Target Selection

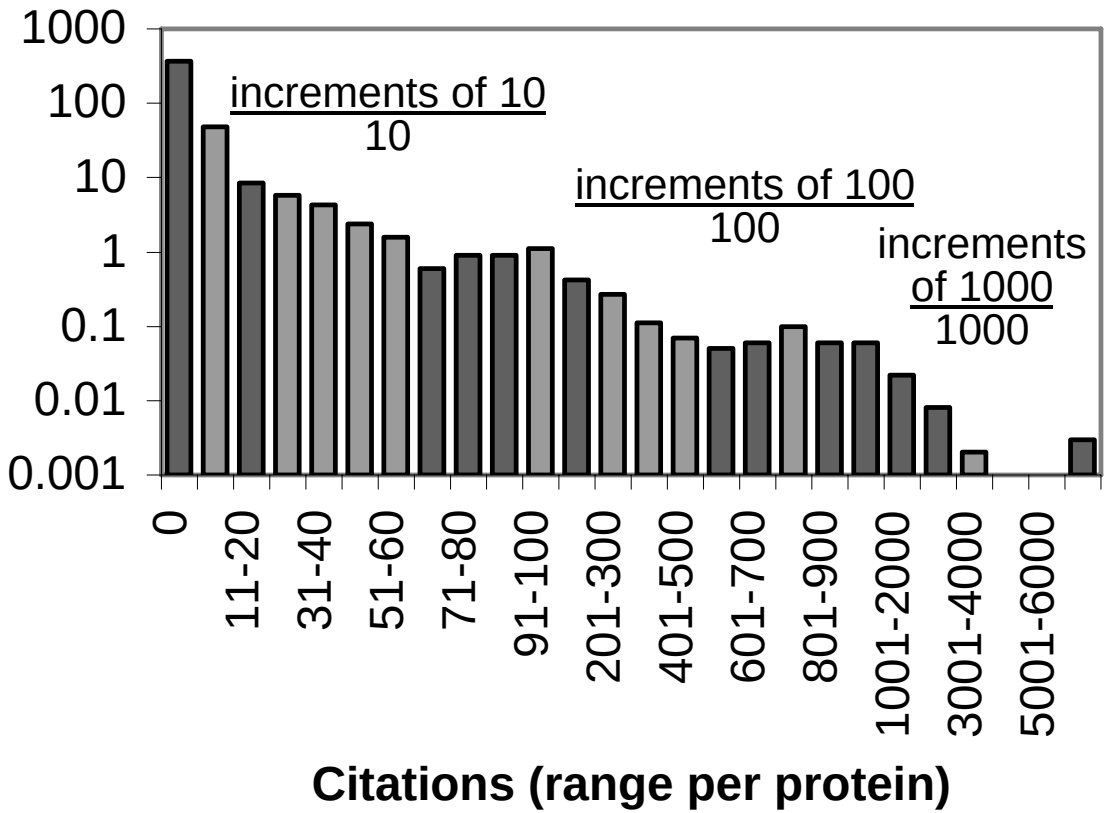
Null Selection Case

- Random selection of candidates?
  - much might be learned by a truly unbiased approach....
  - 1,100 candidates would be 5% of total: a good sampling if broad biomarker patterns are really there
- Presumably we can do better than random...

Collection of Candidates

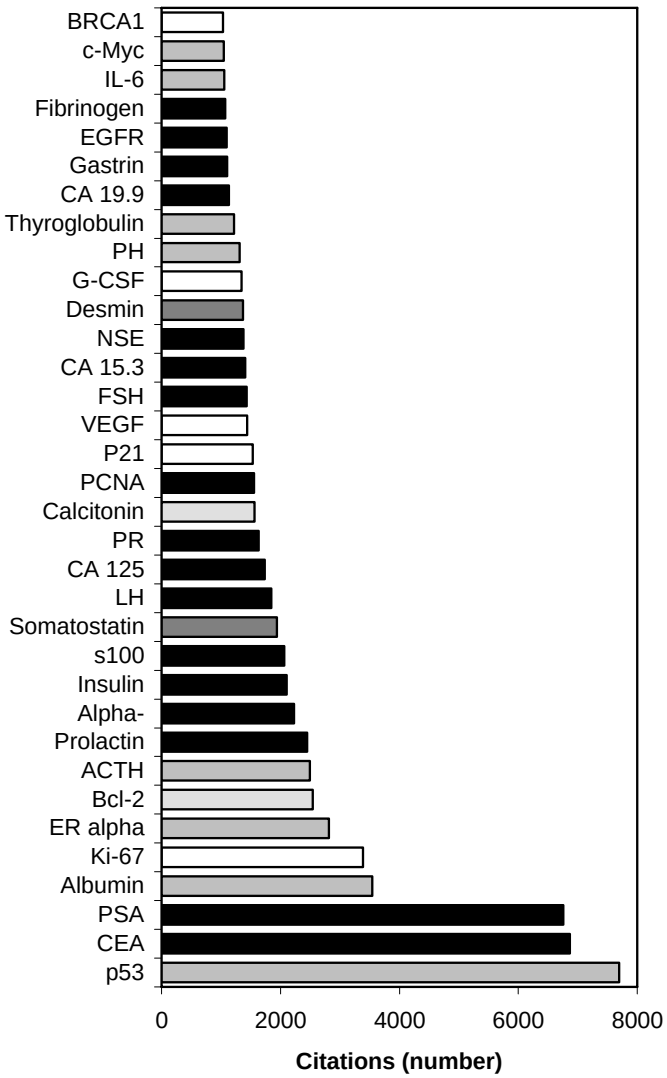
- Literature (Polanski & Anderson, 1200 candidates)
- La Baer website (http://hipseq.med.harvard.edu/MEDGENE)
- HPR data, as available
- More extensive analysis of microarray results

Candidate Cancer Biomarker Citation Frequencies



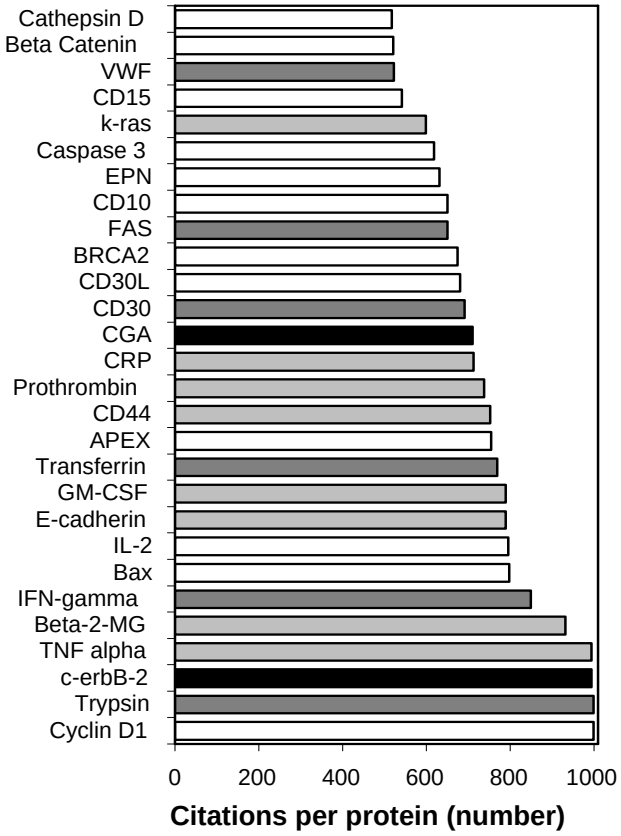
Polanski & Anderson

Candidate Cancer Biomarkers with More Than 1000 Citations



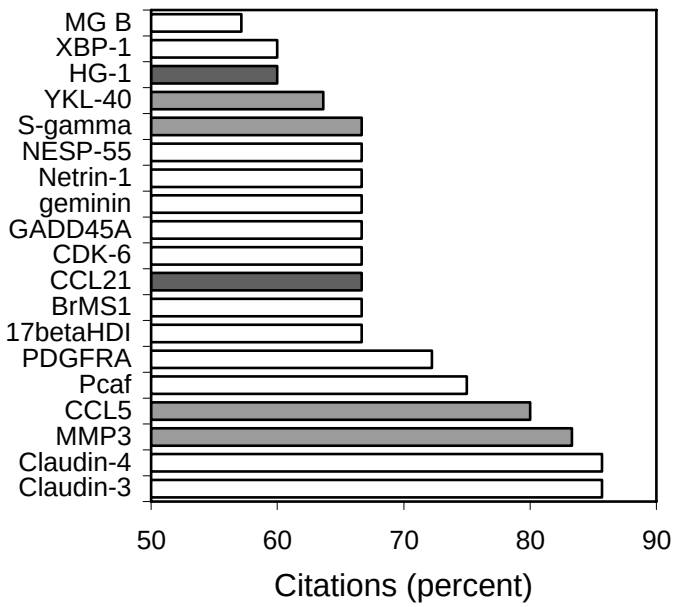
Polanski & Anderson

Candidate Cancer Biomarkers with >500 And <1000 Citations



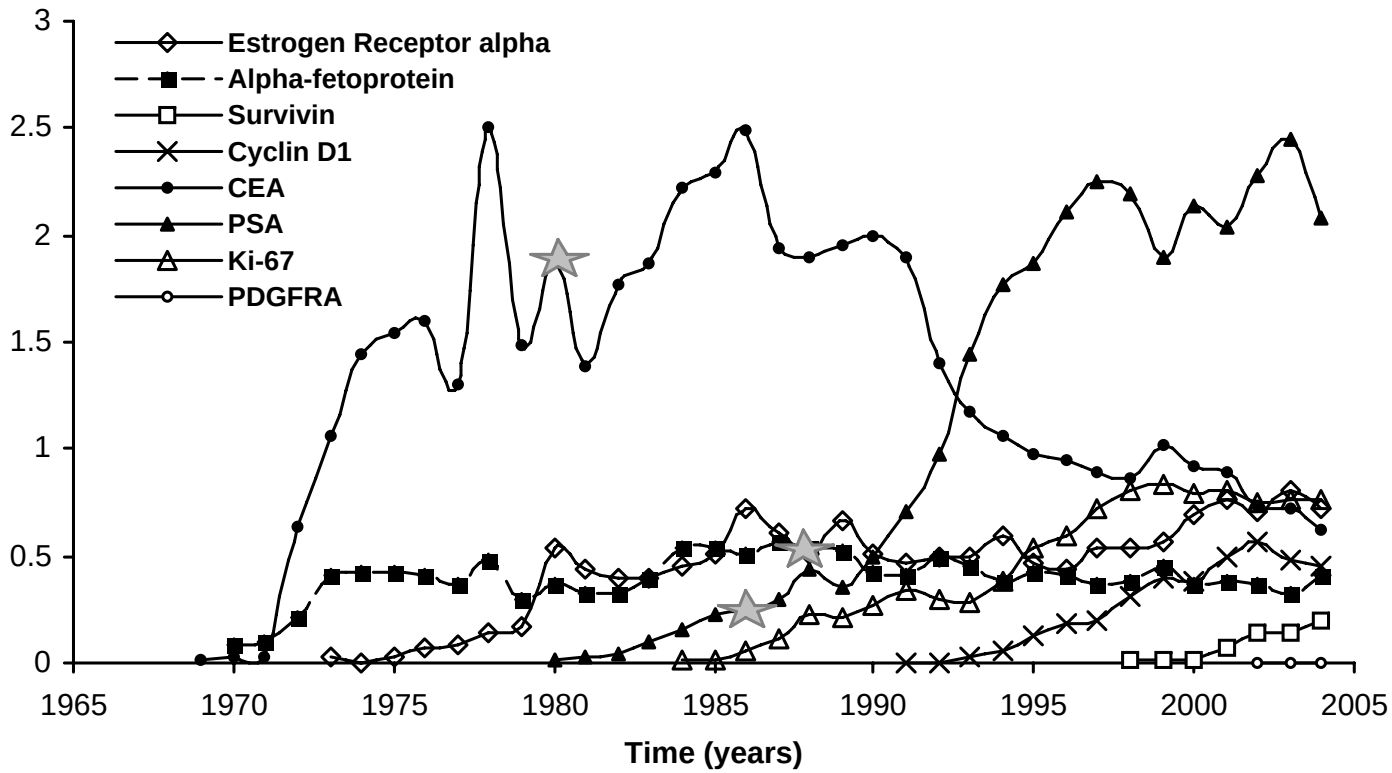
Polanski & Anderson

Candidate Cancer Biomarkers with Mainly Recent Citations



Polanski & Anderson

Time Evolution of Interest in Candidate Cancer Biomarkers



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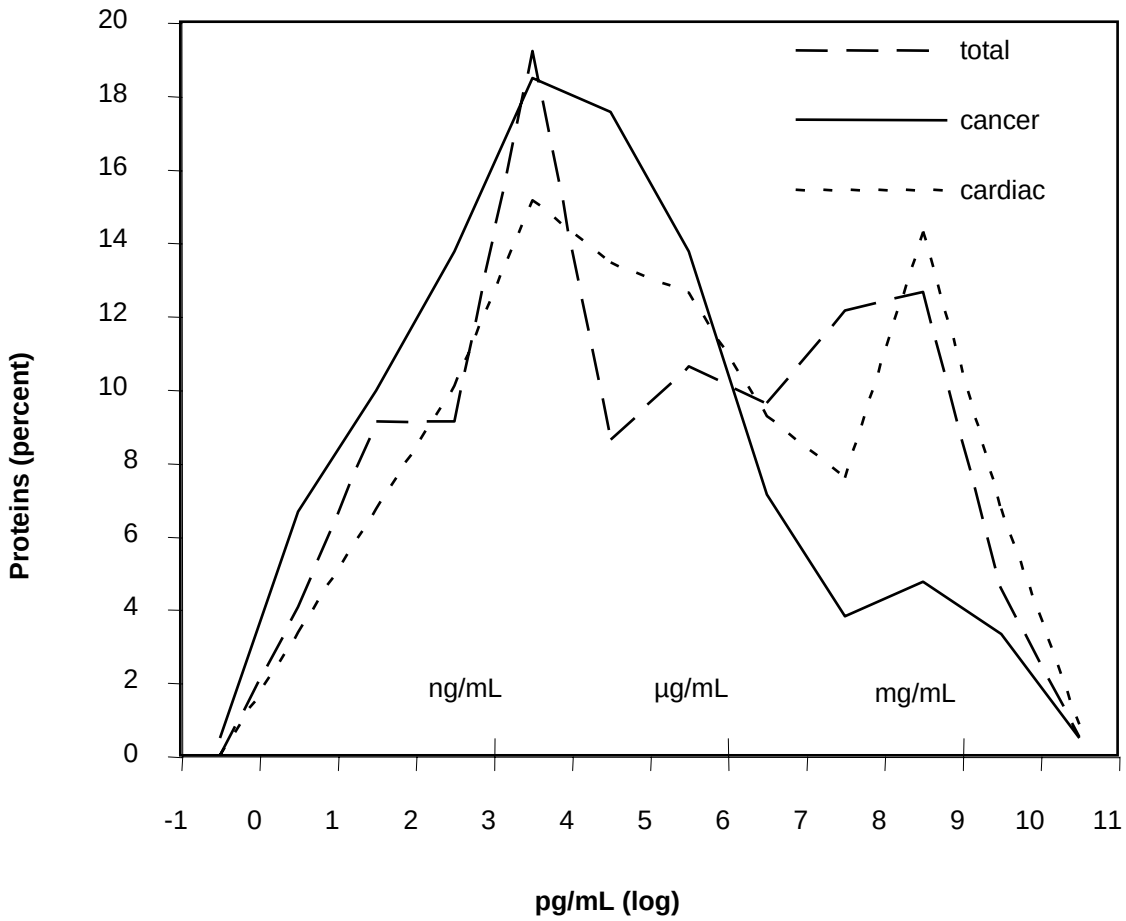
Normal Plasma Concentrations of Candidate Cancer Biomarkers



Polanski & Anderson

La Baer:

http://hipseq.med.harvard.edu/MEDGENE

QuickTime™ and a
TIFF (LZW) decompressor
are needed to see this picture.

Questions

- Level of community input to
  - candidate collection
  - candidate prioritization
- How to prioritize
  - Literature citations?
  - Voting of experts?
  - Pathway analysis?
- How frequently to reprioritize tranches of candidates
- How to avoid looking only under the streetlight (i.e., injections of randomness?)
- How much consistency/coherence is desirable? (e.g., entire pathways or organelles?)