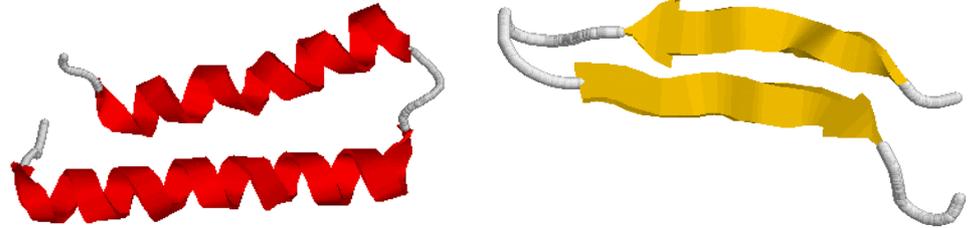


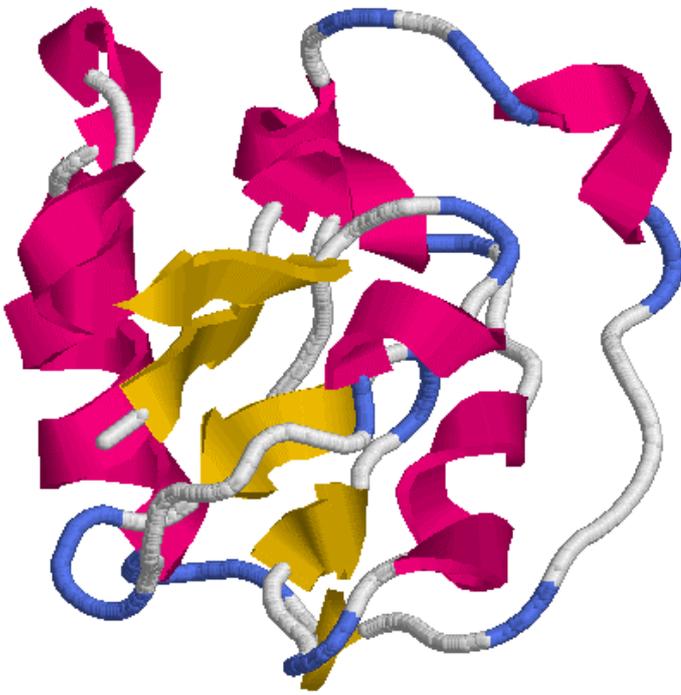
# Niveles de organización en las proteínas

-Ala-Glu-Val-Thr-Asp-Pro-Gly-

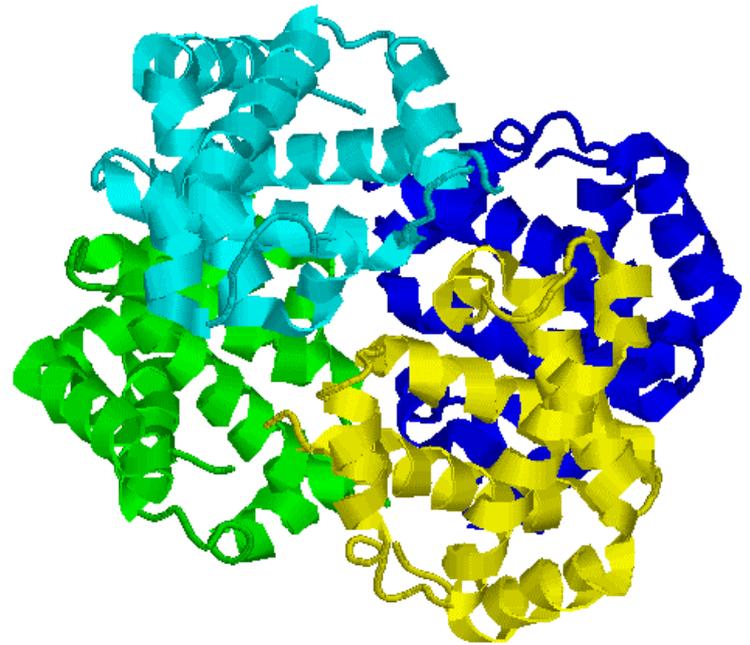
Estructura primaria



Estructura secundaria



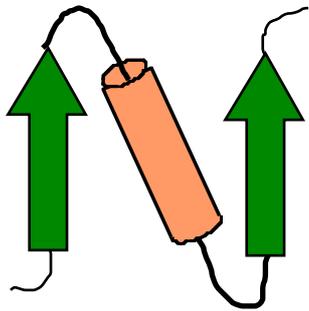
Estructura terciaria



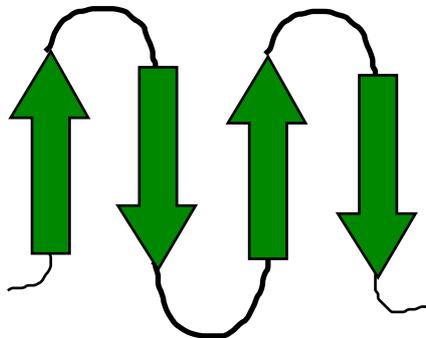
Estructura cuaternaria

# Estructuras supersecundarias

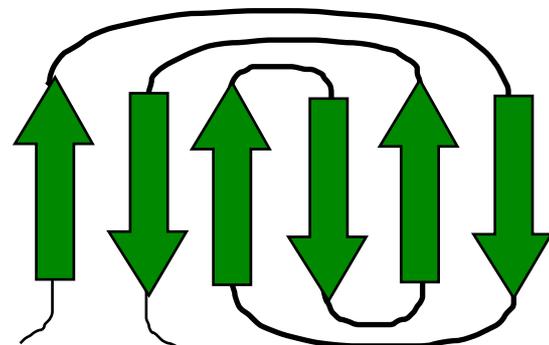
tipo  $\beta\beta$



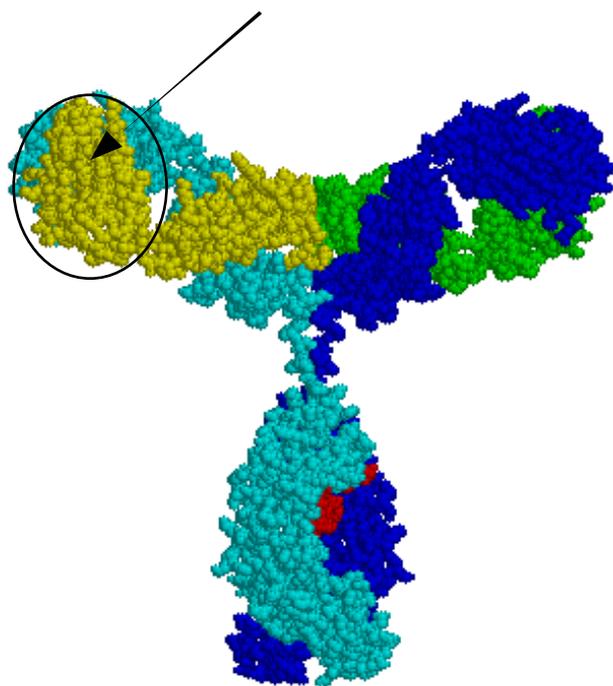
meandros  $\beta$



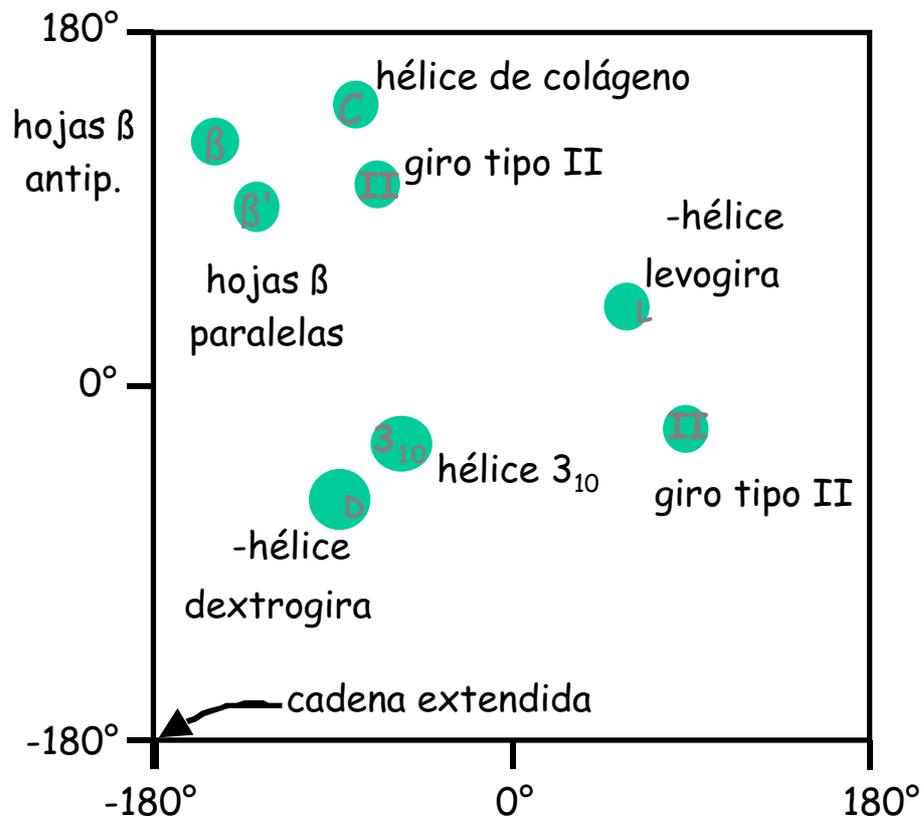
guardas griegas  
o grecas



dominio



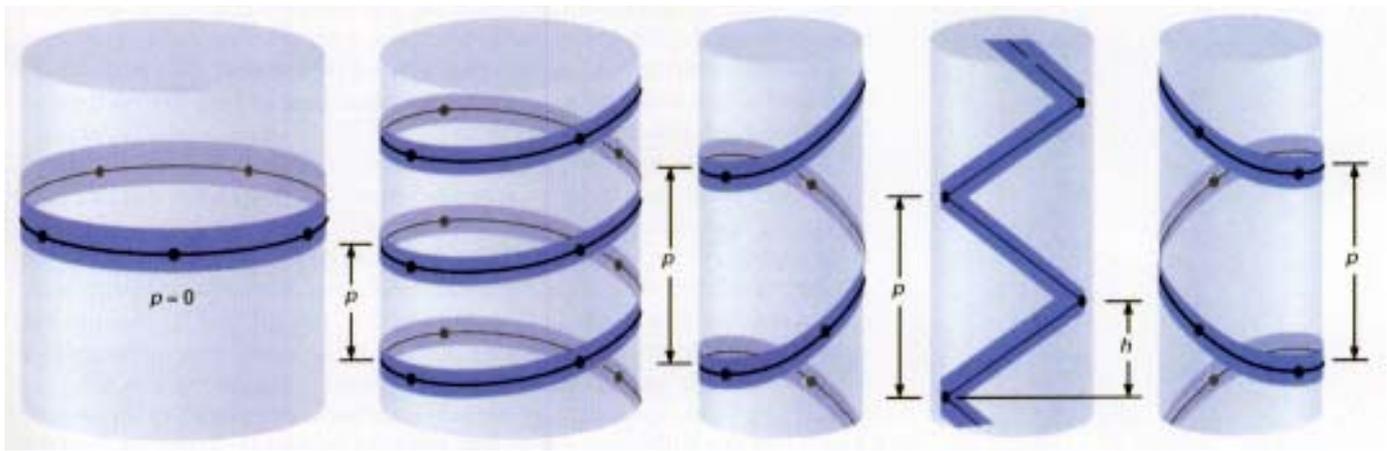
# Estructuras secundarias y diagramas de Ramachandran



## Ángulos $\phi$ y $\psi$ ideales para algunas estructuras secundarias

Conformación	$\phi$ ( $^\circ$ )	$\psi$ ( $^\circ$ )
Hélice (dextrógira)	-57	-47
Hélice (levógira)	+57	+47
Hélice $3_{10}$	-49	-26
Lámina $\beta$ antiparalela	-139	+135
Lámina $\beta$ paralela	-119	+113
Hélice de colágeno	-51	+153
Giro tipo II (segundo residuo)	-60	+120
Giro tipo II (tercer residuo)	+90	0
Cadena extendida	-180	-180

# Parámetros en estructuras helicoidales



$n = 5$   
anillo

$n = 4$   
hélices a derechas

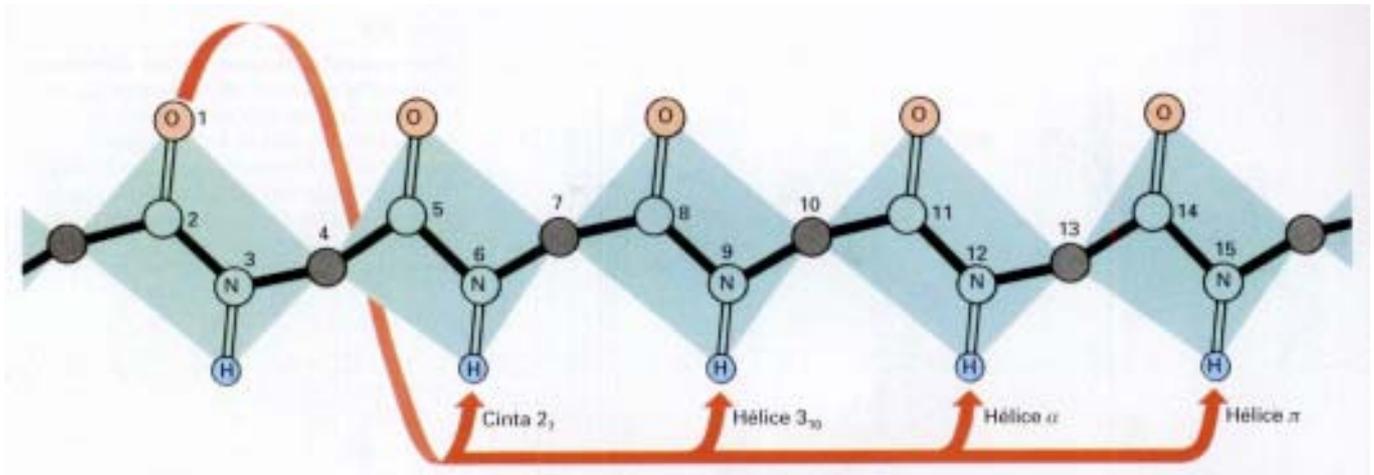
$n = 3$   
cinta plana

$n = -3$   
hélice a izquierdas

$p = n \times h$

$n$  = número de residuos por vuelta  
 $p$  = paso de hélice  
 $h$  = elevación

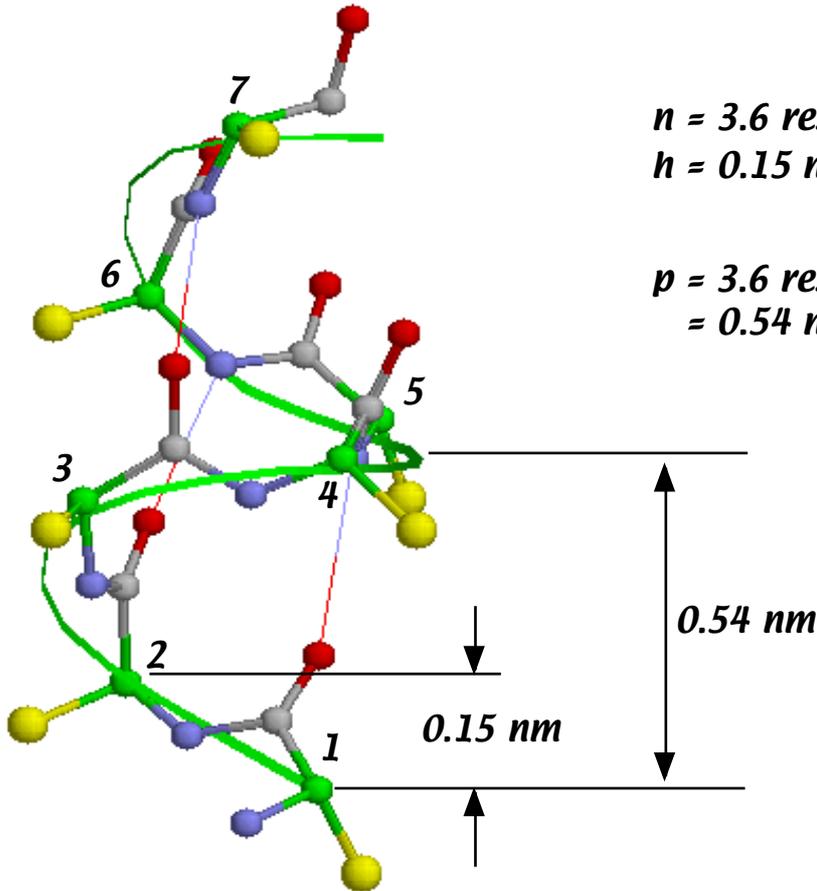
## Puentes de hidrógeno en las hélices



### Parámetros de algunas estructuras secundarias polipeptídicas

Tipo de estructura	Residuos/vuelta	Elevación (nm)	Nº de átomos en un anillo por puente de hidrógeno	(°)	(°)
Lámina $\beta$ antiparalela	2.0	0.34	--	-139	+135
Lámina $\beta$ paralela	2.0	0.32	--	-119	+113
Hélice $3_{10}$	3.0	0.20	10	-49	-26
Hélice $(3.6_{13})$	3.6	0.15	13	-57	-47
Hélice $\pi$ $(4.4_{16})$	4.4	0.12	16	-57	-70

# La hélice alfa



$n = 3.6$  residuos por vuelta  
 $h = 0.15$  nm

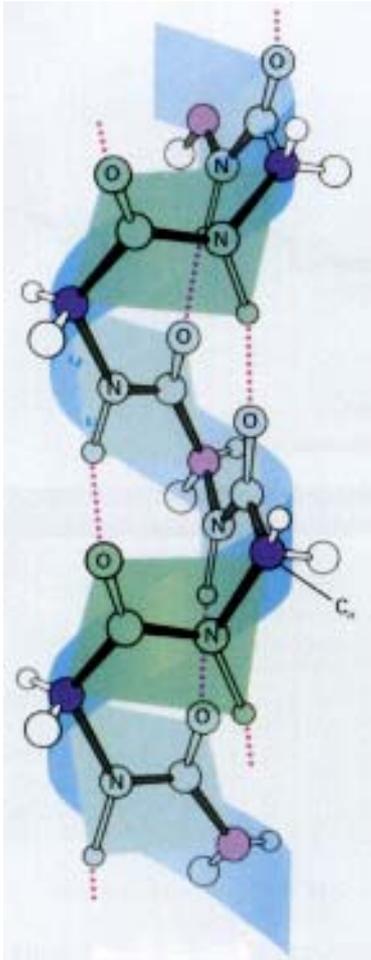
$p = 3.6 \text{ res/vuelta} \times 0.15 \text{ nm/res} =$   
 $= 0.54 \text{ nm/vuelta}$

## Preferencia relativa de posición en una hélice

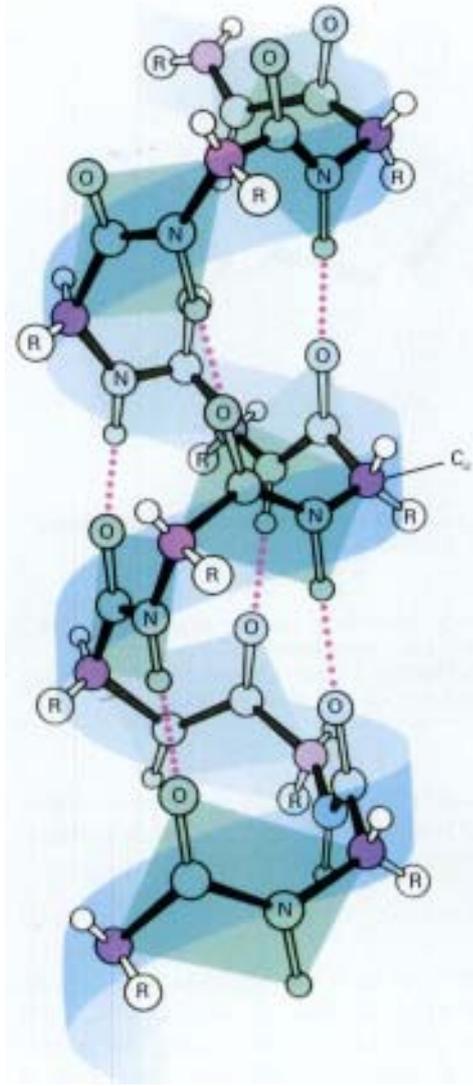
Aminoácido	N-terminal	Central	C-terminal
Pro	0,8	<u>0,3</u>	0,7
Gly	<b>1,8</b>	<u>0,5</u>	<b>3,9</b>
Ser	<b>2,3</b>	0,6	0,8
Tyr	0,8	0,8	0,8
Asn	<b>3,5</b>	0,9	1,6
Asp	<b>2,1</b>	1,0	0,7
Ala	0,5	<b>1,8</b>	0,8
Leu	<u>0,2</u>	1,2	0,7
Val	<u>0,1</u>	1,2	<u>0,2</u>

Datos obtenidos de 215 hélices de 45 proteínas

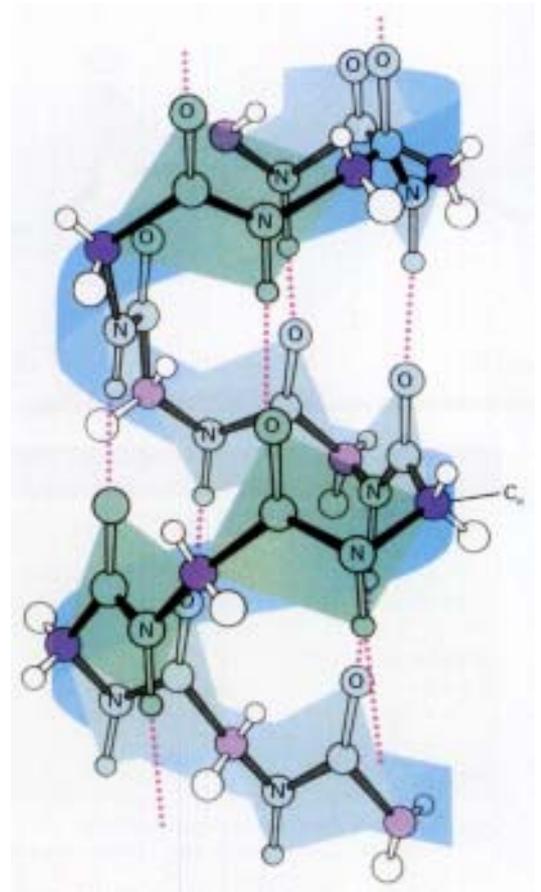
# La hélice $3_{10}$ , $3,6_{13}$ (alfa) Y $4.4_{16}$ ( $\pi$ )



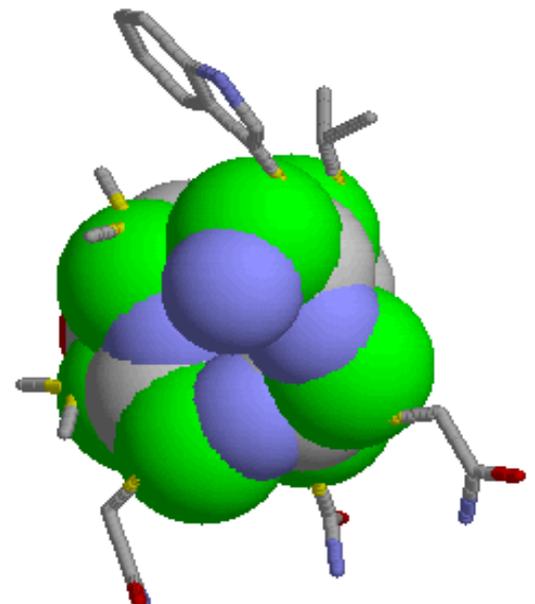
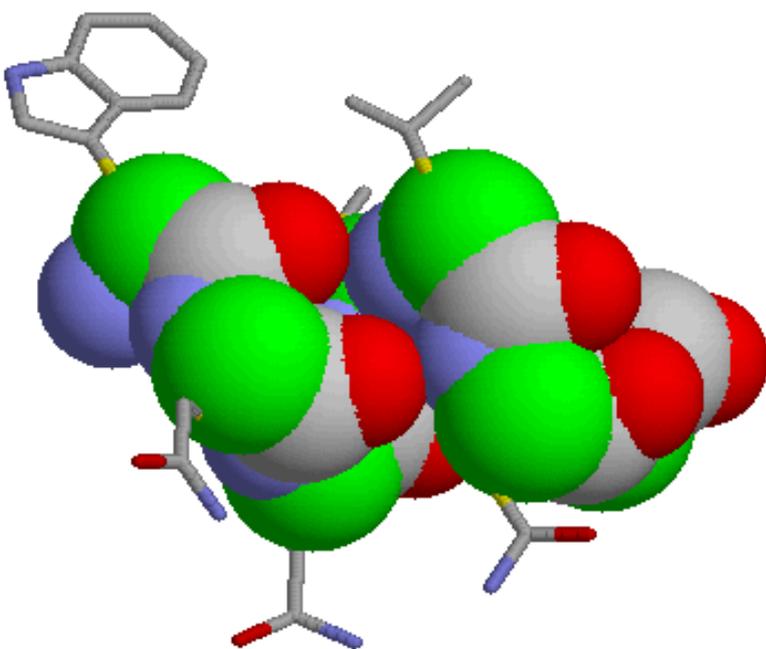
La hélice  $3_{10}$



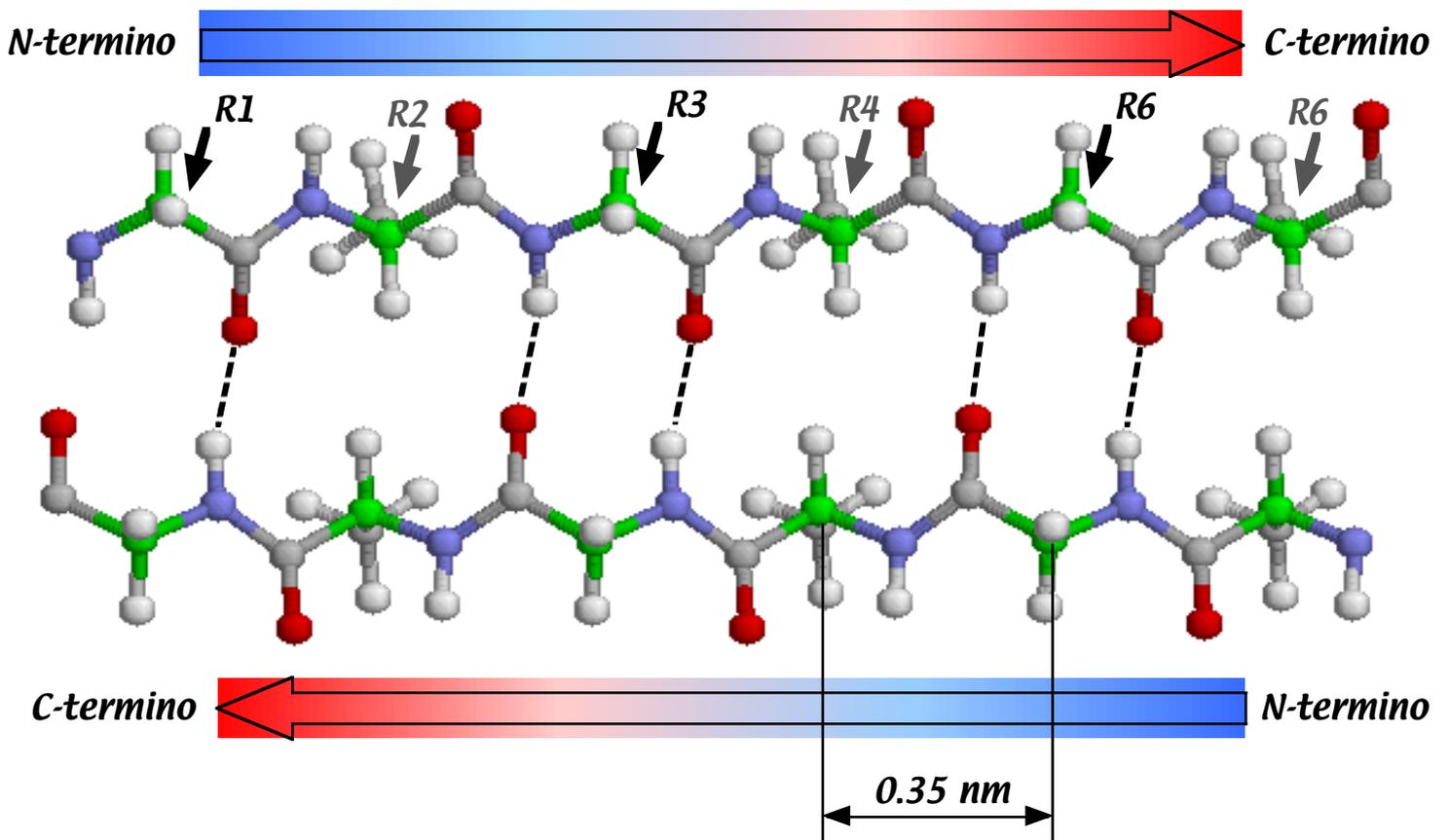
La hélice  $3,6_{13}$  (alfa)



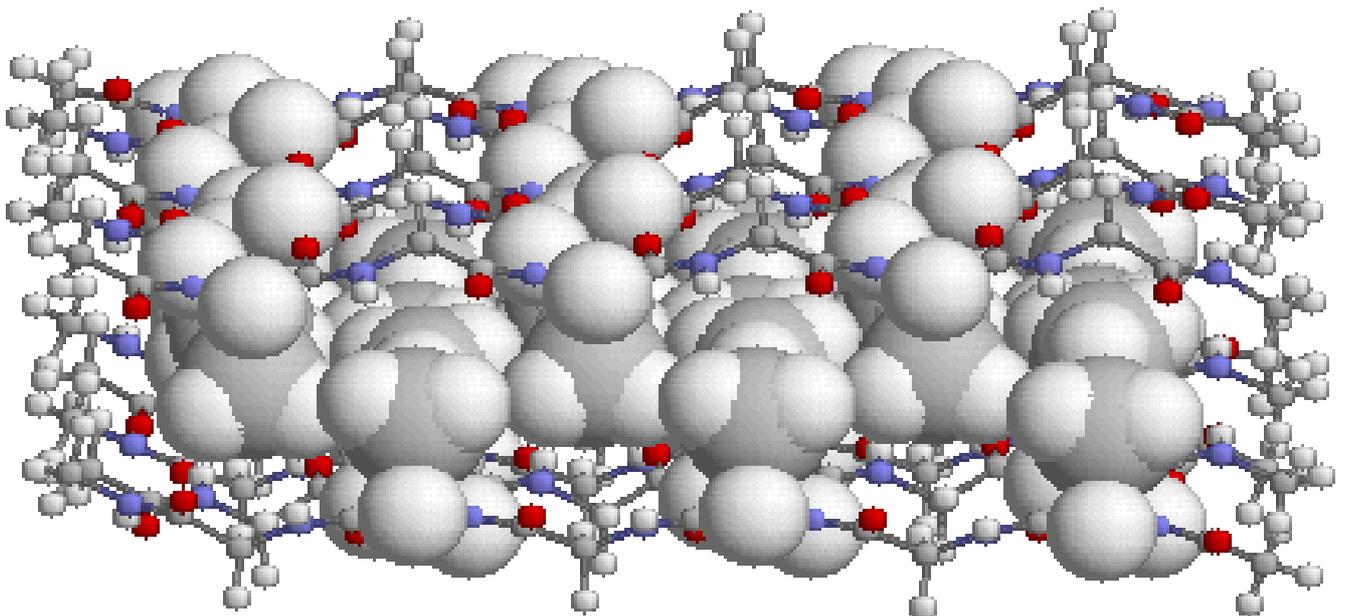
La hélice  $4.4_{16}$  ( $\pi$ )



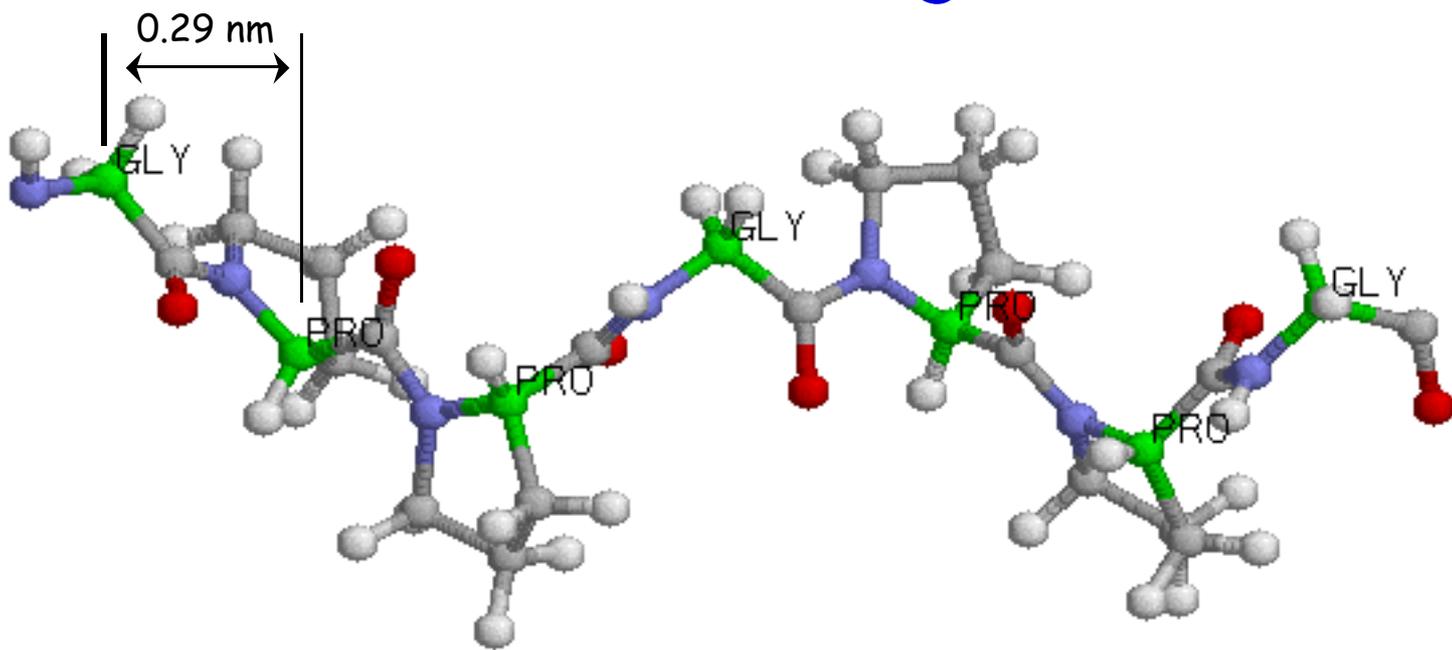
## La hoja beta antiparalela



## La fibroína de la seda

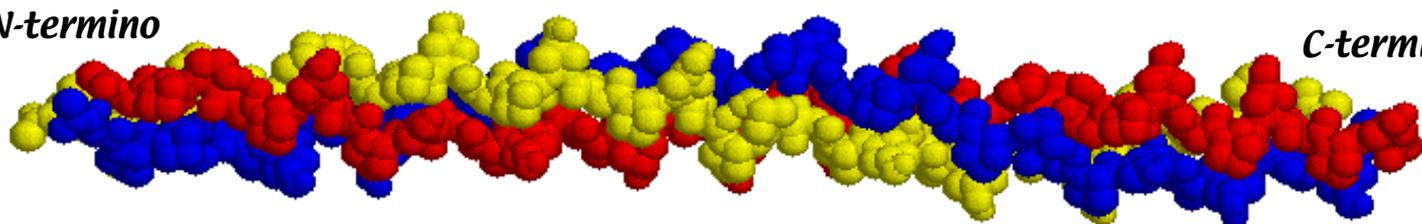


# La hélice de colágeno

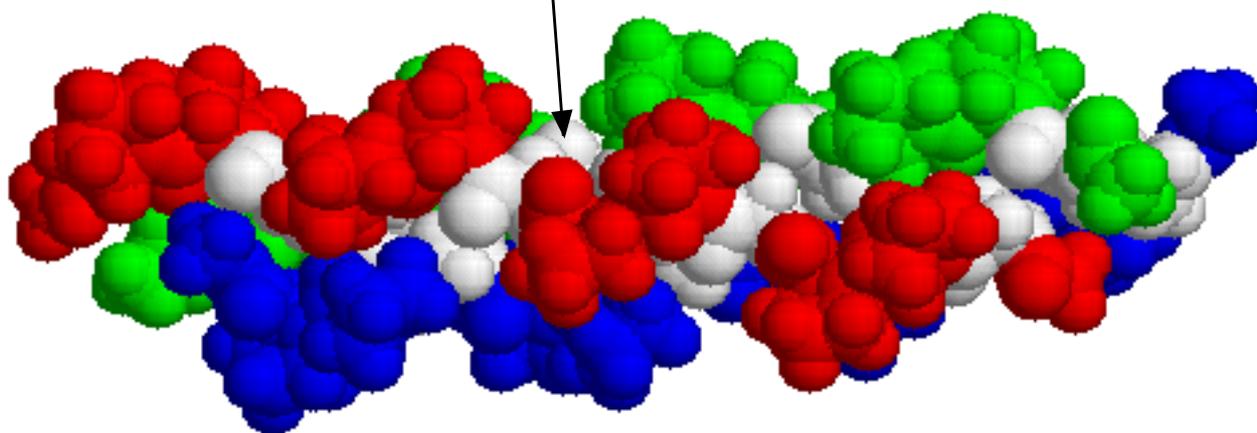


*N-termino*

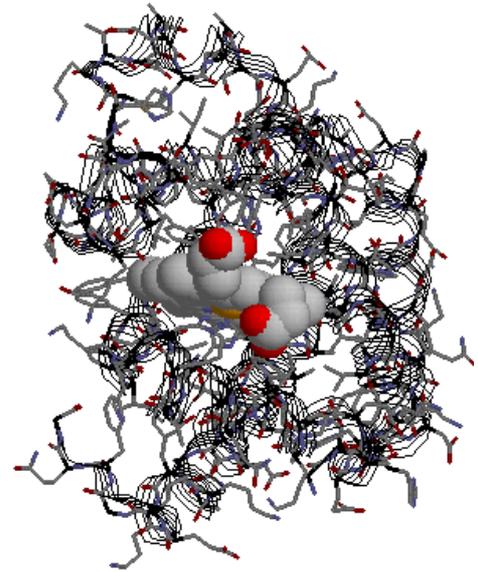
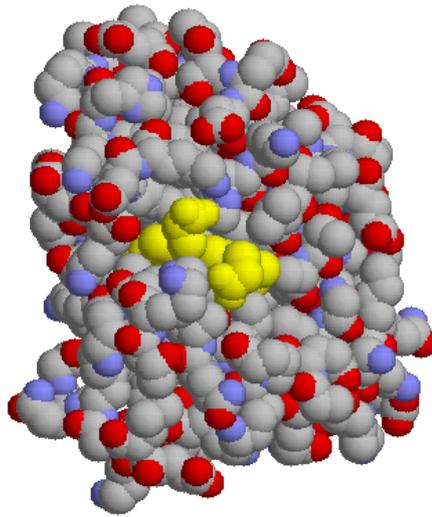
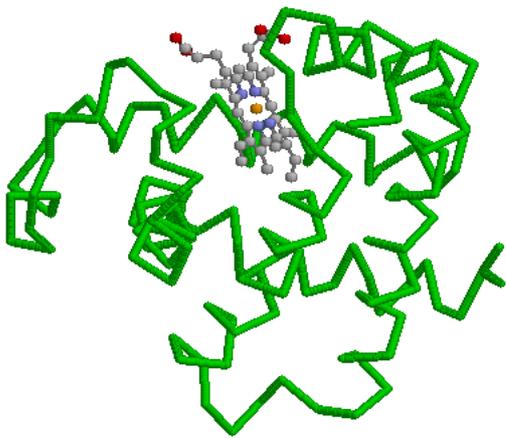
*C-termino*



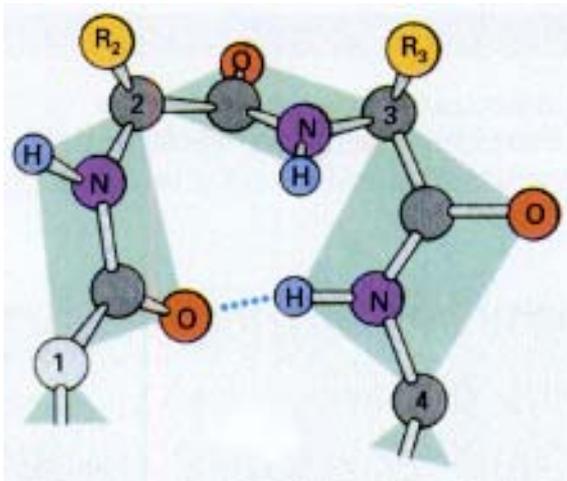
*Residuos de glicina*



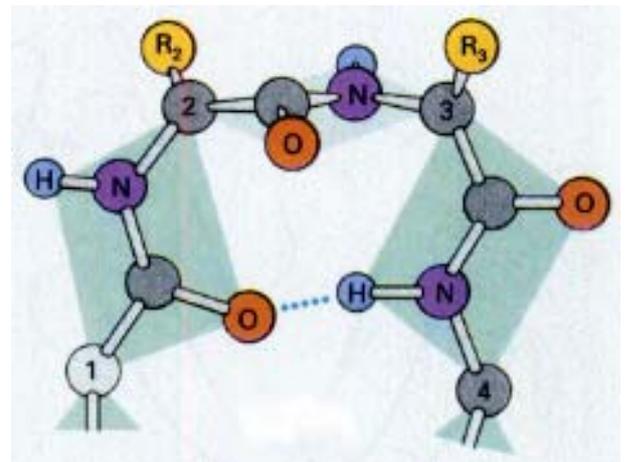
# La estructura terciaria



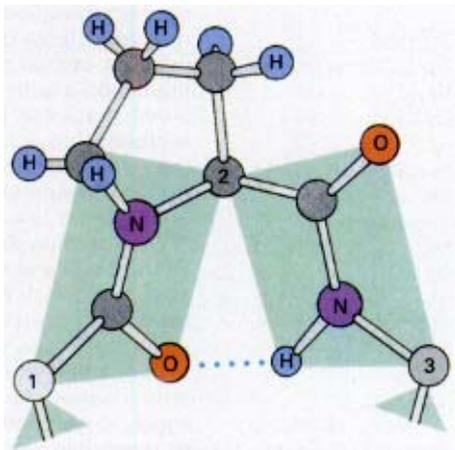
## Los giros reversos



*giro tipo I*



*giro tipo II*



*giro tipo*

*Tipo I:  $n = 3$ , cualquier Aa excepto Pro*

*Tipo II:  $n = 2$  Gly y  $n = 3$  Pro*

*Tipo III: un fragmento de helice 310*

*Tipo :  $n = 1$ , Pro*