



Viewing mak_mb_1-284_FFX1H-multi.table

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All-Atom Contacts	Clashscore, all atoms:	0		100 th percentile* (N=1784, all resolutions)
	Clashscore is the number of serious steric overlaps (> 0.4 Å) per 1000 atoms.			
Protein Geometry	Poor rotamers	20	7.75%	Goal: <1%
	Ramachandran outliers	10	3.55%	Goal: <0.05%
	Ramachandran favored	249	88.30%	Goal: >98%
	MolProbity score [^]	1.77		87 th percentile* (N=27675, 0Å - 99Å)
	Cβ deviations >0.25Å	4	1.48%	Goal: 0
	Bad backbone bonds:	0 / 2392	0.00%	Goal: 0%
	Bad backbone angles:	23 / 3228	0.71%	Goal: <0.1%

In the two column results, the left column gives the raw count, right column gives the percentage.

* 100th percentile is the best among structures of comparable resolution; 0th percentile is the worst. For clashscore the comparative set of structures was selected in 2004, for MolProbity score in 2006.

[^] MolProbity score combines the clashscore, rotamer, and Ramachandran evaluations into a single score, normalized to be on the same scale as X-ray resolution.

#	Alt Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	C β deviation	Bond lengths	Bond angles
Avg: Clashscore: 100.17 Outliers: 0 282 Poor rotamers: 20 of 258 Outliers: 4 of 271 Outliers: 0 of 284 Outliers: 22 of 284								
1	MET	120.85	-	-	6.4% (<i>ptm</i>) chi angles: 56,151.7,300.8	0.114Å	-	-
2	ASN	75.98	-	Allowed (0.18%) General / -159.9,30.3	10.7% (<i>p-10</i>) chi angles: 56.5,290	0.041Å	-	-
3	ARG	122.54	-	Favored (3.94%) General / -133.5,21.2	9.5% (<i>ttp-105</i>) chi angles: 209,161.4,82.7,263.1	0.09Å	-	-
4	TYR	141.56	-	Favored (40.05%) General / -141.5,148.8	91% (<i>m-85</i>) chi angles: 299.8,271.4	0.096Å	-	-

5	THR 111.38	-	Favored (12.7%) General / -131.1,171.9	9.1% (<i>t</i>) chi angles: 193	0.139Å	-	-
6	THR 92.69	-	Favored (28.72%) General / 51.5,45.0	5% (<i>m</i>) chi angles: 316.9	0.125Å	-	-
7	MET 82.7	-	Favored (7.04%) General / -83.5,86.8	71.9% (<i>mtm</i>) chi angles: 291.6,194.5,281.1	0.068Å	-	-
8	ARG 108.28	-	Favored (18.68%) General / -101.2,107.3	8.6% (<i>tpm_?</i>) chi angles: 178.8,57.6,269.5,174.6	0.073Å	-	-
9	GLN 47.93	-	Favored (52.56%) General / -66.4,134.4	49.1% (<i>tt0</i>) chi angles: 185.1,167.5,334.8	0.048Å	-	-
10	LEU 62.56	-	Favored (9.33%) General / -106.8,-29.7	27.5% (<i>mt</i>) chi angles: 312.5,177.8	0.076Å	-	-
11	GLY 22.01	-	Favored (28.44%) Glycine / 169.4,-156.9	-	-	-	-
12	ASP 38.06	-	Favored (45.5%) General / -140.7,152.7	0.4% chi angles: 266.6,249.2	0.066Å	-	-
13	GLY 29.03	-	Favored (4.77%) Glycine / -145.3,-148.2	-	-	-	-
14	THR 66.43	-	Allowed (0.15%) General / -35.7,-67.6	4.5% (<i>m</i>) chi angles: 284.4	0.079Å	-	-
15	TYR 98.21	-	Favored (22.43%) General / -73.5,-50.3	57.6% (<i>m-85</i>) chi angles: 307.8,278.8	0.094Å	-	-
16	GLY 33.75	-	Favored (22.21%) Glycine / 153.6,-150.5	-	-	-	-
			Favored				

17	SER	27.67	-	(26.42%) General / -52.1,137.9	6.4% (<i>m</i>) chi angles: 313.3	0.079Å	-	-
18	VAL	33.91	-	Favored (69.9%) Isoleucine or valine / -112.6,125.5	78.5% (<i>t</i>) chi angles: 172.6	0.074Å	-	-
19	LEU	123.69	-	Favored (46.4%) General / -137.0,147.7	6.4% (<i>tt</i>) chi angles: 174.9,143.1	0.143Å	-	-
20	MET	152.56	-	Favored (29.59%) General / -112.7,152.0	0% chi angles: 79.3,92.8,199	0.049Å	-	-
#	Alt Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
Avg: 100.17				Clashscore: 0	Outliers: 10 of 282	Poor rotamers: 20 of 258	Outliers: 4 of 271	Outliers: 0 of 284
21	GLY	22.38	-	Favored (32.25%) Glycine / -163.2,-173.7	-	-	-	-
22	LYS	102.96	-	Favored (41.74%) General / -116.0,146.9	22.7% (<i>ttmm</i>) chi angles: 179.9,171.5,287.3,302.9	0.039Å	-	-
23	SER	90.22	-	Favored (27.51%) General / -75.8,124.6	32.2% (<i>t</i>) chi angles: 184.4	0.031Å	-	-
24	ASN	80.28	-	Favored (44.1%) General / -85.5,2.6	0.1% chi angles: 222,118.6	0.093Å	-	-
25	GLU	79.44	-	Favored (11.61%) General / -118.7,1.1	1.9% (<i>pt-20</i>) chi angles: 62.4,143.2,39.1	0.033Å	-	-
26	SER	49.52	-	OUTLIER (0.02%) General / -167.5,3.2	84.9% (<i>p</i>) chi angles: 61.1	0.065Å	-	-
27	GLY	24.6	-	Favored (2%) Glycine / 76.5,-23.1	-	-	-	-
				Allowed (0.14%)	42.1% (<i>mt-10</i>) chi angles:			

28	GLU 55.51	-	General / -41.9,149.3	293.9,169.7,102.7	0.138Å	-	-
29	LEU 144.63	-	Favored (32.84%) General / -97.0,139.5	87.4% (<i>mt</i>) chi angles: 296.6,180.3	0.026Å	-	-
30	VAL 47.46	-	Favored (28.42%) Isoleucine or valine / -123.5,146.7	20.4% (<i>m</i>) chi angles: 292.6	0.049Å	-	-
31	ALA 34.35	-	Favored (11.78%) General / -116.4,104.8	-	0.024Å	-	-
32	ILE 48.33	-	Favored (47.55%) Isoleucine or valine / -95.5,123.2	60.6% (<i>mt</i>) chi angles: 288.8,176.8	0.134Å	-	-
33	LYS 58.43	-	Favored (28.74%) General / -111.5,115.2	83.7% (<i>mttt</i>) chi angles: 277,182.7,170.6,174.5	0.06Å	-	-
34	ARG 162.5	-	Favored (31.88%) General / -86.1,138.5	38.8% (<i>ttm180</i>) chi angles: 186.3,183.3,287.9,146.9	0.133Å	-	-
35	MET 178.27	-	Favored (31.93%) General / -117.9,118.4	9.4% (<i>ptm</i>) chi angles: 60.9,155.8,271.4	0.141Å	-	-
36	LYS 178.26	-	Favored (39.85%) General / -74.1,152.8	15.2% (<i>pttm</i>) chi angles: 66.5,207.2,173.1,289.5	0.047Å	-	-
37	ARG 130.87	-	Favored (28.38%) General / -157.0,168.1	15.6% (<i>ptt180</i>) chi angles: 66.5,169.1,192.5,141.9	0.05Å	-	-
38	LYS 152.34	-	Favored (2.54%) General / -155.4,106.2	33.5% (<i>tptt</i>) chi angles: 165.4,51.8,191.2,165.3	0.105Å	-	-
39	PHE 315.91	-	Favored (5.84%) General / -118.2,175.1	22.1% (<i>t80</i>) chi angles: 184.3,49	0.095Å	-	-

40	TYR	288.27	-	(10.4%) General / -163.7,147.9	73.5% (<i>t80</i>) chi angles: 184.2,70.7	0.063Å	-	-
#	Alt Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
Avg: 100.17				Clashscore: 0	Outliers: 10 of 282	Poor rotamers: 20 of 258	Outliers: 4 of 271	Outliers: 0 of 284
41	SER	192	-	Favored (2.26%) General / -163.8,-170.7	12.1% (<i>t</i>) chi angles: 191.1	0.057Å	-	-
42	TRP	154.01	-	Favored (43.23%) General / -77.3,-40.8	58.7% (<i>t-105</i>) chi angles: 184.8,268.7	0.069Å	-	OUTLIER(S) worst is CE3- CD2-CG: 4.486 σ
43	ASP	194.63	-	Favored (10.64%) General / -84.2,173.9	9.1% (<i>p-10</i>) chi angles: 66.7,292.9	0.034Å	-	-
44	GLU	107.11	-	Favored (11.21%) General / -121.6,18.0	0.3% chi angles: 220,300.6,274.5	0.051Å	-	-
45	CYS	99.82	-	Favored (7.68%) General / -83.7,63.8	7.2% (<i>t</i>) chi angles: 199.1	0.106Å	-	-
46	MET	306.03	-	Favored (18.02%) General / -57.6,150.9	0% chi angles: 188,98.1,295.2	0.042Å	-	OUTLIER(S) worst is C-N- CA: 6.681 σ
47	ASN	165.14	-	OUTLIER (0%) General / -54.8,38.7	1.9% (<i>m120</i>) chi angles: 305.4,47.4	0.04Å	-	-
48	LEU	95.21	-	Favored (70.95%) General / -71.5,-36.4	10.4% (<i>mp</i>) chi angles: 281.1,63.4	0.124Å	-	-
49	ARG	87.22	-	Favored (72.01%) General / -54.6,-43.2	8.7% (<i>ptt-85</i>) chi angles: 41.6,159,194.4,282.7	0.086Å	-	-
50	GLU	72.42	-	Favored (57.72%) General / -73.5,-44.4	66.9% (<i>mm-40</i>) chi angles: 304.5,304.8,143.7	0.054Å	-	-
				Favored				

51	VAL	103.21	-	(38.9%) Isoleucine or valine / -69.4,-28.6	25.6% (<i>m</i>) chi angles: 302	0.275Å	-	-
52	LYS	95.64	-	Favored (83.64%) General / -61.2,-37.6	79.8% (<i>tttt</i>) chi angles: 197.1,176.2,181.8,179.1	0.099Å	-	-
53	SER	77.79	-	Favored (75.69%) General / -66.8,-33.5	0.6% chi angles: 264	0.21Å	-	-
54	LEU	73	-	Favored (68.91%) General / -61.6,-27.8	89% (<i>mt</i>) chi angles: 300,178.9	0.161Å	-	-
55	LYS	74.08	-	Favored (3.09%) General / -66.3,-1.2	44.2% (<i>tttp</i>) chi angles: 200.6,183.6,170.5,70.4	0.133Å	-	-
56	LYS	80.34	-	Favored (39.35%) General / -83.7,2.1	39.9% (<i>mtmt</i>) chi angles: 286.5,165.1,279,176.8	0.089Å	-	-
57	LEU	118.54	-	Favored (2.7%) General / -98.0,80.1	26.6% (<i>mt</i>) chi angles: 312.9,177.7	0.054Å	-	-
58	ASN	71.43	-	Favored (52.93%) General / -117.0,136.5	49% (<i>t30</i>) chi angles: 185.3,17.7	0.046Å	-	-
59	HIS	55.5	-	OUTLIER (0.03%) General / 174.5,131.7	1.6% (<i>t-80</i>) chi angles: 156.7,286.7	0.105Å	-	OUTLIER(S) worst is CA-CB- CG: 9.408 σ
60	ALA	50.59	-	Favored (30.26%) General / -48.2,-50.2	-	0.096Å	-	-
<div> <div>#</div> <div>Alt Res</div> <div>High B</div> <div>Clash > 0.4Å</div> <div>Ramachandran</div> <div>Rotamer</div> <div>Cβ deviation</div> <div>Bond lengths</div> <div>Bond angles</div> </div> <div> <div>Avg: 100.17</div> <div>Clashscore: 0</div> <div>Outliers: 10 of 282</div> <div>Poor rotamers: 20 of 258</div> <div>Outliers: 4 of 271</div> <div>Outliers: 0 of 284</div> <div>Outliers: 22 of 284</div> </div>								
61	ASN	112.81	-	Allowed (1.19%) General / -91.1,44.4	5.9% (<i>p-10</i>) chi angles: 45.9,320	0.183Å	-	OUTLIER(S) worst is CA-CB- CG: 4.359 σ
				Favored (29.86%)	21.8% (<i>m</i>)			

62	VAL	108.45	-	Isoleucine or valine / -136.0,165.3	chi angles: 303	0.183Å	-	-
63	ILE	120.35	-	Favored (35.49%) Isoleucine or valine / -74.6,131.1	19.5% (<i>mm</i>) chi angles: 288.4,291.5	0.108Å	-	-
64	LYS	104.31	-	Favored (48.04%) General / -63.8,131.5	49.5% (<i>mtmt</i>) chi angles: 296.8,174.4,280.3,181.6	0.117Å	-	-
65	LEU	70.78	-	Favored (25.54%) General / -92.4,113.3	29.8% (<i>tp</i>) chi angles: 176.3,52.9	0.028Å	-	-
66	LYS	87.57	-	Allowed (0.53%) General / -91.2,-73.7	81.9% (<i>tttt</i>) chi angles: 192.5,180.2,172,176.2	0.125Å	-	-
67	GLU	57.51	-	Favored (12.95%) General / -128.4,170.6	47% (<i>mt-10</i>) chi angles: 293.2,190.8,298.4	0.053Å	-	-
68	VAL	44.32	-	Favored (44.31%) Isoleucine or valine / -138.1,137.7	71.5% (<i>t</i>) chi angles: 179.4	0.063Å	-	-
69	ILE	48.98	-	Favored (36.55%) Isoleucine or valine / -126.8,154.2	23.9% (<i>mt</i>) chi angles: 289.5,185.8	0.133Å	-	-
70	ARG	150.58	-	Allowed (0.64%) General / -151.9,40.4	8% (<i>ttp85</i>) chi angles: 197.3,167.3,91.1,119.7	0.091Å	-	-
71	GLU	104.99	-	Favored (2.44%) General / -66.6,108.4	23.8% (<i>mt-10</i>) chi angles: 288.1,153.7,41.2	0.062Å	-	-
72	ASN	63.62	-	Favored (19.8%) General / 49.0,49.2	2.7% (<i>p30</i>) chi angles: 45.2,86.8	0.214Å	-	OUTLIER(S) worst is CA-CB- CG: 4.118 σ
73	ASP	85.73	-	Favored (15.96%) General / 60.2,26.5	8.4% (<i>t0</i>) chi angles: 209.5,29.1	0.209Å	-	-
74	HIS	115.04	-	Favored (5.7%) General / -91.3,78.8	70.4% (<i>m80</i>) chi angles: 292.9,74.2	0.067Å	-	-

75	LEU	119.69	-	Favored (16.57%) General / -71.0,120.5	0.1% chi angles: 198.9,321.9	0.04Å	-	-	
76	TYR	118.93	-	Favored (48.37%) General / -126.7,151.3	90.8% (<i>m-85</i>) chi angles: 301,275	0.094Å	-	-	
77	PHE	131.62	-	Favored (30.24%) General / -112.7,116.5	37.5% (<i>m-85</i>) chi angles: 309.5,296.3	0.057Å	-	-	
78	ILE	107.3	-	Favored (5.12%) Isoleucine or valine / -93.6,95.2	19.2% (<i>mm</i>) chi angles: 314.5,304.1	0.038Å	-	-	
79	PHE	75.22	-	Favored (10.61%) General / -98.1,167.9	51.1% (<i>m-85</i>) chi angles: 288.1,296.4	0.079Å	-	-	
80	GLU	55.63	-	Favored (55.71%) General / -67.2,144.8	67.1% (<i>tt0</i>) chi angles: 184.8,177.5,24.9	0.13Å	-	-	
#	Alt	Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
		Avg: 100.17	Clashscore: 0	Outliers: 10 of 282	Poor rotamers: 20 of 258	Outliers: 4 of 271	Outliers: 0 of 284	Outliers: 22 of 284	
81	TYR	72.26	-	Favored (24.79%) General / -95.4,145.9	53.8% (<i>t80</i>) chi angles: 174.4,91	0.08Å	-	-	
82	MET	98.43	-	Favored (23.77%) General / -146.3,136.6	5.6% (<i>mtt</i>) chi angles: 262.3,190.6,157.6	0.047Å	-	-	
83	LYS	124.87	-	Favored (74.02%) General / -64.9,-48.5	44.7% (<i>tttm</i>) chi angles: 175.5,183.8,165,288.4	0.063Å	-	-	
84	GLU	129.87	-	Favored (26.4%) General / -89.1,144.1	9.4% (<i>mm-40</i>) chi angles: 315.2,311.1,356.8	0.043Å	-	-	
				Favored (20.32%)	10.8% (<i>p30</i>)				

85	ASN 73.27	-	General / -114.0,159.1	chi angles: 65,85.7	0.029Å	-	-
86	LEU 61.74	-	Favored (75.16%) General / -59.6,-35.9	35.9% (<i>tp</i>) chi angles: 186.9,65.9	0.144Å	-	-
87	TYR 139.42	-	Favored (50.25%) General / -66.4,-52.1	58.9% (<i>t80</i>) chi angles: 172.7,88.7	0.109Å	-	-
88	GLN 121.32	-	Favored (77.96%) General / -63.1,-34.6	26.4% (<i>mm100</i>) chi angles: 289.6,310.4,129.6	0.113Å	-	-
89	LEU 109.27	-	Favored (88.57%) General / -61.0,-47.0	28.2% (<i>tp</i>) chi angles: 188.2,55.9	0.053Å	-	-
90	MET 238.88	-	Favored (2.38%) General / -130.9,-24.6	1.4% (<i>ppp?</i>) chi angles: 43,63.6,54.8	0.2Å	-	-
91	LYS 62.44	-	Favored (45.59%) General / -78.8,-23.1	47.6% (<i>mttp</i>) chi angles: 278.2,181,162.6,64.2	0.184Å	-	-
92	ASP 80.39	-	Allowed (0.36%) General / -103.2,-91.1	73.9% (<i>m-20</i>) chi angles: 292.6,356.3	0.177Å	-	-
93	ARG 157	-	Favored (79.12%) General / -68.9,-37.5	45.5% (<i>tpt85</i>) chi angles: 182.1,52.2,182.6,79.7	0.208Å	-	-
94	ASN 63.35	-	Allowed (1.92%) General / -125.5,80.8	66.7% (<i>m-20</i>) chi angles: 300,343.2	0.049Å	-	-
95	LYS 131.89	-	Favored (2.47%) General / -81.2,14.3	61.5% (<i>mttp</i>) chi angles: 295.5,179.7,169.8,70.1	0.035Å	-	-
96	LEU 101.75	-	Favored (8.45%) General / -124.8,11.7	2.5% (<i>mm?</i>) chi angles: 295.3,317.7	0.037Å	-	-
			Favored				

97	PHE	143.47	-	(65.17%) Pre-proline / -55.0,128.7	32.3% (<i>m-85</i>) chi angles: 278.2,283.9	0.075Å	-	-
98	PRO	132.14	-	Favored (61.07%) Trans-proline / -65.0,156.7	22.7% (<i>Cg_exo</i>) chi angles: 324.4	0.08Å	-	-
99	GLU	74.15	-	Favored (11.1%) General / -44.9,-47.6	3.4% (<i>tm-20</i>) chi angles: 190,303.8,309	0.042Å	-	-
100	SER	68.36	-	Favored (24.04%) General / -47.2,-47.3	66% (<i>p</i>) chi angles: 57	0.089Å	-	-
#	Alt Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
Avg: Clashscore: 100.17 0 Outliers: 282 Poor rotamers: 20 of 258 Outliers: 4 of 271 Outliers: 0 of 284 Outliers: 22 of 284								
101	VAL	45.37	-	Favored (64.67%) Isoleucine or valine / -68.9,-34.5	39.9% (<i>t</i>) chi angles: 185	0.12Å	-	-
102	ILE	50.83	-	Favored (74.69%) Isoleucine or valine / -71.2,-40.6	33.5% (<i>mt</i>) chi angles: 310.8,176	0.123Å	-	-
103	ARG	62.74	-	Favored (86.22%) General / -57.9,-44.0	72.2% (<i>ttt180</i>) chi angles: 186.4,182.9,176.3,197.3	0.039Å	-	-
104	ASN	84.34	-	Favored (91.81%) General / -60.3,-45.9	0.5% chi angles: 147.4,83.9	0.133Å	-	-
105	ILE	109.83	-	Favored (77.21%) Isoleucine or valine / -70.9,-41.5	2% (<i>pp</i>) chi angles: 67.8,100.8	0.263Å	-	-
106	MET	71.57	-	Favored (91.33%) General / -65.6,-42.6	16.2% (<i>ttt</i>) chi angles: 192.6,192.7,180.2	0.115Å	-	-
107	TYR	46.13	-	Favored (70.69%) General / -58.5,-51.2	86.5% (<i>t80</i>) chi angles: 174.9,79.9	0.067Å	-	-

108	GLN 112.1	-	Favored (37.61%) General / -80.6,-26.8	0.3% chi angles: 105.1,190.8,252.5	0.239Å	-	-
109	ILE 106.79	-	Favored (79.64%) Isoleucine or valine / -69.9,-41.7	6.9% (<i>pt</i>) chi angles: 68.2,191.6	0.221Å	-	-
110	LEU 120.92	-	Favored (79.37%) General / -57.3,-41.3	57.5% (<i>tp</i>) chi angles: 174.4,64.5	0.039Å	-	-
111	GLN 100.51	-	Favored (85.3%) General / -60.1,-39.1	10.7% (<i>tp-100</i>) chi angles: 182.9,62,248.7	0.063Å	-	-
112	GLY 23.69	-	Favored (96.02%) Glycine / -60.1,-45.4	-	-	-	-
113	LEU 144.54	-	Favored (86.82%) General / -64.6,-37.2	2.7% (<i>mm?</i>) chi angles: 284,315.4	0.136Å	-	-
114	ALA 27.48	-	Favored (72.25%) General / -63.0,-31.2	-	0.063Å	-	-
115	PHE 46.75	-	Favored (14.5%) General / -81.6,-46.4	87.2% (<i>t80</i>) chi angles: 181.7,75.7	0.052Å	-	-
116	ILE 141.84	-	Favored (18.46%) Isoleucine or valine / -77.4,-32.2	1.6% (<i>pp</i>) chi angles: 67.4,107.3	0.199Å	-	-
117	HIS 52.21	-	Favored (71.2%) General / -64.3,-30.1	43.7% (<i>m170</i>) chi angles: 294.9,151.7	0.159Å	-	-
118	LYS 112.81	-	Allowed (1.22%) General / -76.3,12.4	57.7% (<i>mttp</i>) chi angles: 296.4,180.2,182.9,77.6	0.088Å	-	-
119	HIS 104.68	-	Favored (10.98%) General / -119.7,0.6	48.7% (<i>m80</i>) chi angles: 292.3,67.2	0.058Å	-	-

120	GLY	31.07	-	Favored (71.28%) Glycine / 84.9,13.8	-	-	-	-
#	Alt Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
		Avg: 100.17	Clashscore: 0	Outliers: 10 of 282	Poor rotamers: 20 of 258	Outliers: 4 of 271	Outliers: 0 of 284	Outliers: 22 of 284
121	PHE	92.16	-	Favored (12.2%) General / -114.8,166.0	60.6% (<i>m-85</i>) chi angles: 283.9,85.8	0.047Å	-	-
122	PHE	118.34	-	Favored (18.14%) General / -131.8,168.2	7.7% (<i>m-85</i>) chi angles: 321.2,107.1	0.071Å	-	-
123	HIS	101.44	-	Favored (4.59%) General / -99.1,-49.2	65.6% (<i>t-80</i>) chi angles: 188.5,280.2	0.109Å	-	OUTLIER(S) worst is C-N- CA: 4.795 σ
124	ARG	162.53	-	Allowed (0.38%) General / 65.5,-49.2	87.2% (<i>mtt180</i>) chi angles: 303.1,163.2,168.3,179.5	0.146Å	-	-
125	ASP	185.43	-	Allowed (1.13%) General / -87.3,43.8	40.1% (<i>t0</i>) chi angles: 195,19.5	0.051Å	-	-
126	MET	119.2	-	Favored (52.68%) General / -68.7,136.3	79.8% (<i>mmm</i>) chi angles: 294.2,283.3,283.3	0.054Å	-	-
127	LYS	130.86	-	Allowed (0.28%) Pre-proline / 173.0,163.3	24.4% (<i>pttt</i>) chi angles: 57.8,210,186.9,188.9	0.049Å	-	-
128	PRO	92.38	-	Favored (55.28%) Trans-proline / -55.7,-26.3	0.4% chi angles: 320	0.049Å	-	-
129	GLU	154.2	-	Favored (71.21%) General / -61.9,-30.9	10.5% (<i>tm-20</i>) chi angles: 188.6,277.8,313.5	0.096Å	-	-
130	ASN	206.52	-	Favored (57.38%) General / -92.5,1.2	1.8% (<i>m-80</i>) chi angles: 268,237.4	0.074Å	-	-
				Favored				

131	LEU	75.91	-	(6.68%) General / -112.6,97.6 Favored	36.9% (<i>mt</i>) chi angles: 302.9,189	0.032Å	-	-
132	LEU	104.19	-	(24.82%) General / -105.7,151.1 Favored	2% (<i>mm?</i>) chi angles: 298.8,319	0.03Å	-	-
133	CYS	59.83	-	(6.72%) General / -139.2,179.1 Allowed	82.9% (<i>m</i>) chi angles: 300.7	0.03Å	-	-
134	MET	116.04	-	(0.05%) General / -178.2,109.0 Favored	29.7% (<i>ttp</i>) chi angles: 188.4,155.1,67.2	0.05Å	-	-
135	GLY	167.49	-	(22.95%) Glycine / 87.2,-150.7 Favored	-	-	-	-
136	PRO	325.01	-	(21.79%) Trans-proline / -57.2,157.3 Allowed	14.9% (<i>Cg_exo</i>) chi angles: 323.6	0.059Å	-	-
137	GLU	143.41	-	(0.36%) General / -69.7,72.4 Favored	17% (<i>mp0</i>) chi angles: 287.4,58.2,220	0.085Å	-	-
138	LEU	126.97	-	(4.44%) General / -96.1,87.1 Favored	2.2% (<i>tm?</i>) chi angles: 191.8,295.5	0.027Å	-	-
139	VAL	62.8	-	(27.07%) Isoleucine or valine / -70.9,135.9 Favored	12% (<i>t</i>) chi angles: 191.7	0.043Å	-	-
140	LYS	85.48	-	(11.25%) General / -124.8,107.8 Favored	45.8% (<i>mttm</i>) chi angles: 285.8,179.4,169.6,276	0.039Å	-	-

#	Alt	Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
Avg:				Clashscore:	Outliers: 10 of	Poor rotamers: 20 of	Outliers:	Outliers:	Outliers: 22
100.17				0	282	258	4 of 271	0 of 284	of 284

141	ILE	68.25	-	(25.64%) Isoleucine or valine / -74.0,136.3 Favored	57.5% (<i>mt</i>) chi angles: 302.7,163.3	0.033Å	-	-
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142	ALA	63.87	-	Favored (3.27%) General / -93.2,-173.5	-	0.074Å	-	OUTLIER(S) worst is C-N- CA: 6.571 σ
143	ASP	98.55	-	OUTLIER (0%) General / 42.1,11.7	2.2% (<i>m-20</i>) chi angles: 315.2,349.4	0.177Å	-	-
144	PHE	110.37	-	Favored (4.11%) General / -42.8,131.0	83.6% (<i>m-85</i>) chi angles: 294,285.4	0.129Å	-	-
145	GLY	55.09	-	Favored (4.84%) Glycine / 78.4,-19.4	-	-	-	-
146	LEU	75.28	-	Favored (68.05%) General / -66.5,-27.8	39.3% (<i>mt</i>) chi angles: 304.5,187.4	0.127Å	-	-
147	ALA	45.98	-	Allowed (1.96%) General / -76.2,10.5	-	0.088Å	-	-
148	ARG	46.63	-	Favored (3.84%) General / -110.7,-43.4	41.6% (<i>ttt-85</i>) chi angles: 170.8,182.1,170.3,248.8	0.04Å	-	-
149	GLU	95.79	-	Favored (44.3%) General / -79.7,-21.7	2.8% (<i>mm-40</i>) chi angles: 313,335.1,318.7	0.152Å	-	OUTLIER(S) worst is CB- CG-CD: 4.363 σ
150	LEU	173.77	-	Favored (34.72%) General / -82.6,-22.3	27.4% (<i>tp</i>) chi angles: 190.2,66.1	0.089Å	-	-
151	ARG	227.42	-	Favored (10.42%) General / -86.0,72.7	57.3% (<i>ttt180</i>) chi angles: 182.9,176.3,161.5,196.7	0.105Å	-	-
152	SER	183.61	-	Allowed (0.82%) General / -94.5,-161.1	99.9% (<i>p</i>) chi angles: 64.5	0.131Å	-	-
153	GLN	195.99	-	OUTLIER (0.03%) Pre-proline / 65.5,-175.1	27% (<i>mt-30</i>) chi angles: 308,162.6,249.3	0.042Å	-	-
154	PRO	161.71	-	Favored (80.86%)	15.3% (<i>Cg_exo</i>)	0.084Å	-	-

					Trans-proline / -66.2,152.6	chi angles: 323.6			
155	PRO	167.17	-		Allowed (0.5%) Trans-proline / -67.9,80.5	84.1% (<i>Cg_exo</i>) chi angles: 331	0.05Å	-	-
156	TYR	220.91	-		Favored (3.7%) General / -76.0,-177.0	36.1% (<i>m-85</i>) chi angles: 307.7,119.8	0.07Å	-	-
157	THR	255.06	-		Favored (28.85%) General / -51.2,133.0	15% (<i>p</i>) chi angles: 46.1	0.088Å	-	-
158	ASP	215.56	-		Favored (10.72%) General / -69.2,117.3	20.3% (<i>p-10</i>) chi angles: 53.2,337.3	0.161Å	-	OUTLIER(S) worst is CA-CB-CG: 7.533 σ
159	TYR	94.05	-		Favored (72.93%) General / -58.8,-35.5	2.8% (<i>m-85</i>) chi angles: 326.3,286.5	0.111Å	-	OUTLIER(S) worst is C-N-CA: 4.136 σ
160	VAL	115.39	-		OUTLIER (0.09%) Isoleucine or valine / -83.4,52.0	30.9% (<i>m</i>) chi angles: 300.9	0.15Å	-	-
#	Alt Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles	
Avg: 100.17			Clashscore: 0	Outliers: 10 of 282	Poor rotamers: 20 of 258	Outliers: 4 of 271	Outliers: 0 of 284	Outliers: 22 of 284	
161	SER	372.88	-		Favored (5.16%) General / -136.3,-178.4	1.9% (<i>t</i>) chi angles: 205.9	0.081Å	-	OUTLIER(S) worst is C-N-CA: 7.779 σ
162	THR	249.19	-		OUTLIER (0%) General / 154.1,110.4	52.6% (<i>m</i>) chi angles: 295.2	0.122Å	-	-
163	ARG	193.1	-		Favored (59.54%) General / -78.9,-9.5	0% chi angles: 107.8,280.4,68.6,211.6	0.389Å	-	-
164	TRP	98.45	-		Favored (66.8%) General / -61.5,-24.7	27.2% (<i>m0</i>) chi angles: 301.3,327.5	0.113Å	-	OUTLIER(S) worst is CE3-CD2-CG: 4.081 σ
165	TYR	130.24	-		Favored (20.3%) General / -112.2,15.9	3.9% (<i>m-85</i>) chi angles: 323.2,281.7	0.034Å	-	-

166	ARG	83.31	-	Favored (55.37%) General / -110.0,131.1	0% chi angles: 194.2,149.4,272.3,22.6	0.088Å	-	OUTLIER(S) worst is CD- NE-CZ: 7.698 σ
167	ALA	53.73	-	Favored (92.3%) Pre-proline / -71.2,156.0	-	0.041Å	-	-
168	PRO	81.45	-	Favored (52.29%) Trans-proline / -66.6,-21.3	67.1% (<i>Cg_endo</i>) chi angles: 27.9	0.141Å	-	-
169	GLU	144.21	-	Favored (49.86%) General / -51.2,-51.9	1.6% (<i>mp0</i>) chi angles: 311.8,82.3,278.4	0.143Å	-	-
170	VAL	48.56	-	Favored (7.34%) Isoleucine or valine / -83.9,-27.4	59.9% (<i>t</i>) chi angles: 181	0.154Å	-	-
171	LEU	65.21	-	Favored (76.44%) General / -63.9,-33.8	41.9% (<i>mt</i>) chi angles: 302.4,167.4	0.116Å	-	-
172	LEU	98.07	-	Allowed (1.32%) General / -81.9,18.4	81.5% (<i>mt</i>) chi angles: 295,168.6	0.077Å	-	-
173	ARG	85.05	-	Favored (2.68%) General / 75.5,16.0	26.7% (<i>mtt-85</i>) chi angles: 305.1,176.1,213.4,294.7	0.186Å	-	-
174	SER	47.27	-	Favored (50.93%) General / -66.2,149.0	32.1% (<i>t</i>) chi angles: 184.4	0.066Å	-	-
175	SER	52.71	-	Favored (44.9%) General / -98.5,8.4	8.7% (<i>t</i>) chi angles: 193.5	0.138Å	-	-
176	VAL	49.45	-	Allowed (0.68%) Isoleucine or valine / -85.3,69.9	58.7% (<i>t</i>) chi angles: 180.8	0.088Å	-	-
177	TYR	71.28	-	Favored (8.01%) General / -82.1,67.3	0.8% chi angles: 297,212.7	0.091Å	-	OUTLIER(S) worst is CA-CB- CG: 5.125 σ

178	SER	36.8	-	(2.32%) General / -96.7,-171.7	13.7% (<i>t</i>) chi angles: 190.5	0.118Å	-	-
179	SER	54.02	-	Favored (11.39%) Pre-proline / -57.5,-31.8	34.9% (<i>p</i>) chi angles: 53	0.223Å	-	-
180	PRO	160.75	-	Favored (62.41%) Trans-proline / -64.6,-18.3	93.8% (<i>Cg_exo</i>) chi angles: 329.8	0.084Å	-	-
#	Alt Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
Avg: 100.17				Clashscore: 0	Outliers: 10 of 282	Poor rotamers: 20 of 258	Outliers: 4 of 271	Outliers: 0 of 284
181	ILE	84.37	-	Favored (73.78%) Isoleucine or valine / -63.8,-35.6	3.2% (<i>tt</i>) chi angles: 212.6,184.1	0.164Å	-	-
182	ASP	46.81	-	Favored (40.39%) General / -78.4,-38.8	69.8% (<i>m-20</i>) chi angles: 299.6,313.4	0.077Å	-	-
183	VAL	90	-	Favored (49.17%) Isoleucine or valine / -72.0,-34.0	0.7% chi angles: 88.6	0.23Å	-	-
184	TRP	68.1	-	Favored (50.47%) General / -51.1,-51.7	21.6% (<i>t-105</i>) chi angles: 170.6,275.8	0.045Å	-	OUTLIER(S) worst is CE3- CD2-CG: 4.412 σ
185	ALA	39.23	-	Favored (73.94%) General / -63.4,-32.5	-	0.08Å	-	-
186	VAL	87.88	-	Favored (82.77%) Isoleucine or valine / -62.2,-39.1	89.4% (<i>t</i>) chi angles: 175.3	0.143Å	-	-
187	GLY	23.87	-	Favored (59.2%) Glycine / -69.4,-45.7	-	-	-	-
188	SER	80.49	-	Favored (74.96%) General / -69.5,-34.8	88.7% (<i>p</i>) chi angles: 65.6	0.229Å	-	-

189	ILE	104.73	-	Favored (13.52%) Isoleucine or valine / -78.2,-22.7	1.1% (<i>tt</i>) chi angles: 217.1,150.2	0.235Å	-	-
190	MET	76.74	-	Favored (86.91%) General / -61.7,-47.1	1.4% (<i>tmt?</i>) chi angles: 165.3,260.1,198.1	0.045Å	-	-
191	ALA	38.45	-	Favored (72.81%) General / -62.3,-32.1	-	0.069Å	-	-
192	GLU	81.18	-	Favored (52.29%) General / -51.4,-38.2	6% (<i>mt-10</i>) chi angles: 272.1,210.3,250.5	0.137Å	-	-
193	LEU	100.82	-	Favored (10.56%) General / -87.2,-45.6	0.5% chi angles: 236.9,169.3	0.158Å	-	-
194	TYR	110.64	-	Favored (77.68%) General / -67.1,-34.5	80.9% (<i>m-85</i>) chi angles: 295,107.1	0.179Å	-	-
195	MET	100.32	-	Favored (20.18%) General / -89.0,-28.5	17.7% (<i>mtm</i>) chi angles: 281.4,215,284	0.102Å	-	-
196	LEU	64.95	-	Favored (11.17%) General / 65.8,18.6	46.6% (<i>mt</i>) chi angles: 308.3,175	0.13Å	-	-
197	ARG	159.65	-	Allowed (1.18%) Pre-proline / -126.9,179.6	83% (<i>mtt85</i>) chi angles: 294.4,169.3,174.3,86.8	0.116Å	-	-
198	PRO	149.32	-	Favored (7.41%) Trans-proline / -85.6,140.8	93.5% (<i>Cg_endo</i>) chi angles: 32.2	0.06Å	-	-
199	LEU	63.87	-	Favored (44.38%) General / -63.2,-54.0	32.2% (<i>tp</i>) chi angles: 180.7,53.2	0.062Å	-	-
200	PHE	104.47	-	Favored (53.53%) Pre-proline / -110.6,115.7	34.5% (<i>m-85</i>) chi angles: 311.6,291.8	0.076Å	-	-

Clash >

Cβ Bond

#	Alt	Res	High B	0.4Å	Ramachandran	Rotamer	deviation	lengths	Bond angles
Avg: Clashscore: Outliers: 10 of Poor rotamers: 20 of Outliers: Outliers: Outliers: 22									
100.17 0 282 258 4 of 271 0 of 284 of 284									
201	PRO	120.22	-	Favored (4.97%) Trans-proline / -86.3,63.3	39.5% (<i>Cg_endo</i>) chi angles: 36.6	0.048Å	-	-	-
202	GLY	58.57	-	Favored (37.81%) Glycine / -77.8,151.6	-	-	-	-	-
203	THR	51.8	-	Allowed (0.59%) General / -112.2,-80.0	32.4% (<i>p</i>) chi angles: 51.7	0.106Å	-	-	-
204	SER	40.49	-	Favored (4.49%) General / -78.6,-175.7	85.3% (<i>p</i>) chi angles: 68.2	0.104Å	-	-	-
205	GLU	111.65	-	Favored (54.15%) General / -74.3,-44.1	1.1% (<i>pm0</i>) chi angles: 78.2,298.3,223.7	0.108Å	-	OUTLIER(S) worst is CB- CG-CD: 4.079 σ	-
206	VAL	87.48	-	Favored (71.51%) Isoleucine or valine / -70.6,-37.9	8% (<i>p</i>) chi angles: 70.1	0.21Å	-	-	-
207	ASP	38.64	-	Favored (98.91%) General / -63.4,-42.4	3.7% (<i>t70</i>) chi angles: 170.6,101.2	0.181Å	-	-	-
208	GLU	73.5	-	Favored (87.37%) General / -58.8,-46.6	5.8% (<i>tp10</i>) chi angles: 193.6,76.7,86.4	0.071Å	-	-	-
209	ILE	100.7	-	Favored (58.54%) Isoleucine or valine / -64.9,-32.5	2.8% (<i>pt</i>) chi angles: 74.7,196.5	0.294Å	-	-	-
210	PHE	55.62	-	Favored (84.05%) General / -66.2,-36.8	3.3% (<i>m-30</i>) chi angles: 282.4,33	0.15Å	-	-	-
211	LYS	121.96	-	Favored (85.75%) General / -67.4,-39.8	25% (<i>mmtp</i>) chi angles: 307.5,299.5,159.7,58.2	0.123Å	-	-	-

212	ILE	51.7	-	Favored (90.72%) Isoleucine or valine / -65.3,-41.2	64.6% (<i>mt</i>) chi angles: 294.2,160.3	0.079Å	-	-
213	CYS	80.34	-	Favored (78.41%) General / -60.6,-36.4	19.1% (<i>t</i>) chi angles: 191.9	0.067Å	-	-
214	GLN	42.02	-	Favored (86.96%) General / -67.1,-40.1	64.2% (<i>tt0</i>) chi angles: 186.1,181.6,4.3	0.049Å	-	-
215	VAL	62.96	-	Favored (13.41%) Isoleucine or valine / -92.4,-42.4	21.1% (<i>t</i>) chi angles: 188.5	0.12Å	-	-
216	LEU	143.05	-	Favored (30.39%) General / -96.8,-8.8	3.9% (<i>mm?</i>) chi angles: 284.8,300.3	0.076Å	-	-
217	GLY	34.22	-	Favored (31.39%) Glycine / 82.1,162.8	-	-	-	-
218	THR	107.99	-	Favored (77.18%) Pre-proline / -57.3,141.6	10% (<i>t</i>) chi angles: 184	0.12Å	-	-
219	PRO	163.19	-	Favored (60.85%) Trans-proline / -69.6,157.4	23.8% (<i>Cg_exo</i>) chi angles: 343.1	0.082Å	-	-
220	LYS	87.02	-	Favored (7.5%) General / -133.8,177.7	10.6% (<i>mtmm</i>) chi angles: 294,147.3,306.4,313.5	0.063Å	-	-
#	Alt Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
		Avg: 100.17	Clashscore: 0	Outliers: 10 of 282	Poor rotamers: 20 of 258	Outliers: 4 of 271	Outliers: 0 of 284	Outliers: 22 of 284
221	LYS	64.24	-	Favored (15.66%) General / -78.1,3.2	99.4% (<i>mttt</i>) chi angles: 294.4,185.2,176.2,181.7	0.135Å	-	-
222	SER	30.83	-	Favored (16.11%) General / -88.8,-36.3	60.9% (<i>p</i>) chi angles: 56.2	0.043Å	-	-

223	ASP	54.76	-	Favored (5.66%) General / -119.3,-27.3	7% (<i>p30</i>) chi angles: 44.5,23.8	0.137Å	-	-
224	TRP	98.08	-	Favored (74.83%) Pre-proline / -131.3,64.9	14.1% (<i>t90</i>) chi angles: 188.1,24.9	0.107Å	-	OUTLIER(S) worst is CE3- CD2-CG: 4.107 σ
225	PRO	178.48	-	Favored (20.66%) Trans-proline / -73.6,-20.2	4.5% (<i>Cg_exo</i>) chi angles: 358.9	0.062Å	-	-
226	GLU	206.26	-	Favored (30.91%) General / -84.3,-21.4	0.3% chi angles: 72.7,93.1,64.1	0.101Å	-	-
227	GLY	59.86	-	Allowed (0.19%) Glycine / -146.3,-13.2	-	-	-	-
228	TYR	143.22	-	Favored (81.15%) General / -61.0,-48.6	15.1% (<i>t80</i>) chi angles: 179.3,42.8	0.116Å	-	-
229	GLN	117.14	-	Favored (45.07%) General / -88.1,-12.1	0.3% chi angles: 211.2,247.4,260.9	0.078Å	-	-
230	LEU	137.99	-	Favored (9.61%) General / -106.8,-29.3	35.7% (<i>tp</i>) chi angles: 184.6,55.5	0.08Å	-	-
231	ALA	46.68	-	Favored (55.28%) General / -65.6,135.6	-	0.011Å	-	OUTLIER(S) worst is C-N- CA: 4.17 σ
232	SER	81.95	-	OUTLIER (0.03%) General / -65.6,52.6	18% (<i>m</i>) chi angles: 307	0.076Å	-	-
233	SER	101.41	-	OUTLIER (0.02%) General / -169.4,4.6	4.2% (<i>t</i>) chi angles: 201.1	0.096Å	-	-
234	MET	83.15	-	Favored (46.51%) General / -71.7,148.3	2% (<i>tmt?</i>) chi angles: 189.3,262.8,179.7	0.027Å	-	-

235	ASN	51.51	-	Favored (50.97%) General / -135.7,152.2	9.4% (<i>m120</i>) chi angles: 307.2,148.1	0.1Å	-	OUTLIER(S) worst is CA-CB- CG: 6.896 σ
236	PHE	100.01	-	Favored (60.54%) General / -74.9,-17.7	3.7% (<i>t80</i>) chi angles: 181.8,26	0.072Å	-	OUTLIER(S) worst is CA-CB- CG: 7.134 σ
237	ARG	101.41	-	Favored (52.37%) General / -78.0,-5.8	22.7% (<i>tpt180</i>) chi angles: 196.6,63.7,175.7,184.2	0.109Å	-	-
238	PHE	88.49	-	Favored (89.57%) Pre-proline / -60.0,132.3	15.7% (<i>m-30</i>) chi angles: 294.6,352.7	0.092Å	-	-
239	PRO	66.87	-	Favored (42.39%) Trans-proline / -57.5,131.1	9% (<i>Cg_exo</i>) chi angles: 322.7	0.07Å	-	-
240	GLN	82.84	-	Favored (8.8%) General / -86.2,64.9	21.4% (<i>mm-40</i>) chi angles: 297.4,298.6,265.8	0.059Å	-	-
#	Alt Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
Avg: 100.17				Clashscore: 0	Outliers: 10 of 282	Poor rotamers: 20 of 258	Outliers: 4 of 271	Outliers: 0 of 284
241	CYS	64.35	-	Favored (56.33%) General / -62.9,144.8	74.2% (<i>m</i>) chi angles: 298.5	0.063Å	-	-
242	VAL	187.58	-	Favored (73.54%) Pre-proline / -77.5,146.4	72.9% (<i>t</i>) chi angles: 172	0.11Å	-	-
243	PRO	102.93	-	Favored (17.28%) Trans-proline / -77.6,138.5	92.5% (<i>Cg_endo</i>) chi angles: 30.3	0.082Å	-	-
244	ILE	124.9	-	Favored (19.85%) Isoleucine or valine / -74.5,-26.1	26.5% (<i>pt</i>) chi angles: 65.5,163.2	0.244Å	-	-
245	ASN	248.96	-	OUTLIER (0.03%) General / 91.6,140.0	12.3% (<i>t-20</i>) chi angles: 197,288.5	0.077Å	-	-

246	LEU	79.61	-	Favored (75.68%) General / -61.6,-34.5	42.8% (<i>mt</i>) chi angles: 287.8,161.5	0.123Å	-	-
247	LYS	52.67	-	Favored (59.93%) General / -75.2,-19.1	11.1% (<i>tptp</i>) chi angles: 185.3,63.1,217.7,71.6	0.091Å	-	-
248	THR	26.78	-	Favored (36.05%) General / -78.1,-41.2	12.5% (<i>m</i>) chi angles: 312.4	0.028Å	-	-
249	LEU	79.67	-	Favored (68.09%) General / -72.4,-39.3	28.7% (<i>tp</i>) chi angles: 181.6,52.4	0.08Å	-	-
250	ILE	280.92	-	Favored (30.91%) Pre-proline / -109.3,98.3	5.3% (<i>tt</i>) chi angles: 206,154.6	0.168Å	-	-
251	PRO	185.18	-	Allowed (1.72%) Trans-proline / -68.7,-46.6	73.4% (<i>Cg_exo</i>) chi angles: 332.8	0.086Å	-	-
252	ASN	177.34	-	Favored (7.75%) General / -86.8,88.8	17.3% (<i>p-10</i>) chi angles: 55.9,321.7	0.078Å	-	-
253	ALA	39.08	-	Favored (4.18%) General / -164.1,134.3	-	0.09Å	-	-
254	SER	25.21	-	Favored (6.32%) General / -67.9,171.8	46.3% (<i>p</i>) chi angles: 75.9	0.076Å	-	-
255	ASN	23.95	-	Favored (92.83%) General / -65.0,-39.1	24.4% (<i>p-10</i>) chi angles: 58.6,333.7	0.113Å	-	-
256	GLU	60.99	-	Favored (58.9%) General / -74.6,-42.3	0% chi angles: 209.7,324.2,260.9	0.032Å	-	-
257	ALA	26.77	-	Favored (90.99%) General / -58.9,-43.2	-	0.051Å	-	-

258	ILE	129.94	-	Favored (60.44%) Isoleucine or valine / -71.0,-35.8	0.4% chi angles: 226.1,290	0.236Å	-	-
259	GLN	110.79	-	Favored (75.84%) General / -59.2,-50.0	11.2% (<i>tp-100</i>) chi angles: 179,54,240.3	0.081Å	-	-
260	LEU	50.38	-	Favored (97.59%) General / -63.9,-41.7	25.8% (<i>tp</i>) chi angles: 183.6,51.7	0.105Å	-	-
#	Alt Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
Avg: 100.17				Clashscore: 0	Outliers: 10 of 282	Poor rotamers: 20 of 258	Outliers: 4 of 271	Outliers: 0 of 284
261	MET	104.79	-	Favored (91.23%) General / -65.8,-39.6	21.9% (<i>ptm</i>) chi angles: 79.5,189.7,290.8	0.215Å	-	-
262	THR	108.82	-	Favored (94.56%) General / -64.4,-39.8	38.7% (<i>m</i>) chi angles: 305.9	0.113Å	-	-
263	GLU	43.24	-	Favored (87.07%) General / -58.8,-41.7	21% (<i>tt0</i>) chi angles: 200.1,169.7,113.3	0.046Å	-	-
264	MET	86.39	-	Favored (59.24%) General / -74.2,-23.9	49.8% (<i>mtt</i>) chi angles: 296.8,192.2,177.6	0.088Å	-	-
265	LEU	137.5	-	Favored (33.81%) General / -105.4,9.0	35.2% (<i>mt</i>) chi angles: 300.3,163.9	0.099Å	-	-
266	ASN	49.24	-	Favored (4.89%) General / -47.2,140.9	20.6% (<i>m-80</i>) chi angles: 272.5,296.9	0.092Å	-	-
267	TRP	125.97	-	Favored (87.99%) General / -59.9,-46.9	0.1% chi angles: 331,263.5	0.157Å	-	OUTLIER(S) worst is CE3- CD2-CG: 4.513 σ
268	ASP	68.42	-	Favored (84.62%) Pre-proline /	57.4% (<i>t0</i>) chi angles: 189.8,359.4	0.029Å	-	-

				-75.9,127.8				
				Favored				
269	PRO	77.95	-	(45.42%)	69.8% (<i>Cg_endo</i>)	0.068Å	-	-
				Trans-proline /	chi angles: 28.1			
				-68.1,-17.6				
				Favored				
270	LYS	63.83	-	(60.03%)	72.9% (<i>mttt</i>)	0.091Å	-	-
				General /	chi angles:			
				-78.8,-12.5	293.5,155.9,174.8,167			
				Favored				
271	LYS	110.02	-	(41.17%)	2.6% (<i>mppt?</i>)	0.133Å	-	-
				General /	chi angles:			
				-100.7,2.2	269,85.2,81.8,180.3			
				Favored				
272	ARG	196.37	-	(56.96%)	67.7% (<i>mtt180</i>)	0.035Å	-	-
				Pre-proline /	chi angles:			
				-83.0,148.5	296.5,179.3,195.9,141.2			
				Favored				
273	PRO	153.98	-	(20.4%)	33.5% (<i>Cg_endo</i>)	0.038Å	-	-
				Trans-proline /	chi angles: 37.1			
				-76.9,140.4				
				Favored				
274	THR	90.98	-	(14.42%)	15.1% (<i>t</i>)	0.189Å	-	-
				General /	chi angles: 188.1			
				-60.1,156.7				
				Favored				
275	ALA	29.72	-	(59.46%)	-	0.166Å	-	-
				General /				
				-73.8,-10.2				
				Favored				
276	SER	28.23	-	(20.56%)	15% (<i>m</i>)	0.102Å	-	-
				General /	chi angles: 308.8			
				-87.7,-30.1				
				Favored				
277	GLN	81.85	-	(53.91%)	24.8% (<i>tt0</i>)	0.051Å	-	-
				General /	chi angles:			
				-71.1,-48.2	159.7,188.8,357.4			
				Favored				
278	ALA	29.63	-	(67.83%)	-	0.138Å	-	-
				General /				
				-61.7,-26.1				
				Favored				
279	LEU	43.84	-	(71.28%)	80.8% (<i>mt</i>)	0.131Å	-	-
				General /	chi angles: 288,172.7			
				-62.9,-30.1				
				Favored				
280	LYS	91.69	-	(9.52%)	6.9% (<i>tptp</i>)	0.145Å	-	-
				General /	chi angles:			
					189.3,64.3,226.1,72.7			

-121.2,-4.1								
#	Alt Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
Avg: 100.17			Clashscore: 0	Outliers: 10 of 282	Poor rotamers: 20 of 258	Outliers: 4 of 271	Outliers: 0 of 284	Outliers: 22 of 284
281	HIS	59.56	-	Favored (3.69%) Pre-proline / -43.4,125.5	54.5% (<i>t</i> -80) chi angles: 197.9,289.2	0.134Å	-	-
282	PRO	62.66	-	Favored (2.66%) Trans-proline / -45.5,-26.3	83% (<i>Cg</i> - <i>exo</i>) chi angles: 330.8	0.205Å	-	OUTLIER(S) worst is N-CA- C: 4.194 σ
283	TYR	42.21	-	Favored (36.13%) General / -70.1,-6.8	10.4% (<i>t</i> 80) chi angles: 202.2,62.8	0.095Å	-	-
284	PHE	29.26	-	-	16.8% (<i>m</i> -85) chi angles: 311.8,306.1	0.058Å	-	-

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