

BCH 258 lecture notes Mon. Aug 31, 2009

In class work/demo: brass Kendrew models:

Ala-poly-peptide, parallel & antiparallel β -strands, α -helix;
note chain direction, pattern of possible H-bonds

Demo: connect fragments to make 4 residue sections:

1) in parallel strand orientation (3 strands)

2) in antiparallel strand orientation: (3 strands)

Note: narrow H-bond pair and wide H-bond pair.

(refer to handout sheet to help see this distinction)

care needed: keep the peptide group planar!

2) α -helix, about 3 turns.

Homework: re WorkSheet 4: Making Kinemages (PDB access)

1ADF by "alpha-hemolysin", 1AD1 and 1IG5 by code, Molikin color, animate, text
(Windows (Parallels) Unhide file.ext)

β -strand: one extended chain; β -sheet: multiple, H-bonded β -strands

ϕ, ψ in broad optimum near $-120^\circ, 140^\circ$ (upper left in plot)

sidechains alternate up & down; peptides alternate sideways

Twist : always RH (along chain), 5° to 30° /residue

[p.2]:

Antiparallel β : $\uparrow\downarrow$ H-bonds perpendicular to strand, alternate wide and narrow pairs

Can be just 2 strands; often irregular (β bulges)

Often one side buried one exposed, so alternate "HP"

Parallel β : $\uparrow\uparrow$ H-bonds slanted, evenly spaced

≥ 4 or 5 strands; shielded by mc on both sides, so both Hydrophobic

more regular than $\uparrow\downarrow \beta$ (needs cooperativity to be stable?)

mix of $\uparrow\uparrow$ and $\uparrow\downarrow$ less favored

α -helix [p. 2] – repeating ϕ, ψ near $-55^\circ, -50^\circ$ "classic" (lower left on rama plot)

commonest & most regular -[p2 notes] H-bond CO(i) to NH(i+4)

righthanded spiral: R thumb = direction, follow spiral with fingers

end view: characteristic offset almost-square pattern,

3.6 residues/turn; 5.4 Å per turn, $\sim 5\text{Å}$ across mainchain

$C\alpha$ - $C\beta$ vectors pinwheel, not radial

From side, $C\beta$ slants to N-term, so sidechain interacts most with previous turn

CO's point to C-term, NH's to N-term

helix dipole produced by peptide polarity,

so negative sidechain and phosphate binding common at N-term of helix

helix center satisfies all H-bonds, but 3 free NH at beginning; 3 free CO at end

most have buried hydrophobic side & exposed polar side \rightarrow 3.5 res "HP" period

["H" Hydrophobic, "P" Polar]

3_{10} helix – 3 residues/turn, H-bond CO(i) to NH(i+3), righthanded

end view: triangle. Less stable than α , but common as 1 turn at ends.

Helix N-caps & C-caps – residue half in & half out of helix

Sidechain of N-cap often H-bonds to free NH at cap+3 or 4, so Asn, Ser, etc. good

C-cap often Gly with $+\phi$ ($L\alpha$ conf.)

Non-repetitive structure (NOT random!) or “coil”: α , β , $L\alpha$, conf's in various orders

Lots of sc-mc H-bonds

~2 types: links between secondary str's, or compact, convoluted loops

Tight turns : in loops, or connect $\uparrow\downarrow\beta$; change chain direction

4-residue square corner; CO(1) may H-bond to NH(4)

central peptide perpendicular to approx. plane of turn

Type I (“common” turn): central CO on side opposite $C\beta(2)\&(3)$; any sidechain

Type II (“Gly” turn): central CO on same side as $C\beta(2)\&(3)$; res. 3 should be Gly

Turns non-planar, handed: actually need type I' (mirror of I) to match

The β -sheet twist and work well for a β -hairpin; Gly-Gly or Gly-Asp best

Water – a few internal; at active site may mimic substrate

\leq one layer well-ordered on outside, esp. around polar groups

crystal or domain contacts often through 1 layer of ordered water

Structural Motifs : small, favored clusterings of 2-4 pieces of sec. str.; strong

General preference for contact of near neighbors in sequence

Helix hairpin : successive $\uparrow\downarrow$ helices; pack best at $\sim 15\text{-}20^\circ$ angle

Hydrophobic patches; spiral ridges of sidechains; coiled-coil

$\sim 90^\circ$ helix contacts: “EF hand” Ca^{++} -binding; “helix-turn-helix” DNA-binding

β -hairpin : successive $\uparrow\downarrow$ β strands; shortest with tight turn



crossover or $\beta\alpha\beta$ connection : successive $\uparrow\uparrow$ β -strands

$\gg 99\%$ righthanded; determines architecture of α/β folds

Greek key β :



SS β -cross : 2 touching SS spirals (1L,1R) on adjacent β hairpin strands