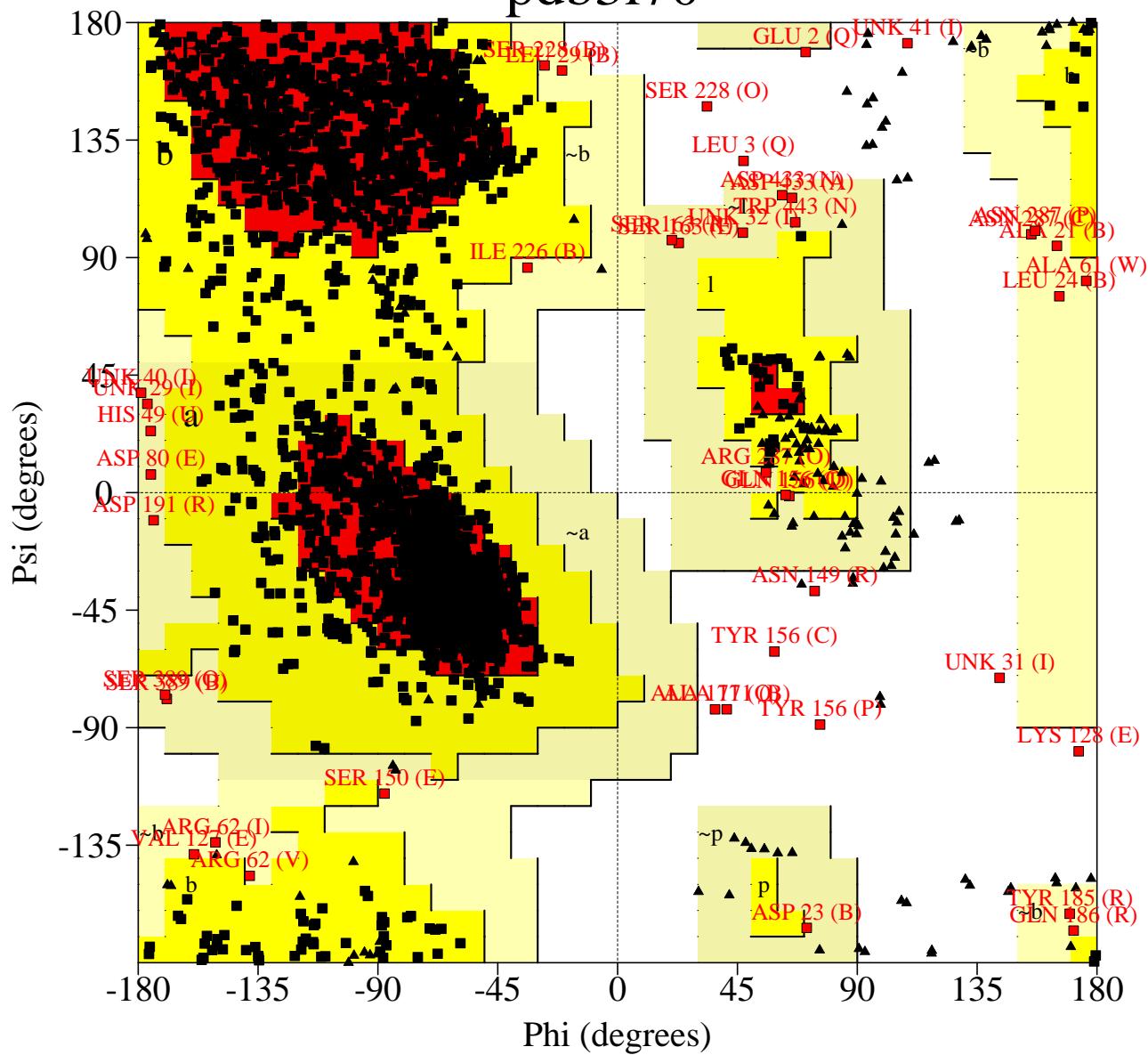


Ramachandran Plot

pdb3l70



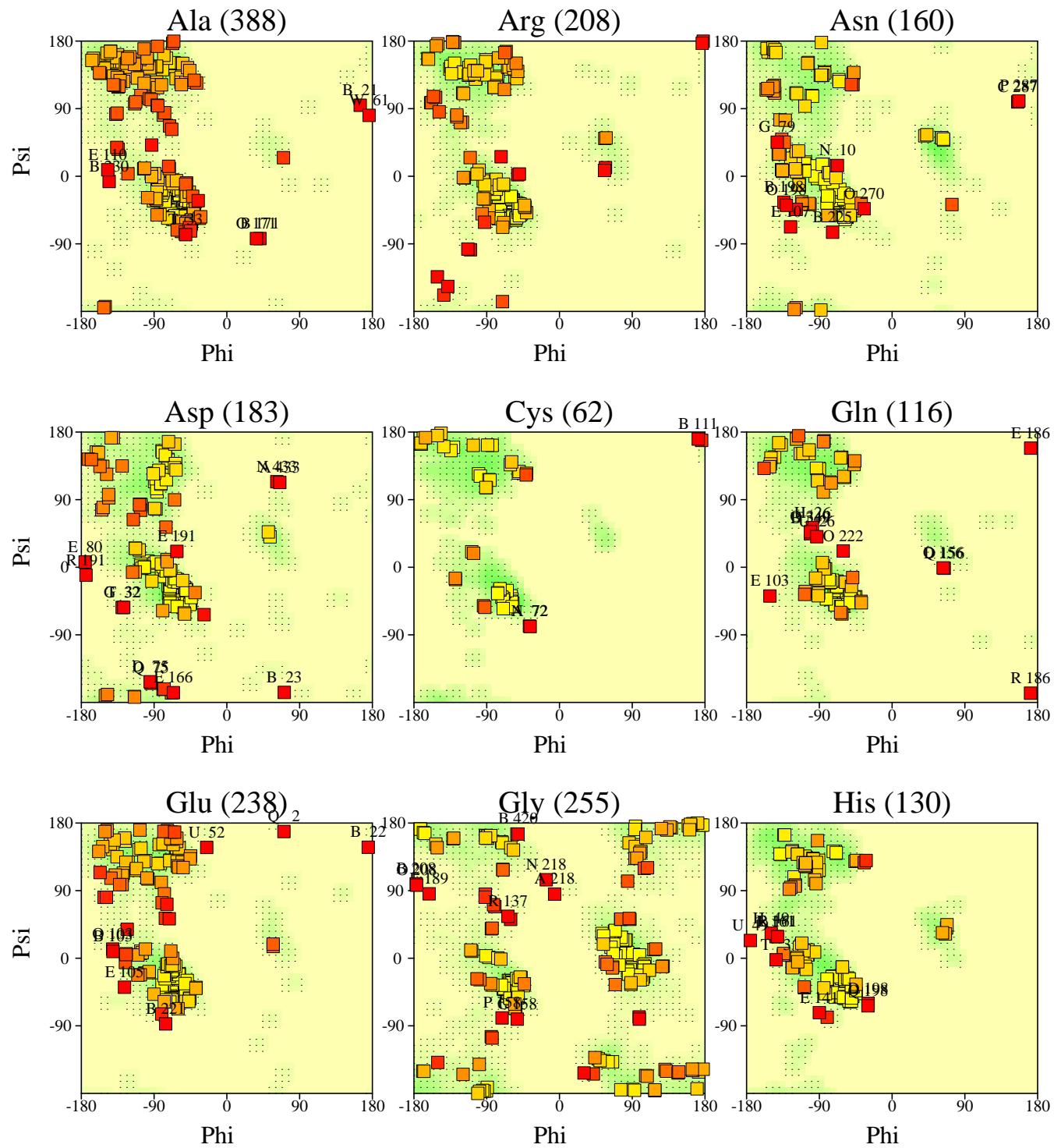
Plot statistics

Residues in most favoured regions [A,B,L]	3108	86.9%
Residues in additional allowed regions [a,b,l,p]	425	11.9%
Residues in generously allowed regions [~a,~b,~l,~p]	31	0.9%
Residues in disallowed regions	11	0.3%
Number of non-glycine and non-proline residues	3575	100.0%
Number of end-residues (excl. Gly and Pro)	37	
Number of glycine residues (shown as triangles)	262	
Number of proline residues	195	
Total number of residues	4069	

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.

Ramachandran plots for all residue types

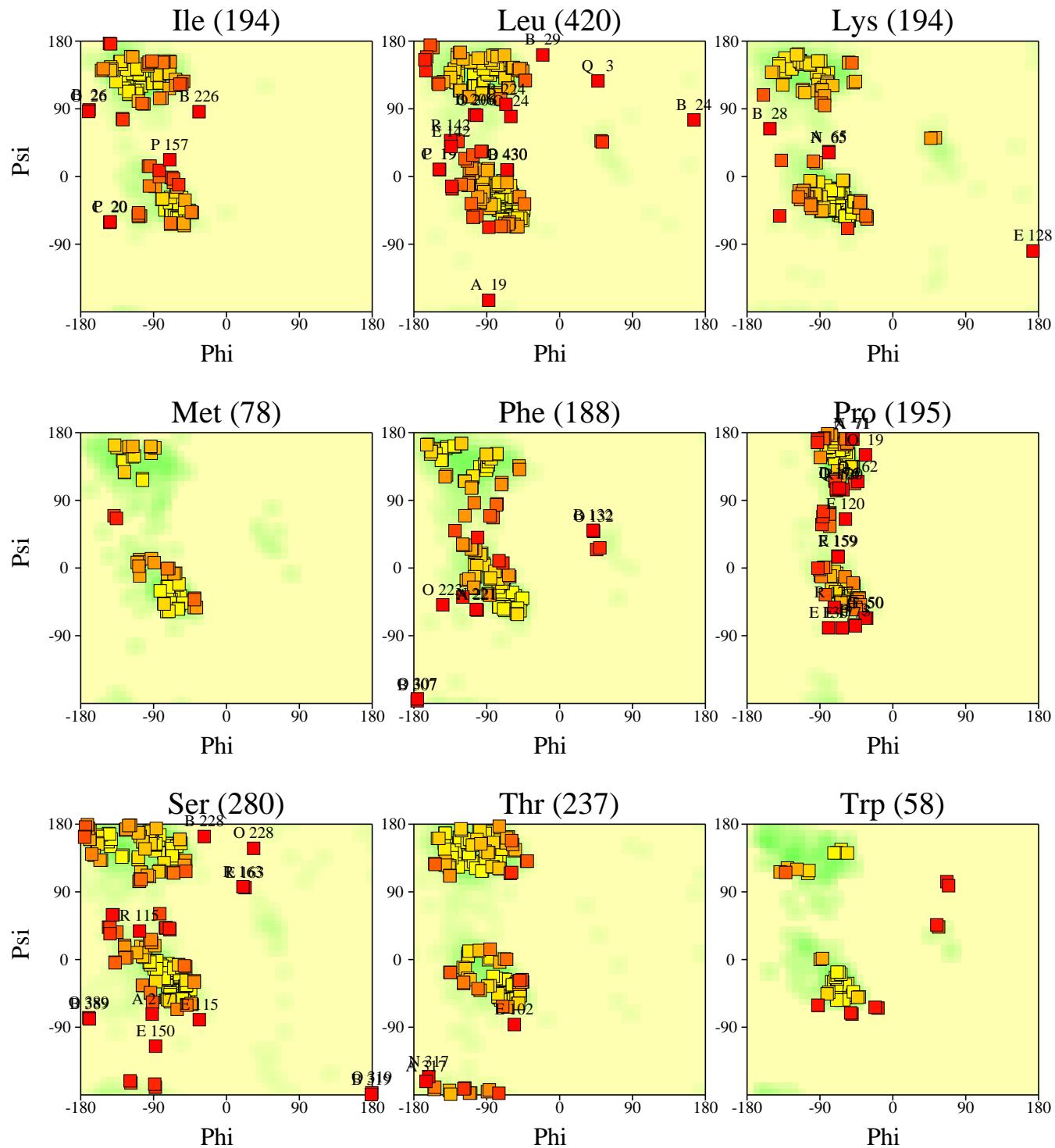
pdb3l70



Numbers of residues are shown in brackets. Those in unfavourable conformations (score < -3.00) are labelled.
Shading shows favourable conformations as obtained from an analysis of 163 structures at resolution 2.0Å or better.

Ramachandran plots for all residue types

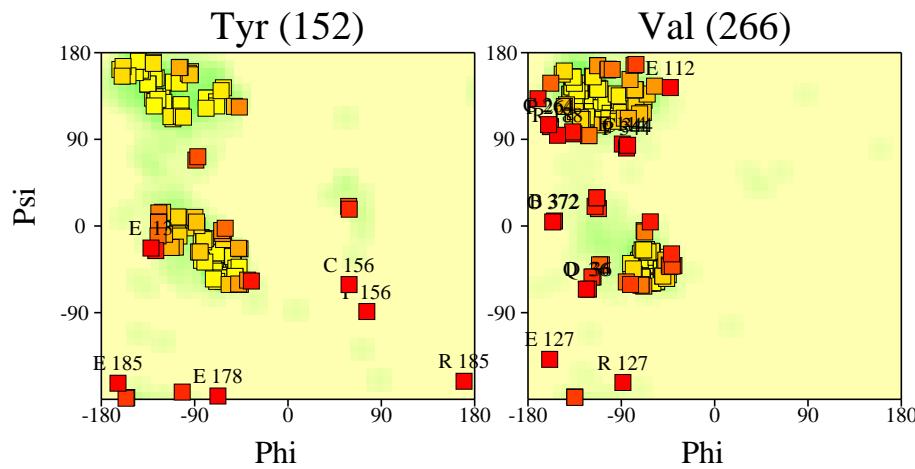
pdb3l70



Numbers of residues are shown in brackets. Those in unfavourable conformations (score < -3.00) are labelled.
Shading shows favourable conformations as obtained from an analysis of 163 structures at resolution 2.0Å or better.

Ramachandran plots for all residue types

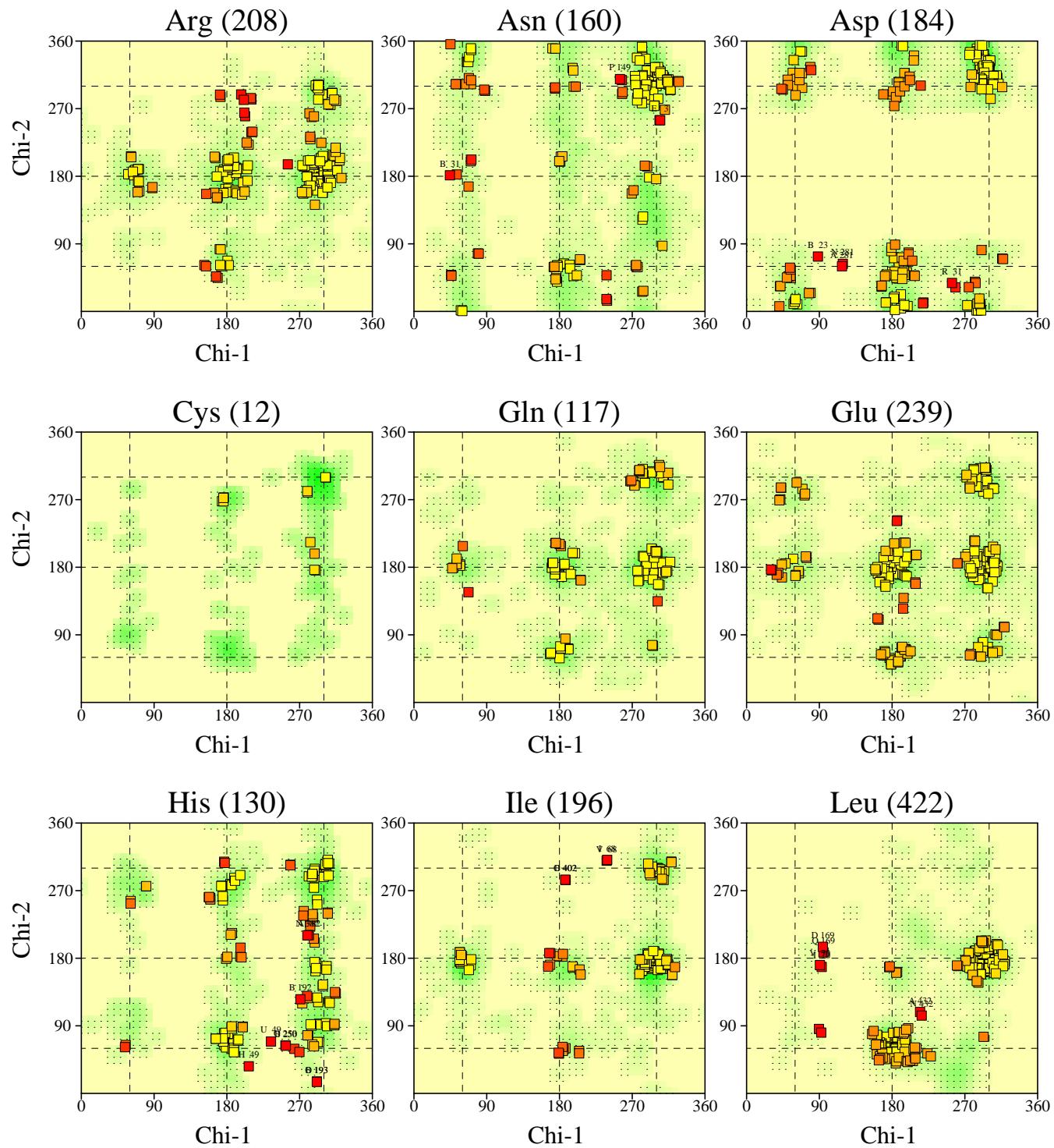
pdb3l70



Numbers of residues are shown in brackets. Those in unfavourable conformations (score < -3.00) are labelled.
Shading shows favourable conformations as obtained from an analysis of 163 structures at resolution 2.0 Å or better.

Chi1-Chi2 plots

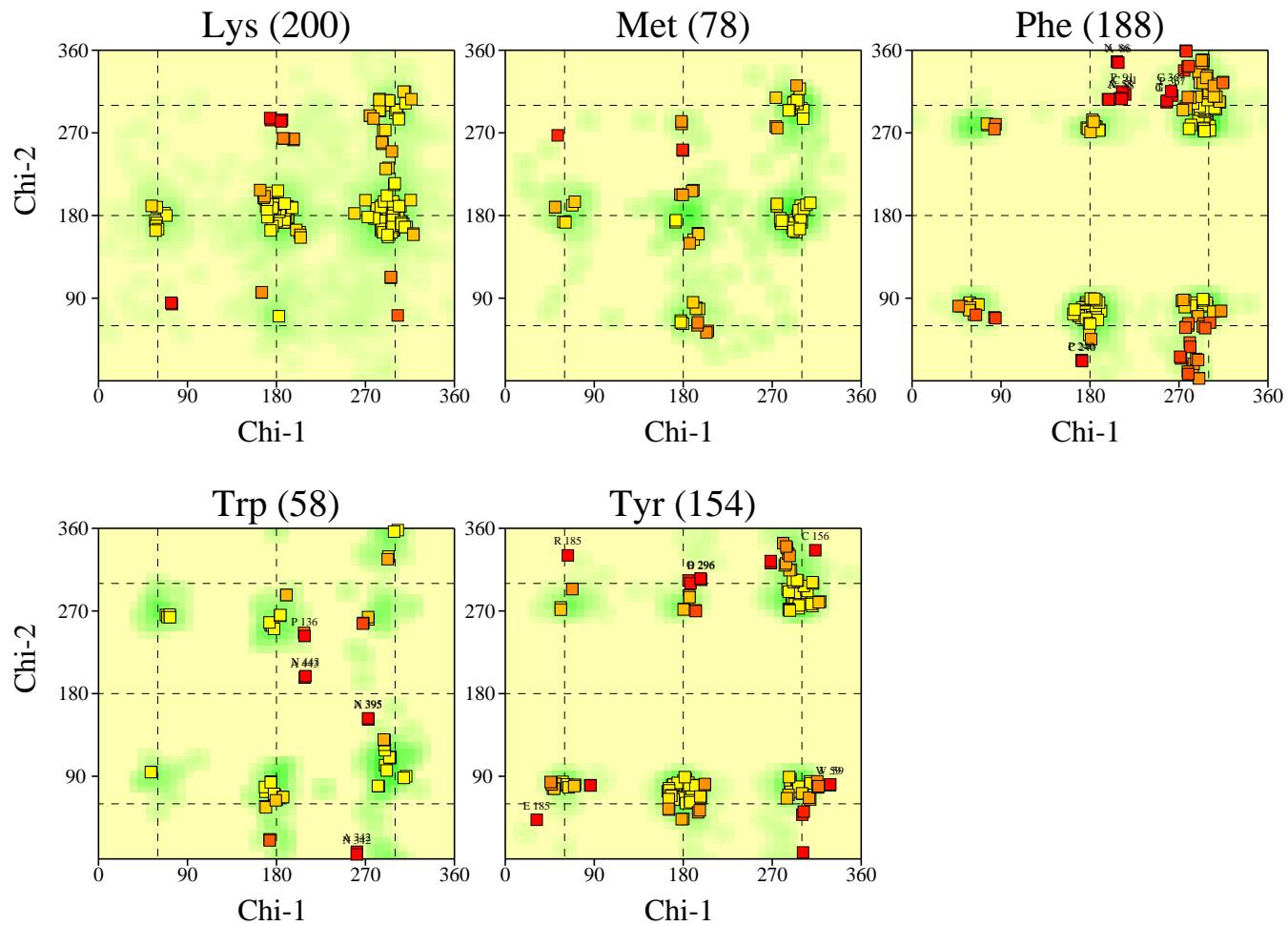
pdb3l70



Numbers of residues are shown in brackets. Those in unfavourable conformations ($\text{score} < -3.00$) are labelled.
Shading shows favourable conformations as obtained from an analysis of 163 structures at resolution 2.0Å or better.

Chi1-Chi2 plots

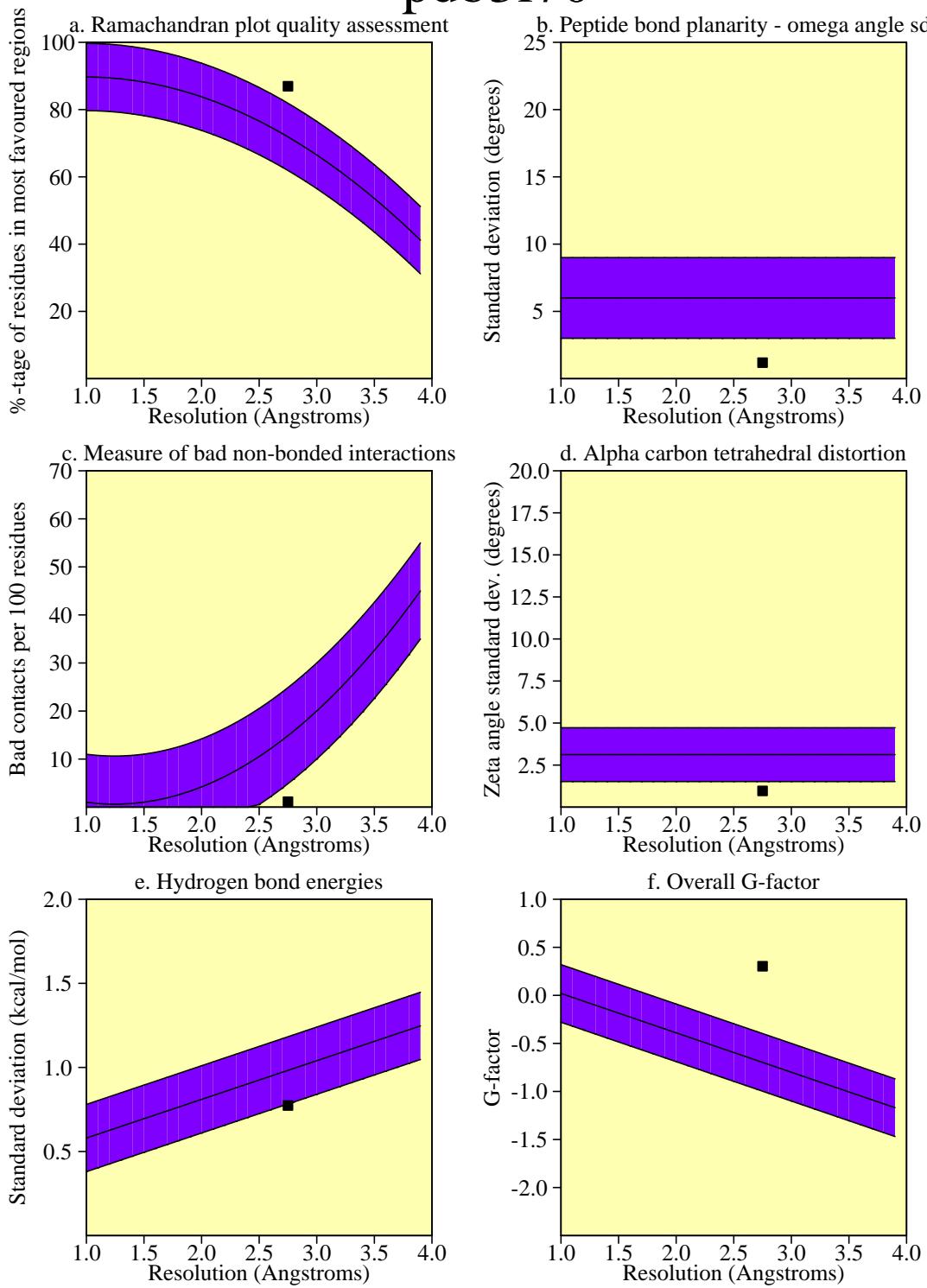
pdb3l70



Numbers of residues are shown in brackets. Those in unfavourable conformations (score < -3.00) are labelled.
Shading shows favourable conformations as obtained from an analysis of 163 structures at resolution 2.0A or better.

Main-chain parameters

pdb3l70

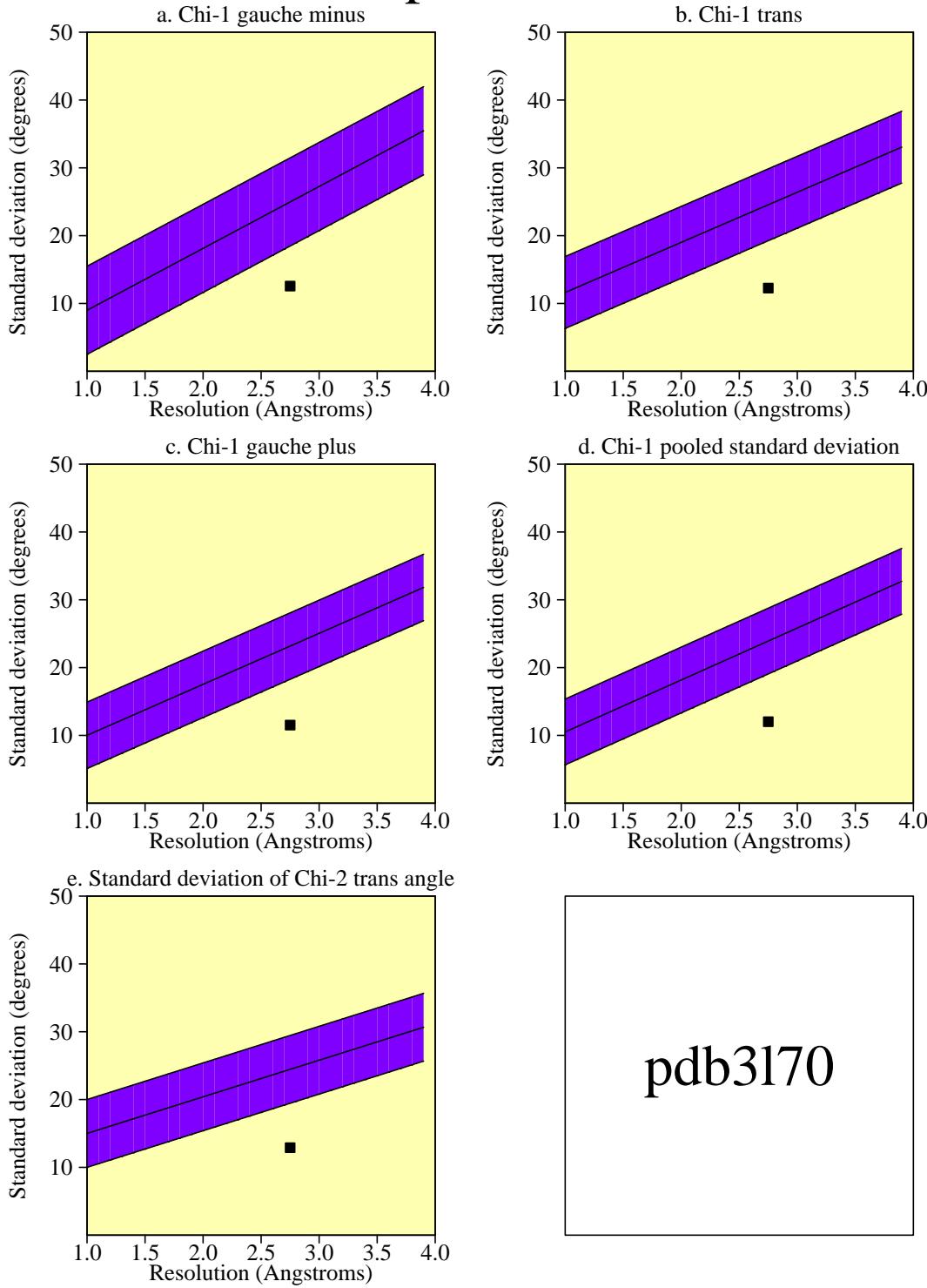


Plot statistics

Stereochemical parameter	No. of data pts	Parameter value	Comparison values	No. of band widths from mean	
			Typical value	Band width	
a. %-tage residues in A, B, L	3575	86.9	71.9	10.0	1.5 BETTER
b. Omega angle st dev	4040	1.2	6.0	3.0	-1.6 BETTER
c. Bad contacts / 100 residues	46	1.1	14.9	10.0	-1.4 BETTER
d. Zeta angle st dev	3791	1.0	3.1	1.6	-1.3 BETTER
e. H-bond energy st dev	2718	0.8	1.0	0.2	-1.0 BETTER
f. Overall G-factor	4069	0.3	-0.7	0.3	3.3 BETTER

Side-chain parameters

pdb3l70



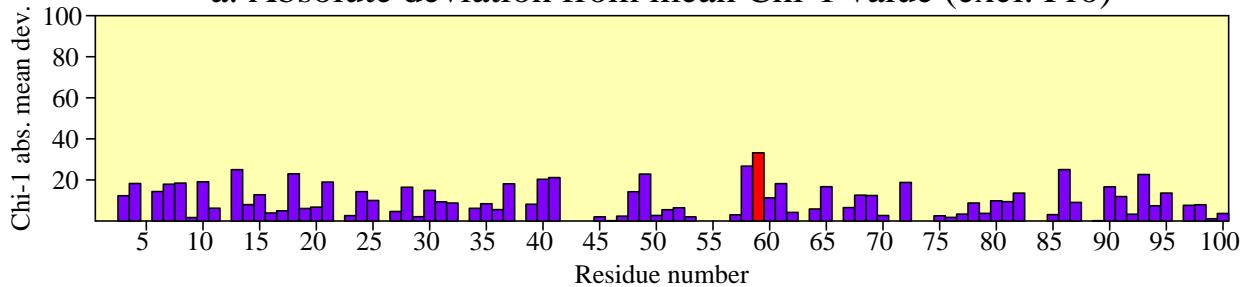
Plot statistics

Stereochemical parameter	No. of data pts	Parameter value	Comparison values	No. of band widths from mean	
			Typical value	Band width	
a. Chi-1 gauche minus st dev	461	12.6	25.0	6.5	-1.9 BETTER
b. Chi-1 trans st dev	1063	12.3	24.6	5.3	-2.3 BETTER
c. Chi-1 gauche plus st dev	1659	11.5	23.2	4.9	-2.4 BETTER
d. Chi-1 pooled st dev	3183	12.0	23.9	4.8	-2.5 BETTER
e. Chi-2 trans st dev	1051	12.9	24.5	5.0	-2.3 BETTER

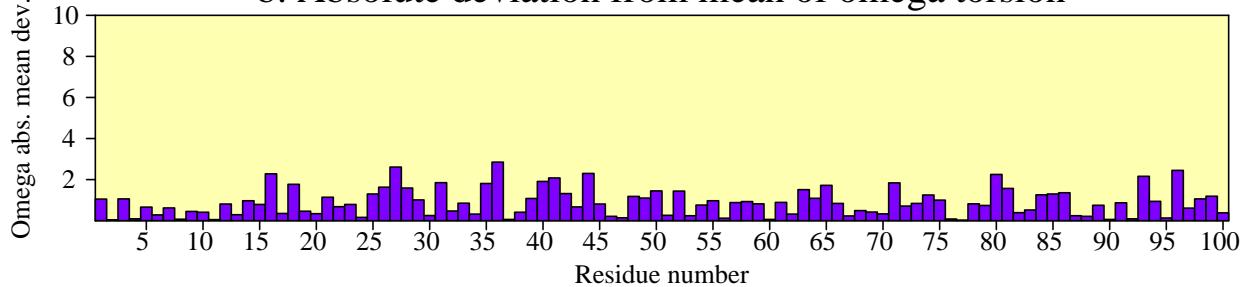
pdb3l70

Residue properties pdb3170

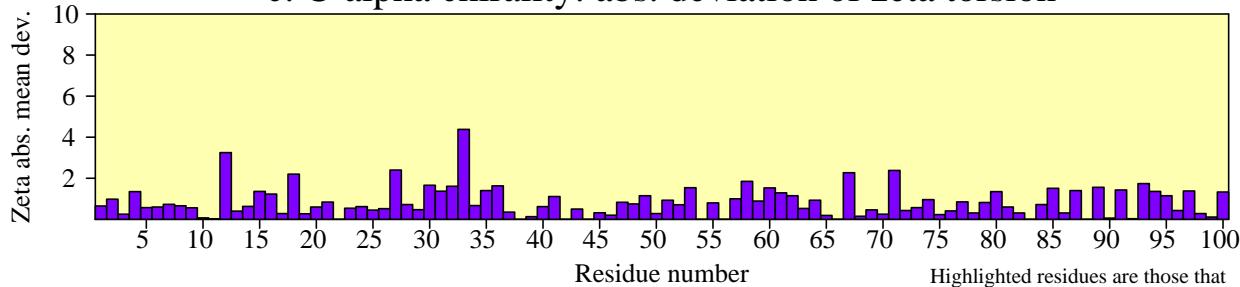
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion



c. C-alpha chirality: abs. deviation of zeta torsion



Highlighted residues are those that deviate by more than 2.0 st. devs. from ideal

d. Secondary structure & estimated accessibility

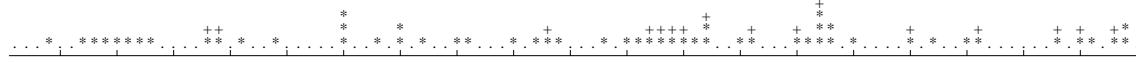


e. Sequence & Ramachandran regions ▲ Most favoured ■ Allowed ■ Generous ■ Disallowed

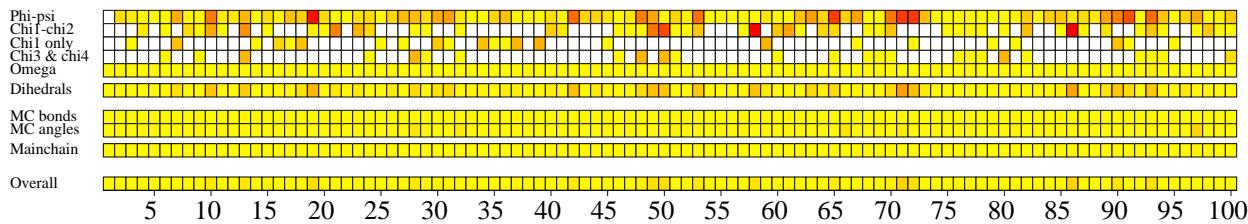
Figure 1. Schematic diagram of the experimental setup. The top part shows the optical path from the laser source to the sample stage. The bottom part shows the sample stage with a schematic of the beam splitter and lenses used for imaging.

AATYAQTLQNI PETNVTLDNGLRVASEES SQPTCTVGWVIGAGSRYENEKNNGAGYFVEHLAFKGTKRCPAAFEKEVESMGAHFNGYTSREQTAFYIK

f. Max. deviation (see listing)

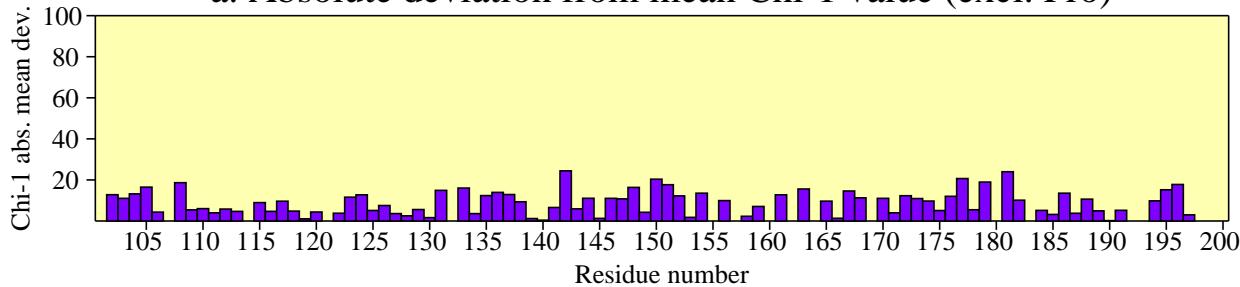


g. G-factors

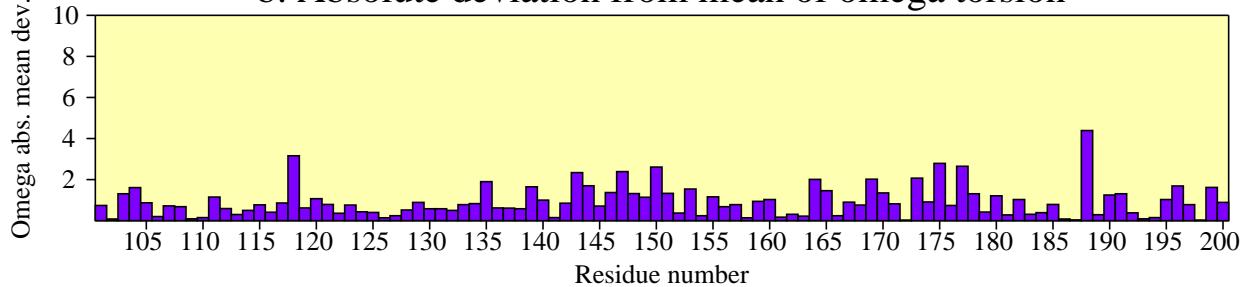


Residue properties pdb3170

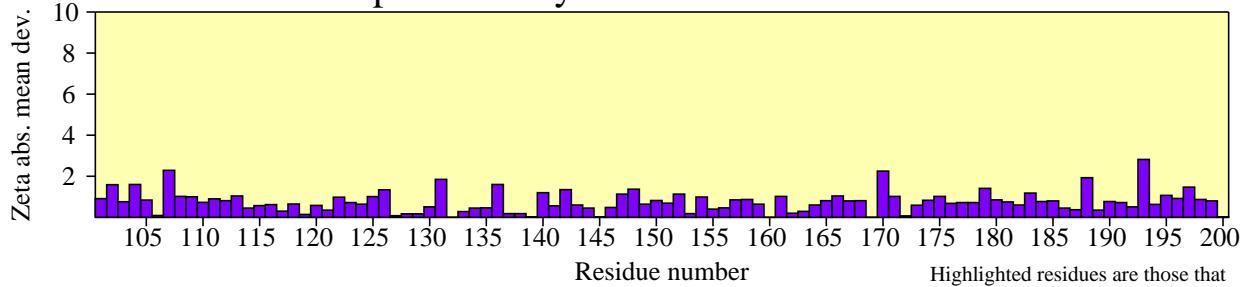
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion



c. C-alpha chirality: abs. deviation of zeta torsion



Highlighted residues are those that deviate by more than 2.0 st. devs. from ideal

d. Secondary structure & estimated accessibility



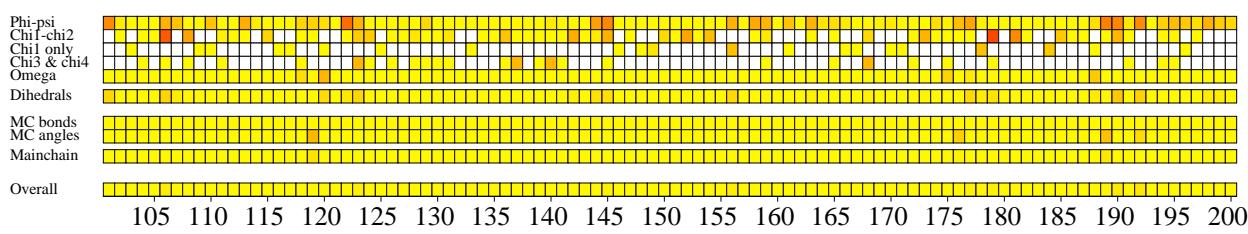
e. Sequence & Ramachandran regions ▲ Most favoured ■ Allowed ■ Generous ■ Disallowed

AI SKDMKPKVVEI LADVVONCAI EESO I EKRGVU LQEI K EMDNDMTNVT FIDYI HATA FOGTAL ARTVEGTTENI KHI TRADI ASY IDTHEKA PRMVII AAA

f. Max. deviation (see listing)



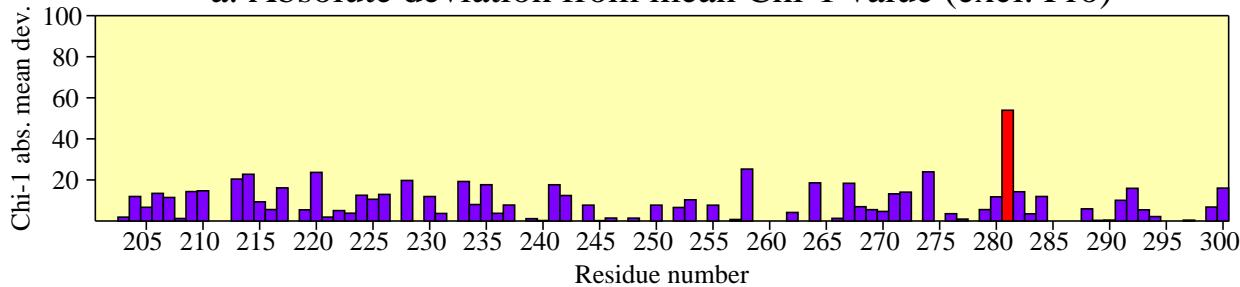
g. G-factors



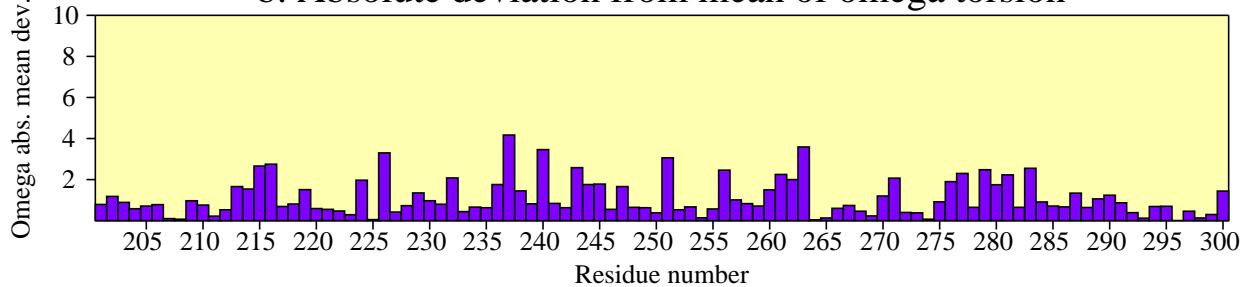
Residue properties

pdb3l70

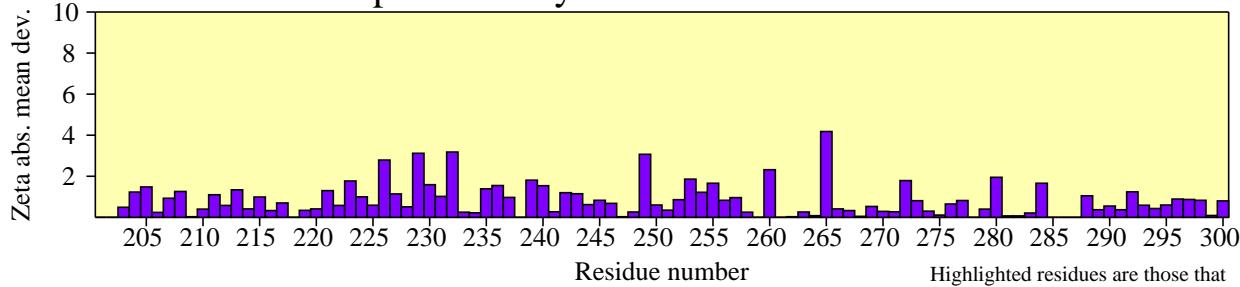
a. Absolute deviation from mean Chi-1 value (excl. Pro)



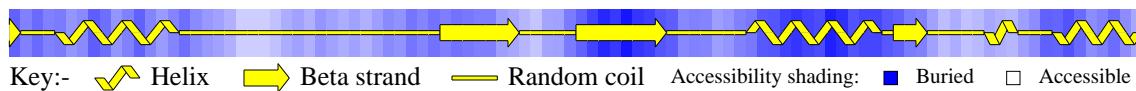
b. Absolute deviation from mean of omega torsion



c. C-alpha chirality: abs. deviation of zeta torsion



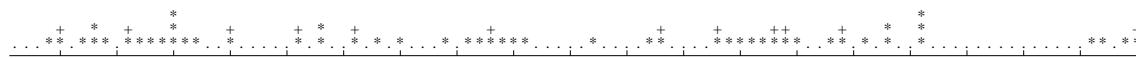
d. Secondary structure & estimated accessibility



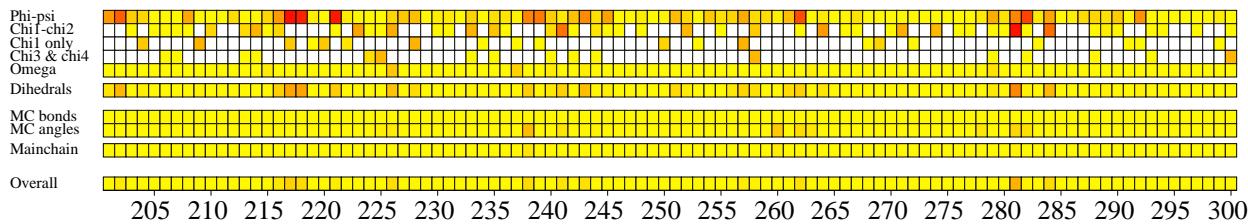
e. Sequence & Ramachandran regions



f. Max. deviation (see listing)



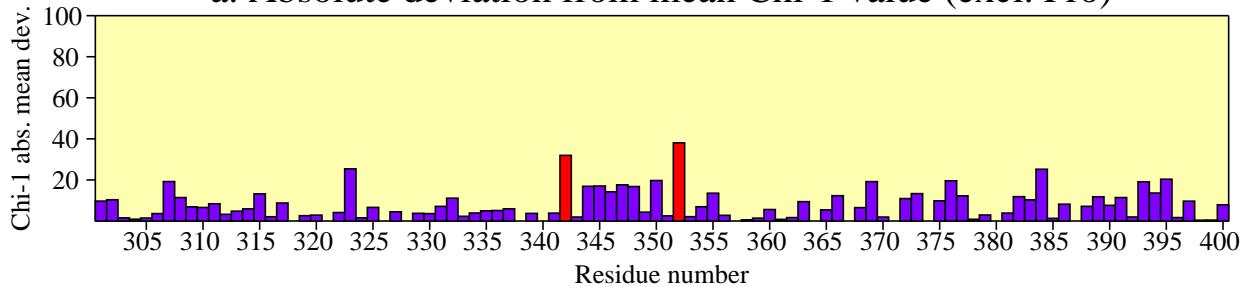
g. G-factors



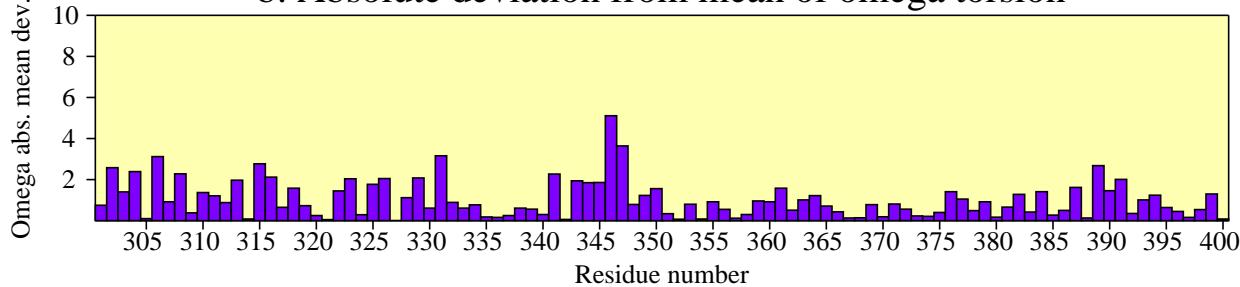
Residue properties

pdb3l70

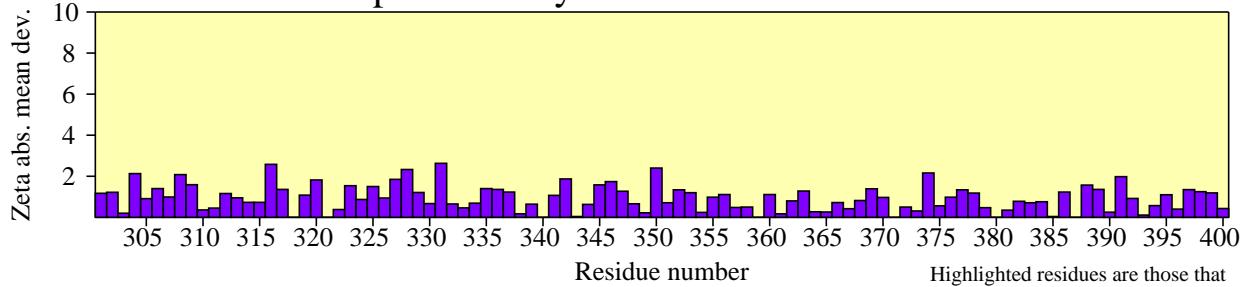
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion



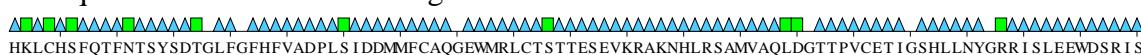
c. C-alpha chirality: abs. deviation of zeta torsion



d. Secondary structure & estimated accessibility



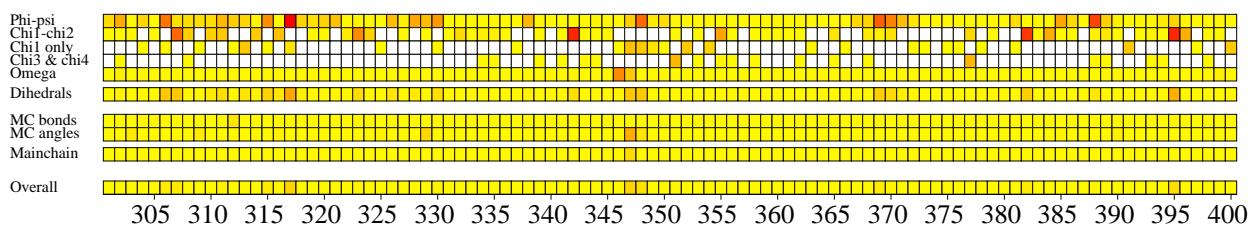
e. Sequence & Ramachandran regions



f. Max. deviation (see listing)



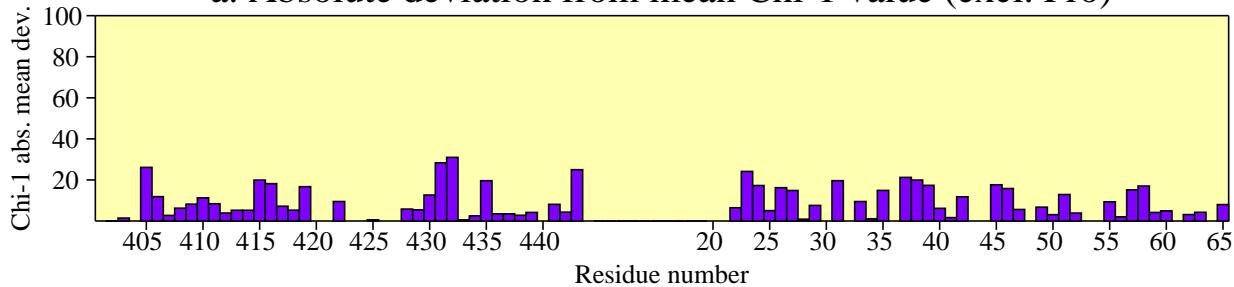
g. G-factors



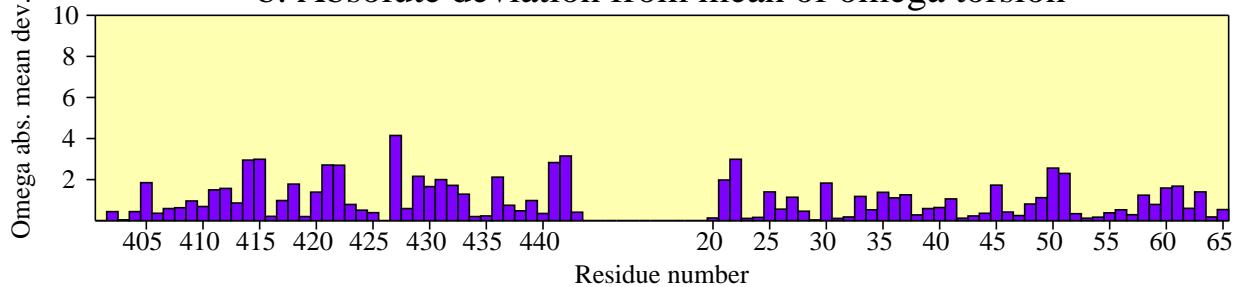
Residue properties

pdb3l70

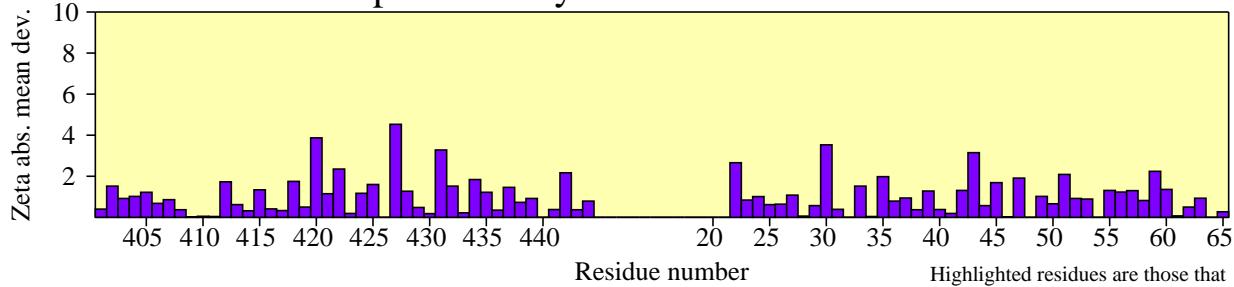
a. Absolute deviation from mean Chi-1 value (excl. Pro)



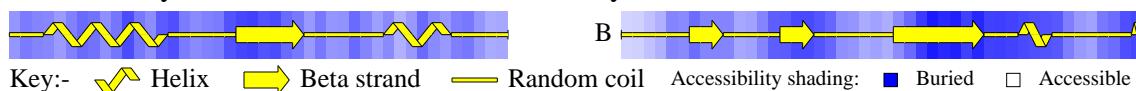
b. Absolute deviation from mean of omega torsion



c. C-alpha chirality: abs. dev. of zeta torsion



d. Secondary structure & estimated accessibility



e. Sequence & Ramachandran regions

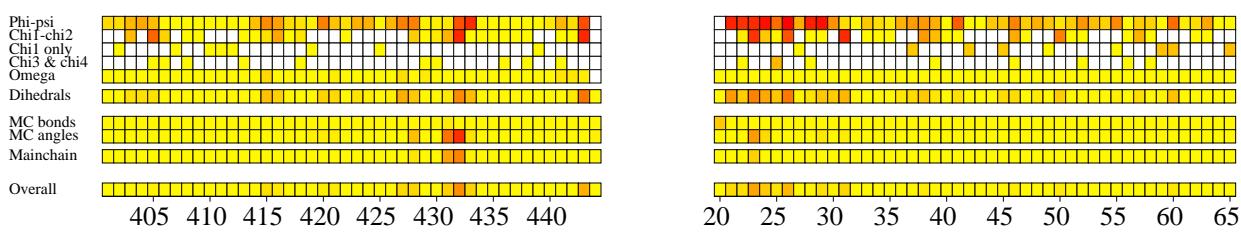


GAEDLEITKLPNGLIASLENFSPASRIGVFIKAGSRYETTANLGT

f. Max. deviation (see listing)



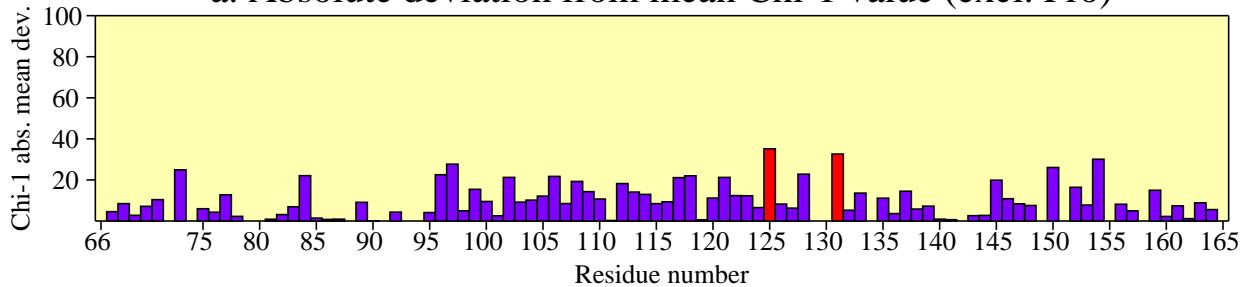
g. G-factors



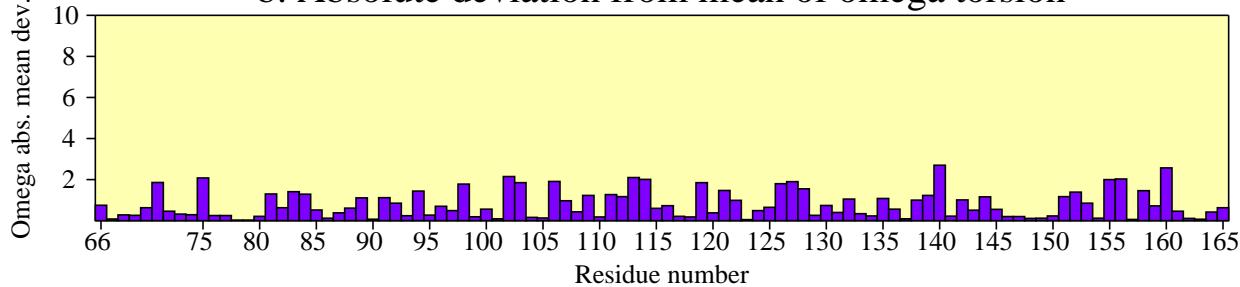
Residue properties

pdb3l70

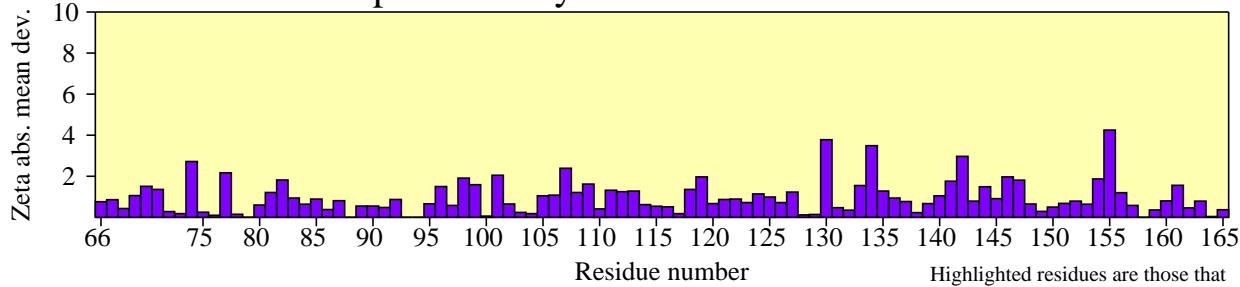
a. Absolute deviation from mean Chi-1 value (excl. Pro)



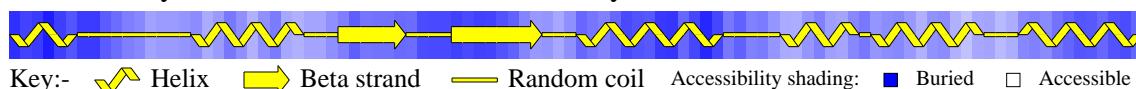
b. Absolute deviation from mean of omega torsion



c. C-alpha chirality: abs. deviation of zeta torsion



d. Secondary structure & estimated accessibility



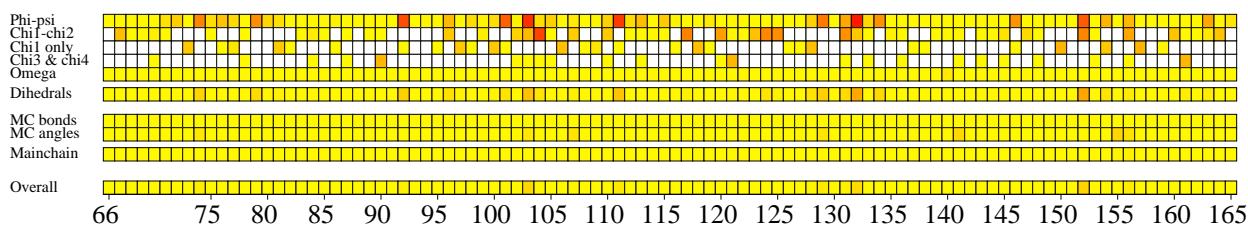
e. Sequence & Ramachandran regions



f. Max. deviation (see listing)



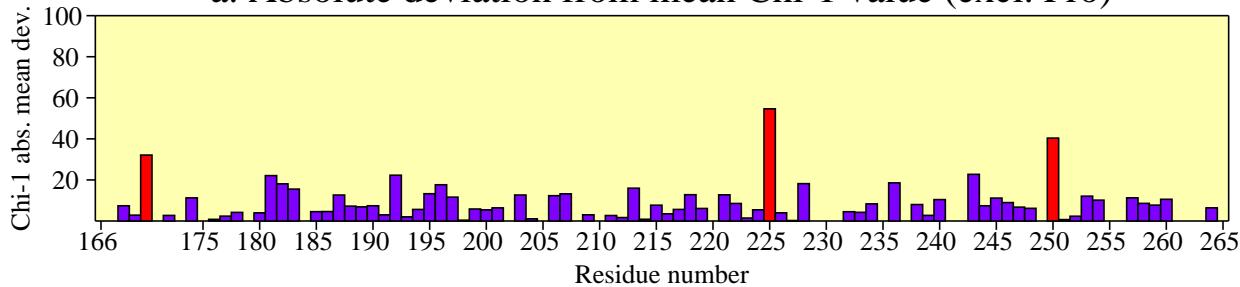
g. G-factors



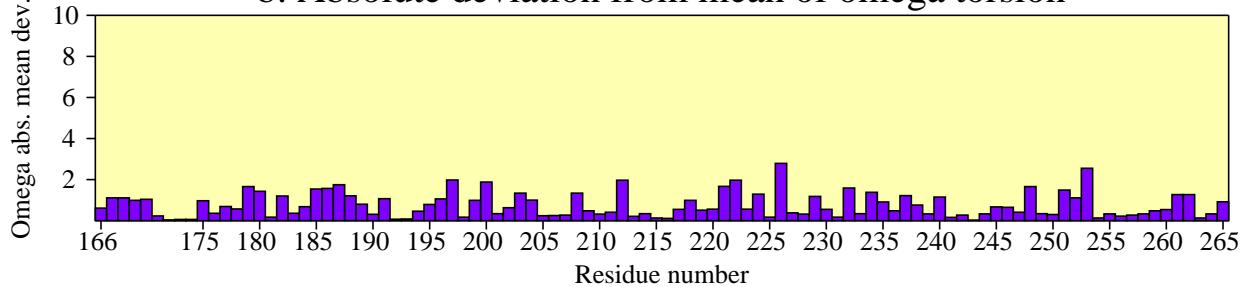
Residue properties

pdb3l70

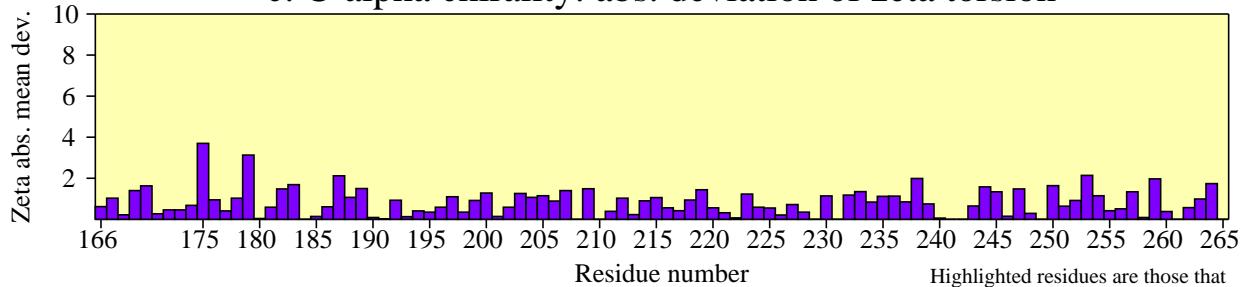
a. Absolute deviation from mean Chi-1 value (excl. Pro)



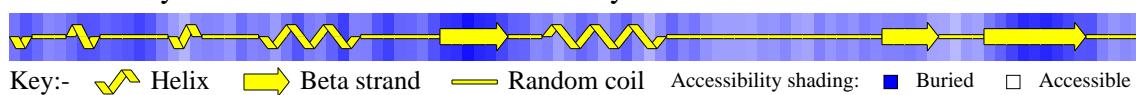
b. Absolute deviation from mean of omega torsion



c. C-alpha chirality: abs. deviation of zeta torsion



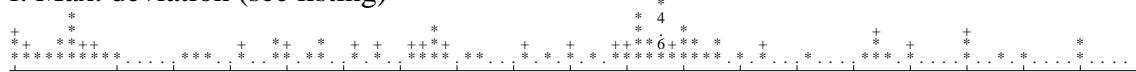
d. Secondary structure & estimated accessibility



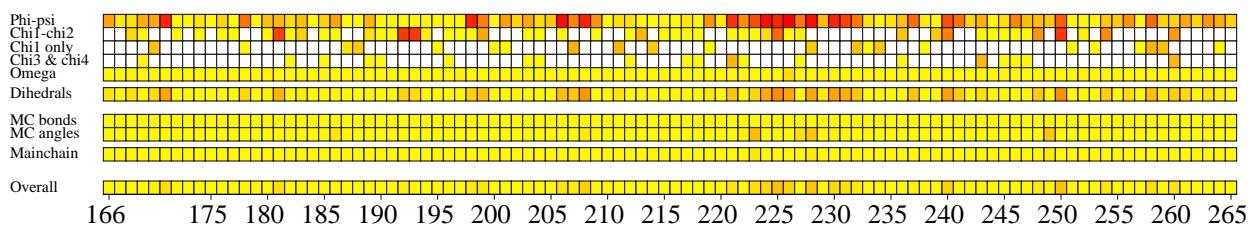
e. Sequence & Ramachandran regions



f. Max. deviation (see listing)



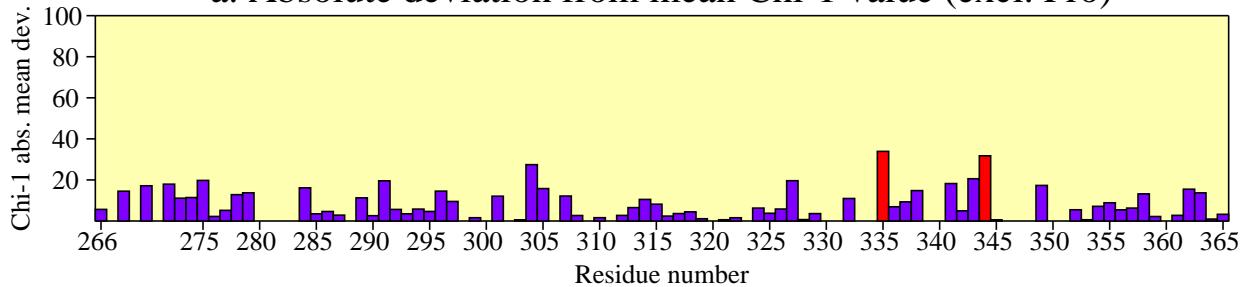
g. G-factors



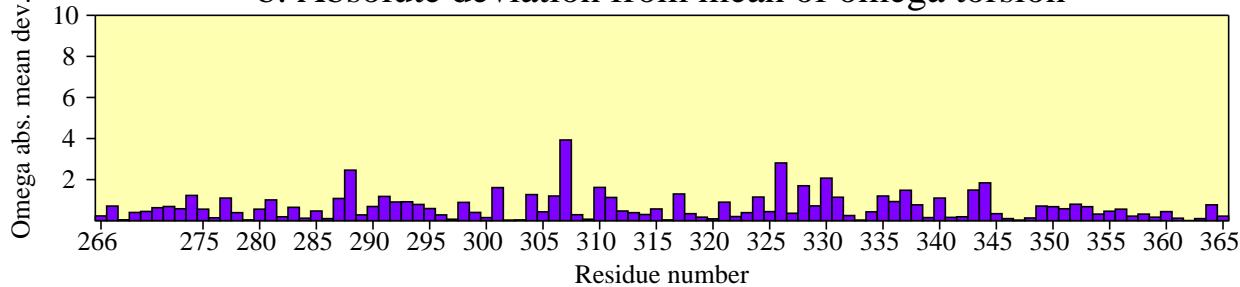
Residue properties

pdb3l70

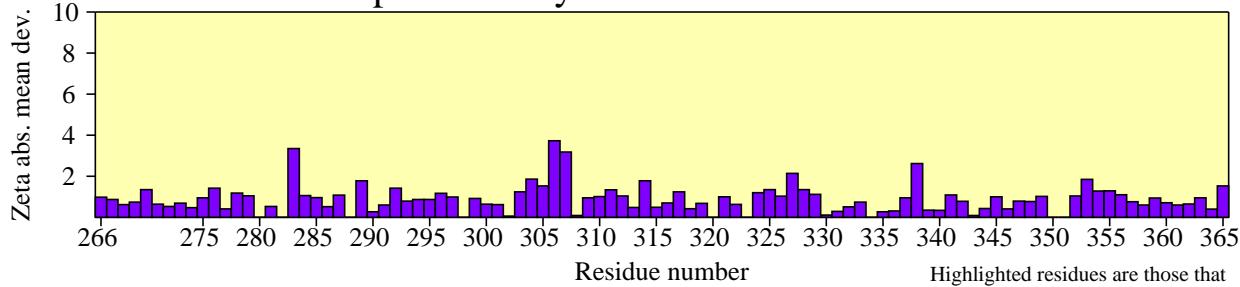
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion



c. C-alpha chirality: abs. deviation of zeta torsion



d. Secondary structure & estimated accessibility



e. Sequence & Ramachandran regions

▲ Most favoured □ Allowed ■ Generous ■ Disallowed

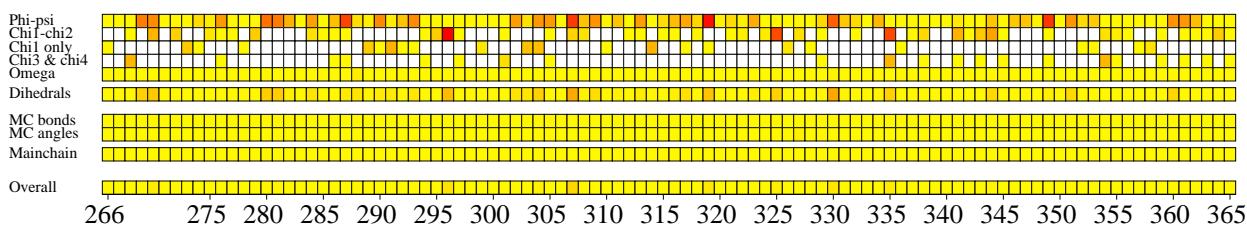
SAEANAFSVLQHVLGAGPLIKRGSSVT SKLYQGVAKATTQPF DASAFNVNYS DSGLFGFYTI SQA HAGEVIR AAMNQLK AAAQGGVTEEDVTKAKNQLK

f. Max. deviation (see listing)

*
+
**

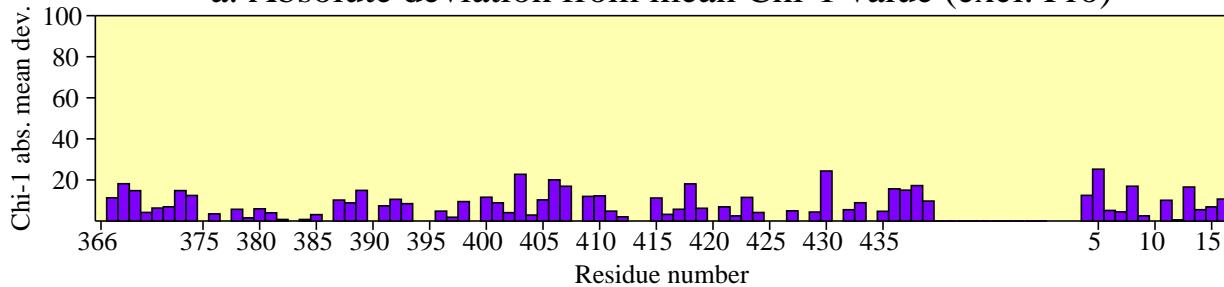
.....

g. G-factors

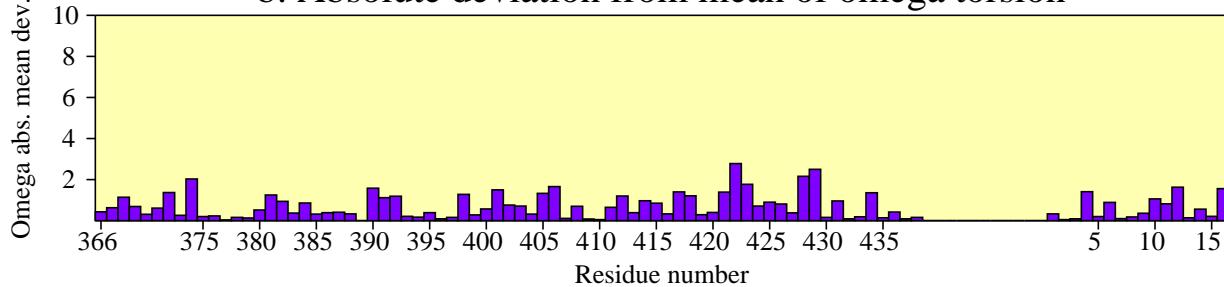


Residue properties pdb3170

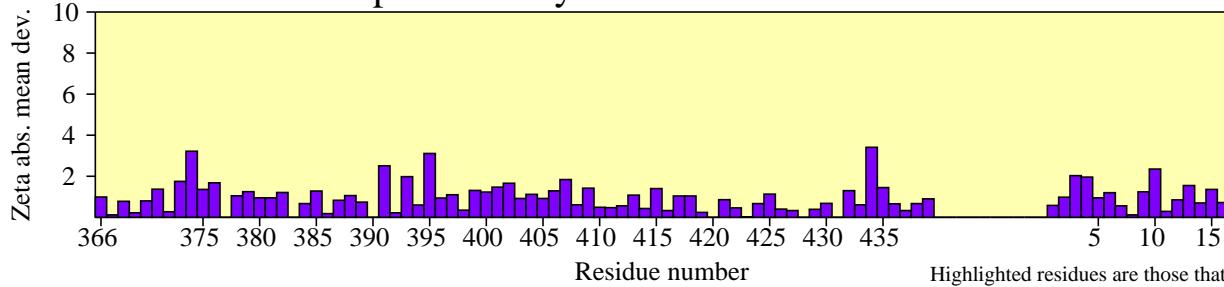
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion



c. C-alpha chirality: abs. deviation of zeta torsion



Highlighted residues are those that deviate by more than 2.0 st. devs. from ideal

d. Secondary structure & estimated accessibility



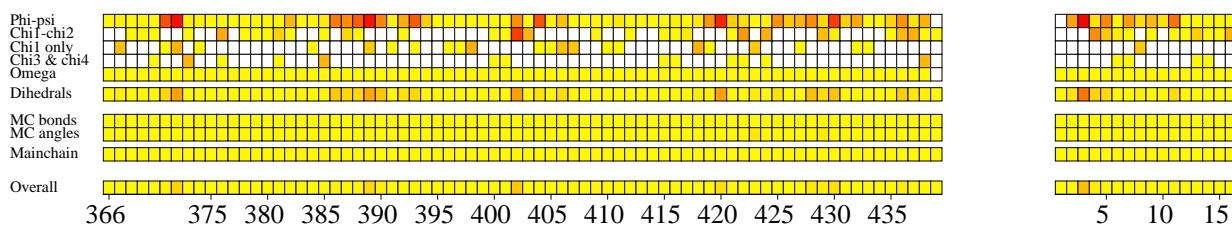
e. Sequence & Ramachandran regions ▲ Most favoured ■ Allowed □ Generous ▨ Disallowed



f. Max. deviation (see listing)



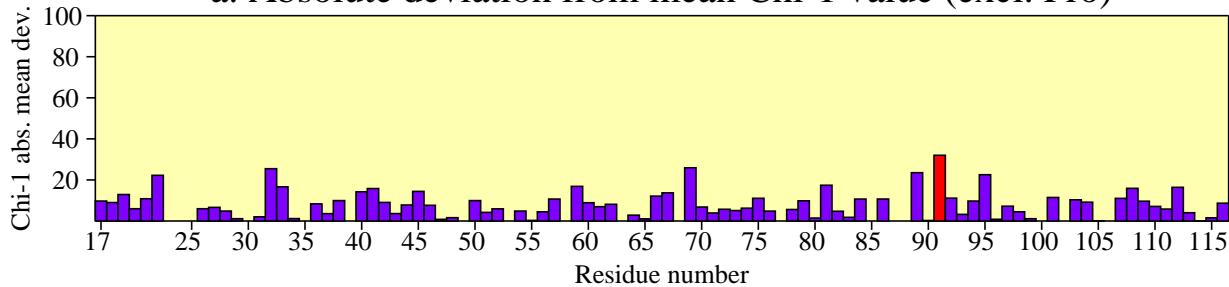
g. G-factors



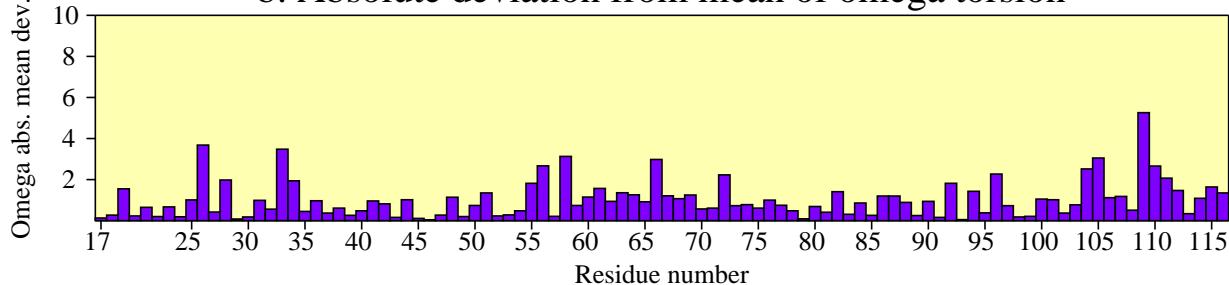
Residue properties

pdb3l70

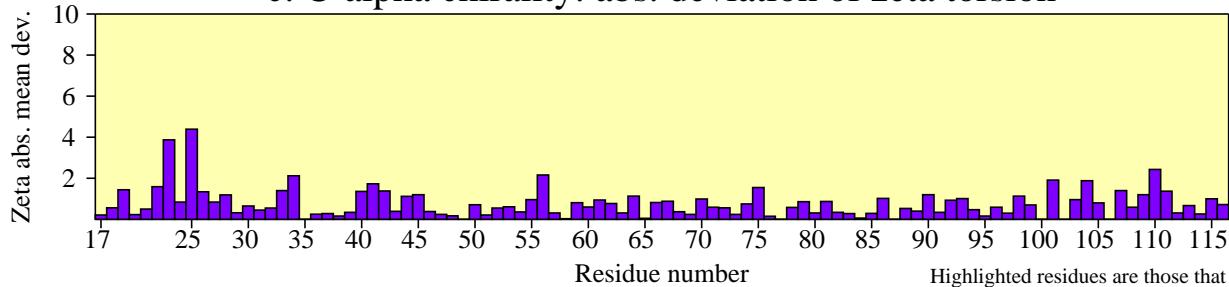
a. Absolute deviation from mean Chi-1 value (excl. Pro)



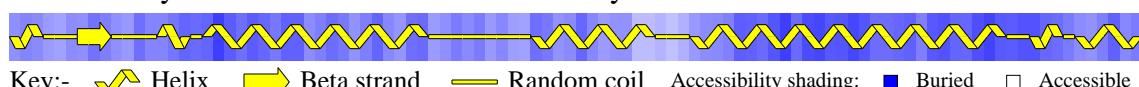
b. Absolute deviation from mean of omega torsion



c. C-alpha chirality: abs. dev. of zeta torsion



d. Secondary structure & estimated accessibility



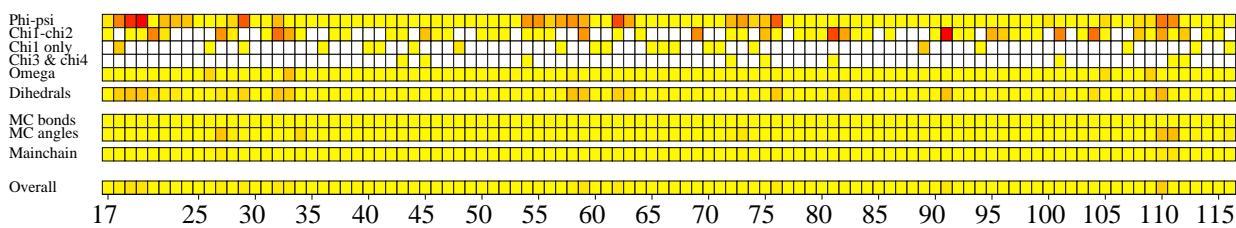
e. Sequence & Ramachandran regions



f. Max. deviation (see listing)



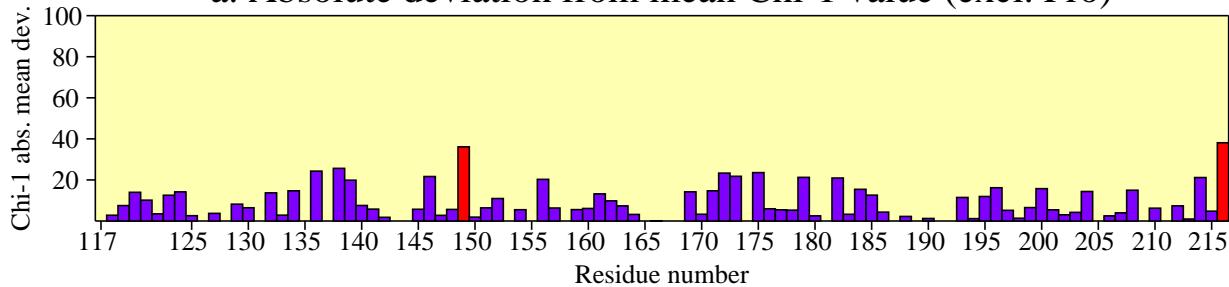
g. G-factors



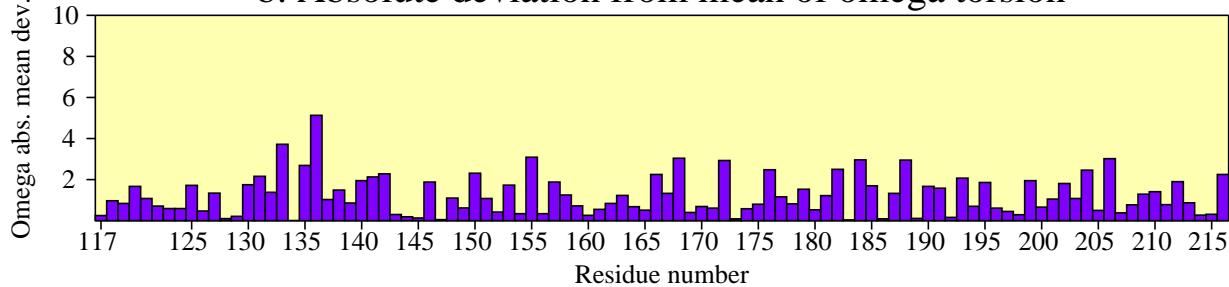
Residue properties

pdb3l70

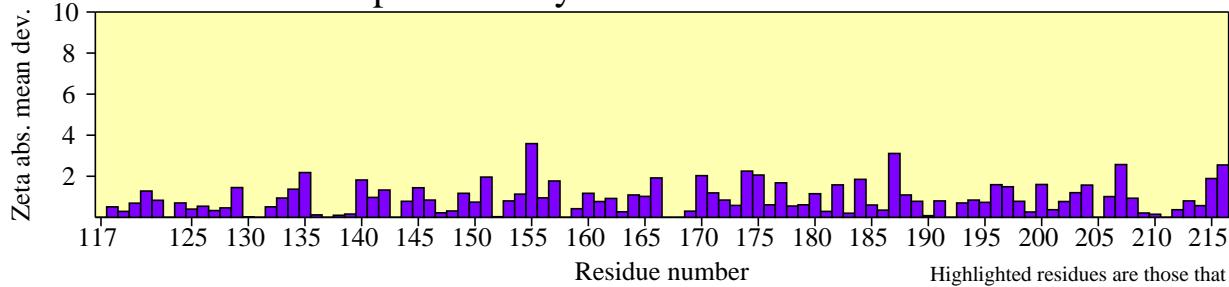
a. Absolute deviation from mean Chi-1 value (excl. Pro)



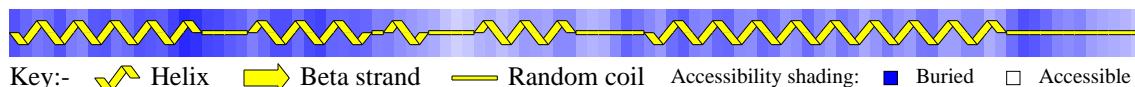
b. Absolute deviation from mean of omega torsion



c. C-alpha chirality: abs. deviation of zeta torsion



d. Secondary structure & estimated accessibility



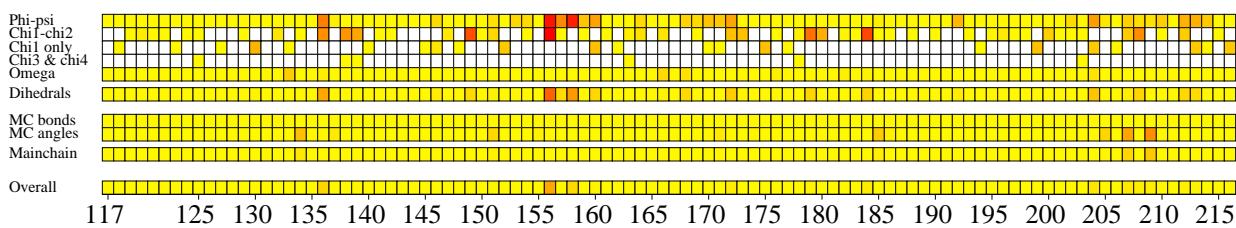
e. Sequence & Ramachandran regions



f. Max. deviation (see listing)



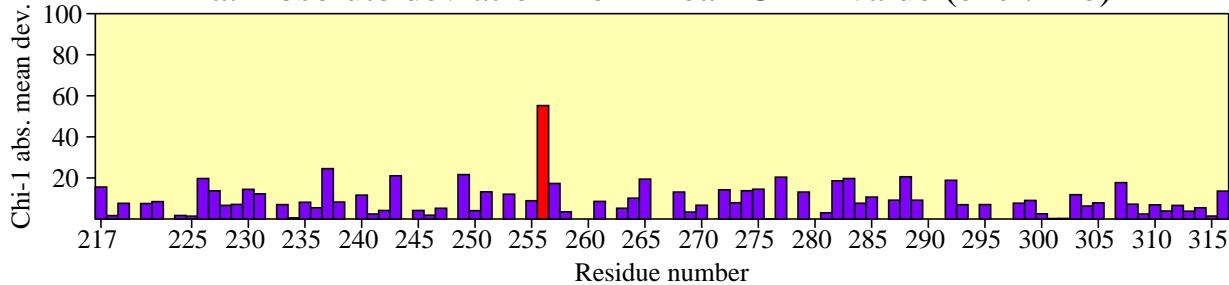
g. G-factors



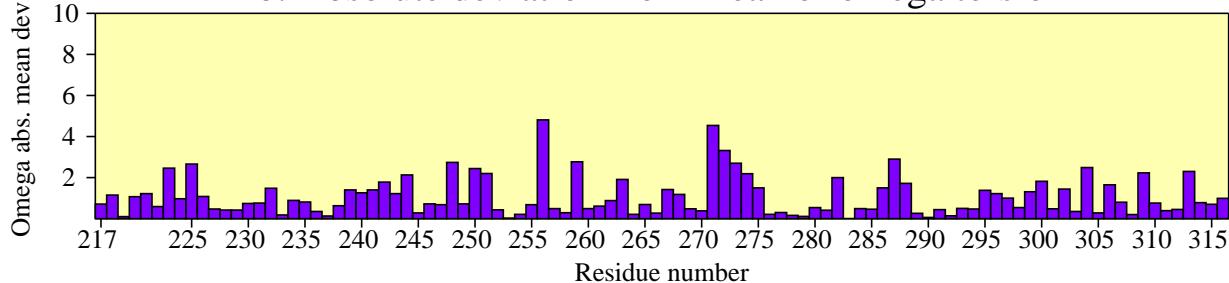
Residue properties

pdb3l70

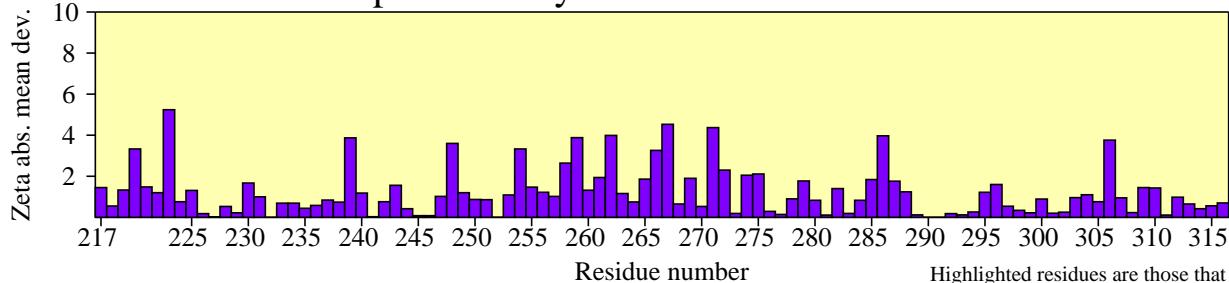
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion

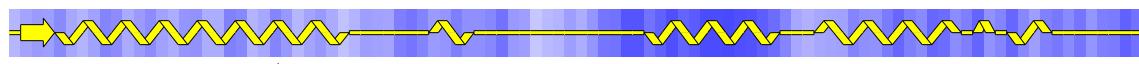


c. C-alpha chirality: abs. deviation of zeta torsion



Highlighted residues are those that deviate by more than 2.0 st. devs. from ideal

d. Secondary structure & estimated accessibility



Key:- Helix Beta strand Random coil Accessibility shading: Buried Accessible

e. Sequence & Ramachandran regions

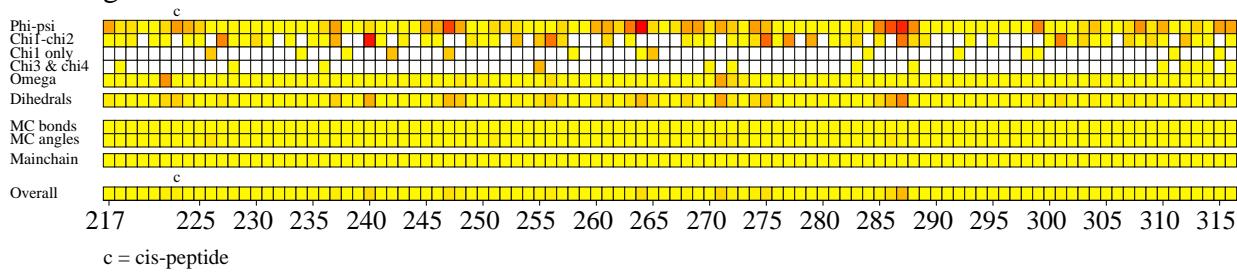
Most favoured Allowed Generous Disallowed

DK I P F H P Y Y S F K D I L G L T L M L T P F L T L A F S P N L L G D P E N F T P A N P L V T P P H I K P E W Y F L F A Y A I L R S I P N K L G G V L A A S V L I L F L I P F L H K S K Q R T M

f. Max. deviation (see listing)

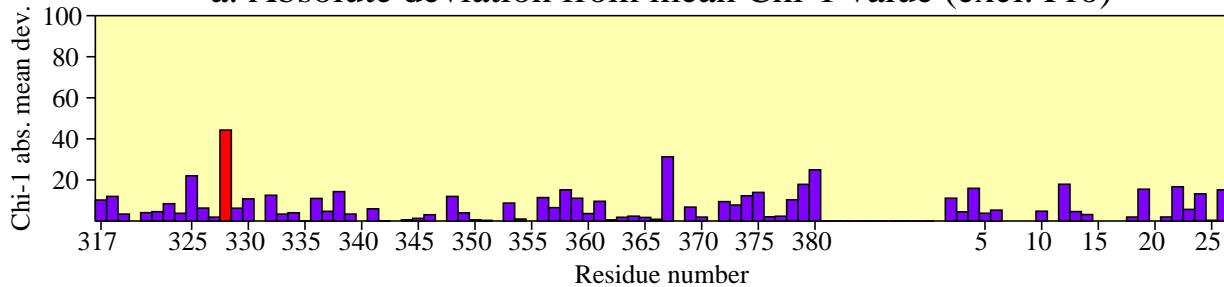


g. G-factors

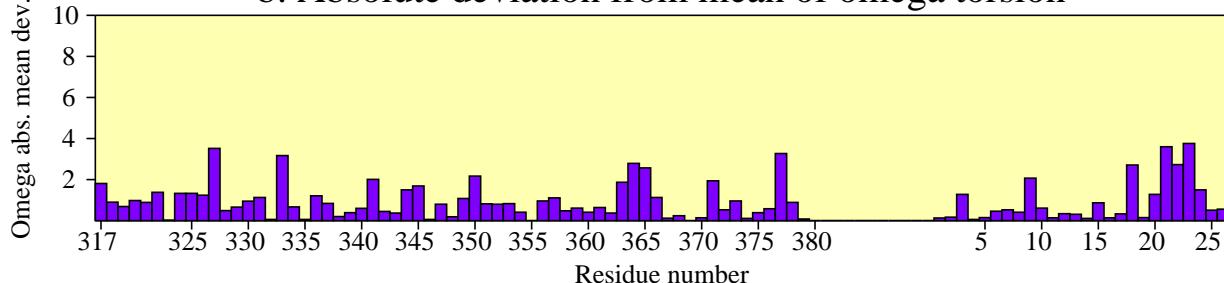


Residue properties pdb3170

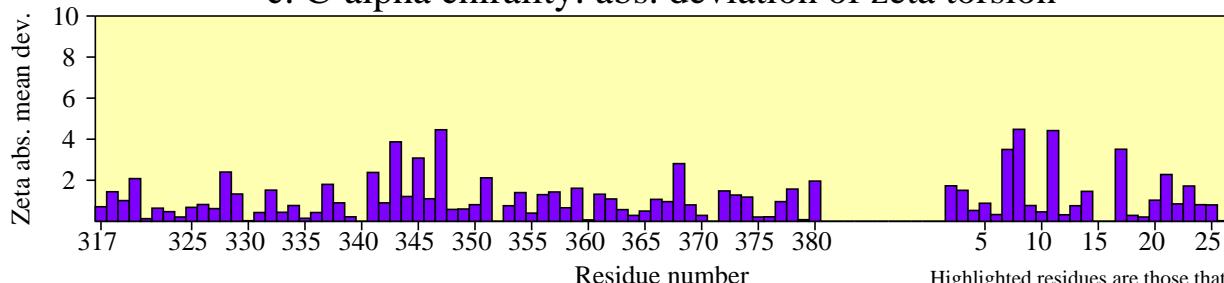
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion



c. C-alpha chirality: abs. deviation of zeta torsion



Highlighted residues are those that deviate by more than 2.0 st. devs. from ideal

d. Secondary structure & estimated accessibility



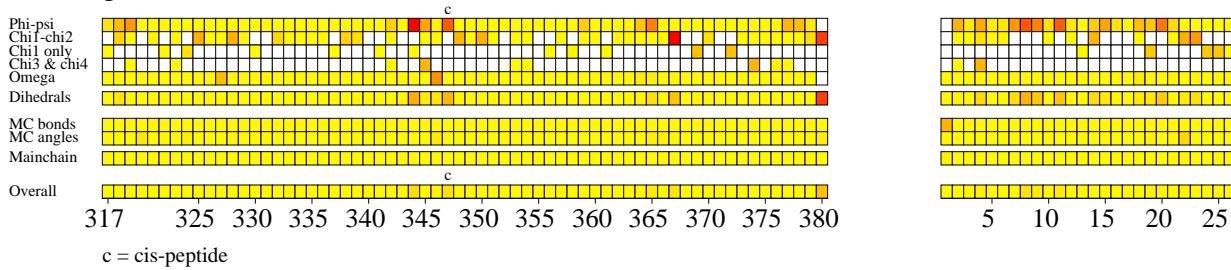
Key: Helix Beta strand Random coil Accessibility shading: Buried Accessible



f Max deviation (see listing)

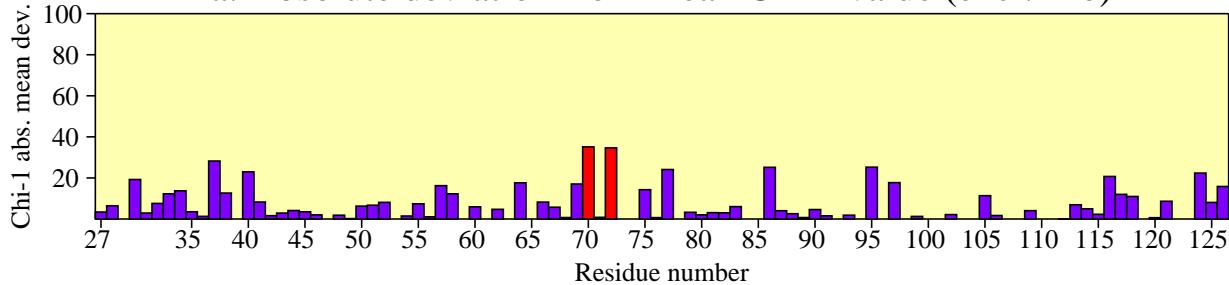


g. G-factors

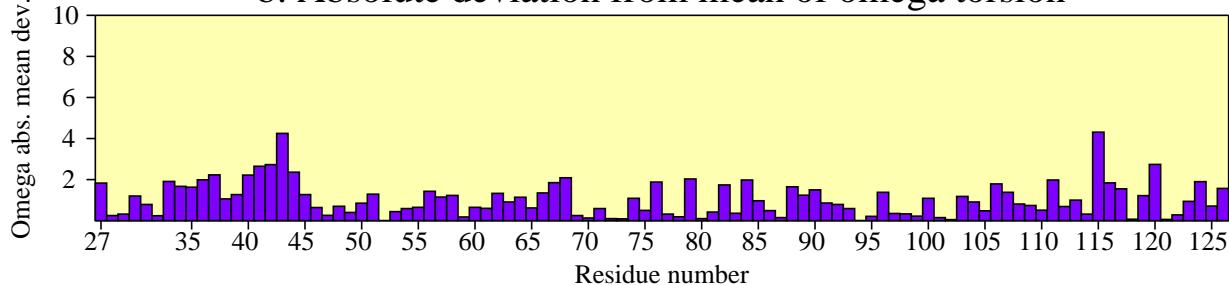


Residue properties pdb3170

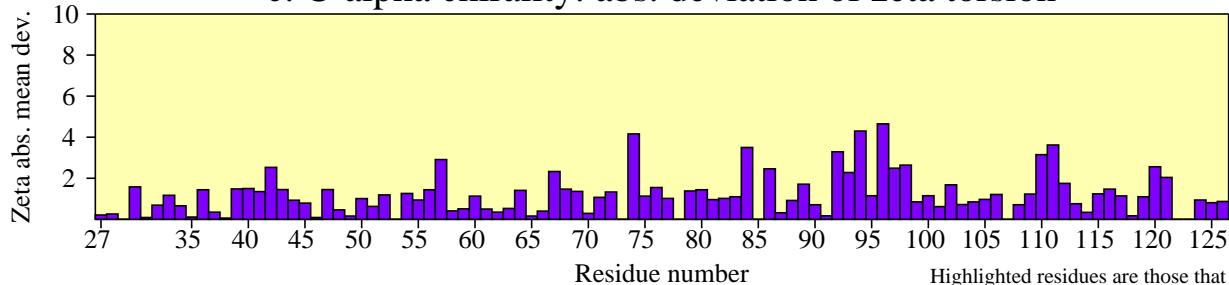
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion

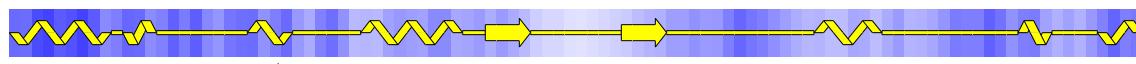


c. C-alpha chirality: abs. deviation of zeta torsion



Highlighted residues are those that deviate by more than 2.0 st. devs. from ideal

d. Secondary structure & estimated accessibility



Key:-  Helix  Beta strand  Random coil Accessibility shading:  Buried  Accessible

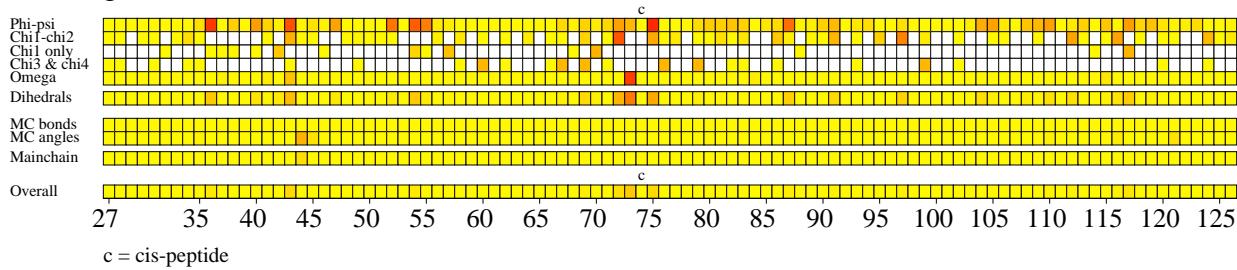
e. Sequence & Ramachandran regions ▲ Most favoured ■ Allowed ■ Generous ■ Disallowed

RRGFQVYKQVCSACHSMDDYVAFRNL IGVTHTEAEAKALAAEVEVQDGPDENGE FMR PKG I SDYFPKPYPNPEAARAANNGAL PPDLSY I VNARHGGEDY

f. Max. deviation (see listing)

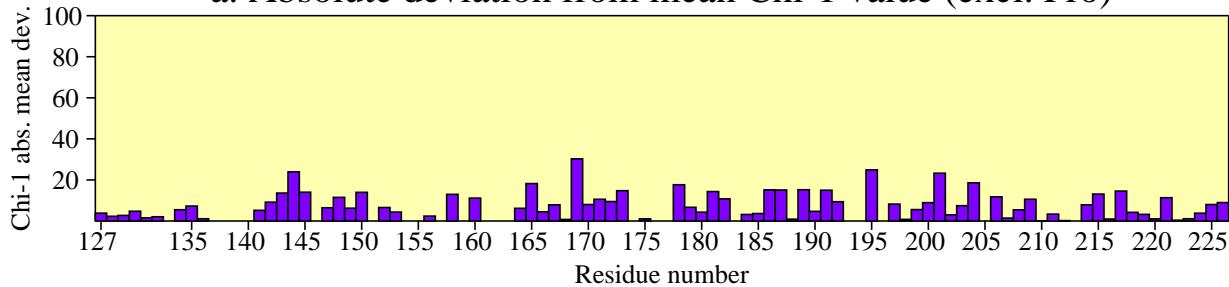


g. G-factors

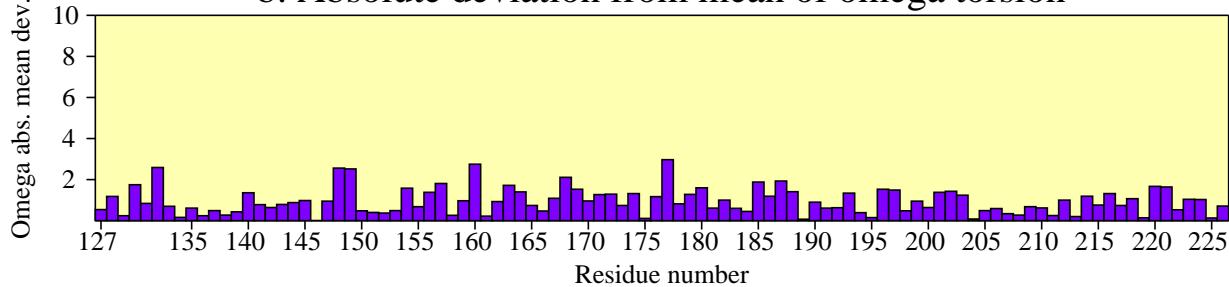


Residue properties pdb3170

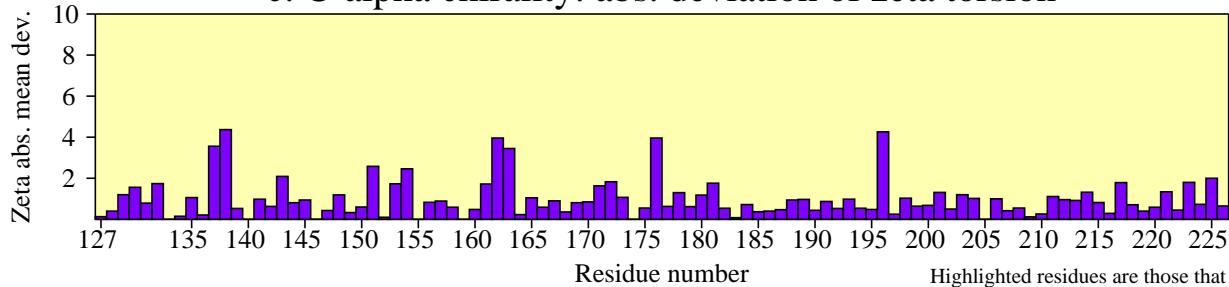
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion

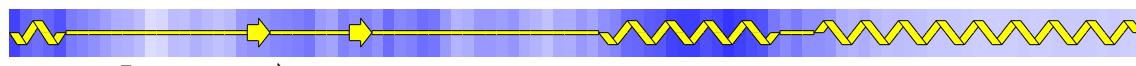


c. C-alpha chirality: abs. deviation of zeta torsion



Highlighted residues are those that deviate by more than 2.0 st. devs. from ideal

d. Secondary structure & estimated accessibility



Key:- Helix Beta strand Random coil Accessibility shading: Buried Accessible

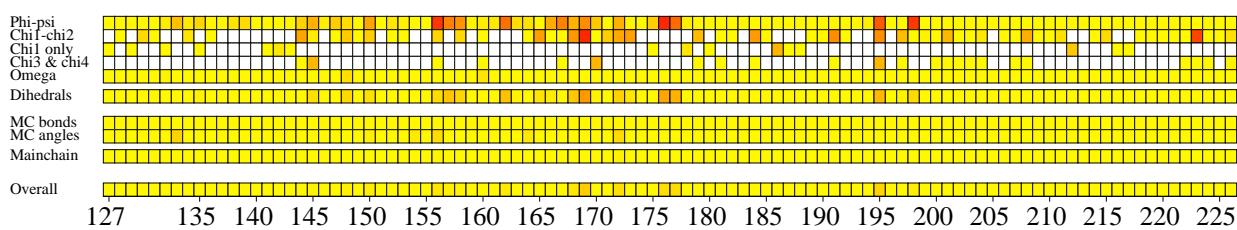
e. Sequence & Ramachandran regions ▲ Most favoured ■ Allowed ■ Generous ■ Disallowed

VFSLLTGCDPAGVVVREGLHYNPYFPQQA1GMAPP1YNE1ILEYDDGTPATMSQ1AKDVCFLRWAAEPEHDQRKRMGLKMILLISALLTSLLYYMKRHK

f. Max. deviation (see listing)

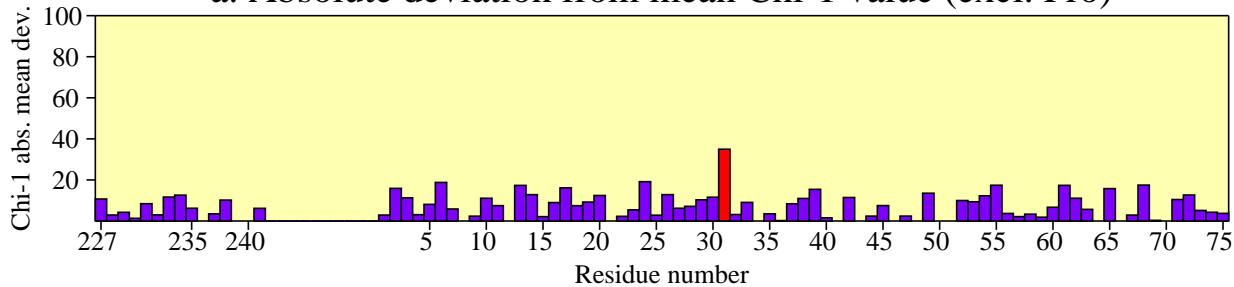


g. G-factors

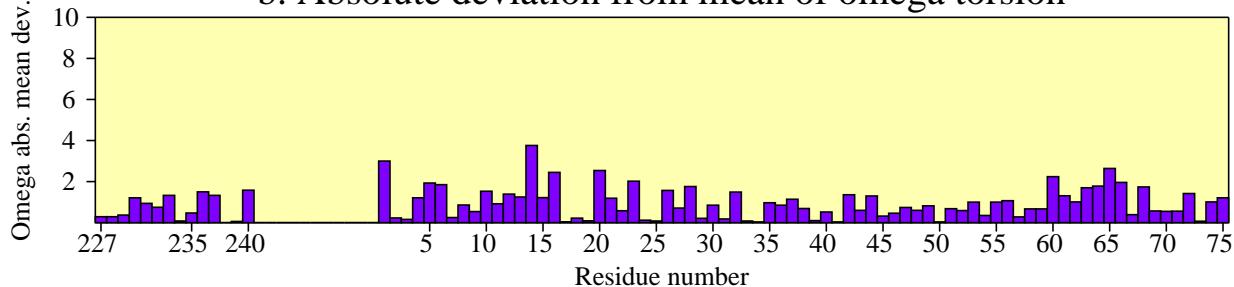


Residue properties pdb3170

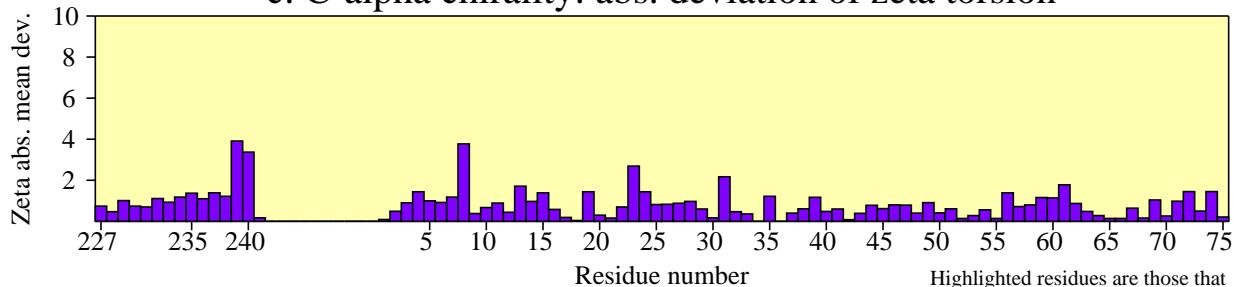
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion

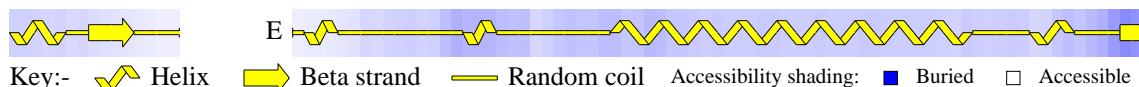


c. C-alpha chirality: abs. deviation of zeta torsion



Highlighted residues are those that deviate by more than 2.0 st. devs. from ideal

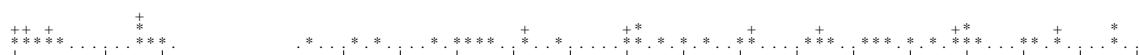
d. Secondary structure & estimated accessibility



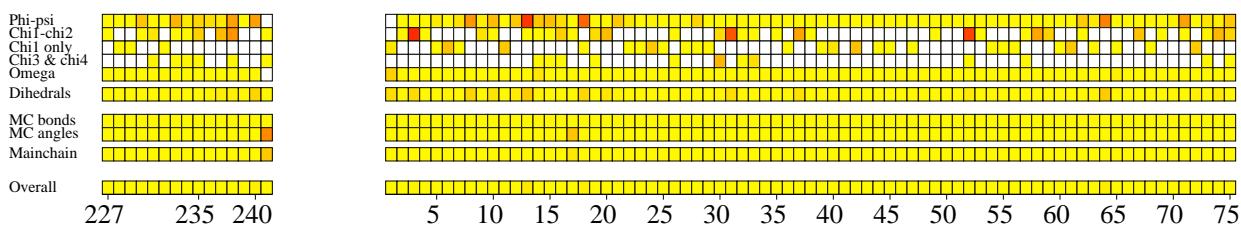
e. Sequence & Ramachandran regions ▲ Most favoured ■ Allowed ■ Generous ■ Disallowed



f. Max. deviation (see listing)



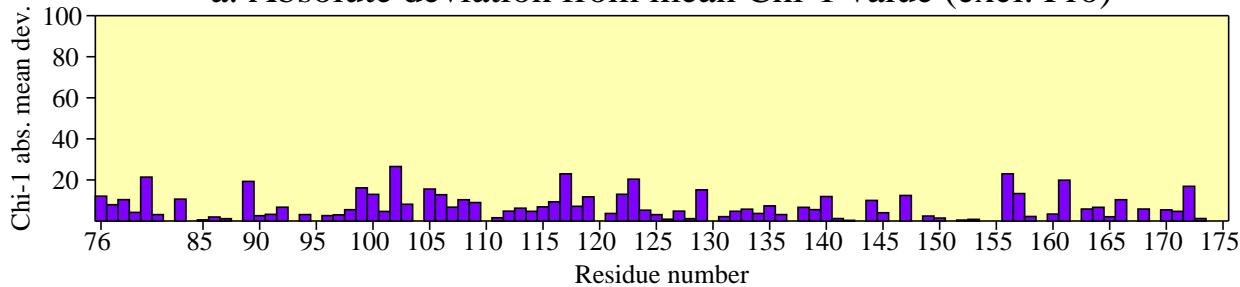
g. G-factors



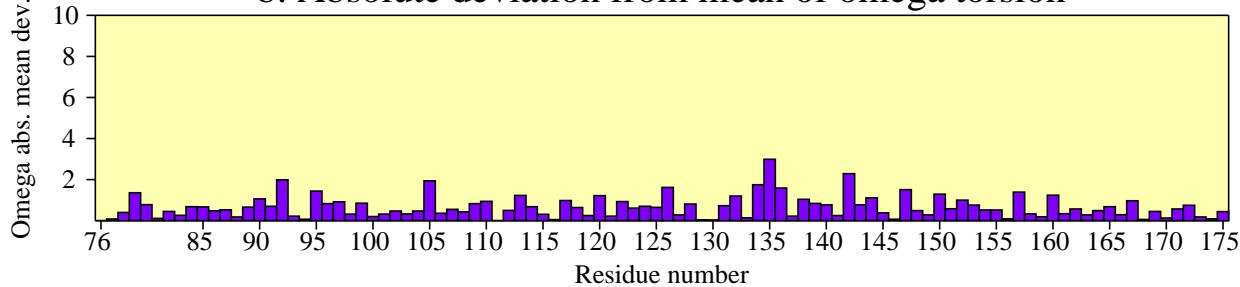
Residue properties

pdb3l70

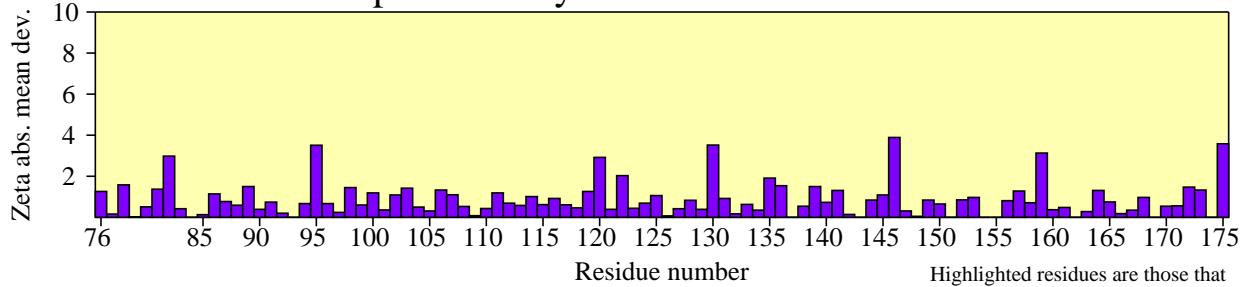
a. Absolute deviation from mean Chi-1 value (excl. Pro)



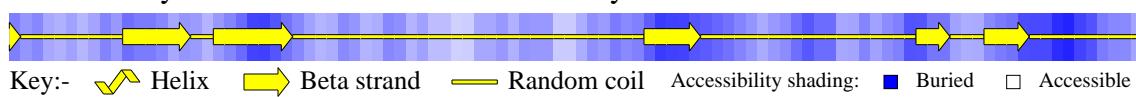
b. Absolute deviation from mean of omega torsion



c. C-alpha chirality: abs. deviation of zeta torsion



d. Secondary structure & estimated accessibility



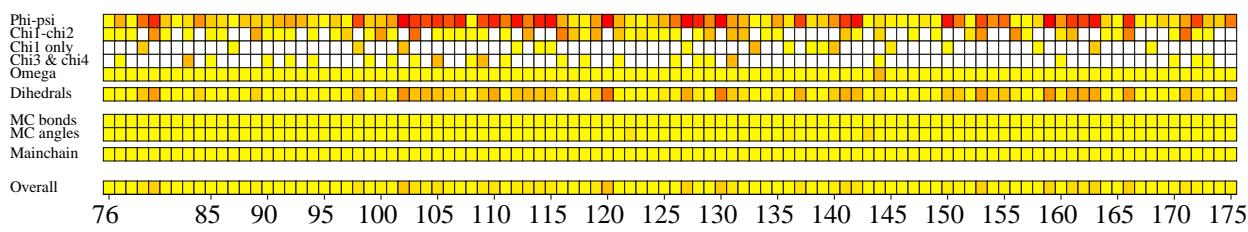
e. Sequence & Ramachandran regions



f. Max. deviation (see listing)



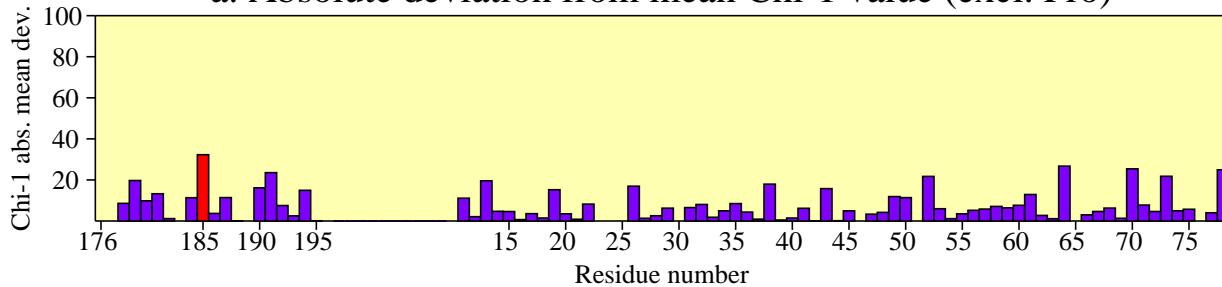
g. G-factors



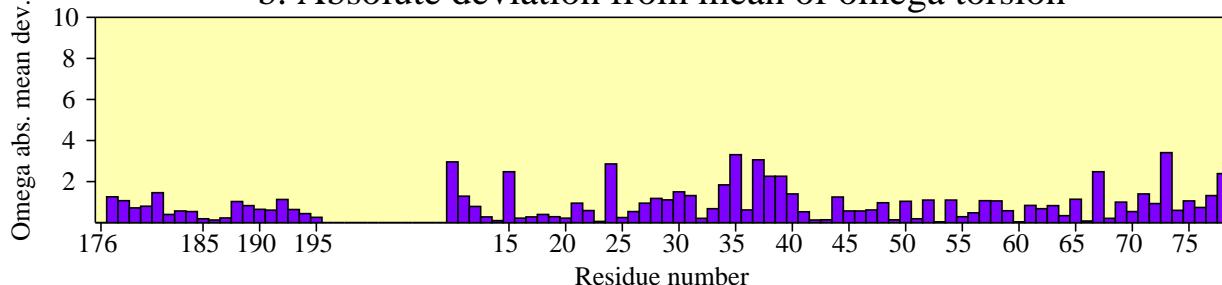
Residue properties

pdb3l70

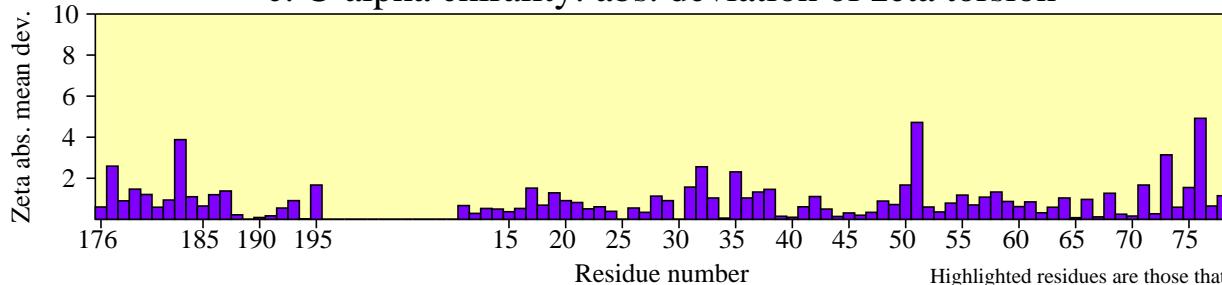
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion



c. C-alpha chirality: abs. deviation of zeta torsion



Highlighted residues are those that deviate by more than 2.0 st. devs. from ideal

d. Secondary structure & estimated accessibility



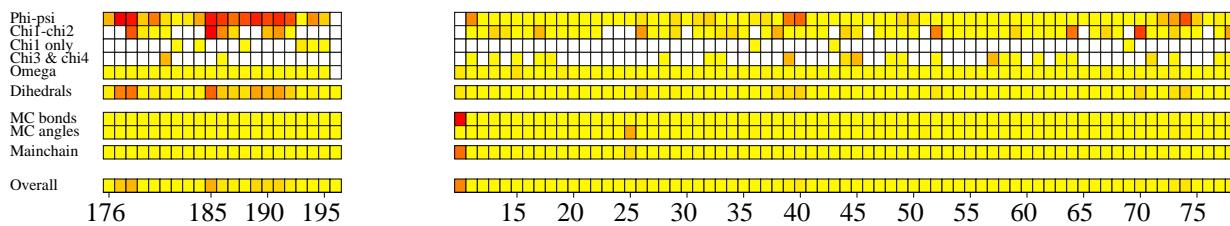
e. Sequence & Ramachandran regions



f. Max. deviation (see listing)



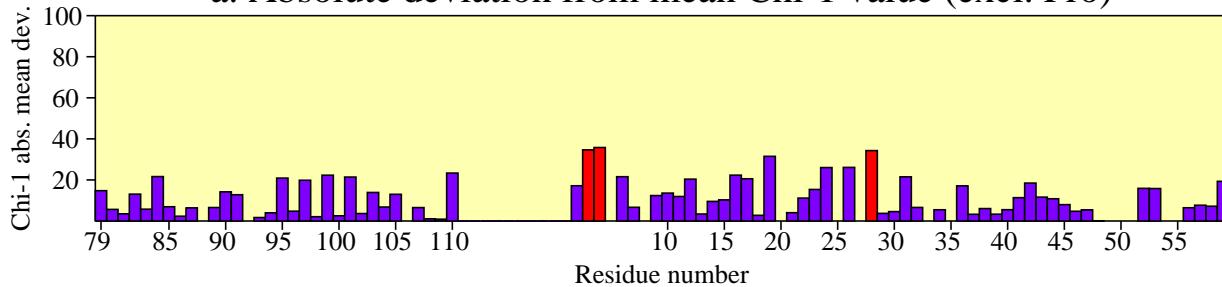
g. G-factors



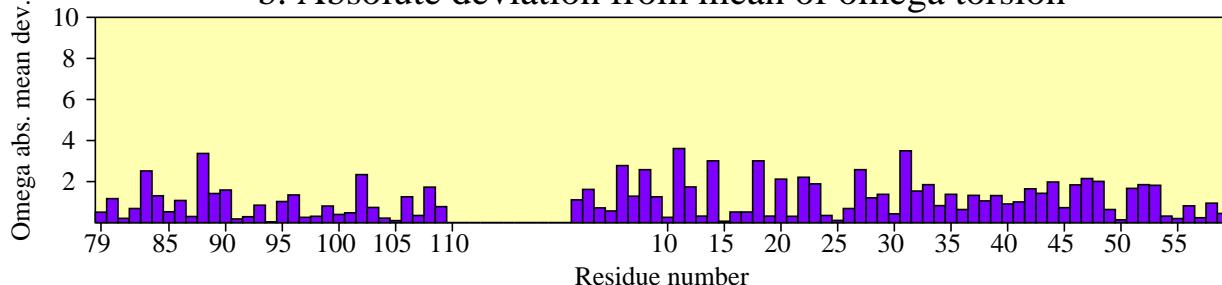
Residue properties

pdb3l70

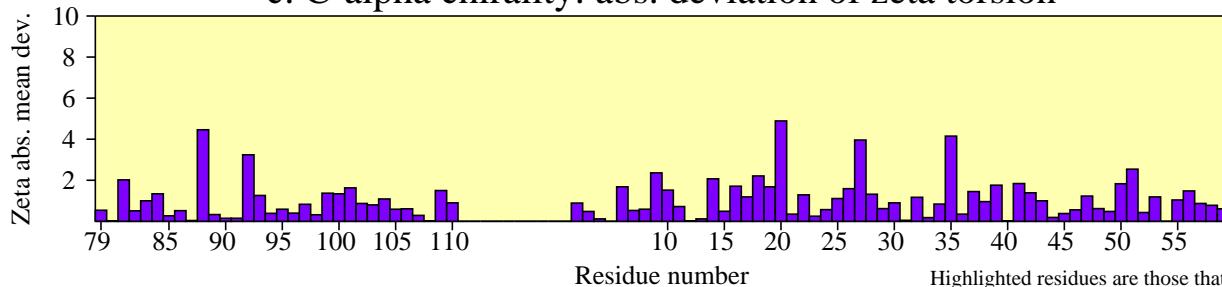
a. Absolute deviation from mean Chi-1 value (excl. Pro)



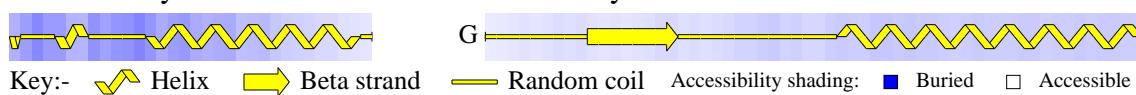
b. Absolute deviation from mean of omega torsion



c. C-alpha chirality: abs. dev. of zeta torsion



d. Secondary structure & estimated accessibility



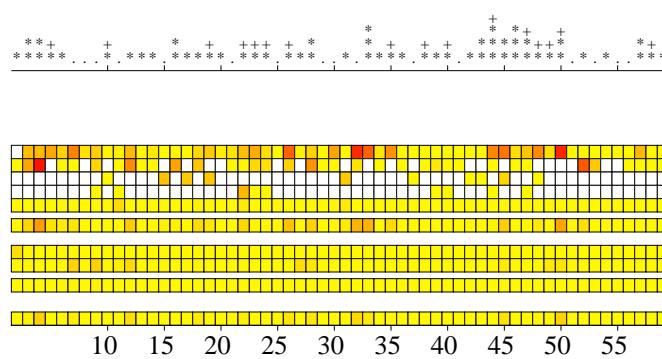
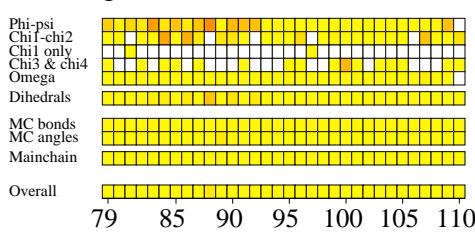
e. Sequence & Ramachandran regions



f. Max. deviation (see listing)



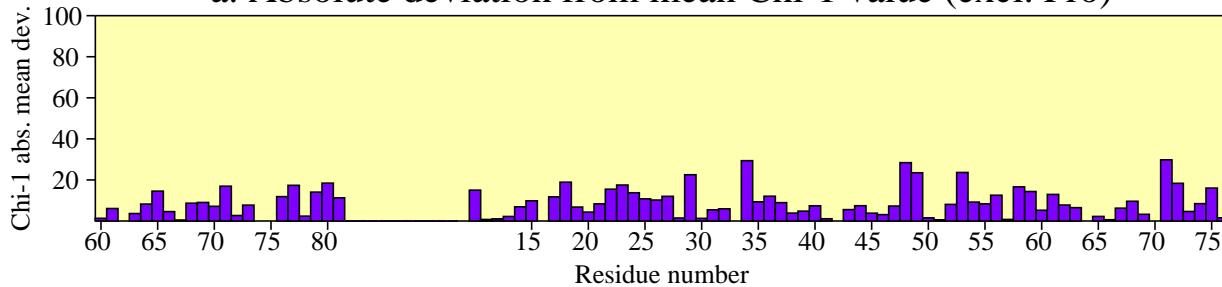
g. G-factors



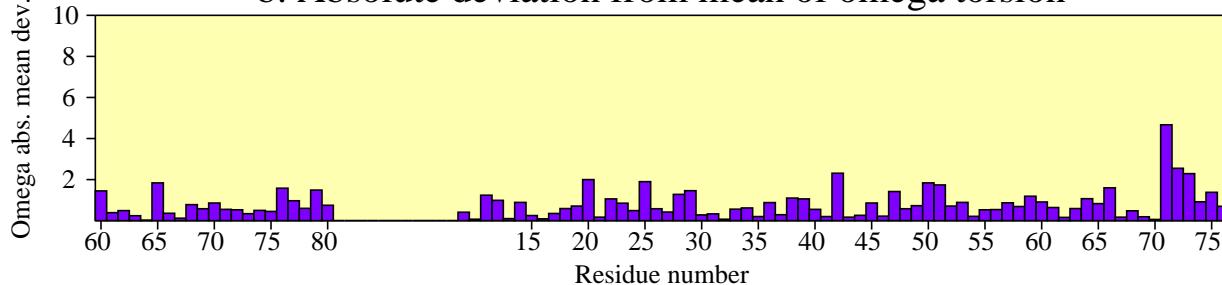
Residue properties

pdb3l70

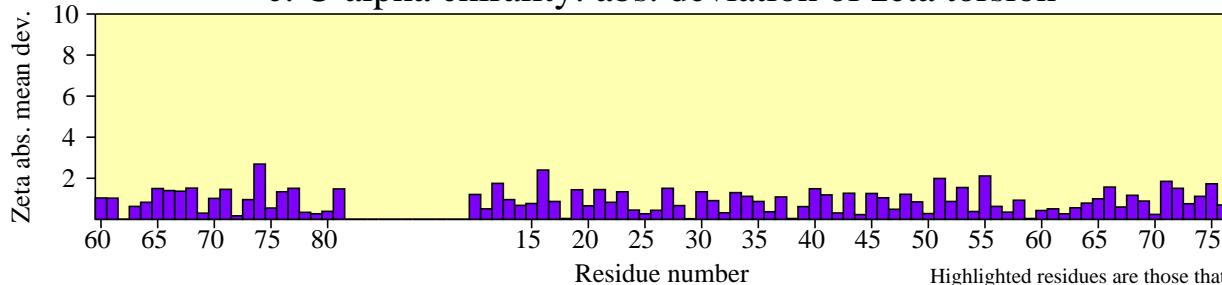
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion

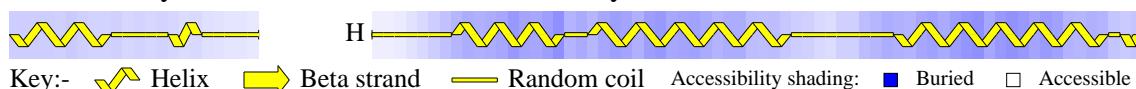


c. C-alpha chirality: abs. deviation of zeta torsion



Highlighted residues are those that deviate by more than 2.0 st. devs. from ideal

d. Secondary structure & estimated accessibility



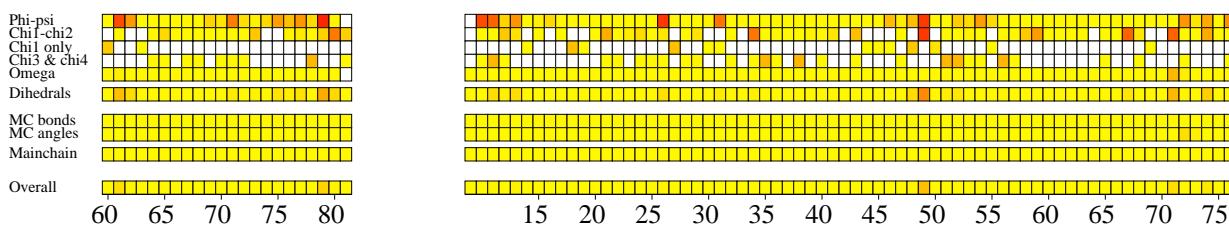
e. Sequence & Ramachandran regions



f. Max. deviation (see listing)



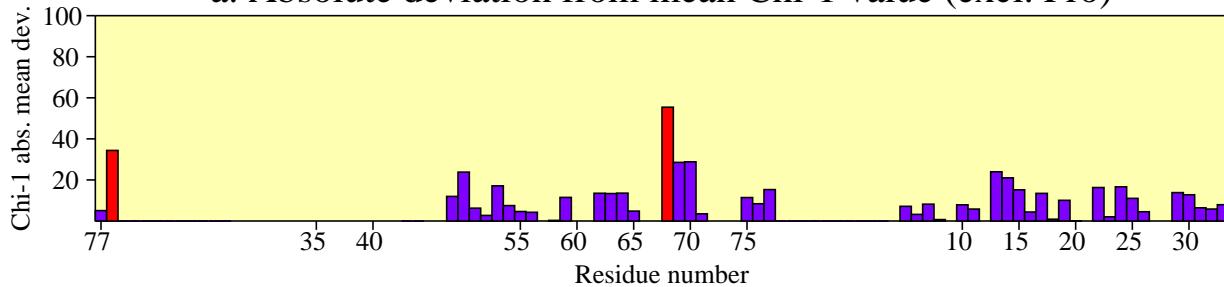
g. G-factors



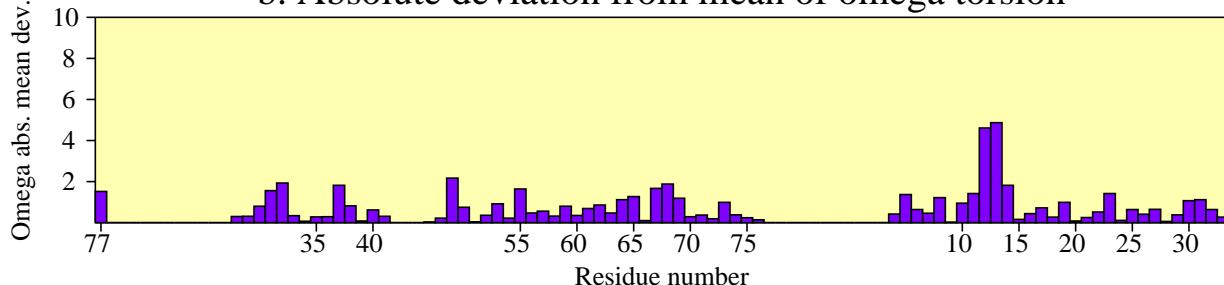
Residue properties

pdb3l70

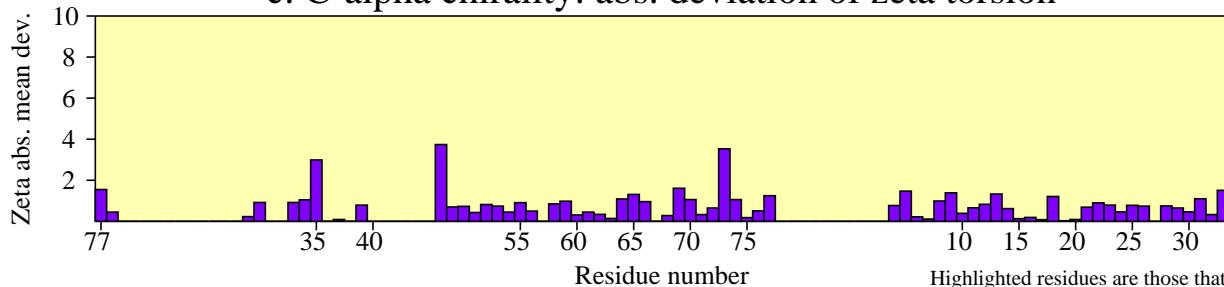
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion

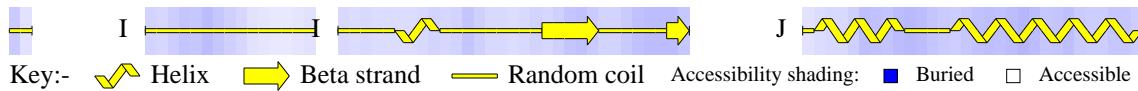


c. C-alpha chirality: abs. deviation of zeta torsion



Highlighted residues are those that deviate by more than 2.0 st. devs. from ideal

d. Secondary structure & estimated accessibility



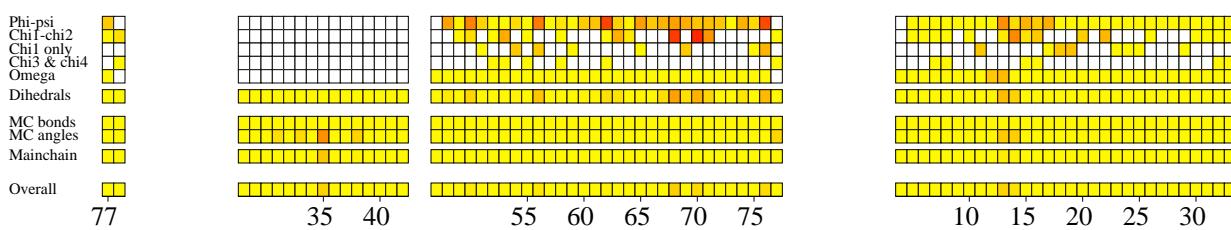
e. Sequence & Ramachandran regions



f. Max. deviation (see listing)

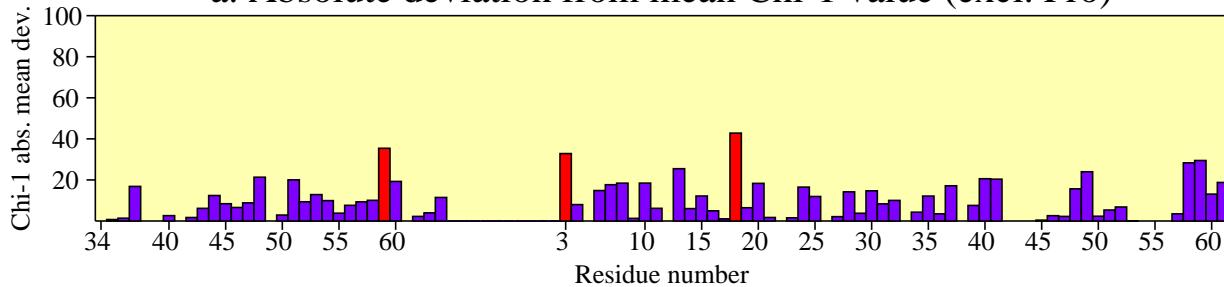


g. G-factors

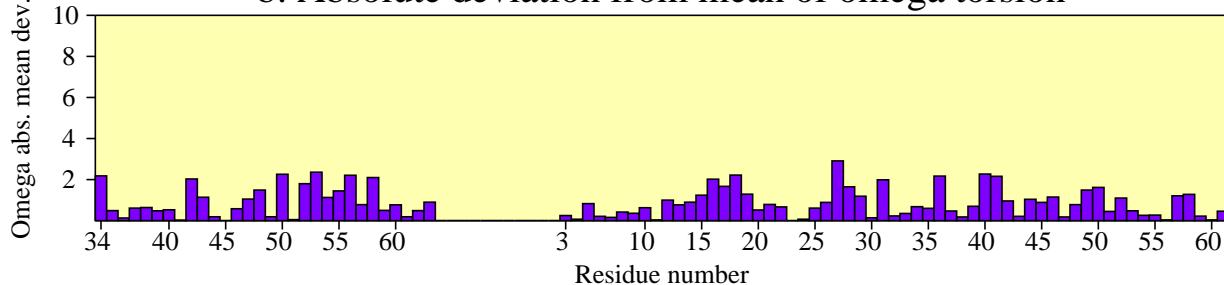


Residue properties pdb3170

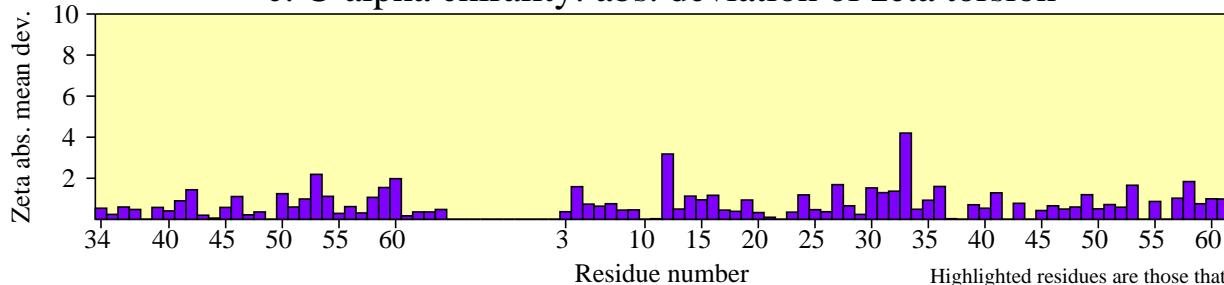
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion

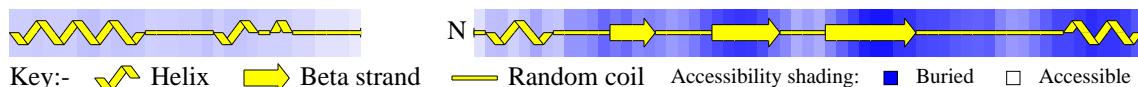


c. C-alpha chirality: abs. deviation of zeta torsion



Highlighted residues are those that deviate by more than 2.0 st. devs. from ideal

d. Secondary structure & estimated accessibility



e. Sequence & Ramachandran regions ▲ Most favoured ■ Allowed ■ Generous ■ Disallowed

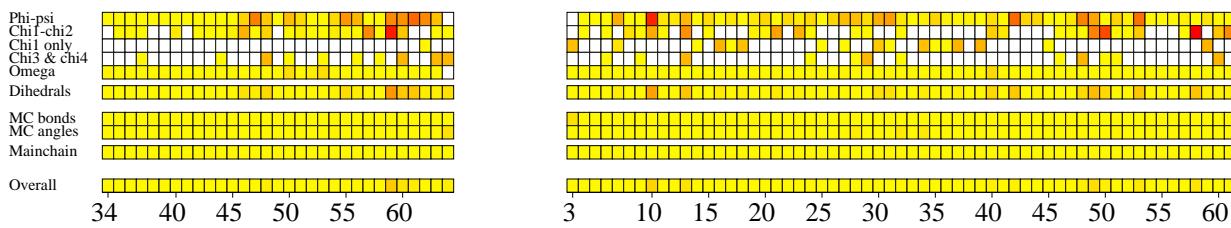
e. Sequence & Ramachandran

AEDQGADALEFHILNECKLWVLLKHKXEASEE

TYA QTL ON LRETINVTTLDNCLRYA SEES SQTGTCVQVYLACGSRVEKEKNICAGYEVH

f. Max. deviation (see listing)

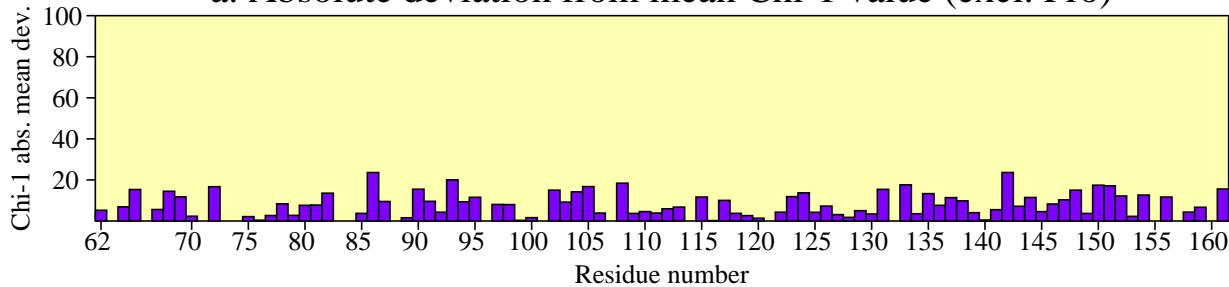
g. G-factors



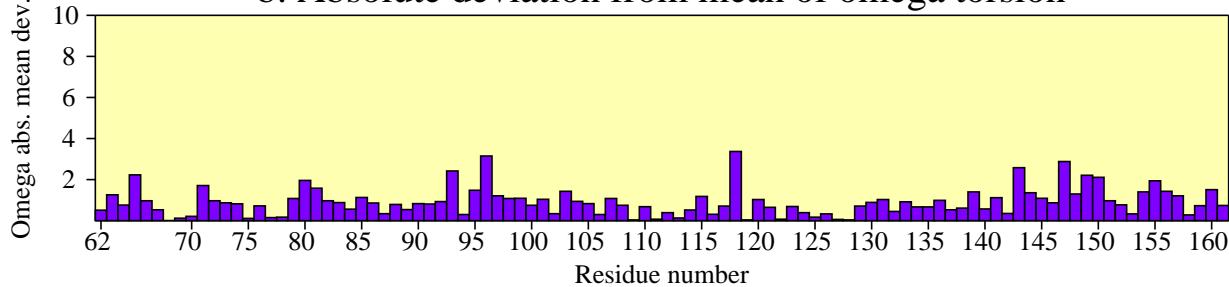
Residue properties

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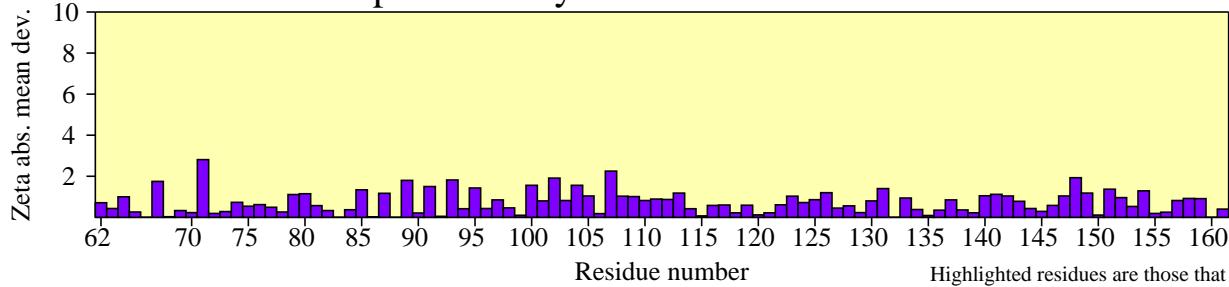
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion



c. C-alpha chirality: abs. deviation of zeta torsion



d. Secondary structure & estimated accessibility



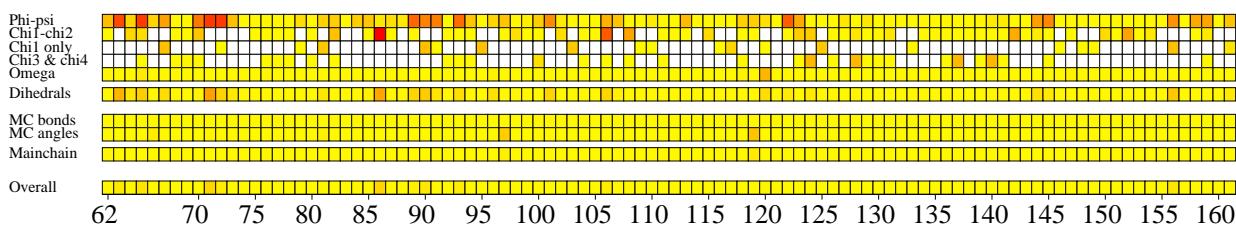
e. Sequence & Ramachandran regions



f. Max. deviation (see listing)



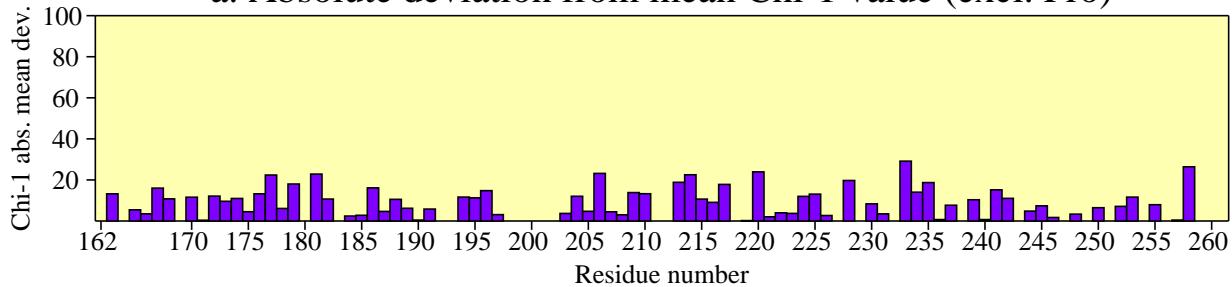
g. G-factors



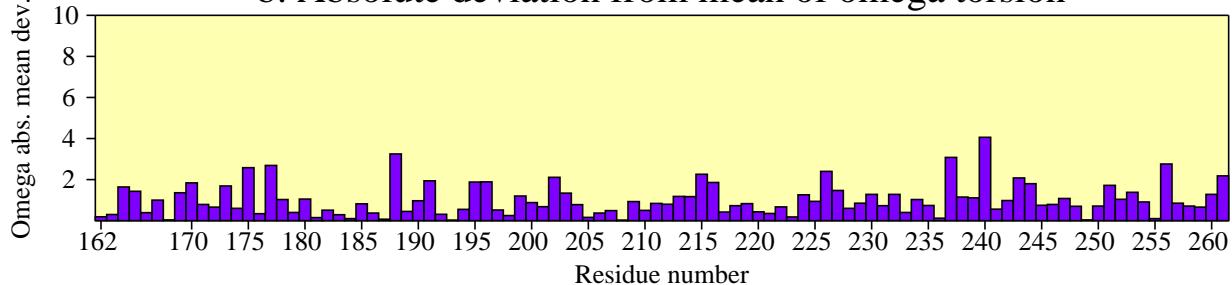
Residue properties

pdb3l70

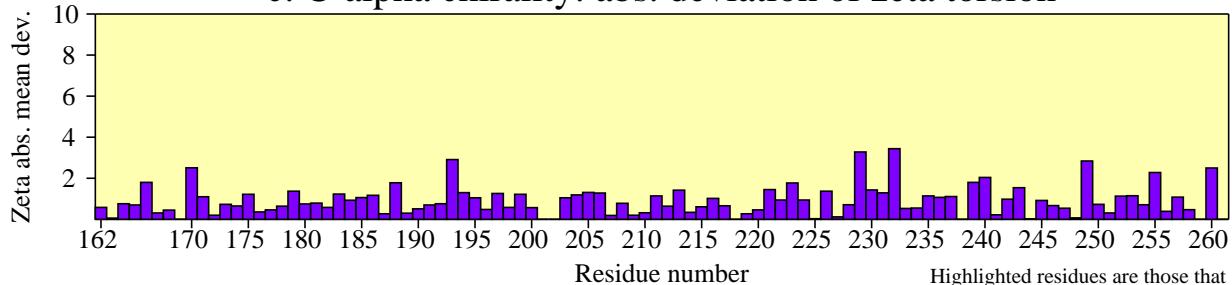
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion

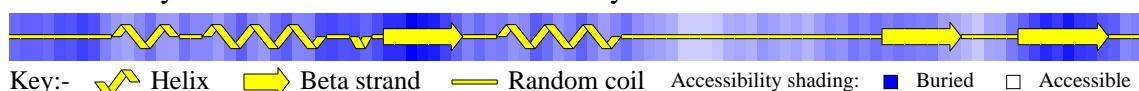


c. C-alpha chirality: abs. deviation of zeta torsion



Highlighted residues are those that deviate by more than 2.0 st. devs. from ideal

d. Secondary structure & estimated accessibility



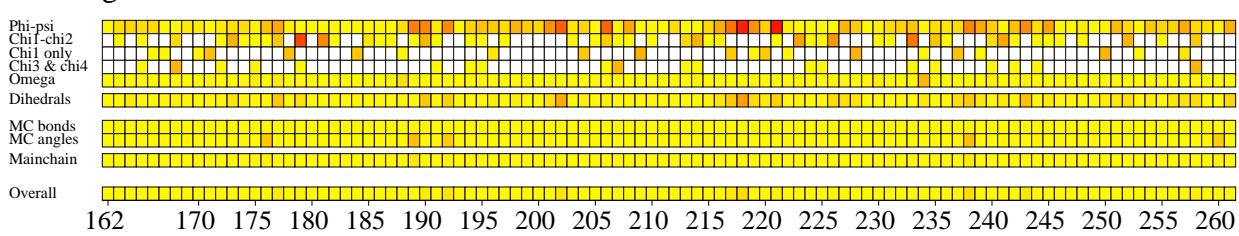
e. Sequence & Ramachandran regions



f. Max. deviation (see listing)



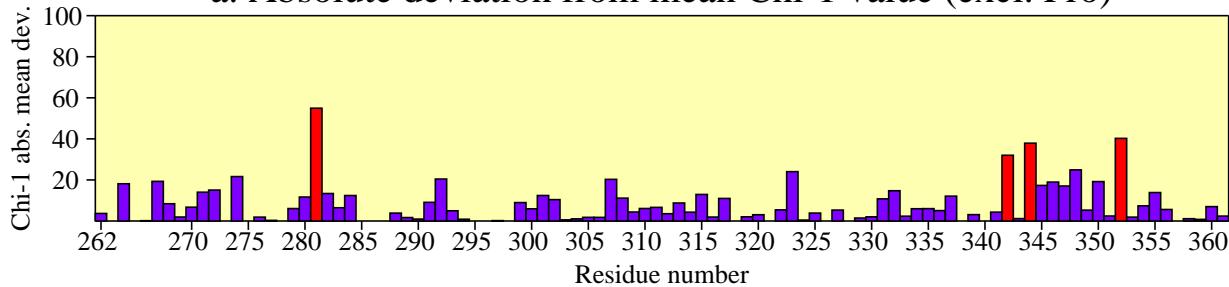
g. G-factors



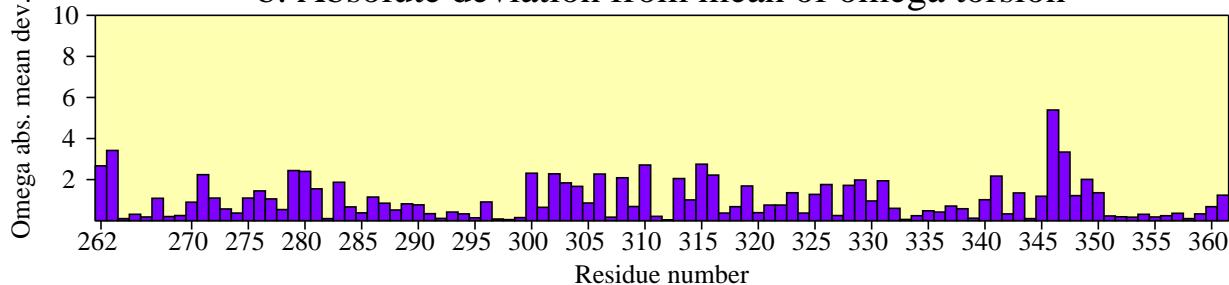
Residue properties

pdb3l70

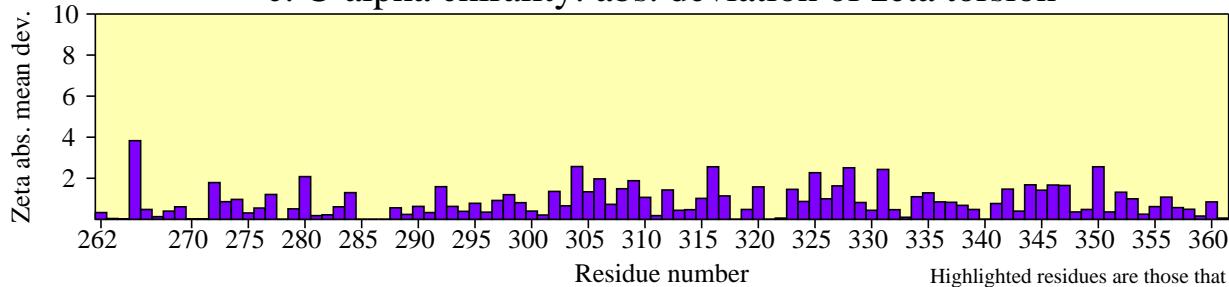
a. Absolute deviation from mean Chi-1 value (excl. Pro)



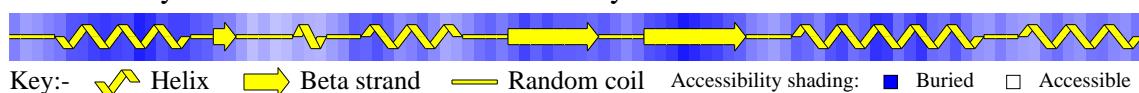
b. Absolute deviation from mean of omega torsion



c. C-alpha chirality: abs. deviation of zeta torsion



d. Secondary structure & estimated accessibility



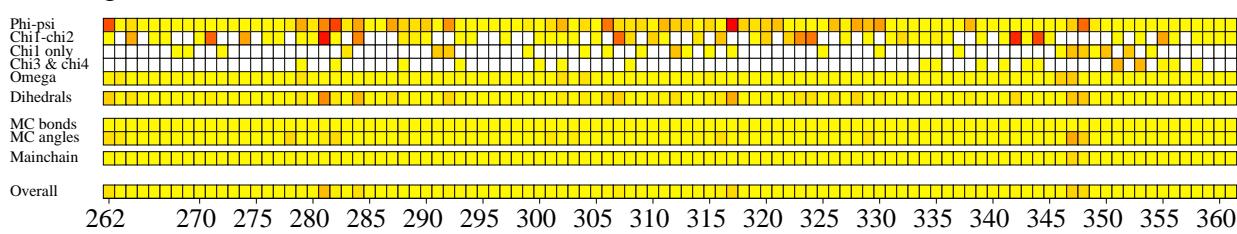
e. Sequence & Ramachandran regions



f. Max. deviation (see listing)



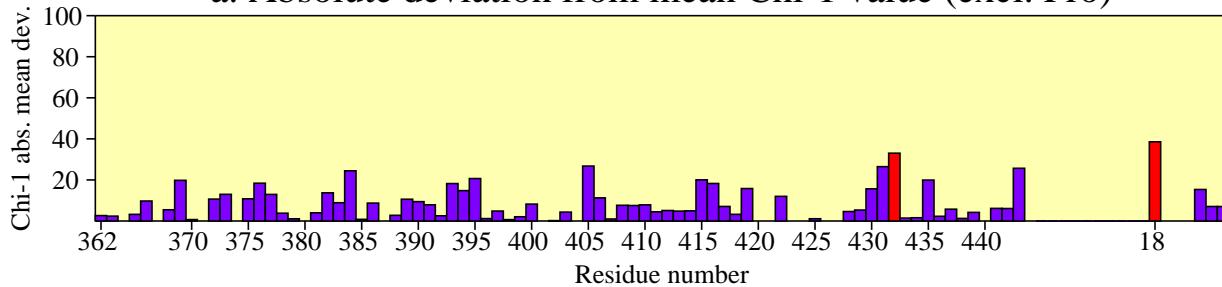
g. G-factors



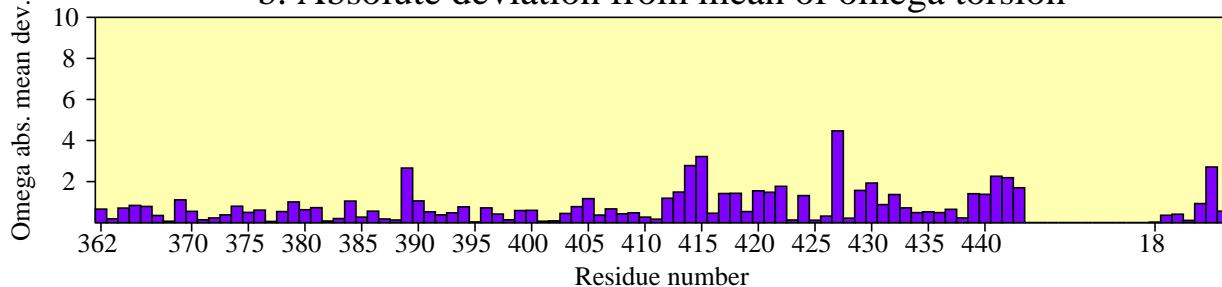
Residue properties

pdb3l70

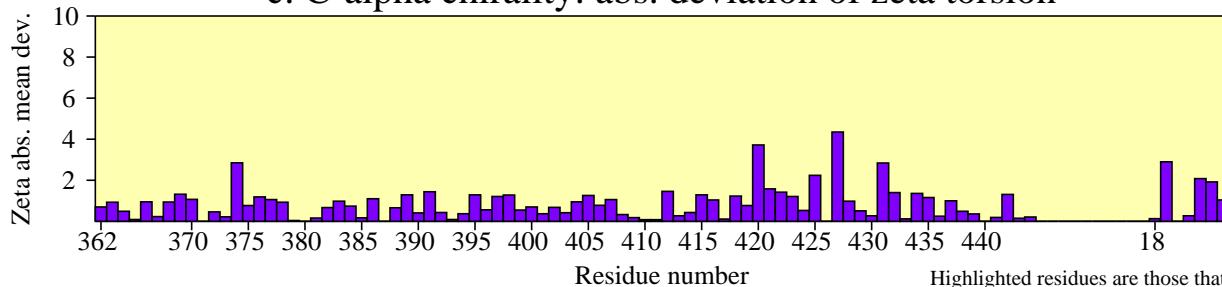
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion



c. C-alpha chirality: abs. dev. of zeta torsion



d. Secondary structure & estimated accessibility



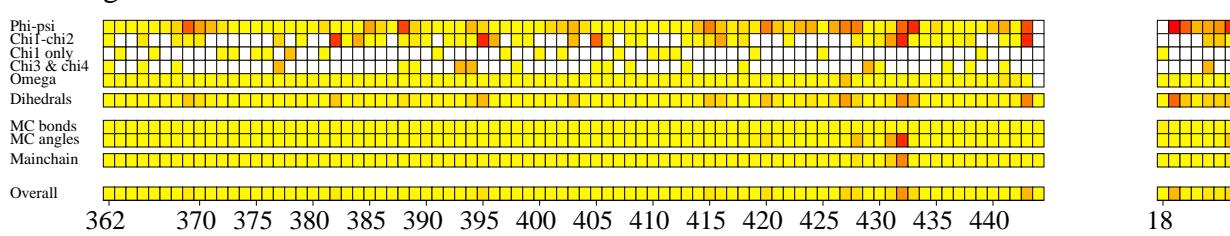
e. Sequence & Ramachandran regions



f. Max. deviation (see listing)

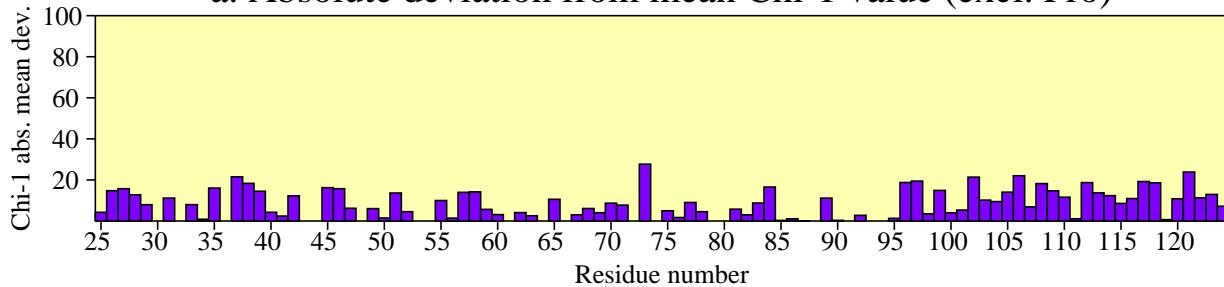


g. G-factors

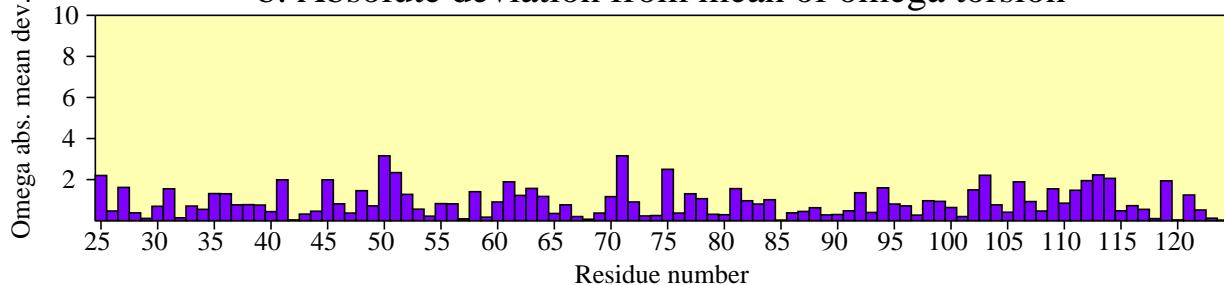


Residue properties pdb3170

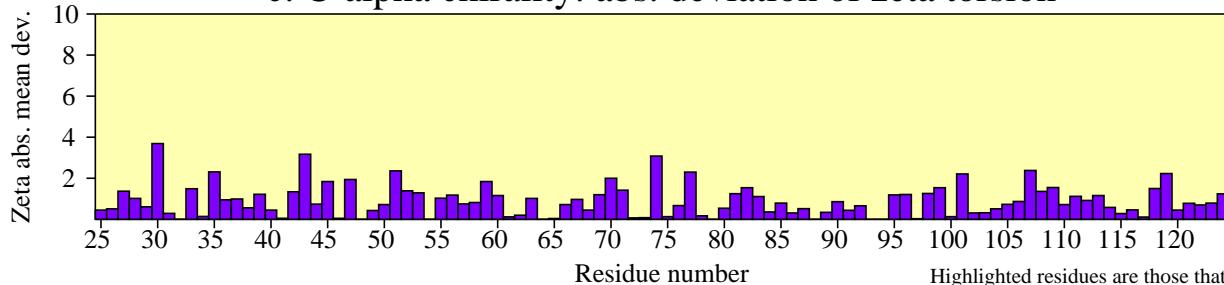
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion

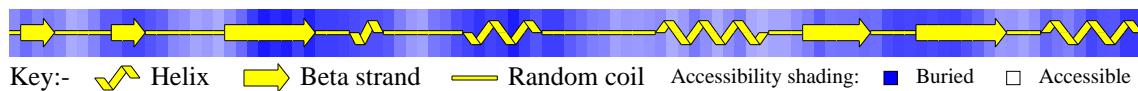


c. C-alpha chirality: abs. deviation of zeta torsion



Highlighted residues are those that deviate by more than 2.0 st. devs. from ideal

d. Secondary structure & estimated accessibility

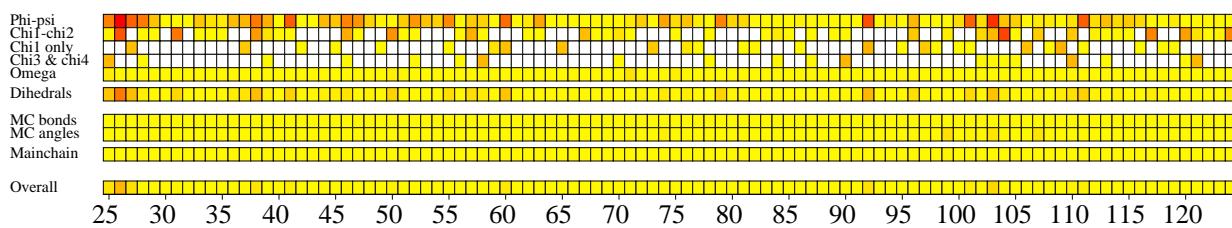


e. Sequence & Ramachandran regions ▲ Most favoured ■ Allowed ■ Generous ■ Disallowed

EITKLPNGLIASLENFSPASRIGVFIAGSRYETTANLGTAAHLLRLASPLTTKGASSFRITRGIEAVVGSLSVYSTREKMTYCVCELRDHVDVTVMYEYL

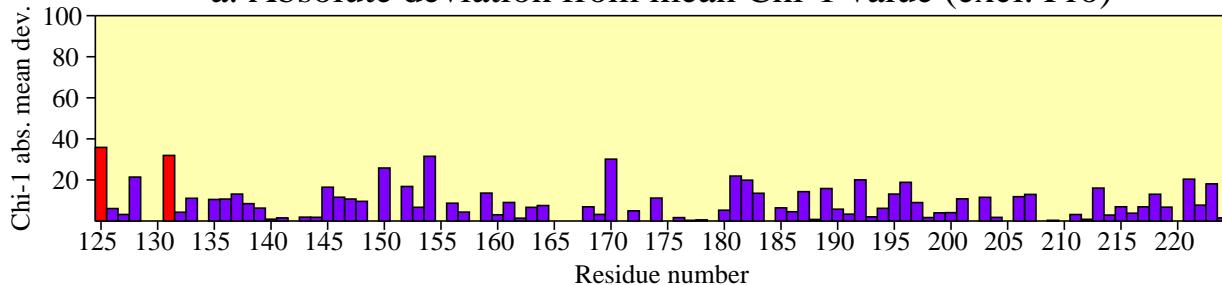
f. Max. deviation (see listing)

g. G-factors

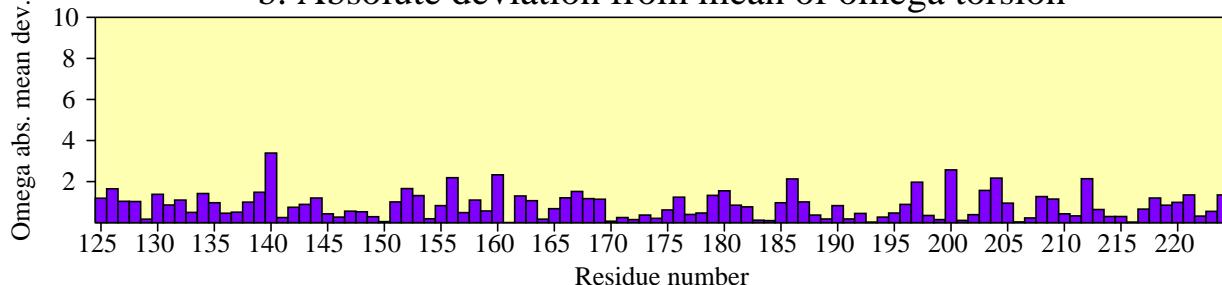


Residue properties pdb3170

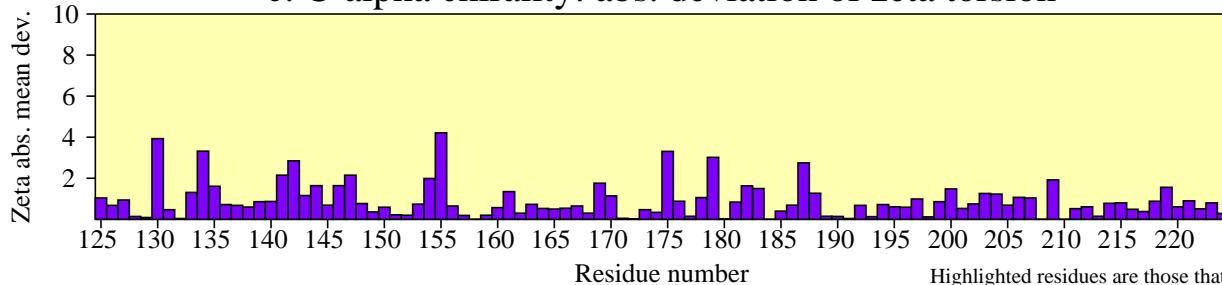
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion

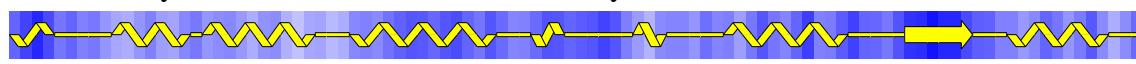


c. C-alpha chirality: abs. deviation of zeta torsion



Highlighted residues are those that deviate by more than 2.0 st. devs. from ideal

d. Secondary structure & estimated accessibility



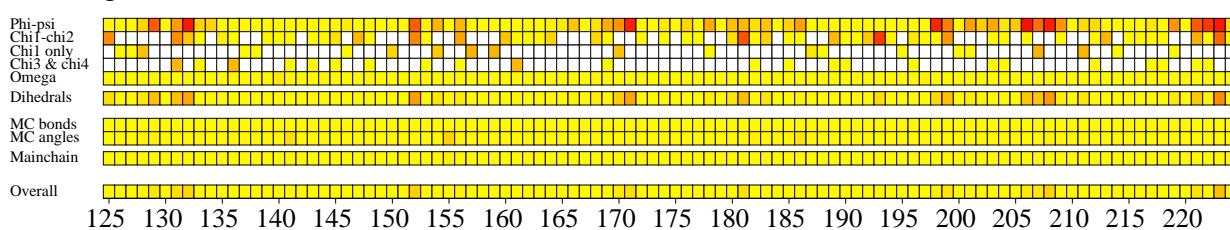
Key:- Helix Beta strand Random coil Accessibility shading: Buried Accessible

e. Sequence & Ramachandran regions ▲ Most favoured ■ Allowed ■ Generous ■ Disallowed

f Max deviation (see listing)



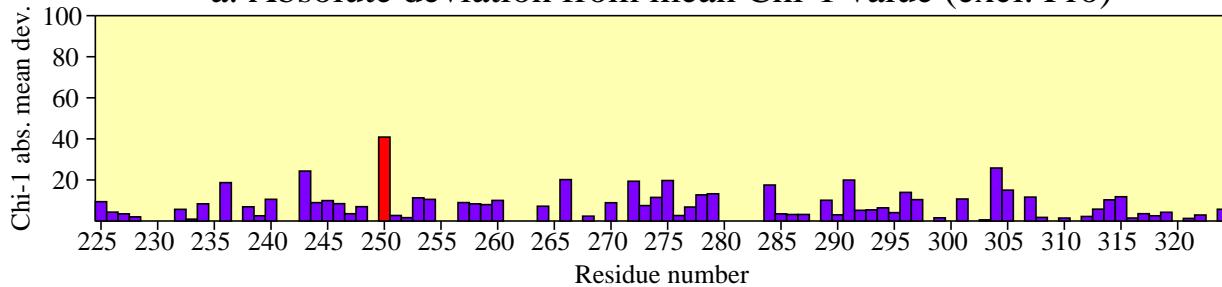
g, G-factors



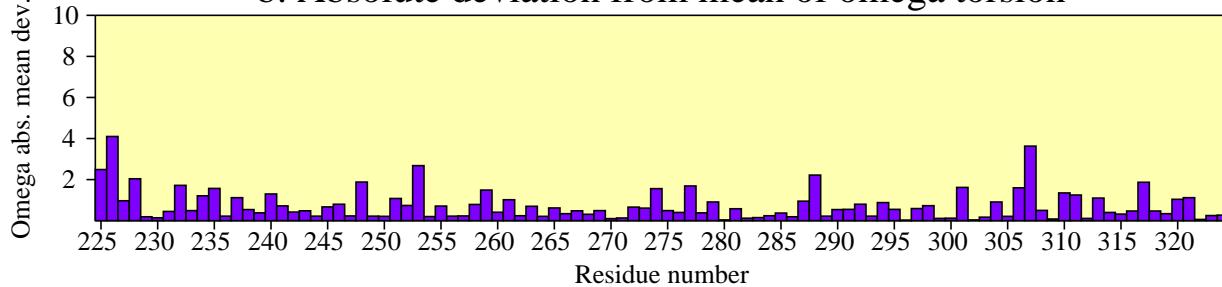
Residue properties

pdb3l70

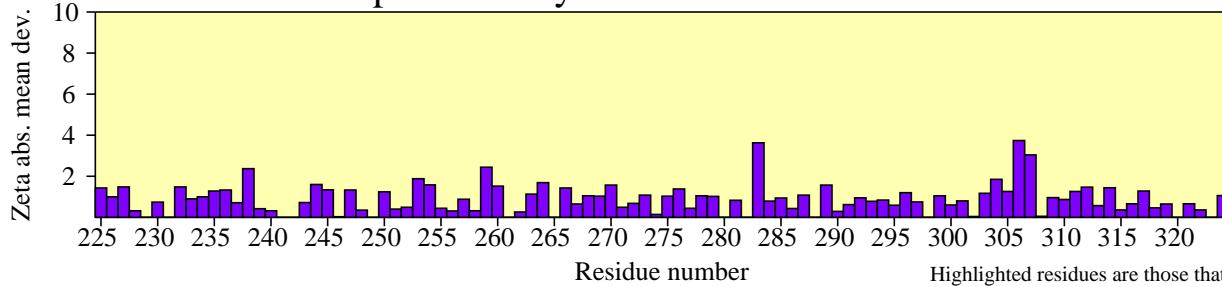
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion



c. C-alpha chirality: abs. deviation of zeta torsion



d. Secondary structure & estimated accessibility



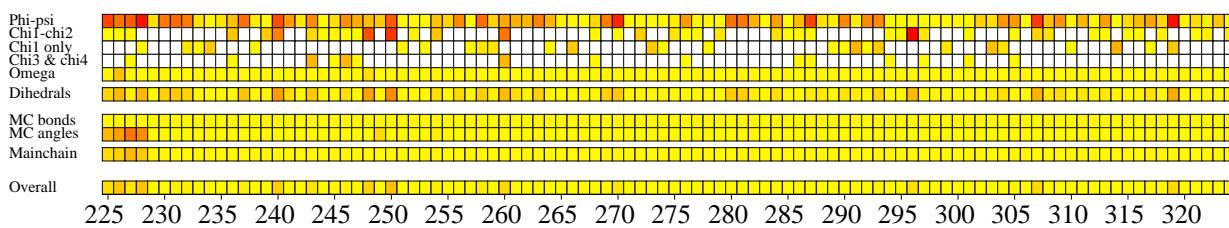
e. Sequence & Ramachandran regions



f. Max. deviation (see listing)



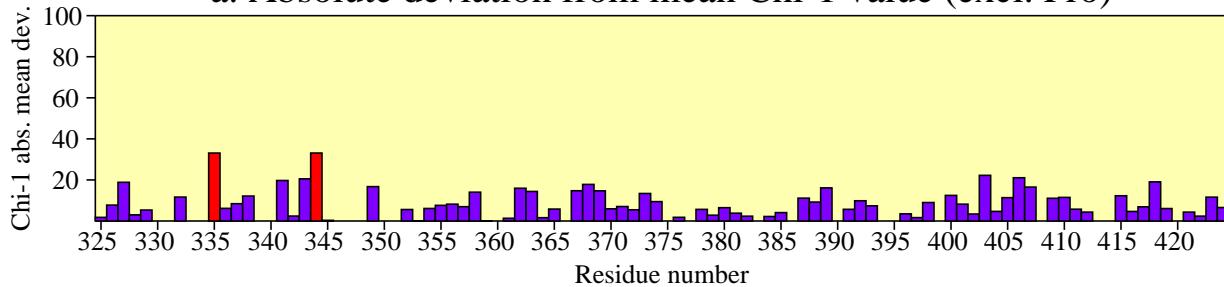
g. G-factors



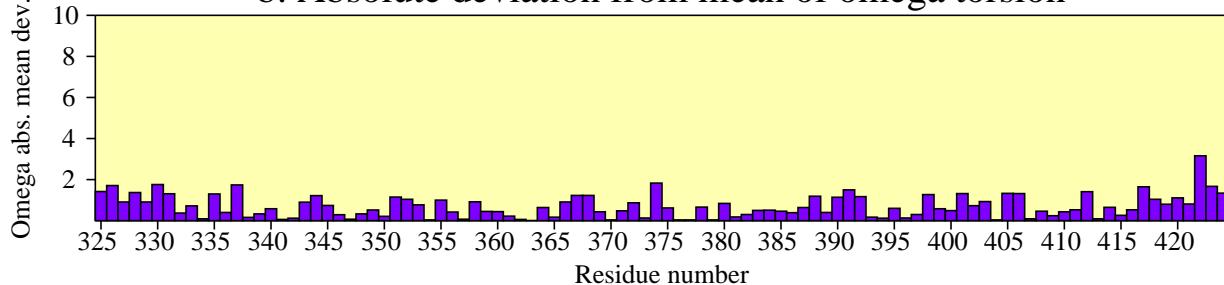
Residue properties

pdb3l70

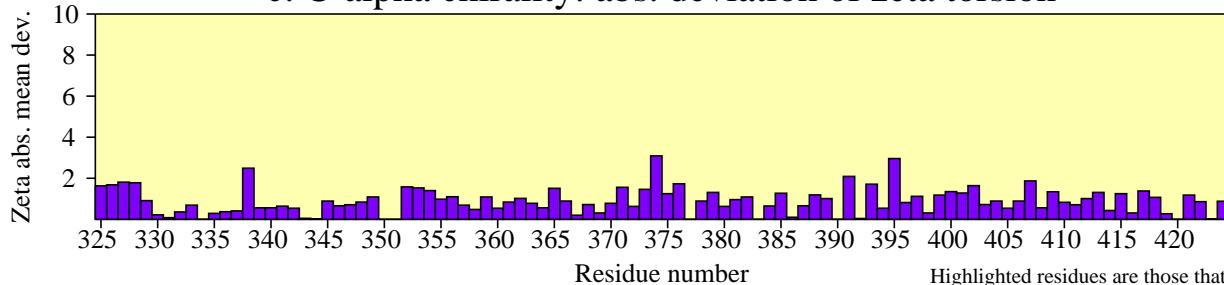
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion

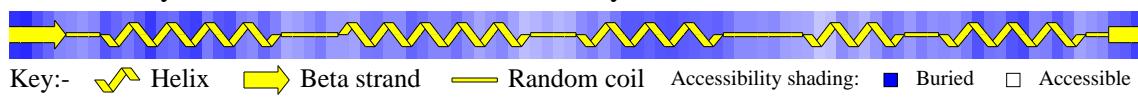


c. C-alpha chirality: abs. deviation of zeta torsion



Highlighted residues are those that deviate by more than 2.0 st. devs. from ideal

d. Secondary structure & estimated accessibility



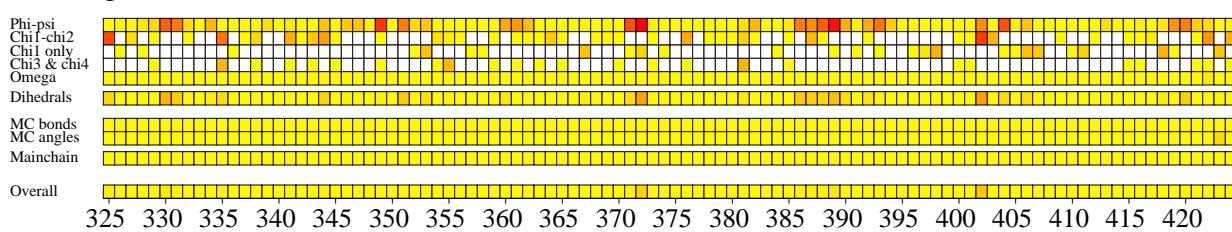
e. Sequence & Ramachandran regions



f. Max. deviation (see listing)

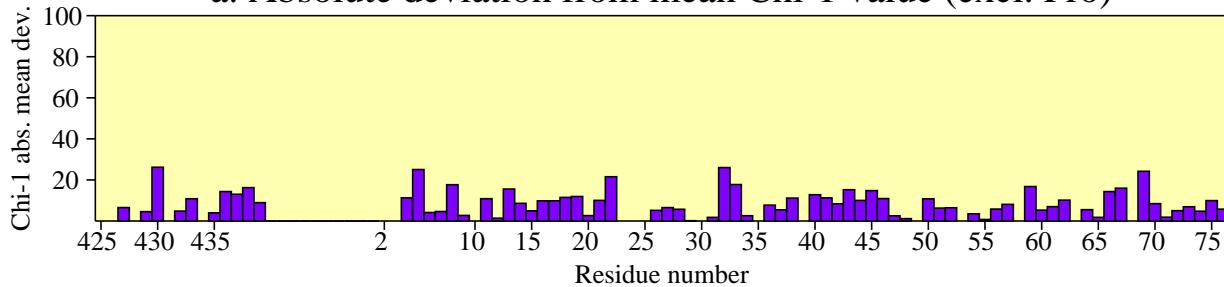


g. G-factors

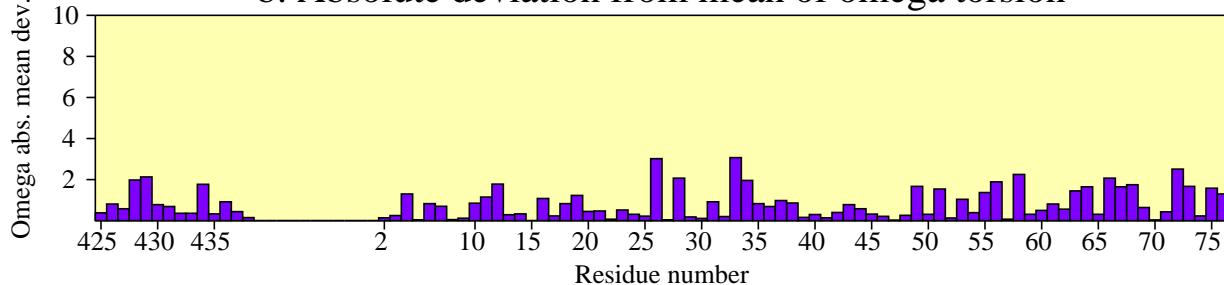


Residue properties pdb3170

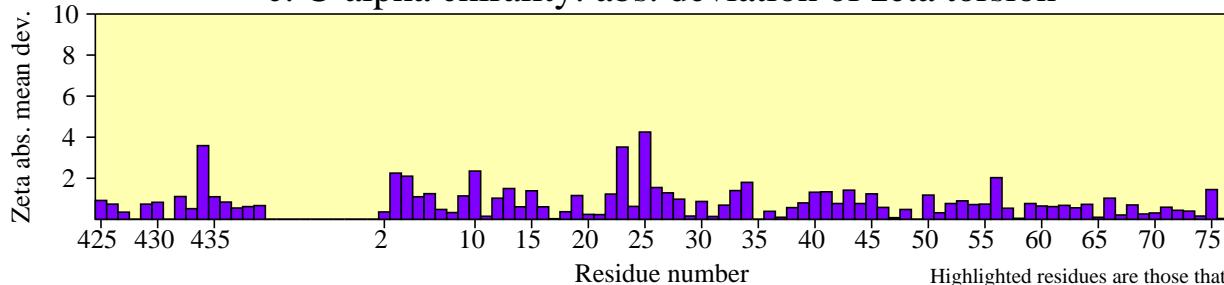
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion

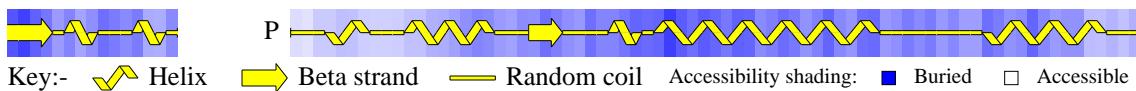


c. C-alpha chirality: abs. deviation of zeta torsion



Highlighted residues are those that deviate by more than 2.0 st. devs. from ideal

d. Secondary structure & estimated accessibility



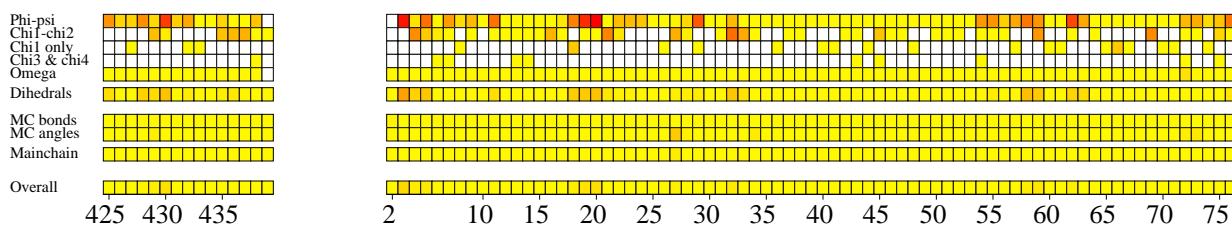
e. Sequence & Ramachandran regions ▲ Most favoured ■ Allowed ■ Generous ■ Disallowed



f. Max. deviation (see listing)



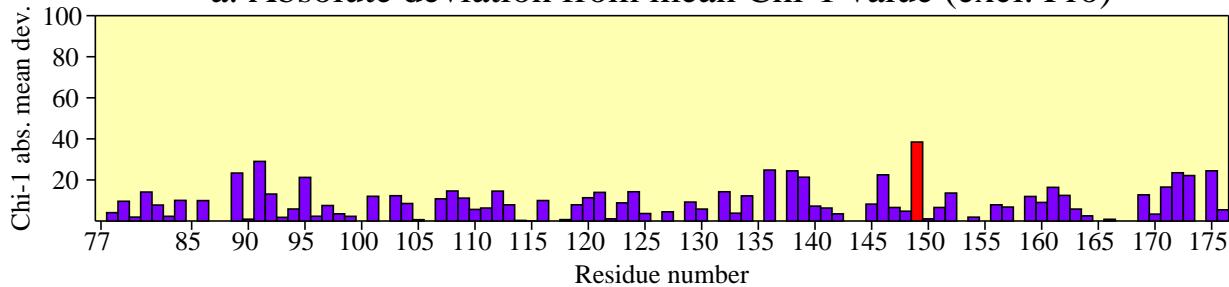
g. G-factors



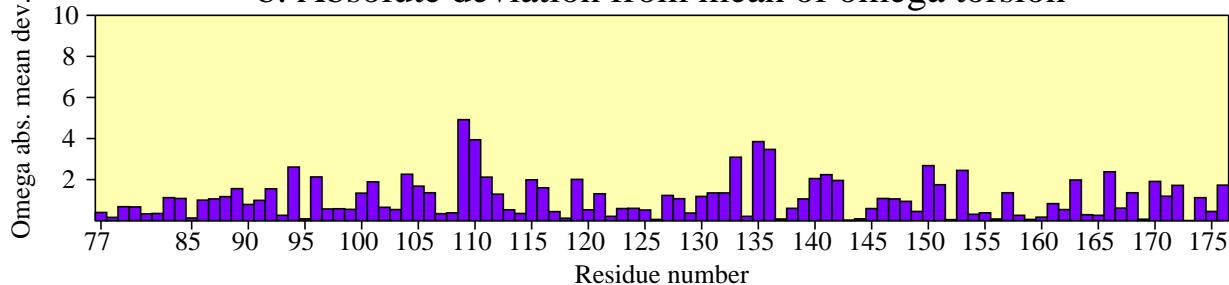
Residue properties

pdb3l70

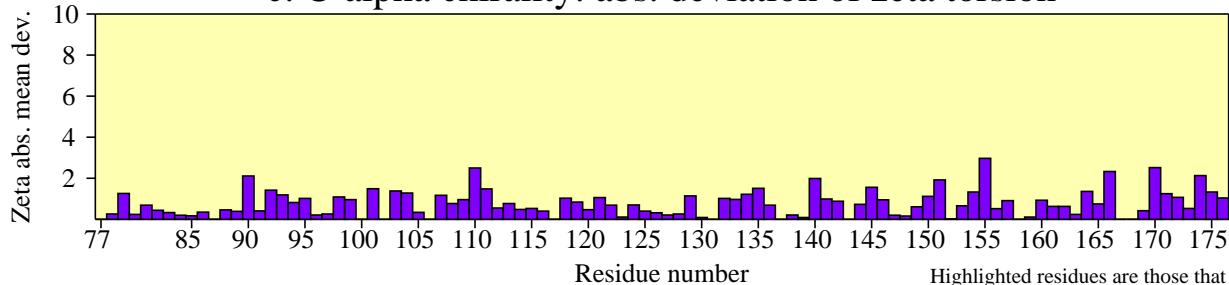
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion



c. C-alpha chirality: abs. deviation of zeta torsion



d. Secondary structure & estimated accessibility



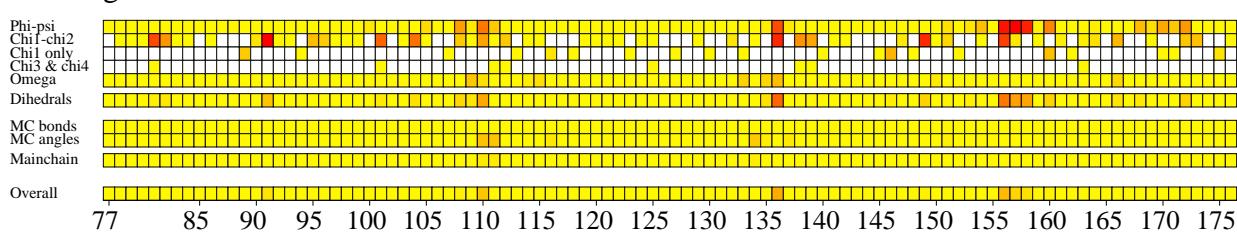
e. Sequence & Ramachandran regions



f. Max. deviation (see listing)

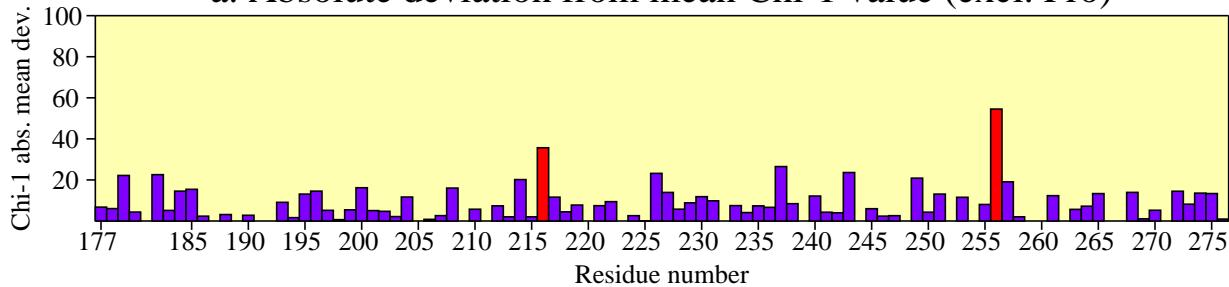


g. G-factors

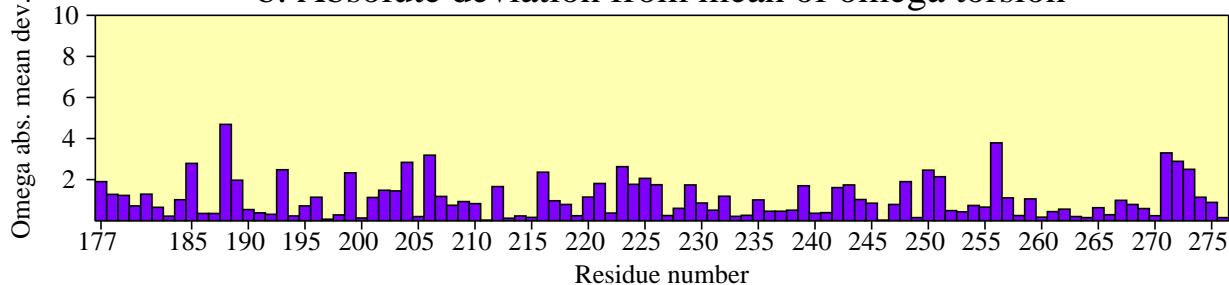


Residue properties pdb3170

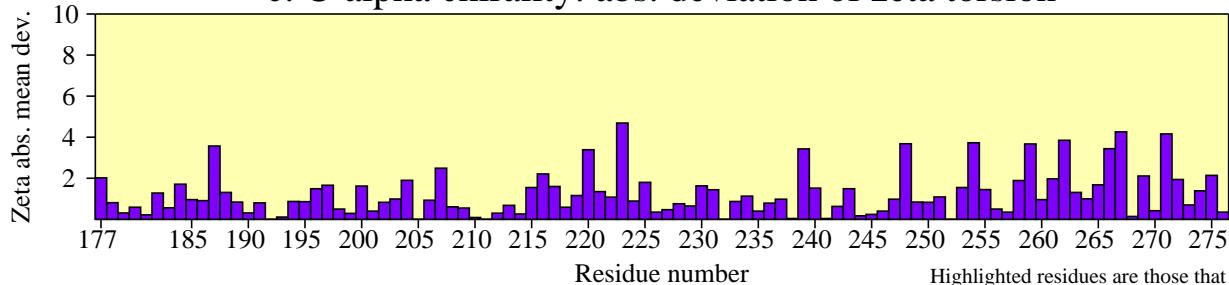
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion



c. C-alpha chirality: abs. deviation of zeta torsion



Highlighted residues are those that deviate by more than 2.0 st. devs. from ideal

d. Secondary structure & estimated accessibility

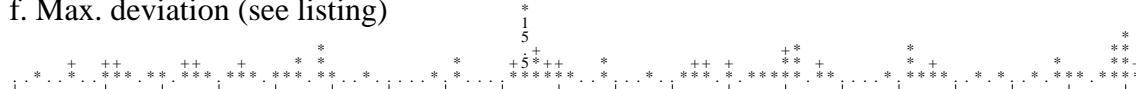


Key:- Helix Beta strand Random coil Accessibility shading: Buried Accessible

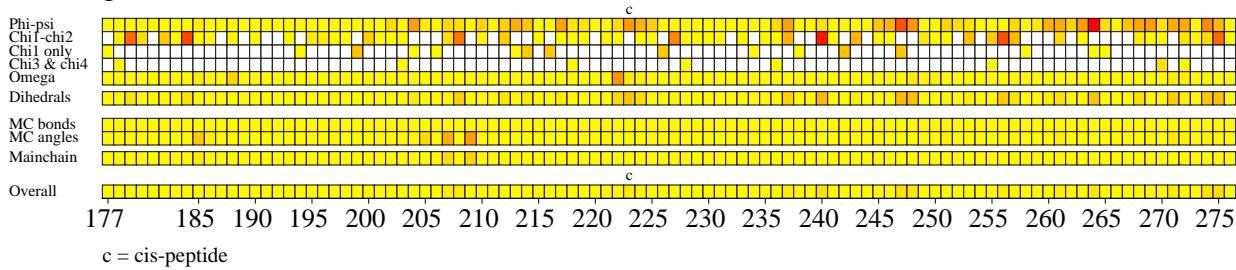
e. Sequence & Ramachandran regions ▲ Most favoured ■ Allowed ■ Generous ■ Disallowed

TRFFALHFLLPFAIAGITIILHHTLHESGSNNPLGISSDSDKIPFHPPYYSFKDILGLTLMTPFLTLAIFSPNLLGDPEFNPANPLVTPPHIKPEWYEL

f. Max. deviation (see listing)



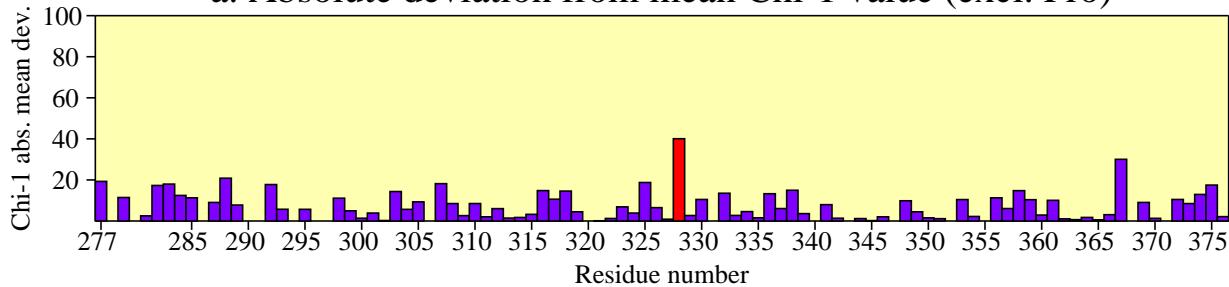
g. G-factors



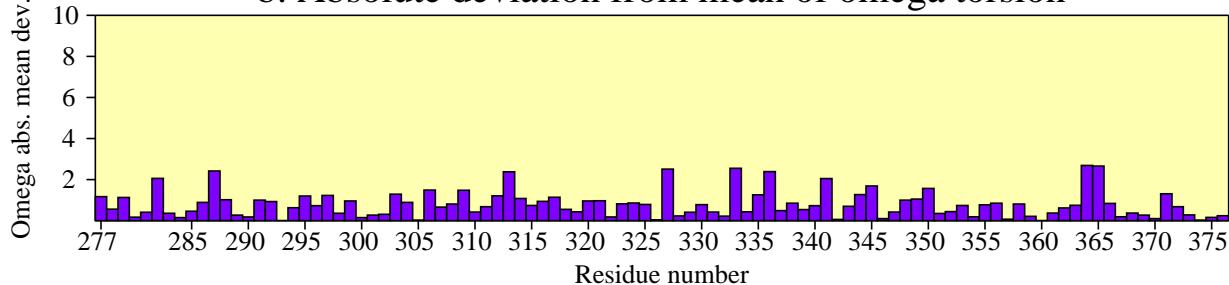
Residue properties

pdb3l70

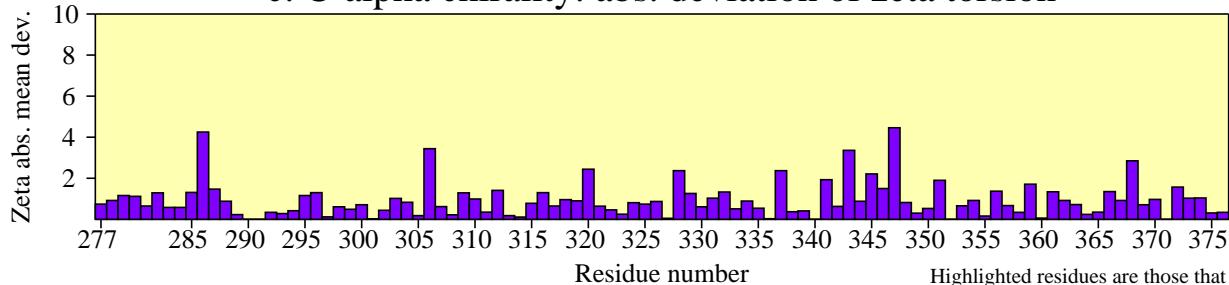
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion



c. C-alpha chirality: abs. deviation of zeta torsion



d. Secondary structure & estimated accessibility



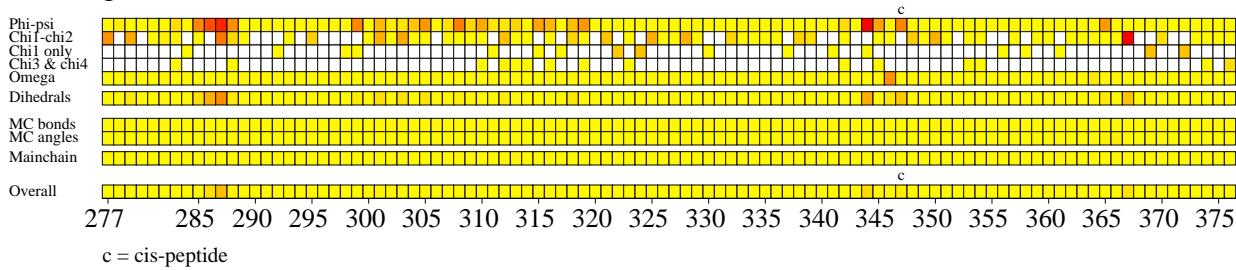
e. Sequence & Ramachandran regions



f. Max. deviation (see listing)

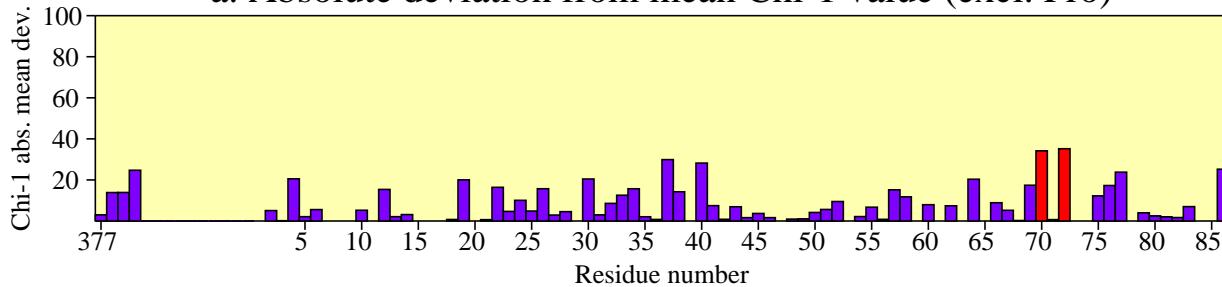


g. G-factors

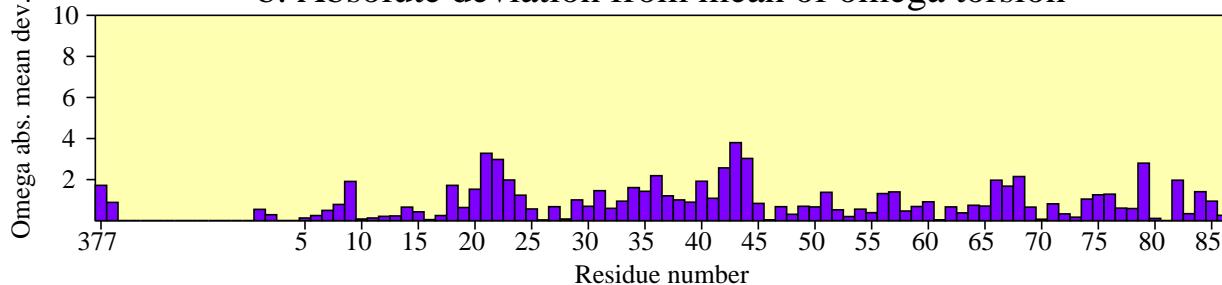


Residue properties pdb3170

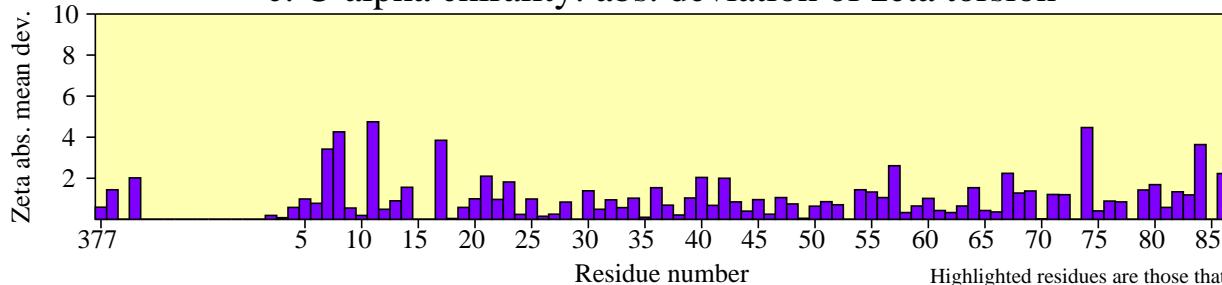
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion



c. C-alpha chirality: abs. deviation of zeta torsion



Highlighted residues are those that deviate by more than 2.0 st. devs. from ideal

d. Secondary structure & estimated accessibility



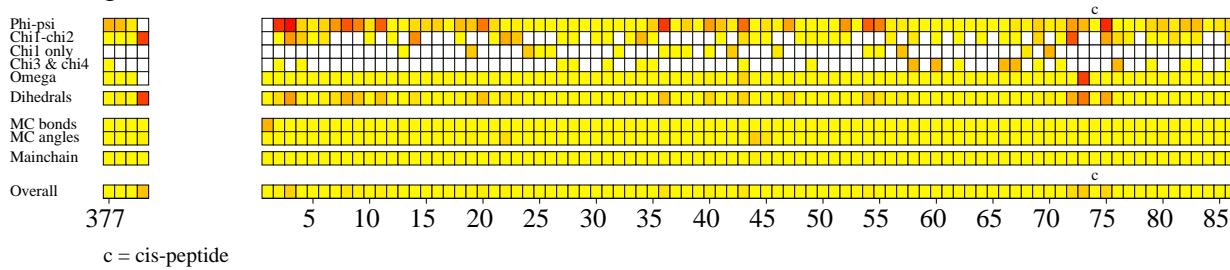
e. Sequence & Ramachandran regions ▲ Most favoured ■ Allowed □ Generous ▨ Disallowed



f. Max. deviation (see listing)



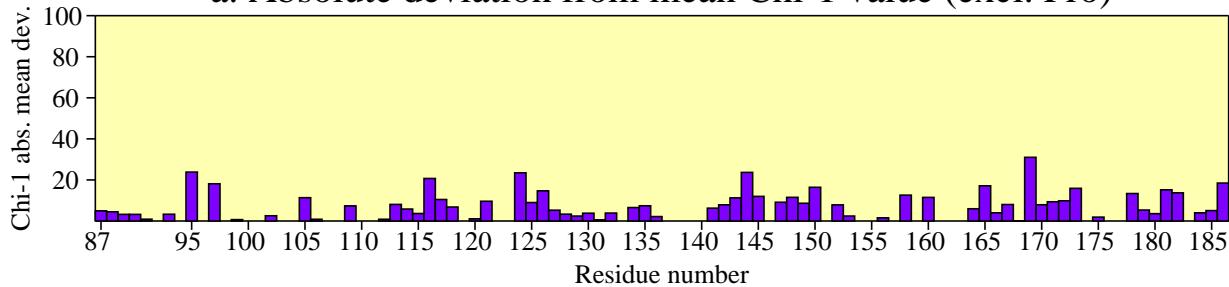
g. G-factors



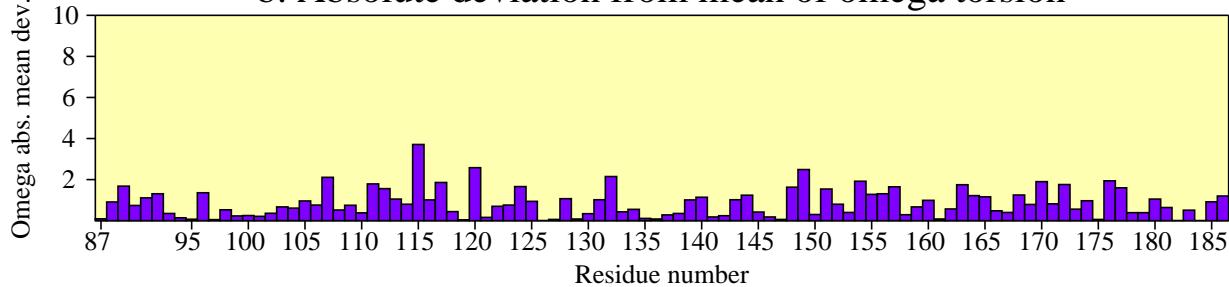
Residue properties

pdb3l70

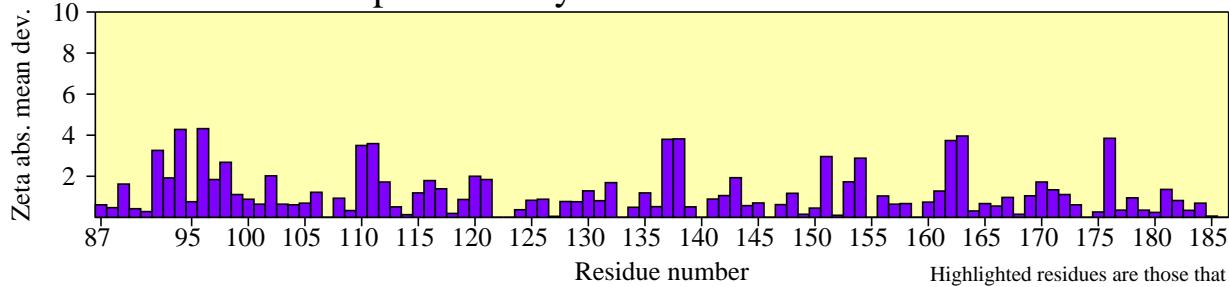
a. Absolute deviation from mean Chi-1 value (excl. Pro)



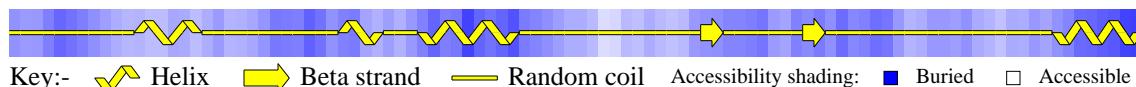
b. Absolute deviation from mean of omega torsion



c. C-alpha chirality: abs. deviation of zeta torsion



d. Secondary structure & estimated accessibility



Key:- Helix Beta strand Random coil Accessibility shading: Buried Accessible

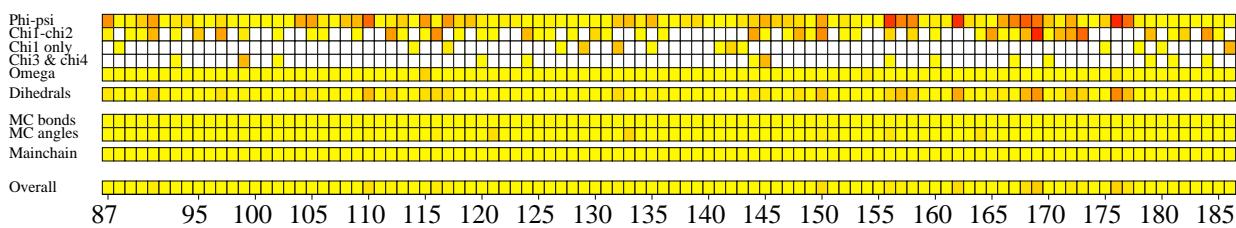
e. Sequence & Ramachandran regions



f. Max. deviation (see listing)

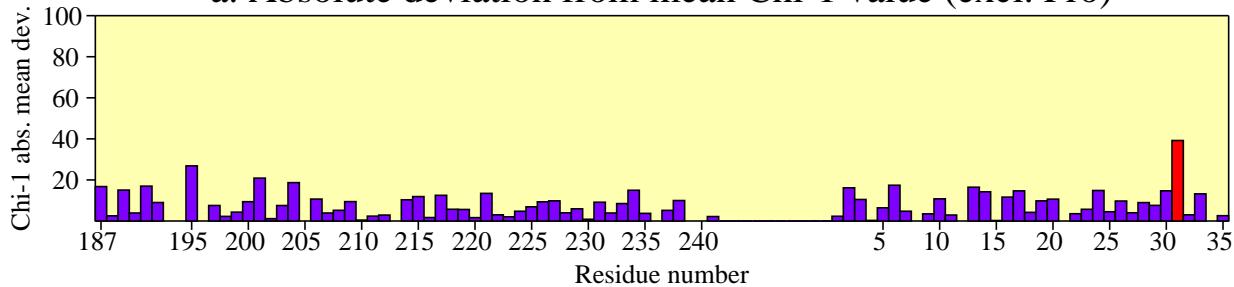


g. G-factors

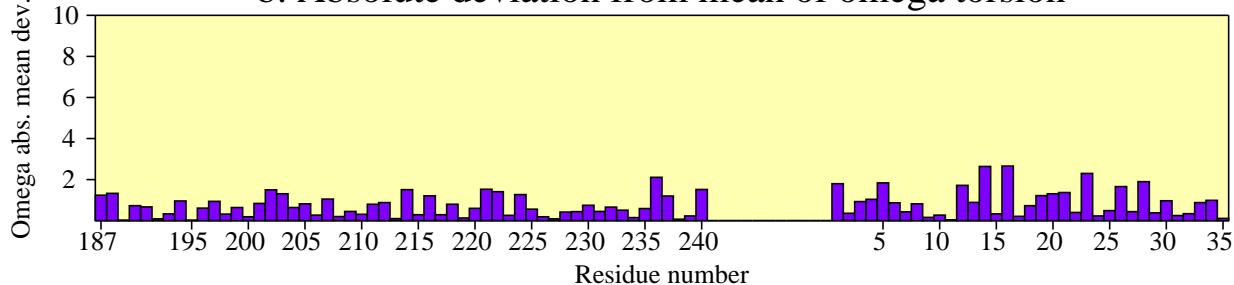


Residue properties pdb3170

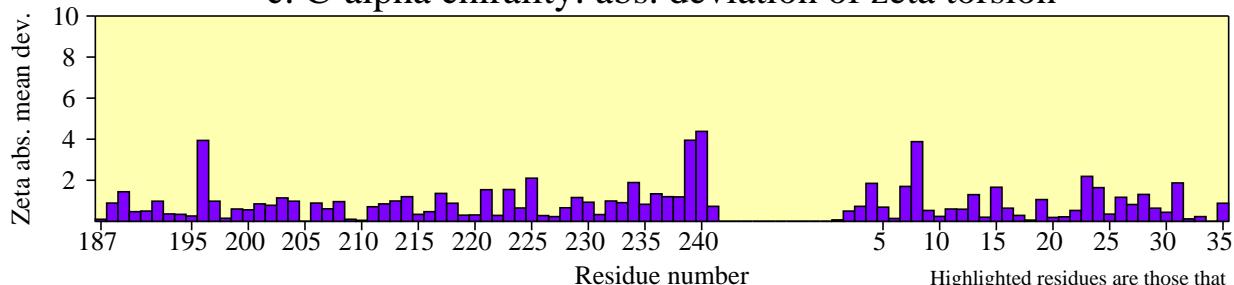
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion



c. C-alpha chirality: abs. deviation of zeta torsion



Highlighted residues are those that deviate by more than 2.0 st. devs. from ideal

d. Secondary structure & estimated accessibility



Key:-  Helix  Beta strand  Random coil

Accessibility shading: Buried Accessible

e. Sequence & Ramachandran regions ▲ Most favoured

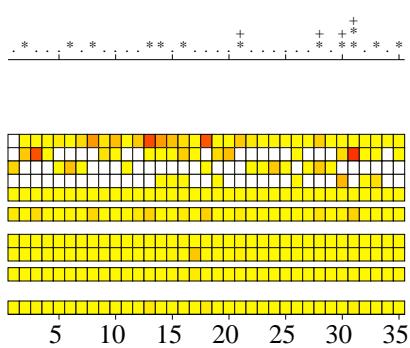
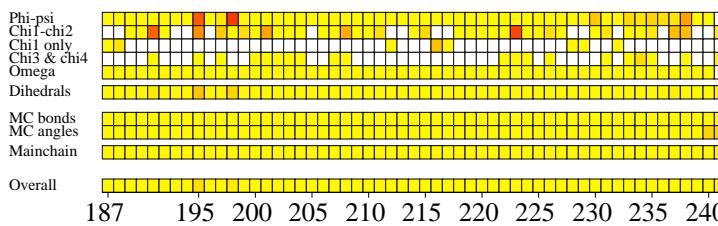


VHNDVTVRDESAYPREDVMADTTSQTSSEDRKGEG

f. Max. deviation (see listing)

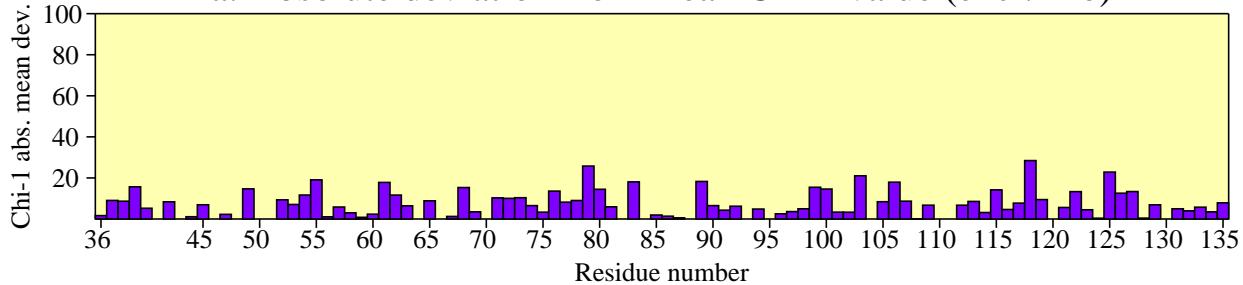


g. G-factors

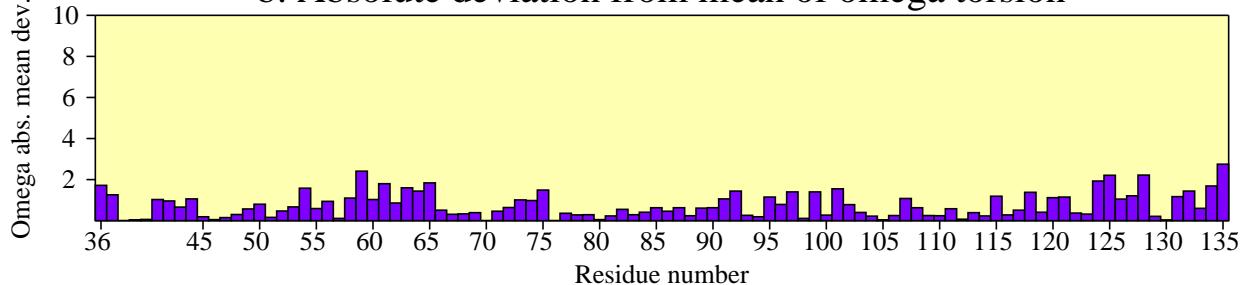


Residue properties pdb3170

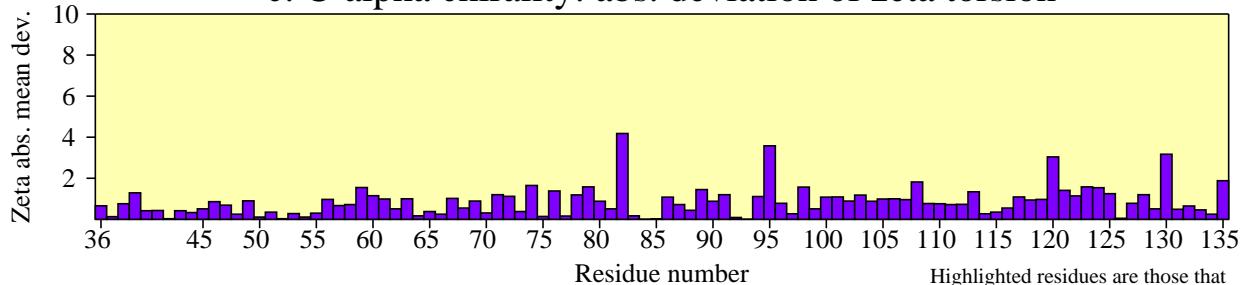
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion

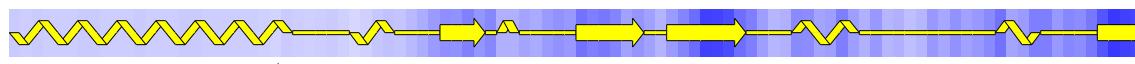


c. C-alpha chirality: abs. deviation of zeta torsion



Highlighted residues are those that deviate by more than 2.0 st. devs. from ideal

d. Secondary structure & estimated accessibility

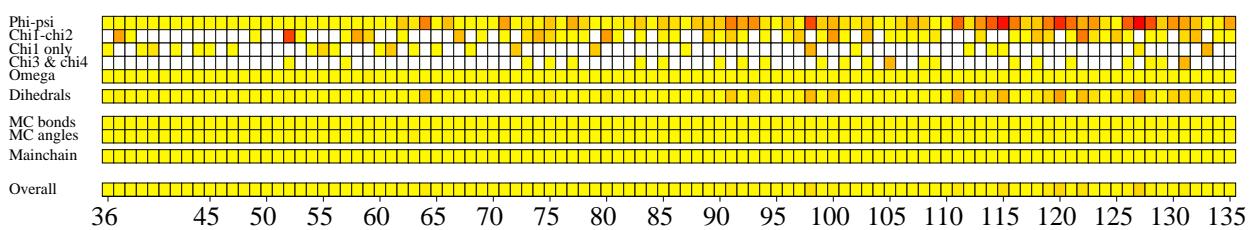


Key:-  Helix  Beta strand  Random coil Accessibility shading:  Buried  Accessible

e. Sequence & Ramachandran regions ▲ Most favoured ■ Allowed ■ Generous ■ Disallowed

f. Max. deviation (see listing)

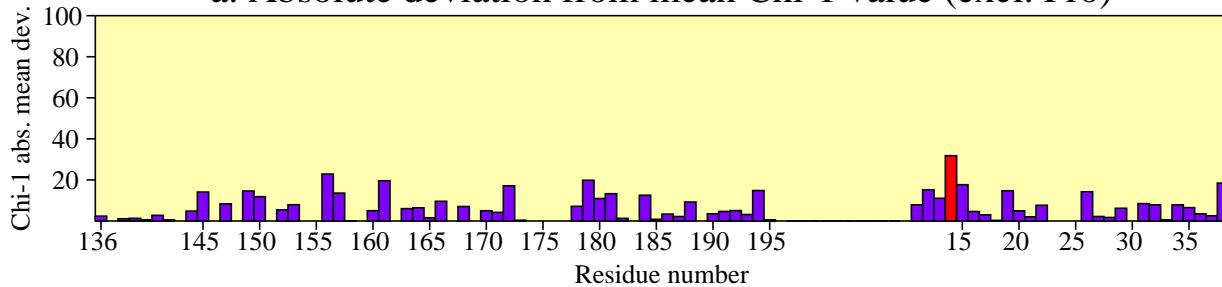
g. G-factors



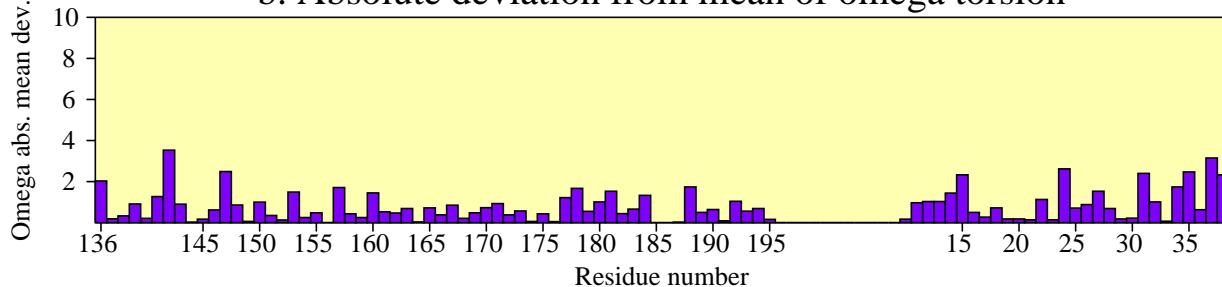
Residue properties

pdb3l70

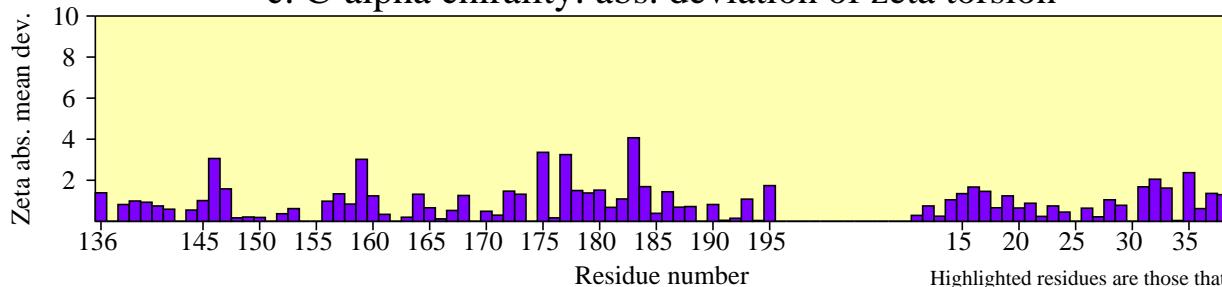
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion

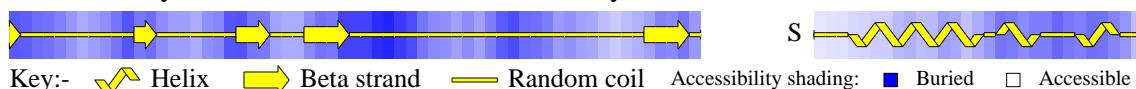


c. C-alpha chirality: abs. deviation of zeta torsion



Highlighted residues are those that deviate by more than 2.0 st. devs. from ideal

d. Secondary structure & estimated accessibility



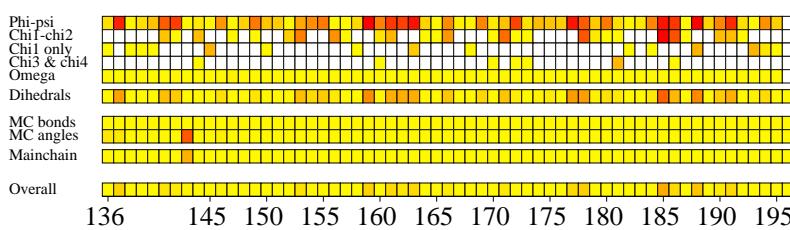
e. Sequence & Ramachandran regions



f. Max. deviation (see listing)



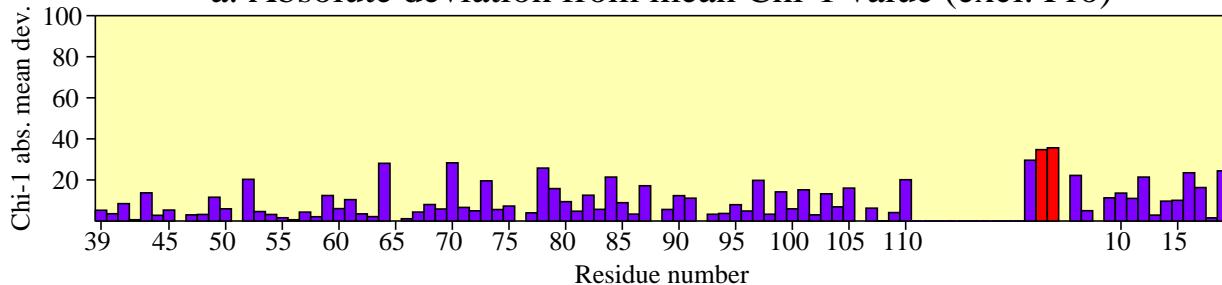
g. G-factors



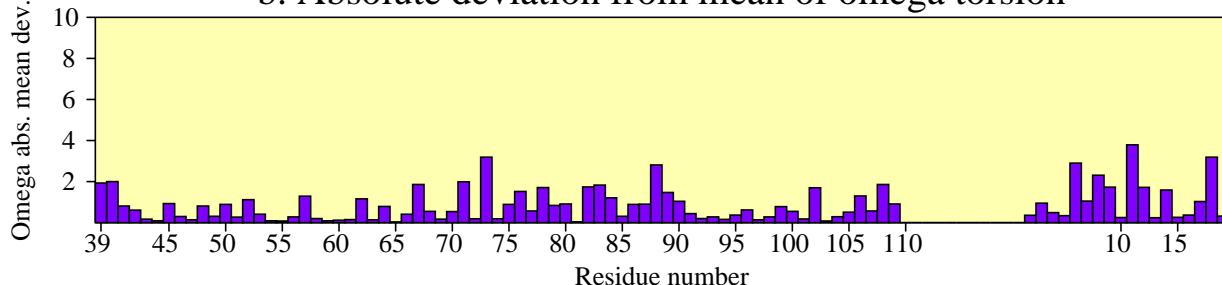
Residue properties

pdb3l70

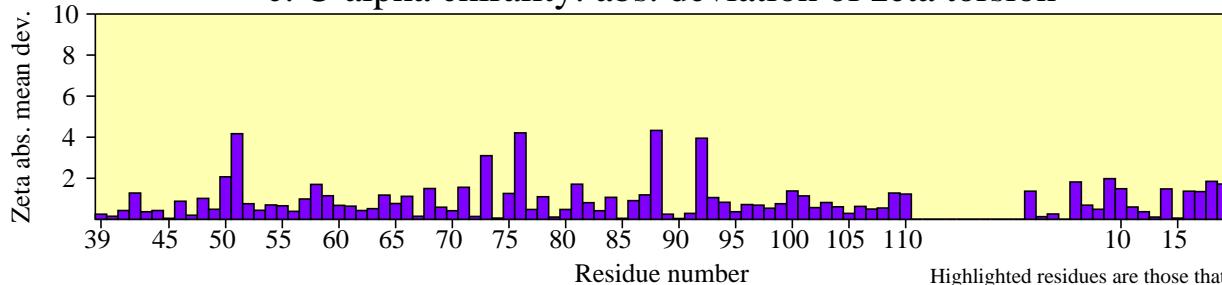
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion

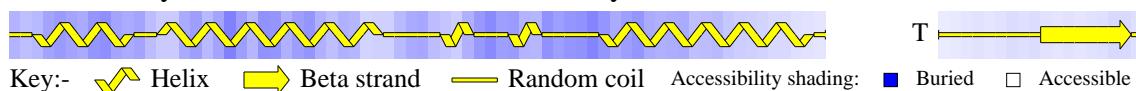


c. C-alpha chirality: abs. deviation of zeta torsion



Highlighted residues are those that deviate by more than 2.0 st. devs. from ideal

d. Secondary structure & estimated accessibility



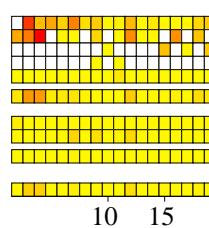
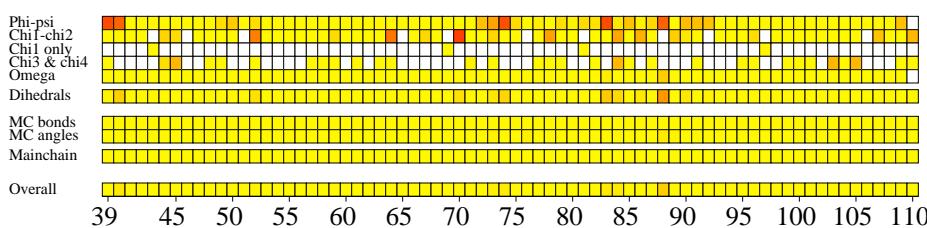
e. Sequence & Ramachandran regions



f. Max. deviation (see listing)



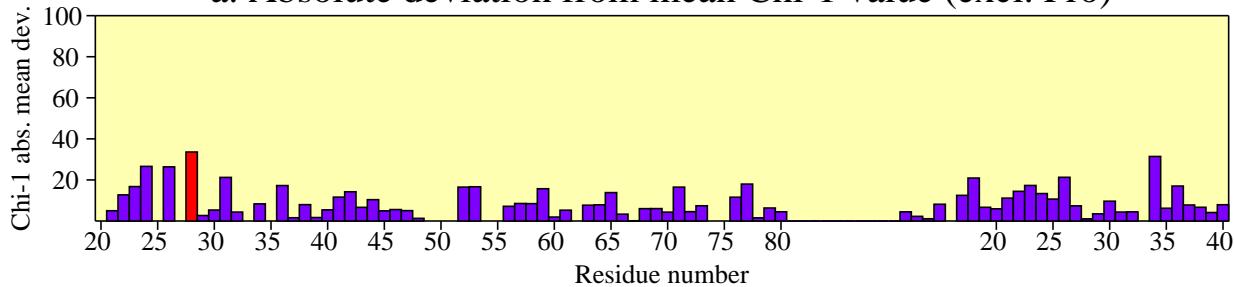
g. G-factors



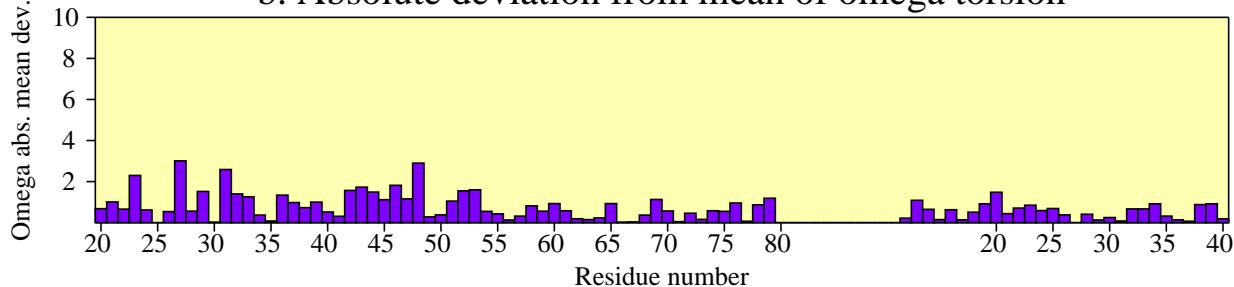
Residue properties

pdb3l70

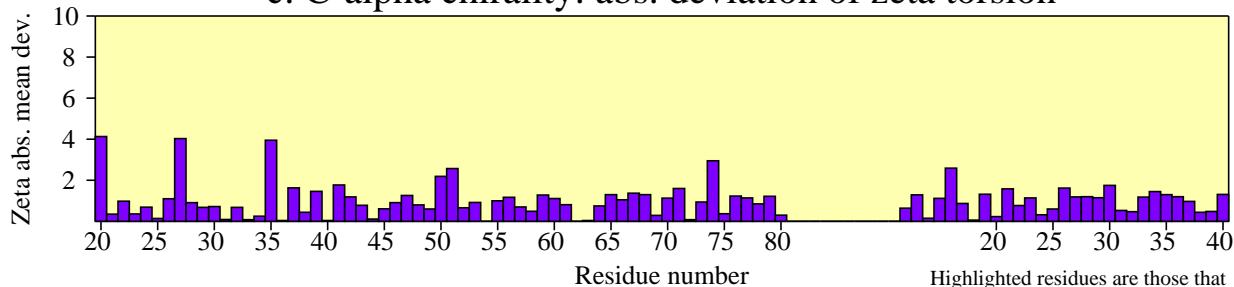
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion



c. C-alpha chirality: abs. deviation of zeta torsion



Highlighted residues are those that deviate by more than 2.0 st. devs. from ideal

d. Secondary structure & estimated accessibility



Accessibility shading: Buried Accessible

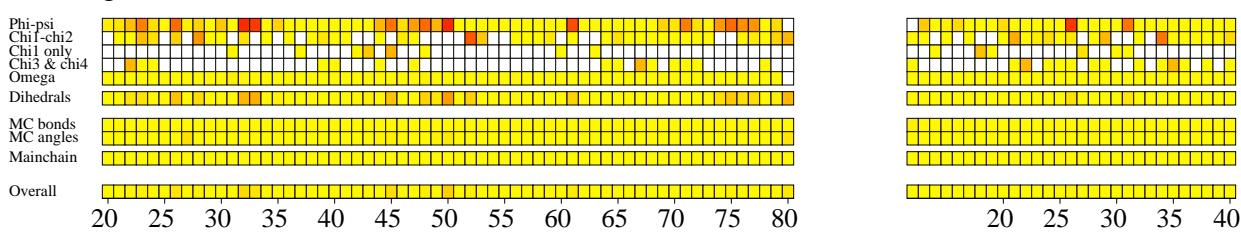
e. Sequence & Ramachandran regions



f. Max. deviation (see listing)



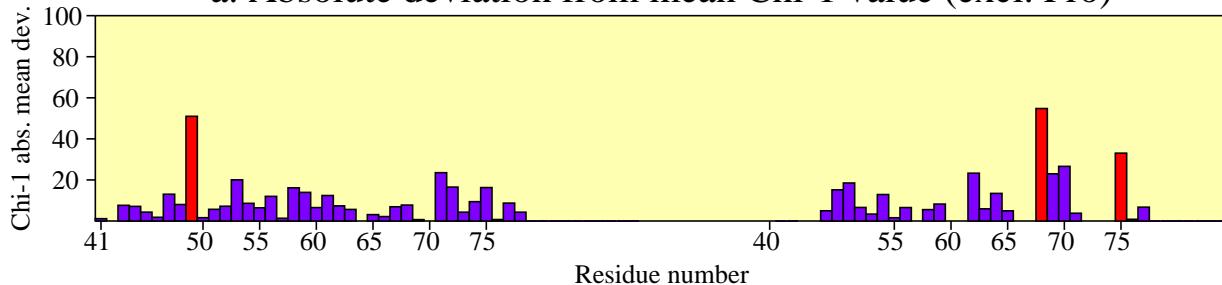
g. G-factors



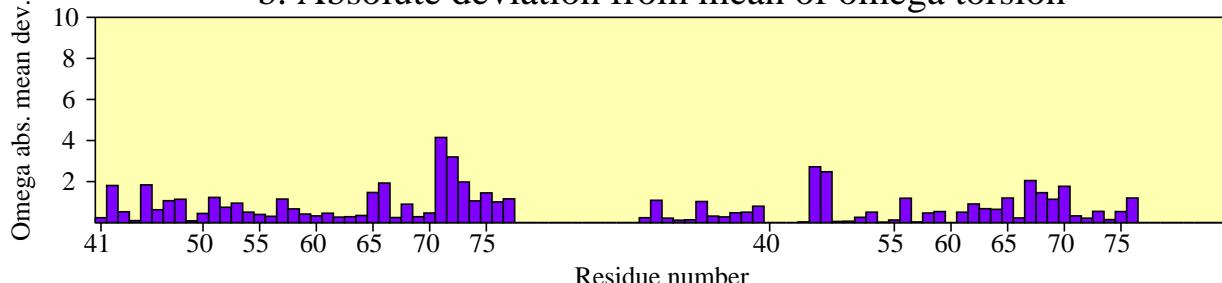
Residue properties

pdb3l70

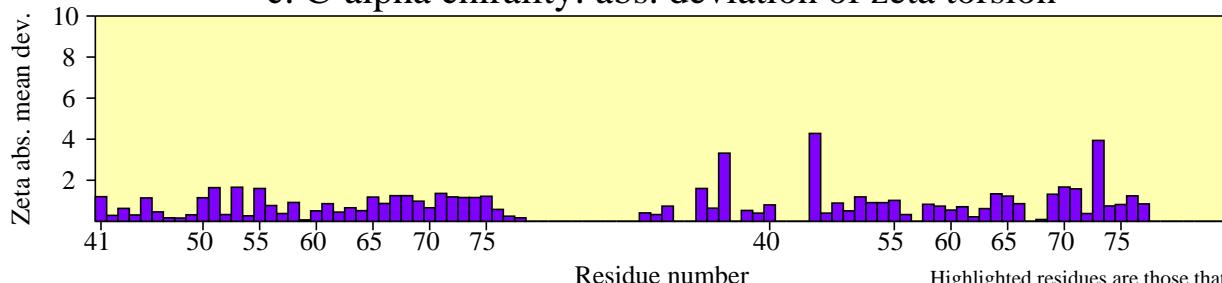
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion

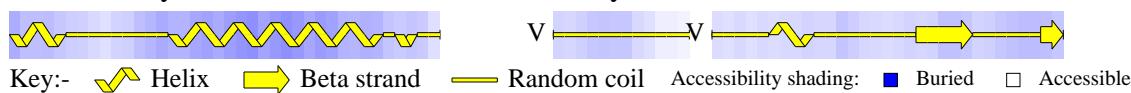


c. C-alpha chirality: abs. deviation of zeta torsion



Highlighted residues are those that deviate by more than 2.0 st. devs. from ideal

d. Secondary structure & estimated accessibility



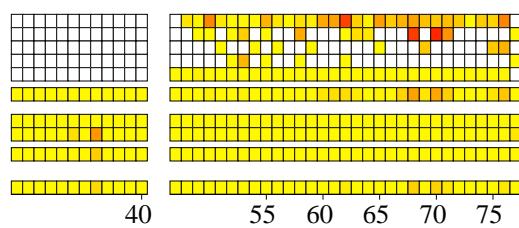
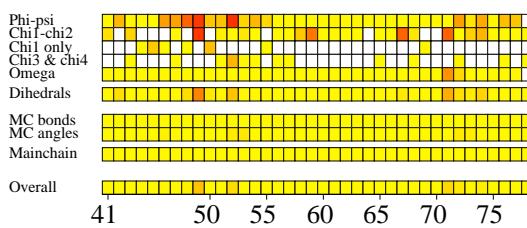
e. Sequence & Ramachandran regions



f. Max. deviation (see listing)

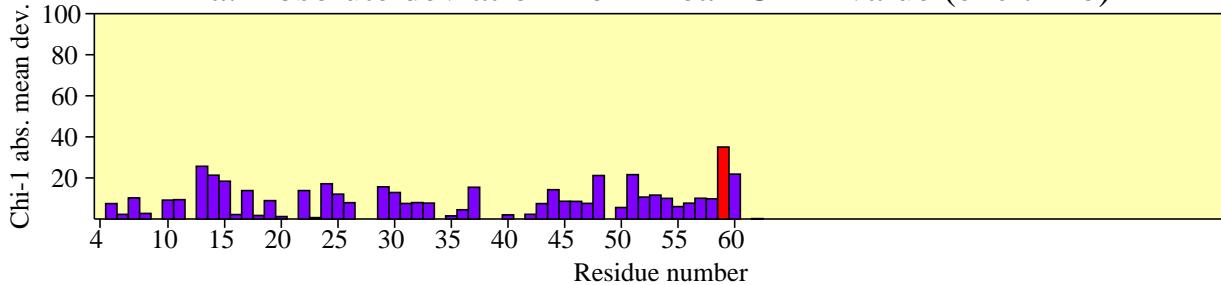


g. G-factors

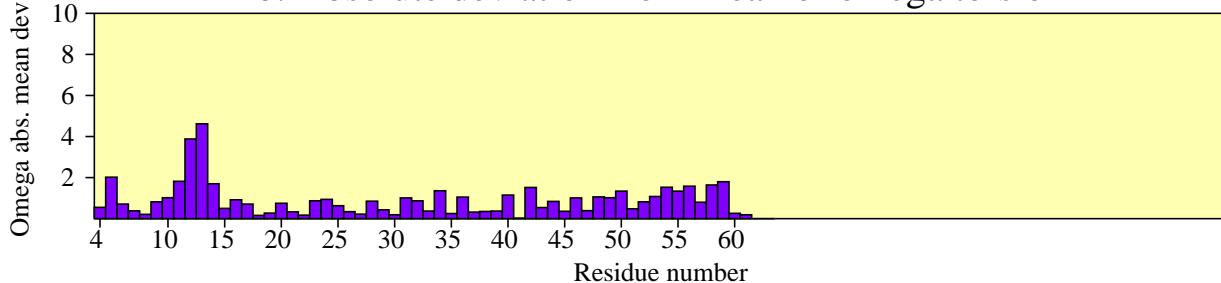


Residue properties pdb3170

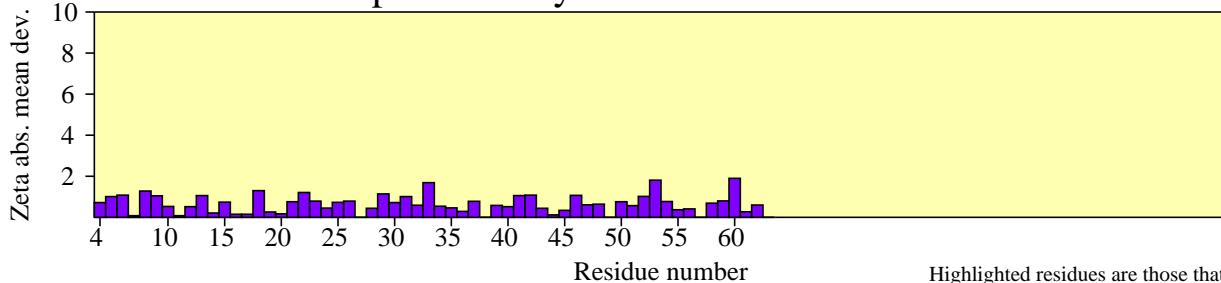
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion



c. C-alpha chirality: abs. deviation of zeta torsion



Highlighted residues are those that deviate by more than 2.0 st. devs. from ideal

d. Secondary structure & estimated accessibility



Key:- Helix Beta strand Random coil Accessibility shading: Buried Accessible

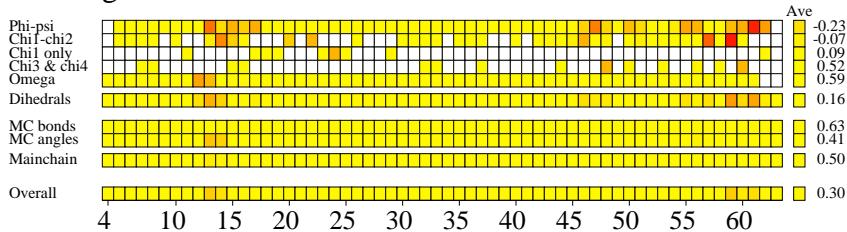
e. Sequence & Ramachandran regions ▲ Most favoured ■ Allowed ■ Generous ■ Disallowed



f. Max. deviation (see listing)

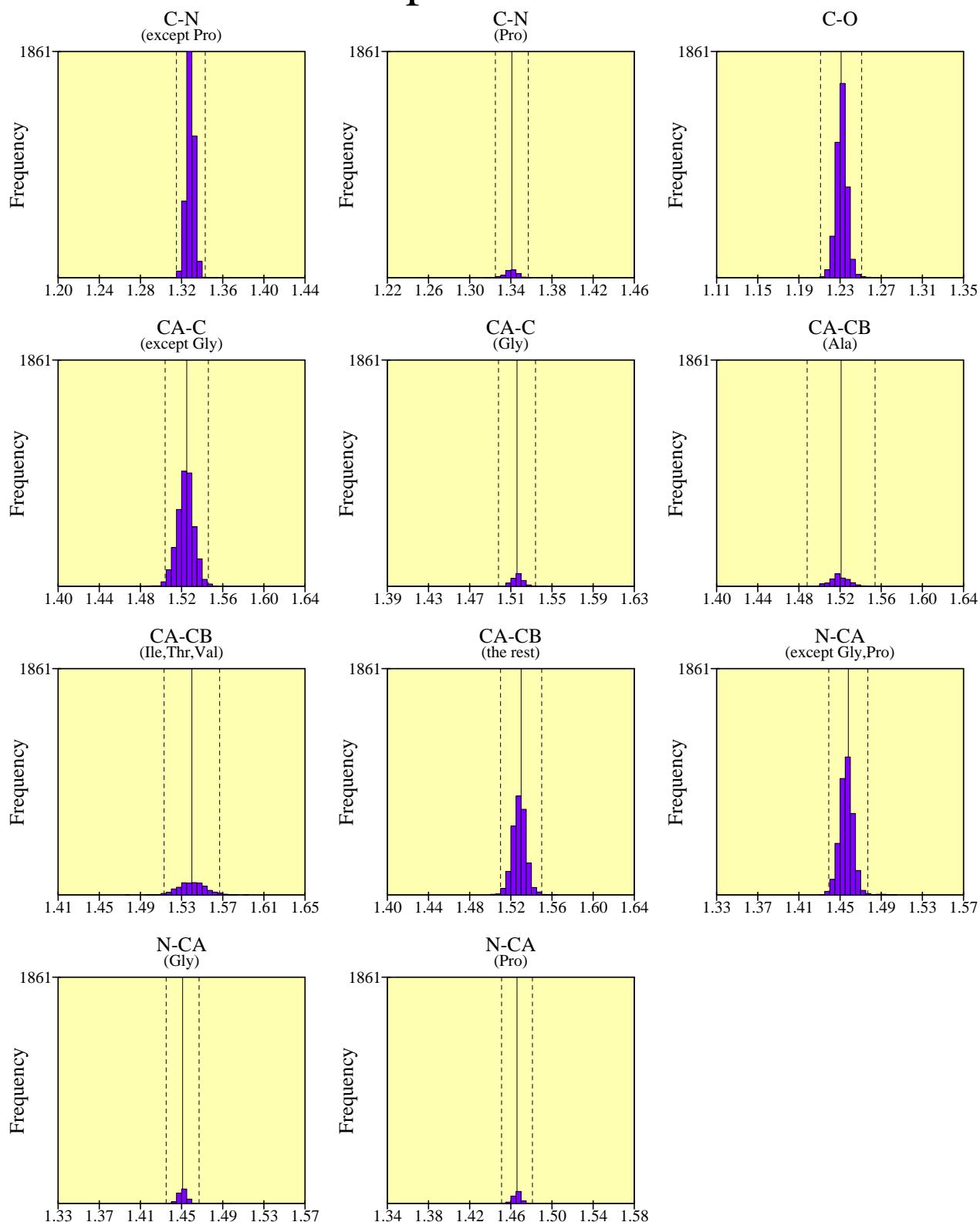


g. G-factors



Main-chain bond lengths

pdb3170

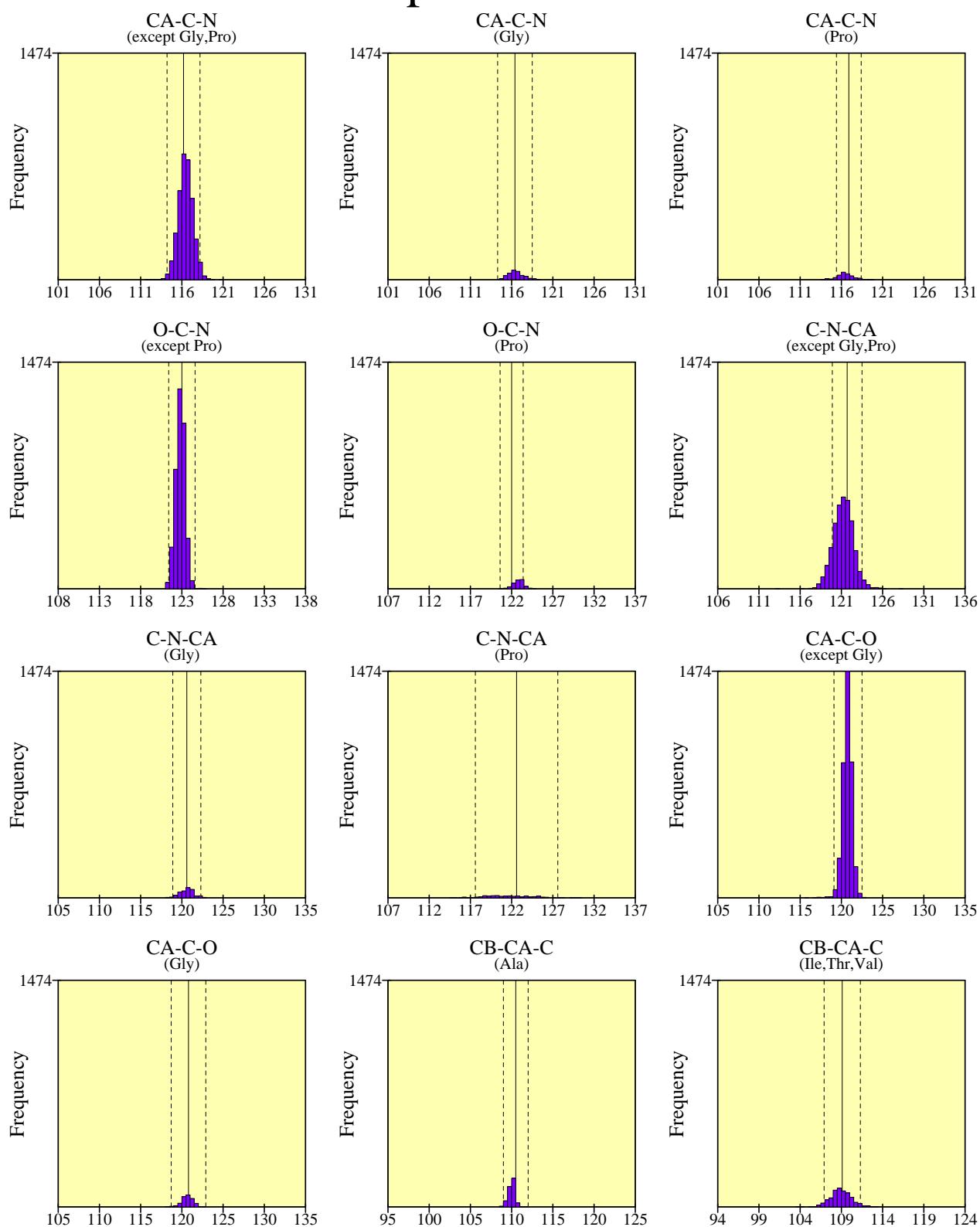


Black bars > 2.0 st. devs. from mean.

Solid and dashed lines represent the mean and standard deviation values as per Engh & Huber small-molecule data.

Main-chain bond angles

pdb3170

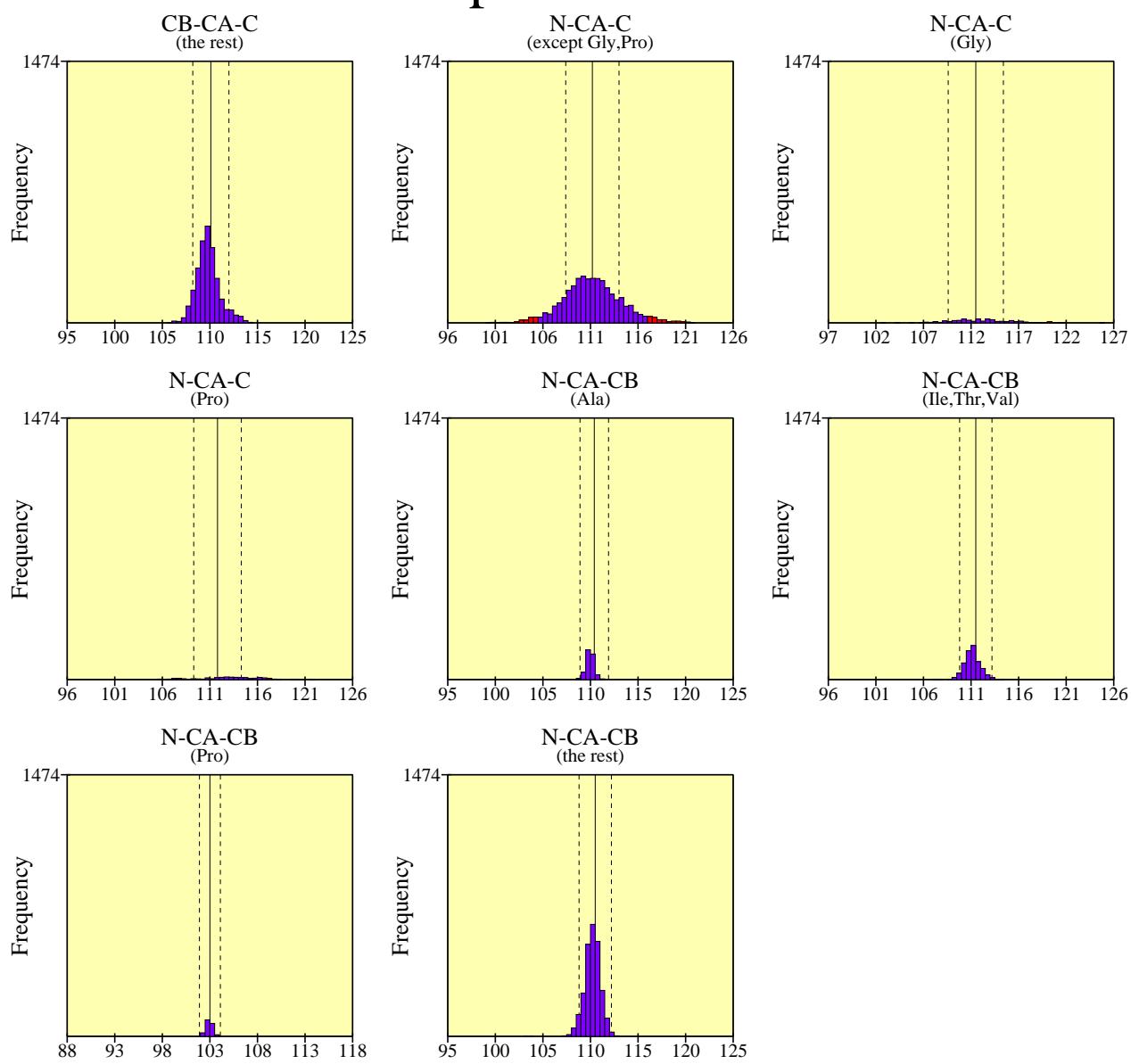


Black bars > 2.0 st. devs. from mean.

Solid and dashed lines represent the mean and standard deviation values as per Engh & Huber small-molecule data.

Main-chain bond angles

pdb3170

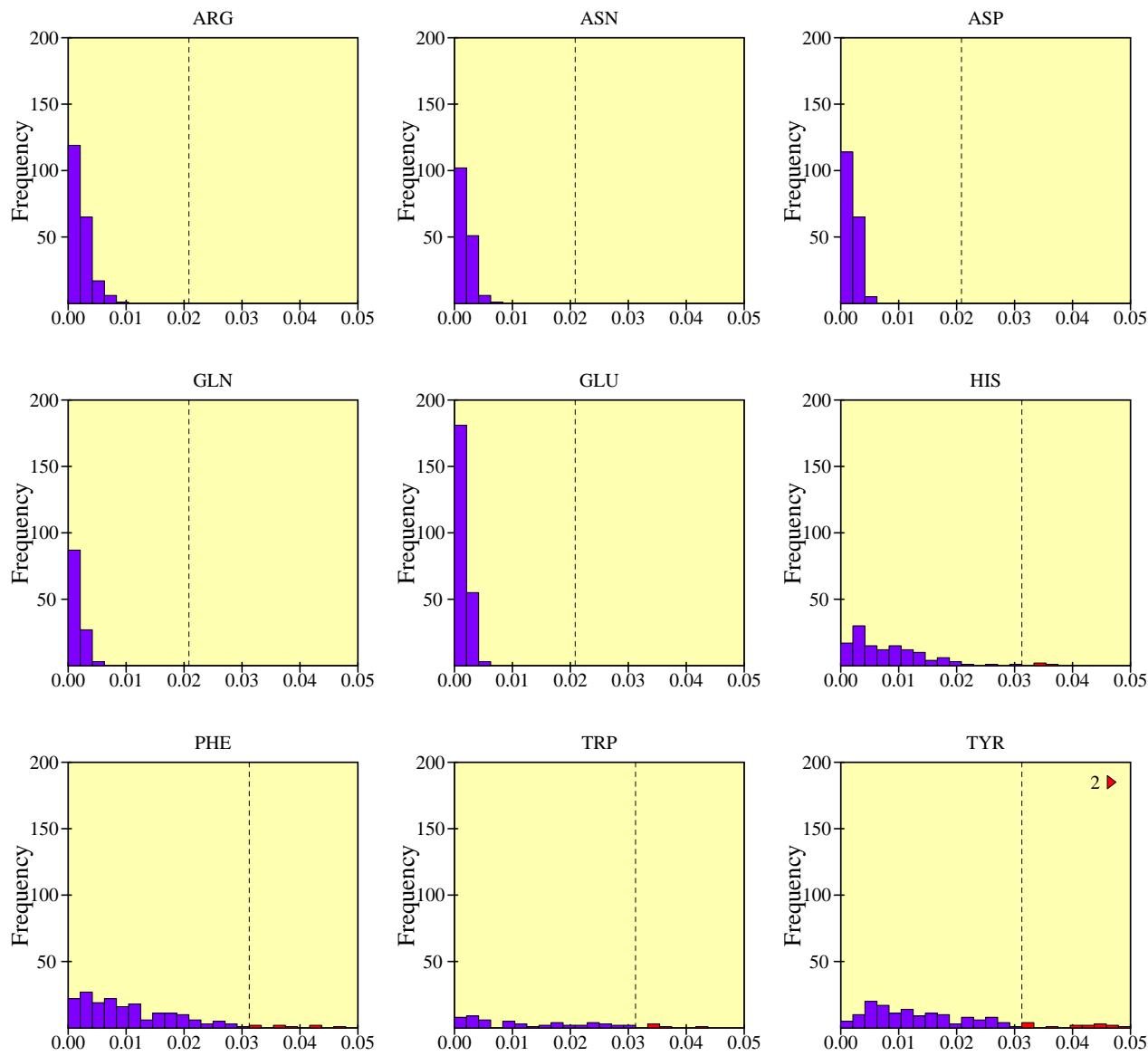


Black bars > 2.0 st. devs. from mean.

Solid and dashed lines represent the mean and standard deviation values as per Engh & Huber small-molecule data.

RMS distances from planarity

pdb3170



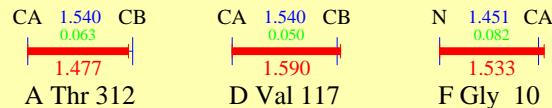
Histograms showing RMS distances of planar atoms from best-fit plane.
Black bars indicate large deviations from planarity: RMS dist > 0.03 for rings, and > 0.02 otherwise.

► signifies data points off the graph in the direction shown.

Distorted geometry

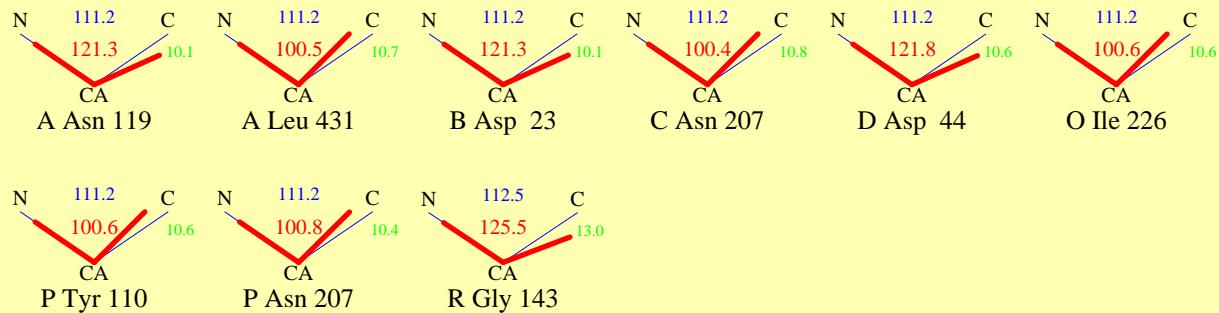
pdb3170

Main-chain bond lengths



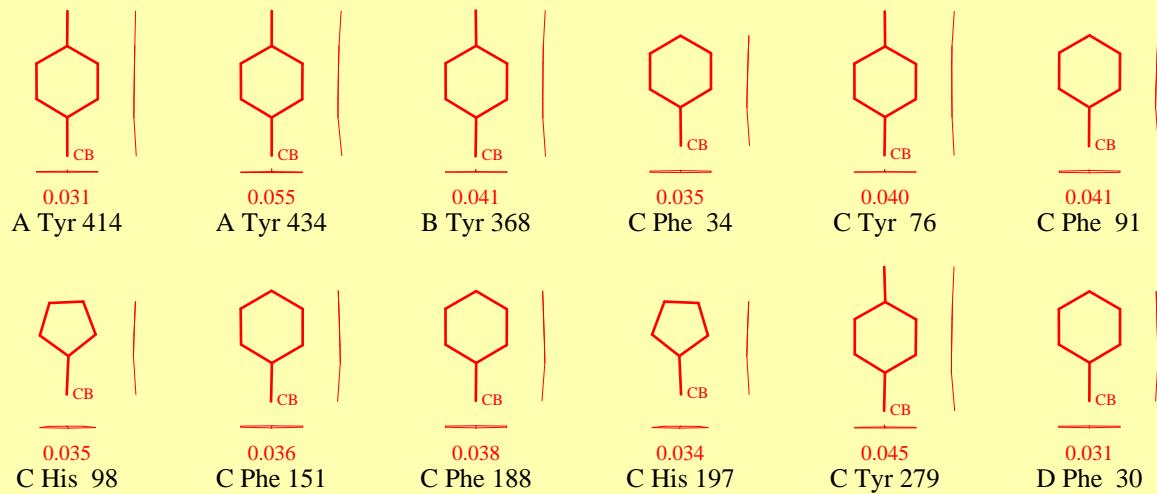
Bonds differing by > 0.05Å from small-molecule values. Values shown: "ideal", difference, actual

Main-chain bond angles



Bond angles differing by > 10.0 degrees from small-molec values. Values shown: "ideal", actual, diff.

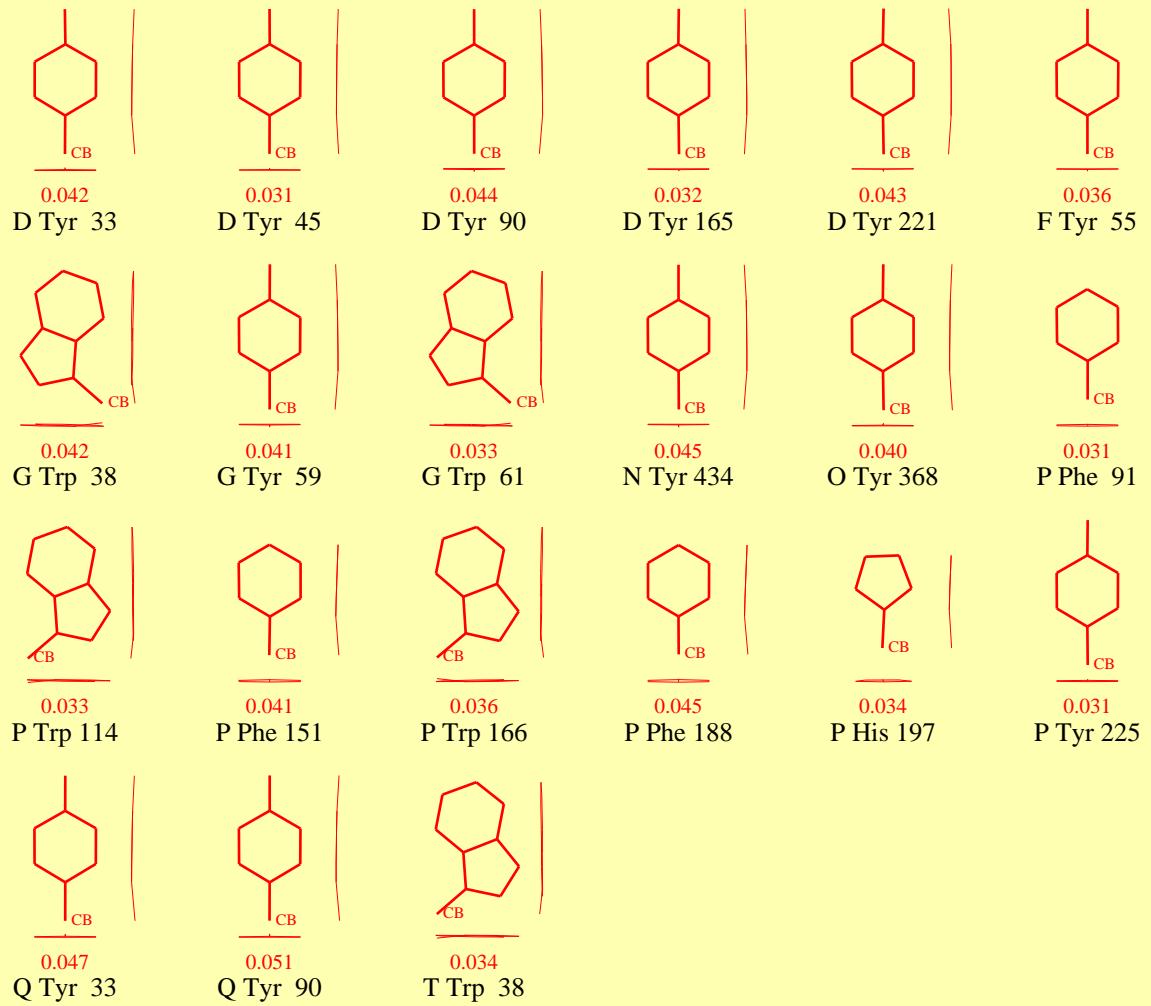
Planar groups



Distorted geometry

pdb3l70

Planar groups (contd)



Sidechains with RMS dist. from planarity > 0.03Å for rings, or > 0.02Å otherwise. Value shown is RMS dist.