

Identifying the antibody specificity repertoire

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You have a unique antibody repertoire that changes as immune responses occur

Immune factors



Pathogens

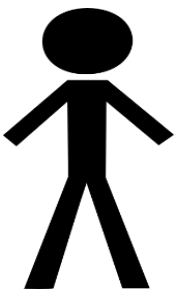
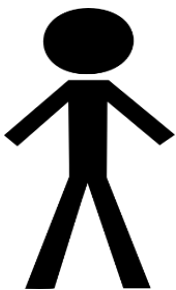


Allergens



Environmental

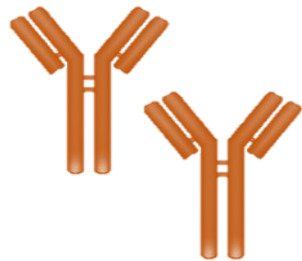
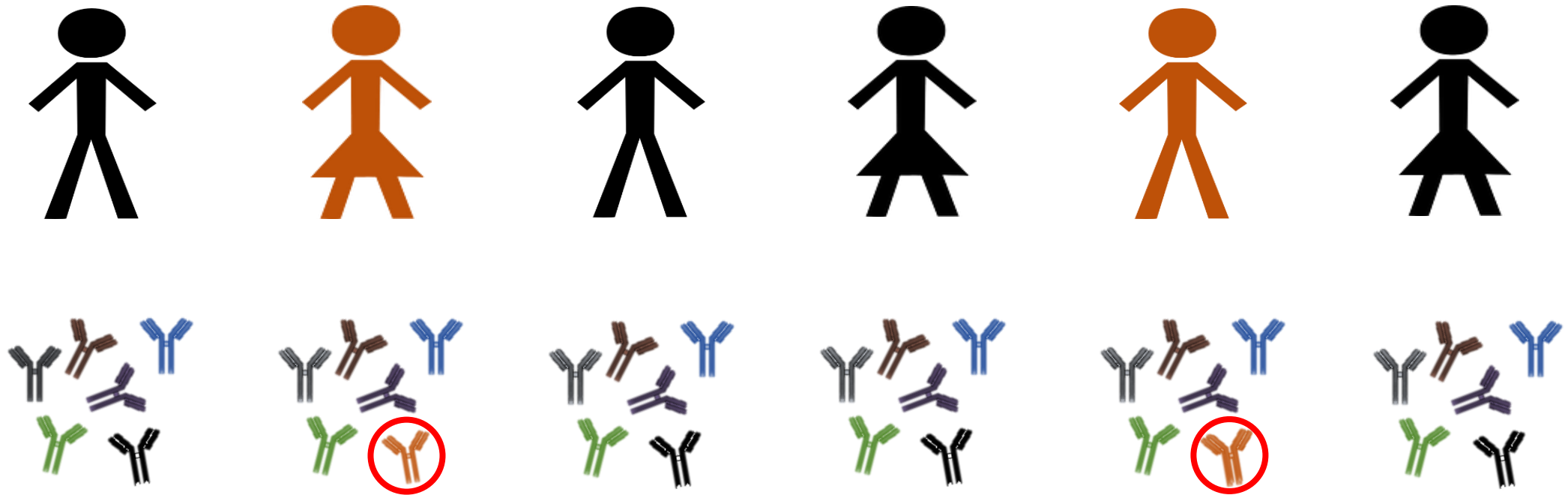
You



Antibody repertoire



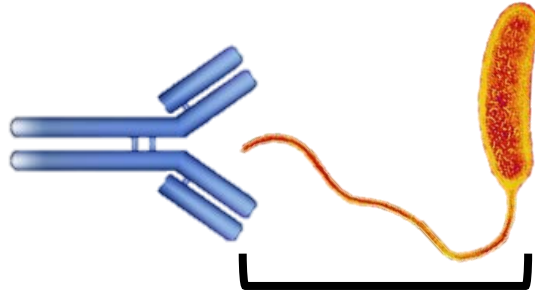
By comparing patient's serums, antibodies can be isolated as disease specific



Potential Biomarkers:

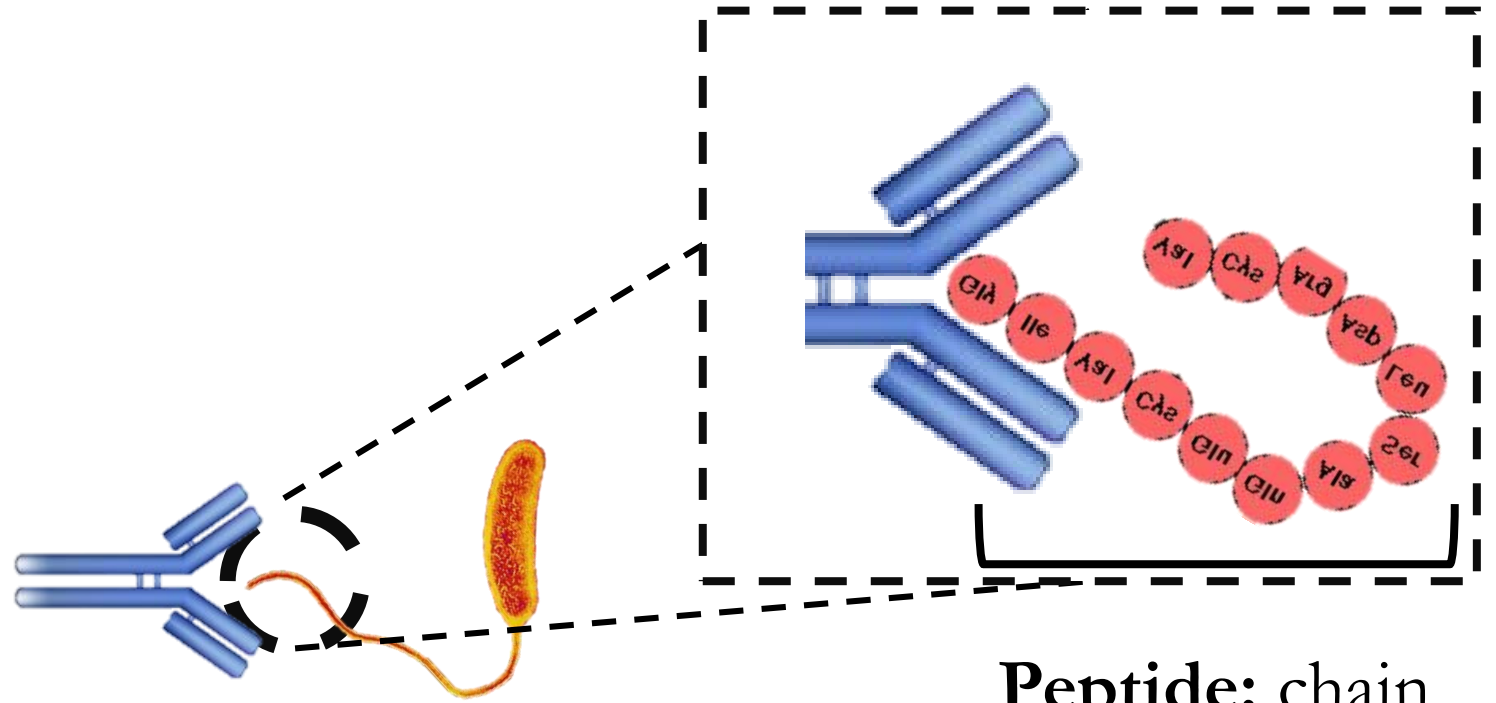
- develop therapeutics
- diagnostic tools
- mechanisms of pathogenesis

All antibodies bind to a unique antigen dependent on their affinity



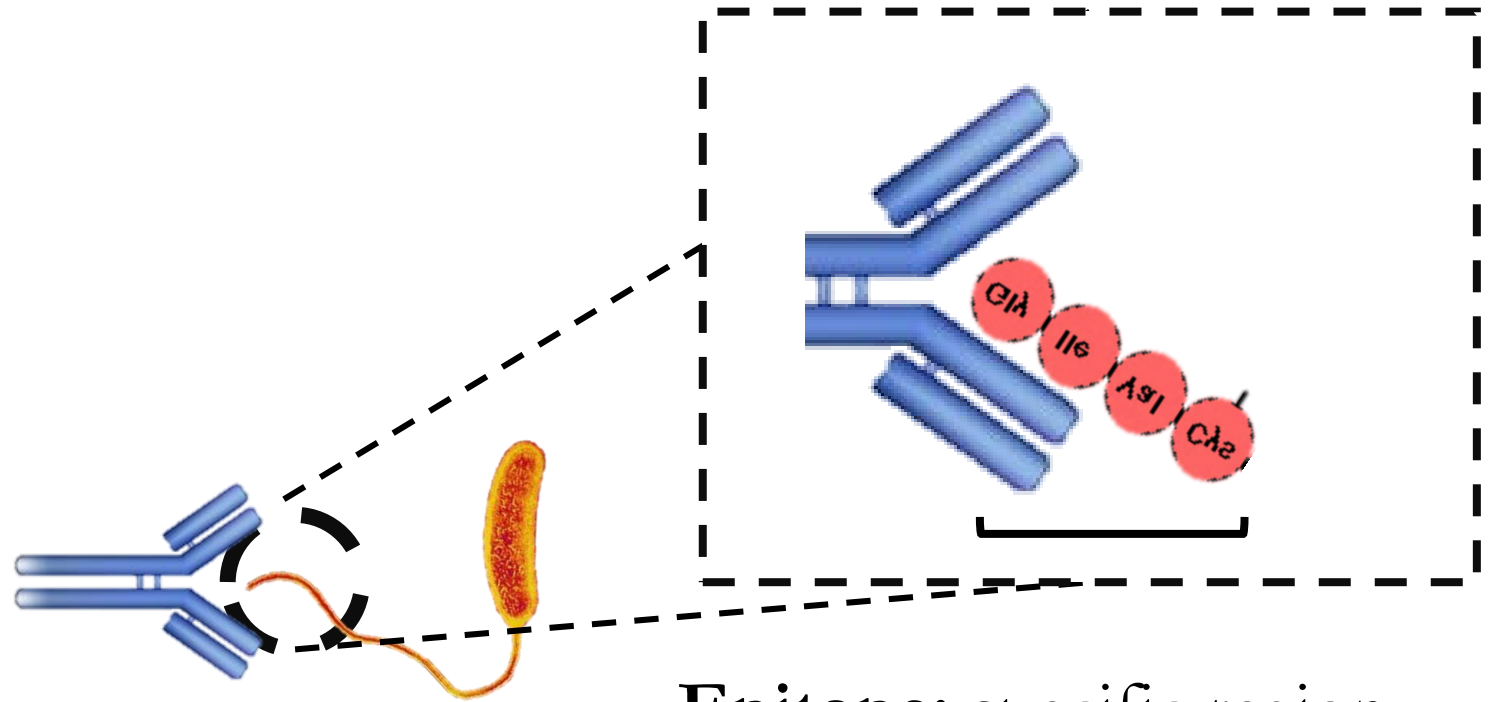
Antigen: a foreign substance
that induces an immune response

All antibodies bind to a unique antigen dependent on their affinity



Peptide: chain
of amino acids

All antibodies bind to a unique antigen dependent on their affinity



Epitope: specific region
responsible for antibody binding

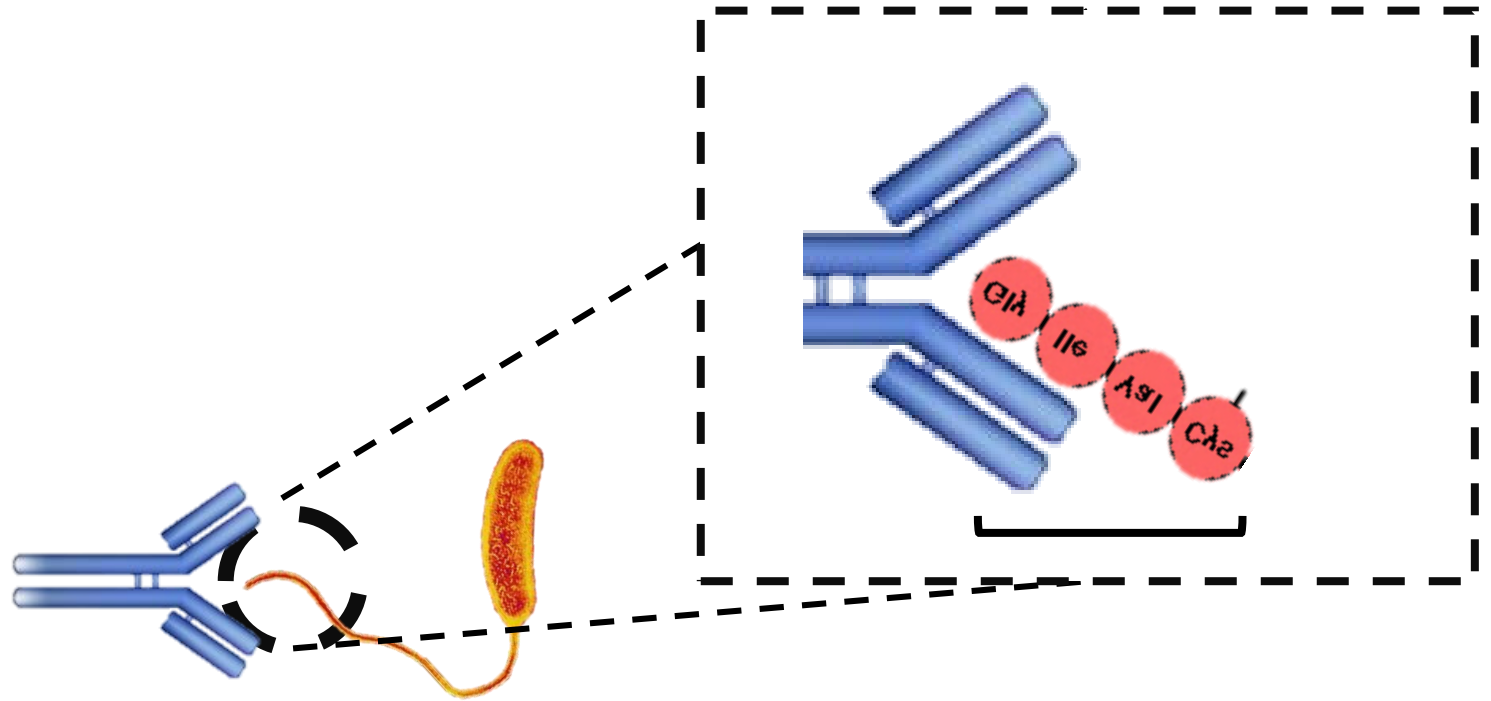
All antibodies bind to a unique antigen dependent on their affinity

Definitions to remember:

-**Antigen:** cause of immune response

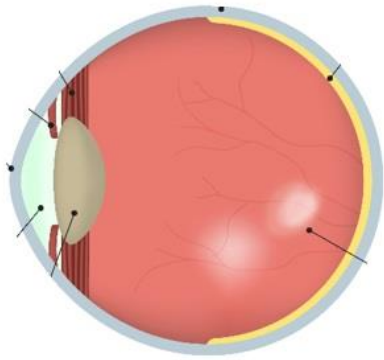
-**Peptide:** chain of amino acids

-**Epitope:** amino acids responsible for binding



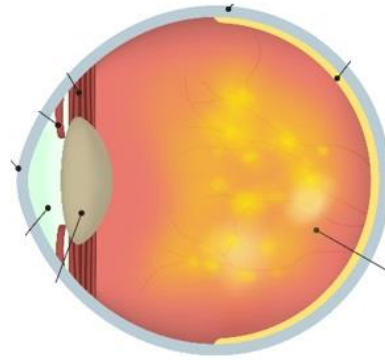
Summer Project: Determine candidates for motifs which are specific to the disease Aged Macular Degeneration (AMD)

Healthy eye



Macula

Eye with AMD



Damaged
Macula

Wet AMD:

- Neo Vascular
- caused by swelling of blood vessels

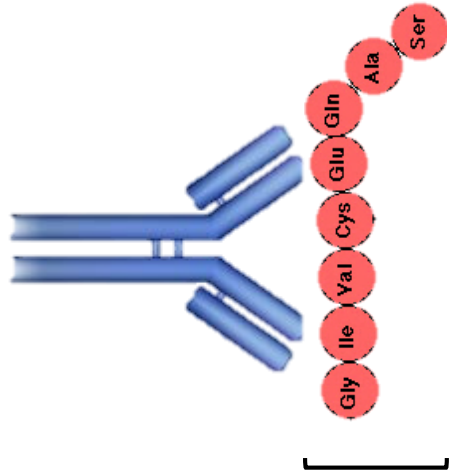
Dry AMD:

- Geographic Atrophy
- caused by aggregation of Drusen

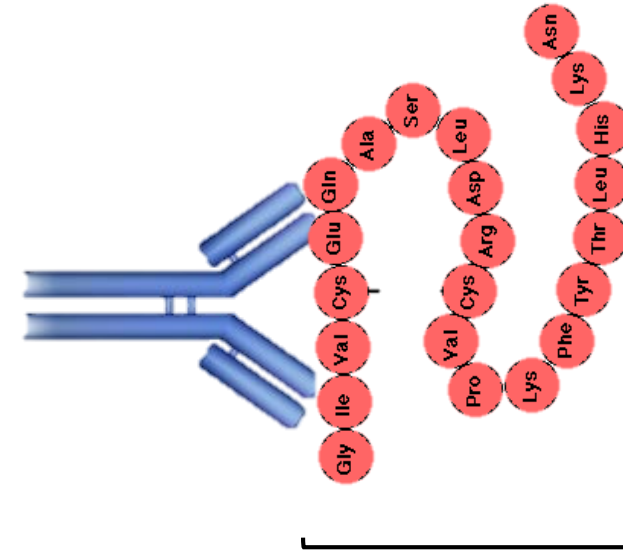
Life with AMD on the right



Research Goal: Develop a systematic method of obtaining disease specific and medically relevant biomarkers



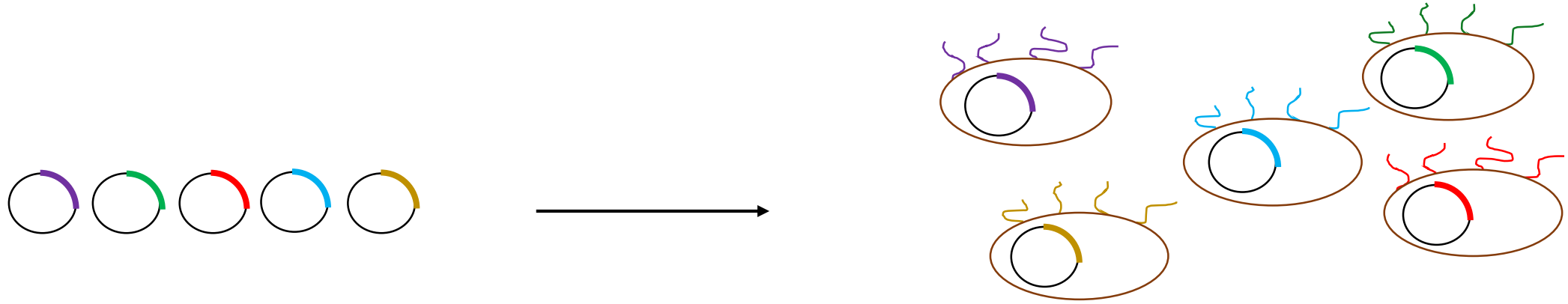
Identify disease specific peptide



Determine complimentary antigen

Accomplish with bacterial display

Engineering bacteria to display peptides for antibody identification



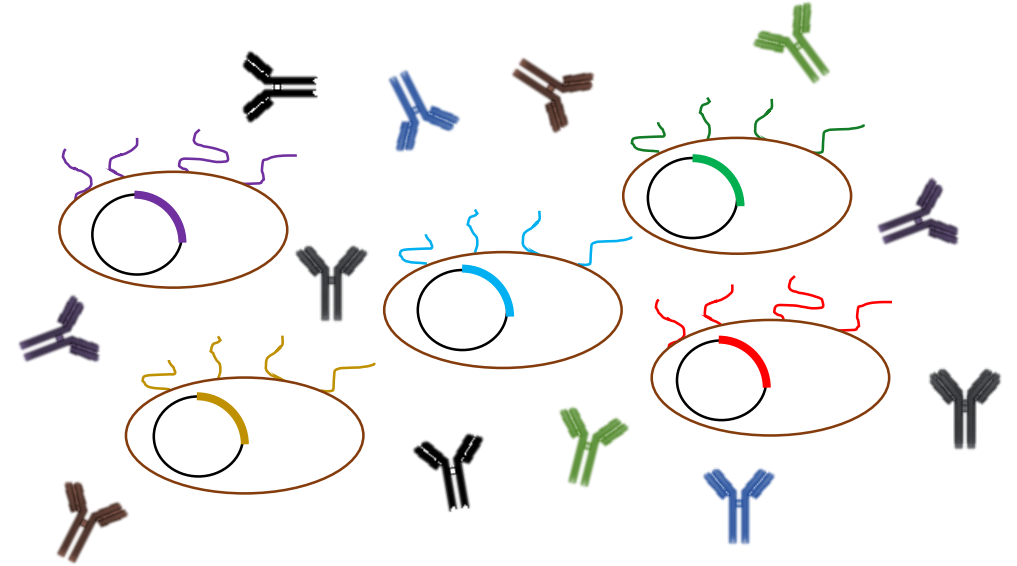
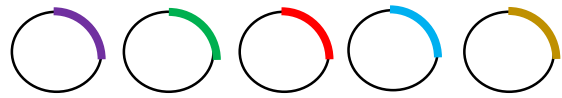
Library of peptides

- 7.6 billion unique peptides
- 12 amino acids in length

Engineer bacteria to display peptide library

- Cells display a unique peptide
- Screen for antibody binding

Engineering bacteria to display peptides for antibody identification

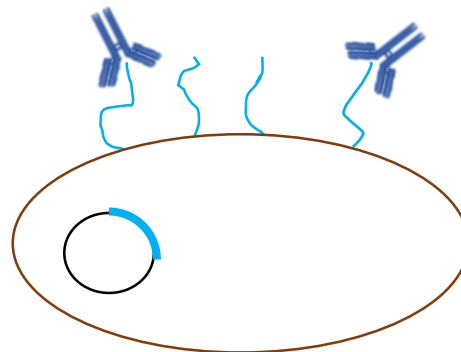


Library of peptides

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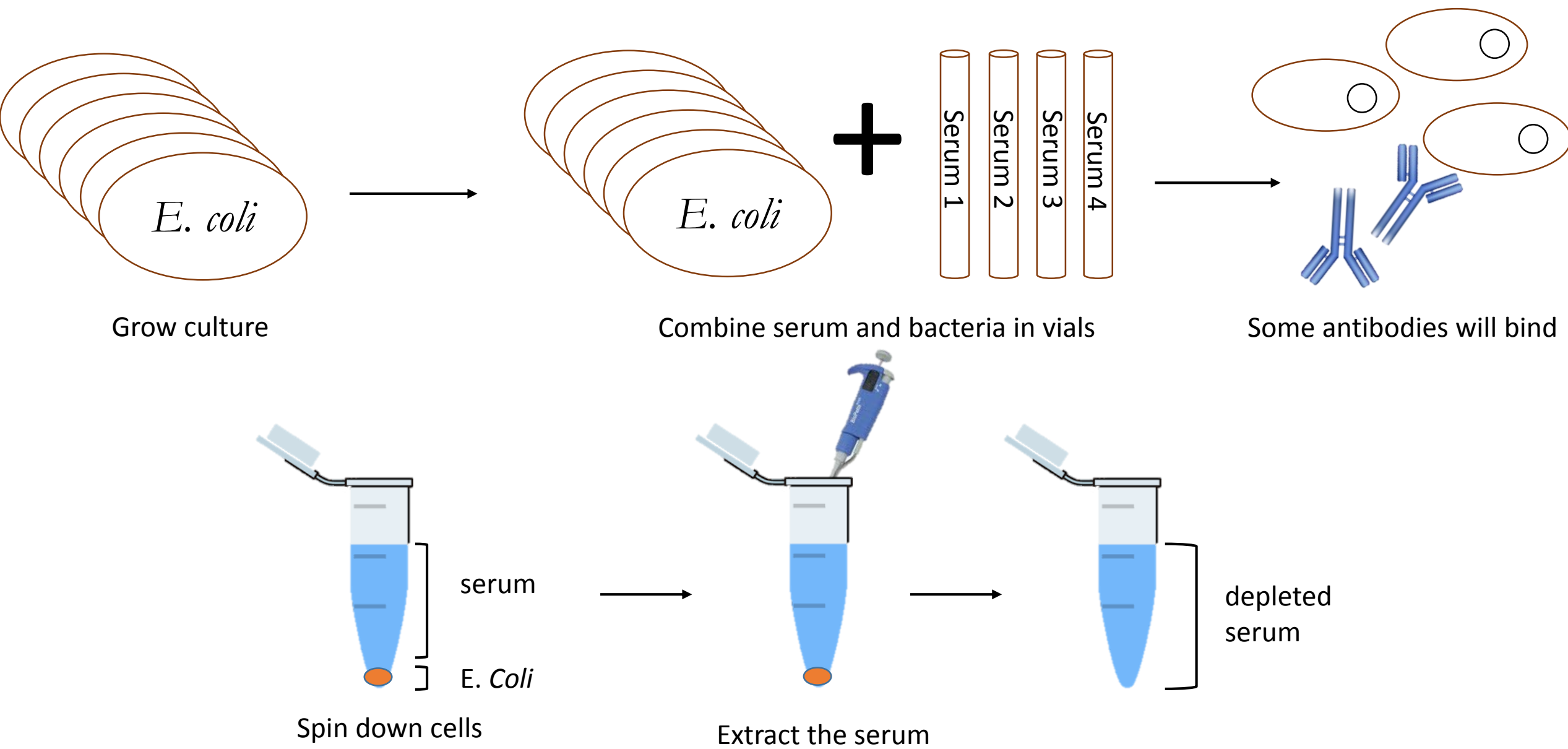
Engineer bacteria to display peptide library

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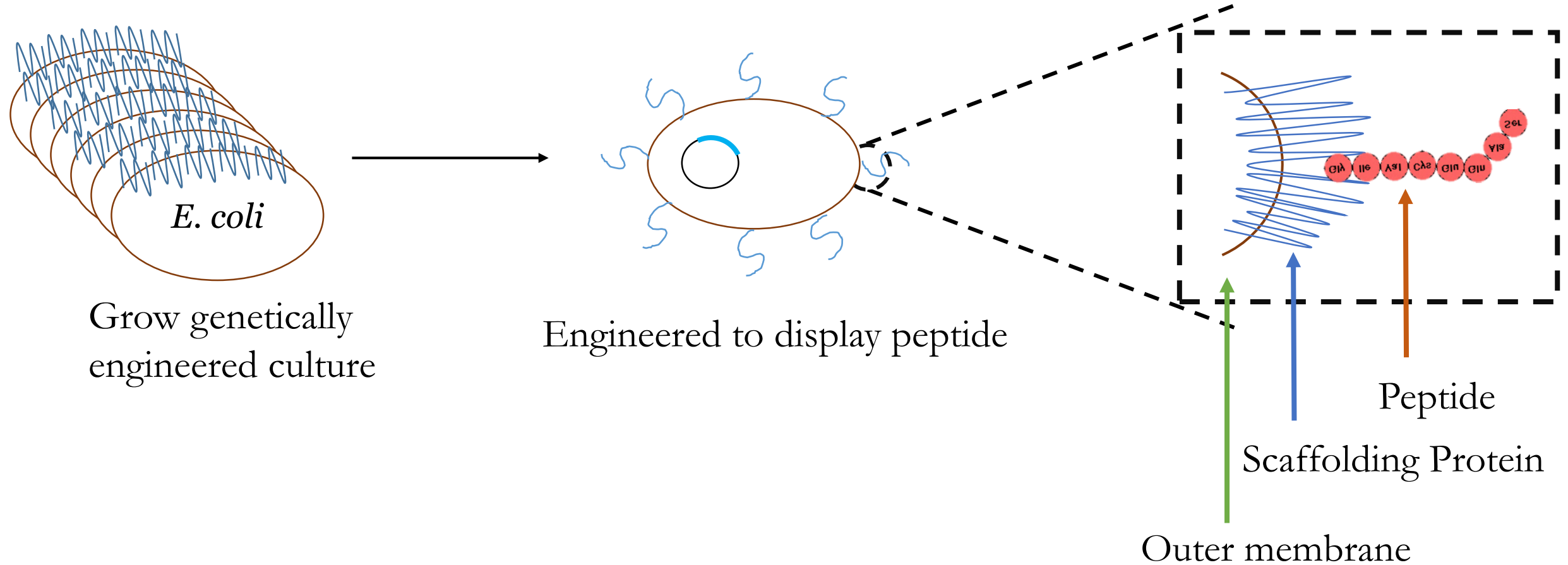


Isolate and sequence
these antibody-peptide interactions

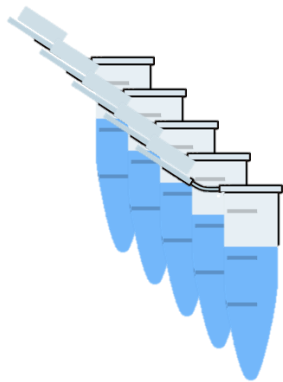
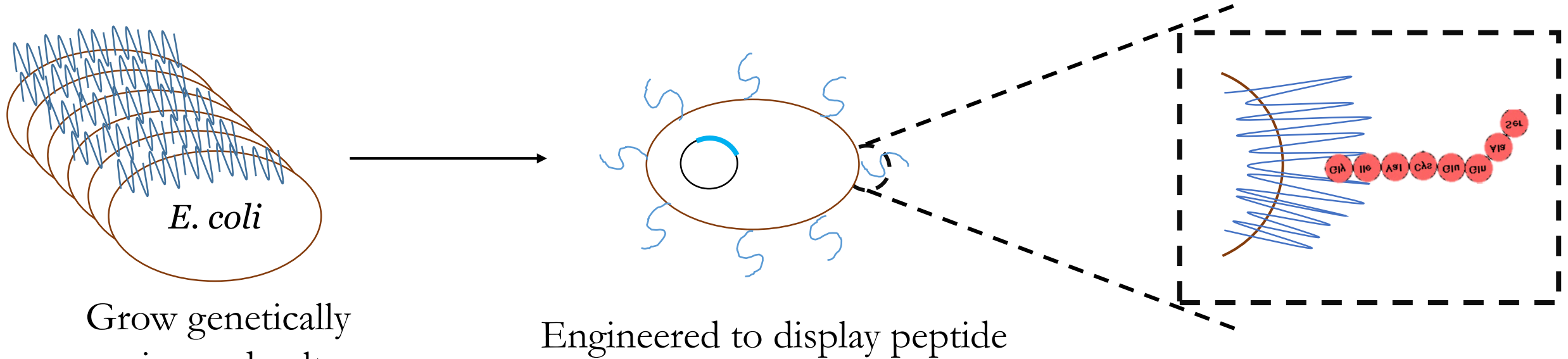
Deplete patient's serum of antibodies that would naturally bind to *E. coli* cells



Combine patient's serum with a vast library of peptides and magnetically separate cells that bound to antibodies



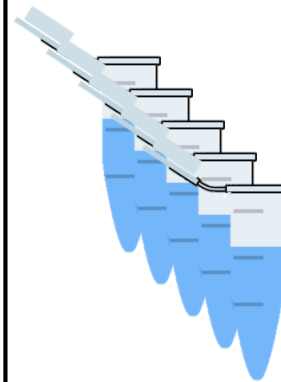
Combine patient's serum with a vast library of peptides and magnetically separate cells that bound to antibodies



Primary Binding Event:

- Peptide Library
- Patient Serum

- Incubate 45 minutes

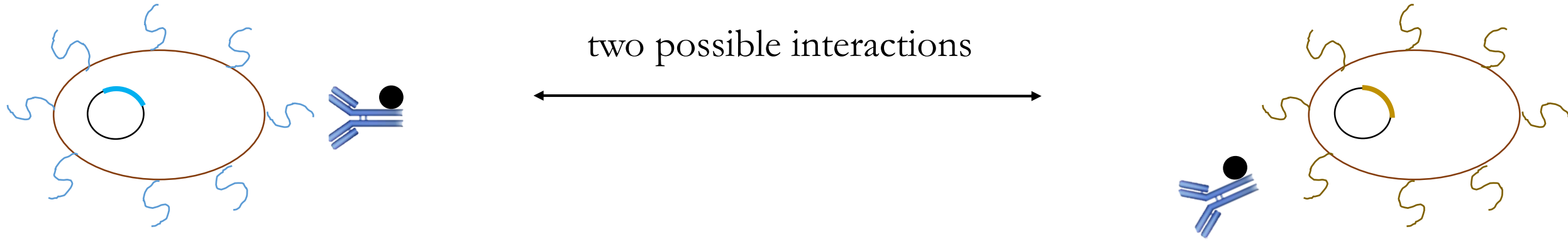


Secondary Binding Event:

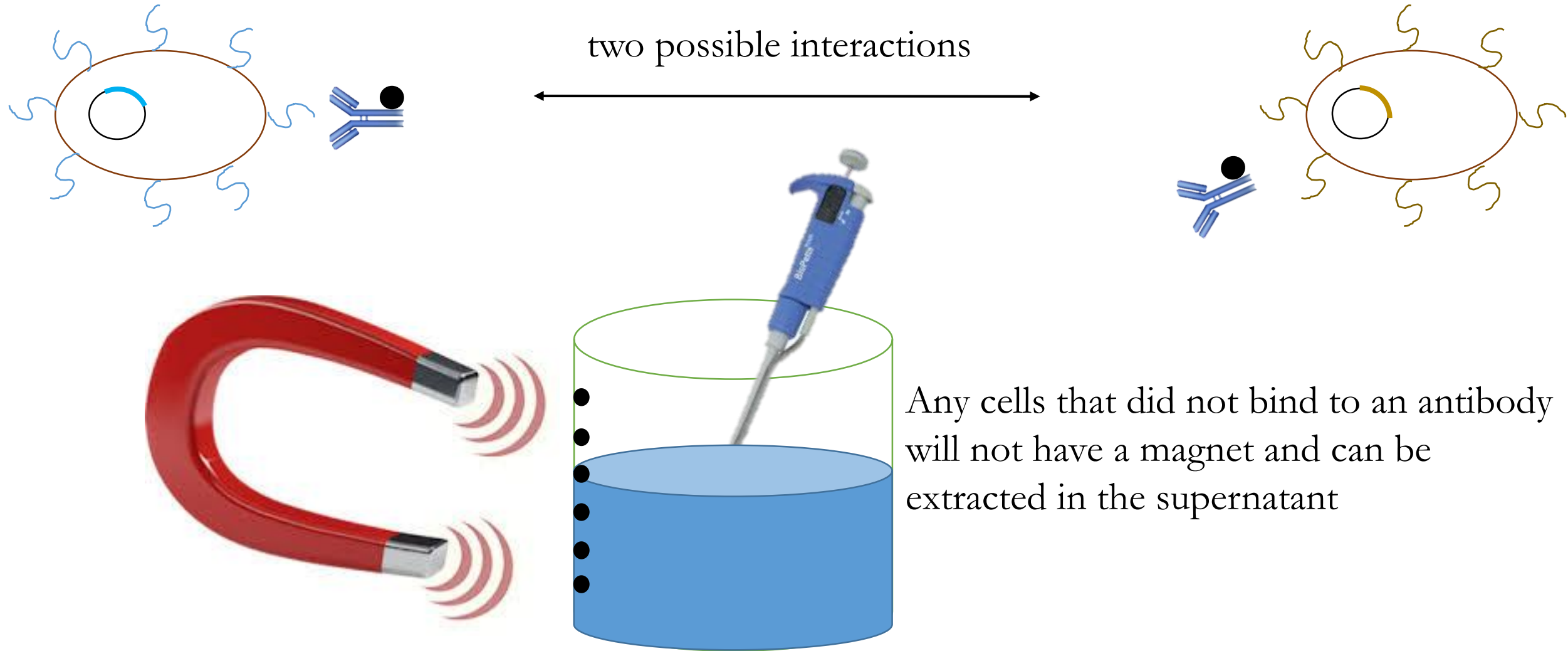
- Peptide Library
- Patient Serum
- Magnetic Beads

- Incubate 45 minutes

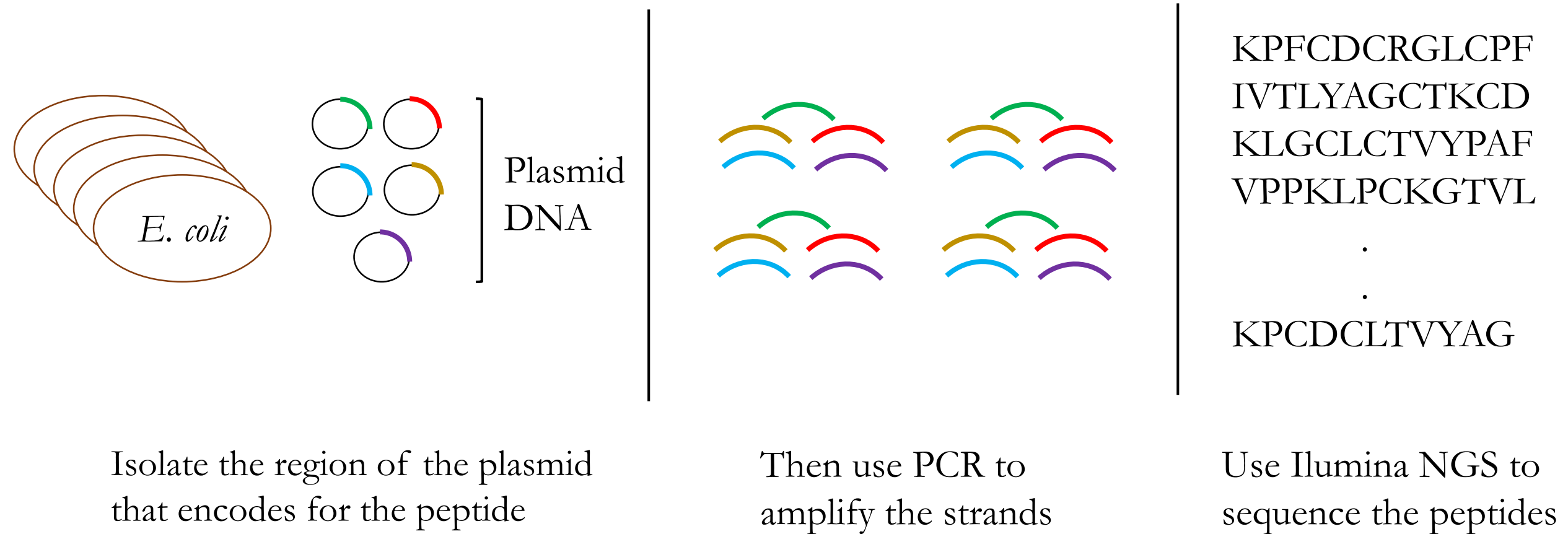
Separate cells that bound with antibodies from cells that didn't bind
to antibodies via magnetic separation



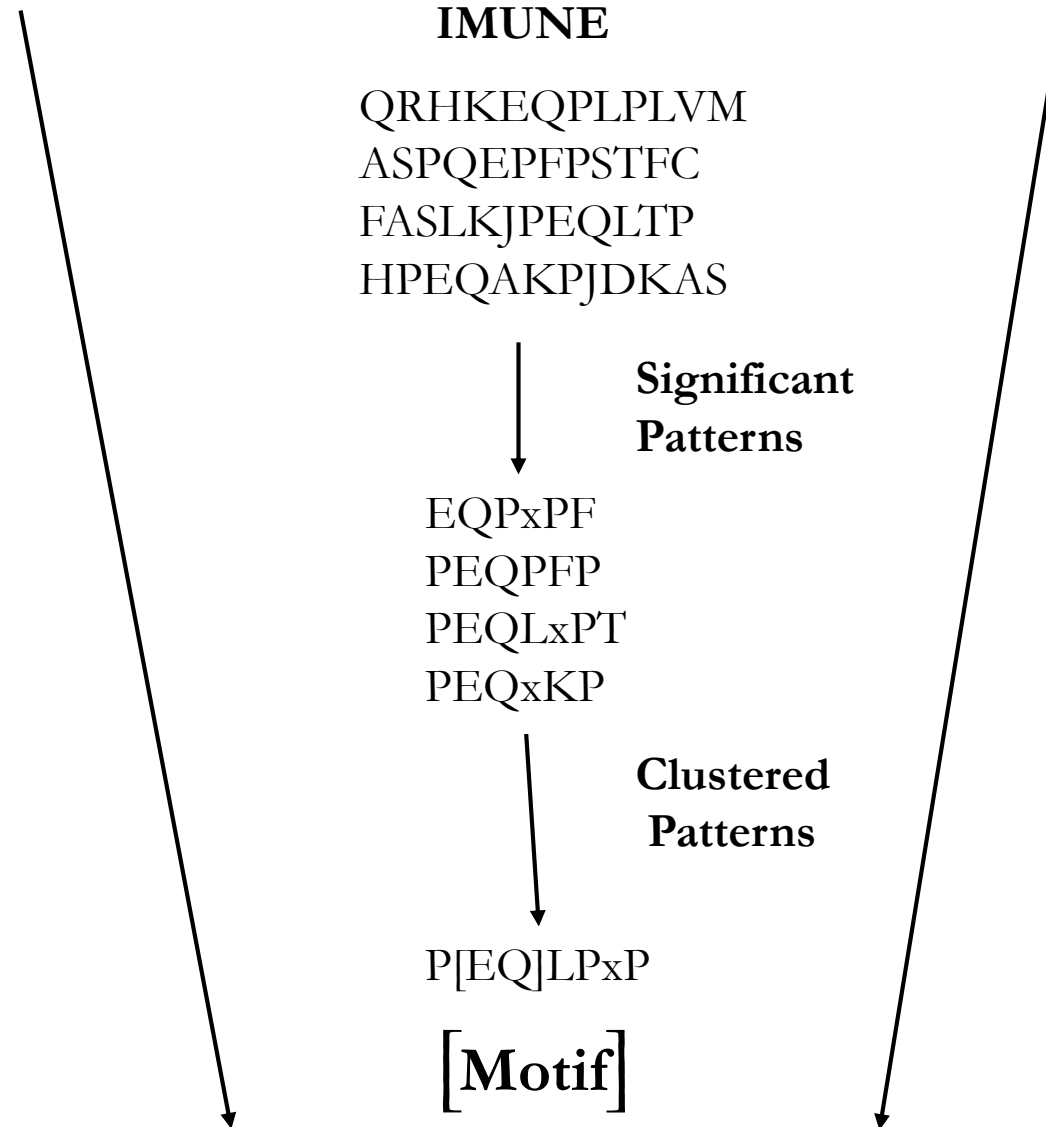
Separate cells that bound with antibodies from cells that didn't bind to antibodies via magnetic separation



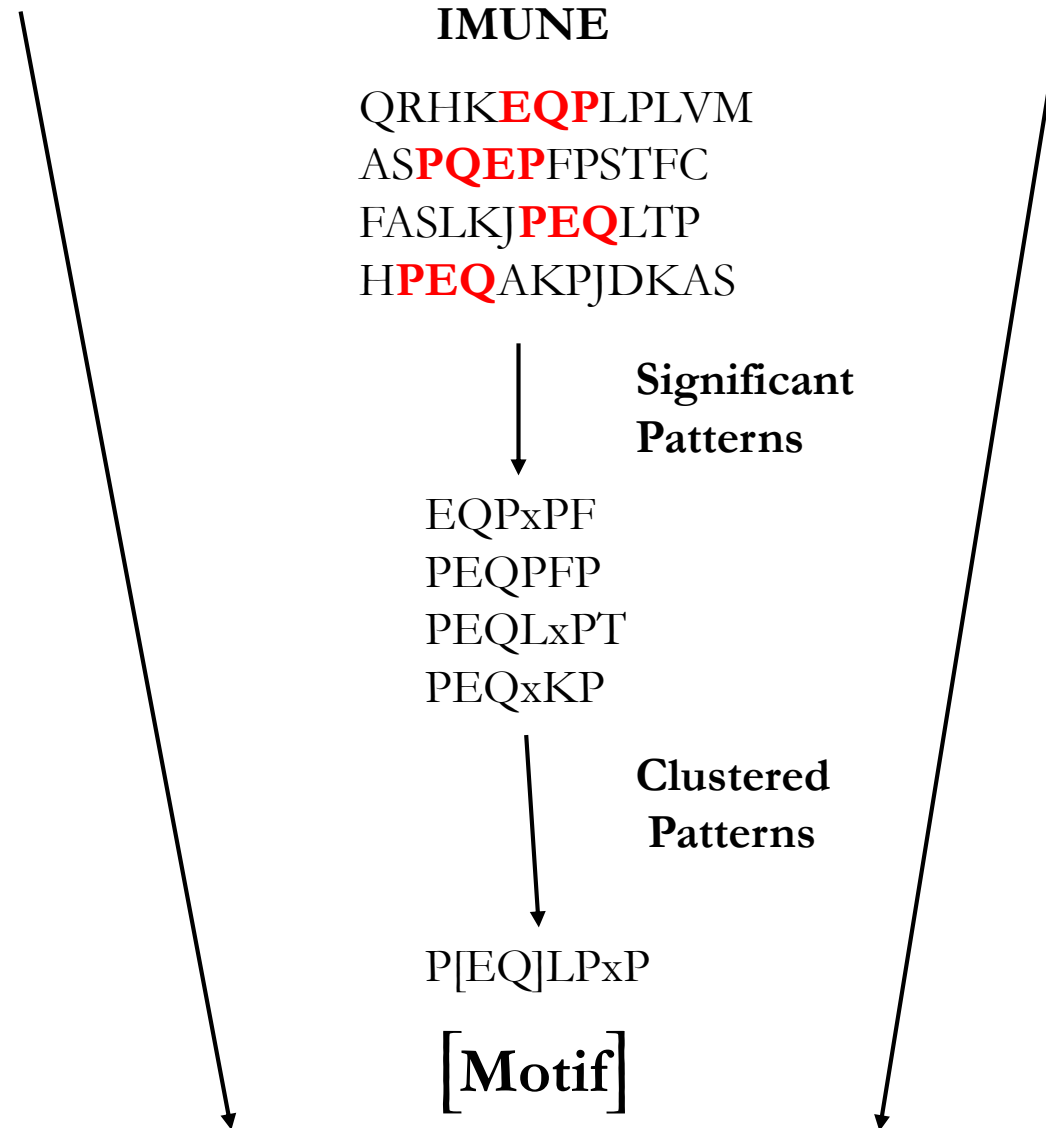
Isolate library DNA so that the peptide can be sequenced and the genetic information accessed



Process the data by converting peptide sequences
into amino acids using bioinformatics



Process the data by converting peptide sequences
into amino acids using bioinformatics



Assess the data by organizing patients into groups
and comparing groups for unique sequences



Group 1:

Diseased Patients

AVCDCFWPRPGW
YEPWRDGFVDCG
HWFLSGHEQGWF
YEPTPWVFKLMF
WPRPGWRDFVDC
HRVGREPCDCWH

List of epitopes

Group 2:

Healthy Patients

HRVGREPCDCWH
KCDCVLPFWHRT
YEPTPWVFKLMF
AVCDCFWPRPGW
TVYALPCDCMFH
CPLFMAHDCDWL

List of epitopes

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Group 1:

Diseased Patients



AVCDCVALWPGW
YEPWRDGFVDCG
HWFLSGHEQGWF
YEPTPWWFKLMF
WPRPGWRDFVDC
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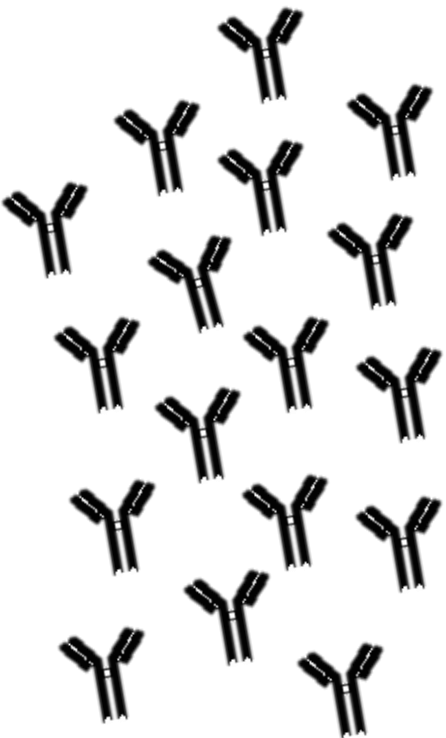
HRVGREPCDCWH
KCDCVLPFWHRT
YEPTPWWFKLMF
AVCDCVALWPGW
TVYALPCDCMFH
CPLFMAHDCDWL

Comparison Algorithm



Group 2:

Healthy Patients

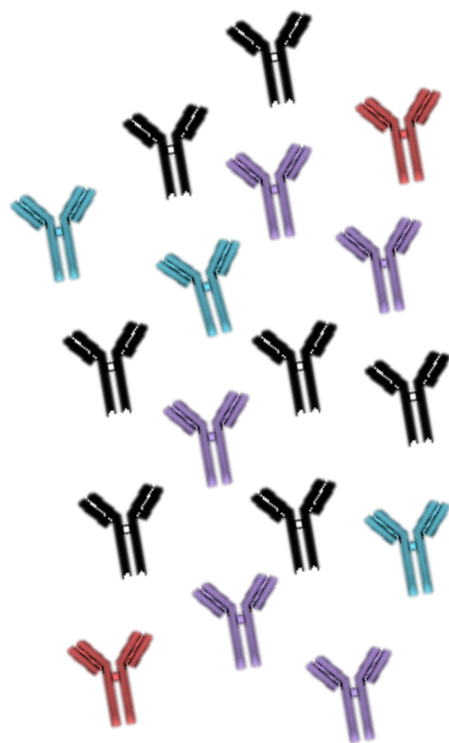


Assess the data by organizing patients into groups
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Diseased Patients



AVCDCVALWPGW
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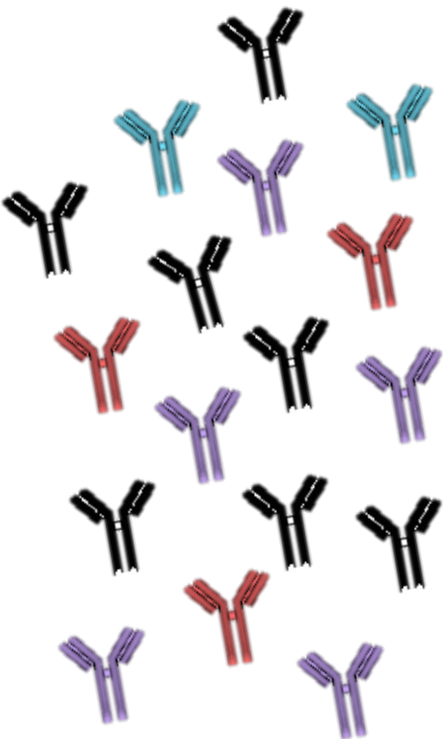
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KCDCVLPFWHRT
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AVCDCVALWPGW
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Comparison Algorithm



Group 2:

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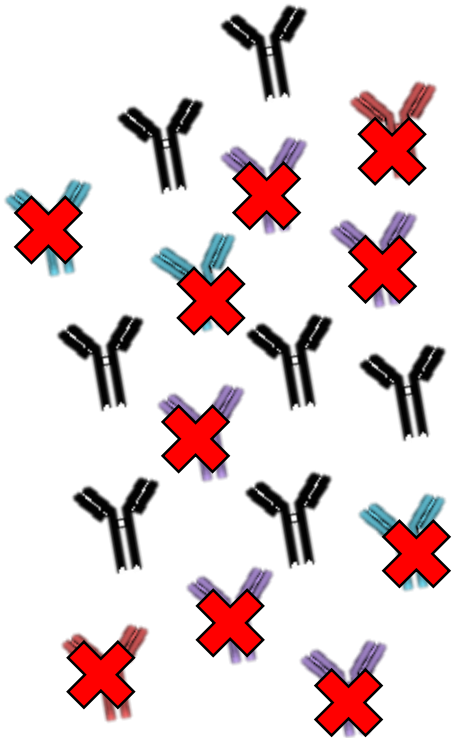


Assess the data by organizing patients into groups
and comparing groups for unique sequences



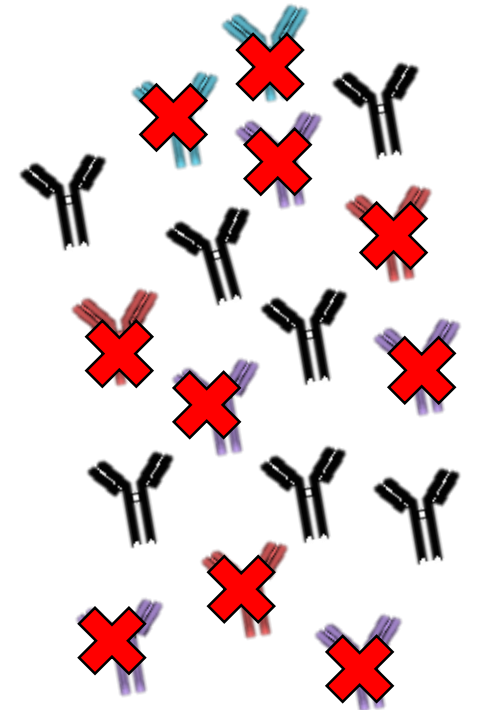
Group 1:

Diseased Patients



Group 2:

Healthy Patients



AVCDCVALWTPGW	HRVGREPCDCWH
YEPWRDGFVDCG	KCDCVLPFWHRT
HWFLSGHEQGWF	YEPTPWWTFLMF
YEPTPWWTFLMF	AVCDCVALWTPGW
WPRPGWRDFVDC	TVYALPCDCMFH
HRVGREPCDCWH	CPLFMAHDCDWL

Comparison Algorithm

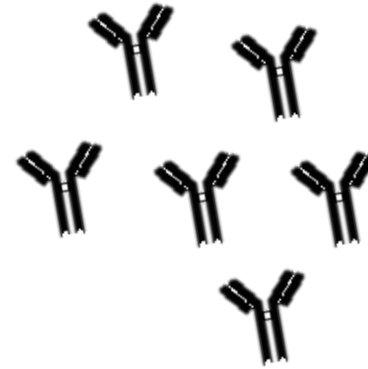
Assess the data by organizing patients into groups
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Group 1:

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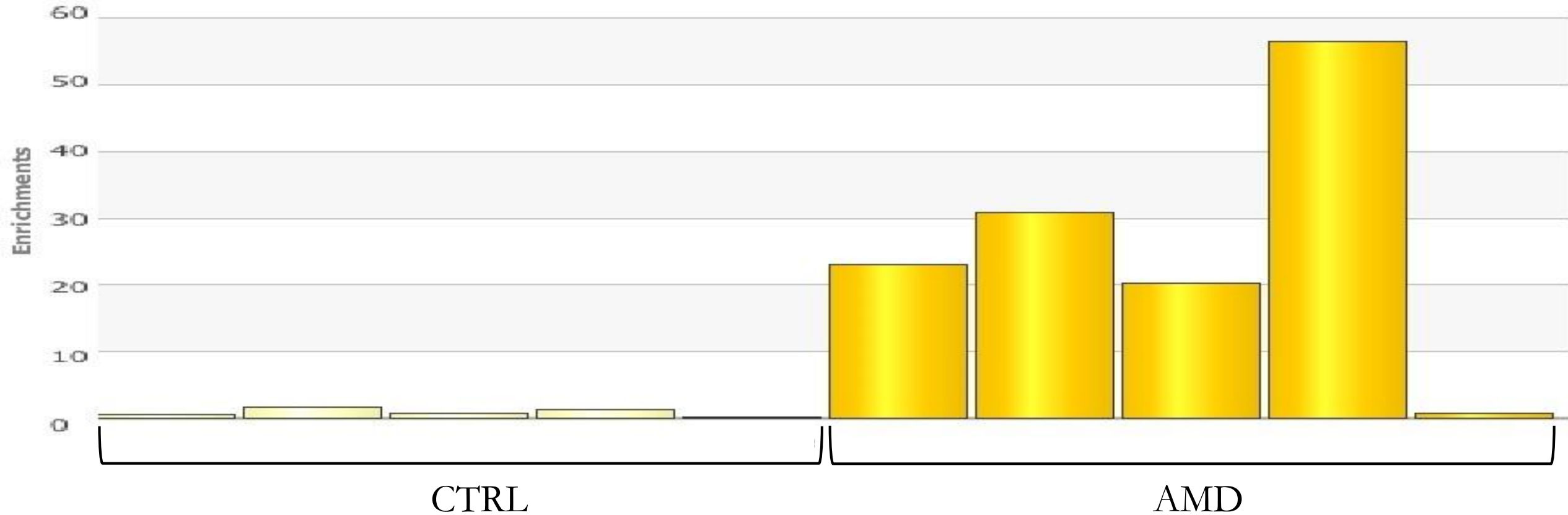


Potential disease specific epitopes/antibodies

Compare motif enrichment across patients to find AMD-specific reactivity

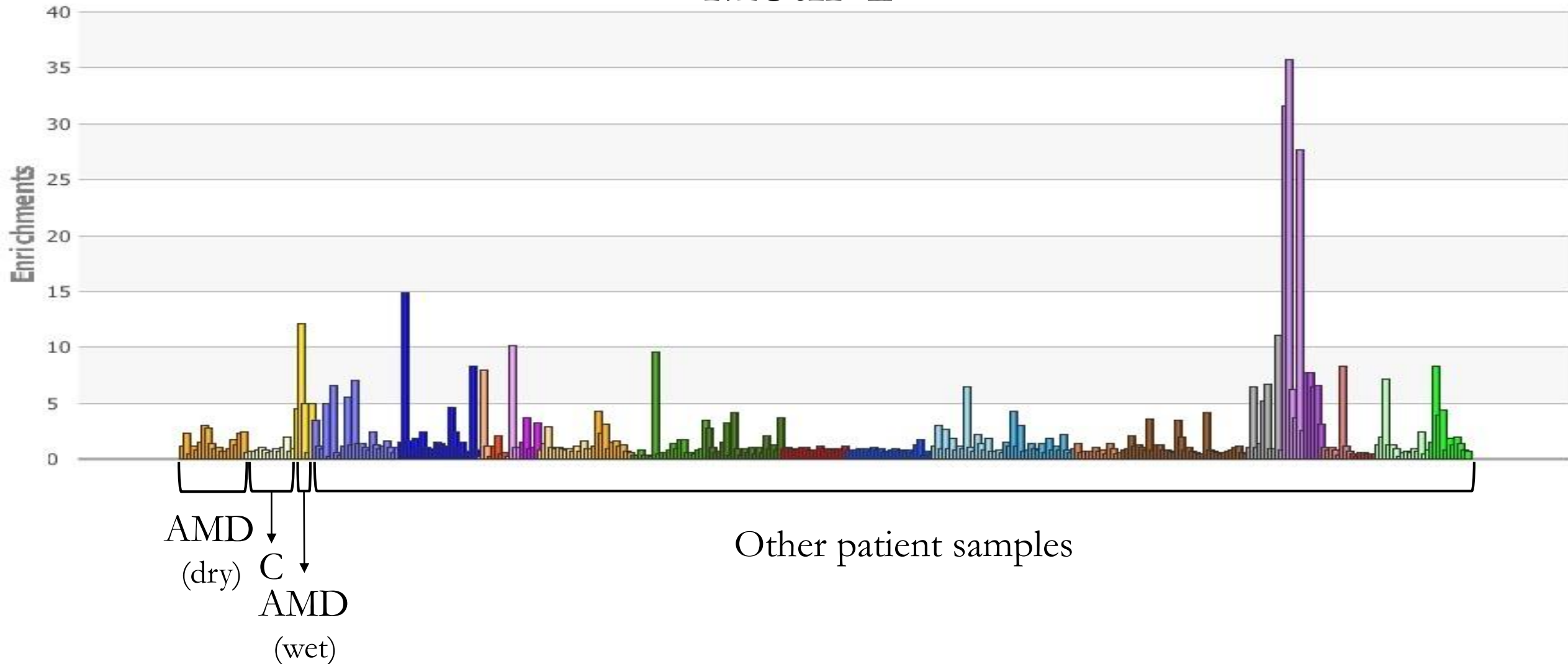
Enrichment =
Observed/Expected

Motif 1



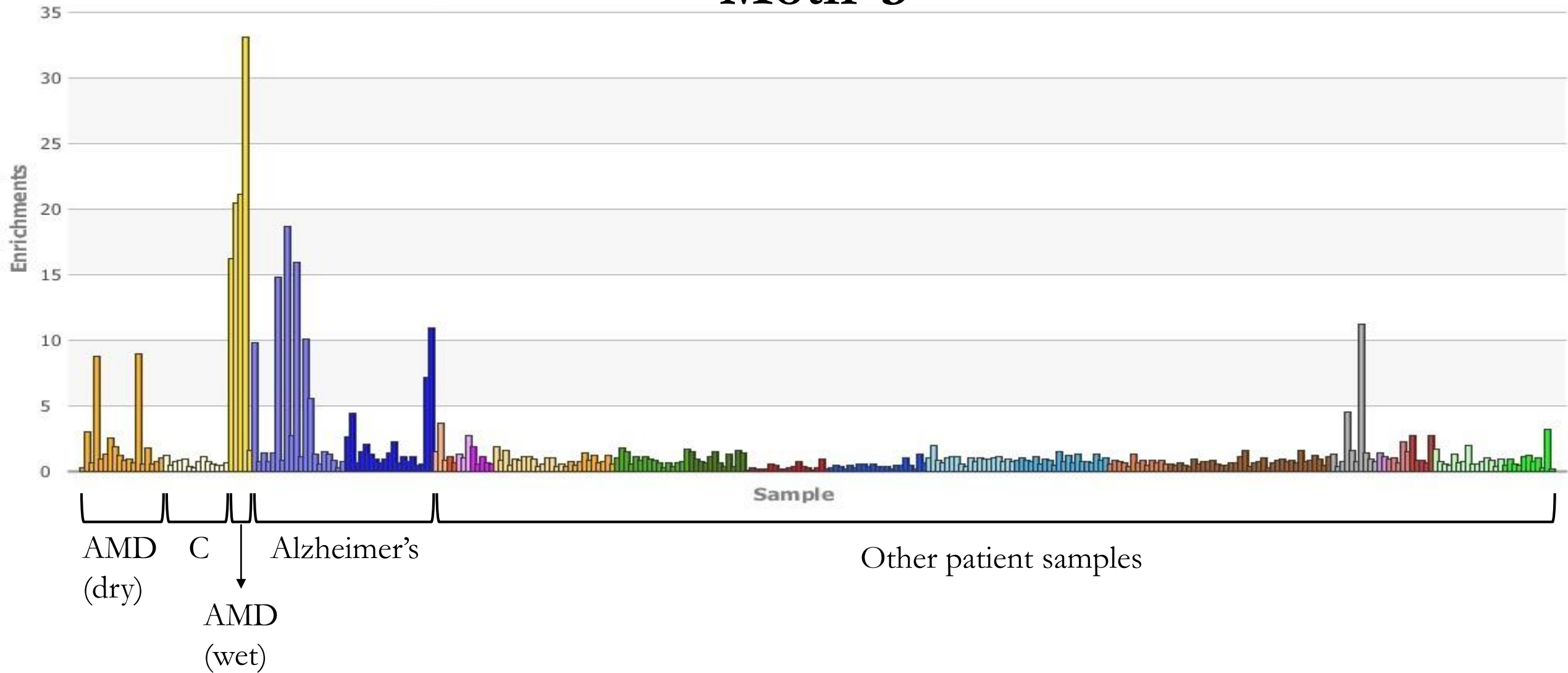
Utilizing the database allows us to eliminate motifs that appear
AMD specific but are enriched in other samples

Motif 2



Interesting motif that shows potential AMD specificity

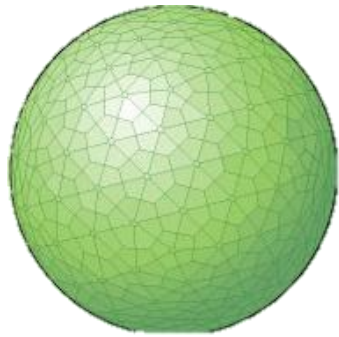
Motif 3



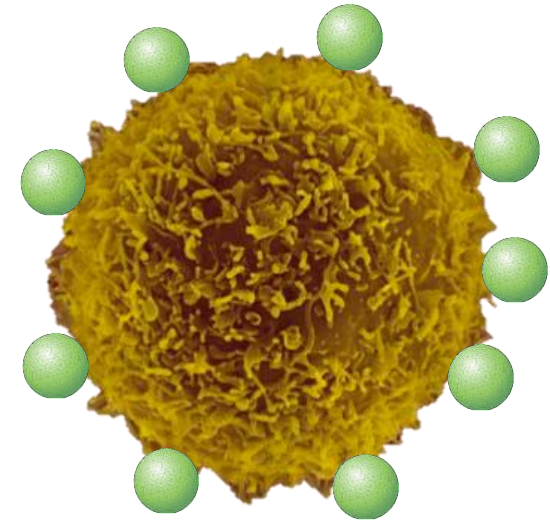
Use protein databases, BLAST, to search for a possible antigen for the peptide

Antigen-to-Protein Identification

Epitope for Human Rhinovirus: ExLVVPNI



Capsid
(antigen)

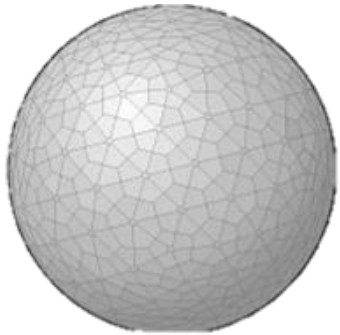


Rhinovirus
(common cold)

In the future we hope to discover a primary candidate disease specific epitope

AMD motif candidate

-Currently not close to realistically searching this database for a protein that is specific to AMD



Unknown Antigen



Acknowledgements

Gorman Program

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- Joel Bozekowski
- Michael Paul

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- Arica Lubin
- Kelly Ibsen
- So many more

