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All-Atom Contacts	Clashscore, all atoms:	1.42		99th percentile* (N=1784, all resolutions)
	Clashscore is the number of serious steric overlaps (> 0.4 Å) per 1000 atoms.			
Protein Geometry	Poor rotamers	3	2.61%	Goal: <1%
	Ramachandran outliers	1	0.74%	Goal: <0.05%
	Ramachandran favored	124	91.85%	Goal: >98%
	MolProbity score^	1.68		90th percentile* (N=27675, 0Å - 99Å)
	Cβ deviations >0.25Å	0	0.00%	Goal: 0
	Bad backbone bonds:	0 / 1123	0.00%	Goal: 0%
	Bad backbone angles:	7 / 1530	0.46%	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: 81.34	Clashscore: 1.42	Outliers: 1 of 135	Poor rotamers: 3 of 115	Outliers: 0 of 128	Outliers: 0 of 137	Outliers: 7 of 137
621		LEU	38.1	0.538Å N with 687 ASP OD2	-	14.7% (*mt*) chi angles: 273,174.4	0.13Å	-	-
622		HIS	116.2	-	Favored (25.34%) General / -54.3,142.8	1.8% (*p80*) chi angles: 31.9,83.1	0.118Å	-	OUTLIER(S) worst is CA-CB-CG: 5.941 σ
623		GLN	69.75	-	Favored (10.3%) General / -50.9,143.3	42% (*tp60*) chi angles: 184.9,59.3,77.1	0.053Å	-	-
624		GLY	20.13	-	Favored (15.12%) Glycine / 138.0,177.3	-	-	-	OUTLIER(S) worst is C-N-CA: 4.497 σ

625	GLU	93.64	-	Favored (11.14%) General / -63.1,162.8	26% (*mp0*) chi angles: 296,61.4,19	0.097Å	-	OUTLIER(S) worst is CB-CG-CD: 5.693 σ
626	ASN	52.63	-	Favored (52.14%) General / -130.8,146.2	74% (*m-20*) chi angles: 285.7,311.6	0.056Å	-	-
627	LEU	56.09	-	Favored (39.44%) General / -121.2,122.2	13.5% (*tp*) chi angles: 179.3,81	0.04Å	-	-
628	PHE	132.53	-	Favored (19.17%) General / -105.1,107.9	62.9% (*t80*) chi angles: 185.7,267.3	0.066Å	-	-
629	GLU	64.34	-	Favored (28.34%) General / -99.7,144.8	78.4% (*mt-10*) chi angles: 302.1,166.2,5.6	0.16Å	-	-
630	LEU	55.14	-	Favored (17.66%) General / -136.2,120.2	49.3% (*mt*) chi angles: 293.3,185.7	0.075Å	-	-
631	HIS	80.09	0.413Å CE1 with 677 ASP OD1	Favored (32.97%) General / -112.7,117.7	28.5% (*t-80*) chi angles: 186.9,300.5	0.057Å	-	-
632	ILE	93.48	-	Favored (40.37%) Isoleucine or valine / -87.2,124.0	46.6% (*mm*) chi angles: 302.2,304.4	0.044Å	-	-
633	HIS	94.51	-	Allowed (0.68%) General / -77.1,-67.7	59% (*t60*) chi angles: 188.5,83.3	0.046Å	-	-
634	GLN	61.67	-	Favored (30.67%) General / -159.2,166.7	86.4% (*mt-30*) chi angles: 291.1,174.4,298.9	0.095Å	-	-
635	ALA	44.85	-	Favored (55.86%) General / -111.1,129.7	-	0.1Å	-	-
636	PHE	102.54	-	Favored (43.98%) General / -107.1,138.1	67.8% (*t80*) chi angles: 185.7,70.1	0.027Å	-	-

#	Alt	Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
637		LEU	92.95	-	Favored (45.18%) General / -108.4,138.2	7.1% (*mp*) chi angles: 287.1,76.9	0.092Å	-	-
638		THR	114.84	-	Allowed (1.99%) General / -64.1,173.2	7% (*t*) chi angles: 194.2	0.13Å	-	-
639		SER	70.56	-	Favored (95.81%) General / -63.9,-40.1	61.9% (*p*) chi angles: 56.4	0.129Å	-	-
640		ALA	44.87	-	Favored (73.37%) General / -55.5,-49.2	-	0.086Å	-	-

#	Alt	Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
			Avg: 81.34	Clashscore: 1.42	Outliers: 1 of 135	Poor rotamers: 3 of 115	Outliers: 0 of 128	Outliers: 0 of 137	Outliers: 7 of 137
641		ALA	58.54	-	Favored (74.38%) General / -67.2,-32.9	-	0.104Å	-	-
642		LEU	141.39	-	Favored (94.53%) General / -63.0,-39.4	23.9% (*tp*) chi angles: 191.7,66.4	0.063Å	-	-
643		ALA	43.44	-	Favored (22.15%) General / -85.8,-31.8	-	0.081Å	-	-
644		GLN	75.48	-	Favored (59.96%) General / -74.8,-10.9	25.5% (*mt-30*) chi angles: 297.3,170.9,132.5	0.101Å	-	-
645		ALA	55.96	-	Favored (67.54%) General / -60.7,-27.1	-	0.11Å	-	-
646		GLY	45.12	-	Favored (13.37%) Glycine / 94.2,26.7	-	-	-	-
647		ASP	64.91	-	Favored (4.14%) General / 56.1,20.0	29.3% (*m-20*) chi angles: 307,335.2	0.177Å	-	-
					Favored				

648	THR 108.4	-	(49.07%) General / -112.4,138.4	95.3% (*m*) chi angles: 299.8	0.075Å	-	-
649	GLN 73.46	-	Favored (14.58%) Pre-proline / -63.2,115.0	41.9% (*mt-30*) chi angles: 292.9,174.5,253	0.04Å	-	-
650	PRO 83.32	-	Favored (31.84%) Trans-proline / -77.1,152.9	89.2% (*Cg_endo*) chi angles: 31.9	0.027Å	-	-
651	THR 110.27	-	Favored (21.82%) General / -122.2,115.1	90% (*m*) chi angles: 302.2	0.057Å	-	-
652	THR 44.26	-	Favored (15.77%) General / -130.4,169.2	72.8% (*p*) chi angles: 59.9	0.032Å	-	-
653	PHE 67.73	-	Favored (26.21%) General / -155.6,150.2	26.8% (*p90*) chi angles: 66.3,283.5	0.051Å	-	-
654	CYS 51.54	-	Favored (5.25%) General / -108.2,176.1	29% (*p*) chi angles: 61.9	0.112Å	-	-
655	THR 124.52	-	Favored (4.9%) General / -166.7,143.9	14% (*t*) chi angles: 186.7	0.051Å	-	-
656	TYR 67.33	-	Favored (16.58%) General / -150.4,171.7	53.5% (*p90*) chi angles: 60.3,91.5	0.043Å	-	-
657	SER 73.86	-	Favored (3.98%) General / -129.2,-176.8	33.9% (*t*) chi angles: 183.4	0.041Å	-	OUTLIER(S) worst is C-N-CA: 4.211 σ
658	PHE 60.88	-	Favored (3.22%) General / -164.4,131.7	82.6% (*t80*) chi angles: 176.6,84.2	0.112Å	-	-
659	TYR 78.28	-	Favored (23.01%) General / 58.9,33.4	26.1% (*t80*) chi angles: 197.2,92.1	0.103Å	-	-
660	ASP 47.8	-	Favored (12.98%) General / 48.1,40.1	4.7% (*m-20*) chi angles: 302.3,13.8	0.191Å	-	-

#	Alt	Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
			Avg: 81.34	Clashscore: 1.42	Outliers: 1 of 135	Poor rotamers: 3 of 115	Outliers: 0 of 128	Outliers: 0 of 137	Outliers: 7 of 137
661		PHE	71.15	-	Favored (11.05%) General / -78.1,174.5	25.7% (*m-85*) chi angles: 281.9,303.2	0.076Å	-	-
662		GLU	77.3	0.485Å HG3 with 664 HIS CE1	Favored (11.14%) General / -48.9,125.8	23.3% (*pt-20*) chi angles: 65.3,172.5,22.8	0.068Å	-	-
663		THR	100.09	-	Favored (10.46%) General / -71.0,115.7	22.7% (*p*) chi angles: 49.4	0.063Å	-	-
664		HIS	37.23	0.485Å CE1 with 662 GLU HG3	Favored (33%) General / -89.9,122.5	68% (*m80*) chi angles: 297.8,75.3	0.049Å	-	-
665		CYS	78.71	-	Favored (38.14%) General / -77.9,133.1	12% (*p*) chi angles: 52.4	0.025Å	-	-
666		THR	45.77	-	Favored (91.72%) Pre-proline / -69.9,156.5	76.1% (*p*) chi angles: 60.1	0.092Å	-	-
667		PRO	82.06	-	Favored (33.22%) Trans-proline / -63.5,131.8	41% (*Cg_endo*) chi angles: 23.9	0.034Å	-	-
668		LEU	99.99	-	Favored (36.47%) General / -78.8,131.4	7% (*mp*) chi angles: 289.1,75	0.069Å	-	-
669		SER	34.99	-	Favored (39.89%) General / -135.8,160.0	21.1% (*t*) chi angles: 188.3	0.02Å	-	-
670		VAL	36.25	-	Favored (12.42%) Isoleucine or valine / -96.8,143.4	72% (*t*) chi angles: 173.8	0.136Å	-	-
671		GLY	40.97	-	Favored (7.54%) Glycine / 137.8,157.5	-	-	-	-

#	Alt	Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
672		PRO	169.99	-	Favored (20.49%) Trans-proline / -64.3,-41.6	94.1% (*Cg_exo*) chi angles: 329.2	0.061Å	-	-
673		GLN	139.8	-	Favored (62.51%) Pre-proline / -136.2,69.6	25.3% (*tp60*) chi angles: 196.8,77.5,10.3	0.048Å	-	-
674		PRO	77.1	-	Favored (11.69%) Trans-proline / -79.5,135.2	65.1% (*Cg_endo*) chi angles: 34	0.049Å	-	-
675		LEU	70.84	-	Favored (6.3%) General / -67.7,114.4	80.4% (*mt*) chi angles: 290.9,167.4	0.077Å	-	-
676		TYR	55.87	-	Favored (66.24%) General / -71.9,-42.9	98.5% (*m-85*) chi angles: 297.2,279.2	0.104Å	-	-
677		ASP	46.2	0.413Å OD1 with 631 HIS CE1	Allowed (0.47%) General / 37.5,44.1	33.7% (*m-20*) chi angles: 282.8,311.2	0.216Å	-	-
678		PHE	55.18	-	Favored (32.28%) General / -95.0,118.7	71.7% (*t80*) chi angles: 179.6,67.7	0.037Å	-	-
679		THR	46.88	-	Favored (28.35%) General / -112.8,115.3	45.8% (*m*) chi angles: 305.2	0.05Å	-	-
680		SER	87.33	-	Favored (34.85%) General / -106.6,143.4	20.2% (*t*) chi angles: 188.6	0.054Å	-	-
#	Alt	Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
			Avg: 81.34	Clashscore: 1.42	Outliers: 1 of 135	Poor rotamers: 3 of 115	Outliers: 0 of 128	Outliers: 0 of 137	Outliers: 7 of 137
681		GLN	55.82	-	Favored (18.83%) General / -156.6,143.7	12.8% (*pt20*) chi angles: 70.6,185,32.2	0.041Å	-	-
682		TYR	89.63	-	Favored (13.05%) General / -157.6,138.2	2.6% (*p90*) chi angles: 36.2,76.8	0.033Å	-	-
					Favored				

683	VAL	40.3	-	(38.75%) Isoleucine or valine / -85.3,128.8	60% (*t*) chi angles: 181.1	0.057Å	-	-
684	MET	86.14	-	Favored (3.39%) General / -155.2,112.9	13.6% (*tpp*) chi angles: 194.3,48,44.1	0.023Å	-	-
685	GLU	130.39	-	Favored (5.91%) General / -92.6,87.4	8.7% (*mp0*) chi angles: 317,70.1,34.9	0.043Å	-	-
686	THR	91.25	-	Favored (14.08%) General / -152.6,133.5	98.6% (*m*) chi angles: 298.4	0.094Å	-	-
687	ASP	108.83	0.538Å OD2 with 621 LEU N	Allowed (1.91%) General / -117.5,-59.7	0.4% chi angles: 265.8,57.6	0.148Å	-	-
688	SER	47.82	-	Favored (90.86%) General / -61.2,-46.3	77.4% (*p*) chi angles: 58.6	0.153Å	-	-
689	LEU	51.68	-	Favored (59.1%) General / -77.8,-15.4	57.9% (*mt*) chi angles: 307.7,177.4	0.163Å	-	-
690	PHE	116.92	-	Favored (15.77%) General / -73.1,-52.0	4.2% (*t80*) chi angles: 186.7,295.6	0.071Å	-	-
691	LEU	48.45	-	Favored (93.19%) General / -62.7,-39.2	57.4% (*mt*) chi angles: 307.1,180.1	0.111Å	-	-
692	HIS	69.78	-	Favored (89.69%) General / -66.2,-39.7	60.5% (*t-80*) chi angles: 184.1,277.5	0.121Å	-	-
693	TYR	46.82	-	Favored (67.33%) General / -54.0,-50.1	69.2% (*t80*) chi angles: 179.4,268.7	0.1Å	-	-
694	LEU	143.63	-	Favored (25.8%) General / -48.5,-40.2	36.1% (*tp*) chi angles: 180.8,70.9	0.041Å	-	-
				Favored				

#	Alt	Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
695		GLN	67.23	-	(22.47%) General / -87.0,-28.8	29.4% (*mm100*) chi angles: 301.6,306,126	0.1Å	-	-
696		GLU	86.47	-	Favored (19.24%) General / -87.3,-33.5	14.8% (*pt-20*) chi angles: 64.5,173.6,313.4	0.164Å	-	-
697		ALA	33.03	-	Favored (8.14%) General / -154.9,127.8	-	0.121Å	-	-
698		SER	80.78	-	Favored (15.73%) General / -93.5,158.4	44% (*t*) chi angles: 178.3	0.075Å	-	-
699		ALA	41.79	-	Favored (56.18%) General / -67.0,144.4	-	0.049Å	-	-
700		ARG	111.88	-	Favored (55.16%) General / -113.2,133.2	57.5% (*ttt85*) chi angles: 187.6,181.8,183.2,90.5	0.08Å	-	-

#	Alt	Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
			Avg: 81.34	Clashscore: 1.42	Outliers: 1 of 135	Poor rotamers: 3 of 115	Outliers: 0 of 128	Outliers: 0 of 137	Outliers: 7 of 137
701		LEU	74.18	-	Favored (8.67%) General / -132.3,107.6	10.9% (*tp*) chi angles: 195.1,80.3	0.045Å	-	-
702		ASP	51.95	-	Favored (54.54%) General / -112.1,125.8	60.5% (*m-20*) chi angles: 298.7,351.1	0.02Å	-	-
703		ILE	100.62	-	Favored (20.36%) Isoleucine or valine / -95.0,108.1	18.8% (*tt*) chi angles: 186.7,173.2	0.183Å	-	-
704		HIS	61.86	-	Favored (44.63%) General / -109.7,139.5	2.1% (*p-80*) chi angles: 31.3,272.7	0.034Å	-	-
705		GLN	55.38	-	Favored (35.11%) General / -82.5,130.4	14.6% (*tt0*) chi angles: 192.1,186.5,122.5	0.063Å	-	-

706	ALA 46.22	-	Favored (2.78%) General / -113.7,88.2	-	0.059Å	-	-
707	MET 100.62	-	Favored (14.45%) General / -85.2,168.8	22.7% (*ptp*) chi angles: 70.6,185.5,74.8	0.103Å	-	-
708	ALA 30.22	-	Favored (69.51%) General / -67.9,-30.2	-	0.113Å	-	-
709	SER 48.93	-	Favored (19.11%) General / -88.3,-31.2	41.2% (*p*) chi angles: 53.8	0.056Å	-	-
710	GLU 61.29	-	Favored (3.82%) General / -165.5,-176.1	14.6% (*tt0*) chi angles: 211.6,184.1,320.7	0.082Å	-	-
711	HIS 82.81	-	Favored (36.88%) General / -137.9,136.3	42.4% (*m80*) chi angles: 305.7,76	0.154Å	-	-
712	SER 45.61	-	Favored (47.12%) General / -138.8,156.7	12.9% (*t*) chi angles: 190.7	0.047Å	-	-
713	THR 77.82	-	Favored (18.19%) General / -105.2,107.3	97.6% (*m*) chi angles: 299.2	0.054Å	-	-
714	LEU 180.94	-	Favored (38.37%) General / -78.8,-38.4	61.5% (*tp*) chi angles: 175.9,60.8	0.105Å	-	-
715	ALA 62.75	-	Favored (41.26%) General / -148.4,155.4	-	0.096Å	-	-
716	ALA 49.31	-	Favored (50.7%) General / -132.7,153.9	-	0.061Å	-	-
717	GLY 22.06	-	Favored (21.15%) Glycine /	-	-	-	-

#	Alt	Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
					-148.5,149.2				
718		TRP	158.33	-	Favored (3.59%) General / -110.7,91.3	38.7% (*t-105*) chi angles: 193.7,271.3	0.107Å	-	OUTLIER(S) worst is CE3-CD2-CG: 4.225 σ
719		ILE	106.65	-	Allowed (1.87%) Isoleucine or valine / -90.5,81.7	15.7% (*tt*) chi angles: 184.4,175.6	0.204Å	-	-
720		CYS	84.05	-	Favored (11.9%) General / -97.6,165.6	2.9% (*t*) chi angles: 206.9	0.09Å	-	-

#	Alt	Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
			Avg: 81.34	Clashscore: 1.42	Outliers: 1 of 135	Poor rotamers: 3 of 115	Outliers: 0 of 128	Outliers: 0 of 137	Outliers: 7 of 137
721		PHE	72.36	-	Allowed (1.94%) General / -132.7,81.3	21.3% (*m-85*) chi angles: 309,306.4	0.036Å	-	-
722		ASP	109.07	-	Favored (62.22%) General / -51.2,-47.1	17.2% (*p-10*) chi angles: 64,312.6	0.05Å	-	-
723		ARG	79.32	-	Favored (61.08%) General / -73.9,-16.9	31.6% (*mmm180*) chi angles: 296.7,297.9,295.6,156.9	0.145Å	-	-
724		VAL	49.38	-	Favored (25.58%) Isoleucine or valine / -69.6,-22.9	70.7% (*t*) chi angles: 173.7	0.15Å	-	-
725		LEU	156.87	-	Favored (87.15%) General / -62.7,-37.6	30.5% (*tp*) chi angles: 188.6,66.9	0.033Å	-	-
726		GLU	103.33	-	Allowed (1.17%) General / -98.3,-63.0	18.1% (*tt0*) chi angles: 184.4,201.6,293.5	0.06Å	-	-
727		THR	60.75	-	Favored (48.94%) General / -110.1,136.7	38.7% (*p*) chi angles: 53.2	0.122Å	-	-
					Favored (66.01%)				OUTLIER(S)

728	VAL 120.12	-	Isoleucine or valine / -114.0,131.4	31.6% (*m*) chi angles: 297	0.073Å	-	worst is C-N-CA: 5.026 σ
729	GLU 78.6	-	OUTLIER (0%) General / 150.0,-167.2	12.9% (*mt-10*) chi angles: 262,187.5,6.4	0.229Å	-	-
730	LYS 122.19	-	Allowed (0.97%) General / -72.2,77.0	68.4% (*mttm*) chi angles: 290.4,184.7,178.3,298.2	0.063Å	-	-
731	VAL 111.58	-	Favored (27.89%) Isoleucine or valine / -94.3,112.9	7.3% (*p*) chi angles: 58.7	0.139Å	-	-
732	HIS 75.19	-	Favored (20.18%) General / -71.4,122.3	84.7% (*t60*) chi angles: 182.3,64.2	0.085Å	-	-
733	GLY 20.13	-	Favored (18.73%) Glycine / -130.1,176.4	-	-	-	-
734	LEU 49.75	-	Favored (42.56%) General / -147.1,155.9	85.7% (*mt*) chi angles: 301.4,176.3	0.11Å	-	-
735	ALA 37.22	-	Favored (47.17%) General / -119.5,144.1	-	0.036Å	-	-
736	THR 90.01	-	Favored (27.34%) General / -87.4,143.2	36.5% (*p*) chi angles: 52.7	0.07Å	-	-
737	LEU 73.55	-	Favored (49.61%) General / -113.8,123.3	97.5% (*mt*) chi angles: 297.3,175.9	0.05Å	-	-
738	ILE 87.79	-	Favored (52.98%) Isoleucine or valine / -110.5,134.4	4.7% (*mp*) chi angles: 297.6,83.3	0.064Å	-	-
739	GLY 39.66	-	Favored (43.75%) Glycine / -64.0,156.8	-	-	-	-

Favored

#	Alt	Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
740		ALA	33.6	-	(47.65%) General / -78.5,-22.3	-	0.077Å	-	-
			Avg: 81.34	Clashscore: 1.42	Outliers: 1 of 135	Poor rotamers: 3 of 115	Outliers: 0 of 128	Outliers: 0 of 137	Outliers: 7 of 137
741		GLY	72.45	-	Favored (35.03%) Glycine / -77.0,-36.6	-	-	-	-
742		GLY	302.96	-	Favored (3.7%) Glycine / 108.6,113.9	-	-	-	-
743		GLU	336.37	-	Favored (3.28%) General / -175.4,168.4	14.1% (*pt-20*) chi angles: 61.6,172.4,313.2	0.077Å	-	OUTLIER(S) worst is C-N-CA: 4.397 σ
744		GLU	170.94	-	Allowed (0.23%) General / -78.4,26.0	97.8% (*mt-10*) chi angles: 292.7,180.8,359.1	0.157Å	-	-
745		PHE	115.64	-	Allowed (0.4%) General / -33.8,-59.6	84.3% (*t80*) chi angles: 182.7,74.2	0.158Å	-	-
746		GLY	39.67	-	Favored (40.03%) Glycine / 175.7,-167.9	-	-	-	-
747		VAL	30.27	-	Favored (44.74%) Isoleucine or valine / -137.4,138.8	59% (*t*) chi angles: 180.9	0.065Å	-	-
748		LEU	47.29	-	Favored (41.23%) General / -101.1,136.2	29.6% (*tp*) chi angles: 188.8,67.6	0.073Å	-	-
749		GLU	76.92	-	Favored (24.98%) General / -105.1,112.0	37.7% (*tt0*) chi angles: 183.5,201.7,353.7	0.039Å	-	-
750		TYR	64.12	-	Favored (6.11%) General / -134.9,179.8	44.1% (*p90*) chi angles: 57.7,84.3	0.055Å	-	-
751		TRP	66.7	-	Favored (32.93%)	64.3% (*p-90*)	0.064Å	-	-

			General / -156.7,156.2	chi angles: 52.6,268.4			
752	MET 126.29	-	Favored (18.92%) General / -127.3,165.9	0% chi angles: 59.1,290.5,184.1	0.071Å	-	-
753	ARG 135.06	-	Favored (7.79%) General / -161.8,137.8	0.2% chi angles: 56.8,133.9,259.8,186.9	0.103Å	-	-
754	LEU 193.6	-	Favored (29.42%) General / -118.4,117.6	9.8% (*tt*) chi angles: 180.7,151.6	0.025Å	-	-
755	ARG 144.16	-	Favored (42.87%) General / -148.6,160.7	8.8% (*ptm-85*) chi angles: 65.9,174.4,291.2,294	0.152Å	-	-
756	PHE 109.12	-	Favored (79.54%) Pre-proline / -66.4,122.0	55.2% (*t80*) chi angles: 167.5,75.6	0.104Å	-	-
757	PRO 61.62	-	-	42.8% (*Cg_endo*) chi angles: 24.2	0.098Å	-	-

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