete genome, strain: 8380	911	911	100%	0.0	100%	AP014839.2
Pseudomonas aeruginosa strain S04 90 genome	911	911	100%	0.0	100%	CP011369.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Pseudomonas aeruginosa strain Carb01 63, complete genome	911	911	100%	0.0	100%	CP011317.1
Achromobacter xylosoxidans genome assembly NCTC10807, chromosome : 1	911	911	100%	0.0	100%	LN831029.1
Pseudomonas aeruginosa strain FRD1, complete genome	911	911	100%	0.0	100%	CP010555.1
Burkholderia cepacia strain DDS 7H-2 chromosome 1, complete sequence	911	911	100%	0.0	100%	CP007787.1
Pseudomonas aeruginosa LESlike4 sequence	911	911	100%	0.0	100%	CP006985.1
Pseudomonas aeruginosa PA38182, complete genome	911	911	100%	0.0	100%	HG530068.1
Pseudomonas aeruginosa SCV20265, complete genome	911	911	100%	0.0	100%	CP006931.1
Achromobacter xylosoxidans NH44784-1996 complete genome	911	911	100%	0.0	100%	HE798385.1
Pseudomonas aeruginosa DK2, complete genome	911	911	100%	0.0	100%	CP003149.1
Tistrella mobilis KA081020-065 plasmid pTM3, complete sequence	911	911	100%	0.0	100%	CP003239.1
Stenotrophomonas maltophilia D457 complete genome	911	911	100%	0.0	100%	HE798556.1
Parvibaculum lavamentivorans DS-1, complete genome	911	911	100%	0.0	100%	CP000774.1
Cupriavidus metallidurans CH34, complete genome	911	911	100%	0.0	100%	CP000352.1
Pseudomonas aeruginosa strain C genomic sequence, gene island PAGI-2(C)	911	911	100%	0.0	100%	AF440523.1
Pseudomonas aeruginosa LESlike1 sequence	905	905	100%	0.0	99%	CP006984.1
Pseudomonas aeruginosa LESB65 sequence	905	905	100%	0.0	99%	CP006983.1
Pseudomonas aeruginosa LES400 sequence	905	905	100%	0.0	99%	CP006982.1
Pseudomonas aeruginosa LESlike7 sequence	905	905	100%	0.0	99%	CP006981.1
Pseudomonas aeruginosa LESlike5 sequence	905	905	100%	0.0	99%	CP006980.1
Pseudomonas aeruginosa LES431, complete genome	905	905	100%	0.0	99%	CP006937.1
Pseudomonas aeruginosa LESB58 complete genome sequence	905	905	100%	0.0	99%	FM209186.1
Acidovorax ebreus TPSY, complete genome	595	595	100%	3e-166	88%	CP001392.1
Cupriavidus necator strain NH9 plasmid pENH91, complete sequence	538	538	100%	5e-149	86%	CP017760.1
Achromobacter xylosoxidans A8 plasmid pA81, complete sequence	538	538	100%	5e-149	86%	CP002288.1
Achromobacter xylosoxidans plasmid pA81, strain A8	538	538	100%	5e-149	86%	AJ515144.2

Alignments

Pseudomonas aeruginosa strain 1242, complete genome

Sequence ID: **CP022002.1** Length: 7050510 Number of Matches: 1
Range 1: 4951056 to 4951548

Score	Expect	Identities	Gaps	Strand	Frame
911 bits(493)	0.0()	493/493(100%)	0/493(0%)	Plus/Plus	

Features:
Cd(II)/Pb(II)-responsive transcriptional regulatorcopper-translocating P-type ATPase

```
Query  1        TCAGGCGGGCTCGGCCAAGCTGTTGAGAATGCCGCACTCGCGCGAGGTTCGGGCGCTATC  60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4951056  TCAGGCGGGCTCGGCCAAGCTGTTGAGAATGCCGCACTCGCGCGAGGTTCGGGCGCTATC  4951115

Query  61       GCAGGAGCGTCGCAGATCCATTAACTCGCGCTCCAAGGCGCGCAATTCCTTCATCTTGGT  120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4951116  GCAGGAGCGTCGCAGATCCATTAACTCGCGCTCCAAGGCGCGCAATTCCTTCATCTTGGT  4951175

Query  121      CCGCACTTGCGCGATATGAGCGTCGACCAGCGCGTTCACCTCGCCGCAGCCCAACTCTGG  180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4951176  CCGCACTTGCGCGATATGAGCGTCGACCAGCGCGTTCACCTCGCCGCAGCCCAACTCTGG  4951235

Query  181      CCGATCCCGTAAGTTCAGCAGTTGACGGATCTCATCCAGCGTCATGTCCTTCGCCCGGCA  240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4951236  CCGATCCCGTAAGTTCAGCAGTTGACGGATCTCATCCAGCGTCATGTCCTTCGCCCGGCA  4951295

Query  241      GCGGCGGATGAACAGCAAGCGCTGCAAATGGACTTCGTCATAGAGCCTGAAGTTGCCCTC  300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4951296  GCGGCGGATGAACAGCAAGCGCTGCAAATGGACTTCGTCATAGAGCCTGAAGTTGCCCTC  4951355

Query  301      GCTACGTGCAGGCTCGGGCAGCAAGCCTTCTGACTCGTAAAAGCGCACGGTCTGCACCAA  360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4951356  GCTACGTGCAGGCTCGGGCAGCAAGCCTTCTGACTCGTAAAAGCGCACGGTCTGCACCAA  4951415

Query  361      GCAATCTGCCTTCTTGCCCAGTTCACCGATCCGCATCATGGTTGCTTCCTATAAAAAACT  420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4951416  GCAATCTGCCTTCTTGCCCAGTTCACCGATCCGCATCATGGTTGCTTCCTATAAAAAACT  4951475

Query  421      TGACTCTATATCTACTAGAGGTTTTCTAATGATGGCATCCGGGGAAAACCTTGTCAATGA  480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4951476  TGACTCTATATCTACTAGAGGTTTTCTAATGATGGCATCCGGGGAAAACCTTGTCAATGA  4951535

Query  481      AGAGCGATCTATG  493
                |||||||||||||
Sbjct  4951536  AGAGCGATCTATG  4951548
```

Pseudomonas aeruginosa strain 1207, complete genome
Sequence ID: **CP022001.1** Length: 7411863 Number of Matches: 2
Range 1: 4537245 to 4537737

Score	Expect	Identities	Gaps	Strand	Frame
911 bits(493)	0.0()	493/493(100%)	0/493(0%)	Plus/Plus	

Features:
Cd(II)/Pb(II)-responsive transcriptional regulatorcopper-translocating P-type ATPase

```
Query  1        TCAGGCGGGCTCGGCCAAGCTGTTGAGAATGCCGCACTCGCGCGAGGTTCGGGCGCTATC  60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4537245  TCAGGCGGGCTCGGCCAAGCTGTTGAGAATGCCGCACTCGCGCGAGGTTCGGGCGCTATC  4537304

Query  61       GCAGGAGCGTCGCAGATCCATTAACTCGCGCTCCAAGGCGCGCAATTCCTTCATCTTGGT  120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4537305  GCAGGAGCGTCGCAGATCCATTAACTCGCGCTCCAAGGCGCGCAATTCCTTCATCTTGGT  4537364

Query  121      CCGCACTTGCGCGATATGAGCGTCGACCAGCGCGTTCACCTCGCCGCAGCCCAACTCTGG  180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4537365  CCGCACTTGCGCGATATGAGCGTCGACCAGCGCGTTCACCTCGCCGCAGCCCAACTCTGG  4537424

Query  181      CCGATCCCGTAAGTTCAGCAGTTGACGGATCTCATCCAGCGTCATGTCCTTCGCCCGGCA  240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4537425  CCGATCCCGTAAGTTCAGCAGTTGACGGATCTCATCCAGCGTCATGTCCTTCGCCCGGCA  4537484

Query  241      GCGGCGGATGAACAGCAAGCGCTGCAAATGGACTTCGTCATAGAGCCTGAAGTTGCCCTC  300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4537485  GCGGCGGATGAACAGCAAGCGCTGCAAATGGACTTCGTCATAGAGCCTGAAGTTGCCCTC  4537544

Query  301      GCTACGTGCAGGCTCGGGCAGCAAGCCTTCTGACTCGTAAAAGCGCACGGTCTGCACCAA  360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4537545  GCTACGTGCAGGCTCGGGCAGCAAGCCTTCTGACTCGTAAAAGCGCACGGTCTGCACCAA  4537604

Query  361      GCAATCTGCCTTCTTGCCCAGTTCACCGATCCGCATCATGGTTGCTTCCTATAAAAAACT  420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4537605  GCAATCTGCCTTCTTGCCCAGTTCACCGATCCGCATCATGGTTGCTTCCTATAAAAAACT  4537664

Query  421      TGACTCTATATCTACTAGAGGTTTTCTAATGATGGCATCCGGGGAAAACCTTGTCAATGA  480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4537665  TGACTCTATATCTACTAGAGGTTTTCTAATGATGGCATCCGGGGAAAACCTTGTCAATGA  4537724

Query  481      AGAGCGATCTATG  493
                |||||||||||||
Sbjct  4537725  AGAGCGATCTATG  4537737
```

Range 2: 5285363 to 5285855

Score	Expect	Identities	Gaps	Strand	Frame
911 bits(493)	0.0()	493/493(100%)	0/493(0%)	Plus/Plus	

Features:
Cd(II)/Pb(II)-responsive transcriptional regulatorcopper-translocating P-type ATPase

```
Query  1        TCAGGCGGGCTCGGCCAAGCTGTTGAGAATGCCGCACTCGCGCGAGGTTCGGGCGCTATC  60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5285363  TCAGGCGGGCTCGGCCAAGCTGTTGAGAATGCCGCACTCGCGCGAGGTTCGGGCGCTATC  5285422

Query  61       GCAGGAGCGTCGCAGATCCATTAACTCGCGCTCCAAGGCGCGCAATTCCTTCATCTTGGT  120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5285423  GCAGGAGCGTCGCAGATCCATTAACTCGCGCTCCAAGGCGCGCAATTCCTTCATCTTGGT  5285482

Query  121      CCGCACTTGCGCGATATGAGCGTCGACCAGCGCGTTCACCTCGCCGCAGCCCAACTCTGG  180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5285483  CCGCACTTGCGCGATATGAGCGTCGACCAGCGCGTTCACCTCGCCGCAGCCCAACTCTGG  5285542

Query  181      CCGATCCCGTAAGTTCAGCAGTTGACGGATCTCATCCAGCGTCATGTCCTTCGCCCGGCA  240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5285543  CCGATCCCGTAAGTTCAGCAGTTGACGGATCTCATCCAGCGTCATGTCCTTCGCCCGGCA  5285602

Query  241      GCGGCGGATGAACAGCAAGCGCTGCAAATGGACTTCGTCATAGAGCCTGAAGTTGCCCTC  300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5285603  GCGGCGGATGAACAGCAAGCGCTGCAAATGGACTTCGTCATAGAGCCTGAAGTTGCCCTC  5285662

Query  301      GCTACGTGCAGGCTCGGGCAGCAAGCCTTCTGACTCGTAAAAGCGCACGGTCTGCACCAA  360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5285663  GCTACGTGCAGGCTCGGGCAGCAAGCCTTCTGACTCGTAAAAGCGCACGGTCTGCACCAA  5285722

Query  361      GCAATCTGCCTTCTTGCCCAGTTCACCGATCCGCATCATGGTTGCTTCCTATAAAAAACT  420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5285723  GCAATCTGCCTTCTTGCCCAGTTCACCGATCCGCATCATGGTTGCTTCCTATAAAAAACT  5285782

Query  421      TGACTCTATATCTACTAGAGGTTTTCTAATGATGGCATCCGGGGAAAACCTTGTCAATGA  480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5285783  TGACTCTATATCTACTAGAGGTTTTCTAATGATGGCATCCGGGGAAAACCTTGTCAATGA  5285842

Query  481      AGAGCGATCTATG  493
                |||||||||||||
Sbjct  5285843  AGAGCGATCTATG  5285855
```

Pseudomonas aeruginosa C-NN2 isolate early isolate NN2 (clone C) genome assembly, chromosome: I
Sequence ID: **LT883143.1** Length: 6902967 Number of Matches: 1
Range 1: 2503098 to 2503590

Score	Expect	Identities	Gaps	Strand	Frame
911 bits(493)	0.0()	493/493(100%)	0/493(0%)	Plus/Minus	

Features:
Lead, cadmium, zinc and mercury transporting ATPase; Copp...Transcriptional regulator, MerR family

```
Query  1        TCAGGCGGGCTCGGCCAAGCTGTTGAGAATGCCGCACTCGCGCGAGGTTCGGGCGCTATC  60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2503590  TCAGGCGGGCTCGGCCAAGCTGTTGAGAATGCCGCACTCGCGCGAGGTTCGGGCGCTATC  2503531

Query  61       GCAGGAGCGTCGCAGATCCATTAACTCGCGCTCCAAGGCGCGCAATTCCTTCATCTTGGT  120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2503530  GCAGGAGCGTCGCAGATCCATTAACTCGCGCTCCAAGGCGCGCAATTCCTTCATCTTGGT  2503471

Query  121      CCGCACTTGCGCGATATGAGCGTCGACCAGCGCGTTCACCTCGCCGCAGCCCAACTCTGG  180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2503470  CCGCACTTGCGCGATATGAGCGTCGACCAGCGCGTTCACCTCGCCGCAGCCCAACTCTGG  2503411

Query  181      CCGATCCCGTAAGTTCAGCAGTTGACGGATCTCATCCAGCGTCATGTCCTTCGCCCGGCA  240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2503410  CCGATCCCGTAAGTTCAGCAGTTGACGGATCTCATCCAGCGTCATGTCCTTCGCCCGGCA  2503351

Query  241      GCGGCGGATGAACAGCAAGCGCTGCAAATGGACTTCGTCATAGAGCCTGAAGTTGCCCTC  300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2503350  GCGGCGGATGAACAGCAAGCGCTGCAAATGGACTTCGTCATAGAGCCTGAAGTTGCCCTC  2503291

Query  301      GCTACGTGCAGGCTCGGGCAGCAAGCCTTCTGACTCGTAAAAGCGCACGGTCTGCACCAA  360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2503290  GCTACGTGCAGGCTCGGGCAGCAAGCCTTCTGACTCGTAAAAGCGCACGGTCTGCACCAA  2503231

Query  361      GCAATCTGCCTTCTTGCCCAGTTCACCGATCCGCATCATGGTTGCTTCCTATAAAAAACT  420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2503230  GCAATCTGCCTTCTTGCCCAGTTCACCGATCCGCATCATGGTTGCTTCCTATAAAAAACT  2503171

Query  421      TGACTCTATATCTACTAGAGGTTTTCTAATGATGGCATCCGGGGAAAACCTTGTCAATGA  480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2503170  TGACTCTATATCTACTAGAGGTTTTCTAATGATGGCATCCGGGGAAAACCTTGTCAATGA  2503111

Query  481      AGAGCGATCTATG  493
                |||||||||||||
Sbjct  2503110  AGAGCGATCTATG  2503098
```

Bordetella genomosp. 13 strain AU7206, complete genome

Sequence ID: **CP021111.1** Length: 5380929 Number of Matches: 1

Range 1: 4154245 to 4154737

Score	Expect	Identities	Gaps	Strand	Frame
911 bits(493)	0.0()	493/493(100%)	0/493(0%)	Plus/Minus	

Features:

copper-translocating P-type ATPaseCd(II)/Pb(II)-responsive transcriptional regulator

```
Query  1        TCAGGCGGGCTCGGCCAAGCTGTTGAGAATGCCGCACTCGCGCGAGGTTCGGGCGCTATC  60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4154737  TCAGGCGGGCTCGGCCAAGCTGTTGAGAATGCCGCACTCGCGCGAGGTTCGGGCGCTATC  4154678

Query  61       GCAGGAGCGTCGCAGATCCATTAACTCGCGCTCCAAGGCGCGCAATTCCTTCATCTTGGT  120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4154677  GCAGGAGCGTCGCAGATCCATTAACTCGCGCTCCAAGGCGCGCAATTCCTTCATCTTGGT  4154618

Query  121      CCGCACTTGCGCGATATGAGCGTCGACCAGCGCGTTCACCTCGCCGCAGCCCAACTCTGG  180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4154617  CCGCACTTGCGCGATATGAGCGTCGACCAGCGCGTTCACCTCGCCGCAGCCCAACTCTGG  4154558

Query  181      CCGATCCCGTAAGTTCAGCAGTTGACGGATCTCATCCAGCGTCATGTCCTTCGCCCGGCA  240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4154557  CCGATCCCGTAAGTTCAGCAGTTGACGGATCTCATCCAGCGTCATGTCCTTCGCCCGGCA  4154498

Query  241      GCGGCGGATGAACAGCAAGCGCTGCAAATGGACTTCGTCATAGAGCCTGAAGTTGCCCTC  300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4154497  GCGGCGGATGAACAGCAAGCGCTGCAAATGGACTTCGTCATAGAGCCTGAAGTTGCCCTC  4154438

Query  301      GCTACGTGCAGGCTCGGGCAGCAAGCCTTCTGACTCGTAAAAGCGCACGGTCTGCACCAA  360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4154437  GCTACGTGCAGGCTCGGGCAGCAAGCCTTCTGACTCGTAAAAGCGCACGGTCTGCACCAA  4154378

Query  361      GCAATCTGCCTTCTTGCCCAGTTCACCGATCCGCATCATGGTTGCTTCCTATAAAAAACT  420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4154377  GCAATCTGCCTTCTTGCCCAGTTCACCGATCCGCATCATGGTTGCTTCCTATAAAAAACT  4154318

Query  421      TGACTCTATATCTACTAGAGGTTTTCTAATGATGGCATCCGGGGAAAACCTTGTCAATGA  480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4154317  TGACTCTATATCTACTAGAGGTTTTCTAATGATGGCATCCGGGGAAAACCTTGTCAATGA  4154258

Query  481      AGAGCGATCTATG  493
                |||||||||||||
Sbjct  4154257  AGAGCGATCTATG  4154245
```

Pseudomonas aeruginosa strain W45909, complete genome

Sequence ID: **CP008871.2** Length: 6777566 Number of Matches: 1

Range 1: 2740844 to 2741336

Score	Expect	Identities	Gaps	Strand	Frame
911 bits(493)	0.0()	493/493(100%)	0/493(0%)	Plus/Minus	

Features:

copper-translocating P-type ATPaseCd(II)/Pb(II)-responsive transcriptional regulator

```
Query  1        TCAGGCGGGCTCGGCCAAGCTGTTGAGAATGCCGCACTCGCGCGAGGTTCGGGCGCTATC  60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2741336  TCAGGCGGGCTCGGCCAAGCTGTTGAGAATGCCGCACTCGCGCGAGGTTCGGGCGCTATC  2741277

Query  61       GCAGGAGCGTCGCAGATCCATTAACTCGCGCTCCAAGGCGCGCAATTCCTTCATCTTGGT  120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2741276  GCAGGAGCGTCGCAGATCCATTAACTCGCGCTCCAAGGCGCGCAATTCCTTCATCTTGGT  2741217

Query  121      CCGCACTTGCGCGATATGAGCGTCGACCAGCGCGTTCACCTCGCCGCAGCCCAACTCTGG  180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2741216  CCGCACTTGCGCGATATGAGCGTCGACCAGCGCGTTCACCTCGCCGCAGCCCAACTCTGG  2741157

Query  181      CCGATCCCGTAAGTTCAGCAGTTGACGGATCTCATCCAGCGTCATGTCCTTCGCCCGGCA  240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2741156  CCGATCCCGTAAGTTCAGCAGTTGACGGATCTCATCCAGCGTCATGTCCTTCGCCCGGCA  2741097

Query  241      GCGGCGGATGAACAGCAAGCGCTGCAAATGGACTTCGTCATAGAGCCTGAAGTTGCCCTC  300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2741096  GCGGCGGATGAACAGCAAGCGCTGCAAATGGACTTCGTCATAGAGCCTGAAGTTGCCCTC  2741037

Query  301      GCTACGTGCAGGCTCGGGCAGCAAGCCTTCTGACTCGTAAAAGCGCACGGTCTGCACCAA  360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2741036  GCTACGTGCAGGCTCGGGCAGCAAGCCTTCTGACTCGTAAAAGCGCACGGTCTGCACCAA  2740977

Query  361      GCAATCTGCCTTCTTGCCCAGTTCACCGATCCGCATCATGGTTGCTTCCTATAAAAAACT  420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2740976  GCAATCTGCCTTCTTGCCCAGTTCACCGATCCGCATCATGGTTGCTTCCTATAAAAAACT  2740917

Query  421      TGACTCTATATCTACTAGAGGTTTTCTAATGATGGCATCCGGGGAAAACCTTGTCAATGA  480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Sbjct  2740916  TGACTCTATATCTACTAGAGGTTTTCTAATGATGGCATCCGGGGAAAACCTTGTCAATGA  2740857

Query  481      AGAGCGATCTATG  493
                |||||||||||||
Sbjct  2740856  AGAGCGATCTATG  2740844
```

LB Trial 3

1:30	0	1000	1500	2000									
	1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	
A	0.065	0.069	0.072	0.071									595
B	0.058	0.067	0.073	0.072									595
C	0.063	0.077	0.073	0.073									595
D	0.073	0.078	0.068	0.07									595
E													595
F													595
G													595
H													595

2:30

	1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	
A	0.071	0.073	0.076	0.074									595
B	0.061	0.069	0.078	0.08									595
C	0.068	0.079	0.079	0.077									595
D	0.076	0.081	0.07	0.073									595
E													595
F													595
G													595
H													595

3:30

	1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	
A	0.078	0.076	0.082	0.078									595
B	0.066	0.072	0.085	0.088									595
C	0.072	0.082	0.084	0.08									595
D	0.08	0.085	0.074	0.081									595
E													595
F													595
G													595
H													595

4:30

	1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	
A	0.083	0.078	0.087	0.08									595
B	0.069	0.077	0.09	0.091									595
C	0.074	0.085	0.09	0.084									595
D	0.084	0.089	0.079	0.085									595
E													595
F													595
G													595
H													595

5:30

	1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	
A	0.086	0.081	0.09	0.081									595
B	0.072	0.083	0.092	0.093									595
C	0.078	0.089	0.095	0.088									595
D	0.086	0.092	0.084	0.089									595
E													595
F													595
G													595
H													595

	0	1000	1500	2000
1:30	0.06475	0.07275	0.0715	0.0715
2:30	0.069	0.0755	0.07575	0.076
3:30	0.074	0.07875	0.08125	0.08175
4:30	0.0775	0.08225	0.0865	0.085
5:30	0.0805	0.08625	0.09025	0.08775

LB Trial 3a

1:30	0	1000	1500		1500-2	2000							
	1	2	3	4	5	6	7	8	9	10	11	12	
A													595
B													595
C													595
D													595
E	0.072	0.095	0.086	N	0.104	0.091							595
F	0.093	0.087	0.08	N	0.079	0.091							595
G	0.079	0.084	0.094	N	0.093	0.097							595
H	0.07	0.086	0.09	N	0.092	0.102							595

2:30

	1	2	3	4	5	6	7	8	9	10	11	12	
A													595
B													595
C													595
D													595
E	0.077	0.11	0.103	N	0.109	0.105							595
F	0.099	0.098	0.1	N	0.095	0.104							595
G	0.091	0.096	0.108	N	0.101	0.109							595
H	0.078	0.101	0.104	N	0.102	0.111							595

3:30

	1	2	3	4	5	6	7	8	9	10	11	12	
A													595
B													595
C													595
D													595
E	0.082	0.116	0.113	N	0.109	0.109							595
F	0.101	0.099	0.111	N	0.101	0.108							595
G	0.099	0.099	0.113	N	0.104	0.113							595
H	0.087	0.105	0.11	N	0.103	0.115							595

4:30

	1	2	3	4	5	6	7	8	9	10	11	12	
A													595
B													595
C													595
D													595
E	0.087	0.117	0.116	N	0.107	0.109							595
F	0.102	0.1	0.113	N	0.102	0.109							595
G	0.102	0.1	0.114	N	0.103	0.114							595
H	0.095	0.106	0.112	N	0.103	0.116							595

5:30

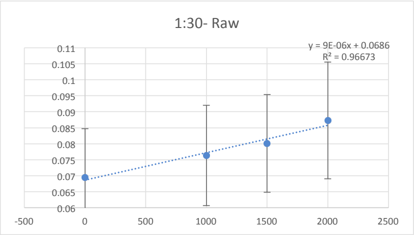
	1	2	3	4	5	6	7	8	9	10	11	12	
A													595
B													595
C													595
D													595
E	0.092	0.115	0.116	N	0.106	0.107							595
F	0.103	0.099	0.113	N	0.101	0.108							595
G	0.103	0.099	0.113	N	0.102	0.112							595
H	0.099	0.106	0.111	N	0.101	0.115							595

	0	1000	1500	1500-2	2000
1:30	0.0785	0.088	0.0875	0.092	0.09525
2:30	0.08625	0.10125	0.10375	0.10175	0.10725
3:30	0.09225	0.10475	0.11175	0.10425	0.11125
4:30	0.0965	0.10575	0.11375	0.10375	0.112
5:30	0.09925	0.10475	0.11325	0.1025	0.1105

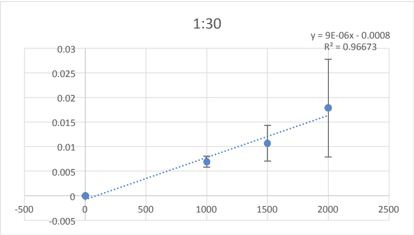
	0	1000	1500	2000
1:30	0.0785	0.088	0.092	0.09525
2:30	0.08625	0.10125	0.10175	0.10725
3:30	0.09225	0.10475	0.10425	0.11125
4:30	0.0965	0.10575	0.10375	0.112
5:30	0.09925	0.10475	0.1025	0.1105

LB Standard Curves

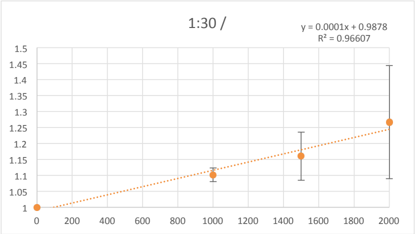
1:30-RAW	0	1000	1500	2000
Trial 1	0.057	0.06275	0.071	0.083
Trial 2	0.0865	0.0935	0.09775	0.10725
Trial 3	0.06475	0.07275	0.0715	0.0715
Average	0.06941667	0.07633333	0.08008333	0.08725
St. Dev.	0.01529365	0.01568505	0.01530182	0.01825



1:30	0	1000	1500	2000
Trial 1	0	0.00575	0.014	0.026
Trial 2	0	0.007	0.01125	0.02075
Trial 3	0	0.008	0.00675	0.00675
Average	0	0.00691667	0.01066667	0.01783333
St. Dev.	0	0.00112731	0.00366003	0.00995092



1:30	0	1000	1500	2000
Trial 1	1	1.10087719	1.24561404	1.45614035
Trial 2	1	1.08092486	1.1300578	1.23988439
Trial 3	1	1.12355212	1.1042471	1.1042471
Average	1	1.10178472	1.15997298	1.26675728
St. Dev.	0	0.02132812	0.07528174	0.17747909



1:30-RAW	0	1000	1500	2000
Trial 1	0.057	0.06275	0.071	0.083
Trial 2	0.0865	0.0935	0.09775	0.10725
Trial 3a	0.0785	0.088	0.092	0.09525
Average	0.074	0.08141667	0.08691667	0.09516667
St. Dev.	0.01525615	0.01639804	0.01408087	0.01212521

0.0625	0	1000	1500	2000
Trial 1	0	0.00575	0.014	0.026
Trial 2	0	0.007	0.01125	0.02075
Trial 3a	0	0.0095	0.0135	0.01675
Average	0	0.00741667	0.01291667	0.02116667
St. Dev.	0	0.00190941	0.00146487	0.00463906