

- **Announcements**
- **Quiz (last one!)**
- **Pre-lab Lecture**
 - ❖ **DMMB assay**
 - ❖ **More about ELISA**
 - ❖ **qPCR analysis**
 - ❖ **Today in Lab (M3D6)**

Announcements

- Lec 7: Atissa on proposal; Lec 8: special topics
- Next time: finish report + clean up; WAC survey
- **Mod 3 research proposal**
 - feedback on your wiki page today/tonight
- **Mod 3 report**
 - no separate Methods section needed: *do* state any unique conditions along the way in Results section/captions
 - **required** analysis: viability (incl. stats), qPCR (incl. RNA amount and cell counts), ELISA (incl. standard curves)
 - **optional/if relevant** analysis: PG assay; general bead, cell, and media appearance on D2, D3, and/or D4

DMMB assay

- Measure GAGs with cationic dye
- Absorbance shift due to complex $A_{595} \downarrow$
 - fades quickly! (pipet upstairs)
 - at low pH, selects for sulfates over carboxyls
 - thus a correction for alginate
 - standard curve made with chondroitin-6 sulfate
- Typically normalize to cell amount (cf DNA content in qPCR)... maybe next year

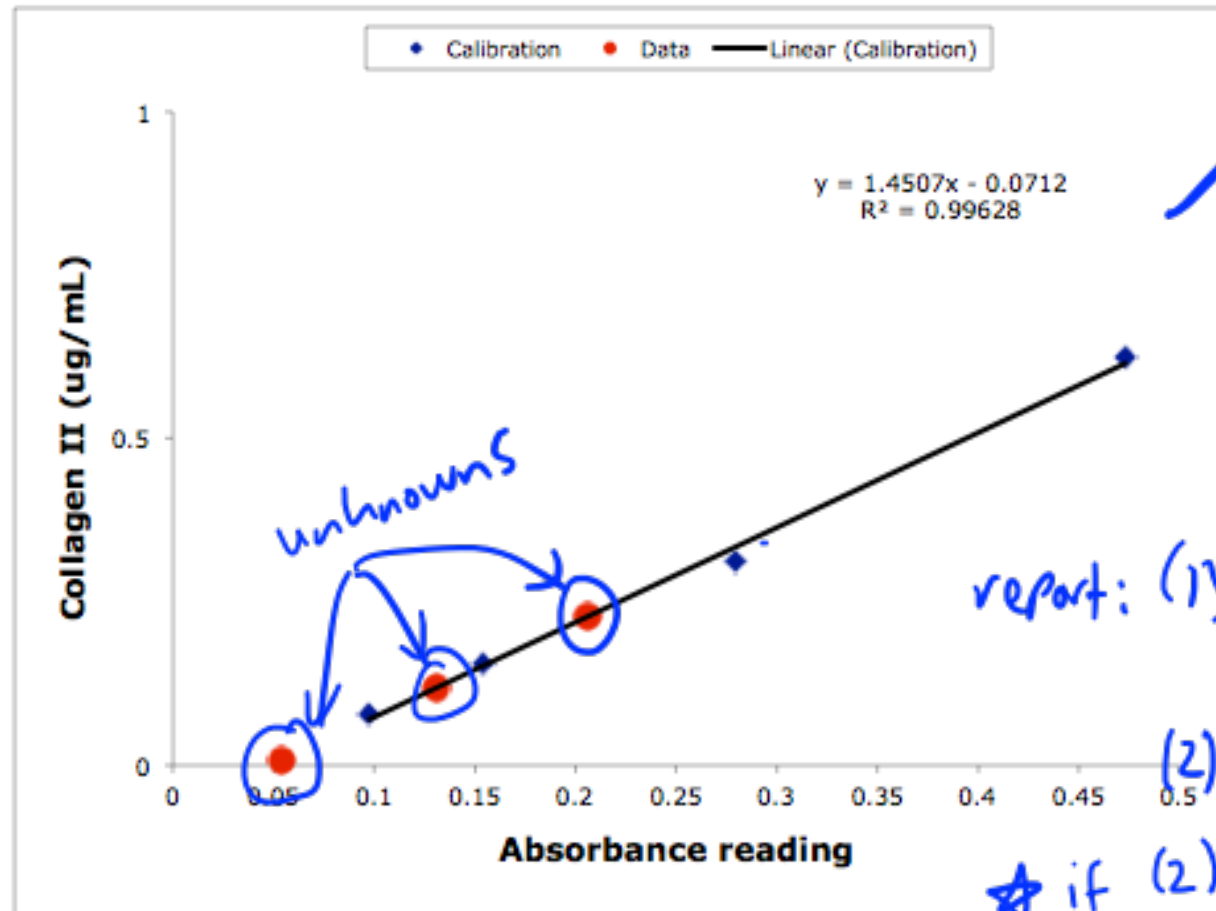
ELISA protocol

- Direct ELISA uses labeled primary antibody
- Indirect ELISA – why use a secondary antibody?
 - signal amplification
 - flexibility/efficiency (t, s) → use w/ many 1^o Abs
 - but may be more cross-reactive
- Development process – what/why/how
 - 2^o Ab – AP conjugated
 - provide substrate: pNPP → colorimetric rxn. in soln; A420
 - development time is key → detect low [protein] → long enough
 - ↘ not oversaturate everything → not too long

ELISA Outcomes

Outcome	Possible Explanations
High reading in "blank" samples	<ul style="list-style-type: none">• cross-contamination of wells or global in PBS• skipped block step• incomplete washes
No signal at all (including standards)	<ul style="list-style-type: none">• wrong or old/bad Abs• flipped plates at 1st Abs step• too high [Tween]
Saturated signal for some samples <u>↳ expt'l</u>	too concentrated → run dilution series usually

ELISA (and PG) analysis



~~exclude non-linear standards/measurements~~

~4 usable

report: (1) CN II:I ratios

(2) absolute [CN]

★ if (2) is very low, then (1) is meaningless

qPCR analysis

efficiency of each primer set

CNII or CNI

change in crossing point (CP/CT)

control = Sample A (-FN)

Sample = Sample B (+FN)

$$\text{ratio} = \frac{(E_{\text{target}})^{\Delta C P_{\text{target}}(\text{control} - \text{sample})}}{(E_{\text{ref}})^{\Delta C P_{\text{ref}}(\text{control} - \text{sample})}}$$

18S rDNA

we can know expression of CNII A vs. CNII B BUT NOT CNII A vs. CNII A in absolute sense

if $E_{\text{tar}} = 2.0$ $\Delta C P_{\text{tar}} = 2$ $\text{ratio} = \frac{2^2}{2^0} = 4\text{-fold change}$
 $E_{\text{ref}} = 2.0$ $\Delta C P_{\text{ref}} = 0$

Equation 1 from M.W. Pfaffl, *Nucleic Acids Res* 29:2002 (2001)

Today in Lab (M3D6)

- Finish ELISA – includes 90 min incubation
- Meanwhile... *figure out how much DEV SOLN your super-group needs!*
 - DMMB assay staggered (15-20 min of work)
 - qPCR analysis
 - finish viability analysis if you haven't already
 - cross-group research discussion
 - (optional: start clean-up)