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All-Atom Contacts	Clashscore, all atoms:	1.42	99 th percentile* (N=1784, all resolutions)	
	Clashscore is the number of serious steric overlaps (> 0.4 Å) per 1000 atoms.			
Protein Geometry	Poor rotamers	7	6.09%	Goal: <1%
	Ramachandran outliers	1	0.74%	Goal: <0.05%
	Ramachandran favored	111	82.22%	Goal: >98%
	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.

* 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: 81.34	Clashscore: 1.42	Outliers: 1 of 135	Poor rotamers: 7 of 115	Outliers: 2 of 128	Outliers: 0 of 137	Outliers: 11 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 σ
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 / -31.5,117.0	0.9% chi angles: 329.2,75.2,262	0.094Å	-	-
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 σ
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	35.7% (<i>mt-30</i>) chi angles: 285.6,189.3,252.2	0.083Å	-	-
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	-	-
				Favored				

637	LEU	92.95	-	(54.5%) General / -121.5,138.0 Favored	2.8% (<i>mp</i>) chi angles: 252.5,61.9	0.046Å	-	-
638	THR	114.84	-	(6.68%) General / -78.4,179.9 Favored	4.4% (<i>t</i>) chi angles: 198.8	0.16Å	-	-
639	SER	70.56	-	(80.28%) General / -68.5,-37.7 Favored	85.2% (<i>p</i>) chi angles: 61.1	0.13Å	-	-
640	ALA	44.87	-	(76.39%) General / -65.2,-33.6	-	0.082Å	-	-
#	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: 2 of 128	Outliers: 0 of 137	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: 4.017 σ
648	THR	108.4	-	Favored (4.41%)	96.4% (<i>m</i>)	0.133Å	-	-

				General / -115.7,178.1	chi angles: 299.5			
649	GLN	73.46	-	Favored (2.01%) Pre-proline / -96.0,95.6	37.8% (<i>mt-30</i>) 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% (<i>p</i>) 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% (<i>p</i>) 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
		Avg: 81.34	Clashscore: 1.42	Outliers: 1 of 135	Poor rotamers: 7 of 115	Outliers: 2 of 128	Outliers: 0 of 137	Outliers: 11 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% (<i>p</i>) chi angles: 41.6	0.038Å	-	-
666	THR	45.77	-	Favored (3.89%) Pre-proline / -69.5,173.5	74.8% (<i>p</i>) 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% (<i>t</i>) 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	-	-
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	-	-
#	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: 2 of 128	Outliers: 0 of 137	Outliers: 11 of 137
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>p90</i>) 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	-	-
684	MET	86.14	-	Allowed (0.88%) General / -160.0,89.8	31.8% (<i>tpp</i>) chi angles: 188.2,48.4,56.7	0.032Å	-	OUTLIER(S) worst is C-N- CA: 5.227 σ
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% (<i>p</i>) 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% (<i>mm100</i>) chi angles: 307.9,316.7,129.4	0.153Å	-	-
696	GLU	86.47	-	Favored (11.75%) General / -105.4,-26.9	5.3% (<i>pt-20</i>) chi angles: 75.6,210.6,327.9	0.092Å	-	-
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% (<i>ttt85</i>) chi angles: 182.1,188.6,170.3,90	0.144Å	-	-
#	Alt Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	C β deviation	Bond lengths	Bond angles
Avg:			Clashscore:	Outliers: 1 of	Poor rotamers: 7 of	Outliers:	Outliers:	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 /	18.9% (<i>tt0</i>) chi angles: 187.7,183.4,115.7	0.04Å	-	-

706	ALA	46.22	-	-96.3,98.1 Favored (9.91%) General / -84.4,67.6	-	0.033Å	-	-
707	MET	100.62	-	Allowed (0.13%) General / -85.1,-150.8	3.9% (<i>ppp?</i>) chi angles: 60.9,94.7,81.2	0.32Å	-	OUTLIER(S) worst is C-CA- CB: 4.678 σ
708	ALA	30.22	-	Favored (7.27%) General / -78.3,-53.5	-	0.068Å	-	-
709	SER	48.93	-	Allowed (1.78%) General / -98.5,-59.3	56.2% (<i>p</i>) chi angles: 55.4	0.098Å	-	-
710	GLU	61.29	-	Favored (38.74%) General / -76.5,145.9	0.3% chi angles: 225.7,305.6,278.7	0.051Å	-	-
711	HIS	82.81	-	Allowed (0.96%) General / -146.2,5.0	76.7% (<i>m80</i>) chi angles: 297.9,81.9	0.059Å	-	-
712	SER	45.61	-	Favored (6.86%) General / -88.1,177.6	19.2% (<i>m</i>) chi angles: 306.5	0.033Å	-	-
713	THR	77.82	-	Favored (20.98%) General / -62.5,124.5	99.9% (<i>m</i>) chi angles: 298.5	0.025Å	-	-
714	LEU	180.94	-	Favored (14.72%) General / -102.8,-19.4	19.1% (<i>tp</i>) chi angles: 189.5,51.4	0.082Å	-	-
715	ALA	62.75	-	Favored (15.37%) General / -156.1,139.0	-	0.032Å	-	-
716	ALA	49.31	-	Favored (36.08%) General / -93.2,122.9	-	0.091Å	-	-
717	GLY	22.06	-	Favored (11.95%) Glycine /	-	-	-	-

718	TRP	158.33	-	-112.1,134.3 Favored (55.45%) General / -109.0,129.4	9.6% (<i>t-105</i>) chi angles: 204.6,276.9	0.045Å	-	OUTLIER(S) worst is CE3- CD2-CG: 4.848 σ	
719	ILE	106.65	-	Allowed (0.29%) Isoleucine or valine / -137.9,72.2	9.5% (<i>tt</i>) chi angles: 186.9,182	0.157Å	-	-	
720	CYS	84.05	-	Favored (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: 2 of 128	Outliers: 0 of 137	Outliers: 11 of 137	
721	PHE	72.36	-	Allowed (0.78%) General / -104.6,50.8	16.2% (<i>m-85</i>) 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% (<i>mmm180</i>) 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	27.9% (<i>m</i>) chi angles: 295.5	0.173Å	-	-	

729	GLU	78.6	-	/ -77.0,80.5 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	-	-
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	-	-	-	-
740	ALA	33.6	-	Favored (69.41%) General /	-	0.105Å	-	-

-60.5,-29.9

#	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: 2 of 128	Outliers: 0 of 137	Outliers: 11 of 137
741	GLY	72.45	-	Favored (73.63%) Glycine / -83.3,6.1	-	-	-	-
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% (<i>pp20?</i>) 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 /	0.6% chi angles: 29,275.9	0.063Å	-	OUTLIER(S) worst is CE3- CD2-CG: 4.135 σ

752	MET 126.29	-	-152.2,132.8 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	-	-
754	LEU 193.6	-	Favored (31.72%) General / -90.3,120.7	1.2% (<i>tt</i>) chi angles: 174.9,128.1	0.045Å	-	-
755	ARG 144.16	-	Allowed (0.33%) General / 179.7,150.1	8.6% (<i>ptm-85</i>) 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	-	-

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