



# Viewing TGFBI\_sm\_252-373H-multi.table

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All-Atom Contacts	Clashscore, all atoms:	77.85		0 <sup>th</sup> percentile* (N=1784, all resolutions)
	Clashscore is the number of serious steric overlaps (> 0.4 Å) per 1000 atoms.			
Protein Geometry	Poor rotamers	4	4.04%	Goal: <1%
	Ramachandran outliers	5	4.17%	Goal: <0.05%
	Ramachandran favored	97	80.83%	Goal: >98%
	MolProbity score^	3.54		8 <sup>th</sup> percentile* (N=27675, 0Å - 99Å)
	Cβ deviations >0.25Å	3	2.68%	Goal: 0
	Bad backbone bonds:	4 / 914	0.44%	Goal: 0%
	Bad backbone angles:	15 / 1243	1.21%	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: 56.97	Clashscore: 77.85	Outliers: 5 of 120	Poor rotamers: 4 of 99	Outliers: 3 of 112	Outliers: 2 of 122	Outliers: 10 of 122
A 252	THR	50	-	-	93.2% ( <i>m</i> ) chi angles: 300.2	0.071Å	-	-
A 253	PHE	50	0.843Å HB3 with A 257 ARG HB3	Favored (2.97%) General / -133.8,42.1	45.3% ( <i>m-85</i> ) chi angles: 309.9,281.7	0.161Å	-	-
A 254	GLU	50	-	Favored (65.46%) General / -67.5,-22.3	12.4% ( <i>pt-20</i> ) chi angles: 59.7,179.5,65.7	0.059Å	-	-
A 255	THR	50	-	Favored (29.95%) General / -83.6,-26.4	13.8% ( <i>t</i> ) chi angles: 190.1	0.086Å	-	-

A 256	LEU	50	0.427Å HB2 with A 285 PHE CZ	Allowed (0.62%) General / -138.3,-53.6	3.3% ( <i>tm?</i> ) chi angles: 189.2,281.4	0.083Å	-	-
A 257	ARG	50	0.843Å HB3 with A 253 PHE HB3	Favored (64.2%) General / -73.7,-32.9	50.7% ( <i>ttm-85</i> ) chi angles: 174.3,190.6,298.7,279.3	0.112Å	-	-
A 258	ALA	50	-	Favored (66.91%) General / -57.7,-31.9	-	0.059Å	-	-
A 259	ALA	50	0.454Å HA with A 262 ALA HB3	Favored (61.26%) General / -72.8,-19.9	-	0.019Å	-	-
A 260	VAL	50	0.771Å HB with A 269 LEU HD12	Allowed (0.81%) Isoleucine or valine / -52.0,-61.0	19.4% ( <i>m</i> ) chi angles: 303.9	0.151Å	-	OUTLIER(S) worst is CA- CB-CG2: 4.6 σ
A 261	ALA	50	-	Favored (64.57%) General / -73.4,-32.8	-	0.048Å	-	-
A 262	ALA	50	0.454Å HB3 with A 259 ALA HA	Favored (40.85%) General / -76.8,-3.9	-	0.032Å	-	-
A 263	SER	50	-	Favored (14.34%) General / -114.0,21.9	32.8% ( <i>t</i> ) chi angles: 183.9	0.018Å	-	-
A 264	GLY	50	-	Favored (92.93%) Glycine / 64.2,36.2	-	-	-	-
A 265	LEU	50	0.733Å HD12 with A 260 VAL HA	Favored (20.08%) General / -108.9,0.2	7% ( <i>mt</i> ) chi angles: 323.5,175.3	0.07Å	-	-
A 266	ASN	50	-	Favored (16.24%) General / -50.8,-55.6	26.5% ( <i>t-20</i> ) chi angles: 184.8,300.2	0.054Å	-	-
A 267	THR	50	-	Favored (62.23%) General /	66.8% ( <i>p</i> ) chi angles: 59.5	0.031Å	-	-

A 268	MET	50	0.549Å HG2 with A 265 LEU HA	-71.7,-17.8 Favored (7.39%) General / -93.9,-46.0	20.4% ( <i>ptp</i> ) chi angles: 74.2,181.9,62.5	0.138Å	-	-
A 269	LEU	50	0.771Å HD12 with A 260 VAL HB	Favored (30.02%) General / -70.5,-51.3	35.7% ( <i>mt</i> ) chi angles: 287.8,184.2	0.08Å	-	-
A 270	GLU	50	0.485Å CD with A 270 GLU O	Allowed (1.57%) General / -98.2,36.5	14.7% ( <i>tm-20</i> ) chi angles: 185.6,283,325.1	0.129Å	-	-
A 271	GLY	50	-	Allowed (0.27%) Glycine / -53.4,-74.8	-	-	-	-
#	Alt Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
		Avg: 56.97	Clashscore: 77.85	Outliers: 5 of 120	Poor rotamers: 4 of 99	Outliers: 3 of 112	Outliers: 2 of 122	Outliers: 10 of 122
A 272	ASN	50	-	OUTLIER (0.01%) General / -178.8,81.7	28.7% ( <i>t-20</i> ) chi angles: 187.3,301.5	0.066Å	-	-
A 273	GLY	50	-	Favored (7.56%) Glycine / 150.5,157.0	-	-	-	-
A 274	GLN	50	-	Favored (2.3%) General / -59.5,113.6	18.3% ( <i>pt20</i> ) chi angles: 64,176.3,61.8	0.046Å	-	-
A 275	TYR	99.99	0.4Å CD1 with A 269 LEU O	Favored (53.78%) General / -116.5,126.8	55.8% ( <i>p90</i> ) chi angles: 62.6,271	0.022Å	-	-
A 276	THR	50	0.513Å CG2 with A 312 LEU HB2	Favored (35.53%) General / -93.8,121.7	4.7% ( <i>t</i> ) chi angles: 175.2	0.033Å	-	-
A 277	LEU	50	-	Favored (12.97%) General / -134.2,114.4	8.9% ( <i>tt</i> ) chi angles: 188.4,157.9	0.075Å	-	-
A 278	LEU	50	0.629Å HA with A 365 HIS O	Allowed (1.28%) General /	71.3% ( <i>mt</i> ) chi angles: 298.5,169	0.069Å	-	-

A 279	ALA	50	0.646Å HB3 with A 257 ARG HH21	-73.0,84.8 Favored (61.6%) Pre-proline / -99.0,111.8	-	0.158Å	-	OUTLIER(S) worst is N-CA- CB: 4.005 $\sigma$
A 280	PRO	50	0.69Å HB3 with A 367 ILE HG13	Favored (27.22%) Trans-proline / -58.7,157.7	55.4% ( <i>Cg_endo</i> ) chi angles: 25.6	0.043Å	-	-
A 281	THR	50	0.553Å HB with A 283 GLU HG2	Favored (43.06%) General / -69.1,153.8	0.1% chi angles: 18.6	0.047Å	-	-
A 282	ASN	50	-	Favored (50.73%) General / -54.9,-28.4	52.2% ( <i>t30</i> ) chi angles: 184.7,58	0.028Å	-	-
A 283	GLU	50	0.553Å HG2 with A 281 THR HB	Favored (73.04%) General / -69.9,-34.1	12.3% ( <i>pt-20</i> ) chi angles: 65.3,177.9,64.1	0.058Å	-	-
A 284	ALA	50	-	Favored (97.15%) General / -64.0,-42.1	-	0.057Å	-	-
A 285	PHE	50	0.929Å CD2 with A 296 ILE HD12	Favored (97.98%) General / -62.6,-43.8	2.6% ( <i>m-85</i> ) chi angles: 260.8,68.5	0.036Å	-	-
A 286	GLU	50	0.809Å HA with A 293 LEU HD12	Favored (61.71%) General / -71.8,-24.3	12.7% ( <i>pt-20</i> ) chi angles: 63.7,181.3,65.4	0.192Å	-	-
A 287	LYS	50	-	Favored (88.13%) General / -66.8,-41.1	27.9% ( <i>tptp</i> ) chi angles: 185.1,61.5,183.2,64.8	0.028Å	-	-
A 288	ILE	50	1.034Å HD11 with A 296 ILE HD13	Favored (67.21%) Pre-proline / -57.9,124.1	20.6% ( <i>pt</i> ) chi angles: 66.8,181.9	0.093Å	-	-
A 289	PRO	50	-	Allowed (0.34%) Trans-proline / -73.1,-167.3	68.5% ( <i>Cg_endo</i> ) chi angles: 33.6	0.019Å	-	-
A 290	SER	50	-	Allowed (0.18%) General / -73.1,-156.8	70.4% ( <i>m</i> ) chi angles: 297.3	0.049Å	-	-

A 291	GLU	50	0.461Å O with A 295 ARG HG3	53.5,-156.9 Favored (3.68%) General / -91.4,22.8	11.9% ( <i>pt</i> -20) chi angles: 62.2,176.8,64	0.034Å	-	-	
#	Alt	Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
			Avg: 56.97	Clashscore: 77.85	Outliers: 5 of 120	Poor rotamers: 4 of 99	Outliers: 3 of 112	Outliers: 2 of 122	Outliers: 10 of 122
A 292	THR	50	0.768Å HG22 with A 288 ILE HD12	Favored (71.85%) General / -70.3,-33.7	47.3% ( <i>m</i> ) chi angles: 305.1	0.029Å	-	-	
A 293	LEU	50	0.809Å HD12 with A 286 GLU HA	Favored (88.32%) General / -66.3,-38.7	6.3% ( <i>tt</i> ) chi angles: 189.7,167.7	0.149Å	-	-	
A 294	ASN	50	-	Favored (76.21%) General / -69.9,-38.6	54% ( <i>t</i> 30) chi angles: 185.8,55.9	0.078Å	-	-	
A 295	ARG	50	0.461Å HG3 with A 291 GLU O	Favored (79.59%) General / -68.9,-38.6	77.2% ( <i>mtp</i> 85) chi angles: 293.3,178.2,68.4,82.6	0.025Å	-	-	
A 296	ILE	50	1.034Å HD13 with A 288 ILE HD11	Favored (17.62%) Isoleucine or valine / -74.0,-20.2	37.5% ( <i>pt</i> ) chi angles: 65.2,175.1	0.046Å	-	OUTLIER(S) worst is CB- CG1-CD1: 4.517 σ	
A 297	LEU	50	-	Favored (59.32%) General / -75.9,-31.5	8.4% ( <i>tp</i> ) chi angles: 197.9,81.9	0.051Å	-	-	
A 298	GLY	50	0.492Å C with A 300 PRO HD2	Favored (38.63%) Glycine / -68.5,142.3	-	-	-	-	
A 299	ASP	99.99	0.515Å OD1 with A 300 PRO HD3	Favored (73.8%) Pre-proline / -60.5,-40.2	15.3% ( <i>p</i> -10) chi angles: 66.9,312.7	0.078Å	-	-	
A 300	PRO	99.99	0.515Å HD3 with A 299 ASP OD1	Favored (13.19%) Trans-proline / -61.5,123.7 Allowed	85.6% ( <i>Cg_endo</i> ) chi angles: 33 21.1% ( <i>pm</i> 0)	0.041Å	-	-	

A 301	GLU	99.99	-	(0.36%) General / -118.8,-141.3	chi angles: 66.4,283.6,4.6	0.219Å	-	-
A 302	ALA	50	-	OUTLIER (0%) General / 163.6,-35.0	-	0.111Å	-	-
A 303	LEU	50	0.424Å CD1 with A 256 LEU HD21	Favored (67.73%) General / -58.0,-32.2	14.4% ( <i>mt</i> ) chi angles: 274.7,162.4	0.043Å	-	-
A 304	ARG	50	0.561Å O with A 307 LEU HD22	Favored (92.24%) General / -64.0,-44.6	78.2% ( <i>ttt-85</i> ) chi angles: 183.7,178.1,178,277.8	0.032Å	-	-
A 305	ASP	50	-	Favored (81.24%) General / -62.1,-36.3	38.4% ( <i>t70</i> ) chi angles: 183.4,59.2	0.014Å	-	-
A 306	LEU	99.99	0.658Å O with A 372 ILE HD11	Favored (6.91%) General / -109.9,30.2	80.6% ( <i>mt</i> ) chi angles: 296.9,169.6	0.037Å	-	-
A 307	LEU	50	0.561Å HD22 with A 304 ARG O	Favored (70.35%) General / -62.3,-29.4	2.4% ( <i>pt?</i> ) chi angles: 78.3,170.7	0.035Å	-	-
A 308	ASN	50	0.886Å HA with A 311 ILE HG22	Favored (74.07%) General / -56.4,-40.1	31.8% ( <i>m120</i> ) chi angles: 292.1,118.5	0.079Å	-	-
A 309	ASN	50	0.424Å ND2 with A 333 THR HG21	Favored (70.25%) General / -65.5,-29.6	27.5% ( <i>t-20</i> ) chi angles: 188,300.7	0.054Å	-	-
A 310	HIS	50	0.813Å HB2 with A 372 ILE HD12	Favored (24.62%) General / -87.3,-23.4	0.3% chi angles: 218.7,351.9	0.082Å	OUTLIER(S) worst is CG-- ND1: 4.608 σ	OUTLIER(S) worst is CB- CG-CD2: 4.284 σ
A 311	ILE	50	0.886Å HG22 with A 308 ASN HA	Favored (56.41%) Isoleucine or valine / -102.3,126.7	9% ( <i>tp</i> ) chi angles: 184.2,63.9	0.055Å	-	-

#	Alt Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
Avg:		Clashscore:	Outliers: 5 of	Poor rotamers: 4 of	Outliers: 3 of 112	Outliers: 2 of 122	Outliers: 10 of 122	
56.97		77.85	120	99				

A 312	LEU	99.99	0.819Å HG with A 329 THR HA	Favored (5.8%) General / -144.7,111.5	4.6% ( <i>mp</i> ) chi angles: 295.9,63.6	0.055Å	-	OUTLIER(S) worst is CD1- CG-CD2: 4.994 σ
A 313	LYS	99.99	-	Favored (43.15%) General / -74.0,135.6	99.3% ( <i>mttt</i> ) chi angles: 293.8,181.9,179.1,180.2	0.038Å	-	-
A 314	SER	50	-	Allowed (0.49%) General / 57.7,72.9	43.3% ( <i>t</i> ) chi angles: 181	0.036Å	-	-
A 315	ALA	50	-	Favored (4.98%) General / -128.2,98.1	-	0.024Å	-	-
A 316	MET	50	-	Favored (26.33%) General / -87.0,146.0	25.7% ( <i>ptp</i> ) chi angles: 62.3,181.3,69.1	0.016Å	-	-
A 317	CYS	50	0.746Å HB2 with A 357 ILE CD1	Favored (29.88%) General / -58.4,147.9	9.6% ( <i>t</i> ) chi angles: 196.2	0.195Å	-	-
A 318	ALA	50	-	Favored (78.5%) General / -58.6,-38.7	-	0.026Å	-	-
A 319	GLU	50	0.647Å HG2 with A 317 CYS SG	Favored (64.94%) General / -58.2,-28.5	12.5% ( <i>pt-20</i> ) chi angles: 67,181.3,58.8	0.04Å	-	-
A 320	ALA	50	-	Favored (71.88%) General / -61.1,-32.2	-	0.019Å	-	-
A 321	ILE	50	0.889Å HG13 with A 322 VAL H	Allowed (0.18%) Isoleucine or valine / -113.3,-86.8	23.8% ( <i>pt</i> ) chi angles: 57.2,162.1	0.154Å	-	-
A 322	VAL	50	0.889Å H with A 321 ILE HG13	Favored (41.05%) Isoleucine or valine / -130.6,154.7	14.7% ( <i>p</i> ) chi angles: 64	0.101Å	-	-
A 323	ALA	50	-	Favored (21.83%) General /	-	0.047Å	-	-

A 324	GLY	50	-	General / -88.9,111.2 Allowed (0.63%) Glycine / 113.9,74.4	-	-	-	-
A 325	LEU	50	0.846Å HG with A 326 SER H	Favored (2.3%) General / -130.5,-170.2	38% ( <i>tp</i> ) chi angles: 186.8,60.6	0.085Å	-	-
A 326	SER	50	0.846Å H with A 325 LEU HG	Favored (21.03%) General / -122.1,162.5	87.8% ( <i>p</i> ) chi angles: 65.5	0.058Å	-	-
A 327	VAL	50	0.58Å CG1 with A 335 LEU HB2	Favored (3.74%) Isoleucine or valine / -126.0,96.6	12.1% ( <i>p</i> ) chi angles: 66.1	0.138Å	-	-
A 328	GLU	50	0.453Å HA with A 333 THR O	Favored (37.68%) General / -78.8,141.5	57.6% ( <i>tt0</i> ) chi angles: 188.2,189.6,334.4	0.098Å	-	-
A 329	THR	50	0.819Å HA with A 312 LEU HG	Favored (23.23%) General / -105.7,152.4	6.3% ( <i>p</i> ) chi angles: 79.7	0.021Å	-	-
A 330	LEU	50	0.592Å HD22 with A 308 ASN ND2	Favored (75.45%) General / -56.0,-41.9	7.4% ( <i>tt</i> ) chi angles: 187.4,162.8	0.028Å	-	-
A 331	GLU	50	-	Favored (67.03%) General / -54.3,-39.4	14.9% ( <i>tt0</i> ) chi angles: 193,199.3,281.7	0.085Å	-	-
#	Alt Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
		Avg: 56.97	Clashscore: 77.85	Outliers: 5 of 120	Poor rotamers: 4 of 99	Outliers: 3 of 112	Outliers: 2 of 122	Outliers: 10 of 122
A 332	GLY	50	-	Allowed (0.34%) Glycine / 120.2,72.1	-	-	-	-
A 333	THR	50	0.453Å O with A 328 GLU HA	Favored (8.14%) General / -149.5,121.3	72.4% ( <i>p</i> ) chi angles: 63.7	0.07Å	-	-
A	THR	50	-	Favored (11.03%) General / -149.5,121.3	66.8% ( <i>p</i> ) chi angles: 63.7	0.021Å	-	-



A 334	THR	50	-	(11.92%) General / -101.5,101.4	66.0% ( <i>p</i> ) chi angles: 57.3	0.021Å	-	-
A 335	LEU	50	0.58Å HB2 with A 327 VAL CG1	Favored (9.99%) General / -88.4,171.6	7.1% ( <i>mp</i> ) chi angles: 287.2,58.6	0.032Å	-	-
A 336	GLU	50	0.414Å O with A 346 ILE HA	Favored (25.92%) General / -106.3,112.8	10.5% ( <i>pt-20</i> ) chi angles: 57,175.3,70.9	0.014Å	-	-
A 337	VAL	50	0.454Å HG22 with A 346 ILE HD13	Favored (15.32%) Isoleucine or valine / -95.3,104.0	16% ( <i>t</i> ) chi angles: 190.2	0.04Å	-	-
A 338	GLY	50	-	Favored (16.49%) Glycine / -112.6,140.8	-	-	-	-
A 339	CYS	50	-	Allowed (1.03%) General / -121.5,-66.6	81.6% ( <i>m</i> ) chi angles: 299.8	0.025Å	-	-
A 340	SER	50	-	Favored (39.15%) General / -61.9,149.9	32.6% ( <i>t</i> ) chi angles: 184.1	0.041Å	-	-
A 341	GLY	50	-	Favored (67.71%) Glycine / 58.4,32.1	-	-	-	-
A 342	ASP	99.99	0.491Å OD2 with A 345 THR HG23	Favored (13.74%) General / -165.7,156.8	38.3% ( <i>t70</i> ) chi angles: 184.7,63.7	0.083Å	-	-
A 343	MET	99.99	0.462Å C with A 344 LEU HG	Favored (52.73%) General / -77.7,-34.7	23.8% ( <i>ptp</i> ) chi angles: 58.6,185.5,67	0.111Å	-	-
A 344	LEU	99.99	0.559Å HB3 with A 352 ILE HG13	OUTLIER (0.01%) General / 177.9,69.9	0% chi angles: 335,133.7	0.241Å	-	OUTLIER(S) worst is O-C- N: 4.582 $\sigma$
A 345	THR	50	0.663Å HB with A 348 GLY O	Favored (57.03%) General / -116.1,131.1	26.5% ( <i>p</i> ) chi angles: 71.5	0.564Å	-	-

A 346	ILE	50	0.542Å HD11 with A 327 VAL CG1	Favored (2.07%) Isoleucine or valine / -137.6,101.4	8.8% ( <i>tp</i> ) chi angles: 184.7,60.6	0.108Å	-	-
A 347	ASN	50	-	Favored (13.93%) General / 56.8,28.2	65.3% ( <i>t30</i> ) chi angles: 191.3,28.2	0.057Å	-	-
A 348	GLY	99.99	0.663Å O with A 345 THR HB	Favored (36.76%) Glycine / 163.1,-166.0	-	-	-	-
A 349	LYS	99.99	-	Favored (47.25%) General / -123.1,147.0	22.8% ( <i>pttp</i> ) chi angles: 61.3,179.4,181.6,65.2	0.031Å	-	-
A 350	ALA	99.99	-	Favored (29.11%) General / 51.3,44.0	-	0.05Å	-	-
A 351	ILE	99.99	0.895Å HD11 with A 371 LEU HG	Favored (11.62%) Isoleucine or valine / -101.0,-47.3	18.3% ( <i>tt</i> ) chi angles: 182.5,166.1	0.112Å	-	OUTLIER(S) worst is CA-C- O: 4.33 σ
<div> <div>#</div> <div>Alt Res</div> <div>High B</div> <div>Clash &gt; 0.4Å</div> <div>Ramachandran</div> <div>Rotamer</div> <div>Cβ deviation</div> <div>Bond lengths</div> <div>Bond angles</div> </div> <div> <div>Avg: 56.97</div> <div>Clashscore: 77.85</div> <div>Outliers: 5 of 120</div> <div>Poor rotamers: 4 of 99</div> <div>Outliers: 3 of 112</div> <div>Outliers: 2 of 122</div> <div>Outliers: 10 of 122</div> </div>								
A 352	ILE	99.99	0.988Å HA with A 367 ILE HA	Allowed (0.12%) Isoleucine or valine / -94.7,-164.4	21.8% ( <i>pt</i> ) chi angles: 56.4,181.5	0.228Å	-	-
A 353	SER	50	-	OUTLIER (0.01%) General / -178.2,-55.5	0.3% chi angles: 240.5	0.06Å	-	-
A 354	ASN	50	-	Favored (2.19%) General / -123.1,83.9	50.9% ( <i>t30</i> ) chi angles: 183.8,58.8	0.056Å	-	-
A 355	LYS	50	0.846Å HD3 with A 352 ILE HD12	Allowed (1.81%) General / -69.7,102.1	28.9% ( <i>mmmt</i> ) chi angles: 296,294.8,275.3,178.1	0.019Å	-	-

A 356	ASP	50	0.604Å O with A 357 ILE HG22	Favored (51.18%) General / -76.8,-39.5	40.3% ( <i>t0</i> ) chi angles: 185,327.8	0.079Å	-	-
A 357	ILE	50	0.746Å CD1 with A 317 CYS HB2	Allowed (0.27%) Isoleucine or valine / 74.4,-60.0	8% ( <i>tp</i> ) chi angles: 185.7,56.7	0.261Å	-	OUTLIER(S) worst is CA- CB-CG2: 5.865 σ
A 358	LEU	50	-	Favored (18.32%) General / -104.8,107.4	55.4% ( <i>tp</i> ) chi angles: 182.3,64.4	0.052Å	-	-
A 359	ALA	50	0.476Å HB2 with A 364 ILE HG23	Favored (10.89%) General / -80.1,175.2	-	0.016Å	-	-
A 360	THR	50	-	Favored (66.81%) General / -68.5,-28.2	80.5% ( <i>p</i> ) chi angles: 60.4	0.03Å	-	-
A 361	ASN	50	-	Favored (3.12%) General / -136.8,14.9	52.7% ( <i>t30</i> ) chi angles: 184.2,47.3	0.064Å	-	-
A 362	GLY	50	0.438Å C with A 359 ALA HB3	Allowed (0.71%) Glycine / 178.6,-120.5	-	-	-	-
A 363	VAL	50	0.532Å HG13 with A 357 ILE O	Favored (41.77%) Isoleucine or valine / -129.2,143.2	85.6% ( <i>t</i> ) chi angles: 175	0.063Å	-	-
A 364	ILE	50	0.84Å HB with A 366 TYR CE1	Favored (17.55%) Isoleucine or valine / -143.7,130.8	20.9% ( <i>pt</i> ) chi angles: 52.7,178.9	0.09Å	-	-
A 365	HIS	50	0.821Å HB3 with A 355 LYS HZ2	Favored (11.54%) General / -146.7,123.9	32.6% ( <i>m170</i> ) chi angles: 294.9,139.4	0.317Å	OUTLIER(S) worst is CG-- ND1: 5.648 σ	OUTLIER(S) worst is C-CA- CB: 4.998 σ
A 366	TYR	50	0.84Å CE1 with A 364 ILE HB	Favored (56.37%) General / -114.4,128.5	3.1% ( <i>m-30</i> ) chi angles: 290,23.2	0.17Å	-	OUTLIER(S) worst is CG- CD1-CE1: 5.266 σ
A	ILE	50	0.988Å HA with A	Favored (28.72%) Isoleucine or	38.1% ( <i>nt</i> )	0.145Å	-	-

A 367	ILE	50	0.636Å HB2 with A 352 ILE O	Favored (65.61%) General / -64.0,-20.1	9.7% ( <i>t0</i> ) chi angles: 56.7,168.2	0.055Å	-	-	
A 368	ASP	50	0.853Å HG2 with A 351 ILE HA	Allowed (0.3%) General / -123.5,-138.1	12% ( <i>pt-20</i> ) chi angles: 66.4,177,61.8	0.137Å	-	-	
A 369	GLU	50	0.416Å N with A 369 GLU HG3	Favored (49.02%) General / -121.1,143.6	9.9% ( <i>tt</i> ) chi angles: 185.3,154.8	0.112Å	-	-	
A 370	LEU	50	0.895Å HG with A 351 ILE HD11	Favored (5.46%) General / -123.7,177.9	1.2% ( <i>mt</i> ) chi angles: 245.5,170.5	0.055Å	-	-	
A 371	LEU	50							
#	Alt	Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
			Avg: 56.97	Clashscore: 77.85	Outliers: 5 of 120	Poor rotamers: 4 of 99	Outliers: 3 of 112	Outliers: 2 of 122	Outliers: 10 of 122
A 372	ILE	99.99	0.813Å HD12 with A 310 HIS HB2	OUTLIER (0.08%) Pre-proline / 59.5,149.3		3.1% ( <i>tt</i> ) chi angles: 187.3,192	0.184Å	-	-
A 373	PRO	99.99	0.484Å HD2 with A 372 ILE CG1	-		61% ( <i>Cg_endo</i> ) chi angles: 27.3	0.035Å	-	-

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