

Viewing TGFBI_sm_252-373-FFX1FH_reg-multi.table

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All-Atom	Clashscore, all atoms: 1.42			99 th percentile* (N=1784, all resolutions)			
Contacts	Clashscore is the number of serious steric overlaps (> 0.4 Å) per 1000 atoms.						
	Poor rotamers	7	6.09%	Goal: <1%			
	Ramachandran outliers	1	0.74%	Goal: <0.05%			
	Ramachandran favored	111 82.22%		Goal: >98%			
Protein Geometry	MolProbity score [^]	2.18		66 th percentile* (N=27675, 0Å - 99Å)			
	Cβ deviations >0.25Å	2	1.56%	Goal: 0			
	Bad backbone bonds:	0 / 1123	0.00%	Goal: 0%			
	Bad backbone angles:	11 / 1530	0.72%	Goal: <0.1%			

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

[^] 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
			0		Outliers: 1 of	Poor rotamers: 7 of			Outliers: 11
			81.34	1.42	135	115	2 of 128	0 of 137	of 137
621		LEU	38.1	0.405Å N with 687 ASP OD2	-	23.3% (<i>mt</i>) chi angles: 301.4,192.2	0.269Å	-	OUTLIER(S) worst is C- CA-CB: 4.312 σ
622		HIS	116.2	-	Favored (27.59%) General / -83.3,148.1	3.3% (<i>p80</i>) chi angles: 87.4,78.3	0.06Å	-	OUTLIER(S) worst is CA- CB-CG: 6.233
623		GLN	69.75	-	Favored (4.28%) General / -63.6,115.0	24.7% (<i>tp60</i>) chi angles: 175.2,48.7,78.4	0.031Å	-	-
624		GLY	20.13	-	Favored (24.17%) Glycine / 132.7,-162.9	-	-	-	OUTLIER(S) worst is C-N- CA: 4.234 σ
625		GLU	93.64	-	Allowed (0.18%) General /	0.9% chi angles:	0.094Å	-	-

^{* 100&}lt;sup>th</sup> 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.

626	ASN 52.63	-	Favored (4.19%) General / -142.7,103.3	54.7% (<i>m-20</i>) chi angles: 275.1,331.9	0.103Å	-	OUTLIER(S) worst is CA- CB-CG: 5.413
627	LEU 56.09	-	Favored (34.84%) General / -85.2,129.3	25.5% (<i>tp</i>) chi angles: 180.4,74.1	0.057Å	-	-
628	PHE 132.53	-	Favored (8.42%) General / -108.2,98.9	11.2% (<i>t80</i>) chi angles: 180.6,218.3	0.03Å	-	-
629	GLU 64.34	-	Favored (46.02%) General / -73.1,146.0	86.4% (<i>mt-10</i>) chi angles: 299.2,178.1,12.6	0.081Å	-	-
630	LEU 55.14	-	Allowed (1.48%) General / -141.5,61.1	17.8% (<i>mt</i>) chi angles: 276.7,164.4	0.064Å	-	-
631	HIS 80.09	-	Favored (16.05%) General / -87.1,104.1	47.4% (<i>t-80</i>) chi angles: 178.4,276	0.029Å	-	-
632	ILE 93.48	-	Favored (29.77%) Isoleucine or valine / -85.7,117.0	34.1% (<i>mm</i>) chi angles: 306.9,307	0.051Å	-	-
633	HIS 94.51	-	Allowed (0.3%) General / -88.8,-80.0	24.9% (<i>t60</i>) chi angles: 177.6,44.5	0.131Å	-	-
634	GLN 61.67	-	Favored (14.35%) General / -135.6,171.5	50% (<i>mt-30</i>) chi angles: 286.5,191.9,71.8	0.051Å	-	-
635	ALA 44.85	-	Favored (9.96%) General / -130.4,108.4	-	0.056Å	-	-
636	PHE 102.54	0.495Å O with 746 GLY HA2	Favored (57.95%) General / -59.0,137.4	11.3% (<i>t80</i>) chi angles: 157.3,78	0.078Å	-	-
637	LEU 92.95	-	Favored (54.5%) General / -121.5,138.0	2.8% (<i>mp</i>) chi angles: 252.5,61.9	0.046Å	-	-

638	THR	114.84	-	Favored (6.68%) General / -78.4,179.9	4.4% (<i>t</i>) chi angles: 198.8	0.16Å	-	-
639	SER	70.56	-	Favored (80.28%) General / -68.5,-37.7	85.2% (<i>p</i>) chi angles: 61.1	0.13Å	-	-
640	ALA	44.87	-	Favored (76.39%) General / -65.2,-33.6	-	0.082Å	-	-
# A	lt Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	C β deviation	Bond lengths	Bond angles
		Avg: 81.34	Clashscore: 1.42	Outliers: 1 of 135	Poor rotamers: 7 of 115		Outliers:	Outliers: 11 of 137
641	ALA	58.54	-	Favored (89.89%) General / -64.9,-38.1	-	0.079Å	-	-
642	LEU	141.39	-	Favored (84.74%) General / -61.0,-38.0	59.1% (<i>tp</i>) chi angles: 181.2,63.9	0.071Å	-	-
643	ALA	43.44	-	Favored (83.63%) General / -63.0,-36.5	-	0.097Å	-	-
644	GLN	75.48	-	Favored (55.4%) General / -79.1,-17.2	16.9% (<i>mt-30</i>) chi angles: 289,157.5,114.7	0.106Å	-	-
645	ALA	55.96	-	Favored (49.7%) General / -77.6,-24.2	-	0.044Å	-	-
646	GLY	45.12	-	Favored (72.45%) Glycine / 73.0,25.9	-	-	-	-
647	ASP	64.91	-	Favored (4.15%) General / 51.2,28.4	12.7% (<i>m-20</i>) chi angles: 301.3,5.9	0.158Å	-	OUTLIER(S) worst is C-N-CA: 4.017σ
648	THR	108.4	-	Favored (4.41%) General / -115.7,178.1	96.4% (<i>m</i>) chi angles: 299.5	0.133Å	-	-
				Favored (2.01%)	37.8% (mt-30)			

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649	GLN 73.46	-	Pre-proline / -96.0,95.6	chi angles: 296.6,186.1,251	0.031Å	-	-
650	PRO 83.32	-	Favored (24.14%) Trans-proline / -79.0,151.7	82.9% (<i>Cg_endo</i>) chi angles: 29.9	0.07Å	-	-
651	THR 110.27	0.437Å HA with 669 SER O	Favored (35.58%) General / -93.2,122.5	88.9% (<i>m</i>) chi angles: 302.1	0.058Å	-	-
652	THR 44.26	-	Favored (44.94%) General / -133.4,157.7	62% (p) chi angles: 62.8	0.029Å	-	-
653	PHE 67.73	-	Favored (30.62%) General / -155.9,167.4	15.3% (<i>p90</i>) chi angles: 76.9,284.1	0.024Å	-	-
654	CYS 51.54	-	Favored (44.98%) General / -131.9,157.1	2.3% (p) chi angles: 42.9	0.122Å	-	-
655	THR 124.52	-	Favored (50.47%) General / -133.5,145.8	2.9% (<i>t</i>) chi angles: 200.9	0.103Å	-	-
656	TYR 67.33	-	Favored (14.38%) General / -164.0,172.1	23.1% (<i>p90</i>) chi angles: 74,101.8	0.062Å	-	-
657	SER 73.86	-	Favored (5.96%) General / -155.4,-176.5	23% (<i>t</i>) chi angles: 187.6	0.101Å	-	-
658	PHE 60.88	-	Allowed (0.07%) General / 178.2,133.5	74.1% (<i>t80</i>) chi angles: 185.3,72.9	0.075Å	-	-
659	TYR 78.28	-	Favored (8.06%) General / 65.2,35.1	12% (<i>t80</i>) chi angles: 201.5,97.8	0.168Å	-	-
660	ASP 47.8	-	Favored (23.44%) General / 57.7,33.6	22.9% (<i>m-20</i>) chi angles: 310.8,320.8	0.134Å	-	-
# /	Alt Res High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles

2/13/2013	Avg: 81.34	Clashscore: 1.42		Poor rotamers: 7 of 115	Outliers:	Outliers: 0 of 137	Outliers: 1 of 137
661	PHE 71.15	-	Favored (11.63%) General / -79.3,174.4	17.1% (<i>m-85</i>) chi angles: 273.5,255.8	0.095Å	-	-
662	GLU 77.3	-	Allowed (0.05%) General / -39.6,149.8	21.7% (<i>pt-20</i>) chi angles: 66.4,189.7,351.6	0.072Å	-	-
663	THR 100.09	-	Favored (5.83%) General / -74.8,105.4	30.8% (<i>p</i>) chi angles: 51.4	0.029Å	-	-
664	HIS 37.23	-	Favored (35.12%) General / -81.7,139.0	78.5% (<i>m80</i>) chi angles: 297.6,83.7	0.081Å	-	-
665	CYS 78.71	-	Favored (36.25%) General / -138.2,136.1	1.9% (p) chi angles: 41.6	0.038Å	-	-
666	THR 45.77	-	Favored (3.89%) Pre-proline / -69.5,173.5	74.8% (p) chi angles: 61.7	0.046Å	-	-
667	PRO 82.06	-	Favored (53.61%) Trans-proline / -69.0,159.5	46.8% (<i>Cg_endo</i>) chi angles: 24.7	0.033Å	-	-
668	LEU 99.99	-	Favored (26.82%) General / -86.3,119.7	11.1% (<i>mp</i>) chi angles: 275.3,63.7	0.038Å	-	-
669	SER 34.99	0.437Å O with 651 THR HA	Favored (16.74%) General / -95.6,155.4	23.2% (<i>t</i>) chi angles: 187.3	0.075Å	-	-
670	VAL 36.25	-	Favored (13.25%) Isoleucine or valine / -129.2,105.9	77.3% (t) chi angles: 172.3	0.095Å	-	-
671	GLY 40.97	-	Favored (7.57%) Glycine / 149.4,157.2	-	-	-	-
672	PRO 169.99	-	Favored (57.6%) Trans-proline / -63.6,-35.7	81.7% (<i>Cg_exo</i>) chi angles: 330.7	0.074Å	-	-

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673	GLN 139.8	-	Favored (28.67%) Pre-proline / -97.7,105.8	13.7% (<i>tp60</i>) chi angles: 174.9,57.4,94	0.043Å	-	-
674	PRO 77.1	-	Favored (9.3%) Trans-proline / -86.4,154.3	88.1% (<i>Cg_endo</i>) chi angles: 31.8	0.029Å	-	-
675	LEU 70.84	-	Favored (49.66%) General / -123.3,144.1	3.1% (<i>mt</i>) chi angles: 267.9,152	0.071Å	-	-
676	TYR 55.87	-	Allowed (0.72%) General / -132.8,-65.3	30.9% (<i>m-85</i>) chi angles: 299.7,307.5	0.1Å	-	-
677	ASP 46.2	-	Favored (24.68%) General / 50.9,47.4	3.4% (<i>m-20</i>) chi angles: 286.1,261.5	0.188Å	-	-
678	PHE 55.18	-	Favored (4.1%) General / -77.9,87.1	84.7% (<i>t80</i>) chi angles: 182.6,74.4	0.045Å	-	-
679	THR 46.88	-	Favored (8.14%) General / -81.6,69.0	49.3% (<i>m</i>) chi angles: 305	0.057Å	-	-
680	SER 87.33	-	Favored (19.21%) General / -83.7,165.1	16.5% (<i>t</i>) chi angles: 189.6	0.037Å	-	-
# A	lt Res High E	3 Clash > 0.4Å	Ramachandran	Rotamer	C β deviation	Bond lengths	Bond angles
	Avg: 81.34		: Outliers: 1 of 135	Poor rotamers: 7 of 115		Outliers:	Outliers: 11
681	GLN 55.82	-	Allowed (1.04%) General / -177.4,154.9	21.3% (<i>pt20</i>) chi angles: 58.6,184.4,358.2	0.063Å	-	-
682	TYR 89.63	-	Favored (4.95%) General / -146.5,-175.9	11.9% (<i>p</i> 90) chi angles: 56.5,71.9	0.141Å	-	-
683	VAL 40.3	-	Favored (26.44%) Isoleucine or valine / -121.3,146.4	84.9% (<i>t</i>) chi angles: 174.9	0.082Å	-	-
			Allowed	31.8% (<i>tpp</i>)			OUTLIER(S)

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684	MET 86.14	-	(0.88%) General / -160.0,89.8	chi angles: 188.2,48.4,56.7	0.032Å	-	worst is C-N-CA: 5.227σ
685	GLU 130.39	-	OUTLIER (0.04%) General / -66.8,49.9	4.4% (<i>mp0</i>) chi angles: 305.2,94.8,306.4	0.051Å	-	-
686	THR 91.25	-	Favored (42.68%) General / -150.4,161.3	17.3% (<i>m</i>) chi angles: 311.3	0.051Å	-	-
687	ASP 108.83	0.405Å OD2 with 621 LEU N	Allowed (0.74%) General / -108.6,-72.1	42.2% (<i>m-20</i>) chi angles: 293.4,4.2	0.06Å	-	OUTLIER(S) worst is CA- CB-CG: 4.218 σ
688	SER 47.82	-	Favored (28.17%) General / -47.6,-48.6	70.7% (p) chi angles: 57.7	0.119Å	-	-
689	LEU 51.68	-	Favored (84.31%) General / -67.7,-39.4	66% (<i>mt</i>) chi angles: 305.2,180.7	0.127Å	-	-
690	PHE 116.92	-	Favored (89.54%) General / -66.5,-41.0	70.4% (<i>t80</i>) chi angles: 175.3,267.2	0.083Å	-	-
691	LEU 48.45	-	Favored (60.59%) General / -74.2,-27.0	53.7% (<i>mt</i>) chi angles: 302.7,169.8	0.11Å	-	-
692	HIS 69.78	-	Favored (91.19%) General / -64.7,-44.1	66.3% (<i>t-80</i>) chi angles: 192.8,283.4	0.074Å	-	-
693	TYR 46.82	-	Favored (84.39%) General / -63.5,-36.6	11.2% (<i>t80</i>) chi angles: 193.4,288.2	0.083Å	-	-
694	LEU 143.63	-	Favored (69.77%) General / -54.7,-41.0	53% (<i>tp</i>) chi angles: 180.3,57.9	0.051Å	-	-
695	GLN 67.23	-	Favored (33.61%) General / -82.6,-25.0	17.7% (mm100) chi angles: 307.9,316.7,129.4	0.153Å	-	-
696	GLU 86.47	-	Favored (11.75%) General /	5.3% (<i>pt-20</i>) chi angles: 75.6,210.6,327.9	0.092Å	-	-

-105.4,-26.9

			-105.4,-26.9				
697	ALA 33.03	-	Allowed (1.73%) General / -140.1,50.1	-	0.062Å	-	-
698	SER 80.78	-	Favored (2.18%) General / -45.3,142.2	18.2% (<i>t</i>) chi angles: 169.4	0.063Å	-	-
699	ALA 41.79	-	Favored (33.47%) General / -62.5,152.8	-	0.014Å	-	OUTLIER(S) worst is C-N- CA: 4.33 σ
700	ARG 111.88	-	Favored (51.14%) General / -134.2,151.1	52.2% (ttt85) chi angles: 182.1,188.6,170.3,90	0.144Å	-	-
# Al	t Res High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
	O		Outliers: 1 of				Outliers: 11
	81.34	1.42	135	115	2 of 128	0 of 137	of 137
701	LEU 74.18	-	Favored (4.71%) General / -148.0,110.6	13.7% (<i>tp</i>) chi angles: 172.6,79.9	0.081Å	-	-
702	ASP 51.95	-	Favored (39.69%) General / -104.4,139.2	87.8% (<i>m-20</i>) chi angles: 288.5,353.4	0.039Å	-	-
703	ILE 100.62	-	Favored (15.2%) Isoleucine or valine / -103.2,143.5	15.8% (<i>tt</i>) chi angles: 197.1,169.3	0.111Å	-	-
704	HIS 61.86	-	Favored (51.63%) General / -130.6,144.8	23.9% (<i>m-70</i>) chi angles: 320.3,284.5	0.144Å	-	-
705	GLN 55.38	-	Favored (9.99%) General / -96.3,98.1	18.9% (<i>tt0</i>) chi angles: 187.7,183.4,115.7	0.04Å	-	-
706	ALA 46.22	-	Favored (9.91%) General / -84.4,67.6	-	0.033Å	-	-
707	MET 100.62	-	Allowed (0.13%) General /	3.9% (ppp?) chi angles: 60.9,94.7,81.2	0.32Å	-	OUTLIER(S) worst is C- CA-CB: 4.678

OUTLIER(S)

worst is CE3-

CD2-CG:

 4.848σ

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ALA 30.22

SER 48.93

GLU 61.29

HIS 82.81

SER 45.61

THR 77.82

LEU 180.94

ALA 62.75

ALA 49.31

GLY 22.06

TRP 158.33

ILE 106.65

Glycine / -112.1,134.3 Favored

(55.45%)

General /

-109.0,129.4

Allowed (0.29%)

Isoleucine or

valine / -137.9,72.2

$http://molprobity.biochem.duke.edu/viewtable.php? MolProbSID=lq9vvrrl2fb9jj2k3vgfallk2eig273q\&file=/Library/WebServer/Documents/moltbx/public_html/data/$	9/13

9.6% (*t*-105)

chi angles: 204.6,276.9

9.5% (tt)

chi angles: 186.9,182

0.045Å

0.157Å

Favored

720	CYS	84.05	-	(41.23%) General / -75.1,146.8	18.2% (<i>t</i>) chi angles: 192.2	0.026Å	-	-
#	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: 7 of 115		Outliers:	Outliers: 11 of 137
721	PHE	72.36	-	Allowed (0.78%) General / -104.6,50.8	16.2% (<i>m</i> -85) chi angles: 310,309.6	0.057Å	-	-
722	ASP	109.07	-	Favored (69.44%) General / -55.4,-38.8	18.2% (<i>p-10</i>) chi angles: 64,315.4	0.049Å	-	-
723	ARG	79.32	-	Favored (60.37%) General / -75.6,-13.9	25.7% (mmm180) chi angles: 304.1,306.9,303.3,149.2	0.116Å	-	-
724	VAL	49.38	-	Favored (9.86%) Isoleucine or valine / -80.8,-6.6	24% (<i>t</i>) chi angles: 187.1	0.136Å	-	-
725	LEU	156.87	-	Favored (58.66%) General / -79.3,-15.0	30.9% (<i>tp</i>) chi angles: 188.4,67.1	0.039Å	-	-
726	GLU	103.33	-	Allowed (0.4%) General / -134.7,-85.9	15.2% (<i>tt0</i>) chi angles: 186.1,206.6,312.1	0.129Å	-	-
727	THR	60.75	-	Favored (4.86%) General / -78.7,82.8	31.8% (<i>p</i>) chi angles: 51.5	0.064Å	-	-
728	VAL	120.12	-	Allowed (0.71%) Isoleucine or valine / -77.0,80.5	27.9% (<i>m</i>) chi angles: 295.5	0.173Å	-	-
729	GLU	78.6	-	Allowed (1.05%) General / -156.0,-160.8	0.8% chi angles: 227.4,303.8,292	0.178Å	-	-
730	LYS	122.19	-	Allowed (1.25%) General / -75.8,59.8	43.5% (<i>mttm</i>) chi angles: 293.7,156.9,185,286.3	0.06Å	-	-

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731	VAL 111.58	-	Allowed (1.87%) Isoleucine or valine / -83.8,83.8	11.8% (<i>p</i>) chi angles: 61.9	0.202Å	-	-
732	HIS 75.19	-	Allowed (1.02%) General / -39.3,135.4	22.5% (<i>t60</i>) chi angles: 156.5,81.4	0.121Å	-	-
733	GLY 20.13	-	Favored (16.62%) Glycine / -123.1,177.1	-	-	-	-
734	LEU 49.75	-	Favored (45.9%) General / -127.1,153.5	95% (<i>mt</i>) chi angles: 297.9,174.8	0.037Å	-	-
735	ALA 37.22	-	Favored (14.32%) General / -147.2,128.0	-	0.048Å	-	-
736	THR 90.01	-	Favored (31.66%) General / -82.1,126.1	19.5% (<i>p</i>) chi angles: 48.1	0.065Å	-	-
737	LEU 73.55	-	Favored (14.29%) General / -103.8,104.3	2.6% (<i>mt</i>) chi angles: 328.4,179	0.049Å	-	-
738	ILE 87.79	-	Favored (41.72%) Isoleucine or valine / -88.4,125.0	4.8% (<i>mp</i>) chi angles: 296,91.5	0.044Å	-	-
739	GLY 39.66	-	Favored (34.67%) Glycine / -97.0,-178.4	-	-	-	-
			Favored				
740	ALA 33.6	-	(69.41%) General / -60.5,-29.9	-	0.105Å	-	-
	ALA 33.6	- Clash > 0.4Å	General /	Rotamer	0.105Å Cβ deviation	Bond lengths	- Bond angles
	t Res High B	0.4Å	General / -60.5,-29.9	Rotamer Poor rotamers: 7 of 115	Cβ deviation	lengths Outliers: 0	

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742	GLY 302.96	-	Favored (58.51%) Glycine / 72.4,38.3	-	-	-	-
743	GLU 336.37	-	Favored (18.46%) General / -117.1,162.0	16.3% (<i>pt-20</i>) chi angles: 64.3,185.4,297.6	0.106Å	-	-
744	GLU 170.94	-	Favored (7.25%) General / -88.1,63.4	1.7% (pp20?) chi angles: 68,103.5,199.3	0.109Å	-	-
745	PHE 115.64	-	Favored (63.41%) General / -51.7,-48.8	57.4% (<i>t80</i>) chi angles: 181.9,92.7	0.095Å	-	-
746	GLY 39.67	0.495Å HA2 with 636 PHE O	Favored (22.73%) Glycine / -135.4,156.6	-	-	-	-
747	VAL 30.27	-	Favored (13.82%) Isoleucine or valine / -130.7,107.2	90.6% (<i>t</i>) chi angles: 177.9	0.049Å	-	-
748	LEU 47.29	-	Favored (44.99%) General / -74.0,144.6	7.7% (<i>tp</i>) chi angles: 205.1,76.7	0.071Å	-	-
749	GLU 76.92	-	Favored (33.16%) General / -115.5,118.4	0.1% chi angles: 191.1,300.1,276.1	0.062Å	-	-
750	TYR 64.12	-	Favored (28.88%) General / -150.3,166.8	33.1% (<i>p90</i>) chi angles: 61.5,101.1	0.073Å	-	-
751	TRP 66.7	-	Favored (13.86%) General / -152.2,132.8	0.6% chi angles: 29,275.9	0.063Å	-	OUTLIER(S) worst is CE3-CD2-CG: 4.135σ
752	MET 126.29	-	Favored (29.16%) General / -137.1,164.1	0% chi angles: 71,288.8,155.6	0.079Å	-	-
753	ARG 135.06	-	Allowed (0.09%) General / -176.9,112.4	0.3% chi angles: 41.8,131.2,283.4,185.8	0.08Å	-	-

2/19/2015			Viewing TGFBI_sm_25	52-373-FFX1FH_reg-multi.table - Mo	lProbity		
754	LEU 193.6	-	Favored (31.72%) General / -90.3,120.7	1.2% (tt) chi angles: 174.9,128.1	0.045Å	-	-
755	ARG 144.16	-	Allowed (0.33%) General / 179.7,150.1	8.6% (ptm-85) chi angles: 53.4,184.8,294.2,281.2	0.074Å	-	-
756	PHE 109.12	-	Favored (7.96%) Pre-proline / -46.5,127.9	53.4% (<i>t80</i>) chi angles: 174.6,91.3	0.096Å	-	-
757	PRO 61.62	-	-	33.7% (<i>Cg_endo</i>) chi angles: 37	0.014Å	-	-

About MolProbity | Website for the Richardson Lab | Using ecloud x-H | Internal reference 4.1-537