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All-Atom Contacts	Clashscore, all atoms:	0.51	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	4	3.33%	Goal: <1%
	Ramachandran outliers	3	2.21%	Goal: <0.05%
	Ramachandran favored	105	77.21%	Goal: >98%
	MolProbity score^	1.84		83 rd percentile* (N=27675, 0Å - 99Å)
	Cβ deviations >0.25Å	1	0.81%	Goal: 0
	Bad backbone bonds:	0 / 1060	0.00%	Goal: 0%
	Bad backbone angles:	15 / 1443	1.04%	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: 62.68	Clashscore: 0.51	Outliers: 3 of 136	Poor rotamers: 4 of 120	Outliers: 1 of 124	Outliers: 0 of 138	Outliers: 15 of 138
A 262	ASN	50	-	-	2% (<i>t</i> 30) chi angles: 219.3,78.9	0.058Å	-	-
A 263	THR	50	-	Favored (23%) General / -80.4,164.6	32.9% (<i>m</i>) chi angles: 306.6	0.091Å	-	-
A 264	ASP	50	-	Favored (5.97%) General / -79.1,96.9	16.4% (<i>t</i> 0) chi angles: 176.2,43.3	0.136Å	-	OUTLIER(S) worst is CA-CB-CG: 5.489 σ
A 265	GLU	50	-	Favored (56.34%) General / -81.3,-15.2	6.5% (<i>mm</i> -40) chi angles: 290.7,283.7,228.8	0.083Å	-	-
A 266	CYS	50	-	Favored (64.52%)	71.4% (<i>m</i>)	0.141Å	-	-

				General / -51.9,-47.3	chi angles: 301.4			
A 267	ALA	50	-	Favored (13.79%) General / -102.7,-23.8	-	0.092Å	-	-
A 268	SER	99.99	-	Favored (53.47%) General / -80.3,-16.9	6.2% (t) chi angles: 197.9	0.199Å	-	-
A 269	GLN	99.99	-	Favored (2.55%) Pre-proline / -145.1,54.6	2.2% (mt-30) chi angles: 258,152,90.9	0.075Å	-	-
A 270	PRO	99.99	-	Favored (4.06%) Trans-proline / -78.8,77.5	4.3% (Cg_endo) chi angles: 41.4	0.039Å	-	-
A 271	CYS	99.99	-	Favored (53.35%) General / -65.3,147.5	31% (t) chi angles: 189.8	0.063Å	-	-
A 272	LEU	99.99	-	Allowed (0.2%) General / -135.5,-111.5	96.5% (mt) chi angles: 297.9,175.9	0.157Å	-	-
A 273	HIS	50	-	Allowed (1.52%) General / 75.4,23.3	16% (m170) chi angles: 280.6,130.7	0.135Å	-	-
A 274	GLY	50	-	Favored (28.11%) Glycine / 96.8,-25.1	-	-	-	-
A 275	GLY	50	-	Favored (52.95%) Glycine / -74.4,171.5	-	-	-	-
A 276	LEU	50	-	Favored (31.54%) General / -119.1,155.4	33.1% (tp) chi angles: 189,62.5	0.103Å	-	-
A 277	CYS	50	-	Favored (20.56%) General / -99.8,152.1	13.9% (t) chi angles: 193.7	0.053Å	-	-
A 278	VAL	50	-	Favored (9.78%) Isoleucine or valine / -147.6,156.6	5.9% (p) chi angles: 75.1	0.091Å	-	-
A 279	ASP	50	-	Allowed (0.1%) General / -82.6,-151.3	3.1% (t70) chi angles: 206,74.3	0.194Å	-	-

A 280	GLY	50	-	Allowed (0.48%) Glycine / 133.0,91.7	-	-	-	-	
A 281	GLU	50	-	Allowed (0.11%) General / -29.0,125.2	65.4% (<i>mm-40</i>) chi angles: 282.7,299,324.4	0.054Å	-	OUTLIER(S) worst is C-N-CA: 4.768 σ	
#	Alt	Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
			Avg: 62.68	Clashscore: 0.51	Outliers: 3 of 136	Poor rotamers: 4 of 120	Outliers: 1 of 124	Outliers: 0 of 138	Outliers: 15 of 138
A 282	ASN	50	-	Allowed (0.19%) General / 83.5,20.5	36.7% (<i>m-80</i>) chi angles: 304.7,275.7	0.125Å	-	-	
A 283	ARG	50	-	OUTLIER (0.02%) General / 172.6,-164.2	7.9% (<i>ptm-85</i>) chi angles: 59.1,175,302.1,294.4	0.08Å	-	-	
A 284	TYR	50	-	Favored (9.18%) General / -166.1,174.6	35.3% (<i>p90</i>) chi angles: 69,99.2	0.042Å	-	-	
A 285	SER	50	-	Favored (9.9%) General / -136.9,175.1	16.3% (<i>m</i>) chi angles: 283.3	0.063Å	-	-	
A 286	CYS	50	-	Favored (10.69%) General / -129.2,173.2	30.8% (<i>m</i>) chi angles: 310	0.065Å	-	-	
A 287	ASN	50	-	Favored (3.72%) General / -146.3,103.8	21% (<i>m-80</i>) chi angles: 307.1,270.7	0.122Å	-	-	
A 288	CYS	99.99	-	Favored (8.26%) General / -67.3,169.8	2.8% (<i>t</i>) chi angles: 207.1	0.038Å	-	-	
A 289	THR	99.99	-	Favored (12.97%) General / -116.8,3.1	14.7% (<i>t</i>) chi angles: 189.1	0.147Å	-	-	
A 290	GLY	99.99	-	Favored (30.24%) Glycine / -172.7,-165.8	-	-	-	-	
A 291	SER	99.99	-	Favored (47.8%) General / -94.7,-4.3	8.3% (<i>t</i>) chi angles: 194.7	0.073Å	-	-	
A				Favored (79.82%)					

292	GLY	50	-	Glycine / -74.1,-15.7	-	-	-	-
A 293	PHE	50	-	Favored (48.69%) General / -133.2,142.6	89.3% (<i>m-85</i>) chi angles: 300,283.2	0.028Å	-	-
A 294	THR	50	-	Allowed (1.04%) General / -139.1,-160.2	15.4% (<i>t</i>) chi angles: 187.5	0.215Å	-	-
A 295	GLY	50	-	Favored (54.17%) Glycine / 81.3,-177.5	-	-	-	-
A 296	THR	50	-	Favored (59.14%) General / -76.8,-10.1	5.4% (<i>t</i>) chi angles: 197	0.243Å	-	-
A 297	HIS	50	-	Favored (8.42%) General / -124.4,4.0	73.8% (<i>m80</i>) chi angles: 300.3,88.5	0.077Å	-	OUTLIER(S) worst is CA-CB- CG: 4.052 σ
A 298	CYS	50	-	Allowed (1.47%) General / 68.3,43.8	3.9% (<i>m</i>) chi angles: 320.2	0.138Å	-	-
A 299	GLU	50	-	Favored (6.4%) General / -104.9,-39.1	2% (<i>pt-20</i>) chi angles: 66.4,219.7,310.2	0.033Å	-	-
A 300	THR	50	-	Favored (40.18%) General / -77.1,140.1	12.7% (<i>m</i>) chi angles: 312.4	0.058Å	-	-
A 301	LEU	50	-	Favored (40.78%) General / -70.3,130.0	36.4% (<i>tp</i>) chi angles: 182.4,70.5	0.064Å	-	-
<div> <div>#</div> <div>Alt Res</div> <div>High B</div> <div>Clash > 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: 62.68</div> <div>Clashscore: 0.51</div> <div>Outliers: 3 of 136</div> <div>Poor rotamers: 4 of 120</div> <div>Outliers: 1 of 124</div> <div>Outliers: 0 of 138</div> <div>Outliers: 15 of 138</div> </div>								
A 302	MET	50	-	Favored (77.04%) Pre-proline / -81.7,125.9	13.2% (<i>tpt</i>) chi angles: 178.7,61,203.9	0.056Å	-	-
A 303	PRO	50	-	Allowed (0.6%) Trans-proline / -87.3,105.2	58.2% (<i>Cg_endo</i>) chi angles: 34.6	0.02Å	-	-

A 304	LEU	50	-	Favored (57.68%) General / -80.5,-15.0	2.5% (<i>mp</i>) chi angles: 298.3,106.3	0.149Å	-	-
A 305	CYS	50	-	Favored (11.48%) General / -88.6,13.7	75.7% (<i>m</i>) chi angles: 298.8	0.066Å	-	-
A 306	TRP	50	-	Favored (63.07%) General / -55.2,-33.5	39.9% (<i>t-105</i>) chi angles: 192.8,271.9	0.094Å	-	OUTLIER(S) worst is CE3- CD2-CG: 4.367 σ
A 307	SER	50	-	Favored (55.77%) General / -92.1,-3.4	89% (<i>p</i>) chi angles: 62.1	0.057Å	-	-
A 308	LYS	50	-	Favored (10.4%) Pre-proline / 54.7,60.2	23.9% (<i>tptp</i>) chi angles: 187,71.5,184.7,78.9	0.11Å	-	-
A 309	PRO	50	0.429Å O with A 311 HIS CE1	Favored (79.78%) Trans-proline / -62.5,-32.9	92.9% (<i>Cg_endo</i>) chi angles: 30.3	0.207Å	-	-
A 310	CYS	50	-	Favored (29.08%) General / -78.7,125.2	70.7% (<i>m</i>) chi angles: 297.5	0.112Å	-	-
A 311	HIS	50	0.429Å CE1 with A 309 PRO O	Favored (2.93%) General / -100.5,-175.5	28.5% (<i>m80</i>) chi angles: 312.3,94.4	0.053Å	-	-
A 312	ASN	50	-	Favored (7.12%) General / 55.2,55.8	2.7% (<i>m-20</i>) chi angles: 303.8,17.1	0.071Å	-	-
A 313	ASN	50	-	Allowed (0.13%) General / 81.0,-37.6	15.4% (<i>m-80</i>) chi angles: 315.4,289.9	0.148Å	-	-
A 314	ALA	50	-	Favored (3.48%) General / -48.1,144.9	-	0.091Å	-	-
A 315	THR	50	-	Favored (8.55%) General / -90.8,172.5	33.1% (<i>p</i>) chi angles: 69	0.116Å	-	-
A 316	CYS	50	-	Allowed (0.98%) General / -162.7,98.0	5.3% (<i>t</i>) chi angles: 201.7	0.061Å	-	-
A 317	GLU	50	-	Favored (50.3%) General / -105.0,133.1	2.5% (<i>mp0</i>) chi angles: 285.2,55.5,255.9	0.05Å	-	-

A 318	ASP	50	-	Favored (27.45%) General / -77.9,161.6	1.4% (<i>t0</i>) chi angles: 222.3,321.5	0.048Å	-	-	
A 319	SER	50	-	Favored (10.79%) General / -167.8,170.4	43% (<i>t</i>) chi angles: 178	0.055Å	-	-	
A 320	VAL	50	-	Favored (14.2%) Isoleucine or valine / -67.7,120.0	77% (<i>t</i>) chi angles: 172.3	0.047Å	-	-	
A 321	ASP	50	-	Allowed (0.08%) General / 84.0,-41.9	10.5% (<i>t70</i>) chi angles: 197.5,74.5	0.197Å	-	-	
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			Avg: 62.68	Clashscore: 0.51	Outliers: 3 of 136	Poor rotamers: 4 of 120	Outliers: 1 of 124	Outliers: 0 of 138	Outliers: 15 of 138
A 322	ASN	50	-	Favored (29.84%) General / -143.5,139.4	29.8% (<i>m-80</i>) chi angles: 281.9,268.3	0.087Å	-	-	
A 323	TYR	50	-	Favored (24.21%) General / -81.9,157.8	50.9% (<i>p90</i>) chi angles: 63.7,86.6	0.027Å	-	-	
A 324	THR	50	-	Favored (20.67%) General / -99.9,108.4	64.4% (<i>p</i>) chi angles: 64.7	0.038Å	-	-	
A 325	CYS	50	-	Favored (32.64%) General / -59.2,148.2	60.1% (<i>m</i>) chi angles: 304.4	0.105Å	-	-	
A 326	HIS	50	-	Favored (3.2%) General / -146.8,99.5	95.1% (<i>m-70</i>) chi angles: 297.7,297.5	0.047Å	-	-	
A 327	CYS	50	-	Allowed (0.16%) General / -46.0,156.2	27% (<i>m</i>) chi angles: 310.7	0.088Å	-	-	
A 328	TRP	50	-	Favored (8.93%) Pre-proline / -99.2,168.9	64.5% (<i>t-105</i>) chi angles: 190.9,257.7	0.114Å	-	OUTLIER(S) worst is CE3- CD2-CG: 4.505 σ	
				Allowed					

A 329	PRO	50	-	(0.11%) Trans-proline / -57.0,102.0	0.5% chi angles: 320.3	0.043Å	-	-
A 330	GLY	50	-	Allowed (0.22%) Glycine / 108.7,-76.5	-	-	-	-
A 331	TYR	50	-	Favored (3.78%) General / -59.7,116.1	52.6% (<i>m</i> -85) chi angles: 305,295.1	0.142Å	-	OUTLIER(S) worst is C-N-CA: 4.248 σ
A 332	THR	50	-	Allowed (0.42%) General / -149.2,-152.0	15% (<i>t</i>) chi angles: 188.3	0.216Å	-	-
A 333	GLY	50	-	Favored (10.31%) Glycine / 98.2,-130.7	-	-	-	-
A 334	ALA	50	-	Favored (8.12%) General / -98.2,-40.9	-	0.041Å	-	-
A 335	GLN	50	-	Favored (2.59%) General / -136.9,35.9	76.6% (<i>mt</i> -30) chi angles: 284.5,188,352.8	0.035Å	-	-
A 336	CYS	50	-	Favored (5.48%) General / 60.4,51.3	36.2% (<i>m</i>) chi angles: 308.3	0.209Å	-	-
A 337	GLU	50	-	Favored (5.04%) General / -116.7,-32.8	0% chi angles: 69.4,296.3,267.6	0.125Å	-	-
A 338	ILE	50	-	Favored (7.34%) Isoleucine or valine / -75.0,148.9	56.6% (<i>mt</i>) chi angles: 299.7,181.6	0.078Å	-	-
A 339	ASP	50	-	Favored (4.38%) General / -108.4,178.8	5.4% (<i>t0</i>) chi angles: 215.1,333.1	0.055Å	-	-
A 340	LEU	50	-	Allowed (1.74%) General / -103.0,79.3	5.1% (<i>tt</i>) chi angles: 198.3,170.7	0.059Å	-	-
A 341	ASN	50	-	Favored (4.19%) General / -75.8,98.5	26.1% (<i>m120</i>) chi angles: 306.3,105.5	0.027Å	-	OUTLIER(S) worst is C-N-CA: 4.286 σ

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A 342	GLU	50	-	Favored (67.06%) General / -57.8,-32.0	9.2% (<i>mp0</i>) chi angles: 307.2,89.9,318.6	0.148Å	-	-
A 343	CYS	50	-	Favored (60.66%) General / -55.3,-30.7	1.3% (<i>m</i>) chi angles: 265.8	0.152Å	-	-
A 344	ASN	50	-	Favored (71.82%) General / -59.8,-33.5	16.2% (<i>t-20</i>) chi angles: 187.8,245.8	0.082Å	-	-
A 345	SER	50	-	Favored (58.29%) General / -78.5,-15.7	52.5% (<i>p</i>) chi angles: 74.9	0.111Å	-	-
A 346	ASN	50	-	Allowed (1.2%) Pre-proline / 60.5,46.5	4.6% (<i>m-80</i>) chi angles: 290,250.6	0.097Å	-	-
A 347	PRO	50	-	Allowed (1.72%) Trans-proline / -81.3,44.3	0.2% chi angles: 44.6	0.061Å	-	-
A 348	CYS	50	-	Favored (17.5%) General / -137.2,121.1	39.6% (<i>m</i>) chi angles: 307.6	0.071Å	-	-
A 349	GLN	50	-	Favored (46.51%) General / -60.1,145.5	22.3% (<i>tt0</i>) chi angles: 182.8,179.2,247.8	0.031Å	-	-
A 350	SER	50	-	Favored (9.16%) General / 58.0,22.8	74.1% (<i>m</i>) chi angles: 294	0.123Å	-	-
A 351	ASN	50	-	Favored (23.46%) General / 59.2,38.2	13.6% (<i>m120</i>) chi angles: 307.1,138.4	0.097Å	-	-
A 352	GLY	50	-	Favored (15.33%) Glycine / -62.6,169.5	-	-	-	-
A 353	GLU	99.99	-	Favored (47.62%) General / -65.8,132.0	5.2% (<i>mm-40</i>) chi angles: 300.2,271,85.7	0.072Å	-	-
A 354	CYS	50	-	Favored (45.8%) General / -138.6,150.0	21.4% (<i>t</i>) chi angles: 191.3	0.146Å	-	-
				Favored 7.3% (<i>p</i>)				

A 355	VAL	99.99	-	(31.56%) Isoleucine or valine / -141.0,141.3	chi angles: 74	0.043Å	-	-	
A 356	GLU	99.99	-	Favored (38.76%) General / -75.0,151.3	1.4% (<i>pm0</i>) chi angles: 41.1,278.8,86.7	0.077Å	-	-	
A 357	LEU	99.99	-	Allowed (0.18%) General / -143.3,-82.2	89.3% (<i>mt</i>) chi angles: 294.7,178.7	0.1Å	-	-	
A 358	SER	50	-	OUTLIER (0.02%) General / -176.5,84.3	94.3% (<i>p</i>) chi angles: 64.9	0.077Å	-	-	
A 359	SER	50	-	Allowed (0.67%) General / 77.2,27.5	15.6% (<i>t</i>) chi angles: 189.9	0.167Å	-	OUTLIER(S) worst is C-N-CA: 5.048 σ	
A 360	GLU	50	-	OUTLIER (0.01%) General / 166.4,135.0	4.4% (<i>tp10</i>) chi angles: 175.4,59.1,124.7	0.087Å	-	-	
A 361	LYS	99.99	-	Favored (6.3%) General / -87.0,-178.6	15.2% (<i>pttp</i>) chi angles: 79.4,186.3,193.4,76.2	0.082Å	-	-	
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A 362	GLN	50	-	Allowed (0.22%) General / -134.1,-110.9	33% (<i>mm-40</i>) chi angles: 283.8,294.5,275.6	0.186Å	-	-	
A 363	TYR	99.99	-	Favored (44.08%) General / -136.3,143.3	5.3% (<i>t80</i>) chi angles: 164.5,100.4	0.105Å	-	-	
A 364	GLY	99.99	-	Favored (32.79%) Glycine / 169.9,-160.0	-	-	-	-	
A 365	ARG	99.99	-	Allowed (0.99%) General / -179.8,161.5	9.6% (<i>tpp180</i>) chi angles: 199.1,65.7,73.9,154.7	0.075Å	-	-	
				Favored (64.38%)					

A 366	ILE	99.99	-	Isoleucine or valine / -130.7,129.9	96.4% (<i>mt</i>) chi angles: 294.1,172	0.068Å	-	-
A 367	THR	99.99	-	Allowed (0.44%) General / -174.4,135.6	1.1% (<i>m</i>) chi angles: 270.9	0.07Å	-	-
A 368	GLY	99.99	-	Favored (38.79%) Glycine / 170.8,174.6	-	-	-	-
A 369	LEU	99.99	-	Favored (65.27%) Pre-proline / -102.2,115.0	24.6% (<i>mt</i>) chi angles: 313.4,179.1	0.057Å	-	-
A 370	PRO	99.99	-	Favored (40.22%) Trans-proline / -68.8,-15.0	82.7% (<i>Cg_exo</i>) chi angles: 328.7	0.058Å	-	-
A 371	SER	99.99	-	Favored (81.6%) General / -65.5,-35.7	34.5% (<i>p</i>) chi angles: 52.9	0.084Å	-	-
A 372	SER	99.99	-	Favored (11.04%) General / -116.9,-10.1	9.3% (<i>p</i>) chi angles: 45.8	0.066Å	-	-
A 373	PHE	99.99	-	Favored (10.37%) General / 63.6,37.5	98.7% (<i>m-85</i>) chi angles: 296.7,274	0.171Å	-	OUTLIER(S) worst is CA-CB- CG: 4.216 σ
A 374	SER	99.99	-	Favored (28.54%) General / -113.7,115.9	40.8% (<i>p</i>) chi angles: 53.8	0.059Å	-	-
A 375	TYR	99.99	-	Favored (4.92%) General / -127.2,-179.5	84.3% (<i>m-85</i>) chi angles: 300.2,266.3	0.086Å	-	-
A 376	HIS	99.99	-	Allowed (0.57%) General / -162.9,87.1	2.6% (<i>t-80</i>) chi angles: 157.5,274.7	0.032Å	-	OUTLIER(S) worst is CA-CB- CG: 5.516 σ
A 377	GLU	99.99	-	Favored (39.61%) General / -110.0,143.7	4.8% (<i>mp0</i>) chi angles: 290.1,57.4,66.9	0.051Å	-	-
A 378	ALA	99.99	-	Favored (23.1%) General / -155.3,147.0	-	0.068Å	-	-

A 379	SER	99.99	-	Favored (2.81%) General / -150.7,100.2	60.7% (<i>p</i>) chi angles: 56.2	0.064Å	-	-
A 380	GLY	99.99	-	Favored (13.59%) Glycine / -118.0,160.9	-	-	-	-
A 381	TYR	99.99	-	Favored (25.09%) General / -108.0,14.6	49.6% (<i>p90</i>) chi angles: 58.7,86.5	0.083Å	-	-
#	Alt Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
		Avg: 62.68	Clashscore: 0.51	Outliers: 3 of 136	Poor rotamers: 4 of 120	Outliers: 1 of 124	Outliers: 0 of 138	Outliers: 15 of 138
A 382	VAL	99.99	-	Favored (51.11%) Isoleucine or valine / -135.0,129.7	95.4% (<i>t</i>) chi angles: 178.2	0.064Å	-	-
A 383	CYS	50	-	Favored (13.81%) General / -63.4,121.5	80% (<i>m</i>) chi angles: 289.1	0.064Å	-	-
A 384	ILE	50	-	Favored (7.42%) Isoleucine or valine / -106.8,-18.1	63.9% (<i>mt</i>) chi angles: 304.8,169.7	0.107Å	-	-
A 385	CYS	50	-	Allowed (0.41%) General / 48.1,-143.7	99.5% (<i>m</i>) chi angles: 290.5	0.281Å	-	OUTLIER(S) worst is C-CA- CB: 4.883 σ
A 386	GLN	50	-	Favored (20.75%) Pre-proline / -148.6,164.6	18.8% (<i>pt20</i>) chi angles: 65.2,183.4,6.9	0.042Å	-	-
A 387	PRO	50	-	Favored (5.18%) Trans-proline / -83.6,130.3	89.8% (<i>Cg_endo</i>) chi angles: 31.9	0.038Å	-	OUTLIER(S) worst is C-N-CA: 5.142 σ
A 388	GLY	50	-	Favored (61.32%) Glycine / -99.4,13.7	-	-	-	-
A 389	PHE	50	-	Favored (7.49%) General / -88.5,88.0	57% (<i>m-85</i>) chi angles: 306.7,271.5	0.042Å	-	-
A 390	THR	50	-	Favored (6.6%) General / -82.2,-177.3	35.6% (<i>p</i>) chi angles: 52.5	0.095Å	-	OUTLIER(S) worst is C-N-CA: 4.973 σ
A				Favored (4.54%)				

391	GLY	50	-	Glycine / -121.5,-15.3	-	-	-	-
A 392	ILE	50	-	Allowed (0.94%) Isoleucine or valine / -125.6,-35.4	9.3% (<i>pt</i>) chi angles: 45,165.2	0.237Å	-	-
A 393	HIS	50	-	Favored (8.21%) General / -125.3,12.5	63.2% (<i>m80</i>) chi angles: 301.7,77.8	0.083Å	-	-
A 394	CYS	50	-	Favored (2.53%) General / 71.7,29.6	53.1% (<i>m</i>) chi angles: 306.7	0.136Å	-	-
A 395	GLU	50	-	Favored (21.65%) General / -85.5,-34.1	0.9% chi angles: 55.2,280.8,81.9	0.199Å	-	-
A 396	GLU	50	-	Favored (9.02%) General / -80.7,177.4	1.6% (<i>mp0</i>) chi angles: 321.5,93.4,73	0.098Å	-	-
A 397	ASP	50	-	Favored (22.18%) General / -155.9,146.8	46.4% (<i>t0</i>) chi angles: 192.1,12.9	0.04Å	-	OUTLIER(S) worst is C-N-CA: 4.202 σ
A 398	VAL	50	-	Allowed (0.31%) Isoleucine or valine / -143.6,-2.1	5.4% (<i>p</i>) chi angles: 75.8	0.125Å	-	-
A 399	ASN	99.99	-	-	7.6% (<i>m120</i>) chi angles: 305,158.9	0.061Å	-	OUTLIER(S) worst is CA-CB- CG: 7.477 σ

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