The Barcode of Life Student Data Portal

Supporting a National Network of Students in Cataloging Multicellular Life with DNA Barcodes

Ralph Imondi, Coastal Marine Biolabs Integrative Biosciences Institute, Ventura Harbor, CA









Our model organizes teaching and learning around student participation in the International Barcode of Life (iBOL) project











A DNA barcode is a short, standardized genomic sequence that delimits species boundaries



Animal species show < 2% *intra*species variation but > 4% divergence from nearest neighbor

Aligned Length = 580 Gaps = 0 Identities = 550 (94%)

P.	clathratus	1		70
P.	nebulifer	1		70
Р.	clathratus	71	A	140
Р.	nebulifer	71		140
P.	clathratus	141		210
P.	nebulifer	141		210
Р.	clathratus	211		280
Р.	nebulifer	211		280
Р.	clathratus	281		350
Р.	nebulifer	281		350
Р.	clathratus	351	CG	420
Р.	nebulifer	351		420
P.	clathratus	421		490
P.	nebulifer	421		490
Р.	clathratus	491	TA	560
Р.	nebulifer	491		560
Р. Р.	clathratus nebulifer	561 561		

A barcode sequence is embedded into a *reference* barcode record and linked to metadata

Specimen Record	
IDENTIFIERS TAXONOMY TAXONOMY SPECIMEN DETAILS COLLECTION DATA	
GGTATTACGCCAAATATACAATGCAATAGT CTCCCCGAATGAACAATAGAGATCTGACTA TTAGCAATATTTTCCCTTCACCTAGCGGGA TTAGCAATATTTTCCCTTCACCTAGCGGGA CCTAGCGGGAGCTTC	
TRACE FILE	

Barcode records are assembled and stored in the Barcode of Life Data Systems (BOLD Systems)





Public Data Portal:

A data retrieval interface that allows for searching over 1.7M public records in BOLD using multiple search criteria including, but not limited to, geography, taxonomy, and depository.



DNA Barcode Education Portal:

A custom platform for educators and students to explore barcode data and contribute novel barcodes to the BOLD database.



Barcode Index Numbers:

A searchable database of Barcode Index Numbers (BINs), sequence clusters that closely approximate species.

Workbench:

An integrated data collection and analysis environment that securely supports the assembly and validation of DNA barcodes and ancillary sequences.

Unknown barcode sequences are queried against a library of *reference* records in BOLD-IDS

••• < > 🗉			l	=			boldsystems.org			Ċ				
	BOLDSYSTEMS	Databases	Taxonomy	dentification	Workbench	Resources								Log In 🔅
	Identification Requ	est										a P	Print	
	Animal Identification [CO] The BOLD Identification Syst forensic applications. Biorocal Databases: Ju Search Databases: Ju Search Databases: Ju Search Databases: Ju Search Carlo Search Control of the nearest matches Septimens as well as a Public Record Barcod Subset of the Species Ju Dublished COI record Subset of the Species Ju Subset of the S	Fungal Identification (ITS) em (IDS) for COI accept I=2015 Jul=2014 Jul- on BOLD (4,708,558 5E and does not provide a registration of the second second and does not provide a Records (2,666,832) and does not provide a record pattabase (1,666 Ibrary with a minimum is a sit provides maximum mat: TCTTAGCGCACCACCACCAC ANTTATCATTGGCGCCTCACCACCAC CATTATCATTGGCGCCTCACCACCACCACCACCACCACCACCACCACCACCACC	Plant Identi IrbcL & mat is sequences from th aquences in the sequence length reserved by only or reserved by only or intervention of the sequences in the sequences intervention of the sequences in the sequences in the sequences intervention of the sequences in the s	fication KI and the S ¹ region of the mit ul=2011 Jul=2010 Jul gth of 500bp (warning ne or two specimens a species/64041 Internet to a taxon. Species/17,982 Internet Species/17,982 Internet Internet Comparison Internet Comparison Inte	ochondrial Cytochrom II-2009 : unvalidated library a well as all species w irm Species) Solop. This library is Solop. This Bibrary is Solop. This Bibrary is Solop. This Bibrary is Solop. This Bibrary is both public and priva de region of COI. TTTCGTAATAA SOCGCTCCCG CCACGCCCGGAG AATTTTAATAA CGAAATTTAA	e c oxidase subunit i nd includes records i th interim taxonomy ncludes many specie: a collection of recor te records. This libra	I gene and returns a species-let without species level . This search only returns a list s represented by only one or tw ds from the published projects ury is intended for short	vel identification when one	e is possible. Further	validation with independent	nt genetic markers will be CE VN SOU	desirable in some		feedback

	RESOURCES	ORGANIZATION	
Public Data Portal	Documentation		
Publications			
	Data Releases		

The BOLD ID System presents the probability of placement in a taxonomic group

					boldsyste	ns.org	Ċ		▲ ₽
	BOLDSYSTEM	IS Databases	Taxonomy	Identification Workbe	ench Resources				Lo
	Specimen Identi	fication Reque	st						Print
	 Query: unknown fish t 	issue					Top Hit:	Chordata - Perciformes - Paralabrax cl	athratus (100%)
	Search Result:								
	The submitted see	quence has been m	natched to Parala	<i>brax clathratus</i> . This ident	fication is solid unless there is	a very closely allied congener	ic species that has not yet been an	alyzed. Such cases are rare.	
	A species page is	s available for this t	axon: Species Pag	e					
	Olasaat matakian								
	Closest matching	Bin (within 3%):	BIN Page						
	For a historybical		ala a ininina tena	ia provided.					
	For a nierarchical	i piacement - a neig	gnbor-joining tree	IS provided: Tree Based Ide	ntification				
	Internet for a firm of an and				01	"			
	Identification Summa	ary:			Sir	niarity Scores of Top 99 Matches:			
	Taxonomic Level	Taxon Assignment	Probability of Placement (%)		× 1	98			
	Phylum	Chordata	100		8	96			
	Class	Actinopterygii	100		arity	94			
	Order	Perciformes	100		Simil	90			
· · · · · · · · · · · · · · · · · · ·	Family	Serranidae	100		· · · ·	88			
	Species	Paralabrax clathratus	100			86	56 67 78 89		
	operio	ranabiliti taanaatii	200				Ranked Matches		
	TOP 20 Matchas							Display option:	Top 20
	TOP 20 Matches .							Display option.	
	Phylum	Cla	155	Order	Family	Genus	Species	Similarity (%)	Status
	Chordata	Actinop	oterygii	Perciformes	Serranidae	Paralabrax	clathratus	100 E	arly-Release
	Chordata	Actinop	otervaji	Perciformes	Serranidae	Paralabrax	clathratus	100 E	arly-Release
	Chordata	Actinop	oterygii	Perciformes	Serranidae	Paralabrax	clathratus	100 E	arly-Release
	Chordata	Actinop	oterygii	Perciformes	Serranidae	Paralabrax	clathratus	100 E	.arly-Release
	Chordata	Actinop	oterygii	Perciformes	Serranidae	Paralabrax	clathratus	100	Published 🚱
	Chordata	Actinop	oterygii	Perciformes	Serranidae	Paralabrax	clathratus	100	Published 🗗
	Chordata	Actinop	oterygii	Perciformes	Serranidae	Paralabrax	clathratus	100	Published 🖬
	Chordata	Actinop	oterygii	Perciformes	Serranidae	Paralabrax	clathratus	100	Published B
	Chordata	Actinop	nerygii	Perciformes	Serranidae	Paralabrax	Clathratus	99.83	Published of
	Chordata	Actinop	nerygii	Perciformes	Serrapidae	Paralabrax	nebulifer	95.29	arty-Release
	Chordata	Actinor	ntervaji	Perciformes	Serranidae	Paralabrax	auroguttatus	95.11	Published P
	Chordata	Actinop	tervaji	Perciformes	Serranidae	Paralabrax	nebulifer	94.94	Published P
	Chordata	Actinop	otervaji	Perciformes	Serranidae	Paralabrax	humeralis	94.94 F	arly-Release
	Chordata	Actinor	otervaji	Perciformes	Serranidae	Paralabrax	humeralis	94.91 F	arly-Release
	Chordata	Actinor	oterygii	Perciformes	Serranidae	Paralabrax	loro	94.87	Private
	Chordata	Actinor	oterygii	Perciformes	Serranidae	Paralabrax	humeralis	94.76	Published 🚱
	Chordata	Actinop	oterygii	Perciformes	Serranidae	Paralabrax	humeralis	94.76	Published 🧬
	Chordata	Actinop	oterygii	Perciformes	Serranidae	Paralabrax	humeralis	94.76	Published 🚱

Sampling Sites For Top Hits (>98% Match)

The student experience binds the concepts and methods of DNA barcoding into an integrated pipeline



field

lab

databasing

The pipeline begins in the field with the collection of specimens and metadata



- Collect target specimens
- Capture images and record specimen metadata





Process specimen tissue

DNA barcodes are generated in the lab using standardized/optimized protocols



- Extract gDNA from tissue
- Use PCR to amplify COI gene segment
- Confirm size of COI amplicon with gel electrophoresis
- Purify amplicon with silicabased spin column
- Submit for bidirectional sequencing

The final segment of the barcoding pipeline involves the online assembly of barcode records



 Assemble reference barcode records with metadata obtained in the field and sequence data generated in the high school science lab

The design of BOLD-SDP was guided by the following considerations



- Class authentication and student identity management
- Class management
- Record assembly workflow
- Sequence editing
- Data validation

BOLDSYSTEMS-SDP STUDENT DATA-PORT@L

- Data visualization and analysis
- Audience-specific user support documentation

Students assemble barcode records through a modular, four-step workflow









New Specimen

A Specimen Identifier

$\bullet \bullet \bullet \bullet < > \square$

onboard page instructions

The Specimen Data for a DNA barcode record consists of 4 parts

Specimer

Instructions

- Specimen Identifier
 Specimen Details (for example, the sex of the specimen and its life
- stage) 3. Taxonomy (what species you've collected), and
- 4. Collection Details (when and where you collected)

your specimen). If you are conducting an investigational study to determine the identity of an unknown sample, you will NOT be able to fill in al fields. You should add notes under the **Specimen Detail** section, provide a provisional species name (if possible) in the notes field of the **Taxonomy section**.

and provide information for the collector, collection date, and any other details on where the sample was obtained in the **Collection Details** section (e.g. supermarket, restaurant, commercial fishing vessel etc.)

Specimen Identifier

The Specimen Identifier allows you to link your DNA barcode record to the actual source specimen. On BOLD, this identifier is called the Sample ID. Each Sample ID is unique to a barcode record and allows you to connect your digital barcode record with the collected specimen. Sample IDs can contain a fairly large combination of numbers, letters, and other characters, but they must be unique in BOLD. To avoid duplication, do not use simple or obvious codes (for example, AA, 001, AA01, etc.). It is likely that someone else has used codes like these before.

Year-InstitutionCode-Initials-Number

For example: 12-JFHS-JS-0001

Institution Name: John Frasier High School (JFHS) Student Initials: Jane Smith (JS)

Specimen Details

Include in your record additional information specific to the specimen. Knowledge of your specimen's life stage, sex, mode of reproduction, and other

Sample ID:	
B Specime	n Details
Life Stage:	Adult Immature OUnknown
Sex:	Male Female Hermaphrodite Olnknow
Reproduction:	Sexual Asexual Cyclic Parthenogen
Notes:	
C Taxonon	ny
Phylum *:	Unselected ᅌ
Class:	Unselected 📀
Order:	Unselected ᅌ
Family:	Unselected ᅌ
Subfamily:	Unselected 📀
Tribe:	Unselected 📀
Genus:	Unselected ᅌ
Species:	Unselected ᅌ
Identification Method	d la
(morphology, barcode, etc):	

boldsystems.org

D Collection Details

Taxonomy Notes:

Collected By:			
Date (dd/mm/yyyy):	1	1	
Country/Ocean *:	Unselected		0
Province/State:	Unselected	0	
Region:			
Exact Site:			
Latitude (D.d):			
Longitude (D.d):			
Elevation:			• meters feet
Depth:			ometers feet
Coordinate			ometers feet
Accuracy.			
Submit Cancel			



Ċ

attribution pane

course information

data input fields

Ô Ô



Upload Images

Image

Instructions

Specimen Identifier

Enter your Sample ID to connect your photo to the appropriate specimen. If you forgot the Sample ID of the specimen that you are working on, click the <Lookup> button to find its ID in your record list.

Image

•

Attach Image - Select the image that you wish to attach to your record (as a .jpg or .JPG file). You can attach up to 10 images per specimen. It is common scientific practice to include in the image an object of known size that provides an indication of scale (for example, a coin, a paper clip, or a ruler).

View Metadata - Describe the orientation of your specimen in the photo (for example, dorsal view, ventral view, lateral view, oral view, aboral view, etc.) or any other specific characteristic of your photo that you wish to point-out.

Caption - Include a short caption that best describes your specimen. If necessary, consult your teacher for guidance.

Photographer - Enter the name(s) of the person(s) responsible for taking and editing the photo.

Δ	Chaoiman	Idoptific
А	Specimen	Identifie

Sample ID:

B Image

Attach Image:	Choose File	no file selected
, main ager	CHOOSE Flie	no nie selecieu

View Metadata:

Caption:

Photographer:





Lookup

Student r	ione	\$
Ad	d Student 🛨	
Course		
Teachers:	Dean Chan	
	James Clement	
	Karen James	
	Mallory M Page	
Institution:	Centennial Collegiate Vocational School	
Courses	Liniversity Biology	



Upload Trace Files

Trace Files

Instructions

O Specimen Identifier

Enter your Sample ID to connect your traces with the appropriate specimen. If you forgot the Sample ID of the specimen that you are working on, click the <Lookup> button to find its ID in your record list.

PCR Primers

Different PCR primer pairs are often used to generate DNA barcode sequences from different organisms. Be sure to select the correct primers used to generate a barcode for this specimen.

C Attach Trace Files

Be sure to add both forward and reverse trace files to your record, and to select the correct primers that were used to generate each trace file.

Sample ID: B PCR Primers Forward: LepF1 ¢ Reverse: LepR1 ¢ C Attach Trace Files Forward: Sequencing Primer M13F-20 ¢ Choose File no file selected Reverse: Sequencing Primer M13R ¢ Choose File no file selected		
B PCR Primers Forward: LepF1 + Reverse: LepR1 + C Attach Trace Files Forward: Sequencing Primer M13F-20 + Choose File no file selected Reverse: Sequencing Primer M13R + Choose File no file selected	Sample ID:	
PCR Primers Forward: LepF1 + Reverse: LepR1 + C Attach Trace Files Forward: Sequencing Primer M13F-20 + Choose File no file selected Reverse: Sequencing Primer M13R + Choose File no file selected		
PCR Primers Forward: LepF1 Reverse: LepR1 C Attach Trace Files Forward: Sequencing Primer M13F-20 Choose File no file selected Reverse: Sequencing Primer M13R Choose File no file selected	-	
Forward: LepF1 Reverse: LepR1 C Attach Trace Files Forward: Sequencing Primer M13F-20 +) Choose File no file selected Reverse: Sequencing Primer M13R +) Choose File no file selected	B PCF	R Primers
Reverse: LepR1 C Attach Trace Files Forward: Sequencing Primer M13F-20 +) Choose File no file selected Reverse: Sequencing Primer M13R +) Choose File no file selected	Forward:	LepF1
C Attach Trace Files Forward: Sequencing Primer M13F-20 Choose File no file selected Reverse: Sequencing Primer M13R \$ Choose File no file selected	Deverses	
C Attach Trace Files Forward: Sequencing Primer M13F-20 + Choose File no file selected Reverse: Sequencing Primer M13R + Choose File no file selected	Reverse:	LepRI
C Attach Trace Files Forward: Sequencing Primer M13F-20 + Choose File no file selected Reverse: Sequencing Primer M13R + Choose File no file selected		
Forward: Sequencing Primer M13F-20 \$ Choose File no file selected Reverse: Sequencing Primer M13R \$ Choose File no file selected		
Forward: Sequencing Primer M13F-20 \$ Choose File no file selected Reverse: Sequencing Primer M13R \$ Choose File no file selected		ch Trace Files
Choose File no file selected Reverse: Sequencing Primer M13R Choose File no file selected	C Atta	ch Trace Files
Reverse: Sequencing Primer M13R \$	C Atta Forward:	ch Trace Files Sequencing Primer M13F-20 +
Reverse: Sequencing Primer M13R \$	C Atta Forward:	ch Trace Files Sequencing Primer M13F-20 +
Choose File no file selected	C Atta Forward:	ch Trace Files Sequencing Primer M13F-20 + Choose File no file selected
	C Atta Forward: Reverse:	ch Trace Files Sequencing Primer M13F-20 + Choose File no file selected Sequencing Primer M13R +
	C Atta Forward: Reverse:	ch Trace Files Sequencing Primer M13F-20 + Choose File no file selected Sequencing Primer M13R + Choose File no file selected

A Specimen Identifier

Cancel

Submit



Student r	one	
Ad	d Student 重	
 Course 		
Instructors:	Dean Chan	
	James Clement	
	Karen James	
	Mallory M Page	
	Centennial Collegiate	
Institution:	Vocational Control	

Lookup



Add Sequence

Sequences

Instructions

O Specimen Identifier

Enter your Sample ID to connect your barcode sequence to the appropriate specimen. If you forgot the Sample ID of the specimen that you are working on, click the <Lookup> button to find its ID in your record list.

Once you enter your Sample ID, a status update will appear showing the information currently contained in the record for this specimen. The absence of a component is indicated by a red x, whereas the presence of a component is denoted by a green checkmark.

Add Sequence

Paste your edited sequence (contig) in the box to attach it to the record. To complete the submission, the sequence must be processed through the steps described below. Each step must be performed in the order in which it appears below.

C Process Sequence

Sequence processing involves 3 steps which need to be completed in sequence.

I) Primer Trimming

Sample ID:	TEST	-402			
<u>ه</u> 4 ب		🦗 0 🗙	8	0 🗙	

B Add Sequence

A Specimen Identifier

There are two options for uploading a sequence:

1. Use the BOLD-SDP Sequence Editor to trim, assemble, and edit your trace files to generate a sequence.

Lookup 🗸

BOLD Sequence Editor

2. Use a third-party software package to trim, assemble, and edit your trace files. If this approach is used, the sequence will need to be uploaded directly.

Upload Assembled Sequence

bmit Cancel

▼ Student Att	ribution	
Student name:	one	•
Ad	<u>d Student</u>	
 Course 		
Instructors:	Dean Chan	
	Karen James	
	Mallory M Page	
Institution:	Centennial Collegiate Vocational School	
Course:	University Biology	



Add Sequence: Sequence Editor

Sequences assembled using the BOLD Sequence Editor may still contain primer sequences. It is recommended that primers be removed and the reading frame be verified upon submission.



Assembled barcode records appear in a row of class record list with various flags

Sun

Ana

Rec

2

Go Back	Showing Records	1 to 20			Page 1	Records Per Page 50
mary	Project Data : Select					
Specimens, Localities, and	Toject Data . Select	•		Longth [Amb	ial	COI-5P. 20 Specimens. 20
GenBank						Partus Info
		Sample ID 🔻	Process ID V	COI-5PV	Record Flags	Extra Info
	Sebastes atrovirens	<u>RE-264</u>	<u>SDP75001-13</u>	629 [0n]	🕮 🔝 🛃 🙀	
Barcode Gap Analysis	Sebastes atrovirens	<u>RE-270</u>	SDP75002-13	594 [0n]	🌐 ⊡ 🔼 🔛	
Alignment Browser	Sebastes atrovirens	<u>RE-276</u>	SDP75004-13	562 [0n]	🕮 📴 🔼 🔛	
Accumulation Curve	Sebastes atrovirens	<u>RE-272</u>	SDP75005-13	630 [0n]	🛞 🛅 🔼 💥	
ID Engine	Sebastes atrovirens	<u>RE-275</u>	SDP75013-13	626 [0n]	🐵 💷 🔼 💥	
Taxon ID Tree	Sebastes atrovirens	<u>RE-269</u>	SDP75014-13	636 [0n]	🐵 💷 🔼 🔛	
Man Collection Sites	Sebastes atrovirens	<u>RE-268</u>	SDP75015-13	629 [0n]	🐵 💷 🔼 💥	
	Sebastes atrovirens	<u>RE-265</u>	SDP75018-13	644 [0n]	🛞 🔯 🔼 🙀	
Image Gallery	Sebastes atrovirens	<u>RE-267</u>	SDP75019-13	605 [0n]	🐵 💷 🔁 🔛	
ord Flags Legend	Sebastes atrovirens	<u>RE-277</u>	SDP75020-13	604 [0n]		
GPS coordinates present for the	Sebastes carnatus	<u>RE-266</u>	SDP75008-13	626 [0n]	🛞 💷 🔁 🔛	
record. Record contains images of the	Sebastes caurinus	<u>RE-273</u>	SDP75009-13	655 [0n]	🛞 ២ 🔼 🔛	
specimen.	Sebastes chrysomelas	<u>RE-278</u>	SDP75012-13	644 [0n]	🐵 💷 🔼 🔛	
The number of traces present for the sample.	Sebastes mystinus	<u>RE-274</u>	SDP75016-13	568 [0n]	🛞 ២ 2 🔛	
Sequence is Barcode Compliant.	Sebastes mystinus	<u>RE-281</u>	SDP75007-13	604 [0n]		
Stop codons present in	Sebastes mystinus	<u>RE-271</u>	SDP75011-13	600 [0n]		
Contamination present in	Sebastes mystinus	<u>RE-282</u>	SDP75003-13	593 [0n]		
sequence.	Sebastes mystinus	<u>RE-283</u>	SDP75017-13	603 [0n]		
	Sebastes mystinus	<u>RE-279</u>	SDP75010-13	589 [0n]		
	Sebastes serriceps	RE-280	SDP75006-13	637 [0n]	🛞 🔯 🔼 💥	

Completed barcode records migrate through a three-tier validation and publication pathway



Completed barcode records migrate through a three-tier validation and publication pathway



- Preserves the fidelity of records entering the global reference library
- Emphasizes the importance of data standards and data sharing practices
- Highlights the authenticity of the student experience
- Minimizes demands on BOLD data managers
- Establishes a user-designer feedback loop that promotes the continued evolution of the resource

Assembled records appear in a the course management console of BOLD-SDP

Record Approval (Queue						
Show 25 🗘 entries Search:							
Sample ID 🔺	Sequence 🔶	Sequence Length (bp)	Trace Count	Image Count	Sequence Quality	Valida	ition
<u>14-ASP-BMN-</u> Sample 1	SDP02108-14	×	×	×	×	•	×
<u>14-ASP-DD-</u> Sample1	SDP02106-14	×	×	1	×	•	×
<u>14-ASP-MB-</u> Sample1	SDP02105-14	×	×	1	×	*	×
<u>14-ASP-MTN-</u> Example2	SDP02117-14	×	×	1	×	*	×
<u>14-ASP-MTN-</u> Example3	SDP02120-14	×	×	1	×	~	×
<u>14-ASP-MV-0001</u>	SDP02119-14	×	1	1	×	~	×
<u>14-ASP-SF-</u> <u>Sample1</u>	SDP02113-14	×	×	1	×	~	×
<u>14-KHS-LVR-</u> <u>0001</u>	SDP01310-14	COI-5P:626	2	1	*	 Image: A start of the start of	×
<u>14-KHS-LVR-</u> 0002	SDP01315-14	×	×	1	×	~	×
14-LHBS-JV-003	SDP02086-14	COI-5P:518	2	1	*	 Image: A start of the start of	×
<u>14-SPSASP-TM-</u> 0002	SDP02104-14	×	2	1	×	~	×
<u>14-WHS-AC-01</u>	SDP01284-14	COI-5P:662	×	1	*	~	×
<u>15-LBHS-AE-</u> 092900	SDP02159-15	×	×	1	×	~	×
15-LBHS-AHP-	SDP01429-15	×	×	×	×		×

The BOLD-SDP data analysis tools deepen the inquiry component of student library building



Map Collection Sites



Specimen Images



Identification Engine



Taxon ID Tree



Barcode Gap Analysis

Students and teachers in our program have contributed over 1600 records to BOLD Systems

Distribution of schools participating in the Barcoding Life's Matrix program



Apart from active program participants, BOLD-SDP supports student data contributors from ~200 high schools, two- and four-year colleges, technical schools, universities, botanical gardens, gene banks, and science centers

Lessons learned from the design and deployment of BOLD-SDP



The design of a student interface can identify usability gaps and inform enhancements to a parent system



Clear mechanisms for data safeguarding and publication can motivate the participation of other science professionals



Rapid data publication is important for maintaining continuity of the learning experience and student investment

Acknowledgements



- Sujeevan Ratnasingham
- Ola Pierossi
- Mallory Van Wyngaarden
- Catherine Wei
- Dean Chan
- Karina Gonzales

Director of Informatics Lead Data Manager Data and Outreach Manager Lead Software Developer Programmer Analyst Programmer Analyst

BOLD SYSTEMS



- Linda Santschi
- Darcy Duffy

Project Co-PI and Scientific Co-Director Project Coordinator

Funding partners







