Viewing RD3_mb_77-191H-multi.table

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All-Atom Contacts	Clashscore, all atoms:	67.82		1st percentile* (N=1784, all resolutions)
	Clashscore is the number of serious steric overlaps (> 0.4 Å) per 1000 atoms.			
Protein Geometry	Poor rotamers	2	1.89%	Goal: <1%
	Ramachandran outliers	3	2.65%	Goal: <0.05%
	Ramachandran favored	106	93.81%	Goal: >98%
	MolProbity score^	2.92		26th percentile* (N=27675, 0Å - 99Å)
	Cβ deviations >0.25Å	0	0.00%	Goal: 0
	Bad backbone bonds:	0 / 970	0.00%	Goal: 0%
	Bad backbone angles:	9 / 1311	0.69%	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: 109.32	Clashscore: 67.82	Outliers: 3 of 113	Poor rotamers: 2 of 106	Outliers: 0 of 113	Outliers: 0 of 115	Outliers: 9 of 115
77		GLU	50.66	-	-	46% (*mt-10*) chi angles: 288,182.4,63.1	0.054Å	-	-
78		ARG	160.75	1.018Å HE with 122 LEU HD12	Favored (68.56%) General / -64.5,-26.8	90.7% (*mtm-85*) chi angles: 297.5,182.9,296.6,268.3	0.104Å	-	-
79		LEU	235.06	0.894Å HD21 with 123 GLN HG3	OUTLIER (0%) General / -43.9,169.3	7.4% (*mp*) chi angles: 288,64.6	0.133Å	-	-
80		GLN	173.91	0.743Å O with 84 VAL HG23	Favored (57.38%) General / -56.6,-27.2	7.1% (*tp-100*) chi angles: 187.6,69.4,205.4	0.088Å	-	-
					Favored				

81	LEU	57.9	-	(77.62%) General / -57.4,-40.1	76.6% (*mt*) chi angles: 293.7,181	0.087Å	-	-
82	GLU	94.21	0.46Å HG3 with 100 PHE HB3	Favored (87.07%) General / -61.8,-47.0	35.9% (*tt0*) chi angles: 180.4,188.3,301.5	0.125Å	-	-
83	ASP	89.21	-	Favored (97.43%) General / -64.0,-41.6	23.7% (*t70*) chi angles: 196.6,52.5	0.084Å	-	OUTLIER(S) worst is CA-CB-CG: 5.428 σ
84	VAL	34.28	0.743Å HG23 with 80 GLN O	Favored (85.72%) Isoleucine or valine / -63.6,-39.5	94.7% (*t*) chi angles: 175.8	0.094Å	-	-
85	CYS	83.13	0.524Å HA with 88 ILE HG12	Favored (97.72%) General / -60.9,-42.4	86.2% (*m*) chi angles: 289.5	0.109Å	-	-
86	VAL	40.64	0.485Å O with 90 PRO HD3	Favored (67.51%) Isoleucine or valine / -59.0,-51.9	86.9% (*t*) chi angles: 175.1	0.152Å	-	-
87	LYS	85.68	-	Favored (73.23%) General / -66.7,-47.2	23.9% (*ttpp*) chi angles: 181,166.4,88.9,67.4	0.079Å	-	-
88	ILE	101.11	0.718Å HG12 with 84 VAL O	Favored (61.91%) Isoleucine or valine / -67.2,-50.6	49.1% (*pt*) chi angles: 61.6,171.4	0.047Å	-	-
89	HIS	72.47	0.783Å HB3 with 92 TYR HB3	Favored (44.53%) Pre-proline / -122.5,75.1	97.4% (*m-70*) chi angles: 300.1,284.9	0.152Å	-	OUTLIER(S) worst is CD2-NE2-CE1: 4.374 σ
90	PRO	84.27	0.485Å HD3 with 86 VAL O	Favored (10.04%) Trans-proline / -67.8,-40.3	5.7% (*Cg_endo*) chi angles: 8.1	0.126Å	-	-
91	SER	84.26	-	Favored (15.18%) General / -77.7,-49.1	45.5% (*t*) chi angles: 180.7	0.083Å	-	-
92	TYR	83.32	0.783Å HB3 with 89 HIS HB3	Favored (75.39%) General / -63.9,-48.7	34.9% (*t80*) chi angles: 195.4,84	0.076Å	-	-
			0.766Å	Favored				

#	Alt	Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
93		CYS	72.4	HB3 with 96 ALA HB3	(85.06%) General / -63.4,-46.7	88.4% (*m*) chi angles: 293.1	0.109Å	-	-
94		GLY	101.99	0.54Å O with 97 ILE HG13	Favored (20.69%) Glycine / 59.9,-120.0	-	-	-	-
95		PRO	73.9	-	Favored (29.02%) Trans-proline / -66.8,-10.6	75.6% (*Cg_exo*) chi angles: 333.1	0.101Å	-	-
96		ALA	42.56	0.766Å HB3 with 93 CYS HB3	Favored (69.41%) General / -60.8,-29.3	-	0.086Å	-	-

#	Alt	Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
			Avg: 109.32	Clashscore: 67.82	Outliers: 3 of 113	Poor rotamers: 2 of 106	Outliers: 0 of 113	Outliers: 0 of 115	Outliers: 9 of 115
97		ILE	59.59	0.54Å HG13 with 94 GLY O	Favored (31.84%) Isoleucine or valine / -53.9,-37.0	69.9% (*mt*) chi angles: 301.1,165.3	0.105Å	-	-
98		LEU	129.14	0.553Å C with 98 LEU HD13	Favored (82.85%) General / -57.7,-47.3	3.1% (*tm?*) chi angles: 180.3,286.9	0.044Å	-	-
99		ARG	149.8	0.68Å HG2 with 96 ALA O	Favored (87.89%) General / -66.8,-39.4	5.6% (*ptp180*) chi angles: 60.9,183.6,58.6,130.4	0.078Å	-	-
100		PHE	60.42	0.733Å HE2 with 96 ALA HB1	Favored (92.07%) General / -59.4,-45.2	85.8% (*m-85*) chi angles: 289.9,277	0.171Å	-	-
101		ARG	78.31	-	Favored (80.85%) General / -61.4,-36.6	90.3% (*mtt-85*) chi angles: 288.8,180.6,171.3,275.7	0.082Å	-	-
102		GLN	251.23	-	Favored (49.16%) General / -58.1,131.0	97.4% (*mt-30*) chi angles: 293.5,180.3,338.3	0.079Å	-	-
103		LEU	261.05	-	Favored (3.64%) General / -95.4,-176.0	80% (*mt*) chi angles: 301.6,181.4	0.116Å	-	-

104	LEU	145.2	1.066Å HD13 with 107 GLN HE22	Favored (37.27%) General / -104.1,118.7	3.4% (*tt*) chi angles: 192.5,180	0.057Å	-	-
105	ALA	47.21	0.506Å N with 104 LEU HD23	Favored (89.01%) General / -66.5,-39.7	-	0.076Å	-	-
106	GLU	120.37	0.646Å H with 104 LEU CD2	Favored (93.03%) General / -60.3,-45.5	63.5% (*tt0*) chi angles: 186.2,167.7,338.4	0.079Å	-	-
107	GLN	186.21	1.066Å HE22 with 104 LEU HD13	Favored (5.3%) General / -92.3,73.5	1.9% (*mp0*) chi angles: 300.5,79.8,217.7	0.038Å	-	-
108	GLU	87.13	0.907Å HB2 with 109 PRO HD3	Favored (48.19%) Pre-proline / -67.1,-44.0	3% (*mp0*) chi angles: 294,102.9,47.9	0.145Å	-	-
109	PRO	129.3	0.907Å HD3 with 108 GLU HB2	Favored (48.91%) Trans-proline / -65.2,-33.4	87.3% (*Cg_exo*) chi angles: 331.6	0.177Å	-	-
110	GLU	76.26	0.613Å O with 114 VAL HG12	Favored (85.86%) General / -67.3,-39.5	37.8% (*mm-40*) chi angles: 290.1,290.5,6.8	0.097Å	-	-
111	VAL	51.45	0.792Å HG23 with 107 GLN O	Favored (86.26%) Isoleucine or valine / -59.5,-41.9	54.3% (*t*) chi angles: 170.1	0.101Å	-	-
112	GLN	103.7	0.702Å HG2 with 109 PRO O	Favored (84.88%) General / -62.5,-47.2	2.7% (*pt20*) chi angles: 62.3,192.3,222.5	0.04Å	-	-
113	GLU	124.08	0.674Å HG3 with 139 THR HG21	Favored (75.7%) General / -68.6,-43.8	4.6% (*tp10*) chi angles: 190.9,68.4,298.8	0.078Å	-	-
114	VAL	114.59	0.77Å HG22 with 118 PHE CD1	Favored (77.23%) Isoleucine or valine / -67.3,-36.6	8.8% (*p*) chi angles: 60.1	0.08Å	-	-
115	SER	84	0.96Å HA with 118 PHE CZ	Favored (58.84%) General / -57.1,-25.4	47.7% (*t*) chi angles: 179.9	0.087Å	-	-
				Favored				

#	Alt	Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
116		GLN	108.9	-	(78.28%) General / -61.4,-49.1	52.4% (*tt0*) chi angles: 189,165.8,358.3	0.054Å	-	-
			Avg: 109.32	Clashscore: 67.82	Outliers: 3 of 113	Poor rotamers: 2 of 106	Outliers: 0 of 113	Outliers: 0 of 115	Outliers: 9 of 115
117		LEU	232.16	0.514Å HD13 with 118 PHE O	Favored (5.15%) General / -151.8,116.5	1.9% (*tm?*) chi angles: 191.3,297.4	0.109Å	-	-
118		PHE	331.89	0.96Å CZ with 115 SER HA	Favored (15.59%) General / -90.1,161.9	57.1% (*m-85*) chi angles: 306.9,272.6	0.142Å	-	OUTLIER(S) worst is CA-CB-CG: 6.522 σ
119		ARG	355.68	0.636Å HB2 with 121 VAL HG23	OUTLIER (0.03%) General / -173.0,-145.8	42.9% (*mtp180*) chi angles: 277.6,180.1,54.5,167.2	0.19Å	-	-
120		SER	77.46	0.41Å H with 119 ARG HB3	Favored (20.65%) General / -71.2,-3.5	82.9% (*p*) chi angles: 60.8	0.095Å	-	-
121		VAL	45.65	0.636Å HG23 with 119 ARG HB2	Favored (67.13%) Isoleucine or valine / -55.4,-42.5	91.7% (*t*) chi angles: 175.5	0.142Å	-	-
122		LEU	153.19	1.018Å HD12 with 78 ARG HE	Favored (97.91%) General / -63.7,-43.0	2.3% (*mm?*) chi angles: 294.3,298.3	0.101Å	-	-
123		GLN	48.27	0.894Å HG3 with 79 LEU HD21	Favored (88.06%) General / -63.8,-45.8	67.7% (*mt-30*) chi angles: 293.2,183.3,68.1	0.135Å	-	-
124		GLU	62.5	0.553Å O with 128 ARG HB2	Favored (76.74%) General / -66.5,-33.9	40.8% (*mt-10*) chi angles: 286.6,200.1,19.3	0.113Å	-	-
125		VAL	99.92	0.75Å HG12 with 122 LEU O	Favored (98.73%) Isoleucine or valine / -63.4,-44.1	8.1% (*p*) chi angles: 68.8	0.07Å	-	-
126		LEU	126.04	0.613Å HD22 with 129 MET CE	Favored (85.93%) General / -65.0,-45.3	3.2% (*tm?*) chi angles: 180.7,283.3	0.063Å	-	-

#	Alt	Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
127		GLU	82.41	-	Favored (66.65%) General / -67.2,-26.5	8.8% (*mm-40*) chi angles: 284.7,275.1,276.9	0.053Å	-	-
128		ARG	111.84	0.729Å HA with 131 GLN HG2	Favored (69.87%) General / -57.2,-35.6	16.7% (*ttp180*) chi angles: 193,174.5,98.8,179	0.076Å	-	-
129		MET	52.7	0.613Å CE with 126 LEU HD22	Favored (96.02%) General / -60.6,-44.8	52.1% (*mtm*) chi angles: 291.4,167.4,280.1	0.051Å	-	-
130		LYS	79.49	-	Favored (69.78%) General / -72.0,-36.5	45.7% (*mttp*) chi angles: 287.7,168,170.5,51.9	0.073Å	-	-
131		GLN	116.43	0.729Å HG2 with 128 ARG HA	Favored (2.23%) General / -99.1,-172.2	0.7% chi angles: 68.3,161.6,163.1	0.165Å	-	-
132		GLU	80.52	0.722Å O with 131 GLN HG3	Favored (30.71%) General / -65.3,156.8	4.6% (*mm-40*) chi angles: 279.8,271.4,46.4	0.125Å	-	-
133		GLU	132.72	0.555Å HA with 128 ARG HG3	Favored (3.35%) General / -95.5,77.6	78.4% (*mt-10*) chi angles: 296.7,164.6,11.9	0.029Å	-	-
134		GLU	110.54	0.997Å HG2 with 138 LEU HG	Favored (46.8%) General / -78.5,-29.8	44.5% (*tt0*) chi angles: 180,179.3,57.6	0.098Å	-	-
135		ALA	56.37	0.691Å HB3 with 128 ARG HH11	Favored (85.42%) General / -57.7,-43.9	-	0.075Å	-	-
136		HIS	49.22	0.65Å CE1 with 140 ARG HH11	Favored (97.34%) General / -62.8,-44.0	25.6% (*t-80*) chi angles: 199.4,265	0.04Å	-	OUTLIER(S) worst is CD2-NE2-CE1: 4.445 σ
#	Alt	Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
			Avg: 109.32	Clashscore: 67.82	Outliers: 3 of 113	Poor rotamers: 2 of 106	Outliers: 0 of 113	Outliers: 0 of 115	Outliers: 9 of 115
137		LYS	75.5	-	Favored (95.27%) General /	16% (*mtpp*) chi angles: 294.3,166.1,96.6,64.1	0.103Å	-	-

				-63.9,-43.7				
138	LEU	46.43	0.997Å HG with 134 GLU HG2	Favored (98.39%) General / -61.0,-43.8	71.9% (*mt*) chi angles: 292,180.7	0.109Å	-	-
139	THR	44.46	0.674Å HG21 with 113 GLU HG3	Favored (44.46%) General / -63.2,-54.0	96.4% (*m*) chi angles: 299.6	0.077Å	-	-
140	ARG	141.27	0.65Å HH11 with 136 HIS CE1	Allowed (0.56%) General / -63.4,-66.3	16.1% (*mtp180*) chi angles: 288.2,151.5,36,177.3	0.048Å	-	-
141	GLN	79.06	0.481Å O with 145 ARG HB3	Favored (16.67%) General / -74.8,-50.6	51.7% (*mm-40*) chi angles: 289.8,284.3,347.3	0.078Å	-	-
142	TRP	119.1	0.582Å HB2 with 138 LEU O	Favored (50.07%) General / -69.3,-50.0	75.7% (*m95*) chi angles: 287.9,82.5	0.079Å	-	-
143	SER	95.53	0.593Å HB2 with 139 THR O	Favored (4.79%) General / -74.3,-56.5	75.3% (*m*) chi angles: 294.7	0.085Å	-	-
144	LEU	141.71	0.638Å HB3 with 140 ARG O	Favored (88.9%) General / -64.9,-44.7	51.1% (*tp*) chi angles: 182.6,65.9	0.067Å	-	-
145	ARG	157.59	0.73Å HB3 with 146 PRO HD3	Favored (70.73%) Pre-proline / -64.6,-43.4	11.9% (*tpt180*) chi angles: 164.9,65.3,188.5,204.5	0.128Å	-	-
146	PRO	153.21	0.73Å HD3 with 145 ARG HB3	Favored (43.08%) Trans-proline / -66.4,136.4	73.8% (*Cg_exo*) chi angles: 328.1	0.242Å	-	-
147	ARG	112.31	-	Favored (87.56%) General / -65.3,-37.6	40% (*mtp85*) chi angles: 292.2,199.5,82.6,84.2	0.098Å	-	-
148	GLY	33.79	-	Favored (77.52%) Glycine / -66.4,-46.5	-	-	-	-
149	SER	95.93	0.409Å HB2 with 143 SER O	Favored (87.76%) General /	70.2% (*m*) chi angles: 295.9	0.097Å	-	-

#	Alt	Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
					-63.9,-45.8				
150		LEU	139.49	-	Favored (91.04%) General / -64.3,-38.4	61.5% (*tp*) chi angles: 179.4,64.3	0.094Å	-	-
151		ALA	55.07	-	Favored (42.73%) General / -72.7,150.7	-	0.074Å	-	-
152		THR	129.4	-	Favored (47.19%) General / -72.8,139.7	15% (*t*) chi angles: 188.3	0.06Å	-	-
153		PHE	120.33	0.955Å CZ with 155 THR HG22	Favored (21.44%) General / -62.6,124.6	63.8% (*t80*) chi angles: 177.2,90.2	0.049Å	-	-
154		LYS	189.06	-	Allowed (1.31%) General / -150.9,79.2	19.5% (*mttp*) chi angles: 296.7,169.9,179.4,108.2	0.189Å	-	-
155		THR	145.73	0.955Å HG22 with 153 PHE CZ	Favored (3.5%) General / -133.6,-174.4	5.5% (*t*) chi angles: 196.8	0.105Å	-	-
156		ARG	163.42	1.015Å HD3 with 169 ILE HB	Favored (28.23%) General / -84.5,121.9	11.5% (*ptm180*) chi angles: 56.1,167.4,283.6,150	0.079Å	-	-
#	Alt	Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
			Avg: 109.32	Clashscore: 67.82	Outliers: 3 of 113	Poor rotamers: 2 of 106	Outliers: 0 of 113	Outliers: 0 of 115	Outliers: 9 of 115
157		ALA	54.82	-	Favored (72.33%) General / -71.1,-39.1	-	0.05Å	-	-
158		ARG	232.54	-	Favored (28.09%) General / -62.0,154.0	1.8% (*ttp180*) chi angles: 193.6,151.2,102.1,142	0.164Å	-	-
159		ILE	194.89	0.521Å O with 160 SER HB3	Favored (46.8%) Isoleucine or valine / -65.8,-52.7	47.1% (*mm*) chi angles: 299,301.6	0.066Å	-	-
160		SER	131.43	0.786Å HB2 with 156 ARG NH2	Allowed (0.11%) Pre-proline /	47.7% (*t*) chi angles: 179.9	0.086Å	-	-

161	PRO	73.63	-	80.0,167.7 Favored (75.32%) Trans-proline / -67.0,154.2	97.4% (*Cg_exo*) chi angles: 329.4	0.189Å	-	-
162	PHE	92.3	-	Favored (94.86%) General / -64.5,-40.0	72.2% (*m-85*) chi angles: 304.2,272	0.081Å	-	OUTLIER(S) worst is CA- CB-CG: 6.371 σ
163	ALA	29.58	-	Favored (87.57%) General / -58.5,-42.5	-	0.097Å	-	-
164	SER	89.35	-	Favored (58.19%) General / -65.1,138.3	47.6% (*t*) chi angles: 180	0.09Å	-	-
165	ASP	183.88	-	Allowed (1.47%) General / -129.0,72.6	79.7% (*m-20*) chi angles: 290.2,355.6	0.158Å	-	OUTLIER(S) worst is CA- CB-CG: 4.057 σ
166	ILE	142.5	0.983Å HG21 with 169 ILE HD11	Favored (48.54%) Isoleucine or valine / -127.2,140.6	9.9% (*tp*) chi angles: 188.8,68.8	0.081Å	-	-
167	ARG	107.6	0.579Å HG3 with 168 THR HG23	Favored (82.07%) General / -68.3,-39.3	37.6% (*ptt180*) chi angles: 57.1,183.7,173.1,181.1	0.061Å	-	-
168	THR	111	0.579Å HG23 with 167 ARG HG3	Favored (48.16%) General / -124.5,147.7	67.2% (*p*) chi angles: 63.1	0.074Å	-	-
169	ILE	103.88	1.015Å HB with 156 ARG HD3	Favored (32.09%) Isoleucine or valine / -137.6,144.2	31.7% (*mm*) chi angles: 292.6,298.7	0.061Å	-	-
170	SER	80.43	-	Favored (24.07%) General / -100.5,111.8	47.1% (*t*) chi angles: 180.2	0.105Å	-	-
171	GLU	81.97	-	Favored (78.81%) General / -69.2,-38.5	19.2% (*tp10*) chi angles: 184.7,68.7,53.6	0.082Å	-	-
				Favored				OUTLIER(S)

#	Alt	Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
172		ASP	95.87	-	(44.1%) General / -97.4,131.4	15.9% (*p-10*) chi angles: 66.9,315.6	0.113Å	-	worst is CA-CB-CG: 4.473 σ
173		VAL	102.72	-	Favored (37.85%) Isoleucine or valine / -67.1,-27.0	14.4% (*p*) chi angles: 63.2	0.084Å	-	-
174		GLU	60.06	0.773Å O with 177 THR HG22	Favored (46.65%) General / -56.1,-25.6	88.1% (*mt-10*) chi angles: 290.1,188.2,5.1	0.092Å	-	-
175		ARG	132.11	0.558Å O with 178 PRO HD2	Favored (65.42%) General / -60.2,-25.1	15.3% (*ptt180*) chi angles: 65.8,166,186.1,137.6	0.126Å	-	-
176		ASP	51.12	0.657Å O with 179 PRO HD2	Favored (70.04%) General / -63.3,-28.5	94.3% (*m-20*) chi angles: 290.6,338.3	0.064Å	-	OUTLIER(S) worst is CA-CB-CG: 4.563 σ
#	Alt	Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
			Avg: 109.32	Clashscore: 67.82	Outliers: 3 of 113	Poor rotamers: 2 of 106	Outliers: 0 of 113	Outliers: 0 of 115	Outliers: 9 of 115
177		THR	136.17	0.954Å HG23 with 178 PRO HD3	Favored (3.32%) Pre-proline / -68.0,-31.4	8.9% (*t*) chi angles: 183	0.247Å	-	-
178		PRO	132.66	0.954Å HD3 with 177 THR HG23	Favored (66.14%) Trans-proline / -64.5,-20.9	99.2% (*Cg_exo*) chi angles: 329.5	0.201Å	-	-
179		PRO	146.25	0.657Å HD2 with 176 ASP O	Favored (68.74%) Trans-proline / -69.0,155.4	93.8% (*Cg_exo*) chi angles: 329.2	0.174Å	-	-
180		PRO	168.87	0.587Å HD2 with 179 PRO HB3	Favored (75.73%) Trans-proline / -59.2,150.2	73.8% (*Cg_endo*) chi angles: 28.8	0.064Å	-	-
181		LEU	201.83	0.473Å HB2 with 180 PRO O	OUTLIER (0.04%) General / 84.6,129.3	61.6% (*mt*) chi angles: 300,185.2	0.084Å	-	-
182		ARG	99.52	0.498Å HD3 with 185 SER OG	Favored (9.66%) General / -107.8,100.3	95.7% (*mtt180*) chi angles: 302.5,169.1,173.8,184.5	0.199Å	-	-

183	SER	36.49	-	Favored (69.53%) General / -69.6,-31.4	66.1% (*m*) chi angles: 296.5	0.112Å	-	-
184	TRP	72.73	-	Favored (78.06%) General / -64.2,-34.4	60.7% (*p-90*) chi angles: 52.2,271.8	0.034Å	-	-
185	SER	88.42	0.498Å OG with 182 ARG HD3	Favored (62.87%) General / -66.0,-15.3	70.3% (*m*) chi angles: 293.2	0.091Å	-	-
186	MET	152.75	0.417Å HE1 with 189 PHE CE2	Favored (86.02%) Pre-proline / -59.1,142.2	54.4% (*ttp*) chi angles: 192.2,177.6,75.8	0.089Å	-	-
187	PRO	66.37	0.889Å HA with 190 ARG HG3	Favored (60.82%) Trans-proline / -64.6,-29.1	73.7% (*Cg_exo*) chi angles: 332.4	0.174Å	-	-
188	GLU	76.78	-	Favored (94.55%) General / -64.5,-39.8	70.6% (*mm-40*) chi angles: 287.8,303.1,304.4	0.068Å	-	-
189	PHE	61.1	0.417Å CE2 with 186 MET HE1	Favored (67.13%) General / -67.7,-27.8	89% (*m-85*) chi angles: 291,278.3	0.05Å	-	OUTLIER(S) worst is CA-CB-CG: 9.506 σ
190	ARG	135.36	0.889Å HG3 with 187 PRO HA	Favored (73.25%) General / -54.7,-47.9	0.7% chi angles: 300.6,246.7,297.7,100.3	0.135Å	-	-
191	ALA	11.72	-	-	-	0.09Å	-	-