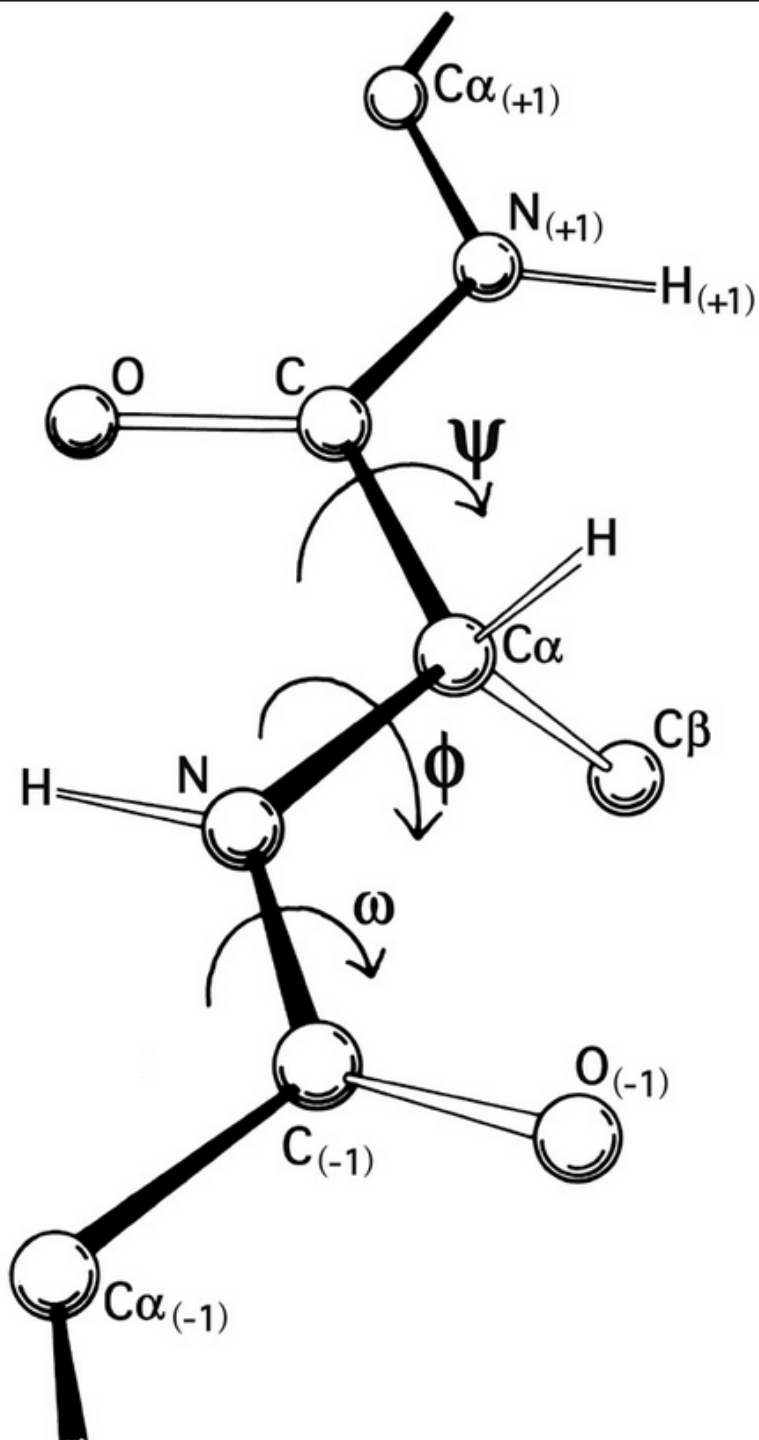


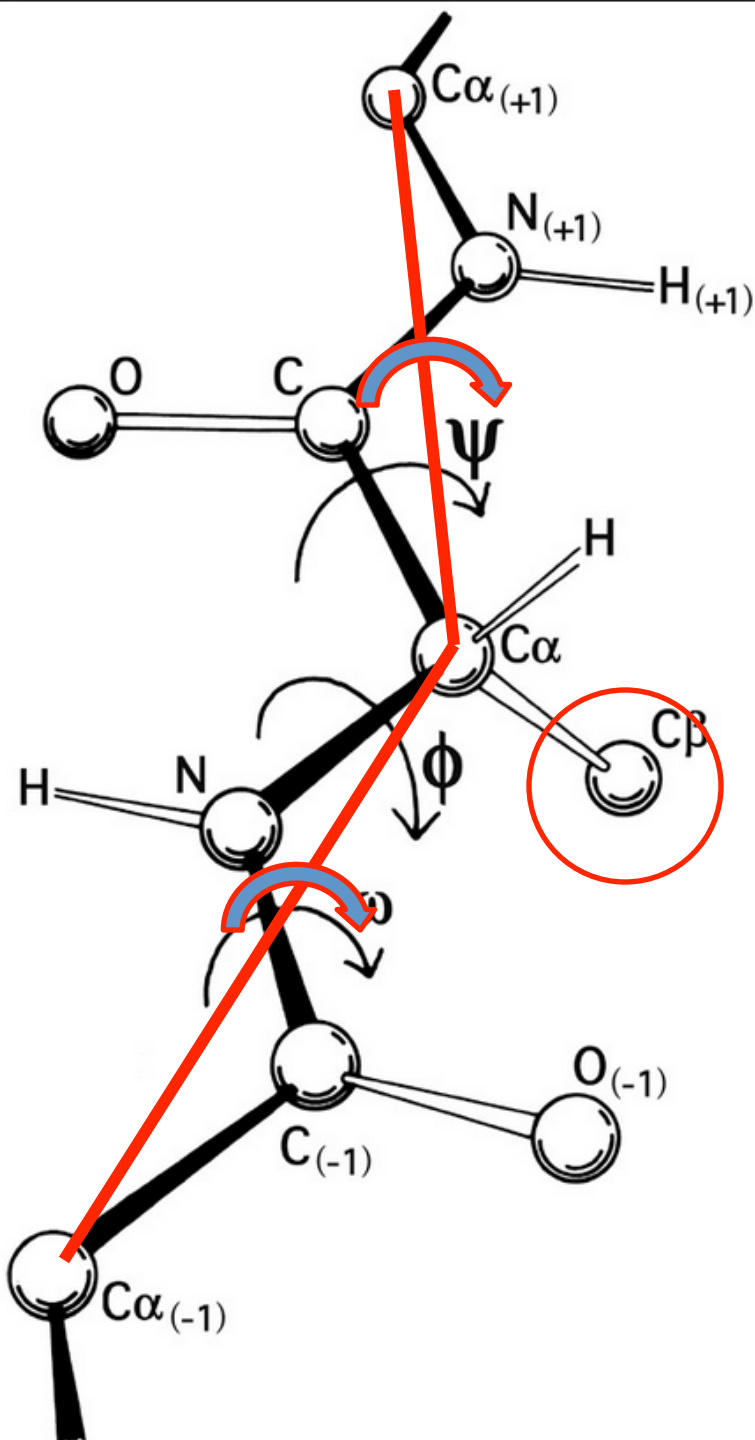
Protein representation



The protein backbone and the dihedral angles

Proteins and their residues

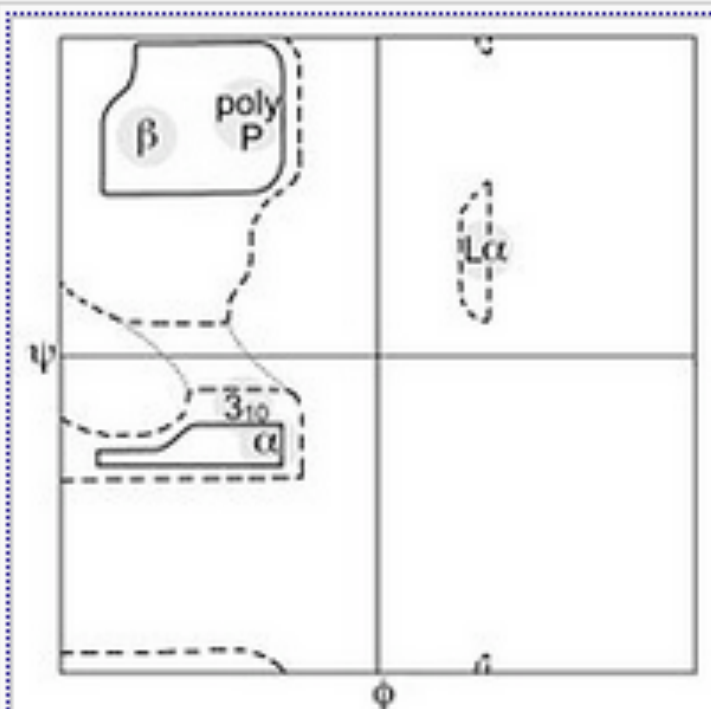
α -Carbon is a term that applies to [proteins](#) and [amino acids](#). It is the backbone carbon before the carbonyl carbon. Therefore, reading along the backbone of a typical protein would give a sequence of N, α -C, carbonyl C, N, α -C, carbonyl C, N, α -C, carbonyl C, etc. (when reading in the N 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.



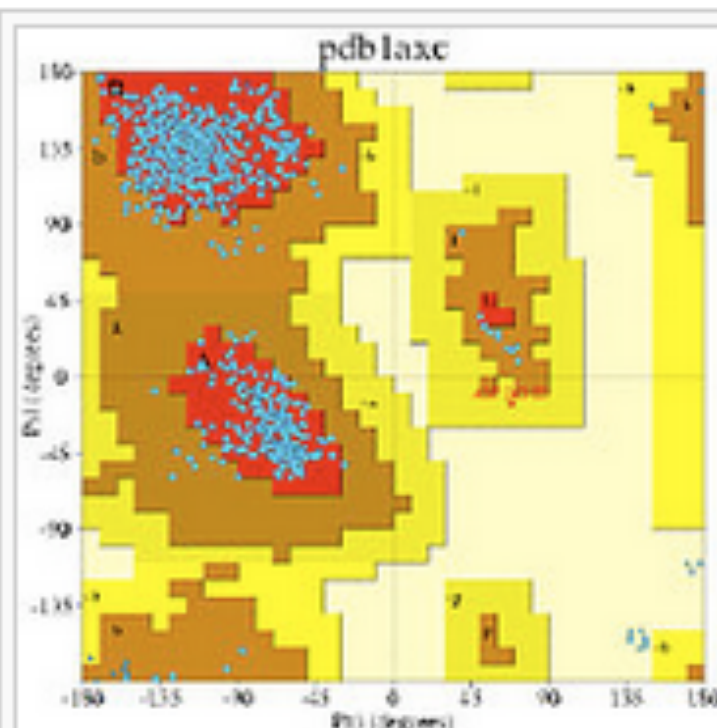
The protein reduced representation and its dihedral angles

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

About PDBsum

Top page

Protein

DNA/RNA

Ligands

Prot-prot

Clefts

Links

Text search

Using RasMol

PROMOTIF

Beta barrels

Beta sheets

Beta-alpha-beta units

Beta hairpins

Psi loops

Beta bulges

Beta strands

Helices

Helix-helix
interactions

Beta turns

Gamma turns

Disulphides

PROSITE patterns

PROCHECK analysis

Main

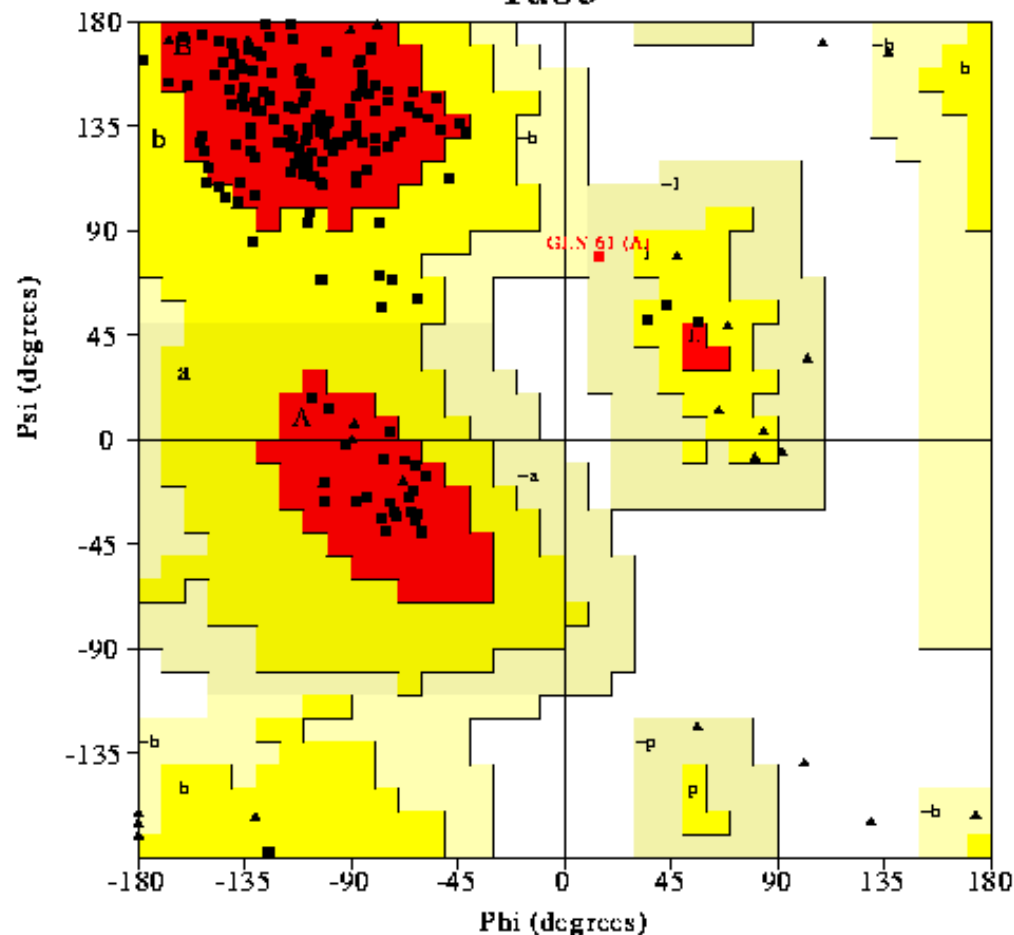
Ramachandran plot

Databases > Structure Databases > PDBsum > Index

PROCHECK

Ramachandran Plot

1abc





PROCHECK and PROCHECK-NMR

- **Home**
- Download
- Manual
- NMR Manual
- References
- Contact

Groups > Thornton > Software > PROCHECK

PROCHECK checks the stereochemical quality of a protein structure, producing a number of PostScript plots analysing its overall and residue-by-residue geometry. It includes **PROCHECK-NMR** for checking the quality of structures solved by NMR.

PROCHECK

Download

PROCHECK is available free. Download details are given [here](#). We request that you complete and sign the **Confidentiality Agreement** (see below) and return by post, fax or e-mail (see [Contact details](#)). Non-academic users can strike out Clause 7 of the agreement.

Confidentiality Agreement



PROCHECK Confidentiality Agreement

Notes

➡ You can upload your structure to [PDBsum](#) to have a full set of **PDBsum** analyses, including PROCHECK plots, generated for it. (Use the **Generate** option in the left-hand menu).

Page last modified: 14 January 2010

<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

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

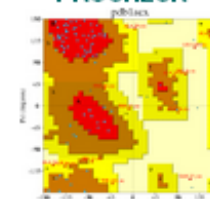
Authors: V.Z.Pletnev, A.P.Kuzin

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

[Links](#)

PROCHECK


[Headers](#)
[References](#)
Protein chain **A**

P01551 (ATXA_STRGL) - Actinoxanthin

Seq:  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

A 108 a.a.

Gene Ontology (GO) functional annotation



Biological process

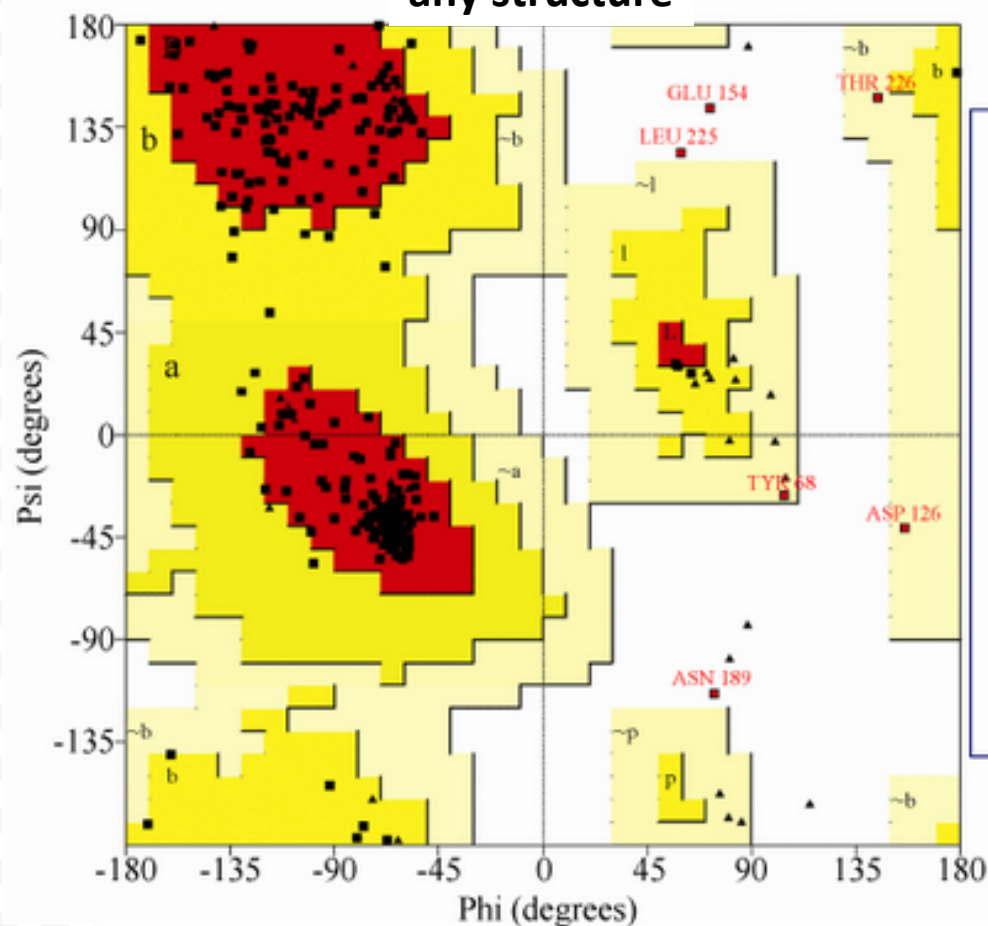
defense response 2 terms

Biochemical function

DNA binding 1 term

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.