



Viewing RPGRIP1_mb_621-757H-multi.table

When finished, you should [close this window](#).

Hint: Use File | Save As... to save a copy of this page.

All-Atom Contacts	Clashscore, all atoms:	68.62		1 st 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	131	97.04%	Goal: >98%
	MolProbity score [^]	2.79		32 nd 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:	23 / 1530	1.50%	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: 68.62	Outliers: 1 of 135	Poor rotamers: 3 of 115	Outliers: 0 of 128	Outliers: 0 of 137	Outliers: 23 of 137
621	LEU	38.1	0.76Å CD1 with 755 ARG HA	-	63.3% (mt) chi angles: 291.8,182.3	0.064Å	-	-
622	HIS	116.2	0.718Å HE1 with 756 PHE HB3	Favored (41.83%) General / -70.9,154.4	0.3% chi angles: 24.2,83.4	0.037Å	-	OUTLIER(S) worst is CD2-NE2-CE1: 4.441 σ
623	GLN	69.75	-	Favored (14.99%) General / -62.1,122.2	61% (mm-40) chi angles: 298.4,282.2,339.3	0.118Å	-	-
624	GLY	20.13	-	Favored (39.92%) Glycine / 167.2,179.0	-	-	-	-

625	GLU	93.64	0.816Å HG3 with 685 GLU OE2	Favored (38.57%) General / -73.0,156.7	1.8% (<i>mp0</i>) chi angles: 281.9,47,70.7	0.079Å	-	-
626	ASN	52.63	0.744Å HA with 757 PRO HD2	Favored (52.34%) General / -127.7,140.0	97.6% (<i>m-20</i>) chi angles: 291.5,342.1	0.145Å	-	-
627	LEU	56.09	0.899Å HB2 with 757 PRO HG3	Favored (44.21%) General / -118.3,123.0	44% (<i>tp</i>) chi angles: 182,68.6	0.104Å	-	-
628	PHE	132.53	0.782Å CE2 with 754 LEU HD21	Favored (30.31%) General / -103.9,115.3	49% (<i>t80</i>) chi angles: 189.1,270.8	0.078Å	-	-
629	GLU	64.34	0.632Å HG2 with 681 GLN HB3	Favored (45.82%) General / -116.7,143.3	79.5% (<i>mt-10</i>) chi angles: 300,162.9,339	0.161Å	-	-
630	LEU	55.14	0.74Å HD21 with 628 PHE CE1	Favored (13.77%) General / -136.2,116.7	82.3% (<i>mt</i>) chi angles: 296.3,181.4	0.094Å	-	-
631	HIS	80.09	0.535Å HB3 with 751 TRP CE2	Favored (56.18%) General / -112.3,128.2	13.5% (<i>t-80</i>) chi angles: 183.7,305.6	0.128Å	-	OUTLIER(S) worst is CD2- NE2-CE1: 4.346 σ
632	ILE	93.48	0.407Å CD1 with 750 TYR HB3	Favored (48.64%) Isoleucine or valine / -109.9,115.0	43.4% (<i>mm</i>) chi angles: 298.2,296.2	0.077Å	-	-
633	HIS	94.51	-	Favored (3.91%) General / -66.8,-59.0	9.7% (<i>t60</i>) chi angles: 198.7,96.8	0.06Å	-	OUTLIER(S) worst is CD2- NE2-CE1: 4.437 σ
634	GLN	61.67	0.827Å CG with 675 LEU HD23	Favored (2.68%) General / -174.2,175.4	91.4% (<i>mt-30</i>) chi angles: 294.8,178.8,306.5	0.219Å	-	-
635	ALA	44.85	-	Favored (44.47%) General / -124.9,125.8	-	0.095Å	-	-
636	PHE	102.54	0.617Å HA with 673 GLN OE1	Favored (17.56%) General /	58.9% (<i>t80</i>) chi angles: 187.1,67.5	0.035Å	-	-

637	LEU	92.95	0.758Å HB3 with 641 ALA HB3	-100.4,155.9 Favored (17.08%) General / -123.6,165.5	5.8% (<i>mp</i>) chi angles: 292.9,64.8	0.09Å	-	-	
638	THR	114.84	0.497Å HG23 with 640 ALA N	Favored (8.48%) General / -94.8,171.9	14% (<i>t</i>) chi angles: 186.7	0.08Å	-	-	
639	SER	70.56	-	Favored (69.47%) General / -57.8,-34.4	40.4% (<i>t</i>) chi angles: 176.8	0.105Å	-	-	
640	ALA	44.87	0.551Å O with 644 GLN HG3	Favored (77.23%) General / -64.4,-48.0	-	0.08Å	-	-	
#	Alt	Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
			Avg: 81.34	Clashscore: 68.62	Outliers: 1 of 135	Poor rotamers: 3 of 115	Outliers: 0 of 128	Outliers: 0 of 137	Outliers: 23 of 137
641	ALA	58.54	0.758Å HB3 with 637 LEU HB3	Favored (90.53%) General / -64.9,-38.3	-	0.104Å	-	-	
642	LEU	141.39	-	Favored (72.29%) General / -60.5,-50.8	22.6% (<i>tp</i>) chi angles: 192.6,60.7	0.052Å	-	-	
643	ALA	43.44	-	Favored (75.2%) General / -69.6,-41.9	-	0.071Å	-	-	
644	GLN	75.48	0.551Å HG3 with 640 ALA O	Favored (67.06%) General / -62.7,-23.3	29.1% (<i>mt-30</i>) chi angles: 290.1,176,130.5	0.041Å	-	-	
645	ALA	55.96	-	Favored (72.9%) General / -54.8,-43.6	-	0.081Å	-	-	
646	GLY	45.12	-	Favored (7.22%) Glycine / 118.5,12.7	-	-	-	-	
647	ASP	64.91	-	Favored (18.66%)	65.7% (<i>m-20</i>)	0.019Å	-	OUTLIER(S) worst is CA-	

				General / 60.8,28.9	chi angles: 295.2,305.1	CB-CG: 6.067 σ		
648	THR	108.4	0.422Å O with 650 PRO HD3	Favored (46.84%) General / -132.1,136.0	15.3% (t) chi angles: 187.8	0.065Å	-	-
649	GLN	73.46	0.609Å HB3 with 670 VAL HG12	Favored (3.96%) Pre-proline / -61.3,111.2	46.9% (mt-30) chi angles: 293,168.8,266.5	0.059Å	-	-
650	PRO	83.32	0.436Å HD2 with 649 GLN HA	Favored (49.91%) Trans-proline / -67.5,139.7	59% (Cg_endo) chi angles: 26.8	0.075Å	-	-
651	THR	110.27	0.935Å HG22 with 670 VAL HG22	Favored (43.74%) General / -118.6,122.9	68.7% (p) chi angles: 63.2	0.086Å	-	-
652	THR	44.26	0.439Å HG22 with 705 GLN HA	Favored (27.94%) General / -142.0,165.3	50.7% (p) chi angles: 65.8	0.092Å	-	-
653	PHE	67.73	0.518Å HE1 with 706 ALA HB2	Favored (33.57%) General / -150.0,151.6	26.8% (p90) chi angles: 61.7,283.3	0.092Å	-	-
654	CYS	51.54	0.925Å HB2 with 701 LEU HD11	Favored (23.31%) General / -116.9,158.8	19.4% (p) chi angles: 54.6	0.065Å	-	-
655	THR	124.52	0.625Å O with 701 LEU HD12	Favored (27.14%) General / -149.2,145.5	8.7% (t) chi angles: 179.9	0.046Å	-	-
656	TYR	67.33	-	Favored (25.78%) General / -154.4,168.7	44.9% (p90) chi angles: 58.3,84.6	0.076Å	-	-
657	SER	73.86	0.935Å HB2 with 663 THR HG22	Favored (37.15%) General / -139.8,144.1	41.3% (t) chi angles: 177.3	0.118Å	-	-
658	PHE	60.88	0.666Å CD2 with 659 TYR HB2	Favored (48.68%) General / -122.2,144.9	84.4% (t80) chi angles: 179.9,83.1	0.116Å	-	OUTLIER(S) worst is CA- CB-CG: 4.534 σ
			0.667Å	Favored	43.4% (t80)			

659	TYR	78.28	HB3 with 661 PHE CE2	(16.99%) General / 54.5,32.6 Favored (27.67%) General / 51.6,45.7	chi angles: 193.2,77	0.061Å	-	-
660	ASP	47.8	-	(27.67%) General / 51.6,45.7	60.6% (<i>t0</i>) chi angles: 188.4,0.5	0.065Å	-	-
#	Alt Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	C β deviation	Bond lengths	Bond angles
		Avg: 81.34	Clashscore: 68.62	Outliers: 1 of 135	Poor rotamers: 3 of 115	Outliers: 0 of 128	Outliers: 0 of 137	Outliers: 23 of 137
661	PHE	71.15	0.667Å CE2 with 659 TYR HB3	Favored (5.1%) General / -97.0,179.0	39.1% (<i>m-85</i>) chi angles: 280.6,288.4	0.152Å	-	OUTLIER(S) worst is CA- CB-CG: 4.664 σ
662	GLU	77.3	-	Favored (57.63%) General / -59.7,135.3	36.4% (<i>tt0</i>) chi angles: 180.1,184.3,297	0.091Å	-	-
663	THR	100.09	0.935Å HG22 with 657 SER HB2	Favored (34.68%) General / -79.3,144.0	58.9% (<i>p</i>) chi angles: 62.6	0.072Å	-	-
664	HIS	37.23	-	Favored (49.57%) General / -113.6,138.9	67.5% (<i>t60</i>) chi angles: 183.5,85.1	0.113Å	-	OUTLIER(S) worst is CD2- NE2-CE1: 4.49 σ
665	CYS	78.71	-	Favored (45.09%) General / -98.5,130.4	19.4% (<i>p</i>) chi angles: 54.6	0.062Å	-	-
666	THR	45.77	0.823Å HG21 with 654 CYS SG	Favored (92.69%) Pre-proline / -68.6,155.6	67.6% (<i>p</i>) chi angles: 59.4	0.05Å	-	-
667	PRO	82.06	-	Favored (19.55%) Trans-proline / -68.1,129.5	16.9% (<i>Cg_endo</i>) chi angles: 16.9	0.138Å	-	-
668	LEU	99.99	0.577Å N with 668 LEU HD12	Favored (35.96%) General / -80.5,140.3	4.4% (<i>mp</i>) chi angles: 297.3,65.4	0.067Å	-	-
669	SER	34.99	-	Favored (26.41%) General / -150.8,146.5	73.7% (<i>m</i>) chi angles: 293.9	0.082Å	-	-

670	VAL	36.25	0.935Å HG22 with 651 THR HG22	Favored (5.04%) Isoleucine or valine / -92.9,147.9	93.1% (<i>t</i>) chi angles: 178.1	0.072Å	-	-
671	GLY	40.97	0.465Å N with 670 VAL HG12	Favored (11.63%) Glycine / 136.6,169.1	-	-	-	-
672	PRO	169.99	-	Allowed (0.28%) Trans-proline / -74.6,-46.0	51.9% (<i>Cg_exo</i>) chi angles: 335.1	0.171Å	-	-
673	GLN	139.8	0.617Å OE1 with 636 PHE HA	Favored (41.33%) Pre-proline / -135.0,82.9	31.1% (<i>tp60</i>) chi angles: 181.7,80.9,10.9	0.139Å	-	-
674	PRO	77.1	-	Favored (22.32%) Trans-proline / -80.2,163.7	13.2% (<i>Cg_endo</i>) chi angles: 15.8	0.113Å	-	-
675	LEU	70.84	0.827Å HD23 with 634 GLN CG	Favored (7.59%) General / -109.1,98.1	65.2% (<i>mt</i>) chi angles: 288.9,179	0.2Å	-	-
676	TYR	55.87	-	Favored (92.95%) General / -59.5,-42.8	97.1% (<i>m-85</i>) chi angles: 293.5,276.1	0.142Å	-	-
677	ASP	46.2	-	Favored (28.9%) General / 51.6,41.5	75% (<i>m-20</i>) chi angles: 289.2,358.1	0.08Å	-	OUTLIER(S) worst is CA- CB-CG: 4.038 σ
678	PHE	55.18	0.577Å CE2 with 680 SER HB3	Favored (47.37%) General / -100.8,126.8	87.2% (<i>t80</i>) chi angles: 176.8,73.5	0.058Å	-	OUTLIER(S) worst is CA- CB-CG: 4.051 σ
679	THR	46.88	-	Favored (23.79%) General / -123.7,116.9	86.3% (<i>m</i>) chi angles: 302.7	0.09Å	-	-
680	SER	87.33	0.577Å HB3 with 678 PHE CE2	Favored (49.83%) General / -116.5,140.0	25.1% (<i>p</i>) chi angles: 78.6	0.165Å	-	-

Alt Res High B Clash > 0.4Å Ramachandran Rotamer Cβ deviation Bond lengths Bond angles

Avg: Clashscore: Outliers: 1 of Poor rotamers: 3 of Outliers: Outliers: Outliers: 23

		81.34	68.62	135	115	0 of 128	0 of 137	of 137
681	GLN	55.82	0.632Å HB3 with 629 GLU HG2	Favored (21.25%) General / -150.7,139.9	15.2% (<i>pt20</i>) chi angles: 62.6,180.8,18	0.073Å	-	-
682	TYR	89.63	0.514Å C with 627 LEU HD12	Favored (30.84%) General / -142.7,138.9	3.6% (<i>p90</i>) chi angles: 37.2,88.7	0.036Å	-	OUTLIER(S) worst is CA- CB-CG: 4.831 σ
683	VAL	40.3	0.587Å HG22 with 627 LEU HD13	Favored (19.72%) Isoleucine or valine / -86.7,110.0	76.8% (<i>t</i>) chi angles: 172.8	0.067Å	-	-
684	MET	86.14	0.617Å CE with 661 PHE HZ	Favored (51.41%) General / -127.1,142.8	19.6% (<i>tpp</i>) chi angles: 189.2,59,41	0.102Å	-	-
685	GLU	130.39	0.816Å OE2 with 625 GLU HG3	Favored (16.58%) General / -112.1,107.6	58% (<i>mp0</i>) chi angles: 295.7,77.8,8.1	0.091Å	-	-
686	THR	91.25	0.851Å HG21 with 689 LEU HB2	Favored (2.2%) General / -162.3,120.7	94.7% (<i>m</i>) chi angles: 299.9	0.086Å	-	-
687	ASP	108.83	-	Favored (2.03%) General / -93.1,-59.5	69% (<i>m-20</i>) chi angles: 296.6,352.6	0.045Å	-	OUTLIER(S) worst is CA- CB-CG: 6.403 σ
688	SER	47.82	-	Favored (34.32%) General / -67.7,-52.7	47.2% (<i>t</i>) chi angles: 180.2	0.076Å	-	-
689	LEU	51.68	0.851Å HB2 with 686 THR HG21	Favored (70.63%) General / -64.1,-29.5	52.4% (<i>mt</i>) chi angles: 294.3,185.6	0.067Å	-	-
690	PHE	116.92	0.407Å CE2 with 658 PHE HZ	Favored (54.12%) General / -60.8,-53.7	29.3% (<i>t80</i>) chi angles: 189.1,281	0.086Å	-	OUTLIER(S) worst is CA- CB-CG: 5.078 σ
691	LEU	48.45	-	Favored (92.33%) General / -62.6,-45.6	87.8% (<i>mt</i>) chi angles: 299.1,180	0.11Å	-	-
692	HIS	69.78	-	Favored (76.3%) General /	90% (<i>m-70</i>) chi angles: 289,272.7	0.061Å	-	OUTLIER(S) worst is CD2- NE2-CE1:

				-63.2,-33.8					4.358 σ
693	TYR	46.82	0.788Å HA with 696 GLU HG2	Favored (98.77%) General / -60.8,-43.0	35.7% (<i>t80</i>) chi angles: 172.9,274.8	0.085Å	-	-	
694	LEU	143.63	0.655Å HD21 with 721 PHE O	Favored (80.75%) General / -56.4,-44.8	43.9% (<i>tp</i>) chi angles: 171.6,67.2	0.137Å	-	-	
695	GLN	67.23	-	Favored (30.41%) General / -73.6,-48.7	26.4% (<i>mm100</i>) chi angles: 304.8,296.8,132.8	0.097Å	-	-	
696	GLU	86.47	0.788Å HG2 with 693 TYR HA	Favored (84.14%) General / -60.1,-47.9	10.6% (<i>pt-20</i>) chi angles: 58.6,167.3,300.8	0.111Å	-	-	
697	ALA	33.03	0.666Å N with 696 GLU HG3	Favored (46.6%) General / -139.7,152.3	-	0.106Å	-	-	
698	SER	80.78	0.602Å HB3 with 718 TRP NE1	Favored (12.16%) General / -121.5,168.0	45.8% (<i>t</i>) chi angles: 180.6	0.066Å	-	-	
699	ALA	41.79	1.002Å HB3 with 719 ILE HG23	Favored (31.03%) General / -81.8,144.5	-	0.061Å	-	-	
700	ARG	111.88	0.64Å HD2 with 700 ARG N	Favored (23.84%) General / -116.9,114.5	0.8% chi angles: 318.7,73.3,179.9,165.4	0.196Å	-	-	
#	Alt	Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	C β deviation	Bond lengths	Bond angles
			Avg: 81.34	Clashscore: 68.62	Outliers: 1 of 135	Poor rotamers: 3 of 115	Outliers: 0 of 128	Outliers: 0 of 137	Outliers: 23 of 137
701	LEU	74.18	0.925Å HD11 with 654 CYS HB2	Favored (16.58%) General / -119.4,110.1	25.7% (<i>tp</i>) chi angles: 179.9,74.1	0.175Å	-	-	
702	ASP	51.95	-	Favored (33.26%) General / -107.6,145.5	82.2% (<i>m-20</i>) chi angles: 296.9,341.1	0.046Å	-		OUTLIER(S) worst is CA- CB-CG: 6.399 σ
				0.72Å Favored (51.05%)					

703	ILE	100.62	CG2 with 715 ALA HB3	Isoleucine or valine / -107.8,116.3	19.9% (<i>tt</i>) chi angles: 185.1,169.3	0.055Å	-	-
704	HIS	61.86	-	Favored (35.69%) General / -114.4,149.7	1.4% (<i>p-80</i>) chi angles: 30.7,261.2	0.068Å	-	OUTLIER(S) worst is CD2- NE2-CE1: 4.329 σ
705	GLN	55.38	0.439Å HA with 652 THR HG22	Favored (36.24%) General / -90.5,127.5	7% (<i>tt0</i>) chi angles: 180.1,176.8,161.1	0.071Å	-	-
706	ALA	46.22	0.518Å HB2 with 653 PHE HE1	Favored (30.78%) General / -102.1,115.5	-	0.091Å	-	-
707	MET	100.62	0.938Å HG3 with 710 GLU H	Favored (11.76%) General / -104.9,164.5	23.9% (<i>ptp</i>) chi angles: 64.5,186,65.8	0.121Å	-	-
708	ALA	30.22	-	Favored (98.9%) General / -62.4,-41.8	-	0.094Å	-	-
709	SER	48.93	-	Favored (8.39%) General / -74.7,-53.9	98.6% (<i>p</i>) chi angles: 64.2	0.066Å	-	-
710	GLU	61.29	0.938Å H with 707 MET HG3	Favored (4.33%) General / -143.0,-175.0	64.6% (<i>tt0</i>) chi angles: 194,167.5,349.9	0.062Å	-	-
711	HIS	82.81	0.557Å H with 710 GLU HG2	Favored (50.94%) General / -129.1,147.5	60.8% (<i>m80</i>) chi angles: 303.9,82.5	0.201Å	-	OUTLIER(S) worst is CD2- NE2-CE1: 4.469 σ
712	SER	45.61	-	Favored (31.23%) General / -153.9,153.0	98.6% (<i>p</i>) chi angles: 64.6	0.112Å	-	-
713	THR	77.82	-	Favored (28.23%) General / -109.9,114.6	62% (<i>m</i>) chi angles: 303.7	0.077Å	-	-
714	LEU	180.94	0.558Å HD23 with 745 PHE CE1	Favored (29.16%) General / -82.0,-35.1	61.1% (<i>tp</i>) chi angles: 179.9,64	0.081Å	-	-

715	ALA	62.75	0.72Å HB3 with 703 ILE CG2	Favored (43.41%) General / -143.4,158.7	-	0.074Å	-	-	
716	ALA	49.31	-	Favored (19.38%) General / -153.3,140.4	-	0.098Å	-	-	
717	GLY	22.06	-	Favored (25.27%) Glycine / -141.3,168.9	-	-	-	-	
718	TRP	158.33	0.602Å NE1 with 698 SER HB3	Favored (28.67%) General / -113.5,115.9	51.7% (<i>t</i> -105) chi angles: 187.9,270.8	0.14Å	-	-	
719	ILE	106.65	1.002Å HG23 with 699 ALA HB3	Favored (43.49%) Isoleucine or valine / -101.0,115.9	20.6% (<i>tt</i>) chi angles: 190.9,166.9	0.101Å	-	-	
720	CYS	84.05	0.518Å HB2 with 698 SER OG	Favored (47.35%) General / -139.5,152.9	49.7% (<i>t</i>) chi angles: 186.4	0.097Å	-	-	
#	Alt	Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
			Avg: 81.34	Clashscore: 68.62	Outliers: 1 of 135	Poor rotamers: 3 of 115	Outliers: 0 of 128	Outliers: 0 of 137	Outliers: 23 of 137
721	PHE	72.36	0.714Å HD1 with 752 MET HE3	Favored (25.05%) General / -117.6,115.4	66.3% (<i>m</i> -85) chi angles: 305.5,285.1	0.126Å	-	OUTLIER(S) worst is CA- CB-CG: 5.959 σ	
722	ASP	109.07	-	Favored (29.33%) General / -76.7,-45.4	20.3% (<i>p</i> -10) chi angles: 59.5,318.9	0.067Å	-	-	
723	ARG	79.32	0.954Å HD2 with 731 VAL HG21	Favored (74.71%) General / -64.0,-33.0	91.1% (<i>mtt</i> 180) chi angles: 294.9,194.4,180.2,192.5	0.066Å	-	-	
724	VAL	49.38	0.554Å HG23 with 721 PHE HB3	Favored (27.43%) Isoleucine or valine / -56.4,-28.9	93.7% (<i>t</i>) chi angles: 175.7	0.082Å	-	-	
725	LEU	156.87	-	Favored (65.59%)	36% (<i>tp</i>)	0.071Å	-	-	

			General / -60.5,-52.3	chi angles: 187.5,61.3			
726	GLU 103.33	-	Favored (4.74%) General / -78.6,-56.0	84.9% (<i>tt0</i>) chi angles: 183.6,179.7,348.1	0.059Å	-	-
727	THR 60.75	0.636Å HG22 with 728 VAL N	Favored (6.53%) General / -111.2,173.0	47.5% (<i>m</i>) chi angles: 305.1	0.052Å	-	-
728	VAL 120.12	0.636Å N with 727 THR HG22	Favored (6.26%) Isoleucine or valine / -147.4,129.0	30.7% (<i>m</i>) chi angles: 296.9	0.062Å	-	-
729	GLU 78.6	0.515Å HG3 with 728 VAL O	OUTLIER (0%) General / 149.0,-156.6	49.7% (<i>mt-10</i>) chi angles: 272.5,168.4,348.7	0.172Å	-	OUTLIER(S) worst is N-CA- CB: 4.051 σ
730	LYS 122.19	0.554Å HD2 with 730 LYS N	Favored (3.57%) General / -75.5,96.8	11.3% (<i>mptt</i>) chi angles: 295,66.1,180.1,176.9	0.079Å	-	-
731	VAL 111.58	0.954Å HG21 with 723 ARG HD2	Favored (37.3%) Isoleucine or valine / -113.6,111.7	7.7% (<i>p</i>) chi angles: 56.7	0.051Å	-	-
732	HIS 75.19	-	Favored (57.79%) General / -66.5,141.7	42.8% (<i>m80</i>) chi angles: 301.4,113	0.067Å	-	OUTLIER(S) worst is CD2- NE2-CE1: 4.415 σ
733	GLY 20.13	0.443Å O with 734 LEU HD23	Favored (33.79%) Glycine / -161.6,162.2	-	-	-	-
734	LEU 49.75	0.443Å HD23 with 733 GLY O	Favored (20.16%) General / -136.0,168.0	62.6% (<i>mt</i>) chi angles: 293.8,183.7	0.129Å	-	-
735	ALA 37.22	-	Favored (45.52%) General / -136.7,146.1	-	0.105Å	-	-
736	THR 90.01	-	Favored (17.86%) General / -94.6,153.4	13.4% (<i>t</i>) chi angles: 186.4	0.08Å	-	-
			Favored				

737	LEU	73.55	0.503Å C with 738 ILE HD12	(54.4%) General / -119.0,135.8	60.3% (<i>mt</i>) chi angles: 288.6,179.7	0.076Å	-	-
738	ILE	87.79	0.541Å N with 738 ILE HD12	Favored (48.18%) Isoleucine or valine / -123.8,140.1	2.5% (<i>mp</i>) chi angles: 297.3,69.3	0.08Å	-	-
739	GLY	39.66	-	Favored (27.57%) Glycine / -77.0,142.4	-	-	-	-
740	ALA	33.6	-	Favored (79.85%) General / -65.4,-46.5	-	0.106Å	-	-
#	Alt Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
Avg: 81.34			Clashscore: 68.62	Outliers: 1 of 135	Poor rotamers: 3 of 115	Outliers: 0 of 128	Outliers: 0 of 137	Outliers: 23 of 137
741	GLY	72.45	-	Favored (99.11%) Glycine / -63.5,-41.9	-	-	-	-
742	GLY	302.96	0.524Å O with 743 GLU HG3	Favored (2.46%) Glycine / 121.1,116.4	-	-	-	-
743	GLU	336.37	0.524Å HG3 with 742 GLY O	Allowed (0.42%) General / -171.5,-165.9	51.3% (<i>mt-10</i>) chi angles: 287.8,180.7,48.8	0.162Å	-	OUTLIER(S) worst is C-N- CA: 10.932 σ
744	GLU	170.94	0.45Å H with 743 GLU HB3	Favored (3.12%) General / -89.5,22.0	93.9% (<i>mt-10</i>) chi angles: 292.5,185.3,1.2	0.101Å	-	-
745	PHE	115.64	0.558Å CE1 with 714 LEU HD23	Allowed (1.96%) General / -43.0,-59.5	49.9% (<i>t80</i>) chi angles: 191.1,83	0.072Å	-	OUTLIER(S) worst is CA- CB-CG: 4.646 σ
746	GLY	39.67	-	Favored (39.49%) Glycine / 170.9,175.4	-	-	-	-
747	VAL	30.27	0.534Å HG12 with	Favored (21.63%) Isoleucine or	91.3% (<i>t</i>)	0.071Å	-	-

			748 LEU N	valine / -119.3,151.6	chi angles: 177			
748	LEU	47.29	0.534Å N with 747 VAL HG12	Favored (49.26%) General / -114.2,139.6	43.2% (<i>tp</i>) chi angles: 186.2,62.5	0.061Å	-	-
749	GLU	76.92	0.426Å CD with 734 LEU HD21	Favored (29.21%) General / -107.0,114.9	35.6% (<i>mm-40</i>) chi angles: 280.7,280.3,353.4	0.109Å	-	-
750	TYR	64.12	0.407Å HB3 with 632 ILE CD1	Favored (32.04%) General / -147.2,164.8	32.9% (<i>p90</i>) chi angles: 57.9,79.9	0.093Å	-	-
751	TRP	66.7	0.535Å CE2 with 631 HIS HB3	Favored (37.88%) General / -145.1,151.0	61.3% (<i>p-90</i>) chi angles: 51.7,265.9	0.068Å	-	-
752	MET	126.29	0.793Å HE1 with 731 VAL HG13	Favored (46.26%) General / -129.0,154.8	0% chi angles: 53.6,290.4,192.3	0.089Å	-	-
753	ARG	135.06	0.537Å HD3 with 629 GLU OE1	Favored (23.25%) General / -152.2,143.4	2.2% (<i>ptm180</i>) chi angles: 58.9,145.4,274.6,205.4	0.152Å	-	-
754	LEU	193.6	0.782Å HD21 with 628 PHE CE2	Favored (11%) General / -135.3,113.2	4.5% (<i>mm?</i>) chi angles: 276.4,295.2	0.191Å	-	-
755	ARG	144.16	0.76Å HA with 621 LEU CD1	Favored (14.24%) General / -149.8,173.0	8.1% (<i>ptm-85</i>) chi angles: 59.2,186.6,294.3,268.2	0.089Å	-	-
756	PHE	109.12	0.718Å HB3 with 622 HIS HE1	Favored (89.99%) Pre-proline / -74.6,125.1	28.4% (<i>t80</i>) chi angles: 162.4,80.8	0.065Å	-	OUTLIER(S) worst is CA- CB-CG: 4.638 σ
757	PRO	61.62	0.899Å HG3 with 627 LEU HB2	-	19.3% (<i>Cg_endo</i>) chi angles: 17.7	0.122Å	-	OUTLIER(S) worst is N-CA- CB: 4.379 σ

About [MolProbity](#) | [Website for the Richardson Lab](#) | Using [ecloud x-H](#) | Internal reference 4.1-537