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All-Atom Contacts	Clashscore, all atoms:	2.52	98 th percentile* (N=1784, all resolutions	
	Clashscore is the number of serious steric overlaps (> 0.4 Å) per 1000 atoms.			
Protein Geometry	Poor rotamers	2	1.69%	Goal: <1%
	Ramachandran outliers	6	4.55%	Goal: <0.05%
	Ramachandran favored	107	81.06%	Goal: >98%
	MolProbity score^	1.93		79 th percentile* (N=27675, 0Å - 99Å)
	Cβ deviations >0.25Å	6	4.92%	Goal: 0
	Bad backbone bonds:	0 / 1024	0.00%	Goal: 0%
	Bad backbone angles:	17 / 1378	1.23%	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	Cβ deviation	Bond lengths	Bond angles
		Avg: Clashscore:		Outliers: 6 of	Poor rotamers: 2 of	Outliers:	Outliers:	Outliers: 1
		64.92	2.52	132	118	6 of 122	0 of 134	of 134
A 768	CYS	50	-	-	4% (<i>m</i>) chi angles: 319.8	0.069Å	-	-
A 769	LYS	50	-	Favored (40.1%) General / -68.9,155.5	27.8% (<i>mmmt</i>) chi angles: 295.6,282.6,287.4,190.1	0.069Å	-	-
A 770	LYS	50	-	Favored (7.2%) General / -52.7,148.5	23.1% (<i>tptp</i>) chi angles: 168.9,62.8,189.7,68.8	0.044Å	-	-

A 771	GLU	50	-	Allowed (0.24%) General / 85.1,-21.3	33.1% (<i>mt-10</i>) chi angles: 308.6,187.7,292.5	0.171Å	-	-
A 772	ALA	50	-	Favored (5.25%) General / -109.7,176.0	-	0.078Å	-	-
A 773	LYS	50	-	OUTLIER (0.02%) General / -161.0,-110.0	21.6% (<i>tptp</i>) chi angles: 176.6,50.7,189.9,59.7	0.221Å	-	-
A 774	GLY	50	-	Favored (3.24%) Glycine / 43.6,-140.1	-	-	-	-
A 775	LEU	50	-	Favored (3.78%) General / -109.2,-45.2	92.8% (<i>mt</i>) chi angles: 295.7,171.8	0.054Å	-	-
A 776	GLN	50	-	Favored (33.19%) General / -86.4,-17.9	23.8% (<i>mm100</i>) chi angles: 304.4,296.7,110.6	0.07Å	-	OUTLIER(worst is C-N-CA: 4.904 σ
A 777	CYS	50	-	OUTLIER (0%) General / 123.3,-51.7	35.4% (<i>m</i>) chi angles: 282.2	0.271Å	-	OUTLIER(worst is CB-CA-N: 5.568 σ
A 778	ASP	50	-	OUTLIER (0%) General / 9.0,-97.5	5.2% (<i>t70</i>) chi angles: 164.5,55	0.208Å	-	-
A 779	THR	50	-	Favored (45.09%) General / -55.0,137.9	41.2% (<i>p</i>) chi angles: 54.2	0.157Å	-	-
A 780	CYS	50	-	Favored (44.9%) General / -62.7,148.9	1.2% (<i>m</i>) chi angles: 331.7	0.067Å	-	-
A 781	ARG	50	-	Favored (39.53%) General / -71.2,156.5	11.6% (<i>ttm-85</i>) chi angles: 191.6,157,291.5,240.5	0.098Å	-	-

A 782	GLU	50	-	Favored (38.44%) General / -56.0,141.8	1.2% (<i>tm-20</i>) chi angles: 210.6,304.6,297.7	0.069Å	-	-	
A 783	ASN	50	-	Favored (2.94%) General / 77.8,3.6	14.1% (<i>t-20</i>) chi angles: 189.9,247.1	0.106Å	-	OUTLIER(worst is CA-CB-CG: 4.666 σ	
A 784	PHE	50	-	Favored (48.76%) General / -135.2,156.6	26.9% (<i>m-85</i>) chi angles: 289.1,69.9	0.042Å	-	-	
A 785	TYR	99.99	-	Favored (43.9%) General / -146.6,158.5	13.5% (<i>p90</i>) chi angles: 80.9,274.5	0.033Å	-	-	
A 786	GLY	50	-	Favored (9.1%) Glycine / 140.5,-138.6	-	-	-	-	
A 787	LEU	50	-	Allowed (0.09%) General / -174.3,96.5	29.7% (<i>tp</i>) chi angles: 175.3,72.3	0.047Å	-	-	
#	Alt	Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
			Avg: 64.92	Clashscore: 2.52	Outliers: 6 of 132	Poor rotamers: 2 of 118	Outliers: 6 of 122	Outliers: 0 of 134	Outliers: 1 of 134
A 788	ASP	99.99	-	Allowed (0.39%) General / 42.7,-116.6	16.4% (<i>t70</i>) chi angles: 191.7,86.6	0.25Å	-	OUTLIER(worst is C-CA-CB: 4.877 σ	
A 789	VAL	99.99	-	Allowed (1.07%) Isoleucine or valine / -44.4,-34.8	4.3% (<i>p</i>) chi angles: 77.5	0.228Å	-	-	
A 790	THR	99.99	-	Favored (7.66%) General / -81.5,81.3	12.1% (<i>t</i>) chi angles: 191.5	0.271Å	-	OUTLIER(worst is C-N-CA: 4.1 σ	
A 791	ASN	50	-	Allowed (0.51%) General / -34.4,122.5	9.7% (<i>m120</i>) chi angles: 299.7,158.7	0.035Å	-	OUTLIER(worst is CA-CB-CG: 6.499 σ	

A 792	CYS	50	-	Allowed (0.33%) General / -59.1,105.5	72.3% (<i>m</i>) chi angles: 301.4	0.082Å	-	-
A 793	LYS	50	-	Favored (13.76%) General / -111.6,163.8	31.8% (<i>mtmt</i>) chi angles: 299.3,170.6,290.8,158.1	0.116Å	-	-
A 794	ALA	50	-	Favored (15.48%) General / -61.2,157.7	-	0.02Å	-	-
A 795	CYS	50	-	Favored (6.09%) General / -52.6,149.4	71.6% (<i>m</i>) chi angles: 297.3	0.097Å	-	-
A 796	ASP	99.99	-	Favored (2.38%) General / -107.9,86.9	5.4% (<i>m-20</i>) chi angles: 314,339.7	0.034Å	-	-
A 797	CYS	50	-	Favored (11.91%) General / -120.3,13.4	27.6% (<i>p</i>) chi angles: 66.7	0.071Å	-	-
A 798	ASP	50	-	Favored (30.85%) General / 55.7,39.6	17.4% (<i>t0</i>) chi angles: 206.5,12.3	0.073Å	-	-
A 799	THR	50	-	OUTLIER (0.03%) General / 53.4,2.5	13.9% (<i>p</i>) chi angles: 45.8	0.328Å	-	-
A 800	ALA	50	-	Allowed (1.12%) General / -90.8,42.9	-	0.058Å	-	-
A 801	GLY	50	-	Favored (3.6%) Glycine / -128.0,121.0	-	-	-	-
A 802	SER	99.99	-	Favored (49.4%) General / -67.3,133.3	35.4% (<i>t</i>) chi angles: 182.7	0.056Å	-	-

A 803	LEU	99.99	-	Favored (40.71%) Pre-proline / -67.0,-42.2	10% (<i>tt</i>) chi angles: 187.6,149.8	0.16Å	-	-
A 804	PRO	99.99	-	Favored (2.25%) Trans-proline / -85.3,121.0	74.3% (<i>Cg_endo</i>) chi angles: 28.6	0.036Å	-	-
A 805	GLY	99.99	-	Favored (8.61%) Glycine / 129.3,155.7	-	-	-	-
A 806	THR	99.99	-	Favored (24.68%) General / -62.9,125.7	13.9% (<i>t</i>) chi angles: 186.7	0.076Å	-	-
A 807	VAL	50	-	Favored (2.83%) Isoleucine or valine / -113.5,-38.4	11% (<i>p</i>) chi angles: 67	0.26Å	-	-
<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: 64.92</div> <div>Clashscore: 2.52</div> <div>Outliers: 6 of 132</div> <div>Poor rotamers: 2 of 118</div> <div>Outliers: 6 of 122</div> <div>Outliers: 0 of 134</div> <div>Outliers: 1 of 134</div> </div>								
A 808	CYS	50	-	Favored (14.42%) General / -147.4,172.1	14.8% (<i>p</i>) chi angles: 74.6	0.034Å	-	-
A 809	ASN	50	-	Favored (12.68%) General / -79.5,108.0	20.9% (<i>t-20</i>) chi angles: 185.6,289.9	0.032Å	-	-
A 810	ALA	50	-	Favored (11.79%) General / -50.6,-29.8	-	0.069Å	-	-
A 811	LYS	50	-	Favored (21%) General / -88.0,-29.1	4.4% (<i>tp tp</i>) chi angles: 188.7,66.4,232.8,73.7	0.067Å	-	-
A 812	THR	50	-	Favored (8.4%) General / -115.8,-24.0	67.3% (<i>p</i>) chi angles: 59.4	0.097Å	-	-

A 813	GLY	50	-	Favored (83%) Glycine / 88.3,-0.0	-	-	-	-
A 814	GLN	50	-	Favored (27.3%) General / -62.2,126.4	47% (<i>tt0</i>) chi angles: 187.9,175.8,313.2	0.036Å	-	-
A 815	CYS	99.99	-	Favored (46.6%) General / -125.3,151.0	18% (<i>t</i>) chi angles: 192.2	0.103Å	-	-
A 816	ILE	99.99	-	OUTLIER (0.09%) Isoleucine or valine / -150.6,23.2	1.8% (<i>pt</i>) chi angles: 79.2,196.1	0.179Å	-	-
A 817	CYS	99.99	-	Favored (32.62%) General / -65.6,156.5	26.4% (<i>t</i>) chi angles: 190.4	0.021Å	-	-
A 818	LYS	99.99	-	Favored (2.44%) Pre-proline / -155.1,117.8	11.9% (<i>pttp</i>) chi angles: 73.2,167.3,204.3,66.2	0.086Å	-	-
A 819	PRO	50	-	Allowed (1.6%) Trans-proline / -79.0,44.0	48.3% (<i>Cg_exo</i>) chi angles: 337.1	0.043Å	-	-
A 820	ASN	50	-	Favored (6.51%) General / 68.5,26.1	70.8% (<i>m-20</i>) chi angles: 304.8,317.7	0.153Å	-	-
A 821	VAL	99.99	-	Favored (2%) Isoleucine or valine / -85.6,166.5	87.8% (<i>t</i>) chi angles: 175.1	0.161Å	-	-
A 822	GLU	50	-	Favored (2.09%) General / -159.3,-167.6	17.3% (<i>tt0</i>) chi angles: 210.9,182.3,0.5	0.074Å	-	-
A 823	GLY	50	-	Favored (32.37%) Glycine / 98.4,179.5	-	-	-	-

A 824	ARG	50	-	Favored (83.81%) General / -63.8,-36.4	44% (<i>ttm-85</i>) chi angles: 176.5,175.3,290,296	0.165Å	-	-
A 825	GLN	50	-	Favored (3.98%) General / -132.5,31.7	18.2% (<i>mp0</i>) chi angles: 303.8,96,325.9	0.037Å	-	-
A 826	CYS	50	-	Allowed (1.95%) General / 64.9,50.5	6.7% (<i>m</i>) chi angles: 316.9	0.139Å	-	-
A 827	ASN	50	-	Favored (14.62%) General / -117.5,16.4	8.2% (<i>m120</i>) chi angles: 316.5,121.8	0.035Å	-	-
				# Alt Res High B Clash > 0.4Å Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
				Avg: 64.92	Clashscore: 2.52	Outliers: 6 of 132	Poor rotamers: 2 of 118	Outliers: 6 of 122
							Outliers: 0 of 134	Outliers: 1 of 134
A 828	LYS	50	-	Favored (6.25%) General / -138.5,179.8	35.5% (<i>mmtm</i>) chi angles: 305.1,294.4,161.5,293.1	0.049Å	-	-
A 829	CYS	50	-	Favored (40.58%) General / -104.3,138.5	0% chi angles: 337.1	0.063Å	-	-
A 830	LEU	99.99	-	Favored (4.26%) General / -47.4,142.2	25.8% (<i>tp</i>) chi angles: 177.9,74.2	0.049Å	-	-
A 831	GLU	50	0.478Å HA with A 831 GLU OE1	Favored (27.77%) General / -63.8,126.5	2.7% (<i>tp10</i>) chi angles: 201.2,60.1,303.2	0.121Å	-	-
A 832	GLY	50	-	Favored (57.03%) Glycine / 98.7,4.4	-	-	-	-
A 833	ASN	50	-	Favored (25.79%) General / -138.2,165.8	9.9% (<i>m120</i>) chi angles: 301.3,76.3	0.065Å	-	-

A 834	PHE 50	-	Favored (9.83%) General / -147.1,176.6	16.7% (<i>p90</i>) chi angles: 74.5,285.3	0.055Å	-	OUTLIER(worst is C-N-CA: 5.607 σ
A 835	TYR 99.99	-	OUTLIER (0%) General / 118.6,-136.5	16.8% (<i>m-30</i>) chi angles: 288.3,345.1	0.309Å	-	OUTLIER(worst is CA-CB-CG 5.077 σ
A 836	LEU 99.99	-	Favored (28.49%) General / 52.2,45.4	18.1% (<i>tp</i>) chi angles: 195.9,64.6	0.133Å	-	-
A 837	ARG 99.99	-	Favored (3.55%) General / -145.2,101.0	57.6% (<i>ttt-85</i>) chi angles: 182.9,195.9,175.2,284.1	0.082Å	-	-
A 838	GLN 99.99	-	Favored (12.11%) General / 46.5,51.2	95.5% (<i>mt-30</i>) chi angles: 291.6,182.4,337.1	0.112Å	-	-
A 839	ASN 99.99	-	Favored (21.37%) General / -118.3,160.6	31.9% (<i>m120</i>) chi angles: 294.2,123.6	0.145Å	-	OUTLIER(worst is CA-CB-CG 4.276 σ
A 840	ASN 99.99	-	Allowed (0.39%) General / -97.6,-83.6	53.1% (<i>t30</i>) chi angles: 184.3,26.1	0.134Å	-	-
A 841	SER 99.99	-	Allowed (1.12%) General / -162.2,103.4	39.9% (<i>t</i>) chi angles: 176.5	0.055Å	-	OUTLIER(worst is C-N-CA: 5.6 σ
A 842	PHE 50	-	Allowed (1.09%) General / 76.6,23.2	8.8% (<i>m-30</i>) chi angles: 311.3,322.5	0.158Å	-	-
A 843	LEU 99.99	-	Allowed (1.73%) General / -69.8,-61.6	40.3% (<i>mt</i>) chi angles: 282.7,174.5	0.128Å	-	-
A 844	CYS 50	-	Favored (3.61%) General / -156.1,116.0	62.3% (<i>m</i>) chi angles: 286.4	0.064Å	-	-

A 845	LEU	99.99	-	Favored (37.62%) Pre-proline / -98.3,151.7	15.1% (<i>tp</i>) chi angles: 195.9,72.1	0.118Å	-	-	
A 846	PRO	50	-	Favored (52.01%) Trans-proline / -72.0,148.8	58.2% (<i>Cg_endo</i>) chi angles: 26.5	0.027Å	-	-	
A 847	CYS	50	-	Favored (73.68%) General / -57.7,-37.6	60.2% (<i>m</i>) chi angles: 304.4	0.152Å	-	-	
#	Alt	Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
			Avg: 64.92	Clashscore: 2.52	Outliers: 6 of 132	Poor rotamers: 2 of 118	Outliers: 6 of 122	Outliers: 0 of 134	Outliers: 1 of 134
A 848	ASN	50	-	Favored (13.76%) General / 61.9,39.3	10% (<i>t-20</i>) chi angles: 187.9,228.6	0.07Å	-	-	
A 849	CYS	50	-	Favored (35.17%) General / -67.3,128.1	43.4% (<i>m</i>) chi angles: 307.3	0.078Å	-	-	
A 850	ASP	99.99	-	Favored (36.67%) General / -79.7,141.1	19.7% (<i>t0</i>) chi angles: 175.2,28.7	0.039Å	-	-	
A 851	LYS	99.99	-	Favored (52.21%) General / -85.0,-12.9	96.5% (<i>mttt</i>) chi angles: 300.1,177.9,179.9,180	0.136Å	-	-	
A 852	THR	99.99	-	Favored (63.12%) General / -74.4,-38.3	2.9% (<i>p</i>) chi angles: 83.2	0.204Å	-	-	
A 853	GLY	50	-	Favored (8.27%) Glycine / -122.0,-6.6	-	-	-	-	
A 854	THR	50	-	Favored (35.67%) General /	84.5% (<i>m</i>) chi angles: 302.8	0.038Å	-	-	

A 855	ILE	50	0.547Å HG13 with A 856 ASN OD1	-81.4,138.1 Favored (17.75%) Isoleucine or valine / -59.6,126.7	9.7% (<i>tp</i>) chi angles: 186.4,67.5	0.103Å	-	-
A 856	ASN	50	0.547Å OD1 with A 855 ILE HG13	Favored (3.29%) General / 57.7,16.1	8.6% (<i>m120</i>) chi angles: 302,72	0.094Å	-	-
A 857	GLY	50	-	Favored (73.43%) Glycine / 69.5,18.3	-	-	-	-
A 858	SER	50	-	Favored (8.46%) General / -51.8,146.2	74.8% (<i>m</i>) chi angles: 294.9	0.048Å	-	-
A 859	LEU	50	-	Favored (46.09%) General / -99.5,5.2	21.1% (<i>tp</i>) chi angles: 190.4,53.8	0.064Å	-	-
A 860	LEU	99.99	-	Favored (42.77%) General / -113.0,144.3	40.9% (<i>tp</i>) chi angles: 184.2,56.8	0.09Å	-	-
A 861	CYS	50	0.479Å HB3 with A 868 CYS SG	Favored (5%) General / -122.1,178.2	29.4% (<i>p</i>) chi angles: 66.1	0.044Å	-	-
A 862	ASN	50	-	Favored (18.29%) General / -58.2,124.1	22.5% (<i>t-20</i>) chi angles: 187.3,279.9	0.026Å	-	-
A 863	LYS	50	-	Favored (66.98%) General / -55.6,-36.5	30.6% (<i>mmmt</i>) chi angles: 308.7,298.5,289.4,182.8	0.114Å	-	-
A 864	SER	50	-	Favored (7.48%) General / -89.1,-48.3	12.7% (<i>t</i>) chi angles: 190.8	0.072Å	-	-
A 865	THR	50	-	Favored (14%) General / -91.4,-36.1	46.2% (<i>p</i>) chi angles: 55.3	0.121Å	-	-

A 866	GLY	50	-	Favored (65.48%) Glycine / 95.0,-1.8	-	-	-	-
A 867	GLN	50	-	Favored (16.03%) General / -73.2,118.3	38.8% (<i>tp60</i>) chi angles: 183.8,55,76.3	0.026Å	-	-
#	Alt Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
		Avg: 64.92	Clashscore: 2.52	Outliers: 6 of 132	Poor rotamers: 2 of 118	Outliers: 6 of 122	Outliers: 0 of 134	Outliers: 1 of 134
A 868	CYS	50	0.535Å HB2 with A 879 CYS SG	Favored (76.8%) Pre-proline / -76.1,161.1	57.1% (<i>m</i>) chi angles: 305.8	0.03Å	-	-
A 869	PRO	50	-	Allowed (1.24%) Trans-proline / -78.2,99.0	60.8% (<i>Cg_endo</i>) chi angles: 27.3	0.045Å	-	-
A 870	CYS	50	-	Favored (58.66%) General / -62.7,139.7	95.5% (<i>m</i>) chi angles: 293.9	0.088Å	-	-
A 871	LYS	50	-	Favored (19.41%) General / -79.5,168.4	19.7% (<i>mtp</i>) chi angles: 291.1,150.4,64.4,68	0.042Å	-	-
A 872	LEU	50	-	Favored (55.76%) General / -56.9,135.8	29% (<i>mt</i>) chi angles: 306.8,188.4	0.059Å	-	-
A 873	GLY	50	-	Favored (82.46%) Glycine / 74.6,10.0	-	-	-	-
A 874	VAL	50	-	Favored (33.5%) Isoleucine or valine / -111.5,139.9	40.3% (<i>t</i>) chi angles: 184.9	0.075Å	-	-
A 875	THR	50	-	Allowed (1.78%)	80.3% (<i>p</i>) chi angles: 61.5	0.163Å	-	-

				General / -128.6,-167.5				
A 876	GLY	50	-	Favored (16.19%) Glycine / 81.9,155.9	-	-	-	-
A 877	LEU	50	-	Favored (79.64%) General / -61.2,-36.3	13.6% (<i>tp</i>) chi angles: 193.8,77	0.057Å	-	-
A 878	ARG	50	-	Favored (43.67%) General / -101.0,7.1	24.9% (<i>ptt-85</i>) chi angles: 58.3,169.2,186.8,282.5	0.142Å	-	-
A 879	CYS	50	0.535Å SG with A 868 CYS HB2	Favored (2.16%) General / 64.0,52.0	40.8% (<i>m</i>) chi angles: 307.5	0.118Å	-	-
A 880	ASN	99.99	-	Favored (5.59%) General / -129.1,24.6	4.5% (<i>t-20</i>) chi angles: 182.4,217	0.052Å	-	OUTLIER(worst is CA-CB-CG 7.204 σ
A 881	GLN	50	-	Favored (39.29%) General / -157.2,161.0	5.9% (<i>pt20</i>) chi angles: 55.4,164.8,120.4	0.028Å	-	-
A 882	CYS	50	-	Favored (17.04%) General / -80.2,170.0	0.8% chi angles: 332.9	0.067Å	-	-
A 883	GLU	50	-	Favored (92.69%) Pre-proline / -71.9,154.3	54.5% (<i>mt-10</i>) chi angles: 287.3,184,305.6	0.057Å	-	-
A 884	PRO	50	-	Favored (47.78%) Trans-proline / -58.0,132.2	8.3% (<i>Cg_exo</i>) chi angles: 322.6	0.047Å	-	-
A 885	HIS	50	0.412Å ND1 with A 885 HIS O	Allowed (0.97%) General / 65.8,55.4	46.9% (<i>t-80</i>) chi angles: 179.7,281.9	0.17Å	-	-
A 886	ARG	99.99	-	Favored (37.52%)	40.4% (<i>mtt-85</i>) chi angles:	0.085Å	-	-

				General / -154.1,156.6	286.2,210.7,192.5,263.6			
A 887	TYR	50	-	Favored (2.27%) General / -137.5,-168.2	5.8% (<i>m-85</i>) chi angles: 321.8,283.8	0.104Å	-	-
#	Alt Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
Avg: Clashscore:				Outliers: 6 of 132	Poor rotamers: 2 of 118	Outliers: 6 of 122	Outliers: 0 of 134	Outliers: 1 of 134
A 888	ASN	99.99	-	Favored (3.58%) General / -149.1,106.0	8.6% (<i>p-10</i>) chi angles: 48.4,302.1	0.035Å	-	-
A 889	LEU	99.99	-	Favored (34.36%) General / -53.2,137.3	7.2% (<i>tt</i>) chi angles: 182.3,140.4	0.043Å	-	-
A 890	THR	99.99	-	Favored (6.84%) General / -126.2,-3.8	1.3% (<i>t</i>) chi angles: 206.6	0.149Å	-	-
A 891	ILE	99.99	-	Favored (35.59%) Isoleucine or valine / -82.7,130.5	32.8% (<i>mm</i>) chi angles: 307.8,307	0.089Å	-	-
A 892	ASP	99.99	-	Favored (10.44%) General / 46.0,51.8	51.9% (<i>t0</i>) chi angles: 187.5,14.9	0.074Å	-	-
A 893	ASN	99.99	-	Favored (23.41%) General / -162.0,168.1	24.7% (<i>m120</i>) chi angles: 288,123.5	0.035Å	-	-
A 894	PHE	99.99	-	Favored (9.61%) General / -118.7,-13.1	2.5% (<i>m-30</i>) chi angles: 299.4,11.4	0.065Å	-	OUTLIER(worst is CA-CB-CG 10.528 σ
A 895	GLN	99.99	-	Allowed (0.32%) General / -136.6,-86.6	16.1% (<i>mp0</i>) chi angles: 287,91.9,30.5	0.204Å	-	OUTLIER(worst is C-N-CA: 6.5 σ

A 896	HIS	50	-	Favored (17.6%) General / -101.1,-14.9	20.2% (<i>t</i> -160) chi angles: 176.9,194.3	0.049Å	-	OUTLIER(worst is CA-CB-CG 7.857 σ
A 897	CYS	50	-	Allowed (0.13%) General / 80.2,-29.2	3.9% (<i>t</i>) chi angles: 205.1	0.219Å	-	-
A 898	GLN	50	-	Favored (12.98%) General / -80.2,-48.5	37.5% (<i>mt</i> -30) chi angles: 304.5,183,257.3	0.084Å	-	-
A 899	MET	50	-	Allowed (0.31%) General / 179.0,-178.3	23.5% (<i>ptp</i>) chi angles: 59.6,187.1,74.3	0.042Å	-	-
A 900	CYS	50	-	Favored (17.59%) General / -96.8,153.9	64.4% (<i>m</i>) chi angles: 302.6	0.037Å	-	-
A 901	GLU	99.99	-	-	2% (<i>pm0</i>) chi angles: 35.2,277.6,303.5	0.047Å	-	-

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