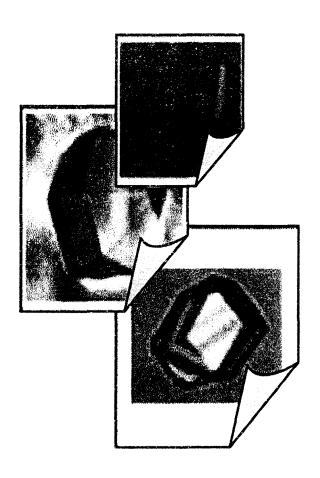
PROTEIN STRUCTURE

NEW APPROACHES TO DISEASE AND THERAPY



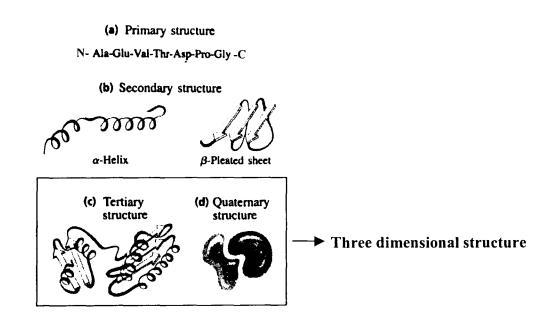
선임연구원 차선신



DNA => Protein

Proteins are composed of 20 amino acids that are connected chemically through amide bonds

The Structure of Proteins is Hierarchical



Protein Engineering

- change amino acids at specific positions in proteins

Asp => Asn : point mutation

Insertion of one to several amino acids

Deletion of one or several amino acids

- make mutant proteins with designed biological characteristics

APOPTOSIS

Two kinds of death in cells

Death by injury – serious effects on life

Cells that are damaged by injury, such as by

- •mechanical damage
- •exposure to toxic chemicals

Death by suicide (programmed cell death or PCD. Apoptosis)

- 1. proper development.
- 2. destroy cells that represent a threat to the integrity of the organism Examples-

Cells infected with viruses
Cells of the immune system
Cells with DNA damage
Cancer cells

Cancer Immunotherapy

- 1. Various immune responses to tumor cells
- 2. Not sufficient to prevent tumor growth
- 3. Augment or supplement natural defense mechanisms <= safe cancer treatment

-190-

Cytokine Therapy

(Many of the bio-venture companies)

- 1. Interferons
 - strengthen immune defense system
- 2. Tumor Necrosis Factor- α (TNF- α)
 - directly kills cancer cells : today's topic

Limitations of TNF-α therapy

- 1. Short half-life necessitates frequent injections
- 2. Adverse side effects: fever, chills, blood-pressure changes, and decreased counts of white blood cells
 - => death of normal cells

The search for a cytokine that selectively affects tumor survival in humans without significant toxicity: *TRAIL*

Generation of thousands of TNF mutants with low toxicity and longer half-life: <u>M3S</u>

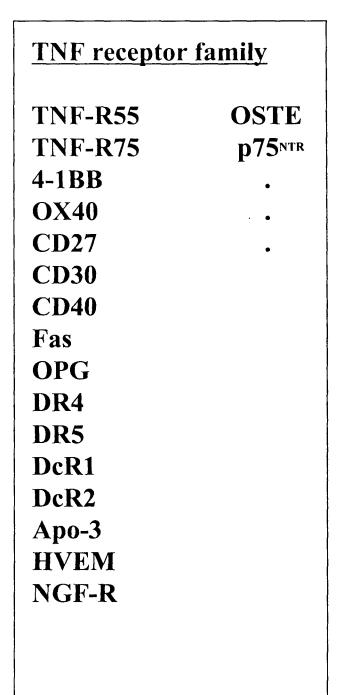
TRAIL belongs to TNF family, a rapidly growing superfamily that interact with a corresponding superfamily of receptors on cell surface

Ligand

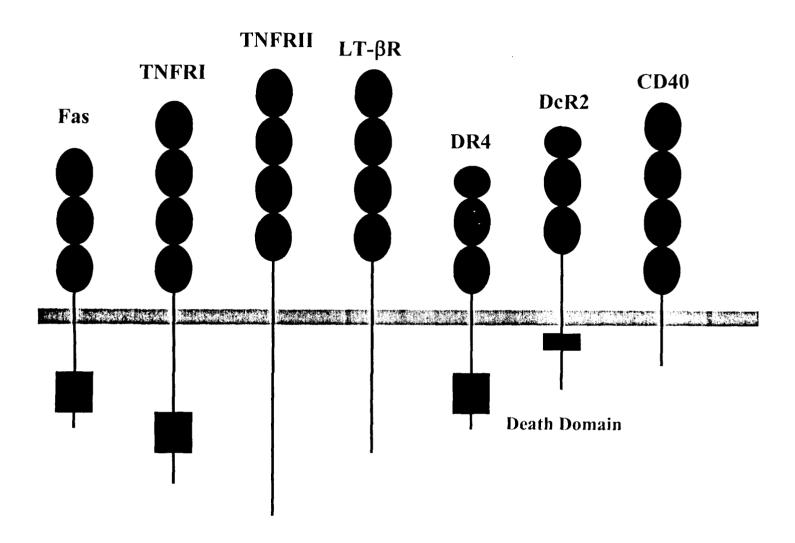
Receptor

TNF family

TNF-α TNF-β LT-β 4-1BBL OX40L CD27L CD30L CD40L **FasL OPGL TRAIL** Apo-3L **TWEAK LIGHT VEGI APRIL**



Signals are transduced through receptors from exterior to interior of cells after binding of ligand



From the structural analyses of TRAIL, TRAIL/DR5 complex, and a TNF-α mutant (M3S)

- 1. Insights into the specific recognition between proteins
 - all the biological processes are mediated by specific interactions between biomolecules
- 2. Rational design of mutants that are more suitable for safe anticancer agents
- 3. Structure-Function relationship
 - => structural genomics

Human TRAIL (Apo-2L)

TNF-Related Apoptosis Inducing Ligand.

Discovered in 1995 (Immunex, Genentech).

Immunex and Genentech have patent on TRAIL gene.

Induces rapid apoptosis in a variety of tumor cell lines.

But, normal cells are not killed by TRAIL.

Administration of TRAIL suppresses transplanted tumors in mice.

No cytotoxicity to normal tissues in vivo mouse and primate models "Magic bullet" so far.

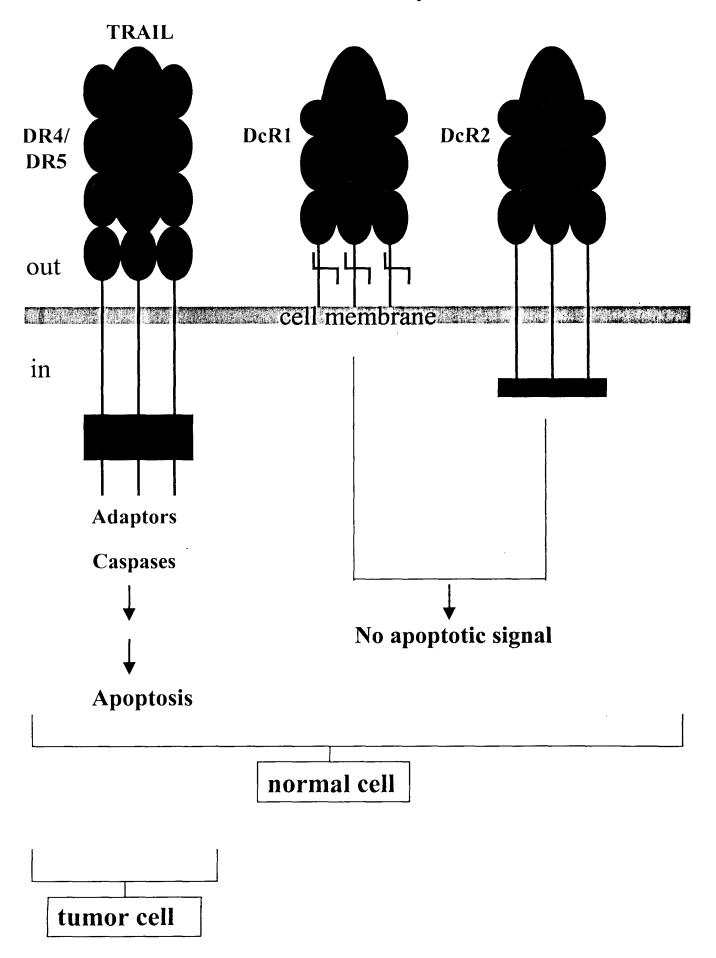
Under a clinical demonstration in U.S.A. (Immunex, Genentech).

Two signalling receptors are identified.

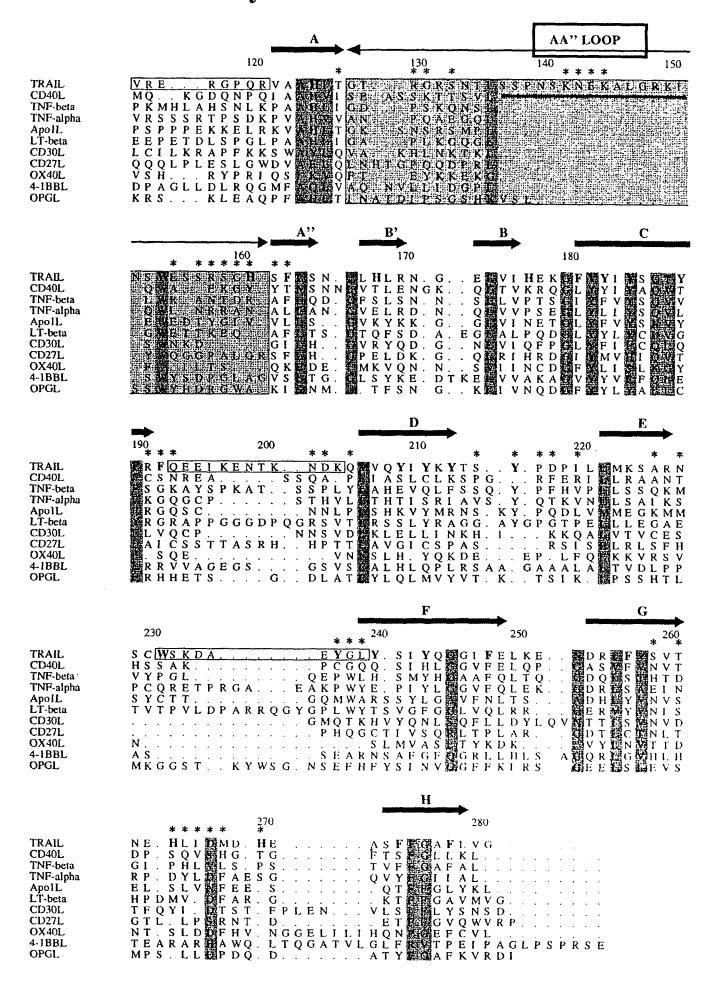
Two non-signalling decoy receptors are identified.

Decoys are mainly expressed in normal cells.

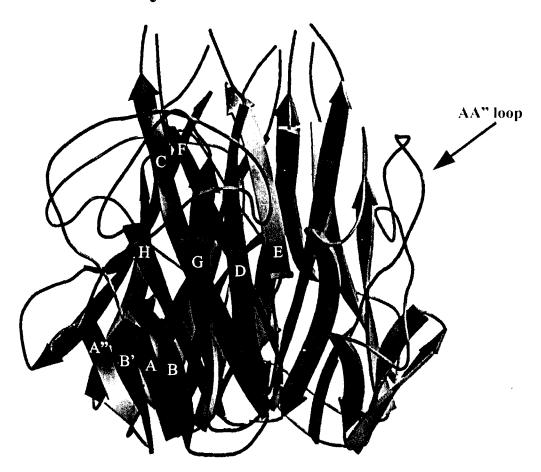
How does TRAIL selectively kills tumor cells



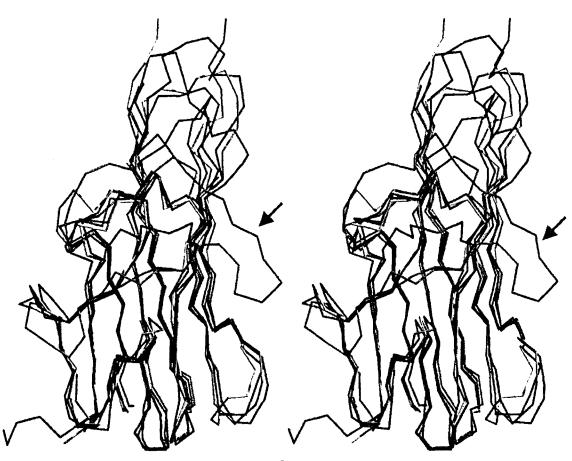
Primary structure of TRAIL

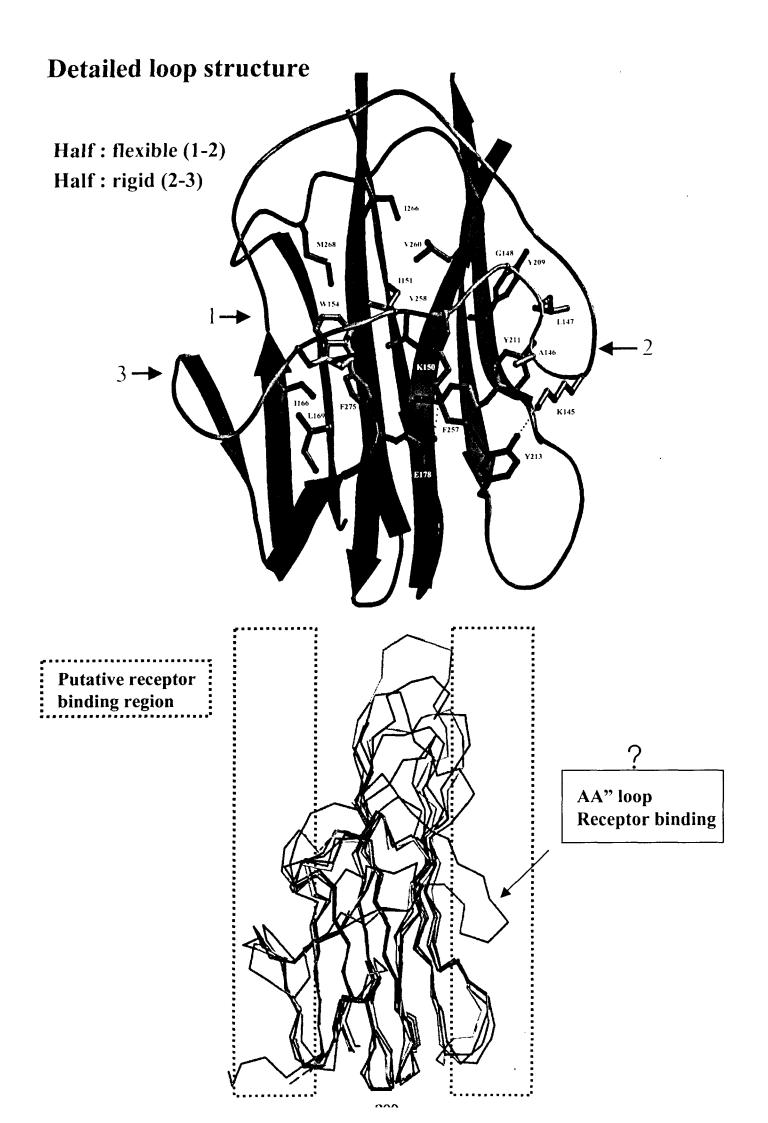


Tertiary Structure of TRAIL

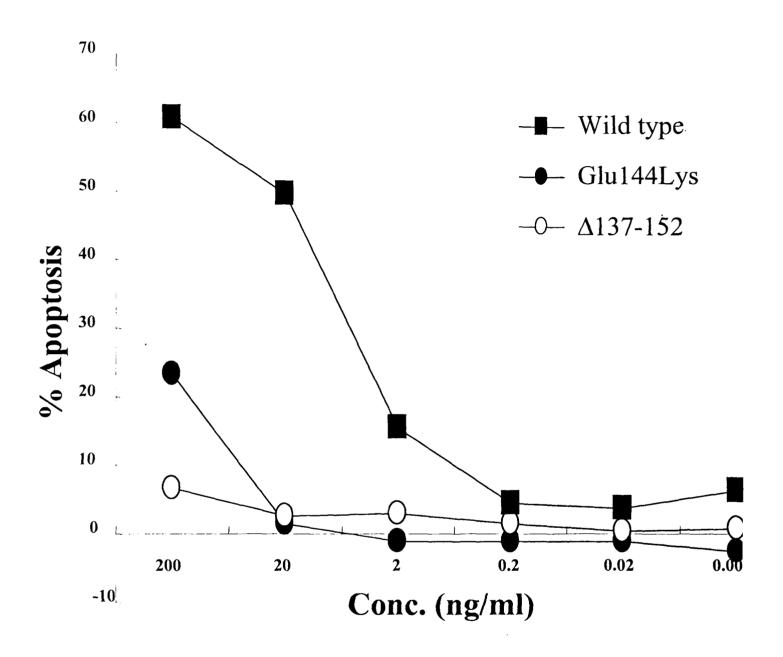


Homotrimeric structure





Mutations on AA" loop



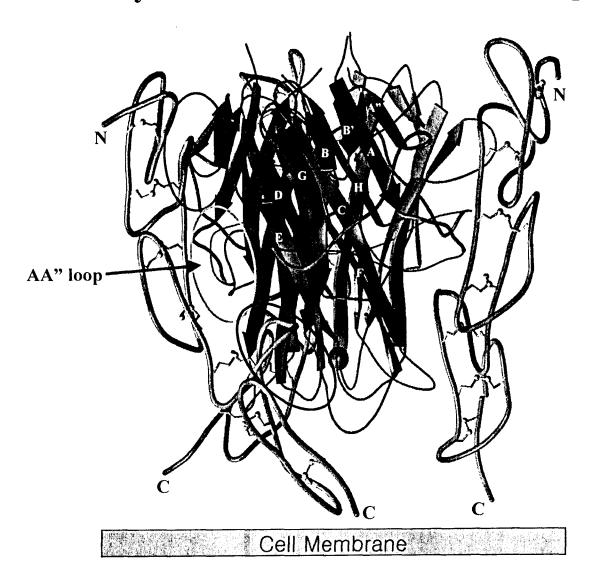
Indirect evidence of the engagement of the loop on the complex formation

Complete understanding of complex formation needs three dimensional structure of the complex

Crystallization of TRAIL/DR5 complex



Tertiary Structure of TRAIL/DR5 complex



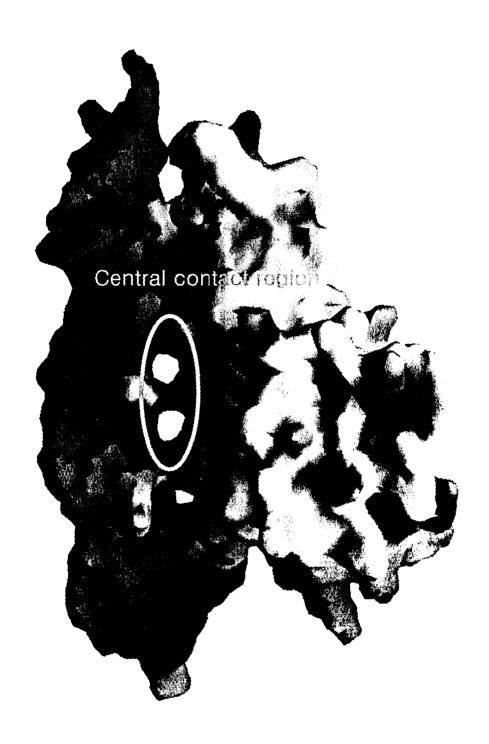
Contact region can be divided into three parts

- Upper, Central, and Lower contact region

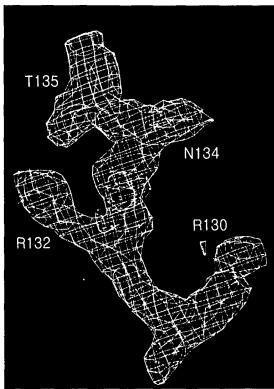
Central Contact Region

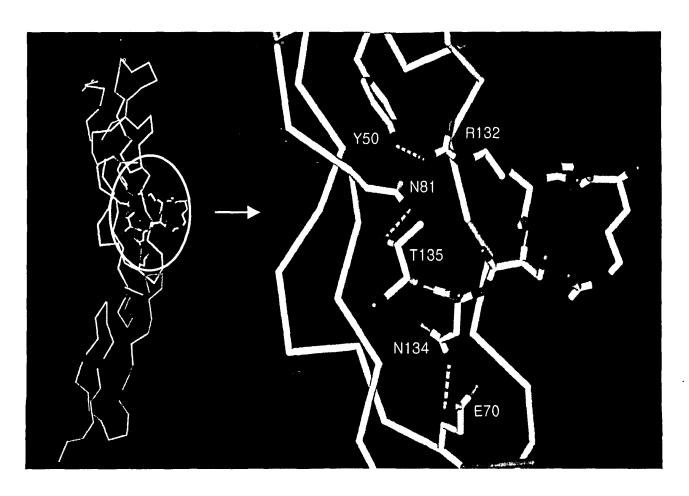
- Involvement of AA" loop in complex formation

Central Contact Region

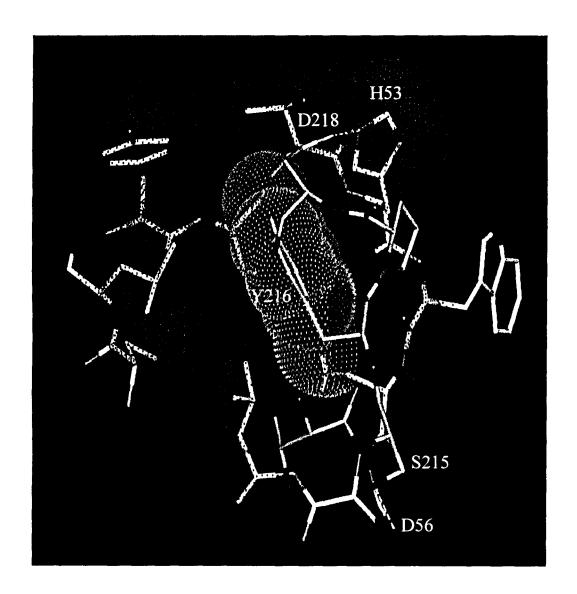








Upper Contact Region



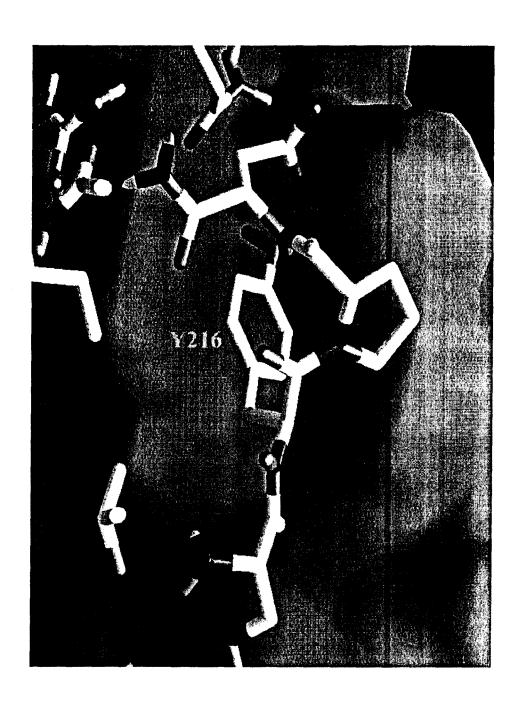
Polar Interactions:

S215 (TRAIL) - D56 (sDR5) D218 (TRAIL) - H53 (sDR5)

Van der Waals surfaces:

Y216 (green dot) fits snugly into a cavity of sDR5 (violet dots)

The protrusion of Y216 into a Small Cavity on DR5



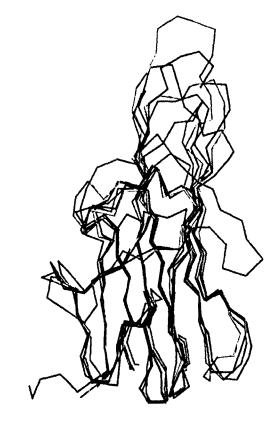
Lower Contact Region



Structural similarity between members

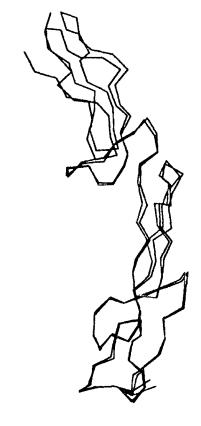
1. Structural similarity between TNF members

TNF-α TNF-β CD40L TRAIL



2. Structural similarity between TNF members

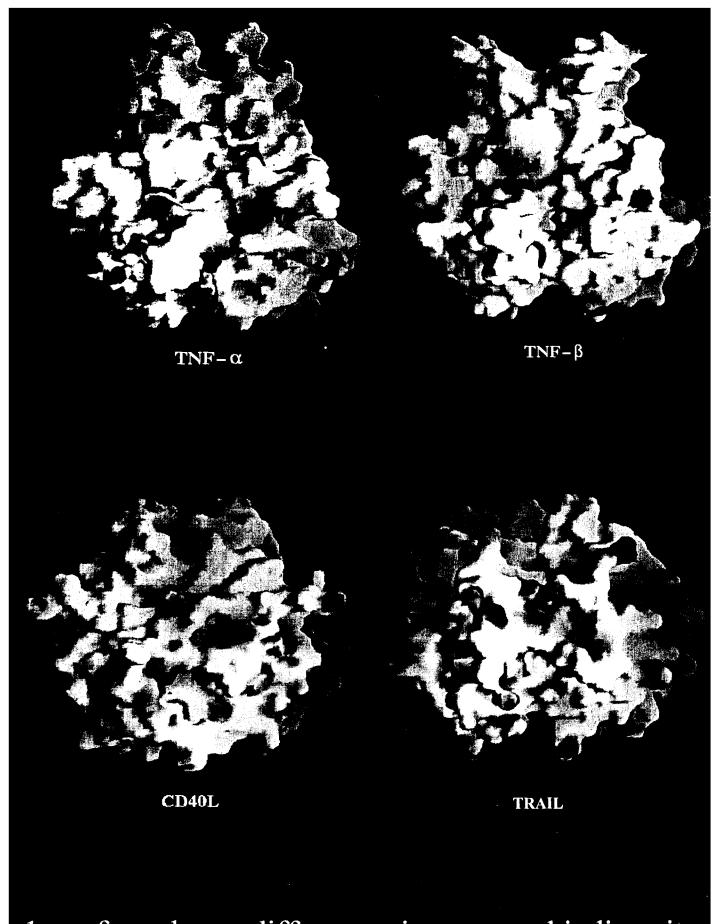
TNFRI DR5



Then, how does specific recognition occur?

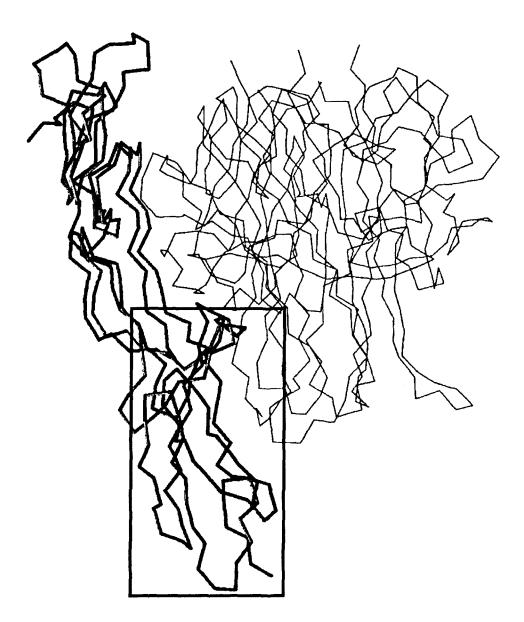
TNF family		TNF receptor family	
TNF-\alpha TNF-\beta LT-\beta 4-1BBL OX40L CD27L CD30L CD40L FasL OPGL TRAIL Apo-3L TWEAK LIGHT VEGI APRIL :	Specific Recognition	TNF-R55 TNF-R75 4-1BB OX40 CD27 CD30 CD40 Fas OPG DR4 DR5 DcR1 DcR2 Apo-3 HVEM NGF-R	OSTE p75NTR

Insights from the structures



2. flexibility of receptor structure

Superposition of TNF/TNFRI and TRAIL/DR5 structures

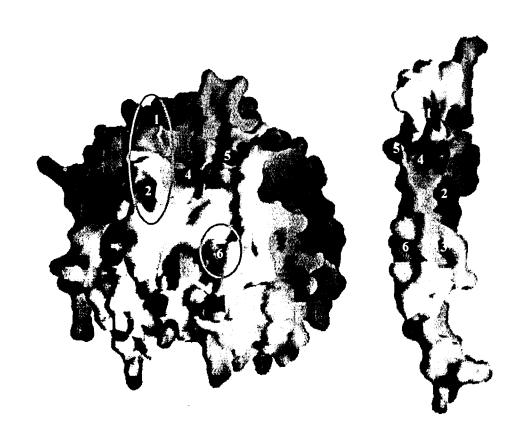


After complex formation, this region Undergoes conformational change

- 3. Insertion of several amino acids into receptor binding site
- generation of new interaction

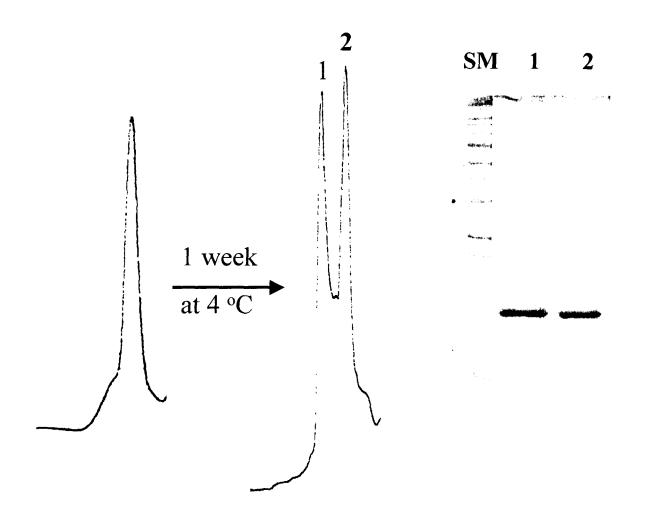
As a results of 1,2, and 3, each pair exhibits exellent electrostactic and geometric complementarity

Ex) TRAIL/DR5 complex



Structures provided ideas in designing mutants that are more suitable for anticancer drugs

Instability of TRAIL trimer



Change of oligomeric state of TRAIL

Trimer => not Trimer (active)

Retention of trimeric conformation of TRAIL is important in cancer treatment

In vivo efficacy test

Immunex

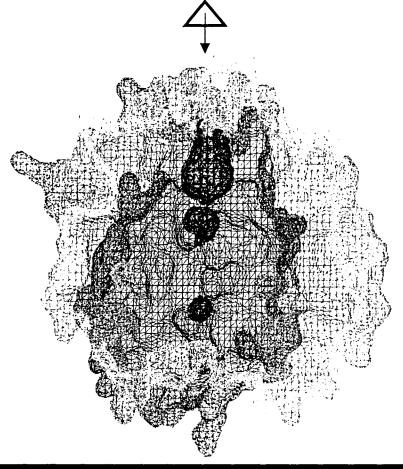
Leucine zipper-TRAIL

- stabilization of trimer

Genentech

Native TRAIL injection of 15 mg/kg

Cavities along the 3-fold axis





Cavity =>
no contact between monomeric TRAILs =>
decreased stability of trimeric TRAIL

Mutations that can fill the cavities

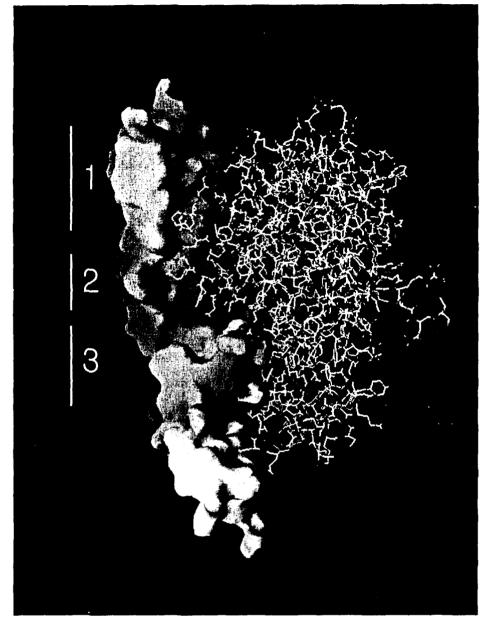
- \Rightarrow stabilize trimeric conformation
- ⇒ Increased therapeutic efficacy

Mutants that are more active => strong binding to receptor

Upper

Central

Lower



1. Tyr
$$\underset{\text{tyr y Tyrosin}}{ \text{HO}} => \text{Trp}$$
 $\underset{\text{trp w Tryptophan}}{ \text{hohology}}$

2. elongation of AA' loop by insertion or cutting the loop