



# Viewing crb1\_sm\_148-260H-multi.table

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All-Atom Contacts	Clashscore, all atoms:	57.49		2 <sup>nd</sup> percentile* (N=1784, all resolutions)
	Clashscore is the number of serious steric overlaps (> 0.4 Å) per 1000 atoms.			
Protein Geometry	Poor rotamers	11	11.70%	Goal: <1%
	Ramachandran outliers	12	10.81%	Goal: <0.05%
	Ramachandran favored	74	66.67%	Goal: >98%
	MolProbity score^	3.91		3 <sup>rd</sup> percentile* (N=27675, 0Å - 99Å)
	Cβ deviations >0.25Å	5	4.90%	Goal: 0
	Bad backbone bonds:	7 / 859	0.81%	Goal: 0%
	Bad backbone angles:	15 / 1169	1.28%	Goal: <0.1%

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

\* 100<sup>th</sup> percentile is the best among structures of comparable resolution; 0<sup>th</sup> percentile is the worst. For clashscore the comparative set of structures was selected in 2004, for MolProbity score in 2006.

<sup>^</sup> 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: 53.98	Clashscore: 57.49	Outliers: 12 of 111	Poor rotamers: 11 of 94	Outliers: 5 of 102	Outliers: 4 of 113	Outliers: 13 of 113
A 148	ASP	50	-	-	18.8% (t0) chi angles: 172.6,24.9	0.05Å	-	-
A 149	HIS	99.99	-	Favored (21.37%) General / -124.2,163.5	34.9% (p80) chi angles: 65.7,81.9	0.042Å	OUTLIER(S) worst is CG--ND1: 4.432 σ	-
A 150	ASP	99.99	0.409Å O with A 150 ASP OD1	Favored (38.49%) General / -125.7,123.2	11% (p30) chi angles: 49.7,34.7	0.096Å	-	OUTLIER(S) worst is CA-CB-CG: 4.684 σ
A 151	GLU	99.99	0.932Å HG3 with A 154 SER HB3	Allowed (0.17%) General / -50.8,107.3	12.3% (pm0) chi angles: 65.9,285.6,350.8	0.425Å	-	OUTLIER(S) worst is CA-CB-CG: 4.511 σ

A 152	CYS	50	0.842Å CB with A 151 GLU HA	OUTLIER (0.02%) General / 83.4,-78.1	25.8% ( <i>m</i> ) chi angles: 310.9	0.366Å	-	OUTLIER(S) worst is N-CA- CB: 9.053 $\sigma$
A 153	ALA	50	0.609Å H with A 151 GLU HB2	Allowed (0.7%) General / -151.7,19.4	-	0.046Å	-	-
A 154	SER	50	0.932Å HB3 with A 151 GLU HG3	Favored (2.41%) General / -131.5,87.0	13.1% ( <i>t</i> ) chi angles: 166.8	0.164Å	-	-
A 155	SER	50	-	Favored (5.68%) Pre-proline / -102.6,95.1	44.1% ( <i>t</i> ) chi angles: 180.9	0.026Å	-	-
A 156	PRO	50	0.689Å O with A 158 GLN HG3	Favored (9.92%) Trans-proline / -72.2,-32.9	42.1% ( <i>Cg_endo</i> ) chi angles: 36.1	0.034Å	-	-
A 157	CYS	50	0.714Å HB3 with A 161 ALA HB3	Allowed (0.77%) General / -47.2,-24.8	61.1% ( <i>m</i> ) chi angles: 303.9	0.154Å	-	-
A 158	GLN	50	0.689Å HG3 with A 156 PRO O	OUTLIER (0.04%) General / 71.2,-103.8	98.1% ( <i>mt-30</i> ) chi angles: 295.5,176.5,331.8	0.052Å	-	-
A 159	ASN	50	-	Favored (3.55%) General / -130.5,40.1	33.4% ( <i>m120</i> ) chi angles: 293.3,117.1	0.051Å	-	-
A 160	GLY	50	0.469Å O with A 178 TYR CZ	OUTLIER (0.07%) Glycine / 173.0,88.9	-	-	-	-
A 161	ALA	50	0.814Å HB1 with A 173 PHE O	OUTLIER (0.02%) General / 165.9,-179.0	-	0.026Å	-	-
A 162	VAL	50	0.8Å HB with A 173 PHE HB2	Favored (43.45%) Isoleucine or valine / -105.9,135.6	91.5% ( <i>t</i> ) chi angles: 175.4	0.076Å	-	-
A 163	CYS	50	-	Favored (41.14%) General /	0.5% chi angles: 94.8	0.02Å	-	-

A 164	GLN	50	-	-116.1,121.1 Favored (20.13%) General / -120.8,162.2	52.2% ( <i>tt0</i> ) chi angles: 189.1,179.9,55	0.092Å	-	-	
A 165	ASP	50	-	Favored (43.35%) General / -100.7,134.7	43.6% ( <i>t0</i> ) chi angles: 192.8,337.5	0.104Å	-	-	
A 166	GLY	50	-	Favored (19.08%) Glycine / -124.5,160.5	-	-	-	-	
A 167	ILE	50	-	Favored (18.09%) Isoleucine or valine / -64.3,123.9	47.4% ( <i>pt</i> ) chi angles: 61.6,169.9	0.042Å	-	-	
#	Alt	Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
			Avg: 53.98	Clashscore: 57.49	Outliers: 12 of 111	Poor rotamers: 11 of 94	Outliers: 5 of 102	Outliers: 4 of 113	Outliers: 13 of 113
A 168	ASP	50	-	-	Allowed (0.39%) General / 76.9,-41.3	47.8% ( <i>t0</i> ) chi angles: 184.2,334.2	0.044Å	-	OUTLIER(S) worst is CA- CB-CG: 4.402 σ
A 169	GLY	50	-	-	Favored (22.88%) Glycine / -129.7,161.9	-	-	-	-
A 170	TYR	50	0.512Å CG with A 151 GLU OE2	-	Favored (19.23%) General / -98.4,152.7	54.6% ( <i>p90</i> ) chi angles: 61.6,269	0.069Å	-	-
A 171	SER	50	-	-	Favored (54.42%) General / -116.2,134.9	40.5% ( <i>t</i> ) chi angles: 181.4	0.078Å	-	-
A 172	CYS	50	0.43Å HB3 with A 184 ASP HB3	-	Favored (45.71%) General / -130.7,133.0	3.8% ( <i>t</i> ) chi angles: 163.4	0.011Å	-	-
A 173	PHE	50	0.814Å O with A 161 ALA HB1	-	Favored (22.5%) General / -83.0,158.6	1.6% ( <i>m-30</i> ) chi angles: 293.3,31.8	0.046Å	-	-
			0.437Å		Favored				

A 174	CYS	50	HB2 with A 178 TYR HB2	(26.59%) General / -98.3,145.5	0.5% chi angles: 26.2	0.097Å	-	-
A 175	VAL	50	0.869Å HG22 with A 176 PRO HD2	Favored (30.15%) Pre-proline / -98.3,145.6	0.5% chi angles: 90.4	0.146Å	-	-
A 176	PRO	50	0.869Å HD2 with A 175 VAL HG22	OUTLIER (0%) Trans-proline / 19.2,-88.4	88.2% (Cg_exo) chi angles: 328.9	0.177Å	-	OUTLIER(S) worst is CA-N- CD: 5.473 $\sigma$
A 177	GLY	50	-	Allowed (0.33%) Glycine / -120.9,79.9	-	-	-	-
A 178	TYR	50	0.818Å CE1 with A 175 VAL HG12	Favored (20.66%) General / -101.9,152.7	2.3% ( <i>m-85</i> ) chi angles: 265.6,42.1	0.034Å	-	-
A 179	GLN	50	0.609Å HG3 with A 185 LEU HB2	Allowed (0.08%) General / -89.5,-130.1	15.9% ( <i>pt20</i> ) chi angles: 61,170.5,64.9	0.085Å	-	OUTLIER(S) worst is OE1- CD-NE2: 4.5 $\sigma$
A 180	GLY	50	0.73Å HA2 with A 185 LEU HD12	Favored (31.12%) Glycine / 90.3,155.4	-	-	-	-
A 181	ARG	50	-	Favored (80.35%) General / -68.1,-36.8	30.1% ( <i>ptt-85</i> ) chi angles: 61.8,173.9,180.6,281.2	0.061Å	-	-
A 182	HIS	50	-	Favored (14.09%) General / -118.1,16.3	57% ( <i>m170</i> ) chi angles: 297.7,160.2	0.039Å	OUTLIER(S) worst is CG-- ND1: 4.584 $\sigma$	-
A 183	CYS	50	0.529Å HA with A 179 GLN O	Allowed (0.1%) General / 74.4,69.2	0.1% chi angles: 224.6	0.022Å	-	-
A 184	ASP	99.99	0.43Å HB3 with A 172 CYS HB3	Allowed (0.52%) General / -151.7,9.0	20.5% ( <i>p-10</i> ) chi angles: 59.9,319.7	0.06Å	-	OUTLIER(S) worst is CA- CB-CG: 4.286 $\sigma$
A 185	LEU	50	0.73Å HD12 with A 180 GLY HA2	Favored (39.34%) General / -120.0,151.2	83% ( <i>mt</i> ) chi angles: 298.6,171.4	0.041Å	-	-
				Favored				

A 186	GLU	50	0.68Å HB2 with A 178 TYR CZ	(48.16%) General / -101.5,127.5	13.7% ( <i>tm</i> -20) chi angles: 181.8,284.8,329.9	0.101Å	-	-
A 187	VAL	50	0.495Å HB with A 179 GLN HB3	Favored (3.75%) Isoleucine or valine / -98.5,156.1	2.6% ( <i>p</i> ) chi angles: 49.6	0.073Å	-	-
#	Alt Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
		Avg: 53.98	Clashscore: 57.49	Outliers: 12 of 111	Poor rotamers: 11 of 94	Outliers: 5 of 102	Outliers: 4 of 113	Outliers: 13 of 113
A 188	ASP	50	1.086Å HA with A 203 ASN ND2	Favored (6.05%) General / -80.8,86.1	14.2% ( <i>t0</i> ) chi angles: 203.3,331.6	0.331Å	-	-
A 189	GLU	50	0.87Å HG3 with A 208 TYR HD1	Favored (62.48%) General / -71.2,-15.6	4.1% ( <i>pm0</i> ) chi angles: 41.8,253.4,40.4	0.094Å	-	-
A 190	CYS	50	-	Favored (38.71%) General / -69.1,-7.7	0.1% chi angles: 111.7	0.045Å	-	-
A 191	ALA	50	-	Favored (20.56%) General / -89.7,-26.6	-	0.021Å	-	-
A 192	SER	50	-	Favored (14.26%) General / -109.7,-14.9	19.8% ( <i>m</i> ) chi angles: 284.5	0.053Å	-	-
A 193	ASP	50	0.508Å HB2 with A 208 TYR CZ	Favored (32.69%) Pre-proline / -134.3,58.8	27.1% ( <i>m</i> -20) chi angles: 304.2,287.7	0.067Å	-	-
A 194	PRO	50	-	Favored (2.33%) Trans-proline / -71.5,5.5	87.6% ( <i>Cg_endo</i> ) chi angles: 32.9	0.026Å	-	-
A 195	CYS	50	0.528Å HB3 with A 199 ALA HB3	Favored (17.36%) General / 62.4,30.9	0.5% chi angles: 249.9	0.106Å	-	-
A 196	LYS	99.99	0.795Å HD2 with A	OUTLIER (0.02%) General /	48.5% ( <i>mtpt</i> ) chi angles:	0.066Å	-	-

220 ASN HB3				79.9,-144.4	289.7,172.4,83.8,171.9			
A 197	ASN	50	-	Favored (4.24%) General / -111.9,34.4	11.5% ( <i>p30</i> ) chi angles: 63.2,83.3	0.072Å	-	-
A 198	GLU	99.99	-	Allowed (1%) General / -146.1,34.5	80.1% ( <i>mm-40</i> ) chi angles: 292.9,302.1,319.2	0.033Å	-	-
A 199	ALA	50	0.528Å HB3 with A 195 CYS HB3	Allowed (0.49%) General / -173.0,131.1	-	0.043Å	-	-
A 200	THR	50	0.488Å HG22 with A 211 ILE HB	Favored (5.11%) General / -72.6,107.4	0.6% chi angles: 217.5	0.147Å	-	OUTLIER(S) worst is CA- CB-CG2: 4.502 σ
A 201	CYS	50	-	Favored (58.22%) General / -63.9,137.8	0.5% chi angles: 100.6	0.029Å	-	-
A 202	LEU	50	-	Favored (2.99%) General / -135.1,93.4	40.2% ( <i>mt</i> ) chi angles: 284.9,180	0.089Å	-	-
A 203	ASN	50	1.086Å ND2 with A 188 ASP HA	Favored (12.3%) General / -63.1,120.9	24.7% ( <i>t-20</i> ) chi angles: 184.9,298.6	0.121Å	-	OUTLIER(S) worst is CA- CB-CG: 4.203 σ
A 204	GLU	50	0.589Å HG2 with A 205 ILE H	Favored (3.19%) General / -121.8,-175.8	69.8% ( <i>tt0</i> ) chi angles: 194.1,185.7,359	0.158Å	-	-
A 205	ILE	50	0.589Å H with A 204 GLU HG2	Allowed (0.14%) Isoleucine or valine / -61.1,101.3	1.4% ( <i>pp</i> ) chi angles: 32.6,65.6	0.088Å	-	-
A 206	GLY	50	-	Favored (5.9%) Glycine / 49.4,25.1	-	-	-	-
A 207	ARG	50	0.483Å HG2 with A 205 ILE O	Favored (18.15%) General / -163.4,156.0	41% ( <i>ptt180</i> ) chi angles: 63.5,181.7,179.6,181.1	0.02Å	-	-

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

Avg: Clashscore: Outliers: 12 of Poor rotamers: 11 Outliers: Outliers: 4 Outliers: 13

		53.98	57.49	111	of 94	5 of 102	of 113	of 113
A 208	TYR	50	0.87Å HD1 with A 189 GLU HG3	Favored (46.67%) General / -139.9,156.4	52.2% ( <i>p90</i> ) chi angles: 62.2,274.1	0.041Å	-	-
A 209	THR	50	-	Favored (45.42%) General / -133.6,137.4	67% ( <i>p</i> ) chi angles: 59.5	0.03Å	-	-
A 210	CYS	50	0.499Å HB2 with A 199 ALA HB1	Favored (22.64%) General / -118.2,114.2	1% chi angles: 35	0.096Å	-	-
A 211	ILE	50	0.488Å HB with A 200 THR HG22	Favored (29.27%) Isoleucine or valine / -85.8,116.7	43.6% ( <i>mm</i> ) chi angles: 297.6,303	0.087Å	-	-
A 212	CYS	50	0.63Å HB2 with A 213 PRO HD2	Favored (7.11%) Pre-proline / -118.3,169.9	21.4% ( <i>p</i> ) chi angles: 55.4	0.188Å	-	-
A 213	PRO	50	0.63Å HD2 with A 212 CYS HB2	Favored (89.52%) Trans-proline / -63.8,150.0	80% ( <i>Cg_endo</i> ) chi angles: 29.8	0.034Å	-	-
A 214	HIS	50	-	Allowed (0.18%) General / -72.0,49.1	60.2% ( <i>m170</i> ) chi angles: 297.4,161.6	0.025Å	OUTLIER(S) worst is CG-- ND1: 4.445 $\sigma$	-
A 215	ASN	50	-	Allowed (0.32%) General / -142.8,-41.8	22.9% ( <i>t-20</i> ) chi angles: 189.1,297.4	0.044Å	-	-
A 216	TYR	50	0.529Å CE2 with A 224 GLU HB3	Favored (10.91%) General / -113.7,167.1	42.2% ( <i>m-85</i> ) chi angles: 281.4,79.1	0.055Å	-	-
A 217	SER	50	-	Favored (11.86%) General / -161.2,175.9	32.6% ( <i>t</i> ) chi angles: 184.1	0.038Å	-	-
A 218	GLY	50	-	Favored (16.57%) Glycine / 123.5,-164.7	-	-	-	-
				Favored (65.51%)	0.5%		OUTLIER(S)	

A 219	VAL	50	-	Isoleucine or valine / -68.5,-34.4	chi angles: 112.7	0.135Å	-	worst is CA- CB-CG1: 4.489 $\sigma$
A 220	ASN	50	0.795Å HB3 with A 196 LYS HD2	Favored (17.96%) General / -112.8,6.3	2.2% ( <i>m120</i> ) chi angles: 273.5,145.9	0.362Å	-	OUTLIER(S) worst is N-CA- CB: 7.789 $\sigma$
A 221	CYS	50	-	Allowed (0.93%) General / 40.4,40.8	98.3% ( <i>m</i> ) chi angles: 290.7	0.03Å	-	-
A 222	GLU	50	0.726Å O with A 243 LEU HD21	Favored (13.03%) General / -116.6,2.4	5.1% ( <i>tp10</i> ) chi angles: 198.1,73.8,277.5	0.044Å	-	OUTLIER(S) worst is CA-C- O: 4.339 $\sigma$
A 223	LEU	50	0.811Å HA with A 243 LEU HD21	Favored (16.2%) General / -94.4,104.2	36.4% ( <i>mt</i> ) chi angles: 302.6,166.1	0.042Å	-	-
A 224	GLU	50	0.529Å HB3 with A 216 TYR CE2	OUTLIER (0.03%) General / -62.8,87.3	9.8% ( <i>pt-20</i> ) chi angles: 54.8,175.5,72	0.055Å	-	-
A 225	ILE	50	-	OUTLIER (0%) Isoleucine or valine / 50.7,-179.6	26.3% ( <i>pt</i> ) chi angles: 67.6,178.5	0.129Å	-	-
A 226	ASP	50	-	Favored (18.46%) General / -99.6,154.2	7% ( <i>t0</i> ) chi angles: 208.6,327	0.075Å	-	-
A 227	GLU	50	-	Allowed (1.99%) General / -142.1,24.1	1.3% ( <i>pm0</i> ) chi angles: 48.3,282.5,276.2	0.044Å	-	-
#	Alt Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	C $\beta$ deviation	Bond lengths	Bond angles
		Avg: 53.98	Clashscore: 57.49	Outliers: 12 of 111	Poor rotamers: 11 of 94	Outliers: 5 of 102	Outliers: 4 of 113	Outliers: 13 of 113
A 228	CYS	50	0.404Å HB2 with A 239 CYS HB2	Favored (40.25%) General / -99.2,11.0	0.5% chi angles: 99.7	0.073Å	-	-
A 229	TRP	50	-	Favored (62.54%) General / -62.7,-18.5	65.8% ( <i>p-90</i> ) chi angles: 64.4,268.3	0.032Å	-	-



A 230	SER	50	-	Favored (7.99%) General / -101.2,25.6	69.9% ( <i>m</i> ) chi angles: 297.8	0.026Å	-	-
A 231	GLN	99.99	0.748Å HG3 with A 233 CYS SG	Allowed (0.64%) Pre-proline / -168.9,87.4	7.3% ( <i>tp-100</i> ) chi angles: 185.3,64,263.6	0.038Å	-	-
A 232	PRO	50	0.411Å C with A 234 LEU H	Favored (3.7%) Trans-proline / -70.7,-40.6	77.2% ( <i>Cg_endo</i> ) chi angles: 29.7	0.038Å	-	-
A 233	CYS	50	0.748Å SG with A 231 GLN HG3	Allowed (0.26%) General / 67.6,-35.3	57.4% ( <i>m</i> ) chi angles: 305.7	0.1Å	-	-
A 234	LEU	50	0.411Å H with A 232 PRO C	Allowed (0.07%) General / 59.2,170.8	18% ( <i>tp</i> ) chi angles: 193.8,55	0.101Å	-	-
A 235	ASN	50	-	OUTLIER (0.04%) General / 71.6,-105.0	34.6% ( <i>m120</i> ) chi angles: 294.4,113.9	0.059Å	-	-
A 236	GLY	50	0.597Å O with A 238 THR HG23	Favored (6.13%) Glycine / -113.1,-20.9	-	-	-	-
A 237	ALA	50	0.565Å CB with A 233 CYS HB3	Allowed (1.19%) General / -56.8,112.0	-	0.271Å	-	OUTLIER(S) worst is C-CA- CB: 5.922 σ
A 238	THR	50	0.597Å HG23 with A 236 GLY O	Favored (27.04%) General / -107.9,113.7	34.8% ( <i>p</i> ) chi angles: 52.3	0.083Å	-	-
A 239	CYS	50	0.404Å HB2 with A 228 CYS HB2	Favored (43.69%) General / -75.1,142.1	17.5% ( <i>p</i> ) chi angles: 71.9	0.084Å	-	-
A 240	GLN	50	0.774Å HB3 with A 247 PHE HB3	Favored (54.12%) General / -106.6,128.4	52.9% ( <i>tt0</i> ) chi angles: 182.1,181.5,60.9	0.036Å	-	-
A 241	ASP	50	0.717Å HB3 with A 223 LEU HD13	Favored (5.69%) General / -78.1,98.2	3.2% ( <i>t0</i> ) chi angles: 213.1,317.2	0.109Å	-	-
				Favored				

A 242	ALA	50	-	(31.05%) General / -112.2,150.3	-	0.037Å	-	-
A 243	LEU	50	0.811Å HD21 with A 223 LEU HA	Allowed (0.28%) General / -71.5,58.6	78.8% ( <i>mt</i> ) chi angles: 291.1,178.5	0.033Å	-	-
A 244	GLY	50	-	Allowed (0.18%) Glycine / 172.0,-43.3	-	-	-	-
A 245	ALA	50	-	Allowed (1.67%) General / -163.1,-168.2	-	0.062Å	-	-
A 246	TYR	99.99	0.466Å CE1 with A 231 GLN CB	Favored (39.99%) General / -114.9,147.4	55.3% ( <i>p90</i> ) chi angles: 62.6,88.8	0.061Å	-	-
A 247	PHE	50	0.774Å HB3 with A 240 GLN HB3	Favored (7.17%) General / -117.7,99.8	81.9% ( <i>t80</i> ) chi angles: 181.2,83.2	0.045Å	-	-
#	Alt Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
		Avg: 53.98	Clashscore: 57.49	Outliers: 12 of 111	Poor rotamers: 11 of 94	Outliers: 5 of 102	Outliers: 4 of 113	Outliers: 13 of 113
A 248	CYS	50	-	Allowed (1.19%) General / -71.5,93.6	51.8% ( <i>t</i> ) chi angles: 179.9	0.056Å	-	-
A 249	ASP	50	0.465Å HB2 with A 247 PHE CE2	Favored (6.96%) General / -101.4,172.5	29% ( <i>t70</i> ) chi angles: 188.1,47.4	0.065Å	-	-
A 250	CYS	50	-	Favored (14.84%) General / -113.7,106.7	35.1% ( <i>t</i> ) chi angles: 188.9	0.064Å	-	-
A 251	ALA	50	-	Favored (93.78%) Pre-proline / -66.9,153.6	-	0.069Å	-	-
A 252	PRO	50	-	OUTLIER (0%) Trans-proline / -119.1,-35.8 Favored	16.2% ( <i>Cg_endo</i> ) chi angles: 39.2	0.053Å	-	-

A 253	GLY	50	-	(38.94%) Glycine / -53.3,-29.8	-	-	-	-
A 254	PHE	50	-	Allowed (0.78%) General / -92.6,-68.7	3.9% ( <i>m-85</i> ) chi angles: 325.6,295.2	0.053Å	-	-
A 255	LEU	50	0.58Å HD23 with A 257 ASP H	Favored (18.65%) General / -49.9,136.1	9.5% ( <i>tt</i> ) chi angles: 180.3,153.4	0.103Å	-	-
A 256	GLY	50	-	Favored (5.02%) Glycine / -118.2,33.1	-	-	-	-
A 257	ASP	50	0.58Å H with A 255 LEU HD23	Allowed (0.5%) General / -107.7,-86.4	50.2% ( <i>m-20</i> ) chi angles: 299.8,296.7	0.059Å	-	-
A 258	HIS	50	0.412Å H with A 255 LEU HD21	OUTLIER (0.02%) General / -167.6,-41.5	78.3% ( <i>m80</i> ) chi angles: 298,85.8	0.04Å	OUTLIER(S) worst is CD2-- NE2: 4.028 $\sigma$	-
A 259	CYS	50	-	OUTLIER (0.03%) General / 57.6,94.9	0.6% chi angles: 155.5	0.032Å	-	-
A 260	GLU	99.99	-	-	4.9% ( <i>pm0</i> ) chi angles: 67.1,297.7,336.8	0.182Å	-	-

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