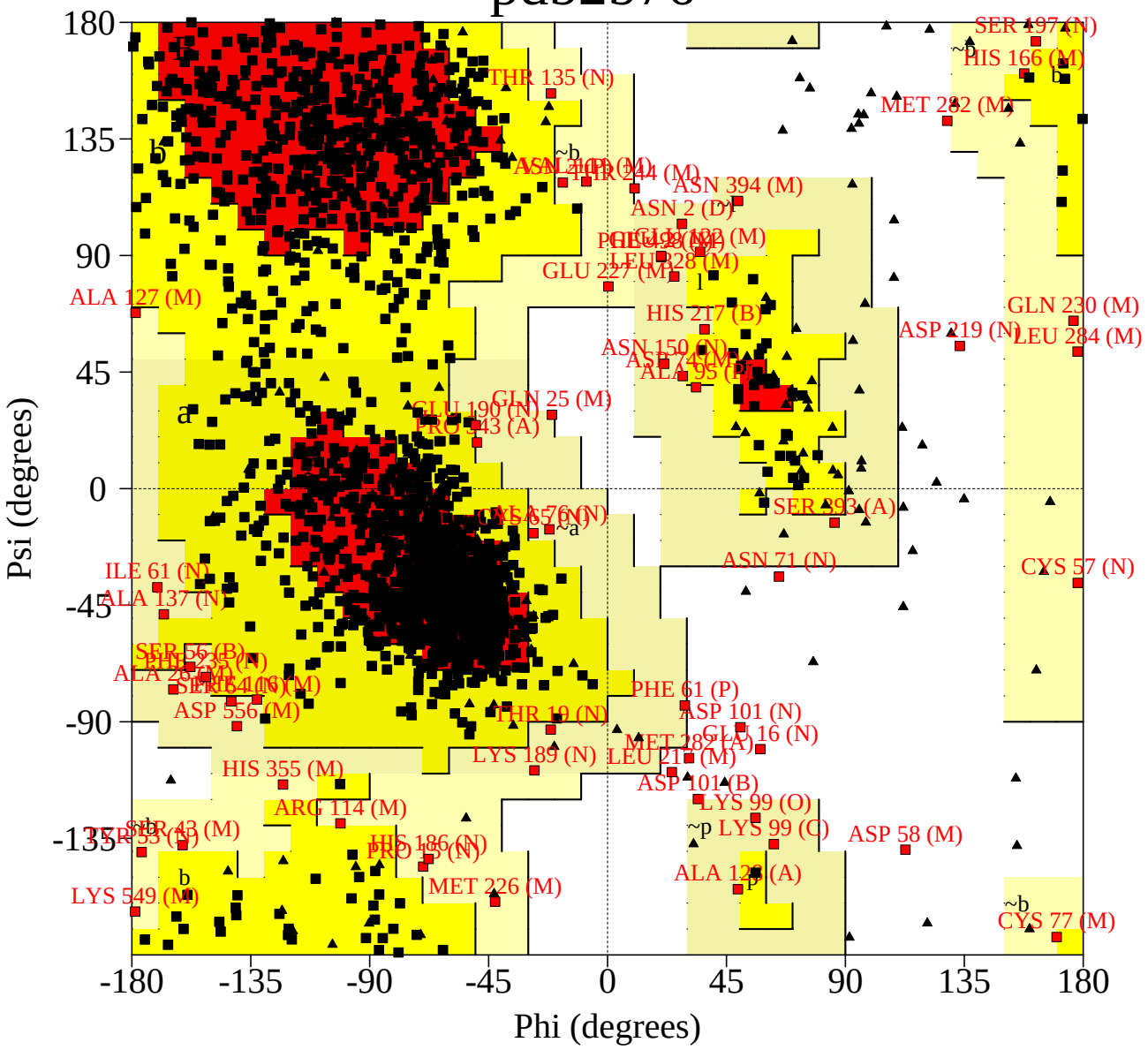
Ramachandran Plot

pdb2b76



Plot statistics

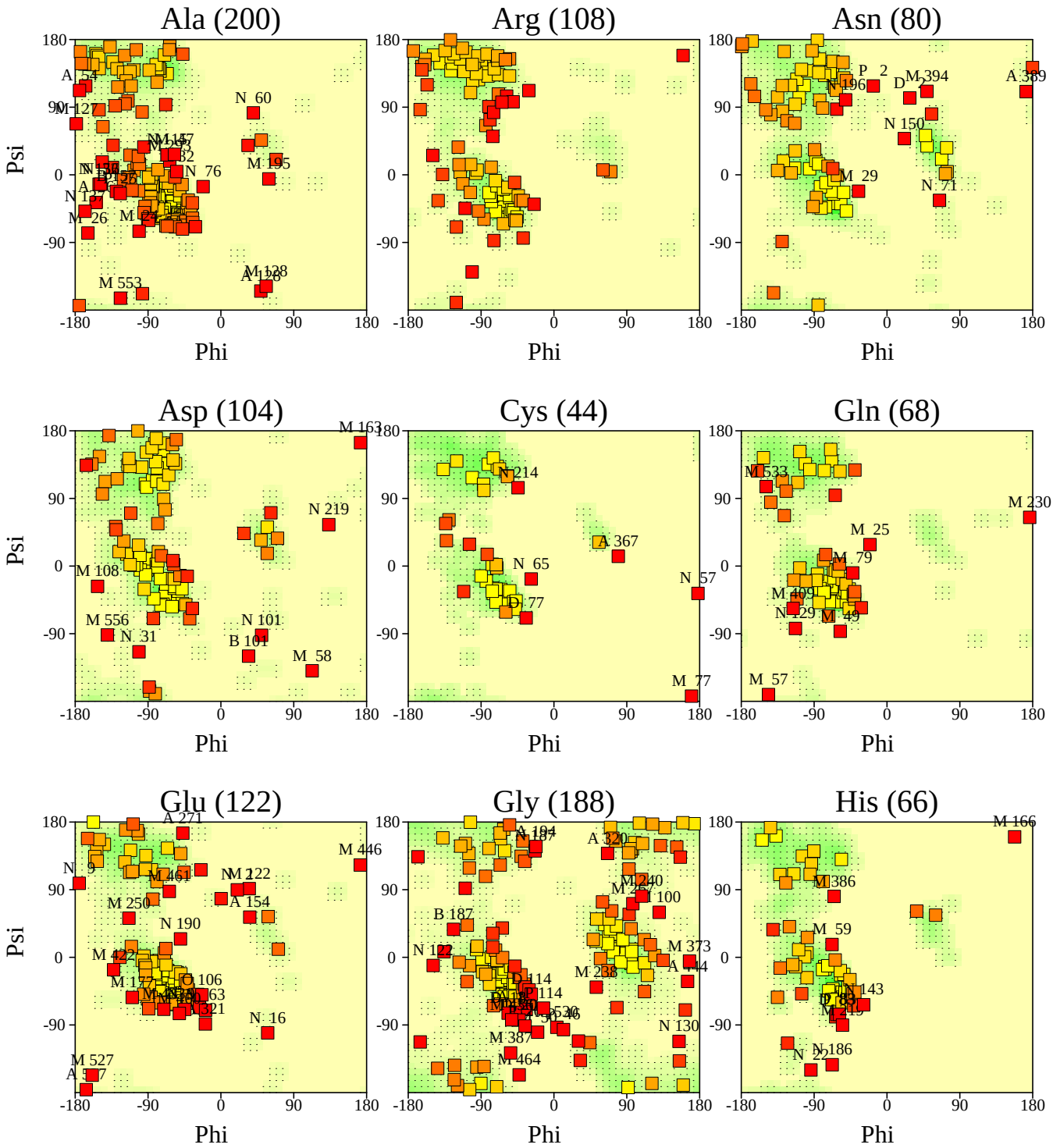
Residues in most favoured regions [A,B,L]	1347	73.8%
Residues in additional allowed regions [a,b,l,p]	421	23.1%
Residues in generously allowed regions [~a,~b,~l,~p]	47	2.6%
Residues in disallowed regions	10	0.5%
	----	------
Number of non-glycine and non-proline residues	1825	100.0%
Number of end-residues (excl. Gly and Pro)	16	
Number of glycine residues (shown as triangles)	188	
Number of proline residues	104	

Total number of residues	2133	

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

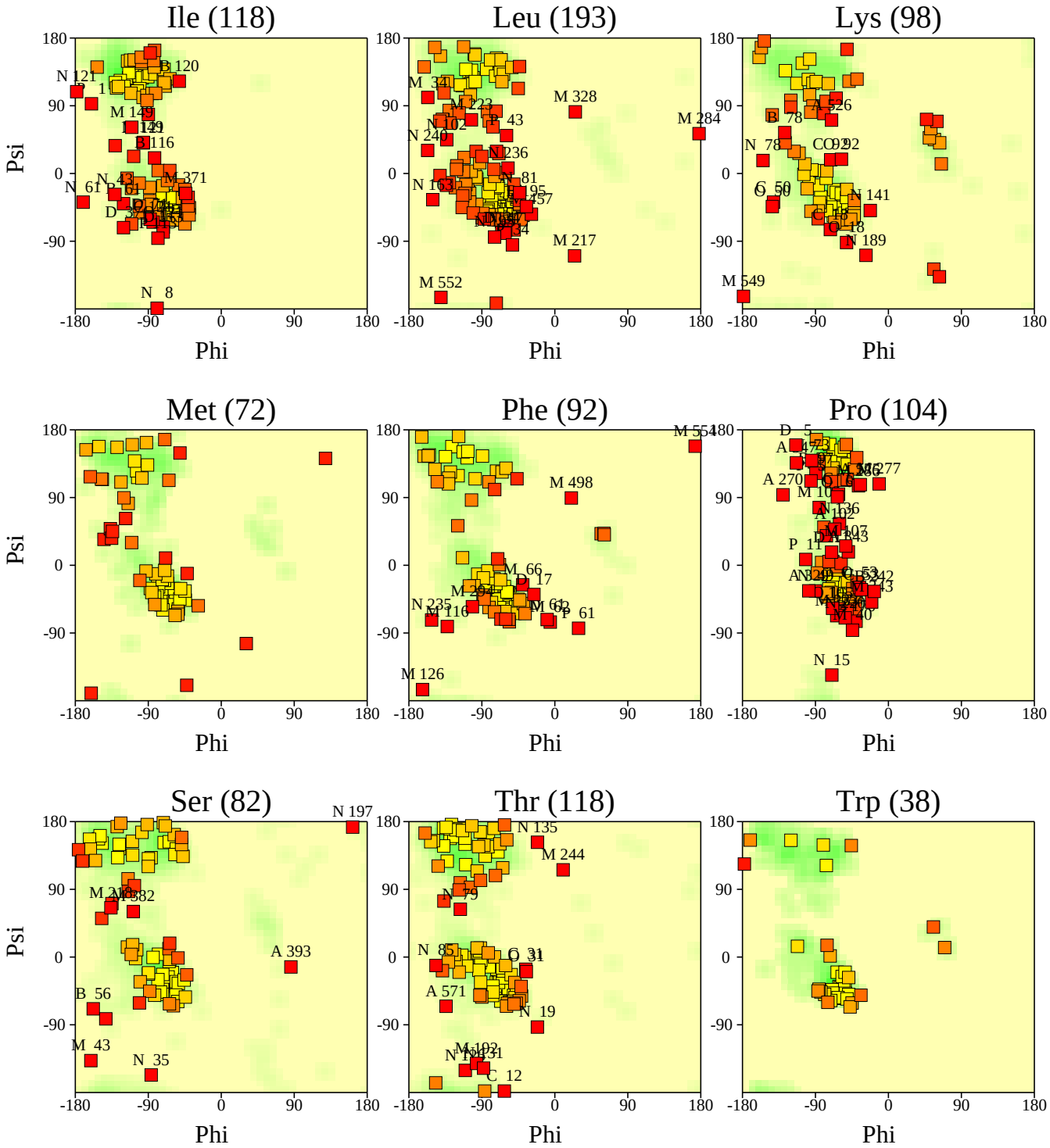
pdb2b76



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.

Ramachandran plots for all residue types

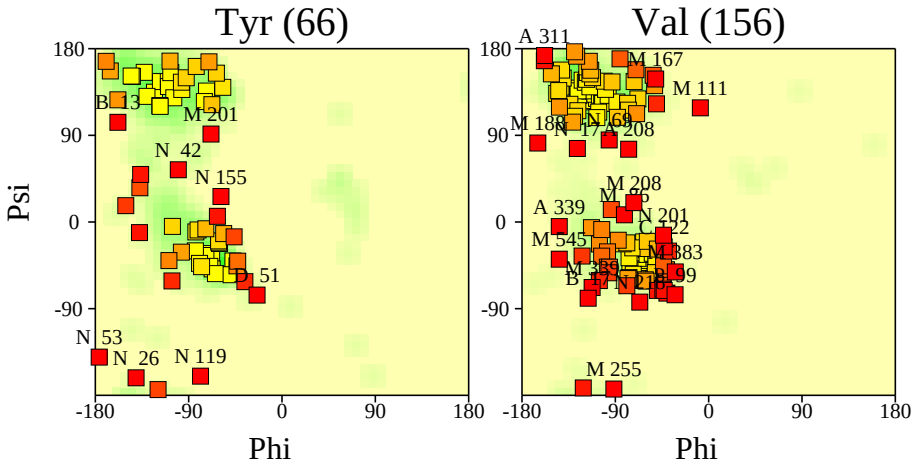
pdb2b76



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.

Ramachandran plots for all residue types

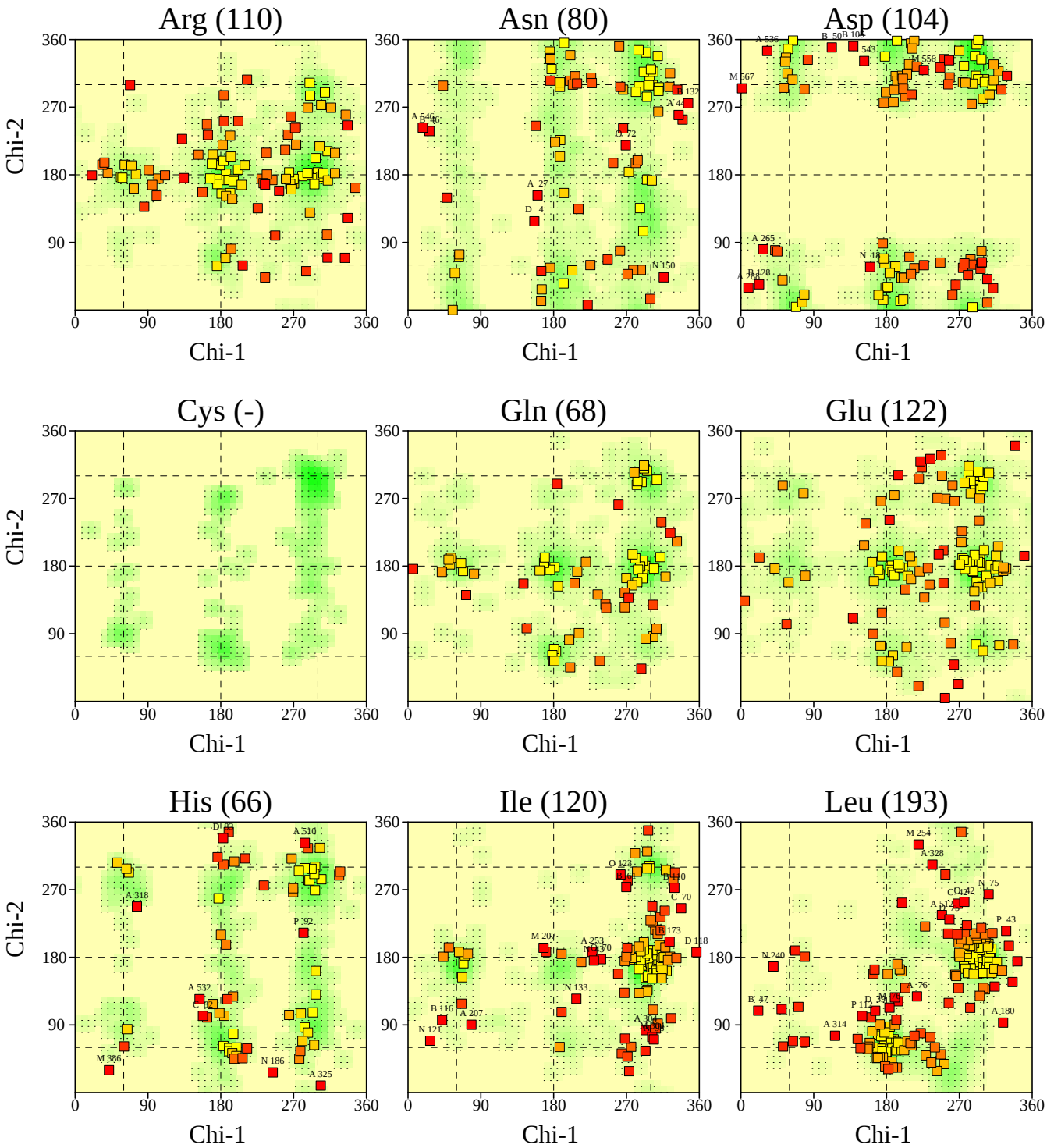
pdb2b76



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.

Chi1-Chi2 plots

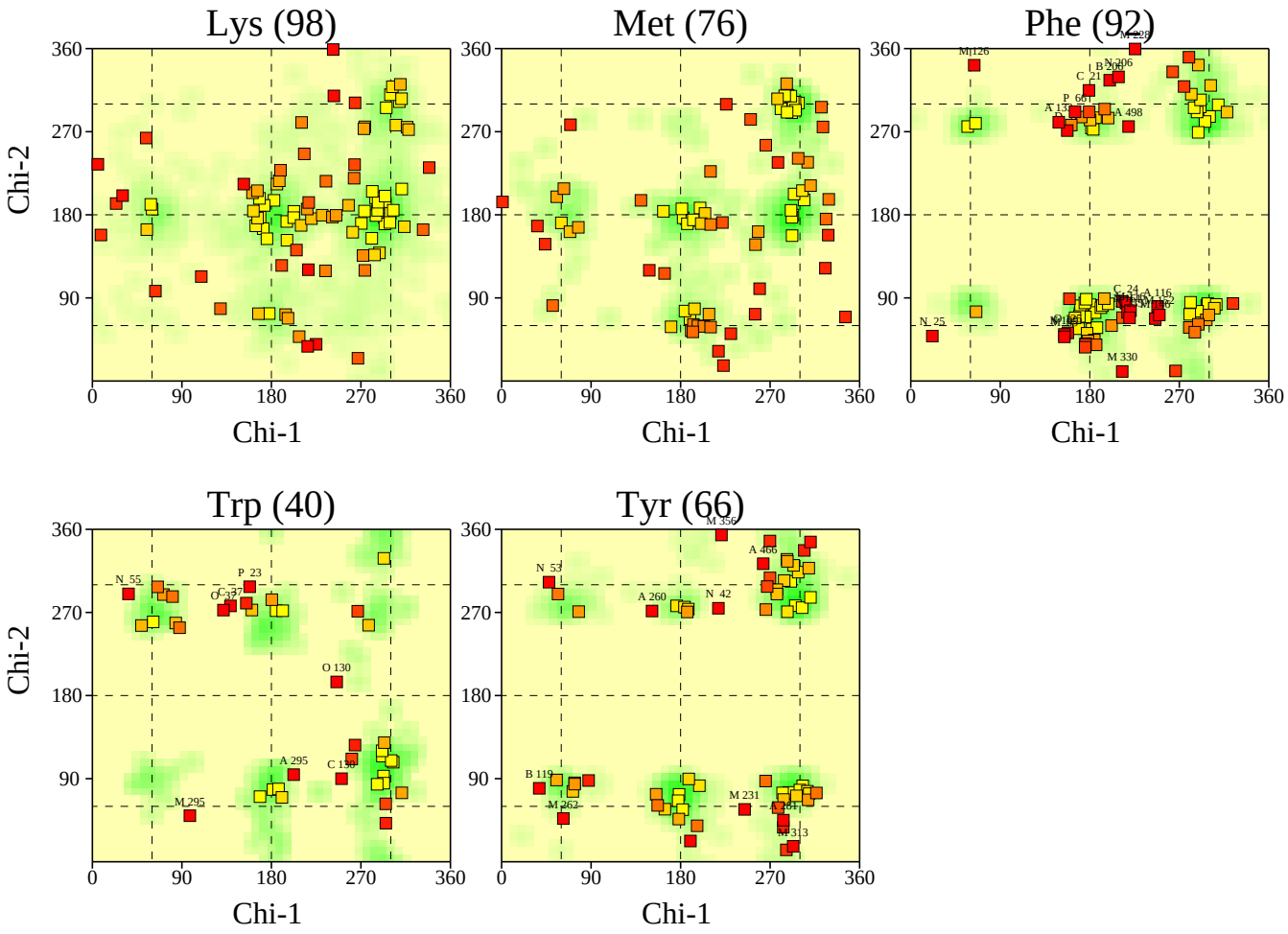
pdb2b76



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.

Chi1-Chi2 plots

pdb2b76

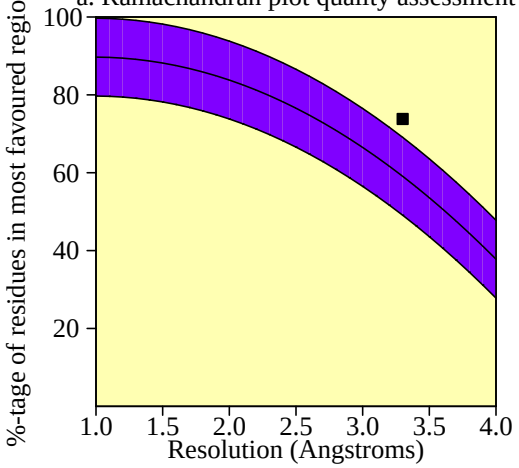


Numbers of residues are shown in brackets. Those in unfavourable conformations (score < -3.00) are labelled.
Shading shows favourable conformations as obtained from an analysis of 163 structures at resolution 2.0A or better.

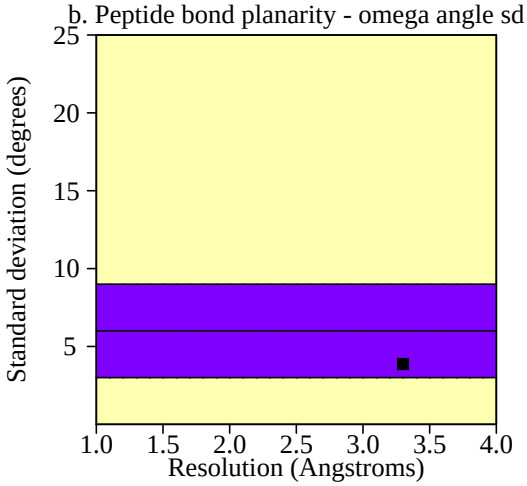
PROCHECK

Main-chain parameters
pdb2b76

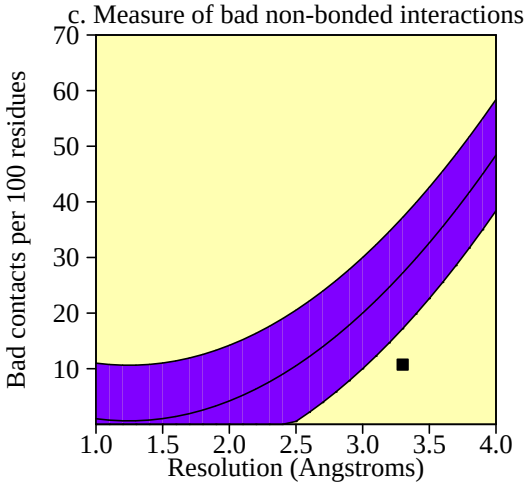
a. Ramachandran plot quality assessment



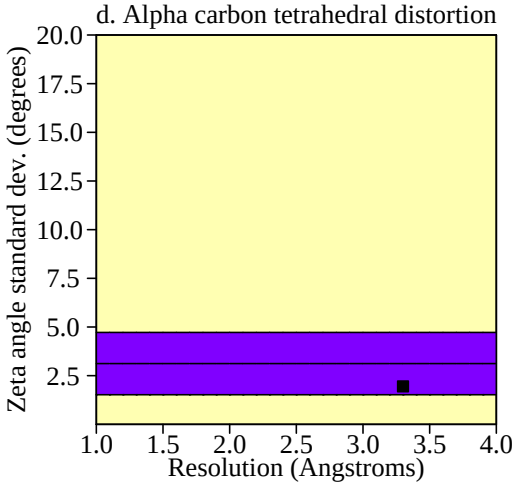
b. Peptide bond planarity - omega angle sd



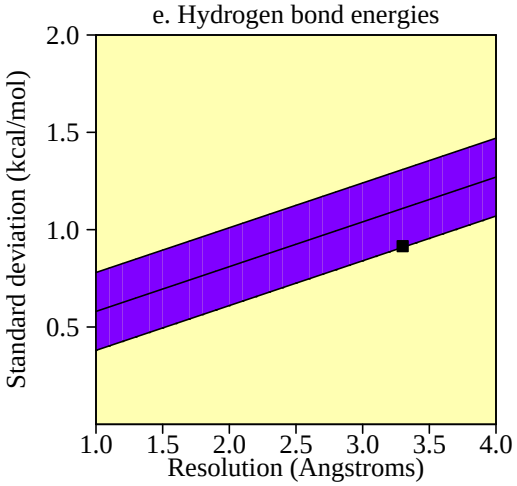
c. Measure of bad non-bonded interactions



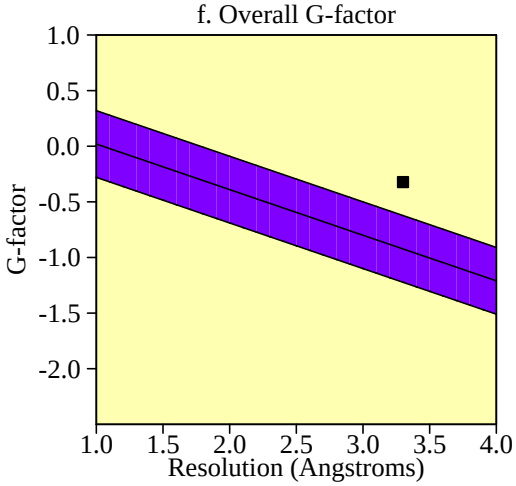
d. Alpha carbon tetrahedral distortion



e. Hydrogen bond energies



f. Overall G-factor



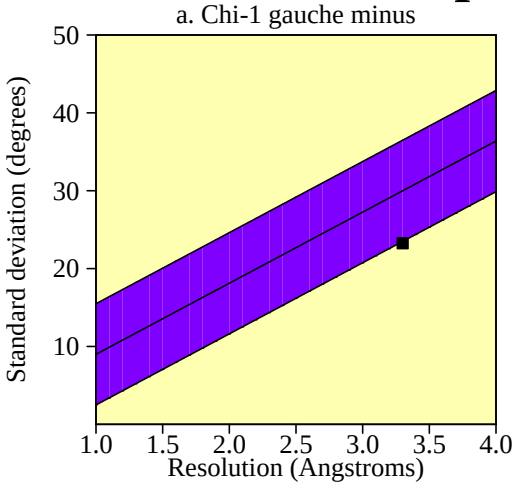
Plot statistics

Stereochemical parameter	No. of data pts	Parameter value	Comparison values: Typical value	Comparison values: Band width	No. of band widths from mean	
a. %-tage residues in A, B, L	1825	73.8	59.1	10.0	1.5	BETTER
b. Omega angle st dev	2125	3.9	6.0	3.0	-0.7	Inside
c. Bad contacts / 100 residues	229	10.7	27.2	10.0	-1.6	BETTER
d. Zeta angle st dev	1945	1.9	3.1	1.6	-0.7	Inside
e. H-bond energy st dev	1281	0.9	1.1	0.2	-1.0	Inside
f. Overall G-factor	2133	-0.3	-0.9	0.3	2.0	BETTER

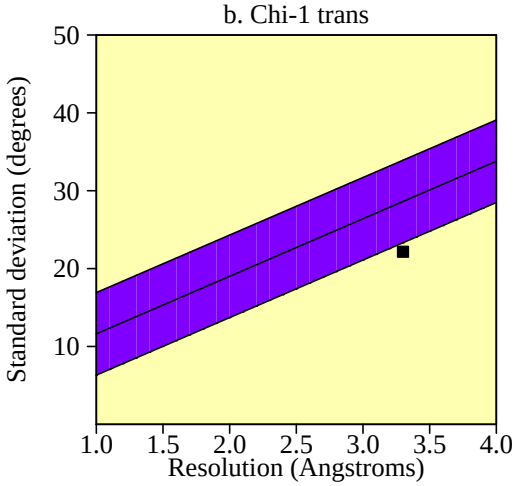
Side-chain parameters

pdb2b76

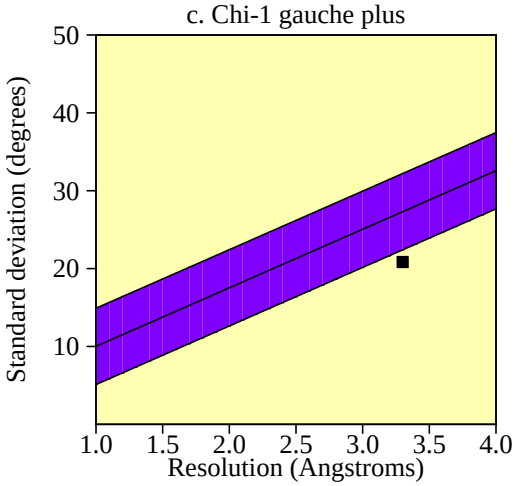
a. Chi-1 gauche minus



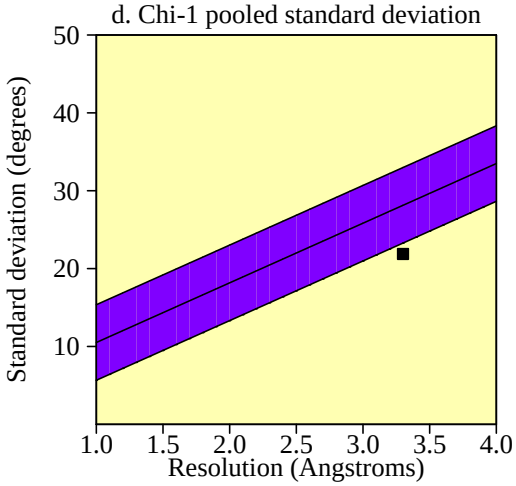
b. Chi-1 trans



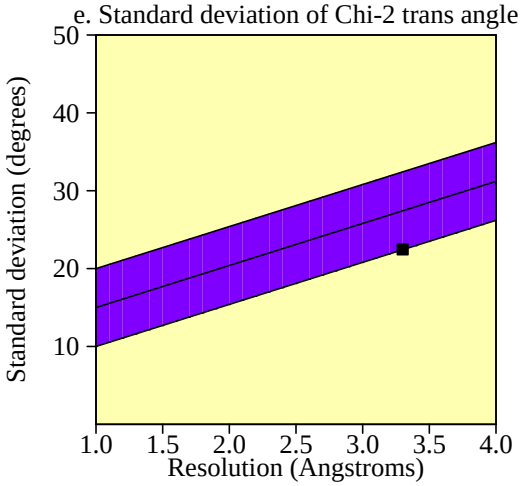
c. Chi-1 gauche plus



d. Chi-1 pooled standard deviation



e. Standard deviation of Chi-2 trans angle



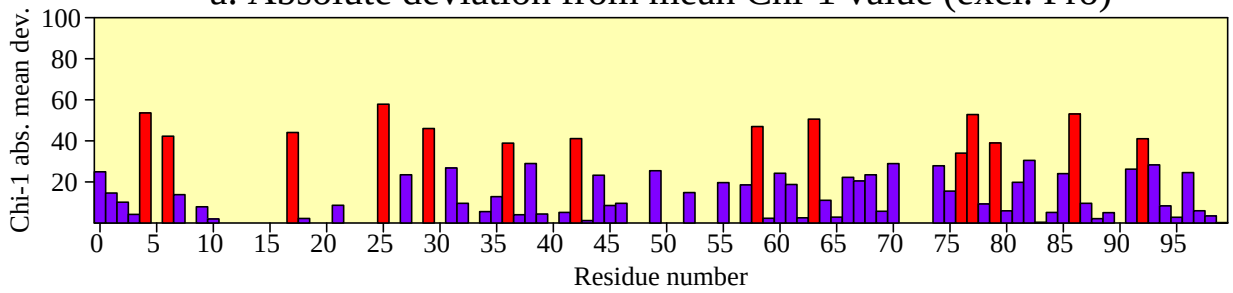
pdb2b76

Plot statistics

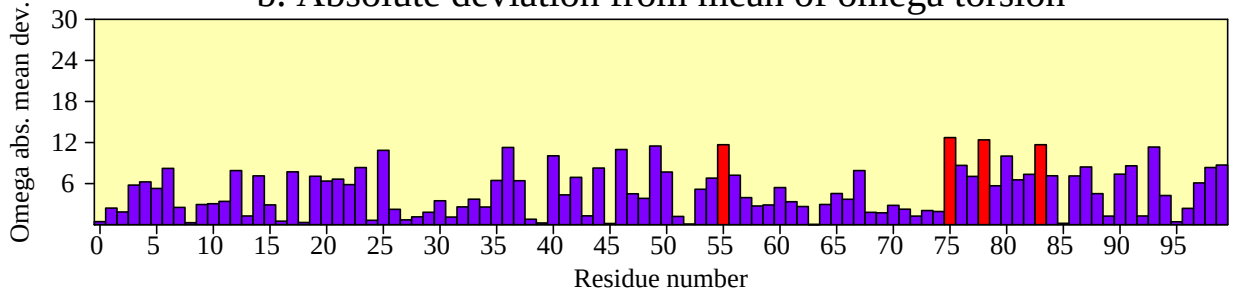
Stereochemical parameter	No. of data pts	Parameter value	Comparison values Typical value	Band width	No. of band widths from mean	
a. Chi-1 gauche minus st dev	251	23.3	30.0	6.5	-1.0	BETTER
b. Chi-1 trans st dev	614	22.2	28.6	5.3	-1.2	BETTER
c. Chi-1 gauche plus st dev	773	20.8	27.3	4.9	-1.3	BETTER
d. Chi-1 pooled st dev	1638	21.9	28.1	4.8	-1.3	BETTER
e. Chi-2 trans st dev	496	22.5	27.4	5.0	-1.0	Inside

Residue properties
pdb2b76

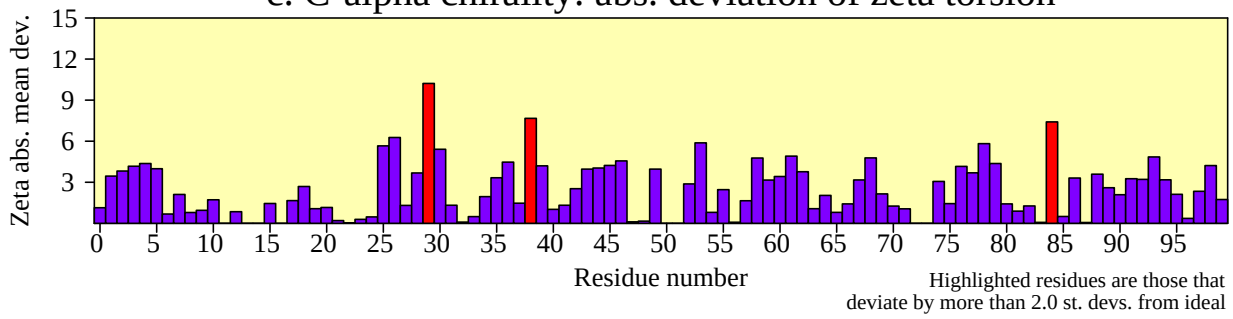
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion

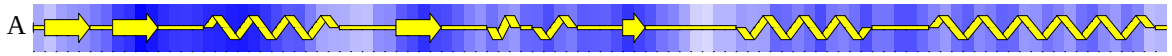


c. C-alpha chirality: abs. deviation of zeta torsion



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

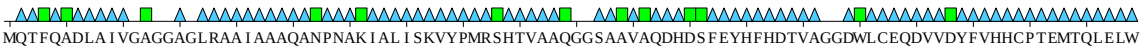
d. Secondary structure & estimated accessibility



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

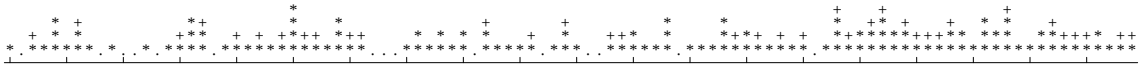
e. Sequence & Ramachandran regions

Most favoured Allowed Generous Disallowed

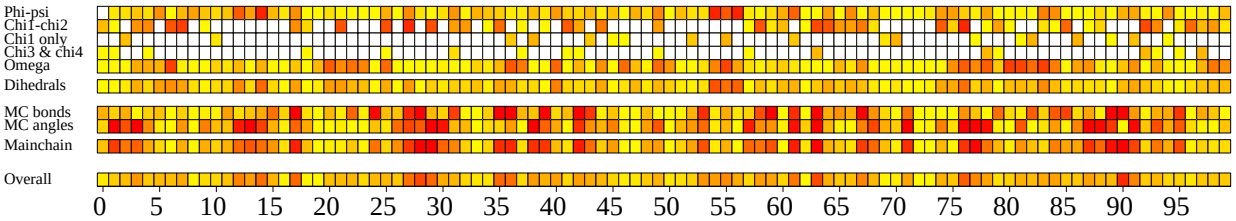


MQTFQADLAIVGAGGAGLRAAIAAAQANPNAKIALISKVYPMRSHTVAAQGGSAAVAQDHDSFEYHFHDTVAGGDWLCEQDVVDYFVHHCPTEMTQLELW

f. Max. deviation (see listing)

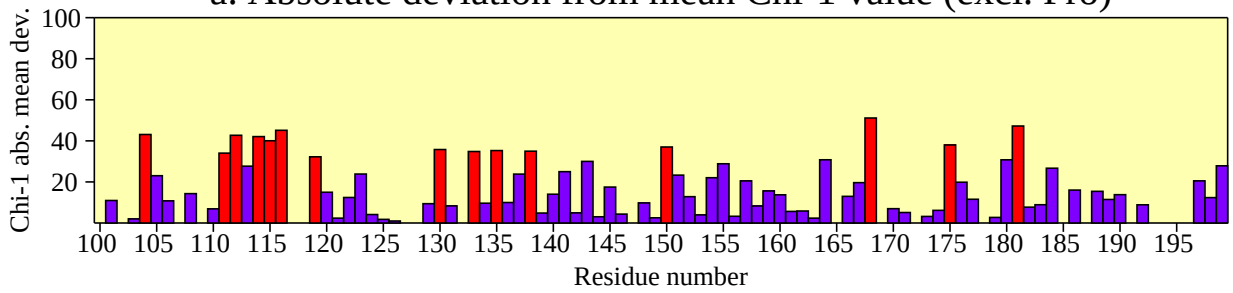


g. G-factors

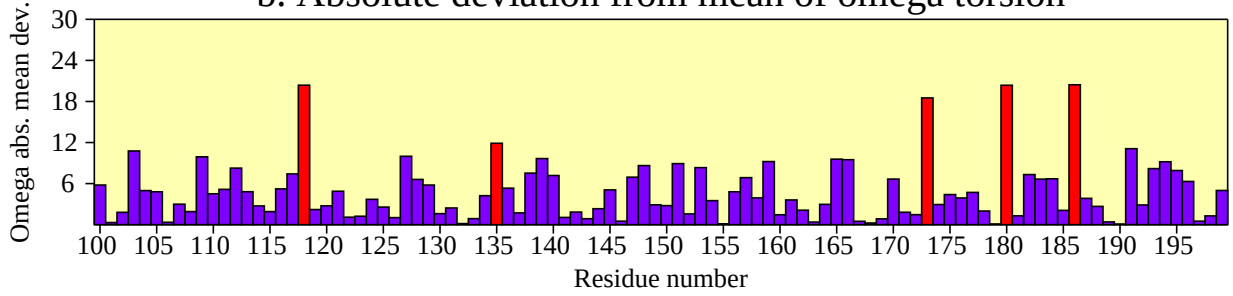


Residue properties
pdb2b76

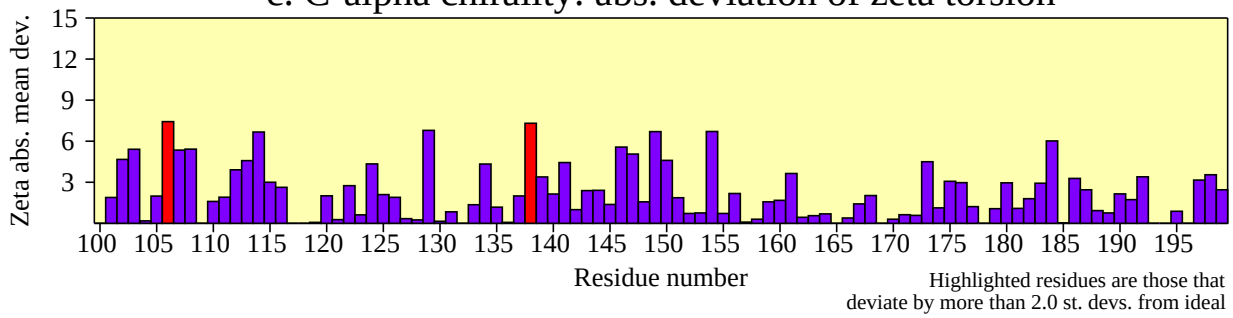
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion

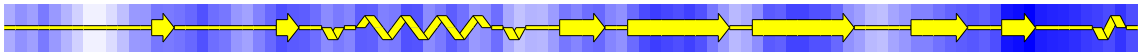


c. C-alpha chirality: abs. deviation of zeta torsion



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

d. Secondary structure & estimated accessibility



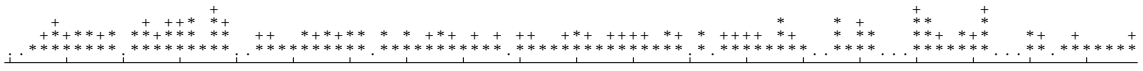
Key:- Helix Beta strand Random coil Accessibility shading: Buried Accessible

e. Sequence & Ramachandran regions

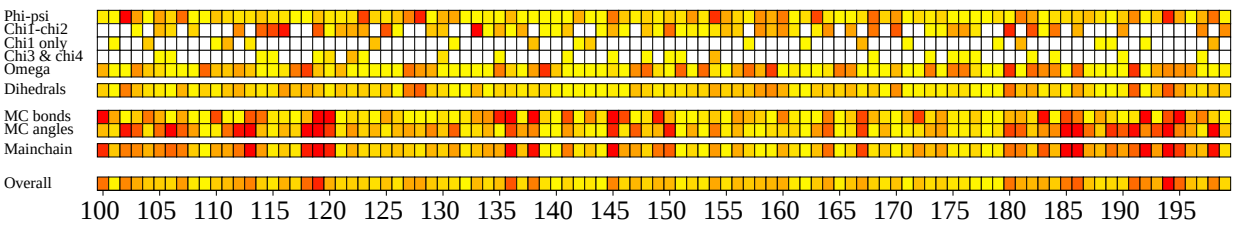
Most favoured Allowed Generous Disallowed

GCPWSRRPDGSVNVRRFGGMKIERTWFAADKTGFHMLHTLFQTSLQFPQIQRFDEHFVLDILVDDGHVRGLVAMNMMEGTLVQIRANAVVMATGGAGRVY

f. Max. deviation (see listing)

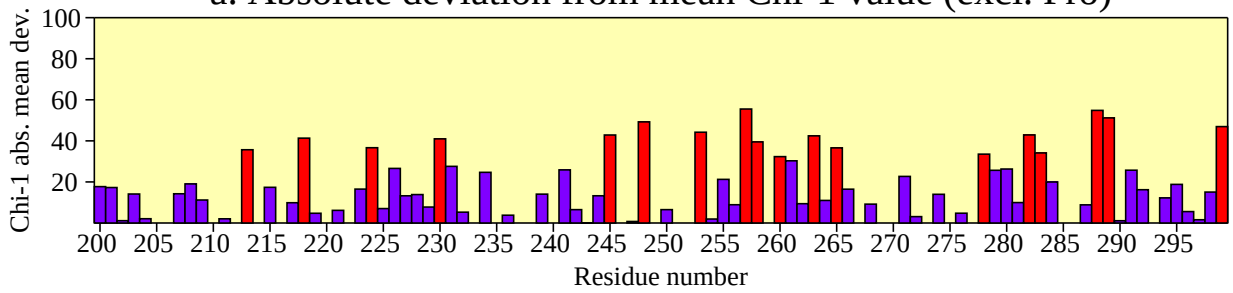


g. G-factors

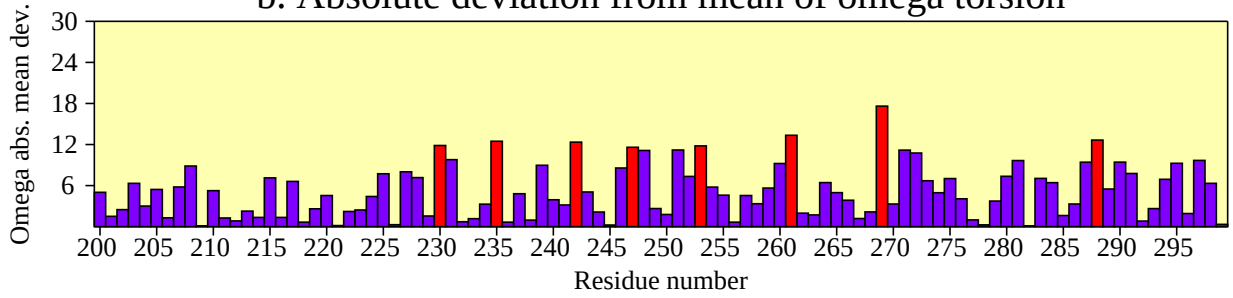


Residue properties
pdb2b76

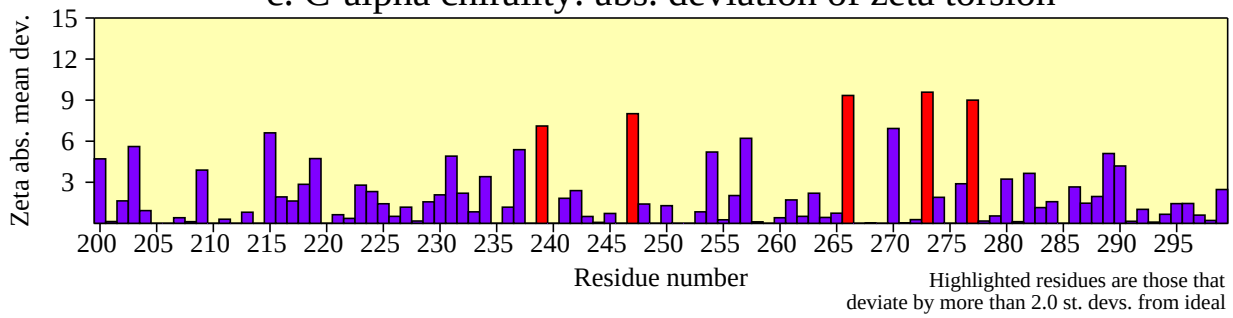
a. Absolute deviation from mean Chi-1 value (excl. Pro)



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

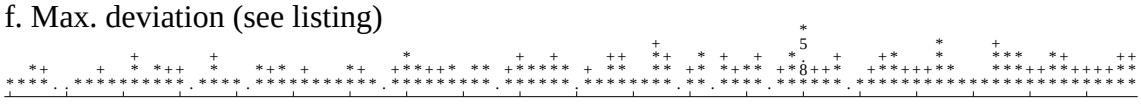
Key:- Helix Beta strand Random coil Accessibility shading: Buried Accessible

e. Sequence & Ramachandran regions

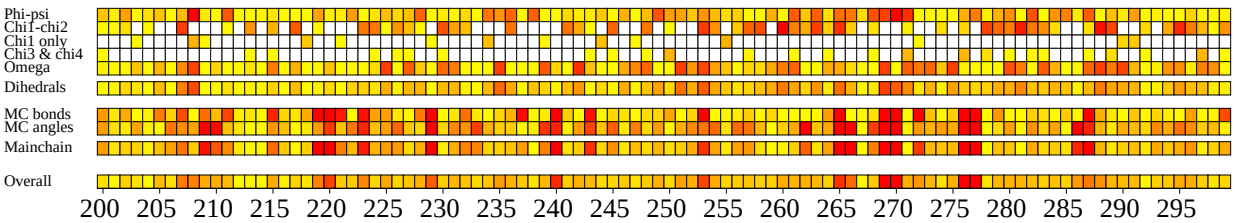
Most favoured Allowed Generous Disallowed

RYNTNGGIVTGDGMGMALSHGVPLRDMEFVQYHPTGLPGSGILMTEGCRGEGGILVNKNGYRYLQDYGMGPETPLGEPKNKYMELGPRDKVSQAFWHEWR

f. Max. deviation (see listing)

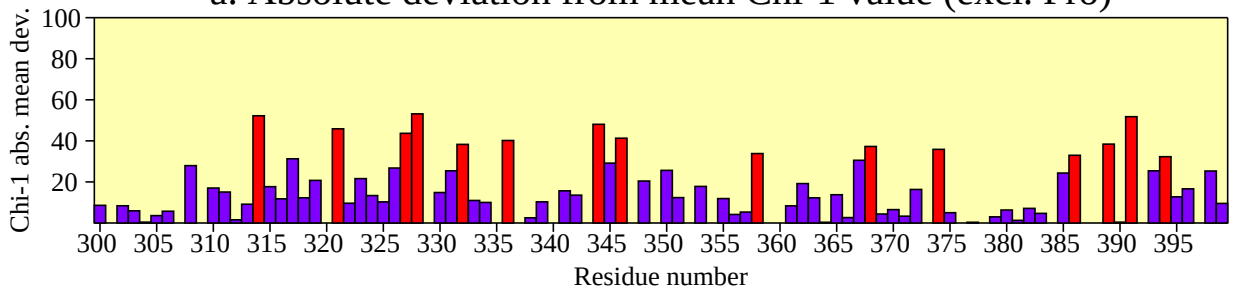


g. G-factors

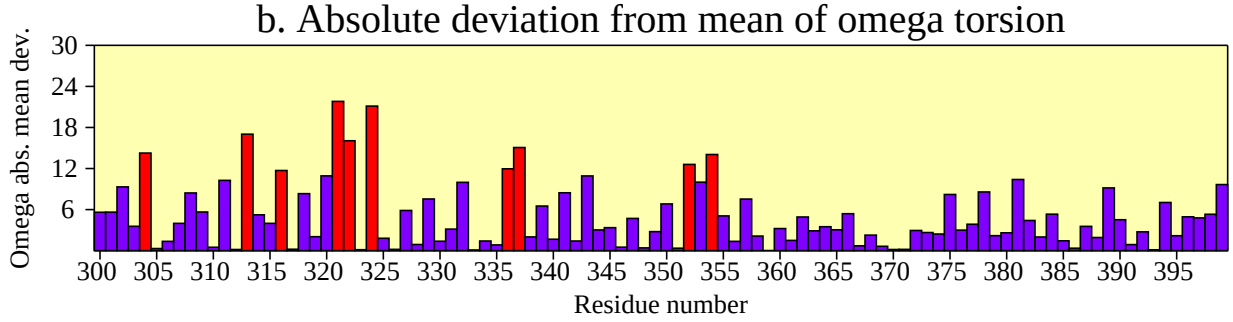


Residue properties
pdb2b76

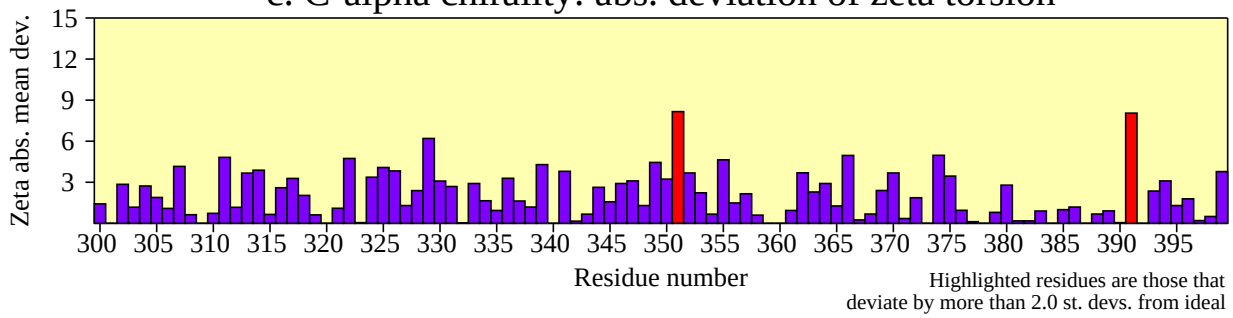
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion

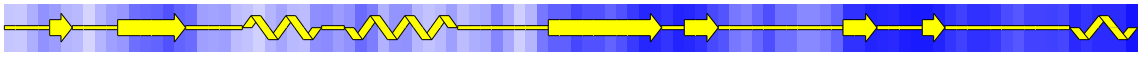


c. C-alpha chirality: abs. deviation of zeta torsion



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

d. Secondary structure & estimated accessibility



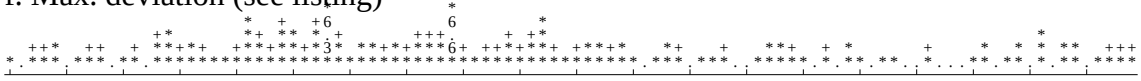
Key:- Helix Beta strand Random coil Accessibility shading: Buried Accessible

e. Sequence & Ramachandran regions

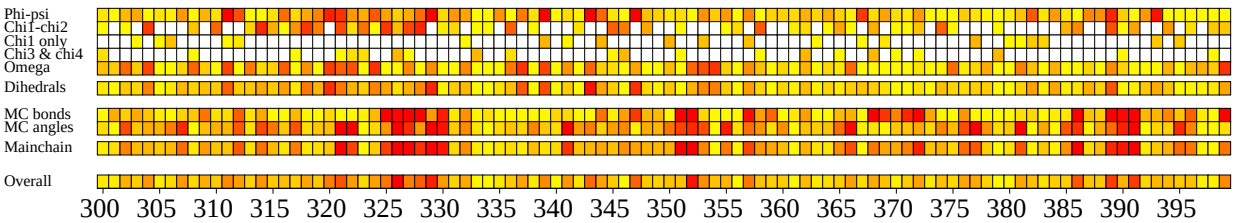
Most favoured Allowed Generous Disallowed

KGNTISTPRGDVVYLDLRHLGEKKLHERLPFICELAKAYVGVDPVKEPIPVRPTAHYTMGGIETDQNCETRIKGLFAVGECSSVGLHGANRLGSNSLAELL

f. Max. deviation (see listing)

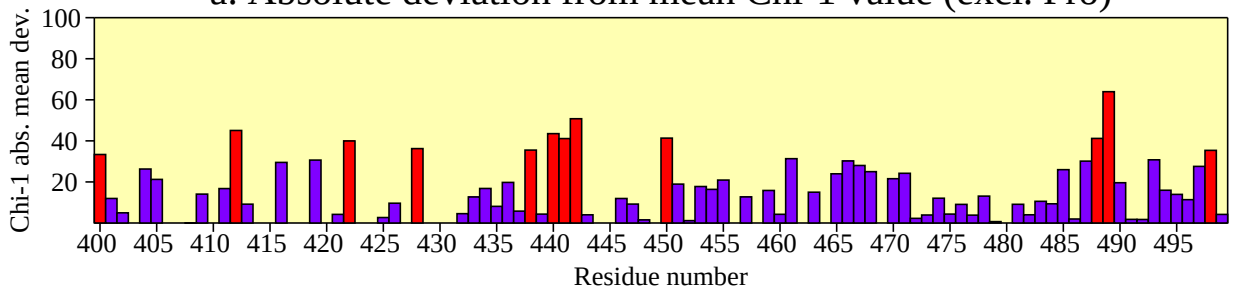


g. G-factors

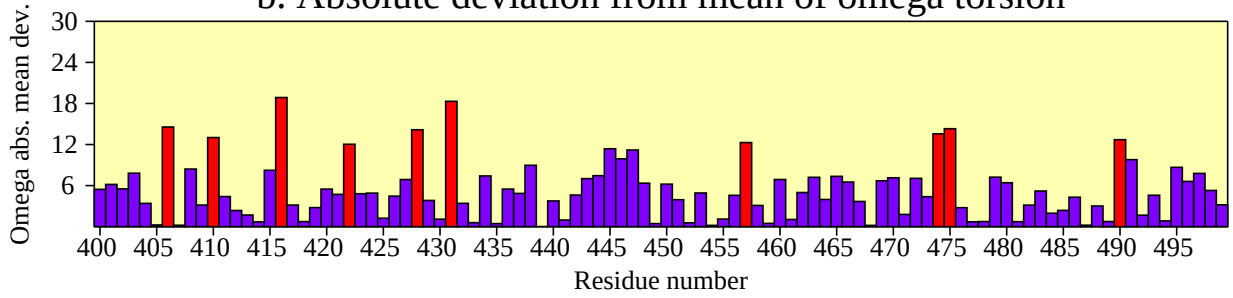


Residue properties
pdb2b76

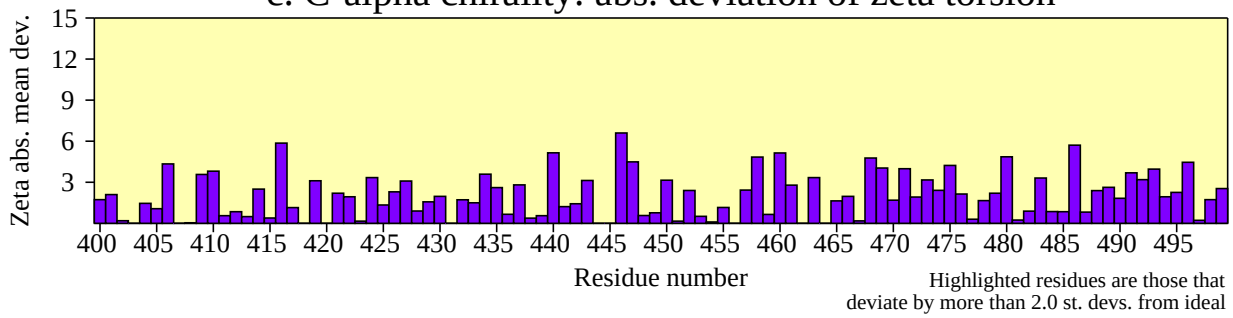
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion



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

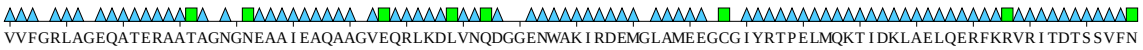


Highlighted residues are those that deviate by more than 2.0 st. devs. from ideal

d. Secondary structure & estimated accessibility

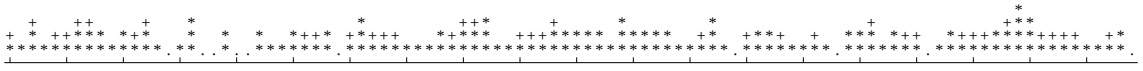
Key:- Helix Beta strand Random coil Accessibility shading: Buried Accessible

e. Sequence & Ramachandran regions Most favoured Allowed Generous Disallowed

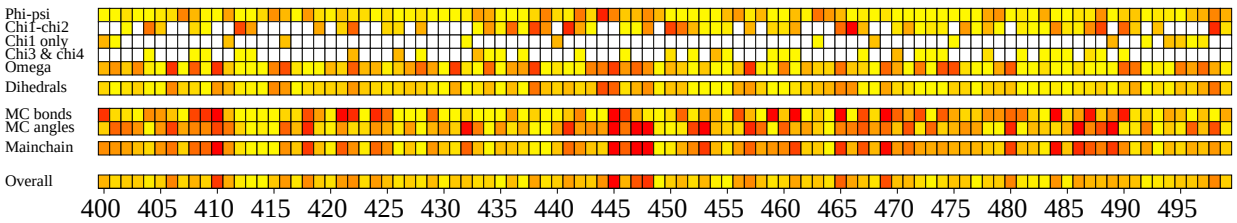


VVFGRLAGEQATERAATAGNGNEAAIEAQAAGVEQRLKDLVNQDGGENWAKIRDEMGLAMEEGCGIYRTPELMQKTIDKLAELQERFKRVRITDTSSVFN

f. Max. deviation (see listing)

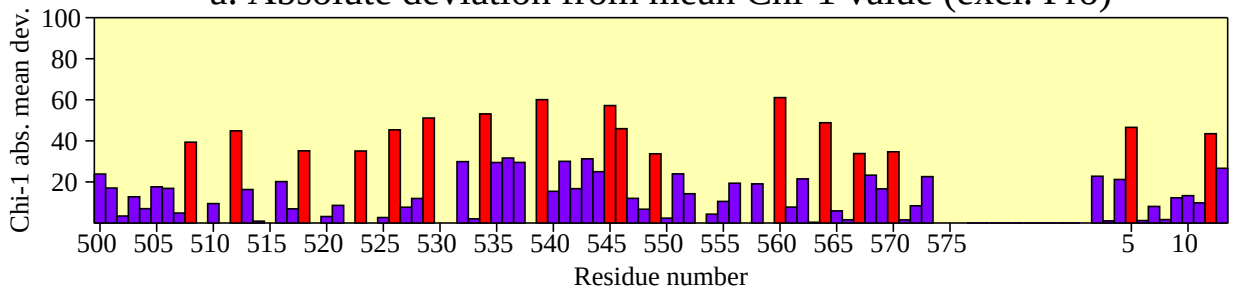


g. G-factors

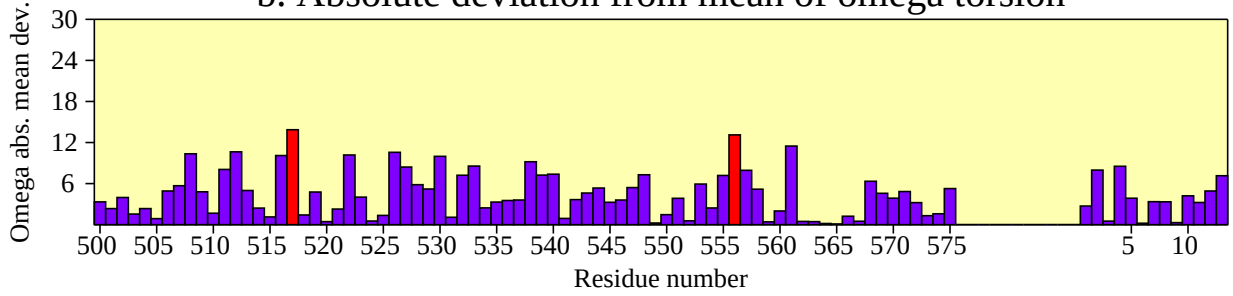


Residue properties
pdb2b76

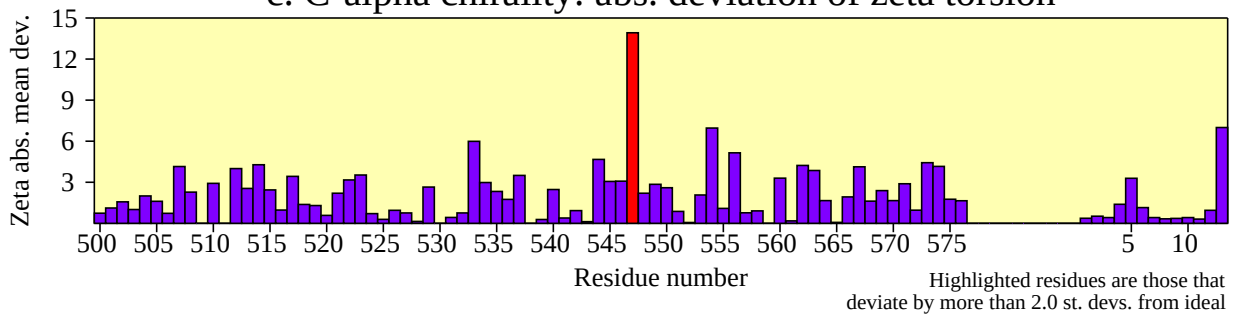
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion

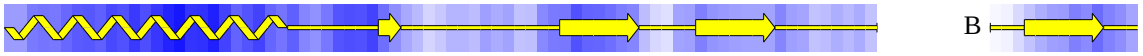


c. C-alpha chirality: abs. deviation of zeta torsion



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

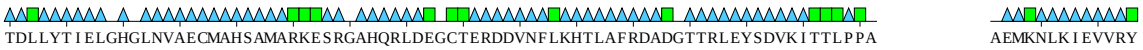
d. Secondary structure & estimated accessibility



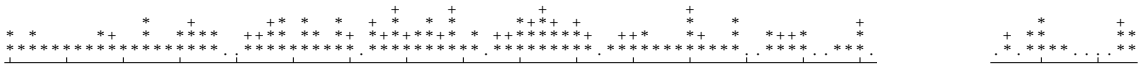
Key:- Helix Beta strand Random coil Accessibility shading: Buried Accessible

e. Sequence & Ramachandran regions

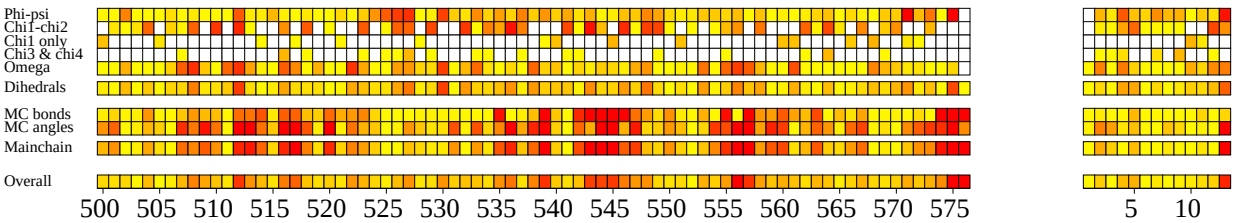
Most favoured Allowed Generous Disallowed



f. Max. deviation (see listing)

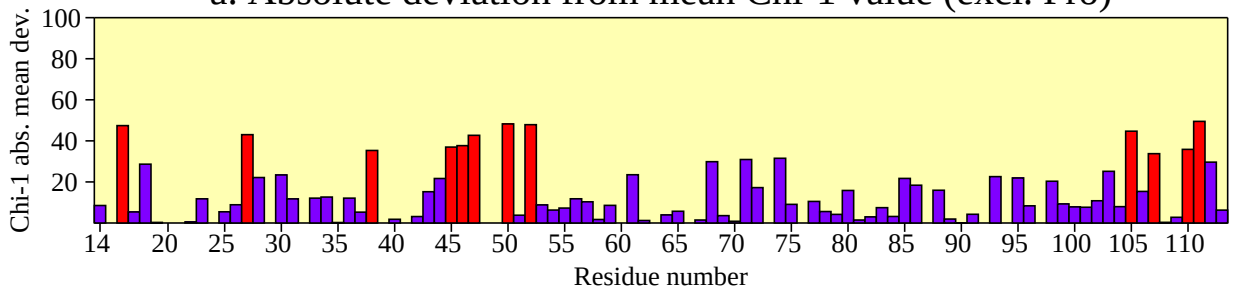


g. G-factors

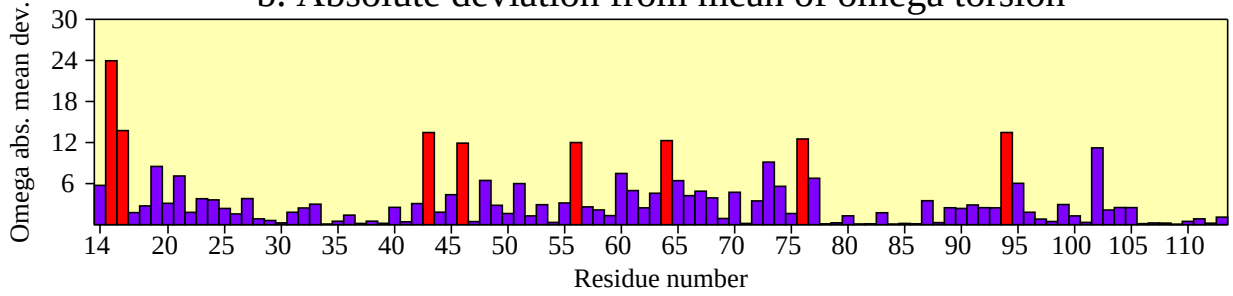


Residue properties
pdb2b76

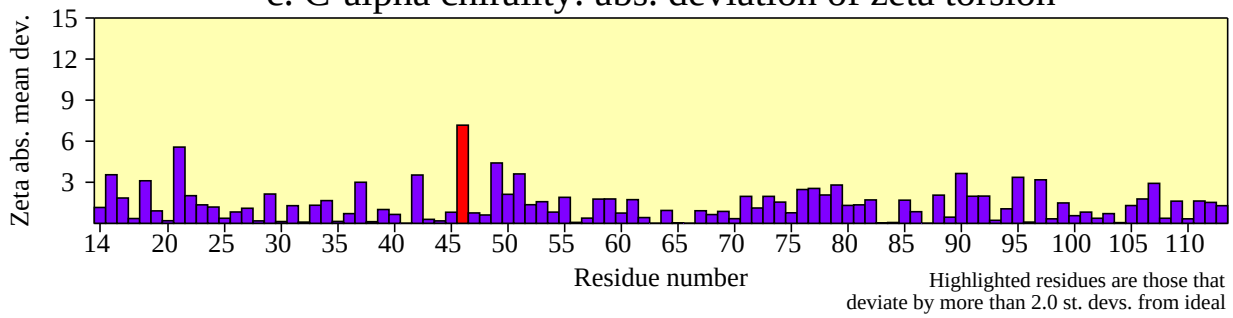
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion

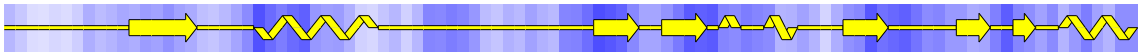


c. C-alpha chirality: abs. deviation of zeta torsion



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

d. Secondary structure & estimated accessibility



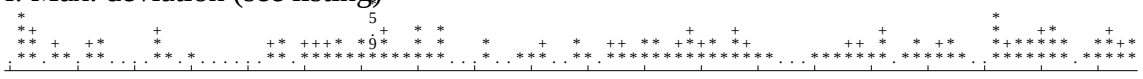
Key:- Helix Beta strand Random coil Accessibility shading: Buried Accessible

e. Sequence & Ramachandran regions

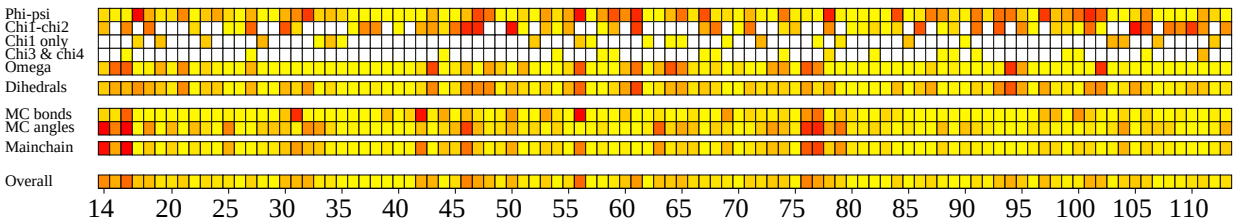
Most favoured Allowed Generous Disallowed

NPEVDTAPHSAFYEVPYDATTSLLDALGYIKDNLAPDLSYRWSCRMAICGSCGMMVNNVPKLACKTFLRDYTDGMKVEALANFPIERDLVVDMTHFIESL

f. Max. deviation (see listing)

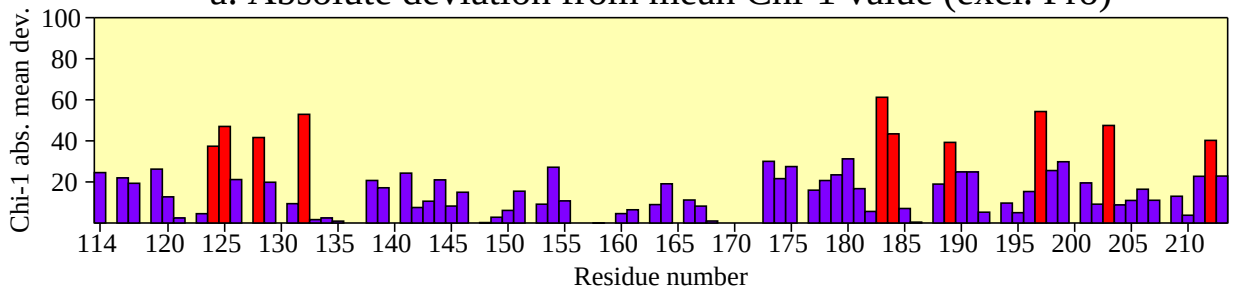


g. G-factors

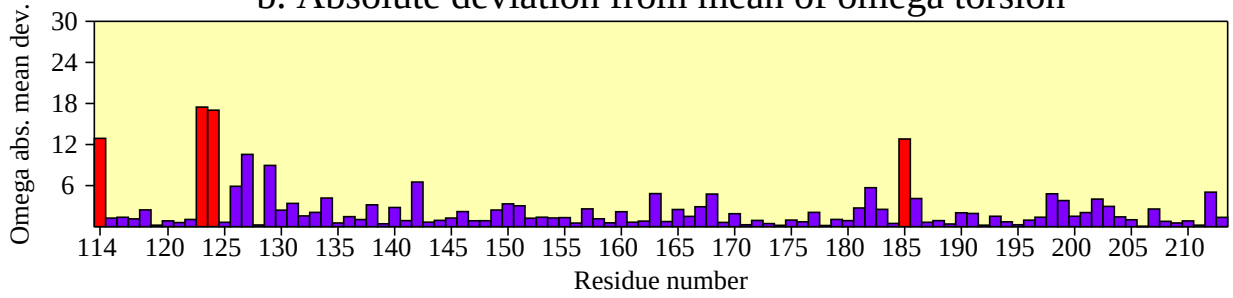


Residue properties
pdb2b76

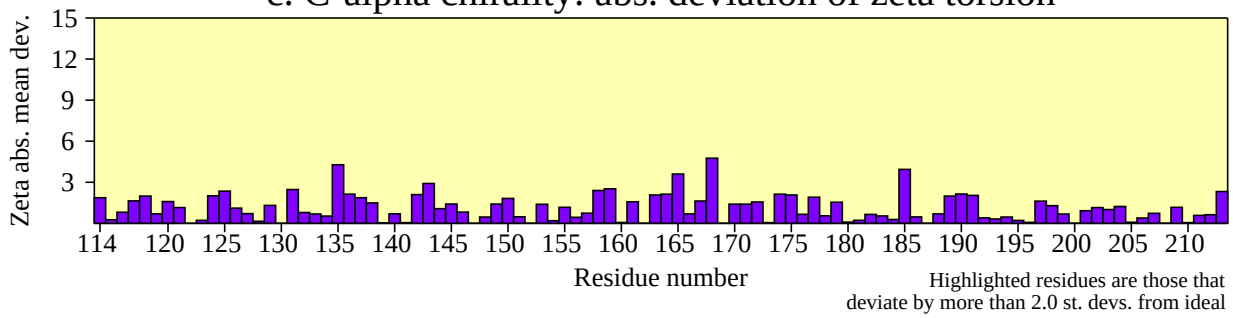
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion

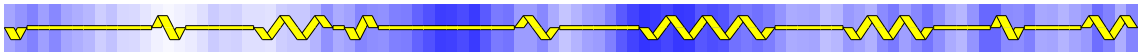


c. C-alpha chirality: abs. deviation of zeta torsion



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

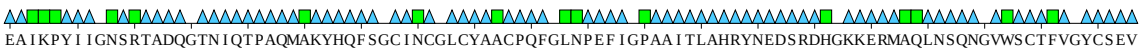
d. Secondary structure & estimated accessibility



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

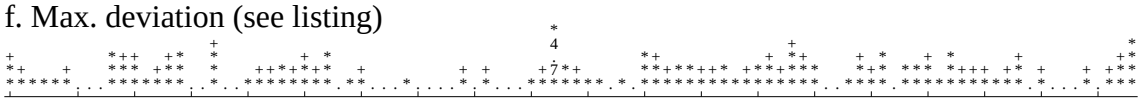
e. Sequence & Ramachandran regions

Most favoured Allowed Generous Disallowed

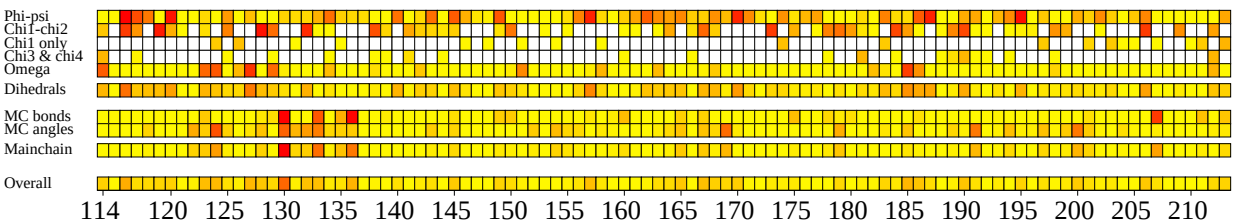


EA I KPY I I GNSRTADQGTN I QT PAQMAKYHQF SGC I NCGLCYAACPQFGLNPEF I GPAA I TLAHRYNEDSRDHGKKERMAQLNSQNGVWSCTFVGYCSEV

f. Max. deviation (see listing)

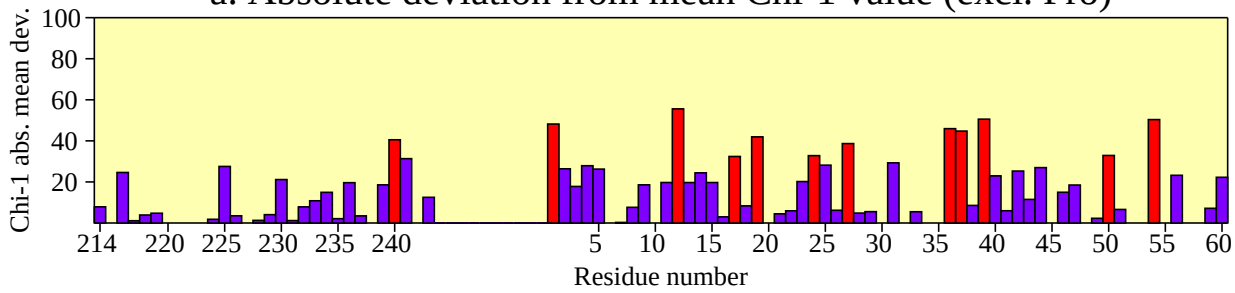


g. G-factors

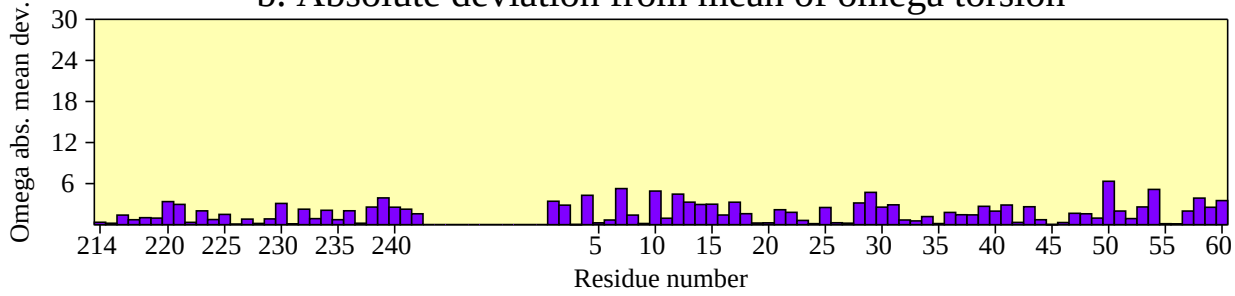


Residue properties
pdb2b76

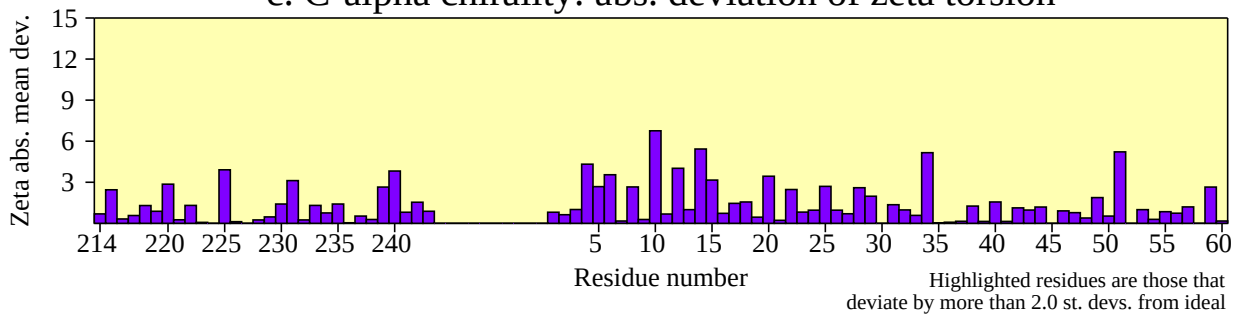
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion

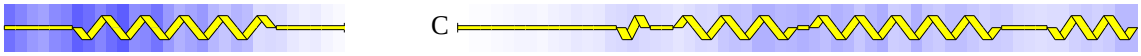


c. C-alpha chirality: abs. deviation of zeta torsion



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

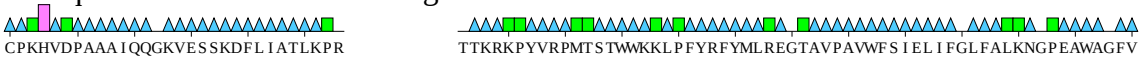
d. Secondary structure & estimated accessibility



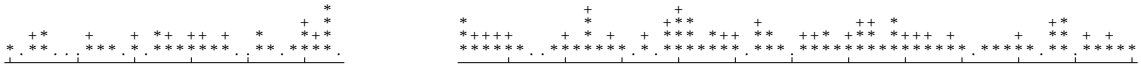
Key:- Helix Beta strand Random coil Accessibility shading: Buried Accessible

e. Sequence & Ramachandran regions

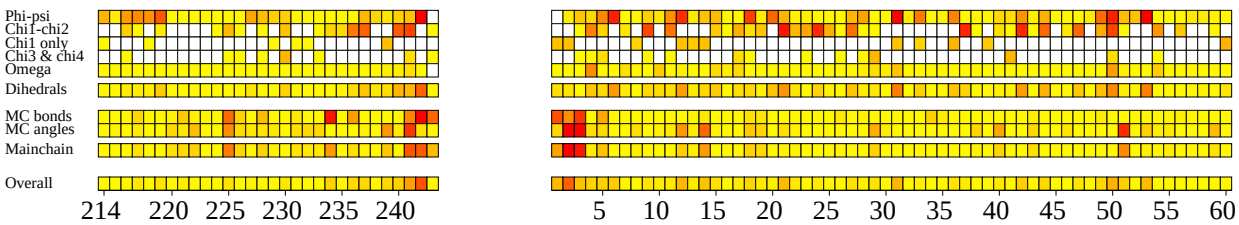
Most favoured Allowed Generous Disallowed



f. Max. deviation (see listing)

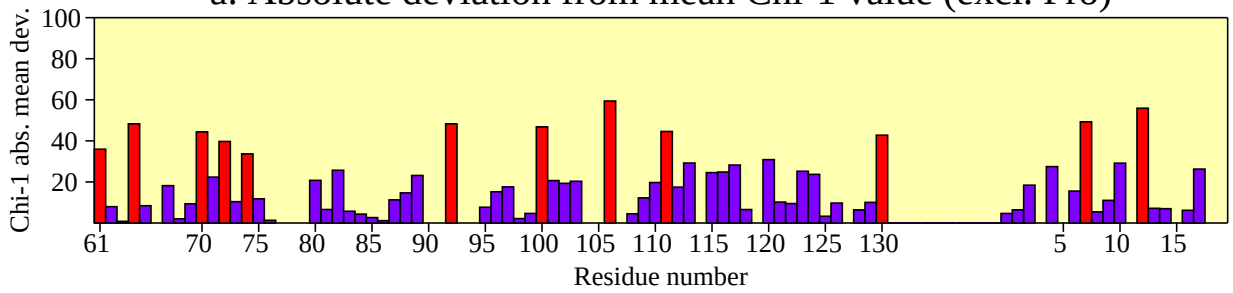


g. G-factors

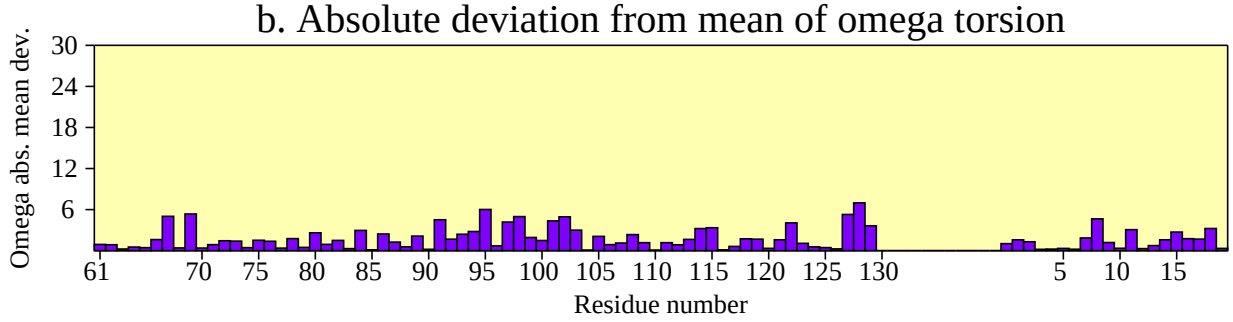


Residue properties
pdb2b76

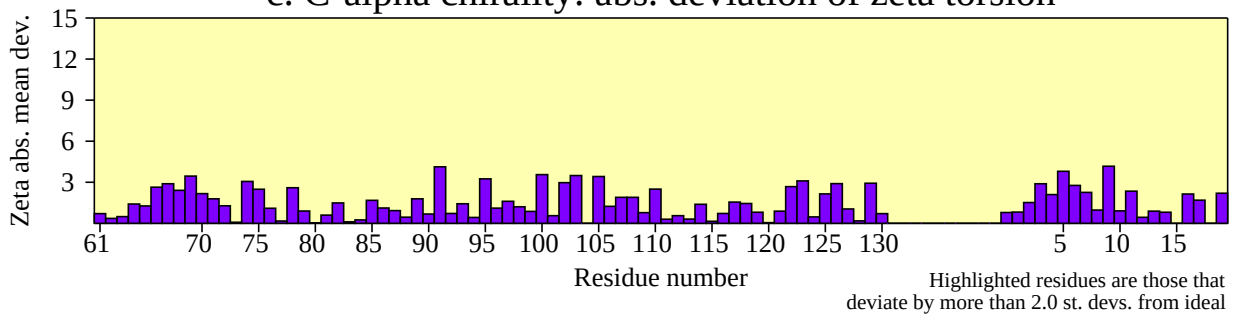
a. Absolute deviation from mean Chi-1 value (excl. Pro)



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

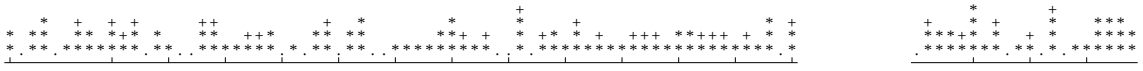
d. Secondary structure & estimated accessibility

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

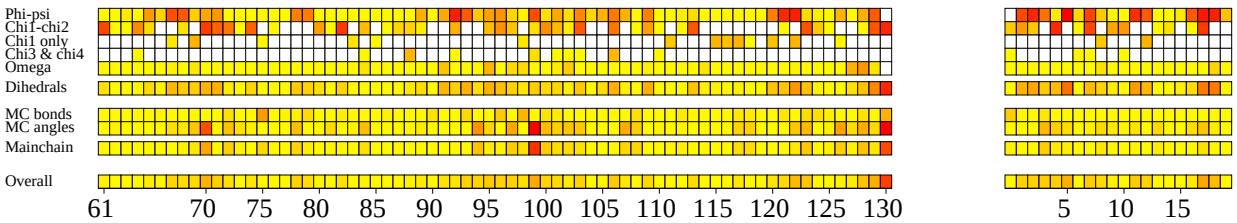
e. Sequence & Ramachandran regions

Most favoured Allowed Generous Disallowed

f. Max. deviation (see listing)

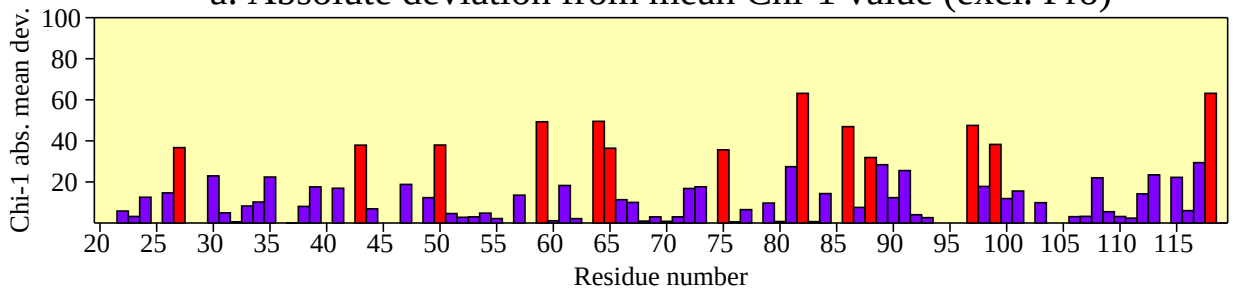


g. G-factors

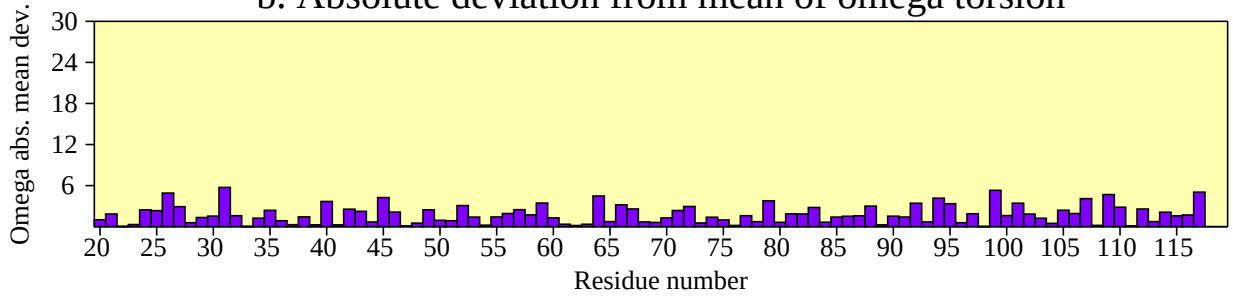


Residue properties
pdb2b76

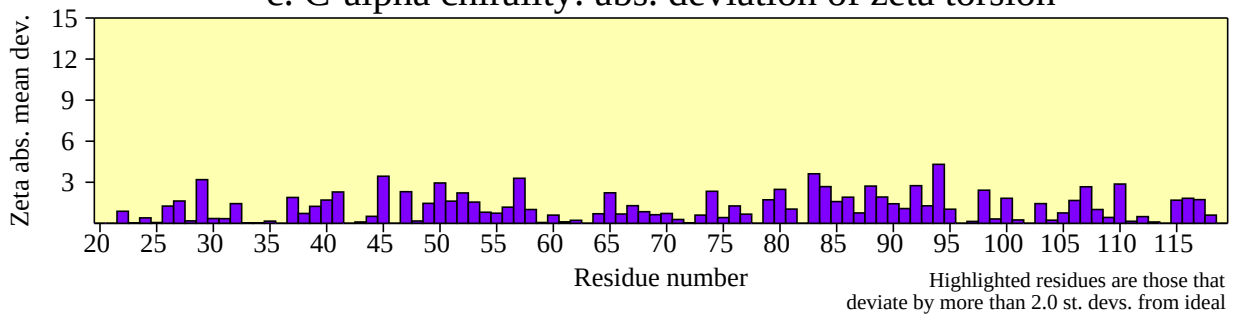
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion



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

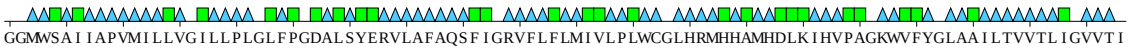


Highlighted residues are those that deviate by more than 2.0 st. devs. from ideal

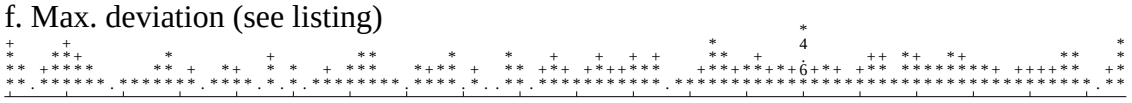
d. Secondary structure & estimated accessibility

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

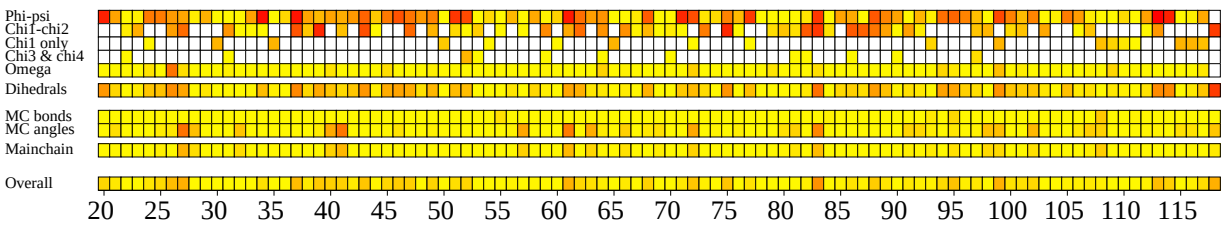
e. Sequence & Ramachandran regions Most favoured Allowed Generous Disallowed



f. Max. deviation (see listing)

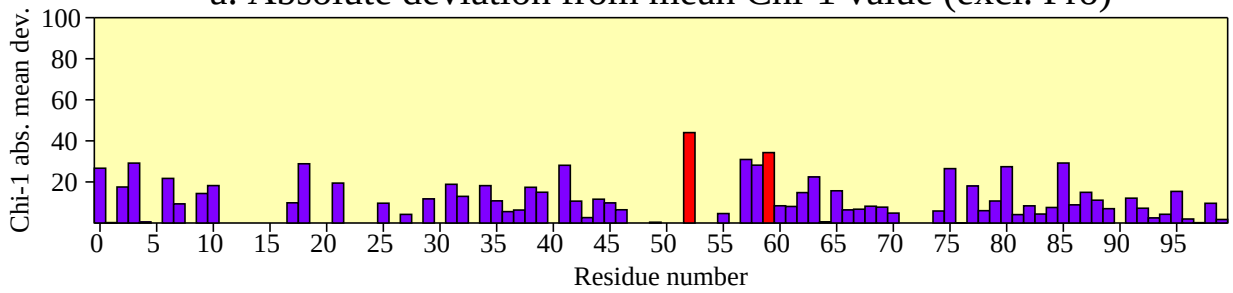


g. G-factors

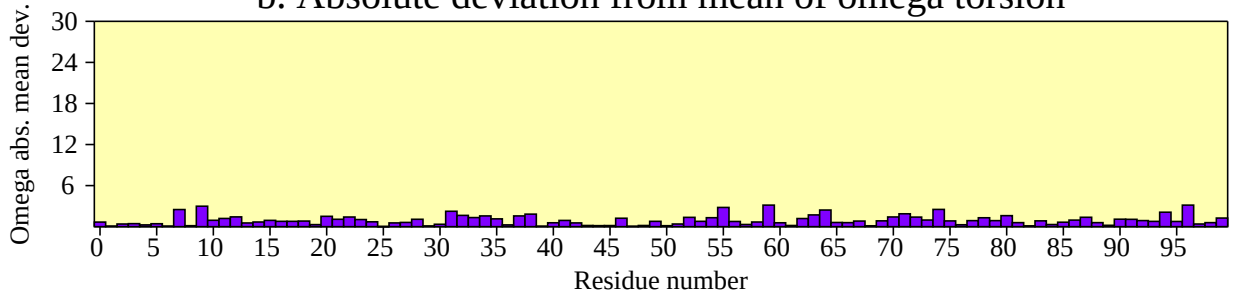


Residue properties
pdb2b76

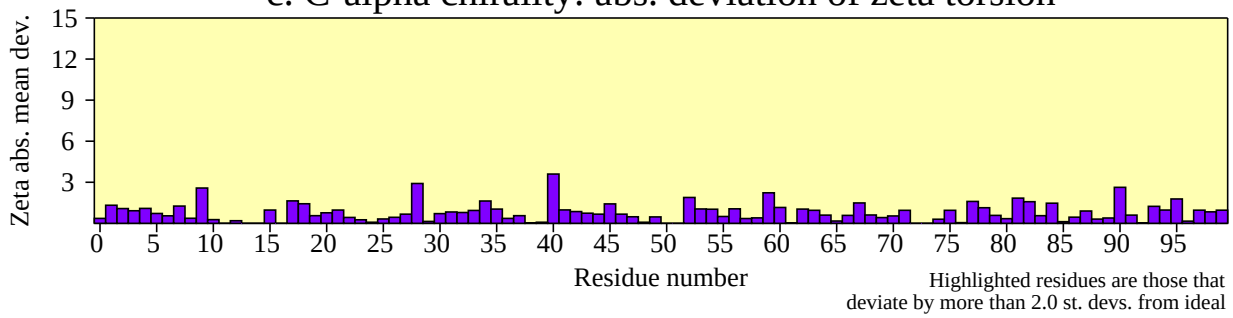
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion

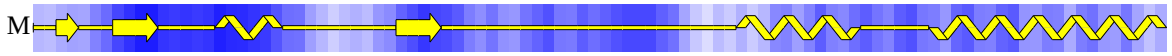


c. C-alpha chirality: abs. deviation of zeta torsion



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

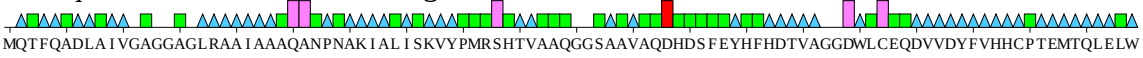
d. Secondary structure & estimated accessibility



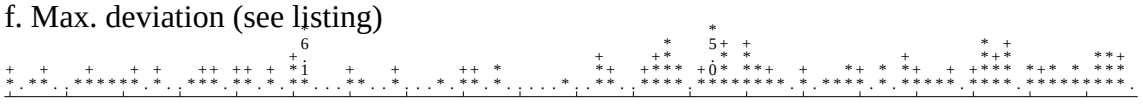
Key:- Helix Beta strand Random coil Accessibility shading: Buried Accessible

e. Sequence & Ramachandran regions

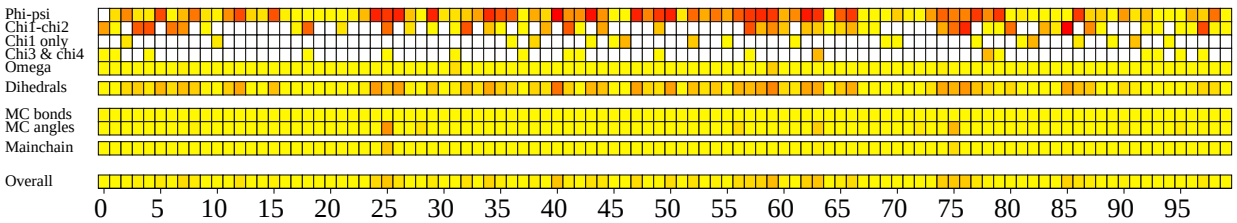
Most favoured Allowed Generous Disallowed



f. Max. deviation (see listing)

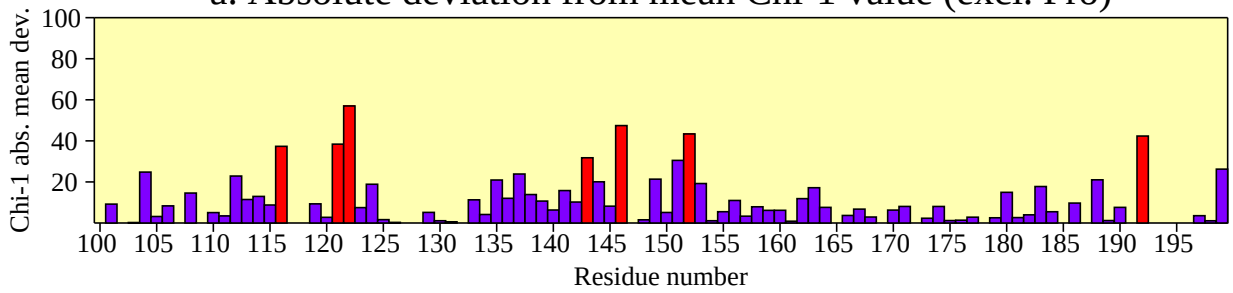


g. G-factors

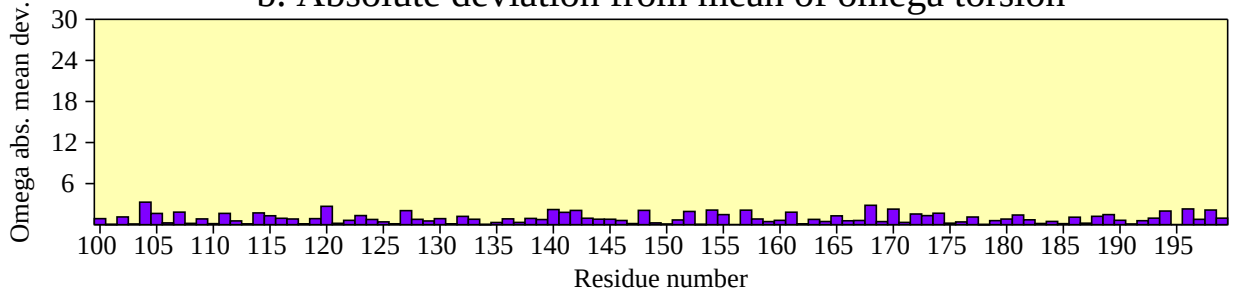


Residue properties
pdb2b76

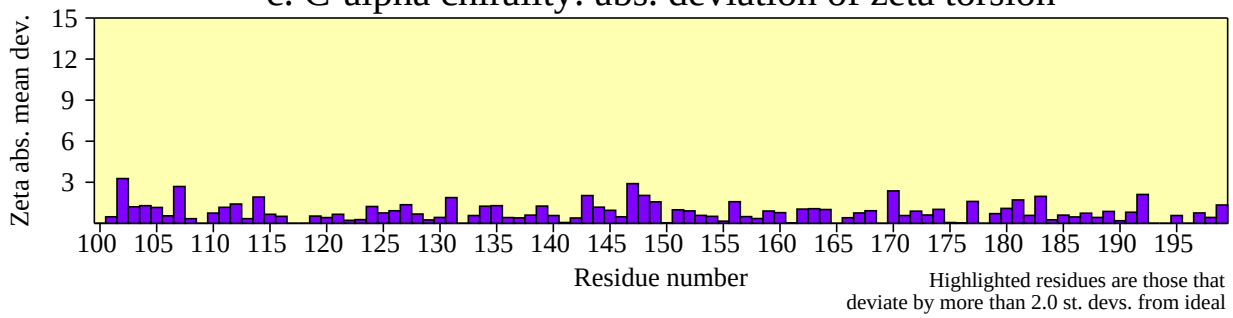
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion

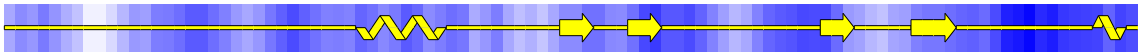


c. C-alpha chirality: abs. deviation of zeta torsion



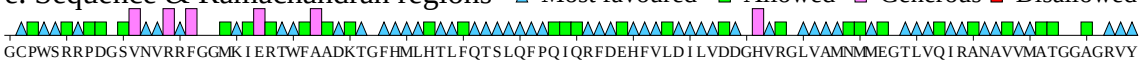
Highlighted residues are those that deviate by more than 2.0 st. devs. from ideal

d. Secondary structure & estimated accessibility



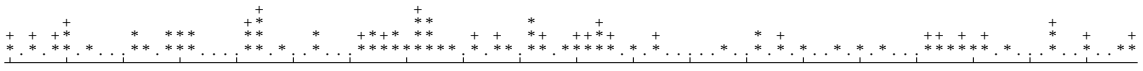
Key:- Helix Beta strand Random coil Accessibility shading: Buried Accessible

e. Sequence & Ramachandran regions Most favoured Allowed Generous Disallowed

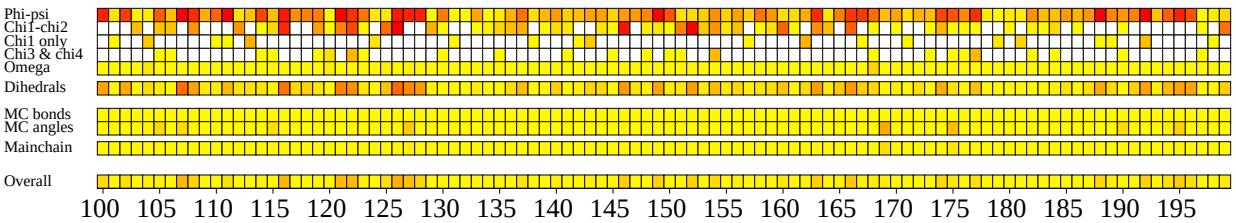


GCPWSRRPDGSVNVRRFGGMKIERTWFAADKTGFHMLHTLFQTSLQFPQIQRFDEHFVLDILVDDGHVRGLVAMNMMEGTLVQIRANAVVMATGGAGRVY

f. Max. deviation (see listing)

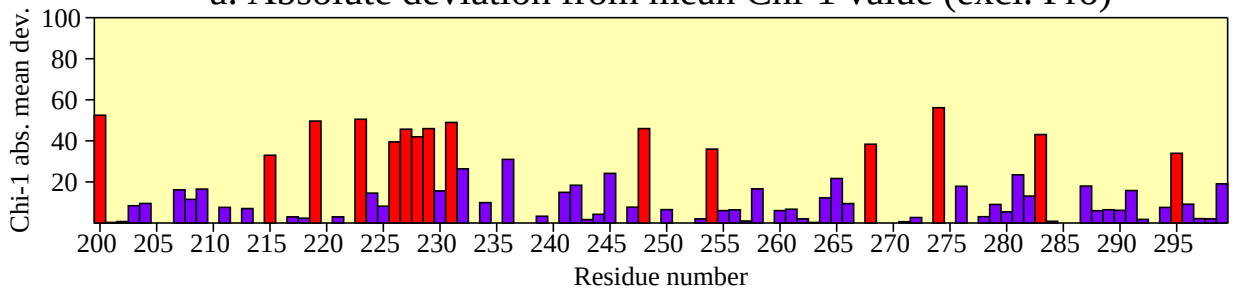


g. G-factors

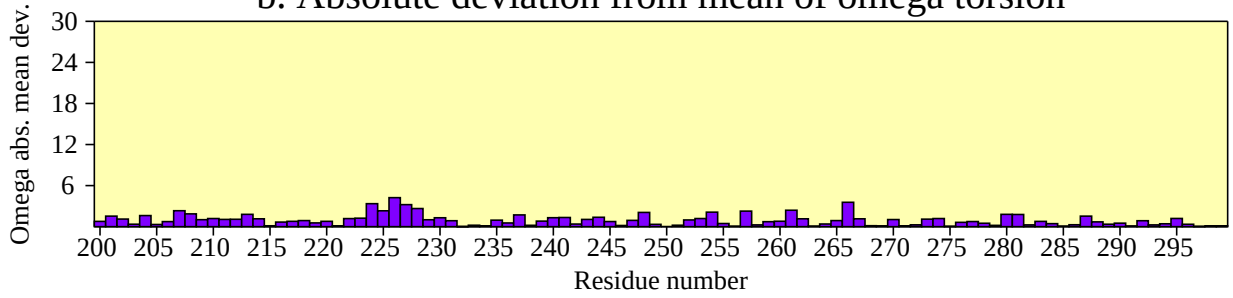


Residue properties
pdb2b76

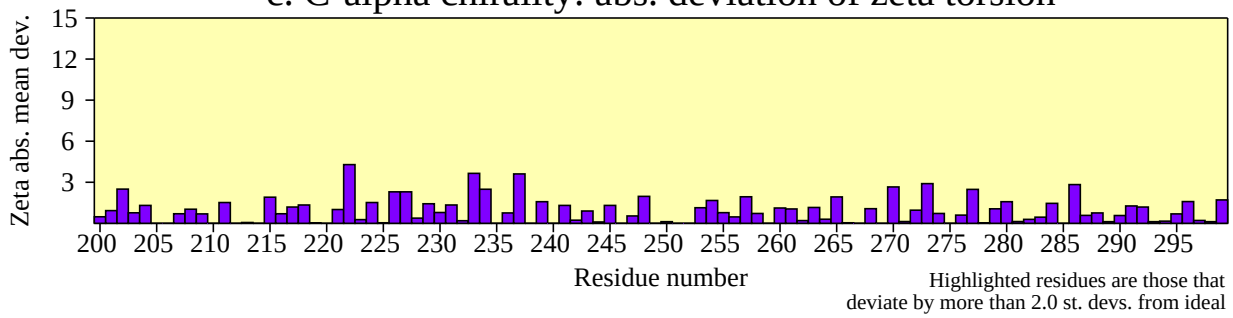
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion

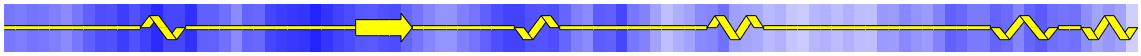


c. C-alpha chirality: abs. deviation of zeta torsion



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

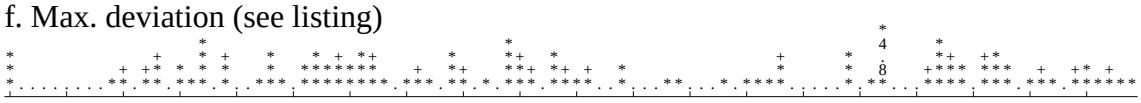
d. Secondary structure & estimated accessibility



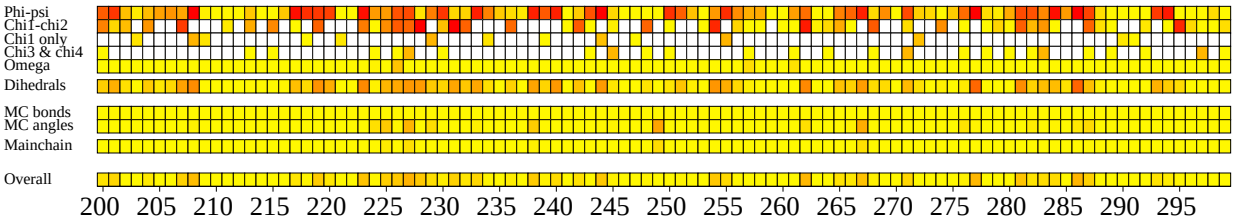
Key:- Helix Beta strand Random coil Accessibility shading: Buried Accessible

e. Sequence & Ramachandran regions Most favoured Allowed Generous Disallowed

f. Max. deviation (see listing)

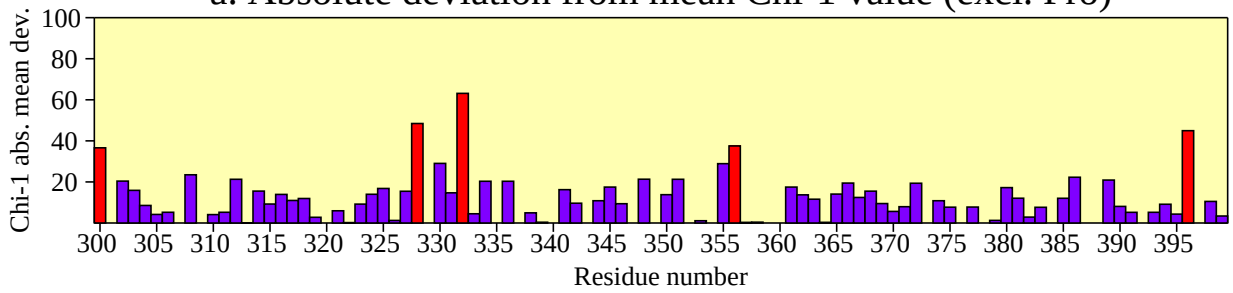


g. G-factors

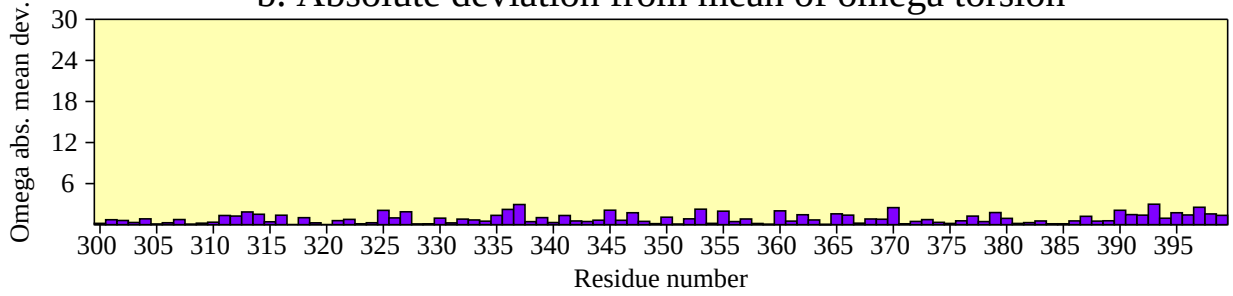


Residue properties
pdb2b76

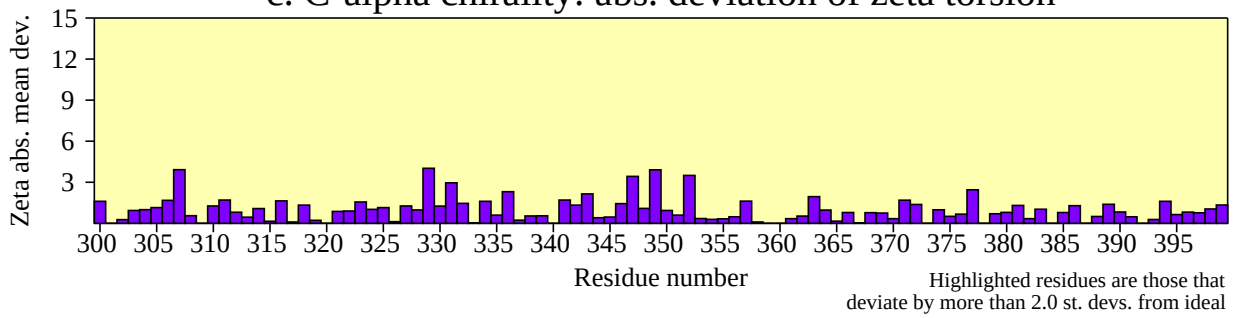
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion

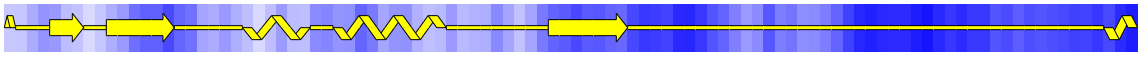


c. C-alpha chirality: abs. deviation of zeta torsion



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

d. Secondary structure & estimated accessibility

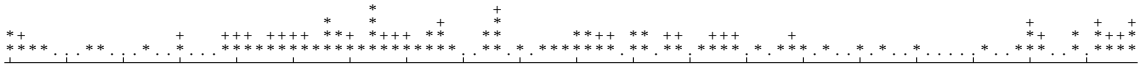


Key:- Helix Beta strand Random coil Accessibility shading: Buried Accessible

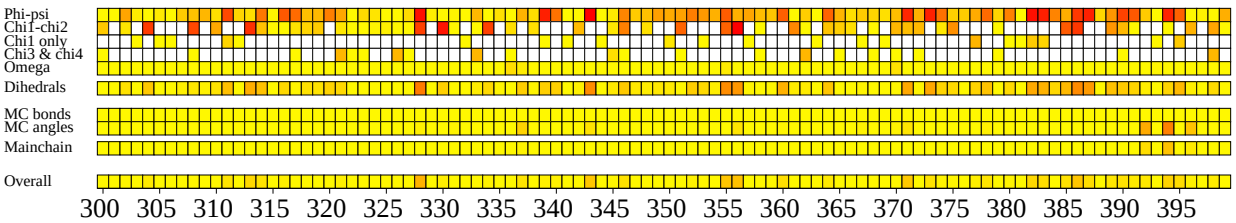
e. Sequence & Ramachandran regions Most favoured Allowed Generous Disallowed

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

f. Max. deviation (see listing)

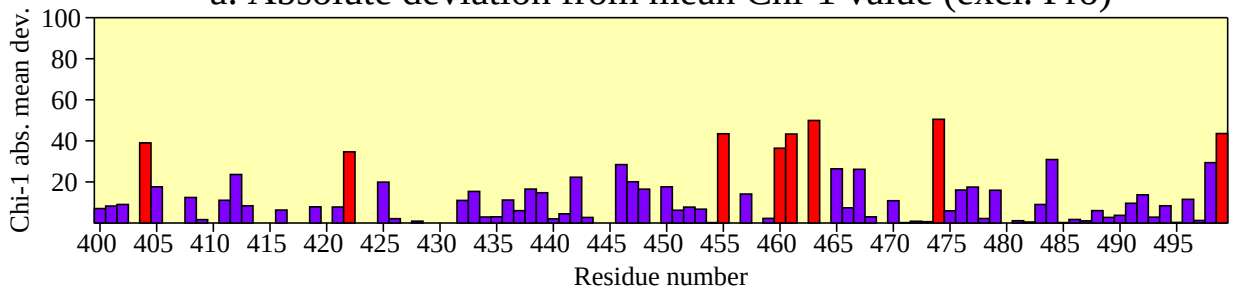


g. G-factors

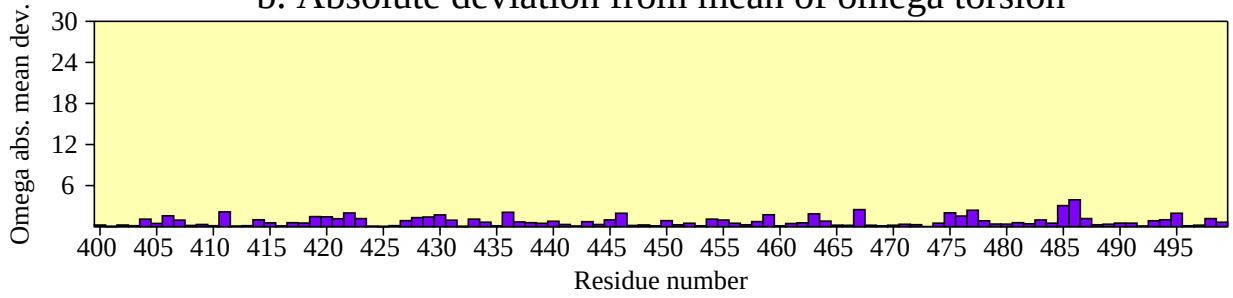


Residue properties
pdb2b76

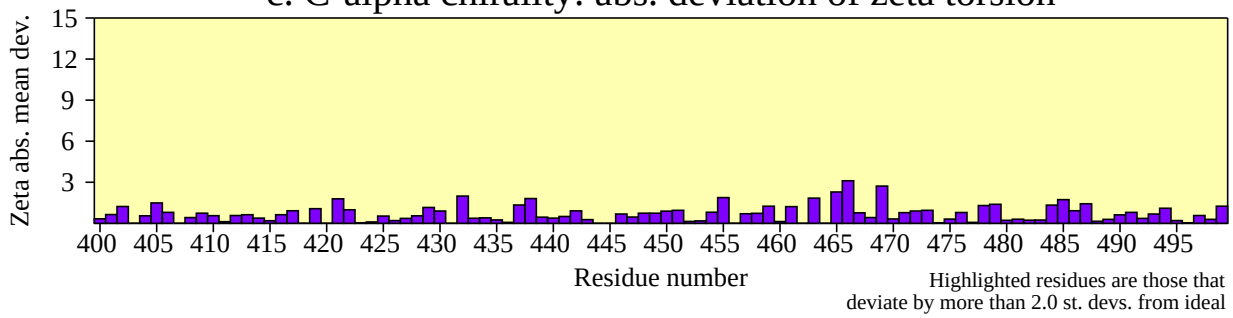
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion



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

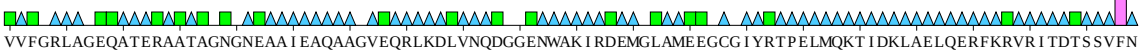


Highlighted residues are those that deviate by more than 2.0 st. devs. from ideal

d. Secondary structure & estimated accessibility

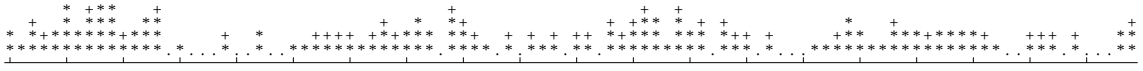
Key:- Helix Beta strand Random coil Accessibility shading: Buried Accessible

e. Sequence & Ramachandran regions Most favoured Allowed Generous Disallowed

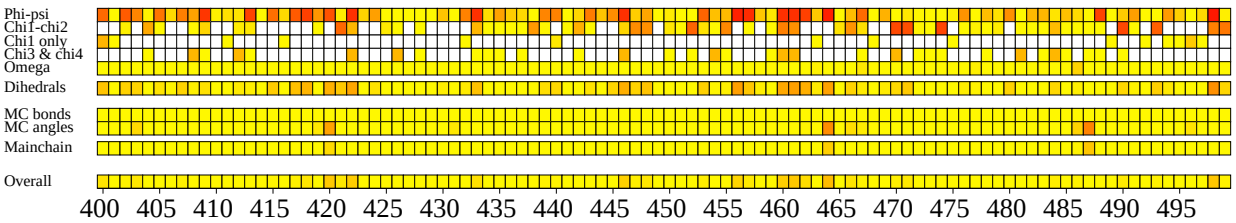


VVFGRLAGEQATERAATAGNGNEAAIEAQAAGVEQRLKDLVNQDGGENWAKIRDEMGLAMEEGCGIYRTPELMQKTIDKLAELQERFKRVRITDTSSVFN

f. Max. deviation (see listing)

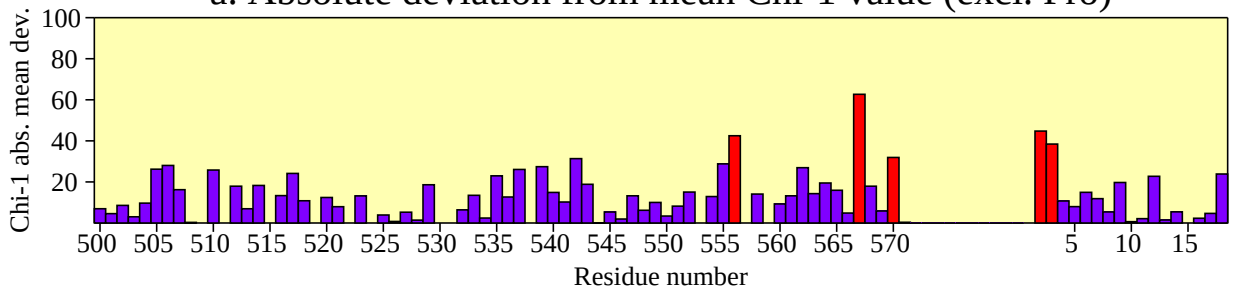


g. G-factors

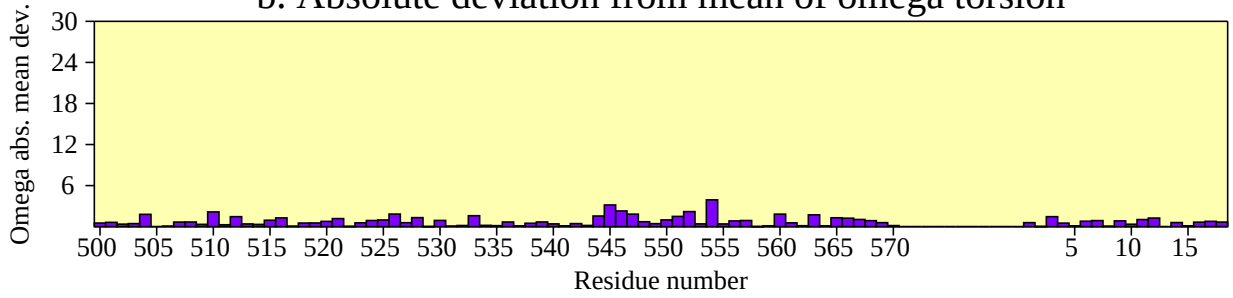


Residue properties
pdb2b76

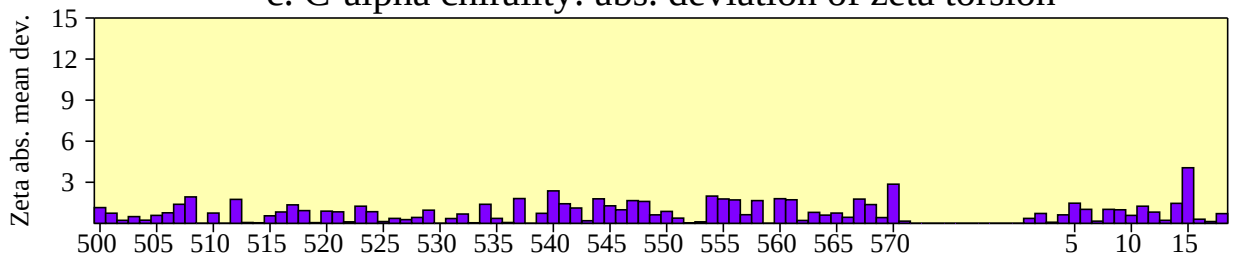
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion

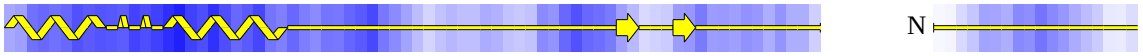


c. C-alpha chirality: abs. deviation of zeta torsion



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

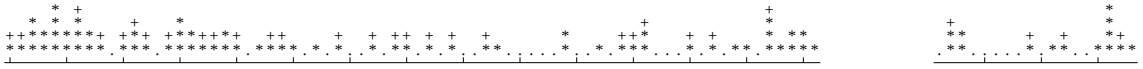
d. Secondary structure & estimated accessibility



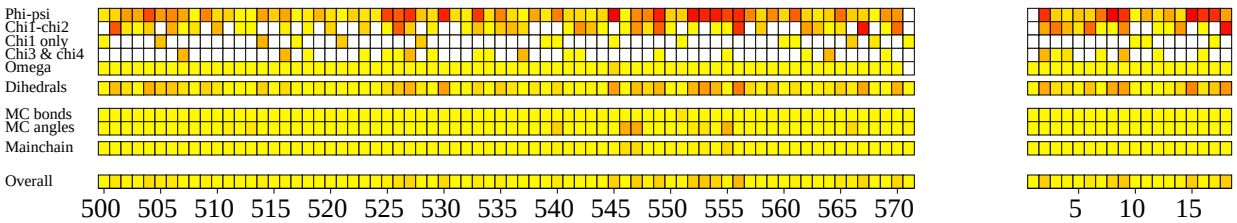
Key:- Helix Beta strand Random coil Accessibility shading: Buried Accessible

e. Sequence & Ramachandran regions Most favoured Allowed Generous Disallowed

f. Max. deviation (see listing)

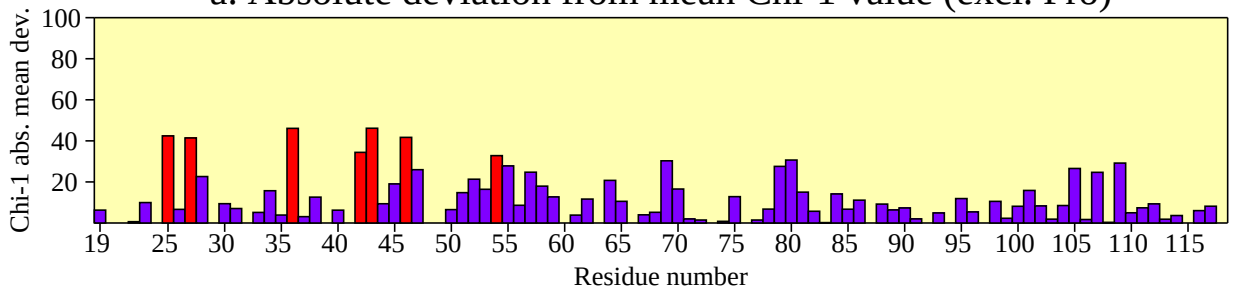


g. G-factors

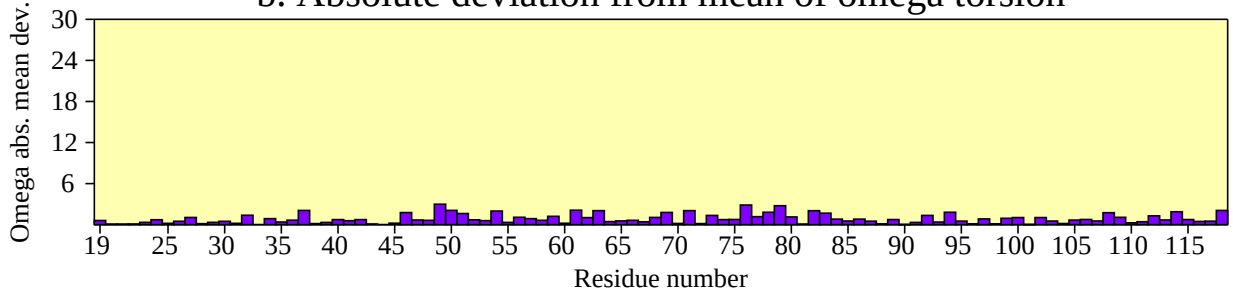


Residue properties
pdb2b76

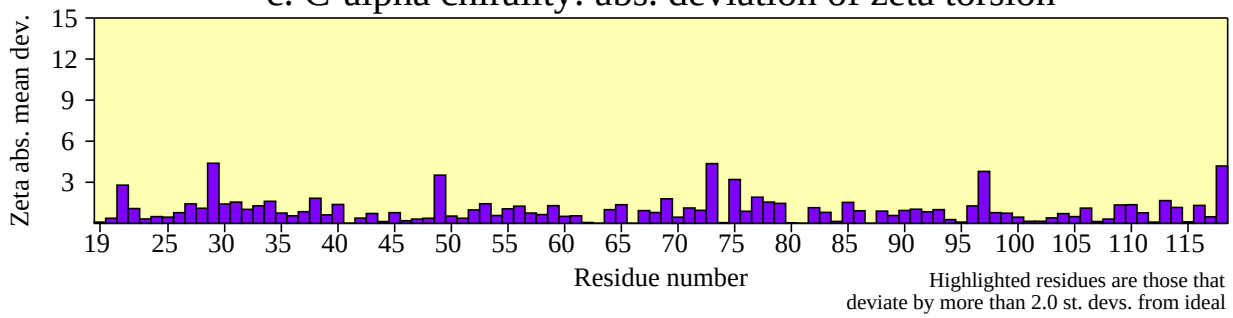
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion

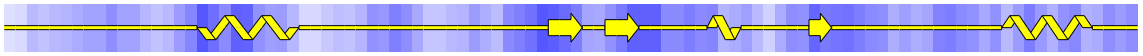


c. C-alpha chirality: abs. deviation of zeta torsion



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

d. Secondary structure & estimated accessibility

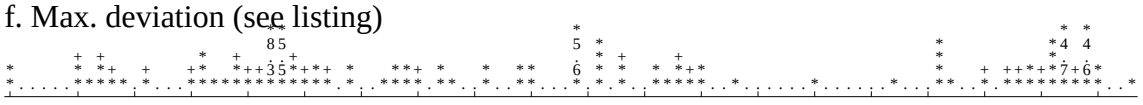


Key:- Helix Beta strand Random coil Accessibility shading: Buried Accessible

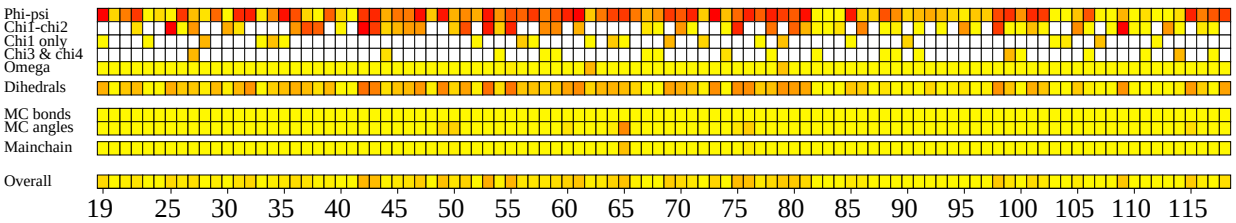
e. Sequence & Ramachandran regions Most favoured Allowed Generous Disallowed

TAPHSAFYEVPYDATTSLLDALGYIKDNLAPDLSYRWSCRMAICGSCGMMVNNVPKLACKTFLRDYTDGMKVEALANFPIERDLVVDMTHFIESLEAIKP

f. Max. deviation (see listing)

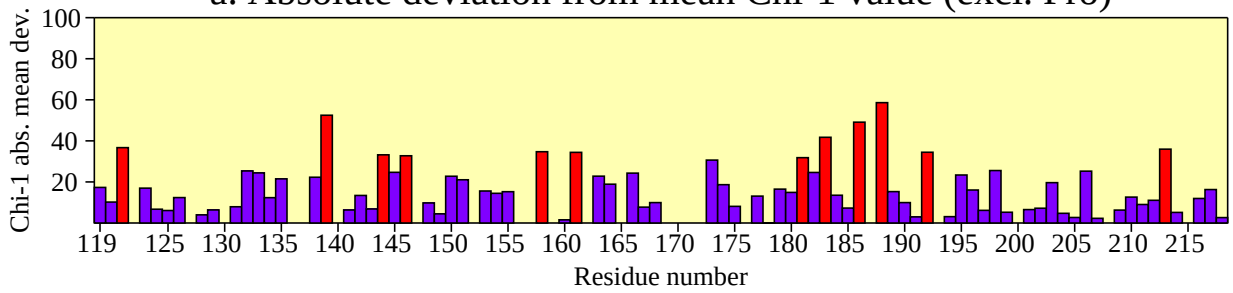


g. G-factors

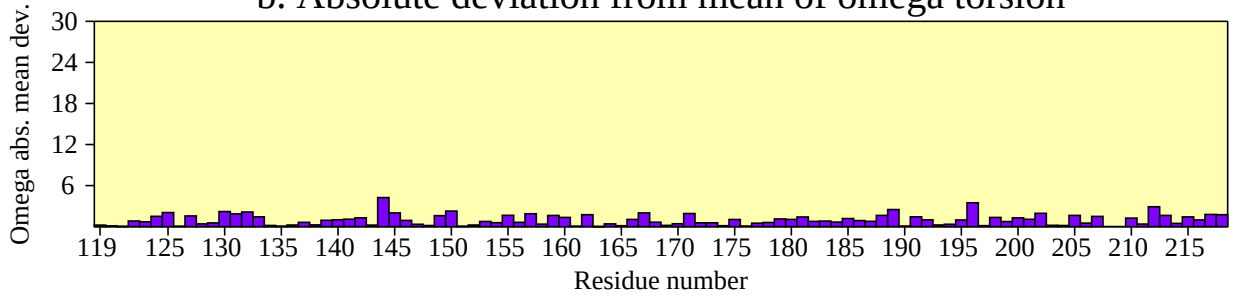


Residue properties
pdb2b76

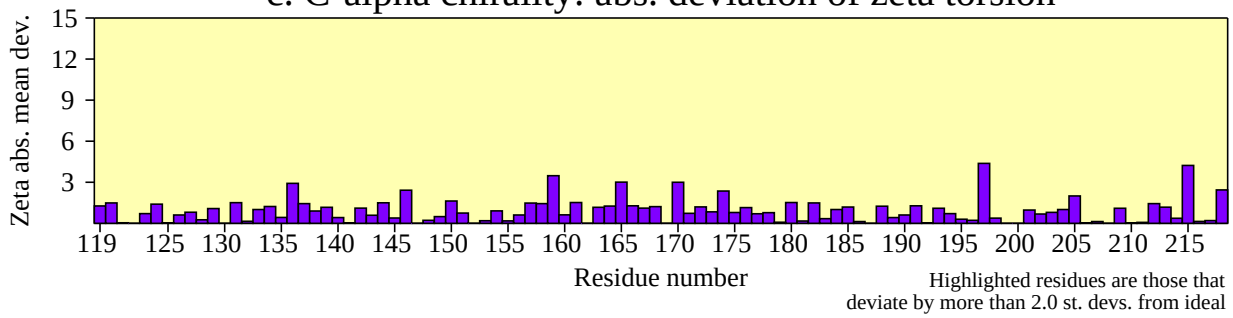
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion

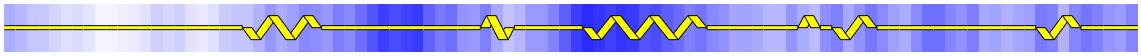


c. C-alpha chirality: abs. deviation of zeta torsion



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

d. Secondary structure & estimated accessibility



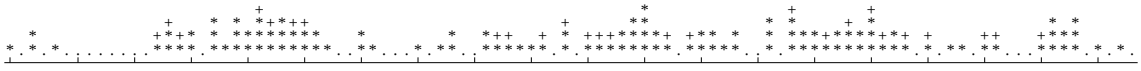
Key:- Helix Beta strand Random coil Accessibility shading: Buried Accessible

e. Sequence & Ramachandran regions

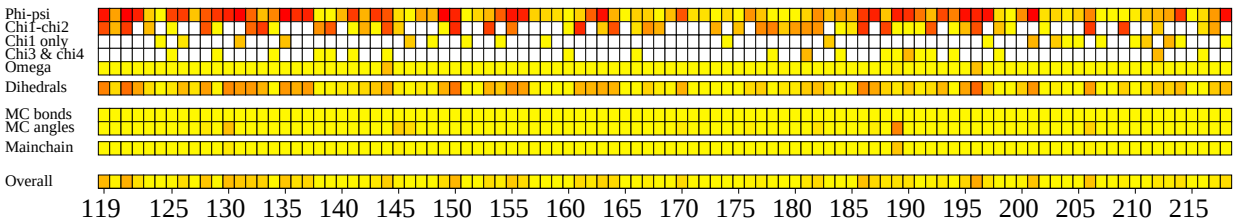
Most favoured Allowed Generous Disallowed

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

f. Max. deviation (see listing)

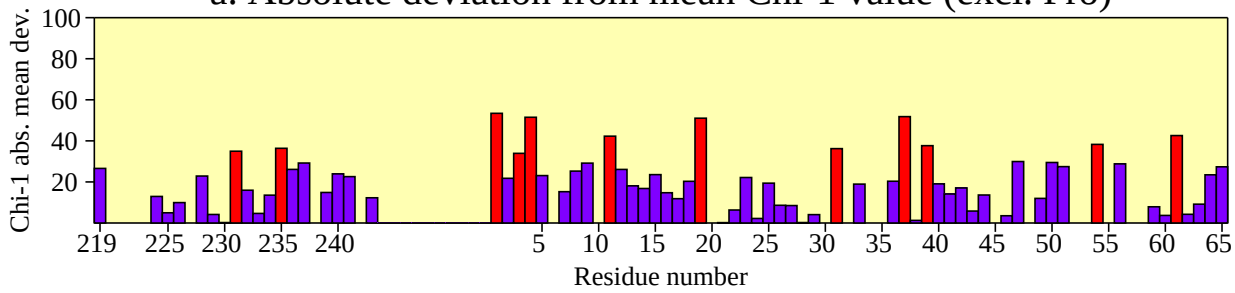


g. G-factors

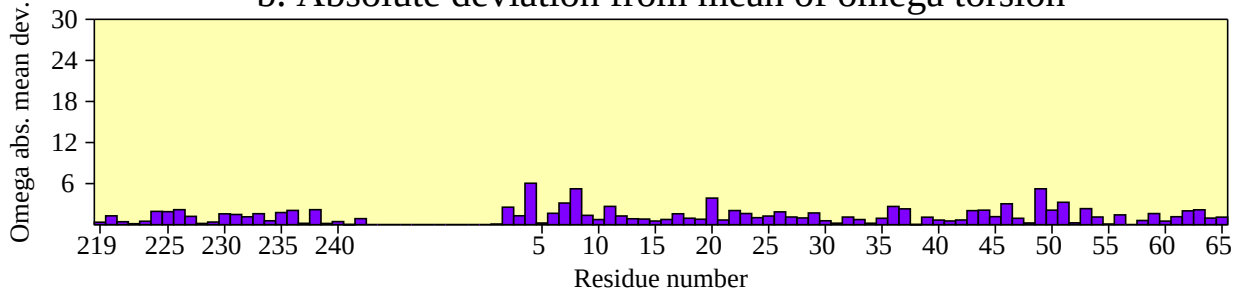


Residue properties
pdb2b76

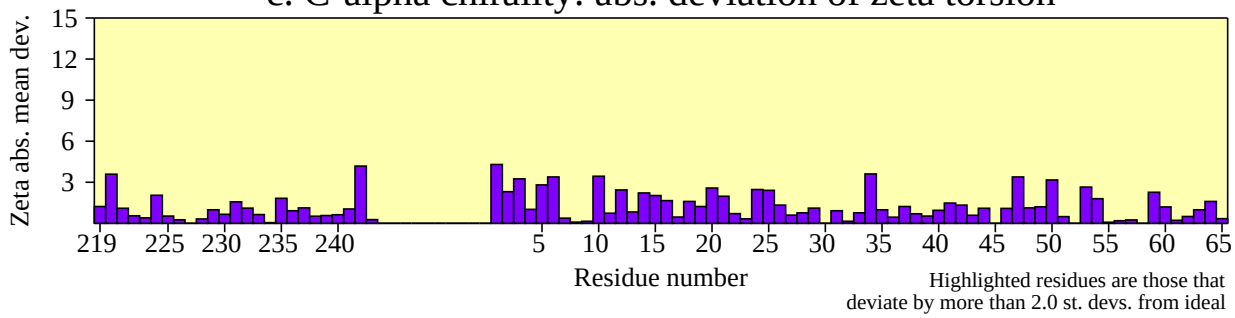
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion



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



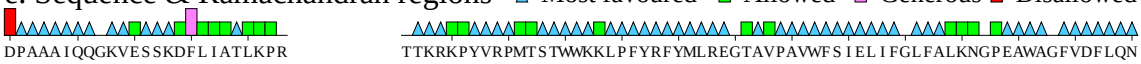
Highlighted residues are those that deviate by more than 2.0 st. devs. from ideal

d. Secondary structure & estimated accessibility

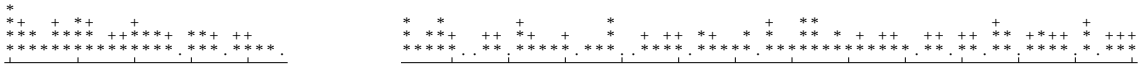
Key:- Helix Beta strand Random coil Accessibility shading: Buried Accessible

e. Sequence & Ramachandran regions

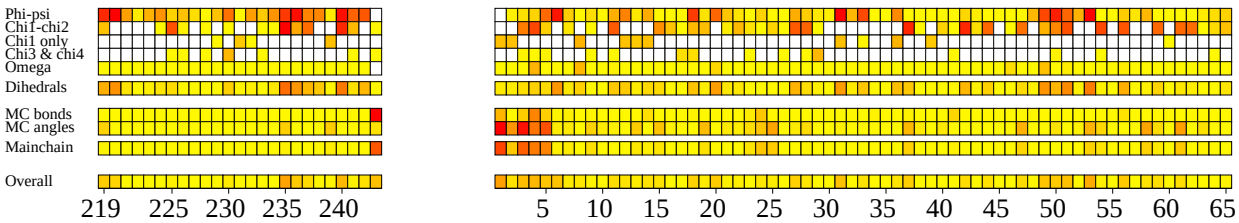
Most favoured Allowed Generous Disallowed



f. Max. deviation (see listing)

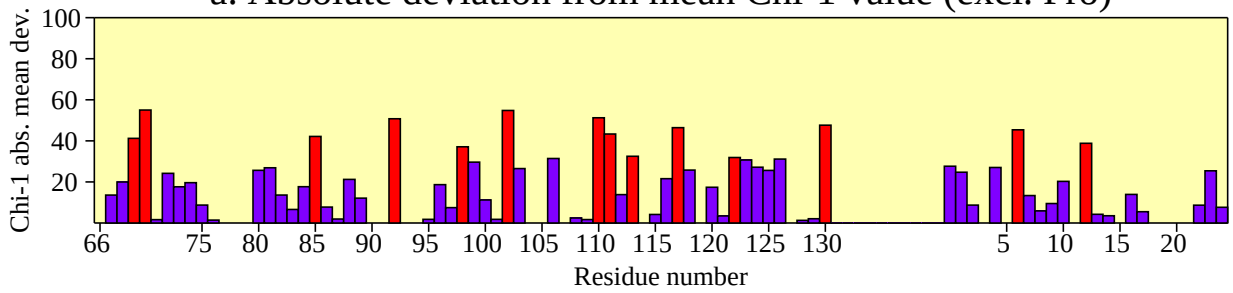


g. G-factors

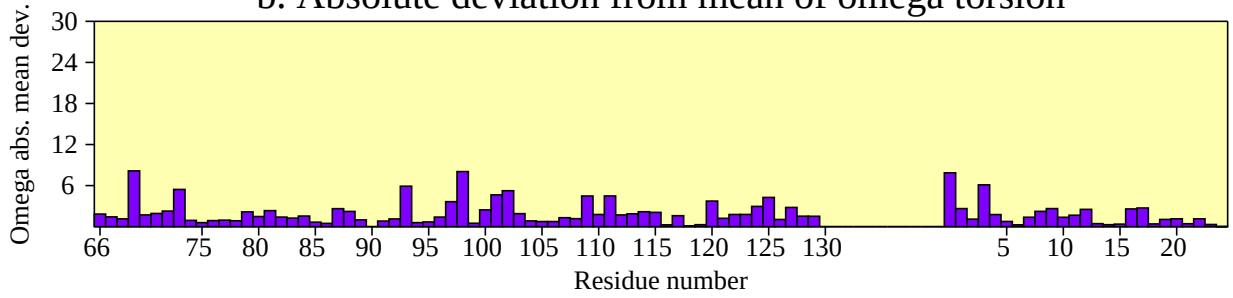


Residue properties
pdb2b76

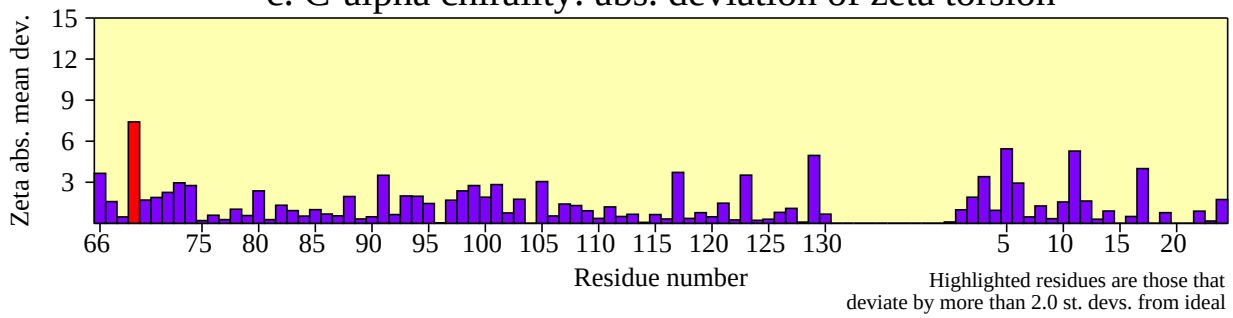
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion



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



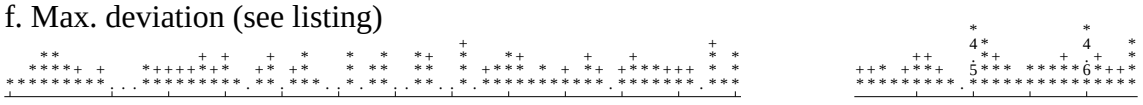
Highlighted residues are those that deviate by more than 2.0 st. devs. from ideal

d. Secondary structure & estimated accessibility

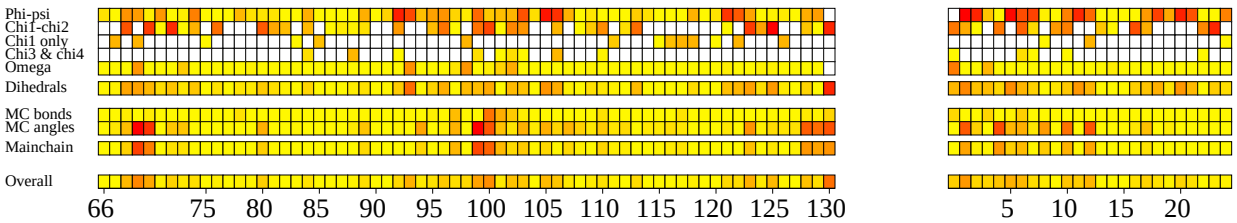
Key:- Helix Beta strand Random coil Accessibility shading: Buried Accessible

e. Sequence & Ramachandran regions Most favoured Allowed Generous Disallowed

f. Max. deviation (see listing)

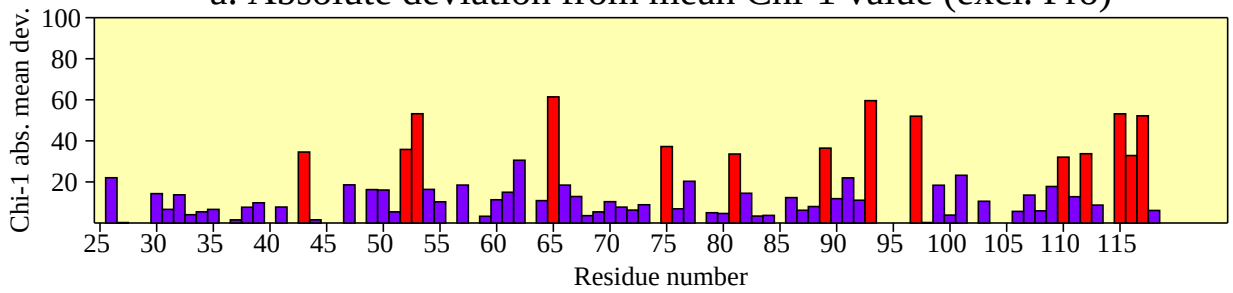


g. G-factors

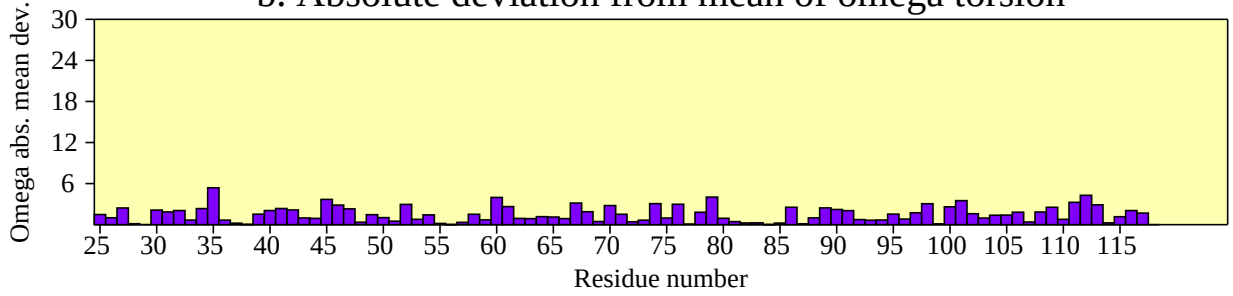


Residue properties
pdb2b76

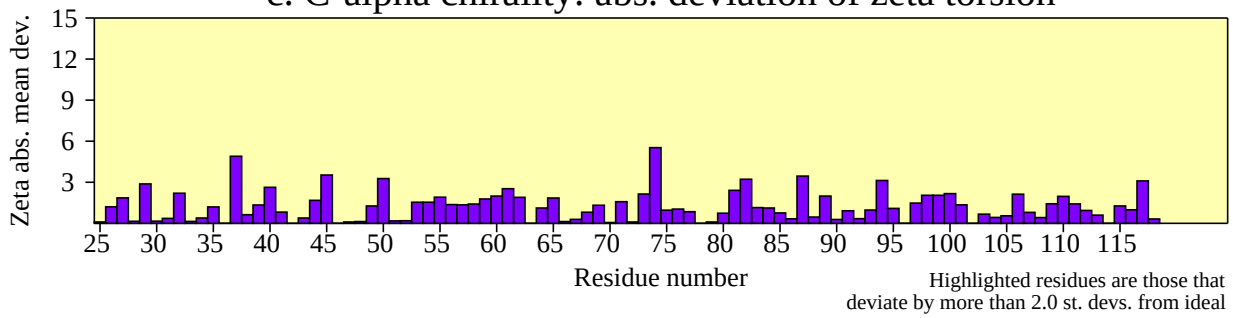
a. Absolute deviation from mean Chi-1 value (excl. Pro)



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

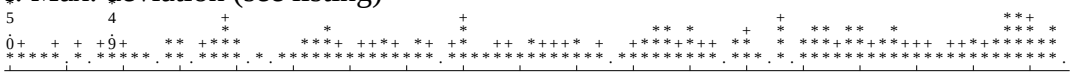
Key:- Helix Beta strand Random coil Accessibility shading: Buried Accessible

e. Sequence & Ramachandran regions

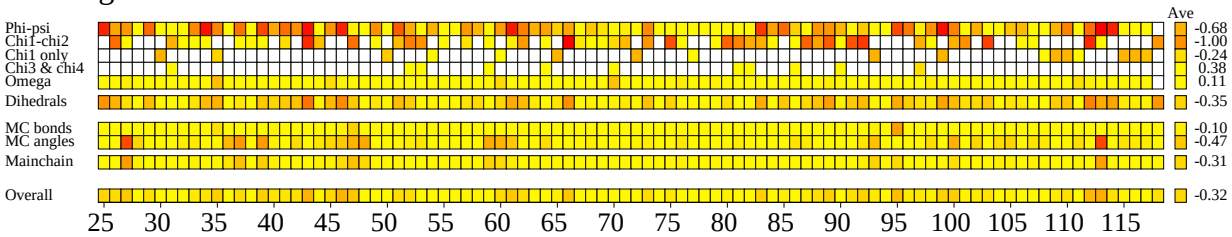
Most favoured Allowed Generous Disallowed

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

f. Max. deviation (see listing)



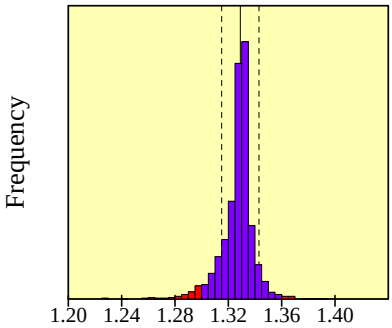
g. G-factors



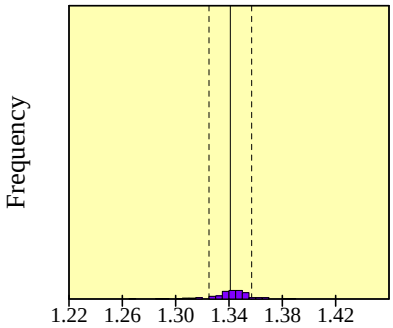
Main-chain bond lengths

pdb2b76

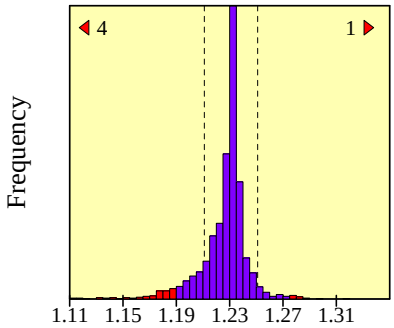
C-N (except Pro)



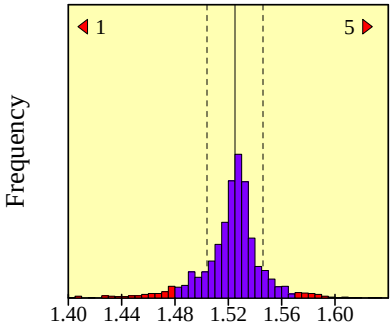
C-N (Pro)



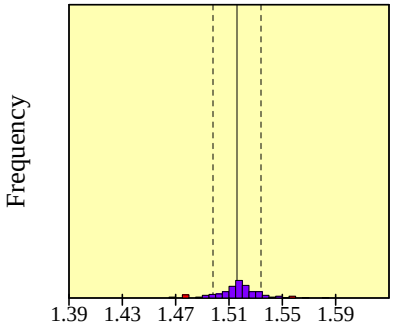
C-O



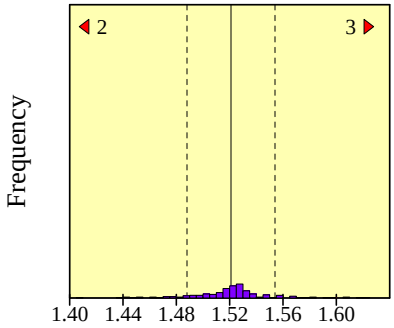
CA-C (except Gly)



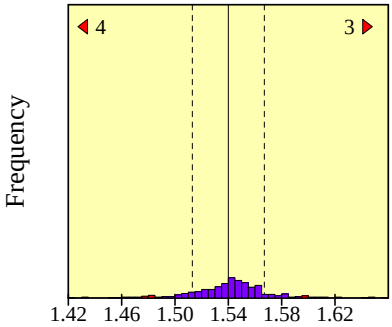
CA-C (Gly)



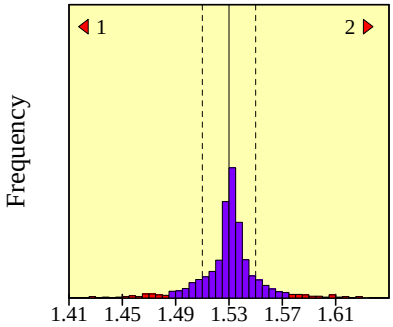
CA-CB (Ala)



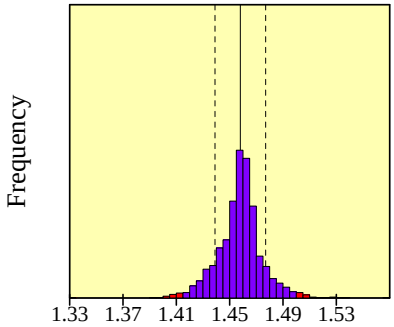
CA-CB (Ile,Thr,Val)



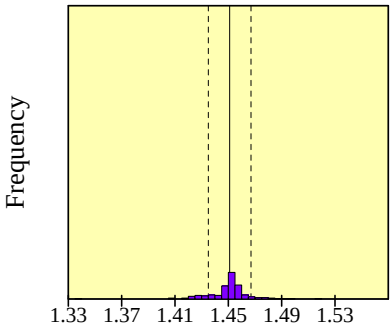
CA-CB (the rest)



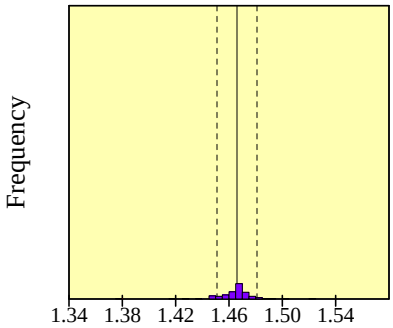
N-CA (except Gly,Pro)



N-CA (Gly)



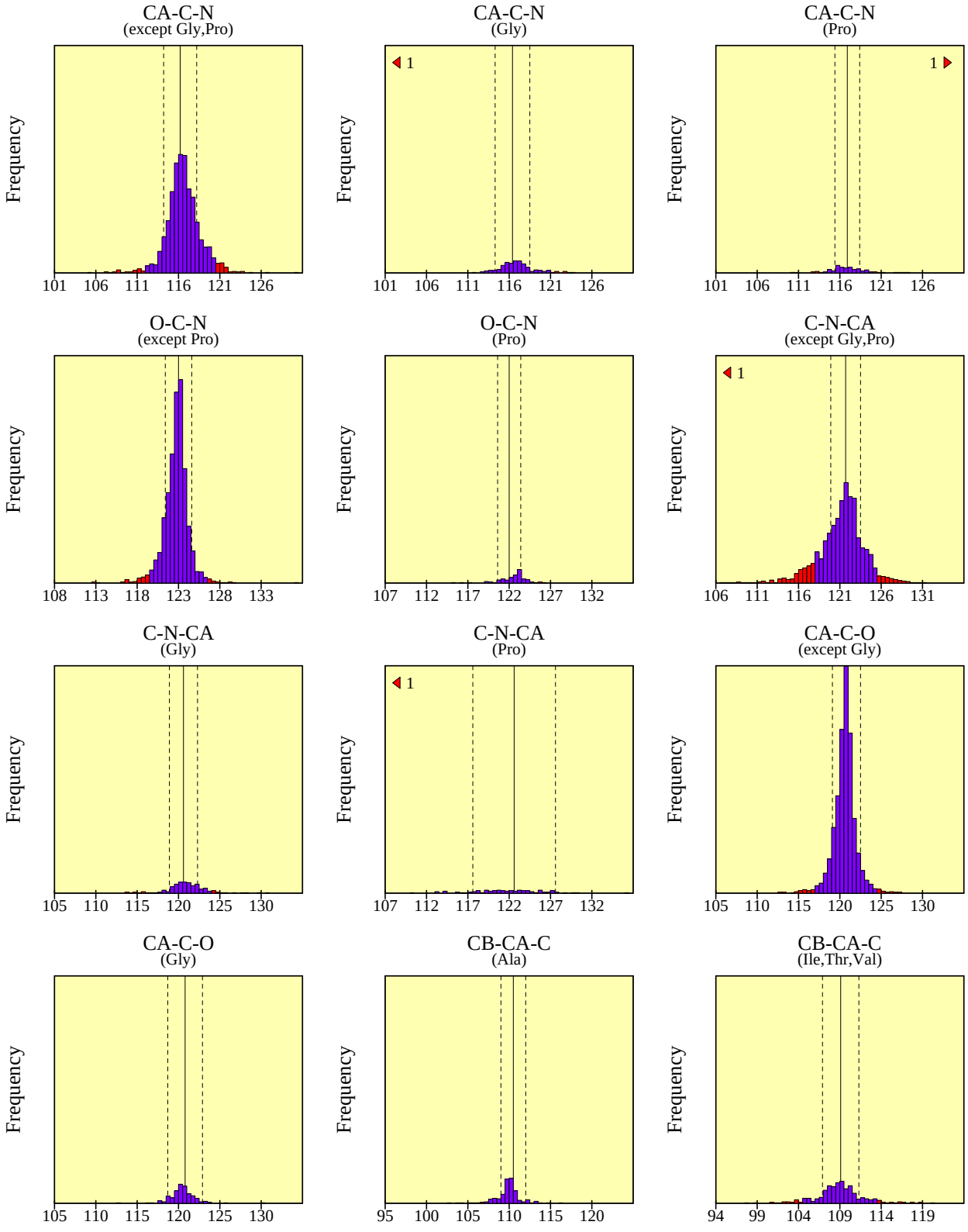
N-CA (Pro)



Black bars > 2.0 st. devs. from mean. ◀ or ▶ signifies data points off the graph in the direction shown.
Solid and dashed lines represent the mean and standard deviation values as per Engh & Huber small-molecule data.

Main-chain bond angles

pdb2b76

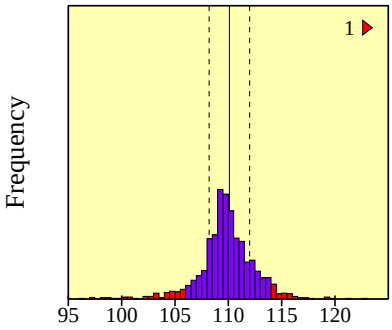


Black bars > 2.0 st. devs. from mean. ◀ or ▶ signifies data points off the graph in the direction shown.
Solid and dashed lines represent the mean and standard deviation values as per Engh & Huber small-molecule data.

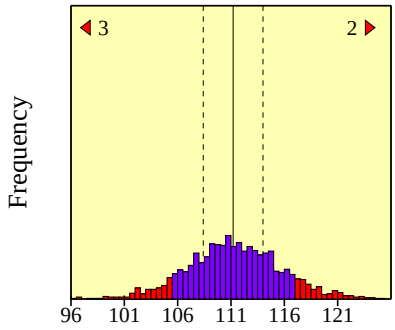
Main-chain bond angles

pdb2b76

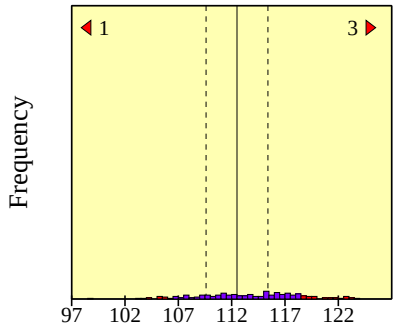
CB-CA-C
(the rest)



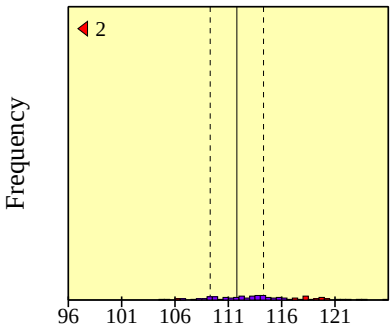
N-CA-C
(except Gly,Pro)



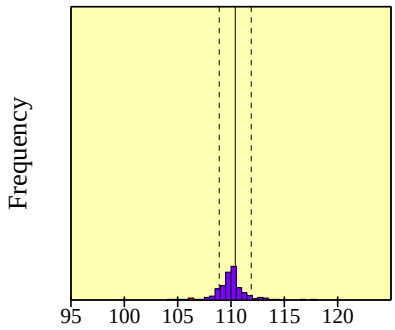
N-CA-C
(Gly)



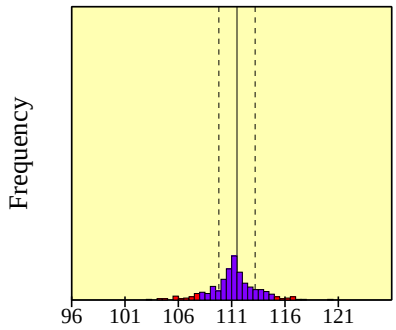
N-CA-C
(Pro)



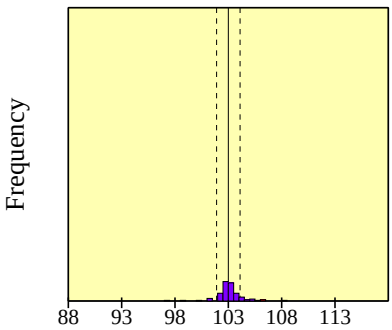
N-CA-CB
(Ala)



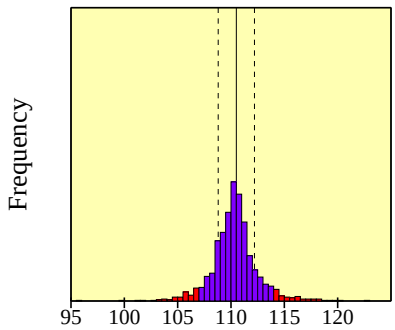
N-CA-CB
(Ile,Thr,Val)



N-CA-CB
(Pro)



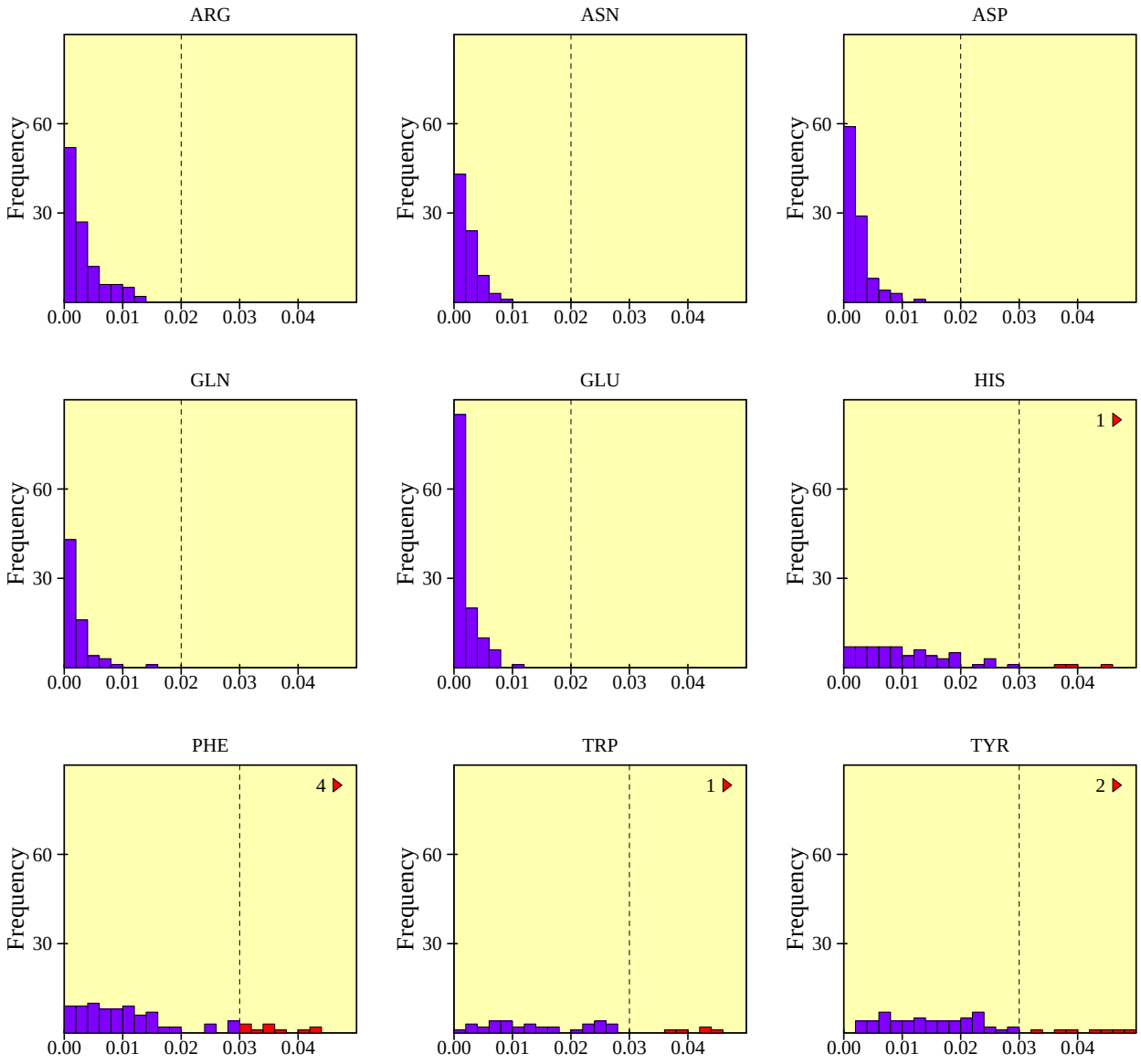
N-CA-CB
(the rest)



Black bars > 2.0 st. devs. from mean. ◀ or ▶ signifies data points off the graph in the direction shown.
Solid and dashed lines represent the mean and standard deviation values as per Engh & Huber small-molecule data.

RMS distances from planarity

pdb2b76

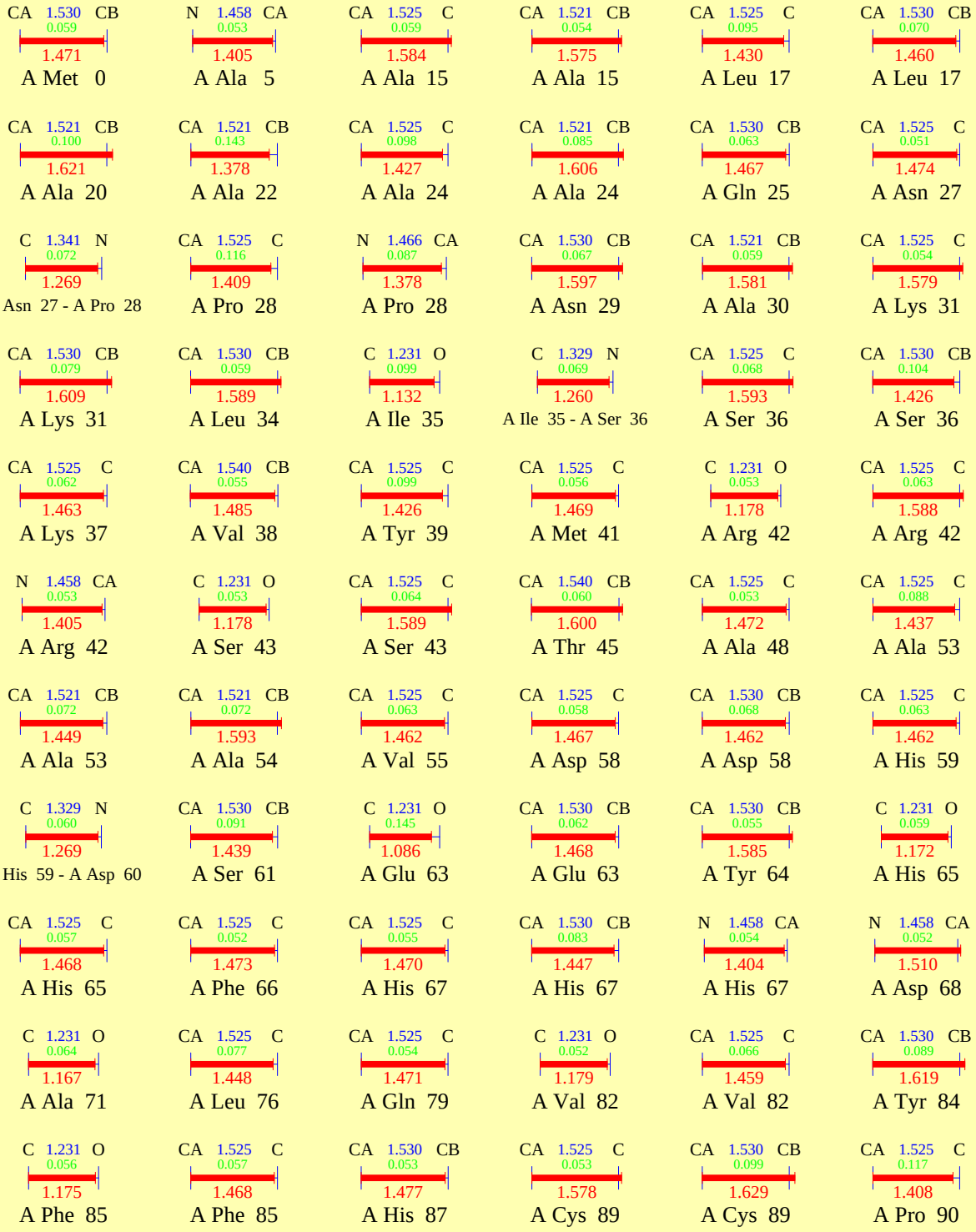


Histograms showing RMS distances of planar atoms from best-fit plane.
Black bars indicate large deviations from planarity: RMS dist > 0.03 for rings, and > 0.02 otherwise.

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

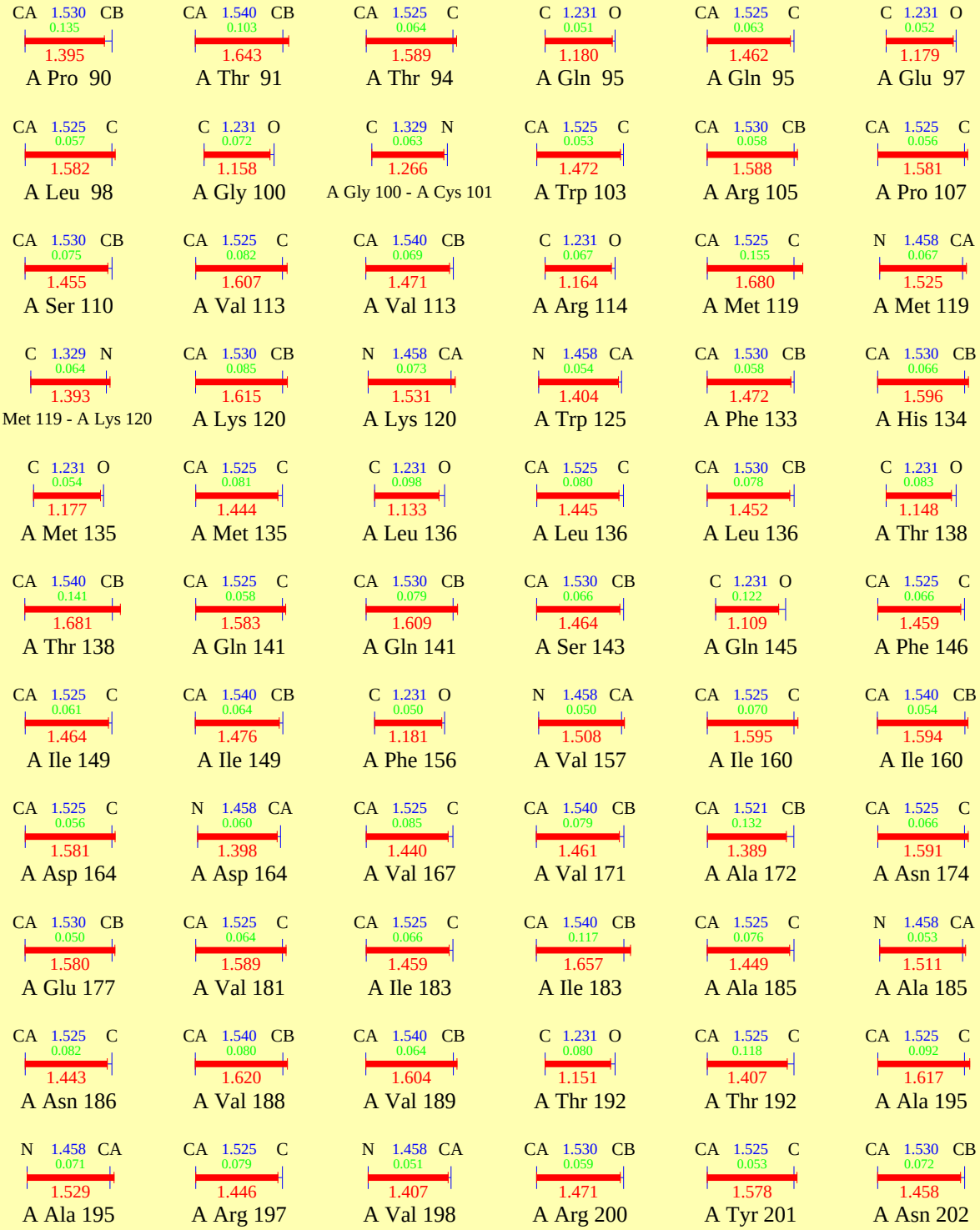
Distorted geometry
pdb2b76

Main-chain bond lengths



Distorted geometry
pdb2b76

Main-chain bond lengths (contd)



Distorted geometry
pdb2b76

Main-chain bond lengths (contd)

C 1.231 O 0.051 1.180 A Gly 205	C 1.231 O 0.063 1.168 A Ile 207	CA 1.525 C 0.064 1.461 A Ile 207	C 1.329 N 0.053 1.382 A Thr 209 - A Gly 210	C 1.329 N 0.064 1.265 A Asp 211 - A Gly 212	CA 1.530 CB 0.079 1.609 A Met 215
CA 1.521 CB 0.095 1.616 A Ala 216	CA 1.525 C 0.109 1.416 A His 219	CA 1.530 CB 0.102 1.428 A His 219	C 1.231 O 0.112 1.119 A Gly 220	C 1.329 N 0.052 1.277 A Gly 220 - A Val 221	CA 1.540 CB 0.136 1.404 A Val 221
CA 1.525 C 0.073 1.452 A Leu 223	CA 1.530 CB 0.053 1.583 A Leu 223	CA 1.525 C 0.052 1.473 A Arg 224	CA 1.530 CB 0.061 1.469 A Asp 225	CA 1.525 C 0.060 1.585 A Phe 228	CA 1.530 CB 0.064 1.594 A Phe 228
C 1.231 O 0.120 1.111 A Val 229	CA 1.525 C 0.051 1.576 A Val 229	CA 1.540 CB 0.074 1.614 A Val 229	C 1.329 N 0.057 1.272 A Val 229 - A Gln 230	CA 1.530 CB 0.060 1.470 A His 232	C 1.231 O 0.066 1.165 A Pro 237
CA 1.525 C 0.059 1.466 A Pro 237	CA 1.530 CB 0.061 1.469 A Pro 237	C 1.231 O 0.134 1.097 A Gly 240	C 1.329 N 0.052 1.277 A Gly 240 - A Ile 241	C 1.231 O 0.090 1.141 A Met 243	CA 1.525 C 0.051 1.576 A Arg 248
CA 1.525 C 0.069 1.594 A Ile 253	CA 1.540 CB 0.124 1.664 A Ile 253	CA 1.530 CB 0.053 1.477 A Asp 265	C 1.329 N 0.066 1.263 A Asp 265 - A Tyr 266	N 1.451 CA 0.113 1.338 A Gly 269	C 1.341 N 0.051 1.290 A Gly 269 - A Pro 270
CA 1.525 C 0.155 1.680 A Pro 270	C 1.329 N 0.061 1.390 A Pro 270 - A Glu 271	CA 1.525 C 0.126 1.651 A Thr 272	CA 1.530 CB 0.141 1.671 A Glu 276	N 1.458 CA 0.126 1.332 A Glu 276	CA 1.525 C 0.183 1.708 A Pro 277
N 1.466 CA 0.058 1.524 A Pro 277	CA 1.530 CB 0.064 1.594 A Asn 279	C 1.231 O 0.127 1.104 A Arg 287	CA 1.525 C 0.056 1.469 A Asp 288	CA 1.525 C 0.051 1.576 A Lys 289	CA 1.525 C 0.051 1.474 A Ser 291
C 1.231 O 0.055 1.176 A His 296	CA 1.530 CB 0.099 1.629 A Arg 299	CA 1.525 C 0.060 1.585 A Asn 302	CA 1.525 C 0.056 1.581 A Thr 303	CA 1.530 CB 0.050 1.480 A Pro 307	N 1.458 CA 0.052 1.406 A Arg 308
CA 1.516 C 0.053 1.569 A Gly 309	CA 1.540 CB 0.118 1.422 A Val 312	CA 1.525 C 0.054 1.579 A Leu 314	CA 1.530 CB 0.055 1.585 A Leu 324	CA 1.525 C 0.116 1.409 A His 325	CA 1.530 CB 0.057 1.473 A Glu 326
N 1.458 CA 0.077 1.535 A Glu 326	CA 1.525 C 0.101 1.626 A Arg 327	CA 1.530 CB 0.059 1.589 A Arg 327	CA 1.525 C 0.057 1.582 A Leu 328	N 1.458 CA 0.111 1.569 A Leu 328	CA 1.525 C 0.060 1.465 A Pro 329

Distorted geometry
pdb2b76

Main-chain bond lengths (contd)

CA 1.530 CB 0.054 1.584 A Pro 329	CA 1.530 CB 0.106 1.636 A Phe 330	CA 1.540 CB 0.066 1.606 A Ile 331	CA 1.525 C 0.062 1.587 A Cys 332	CA 1.521 CB 0.057 1.464 A Ala 335	CA 1.525 C 0.072 1.597 A Val 344
CA 1.530 CB 0.066 1.595 A Glu 346	CA 1.525 C 0.083 1.608 A Pro 347	C 1.231 O 0.051 1.281 A Ile 348	CA 1.525 C 0.089 1.614 A Arg 351	CA 1.530 CB 0.096 1.626 A Arg 351	CA 1.525 C 0.159 1.684 A Pro 352
CA 1.525 C 0.055 1.470 A Thr 353	CA 1.525 C 0.052 1.577 A Thr 357	CA 1.540 CB 0.127 1.413 A Thr 357	CA 1.525 C 0.062 1.463 A Met 358	C 1.231 O 0.050 1.281 A Gly 359	CA 1.540 CB 0.060 1.480 A Ile 361
CA 1.530 CB 0.053 1.582 A Glu 362	CA 1.525 C 0.071 1.596 A Gln 365	CA 1.525 C 0.063 1.462 A Asn 366	CA 1.530 CB 0.108 1.422 A Glu 368	CA 1.540 CB 0.110 1.650 A Thr 369	CA 1.525 C 0.074 1.451 A Arg 370
CA 1.540 CB 0.134 1.674 A Ile 371	C 1.231 O 0.076 1.155 A Lys 372	CA 1.525 C 0.062 1.587 A Lys 372	CA 1.530 CB 0.079 1.609 A Lys 372	CA 1.521 CB 0.077 1.444 A Ala 376	C 1.231 O 0.114 1.117 A His 386
CA 1.530 CB 0.083 1.447 A His 386	C 1.329 N 0.056 1.273 A His 386 - A Gly 387	CA 1.521 CB 0.074 1.595 A Ala 388	C 1.231 O 0.064 1.167 A Asn 389	CA 1.530 CB 0.099 1.431 A Asn 389	C 1.231 O 0.061 1.170 A Arg 390
CA 1.525 C 0.094 1.431 A Arg 390	C 1.231 O 0.093 1.138 A Leu 391	CA 1.530 CB 0.113 1.417 A Leu 391	C 1.231 O 0.057 1.174 A Ser 393	CA 1.525 C 0.052 1.473 A Ser 395	CA 1.530 CB 0.093 1.623 A Leu 396
CA 1.525 C 0.081 1.444 A Leu 399	CA 1.540 CB 0.107 1.433 A Val 400	N 1.458 CA 0.052 1.406 A Val 400	C 1.231 O 0.050 1.181 A Val 401	CA 1.530 CB 0.077 1.453 A Arg 404	CA 1.530 CB 0.061 1.469 A Glu 408
CA 1.525 C 0.091 1.434 A Gln 409	C 1.231 O 0.109 1.122 A Ala 410	CA 1.525 C 0.066 1.459 A Ala 410	CA 1.525 C 0.062 1.463 A Thr 411	C 1.231 O 0.053 1.178 A Asn 419	CA 1.525 C 0.077 1.448 A Asn 421
CA 1.530 CB 0.067 1.597 A Asn 421	C 1.231 O 0.095 1.136 A Glu 422	CA 1.521 CB 0.137 1.658 A Ala 424	CA 1.540 CB 0.107 1.647 A Ile 425	CA 1.525 C 0.080 1.605 A Ala 429	CA 1.521 CB 0.060 1.581 A Ala 429
CA 1.525 C 0.056 1.581 A Val 432	N 1.458 CA 0.066 1.392 A Leu 436	CA 1.525 C 0.054 1.579 A Asn 441	CA 1.525 C 0.057 1.582 A Gln 442	C 1.329 N 0.101 1.228 A Gly 445 - A Glu 446	C 1.329 N 0.053 1.276 A Glu 446 - A Asn 447

Distorted geometry
pdb2b76

Main-chain bond lengths (contd)

CA 1.525 C 0.055 1.580 A Asn 447	CA 1.525 C 0.066 1.459 A Ile 451	CA 1.540 CB 0.072 1.467 A Ile 451	C 1.231 O 0.058 1.173 A Asp 453	CA 1.530 CB 0.056 1.474 A Glu 454	C 1.231 O 0.056 1.175 A Gly 456
CA 1.530 CB 0.090 1.440 A Met 459	C 1.231 O 0.059 1.172 A Glu 461	CA 1.530 CB 0.118 1.648 A Glu 461	C 1.231 O 0.056 1.175 A Ile 465	CA 1.540 CB 0.146 1.394 A Ile 465	CA 1.525 C 0.094 1.431 A Arg 467
CA 1.525 C 0.132 1.393 A Pro 469	CA 1.530 CB 0.057 1.587 A Leu 471	CA 1.525 C 0.066 1.459 A Met 472	CA 1.530 CB 0.061 1.469 A Met 472	CA 1.530 CB 0.085 1.615 A Lys 474	CA 1.525 C 0.073 1.452 A Thr 475
C 1.231 O 0.052 1.179 A Lys 478	CA 1.530 CB 0.051 1.479 A Leu 479	CA 1.525 C 0.090 1.435 A Ala 480	CA 1.530 CB 0.075 1.605 A Glu 481	C 1.231 O 0.069 1.162 A Glu 484	CA 1.525 C 0.121 1.404 A Glu 484
CA 1.530 CB 0.074 1.604 A Glu 484	C 1.231 O 0.054 1.285 A Phe 486	CA 1.530 CB 0.086 1.616 A Lys 487	CA 1.525 C 0.072 1.453 A Val 489	CA 1.540 CB 0.059 1.599 A Val 489	CA 1.530 CB 0.102 1.428 A Arg 490
C 1.231 O 0.072 1.159 A Thr 494	CA 1.530 CB 0.064 1.594 A Asn 499	CA 1.540 CB 0.052 1.592 A Thr 500	C 1.231 O 0.060 1.171 A Tyr 504	C 1.231 O 0.056 1.175 A Glu 507	CA 1.530 CB 0.060 1.590 A Leu 508
C 1.231 O 0.057 1.174 A His 510	C 1.231 O 0.071 1.160 A Leu 512	CA 1.530 CB 0.051 1.581 A Leu 512	C 1.231 O 0.058 1.173 A Asn 513	CA 1.540 CB 0.110 1.430 A Val 514	CA 1.530 CB 0.078 1.608 A Glu 516
CA 1.530 CB 0.053 1.477 A Cys 517	CA 1.525 C 0.055 1.580 A Met 518	CA 1.521 CB 0.053 1.574 A Ala 519	CA 1.530 CB 0.072 1.458 A His 520	CA 1.525 C 0.055 1.470 A Ser 521	CA 1.521 CB 0.119 1.640 A Ala 522
CA 1.530 CB 0.072 1.602 A Met 523	C 1.231 O 0.053 1.178 A Leu 535	CA 1.525 C 0.088 1.437 A Leu 535	CA 1.525 C 0.099 1.426 A Cys 539	C 1.329 N 0.069 1.260 A Cys 539 - A Thr 540	CA 1.525 C 0.075 1.450 A Arg 542
CA 1.530 CB 0.062 1.468 A Arg 542	CA 1.530 CB 0.159 1.689 A Asp 543	C 1.231 O 0.096 1.135 A Asp 544	C 1.231 O 0.087 1.144 A Val 545	CA 1.525 C 0.066 1.459 A Val 545	CA 1.540 CB 0.069 1.609 A Val 545
CA 1.530 CB 0.113 1.643 A Asn 546	CA 1.530 CB 0.089 1.619 A Phe 547	CA 1.530 CB 0.066 1.464 A Leu 548	CA 1.530 CB 0.053 1.477 A His 550	CA 1.521 CB 0.078 1.443 A Ala 553	C 1.329 N 0.072 1.257 A Arg 555 - A Asp 556

Distorted geometry
pdb2b76

Main-chain bond lengths (contd)

CA 1.525 C
0.109
1.633
A Ala 557

N 1.458 CA
0.063
1.521
A Ala 557

N 1.458 CA
0.053
1.511
A Asp 558

CA 1.540 CB
0.082
1.457
A Thr 560

CA 1.540 CB
0.059
1.481
A Thr 561

CA 1.530 CB
0.055
1.585
A Arg 562

CA 1.530 CB
0.093
1.437
A Leu 563

C 1.231 O
0.051
1.180
A Tyr 565

CA 1.530 CB
0.074
1.456
A Asp 567

CA 1.530 CB
0.117
1.413
A Pro 574

CA 1.525 C
0.100
1.425
A Pro 575

C 1.329 N
0.100
1.229
A Pro 575 - A Ala 576

C 1.231 O
0.063
1.168
A Ala 576

CA 1.521 CB
0.174
1.695
A Ala 576

N 1.458 CA
0.054
1.404
A Ala 576

CA 1.525 C
0.059
1.584
B Asn 5

CA 1.540 CB
0.054
1.486
B Val 11

CA 1.525 C
0.070
1.455
B Glu 16

N 1.458 CA
0.051
1.509
B Glu 16

CA 1.530 CB
0.061
1.469
B Tyr 30

C 1.231 O
0.080
1.151
B Asp 31

CA 1.521 CB
0.085
1.436
B Ala 39

C 1.231 O
0.055
1.176
B Tyr 42

CA 1.530 CB
0.079
1.451
B Tyr 42

CA 1.530 CB
0.057
1.473
B Asn 46

CA 1.530 CB
0.057
1.473
B Asp 50

CA 1.530 CB
0.056
1.474
B Tyr 53

C 1.231 O
0.119
1.112
B Ser 56

CA 1.540 CB
0.090
1.450
B Val 69

CA 1.525 C
0.051
1.474
B Asn 71

CA 1.525 C
0.058
1.467
B Cys 77

C 1.231 O
0.051
1.180
B Thr 79

CA 1.521 CB
0.057
1.464
B Ala 92

CA 1.540 CB
0.080
1.460
B Ile 98

CA 1.540 CB
0.066
1.474
B Val 104

CA 1.516 C
0.069
1.585
B Gly 130

N 1.451 CA
0.064
1.515
B Gly 130

CA 1.525 C
0.063
1.462
B Ile 133

CA 1.540 CB
0.061
1.479
B Ile 133

CA 1.525 C
0.052
1.473
B Thr 135

CA 1.540 CB
0.071
1.469
B Thr 135

C 1.231 O
0.063
1.168
B Pro 136

CA 1.530 CB
0.059
1.471
B Pro 136

CA 1.525 C
0.060
1.465
B Leu 175

CA 1.540 CB
0.121
1.419
B Val 207

CA 1.540 CB
0.060
1.480
B Val 213

CA 1.521 CB
0.068
1.453
B Ala 221

C 1.231 O
0.089
1.142
B Asp 234

C 1.231 O
0.056
1.175
B Leu 236

CA 1.540 CB
0.051
1.591
B Ile 237

CA 1.530 CB
0.080
1.610
B Lys 241

C 1.329 N
0.085
1.244
B Pro 242 - B Arg 243

C 1.231 O
0.087
1.318
C Thr 1

CA 1.540 CB
0.081
1.621
C Thr 1

N 1.458 CA
0.058
1.516
C Thr 1

C 1.231 O
0.055
1.286
C Thr 2

C 1.231 O
0.057
1.288
C Lys 3

CA 1.525 C
0.058
1.467
C Thr 75

CA 1.540 CB
0.065
1.475
C Thr 75

CA 1.521 CB
0.068
1.453
C Ala 93

CA 1.540 CB
0.055
1.595
C Ile 96

CA 1.540 CB
0.057
1.597
C Val 98

CA 1.521 CB
0.054
1.467
C Ala 114

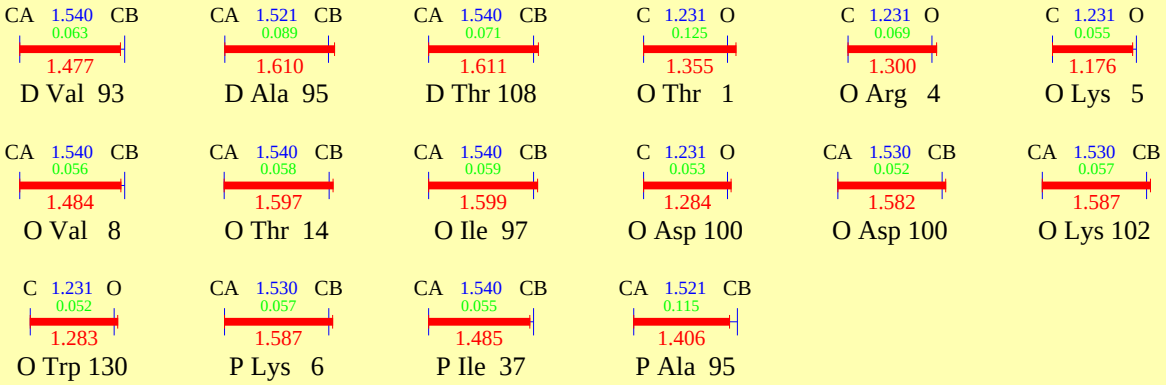
CA 1.540 CB
0.053
1.487
C Val 118

CA 1.530 CB
0.053
1.477
C Trp 130

CA 1.525 C
0.052
1.473
D Pro 3

Distorted geometry
pdb2b76

Main-chain bond lengths (contd)

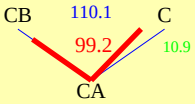


Bonds differing by > 0.05A from small-molecule values. Values shown: "ideal", difference, actual

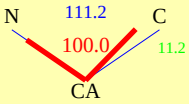
Main-chain bond angles

Distorted geometry
pdb2b76

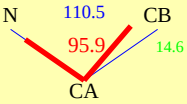
Main-chain bond angles (contd)



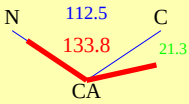
A Asp 265



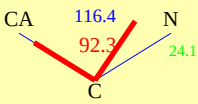
A Tyr 266



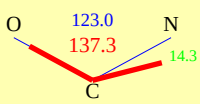
A Tyr 266



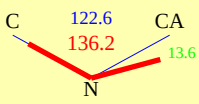
A Gly 269



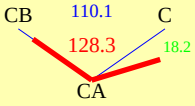
A Gly 269 - A Pro 270



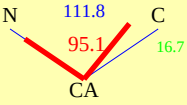
A Gly 269 - A Pro 270



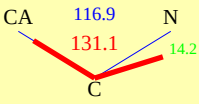
A Gly 269 - A Pro 270



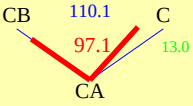
A Pro 270



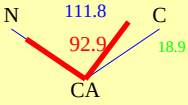
A Pro 270



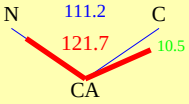
A Pro 270 - A Glu 271



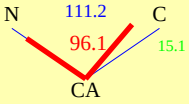
A Glu 276



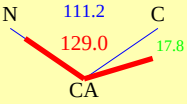
A Pro 277



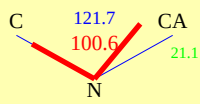
A Asn 302



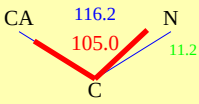
A Val 312



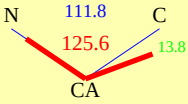
A Glu 321



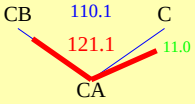
A His 325 - A Glu 326



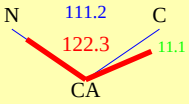
A Glu 326 - A Arg 327



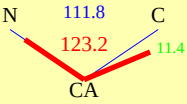
A Pro 329



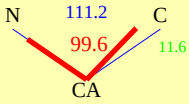
A Phe 330



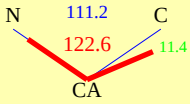
A Val 341



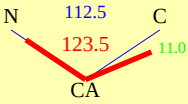
A Pro 343



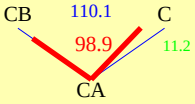
A Glu 346



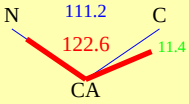
A His 355



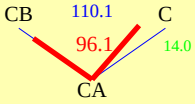
A Gly 360



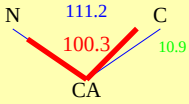
A Asn 366



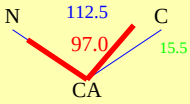
A His 386



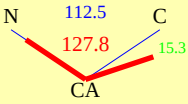
A Leu 391



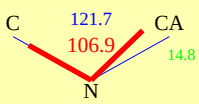
A Ala 410



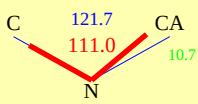
A Gly 418



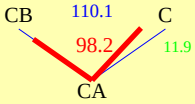
A Gly 445



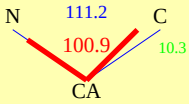
A Glu 446 - A Asn 447



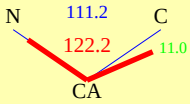
A Asn 447 - A Trp 448



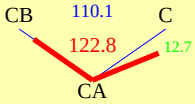
A Trp 448



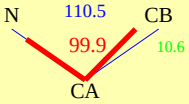
A Val 489



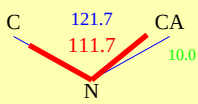
A Thr 492



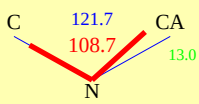
A Cys 517



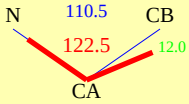
A Cys 517



A Ala 519 - A His 520



A Gly 538 - A Cys 539



A Asp 544

A Val 545

A Phe 547

A Arg 555 - A Asp 556

A Asp 556 - A Ala 557

A Asp 556 - A Ala 557

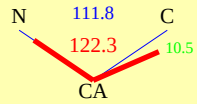
A Thr 560

A Ser 566

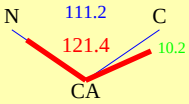
A Leu 573

Distorted geometry
pdb2b76

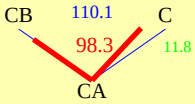
Main-chain bond angles (contd)



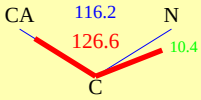
A Pro 575



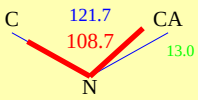
B Met 3



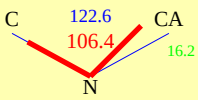
B Tyr 13



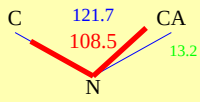
B Tyr 13 - B Asn 14



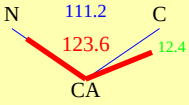
B Tyr 13 - B Asn 14



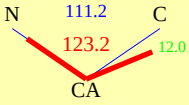
B Asn 14 - B Pro 15



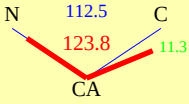
B Pro 15 - B Glu 16



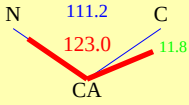
B Asn 46



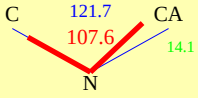
B Ser 124



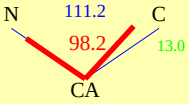
B Gly 169



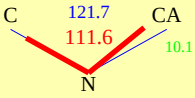
B Lys 241



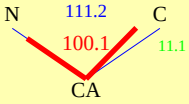
C Thr 1 - C Thr 2



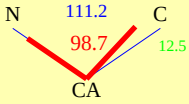
C Thr 2



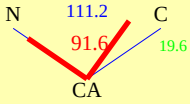
C Thr 2 - C Lys 3



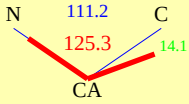
C Ile 70



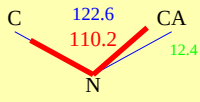
C Ala 94



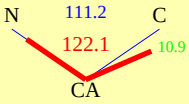
C Lys 99



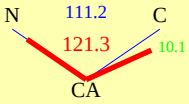
C Trp 130



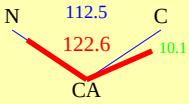
D Leu 39 - D Pro 40



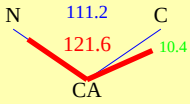
D Phe 61



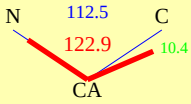
M Gln 25



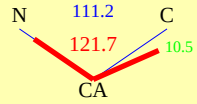
M Gly 169



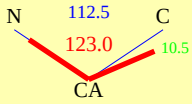
M Glu 227



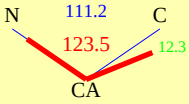
M Gly 267



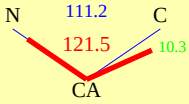
M Asn 394



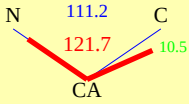
M Gly 464



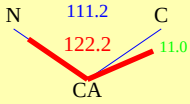
M Lys 487



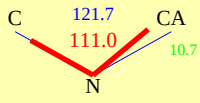
M Asn 546



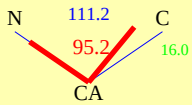
M Phe 547



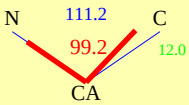
N Lys 189



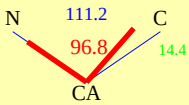
O Ile 68 - O Val 69



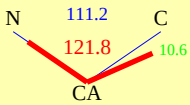
O Ile 70



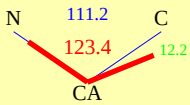
O Ala 94



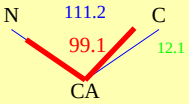
O Lys 99



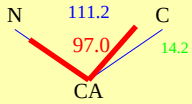
O Met 103



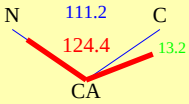
O Leu 128



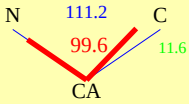
P Ile 1



P Asn 4



P Glu 10



P Val 12

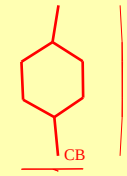
P Ile 27

P Ala 48

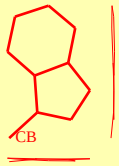
Bond angles differing by > 10.0 degrees from small-molec values. Values shown: "ideal", actual, diff.

Distorted geometry
pdb2b76

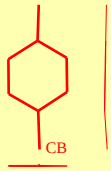
Planar groups



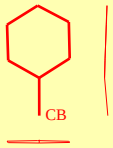
0.037
A Tyr 64



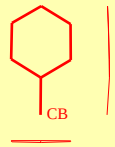
0.043
A Trp 75



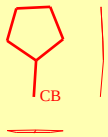
0.033
A Tyr 84



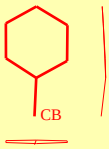
0.043
A Phe 133



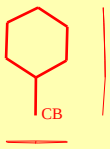
0.034
A Phe 152



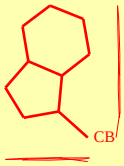
0.045
A His 219



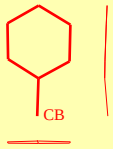
0.060
A Phe 228



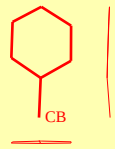
0.034
A Phe 402



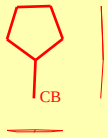
0.046
A Trp 448



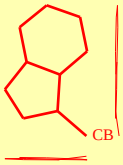
0.043
A Phe 498



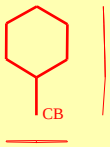
0.040
A Phe 547



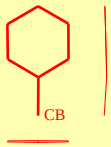
0.036
A His 550



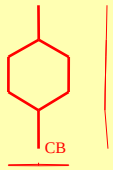
0.044
B Trp 55



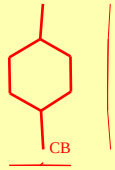
0.033
B Phe 80



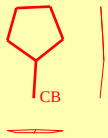
0.032
B Phe 109



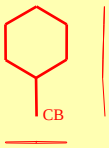
0.038
B Tyr 142



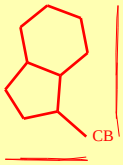
0.045
B Tyr 179



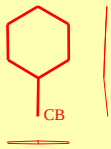
0.055
B His 217



0.031
C Phe 21



0.039
C Trp 113



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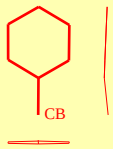
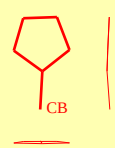
C Phe 125



0.050
D Phe 13



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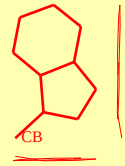
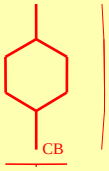
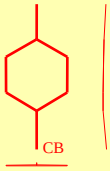
D His 80



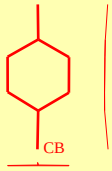
0.053
D Trp 98



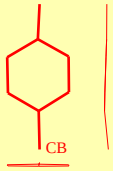
0.043
M Tyr 356



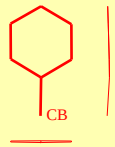
0.050
N Tyr 30



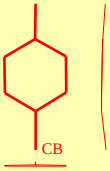
0.053
N Tyr 209



0.047
O Tyr 7



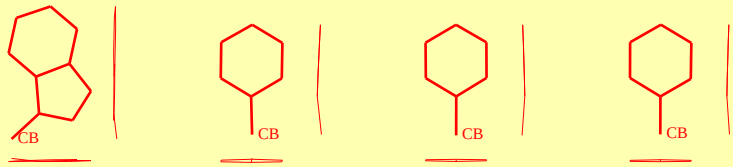
0.031
O Phe 87



0.065
O Tyr 129

Distorted geometry
pdb2b76

Planar groups (contd)



0.038	0.055	0.036	0.034
O Trp 130	P Phe 17	P Phe 66	P Phe 100

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