Tilings and networks

LIP6, Paris

R. Dorantes Gilardi, C. Lesieur and L. Vuillon

M. Achoch, K. Salamatian, March, 2015

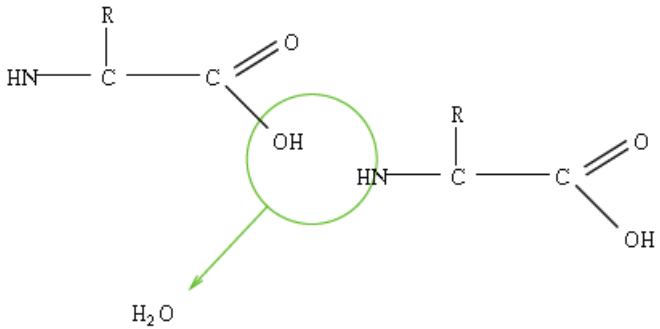
LAMA
Laboratoire de Mathématiques
Université de Savoie

cnrs
dépasser les frontières
UMR 5127

Outline

Proteins

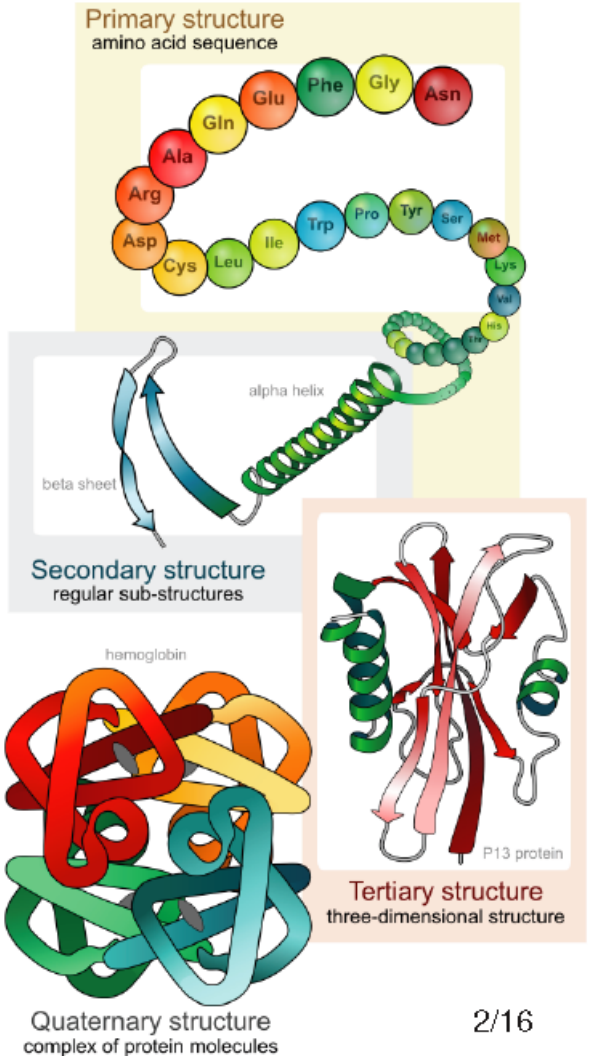
PROTEIN: sequence of amino acids that folds and realises a biological function



R: 20 standard amino acids = protein building blocks

Main chain (backbone), side chain

Information flow: 1D $\longrightarrow$ 3D



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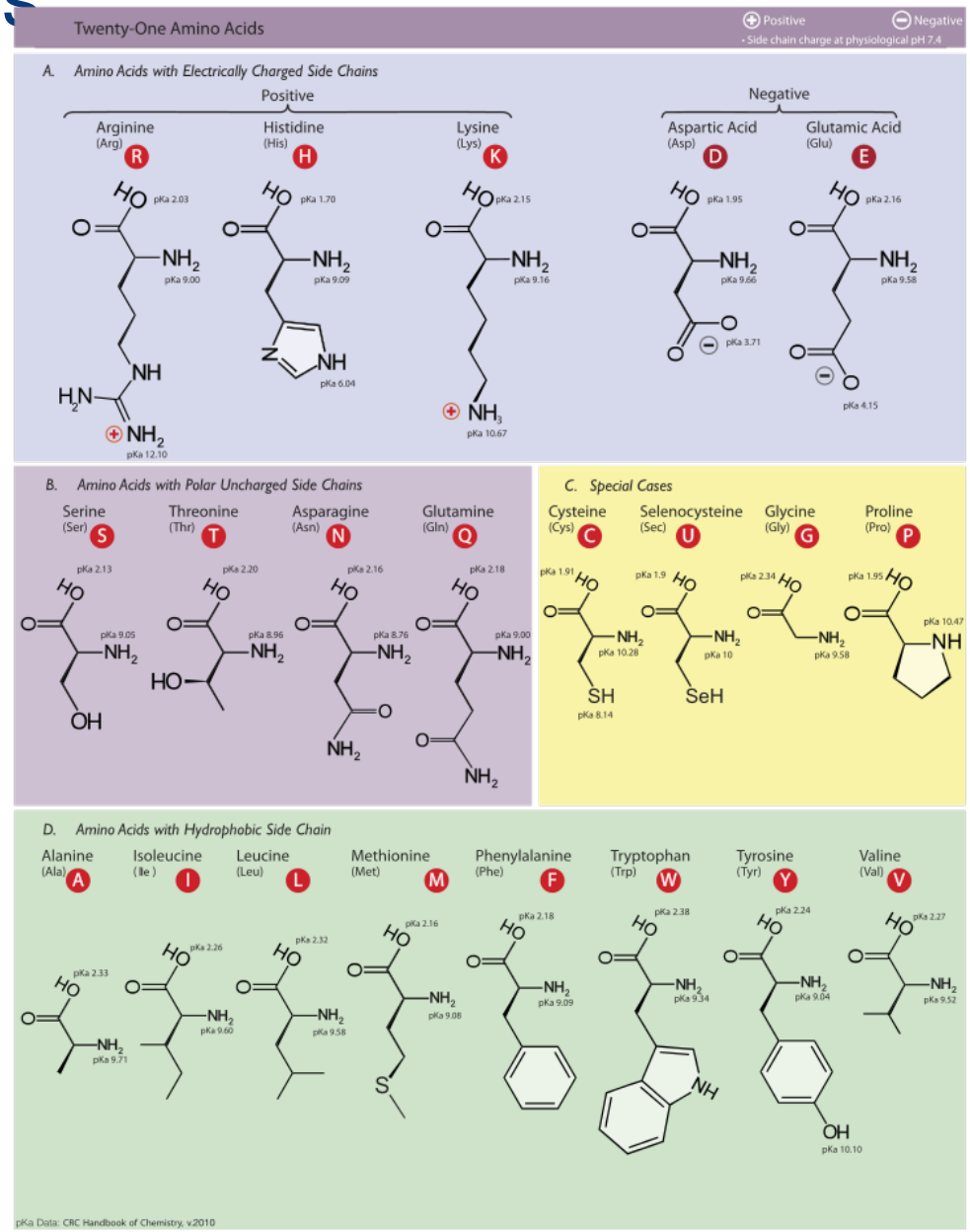
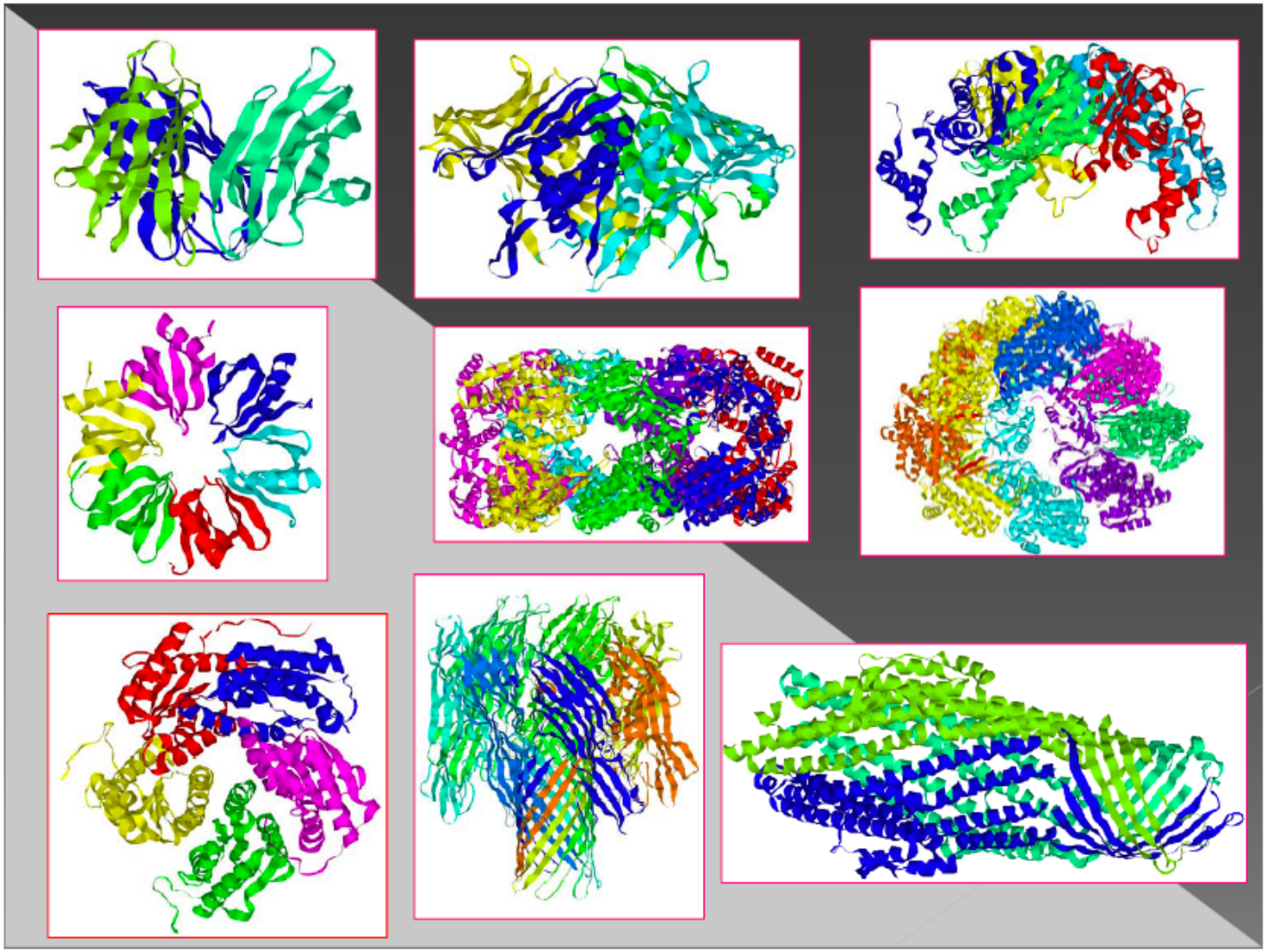
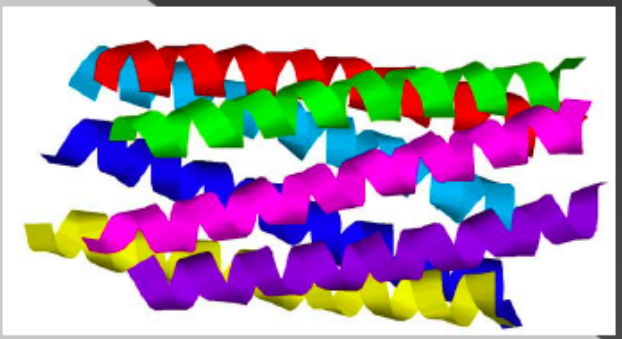
Amino Acids

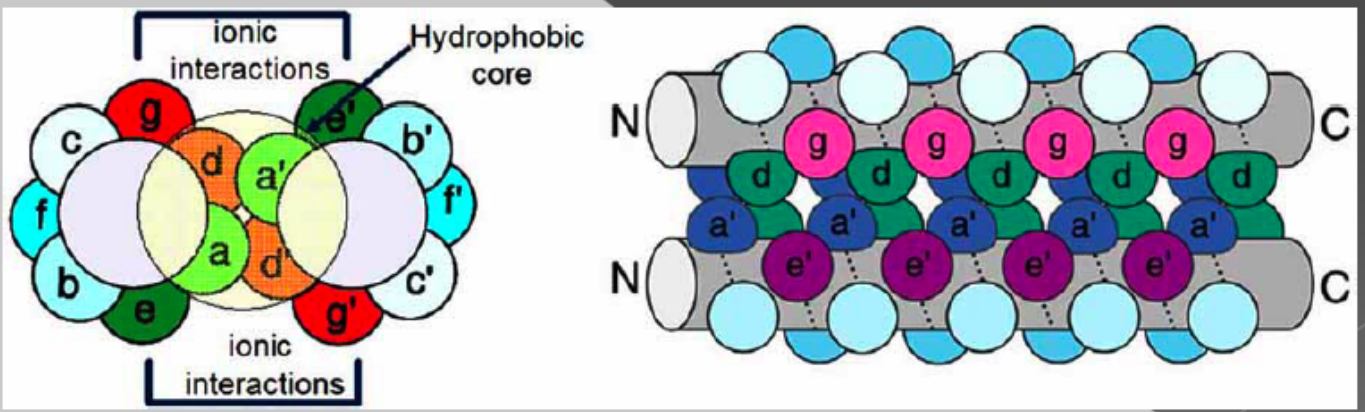

Twenty-One Amino Acids
Positive
Negative
• Side chain charge at physiological pH 7.4
A. Amino Acids with Electrically Charged Side Chains
Positive
Negative
Arginine (Arg) R
Histidine (His) H
Lysine (Lys) K
Aspartic Acid (Asp) D
Glutamic Acid (Glu) E
B. Amino Acids with Polar Uncharged Side Chains
Serine (Ser) S
Threonine (Thr) T
Asparagine (Asn) N
Glutamine (Gln) Q
C. Special Cases
Cysteine (Cys) C
Selenocysteine (Sec) U
Glycine (Gly) G
Proline (Pro) P
D. Amino Acids with Hydrophobic Side Chain
Alanine (Ala) A
Isoleucine (Ile) I
Leucine (Leu) L
Methionine (Met) M
Phenylalanine (Phe) F
Tryptophan (Trp) W
Tyrosine (Tyr) Y
Valine (Val) V
pKa Data: CRC Handbook of Chemistry, v.2010
Dan Cojocari, Department of Medical Biophysics, University of Toronto, 2010



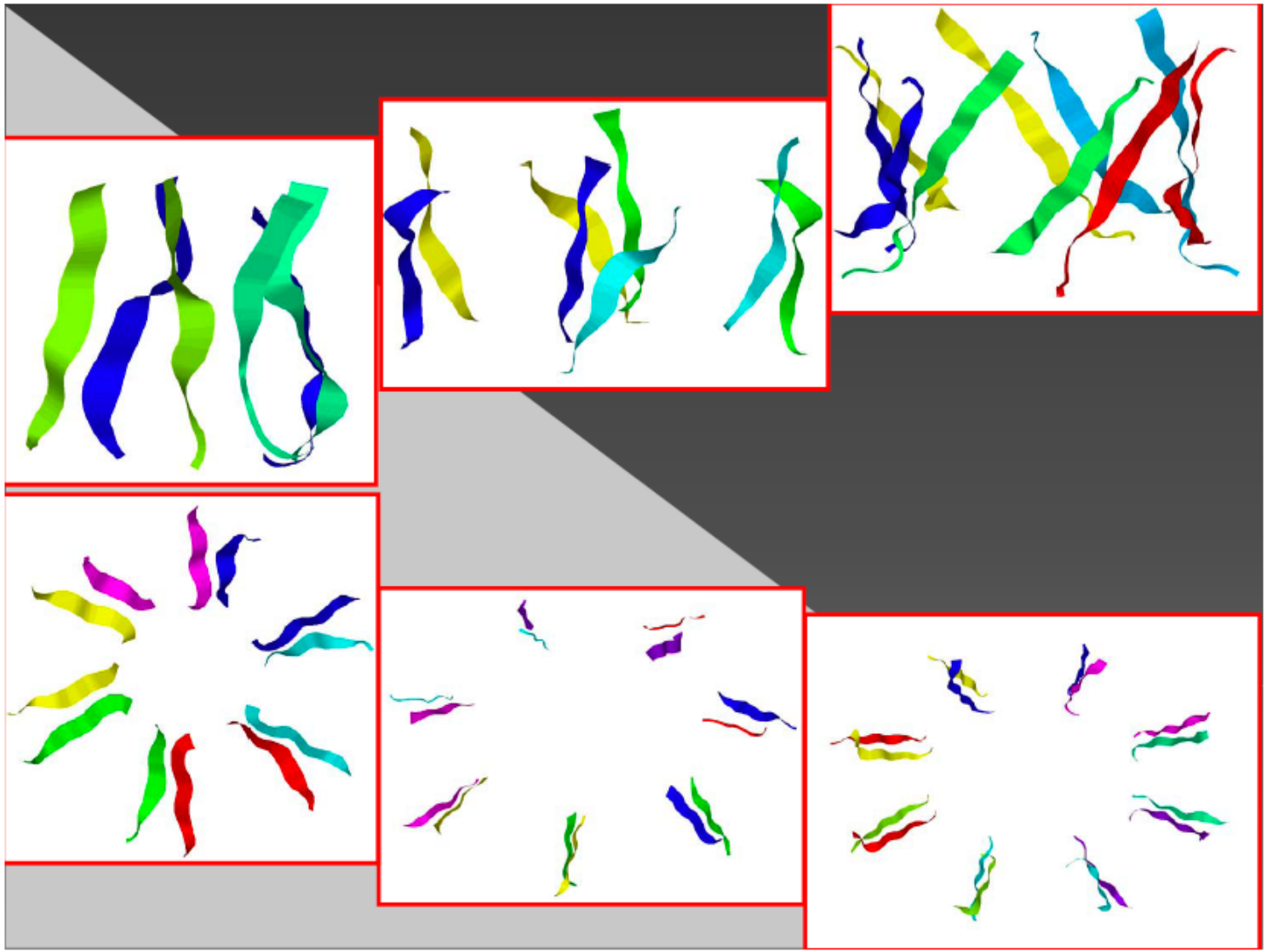
α-coiled interface



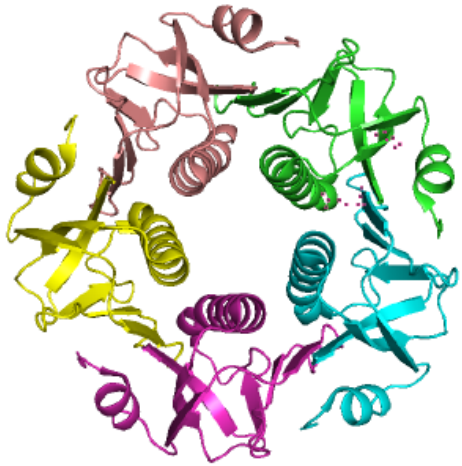
Heptad repeat: « **a**bc**d**efg »

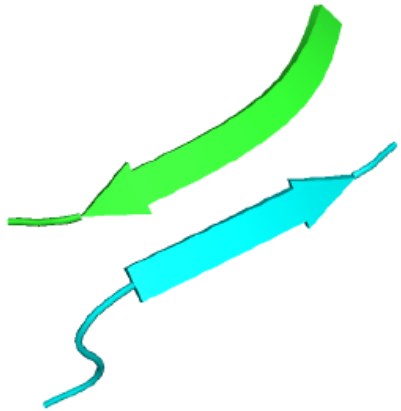


1- Crick FHC (1953). Acta Crystallogr 6: 689–697.
2- Lupas A (1996). Trends Biochem Sci 21: 375-382.



Focus on one interface geometry: two aligned β-strands





D: 96-103, E: 23-31

- ⋆ less understood than α-coil; "planar" geometry: much less constrained than α
- ⋆ many pathologies (Alzheimer, Parkinson, cholera, ...)

classes: continuous β-sheet, β-sandwich Guharoy, Chakrabarti 2007

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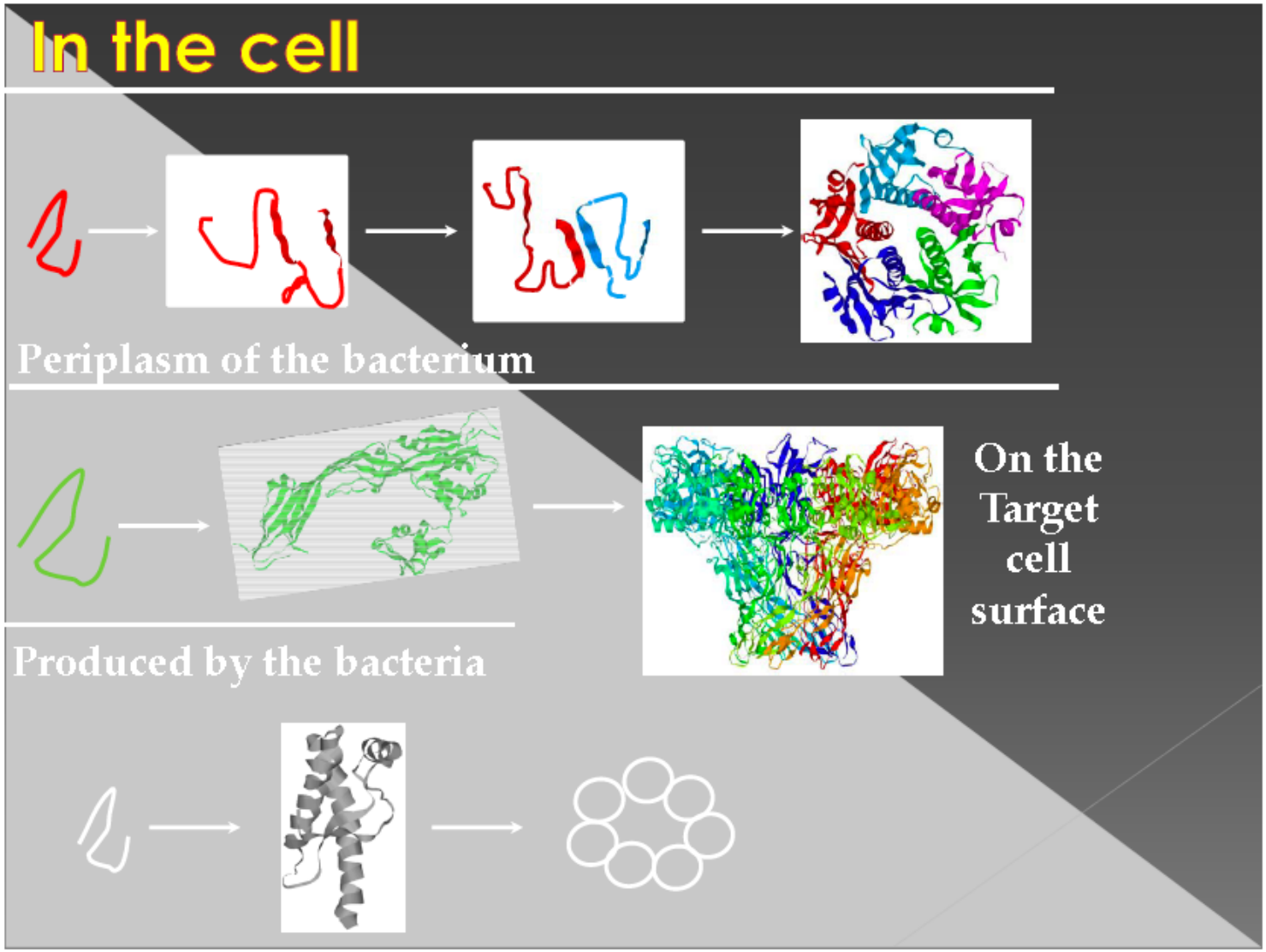
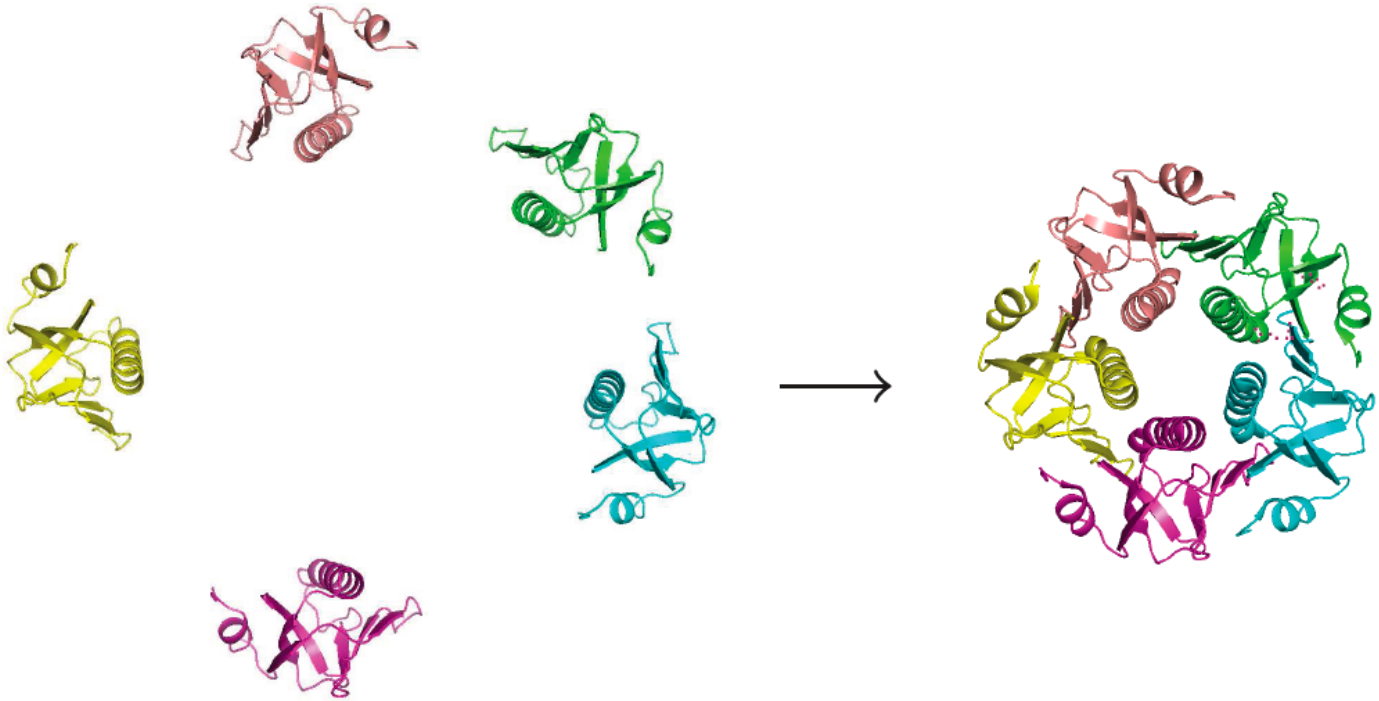
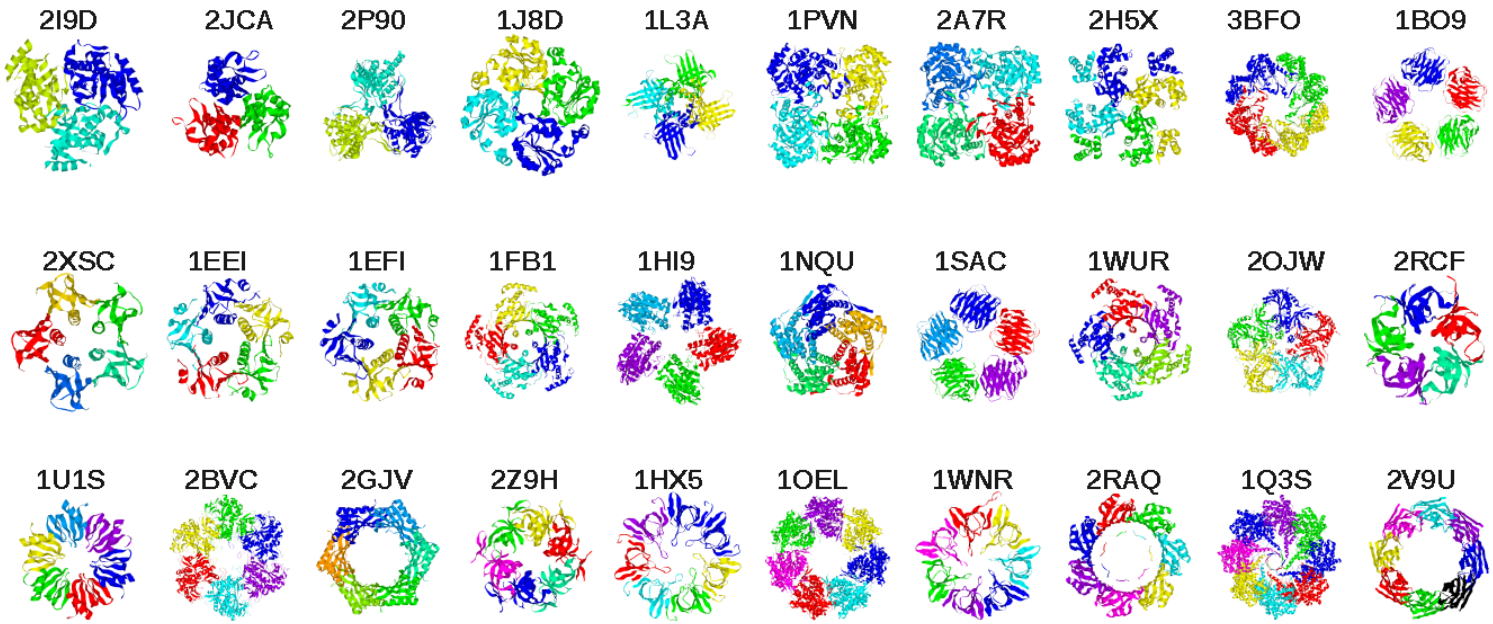

In the cell
Periplasm of the bacterium
On the Target cell surface
Produced by the bacteria

Cyclic



Cyclic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2P90
1J8D
1L3A
1PVN
2A7R
2H5X
3BFO
1BO9
2XSC
1EEI
1EFI
1FB1
1HI9
1NQU
1SAC
1WUR
2OJW
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1OEL
1WNR
2RAQ
1Q3S
2V9U

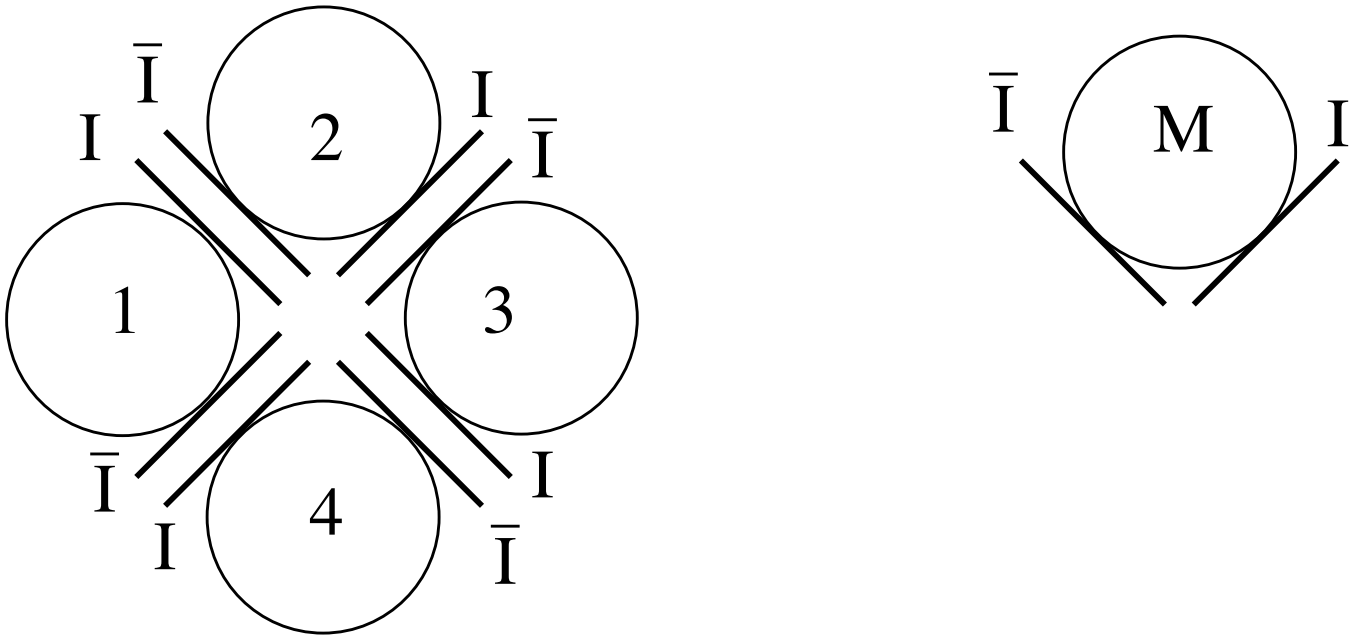


FIGURE: **Abstract view of C_4 symmetry.** A tetramer formed by a single interface between the part I and $\bar{I}$. Each chain is adjacent via the interface to exactly 2 other chains

Lethal

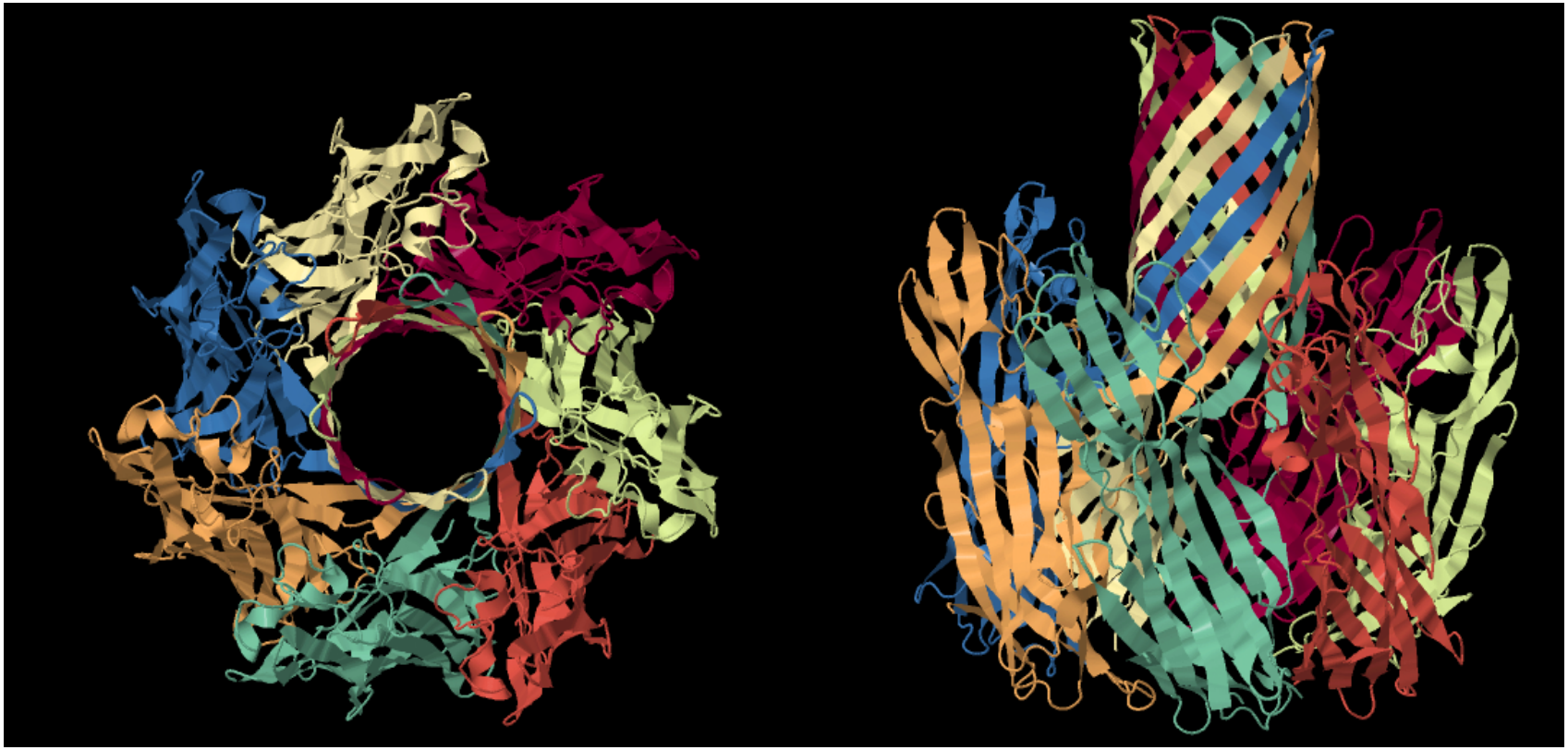
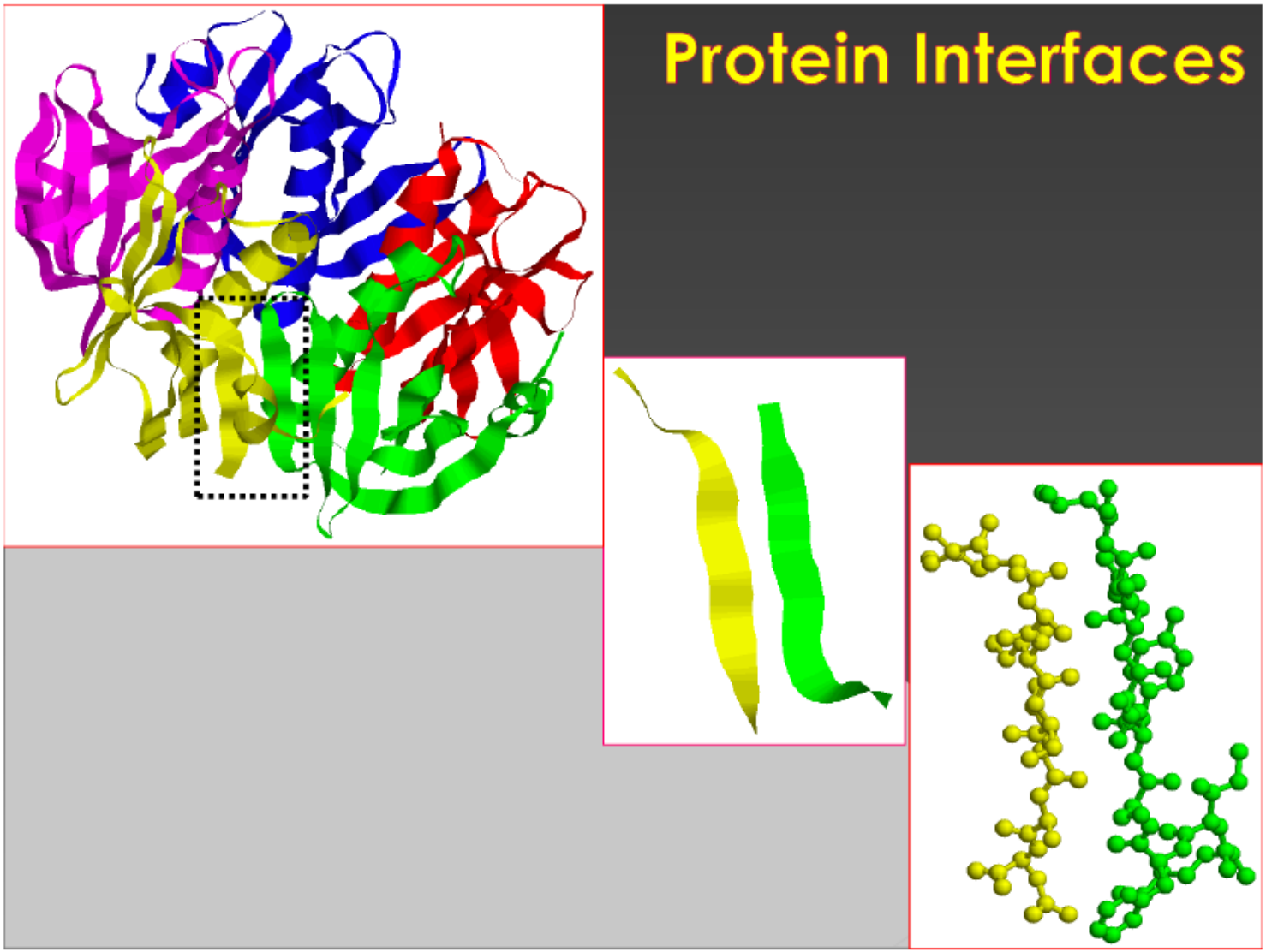
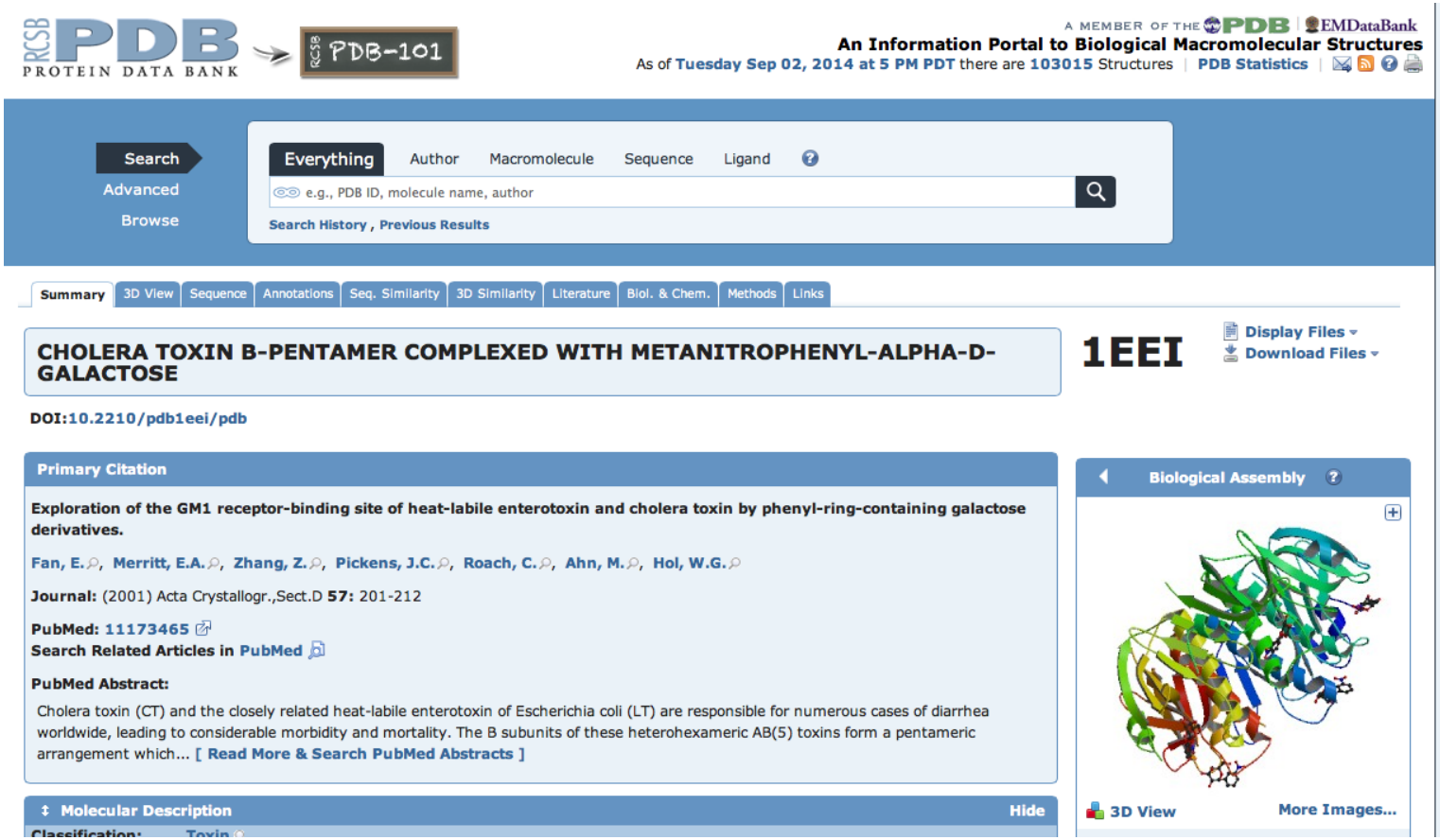
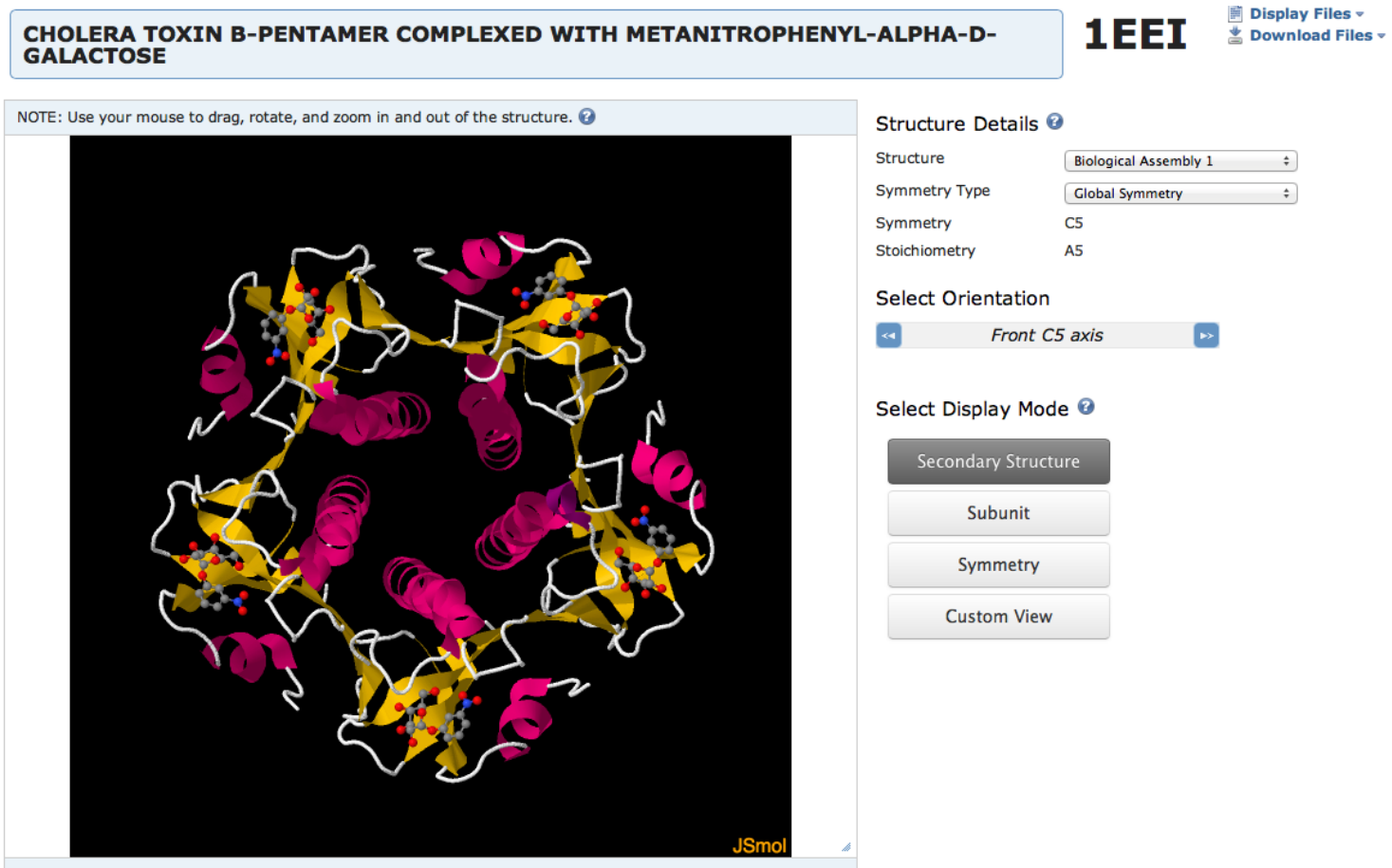


FIGURE: **Heptamer 4H56 in the PDB with each chain adjacent to 2 other chains.** Remark that in the beta barrel the adjacency between pairs of chains is the same as in the other part of the heptamer. This implies an oligomerization with exactly 1 interface.


Protein Interfaces

Protein Data Bank



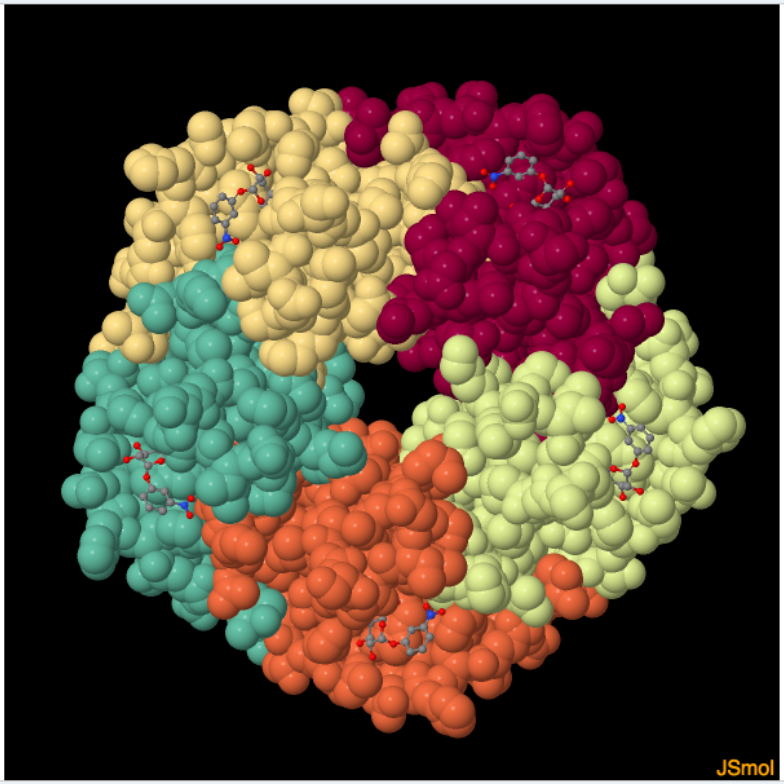

CHOLERA TOXIN B-PENTAMER COMPLEXED WITH METANITROPHENYL-ALPHA-D-GALACTOSE
1EEI
Display Files
Download Files
NOTE: Use your mouse to drag, rotate, and zoom in and out of the structure.
JSmol
Structure Details
Structure
Biological Assembly 1
Symmetry Type
Global Symmetry
Symmetry
C5
Stoichiometry
A5
Select Orientation
Front C5 axis
Select Display Mode
Secondary Structure
Subunit
Symmetry
Custom View

CHOLERA TOXIN B-PENTAMER COMPLEXED WITH METANITROPHENYL-ALPHA-D-GALACTOSE

1EEI

Display Files
Download Files

NOTE: Use your mouse to drag, rotate, and zoom in and out of the structure.



Biological assembly 1 assigned by authors and generated by PISA

Structure Details

Structure	Biological Assembly 1
Symmetry Type	Global Symmetry
Symmetry	C5
Stoichiometry	A5

Select Orientation

Front C5 axis

Select Display Mode

Secondary Structure
Subunit
Symmetry
Custom View

Custom View options

Style	Space Fill
Color	Subunit
Surface	None
Jmol mode	HTML5 (beta)

- [ ] H-Bonds
- [ ] SS Bonds
- [ ] Rotation
- [x] Black Background
- [ ] Polyhedron
- [ ] Axes

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TITLE    2 ALPHA-D-GALACTOSE
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COMPND   2 MOLECULE: PROTEIN (CHOLERA TOXIN B);
COMPND   3 CHAIN: D, E, F, G, H;
COMPND   4 ENGINEERED: YES;
COMPND   5 OTHER_DETAILS: RECEPTOR BINDING SITE ON EACH MONOMER
COMPND   6 OCCUPIED BY METANITROPHENYL-ALPHA-D-GALACTOSIDE
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SOURCE   2 ORGANISM_SCIENTIFIC: VIBRIO CHOLERAE;
SOURCE   3 ORGANISM_TAXID: 666;
SOURCE   4 STRAIN: OGAWA 41 (CLASSICAL BIOTYPE);
SOURCE   5 EXPRESSION_SYSTEM: ESCHERICHIA COLI;
SOURCE   6 EXPRESSION_SYSTEM_TAXID: 562
KEYWDS    TOXIN,ENTEROTOXIN
EXPDTA    X-RAY DIFFRACTION
AUTHOR    E.A.MERRITT,W.G.J.HOL
REVDAT   4   24-FEB-09 1EEI    1       VERSN
REVDAT   3   01-APR-03 1EEI    1       JRNL
REVDAT   2   07-FEB-01 1EEI    1       JRNL
REVDAT   1   16-FEB-00 1EEI    0
JRNL        AUTH   E.FAN,E.A.MERRITT,Z.ZHANG,J.C.PICKENS,C.ROACH,
JRNL        AUTH 2 M.AHN,W.G.HOL
JRNL        TITL   EXPLORATION OF THE GM1 RECEPTOR-BINDING SITE OF
JRNL        TITL 2 HEAT-LABILE ENTEROTOXIN AND CHOLERA TOXIN BY
JRNL        TITL 3 PHENYL-RING-CONTAINING GALACTOSE DERIVATIVES.
JRNL        REF    ACTA CRYSTALLOGR.,SECT.D      V.  57   201 2001
JRNL        REFN                   ISSN 0907-4449
JRNL        PMID   11173465
JRNL        DOI    10.1107/S0907444900016814
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SEQRES   4 F  103  ILE THR PHE LYS ASN GLY ALA THR PHE GLN VAL GLU VAL
SEQRES   5 F  103  PRO GLY SER GLN HIS ILE ASP SER GLN LYS LYS ALA ILE
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ATOM      1  N   THR D   1      38.037  31.348  29.862  1.00 33.00           N
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ATOM      6  OG1 THR D   1      36.841  30.686  32.469  1.00 39.57           O
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ATOM      8  N   PRO D   2      34.892  31.113  28.372  1.00 33.37           N
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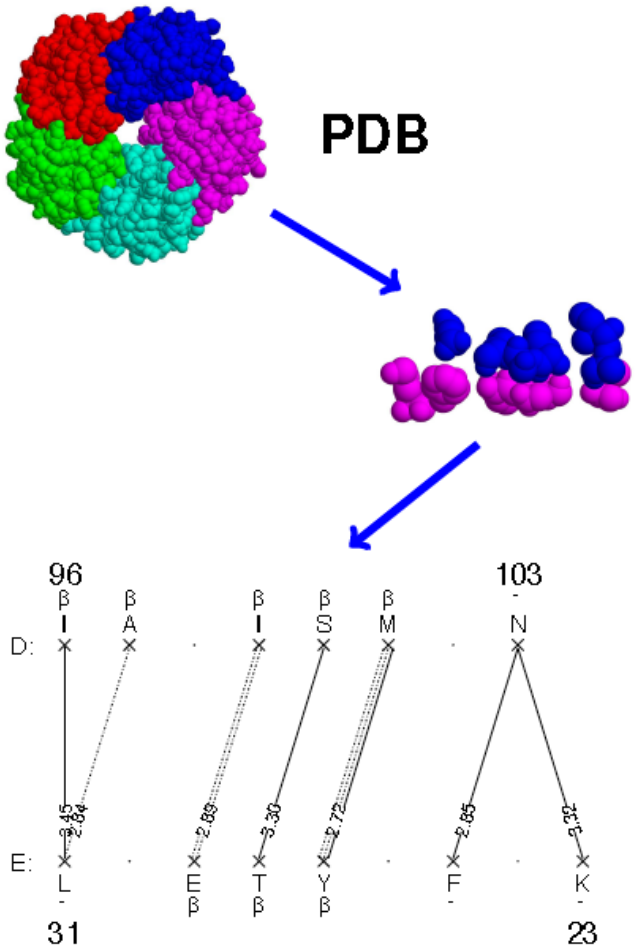
GEMINI



Interactions at the interface

GEMINI

- Interaction patterns
- Large ensembles of data
- Time: 0.1 s/protein

Agence pour la protection des programmes, 2009
G. Feverati, C. Lesieur, Plos ONE 2010
G. Feverati et al., Plos ONE 2012

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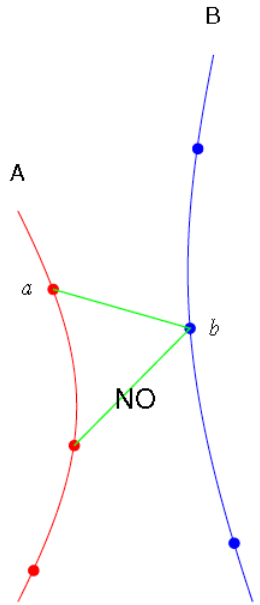
GEMINI



G. Feverati, C. Lesieur, L. Vuillon, International Journal "Information Technologies and Knowledge", 2012

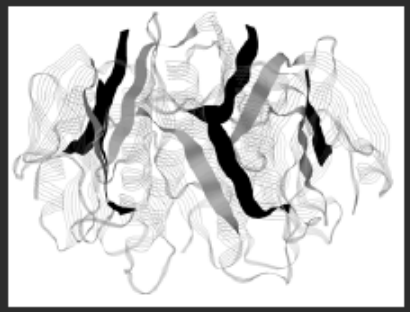
$$R_0 = \{(a,b) \in A \times B \text{ s.t. } d(a,b) \leq d_0\}$$

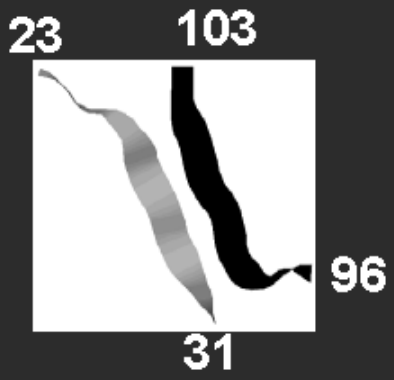
$$L_A = \{(a,b) \in R_0 \text{ s.t. } d(a,b) = min_{c \in B}\{d(a,c)\}\}$$

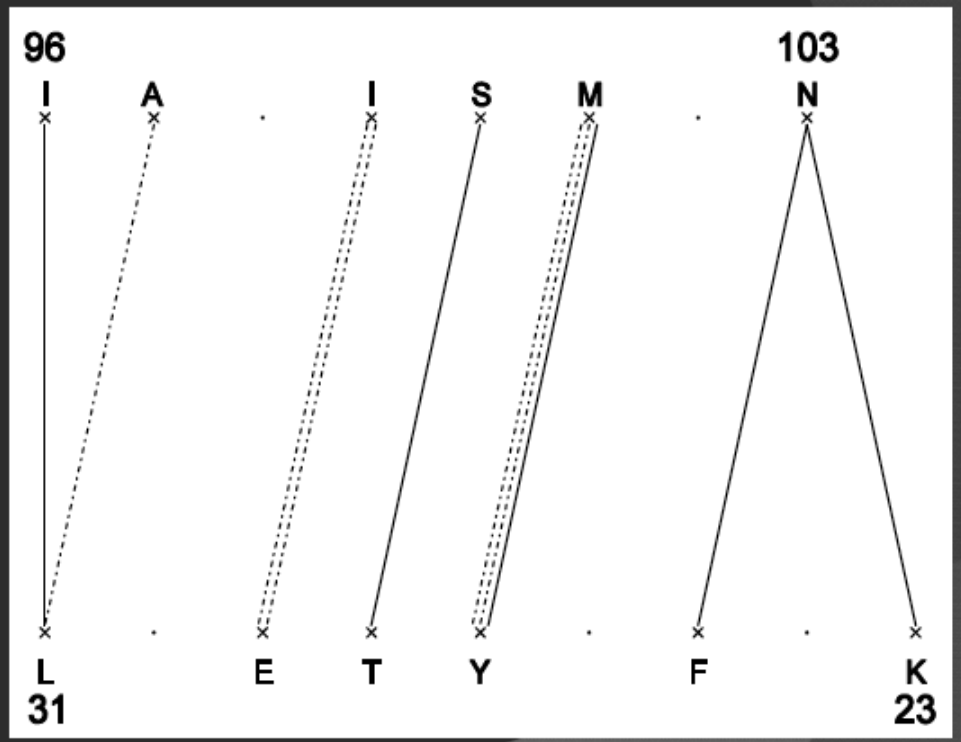
$$L_B = \{(a,b) \in R_0 \text{ s.t. } d(a,b) = \{min_{d \in A}\{d(d,b)\}\}$$

$$S_0 = L_A \cap L_B$$

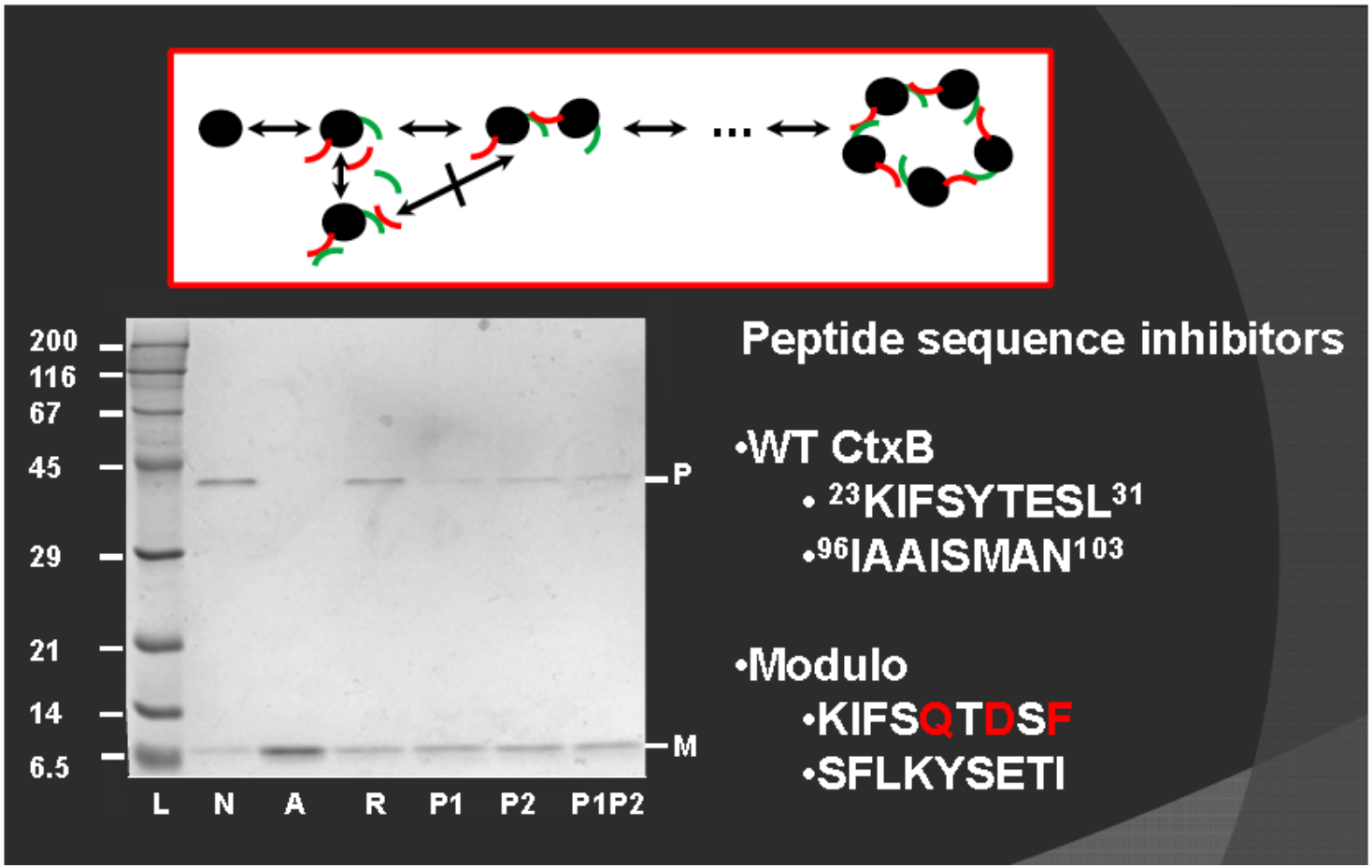
Example: β-interfaces: cholera toxin, Alzheimer, Parkinson...



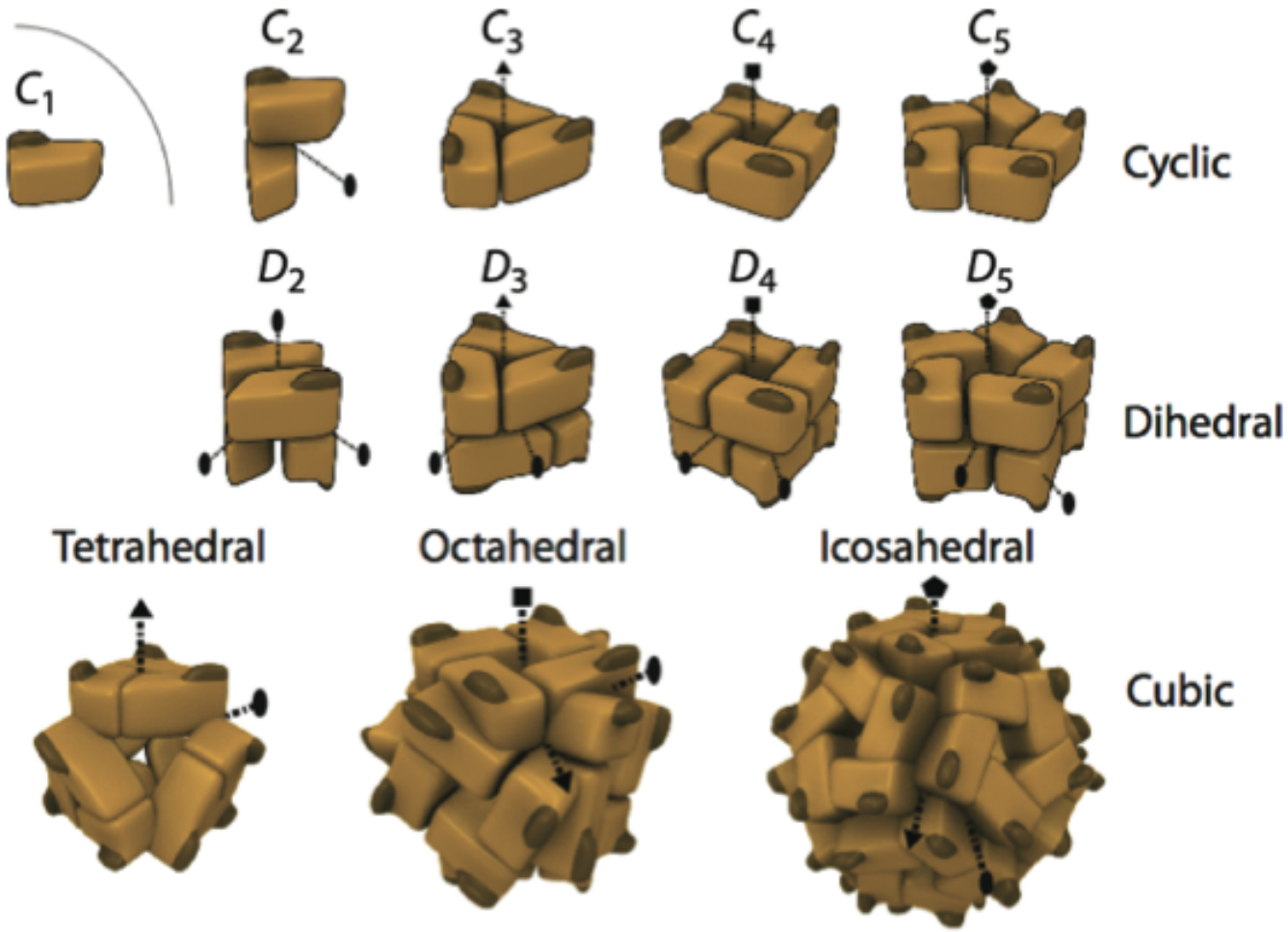




Interfaces and inhibition of the Cholera



Symmetry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C_2
C_3
C_4
C_5
Cyclic
D_2
D_3
D_4
D_5
Dihedral
Tetrahedral
Octahedral
Icosahedral
Cubic

Dihedral

Atomic Model of Mm-cpn in the Closed State

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DOI:10.2210/pdb3los/pdb **EMDataBank** :5137

ENTRY 3LOS SUPERSEDES 3IYE

Primary Citation

Mechanism of folding chamber closure in a group II chaperonin.

Zhang, J., Baker, M.L., Schroder, G.F., Douglas, N.R., Reissmann, S., Jakana, J., Dougherty, M., Fu, C.J., Levitt, M., Ludtke, S.J., Frydman, J., Chiu, W.

Journal: (2010) Nature **463:** 379-383

PubMed: 20090755
PubMedCentral: PMC2834796
DOI: 10.1038/nature08701
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PubMed Abstract:

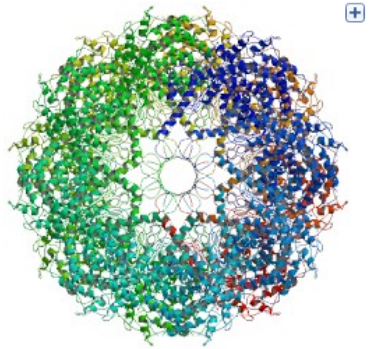
Group II chaperonins are essential mediators of cellular protein folding in eukaryotes and archaea. These oligomeric protein machines, approximately 1 megadalton, consist of two back-to-back rings encompassing a central cavity that accommodates polypeptide substrates. Chaperonin-mediated protein folding is critically dependent... [Read More & Search PubMed Abstracts]

Molecular Description Hide

Classification: Chaperone
Structure Weight: 932652.81

Molecule: Chaperonin
Polymer: 1 **Type:** protein **Length:** 543

Biological Assembly

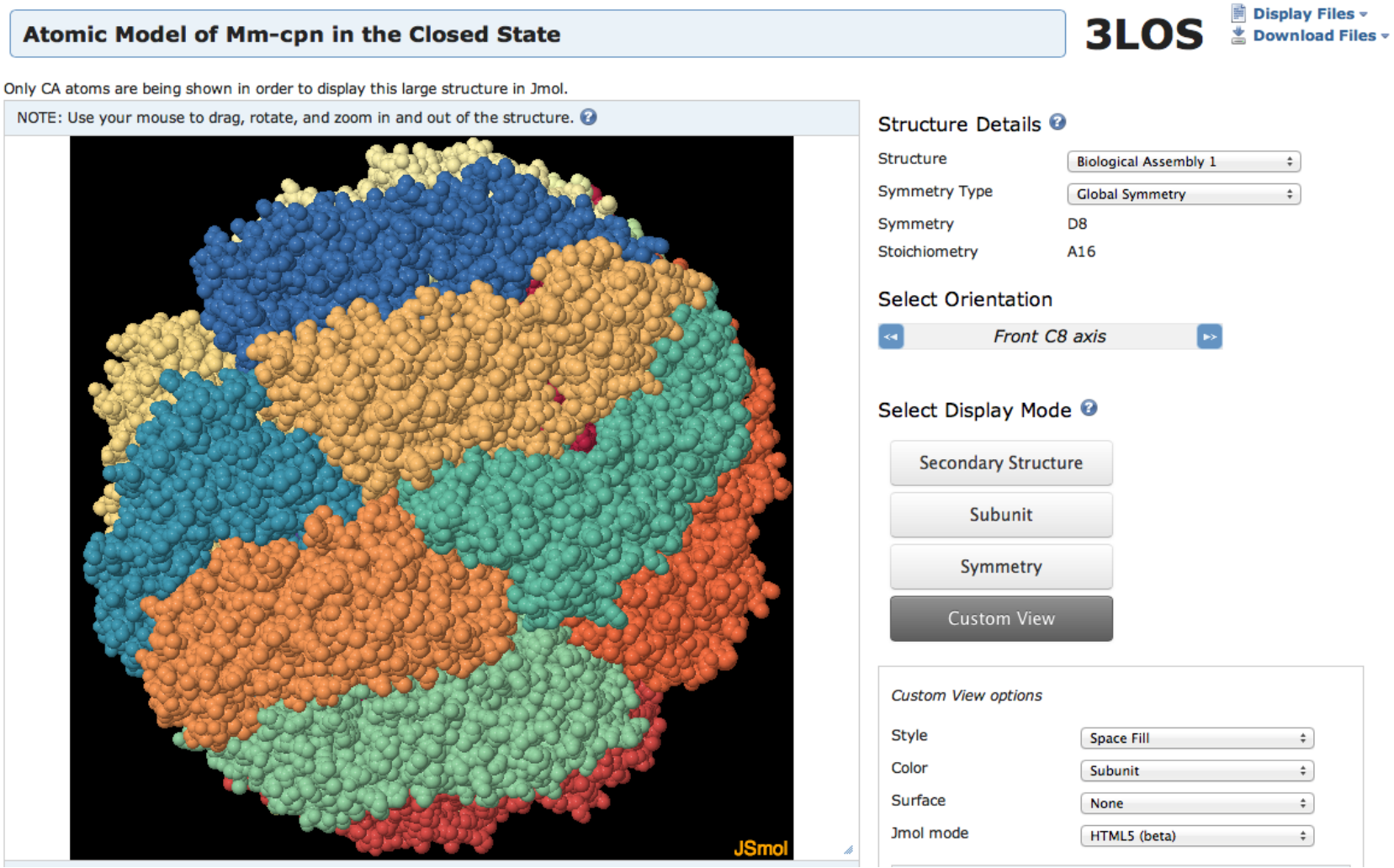


3D View More Images...

Symmetry: **D8** view
Stoichiometry: **Homo 16-mer - A16**
Biological assembly 1 assigned by authors

Downloadable viewers:
Simple Viewer Protein Workshop
Kiosk Viewer

Dihedral


Atomic Model of Mm-cpn in the Closed State
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Only CA atoms are being shown in order to display this large structure in Jmol.
NOTE: Use your mouse to drag, rotate, and zoom in and out of the structure.
JSmol
Structure Details
Structure
Biological Assembly 1
Symmetry Type
Global Symmetry
Symmetry
D8
Stoichiometry
A16
Select Orientation
Front C8 axis
Select Display Mode
Secondary Structure
Subunit
Symmetry
Custom View
Custom View options
Style
Space Fill
Color
Subunit
Surface
None
Jmol mode
HTML5 (beta)

Tetrahedral

Crystal Structure of an archaeal aminopeptidase

1XFO Display Files Download Files

DOI:10.2210/pdb1xfo/pdb

Primary Citation

Crystal structure of a dodecameric tetrahedral-shaped aminopeptidase.

Russo, S., Baumann, U.

Journal: (2004) J.Biol.Chem. **279:** 51275-51281

PubMed: 15375159
DOI: 10.1074/jbc.M409455200
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PubMed Abstract:

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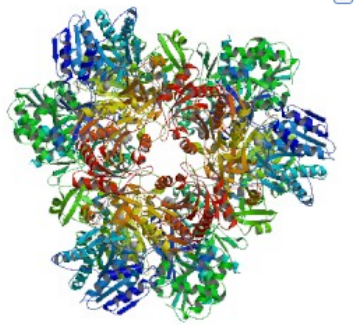
Molecular Description Hide

Classification: Hydrolase
Structure Weight: 158566.63

Molecule:	Frv operon protein FrvX				
Polymer:	1	**Type:**	protein	**Length:**	357
Chains:	A, B, C, D				
EC#:	3.4.11				
Organism:	Pyrococcus horikoshii				
Gene Names:	frvX PH1527				
UniProtKB:	Protein Feature View | Search PDB | O59196				

Biological Assembly



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Symmetry: **T** view
Stoichiometry: **Homo 12-mer - A12**
Biological assembly 1 assigned by authors and generated by PISA,PQS (software)

Downloadable viewers:
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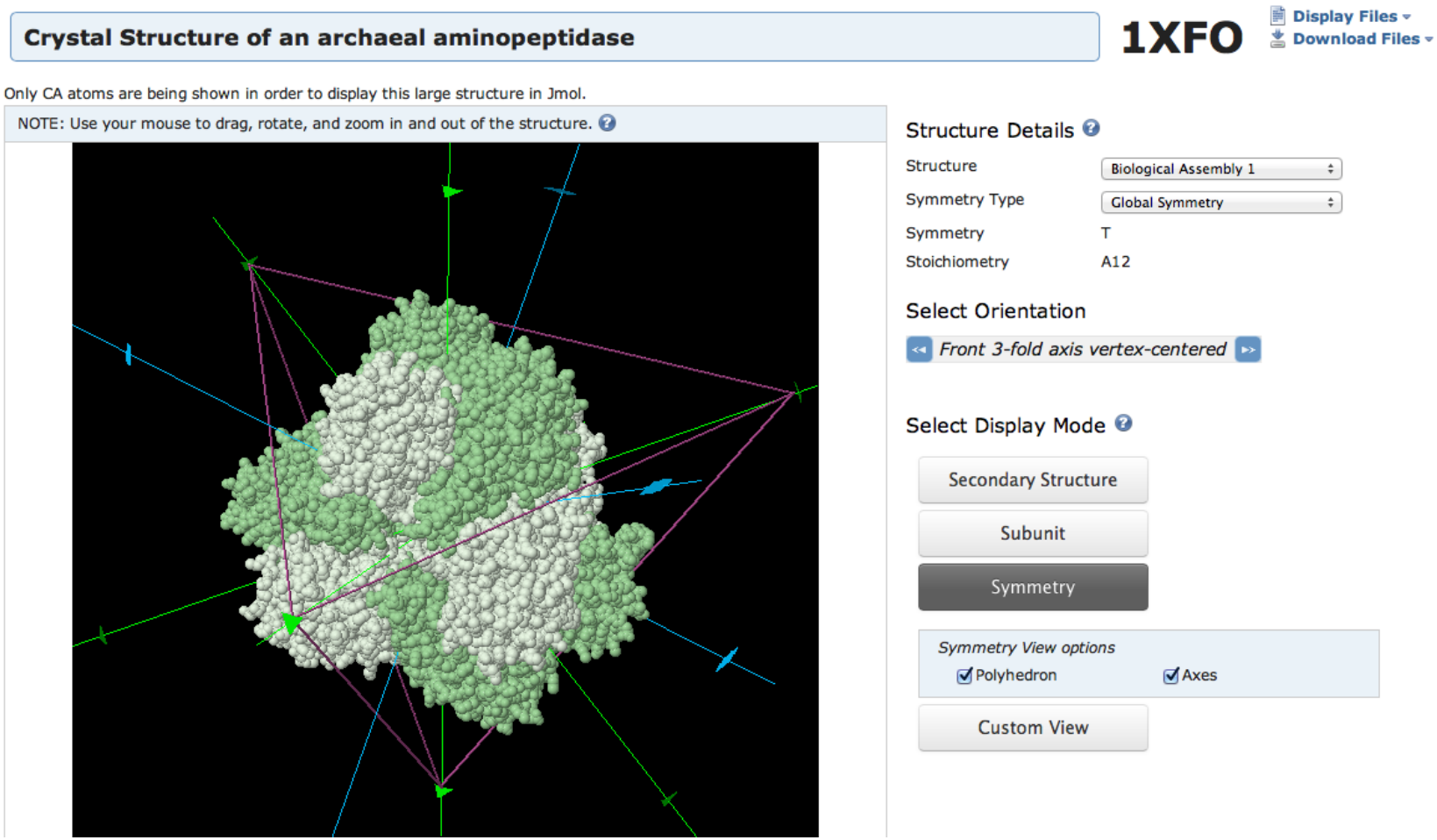
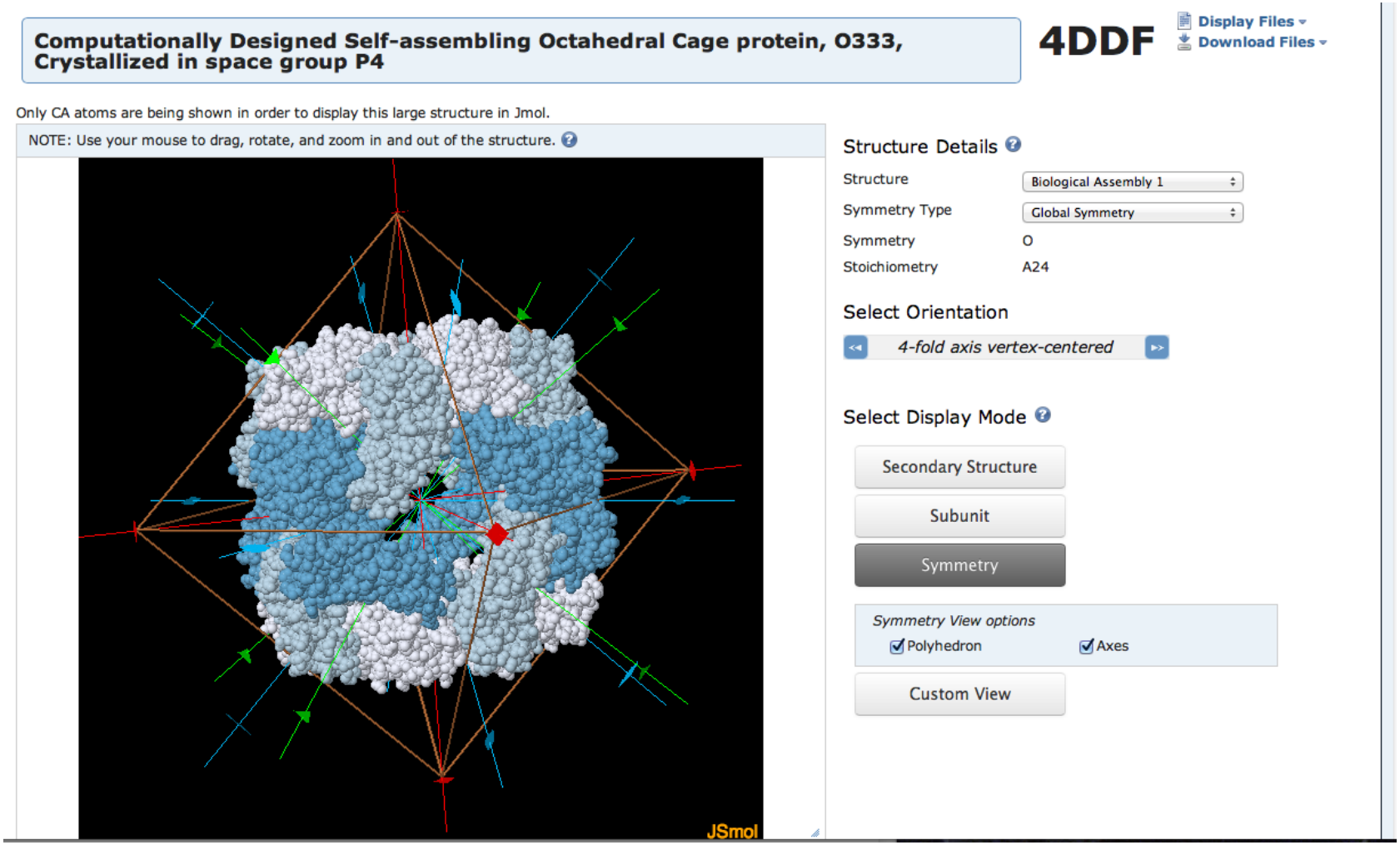
Tetrahedral



Octahedral


Computationally Designed Self-assembling Octahedral Cage protein, O333, Crystallized in space group P4
4DDF
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Only CA atoms are being shown in order to display this large structure in Jmol.
NOTE: Use your mouse to drag, rotate, and zoom in and out of the structure.
JSmol
Structure Details
Structure
Biological Assembly 1
Symmetry Type
Global Symmetry
Symmetry
O
Stoichiometry
A24
Select Orientation
4-fold axis vertex-centered
Select Display Mode
Secondary Structure
Subunit
Symmetry
Symmetry View options
Polyhedron
Axes
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Icosahedral

Life in the extremes: atomic structure of Sulfolobus Turreted Icosahedral Virus

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DOI:10.2210/pdb3j31/pdb **EMDataBank**:5584

Primary Citation

Atomic structure of the 75 MDa extremophile Sulfolobus turreted icosahedral virus determined by CryoEM and X-ray crystallography.

Veesler, D., Ng, T.S., Sendamarai, A.K., Eilers, B.J., Lawrence, C.M., Lok, S.M., Young, M.J., Johnson, J.E., Fu, C.Y.

Journal: (2013) Proc.Natl.Acad.Sci.USA **110:** 5504-5509

PubMed: 23520050
PubMedCentral: PMC3619359
DOI: 10.1073/pnas.1300601110
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PubMed Abstract:

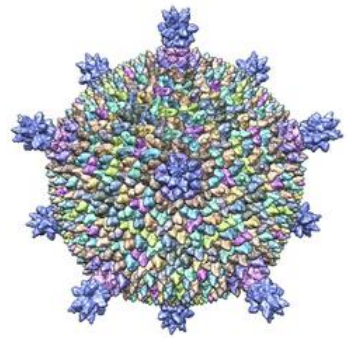
Sulfolobus turreted icosahedral virus (STIV) was isolated in acidic hot springs where it infects the archeon Sulfolobus solfataricus. We determined the STIV structure using near-atomic resolution electron microscopy and X-ray crystallography allowing tracing of structural polypeptide chains and visualization of... [Read More & Search PubMed Abstracts]

Molecular Description Hide

Classification: Virus [VIPERdb]
Structure Weight: 635329.60

Molecule:	A223 penton base				
Polymer:	1	**Type:**	protein	**Length:**	223
Chains:	Q				
Organism:	Sulfolobus turreted icosahedral virus 1				
Gene Name:	A223				

Biological Assembly



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Symmetry: **I** view
Stoichiometry: **Hetero 1020-mer - A900B60C60**
No info available for origin of biological assembly

Downloadable viewers:
Simple Viewer Protein Workshop
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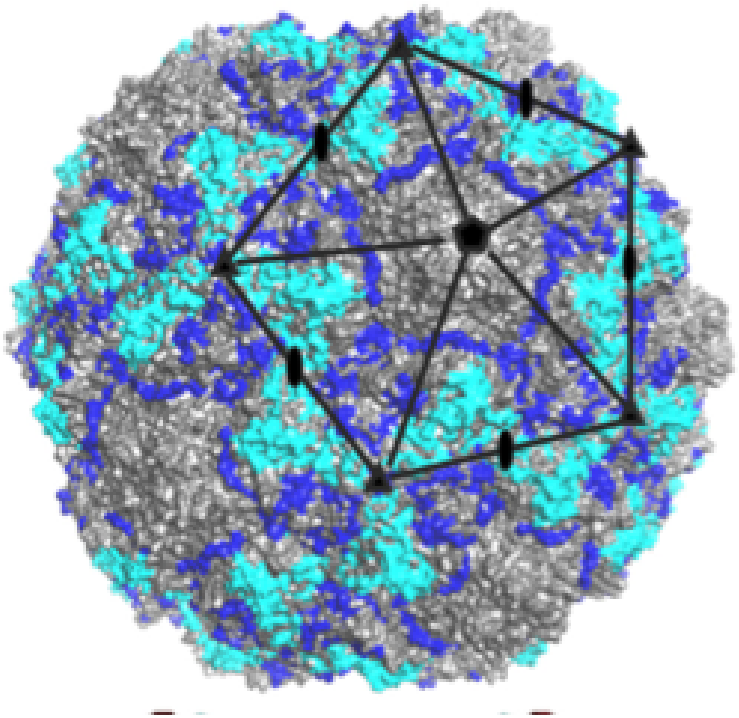
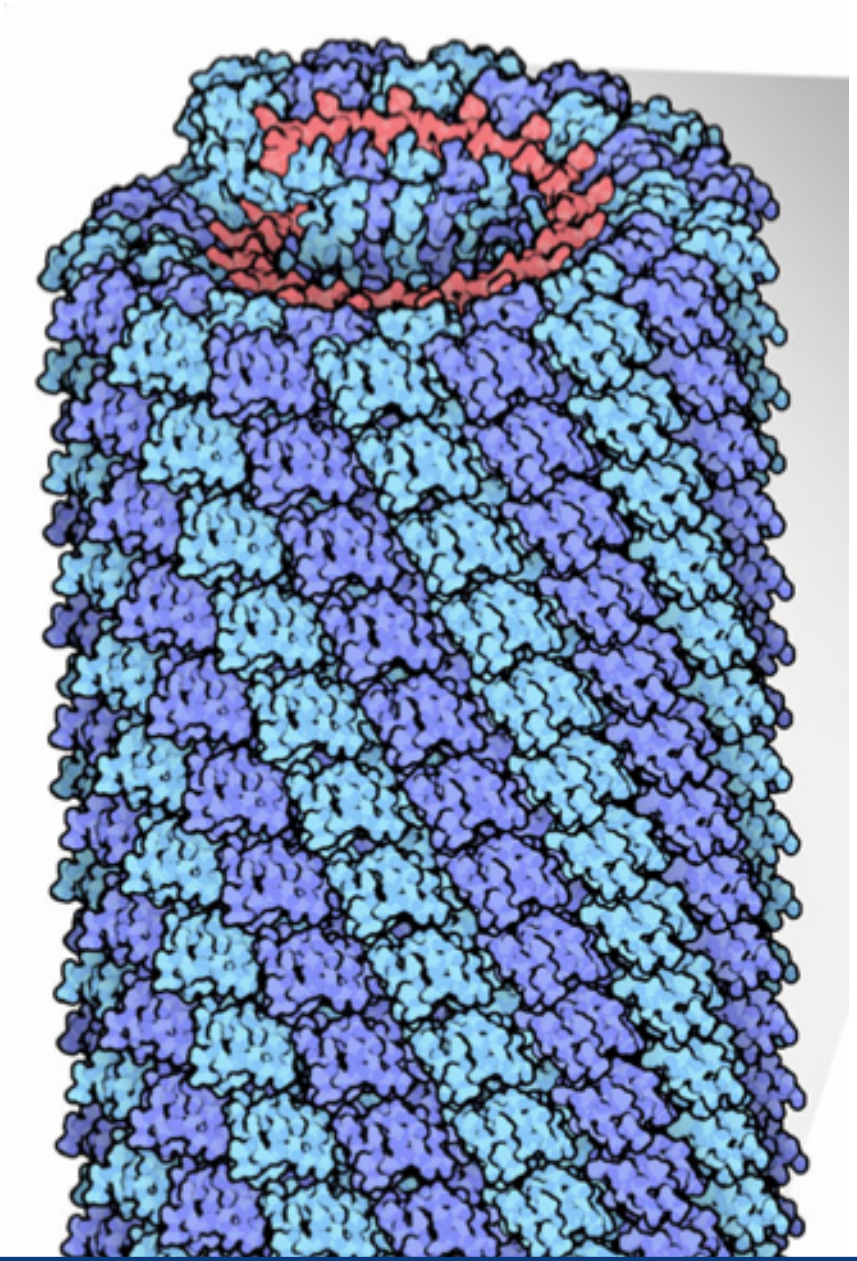
Icosahedral



Fiber !



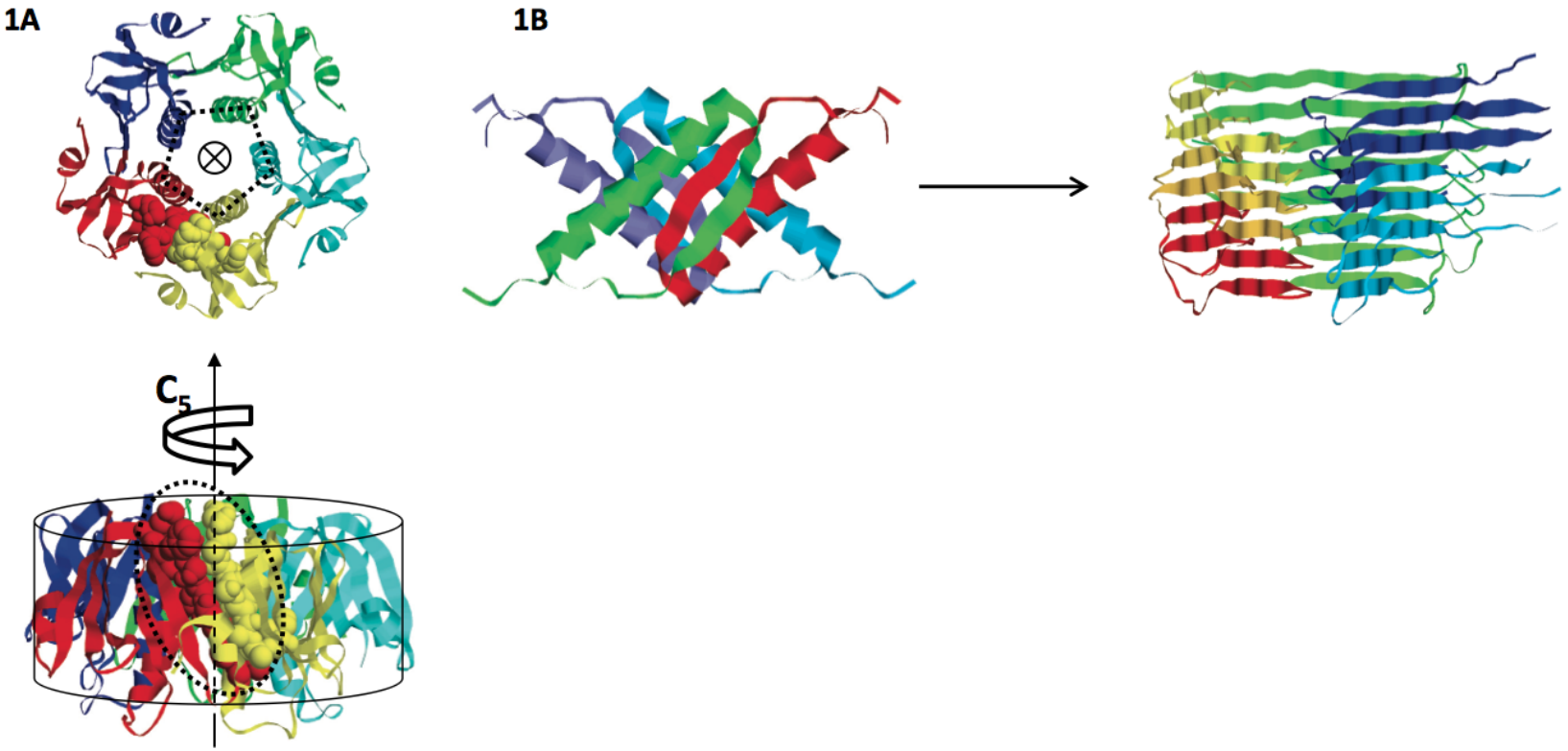
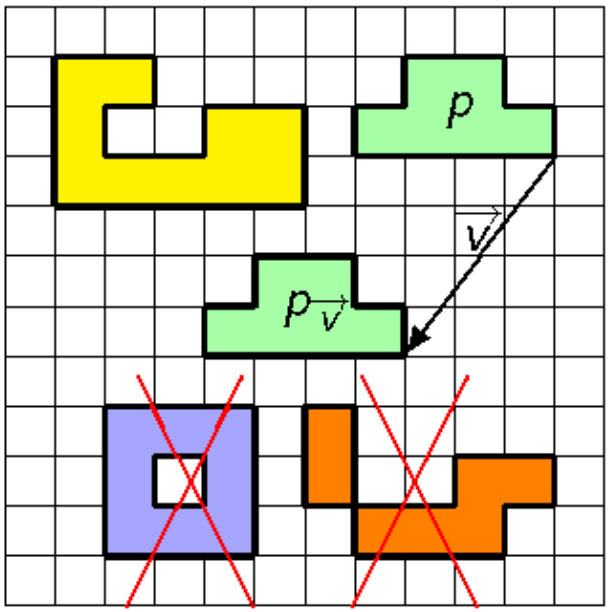


FIGURE: **Protein oligomers and fibers. A. Protein oligomer.** Cholera toxin B pentamer (*CtxB*$_5$) is shown (PDB code 3CHB). **B. Oligomer to fiber transition.** Each monomer is indicated by a different color.

Tilings of the plane

Définition

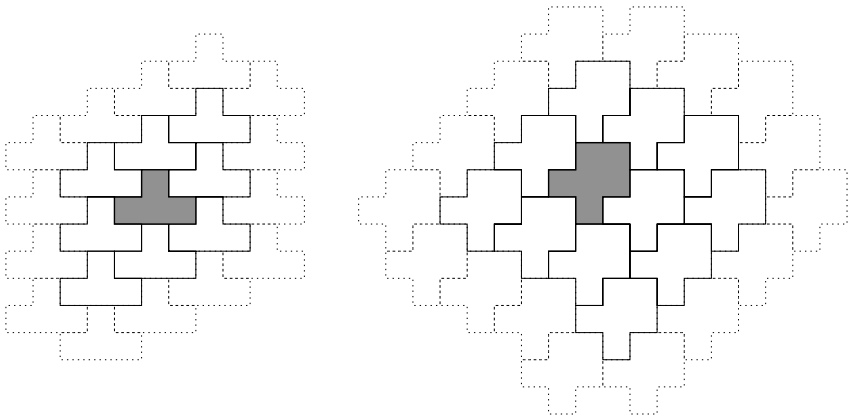
A *polyomino* is the interior of a closed non intersecting path in a square lattice.



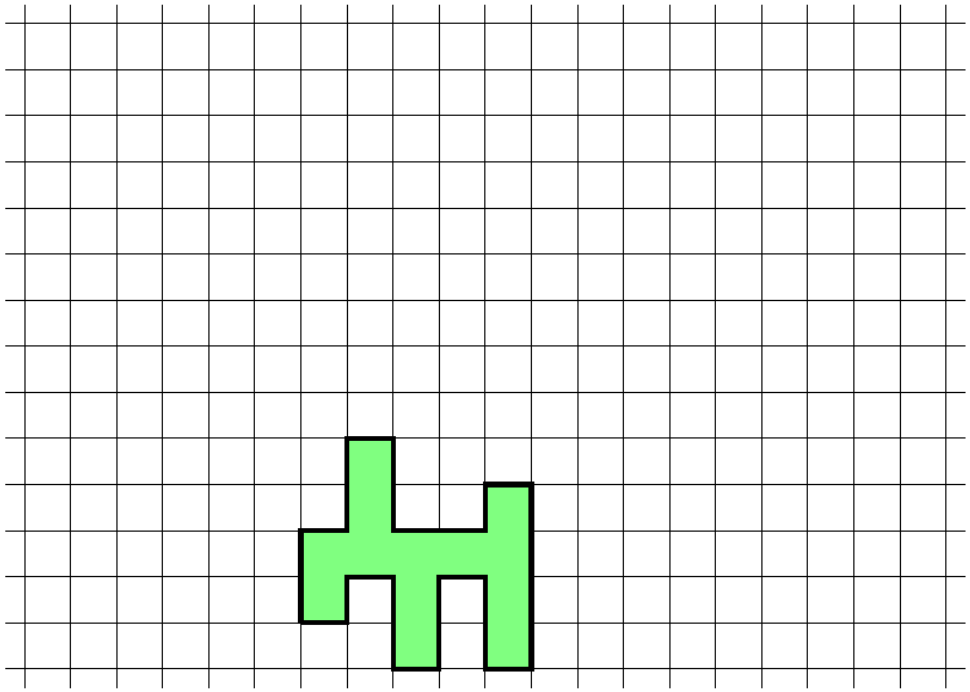
Tilings of the plane

Definitions

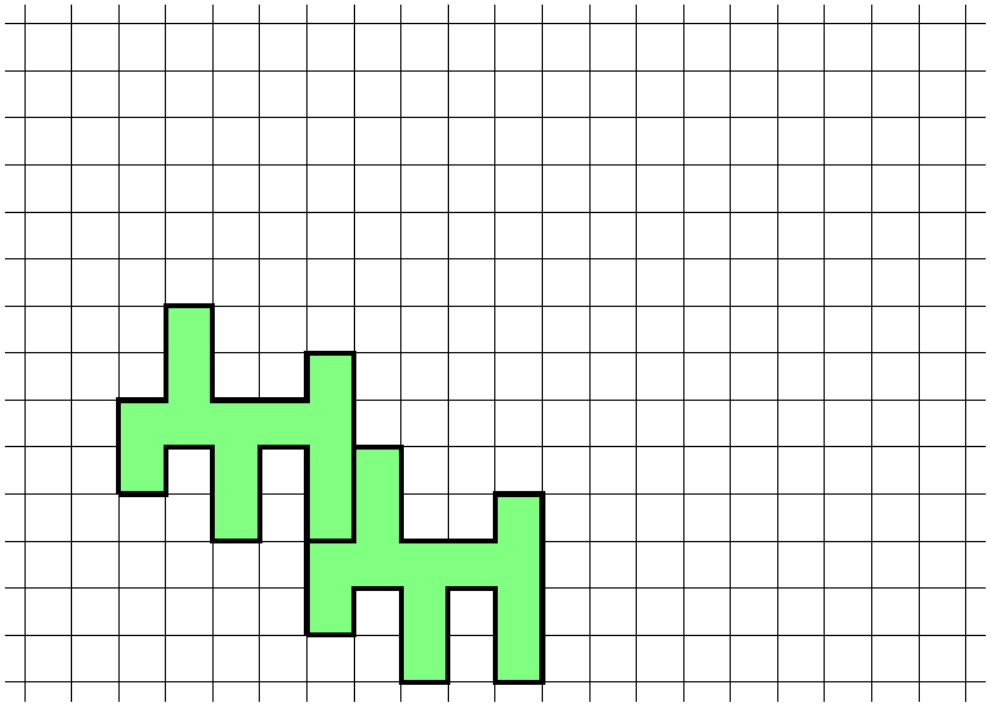
A *tiling by translation* of a polyomino P is a covering of $\mathbb{R}^2$ by translation of copies of P without overlapping or hole.



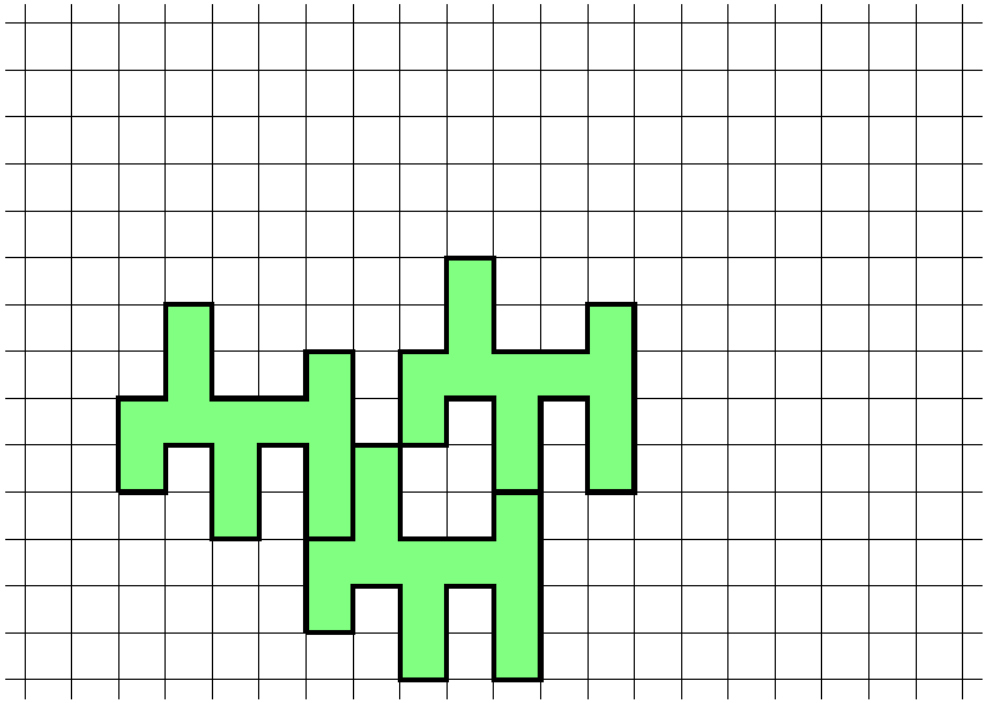
Tilings by translation



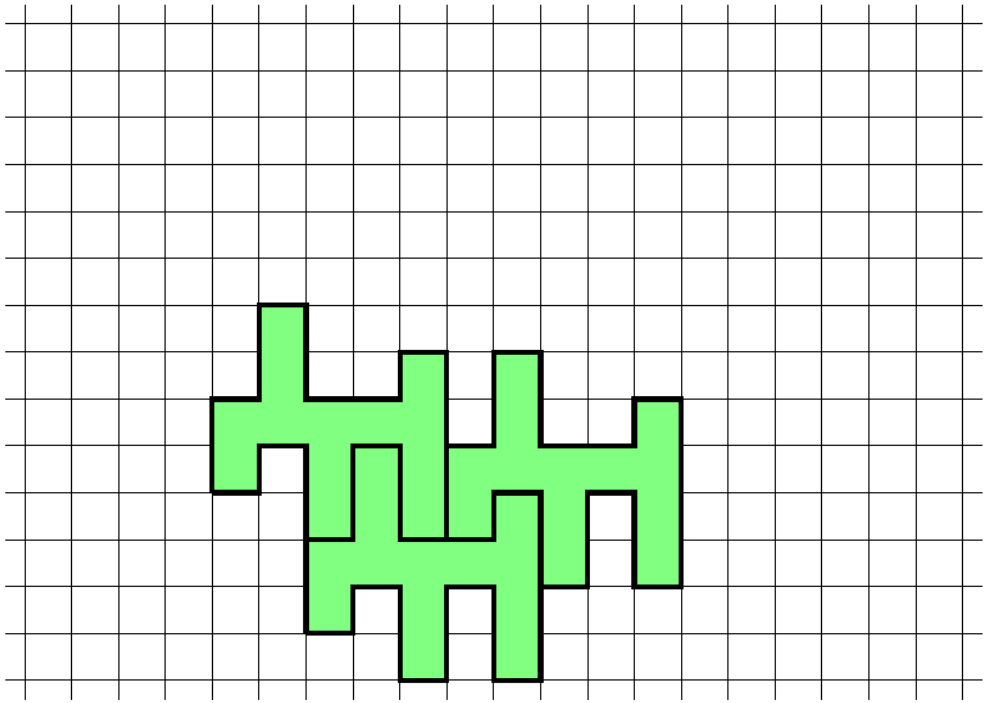
Tilings by translation



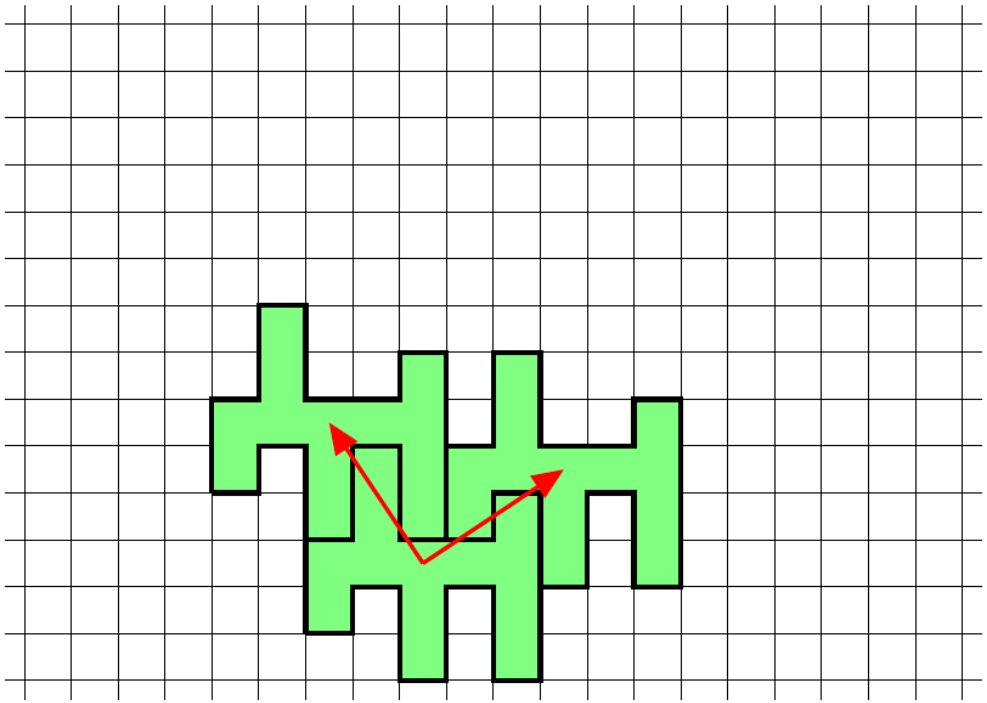
Tilings by translation



Tilings by translation



Tilings by translation



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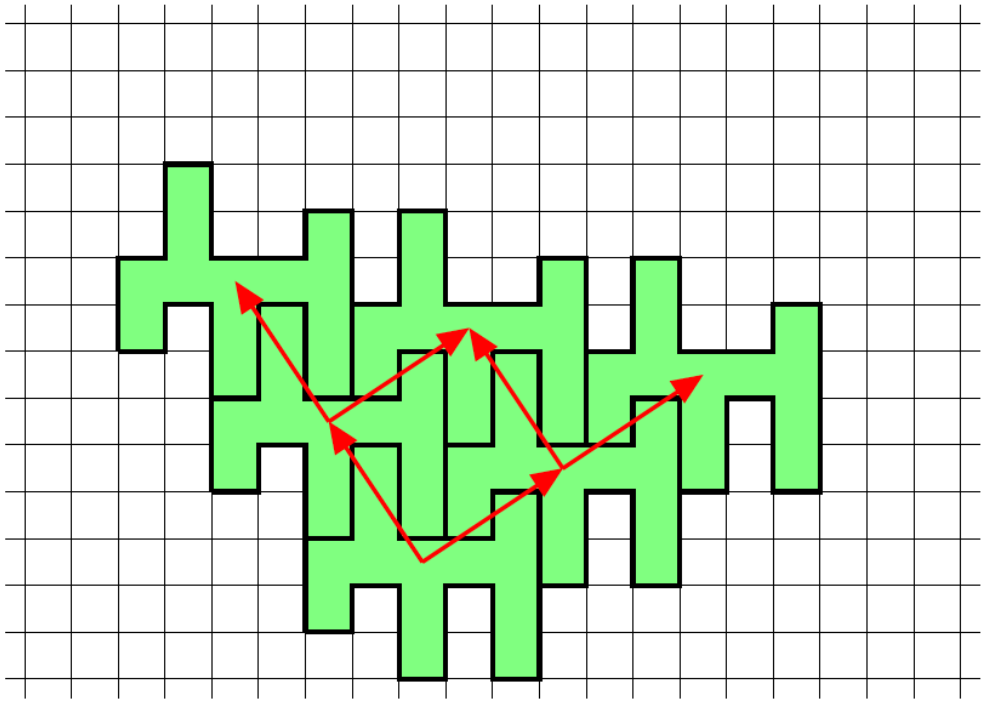

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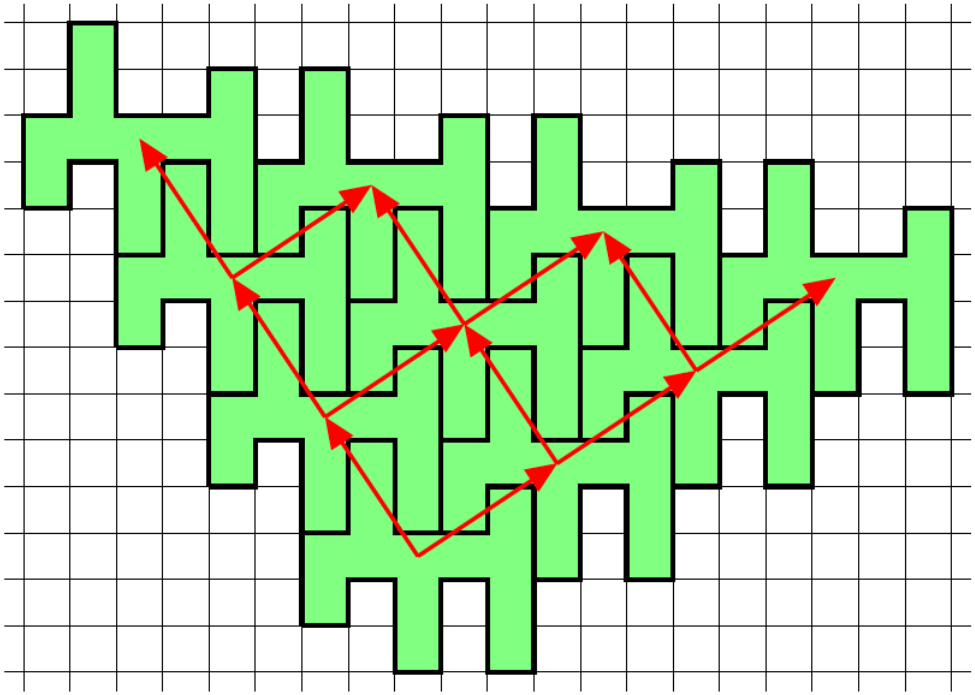

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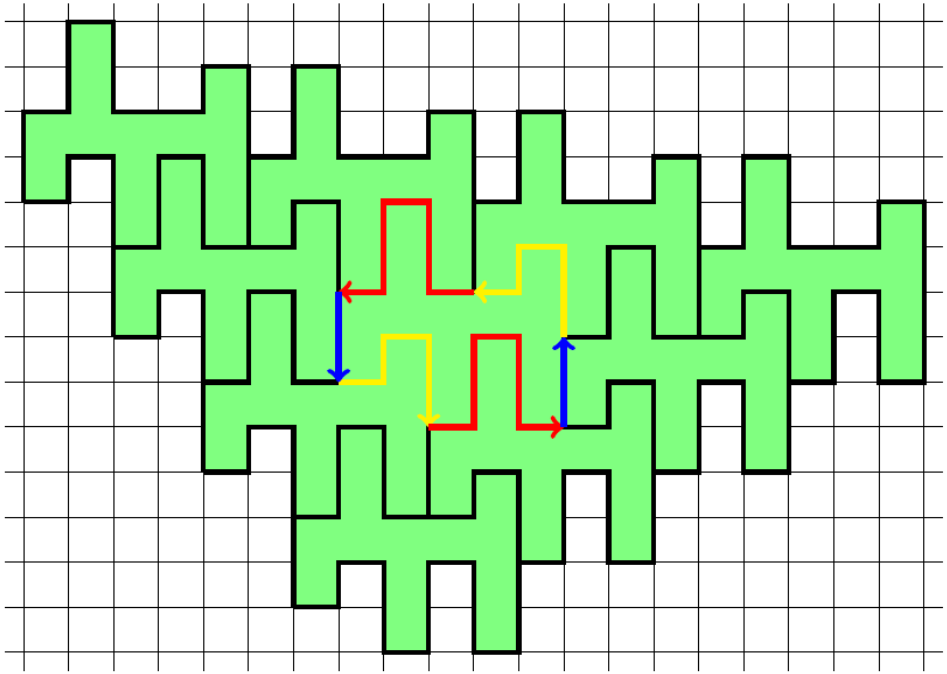
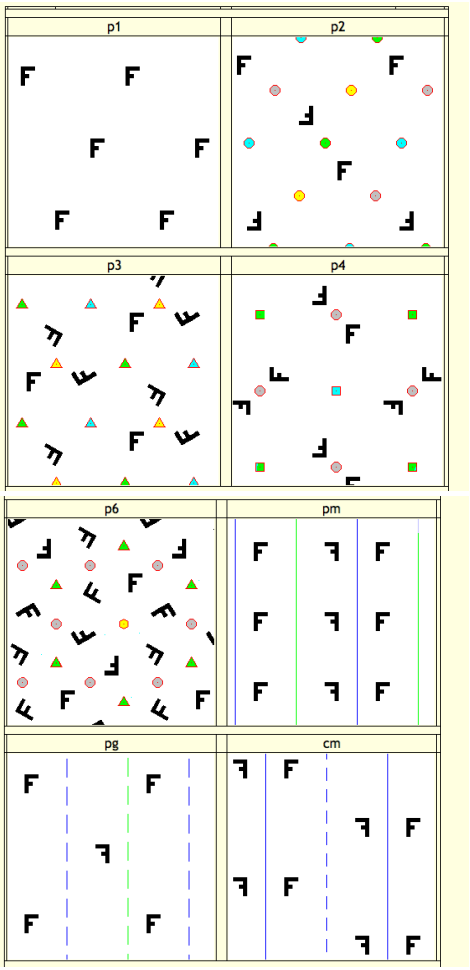


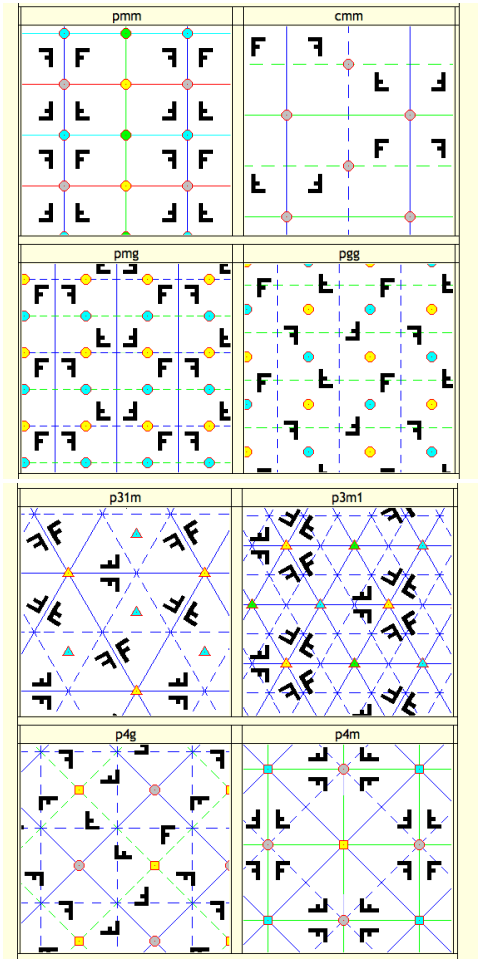
Tilings of the plane

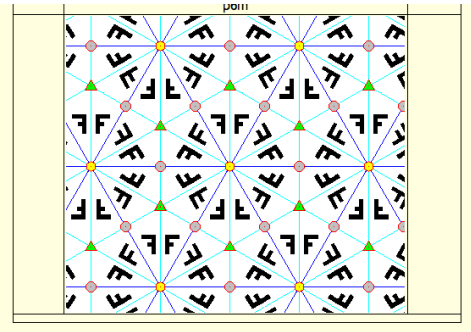
Isometries of the plane : translation, rotation, reflection and glide reflection.
17 crystalographic groups for the plane (Bravais 1847).

The 17 crystallographic groups are represented at the Alhambra of Grenada (by artists around 1350).

Cristallographic groups



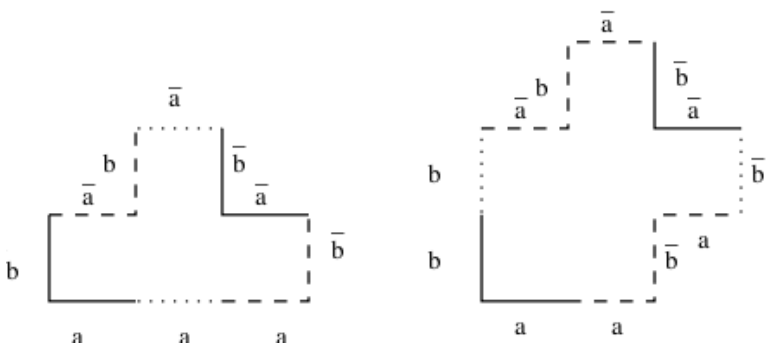




Tilings of the plane by translation

Definitions

Let *bw* be a *boundary word of P*, i.e. a word on the alphabet $\{a, b, \bar{a}, \bar{b}\}$ where a codes left step, b up step, $\bar{a}$ right step and $\bar{b}$ down step which codes the boundary of the polyomino P.



bw is defined up to circular permutations of letters.

Beauquier-Nivat's Theorem

Theorem [Beauquier-Nivat 1991]

A polyomino P tiles the plane by translation if and only if the boundary word bw of P is equal to $XYZ\,\overline{X}\,\overline{Y}\,\overline{Z}$ or $XY\,\overline{X}\,\overline{Y}$ with $X, Y, Z \in \{a, b, \bar{a}, \bar{b}\}^*$ and where $\overline{w} = \overline{w_1 w_2 \cdots w_n} = \overline{w}_n \overline{w}_{n-1} \cdots \overline{w}_1$ with $w_i \in \{a, b, \bar{a}, \bar{b}\}$.

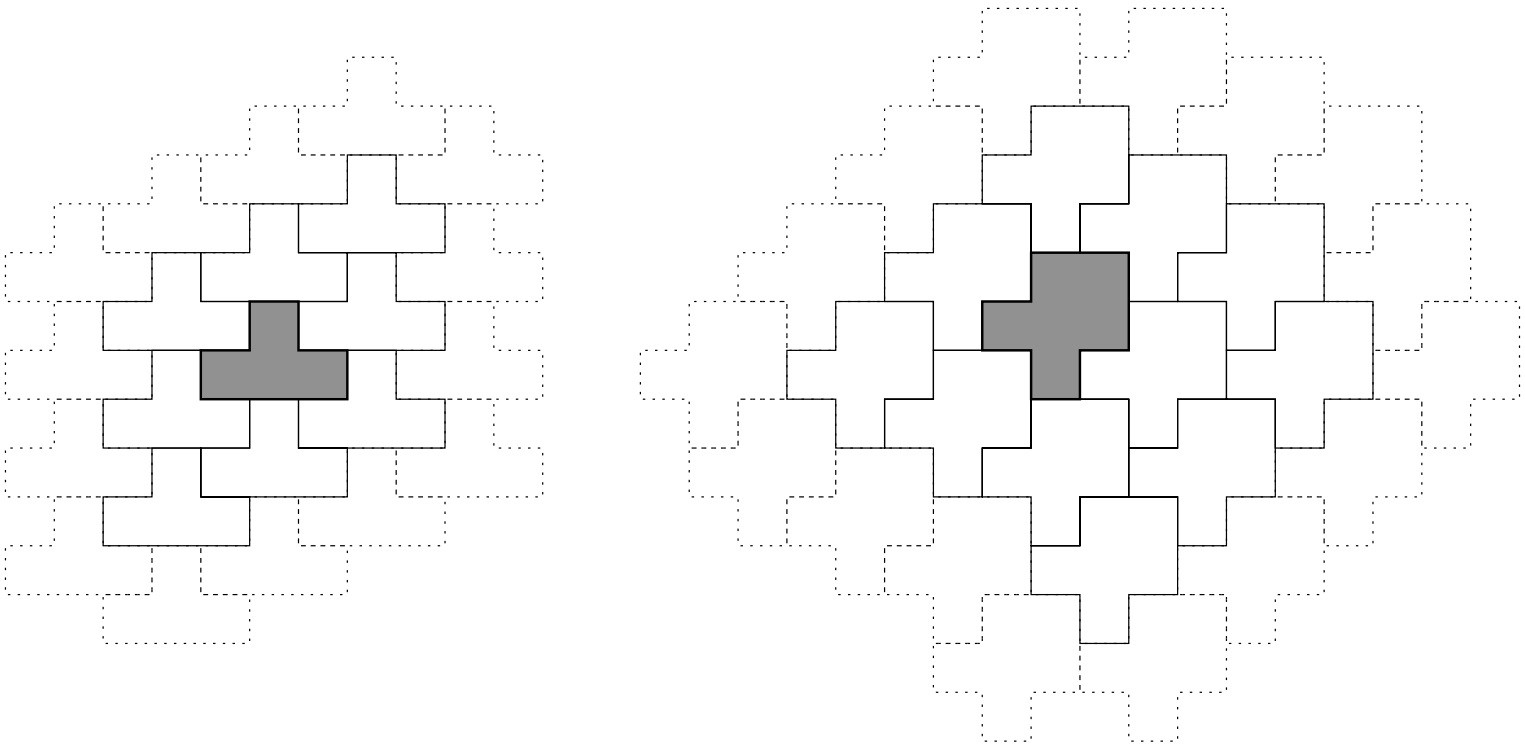
Tiling models

According to Beauquier-Nivat's Theorem, we have 2 ways of tilings the plane by translations :

If the boundary word is $XYZ\ \overline{X}\ \overline{Y}\ \overline{Z}$, we talk about pseudo-hexagon.

If the boundary word is $XY\ \overline{X}\ \overline{Y}$, we talk about pseudo-square.

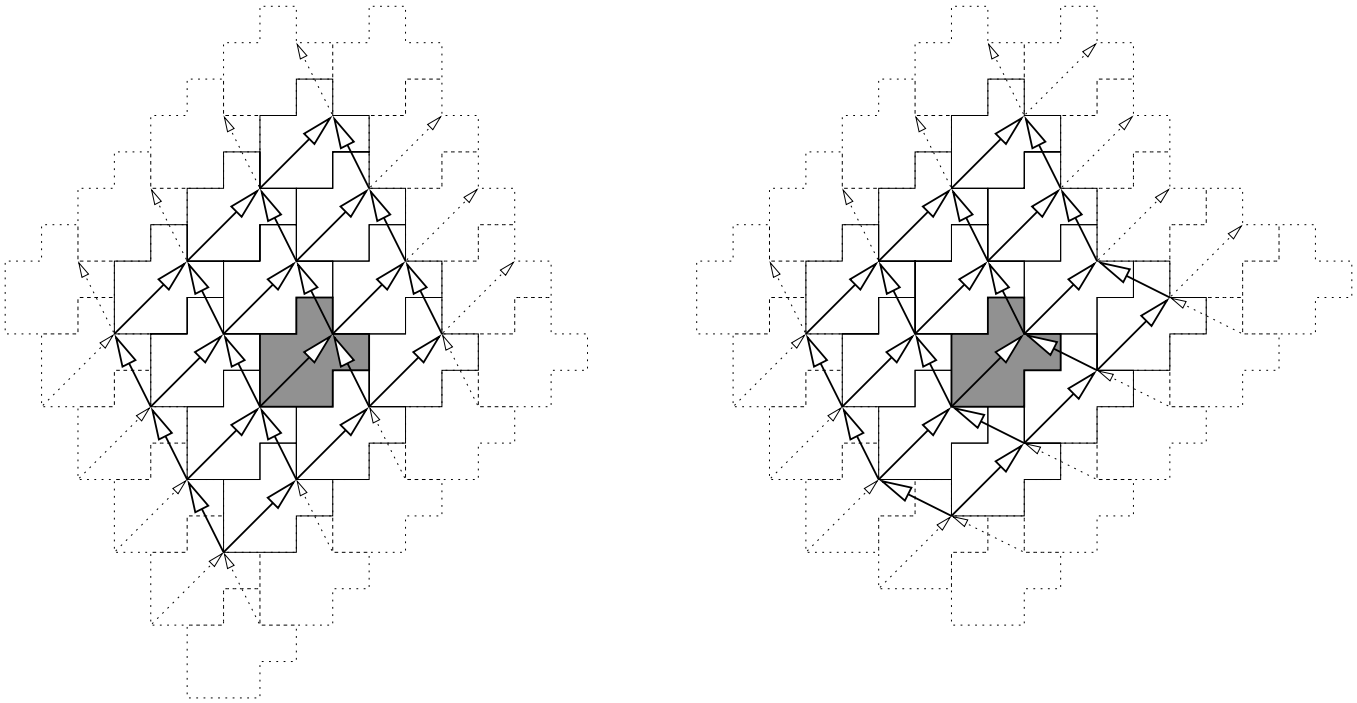
Tilings by translation



Lattice periodic tilings

Definition

A tiling is called *lattice periodic* if it is invariant under the translation by two non-collinear vectors.



a) b)

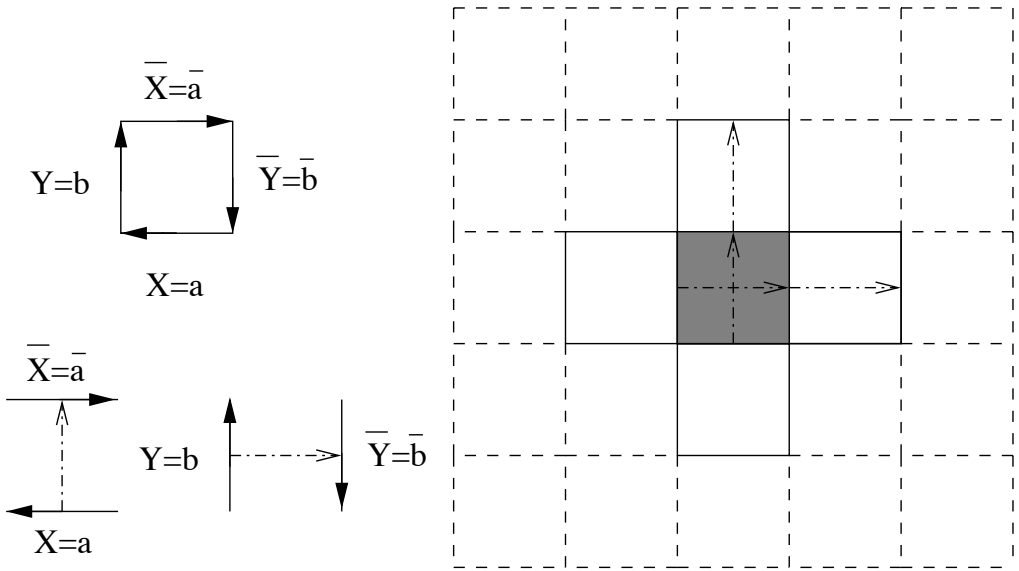


FIGURE: **Tiling by a mino and the 4 adjacent tiles of the grey mino**

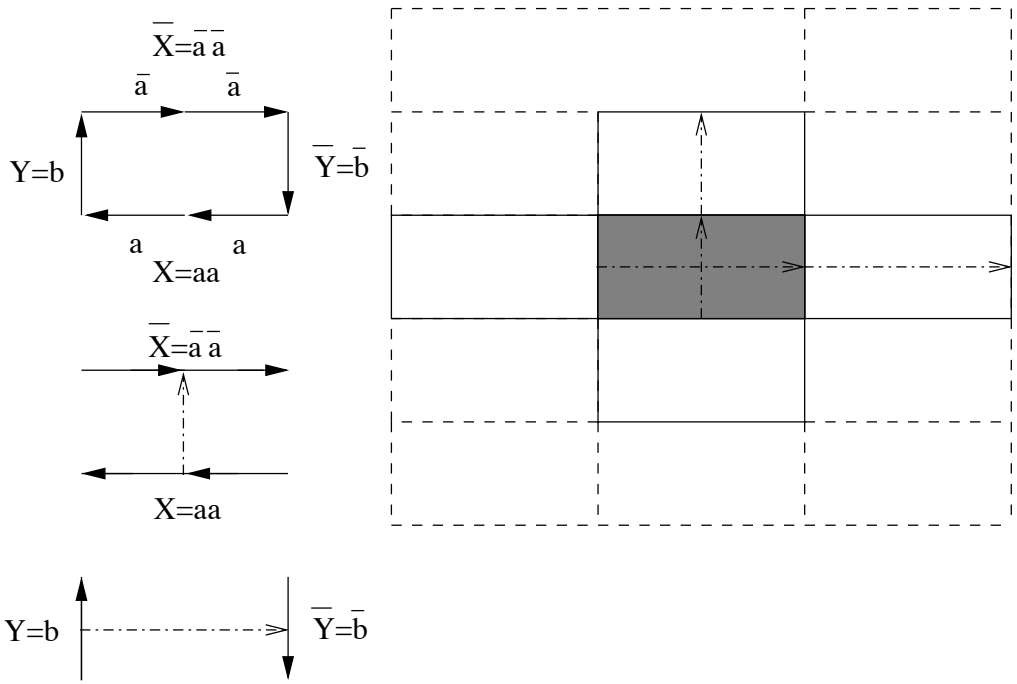


FIGURE: **Tiling of the plane by a domino like a pseudo square and the 4 adjacent tiles of the grey domino**

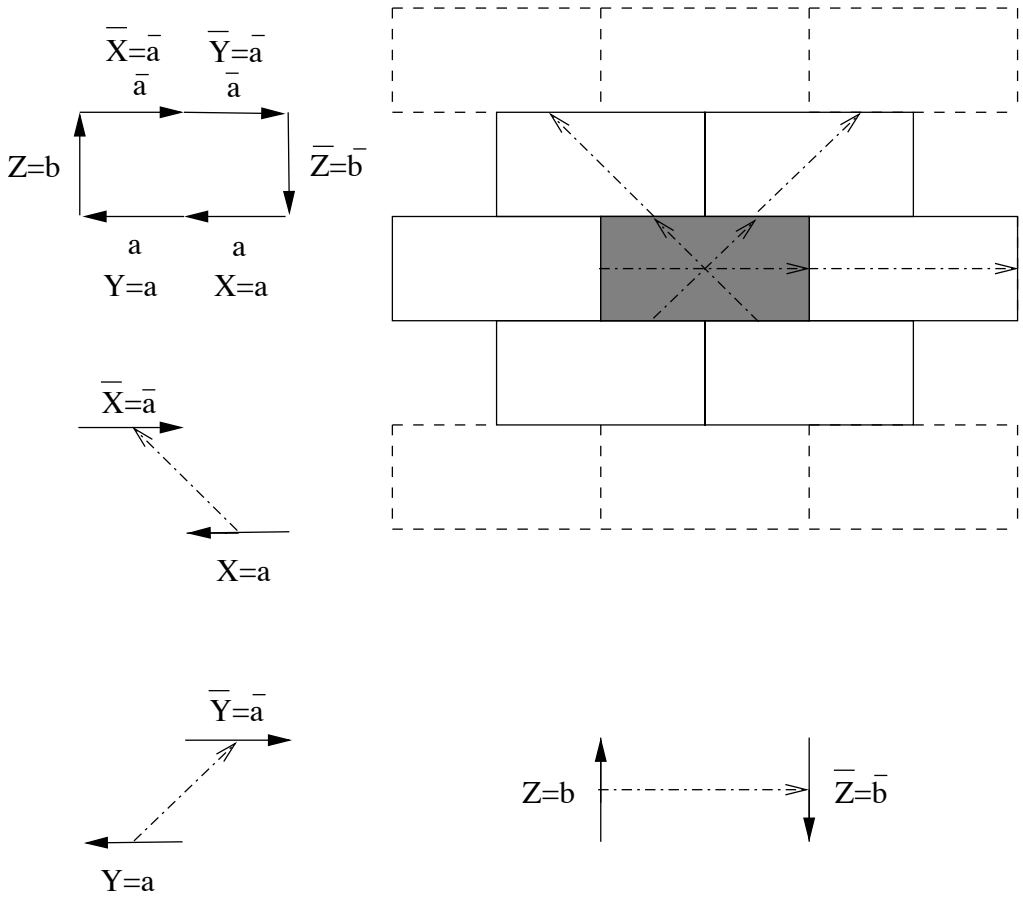


FIGURE: **Tiling of the plane by a domino like a pseudo hexagon and the 6 adjacent tiles of the grey domino**

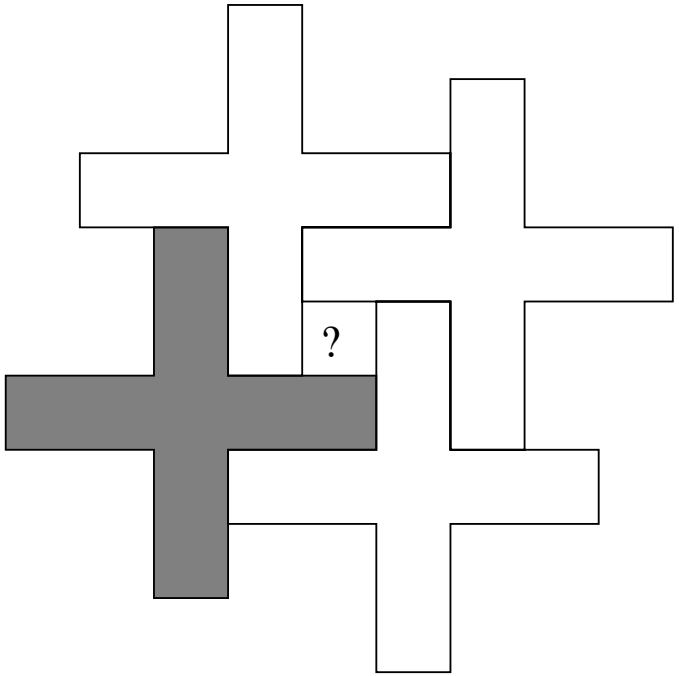


FIGURE: **A thin cross that doesn't tile the plane**

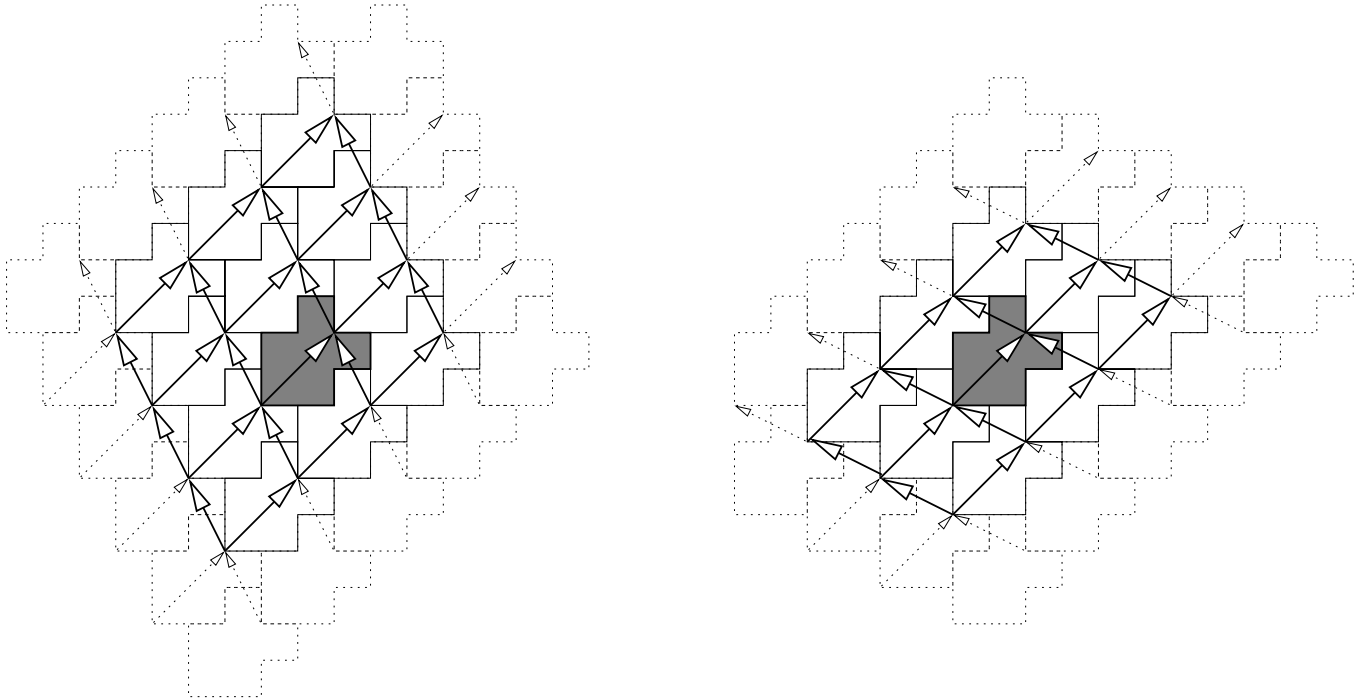


FIGURE: **Two regular tilings of the plane by the same polyomino**

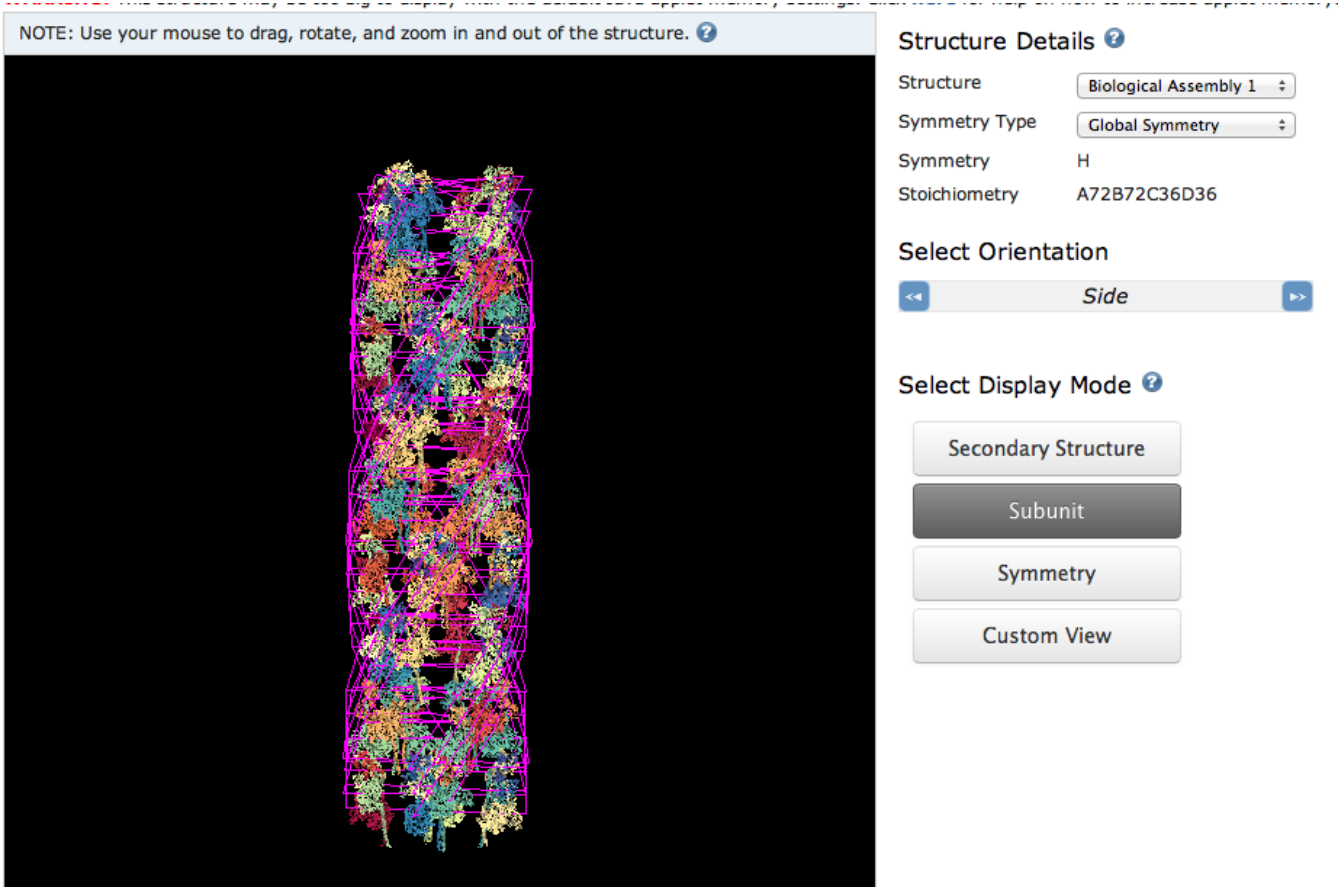


FIGURE: **Spider silk.**

From regular tilings of the plane to tilings of a fiber

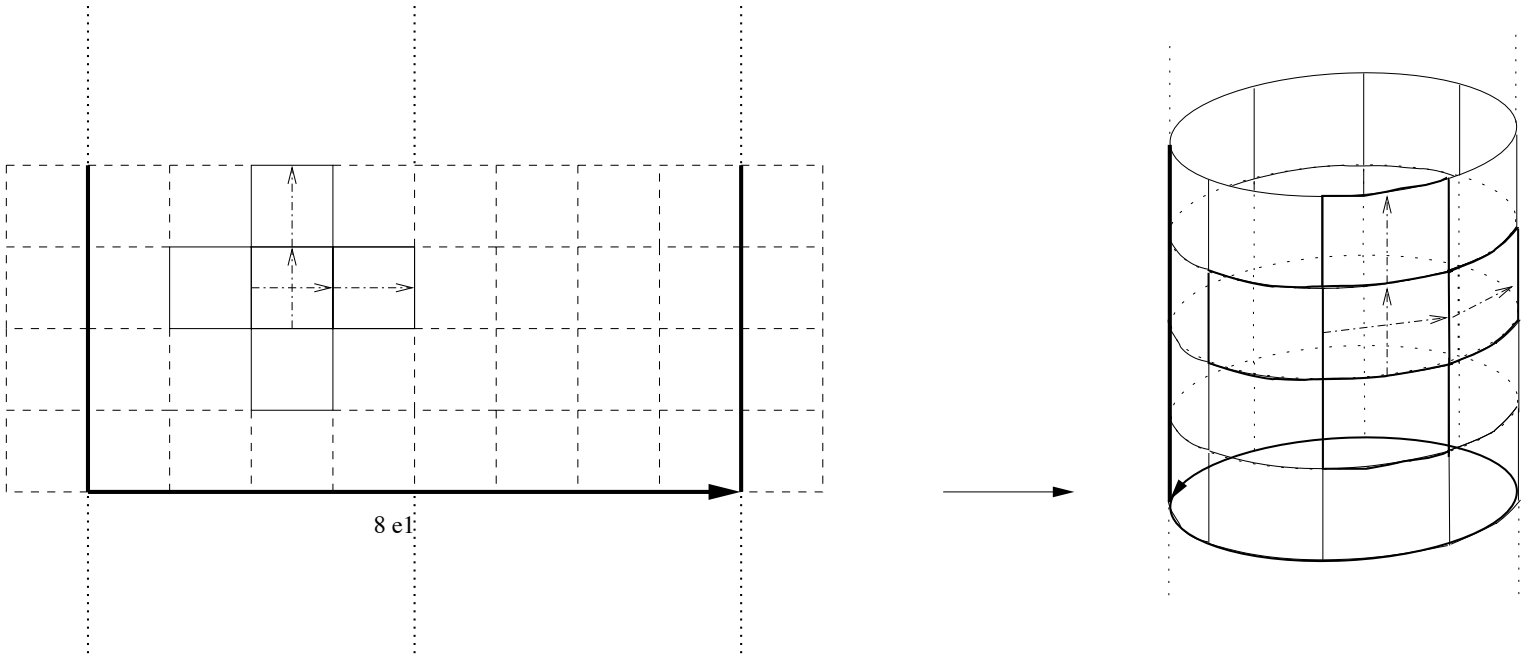


FIGURE: **From tiling to cylinder by using the translation of** 8 **times the vector** $\vec{e}_1$**.**

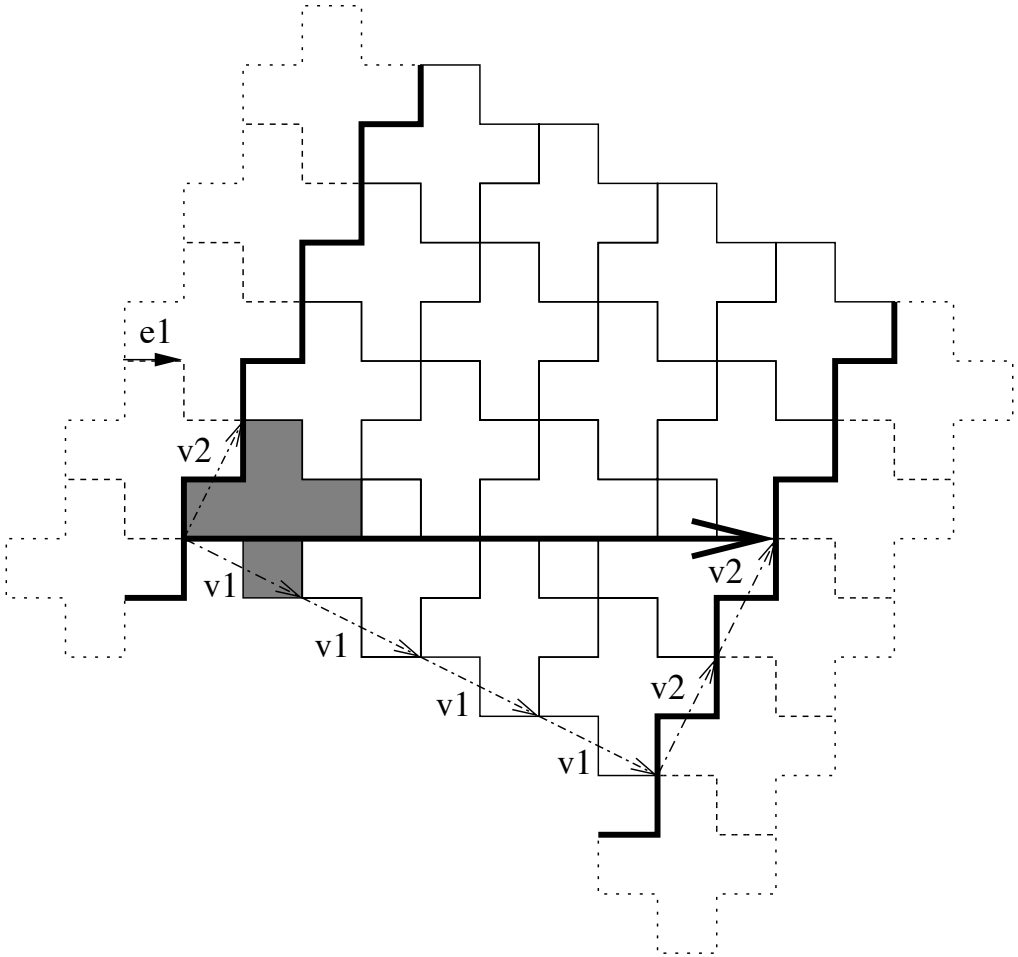


FIGURE: **Two boundaries in correspondence by the translation** $4\vec{v}_1 + 2\vec{v}_2$)

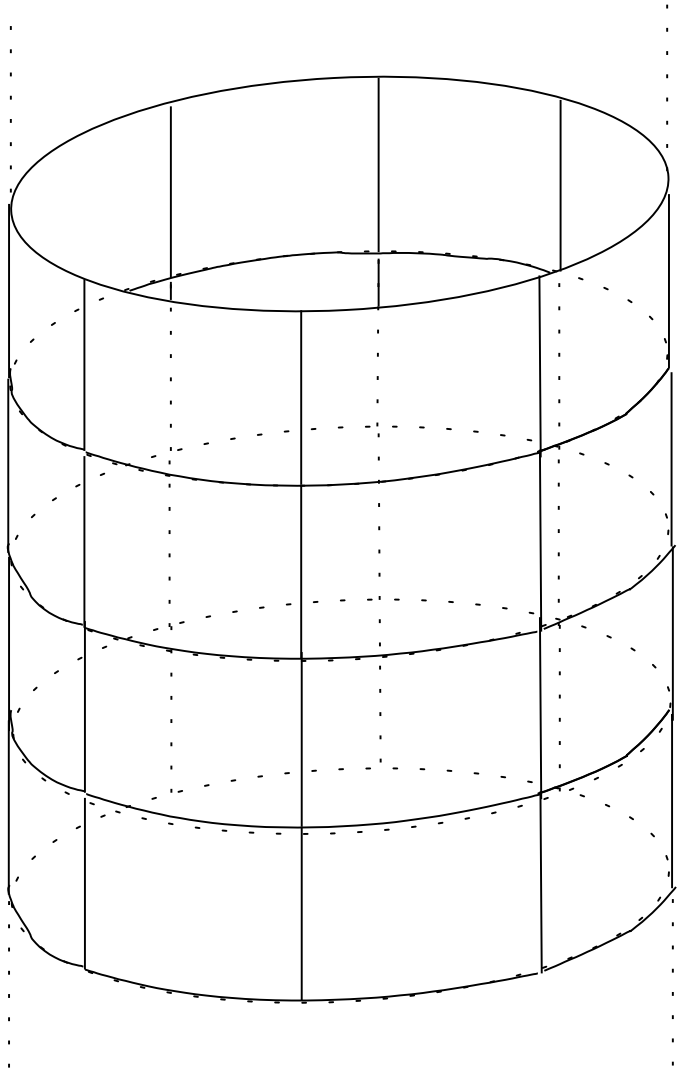


FIGURE: **Fiber with a pseudo square shape.** Each tile is surrounded by 4 tiles.

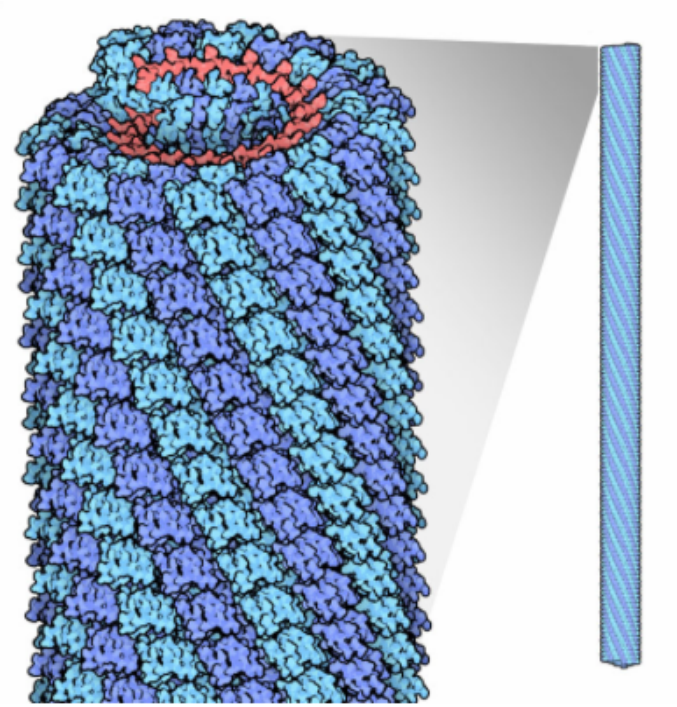


FIGURE: **Tobacco Mosaic Virus.**

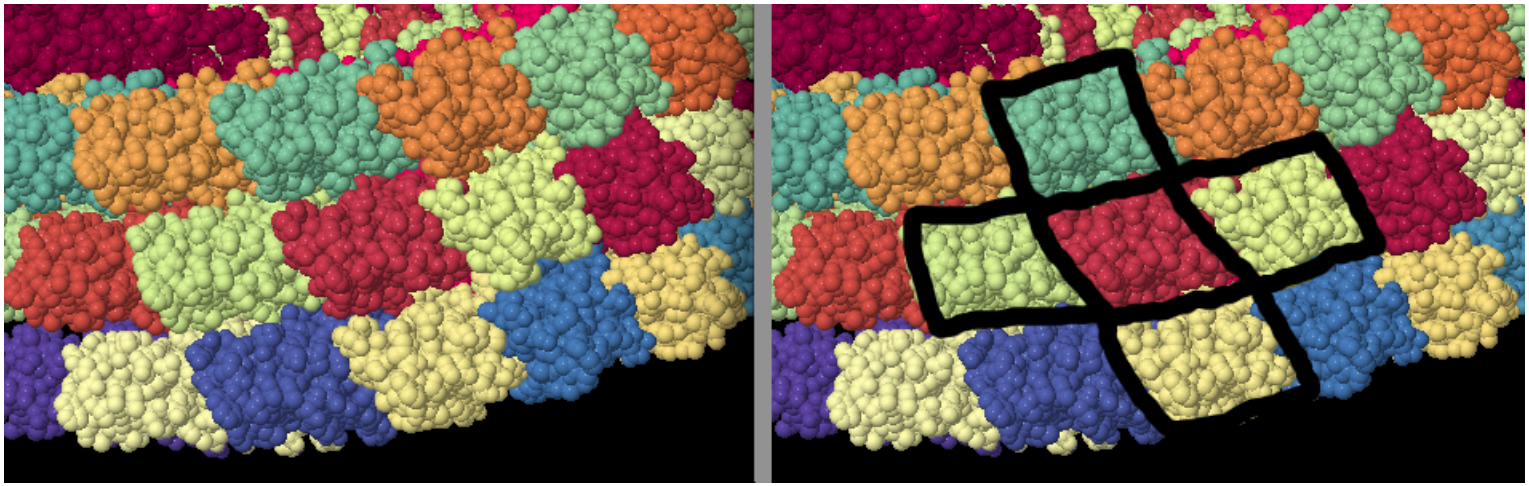


FIGURE: **Tobacco Mosaic Virus : an example of tiling of a fiber with 4 adjacent chains.**

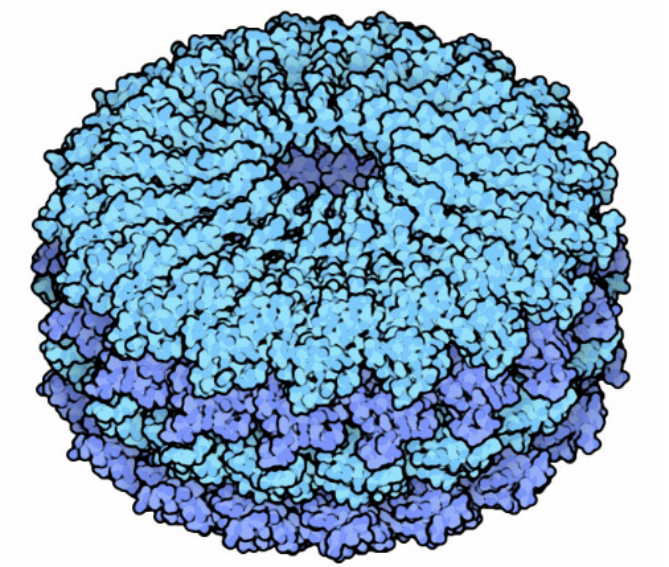


FIGURE: **Tobacco Mosaic Virus : a 17-mer.**

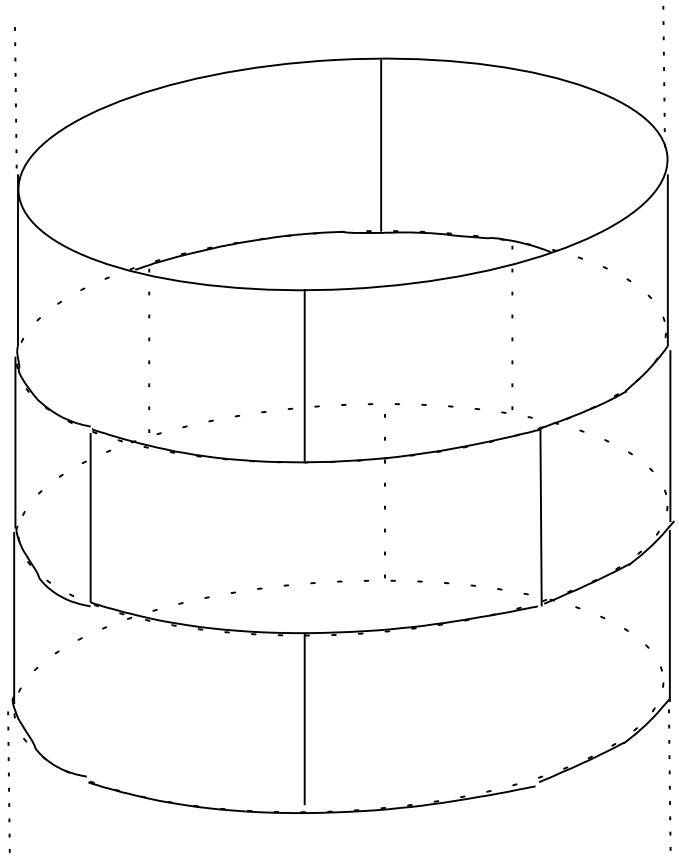


FIGURE: **Fiber with a pseudo hexagon shape.** Each tile is surrounded by 6 tiles. Remark that pseudo hexagon shapes appear in particular when there is a tilt on the fiber.

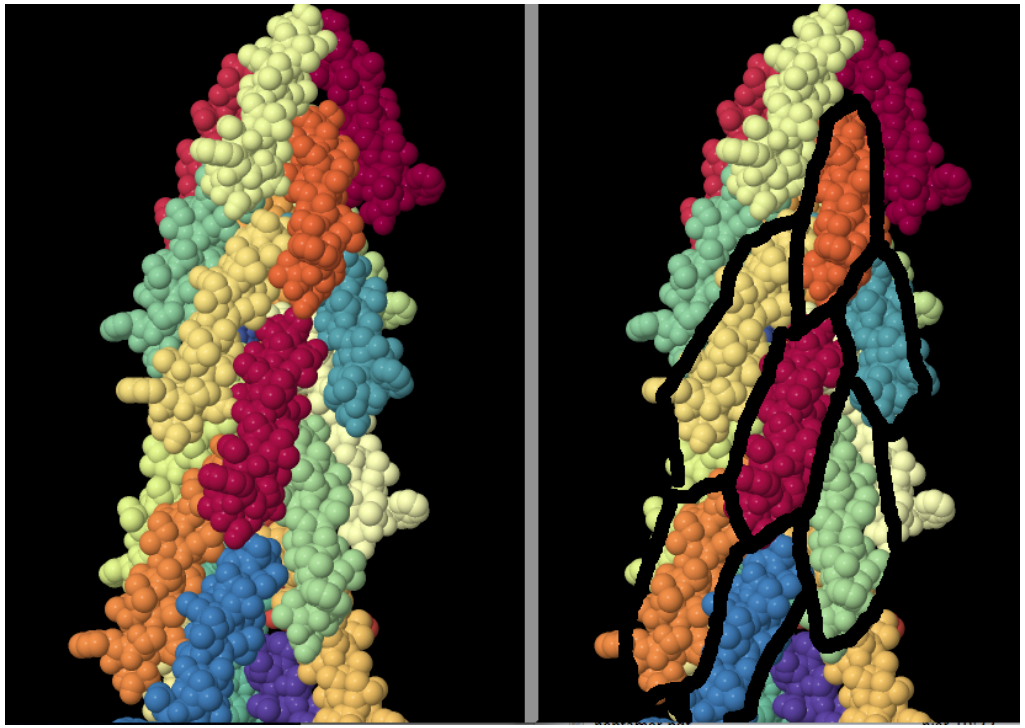


FIGURE: **3J1R : an example of tiling of a fiber with 6 adjacent chains.**

From fold plasticity to fibers : the P53 case

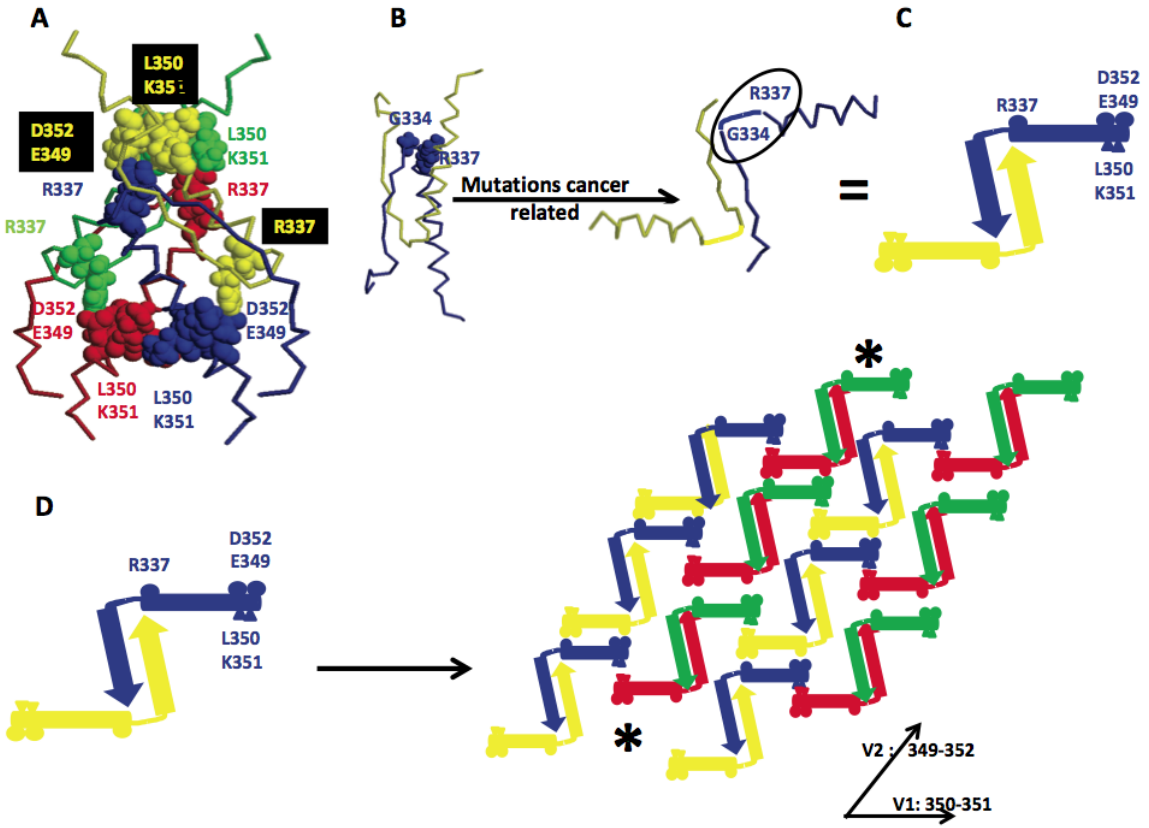


FIGURE: **A. The p53 tetrameric domain is made of 2 dimers.** Each monomer is made of a β-strand followed by a small helix ended by a long α-helix parallel to the β-strand (1SAK). The residue R337 is sensitive to mutation.

Tiling fibers by *n*-mers

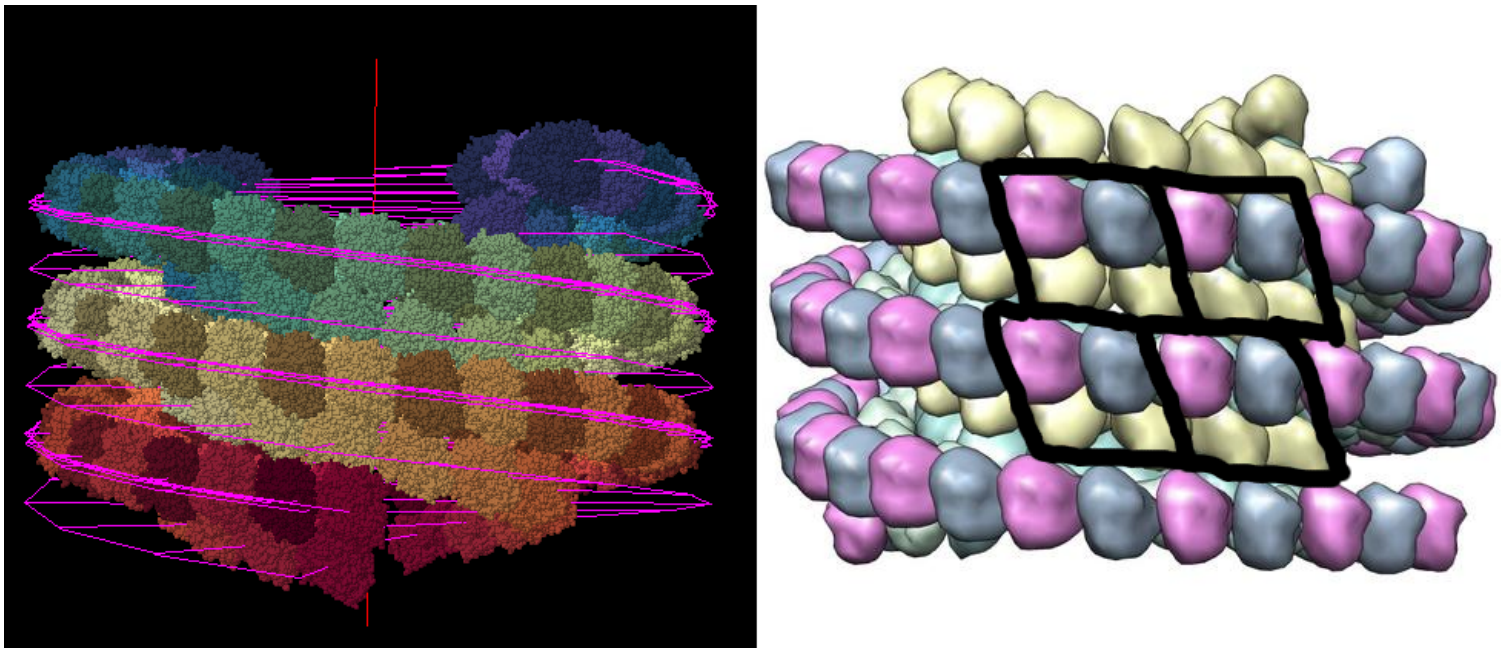


FIGURE: **Fiber 3J2U with a tetramer inside each pseudo hexagon**

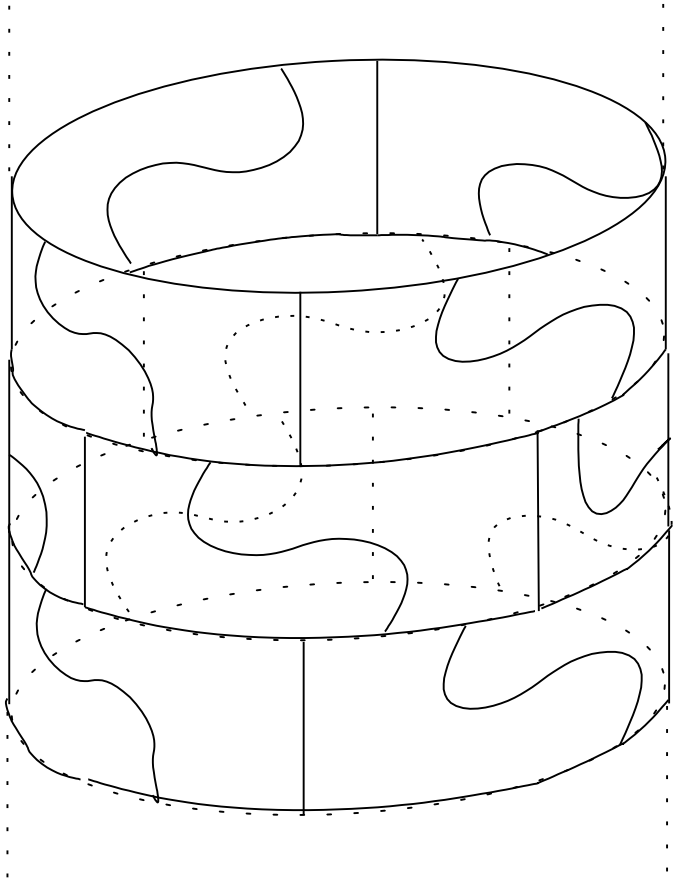


FIGURE: **Fiber with a dimer inside each pseudo hexagon**

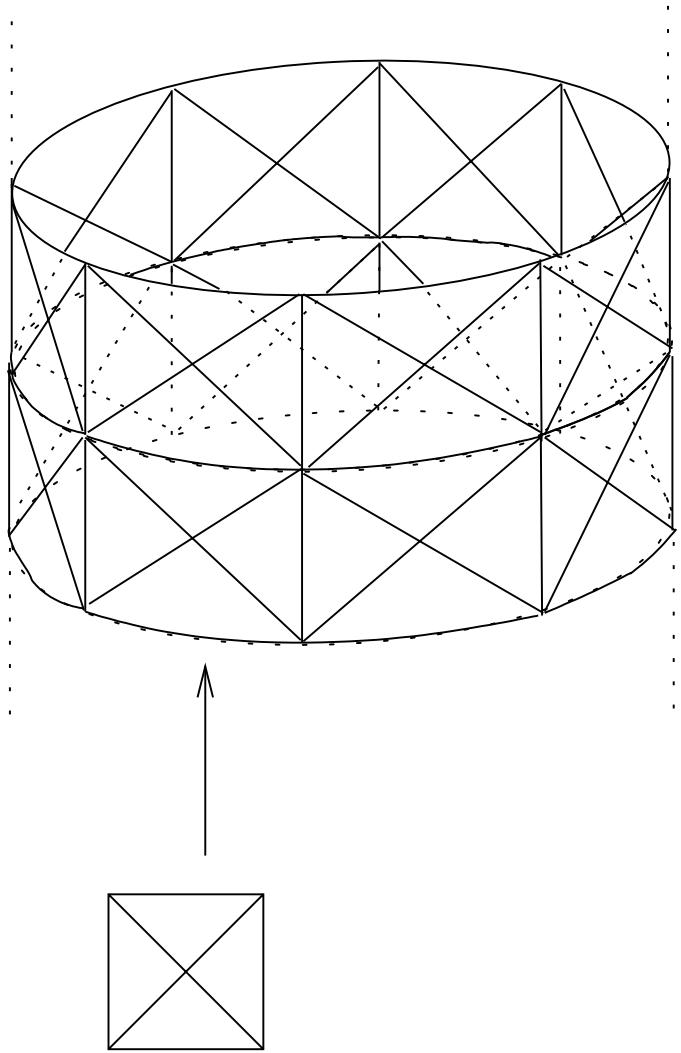


FIGURE: **Replacement of each pseudo square by a tetramer.**

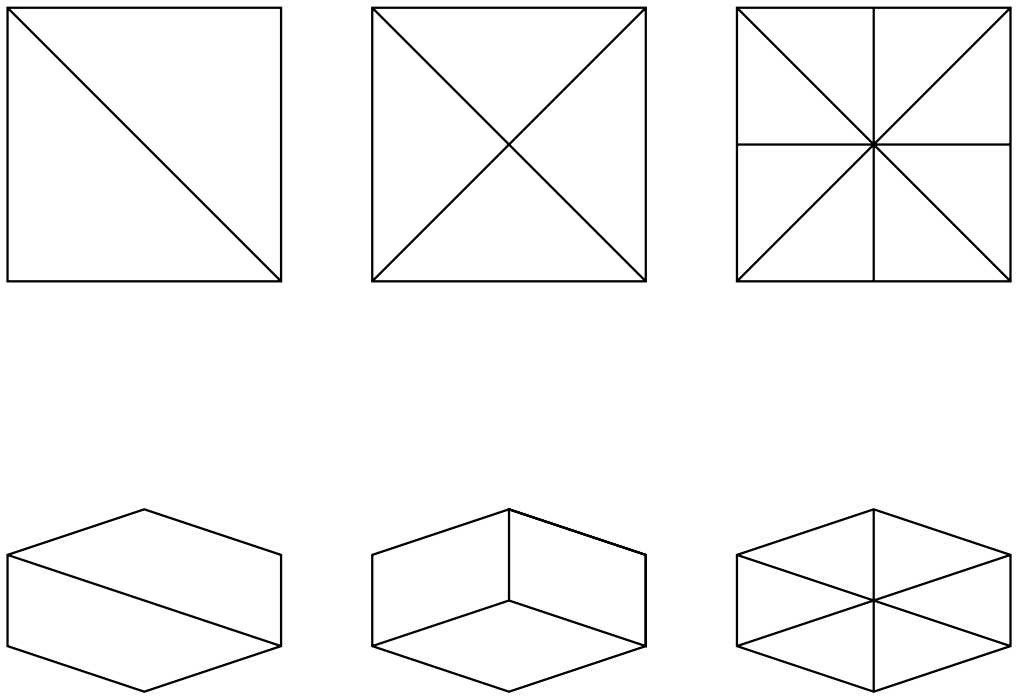


FIGURE: **Replacement of a pseudo square and of a pseudo hexagon.**

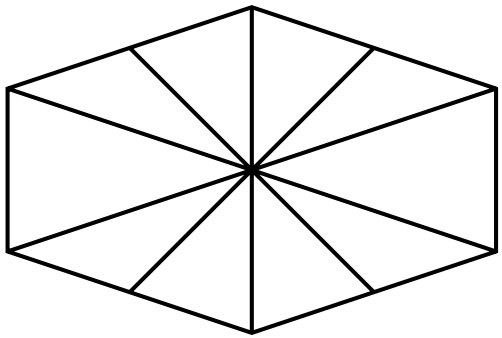


FIGURE: **Replacement of pseudo square by 2 non regular pentamers.**

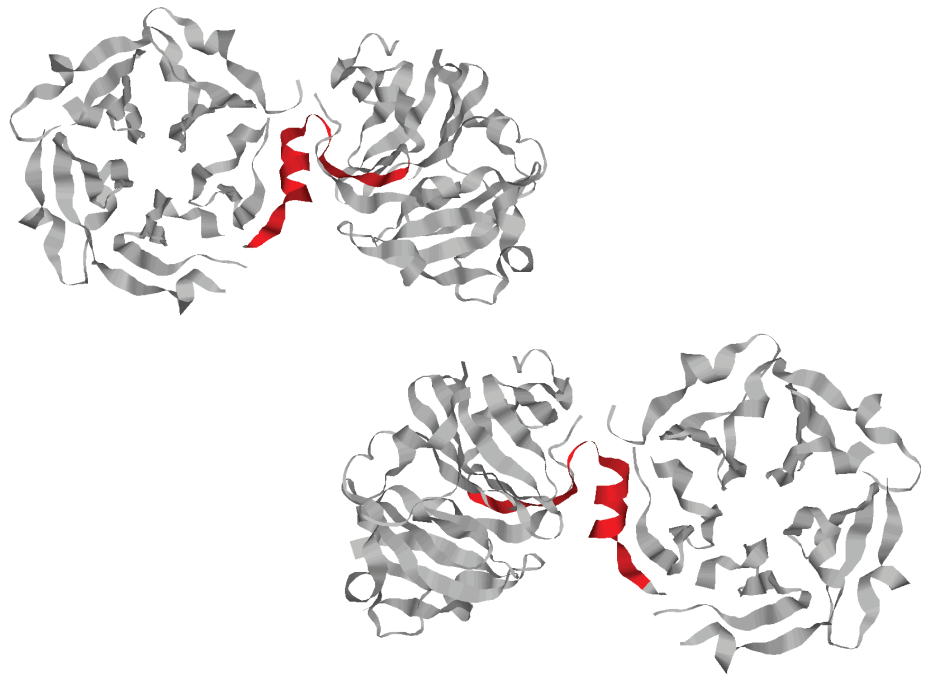


FIGURE: **Double asymmetrical pentamer (Tachylectin).**

PDB of 1SAK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1SAK
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Primary Citation
Refined solution structure of the oligomerization domain of the tumour suppressor p53.
Clore, G.M., Ernst, J., Clubb, R., Omichinski, J.G., Kennedy, W.M., Sakaguchi, K., Appella, E., Gronenborn, A.M.
Journal: (1995) Nat.Struct.Biol. 2: 321-333
PubMed: 7796267
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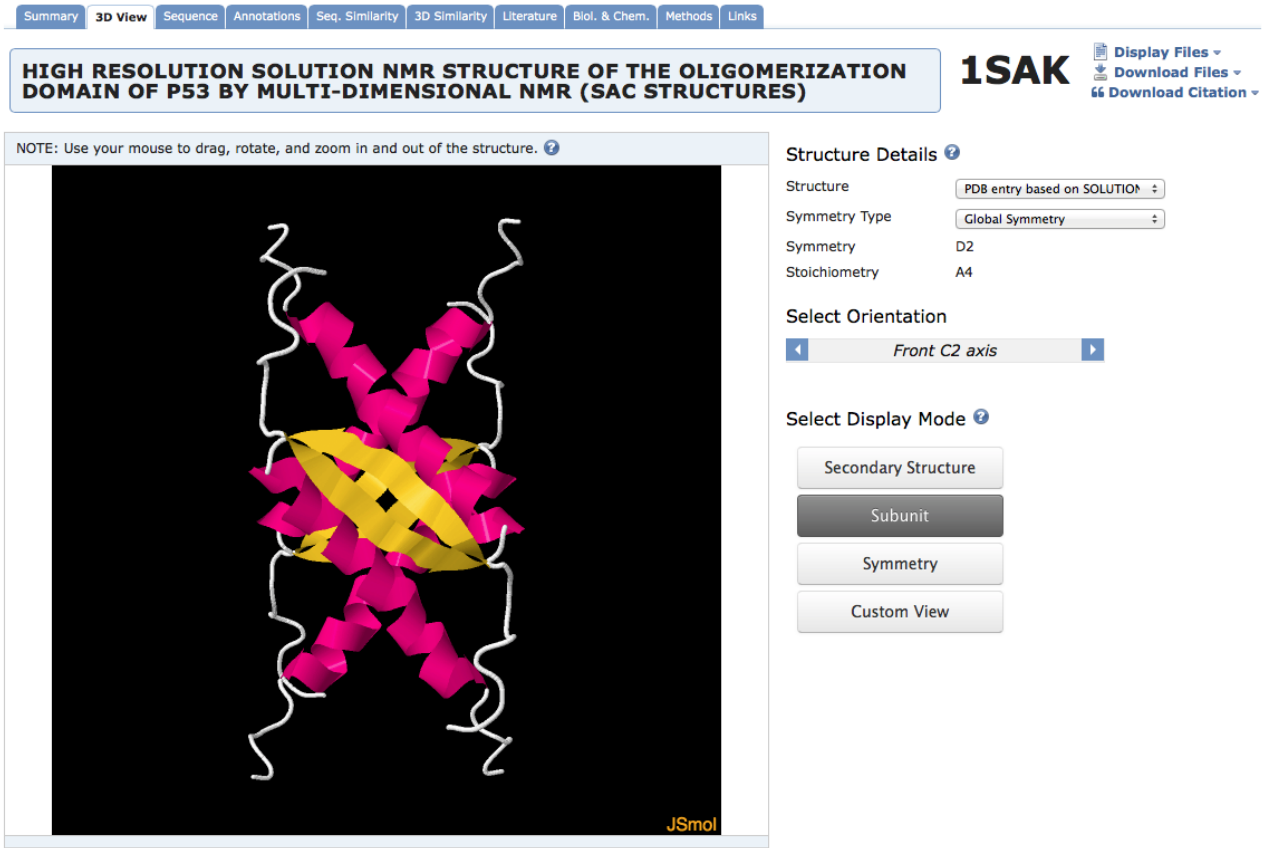
The NMR solution structure of the oligomerization domain of the tumour suppressor p53 (residues 319-360) has been refined. The structure comprises a dimer of dimers, oriented in an approximately orthogonal manner. The present structure determination is based on 4,472 experimental... [Read More & Search PubMed Abstracts]
Structure Image
3D View
More Images...
Symmetry: D2 view
Stoichiometry: Homo 4-mer - A4
Downloadable viewers:
Simple Viewer
Protein Workshop
Kiosk Viewer
Molecular Description
Hide
Classification: Anti Oncogene
Structure Weight: 19794.72
Molecule: TUMOR SUPPRESSOR P53
Polymer: 1 Type: protein Length: 42
Chains: A, B, C, D
Details: MINIMIZED AVERAGE SAC STRUCTURE

PDB of 1SAK


Summary
3D View
Sequence
Annotations
Seq. Similarity
3D Similarity
Literature
Biol. & Chem.
Methods
Links
HIGH RESOLUTION SOLUTION NMR STRUCTURE OF THE OLIGOMERIZATION DOMAIN OF P53 BY MULTI-DIMENSIONAL NMR (SAC STRUCTURES)
1SAK
Display Files
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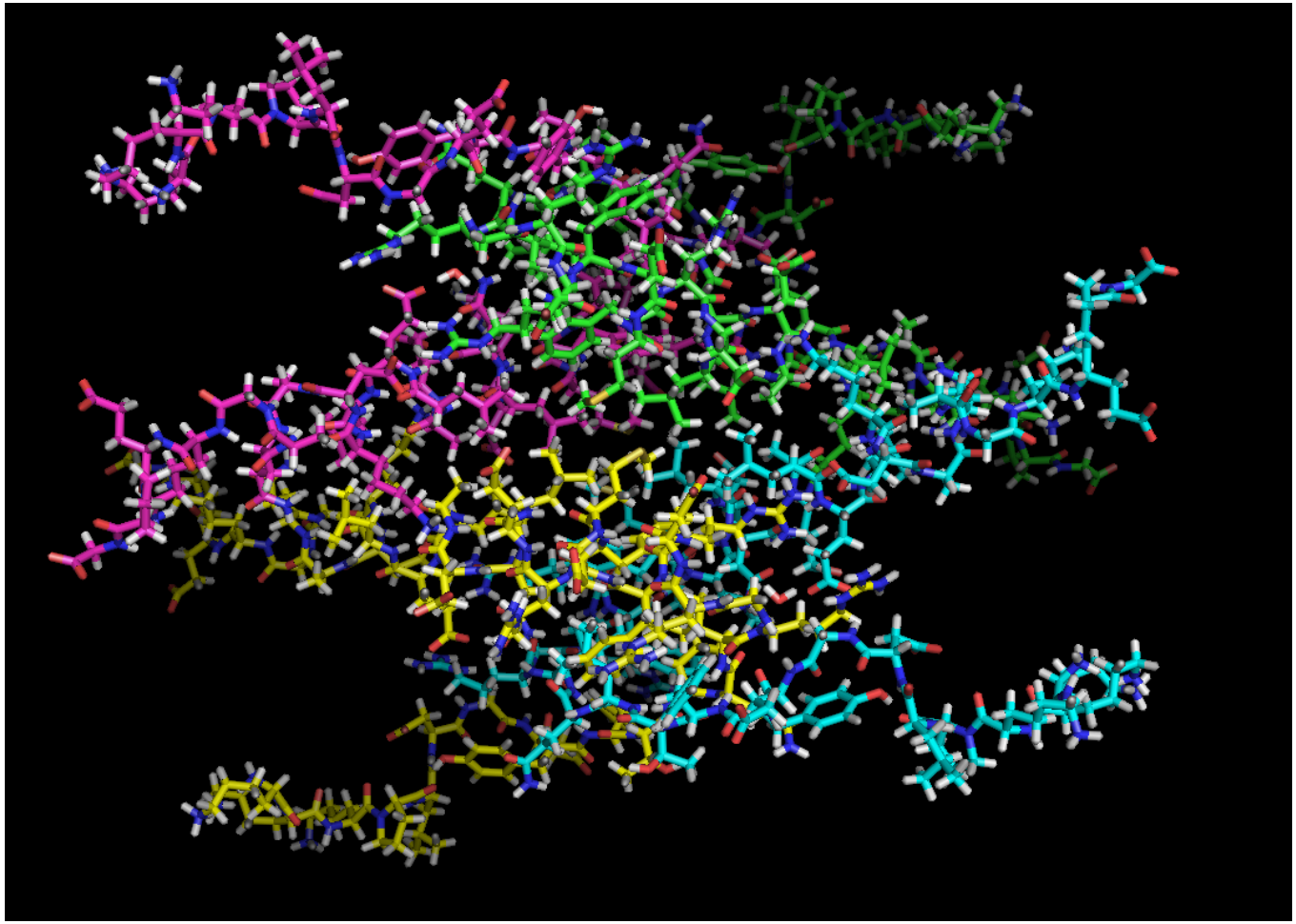
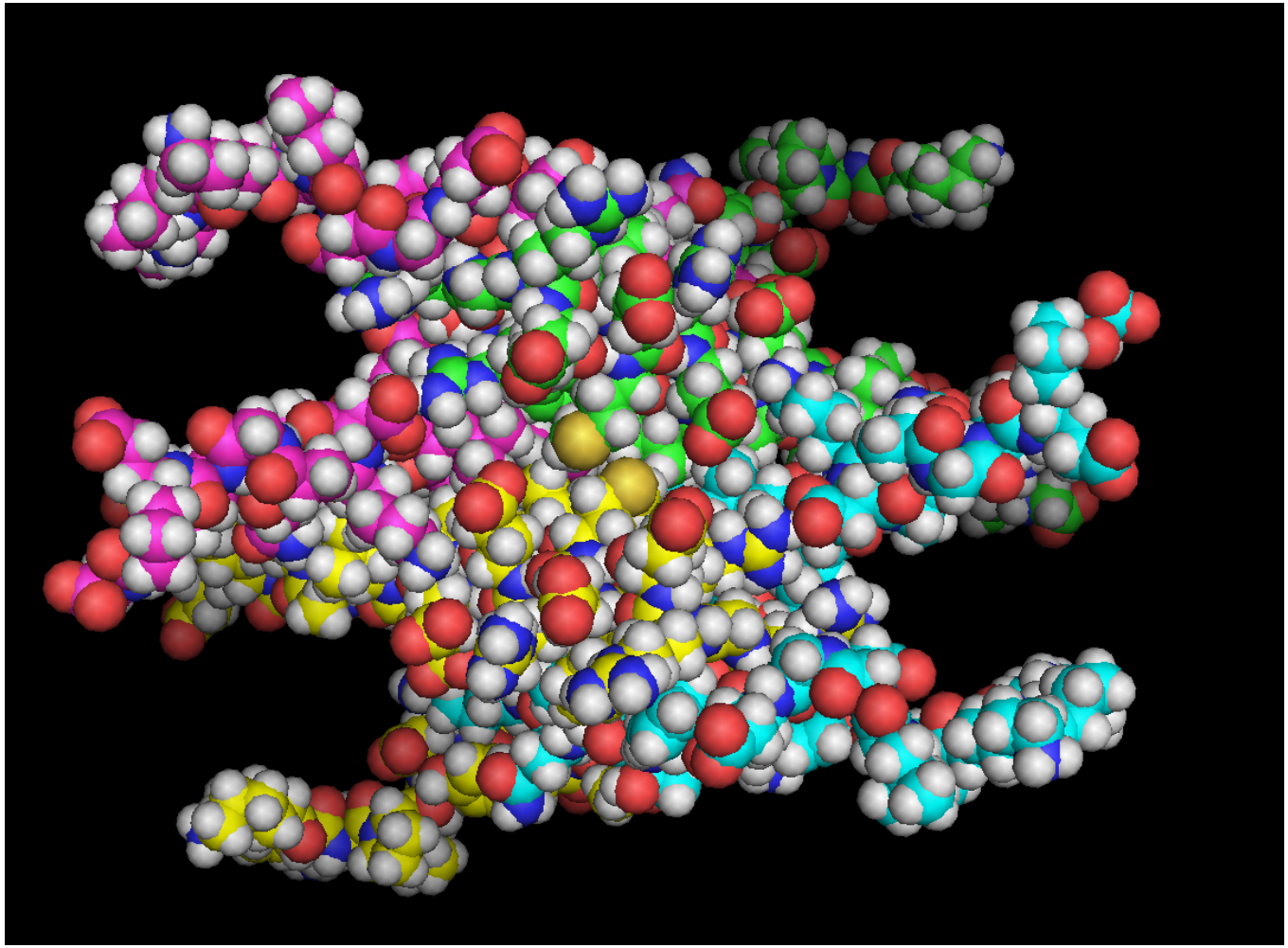
NOTE: Use your mouse to drag, rotate, and zoom in and out of the structure.
JSmol
Structure Details
Structure
PDB entry based on SOLUTION
Symmetry Type
Global Symmetry
Symmetry
D2
Stoichiometry
A4
Select Orientation
Front C2 axis
Select Display Mode
Secondary Structure
Subunit
Symmetry
Custom View

Chain structure of P53

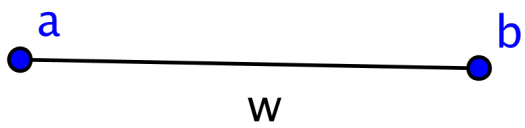


Atomic structure of P53

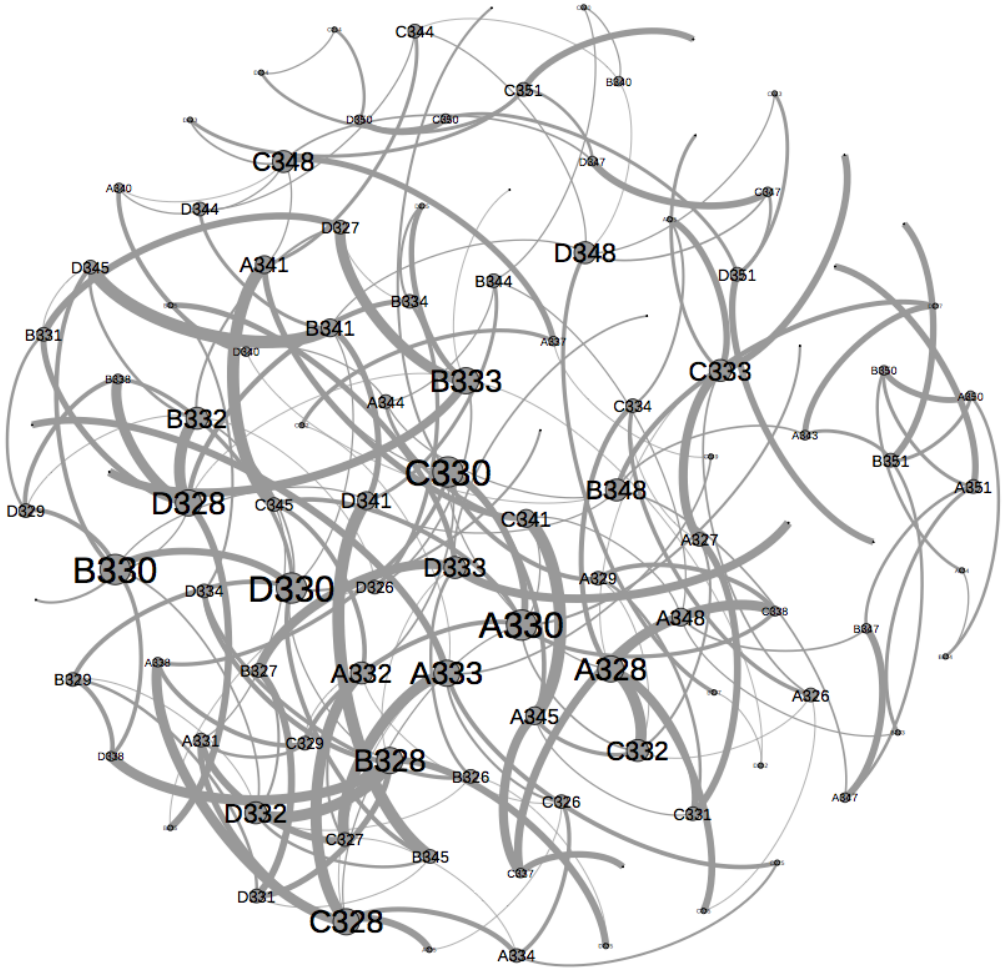


Protein graph

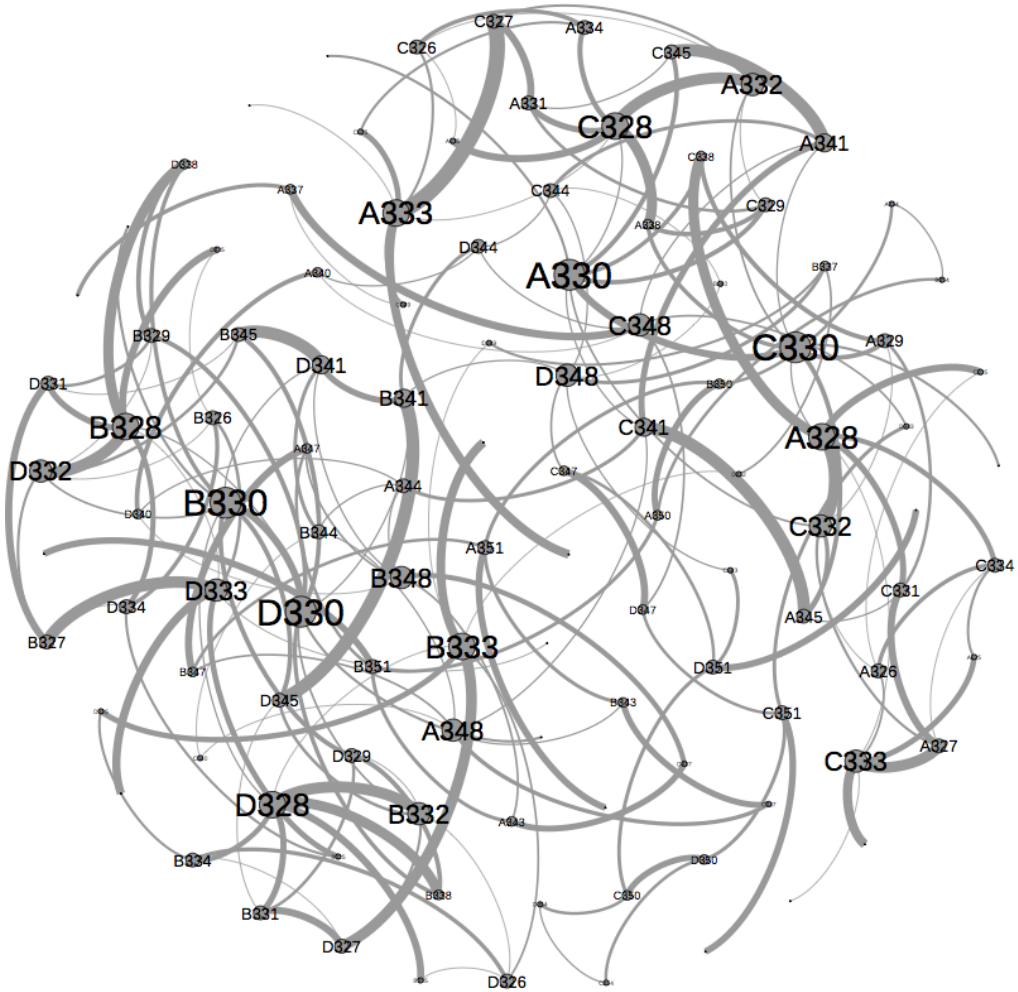
A protein graph (network) is produced by *Spectralpro* (algorithm) considering amino acids as vertices and, for every two vertices there exists an edge if there is an atomic interaction between them. The weight of an edge is the number of atoms involved in the interaction between the two amino acids.



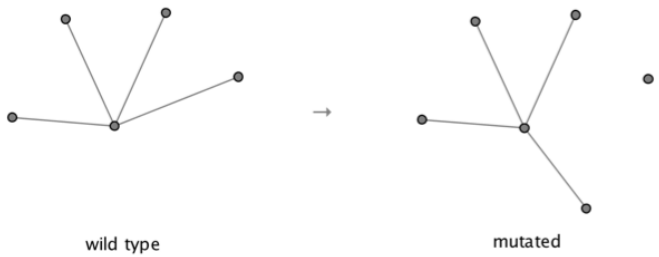
Network structure of P53



Network of mutated G334V in silico using FoldX

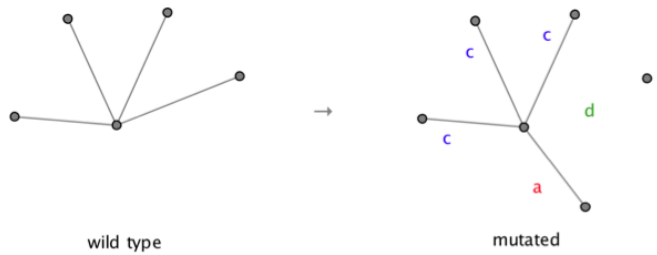


Impact measure



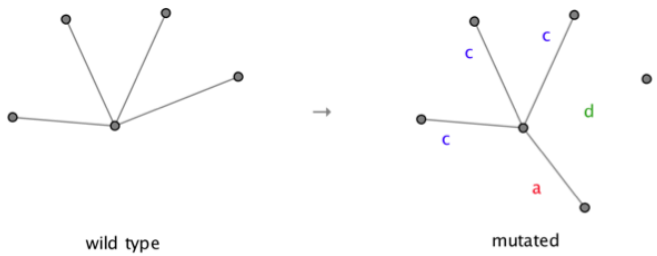
The effect of a mutation is measured by comparing wild type and mutated networks *edges*.

Impact measure



The *Appeared* (a), *disappeared* (d) and *conserved* (c) atomic interactions are counted as in $\frac{a+d}{c}$ and summed over the whole network.

Impact measure

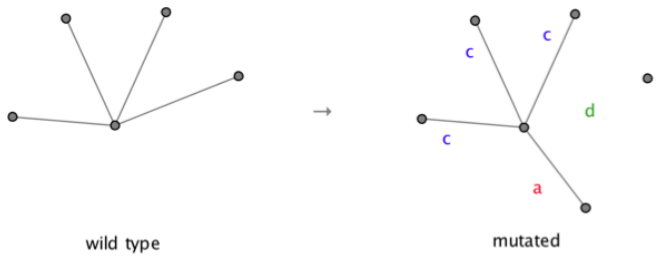


wild type mutated

When two vertices:

- Are no more in interaction (no edge exist between them) after a mutation, or
- They are in interaction only in the mutated network.

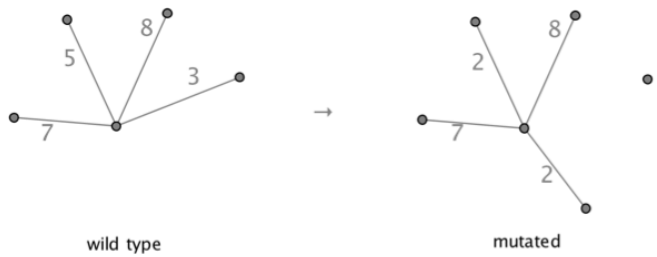
Impact measure



wild type mutated

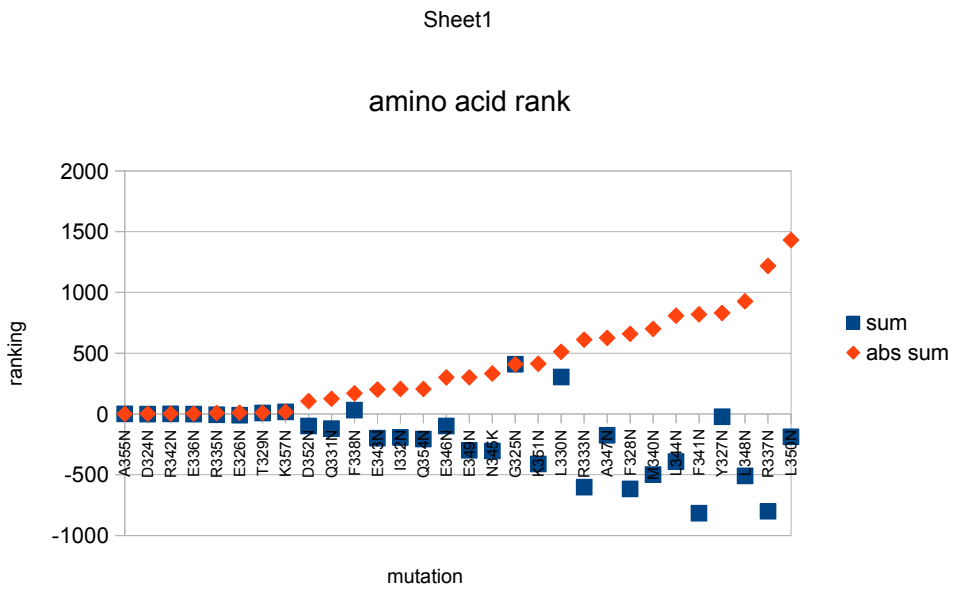
Namely, when $c = 0$, a factor of 100 is considered in the sum.

Impact measure



example

$$\frac{0}{7}+\frac{3}{5}+\frac{0}{8}+100+100 = 200.6$$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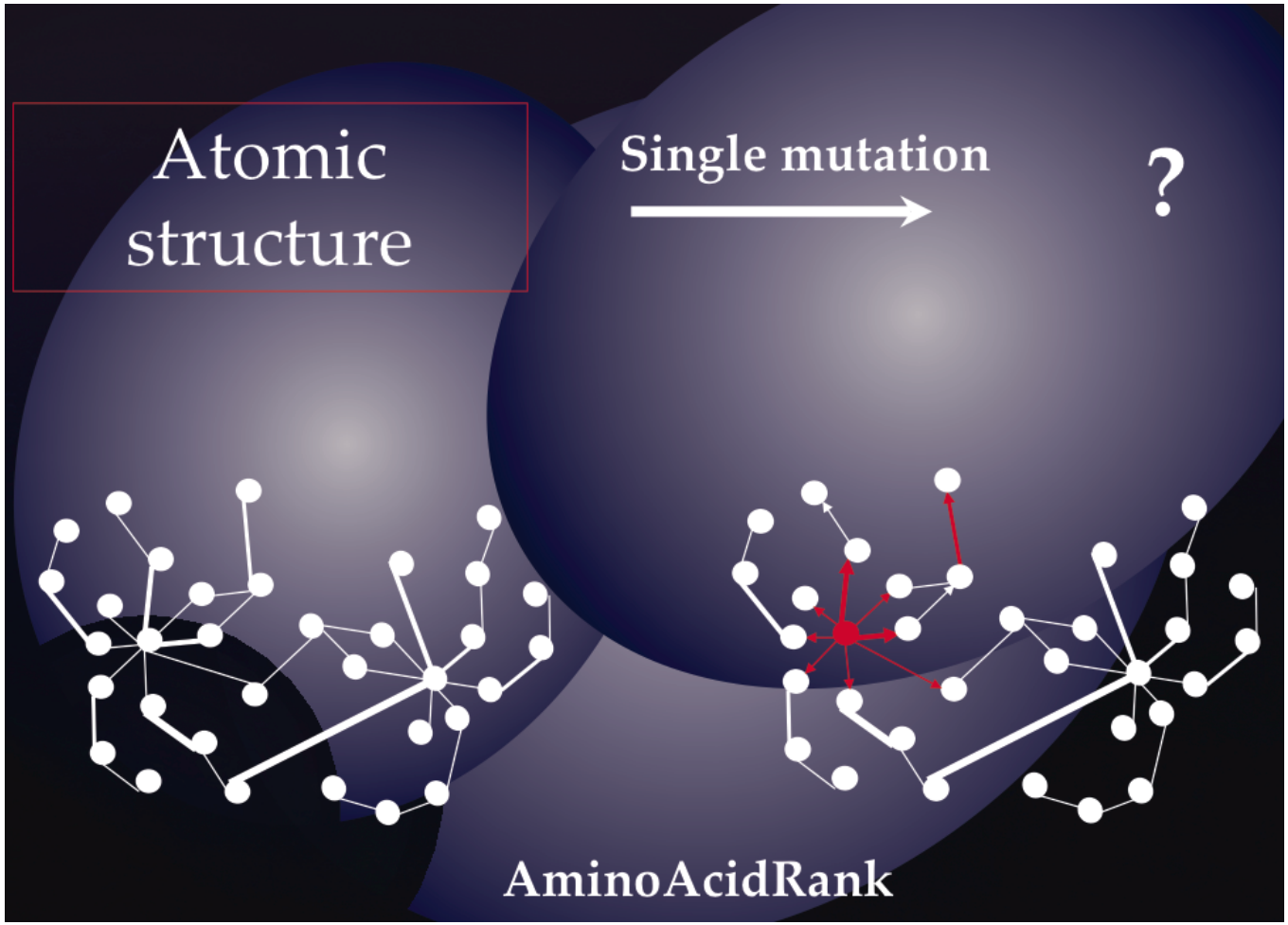
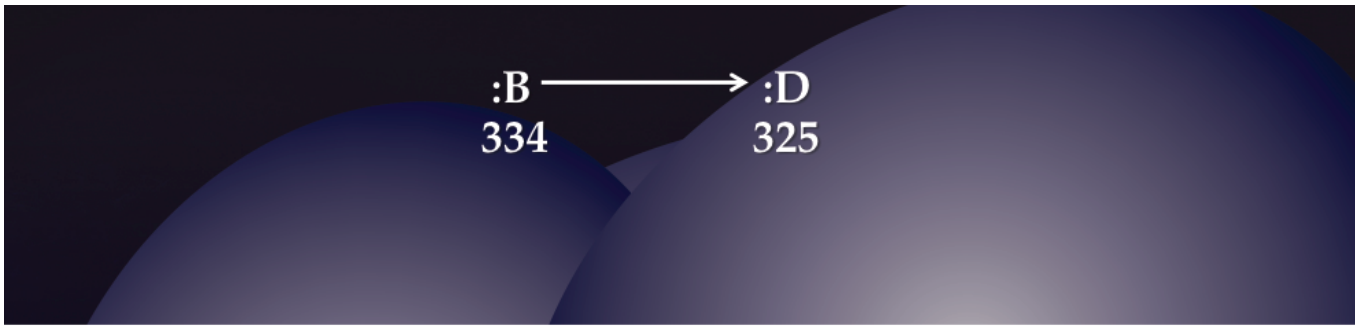
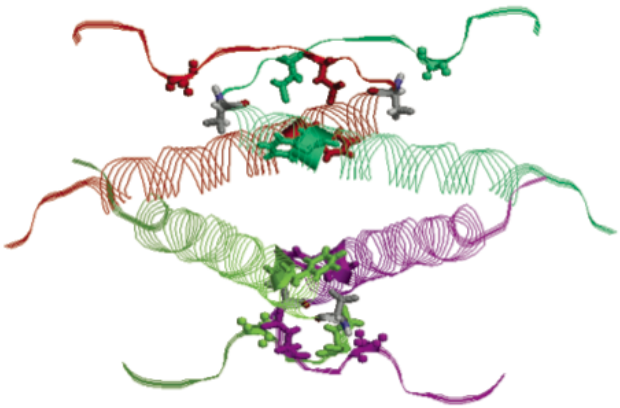
1500
1000
500
0
-500
-1000
ranking
A355N
D324N
R342N
E336N
R335N
E326N
T329N
K357N
D352N
Q331N
F338N
E346N
G325N
L330N
R333N
F328N
F341N
Y327N
R337N
sum
abs sum
mutation

Propagation of the destabilization on the network

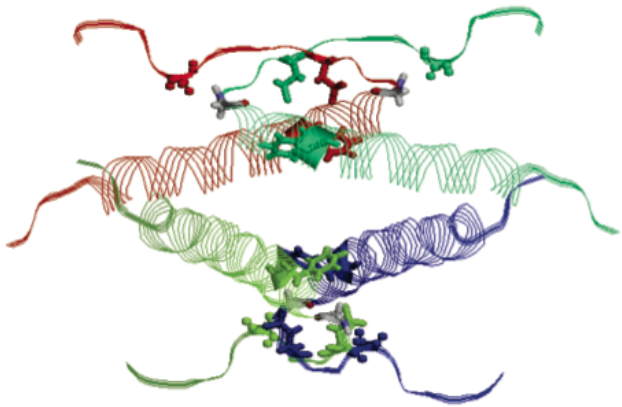




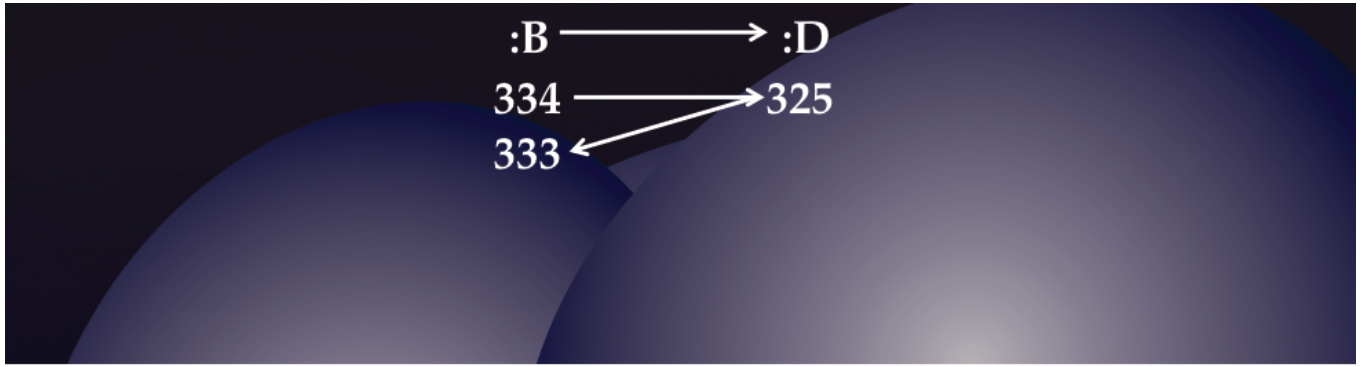
p53 G334V



p53 WILD TYPE



The p53 case


:B
:D
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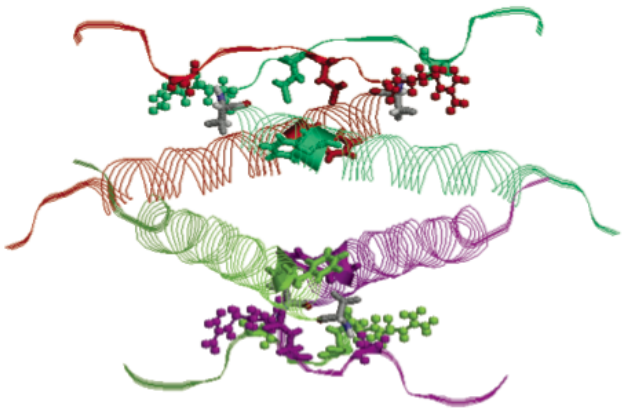
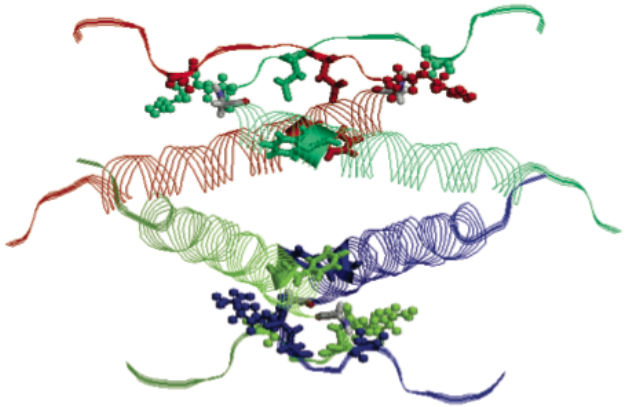
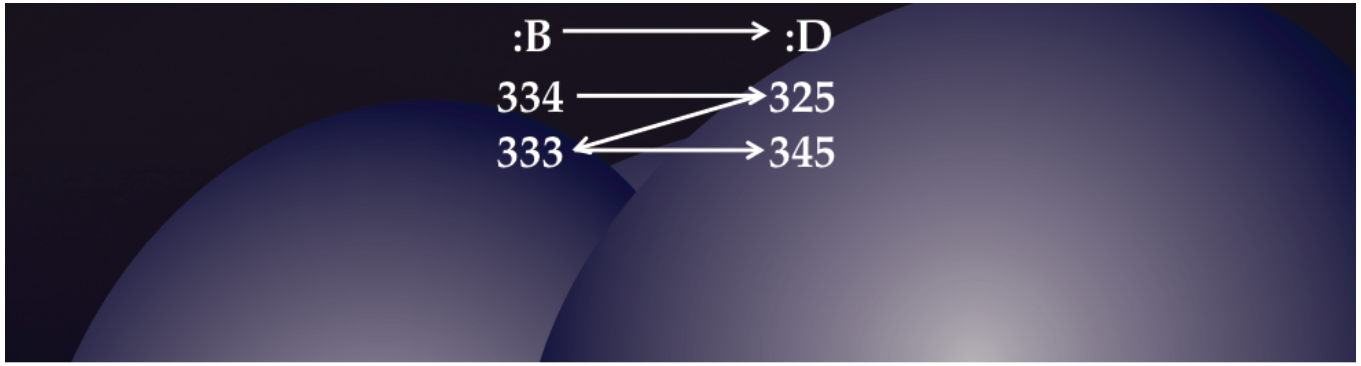
325
333



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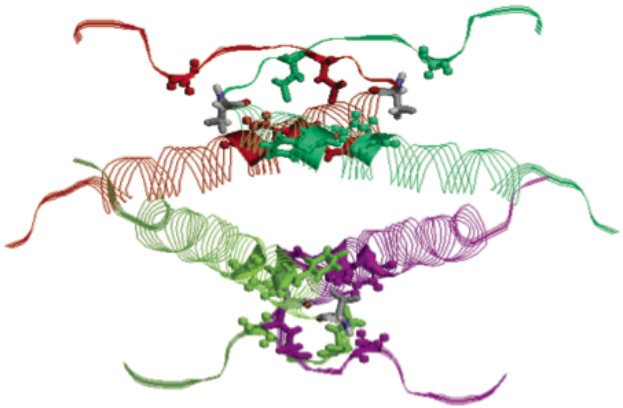

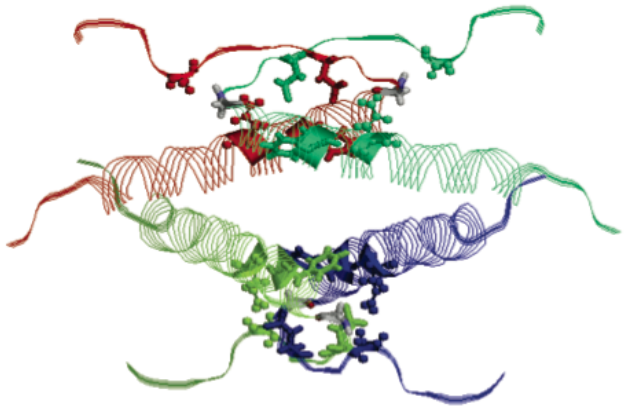

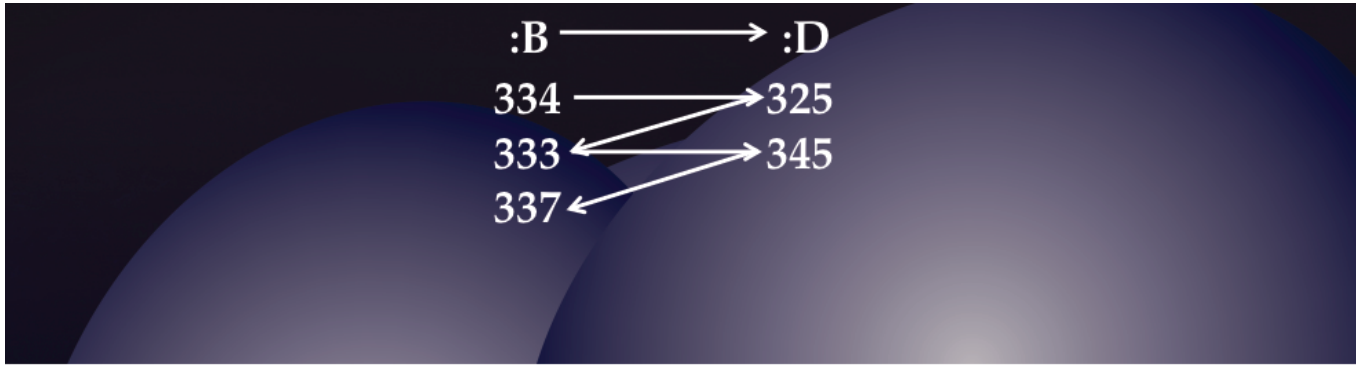
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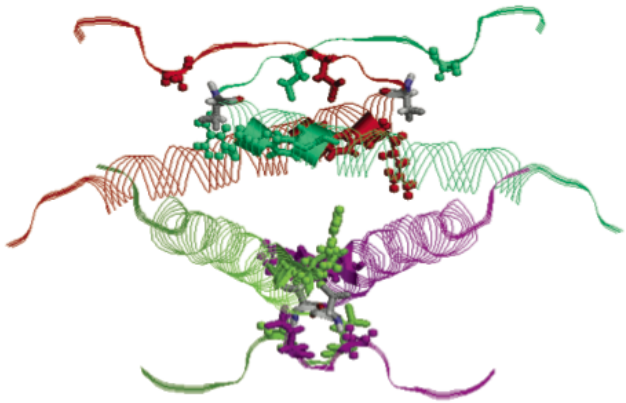

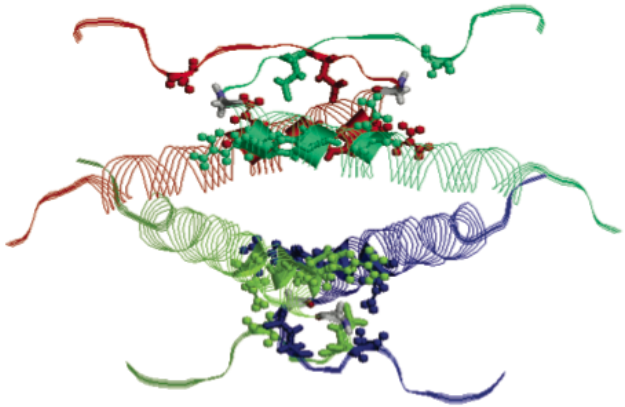

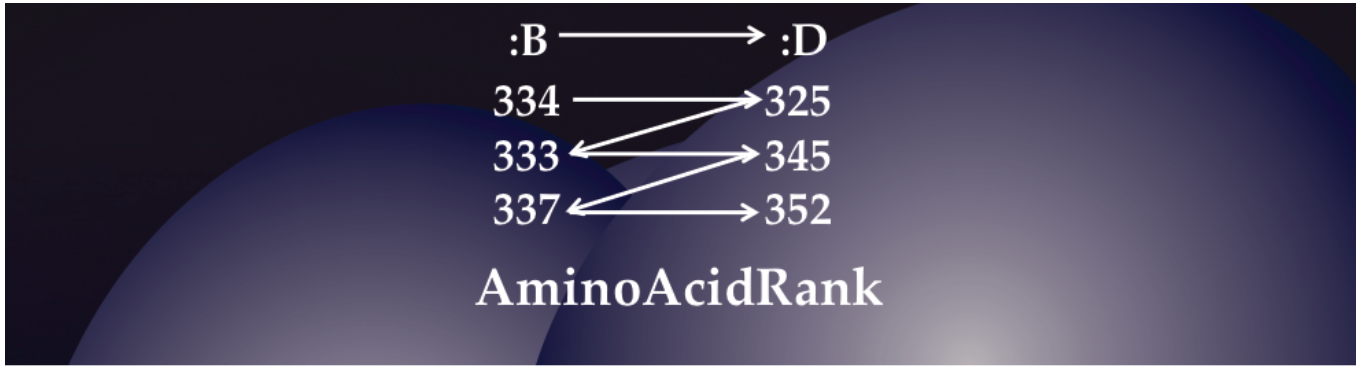
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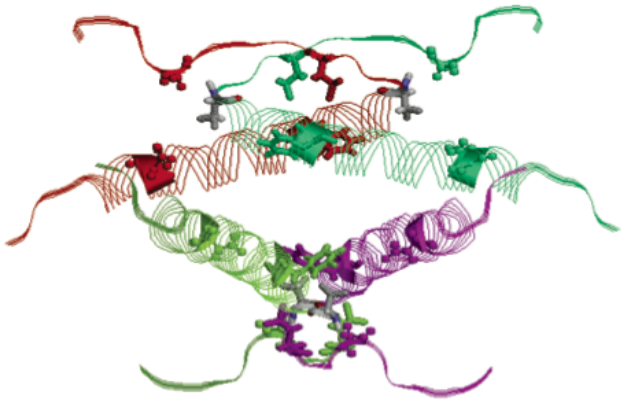
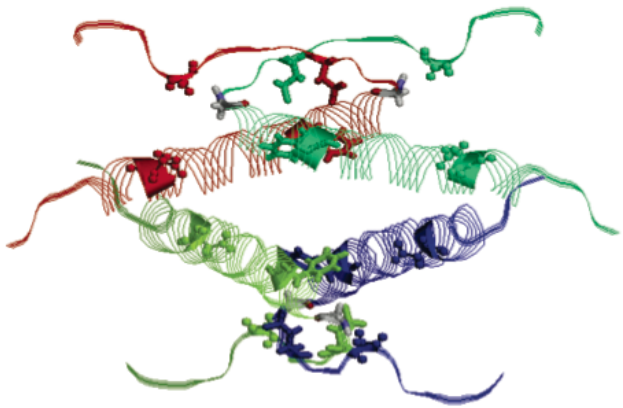
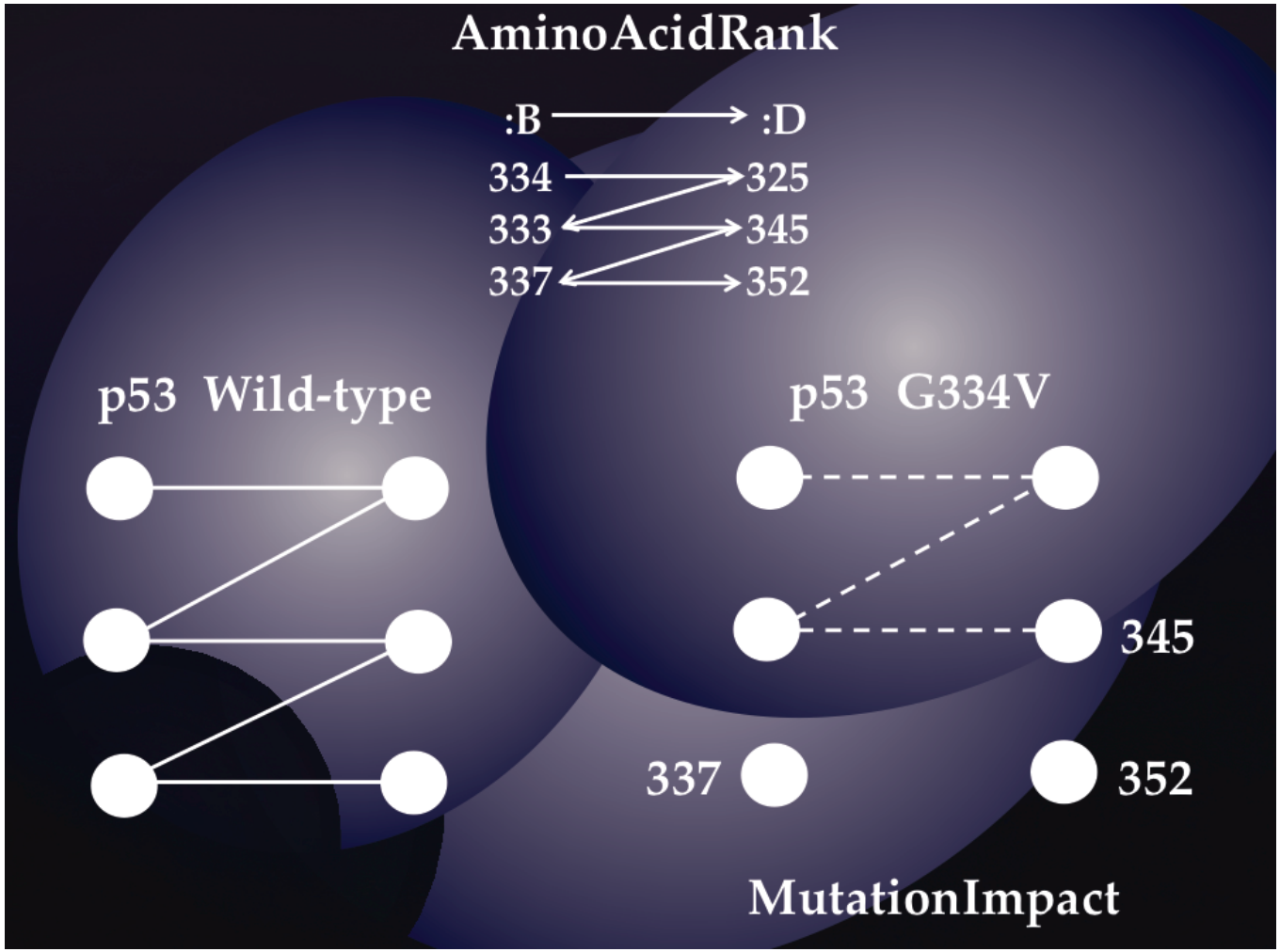
AminoAcidRank



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p53 Wild-type
p53 G334V
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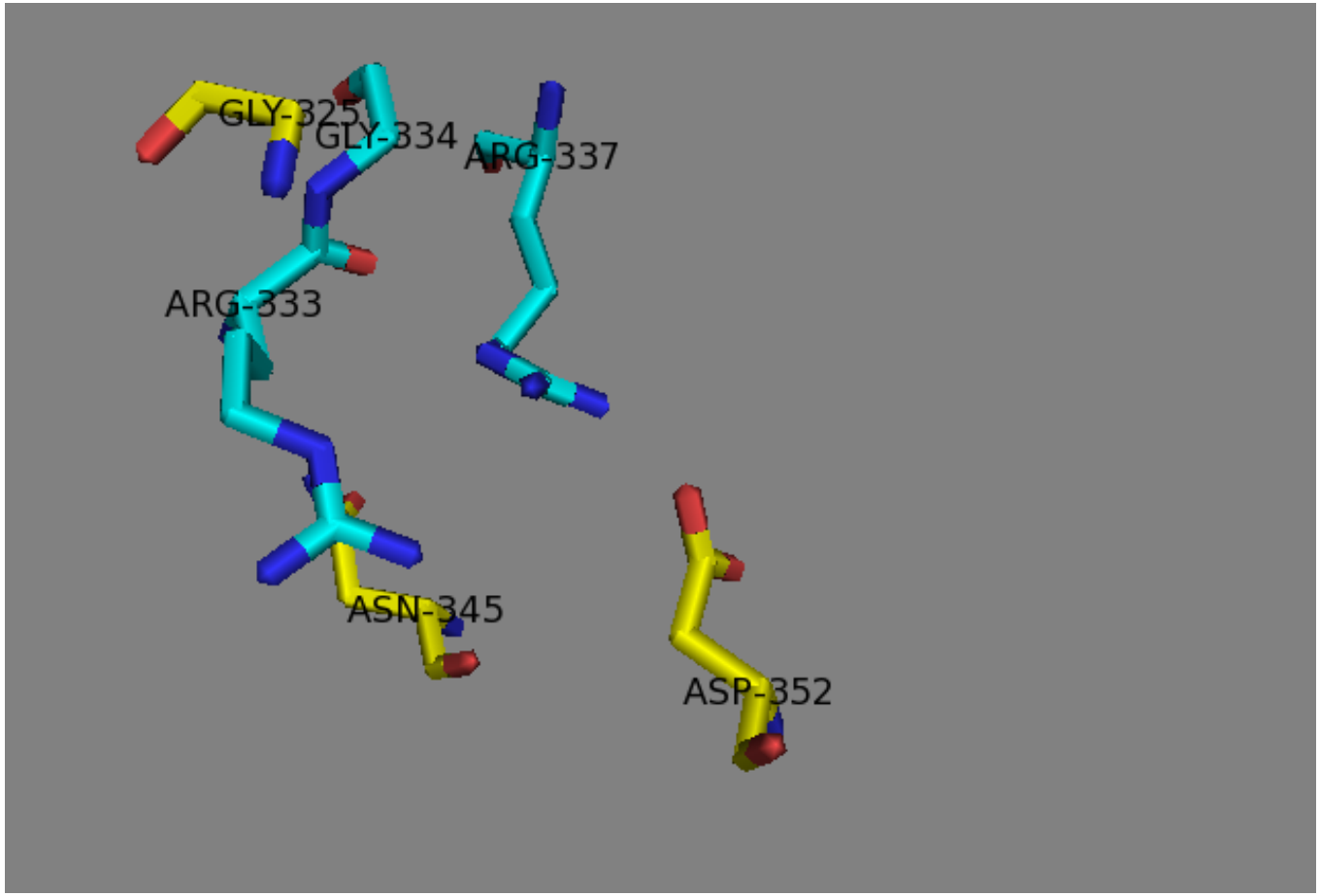
MutationImpact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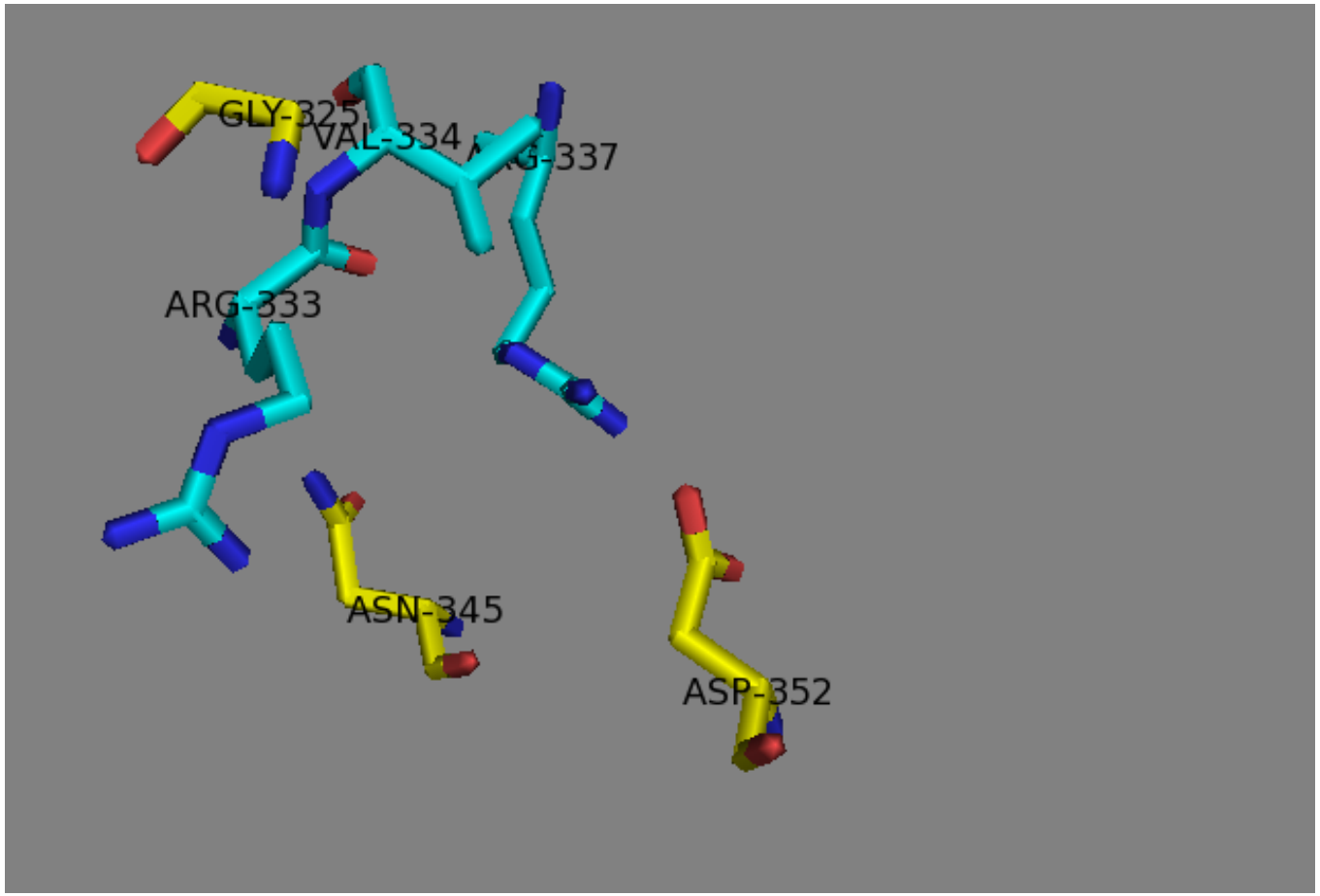
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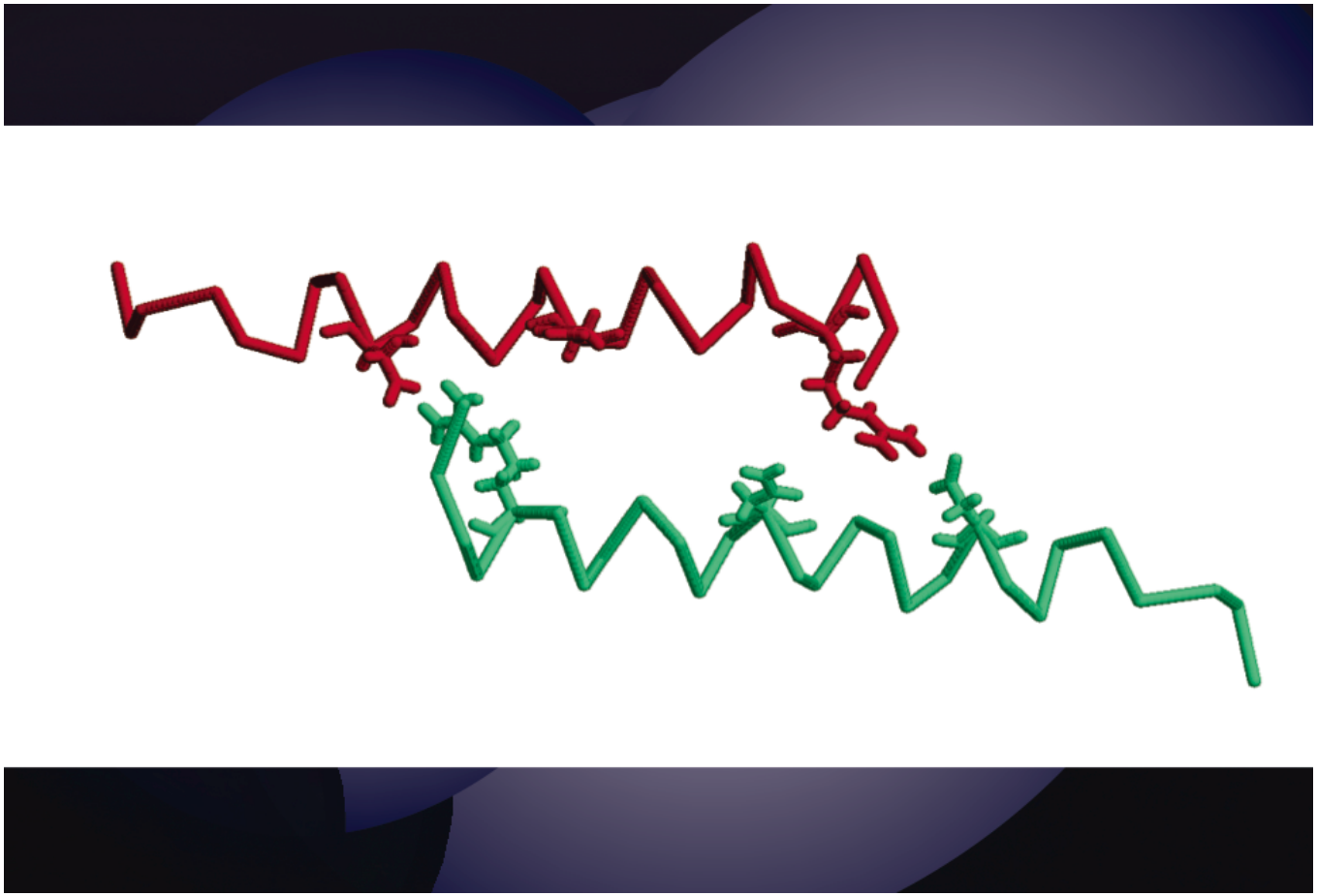

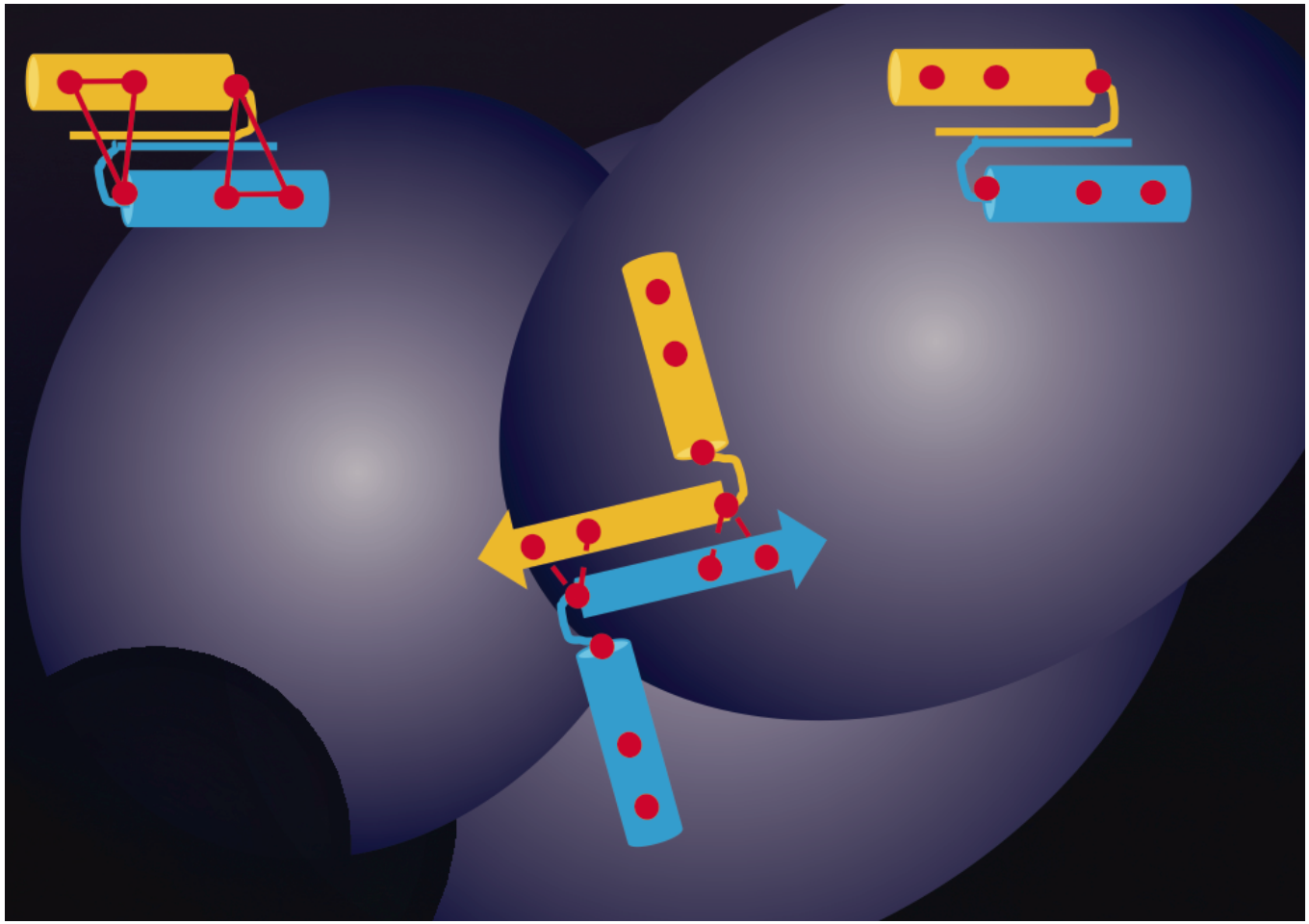

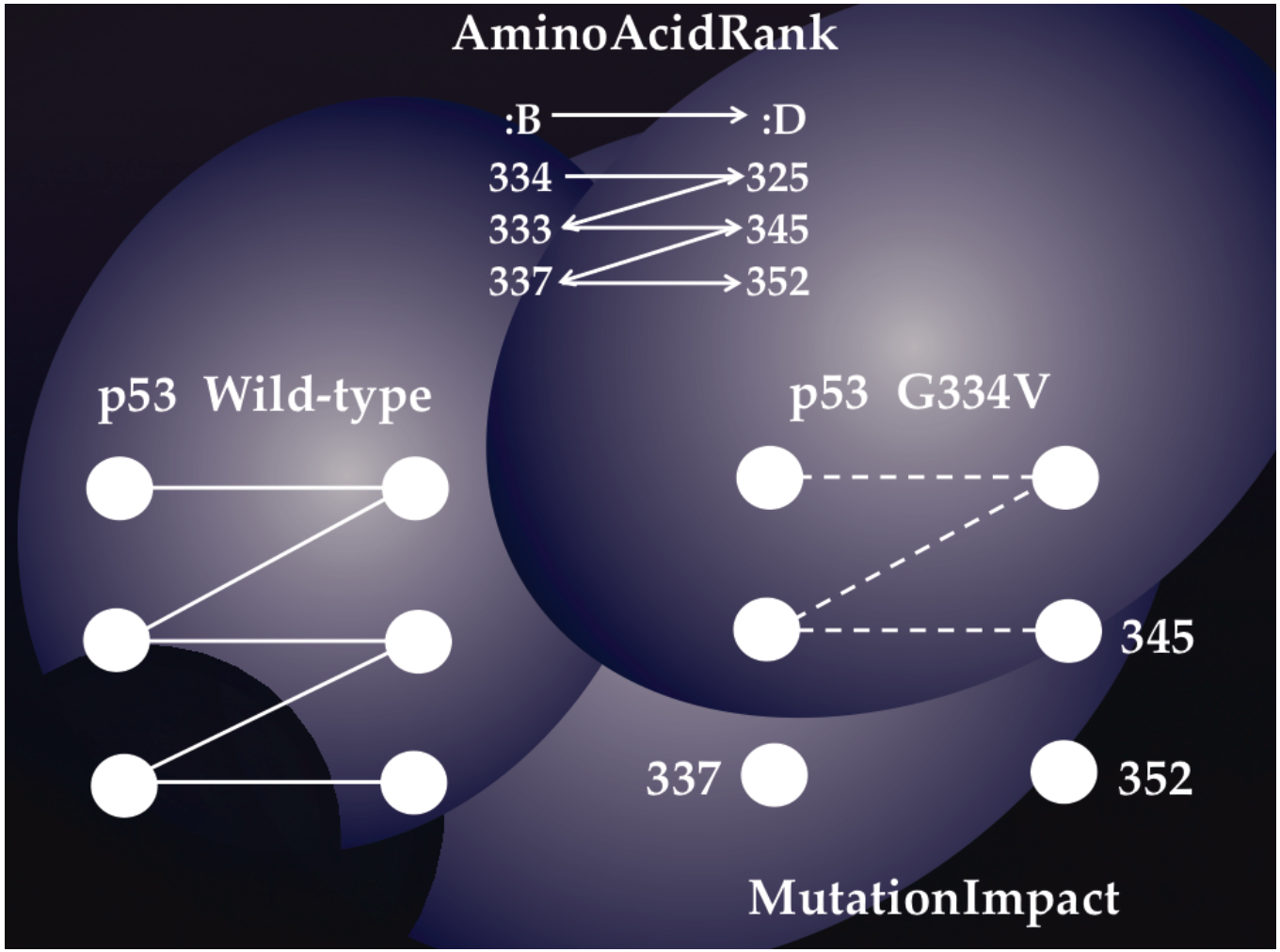
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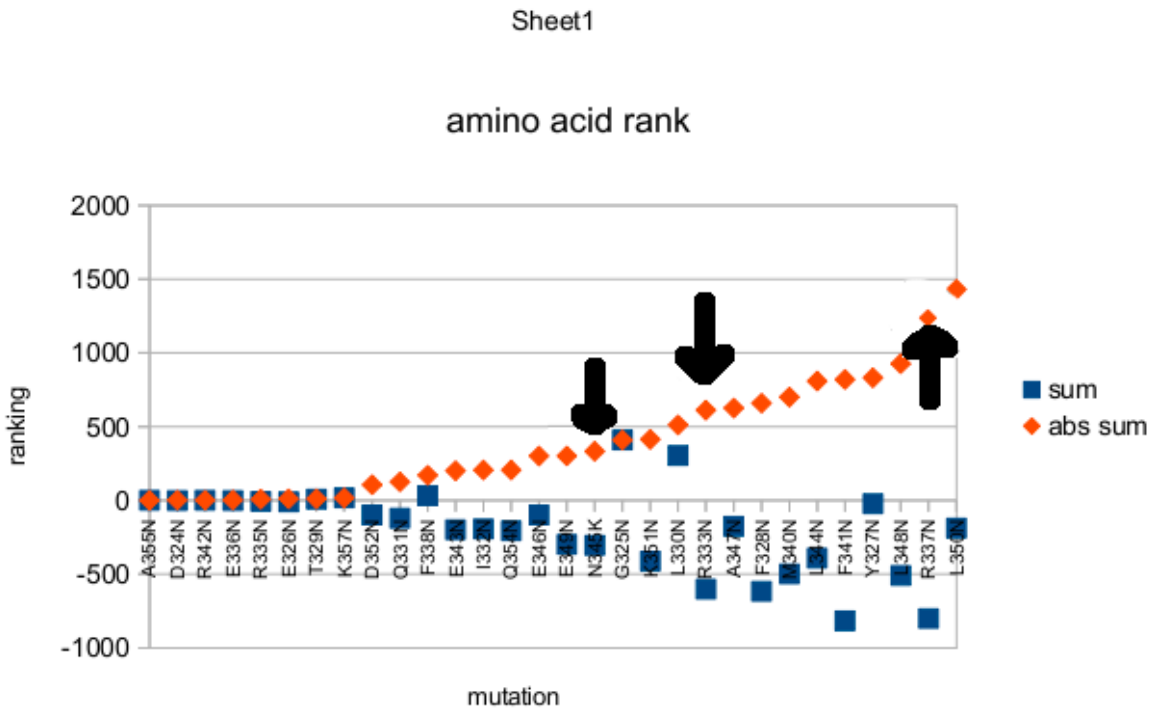
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1000
500
0
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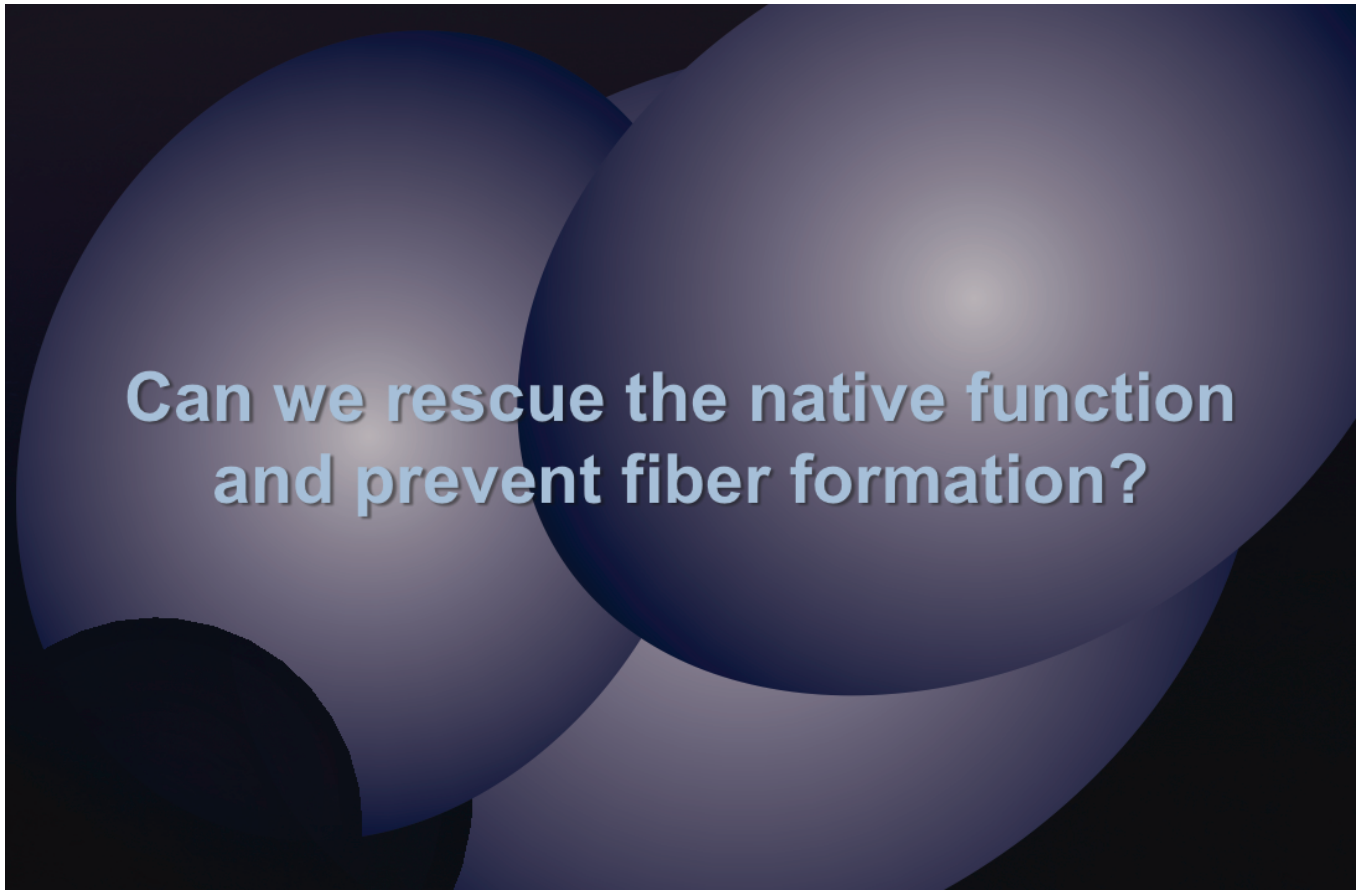
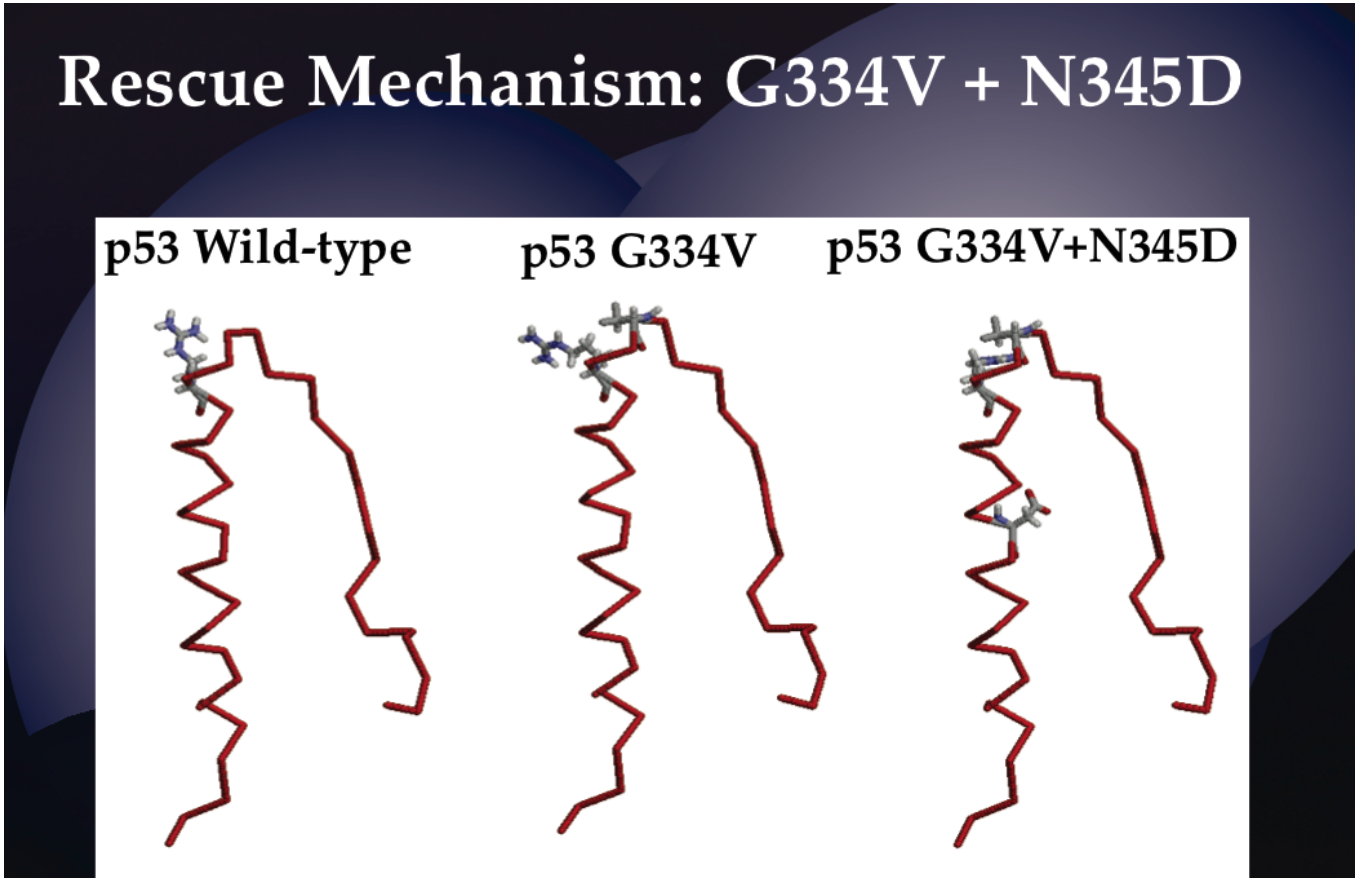
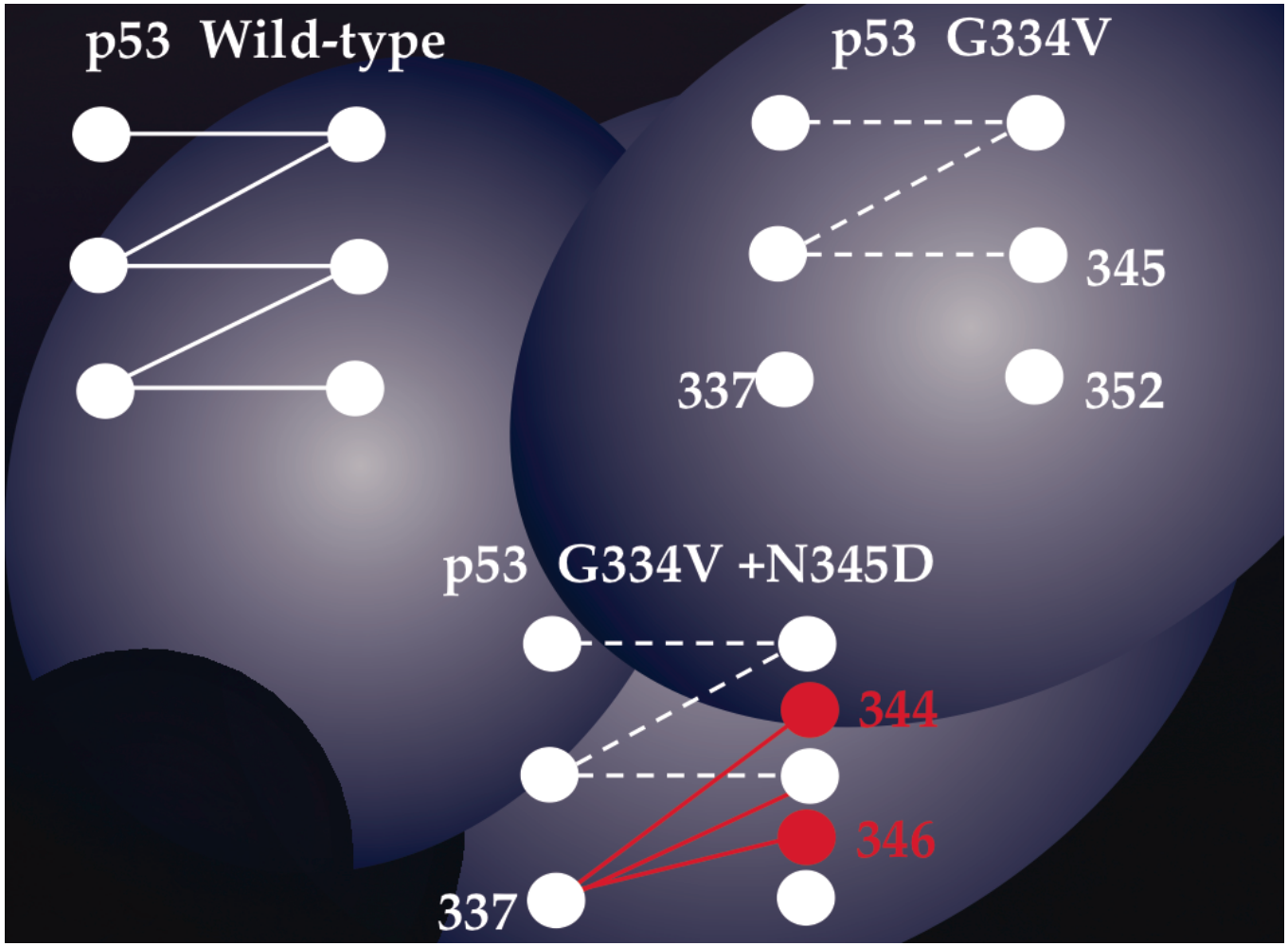
ranking
mutation
sum
abs sum


Can we rescue the native function
and prevent fiber formation?


Rescue Mechanism: G334V + N345D
p53 Wild-type
p53 G334V
p53 G334V+N345D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p53 G334V
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p53 G334V +N345D
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346
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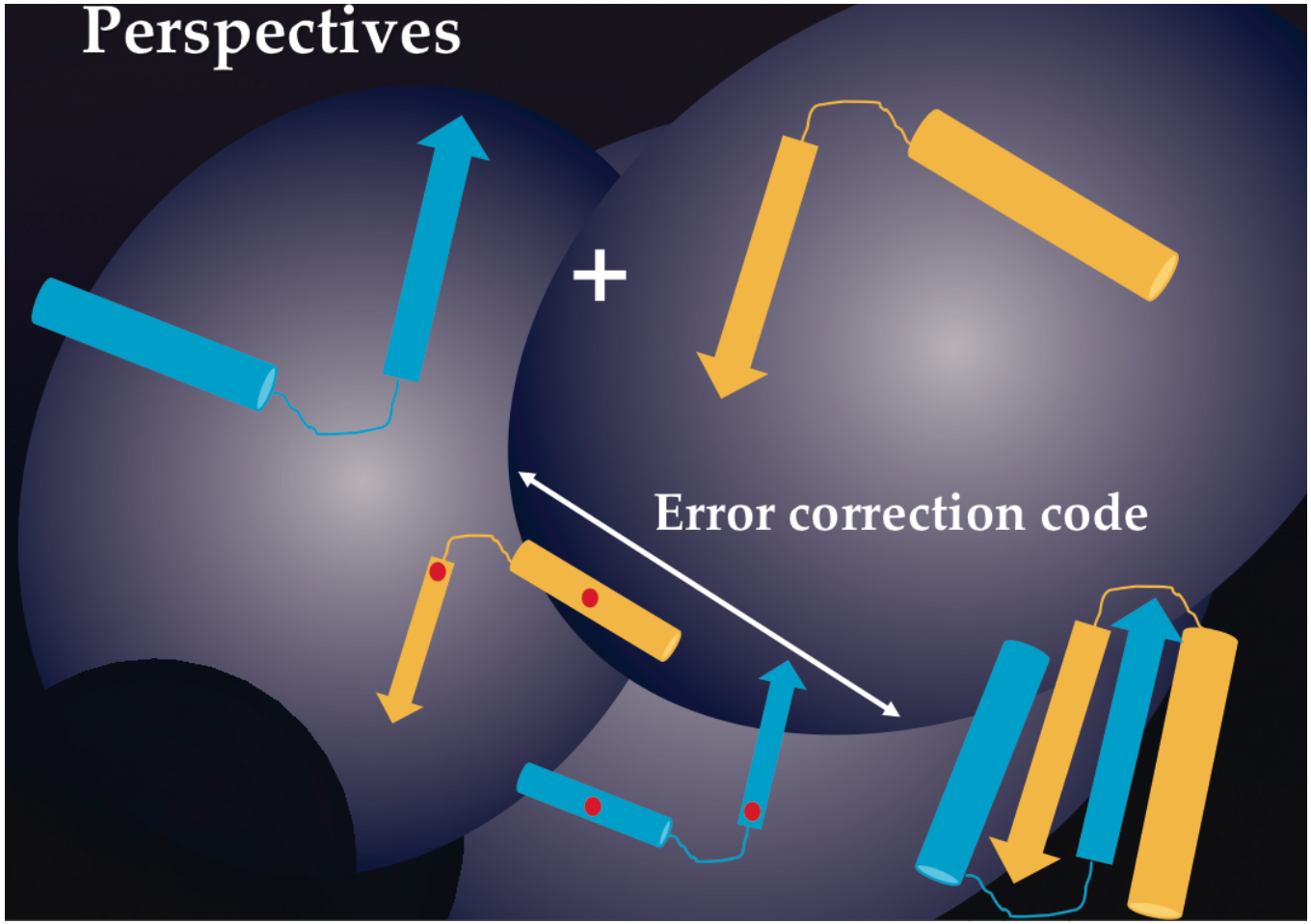
Perspectives
+
Error correction code


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ACADÉMIQUE
RhôneAlpes
UNIVERSITÉ DE SAVOIE
Chambéry
Annecy
Thanks!
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GOBIERNO DE LA REPÚBLICA
ESTADOS UNIDOS MEXICANOS
CONACYT