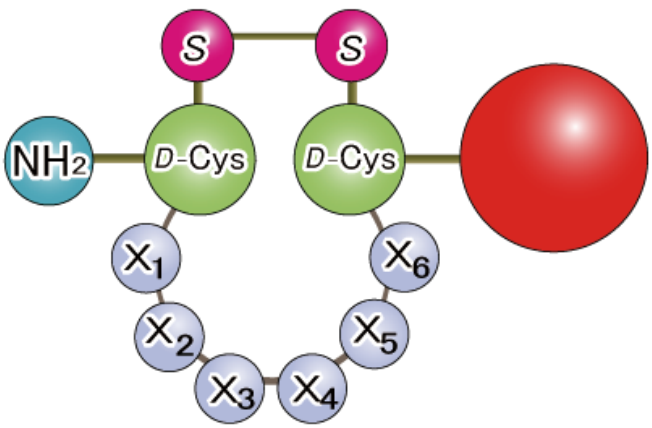
High Quality One cyclic Peptide immobilized on One Bead (OPOB)



Discovery for interacting Sequences

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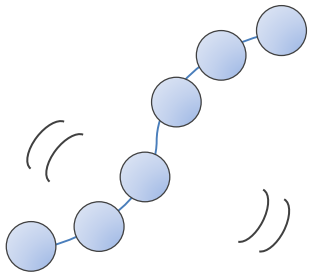
Background

Cyclic peptides library, immobilized on gel-type polymer support, is a reagent for discovery of the sequence that binds to the target molecule.

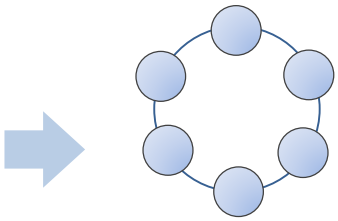
Current deconvolution method for the screened beads is Edman degradation, which is low throughput and free amino terminus is indispensable. Thus we have newly developed a higher throughput method by mass spectrometry in combination with the partial hydrolysis (protocols are in preparation).

Basic architecture of the Peptide-Bead

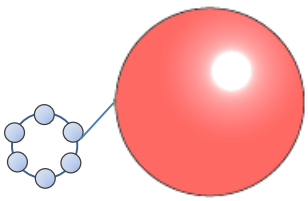
The peptide-beads consisting as the hexamer, constructed by 19 natural and 5 non-proteinogenic amino acids, with two *D*-cysteines to form an intra-molecular disulfide linkage (cyclized).



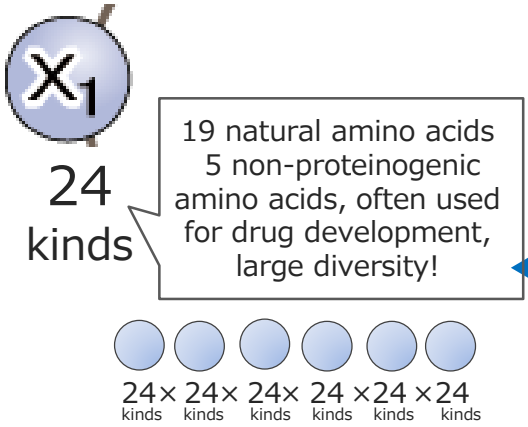
Linear peptide, very flexible structures



Rigid structures (expected higher affinities in recognition); Generally recognition requires 3-4 residues, although 3D structures are indispensable.

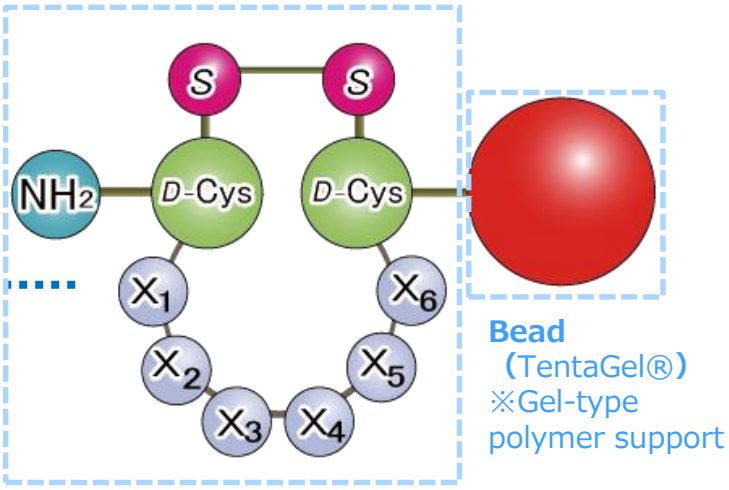


Peptides are immobilized on gel-type-polymer, thus allows assay in aqueous media, easier screening and picking up



Diversity of the sequence

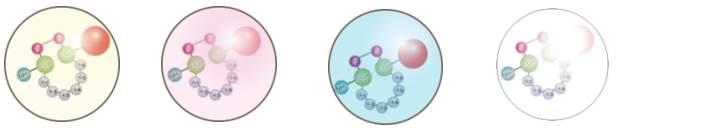
24^6 = **200 millions**



Architecture of immobilized Peptides

※Both termini of hexapeptides two *D*-cysteines are attached and cyclized, preventing enzymatic degradation during assays

Proteins or cells (cell-surface proteins) are recognized, which can be picked up through screening (assays) and deconvoluted.



Sequence A Sequence B Sequence C Sequence D ···

About 200 millions ways

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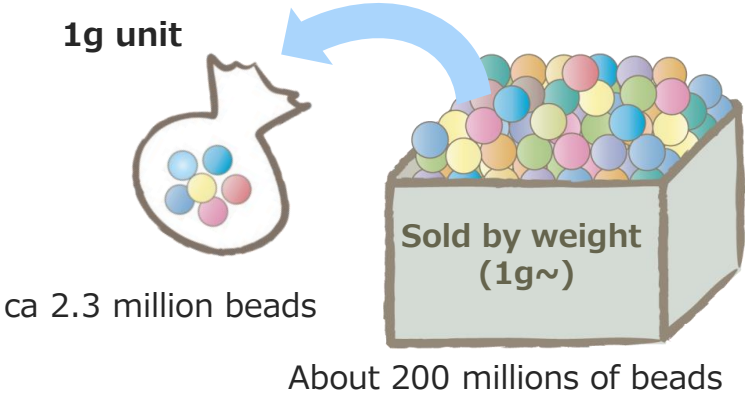
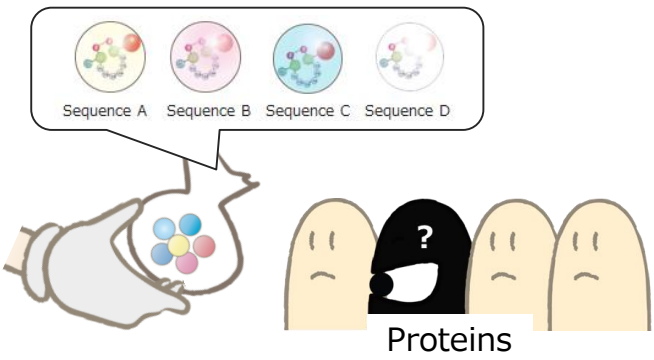
Offer

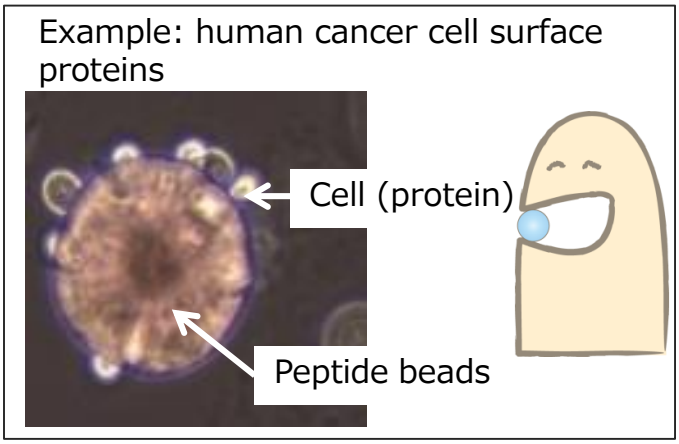
- Min. sales unit: 1 gram beads (equivalent to the dry weight) swelled in aqueous media containing *ca.* 2.3 million beads carrying 2.3 millions of high quality of cyclic octapeptides.

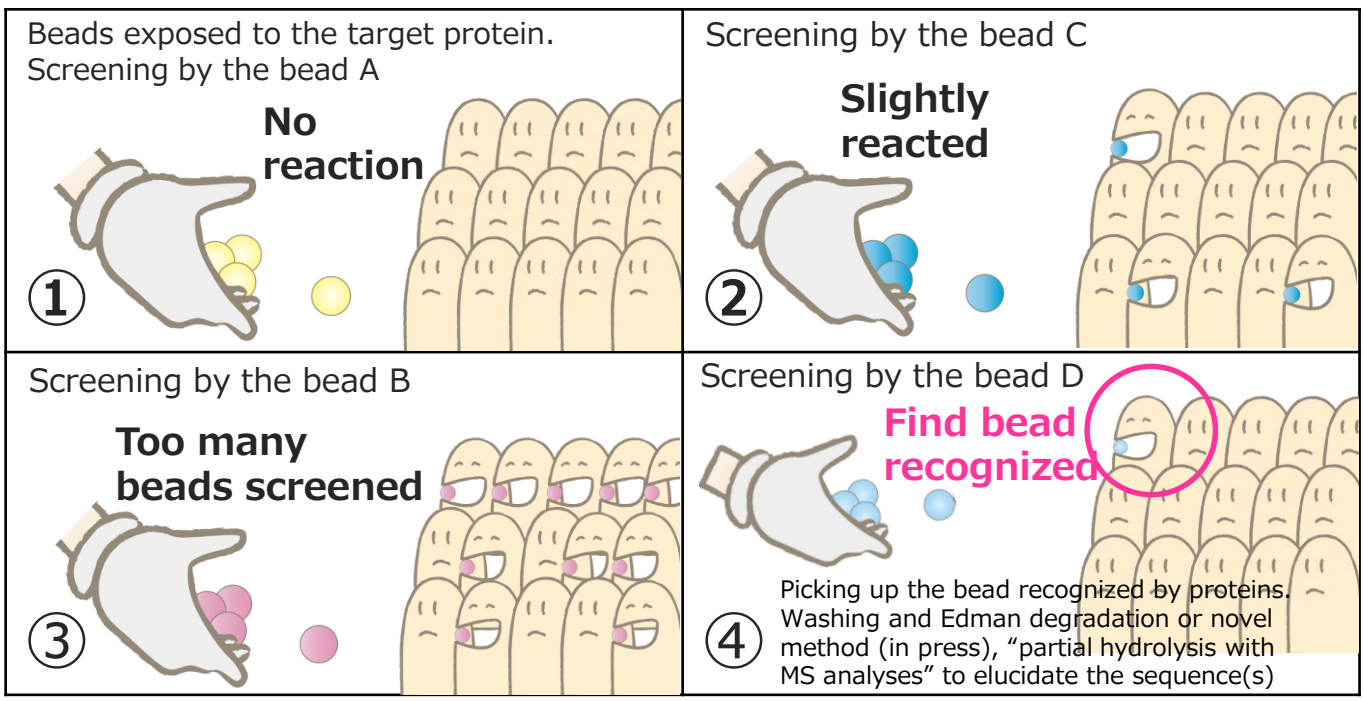


Screening and selection (Image)

Discovery of interacted of recognized beads → picking up → washing → deconvolution (sequence elucidation)



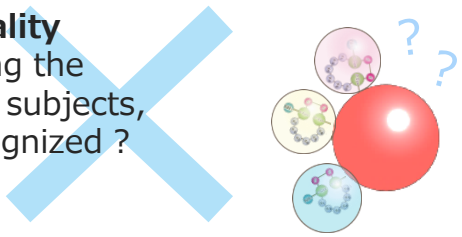




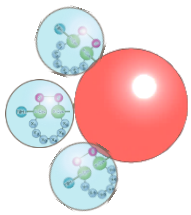
Points

- **Resistant to enzymatic degradations during assays**
  - No inter-molecular cyclization (disulfide).
  - Two *D*-Cys for intra-molecule cyclization.
  - They are atable against endogenous enzymes.
- **High quality: thorough SPLIT & COMBINE procedure allow facile and higher-precision for deconvolution**
  - The polymer support used was gel-type TentaGel ®, swollen in aqueous media and lower non-specific absorption of proteins.
  - Contamination free Cyclic peptides immobilized on beads with the concept of One Peptide on One Bead (**OPOB**).

Conventional mixture: Lower quality
Even finding the interacting subjects, Really recognized ?



High quality OPOB
Immediately find recognition and sequence information



Representative references

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Ito H., Nokihara K., Soutome S., Ohyama T. Screening of peptides that inhibit bacterial binding to fibronectin using combinatorial peptide libraries. Int. J. Pept. Res.Ther. 2006, 12, 275-281.

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