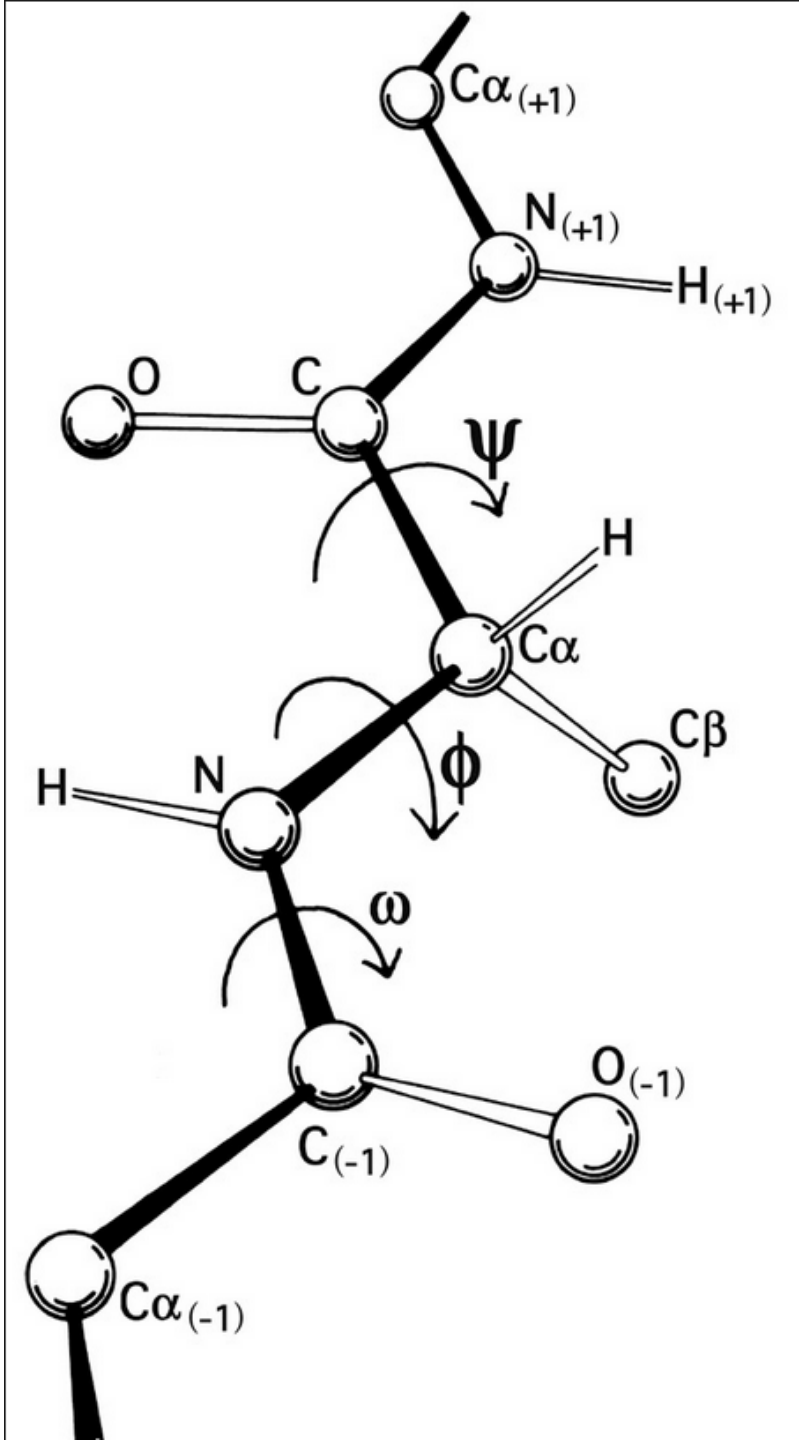
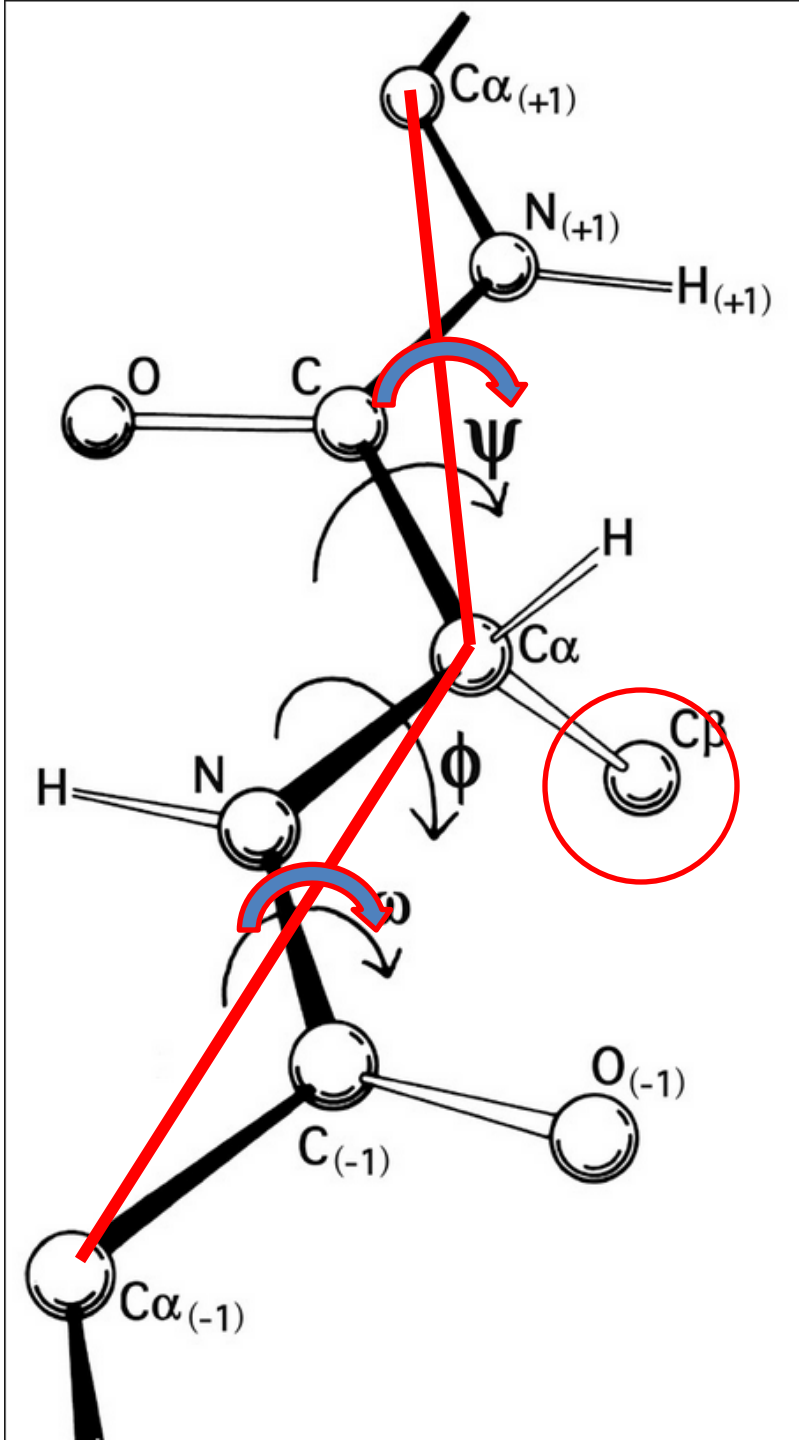
Protein representation



The protein backbone and the dihedral angles

Proteins and their residues

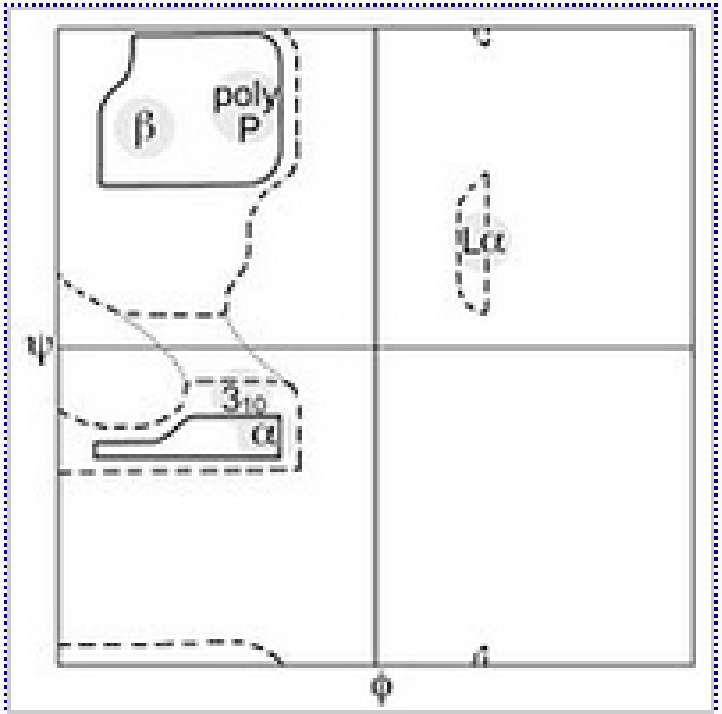
α-Carbon is a term that applies to proteins and amino acids. It is the backbone carbon before the carbonyl carbon. Therefore, reading along the backbone of a typical protein would give a sequence of N, α-C, carbonyl C, N, α-C, carbonyl C, N, α-C, carbonyl C, etc. (when reading in the N to C direction). *The α-carbon is where the different residues are covalently linked attach*. That is, the groups hanging off the chain at the α-carbon are what give to proteins their difference in residues. These groups give the α-carbon its stereogenic properties for every residue except for glycine. Therefore, the α-carbon is a stereocenter for every residue except glycine. Glycine also does not have a β-carbon, while every other residue does.



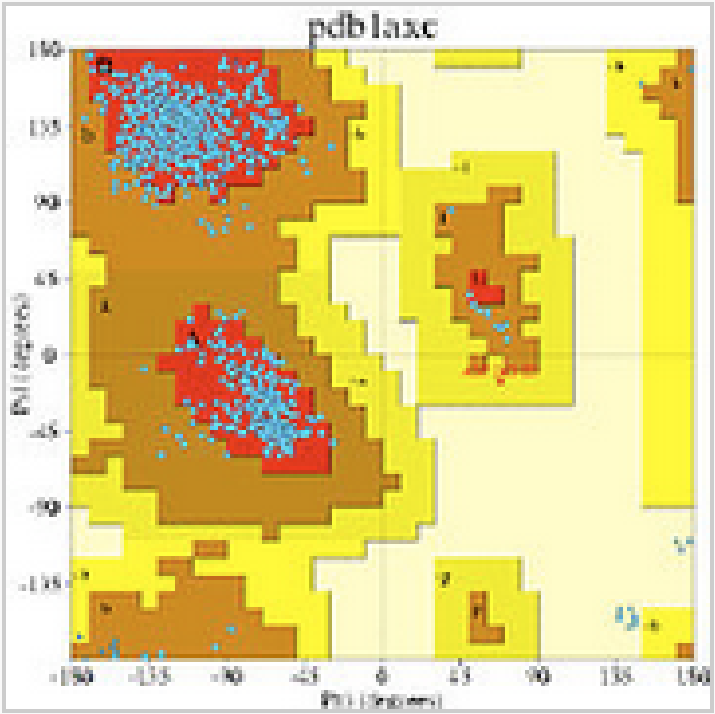
The protein reduced representation and its dihedral angles

The α-carbon of a residue is significant in protein folding. When describing a protein (which is an ethero polymer), one often approximates the location of each residue as the location of its α-carbon. In general, α-carbons of adjacent residues in a protein are about 3.8 ångströms (380 picometers) apart.

The Ramachandran plot

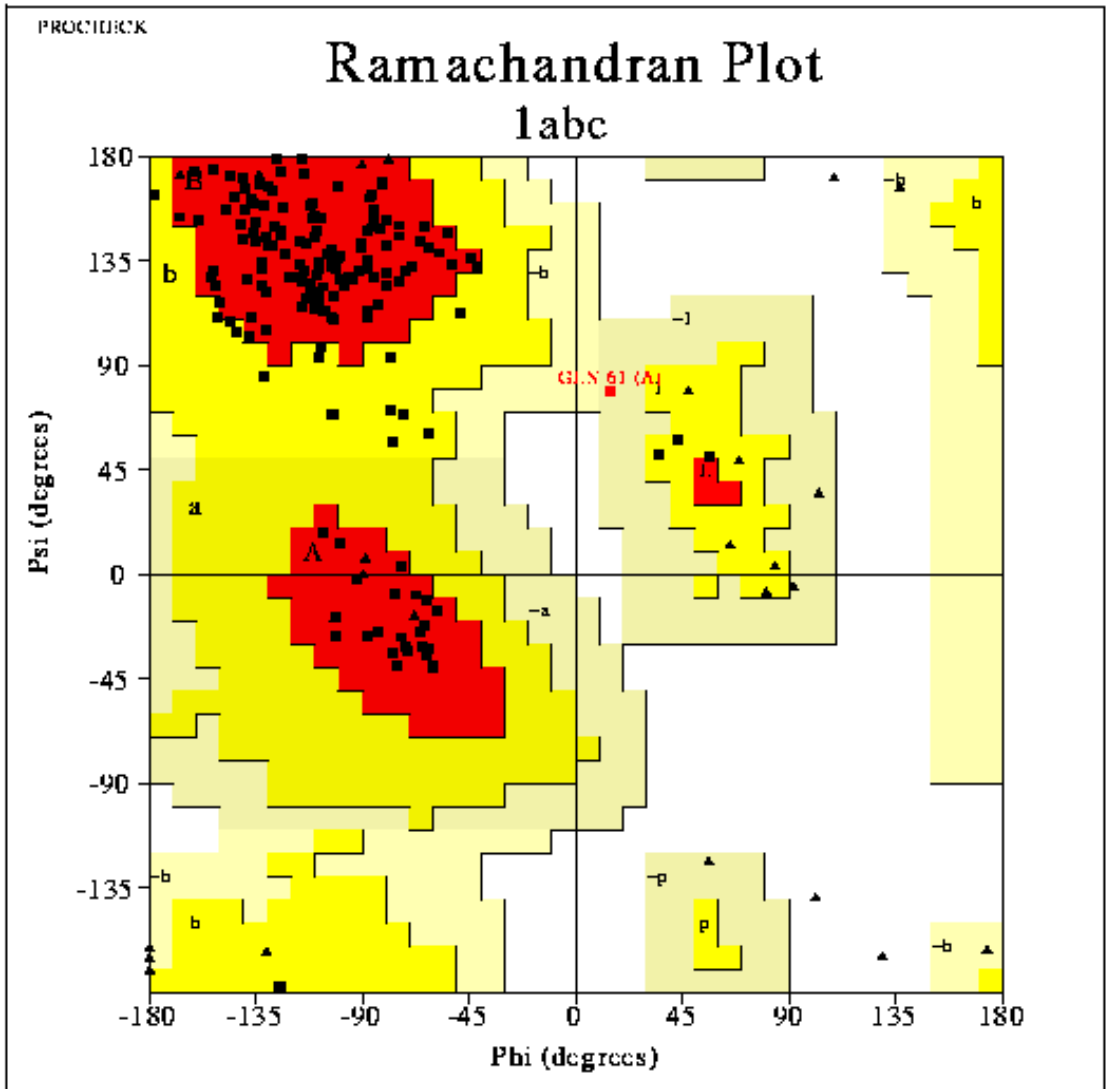


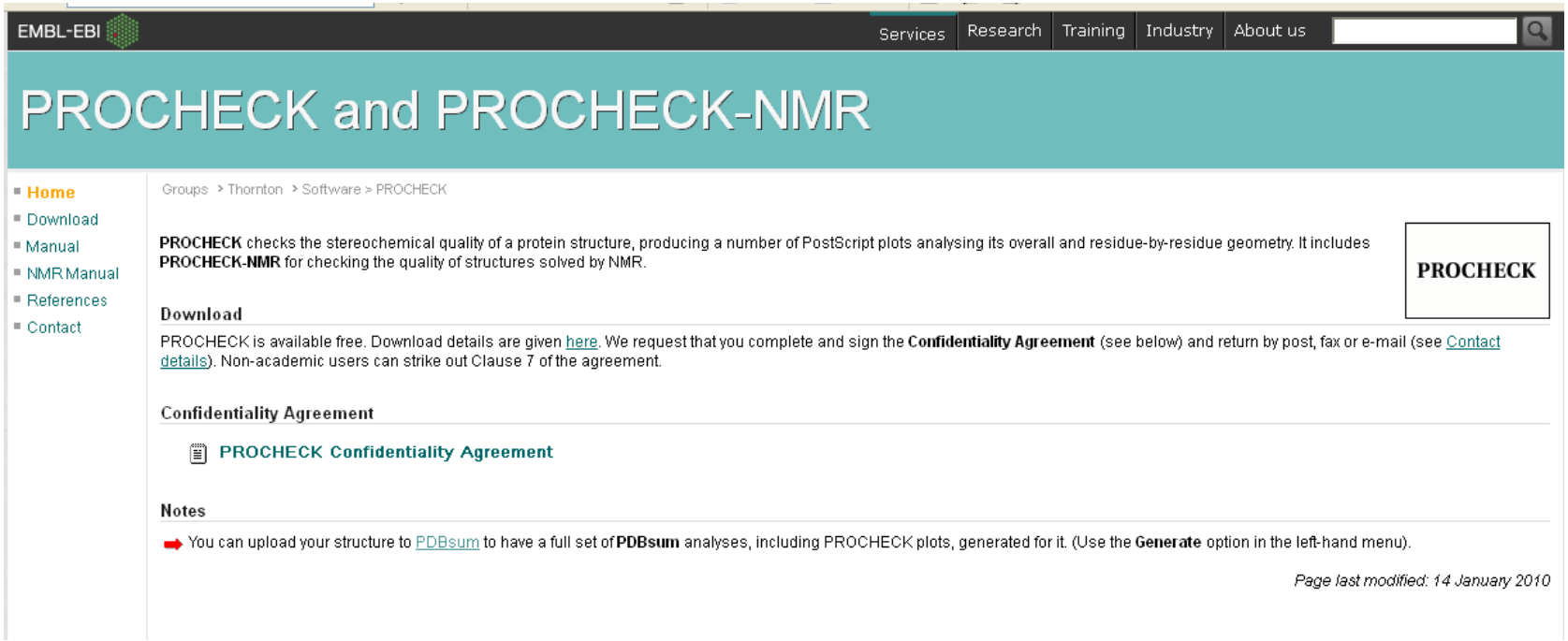
Original hard-sphere, reduced-radius, and relaxed-tau φ,ψ regions from Ramachandran, with updated labels and axes



A Ramachandran plot generated from human PCNA, a trimeric DNA clamp protein that contains both β-sheet and α-helix (PDB ID 1AXC). The red, brown, and yellow regions represent the favored, allowed, and "generously allowed" regions as defined by ProCheck

European Bioinformatics Institute





http://www.ebi.ac.uk/thornton-srv/software/PROCHECK/

PDBsum entry 1acx

Go to PDB code: 1acx go

Top page | Protein | Clefts | Tunnels | Links

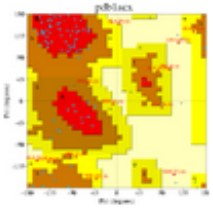
Antibacterial protein PDB id 1acx

PDB id: 1acx

Links

Name: Antibacterial protein
Title: Actinoxanthin structure at the atomic level (russian)
Structure: Actinoxanthin. Chain: a. Engineered: yes
Source: Streptomyces globisporus. Organism_taxid: 1908
Resolution: 2.00Å **R-factor:** not given
Authors: V.Z.Pletnev,A.P.Kuzin
Key ref: V.Z.Pletnev et al. (1982). Actinoxanthin structure at the atomic level (russian). *Bioorg.Khim.*, **8**, 1637.
Date: 17-Dec-82 **Release date:** 09-Mar-83

PROCHECK



Headers
References

Protein chain

P01551 (ATXA_STRGL) - Actinoxanthin

Seq: Neocarzinostat 143 a.a.
Struc: 108 a.a.*

Key: Family — PfamA domain — PfamB domain — Secondary structure — CATH domain

* PDB and UniProt seqs differ at 5 residue positions (black crosses)

Contents
- Protein chain
  - 108 a.a.

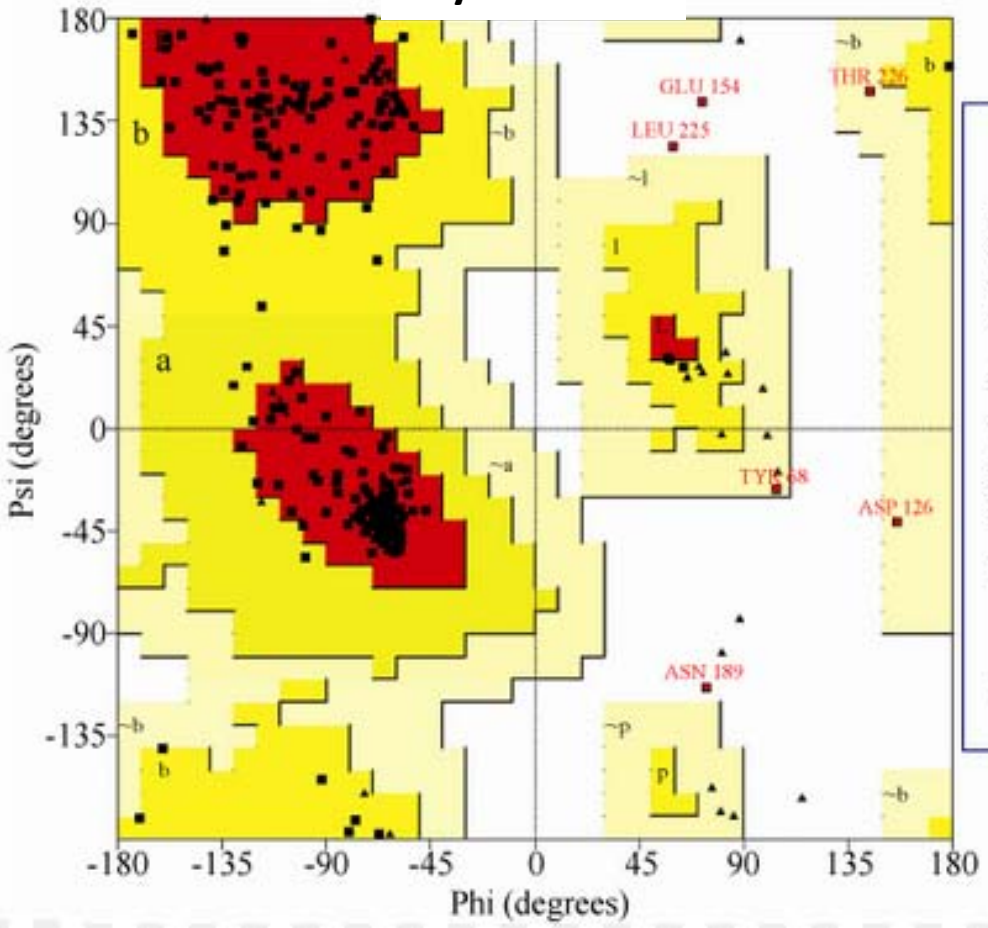
Gene Ontology (GO) functional annotation

Biological process	defense response	2 terms
Biochemical function	DNA binding	1 term

PROCHECK

Ramachandran Plot

any structure



Plot statistics

Residues in most favoured regions [A,B,L]	222	90.2%
Residues in additional allowed regions [a,b,l,p]	21	7.4%
Residues in generously allowed regions [~a,~b,~l,~p]	3	1.2%
Residues in disallowed regions	3	1.2%
Number of non-glycine and non-proline residues	249	100.0%
Number of end-residues (excl. Gly and Pro)	2	
Number of glycine residues (shown as triangles)	33	
Number of proline residues	13	
Total number of residues	297	

Based on an analysis of 118 structures of resolution of at least 2.0 Angstroms and R-factor no greater than 20%, a good quality model would be expected to have over 90% in the most favoured regions.