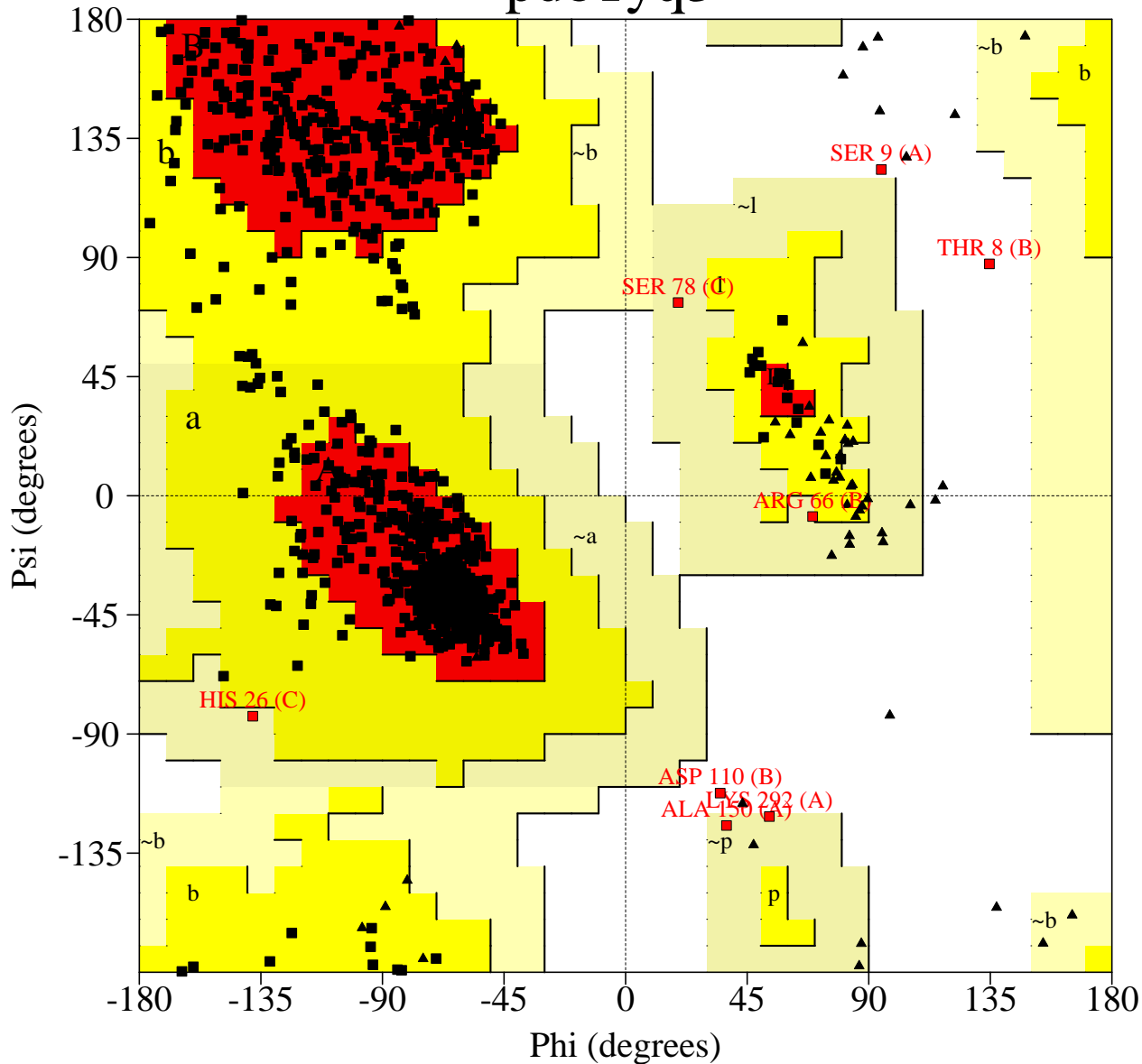


# Ramachandran Plot

## pdb1yq3



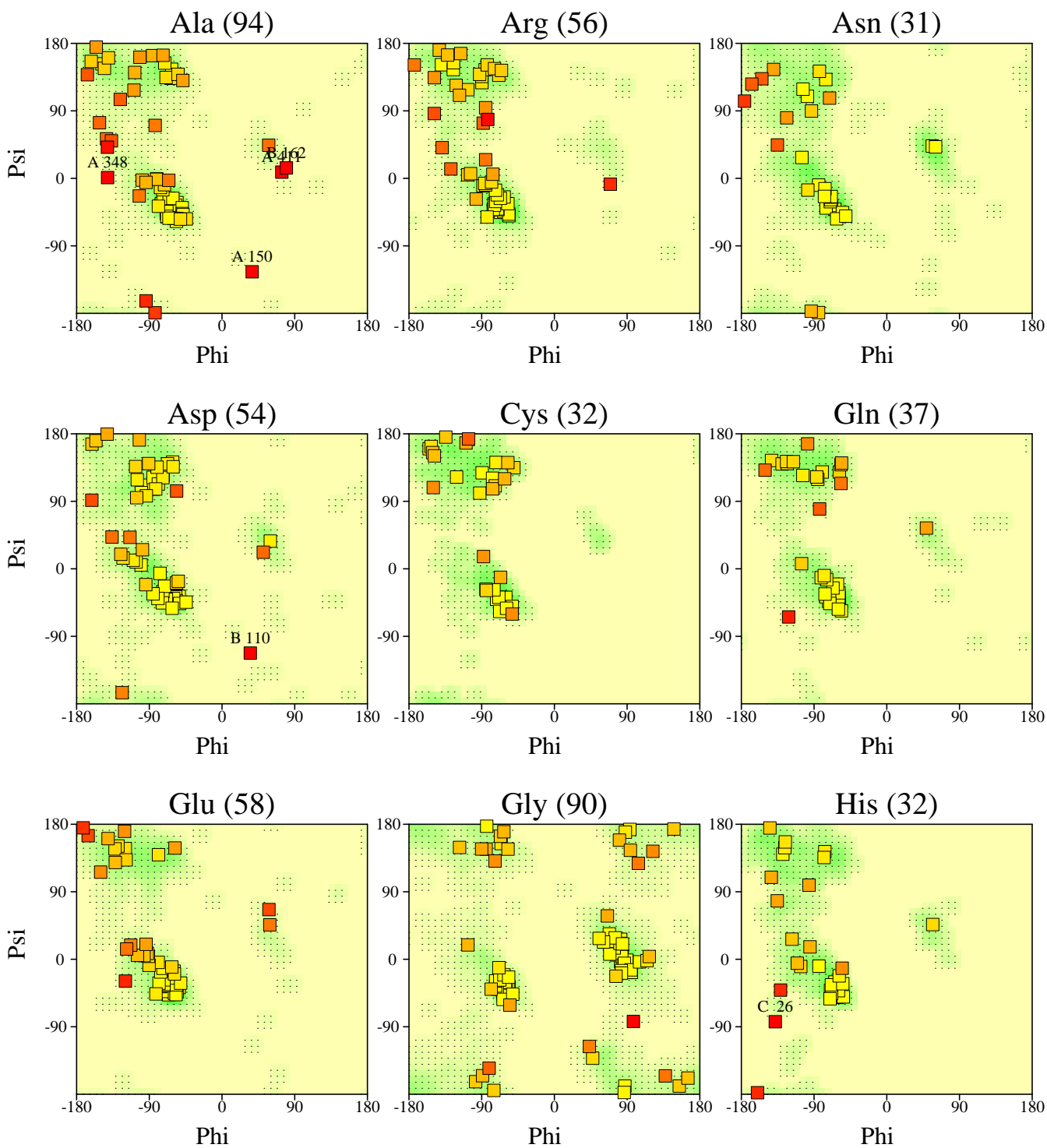
### Plot statistics

Residues in most favoured regions [A,B,L]	842	88.6%
Residues in additional allowed regions [a,b,l,p]	100	10.5%
Residues in generously allowed regions [-a,-b,-l,-p]	5	0.5%
Residues in disallowed regions	3	0.3%
-----		
Number of non-glycine and non-proline residues	950	100.0%
Number of end-residues (excl. Gly and Pro)	8	
Number of glycine residues (shown as triangles)	90	
Number of proline residues	50	
-----		
Total number of residues	1098	

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

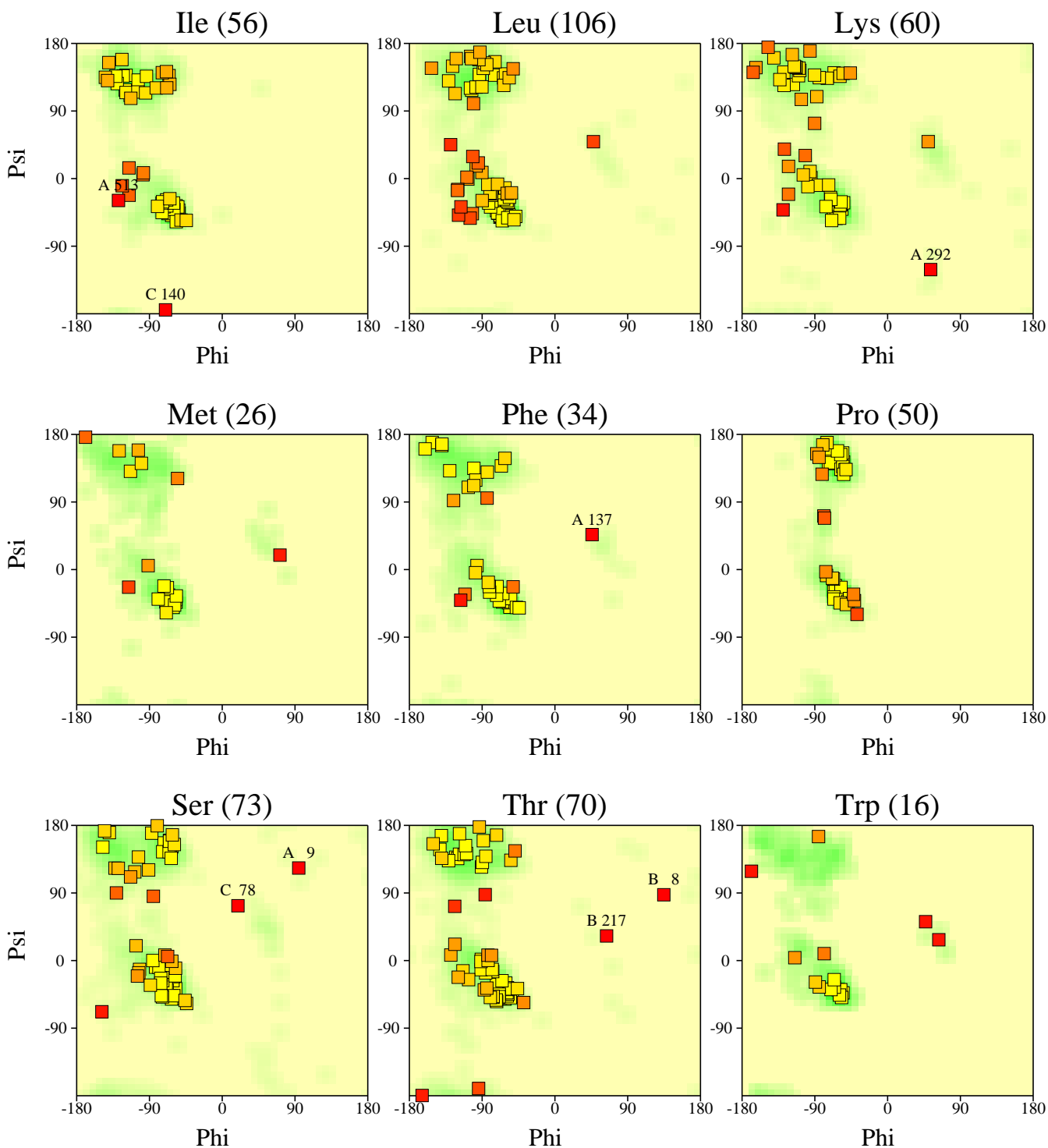
## pdb1yq3



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

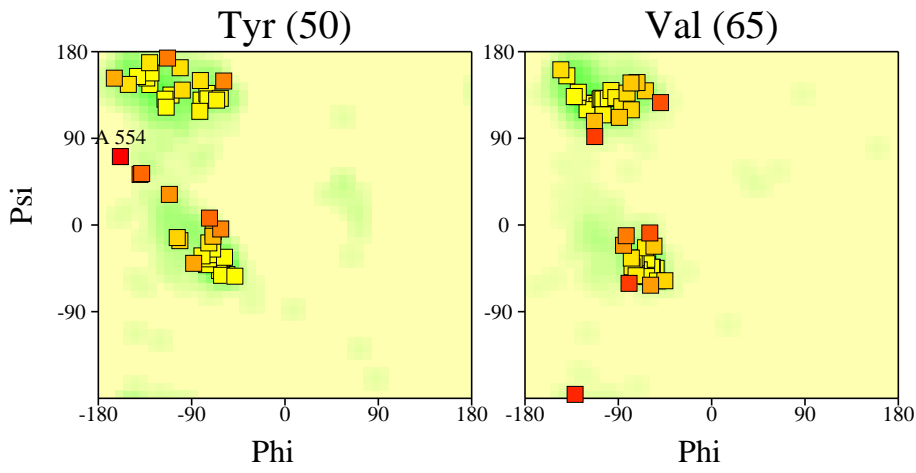
## pdb1yq3



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

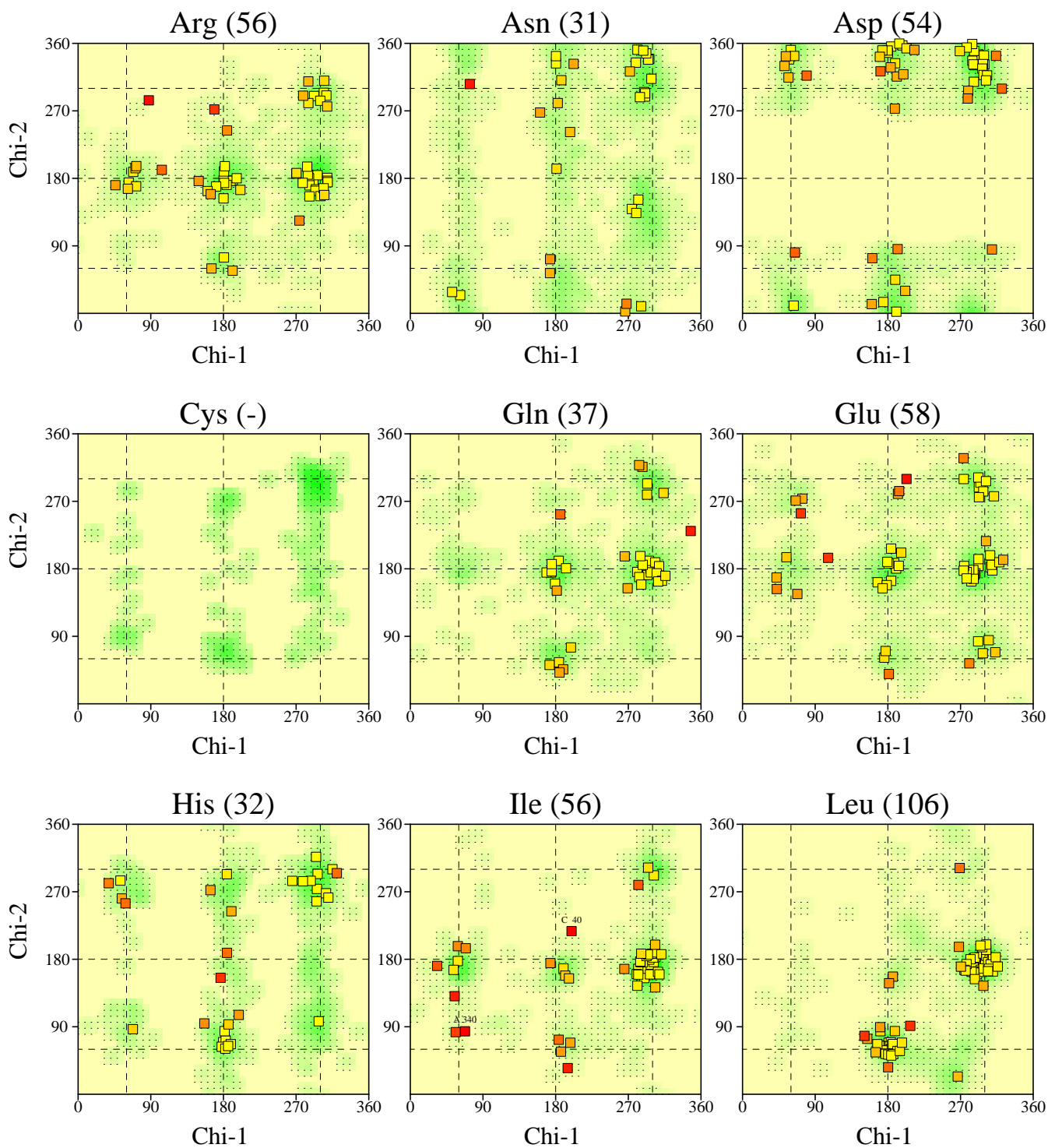
## pdb1yq3



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

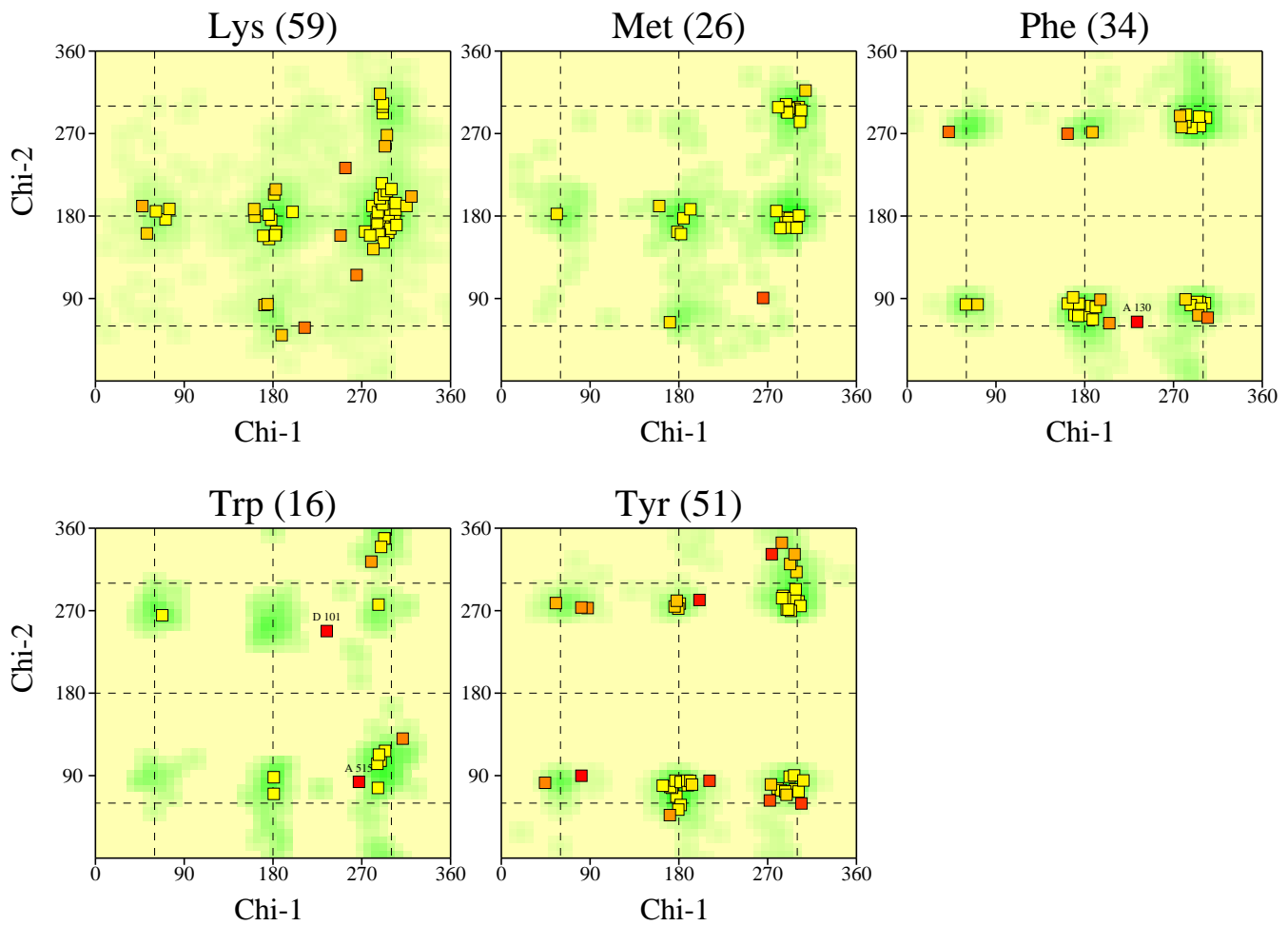
## pdb1yq3



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

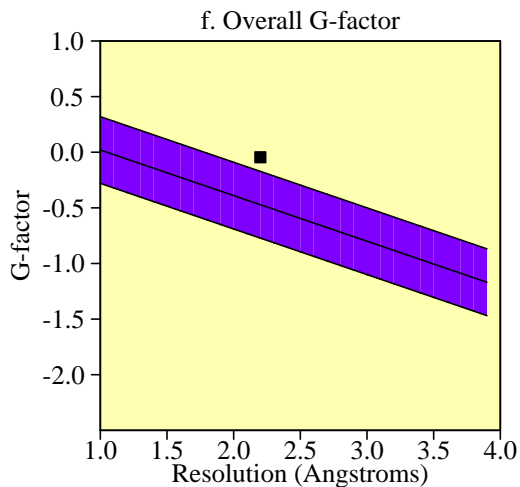
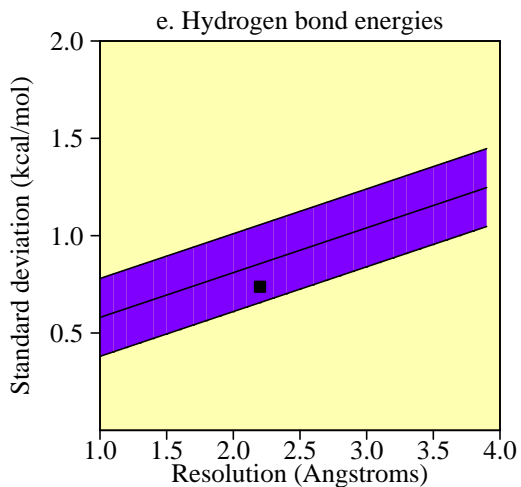
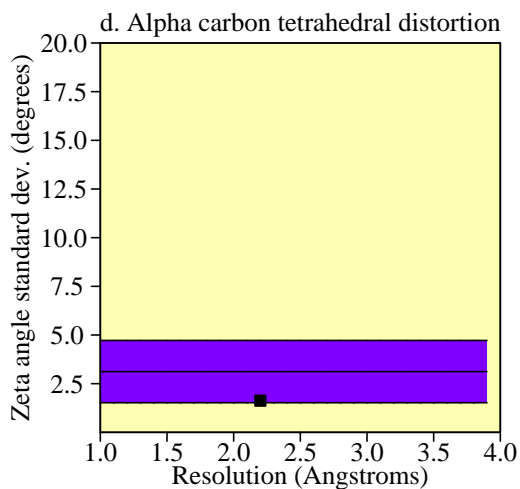
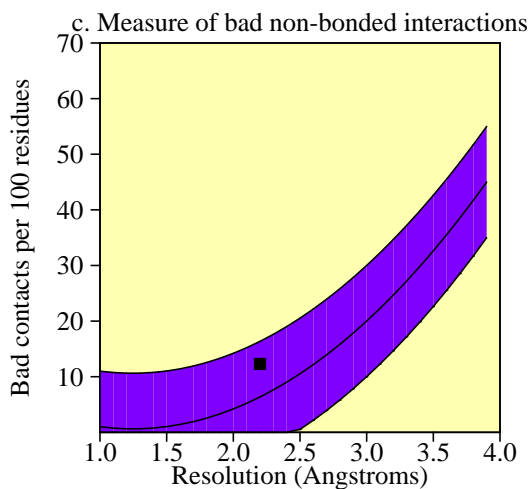
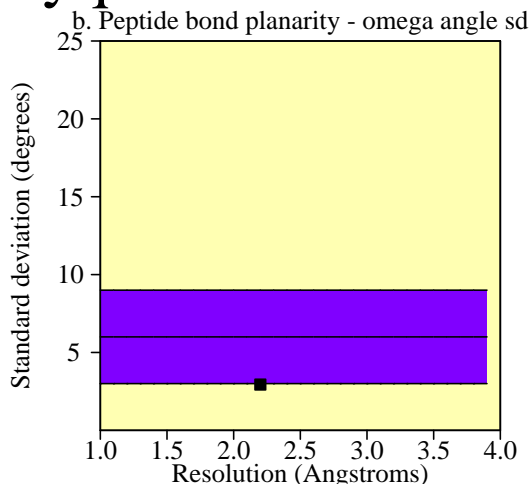
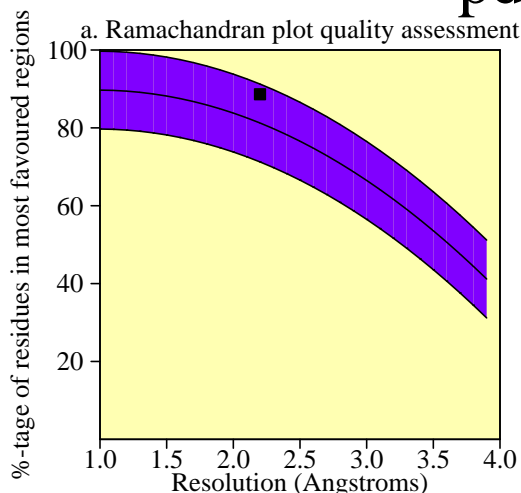
## pdb1yq3



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

# Main-chain parameters

## pdb1yq3

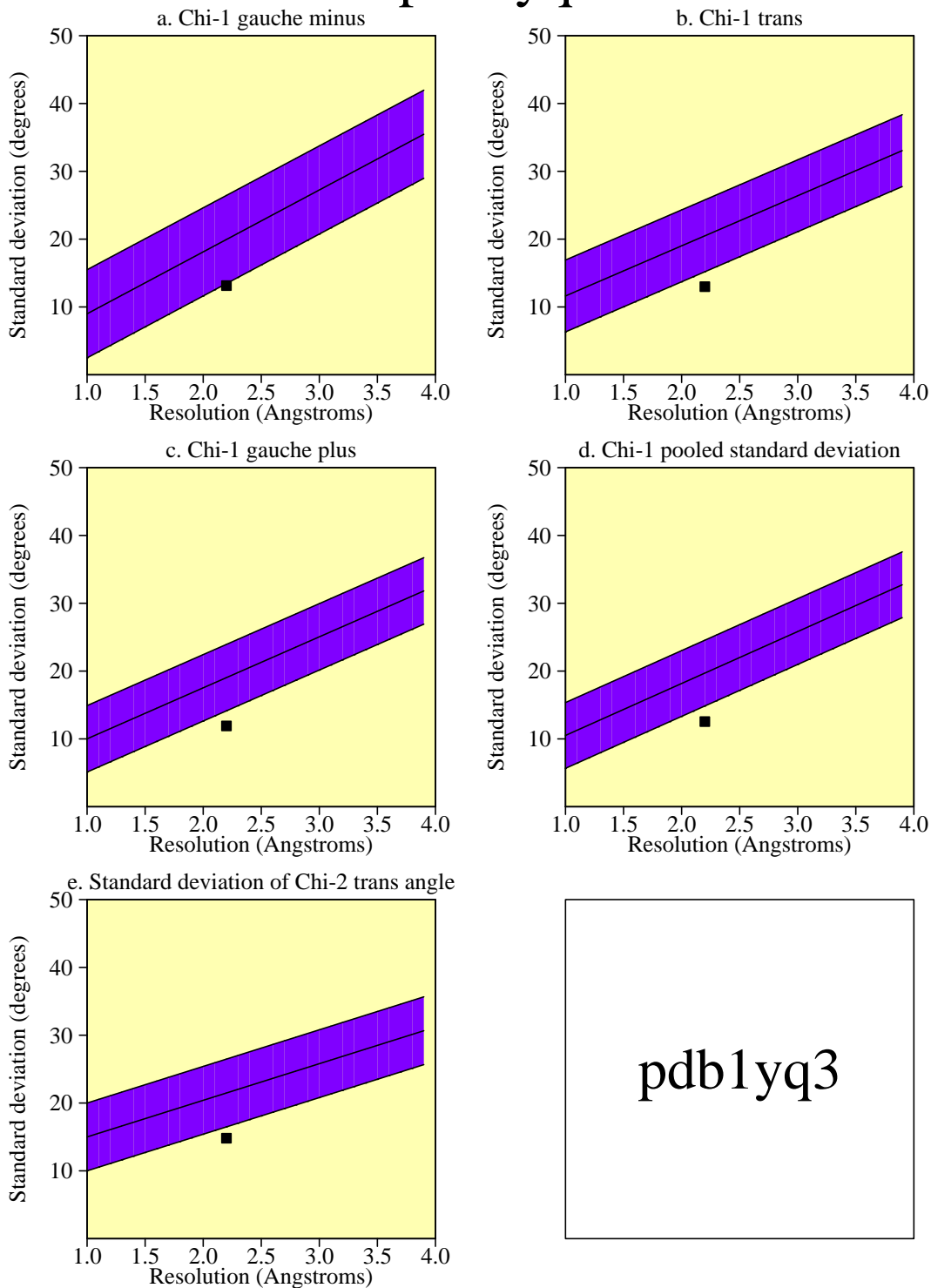


### Plot statistics

Stereochemical parameter	No. of data pts	Parameter value	Comparison values		No. of band widths from mean
			Typical value	Band width	
a. %-tage residues in A, B, L	950	88.6	81.3	10.0	0.7 Inside
b. Omega angle st dev	1092	2.9	6.0	3.0	-1.0 BETTER
c. Bad contacts / 100 residues	135	12.3	6.4	10.0	0.6 Inside
d. Zeta angle st dev	1007	1.6	3.1	1.6	-0.9 Inside
e. H-bond energy st dev	717	0.7	0.9	0.2	-0.6 Inside
f. Overall G-factor	1098	0.0	-0.5	0.3	1.4 BETTER

# Side-chain parameters

## pdb1yq3



pdb1yq3

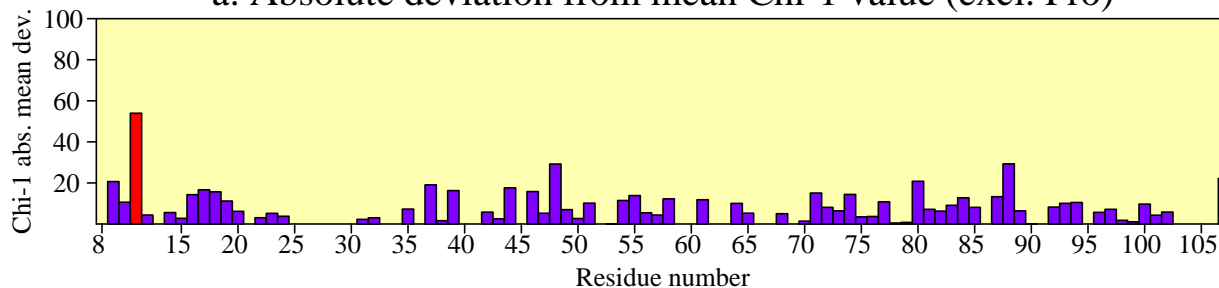
### Plot statistics

Stereochemical parameter	No. of data pts	Parameter value	Comparison values		No. of band widths from mean	
			Typical value	Band width		
a. Chi-1 gauche minus st dev	129	13.1	19.9	6.5	-1.0	BETTER
b. Chi-1 trans st dev	274	13.0	20.5	5.3	-1.4	BETTER
c. Chi-1 gauche plus st dev	453	11.9	19.0	4.9	-1.5	BETTER
d. Chi-1 pooled st dev	856	12.5	19.7	4.8	-1.5	BETTER
e. Chi-2 trans st dev	287	14.8	21.5	5.0	-1.3	BETTER

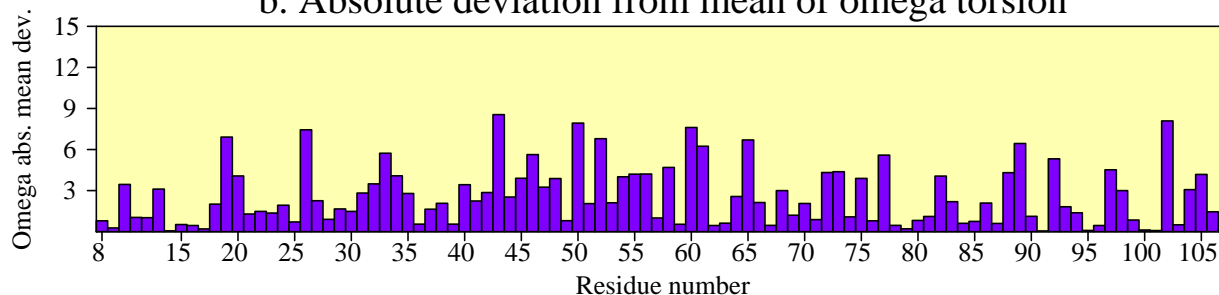


# Residue properties pdb1yq3

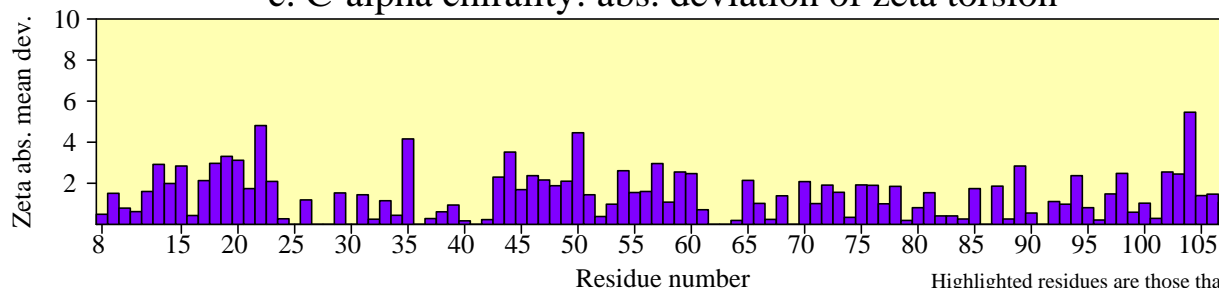
### a. Absolute deviation from mean Chi-1 value (excl. Pro)



### b. Absolute deviation from mean of omega torsion

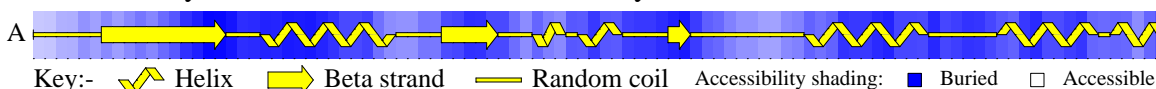


### c. C-alpha chirality: abs. deviation of zeta torsion

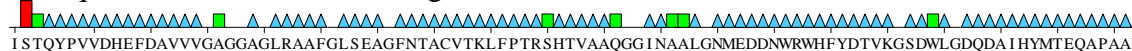


Highlighted residues are those that deviate by more than 2.0 st. devs. from ideal

### d. Secondary structure & estimated accessibility



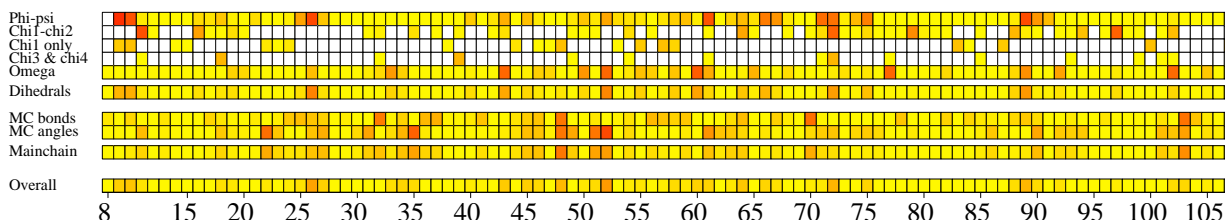
### e. Sequence & Ramachandran regions



### f. Max. deviation (see listing)

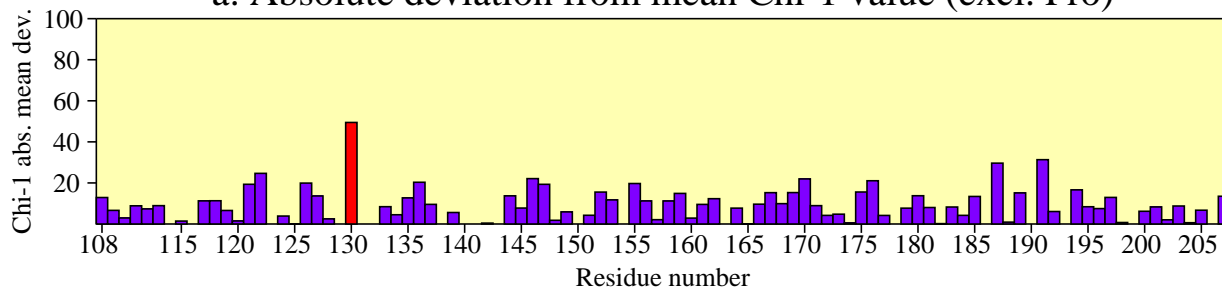


### g. G-factors

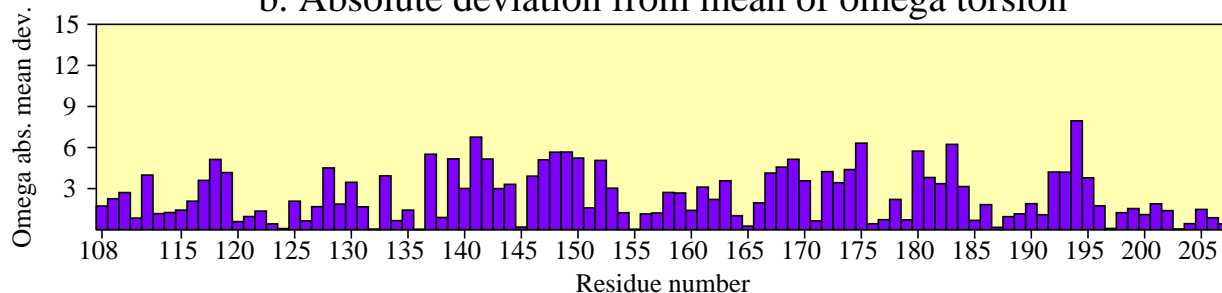


# Residue properties pdb1yq3

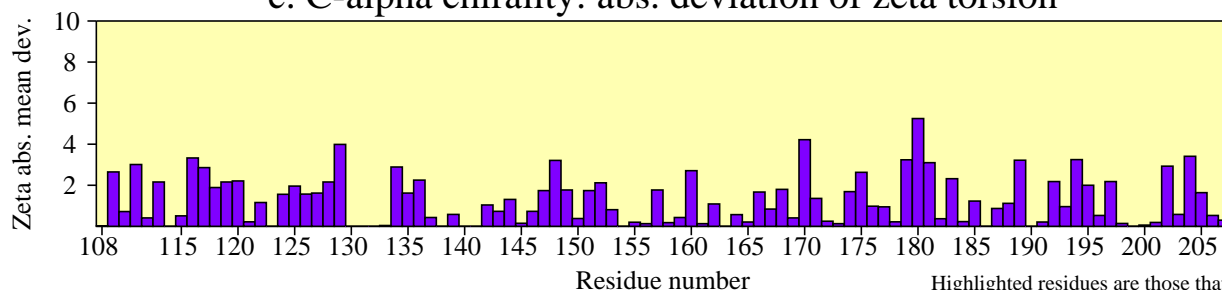
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion

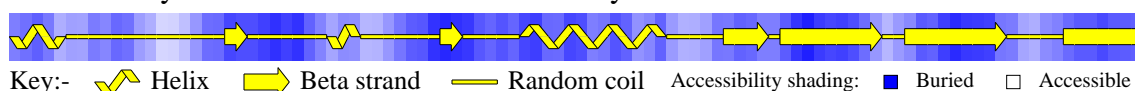


c. C-alpha chirality: abs. deviation of zeta torsion



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

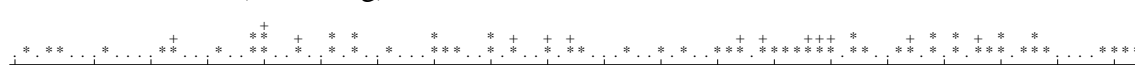
d. Secondary structure & estimated accessibility



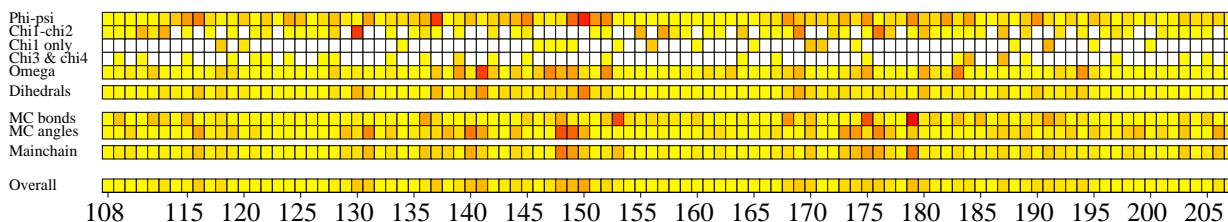
e. Sequence & Ramachandran regions Most favoured Allowed Generous Disallowed



f. Max. deviation (see listing)

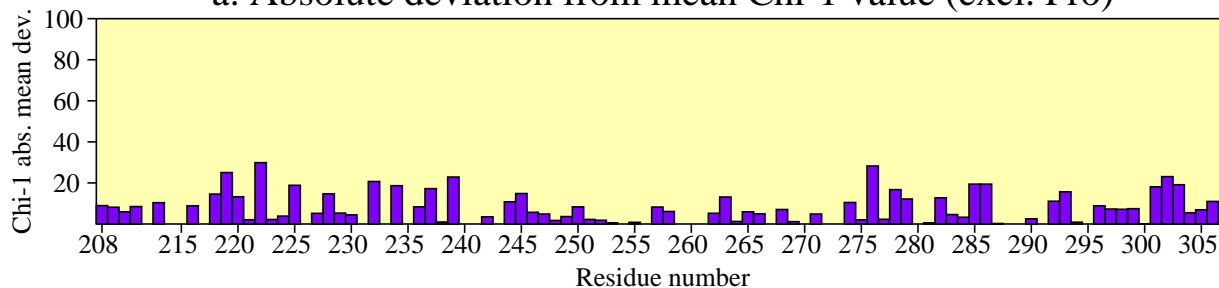


g. G-factors

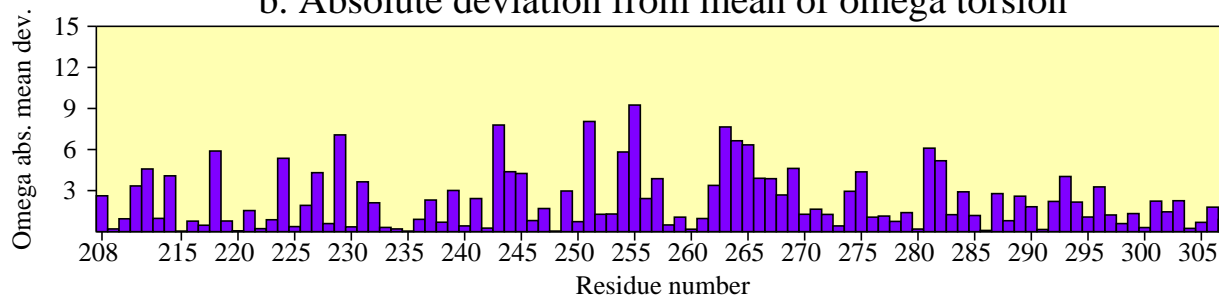


# Residue properties pdb1yq3

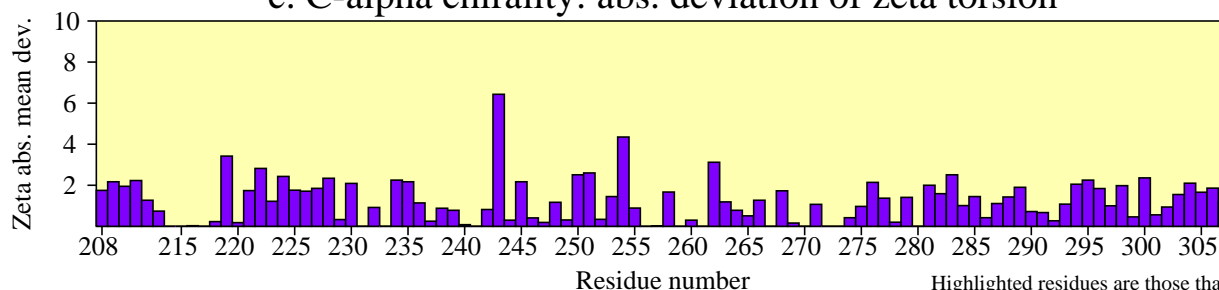
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion

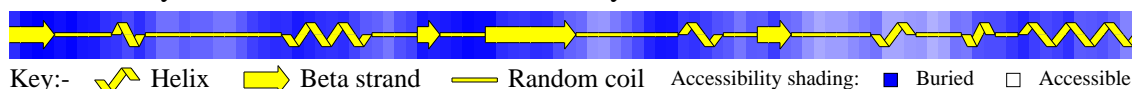


c. C-alpha chirality: abs. deviation of zeta torsion



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

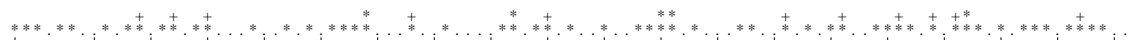
d. Secondary structure & estimated accessibility



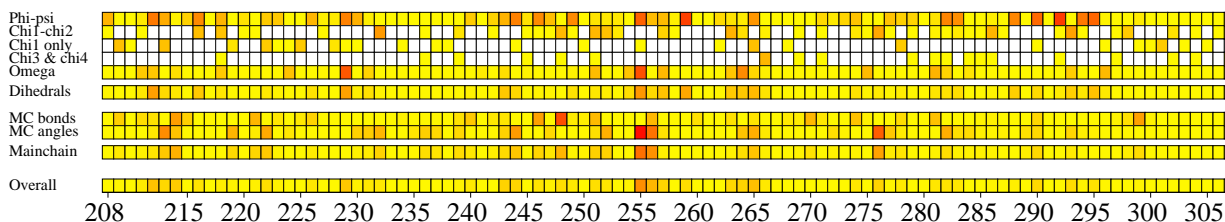
e. Sequence & Ramachandran regions



f. Max. deviation (see listing)

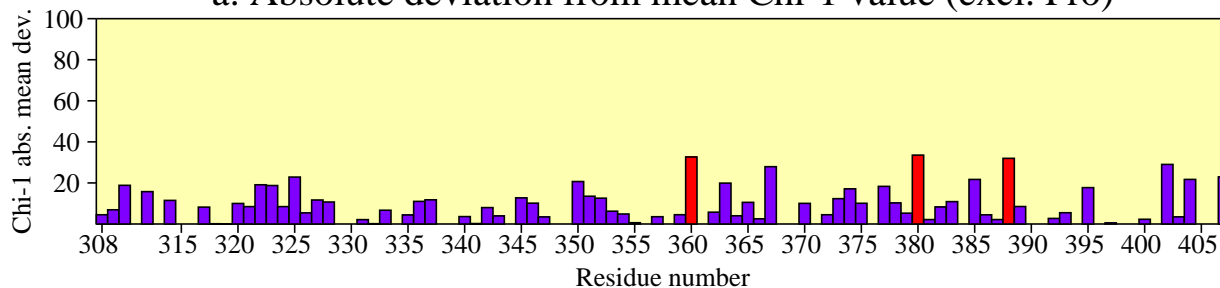


g. G-factors

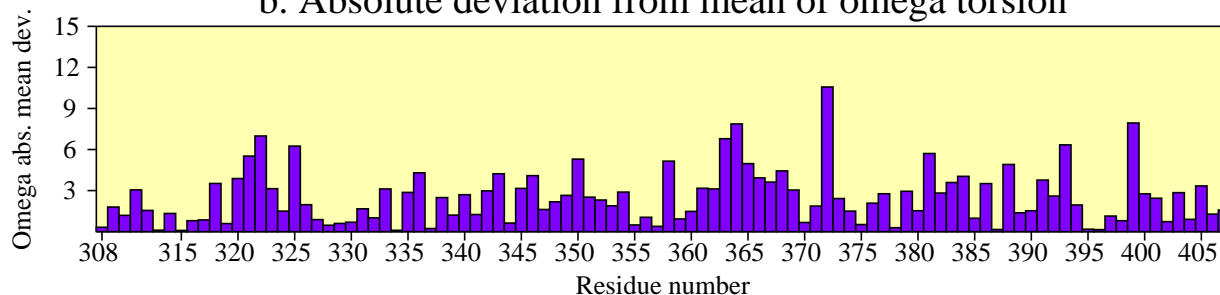


# Residue properties pdb1yq3

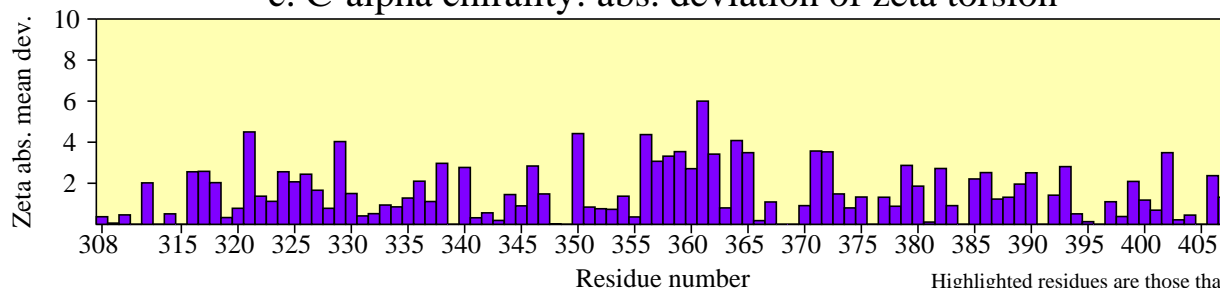
### a. Absolute deviation from mean Chi-1 value (excl. Pro)



### b. Absolute deviation from mean of omega torsion

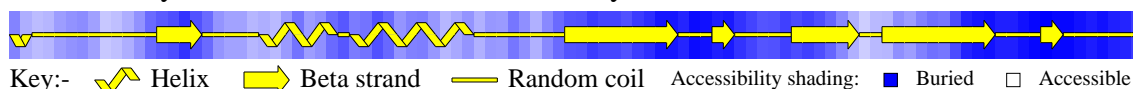


### c. C-alpha chirality: abs. deviation of zeta torsion



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

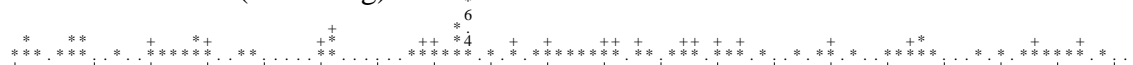
### d. Secondary structure & estimated accessibility



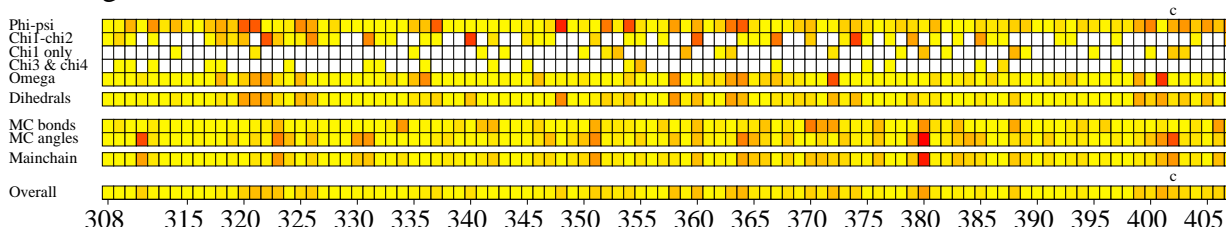
### e. Sequence & Ramachandran regions



### f. Max. deviation (see listing)



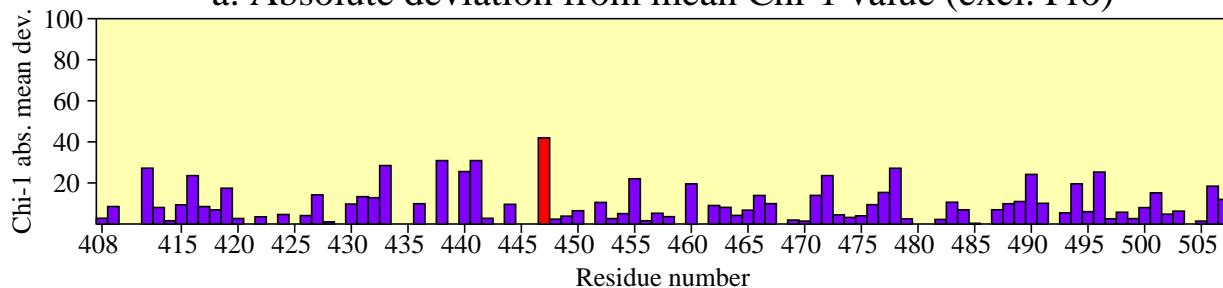
### g. G-factors



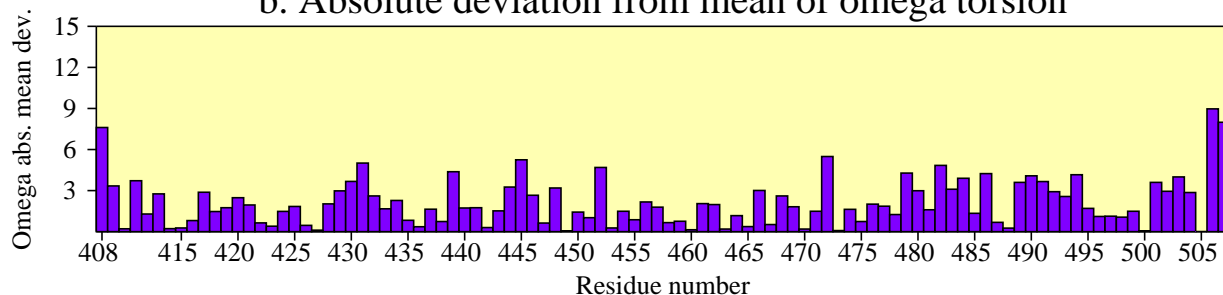
c = cis-peptide

# Residue properties pdb1yq3

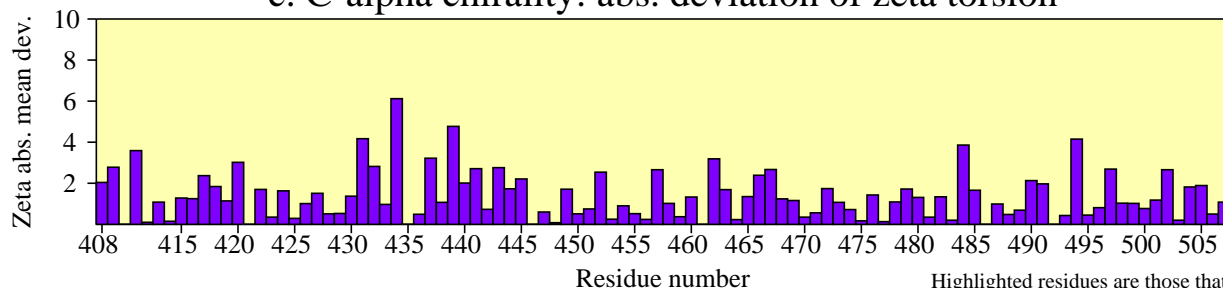
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion

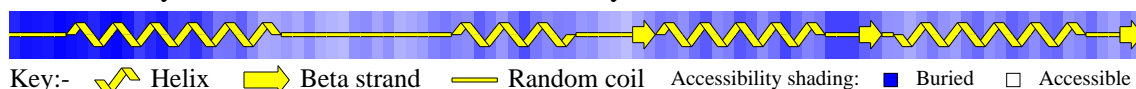


c. C-alpha chirality: abs. deviation of zeta torsion



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

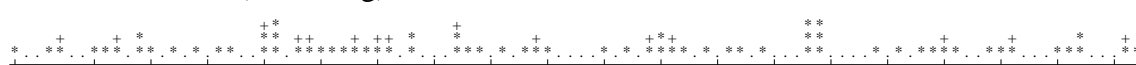
d. Secondary structure & estimated accessibility



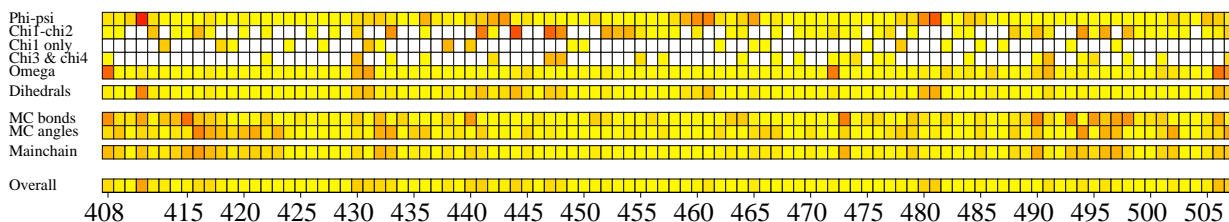
e. Sequence & Ramachandran regions



f. Max. deviation (see listing)

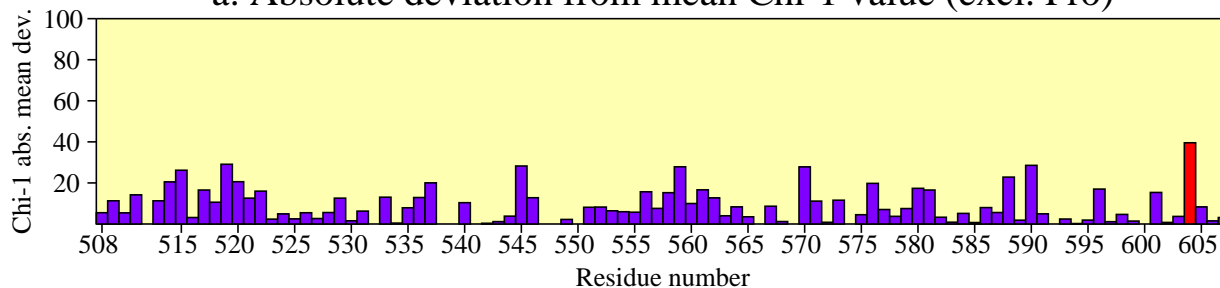


g. G-factors

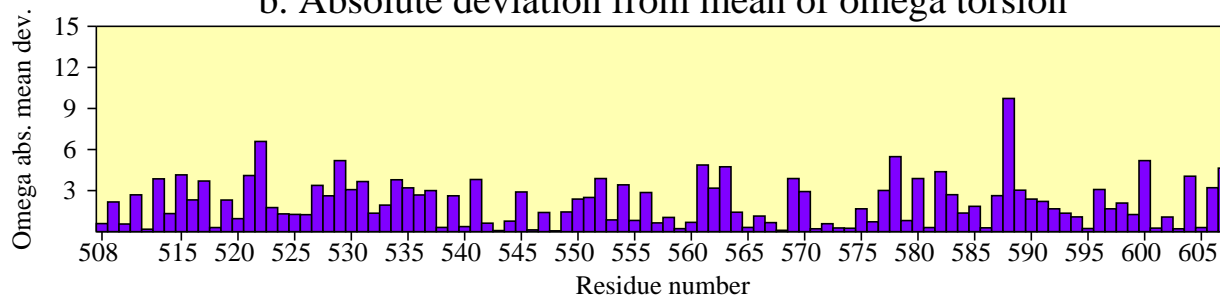


# Residue properties pdb1yq3

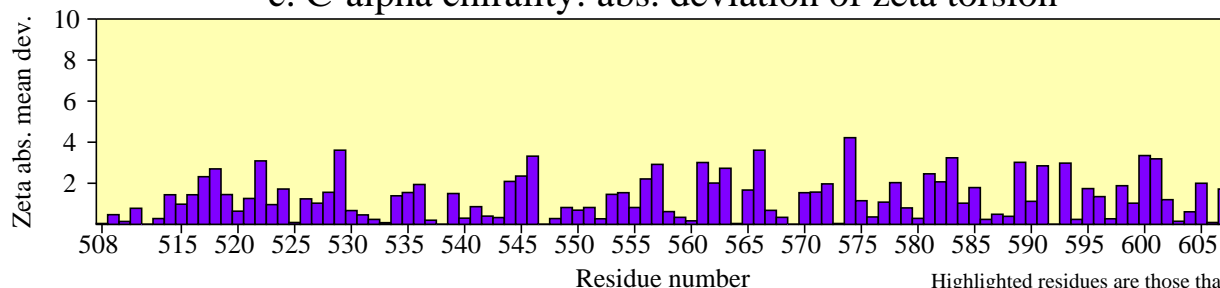
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion

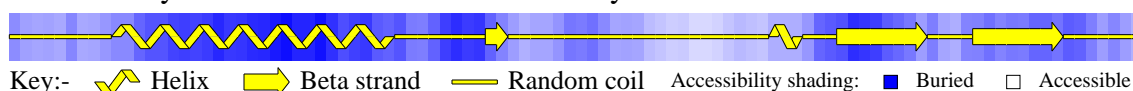


c. C-alpha chirality: abs. deviation of zeta torsion



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

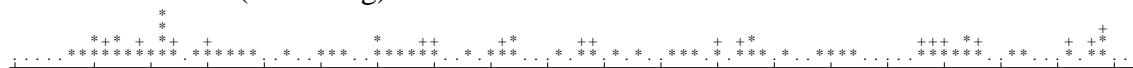
d. Secondary structure & estimated accessibility



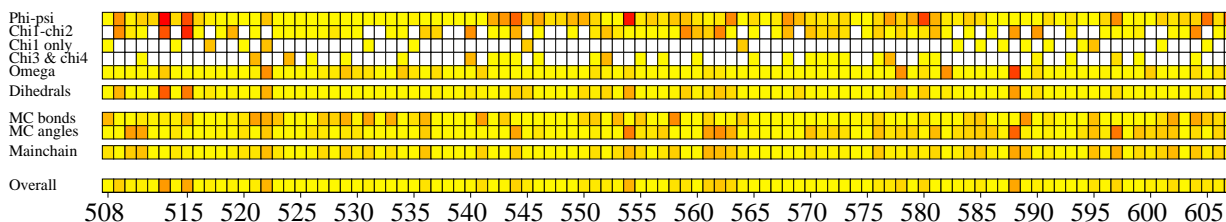
e. Sequence & Ramachandran regions



f. Max. deviation (see listing)



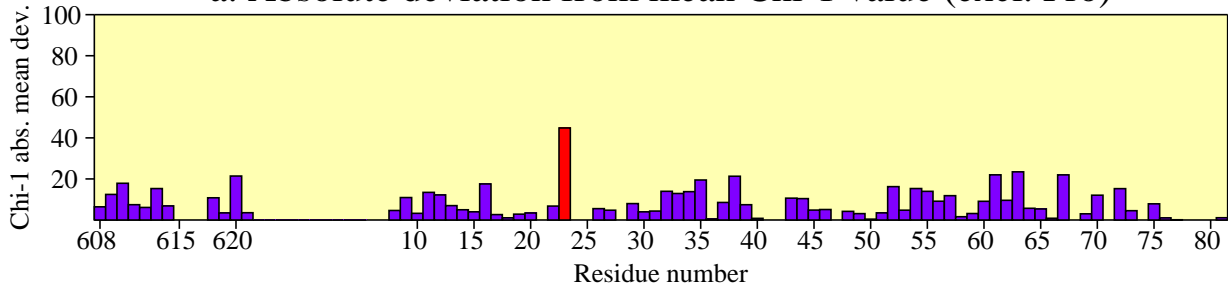
g. G-factors



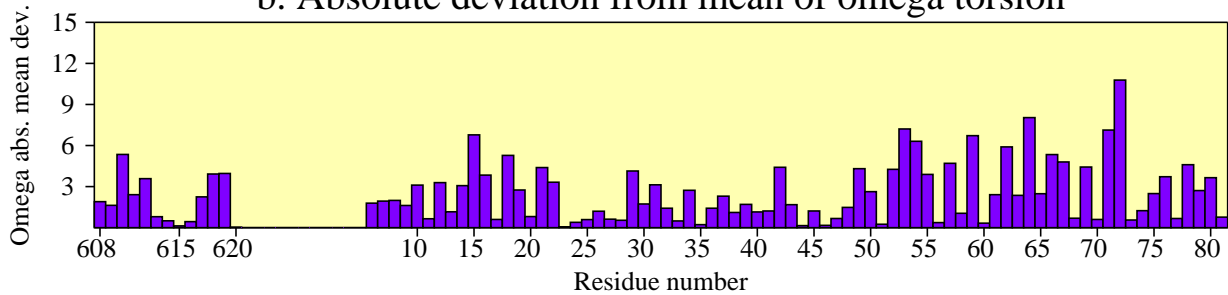
# Residue properties

## pdb1yq3

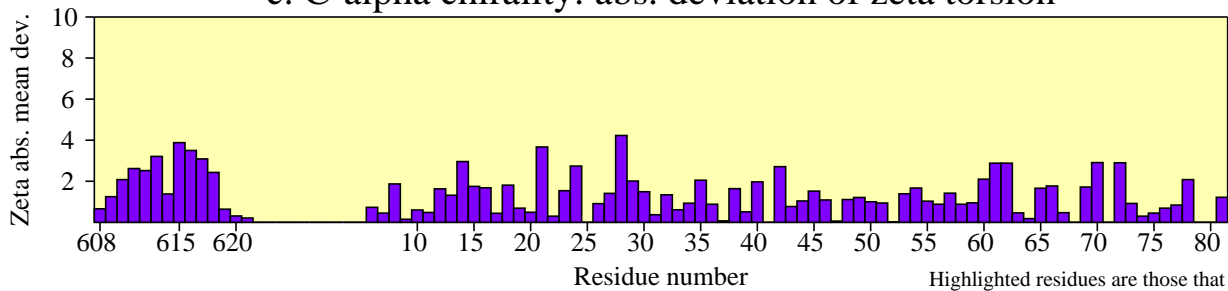
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion

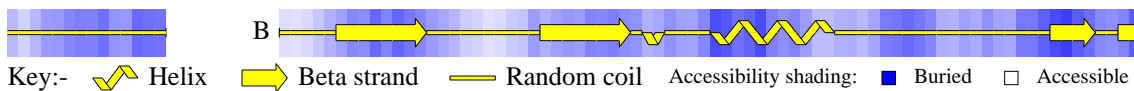


c. C-alpha chirality: abs. deviation of zeta torsion



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

d. Secondary structure & estimated accessibility



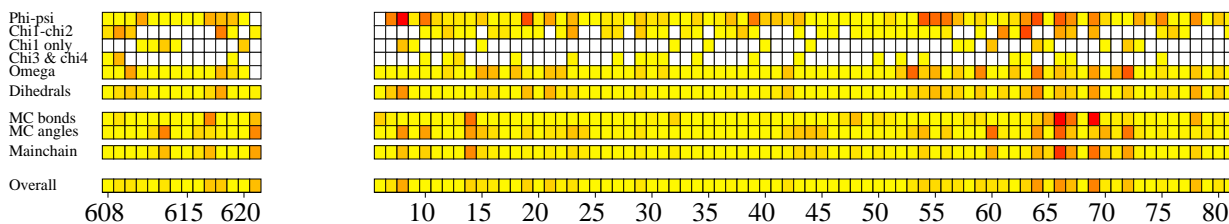
e. Sequence & Ramachandran regions



f. Max. deviation (see listing)

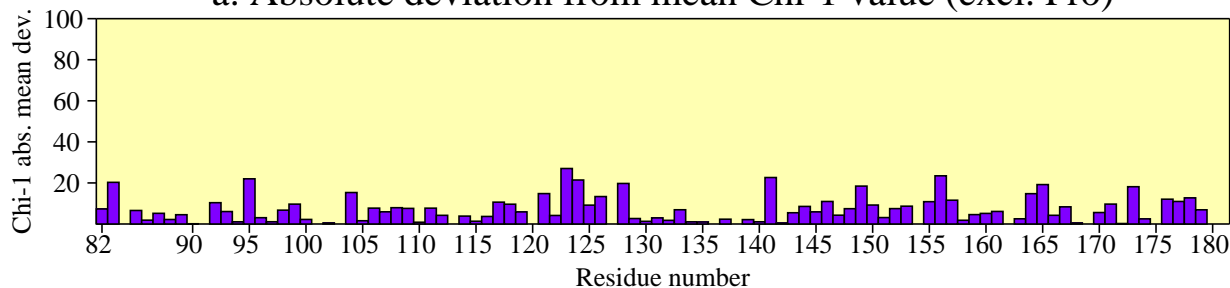


g. G-factors

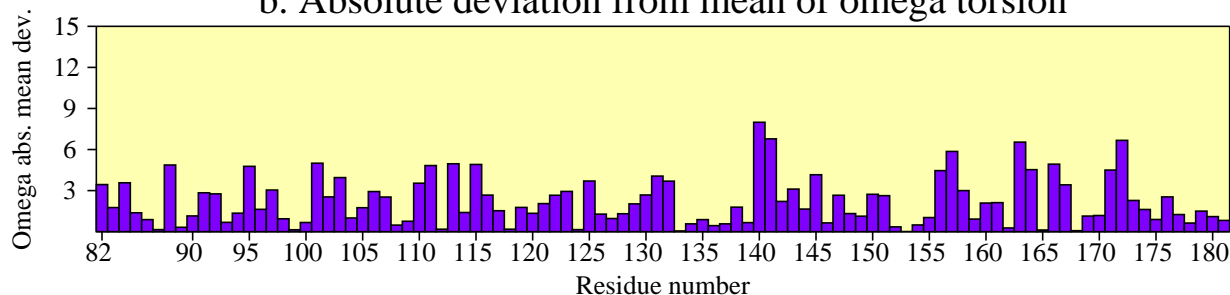


# Residue properties pdb1yq3

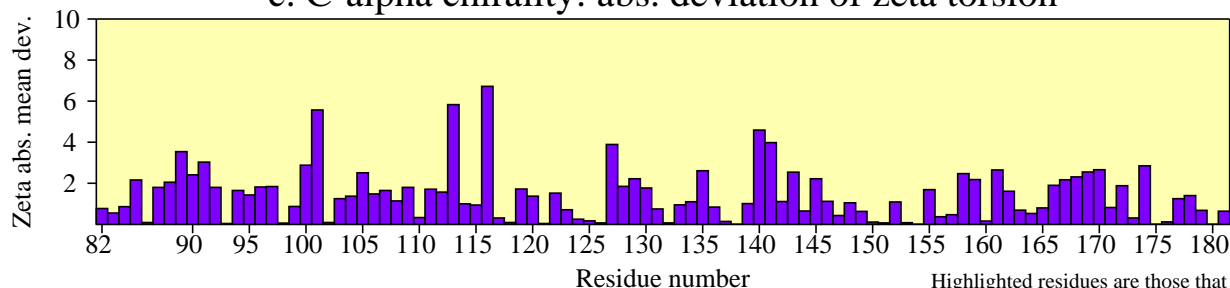
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion

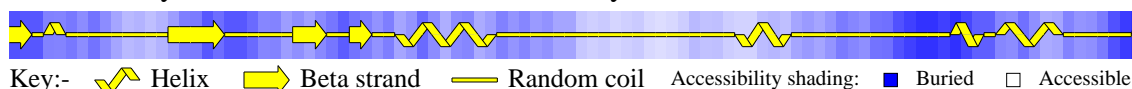


c. C-alpha chirality: abs. deviation of zeta torsion



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

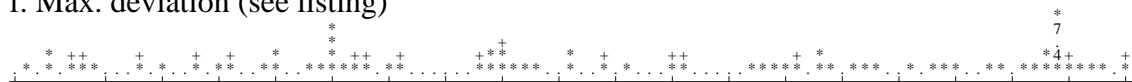
d. Secondary structure & estimated accessibility



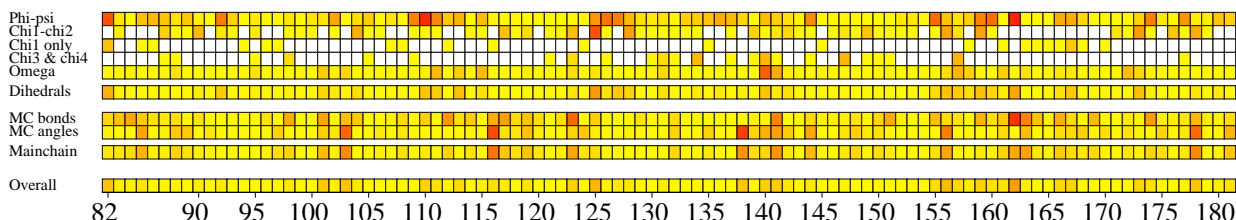
e. Sequence & Ramachandran regions



f. Max. deviation (see listing)



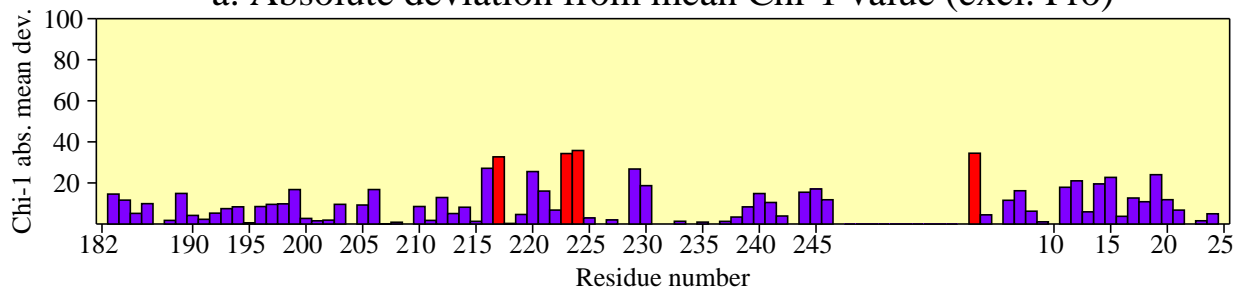
g. G-factors



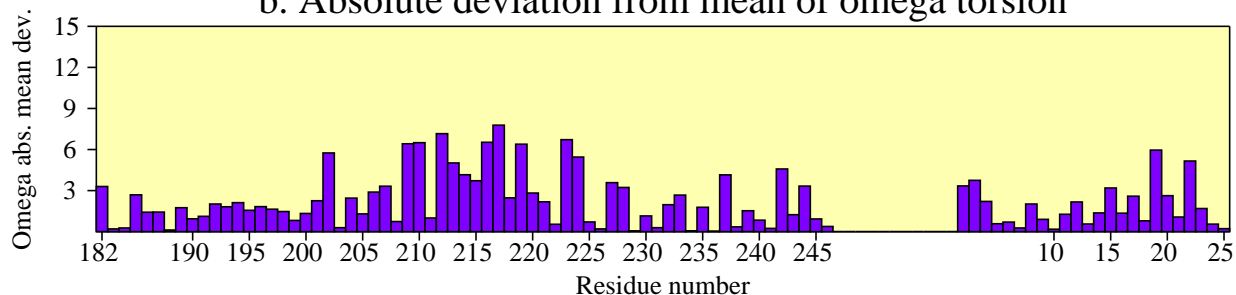


# Residue properties pdb1yq3

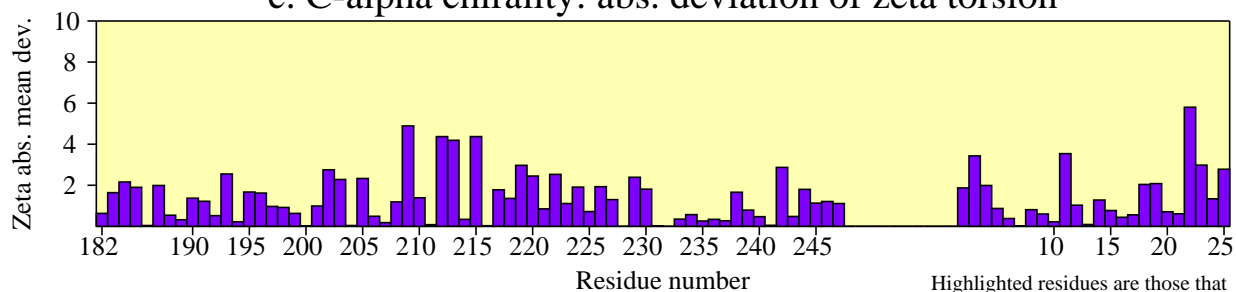
### a. Absolute deviation from mean Chi-1 value (excl. Pro)



### b. Absolute deviation from mean of omega torsion

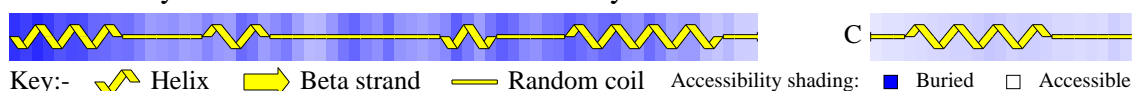


### c. C-alpha chirality: abs. deviation of zeta torsion



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

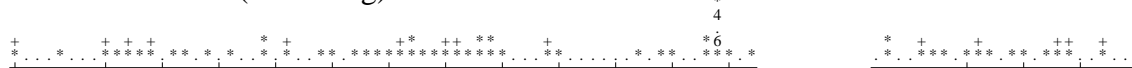
### d. Secondary structure & estimated accessibility



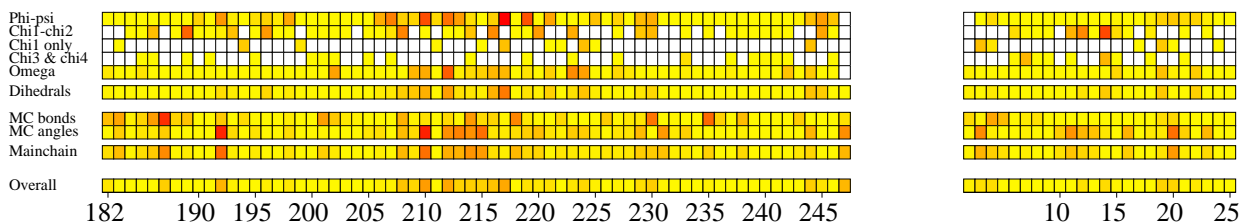
### e. Sequence & Ramachandran regions



### f. Max. deviation (see listing)

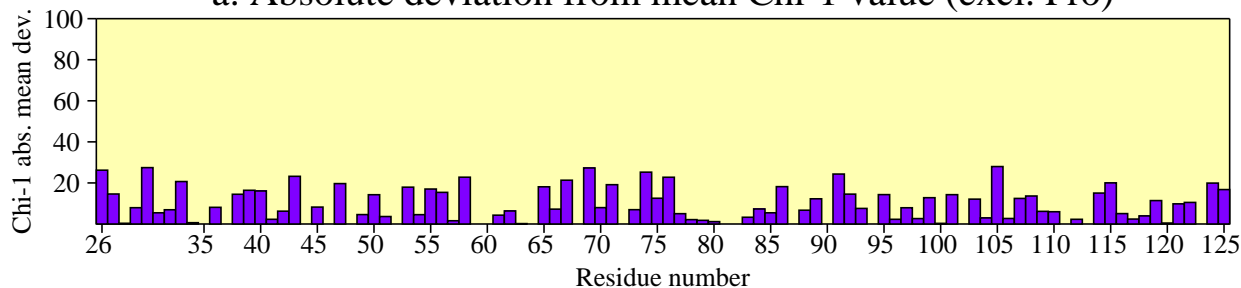


### g. G-factors

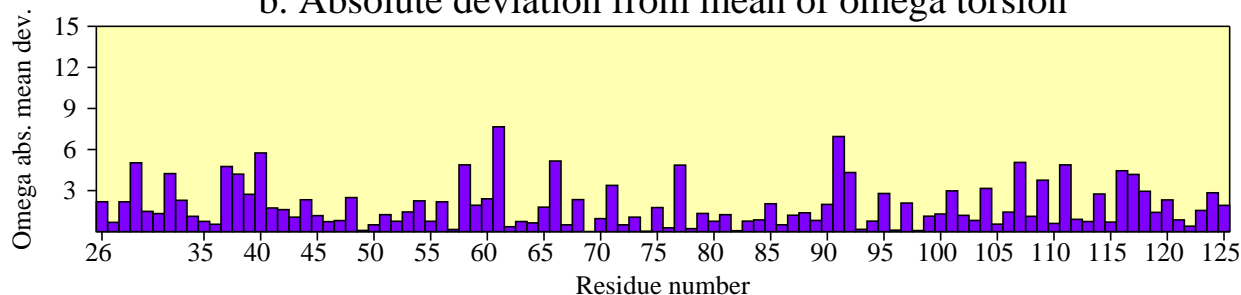


# Residue properties pdb1yq3

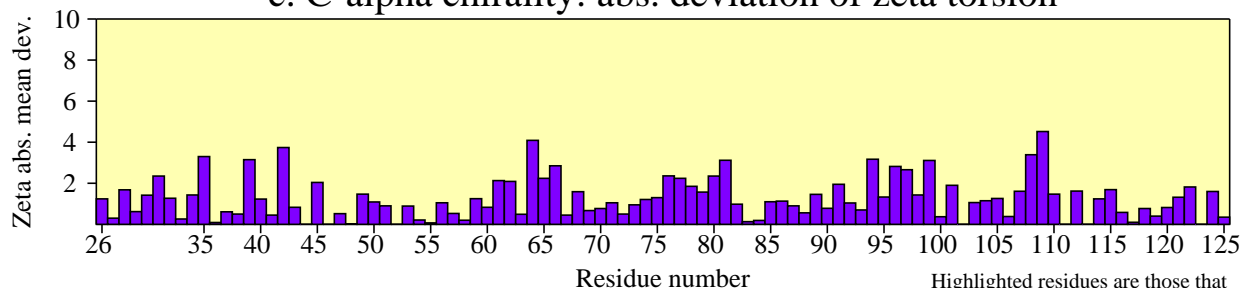
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion

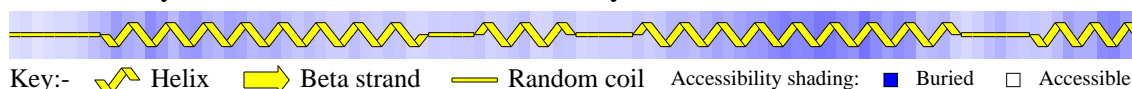


c. C-alpha chirality: abs. deviation of zeta torsion



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

d. Secondary structure & estimated accessibility



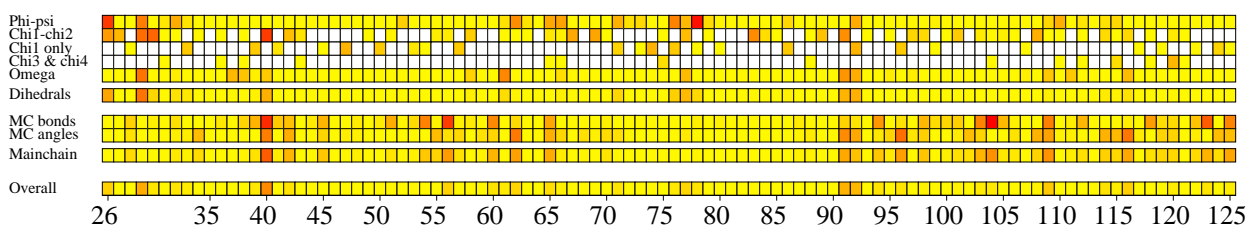
e. Sequence & Ramachandran regions



f. Max. deviation (see listing)



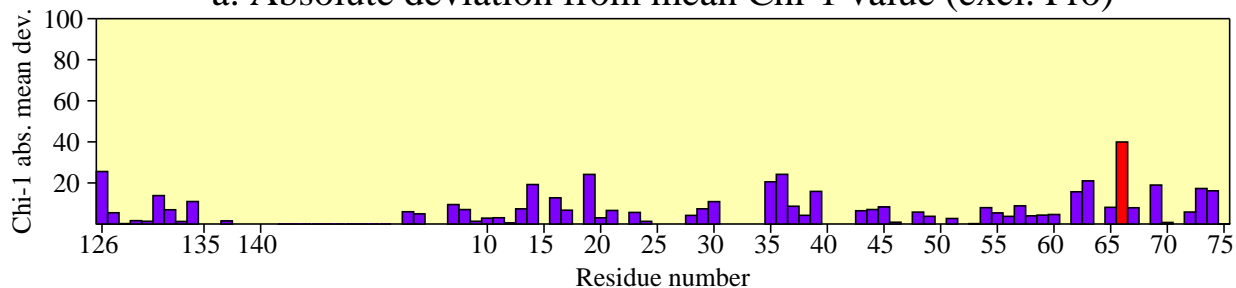
g. G-factors



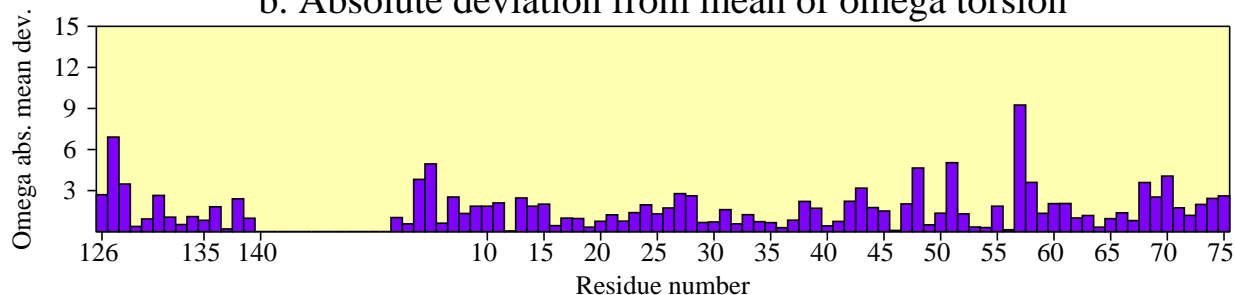
# Residue properties

## pdb1yq3

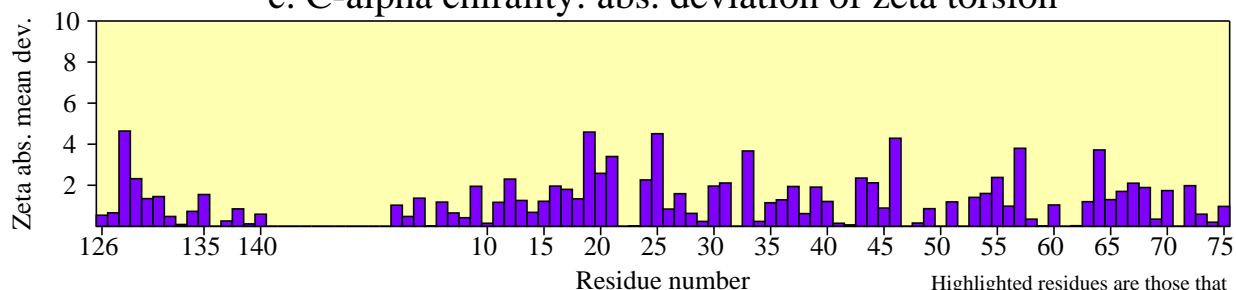
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion



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



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

d. Secondary structure & estimated accessibility



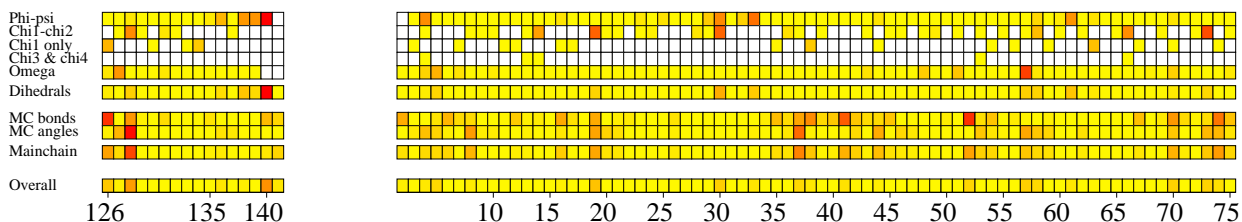
e. Sequence & Ramachandran regions



f. Max. deviation (see listing)

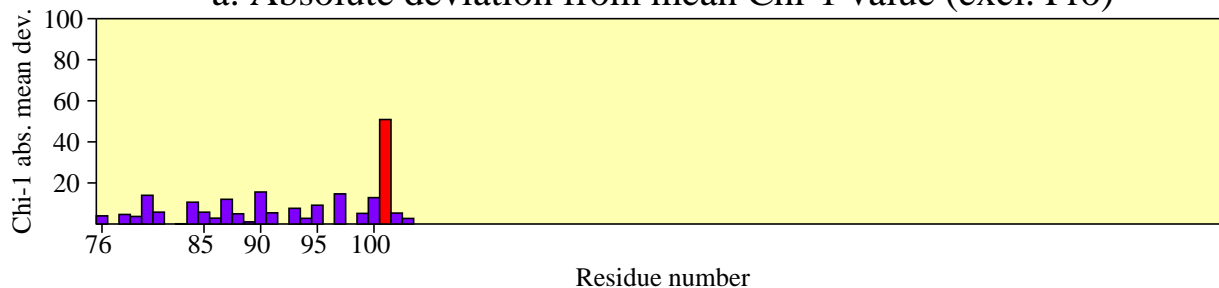


g. G-factors

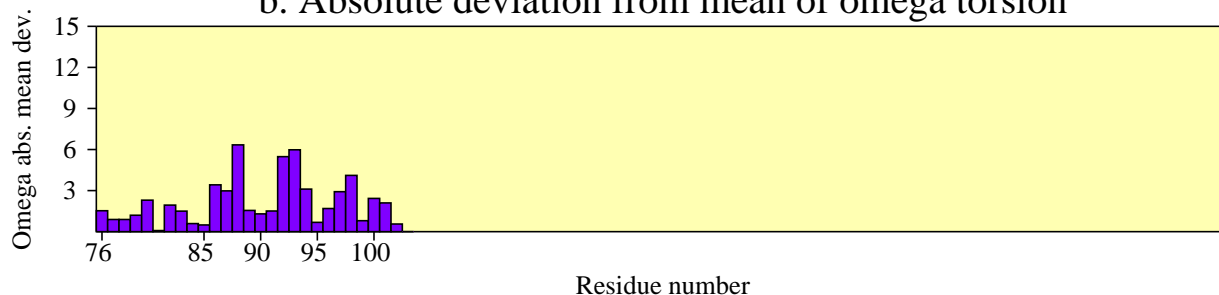


# Residue properties pdb1yq3

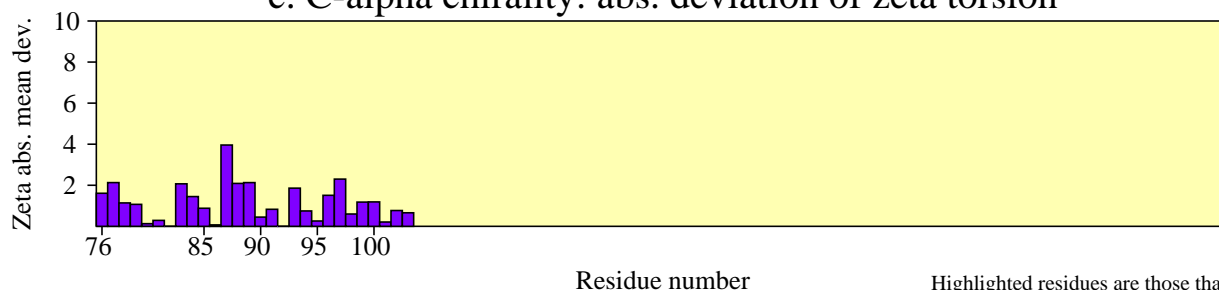
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion



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



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

d. Secondary structure & estimated accessibility



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

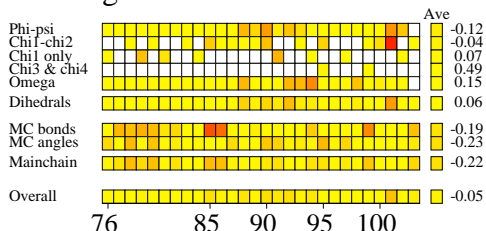
e. Sequence & Ramachandran regions Most favoured Allowed Generous Disallowed



f. Max. deviation (see listing)

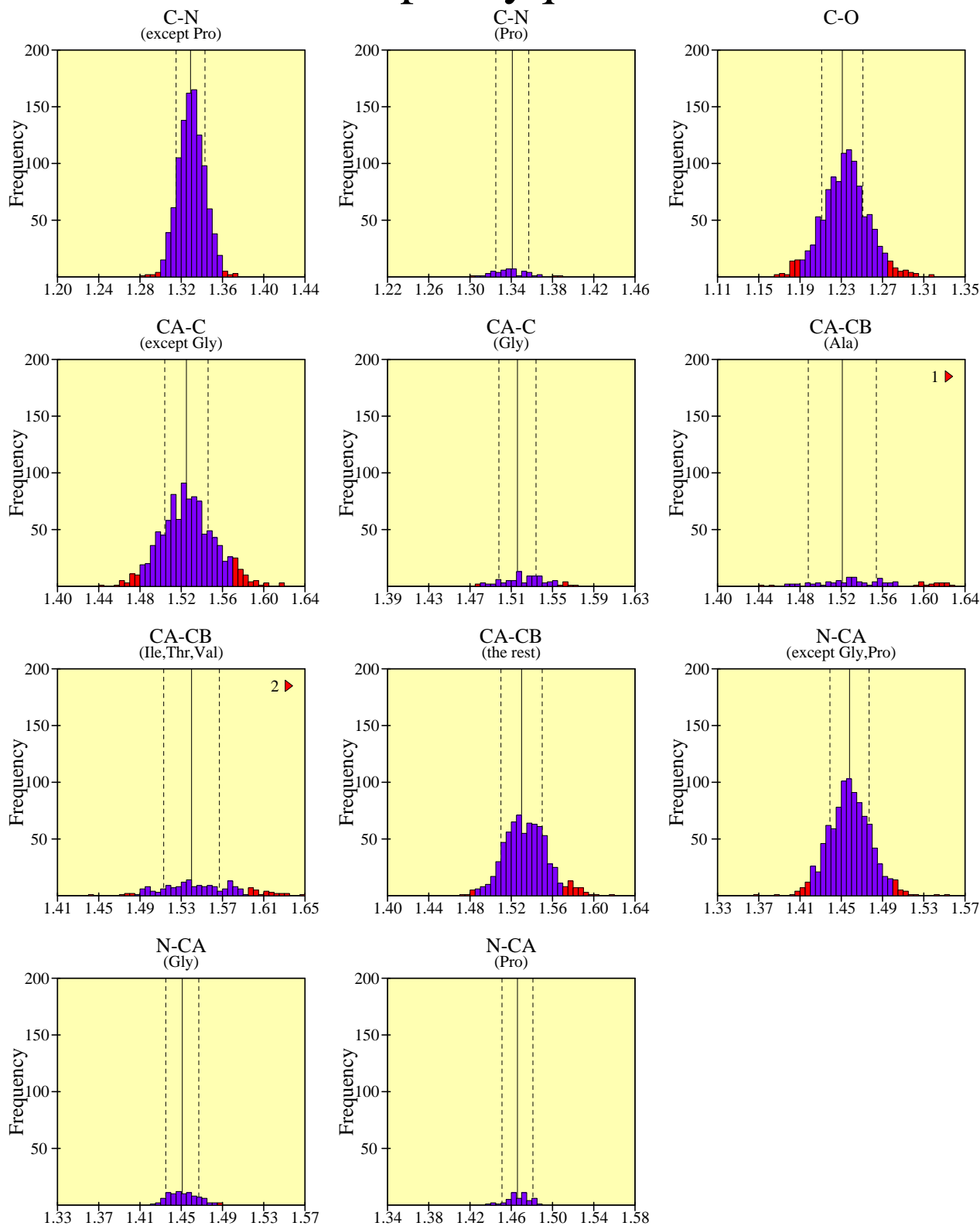


g. G-factors



# Main-chain bond lengths

## pdb1yq3



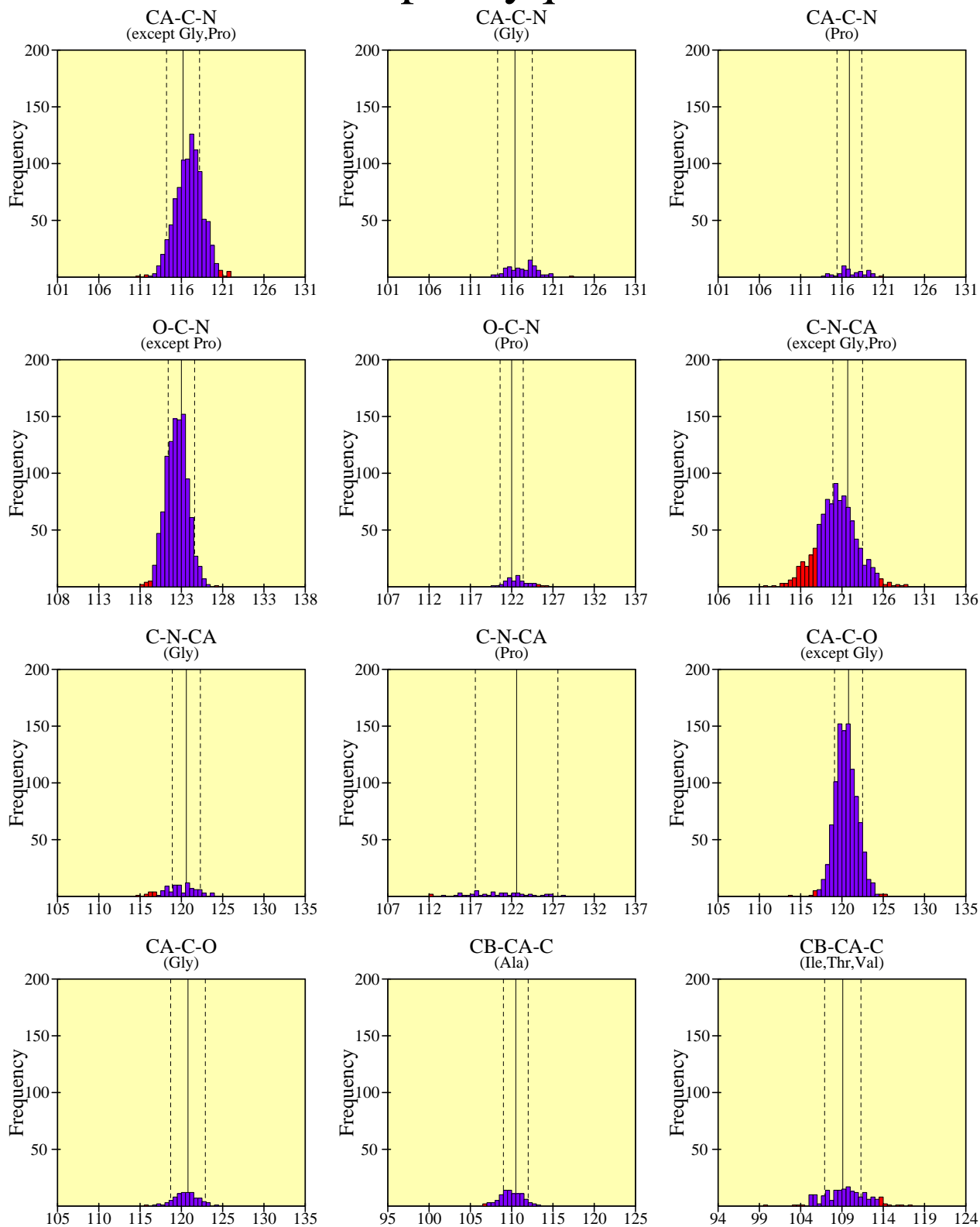
Black bars > 2.0 st. devs. from mean.

◀ 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

## pdb1yq3

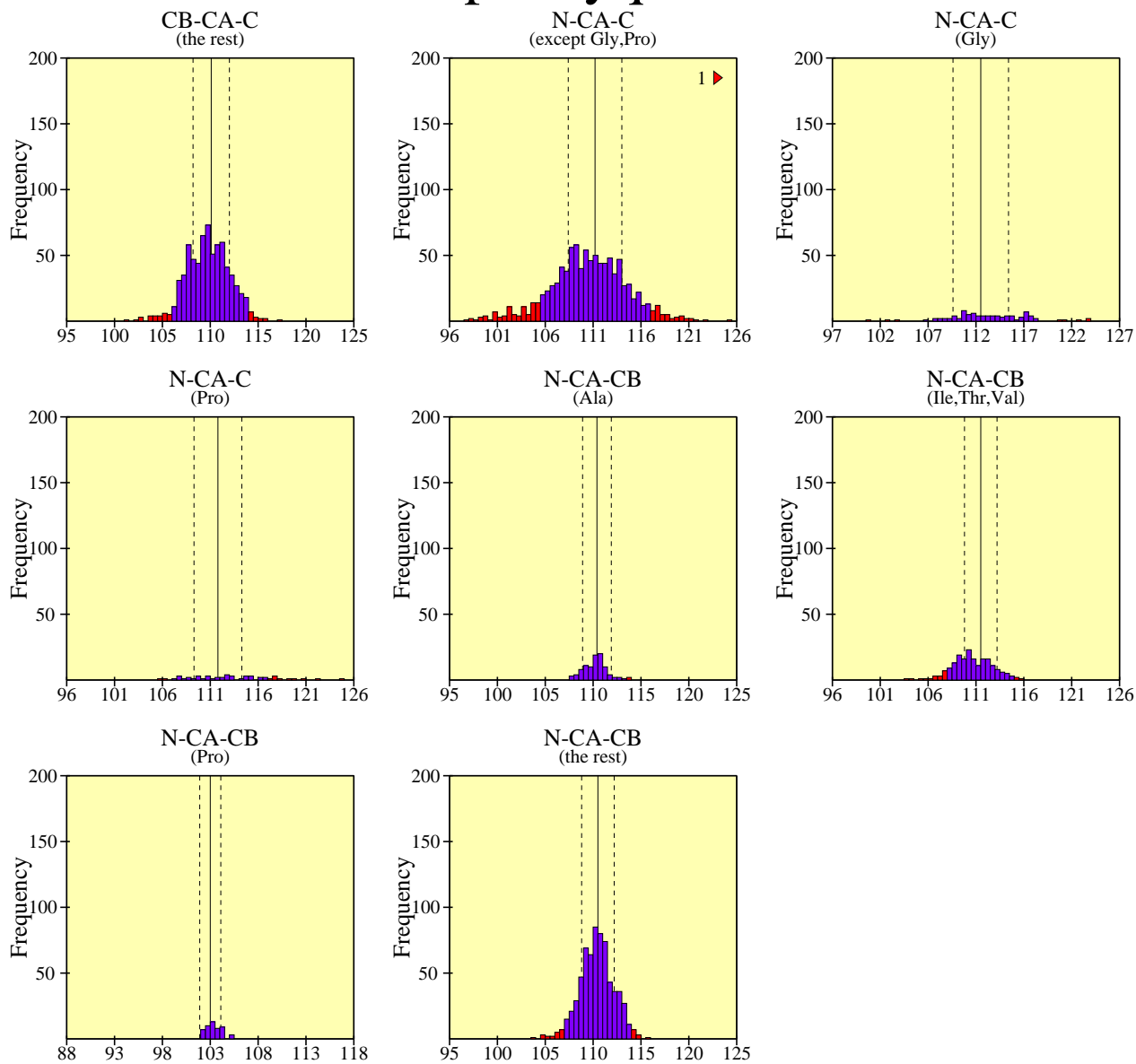


Black bars > 2.0 st. devs. from mean.

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

# Main-chain bond angles

## pdb1yq3



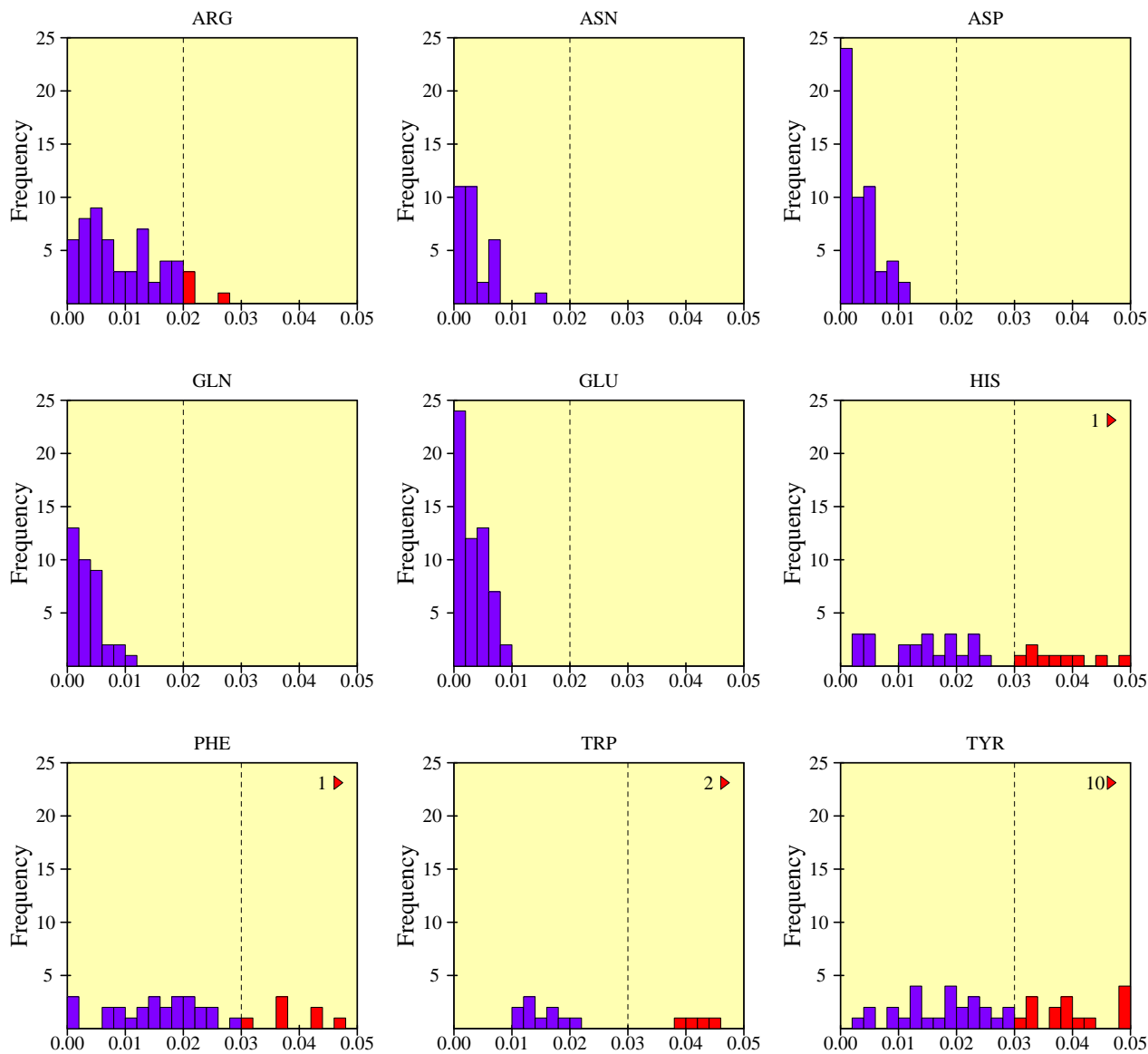
Black bars > 2.0 st. devs. from mean.

◀ 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

## pdb1yq3



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

## pdb1yq3

### Main-chain bond lengths

CA 1.540 CB 0.056 1.596 A Thr 10	CA 1.540 CB 0.055 1.595 A Val 24	C 1.231 O 0.070 1.301 A Arg 32	CA 1.521 CB 0.076 1.597 A Ala 33	CA 1.525 C 0.051 1.576 A Ala 40	C 1.231 O 0.057 1.174 A Ala 45
CA 1.540 CB 0.116 1.656 A Thr 48	CA 1.530 CB 0.058 1.588 A His 56	CA 1.540 CB 0.063 1.603 A Ile 64	CA 1.525 C 0.066 1.591 A Asn 70	CA 1.525 C 0.056 1.469 A Asp 88	CA 1.521 CB 0.143 1.664 A Ala 103
CA 1.530 CB 0.057 1.587 A Pro 104	CA 1.521 CB 0.072 1.593 A Ala 105	C 1.231 O 0.051 1.281 A Glu 109	N 1.458 CA 0.052 1.510 A Gln 136	CA 1.530 CB 0.053 1.582 A Arg 145	C 1.231 O 0.050 1.281 A Cys 148
CA 1.525 C 0.052 1.577 A Ala 150	N 1.458 CA 0.051 1.509 A Arg 152	C 1.231 O 0.089 1.320 A Thr 153	C 1.231 O 0.056 1.175 A Tyr 168	CA 1.525 C 0.060 1.465 A Tyr 168	CA 1.540 CB 0.057 1.483 A Thr 170
CA 1.525 C 0.091 1.616 A Glu 175	N 1.458 CA 0.094 1.552 A Leu 179	CA 1.530 CB 0.056 1.586 A Asn 185	CA 1.540 CB 0.094 1.634 A Val 191	CA 1.540 CB 0.078 1.618 A Ile 192	CA 1.540 CB 0.063 1.603 A Thr 209
CA 1.521 CB 0.087 1.609 A Ala 212	CA 1.530 CB 0.063 1.593 A Asp 246	CA 1.530 CB 0.086 1.616 A Glu 248	C 1.231 O 0.061 1.292 A Gln 251	CA 1.516 C 0.056 1.572 A Gly 256	CA 1.540 CB 0.059 1.599 A Ile 274
CA 1.525 C 0.059 1.584 A Val 290	CA 1.540 CB 0.090 1.630 A Val 299	CA 1.521 CB 0.092 1.613 A Ala 334	C 1.231 O 0.061 1.292 A Ser 341	CA 1.525 C 0.058 1.583 A Glu 342	CA 1.525 C 0.052 1.577 A Ile 346
C 1.231 O 0.063 1.293 A Asp 351	CA 1.540 CB 0.056 1.596 A Val 352	CA 1.540 CB 0.075 1.615 A Ile 357	CA 1.525 C 0.063 1.588 A Leu 360	C 1.231 O 0.052 1.283 A Asn 366	C 1.231 O 0.068 1.299 A Pro 371
CA 1.540 CB 0.084 1.624 A Thr 372	CA 1.540 CB 0.074 1.614 A Thr 380	CA 1.525 C 0.055 1.580 A His 381	CA 1.540 CB 0.058 1.598 A Val 388	N 1.458 CA 0.053 1.405 A Val 388	CA 1.540 CB 0.061 1.479 A Val 389
CA 1.525 C 0.050 1.475 A Ala 406	CA 1.521 CB 0.098 1.619 A Ala 406	CA 1.525 C 0.069 1.456 A Ala 411	CA 1.521 CB 0.051 1.572 A Ala 411	CA 1.530 CB 0.058 1.472 A Leu 414	C 1.231 O 0.086 1.317 A Leu 415
C 1.231 O 0.052 1.179 A Asp 416	CA 1.525 C 0.050 1.475 A Leu 417	CA 1.525 C 0.062 1.463 A Cys 432	C 1.231 O 0.052 1.283 A Ser 440	CA 1.525 C 0.059 1.584 A Ser 440	CA 1.521 CB 0.078 1.599 A Ala 451

# Distorted geometry

## pdb1yq3

### Main-chain bond lengths (contd)

CA 1.525 C 0.064 1.461 A Gln 473	CA 1.525 C 0.059 1.584 A Gln 490	C 1.231 O 0.066 1.297 A Cys 493	C 1.231 O 0.056 1.287 A Lys 495	C 1.231 O 0.069 1.300 A Ser 497	CA 1.530 CB 0.056 1.586 A Gln 498
CA 1.525 C 0.052 1.577 A Leu 506	CA 1.525 C 0.057 1.582 A Thr 508	CA 1.525 C 0.050 1.475 A Arg 511	CA 1.540 CB 0.085 1.625 A Thr 522	CA 1.525 C 0.057 1.582 A Asn 527	CA 1.530 CB 0.060 1.590 A Met 529
CA 1.530 CB 0.065 1.595 A Cys 531	CA 1.540 CB 0.066 1.606 A Thr 535	CA 1.521 CB 0.103 1.624 A Ala 541	CA 1.521 CB 0.051 1.572 A Ala 548	CA 1.525 C 0.058 1.583 A Ala 550	CA 1.525 C 0.066 1.591 A Asp 553
CA 1.525 C 0.054 1.579 A Ser 564	CA 1.525 C 0.054 1.579 A Leu 584	CA 1.525 C 0.051 1.576 A Ser 585	CA 1.540 CB 0.091 1.631 A Val 589	CA 1.540 CB 0.064 1.604 A Thr 595	CA 1.540 CB 0.057 1.483 A Val 601
C 1.231 O 0.059 1.172 A Ile 602	CA 1.530 CB 0.054 1.584 A Arg 604	CA 1.521 CB 0.107 1.628 A Ala 617	C 1.231 O 0.052 1.283 A Tyr 621	CA 1.521 CB 0.052 1.573 B Ala 7	CA 1.525 C 0.061 1.464 B Phe 14
CA 1.530 CB 0.056 1.586 B Cys 65	CA 1.525 C 0.094 1.619 B Arg 66	CA 1.530 CB 0.052 1.582 B Arg 66	CA 1.525 C 0.093 1.618 B Glu 67	CA 1.540 CB 0.108 1.648 B Ile 69	N 1.458 CA 0.071 1.387 B Ile 69
CA 1.521 CB 0.067 1.454 B Ala 74	CA 1.521 CB 0.099 1.620 B Ala 78	CA 1.540 CB 0.063 1.603 B Thr 82	CA 1.525 C 0.065 1.590 B Leu 83	C 1.231 O 0.057 1.288 B Ala 84	CA 1.540 CB 0.070 1.470 B Thr 96
C 1.231 O 0.060 1.291 B Lys 98	CA 1.525 C 0.050 1.575 B Pro 101	CA 1.525 C 0.051 1.474 B Pro 103	CA 1.540 CB 0.062 1.602 B Val 112	CA 1.525 C 0.062 1.587 B Asp 114	C 1.231 O 0.052 1.179 B Ser 116
CA 1.525 C 0.059 1.584 B Asn 117	CA 1.521 CB 0.076 1.597 B Ala 120	CA 1.530 CB 0.052 1.582 B Tyr 122	N 1.458 CA 0.082 1.540 B Lys 123	CA 1.525 C 0.050 1.475 B Lys 132	CA 1.525 C 0.053 1.578 B Gln 141
CA 1.530 CB 0.055 1.585 B Gln 141	CA 1.525 C 0.054 1.471 B Gln 144	N 1.458 CA 0.054 1.512 B Leu 155	C 1.231 O 0.056 1.287 B Ile 159	C 1.231 O 0.054 1.285 B Ala 162	CA 1.521 CB 0.091 1.612 B Ala 162
CA 1.530 CB 0.074 1.604 B Cys 163	CA 1.530 CB 0.054 1.584 B Cys 164	CA 1.525 C 0.051 1.474 B Asn 174	CA 1.525 C 0.052 1.577 B Tyr 178	CA 1.521 CB 0.090 1.611 B Ala 182	CA 1.525 C 0.057 1.582 B Val 183

# Distorted geometry

## pdb1yq3

### Main-chain bond lengths (contd)

CA 1.530 CB 0.056 1.586 B Met 185	N 1.458 CA 0.062 1.520 B Gln 186	CA 1.525 C 0.069 1.594 B Ala 187	CA 1.521 CB 0.101 1.622 B Ala 187	CA 1.530 CB 0.052 1.582 B Arg 189	CA 1.525 C 0.055 1.470 B Ile 192
CA 1.525 C 0.076 1.601 B Arg 214	N 1.458 CA 0.054 1.512 B Cys 215	CA 1.525 C 0.073 1.598 B Ile 218	CA 1.525 C 0.053 1.472 B Pro 226	CA 1.525 C 0.054 1.579 B Asn 230	CA 1.540 CB 0.096 1.444 B Ile 235
CA 1.521 CB 0.098 1.619 B Ala 236	CA 1.525 C 0.058 1.583 C Thr 4	CA 1.521 CB 0.089 1.610 C Ala 5	CA 1.525 C 0.052 1.577 C Ser 28	CA 1.525 C 0.052 1.473 C Trp 32	N 1.458 CA 0.089 1.369 C Ile 40
CA 1.525 C 0.052 1.577 C Thr 41	CA 1.540 CB 0.058 1.598 C Thr 45	N 1.458 CA 0.056 1.402 C Leu 51	CA 1.525 C 0.054 1.471 C Ser 54	CA 1.530 CB 0.055 1.475 C Ser 54	C 1.231 O 0.065 1.166 C Phe 56
CA 1.525 C 0.080 1.605 C Ala 60	CA 1.521 CB 0.052 1.469 C Ala 87	CA 1.525 C 0.053 1.472 C Leu 91	CA 1.525 C 0.064 1.461 C Pro 94	CA 1.540 CB 0.080 1.620 C Ile 103	CA 1.525 C 0.060 1.585 C Arg 104
CA 1.530 CB 0.052 1.582 C Arg 104	N 1.458 CA 0.067 1.525 C Arg 104	C 1.231 O 0.063 1.294 C Gln 118	CA 1.530 CB 0.062 1.592 C Ser 122	C 1.231 O 0.073 1.304 C Gly 123	CA 1.525 C 0.066 1.591 C Val 125
CA 1.540 CB 0.140 1.680 C Val 126	CA 1.540 CB 0.076 1.616 C Ile 128	CA 1.521 CB 0.078 1.443 C Ala 135	C 1.231 O 0.051 1.282 C Ile 140	N 1.458 CA 0.056 1.514 D Ser 2	CA 1.521 CB 0.074 1.595 D Ala 6
CA 1.540 CB 0.076 1.616 D Val 16	CA 1.521 CB 0.053 1.468 D Ala 26	CA 1.540 CB 0.055 1.595 D Val 35	C 1.231 O 0.060 1.291 D Tyr 37	C 1.231 O 0.064 1.167 D Ser 38	CA 1.521 CB 0.079 1.600 D Ala 40
CA 1.525 C 0.080 1.605 D Ala 41	C 1.231 O 0.056 1.287 D Gly 52	C 1.231 O 0.054 1.285 D Val 54	CA 1.540 CB 0.051 1.488 D Thr 56	CA 1.540 CB 0.055 1.595 D Val 59	CA 1.525 C 0.062 1.463 D Thr 70
CA 1.540 CB 0.072 1.612 D Thr 70	CA 1.525 C 0.054 1.579 D Tyr 73	C 1.231 O 0.070 1.301 D Val 74	CA 1.521 CB 0.094 1.615 D Ala 77	CA 1.540 CB 0.072 1.612 D Ile 78	C 1.231 O 0.067 1.298 D Tyr 85
CA 1.525 C 0.068 1.593 D Tyr 85	N 1.458 CA 0.051 1.508 D Phe 86	CA 1.525 C 0.082 1.442 D Met 99	CA 1.540 CB 0.062 1.478 D Ile 103		

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

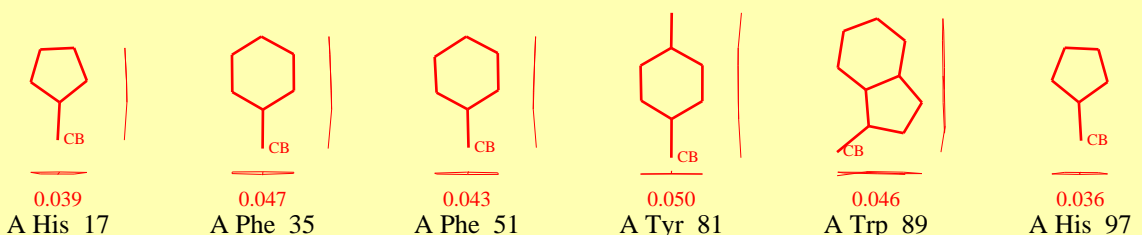
# Distorted geometry pdb1yq3

## Main-chain bond angles



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

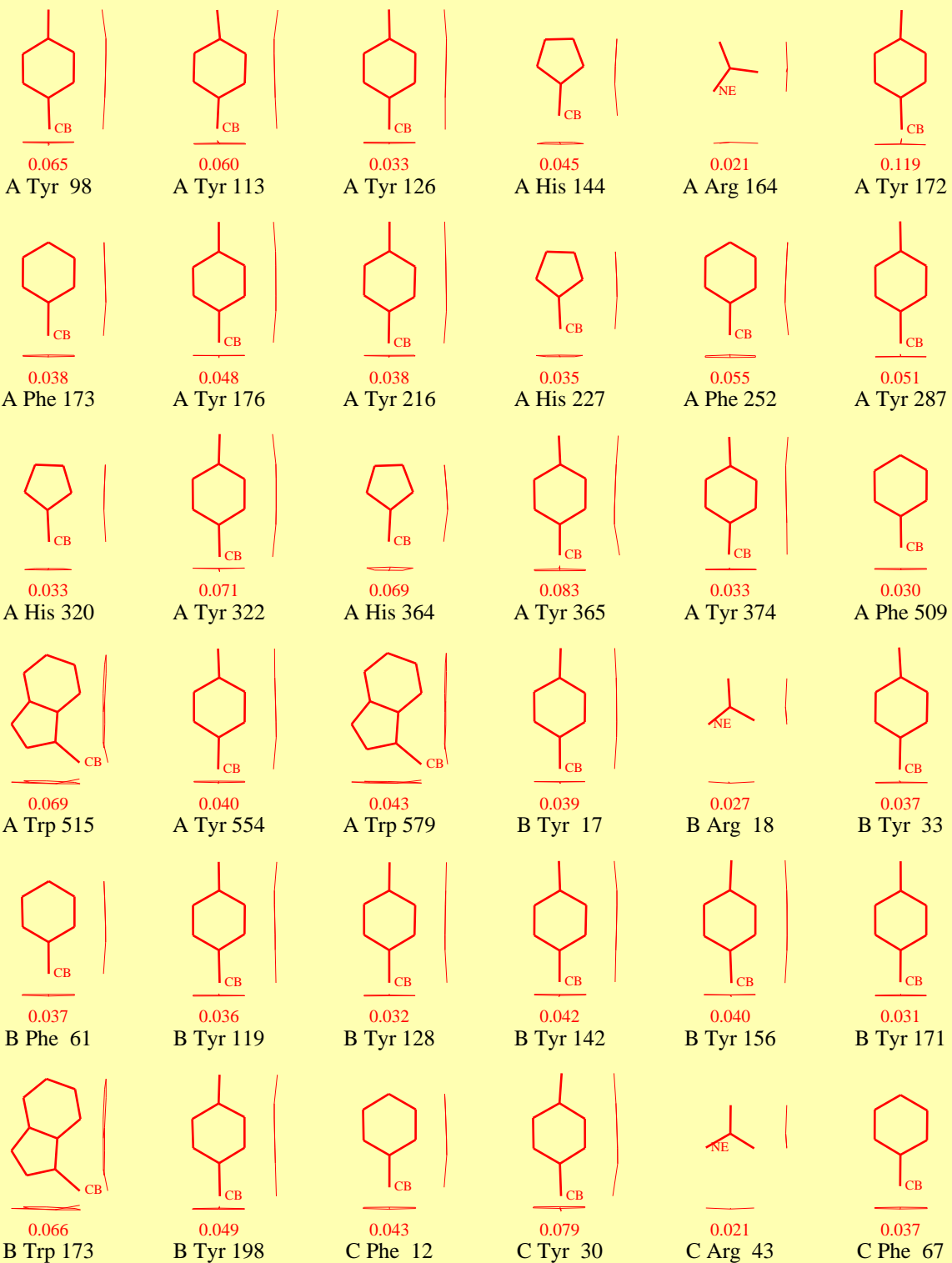
## Planar groups



# Distorted geometry

## pdb1yq3

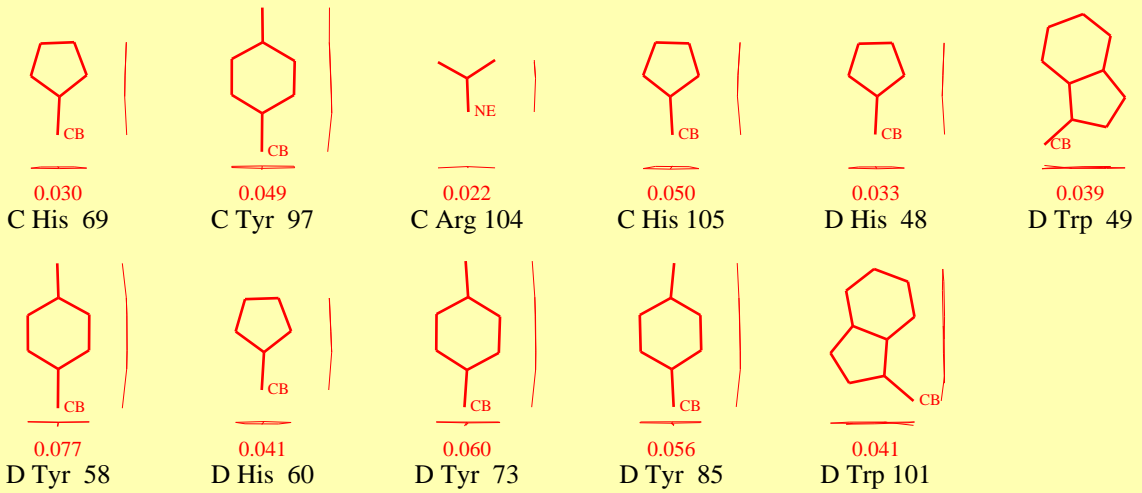
### Planar groups (contd)



# Distorted geometry

## pdb1yq3

### Planar groups (contd)



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