IBC Meeting Agenda
9/11/2025
3:00pm TEAMS

Member Attendees: Rachel Spurbeck, Caitlyn Heil, Addie Moore, Yun Li, Gloria Sivko, David Glasbrenner, Manju Kulkarni, Samuel Fred Harrison, Jacqueline Grible, & Craig Bartling

Guest Attendees: Chloe Hart, Jamison Law, Thomas Mallot

I. Application Reviews

Application: FY25-32
Study title: DARPA MICA – Microsystems Induced Catalysis
PI: Stephanie Napieralski

- **PI and laboratory staff performing the research have been appropriately trained in the safe conduct of the research:** Y
- **Applicable section of the NIH Guidelines:** III-D-2
- **BSL-#** 2
- **Agent characteristics:** While some of the source organisms listed below are BSL-2, all genes, bacteria, and yeast utilized on this project will not have potential to cause any harm. The genes utilized are not virulence factors, are non-toxic, and will not be introduced into any living system. The host organism is a commercial expression strain of *E. coli*. The "agent" in this case will be purified proteins used to catalyze metabolic reactions acellularly.
- **Types of manipulations planned:** Expression of catalytic enzymes and controlling catalytic enzymes by domains which require a physical stimulus for the enzyme to properly function.
- **Source(s) of the nucleic sequences (e.g., species):** Several species will be used as sources of proteins to be expressed: *Streptomyces coelicolor, Paralcaligenes ureilyticus, Picrophilus torridus, Thermatoga maritmia, Deinococcus radiodurans, Bacillus subtilis, Geobacillus sp. CHB1, Neurospora crassa, Botrytis cinerea, Salmonella enterica subsp. enterica serovar Typhimurium, Kryptopterus bicirrhis, Homo sapiens, Chlamydomonas reinhardtii, Hydrogenobacter thermophilus, Thermoanaerobacterium saccharolyticum, Buttiauxella sp. S04-F03, Candida boidinii, Thermotoga neapolitana, Escherichia coli, Derived from the Z domain of immunoglobulin-binding staphylococcal protein A, Streptomyces chattanoogensis, Avena sativa, Drosophila melanogaster, Corynebacterium glutamicum, Vaucheria frigida,* and *Salpingoeca rosetta*
- **Nature of the nucleic acid sequences (e.g., structural gene, oncogene):** The nucleic acid sequences are genes encoding enzymes that support catalysis of reactions such as Ldh or CatBsu, light interactions such as LDB3 or vvd, protein kinases such as NPH1-1, or selective oxidation with XyoA.
- **Host(s) and vector(s) to be used:**

Hosts: *Escherichia coli*
Vectors: Plasmids pAnsa3-1 and pAnsa3-2

- **Transgene expression:** yes, transgenes will be expressed and proteins purified.
- **Protein function:** See table below

Insert Source	**Protein**	**Function**
Streptomyces coelicolor	XyoA	Performs selective oxidation of the terminal primary hydroxyl group of several alditols, with a reduction of O_2 to H_2O_2.
Paralcaligenes ureilyticus	EDC26_10935	Converts D-gluconate to 2-keto-3-deoxygluconate and D-glycerate to pyruvate
Picrophilus torridus	SAMN02745355_0986	Reversible cleavage of KDPG into the three carbon units pyruvate and glyceraldehyde-3-phosphate.
Thermatoga maritmia	Ldh	Catalyzes this reaction > pyruvate + NADH + H^+ = (S)-lactate + NAD^+
Deinococcus radiodurans	Ldh	Catalyzes this reaction > pyruvate + NADH + H^+ = (S)-lactate + NAD^+
Bacillus subtilis	CatBsu	Catalyzes this reaction > 2 H_2O_2 = O_2 + 2 H_2O
Geobacillus sp. CHB1	kat	Catalyzes this reaction > 2 H_2O_2 = O_2 + 2 H_2O
Neurospora crassa	vvd	Binds and affects blue light regulation of the al-3 gene
Neurospora crassa	Vvd- pMagFast2(3x)	Under blue light (488 nm) illumination, dimerizes with pMagHigh1
Neurospora crassa	Vvd- pMagHigh1	Under blue light (488 nm) illumination, dimerizes with pMagFast2(3X)
Neurospora crassa	LightR	Optogenic allosteric regulation of enzyme activity by inserting into flexible loops near the active site
Deinococcus radiodurans	LDB3	Under red light (660 nm) illumination, interacts with their interaction partners PnBphP or FnBphP
Deinococcus radiodurans	PnBphP	Under red light (660 nm) illumination, interacts with their interaction partner LDB3
Deinococcus radiodurans	FnBphP	Under red light (660 nm) illumination, interacts with their interaction partner LDB3
Botrytis cinerea	BcLOV4	Thermoswitch that operates tunably and reversibly within a 27–32°C range
Salmonella enterica subsp. enterica serovar Typhimurium	TlpA	Thermolabile coiled-coil protein that heterodimerizes at a tunable transition temperature within the biocompatible range of 37–42 °C
Salmonella enterica subsp. enterica serovar Typhimurium	TlpA	Thermolabile coiled-coil protein that heterodimerizes at a tunable transition

		temperature within the biocompatible range of 37–42 °C
Kryptopterus bicirrhis	Epg	Electromagnetic perceptive protein
Homo sapiens	FkpA	Rapamycin-mediated dimerization domain
Homo sapiens	Rapt1	Rapamycin-mediated dimerization domain
Chlamydomonas reinhardtii	Peth	Catalyzes this reaction > 2 reduced [2Fe-2S]-[ferredoxin] + NADP$^+$ + H$^+$ = 2 oxidized [2Fe-2S]-[ferredoxin] + NADPH
Hydrogenobacter thermophilus	Fpr	Catalyzes this reaction > 2 oxidized [2Fe-2S]-[protein] + NADPH = 2 reduced [2Fe-2S]-[protein] + NADP$^+$ + H$^+$
Thermoanaerobacterium saccharolyticum	Tsac_0046	Catalyzes this reaction > 2 oxidized [2Fe-2S]-[ferredoxin] + pyruvate + CoA = 2 reduced [2Fe-2S]-[ferredoxin] + acetyl-CoA + CO2 + H
Thermoanaerobacterium saccharolyticum	AdhE	Catalyzes this reaction > a primary alcohol + NAD(P)+ = an aldehyde + NAD(P)H + H+
Thermoanaerobacterium saccharolyticum	AdhA	Catalyzes this reaction > a primary alcohol + NAD$^+$ = an aldehyde + NADH + H$^+$
Buttiauxella sp. S04-F03	acetaldehyde dehydrogenases ADA6-P443C–I440T	Catalyzes the conversion of acetylaldehyde to acetyl-CoA
Candida boidinii	AOD1	Catalyzes this reaction > a primary alcohol + O$_2$ = an aldehyde + H$_2$O$_2$
Thermotoga neapolitana	CTN_0580	Catalyzes this reaction > a primary alcohol + NAD$^+$ = an aldehyde + NADH + H$^+$
Escherichia coli	PflB	Catalyzes this reaction > formate + acetyl-CoA = pyruvate + CoA
Deinococcus radiodurans	BphP	Photoreceptor which exists in two forms that are reversibly interconvertible by light: the R form that absorbs maximally in the red region of the spectrum and the FR form that absorbs maximally in the far-red region. Also has a slight blue shift for the far-red maximum. Could also absorb green light.
Derived from the Z domain of immunoglobulin-binding staphylococcal protein A	Aff6_V18FΔN	Forms “MagRed” when paired with DrbphP
Streptomyces chattanoogensis	AzoF	A reversible, light-controlled on/off switch for protein–protein interactions. In its trans form, it allows proteins to assemble into

		defined complexes (e.g., oligomers, dimers). When exposed to light, AzoF photoisomerizes to the cis form, which disrupts those interactions and causes the complexes to disassemble.
Avena sativa	NPH1-1	Protein kinase that acts as a blue light photoreceptor in a signal-transduction pathway for phototropic responses. Regulates a wide range of physiological activities in plants that maximize the efficiency of photosynthesis, such as chloroplast relocations, stomata opening, and leaf expansion.
Drosophila melanogaster	MagR	Involved in the assembly of mitochondrial iron-sulfur proteins. Probably involved in the binding of an intermediate of Fe/S cluster assembly (By similarity). Required for maintenance of circadian rhythms under constant darkness
Corynebacterium glutamicum	NCgl1221	Mechanosensitive monoatomic ion channel activity
Vaucheria frigida	AUREO1	The LOV domain noncovalently binds a flavin chromophore, which can be stimulated by blue light (λmax ≈ 470 nm) absorption to initiate a photochemical reaction that results in the formation of a covalent adduct between a conserved cysteine and the flavin ring . This results in a change in protein conformation allowing for dimerisation of the LOV domains.
Escherichia coli	MalE	Part of the ABC transporter complex MalEFGK involved in maltose/maltodextrin import. Binds maltose and higher maltodextrins such as maltotriose.
Salpingoeca rosetta	RhoPDE	Binds 2 divalent metal cations per subunit. Site 1 may preferentially bind zinc ions, while site 2 has a preference for magnesium and/or manganese ions.

Move to approve: David Glasbrenner
Second: Craig Bartling
Outcome: Approved with the following stipulations: 1) the strains of *E. coli* hosts are defined 2) describe the read-out method so we know how it works 3) Describe the protein parts A and B are they fused or separated.

Application: FY24-13-A1
Study title: Biological disclosure spray
PI: David Glasbrenner

- **PI and laboratory staff performing the research have been appropriately trained in the safe conduct of the research:** Y
- **Applicable section of the NIH Guidelines:** III-D-2
- **BSL-#** 1 and 2
- **Agent characteristics:** While the some of the source organisms listed below are BSL-2, all genes, bacteria, and yeast utilized on this project will not have potential to cause any harm. The genes utilized are not virulence factors, are non-toxic, and will not be introduced into any living system. The host organisms are commercial expression strains of *E. coli* and *S. cerevisiae*. The "agent" in this case will be purified proteins used as an indicator.
- **Types of manipulations planned:** expression and purification of protein or peptide constructs from genes inserted into expression vectors.
- **Source(s) of the nucleic sequences (e.g., species):** Several species will be used as sources of proteins to be expressed: avian reovirus S1133, human, *Saccharomyces cerevisiae*, *Escherichia coli, Basidiomycete PM1, Coriolopsis trogii, Phytophthora capsica, Coriolopsis gallica, Trametes sp. 48424, Trametes versicolor, Trametes polyzona, Trametes sp. AH28-2, Trametes cinnabarina, Aspergillus oryzae, Trametes pubescens, Thermus thermophilus, Bacillus pumilus, Bacillus vallismortis, Bacillus subtilis cjp3, Bacillus licheniformis, Thioalkalivibrio, Psychrobacter sp.,* uncultured bacterium, *Stenotrophomonas maltophilia, Enterobacter hormaechei, Bordetella bronchiseptica, Vreelandella arctica, Paenibacillus glucanolyticus, Thermus sp. 2.9, Achromobacter xylosoxidans, Citrobacter freundii, Stenotrophomonas maltophilia, Bacillus pumilus ATCC 7061, Halalkalibacter wakoensis, Geothermobacter hydrogeniphilus, Bacillus mojavensis, Thermus thermophilus HB27, Aspergillus niger, Pyrococcus furiosus,* soybean, Chromohalobacter sp. 560, *Aspergillus fumigatus Af293, Pyrococcus abyssi, Thermotoga maritima, Gallus gallus, Pseudonaja textilis, Zootoca vivipara, Taeniopygia guttata, Danio rerio, Calypte anna, Oncorhynchus mykiss, Pelobates fuscus, Cyprinodon variegatus, Gadus morhua, Gasterosteus aculeatus aculeatus,* Wbeta phage, gamma phage, prophage LambdaBa03, AP50c phage, Wip1 phage, *Petromyzon marinus, Lama glama, Cytaeis uchidae, Verrillofungia concinna, Entacmaea quadricolor, Aequorea victoria, Discosoma sp, Oplophorus gracilirostris, Mus musculus*, and synthetic sources.

- **Nature of the nucleic acid sequences (e.g., structural gene, oncogene):** The nucleic acid sequences are genes encoding enzymes such as caspases or prothrombin, enzymatic reporters such as nanoluc, fluorescent reporters such as GFP or mCherry, or binding proteins such as FK506-binding protein or synthetic z-affibodies.
- **Host(s) and vector(s) to be used:**

Hosts: *E. coli* and *S. cerevisiae*
Vectors: 17 custom plasmids for *E. coli* expression based on the following backbones: Twist Biosciences's minimal plasmid backbone, shuffle vectors 1-7, p15A, pBR322, pUC57, and pRS314.

- **Transgene expression:** yes, transgenes will be expressed and proteins purified.
- **Protein function:**

Insert Source	**Protein**	**Function**
human	FKBP12	a peptidyl-prolyl isomerase involved in protein folding and regulation of signaling pathways
	Caspase 4	an inflammatory caspase and plays a role in the immune system
	Caspase 5	an inflammatory caspase and plays a role in the immune system
	FactorX	enzyme in the human blood coagulation cascade
	prothrombin	enzyme in the human blood coagulation cascade
Mus musculus	SRC Homology 3 Domain	binds PPPPLPPKRRR peptide
	scFv-6w10	Putatively bind *B. anthracis*
Oplophorus gracilirostris	Nanoluc	enzymatic reporter for luminescence assays
Discosoma sp	mCherry	fluorescent protein
Aequorea victoria	SCFP3A, mJuniper, mChartreuse, mLemon, and mgold	fluorescent proteins
Entacmaea quadricolor	CyOFP1 and super-TagRFP	fluorescent protein
Verrillofungia concinna	mKO-kappa	fluorescent protein
Cytaeis uchidae	Mstaygold	fluorescent protein
Synthetic	Z-affibodies	Putatively bind *B. anthracis*

	BBP-1	Putatively bind *B. anthracis*
	BBP-2	Putatively bind *B. anthracis*
	MMS128	Putatively bind *B. anthracis*
	MMS133	Putatively bind *B. anthracis*
	Anchor ligan	Putatively bind *B. anthracis*
	PA affinity peptide	Putatively bind *B. anthracis*
	P01(26_72)	Putatively bind *B. anthracis*
	P04(15_72)	Putatively bind *B. anthracis*
	P26(3_72)	Putatively bind *B. anthracis*
	P50(3_72)	Putatively bind *B. anthracis*
	P1	Putatively bind *B. anthracis*
	P2	Putatively bind *B. anthracis*
	P2a	Putatively bind *B. anthracis*
	P2b	Putatively bind *B. anthracis*
	P2c	Putatively bind *B. anthracis*
	P3	Putatively bind *B. anthracis*
Lama glama	Bc1A_A5	Putatively bind *B. anthracis*
	Bc1A_B7	Putatively bind *B. anthracis*
	SODA1_F3	Putatively bind *B. anthracis*
	sdAbs_B12	Putatively bind *B. anthracis*
	sdAbs_G10	Putatively bind *B. anthracis*
	sdAbs_C7	Putatively bind *B. anthracis*
	sdAb_A4	Putatively bind *B. anthracis*
	sdAb_A5	Putatively bind *B. anthracis*

	sdAb_C5	Putatively bind *B. anthracis*
	sdAb_D4	Putatively bind *B. anthracis*
	sdAb_E6	Putatively bind *B. anthracis*
	Nb 632	Putatively bind *B. anthracis*
	Nb 633	Putatively bind *B. anthracis*
	Nb 643	Putatively bind *B. anthracis*
Gamma phage	PlyG-P3	Part of PlyG which putatively bind *B. anthracis*
Petromyzon marinus	VLR4	Putatively bind *B. anthracis*
	BA191	Putatively bind *B. anthracis*
Wip1 phage	RBPwip1(P23+P34)	Phage recognition protein which putatively binds *B. anthracis*
AP50c phage	RBPap50(P28+p29)	Phage recognition protein which putatively binds *B. anthracis*
Prophage LambdaBa03	RBPλ03Δ1-120	part of a phage recognition protein which putatively bind *B. anthracis*
Gamma phage	60aa	Domain of PlyG which putatively bind *B. anthracis*
Wbeta phage	WP14	phage recognition protein which putatively bind *B. anthracis*
Gasterosteus aculeatus aculeatus	Caspase 9	initiation of apoptosis and other nonapoptotic roles including regulation of necroptosis, cellular differentiation, innate immune response, sensory neuron maturation, mitochondrial homeostasis, corticospinal circuit

		organization, and ischemic vascular injury
Gadus morhua	Caspase 9	initiation of apoptosis and other nonapoptotic roles including regulation of necroptosis, cellular differentiation, innate immune response, sensory neuron maturation, mitochondrial homeostasis, corticospinal circuit organization, and ischemic vascular injury
Cyprinodon variegatus	Caspase 9	initiation of apoptosis and other nonapoptotic roles including regulation of necroptosis, cellular differentiation, innate immune response, sensory neuron maturation, mitochondrial homeostasis, corticospinal circuit organization, and ischemic vascular injury
Pelobates fuscus	Caspase 9	initiation of apoptosis and other nonapoptotic roles including regulation of necroptosis, cellular differentiation, innate immune response, sensory neuron maturation, mitochondrial homeostasis, corticospinal circuit organization, and ischemic vascular injury
Oncorhynchus mykiss	Caspase 9	initiation of apoptosis and other nonapoptotic roles including regulation of necroptosis, cellular differentiation, innate immune response, sensory neuron maturation, mitochondrial homeostasis,

		corticospinal circuit organization, and ischemic vascular injury
Calypte anna	Caspase 9	initiation of apoptosis and other nonapoptotic roles including regulation of necroptosis, cellular differentiation, innate immune response, sensory neuron maturation, mitochondrial homeostasis, corticospinal circuit organization, and ischemic vascular injury
Danio rerio	Caspase 9	initiation of apoptosis and other nonapoptotic roles including regulation of necroptosis, cellular differentiation, innate immune response, sensory neuron maturation, mitochondrial homeostasis, corticospinal circuit organization, and ischemic vascular injury
Taeniopygia guttata	Caspase 9	initiation of apoptosis and other nonapoptotic roles including regulation of necroptosis, cellular differentiation, innate immune response, sensory neuron maturation, mitochondrial homeostasis, corticospinal circuit organization, and ischemic vascular injury
Zootoca vivipara	Caspase 9	initiation of apoptosis and other nonapoptotic roles including regulation of necroptosis, cellular differentiation, innate immune response, sensory neuron maturation,

		mitochondrial homeostasis, corticospinal circuit organization, and ischemic vascular injury
Pseudonaja textilis	Caspase 9	initiation of apoptosis and other nonapoptotic roles including regulation of necroptosis, cellular differentiation, innate immune response, sensory neuron maturation, mitochondrial homeostasis, corticospinal circuit organization, and ischemic vascular injury
Gallus gallus	Caspase 9	initiation of apoptosis and other nonapoptotic roles including regulation of necroptosis, cellular differentiation, innate immune response, sensory neuron maturation, mitochondrial homeostasis, corticospinal circuit organization, and ischemic vascular injury
2 engineered variants from *Escherichia coli*	Alkaline Phosphatase	removes phosphate groups from molecules such as nucleotides, proteins, and alkaloids under alkaline conditions.
Escherichia coli	Alkaline Phosphatase	
Thermotoga (Thermotoga maritima)	Alkaline Phosphatase	removes phosphate groups from molecules such as nucleotides, proteins, and alkaloids under alkaline conditions.
Bacillus licheniformis	Alkaline Phosphatase	removes phosphate groups from molecules such as nucleotides, proteins, and alkaloids under alkaline conditions.

Thermus thermophilus	Alkaline Phosphatase	removes phosphate groups from molecules such as nucleotides, proteins, and alkaloids under alkaline conditions.
Pyrococcus abyssi	Alkaline Phosphatase	removes phosphate groups from molecules such as nucleotides, proteins, and alkaloids under alkaline conditions.
Aspergillus fumigatus Af293	Acid Phosphatase	removes phosphate groups from molecules such as nucleotides, proteins, and alkaloids under acidic conditions.
3 Engineered variants from *Escherichia coli*	Beta-lactamase	catalyzes the hydrolysis of the beta-lactam ring in beta-lactam compounds by attacking the amide bond.
Chromohalobacter sp. 560	Beta-lactamase	catalyzes the hydrolysis of the beta-lactam ring in beta-lactam compounds by attacking the amide bond.
Engineered variant of soybean ascorbate peroxidase	APEX2	an engineered peroxidase that catalyzes the H_2O_2-dependent oxidation of biotin-phenol or other phenolic substrates.
Pyrococcus furiosus	β-Galactosidase	hydrolyzes β-galactosides into monosaccharides by cleaving the glycosidic bond between a galactose and its adjoining sugar moiety
Aspergillus niger	β-Glucosidase	hydrolyzes β-glucosidic bonds in β-D-glucosides, releasing glucose and the corresponding aglycone.

Thermus thermophilus HB27	Laccase	a multicopper oxidase that catalyzes the one-electron oxidation of phenols, aromatic amines, and other electron-rich substrates by reducing molecular oxygen to water.
Bacillus mojavensis	Laccase (1548 bp)	a multicopper oxidase that catalyzes the one-electron oxidation of phenols, aromatic amines, and other electron-rich substrates by reducing molecular oxygen to water.
	Laccase (1542 bp)	a multicopper oxidase that catalyzes the one-electron oxidation of phenols, aromatic amines, and other electron-rich substrates by reducing molecular oxygen to water.
Geothermobacter hydrogeniphilus	Laccase	a multicopper oxidase that catalyzes the one-electron oxidation of phenols, aromatic amines, and other electron-rich substrates by reducing molecular oxygen to water.
Halalkalibacter wakoensis	Laccase	a multicopper oxidase that catalyzes the one-electron oxidation of phenols, aromatic amines, and other electron-rich substrates by reducing molecular oxygen to water.
Bacillus pumilus ATCC 7061	Laccase	a multicopper oxidase that catalyzes the one-electron oxidation of phenols, aromatic amines, and other electron-rich substrates by

		reducing molecular oxygen to water.
Stenotrophomonas maltophilia	Laccase	a multicopper oxidase that catalyzes the one-electron oxidation of phenols, aromatic amines, and other electron-rich substrates by reducing molecular oxygen to water.
Citrobacter freundii	Laccase	a multicopper oxidase that catalyzes the one-electron oxidation of phenols, aromatic amines, and other electron-rich substrates by reducing molecular oxygen to water.
Achromobacter xylosoxidans	Laccase (1620 bp)	a multicopper oxidase that catalyzes the one-electron oxidation of phenols, aromatic amines, and other electron-rich substrates by reducing molecular oxygen to water.
	Laccase (1671 bp)	a multicopper oxidase that catalyzes the one-electron oxidation of phenols, aromatic amines, and other electron-rich substrates by reducing molecular oxygen to water.
Thermus sp. 2.9	Laccase	a multicopper oxidase that catalyzes the one-electron oxidation of phenols, aromatic amines, and other electron-rich substrates by reducing molecular oxygen to water.
Paenibacillus glucanolyticus	Laccase	a multicopper oxidase that catalyzes the one-electron oxidation of phenols, aromatic amines, and other

		electron-rich substrates by reducing molecular oxygen to water.
Vreelandella arctica	Laccase	a multicopper oxidase that catalyzes the one-electron oxidation of phenols, aromatic amines, and other electron-rich substrates by reducing molecular oxygen to water.
Bordetella bronchiseptica	Laccase	a multicopper oxidase that catalyzes the one-electron oxidation of phenols, aromatic amines, and other electron-rich substrates by reducing molecular oxygen to water.
Enterobacter hormaechei	Laccase	a multicopper oxidase that catalyzes the one-electron oxidation of phenols, aromatic amines, and other electron-rich substrates by reducing molecular oxygen to water.
Stenotrophomonas maltophilia	Laccase	a multicopper oxidase that catalyzes the one-electron oxidation of phenols, aromatic amines, and other electron-rich substrates by reducing molecular oxygen to water.
uncultured bacterium	Laccase	a multicopper oxidase that catalyzes the one-electron oxidation of phenols, aromatic amines, and other electron-rich substrates by reducing molecular oxygen to water.
Psychrobacter sp.	Laccase	a multicopper oxidase that catalyzes the one-electron oxidation of phenols,

		aromatic amines, and other electron-rich substrates by reducing molecular oxygen to water.
Thioalkalivibrio	Laccase	a multicopper oxidase that catalyzes the one-electron oxidation of phenols, aromatic amines, and other electron-rich substrates by reducing molecular oxygen to water.
Bacillus licheniformis	Laccase	a multicopper oxidase that catalyzes the one-electron oxidation of phenols, aromatic amines, and other electron-rich substrates by reducing molecular oxygen to water.
Bacillus subtilis cjp3	Laccase	a multicopper oxidase that catalyzes the one-electron oxidation of phenols, aromatic amines, and other electron-rich substrates by reducing molecular oxygen to water.
Bacillus vallismortis	Laccase	a multicopper oxidase that catalyzes the one-electron oxidation of phenols, aromatic amines, and other electron-rich substrates by reducing molecular oxygen to water.
Bacillus pumilus	Laccase	a multicopper oxidase that catalyzes the one-electron oxidation of phenols, aromatic amines, and other electron-rich substrates by reducing molecular oxygen to water.
Thermus thermophilus	Laccase	a multicopper oxidase that catalyzes the one-electron

		oxidation of phenols, aromatic amines, and other electron-rich substrates by reducing molecular oxygen to water.
Trametes pubescens	Laccase	a multicopper oxidase that catalyzes the one-electron oxidation of phenols, aromatic amines, and other electron-rich substrates by reducing molecular oxygen to water.
Aspergillus oryzae	Laccase	a multicopper oxidase that catalyzes the one-electron oxidation of phenols, aromatic amines, and other electron-rich substrates by reducing molecular oxygen to water.
Trametes cinnabarina	Laccase	a multicopper oxidase that catalyzes the one-electron oxidation of phenols, aromatic amines, and other electron-rich substrates by reducing molecular oxygen to water.
Trametes versicolor	Laccase	a multicopper oxidase that catalyzes the one-electron oxidation of phenols, aromatic amines, and other electron-rich substrates by reducing molecular oxygen to water.
Trametes sp. AH28-2	Laccase	a multicopper oxidase that catalyzes the one-electron oxidation of phenols, aromatic amines, and other electron-rich substrates by reducing molecular oxygen to water.

Coriolopsis gallica	Laccase	a multicopper oxidase that catalyzes the one-electron oxidation of phenols, aromatic amines, and other electron-rich substrates by reducing molecular oxygen to water.
Trametes polyzona	Laccase	a multicopper oxidase that catalyzes the one-electron oxidation of phenols, aromatic amines, and other electron-rich substrates by reducing molecular oxygen to water.
Basidiomycete PM1	Laccase	a multicopper oxidase that catalyzes the one-electron oxidation of phenols, aromatic amines, and other electron-rich substrates by reducing molecular oxygen to water.
Trametes versicolor	Laccase	a multicopper oxidase that catalyzes the one-electron oxidation of phenols, aromatic amines, and other electron-rich substrates by reducing molecular oxygen to water.
Trametes sp. 48424	Laccase	a multicopper oxidase that catalyzes the one-electron oxidation of phenols, aromatic amines, and other electron-rich substrates by reducing molecular oxygen to water.
Coriolopsis gallica	Laccase	a multicopper oxidase that catalyzes the one-electron oxidation of phenols, aromatic amines, and other electron-rich substrates by

		reducing molecular oxygen to water.
Phytophthora capsici	Laccase	a multicopper oxidase that catalyzes the one-electron oxidation of phenols, aromatic amines, and other electron-rich substrates by reducing molecular oxygen to water.
Coriolopsis trogii	Laccase	a multicopper oxidase that catalyzes the one-electron oxidation of phenols, aromatic amines, and other electron-rich substrates by reducing molecular oxygen to water.
2 engineered variants from *Basidiomycete PM1*	Laccase	a multicopper oxidase that catalyzes the one-electron oxidation of phenols, aromatic amines, and other electron-rich substrates by reducing molecular oxygen to water.
Escherichia coli	maltodextrin-binding protein (MBP)	binds maltodextrin and assist with the purification of proteins
Saccharomyces cerevisiae	Sumo tag	Increases proteins expression and solubility
Escherichia coli	*araC*	native *E. coli* transcription factor that regulates the araBAD operon in response to L-arabinose.
Engineered variant from *Escherichia coli*	*rhaS*	an engineered *E. coli* transcription factor that activates the rhaBAD operon in response to L-mannose

Engineered variant from *Escherichia coli*	*pheS*	α-subunit of phenylalanyl-tRNA synthetase, Cells expressing *pheS** die in the presence of p-Cl-Phe, allowing selection of clones that have lost the marker after recombination – encodes an engineered variant of the alpha subunit of phenylalanyl-tRNA synthetase in E. coli, and is used in counter-selection systems, where incorporation of p-chlorophenylalanine leads to cell death
Escherichia coli	LacI	a lac repressor, which regulates the lac operon by binding to the operator and inhibiting transcription in the absence of lactose or IPTG.
Escherichia coli	DsbA	Assists with the formation of disulfide bonds
Escherichia coli	DsbC	Assists with the formation of disulfide bonds
Escherichia coli	secA	Assists translocation of preproteins across the cytoplasmic membrane
Escherichia coli	ppiD	Chaperones that assists with folding
Saccharomyces cerevisiae	3’ flank of Fur1	homologous recombination at the fur1 site
	CPR5	a peptidyl-prolyl cis-trans isomerase (cyclophilin) that assists in protein folding within the endoplasmic reticulum (ER).

	PDI1	catalyzes the formation and rearrangement of disulfide bonds during protein folding in the ER
	KAR2	an ER-resident Hsp70 chaperone BiP, which binds nascent or misfolded proteins to prevent aggregation and aid in proper folding.
	TDK	catalyzes the phosphorylation of dTMP to dTDP and can confer sensitivity to 5-fluoro-2'-deoxyuridine (FUDR), allowing its use in counter-selection systems.
	ERO1	an ER oxidoreductin that reoxidizes Pdi1, thereby promoting disulfide bond formation in secretory proteins.
	LHS1	a nucleotide exchange factor and co-chaperone of Kar2 that supports protein folding in the ER.
	SIL1	a nucleotide exchange factor for Kar2 that facilitates the release of ADP to promote chaperone cycling during protein folding.
Engineered variant* from avian reovirus S1133	muNS-Mi	this protein is a matrix protein which forms nanospheres. In the virus it encapsulates viral proteins, but in our system, it will encapsulate the enzyme of interest to improve thermal stability. * The

		glycosylation site has been removed.
	Intercoil	a coil domain from the muNS-Mi protein above. This tag allows the protein of interest to be incorporated into the nanospheres. * The glycosylation site has been removed.
Engineered variant of first 38 residues of human a-synuclein	The alpha-helical amino-terminal 38 residues of aSyn	are sufficient to bring about the formation and release of OmpA-labeled extracellular membrane-bound vesicles from *E. coli* cells into the culture media. This gives *E. coli* the ability to secretion proteins and improves production yields

David Glasbrenner: abstained
Move to approve: Caitlyn Heil
Second: Yun Li
Outcome: Approved with the following stipulations: 1) the strains of *E. coli* and *S. cerevisiae* hosts are defined 2) defining the cell-free system to ensure that no plasmids can be transferred to *B. anthracis* 3) and reference the BSC application numbers.

II. Old Business:

NA

III. New Business (review of incidents, inspections/oversight, IBC training, or additional topics):

a. Discussed how the application form works for complex project applications: should we have an attachment option for the gene lists?
b. Reviewed the updated amendment form where exempt categories are defined.
c. Meeting minutes from the last meeting on 08/13/2025 were reviewed and approved by all IBC members present. Caitlyn Heil moved to approve, Yun Li seconded the motion.
d. Voted to approve the addition of Carrie Howland to the IBC.

Meeting adjourned at 3:52 pm

Rachel R. Spurbeck 1/14/2026

Rachel Spurbeck, IBC Chair or Date

Yun Li, IBC Co-Chair

Redaction Disclaimer: Information redacted includes trade secret information, other confidential commercial information, and specific information whose disclosure would directly compromise institutional or national security.