

## Viewing cnga3\_sm\_407-599Hmulti.table

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All-Atom	Clashscore, all atoms:	65.92		1 <sup>st</sup> percentile* (N=1784, all resolutions)
Contacts	Clashscore is the number	of serious s	steric over	laps (> 0.4 Å) per 1000 atoms.
	Poor rotamers	12	1.78%	Goal: <1%
	Ramachandran outliers	16	2.09%	Goal: <0.05%
	Ramachandran favored	652   85.34%		Goal: >98%
Protein Geometry	MolProbity score <sup>^</sup>	3.13		18 <sup>th</sup> percentile <sup>*</sup> (N=27675, 0Å - 99Å)
geometry	Cβ deviations >0.25Å	4	0.55%	Goal: 0
	Bad backbone bonds:	20 / 6252 0.32%		Goal: 0%
	Bad backbone angles:	92 / 8404	1.09%	Goal: <0.1%

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

<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:	Clashscore:	Outliers: 16 of	Poor rotamers: 12 of	Outliers:	Outliers: 12	Outliers: 64
			61.33	65.92	764	676	4 of 728	of 772	of 772
A 407		ASN	50	0.539Å OD1 with A 410 ARG HB2	-	55.3% ( <i>t-20</i> ) chi angles: 182.4,339	0.064Å	-	-
A 408		ALA	50	-	OUTLIER (0.02%) General / -169.4,-38.8	-	0.062Å	-	-
A 409		SER	50	0.678Å HB2 with A 449 LYS HD2	Favored (58.86%) General / -81.2,-6.5	80% ( <i>p</i> ) chi angles: 60	0.123Å	-	-
A 410		ARG	50	0.54Å HH21 with A 447 ASN CG	Favored (64.1%) General /	12.9% ( <i>mtp180</i> ) chi angles: 305.2,211.5,68.4,156.6	0.071Å	-	-

<sup>\* 100&</sup>lt;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.

				-71.8,-29.1				
A 411	ALA	50	-	Favored (63.75%) General / -73.4,-41.0	-	0.05Å	-	-
A 412	GLU	50	-	Favored (81.94%) General / -60.6,-37.6	11.8% ( <i>tm-20</i> ) chi angles: 179.8,287.2,328.8	0.068Å	-	-
A 413	PHE	50	0.448Å CD1 with A 445 TRP HE3	Favored (44.22%) General / -65.1,-53.5	88.9% ( <i>t80</i> ) chi angles: 178.5,82.1	0.035Å	-	-
A 414	GLN	50	0.561Å HA with A 417 ILE HG12	Favored (81.56%) General / -59.5,-38.8	15.6% ( <i>mt-30</i> ) chi angles: 282.6,140.6,20.4	0.016Å	-	-
A 415	ALA	50	-	Favored (80.73%) General / -68.5,-40.6	-	0.039Å	-	-
A 416	LYS	50	-	Favored (8.88%) General / -69.9,-55.8	13.8% ( <i>tppt?</i> ) chi angles: 177.9,49.7,62.1,192.2	0.03Å	-	-
A 417	ILE	50	0.737Å O with A 420 ILE HG12	Favored (33.54%) Isoleucine or valine / -58.1,-28.1	30% ( <i>pt</i> ) chi angles: 69.4,172.7	0.078Å	-	-
A 418	ASP	50	-	Favored (92.98%) General / -65.4,-41.9	44.5% ( <i>t0</i> ) chi angles: 186.9,329.5	0.038Å	-	-
A 419	SER	50	-	Favored (97.46%) General / -61.8,-44.1	40.1% (t) chi angles: 181.5	0.038Å	-	-
A 420	ILE	50	0.737Å HG12 with A 417 ILE O	Favored (65.2%) Isoleucine or valine / -58.7,-37.4	16.4% ( <i>pt</i> ) chi angles: 71.3,180.5	0.072Å	-	OUTLIER(S) worst is CB- CG1-CD1: 4.186 σ
A 421	LYS	50	0.648Å HG3 with A 417 ILE O	Favored (90.34%) General / -65.2,-38.4	30.7% ( <i>mtpp</i> ) chi angles: 294,181,68,63.9	0.047Å	-	-
				Favored				

A 422	GLN	50	-	(54.03%) General / -77.6,-33.0	19% ( <i>mt-30</i> ) chi angles: 298,166.1,183.6	0.087Å	-	-
A 423	TYR	50	0.446Å CE1 with C 453 GLU HG3	Favored (99.6%) General / -62.0,-42.9	71.9% ( <i>t80</i> ) chi angles: 172.6,84.8	0.05Å	-	-
A 424	MET	50	0.993Å SD with A 437 VAL HG11	Favored (70.48%) General / -71.4,-40.7	69.9% ( <i>mtm</i> ) chi angles: 293.7,191.9,299.6	0.05Å	-	-
A 425	GLN	50	-	Favored (79.46%) General / -67.7,-35.7	53.4% ( <i>tt0</i> ) chi angles: 185.3,179.2,57	0.012Å	-	-
A 426	РНЕ	50	-	Favored (79.94%) General / -64.8,-35.1	11% ( <i>t80</i> ) chi angles: 182.8,38.1	0.025Å	-	-
# /	Alt Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
		Avg: 61.33		Outliers: 16 of 764	Poor rotamers: 12 of 676	Outliers: 4 of 728	Outliers: 12 of 772	2 Outliers: 64 of 772
		01.55		7 0 1	0, 0	1 01 / 20		01 / / 2
A 427		99.99	0.989Å	Favored (57.36%) General / -92.0,-1.2	32.8% ( <i>mmt180</i> ) chi angles: 287.3,304.8,183.2,180	0.21Å	-	OUTLIER(S) worst is N-CA- CB: 4.945 σ
			0.989Å HB3 with C	Favored (57.36%) General /	32.8% ( <i>mmt180</i> ) chi angles:		-	OUTLIER(S) worst is N-CA-
427 A	ARG	99.99	0.989Å HB3 with C	Favored (57.36%) General / -92.0,-1.2 Favored (28.26%) General /	32.8% ( <i>mmt180</i> ) chi angles: 287.3,304.8,183.2,180 88.4% ( <i>mttt</i> ) chi angles:	0.21Å	-	OUTLIER(S) worst is N-CA-
427 A 428 A	ARG LYS	99.99 50	0.989Å HB3 with C 473 HIS HE1  -  0.942Å HG21 with A 433 LEU	Favored (57.36%) General / -92.0,-1.2 Favored (28.26%) General / 54.1,38.0 Favored (5.58%) Isoleucine or valine /	32.8% ( <i>mmt180</i> ) chi angles: 287.3,304.8,183.2,180 88.4% ( <i>mttt</i> ) chi angles: 298.3,170.7,185,166.6	0.21Å 0.051Å	-	OUTLIER(S) worst is N-CA-
A 428 A 429	ARG LYS VAL	99.99 50 50	0.989Å HB3 with C 473 HIS HE1  -  0.942Å HG21 with A 433 LEU HD22  0.448Å HG22 with A	Favored (57.36%) General / -92.0,-1.2 Favored (28.26%) General / 54.1,38.0 Favored (5.58%) Isoleucine or valine / -61.0,152.8 Favored (7.51%) General / -57.2,156.3 Favored (82.42%)	32.8% ( <i>mmt180</i> ) chi angles: 287.3,304.8,183.2,180  88.4% ( <i>mttt</i> ) chi angles: 298.3,170.7,185,166.6  12.1% ( <i>p</i> ) chi angles: 62.1	0.21Å 0.051Å 0.168Å	- -	OUTLIER(S) worst is N-CA-

		THR HG22	-65.3,-35.3				
A 433	LEU 50	0.942Å HD22 with A 429 VAL HG21	Favored (63.85%) General / -73.5,-40.7	8.5% (tt) chi angles: 191.4,155.1	0.12Å	-	-
A 434	GLU 50	0.791Å O with A 437 VAL HG12	Favored (93.67%) General / -63.9,-39.2	54.6% ( <i>mt-10</i> ) chi angles: 296.7,182.7,298.2	0.075Å	-	-
A 435	THR 50	0.444Å HG23 with A 431 LYS O	Favored (68.27%) General / -66.1,-49.3	77.9% (p) chi angles: 60.2	0.02Å	-	-
A 436	ARG 50	-	Favored (72.82%) General / -58.2,-36.2	86.8% ( <i>mtm-85</i> ) chi angles: 285.7,187.7,294.2,260.3	0.068Å	-	-
A 437	VAL 50	0.993Å HG11 with A 424 MET SD	Favored (68.54%) Isoleucine or valine / -72.0,-41.3	4.9% (p) chi angles: 76.4	0.175Å	-	-
A 438	ILE 50	0.781Å HG12 with A 434 GLU O	Favored (28.75%) Isoleucine or valine / -58.1,-54.7	41.1% ( <i>mm</i> ) chi angles: 299.1,304.7	0.028Å	-	-
A 439	ARG 50	0.448Å O with A 443 TYR HD2	Favored (77.74%) General / -60.0,-36.6	55.1% (mmm-85) chi angles: 293.6,298,293,278.7	0.033Å	-	-
A 440	TRP 99.99	0.829Å 9 CH2 with A 444 LEU HD22	Favored (42.13%) General / -62.5,-54.3	89.3% ( <i>t</i> 90) chi angles: 184.8,87.4	0.024Å	OUTLIER(S) worst is NE1 CE2: 4.896 σ	OUTLIER(S) worst is CZ2- CH2-CZ3: 5.444 σ
A 441	PHE 50	0.791Å HE2 with A 437 VAL HG22	Favored (61.53%) General / -51.0,-46.1	95.2% ( <i>m-85</i> ) chi angles: 292.2,275.1	0.075Å	-	-
A 442	ASP 50	0.4Å HB2 with A 439 ARG O	Favored (67.79%) General / -53.0,-45.5	51.3% ( <i>m-20</i> ) chi angles: 295.5,296.5	0.044Å	-	-
A 443	TYR 50	0.539Å CD2 with A 573 TYR CE1	Favored (60.59%) General / -75.2,-30.6	95.2% ( <i>m-85</i> ) chi angles: 292.2,274.8	0.027Å	-	-

A 444		LEU	99.99	0.829A HD22 with A 440 TRP CH2	Favored (22.95%) General / -84.8,-33.5	21.3% ( <i>tp</i> ) chi angles: 187.1,74	0.098Å	-	-
A 445	,	TRP	50	0.453Å NE1 with A 444 LEU HD23	Favored (8.95%) General / -119.4,-16.7	51.6% ( <i>m0</i> ) chi angles: 296.7,351.6	0.079Å	OUTLIER(S) worst is NE1 CE2: 4.813 σ	OUTLIER(S) worst is CD2- CE3-CZ3: 4.178 σ
A 446	,	ALA	50	-	Allowed (0.65%) General / 51.6,18.1	-	0.046Å	-	-
#	Alt	Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
			Avg: 61.33	Clashscore: 65.92	Outliers: 16 of 764	Poor rotamers: 12 of 676	Outliers: 4 of 728	Outliers: 12 of 772	Outliers: 64 of 772
A 447	,	ASN	99.99	0.54Å CG with A 410 ARG HH21	Favored (10.13%) General / 56.4,25.9	64.3% ( <i>t</i> -20) chi angles: 184.8,348.6	0.098Å	-	OUTLIER(S) worst is OD1- CG-ND2: 5.744 $\sigma$
A 448		LYS	99.99	-	Allowed (0.73%) General / -106.2,-72.1	29.5% ( <i>tptp</i> ) chi angles: 182.4,64.6,177.9,64.7	0.064Å	-	-
A 449		LYS	99.99	0.678Å HD2 with A 409 SER HB2	Favored (49.15%) General / -125.2,147.2	27.9% ( <i>tptp</i> ) chi angles: 180.1,66.8,182.2,61.8	0.079Å	-	OUTLIER(S) worst is CG- CD-CE: 4.395 σ
A 450	-	THR	99.99	0.721Å HG22 with A 451 VAL H	Allowed (0.82%) General / -119.5,-160.6	48.8% ( <i>m</i> ) chi angles: 305	0.108Å	-	-
A 451	,	VAL	99.99	1.05Å HG22 with A 452 ASP HA	Allowed (0.43%) Isoleucine or valine / -48.1,151.1	6% (p) chi angles: 75	0.168Å	-	-
A 452		ASP	50	1.05Å HA with A 451 VAL HG22	Allowed (1%) General / -104.9,44.8	2.2% ( <i>m-20</i> ) chi angles: 294.9,33.2	0.139Å	-	-
A 453	(	GLU	50	0.823Å HA with A 456 VAL HG22	Allowed (0.61%) General / -40.4,-36.9	27.2% (tt0) chi angles: 193.5,193.3,40.1	0.049Å	-	-
A 454		LYS	50	-	Favored (79.07%) General /	39% (ttpt) chi angles: 186.5,180,64.3,181.3	0.042Å	-	-

				-63.4,-48.1				
A 455	GLU	50	0.766Å HB3 with A 452 ASP HB3	Favored (76.52%) General / -65.6,-47.2	10.8% ( <i>tm-20</i> ) chi angles: 181.5,289.9,325.1	0.055Å	-	-
A 456	VAL	50	0.823Å HG22 with A 453 GLU HA	Favored (84.79%) Isoleucine or valine / -58.1,-43.2	23.1% ( <i>m</i> ) chi angles: 302.6	0.057Å	-	-
A 457	LEU	50	0.485Å HB2 with A 453 GLU O	Favored (84.41%) General / -67.7,-40.6	0.6% chi angles: 254.3,39.5	0.031Å	-	-
A 458	LYS	50	-	Favored (91.56%) General / -61.5,-39.6	28.6% ( <i>tptp</i> ) chi angles: 184.7,62.4,180.5,64.5	0.039Å	-	-
A 459	SER	50	0.646Å O with D 440 TRP CH2	Favored (81.83%) General / -64.3,-35.7	68.7% ( <i>m</i> ) chi angles: 296.1	0.096Å	-	OUTLIER(S) worst is CA-C- O: 5.259 σ
A 460	LEU	50	-	Favored (39.39%) Pre-proline / -70.6,166.1	80.5% ( <i>mt</i> ) chi angles: 298.8,182.5	0.042Å	-	-
A 461	PRO	50	0.782Å HD3 with D 440 TRP CE2	Favored (6.38%) Trans-proline / -87.5,171.2	42.7% ( <i>Cg_endo</i> ) chi angles: 36	0.014Å	-	-
A 462	ASP	50	-	Favored (96.91%) General / -63.9,-43.1	42.1% ( <i>t0</i> ) chi angles: 190.5,329.5	0.015Å	-	-
A 463	LYS	50	0.667Å HE2 with D 508 TYR H	Favored (73.89%) General / -57.9,-37.4	32.4% ( <i>mmmt</i> ) chi angles: 294.8,293.5,296.6,184.8	0.04Å	-	-
A 464	LEU	50	0.654Å HD12 with A 461 PRO HD2	Favored (22.9%) General / -75.5,-48.4	59.3% ( <i>mt</i> ) chi angles: 286.4,177.4	0.038Å	-	-
A 465	LYS	50	0.581Å O with A 470 ILE HG12	Favored (72.81%) General / -61.0,-33.1	54.9% ( <i>mtmt</i> ) chi angles: 294.7,178.6,295.9,178.8	0.136Å	-	-
A		F0	0.722Å	Favored (83.81%)		04408		

466 ALA 50 FIA WILLI A GENERAL / - U.119A - 470 ILE CB -66.6,-36.9

#	Alt Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
		Avg: 61.33	Clashscore: 65.92	Outliers: 16 of 764	Poor rotamers: 12 of 676	Outliers: 4 of 728	Outliers: 12 of 772	Outliers: 64 of 772
A 467	<sub>7</sub> GLU	J 50	0.589Å OE2 with D 433 LEU HD12	Favored (79.53%) General / -68.8,-40.5	15.5% (tt0) chi angles: 206.1,191.3,309.1	0.116Å	-	-
A 468	3 ILE	99.99	0.871Å HA with A 472 VAL HG12	Favored (24.37%) Isoleucine or valine / -119.2,146.1	17.8% ( <i>pt</i> ) chi angles: 51.7,179.6	0.185Å	-	-
A 469	AL/	A 99.99	0.914Å H with A 473 HIS HD2	Allowed (1.8%) General / 66.3,0.8	-	0.078Å	-	-
A 470	) ILE	99.99	0.978Å HD12 with A 496 LEU HA	Allowed (0.75%) Isoleucine or valine / -132.4,-25.7	27.1% ( <i>mm</i> ) chi angles: 299,310.2	0.091Å	-	-
A 471	ASN	N 50	1.003Å HD21 with A 492 VAL HG12	Allowed (0.47%) General / -140.4,-51.1	42.2% ( <i>m-20</i> ) chi angles: 278.7,302.3	0.195Å	-	OUTLIER(S) worst is CA- CB-CG: 4.049 σ
A 472	2 VAI	L 50	0.871Å HG12 with A 468 ILE HA	Favored (82.17%) Isoleucine or valine / -58.6,-41.5	15% (p) chi angles: 63.5	0.065Å	-	-
A 473	3 HIS	5 50	1.002Å HE1 with D 427 ARG HB3	Favored (61.3%) General / -72.7,-25.5	84.1% ( <i>m-70</i> ) chi angles: 288,298.1	0.04Å	OUTLIER(S) worst is CD2 NE2: 7.05 σ	OUTLIER(S) worst is CD2- NE2-CE1: 12.768 σ
A 474	LEU	J 99.99	0.694Å C with A 474 LEU HD23	Favored (38.13%) General / -53.1,132.5	7.2% (tt) chi angles: 184.9,162.9	0.126Å	-	-
A 475	S ASI	99.99	0.527Å N with A 474 LEU HD23	Favored (5.85%) General / -129.7,12.7	29.9% ( <i>t70</i> ) chi angles: 179.1,76.5	0.069Å	-	-
A		R 99.99	0.473Å HB with A	Favored (2.21%)	10.3% (t)	0.074Å	-	-

4/6		J2J MJN HM	-136.0,48.0	CIII aligies. 104.2			
A 477 LE	∪ 99.99	1.1Å HG with A 483 PHE HB3	Allowed (0.81%) General / -134.6,-52.3	10% (tt) chi angles: 185.3,154.6	0.239Å	-	-
A 478 LY	S 50	-	Favored (31.44%) General / -53.1,-29.6	27.1% ( <i>tptp</i> ) chi angles: 180.3,61.9,184.6,69.5	0.035Å	-	-
A 479 LY	S 50	-	Favored (49.45%) General / -89.1,-9.9	26.8% ( <i>tptp</i> ) chi angles: 188.6,61.2,182.7,67.3	0.051Å	-	-
A 480 VA	L 50	1.093Å HG12 with A 477 LEU HA	Favored (23.98%) Isoleucine or valine / -117.0,108.1	11.5% ( <i>p</i> ) chi angles: 66.5	0.141Å	-	-
A 481 AR	G 50	0.715Å HA with A 484 GLN HG2	Favored (7.28%) General / -43.5,-47.1	57.9% (mmm-85) chi angles: 296.1,292.8,296.7,277.2	0.027Å	-	-
A 482 ILI	E 50	0.744Å HG12 with A 480 VAL HG22	Favored (87.84%) Isoleucine or valine / -59.3,-42.6	42.2% ( <i>pt</i> ) chi angles: 65.5,172.5	0.067Å	-	-
A 483 PH	E 50	1.1Å HB3 with A 477 LEU HG	Favored (28.76%) General / -79.7,-40.6	7.1% ( <i>m-30</i> ) chi angles: 278.5,9.7	0.047Å	-	OUTLIER(S) worst is CA- CB-CG: 4.414 σ
A 484 GL	N 50	0.715Å HG2 with A 481 ARG HA	Favored (83.93%) General / -67.8,-38.8	19.8% ( <i>pt20</i> ) chi angles: 65.9,181.7,61.9	0.076Å	-	-
A 485 AS	P 50	-	Favored (4.67%) General / -97.0,26.4	48.7% ( <i>t0</i> ) chi angles: 190.7,338.3	0.039Å	-	-
A 486 CY	'S 99.99	0.624Å SG with A 490 LEU HD23	Favored (27.27%) General / -115.1,155.3	52.7% ( <i>t</i> ) chi angles: 181.3	0.052Å	-	-
# Alt Re	B	Clash > 0.4Å Clashscore:	Ramachandran Outliers: 16 of	<b>Rotamer</b> Poor rotamers: 12 of	<b>C</b> β <b>deviation</b> Outliers: 0	<b>Bond lengths</b> Outliers: 12	Bond angles 2 Outliers: 64

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A 487	GLU 99.99	) -	Favored (8.68%) General / -57.2,120.8	87.8% ( <i>mt-10</i> ) chi angles: 301.3,182.2,337.1	0.064Å	-	-
A 488	ALA 50	0.728Å O with A 492 VAL HG13	Favored (14.29%) General / -54.9,-22.3	-	0.016Å	-	-
A 489	GLY 50	0.497Å O with A 492 VAL HG22	Favored (76.39%) Glycine / -67.5,-45.6	-	-	-	-
A 490	LEU 99.99	0.748Å HD13 with A 591 TYR CD1	Favored (93.9%) General / -65.5,-41.0	35.4% ( <i>tp</i> ) chi angles: 175.6,54.2	0.063Å	-	-
A 491	LEU 99.99	0.838Å HD13 with A 477 LEU HD11	Favored (5.02%) General / -57.2,-59.5	94.3% ( <i>mt</i> ) chi angles: 298.4,175.6	0.075Å	-	-
A 492	VAL 50	1.003Å HG12 with A 471 ASN HD21	Favored (14.91%) Isoleucine or valine / -48.6,-45.5	25.8% ( <i>m</i> ) chi angles: 302	0.023Å	-	-
A 493	GLU 50	-	Favored (68.49%) General / -66.1,-28.0	14.3% ( <i>tm-20</i> ) chi angles: 183.8,285.3,333.8	0.107Å	-	-
A 494	LEU 50	0.701Å HD23 with A 483 PHE CE1	Favored (12.94%) General / -80.0,-48.7	33.9% ( <i>tp</i> ) chi angles: 187.7,59.4	0.033Å	-	OUTLIER(S) worst is CD1- CG-CD2: 4.562 σ
A 495	VAL 50	0.758Å HG21 with A 470 ILE O	Favored (44.55%) Isoleucine or valine / -57.7,-33.2	20.8% ( <i>m</i> ) chi angles: 303.3	0.021Å	-	-
A 496	LEU 50	0.978Å HA with A 470 ILE HD12	Favored (55.61%) General / -64.8,-13.4	8.9% ( <i>tt</i> ) chi angles: 190.5,154.5	0.155Å	-	-
A 497	LYS 50	-	Favored (10.85%) General / -115.9,-18.0	64.5% ( <i>mttp</i> ) chi angles: 295.5,177.2,177.3,63.2	0.054Å	-	-
٨	IFII FO	0 610 Å	Favored	EQ 10/ (mt)	0.006 %		

^ 498	LEU	ΣU	U.U43A HB3 with A 577 PHE HB3	(44.49 /0) General / -58.6,144.1	30.4 /o (IIII.) chi angles: 305.2,173.5	U.UYOA	-	-
A 499	ARG	50	-	Favored (28.15%) Pre-proline / -118.9,124.7	40.1% ( <i>ptt180</i> ) chi angles: 62,179.4,181.4,181.7	0.069Å	-	-
A 500	PRO	50	-	Favored (33.33%) Trans-proline / -68.0,134.9	92.8% ( <i>Cg_endo</i> ) chi angles: 30.9	0.035Å	-	-
A 501	THR	50	-	Favored (30.25%) General / -144.9,142.9	63.4% (p) chi angles: 62.2	0.038Å	-	-
A 502	VAL	50	-	Favored (36.42%) Isoleucine or valine / -115.5,140.6	74% ( <i>t</i> ) chi angles: 174	0.052Å	-	-
A 503	PHE	50	-	Favored (50.81%) General / -127.0,145.2	63.9% ( <i>m-85</i> ) chi angles: 284.3,87.2	0.046Å	-	-
A 504	SER	50	-	Favored (31.54%) Pre-proline / -101.6,158.6	70.2% ( <i>m</i> ) chi angles: 295.9	0.029Å	-	-
A 505	PRO	50	-	Favored (52.29%) Trans-proline / -53.9,132.9	87.8% ( <i>Cg_exo</i> ) chi angles: 331.3	0.109Å	-	-
A 506	GLY		-	Favored (9.88%) Glycine / 100.2,-30.6	-	-	-	-
# /	Alt Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
		Avg: 61.33		Outliers: 16 of 764	Poor rotamers: 12 of 676	Outliers: 0 4 of 728	Outliers: 12 of 772	Outliers: 64 of 772
A 507	ASP	50	0.454Å HA with C 463 LYS HE2	Allowed (0.56%) General / -49.0,155.9	81.1% ( <i>m-20</i> ) chi angles: 283.3,337.3	0.05Å	-	-
A 508	TYR	50	0.673Å H with C 463 LYS HE2	Favored (5.14%) General /	11.4% ( <i>m-30</i> ) chi angles: 282.8,356.5	0.101Å	-	-
				-100 1 74 0				

A 509	ILE	50	0.788Å HB with A 568 ILE HG23	Favored (99.01%) Isoleucine or valine / -60.9,-45.0	69% ( <i>mt</i> ) chi angles: 303.1,168.1	0.091Å	-	-
A 510	CYS	99.99	1.027Å HB3 with A 568 ILE HG22	Favored (28.07%) General / -144.3,138.6	4.8% (t) chi angles: 164.3	0.071Å	-	-
A 511	LYS	50	0.454Å NZ with A 508 TYR HD2	Favored (37.7%) General / -108.1,142.8	68.4% ( <i>mttm</i> ) chi angles: 292.6,179.7,178.2,293.8	0.066Å	-	-
A 512	LYS	50	-	Favored (31.24%) General / -61.9,152.7	38.6% (ttpt) chi angles: 184.7,182,62.4,181.3	0.071Å	-	-
A 513	GLY	50	0.447Å O with A 563 ARG HD2	Favored (4.44%) Glycine / 78.9,-20.6	-	-	-	-
A 514	ASP	50	0.477Å O with A 564 ARG HG2	Favored (43.53%) General / -74.6,139.2	42.5% ( <i>t0</i> ) chi angles: 189,328.5	0.062Å	-	-
A 515	ILE	50	-	Favored (12.76%) Isoleucine or valine / -63.5,121.6	27.2% ( <i>mt</i> ) chi angles: 311.5,178.4	0.032Å	-	-
A 516	GLY	50	-	Favored (10.08%) Glycine / -98.5,130.0	-	-	-	-
A 517	LYS	50	0.53Å HG2 with A 517 LYS O	Favored (9.22%) General / -124.0,19.7	61.9% (tttm) chi angles: 185.6,184.4,177.4,293.2	0.063Å	-	-
A 518	GLU	50	-	Favored (7.59%) General / -169.3,157.6	12.6% ( <i>pt-20</i> ) chi angles: 61.5,180.2,62.4	0.013Å	-	-
A 519	MET	50	-	Favored (8.78%) General / -124.8,173.1 Favored	27.1% (ptm) chi angles: 65.3,172.3,293.2	0.032Å	-	-
Δ	TVD	F0		(52 46%)	90 7% (m-85)	0 071 Å		

520	IIK	<b>5</b> U	-	General / -130.9,149.6	chi angles: 299.1,87.1	U.U/ I <i>A</i>	-	-
A 521	ILE	50	0.645Å HG12 with A 577 PHE HB2	Favored (15.09%) Isoleucine or valine / -121.0,104.3	32% ( <i>pt</i> ) chi angles: 66.9,166.7	0.058Å	-	-
A 522	ILE	50	-	Allowed (0.15%) Isoleucine or valine / -58.2,105.0	62.3% ( <i>mt</i> ) chi angles: 304.9,175.2	0.02Å	-	-
A 523	ASN	50	0.477Å HB3 with A 575 ASP O	Favored (20.01%) General / -76.9,-47.8	48.4% ( <i>t30</i> ) chi angles: 182.1,60.4	0.01Å	-	-
A 524	GLU	50	-	Favored (6.4%) General / -157.0,127.2	11.3% ( <i>tm-20</i> ) chi angles: 179.9,288.4,328.6	0.08Å	-	-
A 525	GLY	50	-	Favored (13.05%) Glycine / 132.8,172.6	-	-	-	-
			0.075 Å	Favored				
A 526	LYS	99.99	0.975Å HG3 with A 540 VAL HG13	(51.03%) General / -122.2,128.3	66.7% (tttt) chi angles: 165.7,169.7,180.8,162.5	0.107Å	-	-
526	LYS Alt Res	99.99 High B	HG3 with A 540 VAL	(51.03%) General /	chi angles:		Bond lengths	- Bond angles
526		High B Avg:	HG3 with A 540 VAL HG13 Clash > 0.4Å	(51.03%) General / -122.2,128.3 Ramachandran	chi angles: 165.7,169.7,180.8,162.5	Cβ deviation	lengths	angles
526		High B	HG3 with A 540 VAL HG13 Clash > 0.4Å Clashscore:	(51.03%) General / -122.2,128.3  Ramachandran Outliers: 16 of	chi angles: 165.7,169.7,180.8,162.5 <b>Rotamer</b> Poor rotamers: 12 of	Cβ deviation Outliers:	<b>lengths</b> Outliers: 12	angles 2 Outliers: 64
526 # A	Alt Res	High B Avg: 61.33	HG3 with A 540 VAL HG13 Clash > 0.4Å Clashscore: 65.92 0.877Å HB3 with A 568 ILE	(51.03%)     General / -122.2,128.3  Ramachandran  Outliers: 16 of     764     Favored     (29.48%)     General /	chi angles: 165.7,169.7,180.8,162.5 <b>Rotamer</b> Poor rotamers: 12 of 676  9.5% (mp)	Cβ deviation Outliers: 4 of 728	<b>lengths</b> Outliers: 12	angles 2 Outliers: 64 of 772 OUTLIER(S) worst is CD1- CG-CD2:
526 # A 527	<b>Alt Res</b> LEU	High B Avg: 61.33	HG3 with A 540 VAL HG13  Clash > 0.4Å  Clashscore: 65.92 0.877Å HB3 with A 568 ILE HD11 0.511Å O with A 568	(51.03%) General / -122.2,128.3  Ramachandran  Outliers: 16 of 764  Favored (29.48%) General / -119.4,156.8  Favored (54.91%) General / -118.4,128.8  Favored (70.26%) Isoleucine or valine / -113.0,127.5	chi angles: 165.7,169.7,180.8,162.5 <b>Rotamer</b> Poor rotamers: 12 of 676  9.5% (mp)	Cβ deviation Outliers: 4 of 728 0.069Å	<b>lengths</b> Outliers: 12	angles 2 Outliers: 64 of 772 OUTLIER(S) worst is CD1- CG-CD2:
526 # A 527 A 528	Alt Res LEU ALA	High B Avg: 61.33 50	HG3 with A 540 VAL HG13  Clash > 0.4Å  Clashscore: 65.92 0.877Å HB3 with A 568 ILE HD11 0.511Å O with A 568 ILE HD12  0.682Å HG22 with A 568 ILE	(51.03%) General / -122.2,128.3  Ramachandran  Outliers: 16 of 764  Favored (29.48%) General / -119.4,156.8  Favored (54.91%) General / -118.4,128.8  Favored (70.26%) Isoleucine or valine /	chi angles: 165.7,169.7,180.8,162.5 <b>Rotamer</b> Poor rotamers: 12 of 676  9.5% ( <i>mp</i> ) chi angles: 281.9,69.5	Cβ deviation Outliers: 4 of 728 0.069Å	<b>lengths</b> Outliers: 12	angles 2 Outliers: 64 of 772 OUTLIER(S) worst is CD1- CG-CD2:

550	VAL JU		valine / -130.1,97.0	U	0.101/1		
A 531	ALA 99.99	0.872Å HB2 with A 566 ALA HB2	Allowed (1.95%) General / -130.4,80.3	-	0.137Å	-	-
A 532	ASP 99.99	-	Favored (11.65%) General / 53.0,31.7	29.4% ( <i>t70</i> ) chi angles: 178.9,77	0.068Å	-	-
A 533	ASP 99.99	-	Favored (31.44%) General / -160.3,165.4	26.1% ( <i>p30</i> ) chi angles: 61.8,29.5	0.02Å	-	-
A 534	GLY 99.99	-	Allowed (0.82%) Glycine / -61.8,105.1	-	-	-	-
A 535	VAL 50	0.608Å HG22 with A 536 THR HG22	OUTLIER (0%) Isoleucine or valine / -10.6,108.9	7.1% (p) chi angles: 58.4	0.01Å	-	-
A 536	THR 99.99	0.608Å HG22 with A 535 VAL HG22	Allowed (1.5%) General / 55.6,15.4	9.9% ( <i>t</i> ) chi angles: 184	0.055Å	-	-
A 537	GLN 99.99	0.534Å HG2 with A 536 THR O	Favored (14.51%) General / 47.9,51.3	18.5% ( <i>pt20</i> ) chi angles: 64.8,180.9,57	0.097Å	-	-
A 538	PHE 99.99	0.475Å CD2 with A 538 PHE O	Favored (14.34%) General / 63.5,32.4	85.3% ( <i>t80</i> ) chi angles: 180.7,81.9	0.055Å	-	-
A 539	VAL 99.99	0.785Å HG12 with A 540 VAL H	Allowed (0.48%) Isoleucine or valine / -119.6,-168.6	63.1% ( <i>t</i> ) chi angles: 180	0.087Å	-	OUTLIER(S) worst is CA- CB-CG1: 4.474 σ
A 540	VAL 99.99	0.975Å HG13 with A 526 LYS HG3	OUTLIER (0.06%) Isoleucine or valine / -158.5,97.4	26.7% (t) chi angles: 164.6	0.381Å	-	OUTLIER(S) worst is N-CA- CB: 5.587 σ
A 541	LEU 50	-	Allowed (1.63%) General /	18.6% ( <i>mt</i> ) chi angles: 292,193.2	0.076Å	-	-
			-59.4,112.1				

A 542	SER	50	-	Allowed (1.05%) General / -124.4,-162.1	20.8% ( <i>t</i> ) chi angles: 188.4	0.068Å	-	-
A 543	ASP	50	-	Favored (20.24%) General / -50.1,135.9	0.3% chi angles: 313.8,44.5	0.116Å	-	-
A 544	GLY	50	-	Favored (73.87%) Glycine / 79.3,18.6	-	-	-	-
A 545	SER	50	-	Favored (28.28%) General / -124.4,160.4	72.6% ( <i>m</i> ) chi angles: 295.6	0.026Å	-	-
A 546	TYR	50	0.615Å CE1 with A 482 ILE HD13	Favored (7.79%) General / -134.8,177.4	45.9% ( <i>p90</i> ) chi angles: 59,275.2	0.048Å	-	-
# A	Alt Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
		Avg: 61.33	Clashscore: 65.92	Outliers: 16 of 764	Poor rotamers: 12 of 676	Outliers: 0 4 of 728	Outliers: 12 of 772	Outliers: 64 of 772
		01.55	05.52	/ U <del>1</del>	07 0	7 01 / 20	01 / / 2	01 / / 2
A 547	PHE	50	0.519Å CE2 with A 527 LEU HD22	Favored (4.1%) General / -173.7,162.6	43.6% ( <i>p</i> 90) chi angles: 60.5,83.6	0.022Å	-	-
	PHE GLY		0.519Å CE2 with A 527 LEU	Favored (4.1%) General /	43.6% ( <i>p90</i> )		-	-
547 A		50 50	0.519Å CE2 with A 527 LEU	Favored (4.1%) General / -173.7,162.6 Favored (62.81%) Glycine /	43.6% ( <i>p90</i> )		-	-
547 A 548	GLY	50 50	0.519Å CE2 with A 527 LEU	Favored (4.1%)     General /     -173.7,162.6  Favored     (62.81%)     Glycine /     75.1,28.1  Favored     (29.19%)     General /	43.6% ( <i>p90</i> ) chi angles: 60.5,83.6  -  6.4% ( <i>pm0</i> ) chi angles:	0.022Å -	-	-
547 A 548 A 549	GLY	50 50 50	0.519Å CE2 with A 527 LEU	Favored (4.1%)     General /     -173.7,162.6      Favored     (62.81%)     Glycine /     75.1,28.1     Favored     (29.19%)     General /     -86.9,-19.2     Favored     (97.65%)     Isoleucine or     valine /     -62.3,-43.1     Favored     (66.23%)     General /     -68.4,-27.5	43.6% ( <i>p90</i> ) chi angles: 60.5,83.6  -  6.4% ( <i>pm0</i> ) chi angles: 70.4,293.3,339.2	0.022Å - 0.053Å	- - -	-
547  A 548  A 549  A 550	GLY GLU ILE SER	<ul><li>50</li><li>50</li><li>50</li><li>50</li></ul>	0.519Å CE2 with A 527 LEU	Favored (4.1%) General / -173.7,162.6  Favored (62.81%) Glycine / 75.1,28.1  Favored (29.19%) General / -86.9,-19.2  Favored (97.65%) Isoleucine or valine / -62.3,-43.1  Favored (66.23%) General / -68.4,-27.5  Favored	43.6% ( <i>p</i> 90) chi angles: 60.5,83.6  -  6.4% ( <i>pm0</i> ) chi angles: 70.4,293.3,339.2  76.9% ( <i>mt</i> ) chi angles: 298.8,177	0.022Å - 0.053Å 0.063Å	-	-

552	122 33,33	584 LEU HD13	Isoleucine or valine / -73.2,-42.2	chi angles: 302.9,177.3	0.000, 1		
A 553	LEU 99.99	0.479Å HD23 with A 554 ASN N	Favored (52.8%) General / -70.0,139.6	6.7% (tt) chi angles: 182.7,164	0.065Å	-	-
A 554	ASN 99.99	0.479Å N with A 553 LEU HD23	Favored (24.51%) General / -118.8,115.5	41% ( <i>p30</i> ) chi angles: 60.9,25.7	0.036Å	-	OUTLIER(S) worst is OD1- CG-ND2: 6.181 σ
A 555	ILE 99.99	0.84Å H with A 560 SER HB3	Favored (28.01%) Isoleucine or valine / -62.8,134.6	37.2% (pt) chi angles: 64,176.5	0.065Å	-	-
A 556	LYS 99.99	-	Favored (50.62%) General / -65.7,133.2	22.7% (pttp) chi angles: 61.9,180,182,64.6	0.024Å	-	-
A 557	GLY 99.99	-	Favored (33.75%) Glycine / 106.2,-21.2	-	-	-	-
A 558	SER 99.99	-	Favored (2.7%) General /	32.1% ( <i>t</i> ) chi angles: 184.5	0.087Å	_	-
330			-151.6,-167.1	cili aligies. 104.5			
A 559	LYS 99.99	-	-151.6,-167.1 Favored (30.42%) General / -115.6,117.5	22.6% ( <i>pttp</i> ) chi angles: 59.8,180.7,181.7,66.3	0.056Å	-	-
A		- 0.84Å HB3 with A 555 ILE H	Favored (30.42%) General / -115.6,117.5 Favored (5.02%) General / -130.5,27.4	22.6% (pttp) chi angles:	0.056Å 0.049Å	-	- OUTLIER(S) worst is O-C- N: 4.559 σ
A 559 A	LYS 99.99	HB3 with A	Favored (30.42%) General / -115.6,117.5 Favored (5.02%) General /	22.6% ( <i>pttp</i> ) chi angles: 59.8,180.7,181.7,66.3 45.1% ( <i>t</i> )		-	worst is O-C-
A 559 A 560	LYS 99.99 SER 99.99	HB3 with A	Favored (30.42%) General / -115.6,117.5 Favored (5.02%) General / -130.5,27.4 Allowed (0.74%) Glycine /	22.6% ( <i>pttp</i> ) chi angles: 59.8,180.7,181.7,66.3 45.1% ( <i>t</i> )		-	worst is O-C-
A 559 A 560 A 561	LYS 99.99 SER 99.99 GLY 50	HB3 with A 555 ILE H - 0.644Å ND2 with A	Favored (30.42%) General / -115.6,117.5 Favored (5.02%) General / -130.5,27.4 Allowed (0.74%) Glycine / 48.5,17.4 Allowed (0.31%) General /	22.6% ( <i>pttp</i> ) chi angles: 59.8,180.7,181.7,66.3  45.1% ( <i>t</i> ) chi angles: 178.7	0.049Å	-	worst is O-C-

л 564	ARG	50	HG2 with A 514 ASP O	General / -59.0,114.3	chi angles: 296.1,296.9,204.3,186.3	0.057Å	-	-
A 565	THR	50	-	Allowed (0.75%) General / -71.9,10.2	63.3% ( <i>p</i> ) chi angles: 64.8	0.021Å	-	-
A 566	ALA	50	0.872Å HB2 with A 531 ALA HB2	Allowed (0.63%) General / -173.3,-170.6	-	0.204Å	-	-
#	Alt Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
		Avg:	Clashscore:	Outliers: 16 of	Poor rotamers: 12 of	Outliers:	Outliers: 12	Outliers: 64
		61.33		764	676	4 of 728	of 772	of 772
A 567	ASN	50	-	Favored (54.23%) General / -121.7,138.7	28.5% ( <i>t-20</i> ) chi angles: 187.7,301.4	0.124Å	-	-
A 568	ILE	50	1.027Å HG22 with A 510 CYS HB3	Favored (74.3%) Isoleucine or valine / -117.4,125.9	8.6% ( <i>tp</i> ) chi angles: 183.2,64.9	0.129Å	-	-
A 569	ARG	50	-	Favored (46.23%) General / -124.8,126.9	50.3% ( <i>ttp180</i> ) chi angles: 184.2,189.1,74.3,213.1	0.114Å	-	-
A 570	SER	50	-	Favored (53%) General / -69.3,137.4	34.4% (t) chi angles: 183.1	0.109Å	-	-
A 571	ILE	50	0.939Å HG12 with A 526 LYS HG2	Favored (3.98%) Isoleucine or valine / -101.1,-34.6	0.8% chi angles: 77.1,123.2	0.071Å	-	-
A 572	GLY	50	0.612Å N with A 571 ILE HG13	Favored (14.71%) Glycine / -118.7,172.9	-	-	-	-
A 573	TYR	50	0.539Å CE1 with A 443 TYR CD2	OUTLIER (0.02%) General / -60.4,90.5	22.6% ( <i>m</i> -85) chi angles: 274.5,272.2	0.028Å	-	-
A 574	SER	50	-	Favored (40.49%) General / -76.0,145.1	53.7% ( <i>m</i> ) chi angles: 299.9	0.062Å	-	-
			~ · 9	Favored				

A 575	ASP	50	0.477A O with A 523 ASN HB3	(6.37%) General / -125.7,100.3	90% ( <i>m-20</i> ) chi angles: 294.2,344	0.005Å	-	-
A 576	LEU	50	-	Favored (9.84%) General / -109.0,167.8	37.2% ( <i>mt</i> ) chi angles: 310.5,176.1	0.111Å	-	-
A 577	PHE	50	0.649Å HB3 with A 498 LEU HB3	Favored (51.56%) General / -126.1,133.8	88.9% ( <i>m-85</i> ) chi angles: 300.1,90	0.044Å	-	-
A 578	CYS	99.99	-	Favored (31.6%) General / -104.5,144.5	52.3% ( <i>t</i> ) chi angles: 180	0.035Å	-	-
A 579	LEU	50	0.556Å HD22 with A 494 LEU HD11	Favored (44.24%) General / -129.0,128.7	30.8% ( <i>tp</i> ) chi angles: 188.6,66.7	0.096Å	-	-
A 580	SER	50	-	Favored (21.27%) General / -83.9,159.8	84% (p) chi angles: 68.6	0.017Å	-	-
A 581	LYS	50	0.727Å HG3 with A 552 ILE HG23	Favored (79.78%) General / -60.1,-37.4	39.2% ( <i>ttpt</i> ) chi angles: 187,179.1,66.9,179.8	0.066Å	-	-
A 582	ASP	50	-	Allowed (0.83%) General / -52.3,-64.4	5.6% ( <i>m-20</i> ) chi angles: 306.4,84.2	0.075Å	-	-
A 583	ASP	50	-	Favored (78.54%) General / -63.6,-34.8	61.9% ( <i>m-20</i> ) chi angles: 294.3,302.7	0.03Å	-	-
A 584	LEU	99.99	0.812Å HD13 with A 552 ILE HG21	Favored (73.82%) General / -61.0,-50.3	10.3% (tt) chi angles: 183.9,150	0.045Å	-	-
A 585	MET	50	0.629Å O with A 589 THR HG23	Favored (69.05%) General / -69.1,-30.7	60.7% ( <i>mtt</i> ) chi angles: 292.3,183.8,173.7	0.026Å	-	-
A 586	GLU	50	-	Favored (45.07%) General / -66.7,-52.4	62.4% (tt0) chi angles: 185.1,189.7,338.7	0.069Å	-	-
щ	Alc D.	High	Clash >	n	D. (	Сβ	Bond	Bond

#	AIT Kes	B	0.4Å	Kamacnandran	коtamer	deviation	lengths	angles
		Avg: 61.33		Outliers: 16 of 764	Poor rotamers: 12 of 676	Outliers: 4 of 728	Outliers: 12 O of 772	outliers: 64 of 772
A 587	, ALA	50	-	Favored (70.58%) General / -61.5,-30.4	-	0.091Å	-	-
A 588	LEU	50	-	Favored (26.72%) General / -86.3,-22.5	48.9% ( <i>mt</i> ) chi angles: 293.2,185.6	0.112Å	-	-
A 589	THR	50	0.629Å HG23 with A 585 MET O	Favored (65.07%) General / -72.8,-31.9	77.8% (p) chi angles: 60.2	0.017Å	-	-
A 590	GLU	50	-	Favored (57.13%) General / -77.0,-32.5	80.4% ( <i>tt0</i> ) chi angles: 180.2,177.5,15.6	0.094Å	-	-
A 591	TYR	50	0.748Å CD1 with A 490 LEU HD13	Favored (65.41%) Pre-proline / -133.8,76.7	90.7% ( <i>m</i> -85) chi angles: 301.5,99.4	0.05Å	-	-
A 592	PRO	50	-	Favored (32.53%) Trans-proline / -60.1,-43.9	82.1% ( <i>Cg_exo</i> ) chi angles: 331.9	0.085Å	-	-
A 593	GLU	50	-	Allowed (0.79%) General / -42.2,-34.6	52.3% ( <i>mm-40</i> ) chi angles: 290.9,289.4,0.6	0.08Å	-	-
A 594	ALA	50	-	Favored (60.22%) General / -74.2,-20.4	-	0.035Å	-	-
A 595	LYS	50	0.412Å O with A 599 GLU HG3	Favored (83.92%) General / -59.5,-39.5	63.6% ( <i>tttp</i> ) chi angles: 183.3,182.1,179.2,63.2	0.022Å	-	-
A 596	LYS	50	-	Favored (80.88%) General / -64.0,-35.5	64% ( <i>tttp</i> ) chi angles: 184.1,180.4,179.1,62.3	0.017Å	-	-
A 597	ALA	50	-	Favored (64.25%) General / -56.5,-52.6	-	0.031Å	-	-

A 598	LEU	50	-	Favored (92.89%) General / -64.8,-39.0	10.5% ( <i>mp</i> ) chi angles: 280.6,63.7	0.026Å	-	-
A 599	GLU	99.99	0.412Å HG3 with A 595 LYS O	-	74.9% ( <i>mt-10</i> ) chi angles: 293.7,191.7,332	0.049Å	-	-
B 407	ASN	99.99	-	-	85% ( <i>m-20</i> ) chi angles: 296.7,336.5	0.058Å	-	-
B 408	ALA	50	-	OUTLIER (0.02%) General / -171.2,-39.6	-	0.063Å	-	-
B 409	SER	50	0.688Å HB2 with B 449 LYS HD2	Favored (58.86%) General / -81.7,-6.2	80.2% (p) chi angles: 60	0.123Å	-	-
B 410	ARG	50	0.541Å HH21 with B 447 ASN CG	Favored (66.01%) General / -71.2,-30.2	10.9% ( <i>mtp180</i> ) chi angles: 302.7,214.3,69.6,156.8	0.073Å	-	-
B 411	ALA	50	-	Favored (63.85%) General / -73.4,-40.9	-	0.052Å	-	-
B 412	GLU	50	-	Favored (81.99%) General / -60.7,-37.5	11.8% ( <i>tm-20</i> ) chi angles: 179.8,287.3,328.8	0.069Å	-	-
B 413	PHE	50	0.45Å CD1 with B 445 TRP HE3	Favored (45.25%) General / -65.1,-53.5	88.8% ( <i>t80</i> ) chi angles: 178.5,82.1	0.037Å	-	-
# A	Alt Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
		Avg: 61.33	Clashscore: 65.92	Outliers: 16 of 764	Poor rotamers: 12 of 676	Outliers: 4 of 728	Outliers: 12 of 772	Outliers: 64 of 772
B 414	GLN		0.544Å HA with B 417 ILE HG12	Favored (81.81%) General / -59.5,-38.7	15.8% ( <i>mt-30</i> ) chi angles: 282.5,140.6,20.1	0.015Å	-	-
В				Favored		9		
415	ALA	50	-	(80.73%) General / -68.5,-40.6 Favored	-	0.039Å	-	-

416				General / -69.9,-55.8	chi angles: 177.9,49.7,62.1,192.2			
B 417	ILE	50	0.736Å O with B 420 ILE HG12	Favored (33.54%) Isoleucine or valine / -58.1,-28.1	30% ( <i>pt</i> ) chi angles: 69.4,172.7	0.078Å	-	-
B 418	ASP	50	-	Favored (92.98%) General / -65.4,-41.9	44.5% ( <i>t0</i> ) chi angles: 186.9,329.5	0.038Å	-	-
B 419	SER	50	-	Favored (97.46%) General / -61.8,-44.1	40.1% (t) chi angles: 181.5	0.038Å	-	-
B 420	ILE	50	0.736Å HG12 with B 417 ILE O	Favored (65.2%) Isoleucine or valine / -58.7,-37.4	16.4% ( <i>pt</i> ) chi angles: 71.3,180.5	0.072Å	-	OUTLIER(S) worst is CB-CG1-CD1: $4.186 \sigma$
B 421	LYS	50	0.672Å HG3 with B 417 ILE O	Favored (90.34%) General / -65.2,-38.4	30.7% ( <i>mtpp</i> ) chi angles: 294,181,68,63.9	0.047Å	-	-
B 422	GLN	50	-	Favored (54.03%) General / -77.6,-33.0	19% ( <i>mt-30</i> ) chi angles: 298,166.1,183.6	0.087Å	-	-
B 423	TYR	50	0.445Å CE1 with D 453 GLU HG3	Favored (99.6%) General / -62.0,-42.9	71.9% ( <i>t80</i> ) chi angles: 172.6,84.8	0.05Å	-	-
B 424	MET	50	1.002Å SD with B 437 VAL HG11	Favored (70.48%) General / -71.4,-40.7	69.9% (mtm) chi angles: 293.7,191.9,299.6	0.05Å	-	-
B 425	GLN	50	-	Favored (79.46%) General / -67.7,-35.7	53.4% ( <i>tt0</i> ) chi angles: 185.3,179.2,57	0.012Å	-	-
B 426	PHE	50	-	Favored (79.94%) General / -64.8,-35.1	11% ( <i>t80</i> ) chi angles: 182.8,38.1	0.025Å	-	-
B 427	ARG 9	99.99	1.003Å HB3 with D 473 HIS HE1	Favored (57.36%) General / -92.0,-1.2	32.8% ( <i>mmt180</i> ) chi angles: 287.3,304.8,183.2,180	0.21Å	-	OUTLIER(S) worst is N-CA-CB: $4.945 \sigma$

B 428	LYS	50	-	Favored (28.26%) General / 54.1,38.0	88.4% ( <i>mttt</i> ) chi angles: 298.3,170.7,185,166.6	0.051Å	-	-
B 429	VAL	50	0.914Å HG21 with B 433 LEU HD22	Favored (5.58%) Isoleucine or valine / -61.0,152.8	12.1% ( <i>p</i> ) chi angles: 62.1	0.168Å	-	-
B 430	THR	50	0.455Å HG22 with B 432 ASP H	Favored (7.51%) General / -57.2,156.3	98.9% ( <i>m</i> ) chi angles: 298.8	0.05Å	-	-
B 431	LYS	50	0.441Å O with B 435 THR HG23	Favored (82.42%) General / -66.9,-36.5	32.8% ( <i>mmmt</i> ) chi angles: 296.3,295.3,295.3,181.1	0.032Å	-	-
B 432	ASP	50	0.455Å H with B 430 THR HG22	Favored (80.59%) General / -65.3,-35.3	85.2% ( <i>m</i> -20) chi angles: 293.9,349.1	0.053Å	-	-
B 433	LEU	50	0.914Å HD22 with B 429 VAL HG21	Favored (63.84%) General /	8.5% ( <i>tt</i> ) chi angles: 191.4,155.1	0.12Å	-	-
			HG21	-73.5,-40.7				
# 4	Alt Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
# A		B	Clash > 0.4Å Clashscore:	Ramachandran	Rotamer Poor rotamers: 12 of 676	deviation	lengths	angles
# A B 434		<b>B</b> Avg: 61.33	Clash > 0.4Å Clashscore:	Ramachandran Outliers: 16 of	Poor rotamers: 12 of	<b>deviation</b> Outliers:	<b>lengths</b> Outliers: 12	<b>angles</b> Outliers: 64
В		<b>B</b> Avg: 61.33	Clash > 0.4Å Clashscore: 65.92 0.786Å O with B 438	Ramachandran Outliers: 16 of 764 Favored (93.61%) General /	Poor rotamers: 12 of 676 54.6% ( <i>mt-10</i> ) chi angles:	deviation Outliers: 0 4 of 728	<b>lengths</b> Outliers: 12	<b>angles</b> Outliers: 64
B 434 B	GLU	<b>B</b> Avg: 61.33 50	Clash > 0.4Å Clashscore: 65.92 0.786Å O with B 438 ILE HG12 0.441Å HG23 with B	Ramachandran Outliers: 16 of 764 Favored (93.61%) General / -63.9,-39.2 Favored (68.27%) General / -66.1,-49.3 Favored (72.82%) General / -58.2,-36.2	Poor rotamers: 12 of 676  54.6% ( <i>mt-10</i> ) chi angles: 296.7,182.7,298.1  77.9% ( <i>p</i> )	deviation Outliers: 0 4 of 728 0.075Å	<b>lengths</b> Outliers: 12	<b>angles</b> Outliers: 64
B 434 B 435	GLU	<b>B</b> Avg: 61.33 50	Clash > 0.4Å Clashscore: 65.92 0.786Å O with B 438 ILE HG12 0.441Å HG23 with B	Ramachandran Outliers: 16 of 764 Favored (93.61%) General / -63.9,-39.2 Favored (68.27%) General / -66.1,-49.3 Favored (72.82%) General /	Poor rotamers: 12 of 676  54.6% ( <i>mt-10</i> ) chi angles: 296.7,182.7,298.1  77.9% ( <i>p</i> ) chi angles: 60.2  86.8% ( <i>mtm-85</i> ) chi angles:	deviation Outliers: 0 4 of 728  0.075Å  0.02Å	<b>lengths</b> Outliers: 12	<b>angles</b> Outliers: 64

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B 438	ILE 50	U./OUA HG12 with B 434 GLU O	(28.75%) Isoleucine or valine / -58.1,-54.7	41.1% ( <i>mm</i> ) chi angles: 299.1,304.7	0.028Å	-	-
B 439	ARG 50	0.437Å O with B 443 TYR HD2	Favored (77.74%) General / -60.0,-36.6	55.1% ( <i>mmm-85</i> ) chi angles: 293.6,298,293,278.7	0.033Å	-	-
B 440	TRP 99.99	0.842Å CH2 with B 444 LEU HD22	Favored (42.13%) General / -62.5,-54.3	89.3% ( <i>t</i> 90) chi angles: 184.8,87.4	0.024Å	OUTLIER(S) worst is NE1 CE2: 4.896 σ	Worst is ( / )_
B 441	PHE 50	0.775Å HE2 with B 437 VAL HG22	Favored (61.2%) General / -51.0,-46.2	95.4% ( <i>m-85</i> ) chi angles: 292.2,275.1	0.073Å	-	-
B 442	ASP 50	0.404Å HB2 with B 439 ARG O	Favored (67.79%) General / -53.0,-45.5	51.3% ( <i>m-20</i> ) chi angles: 295.4,296.5	0.044Å	-	-
B 443	TYR 50	0.552Å CE2 with B 573 TYR CZ	Favored (60.59%) General / -75.2,-30.6	95.2% ( <i>m</i> -85) chi angles: 292.2,274.8	0.027Å	-	-
B 444	LEU 99.99	0.842Å HD22 with B 440 TRP CH2	Favored (22.95%) General / -84.8,-33.5	21.3% ( <i>tp</i> ) chi angles: 187.1,74	0.098Å	-	-
B 445	TRP 50	0.458Å NE1 with B 444 LEU HD23	Favored (8.95%) General / -119.4,-16.7	51.6% ( <i>m0</i> ) chi angles: 296.7,351.6	0.079Å	OUTLIER(S) worst is NE1 CE2: 4.813 σ	OUTLIER(S) worst is CD2- CE3-CZ3: 4.178 σ
B 446	ALA 50	-	Allowed (0.65%) General / 51.6,18.1	-	0.046Å	-	-
B 447	ASN 99.99	0.541Å CG with B 410 ARG HH21	Favored (10.17%) General / 56.4,26.0	64.3% ( <i>t-20</i> ) chi angles: 184.8,348.8	0.097Å	-	OUTLIER(S) worst is OD1- CG-ND2: 5.666 σ
B 448	LYS 99.99	-	Allowed (0.73%) General / -106.2,-72.0	29.5% ( <i>tptp</i> ) chi angles: 182.4,64.6,177.9,64.7	0.065Å	-	-
B 449	LYS 99.99	0.688Å HD2 with B 409 SER HB2	Favored (49.19%) General / -125.3,147.2	27.9% ( <i>tptp</i> ) chi angles: 180.1,66.8,182.2,61.9	0.079Å	-	OUTLIER(S) worst is CG- CD-CE: 4.38
		TUJ JLK I IDZ	-149.9,147.4	100.1,00.0,102.2,01.9			σ

B 450	THR	99.99	0.721Å HG22 with B 451 VAL H	Allowed (0.82%) General / -119.5,-160.6	48.5% ( <i>m</i> ) chi angles: 305	0.108Å	-	-
B 451	VAL	99.99	1.088Å HG22 with B 452 ASP HA	Allowed (0.43%) Isoleucine or valine / -48.1,151.1	6% ( <i>p</i> ) chi angles: 75	0.168Å	-	-
B 452	ASP	50	1.088Å HA with B 451 VAL HG22	Allowed (1%) General / -104.9,44.8	2.2% ( <i>m-20</i> ) chi angles: 294.9,33.2	0.139Å	-	-
B 453	GLU	50	0.835Å HA with B 456 VAL HG22	Allowed (0.61%) General / -40.4,-36.9	27.2% (tt0) chi angles: 193.5,193.3,40.1	0.049Å	-	-
# Al	t Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
		Avg:	Clashscore:	Outliers: 16 of	Poor rotamers: 12 of	Outliers:	Outliers: 12	Outliers: 64
		61.33	65.92	764	676	4 of 728	of 772	of 772
B 454	LYS	50	-	Favored (79.07%) General / -63.4,-48.1	39% (ttpt) chi angles: 186.5,180,64.3,181.3	0.042Å	-	-
B 455	GLU	50	0.752Å HB3 with B 452 ASP HB3	Favored (76.52%) General / -65.6,-47.2	10.8% ( <i>tm-20</i> ) chi angles: 181.5,289.9,325.1	0.055Å	-	-
B 456	VAL	50	0.835Å HG22 with B 453 GLU HA	Favored (84.79%) Isoleucine or valine / -58.1,-43.2	23.1% ( <i>m</i> ) chi angles: 302.6	0.057Å	-	-
B 457	LEU	50	0.476Å HB2 with B 453 GLU O	Favored (84.41%) General / -67.7,-40.6	0.6% chi angles: 254.3,39.5	0.031Å	-	-
B 458	LYS	50	-	Favored (91.56%) General / -61.5,-39.6	28.6% ( <i>tptp</i> ) chi angles: 184.7,62.4,180.5,64.5	0.039Å	-	-
B 459	SER	50	0.641Å O with C 440 TRP CH2	Favored (81.95%) General / -64.2,-35.8	68.2% ( <i>m</i> ) chi angles: 296.2	0.096Å	-	OUTLIER(S) worst is CA-C- O: 5.239 σ
В	1 - 1 1	F0		Favored	80.5% (mt)	0.042 Å		

460	LEU	ΣU	-	(39.39%) Pre-proline / -70.6,166.1	chi angles: 298.8,182.5	U.U4ZA	-	-
В 461	PRO	50	0.778Å HD3 with C 440 TRP CE2	Favored (6.38%) Trans-proline / -87.5,171.2	42.7% ( <i>Cg_endo</i> ) chi angles: 36	0.014Å	-	-
B 462	ASP	50	-	Favored (96.91%) General / -63.9,-43.1	42.1% ( <i>t0</i> ) chi angles: 190.5,329.5	0.015Å	-	-
B 463	LYS	50	0.686Å HE2 with C 508 TYR H	Favored (73.89%) General / -57.9,-37.4	32.4% ( <i>mmmt</i> ) chi angles: 294.8,293.5,296.6,184.8	0.04Å	-	-
B 464	LEU	50	0.669Å HD12 with B 461 PRO HD2	Favored (22.9%) General / -75.5,-48.4	59.3% ( <i>mt</i> ) chi angles: 286.4,177.4	0.038Å	-	-
В 465	LYS	50	0.593Å O with B 470 ILE HG12	Favored (72.81%) General / -61.0,-33.1	54.9% ( <i>mtmt</i> ) chi angles: 294.7,178.6,295.9,178.8	0.136Å	-	-
В 466	ALA	50	0.72Å HA with B 470 ILE CB	Favored (83.81%) General / -66.6,-36.9	-	0.119Å	-	-
В 467	GLU	50	0.599Å OE2 with C 433 LEU HD12	Favored (79.53%) General / -68.8,-40.5	15.5% ( <i>tt0</i> ) chi angles: 206.1,191.3,309.1	0.116Å	-	-
B 468	ILE 9	99.99	0.867Å HA with B 472 VAL HG12	Favored (24.37%) Isoleucine or valine / -119.2,146.1	17.8% ( <i>pt</i> ) chi angles: 51.7,179.6	0.185Å	-	-
B 469	ALA S	99.99	0.977Å H with B 473 HIS HD2	Allowed (1.8%) General / 66.3,0.8	-	0.078Å	-	-
B 470	ILE 9	99.99	0.966Å HD12 with B 496 LEU HA	Allowed (0.75%) Isoleucine or valine / -132.4,-25.7	27.1% ( <i>mm</i> ) chi angles: 299,310.2	0.091Å	-	-
B 471	ASN	50	1.034Å HD21 with B 492 VAL HG12	Allowed (0.47%) General / -140.4,-51.1	42.2% ( <i>m</i> -20) chi angles: 278.7,302.3	0.195Å	-	OUTLIER(S) worst is CA- CB-CG: 4.049

B 472	VAL	50	0.867Å HG12 with B 468 ILE HA	Favored (82.17%) Isoleucine or valine / -58.6,-41.5	15% (p) chi angles: 63.5	0.065Å	-	-
B 473	HIS	50	1.019Å HE1 with C 427 ARG HB3	Favored (61.3%) General / -72.7,-25.5	84.1% ( <i>m-70</i> ) chi angles: 288,298.1	0.04Å	OUTLIER(S) worst is CD2 NE2: 7.05 σ	OUTLIER(S) worst is CD2- NE2-CE1: 12.768 σ
# Alt	Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
		Avg:	Clashscore:	Outliers: 16 of	Poor rotamers: 12 of	Outliers:	Outliers: 12	Outliers: 64
		61.33	65.92	764	676	4 of 728	of 772	of 772
B 474	LEU	99.99	0.696Å C with B 474 LEU HD23	Favored (38.13%) General / -53.1,132.5	7.2% (tt) chi angles: 184.9,162.9	0.126Å	-	-
B 475	ASP	99.99	0.542Å N with B 474 LEU HD23	Favored (5.85%) General / -129.7,12.7	29.9% ( <i>t70</i> ) chi angles: 179.1,76.4	0.069Å	-	-
B 476	THR	99.99	0.49Å HB with B 523 ASN HA	Favored (2.21%) General / -136.0,48.0	10.3% ( <i>t</i> ) chi angles: 184.2	0.074Å	-	-
B 477	LEU	99.99	1.093Å HG with B 483 PHE HB3	Allowed (0.81%) General / -134.6,-52.3	10% (tt) chi angles: 185.3,154.6	0.239Å	-	-
B 478	LYS	50	-	Favored (31.44%) General / -53.1,-29.6	27.1% ( <i>tptp</i> ) chi angles: 180.3,61.9,184.6,69.5	0.035Å	-	-
B 479	LYS	50	-	Favored (49.45%) General / -89.1,-9.9	26.8% ( <i>tptp</i> ) chi angles: 188.6,61.2,182.7,67.3	0.051Å	-	-
B 480	VAL	50	1.051Å HG12 with B 477 LEU HA	Favored (23.98%) Isoleucine or valine / -117.0,108.1	11.5% ( <i>p</i> ) chi angles: 66.5	0.141Å	-	-
B 481	ARG	50	0.724Å HA with B 484 GLN HG2	Favored (7.28%) General / -43.5,-47.1	57.9% (mmm-85) chi angles: 296.1,292.8,296.7,277.2	0.027Å	-	-
В	ΗE	ΕO	0.741Å	Favored	42.2% (pt)	0 0671		

482	ILE SU	HG12 WIUI B 480 VAL HG22	(8/.84%) Isoleucine or valine / -59.3,-42.6	chi angles: 65.5,172.5	U.UU/A	-	-
B 483	PHE 50	1.093Å HB3 with B 477 LEU HG	Favored (28.76%) General / -79.7,-40.6	7.1% ( <i>m</i> -30) chi angles: 278.5,9.7	0.047Å	-	OUTLIER(S) worst is CA- CB-CG: 4.414 σ
B 484	GLN 50	0.724Å HG2 with B 481 ARG HA	Favored (83.93%) General / -67.8,-38.8	19.8% ( <i>pt20</i> ) chi angles: 65.9,181.7,61.9	0.076Å	-	-
B 485	ASP 50	-	Favored (4.67%) General / -97.0,26.4	48.7% ( <i>t0</i> ) chi angles: 190.7,338.3	0.039Å	-	-
B 486	CYS 99.99	0.636Å 9 SG with B 490 LEU HD23	Favored (27.27%) General / -115.1,155.3	52.7% (t) chi angles: 181.3	0.052Å	-	-
B 487	GLU 99.99	) -	Favored (8.68%) General / -57.2,120.8	87.8% ( <i>mt-10</i> ) chi angles: 301.3,182.2,337.1	0.064Å	-	-
B 488	ALA 50	0.722Å O with B 492 VAL HG13	Favored (14.29%) General / -54.9,-22.3	-	0.016Å	-	-
B 489	GLY 50	0.492Å O with B 492 VAL HG22	Favored (76.39%) Glycine / -67.5,-45.6	-	-	-	-
B 490	LEU 99.99	0.748Å 9 HD13 with B 591 TYR CD1	Favored (93.9%) General / -65.5,-41.0	35.4% ( <i>tp</i> ) chi angles: 175.6,54.2	0.063Å	-	-
В 491	LEU 99.99	0.829Å HD13 with B 477 LEU HD11	Favored (5.02%) General / -57.2,-59.5	94.3% ( <i>mt</i> ) chi angles: 298.4,175.6	0.075Å	-	-
B 492	VAL 50	1.034Å HG12 with B 471 ASN HD21	Favored (14.91%) Isoleucine or valine / -48.6,-45.5	25.8% ( <i>m</i> ) chi angles: 302	0.023Å	-	-
B 493	GLU 50	-	Favored (68.49%) General / -66.128.0	14.3% ( <i>tm-20</i> )  chi angles: 183.8.285.3.333.8	0.107Å	-	-

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#	Alt R	Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
			_			Poor rotamers: 12 of			
			61.33	65.92	764	676	4 of 728	of 772	of 772
B 494	L	EU	50	0.689Å HD23 with B 483 PHE CE1	Favored (12.94%) General / -80.0,-48.7	33.9% ( <i>tp</i> ) chi angles: 187.7,59.4	0.033Å	-	OUTLIER(S) worst is CD1- CG-CD2: 4.562 σ
B 495	, V	'AL	50	0.749Å HG21 with B 470 ILE O	Favored (44.55%) Isoleucine or valine / -57.7,-33.2	20.8% ( <i>m</i> ) chi angles: 303.3	0.021Å	-	-
В 496	L	EU	50	0.966Å HA with B 470 ILE HD12	Favored (55.61%) General / -64.8,-13.4	8.9% (tt) chi angles: 190.5,154.5	0.155Å	-	-
B 497	, L	YS	50	-	Favored (10.85%) General / -115.9,-18.0	64.5% ( <i>mttp</i> ) chi angles: 295.5,177.2,177.3,63.2	0.054Å	-	-
B 498	3 L	EU	50	0.639Å HB3 with B 577 PHE HB3	Favored (44.49%) General / -58.6,144.1	58.4% ( <i>mt</i> ) chi angles: 305.2,173.5	0.096Å	-	-
B 499	, А	RG	50	-	Favored (28.15%) Pre-proline / -118.9,124.7	40.1% ( <i>ptt180</i> ) chi angles: 62,179.4,181.4,181.7	0.069Å	-	-
В 500	) P	RO	50	-	Favored (33.33%) Trans-proline / -68.0,134.9	92.8% ( <i>Cg_endo</i> ) chi angles: 30.9	0.035Å	-	-
В 501	Т	HR	50	-	Favored (30.25%) General / -144.9,142.9	63.4% (p) chi angles: 62.2	0.038Å	-	-
B 502	. V	'AL	50	-	Favored (36.42%) Isoleucine or valine / -115.5,140.6	74% ( <i>t</i> ) chi angles: 174	0.052Å	-	-
B 503	в Р	HE	50	-	Favored (50.81%) General / -127.0,145.2	63.9% ( <i>m-85</i> ) chi angles: 284.3,87.2	0.046Å	-	-

B 504	SER	50	-	Favored (31.54%) Pre-proline / -101.6,158.6	70.2% ( <i>m</i> ) chi angles: 295.9	0.029Å	-	-
B 505	PRO	50	-	Favored (52.29%) Trans-proline / -53.9,132.9	87.8% ( <i>Cg_exo</i> ) chi angles: 331.3	0.109Å	-	-
B 506	GLY	50	-	Favored (9.88%) Glycine / 100.2,-30.6	-	-	-	-
B 507	ASP	50	0.443Å HA with D 463 LYS HE2	Allowed (0.56%) General / -49.0,155.9	81.1% ( <i>m-20</i> ) chi angles: 283.3,337.3	0.05Å	-	-
B 508	TYR	50	0.684Å H with D 463 LYS HE2	Favored (5.14%) General / -108.5,94.6	11.4% ( <i>m-30</i> ) chi angles: 282.8,356.5	0.101Å	-	-
B 509	ILE	50	0.806Å HB with B 568 ILE HG23	Favored (99.01%) Isoleucine or valine / -60.9,-45.0	69% ( <i>mt</i> ) chi angles: 303.1,168.1	0.091Å	-	-
В 510	CYS	99.99	1.038Å HB3 with B 568 ILE HG22	Favored (28.07%) General / -144.3,138.6	4.8% ( <i>t</i> ) chi angles: 164.3	0.071Å	-	-
В 511	LYS	50	0.449Å NZ with B 508 TYR HD2	Favored (37.7%) General / -108.1,142.8	68.4% ( <i>mttm</i> ) chi angles: 292.6,179.7,178.2,293.8	0.066Å	-	-
B 512	LYS	50	-	Favored (31.24%) General / -61.9,152.7	38.6% ( <i>ttpt</i> ) chi angles: 184.7,182,62.4,181.3	0.071Å	-	-
B 513	GLY	50	0.446Å O with B 563 ARG HD2	Favored (4.44%) Glycine / 78.9,-20.6	-	-	-	-
# /	Alt Res	High B	Clash > <b>0.4</b> Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
		Avg: 61.33		Outliers: 16 of 764	Poor rotamers: 12 of 676	Outliers: 4 of 728	Outliers: 12 ( of 772	Outliers: 64 of 772
				Favored		-		
B = 1 1	ASP	50	0.477Å	(43.53%)	42.5% ( <i>t0</i> )	0.062Å	-	-

314			ARG HG2	-74.6,139.2	CIII UIIGICS. 102/320.3			
B 515	ILE	50	-	Favored (12.76%) Isoleucine or valine / -63.5,121.6	27.2% ( <i>mt</i> ) chi angles: 311.5,178.4	0.032Å	-	-
В 516	GLY	50	-	Favored (10.08%) Glycine / -98.5,130.0	-	-	-	-
В 517	LYS	50	0.528Å HG2 with B 517 LYS O	Favored (9.22%) General / -124.0,19.7	61.9% ( <i>tttm</i> ) chi angles: 185.6,184.4,177.4,293.2	0.063Å	-	-
В 518	GLU	50	-	Favored (7.59%) General / -169.3,157.6	12.6% ( <i>pt-20</i> ) chi angles: 61.5,180.2,62.4	0.013Å	-	-
В 519	MET	50	-	Favored (8.78%) General / -124.8,173.1	27.1% ( <i>ptm</i> ) chi angles: 65.3,172.3,293.2	0.032Å	-	-
B 520	TYR	50	-	Favored (52.46%) General / -130.9,149.6	90.2% ( <i>m-85</i> ) chi angles: 299.1,87.1	0.071Å	-	-
В 521	ILE	50	0.646Å HG12 with B 577 PHE HB2	Favored (15.09%) Isoleucine or valine / -121.0,104.3	32% ( <i>pt</i> ) chi angles: 66.9,166.7	0.058Å	-	-
В 522	ILE	50	-	Allowed (0.15%) Isoleucine or valine / -58.2,105.0	62.3% ( <i>mt</i> ) chi angles: 304.9,175.2	0.02Å	-	-
B 523	ASN	50	0.49Å HA with B 476 THR HB	Favored (20.01%) General / -76.9,-47.8	48.4% ( <i>t30</i> ) chi angles: 182.1,60.4	0.01Å	-	-
В 524	GLU	50	-	Favored (6.4%) General / -157.0,127.2	11.3% ( <i>tm-20</i> ) chi angles: 179.9,288.5,328.5	0.08Å	-	-
B 525	GLY	50	-	Favored (13.05%) Glycine / 132.8,172.6	-	-	-	-

В 526	LYS	99.99	0.955Å HG3 with B 540 VAL HG13	Favored (51.03%) General / -122.2,128.3	66.7% (tttt) chi angles: 165.7,169.7,180.8,162.5	0.107Å	-	-
В 527	, LEU	50	0.871Å HB3 with B 568 ILE HD11	Favored (29.48%) General / -119.4,156.8	9.5% ( <i>mp</i> ) chi angles: 281.9,69.5	0.069Å	-	OUTLIER(S) worst is CD1- CG-CD2: 4.488 σ
В 528	ALA	50	0.499Å O with B 568 ILE HD12	Favored (54.91%) General / -118.4,128.8	-	0.07Å	-	-
B 529	y VAL	50	0.683Å HG22 with B 568 ILE HD13	Favored (70.26%) Isoleucine or valine / -113.0,127.5	22.5% (t) chi angles: 187.4	0.056Å	-	-
B 530	) VAL	50	-	Favored (3.12%) Isoleucine or valine / -130.1,97.0	7.3% (p) chi angles: 58.8	0.101Å	-	-
В 531	ALA	99.99	0.856Å HB2 with B 566 ALA HB2	Allowed (1.95%) General / -130.4,80.3	-	0.137Å	-	-
В 532	ASP	99.99	-	Favored (11.65%) General / 53.0,31.7	29.4% ( <i>t70</i> ) chi angles: 178.9,77	0.068Å	-	-
В 533	asp ASP	99.99	-	Favored (31.44%) General / -160.3,165.4	26.1% ( <i>p30</i> ) chi angles: 61.8,29.5	0.02Å	-	-
#	Alt Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
		Avg: 61.33	Clashscore: 65.92	Outliers: 16 of 764	Poor rotamers: 12 of 676	Outliers: 4 of 728	Outliers: 12 of 772	Outliers: 64 of 772
В 534	GLY	99.99	<del>-</del>	Allowed (0.82%) Glycine / -61.8,105.1	-	-	-	-
	↓ VAI		- 0.6Å HG22 with B 536 THR	Allowed (0.82%) Glycine /	- 7.1% ( <i>p</i> ) chi angles: 58.4	- 0.01Å	-	-

В 536	THR	99.99	HG22 with B 535 VAL HG22	(1.5%) General / 55.6,15.4	9.9% ( <i>t</i> ) chi angles: 184	0.055Å	-	-
B 537	GLN	99.99	0.517Å HG2 with B 536 THR O	Favored (14.51%) General / 47.9,51.3	18.5% ( <i>pt20</i> ) chi angles: 64.8,180.9,57	0.097Å	-	-
B 538	PHE	99.99	0.475Å CD2 with B 538 PHE O	Favored (14.34%) General / 63.5,32.4	85.3% ( <i>t80</i> ) chi angles: 180.7,81.9	0.055Å	-	-
B 539	VAL	99.99	0.806Å HG12 with B 540 VAL H	Allowed (0.48%)	63.1% ( <i>t</i> ) chi angles: 180	0.087Å	-	OUTLIER(S) worst is CA- CB-CG1: 4.474 σ
В 540	VAL	99.99	0.955Å HG13 with B 526 LYS HG3		26.7% (t) chi angles: 164.6	0.381Å	-	OUTLIER(S) worst is N-CA-CB: $5.587 \sigma$
В 541	LEU	50	-	Allowed (1.63%) General / -59.4,112.1	18.6% ( <i>mt</i> ) chi angles: 292,193.2	0.076Å	-	-
B 542	SER	50	-	Allowed (1.05%) General / -124.4,-162.1	20.8% (t) chi angles: 188.4	0.068Å	-	-
В 543	ASP	50	-	Favored (20.24%) General / -50.1,135.9	0.3% chi angles: 313.8,44.5	0.116Å	-	-
В 544	GLY	50	-	Favored (73.87%) Glycine / 79.3,18.6	-	-	-	-
В 545	SER	50	-	Favored (28.28%) General / -124.4,160.4	72.6% ( <i>m</i> ) chi angles: 295.6	0.026Å	-	-
В 546	TYR	50	0.619Å CE1 with B 482 ILE HD13	Favored (7.79%) General / -134.8,177.4	45.9% ( <i>p90</i> ) chi angles: 59,275.2	0.048Å	-	-
В	PHE	50	0.512Å  CE2 with B	Favored (4.1%)	43.6% ( <i>p90</i> )	0.022Å	-	-
547			527 LEU	General /	chi angles: 60.5,83.6			

517		HD22	-173.7,162.6	,			
B 548	GLY 50	-	Favored (62.81%) Glycine / 75.1,28.1	-	-	-	-
В 549	GLU 50	-	Favored (29.19%) General / -86.9,-19.2	6.4% ( <i>pm0</i> ) chi angles: 70.4,293.3,339.2	0.053Å	-	-
B 550	ILE 50	-	Favored (97.65%) Isoleucine or valine / -62.3,-43.1	76.9% ( <i>mt</i> ) chi angles: 298.8,177	0.063Å	-	-
B 551	SER 50	-	Favored (66.23%) General / -68.4,-27.5	73.4% ( <i>m</i> ) chi angles: 295.3	0.038Å	-	-
В 552	ILE 99.99	0.79Å HG21 with B 584 LEU HD13	Favored (58.47%) Isoleucine or valine / -73.2,-42.2	65.2% ( <i>mt</i> ) chi angles: 302.9,177.3	0.083Å	-	-
B 553	LEU 99.99	0.485Å HD23 with B 554 ASN N	Favored (52.8%) General / -70.0,139.6	6.7% (tt) chi angles: 182.7,164	0.065Å	-	-
# <b>A</b>	lt Res High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
	Avg: 61.33		Outliers: 16 of 764	Poor rotamers: 12 of 676	Outliers: 4 of 728	Outliers: 12 of 772	2 Outliers: 64 of 772
B 554		0.485Å N with B 553 LEU HD23	Favored (24.51%) General / -118.8,115.5	41% ( <i>p30</i> ) chi angles: 60.9,25.7	0.036Å	-	OUTLIER(S) worst is OD1- CG-ND2: 6.181 σ
B 555	ILE 99.99	0.861Å H with B 560 SER HB3	Favored (28.01%) Isoleucine or valine / -62.8,134.6	37.2% ( <i>pt</i> ) chi angles: 64,176.5	0.065Å	-	-
B 556	LYS 99.99	-	Favored (50.62%) General / -65.7,133.2 Favored	22.7% ( <i>pttp</i> ) chi angles: 61.9,180,182,64.6	0.024Å	-	-
В	GLY 99.99		(33.75%)		_		

55,				106.2,-21.2				
B 558	SER 9	99.99	-	Favored (2.7%) General / -151.6,-167.1	32.1% ( <i>t</i> ) chi angles: 184.5	0.087Å	-	-
B 559	LYS 9	99.99	-	Favored (30.42%) General / -115.6,117.5	22.6% ( <i>pttp</i> ) chi angles: 59.8,180.7,181.7,66.3	0.056Å	-	-
В 560	SER 9	99.99	0.861Å HB3 with B 555 ILE H	Favored (5.02%) General / -130.5,27.4	45.1% ( <i>t</i> ) chi angles: 178.7	0.049Å	-	OUTLIER(S) worst is O-C- N: 4.559 σ
В 561	GLY	50	-	Allowed (0.74%) Glycine / 48.5,17.4	-	-	-	-
B 562	ASN	50	0.654Å ND2 with B 563 ARG H	Allowed (0.31%) General / -125.8,-144.1	59% ( <i>t30</i> ) chi angles: 188.9,50.1	0.12Å	-	-
B 563	ARG	50	0.654Å H with B 562 ASN ND2	Favored (22.72%) General / -101.8,150.9	12.2% ( <i>mmt180</i> ) chi angles: 305,301.9,193.1,133.1	0.097Å	-	-
В 564	ARG	50	0.477Å HG2 with B 514 ASP O	Favored (2.5%) General / -59.0,114.3	28.1% ( <i>mmt180</i> ) chi angles: 296.1,296.9,204.3,186.3	0.057Å	-	-
В 565	THR	50	-	Allowed (0.75%) General / -71.9,10.2	63.3% (p) chi angles: 64.8	0.021Å	-	-
В 566	ALA	50	0.856Å HB2 with B 531 ALA HB2	Allowed (0.63%) General / -173.3,-170.6	-	0.204Å	-	-
В 567	ASN	50	-	Favored (54.23%) General / -121.7,138.7	28.5% ( <i>t-20</i> ) chi angles: 187.7,301.4	0.124Å	-	-
B 568	ILE	50	1.038Å HG22 with B 510 CYS HB3	Favored (74.3%) Isoleucine or valine / -117.4,125.9	8.6% ( <i>tp</i> ) chi angles: 183.2,64.9	0.129Å	-	-
B 569	ARG	50	-	Favored (46.23%) General / -124.8,126.9	50.3% ( <i>ttp180</i> ) chi angles: 184.2,189.1,74.3,213.1	0.114Å	-	-

B 570	SER	50	-	Favored (53%) General / -69.3,137.4	34.4% (t) chi angles: 183.1	0.109Å	-	-
В 571	ILE	50	0.945Å HG12 with B 526 LYS HG2	Favored (3.98%) Isoleucine or valine / -101.1,-34.6	0.8% chi angles: 77.1,123.2	0.071Å	-	-
B 572	GLY	50	0.62Å N with B 571 ILE HG13	Favored (14.71%) Glycine / -118.7,172.9	-	-	-	-
B 573	TYR	50	0.552Å CZ with B 443 TYR CE2	OUTLIER (0.02%) General / -60.4,90.5	22.6% ( <i>m-85</i> ) chi angles: 274.5,272.2	0.028Å	-	-
# Alt	Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	<b>C</b> β deviation	Bond lengths	Bond angles
		Avg: 61.33	Clashscore: 65.92	Outliers: 16 of 764	Poor rotamers: 12 of 676	Outliers: 4 of 728	Outliers: 12 of 772	Outliers: 64 of 772
B 574	SER	50	-	Favored (40.49%) General / -76.0,145.1	53.7% ( <i>m</i> ) chi angles: 299.9	0.062Å	-	-
B 575	ASP	50	0.488Å O with B 523 ASN HB3	Favored (6.37%) General / -125.7,100.3	90% ( <i>m-20</i> ) chi angles: 294.2,344	0.005Å	-	-
B 576	LEU	50	-	Favored (9.84%) General / -109.0,167.8	37.2% ( <i>mt</i> ) chi angles: 310.5,176.1	0.111Å	-	-
B 577	PHE	50	0.646Å HB2 with B 521 ILE HG12	Favored (51.56%) General / -126.1,133.8	88.9% ( <i>m-85</i> ) chi angles: 300.1,90	0.044Å	-	-
B 578	CYS	99.99	-	Favored (31.6%) General / -104.5,144.5	52.3% (t) chi angles: 180	0.035Å	-	-
B 579	LEU	50	0.541Å HD22 with B 494 LEU HD11	Favored (44.24%) General / -129.0,128.7	30.8% ( <i>tp</i> ) chi angles: 188.6,66.7	0.096Å	-	-
B 580	SER	50	-	Favored (21.27%) General /	84% (p) chi angles: 68.6	0.017Å	-	-

				-83.9,159.8				
B 581	LYS	50	0.721Å HG3 with B 552 ILE HG23	Favored (79.78%) General / -60.1,-37.4	39.2% ( <i>ttpt</i> ) chi angles: 187,179.1,66.9,179.8	0.066Å	-	-
B 582	ASP	50	-	Allowed (0.83%) General / -52.3,-64.4	5.6% ( <i>m-20</i> ) chi angles: 306.4,84.2	0.075Å	-	-
B 583	ASP	50	-	Favored (78.54%) General / -63.6,-34.8	61.9% ( <i>m-20</i> ) chi angles: 294.3,302.7	0.03Å	-	-
B 584	LEU	99.99	0.79Å HD13 with B 552 ILE HG21	Favored (73.82%) General / -61.0,-50.3	10.3% (tt) chi angles: 183.9,150	0.045Å	-	-
B 585	MET	50	0.624Å O with B 589 THR HG23	Favored (69.05%) General / -69.1,-30.7	60.7% ( <i>mtt</i> ) chi angles: 292.3,183.8,173.7	0.026Å	-	-
В 586	GLU	50	-	Favored (45.07%) General / -66.7,-52.4	62.4% ( <i>tt0</i> ) chi angles: 185.1,189.7,338.7	0.069Å	-	-
В 587	ALA	50	-	Favored (70.58%) General / -61.5,-30.4	-	0.091Å	-	-
B 588	LEU	50	-	Favored (26.72%) General / -86.3,-22.5	48.9% ( <i>mt</i> ) chi angles: 293.2,185.6	0.112Å	-	-
B 589	THR	50	0.624Å HG23 with B 585 MET O	Favored (65.07%) General / -72.8,-31.9	77.8% (p) chi angles: 60.2	0.017Å	-	-
B 590	GLU	50	-	Favored (57.13%) General / -77.0,-32.5	80.4% (tt0) chi angles: 180.2,177.5,15.6	0.094Å	-	-
B 591	TYR	50	0.748Å CD1 with B 490 LEU HD13	Favored (65.41%) Pre-proline / -133.8,76.7	90.7% ( <i>m-85</i> ) chi angles: 301.5,99.4	0.05Å	-	-
В 592	PRO	50	-	Favored (32.53%)	82.1% ( <i>Cg_exo</i> ) chi angles: 331.9	0.085Å	-	-

D				Trans-proline / -60.1,-43.9 Allowed	52.3% ( <i>mm-40</i> )			
B 593	GLU	50	-	(0.79%) General / -42.2,-34.6	chi angles: 290.9,289.4,0.6	0.08Å	-	-
#	Alt Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	$\begin{array}{c} C\beta \\ \text{deviation} \end{array}$	Bond lengths	Bond angles
		Avg: 61.33	Clashscore: 65.92	Outliers: 16 of 764	Poor rotamers: 12 of 676	Outliers: 4 of 728	Outliers: 12 of 772	Outliers: 64 of 772
В 594	ALA	50	-	Favored (60.22%) General / -74.2,-20.4	-	0.035Å	-	-
B 595	LYS	50	0.405Å O with B 599 GLU HG3	Favored (83.92%) General / -59.5,-39.5	63.6% ( <i>tttp</i> ) chi angles: 183.3,182.1,179.2,63.2	0.022Å	-	-
В 596	LYS	50	-	Favored (80.88%) General / -64.0,-35.5	64% ( <i>tttp</i> ) chi angles: 184.1,180.4,179.1,62.3	0.017Å	-	-
B 597	ALA	50	-	Favored (64.25%) General / -56.5,-52.6	-	0.031Å	-	-
В 598	LEU	50	-	Favored (92.89%) General / -64.8,-39.0	10.5% ( <i>mp</i> ) chi angles: 280.6,63.7	0.026Å	-	-
В 599	GLU	99.99	0.405Å HG3 with B 595 LYS O	-	74.9% ( <i>mt-10</i> ) chi angles: 293.7,191.7,332	0.049Å	-	-
C 407	ASN	99.99	-	-	85% ( <i>m-20</i> ) chi angles: 296.7,336.5	0.058Å	-	-
C 408	ALA	50	-	OUTLIER (0.02%) General / -171.2,-39.6	-	0.063Å	-	-
C 409	SER	50	0.675Å HB2 with C 449 LYS HD2	Favored (58.86%) General / -81.7,-6.2	80.2% ( <i>p</i> ) chi angles: 60	0.123Å	-	-
С			0.545Å HH21 with C	Favored (66.01%)	10.9% ( <i>mtp180</i> ) chi angles:			
410	ARG	50	447 ASN CG	General / -71.2,-30.2	302.7,214.3,69.6,156.8	0.073Å	-	-

C 411	ALA	50	-	Favored (63.85%) General / -73.4,-40.9	-	0.052Å	-	-
C 412	GLU	50	-	Favored (81.99%) General / -60.7,-37.5	11.8% ( <i>tm-20</i> ) chi angles: 179.8,287.3,328.8	0.069Å	-	-
C 413	PHE	50	0.454Å CD1 with C 445 TRP HE3	Favored (45.25%) General / -65.1,-53.5	88.8% ( <i>t80</i> ) chi angles: 178.5,82.1	0.037Å	-	-
C 414	GLN	50	0.553Å HA with C 417 ILE HG12	Favored (81.81%) General / -59.5,-38.7	15.8% ( <i>mt-30</i> ) chi angles: 282.5,140.6,20.1	0.015Å	-	-
C 415	ALA	50	-	Favored (80.73%) General / -68.5,-40.6	-	0.039Å	-	-
C 416	LYS	50	-	Favored (9%) General / -69.9,-55.7	13.8% (tppt?) chi angles: 177.9,49.7,62.1,192.2	0.03Å	-	-
C 417	ILE	50	0.74Å O with C 420 ILE HG12	Favored (33.85%) Isoleucine or valine / -58.2,-28.1	30.1% ( <i>pt</i> ) chi angles: 69.3,172.7	0.077Å	-	-
C				Favored				
C 418	ASP	50	-	(92.98%) General / -65.4,-41.9	44.5% ( <i>t0</i> ) chi angles: 186.9,329.5	0.038Å	-	-
	ASP SER	50 50	-	General /		0.038Å 0.038Å	-	-
418 C			- 0.74Å HG12 with C 417 ILE O	General / -65.4,-41.9 Favored (97.46%) General / -61.8,-44.1 Favored (65.2%) Isoleucine or valine /	chi angles: 186.9,329.5 40.1% ( <i>t</i> )		-	- OUTLIER(S) worst is CB- CG1-CD1: 4.186 σ
418 C 419 C 420	SER	50	HG12 with C	General / -65.4,-41.9 Favored (97.46%) General / -61.8,-44.1 Favored (65.2%) Isoleucine or	chi angles: 186.9,329.5 40.1% (t) chi angles: 181.5	0.038Å	- Bond lengths	worst is CB- CG1-CD1:
418 C 419 C 420	SER ILE	50 50 <b>High</b> <b>B</b>	HG12 with C 417 ILE O  Clash > 0.4Å  Clashscore:	General / -65.4,-41.9 Favored (97.46%) General / -61.8,-44.1 Favored (65.2%) Isoleucine or valine / -58.7,-37.4  Ramachandran	chi angles: 186.9,329.5  40.1% (t) chi angles: 181.5  16.4% (pt) chi angles: 71.3,180.5	0.038Å  0.072Å  Cβ deviation	lengths	worst is CB- CG1-CD1: 4.186 σ Bond angles

421	LYS	50	HG3 with C 417 ILE O	(90.34 /o) General / -65.2,-38.4	chi angles: 294,181,68,63.9	0.047A	-	-
C 422	GLN	50	-	Favored (54.03%) General / -77.6,-33.0	19% ( <i>mt-30</i> ) chi angles: 298,166.1,183.5	0.087Å	-	-
C 423	TYR	50	0.445Å CE1 with B 453 GLU HG3	Favored (99.6%) General / -62.0,-42.9	71.9% ( <i>t80</i> ) chi angles: 172.6,84.8	0.05Å	-	-
C 424	MET	50	1.002Å SD with C 437 VAL HG11	Favored (70.48%) General / -71.4,-40.7	69.9% ( <i>mtm</i> ) chi angles: 293.7,191.9,299.6	0.05Å	-	-
C 425	GLN	50	-	Favored (79.46%) General / -67.7,-35.7	53.4% ( <i>tt0</i> ) chi angles: 185.3,179.2,57	0.012Å	-	-
C 426	РНЕ	50	-	Favored (79.94%) General / -64.8,-35.1	11% ( <i>t80</i> ) chi angles: 182.8,38.1	0.025Å	-	-
C 427	ARG	99.99	1.019Å HB3 with B 473 HIS HE1	Favored (57.36%) General / -92.0,-1.2	32.8% (mmt180) chi angles: 287.3,304.8,183.2,180	0.21Å	-	OUTLIER(S) worst is N-CA- CB: 4.945 σ
C 428	LYS	50	-	Favored (28.26%) General / 54.1,38.0	88.4% ( <i>mttt</i> ) chi angles: 298.3,170.7,185,166.6	0.051Å	-	-
C 429	VAL	50	0.926Å HG21 with C 433 LEU HD22	Favored (5.58%) Isoleucine or valine / -61.0,152.8	12.1% ( <i>p</i> ) chi angles: 62.1	0.168Å	-	-
C 430	THR	50	0.449Å HG22 with C 432 ASP H	Favored (7.51%) General / -57.2,156.3	98.9% ( <i>m</i> ) chi angles: 298.8	0.05Å	-	-
C 431	LYS	50	0.437Å O with C 435 THR HG23	Favored (82.42%) General / -66.9,-36.5	32.8% (mmmt) chi angles: 296.3,295.3,295.3,181.1	0.032Å	-	-
C 432	ASP	50	0.449Å H with C 430 THR HG22	Favored (80.59%)  General / -65.3,-35.3	85.2% ( <i>m-20</i> ) chi angles: 293.9,349.1	0.053Å	-	-

		61.33	65.92 0.787Å	764	676	4 of 728	of 772	of 772
# <b>A</b>	lt Res	High B Avg:	Clash > 0.4Å Clashscore:	Ramachandran Outliers: 16 of	<b>Rotamer</b> Poor rotamers: 12 of	<b>C</b> β <b>deviation</b> Outliers:	U	Bond angles Outliers: 64
C 440	TRP	99.99	0.834Å CH2 with C 444 LEU HD22	Favored (42.13%) General / -62.5,-54.3	89.3% ( <i>t</i> 90) chi angles: 184.8,87.3	0.024Å	OUTLIER(S) worst is NE1 CE2: 4.769 σ	OUTLIER(S) worst is CZ2- CH2-CZ3: 5.295 σ
C 439	ARG	50	0.445Å O with C 443 TYR HD2	Favored (77.74%) General / -60.0,-36.6	55.1% ( <i>mmm-85</i> ) chi angles: 293.6,298,293,278.7	0.033Å	-	-
C 438	ILE	50	0.784Å HG12 with C 434 GLU O	Favored (28.75%) Isoleucine or valine / -58.1,-54.7	41.3% ( <i>mm</i> ) chi angles: 299.1,304.7	0.028Å	-	-
C 437	VAL	50	1.002Å HG11 with C 424 MET SD	Favored (68.54%) Isoleucine or valine / -72.0,-41.3	4.9% (p) chi angles: 76.4	0.175Å	-	-
C 436	ARG	50	-	Favored (72.82%) General / -58.2,-36.2	86.8% ( <i>mtm-85</i> ) chi angles: 285.7,187.7,294.2,260.3	0.068Å	-	-
C 435	THR	50	0.437Å HG23 with C 431 LYS O	Favored (68.27%) General / -66.1,-49.3	77.9% (p) chi angles: 60.2	0.02Å	-	-
C 434	GLU	50	0.784Å O with C 438 ILE HG12	Favored (93.68%) General / -63.9,-39.2	54.6% ( <i>mt-10</i> ) chi angles: 296.7,182.7,298.1	0.075Å	-	-
C 433	LEU	50	0.926A HD22 with C 429 VAL HG21	Favored (63.82%) General / -73.5,-40.7	8.5% ( <i>tt</i> ) chi angles: 191.4,155.1	0.12Å	-	-

443	III JU	573 TYR CZ	General / -75.2,-30.6	chi angles: 292.2,274.8	0.02//		
C 444	LEU 99.99	0.834Å HD22 with C 440 TRP CH2	Favored (22.95%) General / -84.8,-33.5	21.3% ( <i>tp</i> ) chi angles: 187.1,74	0.098Å	-	-
C 445	TRP 50	0.454Å HE3 with C 413 PHE CD1	Favored (8.96%) General / -119.3,-16.7	51.6% ( <i>m0</i> ) chi angles: 296.7,351.6	0.079Å	OUTLIER(S) worst is NE1 CE2: 4.757 σ	OUTLIER(S) worst is CD2- CE3-CZ3: 4.172 σ
C 446	ALA 50	-	Allowed (0.66%) General / 51.6,18.1	-	0.046Å	-	-
C 447	ASN 99.99	0.545Å CG with C 410 ARG HH21	Favored (10.17%) General / 56.4,26.0	64.3% ( <i>t-20</i> ) chi angles: 184.8,348.8	0.097Å	-	OUTLIER(S) worst is OD1- CG-ND2: 5.666 σ
C 448	LYS 99.99	-	Allowed (0.73%) General / -106.2,-72.0	29.5% ( <i>tptp</i> ) chi angles: 182.4,64.6,177.9,64.7	0.065Å	-	-
C 449	LYS 99.99	0.675Å HD2 with C 409 SER HB2	Favored (49.27%) General / -125.4,147.2	27.9% ( <i>tptp</i> ) chi angles: 180.1,66.8,182.2,61.9	0.078Å	-	OUTLIER(S) worst is CG- CD-CE: 4.38 $\sigma$
C 450	THR 99.99	0.709Å HG22 with C 451 VAL H	Allowed (0.82%) General / -119.5,-160.6	48.8% ( <i>m</i> ) chi angles: 305	0.108Å	-	-
C 451	VAL 99.99	1.053Å HG22 with C 452 ASP HA	Allowed (0.44%) Isoleucine or valine / -48.1,151.2	6% (p) chi angles: 75	0.168Å	-	-
C 452	ASP 50	1.053Å HA with C 451 VAL HG22	Allowed (1.01%) General / -104.8,44.7	2.2% ( <i>m</i> -20) chi angles: 294.9,33.2	0.14Å	-	-
C 453	GLU 50	0.825Å HA with C 456 VAL HG22	Allowed (0.6%) General / -40.4,-36.9	27.1% (tt0) chi angles: 193.5,193.3,40.1	0.048Å	-	-
C 454	LYS 50	-	Favored (79.14%) General / -63.5,-48.0	39% (ttpt) chi angles: 186.5,179.9,64.3,181.3	0.041Å	-	-

C 455	GLU	50	0.762Å HB3 with C 452 ASP HB3	Favored (75.69%) General / -65.6,-47.4	10.8% ( <i>tm-20</i> ) chi angles: 181.5,289.8,325.2	0.055Å	-	-
C 456	VAL	50	0.825Å HG22 with C 453 GLU HA	Favored (85.34%) Isoleucine or valine / -58.9,-42.3	22.1% ( <i>m</i> ) chi angles: 302.9	0.037Å	-	-
C 457	LEU	50	0.469Å HB2 with C 453 GLU O	Favored (82.27%) General / -68.2,-40.5	0.5% chi angles: 254.3,39.3	0.042Å	-	-
C 458	LYS	50	-	Favored (93.83%) General / -61.1,-40.4	28.6% ( <i>tptp</i> ) chi angles: 184.5,62.4,180.5,64.5	0.04Å	-	-
C 459	SER	99.99	0.653Å O with A 440 TRP CH2	Favored (77.29%) General / -64.6,-34.0	95.4% (p) chi angles: 66.7	0.102Å	-	OUTLIER(S) worst is CA-C- O: 5.595 σ
C 460	LEU	50	-	Favored (38.7%) Pre-proline / -71.6,166.5	81% ( <i>mt</i> ) chi angles: 298.2,182.5	0.042Å	-	-
				71.0,100.5				
# A	Alt Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
# A	Alt Res	<b>B</b> Avg:	<b>0.4Å</b> Clashscore:	Ramachandran Outliers: 16 of	Poor rotamers: 12 of	<b>deviation</b> Outliers:	<b>lengths</b> Outliers: 12	<b>angles</b> 2 Outliers: 64
# A C 461	Alt Res	<b>B</b> Avg: 61.33	<b>0.4Å</b> Clashscore:	Ramachandran		deviation	lengths	angles
С		<b>B</b> Avg: 61.33	0.4Å Clashscore: 65.92 0.778Å HD3 with A	Ramachandran Outliers: 16 of 764 Favored (6.07%) Trans-proline /	Poor rotamers: 12 of 676 42.9% ( <i>Cg_endo</i> )	deviation Outliers: 4 of 728	<b>lengths</b> Outliers: 12	<b>angles</b> 2 Outliers: 64
C 461	PRO	<b>B</b> Avg: 61.33	0.4Å Clashscore: 65.92 0.778Å HD3 with A	Ramachandran Outliers: 16 of 764 Favored (6.07%) Trans-proline / -87.7,171.3 Favored (96.45%) General /	Poor rotamers: 12 of 676  42.9% ( <i>Cg_endo</i> ) chi angles: 35.9  42.1% ( <i>t0</i> )	deviation Outliers: 4 of 728 0.014Å	<b>lengths</b> Outliers: 12	<b>angles</b> 2 Outliers: 64
C 461 C 462	PRO ASP	<b>B</b> Avg: 61.33 50	0.4Å Clashscore: 65.92 0.778Å HD3 with A 440 TRP CE2  - 0.673Å HE2 with A	Ramachandran Outliers: 16 of 764 Favored (6.07%) Trans-proline / -87.7,171.3 Favored (96.45%) General / -64.0,-43.1 Favored (73.75%) General /	Poor rotamers: 12 of 676  42.9% ( <i>Cg_endo</i> ) chi angles: 35.9  42.1% ( <i>t0</i> ) chi angles: 190.5,329.5  32.4% ( <i>mmmt</i> ) chi angles:	deviation Outliers: 4 of 728 0.014Å 0.016Å	<b>lengths</b> Outliers: 12	<b>angles</b> 2 Outliers: 64

465	LYS	50	O with C 470 ILE HG12	(/ <b>2.0 i</b> /o) General / -61.0,-33.1	chi angles: 294.7,178.6,295.9,178.8	0.135A	-	-
C 466	ALA	50	0.723Å HA with C 470 ILE CB	Favored (83.8%) General / -66.6,-36.9	-	0.118Å	-	-
C 467	GLU	50	0.601Å OE2 with A 433 LEU HD12	Favored (79.54%) General / -68.8,-40.5	15.5% ( <i>tt0</i> ) chi angles: 206.1,191.3,309.1	0.116Å	-	-
C 468	ILE 9	99.99	0.892Å HA with C 472 VAL HG12	Favored (24.44%) Isoleucine or valine / -119.2,146.0	17.8% ( <i>pt</i> ) chi angles: 51.7,179.6	0.186Å	-	-
C 469	ALA 9	99.99	0.922Å H with C 473 HIS HD2	Allowed (1.81%) General / 66.3,0.8	-	0.078Å	-	-
C 470	ILE 9	99.99	0.986Å HD12 with C 496 LEU HA	Allowed (0.75%) Isoleucine or valine / -132.4,-25.7	26.9% (mm) chi angles: 299,310.2	0.091Å	-	-
C 471	ASN	50	1.066Å HD21 with C 492 VAL HG12	Allowed (0.47%) General / -140.4,-51.1	42.2% ( <i>m-20</i> ) chi angles: 278.7,302.3	0.195Å	-	OUTLIER(S) worst is CA- CB-CG: 4.049 σ
C 472	VAL	50	0.892Å HG12 with C 468 ILE HA	Favored (82.17%) Isoleucine or valine / -58.6,-41.5	15% ( <i>p</i> ) chi angles: 63.5	0.065Å	-	-
C 473	HIS	99.99	0.989Å HE1 with A 427 ARG HB3	Favored (61.3%) General / -72.7,-25.5	84.1% ( <i>m-70</i> ) chi angles: 288,298.1	0.04Å	OUTLIER(S) worst is CD2 NE2: 7.083 σ	\\/\Crct  c
C 474	LEU 9	99.99	0.684Å C with C 474 LEU HD23	Favored (38.13%) General / -53.1,132.5	7.2% ( <i>tt</i> ) chi angles: 184.9,162.9	0.126Å	-	-
C 475	ASP 9	99.99	0.542Å N with C 474 LEU HD23	Favored (5.85%) General / -129.7,12.7	29.9% ( <i>t70</i> ) chi angles: 179.1,76.4	0.069Å	-	-
C 476	THR	99.99	0.483Å HB with C	Favored (2.21%) General /	10.3% ( <i>t</i> ) chi angles: 184.2	0.074Å	-	-

			JZJ /\J \      /\	-130.0,70.0				
C 477	LEU	99.99	1.097Å HG with C 483 PHE HB3	Allowed (0.81%) General / -134.6,-52.3	10% (tt) chi angles: 185.3,154.6	0.239Å	-	-
C 478	LYS	50	-	Favored (31.44%) General / -53.1,-29.6	27.1% ( <i>tptp</i> ) chi angles: 180.3,61.9,184.6,69.5	0.035Å	-	-
C 479	LYS	50	-	Favored (49.45%) General / -89.1,-9.9	26.8% ( <i>tptp</i> ) chi angles: 188.6,61.2,182.7,67.3	0.051Å	-	-
C 480	VAL	50	1.043Å HG12 with C 477 LEU HA	Favored (23.98%) Isoleucine or valine / -117.0,108.1	11.5% ( <i>p</i> ) chi angles: 66.6	0.141Å	-	-
#	Alt Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
		Avg:	Clashscore:	Outliers: 16 of	Poor rotamers: 12 of	Outliers:	Outliers: 12	Outliers: 64
		61.33	65.92	764	676	4 of 728	of 772	of 772
C 481	ARG	50	0.713Å HA with C 484 GLN HG2	Favored (7.28%) General / -43.5,-47.1	57.9% ( <i>mmm-85</i> ) chi angles: 296.1,292.8,296.7,277.2	0.027Å	-	-
C 482	ILE	50	0.745Å HG12 with C 480 VAL HG22	Favored (87.84%) Isoleucine or valine / -59.3,-42.6	42.2% ( <i>pt</i> ) chi angles: 65.5,172.5	0.067Å	-	-
C 483	PHE	50	1.097Å HB3 with C 477 LEU HG	Favored (28.76%) General / -79.7,-40.6	7.1% ( <i>m-30</i> ) chi angles: 278.5,9.7	0.047Å	-	OUTLIER(S) worst is CA- CB-CG: 4.414 σ
C 484	GLN	50	0.713Å HG2 with C 481 ARG HA	Favored (83.93%) General / -67.8,-38.8	19.8% ( <i>pt20</i> ) chi angles: 65.9,181.7,61.9	0.076Å	-	-
C 485	ASP	50	-	Favored (4.67%) General / -97.0,26.4	48.7% ( <i>t0</i> ) chi angles: 190.7,338.3	0.039Å	-	-
6			0.600 8	Favored				
C			0.639Å SG with C	(27.27%)	52.7% (t)			

C 487	GLU 99.99	) -	Favored (8.68%) General / -57.2,120.8	87.8% ( <i>mt-10</i> ) chi angles: 301.3,182.2,337.1	0.064Å	-	-
C 488	ALA 50	0.723Å O with C 492 VAL HG13	Favored (14.29%) General / -54.9,-22.3	-	0.016Å	-	-
C 489	GLY 50	0.483Å O with C 492 VAL HG22	Favored (76.39%) Glycine / -67.5,-45.6	-	-	-	-
C 490	LEU 99.99	0.749Å HD13 with C 591 TYR CD1	Favored (93.9%) General / -65.5,-41.0	35.4% ( <i>tp</i> ) chi angles: 175.6,54.2	0.063Å	-	-
C 491	LEU 99.99	0.835Å HD13 with C 477 LEU HD11	Favored (5.02%) General / -57.2,-59.5	94.3% ( <i>mt</i> ) chi angles: 298.4,175.6	0.075Å	-	-
C 492	VAL 50	1.066Å HG12 with C 471 ASN HD21	Favored (14.9%) Isoleucine or valine / -48.6,-45.5	25.8% ( <i>m</i> ) chi angles: 302	0.023Å	-	-
C 493	GLU 50	-	Favored (68.45%) General / -66.2,-28.0	14.3% ( <i>tm-20</i> ) chi angles: 183.8,285.4,333.7	0.107Å	-	-
C 494	LEU 50	0.699Å HD23 with C 483 PHE CE1	Favored (12.94%) General / -80.0,-48.7	33.9% ( <i>tp</i> ) chi angles: 187.7,59.4	0.033Å	-	OUTLIER(S) worst is CD1- CG-CD2: 4.562 σ
C 495	VAL 50	0.756Å HG21 with C 470 ILE O	Favored (44.55%) Isoleucine or valine / -57.7,-33.2	20.8% ( <i>m</i> ) chi angles: 303.3	0.021Å	-	-
C 496	LEU 50	0.986Å HA with C 470 ILE HD12	Favored (55.61%) General / -64.8,-13.4	8.9% (tt) chi angles: 190.5,154.5	0.155Å	-	-
C 497	LYS 50	-	Favored (10.85%) General / -115.9,-18.0	64.5% (mttp) chi angles: 295.5,177.2,177.3,63.2	0.054Å	-	-
		0	Favored				
~		0 651 Å	ravoicu				

C 498	LEU	50	HB3 with C 577 PHE HB3	(44.49%) General / -58.6,144.1	58.4% ( <i>mt</i> ) chi angles: 305.2,173.5	0.096Å	-	-
C 499	ARG	50	-	Favored (28.15%) Pre-proline / -118.9,124.7	40.1% ( <i>ptt180</i> ) chi angles: 62,179.4,181.4,181.7	0.069Å	-	-
C 500	PRO	50	-	Favored (33.36%) Trans-proline / -68.0,135.0	92.8% ( <i>Cg_endo</i> ) chi angles: 30.9	0.035Å	-	-
#	Alt Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
		Avg: 61.33	Clashscore: 65.92	Outliers: 16 of 764	Poor rotamers: 12 of 676	Outliers: 4 of 728	Outliers: 12 ( of 772	Outliers: 64 of 772
C 501	THR	50	-	Favored (30.24%) General / -144.9,142.9	63.1% ( <i>p</i> ) chi angles: 62.3	0.038Å	-	-
C 502	VAL	50	-	Favored (36.42%) Isoleucine or valine / -115.5,140.6	74% ( <i>t</i> ) chi angles: 174	0.052Å	-	-
C 503	PHE	50	-	Favored (50.81%) General / -127.0,145.2	63.9% ( <i>m-85</i> ) chi angles: 284.3,87.2	0.046Å	-	-
C 504	SER	50	-	Favored (31.54%) Pre-proline / -101.6,158.6	70.2% ( <i>m</i> ) chi angles: 295.9	0.029Å	-	-
C 505	PRO	50	-	Favored (52.06%) Trans-proline / -53.9,132.9	88.3% ( <i>Cg_exo</i> ) chi angles: 331.4	0.107Å	-	-
C 506	GLY	50	-	Favored (9.88%) Glycine / 100.2,-30.6	-	-	-	-
C 507	ASP	50	0.441Å HA with B 463 LYS HE2	Allowed (0.56%) General / -49.0,155.9	81.1% ( <i>m-20</i> ) chi angles: 283.3,337.3	0.05Å	-	-
C 508	TYR	50	0.686Å H with B 463 IYS HF2	Favored (5.14%) General / -108.5.94.6	11.4% ( <i>m-30</i> ) chi angles: 282.8,356.5	0.101Å	-	-

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C 509	ILE	50	0.801 Å HB with C 568 ILE HG23	Favored (99.01%) Isoleucine or valine / -60.9,-45.0	69% ( <i>mt</i> ) chi angles: 303.1,168.1	0.091Å	-	-
C 510	CYS	99.99	1.016Å HB3 with C 568 ILE HG22	Favored (28.07%) General / -144.3,138.6	4.8% (t) chi angles: 164.3	0.071Å	-	-
C 511	LYS	50	0.457Å NZ with C 508 TYR HD2	Favored (37.7%) General / -108.1,142.8	68.4% ( <i>mttm</i> ) chi angles: 292.6,179.7,178.2,293.8	0.066Å	-	-
C 512	LYS	50	-	Favored (31.24%) General / -61.9,152.7	38.6% ( <i>ttpt</i> ) chi angles: 184.7,182,62.4,181.3	0.071Å	-	-
C 513	GLY	50	0.441 Å O with C 563 ARG HD2	Favored (4.44%) Glycine / 78.9,-20.6	-	-	-	-
C 514	ASP	50	0.479Å O with C 564 ARG HG2	Favored (43.53%) General / -74.6,139.2	42.5% ( <i>t0</i> ) chi angles: 189,328.5	0.062Å	-	-
C 515	ILE	50	-	Favored (12.76%) Isoleucine or valine / -63.5,121.6	27.2% ( <i>mt</i> ) chi angles: 311.5,178.4	0.032Å	-	-
C 516	GLY	50	-	Favored (10.08%) Glycine / -98.5,130.0	-	-	-	-
C 51 <i>7</i>	LYS	50	0.524Å HG2 with C 517 LYS O	Favored (9.22%) General / -124.0,19.7	61.9% (tttm) chi angles: 185.6,184.4,177.4,293.2	0.063Å	-	-
C 518	GLU	50	-	Favored (7.59%) General / -169.3,157.6	12.6% (pt-20) chi angles: 61.5,180.2,62.4	0.013Å	-	-
C 519	MET	50	-	Favored (8.78%) General / -124.8,173.1	27.1% ( <i>ptm</i> ) chi angles: 65.3,172.3,293.2	0.032Å	-	-
C				Favored	90 2% (m-85)	. •		

520	7	ΓYR	50	-	(32.40%) General / -130.9,149.6	chi angles: 299.1,87.1	0.071A	-	-
#	Alt I	Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
			Avg: 61.33	Clashscore: 65.92	Outliers: 16 of 764	Poor rotamers: 12 of 676	Outliers: 0 4 of 728	•	Outliers: 64 of 772
C 521		ILE	50	0.644Å CG1 with C 577 PHE HB2	Favored (15.09%) Isoleucine or valine / -121.0,104.3	32% ( <i>pt</i> ) chi angles: 66.9,166.7	0.058Å	-	-
C 522	1	ILE	50	-	Allowed (0.15%) Isoleucine or valine / -58.2,105.0	62.3% ( <i>mt</i> ) chi angles: 304.9,175.2	0.02Å	-	-
C 523	A	ASN	50	0.483Å HA with C 476 THR HB	Favored (20.01%) General / -76.9,-47.8	48.4% ( <i>t30</i> ) chi angles: 182.1,60.4	0.01Å	-	-
C 524	C	GLU	50	-	Favored (6.4%) General / -157.0,127.2	11.3% ( <i>tm-20</i> ) chi angles: 179.9,288.5,328.5	0.08Å	-	-
C 525	(	GLY	50	-	Favored (13.05%) Glycine / 132.8,172.6	-	-	-	-
C 526	I	LYS	99.99	0.972Å HG2 with C 571 ILE HG12	Favored (51.03%) General / -122.2,128.3	66.7% (tttt) chi angles: 165.7,169.7,180.8,162.5	0.107Å	-	-
C 527	L	.EU	50	0.885Å HB3 with C 568 ILE HD11	Favored (29.48%) General / -119.4,156.8	9.5% ( <i>mp</i> ) chi angles: 281.9,69.5	0.069Å	-	OUTLIER(S) worst is CD1- CG-CD2: 4.488 σ
C 528	A	λLA	50	0.51Å O with C 568 ILE HD12	Favored (54.91%) General / -118.4,128.8	-	0.07Å	-	-
C 529	١	/AL	50	0.695Å HG22 with C 568 ILE HD13	Favored (70.26%) Isoleucine or valine / -113.0,127.5	22.5% ( <i>t</i> ) chi angles: 187.4	0.056Å	-	-
C 530	\	/AL	50	-	Favored (3.12%)	7.3% (p) chi angles: 58.8	0.101Å	-	-

			valine / -130.1,97.0 Allowed	J			
C 531	ALA 99.99	0.87Å HB2 with C 566 ALA HB2	(1.95%) General / -130.4,80.3	-	0.137Å	-	-
C 532	ASP 99.99	-	Favored (11.65%) General / 53.0,31.7	29.4% ( <i>t70</i> ) chi angles: 178.9,77	0.068Å	-	-
C 533	ASP 99.99	-	Favored (31.44%) General / -160.3,165.4	26.1% ( <i>p30</i> ) chi angles: 61.8,29.5	0.02Å	-	-
C 534	GLY 99.99		Allowed (0.82%) Glycine / -61.8,105.1	-	-	-	-
C 535	VAL 50	0.596Å HG22 with C 536 THR HG22	OUTLIER (0%) Isoleucine or valine / -10.6,108.9	7.1% (p) chi angles: 58.4	0.01Å	-	-
C 536	THR 99.99	0.596Å HG22 with C 535 VAL HG22	Allowed (1.5%) General / 55.6,15.4	9.9% (t) chi angles: 184	0.055Å	-	-
C 537	GLN 99.99	0.526Å HG2 with C 536 THR O	Favored (14.51%) General / 47.9,51.3	18.5% ( <i>pt20</i> ) chi angles: 64.8,180.9,57	0.097Å	-	-
C 538	PHE 99.99	0.484Å CD2 with C 538 PHE O	Favored (14.34%) General / 63.5,32.4	85.3% ( <i>t80</i> ) chi angles: 180.7,81.9	0.055Å	-	-
C 539	VAL 99.99	0.791Å HG12 with C 540 VAL H	Allowed (0.48%) Isoleucine or valine / -119.6,-168.6	63.1% ( <i>t</i> ) chi angles: 180	0.087Å	-	OUTLIER(S) worst is CA- CB-CG1: 4.474 σ
C 540	VAL 99.99	0.956Å HG13 with C 526 LYS HG3	OUTLIER (0.06%) Isoleucine or valine / -158.5,97.4	26.7% ( <i>t</i> ) chi angles: 164.6	0.381Å	-	OUTLIER(S) worst is N-CA- CB: 5.587 σ
# <b>Al</b> t	t Res High	Clash >	Ramachandran	Rotamer	Сβ	Bond	Bond
	В	<b>0.4Å</b>			deviation	lengths	angles
	Avg:	Clashscore:	Outliers: 16 of	Poor rotamers: 12 of	f Outliers: (	Outliers: 12	2 Outliers: 64

		01.33	b5.92	/ b <del>4</del>	0/0	4 01 / 20	OI //Z	01//2
C 541	LEU	50	-	Allowed (1.63%) General / -59.4,112.1	18.6% ( <i>mt</i> ) chi angles: 292,193.2	0.076Å	-	-
C 542	SER	50	-	Allowed (1.05%) General / -124.4,-162.1	20.8% ( <i>t</i> ) chi angles: 188.4	0.068Å	-	-
C 543	ASP	50	-	Favored (20.24%) General / -50.1,135.9	0.3% chi angles: 313.8,44.5	0.116Å	-	-
C 544	GLY	50	-	Favored (73.87%) Glycine / 79.3,18.6	-	-	-	-
C 545	SER	50	-	Favored (28.28%) General / -124.4,160.4	72.6% ( <i>m</i> ) chi angles: 295.6	0.026Å	-	-
C 546	TYR	50	0.622Å CE1 with C 482 ILE HD13	Favored (7.79%) General / -134.8,177.4	45.9% ( <i>p</i> 90) chi angles: 59,275.2	0.048Å	-	-
C 547	PHE	50	0.52Å CE2 with C 527 LEU HD22	Favored (4.1%) General / -173.7,162.6	43.6% ( <i>p90</i> ) chi angles: 60.5,83.6	0.022Å	-	-
C 548	GLY	50	-	Favored (62.81%) Glycine / 75.1,28.1	-	-	-	-
C 549	GLU	50	-	Favored (29.19%) General / -86.9,-19.2	6.4% ( <i>pm0</i> ) chi angles: 70.4,293.3,339.2	0.053Å	-	-
C 550	ILE	50	-	Favored (97.65%) Isoleucine or valine / -62.3,-43.1	76.9% ( <i>mt</i> ) chi angles: 298.8,177	0.063Å	-	-
C 551	SER	50	-	Favored (66.23%) General / -68.4,-27.5	73.4% ( <i>m</i> ) chi angles: 295.3	0.038Å	-	-
С		00 00	0.785Å HG21 with C	Favored (58.47%)	65.2% (mt)	0 000 <sup>9</sup>		

552	ILE	99.99	584 LEU HD13	Isoleucine or valine / -73.2,-42.2	chi angles: 302.9,177.3	U.U83A	-	-
C 553	LEU	99.99	0.483Å HD23 with C 554 ASN N	Favored (52.8%) General / -70.0,139.6	6.7% (tt) chi angles: 182.7,164	0.065Å	-	-
C 554	ASN	99.99	0.483Å N with C 553 LEU HD23	Favored (24.51%) General / -118.8,115.5	41% ( <i>p30</i> ) chi angles: 60.9,25.7	0.036Å	-	OUTLIER(S) worst is OD1- CG-ND2: 6.181 σ
C 555	ILE	99.99	0.843Å H with C 560 SER HB3	Favored (28.01%) Isoleucine or valine / -62.8,134.6	37.2% ( <i>pt</i> ) chi angles: 64,176.5	0.065Å	-	-
C 556	LYS	99.99	-	Favored (50.62%) General / -65.7,133.2	22.7% (pttp) chi angles: 61.9,180,182,64.6	0.024Å	-	-
C 557	GLY	99.99	-	Favored (33.75%) Glycine / 106.2,-21.2	-	-	-	-
C 558	SER	99.99	-	Favored (2.7%) General / -151.6,-167.1	32.1% ( <i>t</i> ) chi angles: 184.5	0.087Å	-	-
C 559	LYS	99.99	-	Favored (30.42%) General / -115.6,117.5	22.6% (pttp) chi angles: 59.8,180.7,181.7,66.3	0.056Å	-	-
C 560	SER	99.99	0.843Å HB3 with C 555 ILE H	Favored (5.02%) General / -130.5,27.4	45.1% ( <i>t</i> ) chi angles: 178.7	0.049Å	-	OUTLIER(S) worst is O-C-N: $4.559 \sigma$
# Al	t Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
		Avg: 61.33	Clashscore: 65.92	Outliers: 16 of 764	Poor rotamers: 12 of 676	Outliers: 0	Outliers: 12 of 772	2 Outliers: 64 of 772
C 561	GLY	50	-	Allowed (0.75%) Glycine / 48.6,17.4	-	-	-	-
С			0.645Å	Allowed (0.31%)	59% ( <i>t30</i> )			
562	ASN	50	ND2 with C 563 ARG H	General / -125.8,-144.1	chi angles: 188.9,50.1	0.12Å	-	-

 $http://molprobity.biochem.duke.edu/viewtable.php? MolProbSID=6 tg 76...b75 cr8hl50 shh7q53 s1cc1jkg4/raw\_data/cnga3\_sm\_407-599 H-multi.table$ 

C 563	ARG	50	0.645Å H with C 562 ASN ND2	Favored (22.72%) General / -101.8,150.9	12.2% (mmt180) chi angles: 305,301.9,193.1,133.1	0.097Å	-	-
C 564	ARG	50	0.479Å HG2 with C 514 ASP O	Favored (2.5%) General / -59.0,114.3	28.1% ( <i>mmt180</i> ) chi angles: 296.1,296.9,204.3,186.3	0.057Å	-	-
C 565	THR	50	-	Allowed (0.75%) General / -71.9,10.2	63.3% (p) chi angles: 64.8	0.021Å	-	-
C 566	ALA	50	0.87Å HB2 with C 531 ALA HB2	Allowed (0.63%) General / -173.3,-170.6	-	0.204Å	-	-
C 567	ASN	50	-	Favored (54.23%) General / -121.7,138.7	28.5% ( <i>t-20</i> ) chi angles: 187.7,301.4	0.124Å	-	-
C 568	ILE	50	1.016Å HG22 with C 510 CYS HB3	Favored (74.3%) Isoleucine or valine / -117.4,125.9	8.6% ( <i>tp</i> ) chi angles: 183.2,64.9	0.129Å	-	-
C 569	ARG	50	-	Favored (46.23%) General / -124.8,126.9	50.3% ( <i>ttp180</i> ) chi angles: 184.2,189.1,74.3,213.1	0.114Å	-	-
C 570	SER	50	-	Favored (53%) General / -69.3,137.4	34.4% (t) chi angles: 183.1	0.109Å	-	-
C 571	ILE	50	0.972Å HG12 with C 526 LYS HG2	Favored (3.98%) Isoleucine or valine / -101.1,-34.6	0.8% chi angles: 77.1,123.2	0.071Å	-	-
C 572	GLY	50	0.628Å N with C 571 ILE HG13	Favored (14.71%) Glycine / -118.7,172.9	-	-	-	-
C 573	TYR	50	0.543Å CZ with C 443 TYR CE2	OUTLIER (0.02%) General / -60.4,90.5	22.6% ( <i>m-85</i> ) chi angles: 274.5,272.2	0.028Å	-	-
C 574	SER	50	-	Favored (40.49%) General / -76.0,145.1	53.7% ( <i>m</i> ) chi angles: 299.9	0.062Å	-	-

C 575	ASP	50	0.474Å O with C 523 ASN HB3	Favored (6.37%) General / -125.7,100.3	90% ( <i>m</i> -20) chi angles: 294.2,344	0.005Å	-	-
C 576	LEU	50	-	Favored (9.84%) General / -109.0,167.8	37.2% ( <i>mt</i> ) chi angles: 310.5,176.1	0.111Å	-	-
C 577	PHE	50	0.651Å HB3 with C 498 LEU HB3	Favored (51.56%) General / -126.1,133.8	88.9% ( <i>m-85</i> ) chi angles: 300.1,90	0.044Å	-	-
C 578	CYS	99.99		Favored (31.6%) General / -104.5,144.5	52.3% ( <i>t</i> ) chi angles: 180	0.035Å	-	-
C 579	LEU	50	0.551Å HD22 with C 494 LEU HD11	Favored (44.24%) General / -129.0,128.7	30.8% ( <i>tp</i> ) chi angles: 188.6,66.7	0.096Å	-	-
C 580	SER	50	-	Favored (21.27%) General / -83.9,159.8	84% ( <i>p</i> ) chi angles: 68.6	0.017Å	-	-
							n I	
# Al	t Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	<b>C</b> β <b>deviation</b>	Bond lengths	Bond angles
# Al		B	<b>0.4Å</b> Clashscore:		Rotamer Poor rotamers: 12 of 676	deviation	lengths	angles
# <b>Al</b> C 581		<b>B</b> Avg:	<b>0.4Å</b> Clashscore:	Outliers: 16 of	Poor rotamers: 12 of	<b>deviation</b> Outliers:	<b>lengths</b> Outliers: 12	<b>angles</b> Outliers: 64
С		<b>B</b> Avg: 61.33	<b>0.4Å</b> Clashscore: 65.92 0.728Å HG3 with C 552 ILE	Outliers: 16 of 764 Favored (79.78%) General /	Poor rotamers: 12 of 676 39.2% (ttpt) chi angles:	deviation Outliers: 4 of 728	<b>lengths</b> Outliers: 12	<b>angles</b> Outliers: 64
C 581 C	LYS	B Avg: 61.33	0.4Å Clashscore: 65.92 0.728Å HG3 with C 552 ILE HG23	Outliers: 16 of 764  Favored (79.78%) General / -60.1,-37.4  Allowed (0.83%) General / -52.3,-64.4  Favored (78.54%) General / -63.6,-34.8	Poor rotamers: 12 of 676  39.2% (ttpt) chi angles: 187,179.1,66.9,179.8  5.6% (m-20)	deviation Outliers: 4 4 of 728 0.066Å	<b>lengths</b> Outliers: 12	<b>angles</b> Outliers: 64
C 581 C 582	LYS ASP	B Avg: 61.33 50	0.4Å Clashscore: 65.92 0.728Å HG3 with C 552 ILE HG23 - 0.785Å HD13 with C	Outliers: 16 of 764  Favored (79.78%)  General / -60.1,-37.4  Allowed (0.83%)  General / -52.3,-64.4  Favored (78.54%)  General /	Poor rotamers: 12 of 676  39.2% (ttpt) chi angles: 187,179.1,66.9,179.8  5.6% (m-20) chi angles: 306.4,84.2	deviation Outliers: 4 of 728 0.066Å 0.075Å	<b>lengths</b> Outliers: 12	<b>angles</b> Outliers: 64

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C 586	GLU	50	-	-69.1,-30.7 Favored (45.07%) General / -66.7,-52.4	62.4% (tt0) chi angles: 185.1,189.7,338.7	0.069Å	-	-
C 587	ALA	50	-	Favored (70.58%) General / -61.5,-30.4	<del>-</del>	0.091Å	-	-
C 588	LEU	50	-	Favored (26.72%) General / -86.3,-22.5	48.9% ( <i>mt</i> ) chi angles: 293.2,185.6	0.112Å	-	-
C 589	THR	50	0.625Å HG23 with C 585 MET O	Favored (65.07%) General / -72.8,-31.9	77.8% (p) chi angles: 60.2	0.01 <i>7</i> Å	-	-
C 590	GLU	50	-	Favored (57.13%) General / -77.0,-32.5	80.4% (tt0) chi angles: 180.2,177.5,15.6	0.094Å	-	-
C 591	TYR	50	0.749Å CD1 with C 490 LEU HD13	Favored (65.41%) Pre-proline / -133.8,76.7	90.7% ( <i>m</i> -85) chi angles: 301.5,99.4	0.05Å	-	-
C 592	PRO	50	-	Favored (32.53%) Trans-proline / -60.1,-43.9	82.1% ( <i>Cg_exo</i> ) chi angles: 331.9	0.085Å	-	-
C 593	GLU	50	-	Allowed (0.79%) General / -42.2,-34.6	52.3% ( <i>mm-40</i> ) chi angles: 290.9,289.4,0.6	0.08Å	-	-
C 594	ALA	50	-	Favored (60.22%) General / -74.2,-20.4	-	0.035Å	-	-
C 595	LYS	50	0.412Å O with C 599 GLU HG3	Favored (83.92%) General / -59.5,-39.5	63.6% (tttp) chi angles: 183.3,182.1,179.2,63.2	0.022Å	-	-
C 596	LYS	50	-	Favored (80.88%) General / -64.0,-35.5	64% (tttp) chi angles: 184.1,180.4,179.1,62.3	0.017Å	-	-
C 597	ALA	50	-	Favored (64.25%)	-	0.031Å	-	-

331				-56.5,-52.6 Favored				
C 598	LEU	50	-	(92.89%) General / -64.8,-39.0	10.5% ( <i>mp</i> ) chi angles: 280.6,63.7	0.026Å	-	-
C 599	GLU	99.99	0.412Å HG3 with C 595 LYS O	-	74.9% ( <i>mt-10</i> ) chi angles: 293.7,191.7,332	0.049Å	-	-
D 407	ASN	99.99	-	-	85% ( <i>m-20</i> ) chi angles: 296.7,336.5	0.058Å	-	-
#	Alt Res	High B	Clash > <b>0.4</b> Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
		Avg:	Clashscore:	Outliers: 16 of	Poor rotamers: 12 of		Outliers: 12	Outliers: 64
		61.33	65.92	764	676	4 of 728	of 772	of 772
D 408	ALA	50	-	OUTLIER (0.02%) General / -171.2,-39.6	-	0.063Å	-	-
D 409	SER	50	0.671Å HB2 with D 449 LYS HD2	Favored (58.86%) General / -81.7,-6.2	80.2% (p) chi angles: 60	0.123Å	-	-
D 410	ARC	50	0.546Å HH21 with D 447 ASN CG	Favored (66.01%) General / -71.2,-30.2	10.9% ( <i>mtp180</i> ) chi angles: 302.7,214.3,69.6,156.8	0.073Å	-	-
D 411	ALA	50	-	Favored (63.85%) General / -73.4,-40.9	-	0.052Å	-	-
D 412	GLU	50	-	Favored (81.99%) General / -60.7,-37.5	11.8% ( <i>tm-20</i> ) chi angles: 179.8,287.3,328.8	0.069Å	-	-
D 413	PHE	50	0.445 Å CD1 with D 445 TRP HE3	Favored (45.25%) General / -65.1,-53.5	88.8% ( <i>t80</i> ) chi angles: 178.5,82.1	0.037Å	-	-
D 414	GLN	50	0.558Å HA with D 417 ILE HG12	Favored (81.81%) General / -59.5,-38.7	15.8% ( <i>mt-30</i> ) chi angles: 282.5,140.6,20.1	0.015Å	-	-
				Favored				
D 415	ALA	50	-	(80.73%) General / -68.5,-40.6	-	0.039Å	-	-

D 416	LYS	50	-	Favored (8.88%) General / -69.9,-55.8	13.8% ( <i>tppt</i> ?) chi angles: 177.9,49.7,62.1,192.2	0.03Å	-	-
D 417	ILE	50	0.733Å O with D 420 ILE HG12	Favored (33.54%) Isoleucine or valine / -58.1,-28.1	30% ( <i>pt</i> ) chi angles: 69.4,172.7	0.078Å	-	-
D 418	ASP	50	-	Favored (93.02%) General / -65.4,-41.9	44.6% ( <i>t0</i> ) chi angles: 186.9,329.6	0.038Å	-	-
D 419	SER	50	-	Favored (97.44%) General / -61.8,-44.1	40.5% (t) chi angles: 181.4	0.038Å	-	-
D 420	ILE	50	0.733Å HG12 with D 417 ILE O	Favored (65.2%) Isoleucine or valine / -58.7,-37.4	16.4% ( <i>pt</i> ) chi angles: 71.3,180.5	0.072Å	-	OUTLIER(S) worst is CB-CG1-CD1: $4.186 \sigma$
D 421	LYS	50	0.659Å HG3 with D 417 ILE O	Favored (90.34%) General / -65.2,-38.4	30.7% ( <i>mtpp</i> ) chi angles: 294,181,68,63.9	0.047Å	-	-
D 422	GLN	50	-	Favored (54.03%) General / -77.6,-33.0	19% ( <i>mt-30</i> ) chi angles: 298,166.1,183.5	0.087Å	-	-
D 423	TYR	50	0.446Å CE1 with A 453 GLU HG3	Favored (99.6%) General / -62.0,-42.9	71.9% ( <i>t80</i> ) chi angles: 172.6,84.8	0.05Å	-	-
D 424	MET	50	0.987Å SD with D 437 VAL HG11	Favored (70.48%) General / -71.4,-40.5	69.9% ( <i>mtm</i> ) chi angles: 293.7,191.9,299.6	0.051Å	-	-
D 425	GLN	50	-	Favored (79.45%) General / -67.7,-35.8	53.4% ( <i>tt0</i> ) chi angles: 185.3,179.2,57.1	0.012Å	-	-
D 426	PHE	50	-	Favored (79.9%) General /	11% ( <i>t80</i> ) chi angles: 182.8,38.1	0.025Å	-	-
D	ARG	99 90	1.002Å HR3 with A	-64.7,-35.1 Favored (57.36%)	32.8% ( <i>mmt180</i> )	N 21Å	-	OUTLIER(S)

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ciii angics. 427 General / 473 HIS HE1 287.3,304.8,183.2,180 CB: 4.945 σ -92.0,-1.2 Cβ **Bond Bond** High Clash > Alt Res Ramachandran Rotamer B 0.4Å deviation lengths angles Avg: Clashscore: Outliers: 16 of Poor rotamers: 12 of Outliers: Outliers: 12 Outliers: 64 61.33 65.92 764 676 4 of 728 of 772 of 772 **Favored** 88.4% (mttt) D (28.26%)LYS 0.051Å 50 chi angles: 428 General / 298.3,170.7,185,166.5 54.1,38.0 **Favored** 0.935Å (5.58%)D 12.1% (p)HG21 with D 0.168Å VAL 50 Isoleucine or 429 433 LEU chi angles: 62.1 valine / HD22 -61.0,152.8 **Favored** 0.449Å D 98.9% (m) (7.51%)0.05Å **THR** 50 HG22 with D 430 General / chi angles: 298.8 432 ASP H -57.2,156.3 **Favored** 0.445Å 32.8% (mmmt) D (82.42%)0.032Å LYS 50 O with D 435 chi angles: 431 General / THR HG23 296.3,295.3,295.3,181.1 -66.9,-36.5 Favored 0.449Å D 85.2% (m-20) (80.59%)0.053Å **ASP** 50 H with D 430 432 chi angles: 293.9,349.1 General / THR HG22 -65.3,-35.3 0.935Å **Favored** D 8.5% (tt) HD22 with D (63.81%)0.12Å **LEU** 50 433 429 VAL chi angles: 191.4,155.1 General / HG21 -73.5,-40.7 **Favored** 0.783Å 54.6% (mt-10) D (93.62%)0.075Å **GLU** 50 O with D 438 chi angles: 434 General / ILE HG12 296.7,182.7,298.1 -63.9,-39.2 **Favored** 0.445Å D (68.27%)77.9% (p) 0.02Å THR 50 HG23 with D 435 chi angles: 60.2 General / 431 LYS O -66.1,-49.3 **Favored** 86.8% (mtm-85) D (72.82%)ARG chi angles: 0.068Å 50 436 General / 285.7,187.7,294.2,260.3 -58.2,-36.2 0.987Å **Favored** D 4.9% (p)0.175Å VAL 50 HG11 with D (68.54%)437 chi angles: 76.4 424 MET SD Isoleucine or

		61.33		764 Allowed	676	4 of 728	of 772	of 772
# <b>A</b>	it kes	В	<b>0.4Å</b> Clashscore:	Ramachandran Outliers: 16 of	<b>Rotamer</b> Poor rotamers: 12 of	deviation	O	<b>angles</b> Outliers: 64
447	ASN  It Res	99.99 High	410 ARG HH21 Clash >	General / 56.4,26.0	chi angles: 184.8,348.8	0.09/A <b>C</b> β	Bond	CG-ND2: 5.666 σ <b>Bond</b>
D	ACNI	99.99	0.546Å CG with D	51.6,18.1 Favored (10.17%)	64.3% ( <i>t-20</i> )	0.097Å		OUTLIER(S) worst is OD1-
D 446	ALA	50	-	Allowed (0.66%) General /	-	0.046Å	-	-
D 445	TRP	50	0.445Å HE3 with D 413 PHE CD1	Favored (8.96%) General / -119.3,-16.7	51.6% ( <i>m0</i> ) chi angles: 296.7,351.6	0.079Å	OUTLIER(S) worst is NE1 CE2: 4.757 σ	OUTLIER(S) worst is CD2- CE3-CZ3: 4.172 σ
D 444	LEU	99.99	0.837Å HD22 with D 440 TRP CH2	Favored (22.95%) General / -84.8,-33.5	21.3% ( <i>tp</i> ) chi angles: 187.1,74	0.098Å	-	-
D 443	TYR	50	0.55Å CE2 with D 573 TYR CZ	Favored (60.59%) General / -75.2,-30.6	95.2% ( <i>m-85</i> ) chi angles: 292.2,274.8	0.027Å	-	-
D 442	ASP	50	0.403Å HB2 with D 439 ARG O	Favored (67.79%) General / -53.0,-45.5	51.3% ( <i>m-20</i> ) chi angles: 295.4,296.5	0.044Å	-	-
D 441	PHE	50	0.791Å HE2 with D 437 VAL HG22	Favored (61.2%) General / -51.0,-46.2	95.6% ( <i>m</i> -85) chi angles: 292.3,275.1	0.072Å	-	-
D 440	TRP	99.99	0.837Å CH2 with D 444 LEU HD22	Favored (42.13%) General / -62.5,-54.3	89.3% ( <i>t</i> 90) chi angles: 184.8,87.3	0.024Å	OUTLIER(S) worst is NE1 CE2: 4.769 σ	OUTLIER(S) worst is CZ2- CH2-CZ3: 5.295 σ
D 439	ARG	50	0.456Å O with D 443 TYR HD2	Favored (77.74%) General / -60.0,-36.6	55.1% ( <i>mmm-85</i> ) chi angles: 293.6,298,293,278.7	0.033Å	-	-
D 438	ILE	50	0.783Å HG12 with D 434 GLU O	valine / -72.0,-41.3 Favored (28.75%) Isoleucine or valine / -58.1,-54.7	41.3% ( <i>mm</i> ) chi angles: 299.1,304.7	0.028Å	-	-

D 448	LYS 99.99	-	(0.73%) General / -106.2,-72.0	29.5% ( <i>ιριρ)</i> chi angles: 182.4,64.6,177.9,64.7	0.065Å	-	-
D 449	LYS 99.99	0.671Å HD2 with D 409 SER HB2	Favored (49.27%) General / -125.4,147.2	27.9% ( <i>tptp</i> ) chi angles: 180.1,66.8,182.2,61.9	0.078Å	-	OUTLIER(S) worst is CG- CD-CE: 4.38 σ
D 450	THR 99.99	0.72Å HG22 with D 451 VAL H	Allowed (0.82%) General / -119.5,-160.6	48.8% ( <i>m</i> ) chi angles: 305	0.108Å	-	-
D 451	VAL 99.99	1.03Å HG22 with D 452 ASP HA	Allowed (0.44%) Isoleucine or valine / -48.1,151.2	6% (p) chi angles: 75	0.168Å	-	-
D 452	ASP 50	1.03Å HA with D 451 VAL HG22	Allowed (1.01%) General / -104.8,44.7	2.2% ( <i>m-20</i> ) chi angles: 294.9,33.2	0.14Å	-	-
D 453	GLU 50	0.836Å HA with D 456 VAL HG22	Allowed (0.6%) General / -40.4,-36.9	27.1% (tt0) chi angles: 193.5,193.3,40.1	0.048Å	-	-
D 454	LYS 50	-	Favored (79.14%) General / -63.5,-48.0	39% (ttpt) chi angles: 186.5,179.9,64.3,181.3	0.041Å	-	-
D 455	GLU 50	0.762Å HB3 with D 452 ASP HB3	Favored (75.69%) General / -65.6,-47.4	10.8% ( <i>tm-20</i> ) chi angles: 181.5,289.8,325.2	0.055Å	-	-
D 456	VAL 50	0.836Å HG22 with D 453 GLU HA	Favored (85.34%) Isoleucine or valine / -58.9,-42.3	22.1% ( <i>m</i> ) chi angles: 302.9	0.037Å	-	-
D 457	LEU 50	0.477Å HB2 with D 453 GLU O	Favored (82.27%) General / -68.2,-40.5	0.5% chi angles: 254.3,39.3	0.042Å	-	-
D 458	LYS 50	-	Favored (93.83%) General / -61.1,-40.4	28.6% ( <i>tptp</i> ) chi angles: 184.5,62.4,180.5,64.5	0.04Å	-	-
D 459	SER 99.99	0.652Å O with B 440	Favored (77.29%) General /	95.9% (p) chi angles: 66.7	0.102Å	-	OUTLIER(S) worst is CA-C-

			INF UHZ	-64.6,-34.0	<u>~</u>			U. 3.373 U
D 460	LEU	50	-	Favored (38.7%) Pre-proline / -71.6,166.5	81% ( <i>mt</i> ) chi angles: 298.2,182.5	0.042Å	-	-
D 461	PRO	50	0.774Å HD3 with B 440 TRP CE2	Favored (6.07%) Trans-proline / -87.7,171.3	42.9% ( <i>Cg_endo</i> ) chi angles: 35.9	0.014Å	-	-
D 462	ASP	50	-	Favored (96.45%) General / -64.0,-43.1	42.1% ( <i>t0</i> ) chi angles: 190.5,329.5	0.016Å	-	-
D 463	LYS	50	0.684Å HE2 with B 508 TYR H	Favored (73.75%) General / -57.8,-37.4	32.4% ( <i>mmmt</i> ) chi angles: 294.8,293.5,296.6,184.8	0.04Å	-	-
D 464	LEU	50	0.657Å HD12 with D 461 PRO HD2	Favored (22.9%) General / -75.5,-48.4	59.3% ( <i>mt</i> ) chi angles: 286.4,177.4	0.038Å	-	-
D 465	LYS	50	0.591Å O with D 470 ILE HG12	Favored (72.81%) General / -61.0,-33.1	54.9% ( <i>mtmt</i> ) chi angles: 294.7,178.6,295.9,178.8	0.135Å	-	-
D 466	ALA	50	0.727Å HA with D 470 ILE CB	Favored (83.8%) General / -66.6,-36.9	-	0.118Å	-	-
D 467	GLU	50	0.6Å OE2 with B 433 LEU HD12	Favored (79.54%) General / -68.8,-40.5	15.5% ( <i>tt0</i> ) chi angles: 206.1,191.3,309.1	0.116Å	-	-
# <b>A</b> l	lt Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
		Avg: 61.33	Clashscore: 65.92	Outliers: 16 of 764	Poor rotamers: 12 of 676	Outliers: 4 of 728	Outliers: 12 ( of 772	Outliers: 64 of 772
D 468	ILE	99.99	0.887Å HA with D 472 VAL HG12	Favored (24.44%) Isoleucine or valine / -119.2,146.0	17.8% ( <i>pt</i> ) chi angles: 51.7,179.6	0.186Å	-	-
D 469	ALA	99.99	0.947Å H with D 473 HIS HD2	Allowed (1.81%) General / 66.3,0.8 Allowed	-	0.078Å	-	-

D 470	ILE 99.99	0.973A HD12 with D 496 LEU HA	(0.75%) Isoleucine or valine / -132.4,-25.7	26.9% (mm) chi angles: 299,310.2	0.091Å	-	-
D 471	ASN 50	1.036Å HD21 with D 492 VAL HG12	Allowed (0.47%) General / -140.4,-51.1	42.2% ( <i>m-20</i> ) chi angles: 278.7,302.3	0.195Å	-	OUTLIER(S) worst is CA- CB-CG: 4.049 σ
D 472	VAL 50	0.887Å HG12 with D 468 ILE HA	Favored (82.17%) Isoleucine or valine / -58.6,-41.5	15% (p) chi angles: 63.5	0.065Å	-	-
D 473	HIS 99.99	1.003Å HE1 with B 427 ARG HB3	Favored (61.3%) General / -72.7,-25.5	84.1% ( <i>m-70</i> ) chi angles: 288,298.1	0.04Å	OUTLIER(S) worst is CD2 NE2: 7.083 σ	OUTLIER(S) worst is CD2- NE2-CE1: 12.71 σ
D 474	LEU 99.99	0.699Å 9 C with D 474 LEU HD23	Favored (38.13%) General / -53.1,132.5	7.2% (tt) chi angles: 184.9,162.9	0.126Å	-	-
D 475	ASP 99.99	0.538Å 9 N with D 474 LEU HD23	Favored (5.85%) General / -129.7,12.7	29.9% ( <i>t70</i> ) chi angles: 179.1,76.4	0.069Å	-	-
D 476	THR 99.99	0.485Å HB with D 523 ASN HA	Favored (2.21%) General / -136.0,48.0	10.3% ( <i>t</i> ) chi angles: 184.2	0.074Å	-	-
D 477	LEU 99.99	1.099Å HG with D 483 PHE HB3	Allowed (0.81%) General / -134.6,-52.3	10% ( <i>tt</i> ) chi angles: 185.3,154.6	0.239Å	-	-
D 478	LYS 50	-	Favored (31.44%) General / -53.1,-29.6	27.1% ( <i>tptp</i> ) chi angles: 180.3,61.9,184.6,69.5	0.035Å	-	-
D 479	LYS 50	-	Favored (49.45%) General / -89.1,-9.9	26.8% ( <i>tptp</i> ) chi angles: 188.6,61.2,182.7,67.3	0.051Å	-	-
D 480	VAL 50	1.033Å HG12 with D 477 LEU HA	Favored (23.98%) Isoleucine or valine /	11.5% ( <i>p</i> ) chi angles: 66.6	0.141Å	-	-
D 401	ARG 50	0.722Å HA with D	-117.0,108.1 Favored (7.28%)	57.9% ( <i>mmm-85</i> ) chi angles:	0.027Å	-	-

<del>4</del> 01			404 ULIN HG2	Generai / -43.5,-47.1	296.1,292.8,296.7,277.2			
D 482	ILE	50	0.739Å HG12 with D 480 VAL HG22	Favored (87.84%) Isoleucine or valine / -59.3,-42.6	42.2% ( <i>pt</i> ) chi angles: 65.5,172.5	0.067Å	-	-
D 483	РНЕ	50	1.099Å HB3 with D 477 LEU HG	Favored (28.76%) General / -79.7,-40.6	7.1% ( <i>m</i> -30) chi angles: 278.5,9.7	0.047Å	-	OUTLIER(S) worst is CA- CB-CG: 4.414 σ
D 484	GLN	50	0.722Å HG2 with D 481 ARG HA	Favored (83.93%) General / -67.8,-38.8	19.8% ( <i>pt20</i> ) chi angles: 65.9,181.7,61.9	0.076Å	-	-
D 485	ASP	50	-	Favored (4.67%) General / -97.0,26.4	48.7% ( <i>t0</i> ) chi angles: 190.7,338.3	0.039Å	-	-
D 486	CYS	99.99	0.633Å SG with D 490 LEU HD23	Favored (27.27%) General / -115.1,155.3	52.7% ( <i>t</i> ) chi angles: 181.3	0.052Å	-	-
D		00.00		Favored (8.68%)	87.8% (mt-10)	0.0648		
487	GLU	99.99	-	General / -57.2,120.8	chi angles: 301.3,182.2,337.1	0.064Å	-	-
487	GLU <b>Alt Res</b>	99.99 High B	- Clash > 0.4Å	General /	301.3,182.2,337.1	Сβ	Bond lengths	Bond angles
487		High B	0.4Å	General / -57.2,120.8 Ramachandran	301.3,182.2,337.1	Cβ deviation	lengths	angles
487		<b>High B</b> Avg: 61.33	<b>0.4Å</b> Clashscore:	General / -57.2,120.8 Ramachandran Outliers: 16 of	301.3,182.2,337.1 <b>Rotamer</b> Poor rotamers: 12 of	Cβ deviation Outliers:	<b>lengths</b> Outliers: 12	<b>angles</b> 2 Outliers: 64
487 # A	Alt Res	<b>High B</b> Avg: 61.33	<b>0.4Å</b> Clashscore: 65.92 0.732Å O with D 492	General / -57.2,120.8 Ramachandran Outliers: 16 of 764 Favored (14.29%) General /	301.3,182.2,337.1 <b>Rotamer</b> Poor rotamers: 12 of	Cβ deviation Outliers: 4 of 728	<b>lengths</b> Outliers: 12	<b>angles</b> 2 Outliers: 64
487 # A D 488	Alt Res ALA GLY	High B Avg: 61.33 50	0.4Å Clashscore: 65.92 0.732Å O with D 492 VAL HG13 0.49Å O with D 492	General / -57.2,120.8 Ramachandran Outliers: 16 of 764 Favored (14.29%) General / -54.9,-22.3 Favored (76.39%) Glycine /	301.3,182.2,337.1 <b>Rotamer</b> Poor rotamers: 12 of	Cβ deviation Outliers: 4 of 728	<b>lengths</b> Outliers: 12	<b>angles</b> 2 Outliers: 64
# A D 488 D 489	Alt Res  ALA  GLY  LEU	High B Avg: 61.33 50 50	0.4Å Clashscore: 65.92 0.732Å O with D 492 VAL HG13  0.49Å O with D 492 VAL HG22  0.748Å HD13 with D 591 TYR CD1  0.837Å	General / -57.2,120.8  Ramachandran  Outliers: 16 of 764  Favored (14.29%) General / -54.9,-22.3  Favored (76.39%) Glycine / -67.5,-45.6  Favored (93.9%) General /	301.3,182.2,337.1  Rotamer  Poor rotamers: 12 of 676  -  35.4% (tp)	Cβ deviation Outliers: 4 of 728 0.016Å	<b>lengths</b> Outliers: 12	<b>angles</b> 2 Outliers: 64
# A D 488 D 489	Alt Res  ALA  GLY  LEU	High B Avg: 61.33 50 50	0.4Å Clashscore: 65.92 0.732Å O with D 492 VAL HG13  0.49Å O with D 492 VAL HG22  0.748Å HD13 with D 591 TYR CD1	General / -57.2,120.8  Ramachandran  Outliers: 16 of 764  Favored (14.29%) General / -54.9,-22.3  Favored (76.39%) Glycine / -67.5,-45.6  Favored (93.9%) General / -65.5,-41.0	301.3,182.2,337.1  Rotamer  Poor rotamers: 12 of 676  -  35.4% (tp)	Cβ deviation Outliers: 4 of 728 0.016Å	<b>lengths</b> Outliers: 12	<b>angles</b> 2 Outliers: 64

D 492	VAL	50	1.036Å HG12 with D 471 ASN HD21	Favored (14.9%) Isoleucine or valine / -48.6,-45.5	25.8% ( <i>m</i> ) chi angles: 302	0.023Å	-	-
D 493	GLU	50	-	Favored (68.45%) General / -66.2,-28.0	14.3% ( <i>tm-20</i> ) chi angles: 183.8,285.4,333.7	0.107Å	-	-
D 494	LEU	50	0.694Å HD23 with D 483 PHE CE1	Favored (12.94%) General / -80.0,-48.7	33.9% ( <i>tp</i> ) chi angles: 187.7,59.4	0.033Å	-	OUTLIER(S) worst is CD1- CG-CD2: 4.562 σ
D 495	VAL	50	0.752Å HG21 with D 470 ILE O	Favored (44.55%) Isoleucine or valine / -57.7,-33.2	20.8% (m) chi angles: 303.3	0.021Å	-	-
D 496	LEU	50	0.973Å HA with D 470 ILE HD12	Favored (55.61%) General / -64.8,-13.4	8.9% ( <i>tt</i> ) chi angles: 190.5,154.5	0.155Å	-	-
D 497	LYS	50	-	Favored (10.85%) General / -115.9,-18.0	64.5% ( <i>mttp</i> ) chi angles: 295.5,177.2,177.3,63.2	0.054Å	-	-
D 498	LEU	50	0.636Å HB3 with D 577 PHE HB3	Favored (44.49%) General / -58.6,144.1	58.4% ( <i>mt</i> ) chi angles: 305.2,173.5	0.096Å	-	-
D 499	ARG	50	-	Favored (28.15%) Pre-proline / -118.9,124.7	40.1% ( <i>ptt180</i> ) chi angles: 62,179.4,181.4,181.7	0.069Å	-	-
D 500	PRO	50	-	Favored (33.36%) Trans-proline / -68.0,135.0	92.8% ( <i>Cg_endo</i> ) chi angles: 30.9	0.035Å	-	-
D 501	THR	50	-	Favored (30.24%) General / -144.9,142.9	63.1% ( <i>p</i> ) chi angles: 62.3	0.038Å	-	-
D 502	VAL	50	-	Favored (36.42%) Isoleucine or valine / -115.5,140.6	74% (t) chi angles: 174	0.052Å	-	-

D 503	PHE	50	-	(50.81%) General / -127.0,145.2	63.9% ( <i>m-85</i> ) chi angles: 284.3,87.2	0.046Å	-	-
D 504	SER	50	-	Favored (31.54%) Pre-proline / -101.6,158.6	70.2% ( <i>m</i> ) chi angles: 295.9	0.029Å	-	-
D 505	PRO	50	-	Favored (52.06%) Trans-proline / -53.9,132.9	88.3% ( <i>Cg_exo</i> ) chi angles: 331.4	0.107Å	-	-
D 506	GLY	50	-	Favored (9.88%) Glycine / 100.2,-30.6	-	-	-	-
D 507	ASP	50	0.458Å HA with A 463 LYS HE2	Allowed (0.56%) General / -49.0,155.9	81.1% ( <i>m-20</i> ) chi angles: 283.3,337.3	0.05Å	-	-
# .	Alt Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
		Avg: 61.33		Outliers: 16 of 764	Poor rotamers: 12 of 676	Outliers: 4 of 728	Outliers: 12 of 772	Outliers: 64 of 772
				Favored				
D 508	TYR	50	0.667Å H with A 463 LYS HE2	(5.14%) General / -108.5,94.6	11.4% ( <i>m-30</i> ) chi angles: 282.8,356.5	0.101Å	-	-
	TYR ILE	50 50	H with A 463	(5.14%) General /		0.101Å 0.091Å	-	-
508 D	ILE		H with A 463 LYS HE2  0.814Å HB with D 568 ILE HG23  1.035Å	(5.14%) General / -108.5,94.6 Favored (99.01%) Isoleucine or valine /	chi angles: 282.8,356.5 69% ( <i>mt</i> )		-	-
508 D 509	ILE	50	H with A 463 LYS HE2  0.814Å HB with D 568 ILE HG23  1.035Å HB3 with D 568 ILE	(5.14%) General / -108.5,94.6 Favored (99.01%) Isoleucine or valine / -60.9,-45.0 Favored (28.07%) General /	chi angles: 282.8,356.5  69% ( <i>mt</i> ) chi angles: 303.1,168.1	0.091Å	-	-
508  D 509  D 510	ILE CYS	50 99.99	H with A 463 LYS HE2  0.814Å HB with D 568 ILE HG23  1.035Å HB3 with D 568 ILE HG22  0.455Å NZ with D	(5.14%) General / -108.5,94.6 Favored (99.01%) Isoleucine or valine / -60.9,-45.0 Favored (28.07%) General / -144.3,138.6 Favored (37.7%) General /	69% ( <i>mt</i> ) chi angles: 303.1,168.1  4.8% ( <i>t</i> ) chi angles: 164.3  68.4% ( <i>mttm</i> ) chi angles:	0.091Å 0.071Å	-	-

٠.٠			AKG HDZ	78.9,-20.6				
D 514	ASP	50	0.475Å O with D 564 ARG HG2	Favored	42.6% ( <i>t0</i> ) chi angles: 189,328.5	0.062Å	-	-
D 515	ILE	50	-	Favored (12.76%) Isoleucine or valine / -63.5,121.6	27.2% ( <i>mt</i> ) chi angles: 311.5,178.4	0.032Å	-	-
D 516	GLY	50	-	Favored (10.08%) Glycine / -98.5,130.0	-	-	-	-
D 517	LYS	50	0.533Å HG2 with D 517 LYS O	Favored (9.22%) General / -124.0,19.7	61.9% (tttm) chi angles: 185.6,184.4,177.4,293.2	0.063Å	-	-
D 518	GLU	50	-	Favored (7.59%) General / -169.3,157.6	12.6% ( <i>pt-20</i> ) chi angles: 61.5,180.2,62.4	0.013Å	-	-
D 519	MET	50	-	Favored (8.78%) General / -124.8,173.1	27.1% ( <i>ptm</i> ) chi angles: 65.3,172.3,293.2	0.032Å	-	-
D 520	TYR	50	-	Favored (52.46%) General / -130.9,149.6	90.2% ( <i>m-85</i> ) chi angles: 299.1,87.1	0.071Å	-	-
D 521	ILE	50	0.645Å CG1 with D 577 PHE HB2	Favored (15.09%) Isoleucine or valine / -121.0,104.3	32% ( <i>pt</i> ) chi angles: 66.9,166.7	0.058Å	-	-
D 522	ILE	50	-	Allowed (0.15%) Isoleucine or valine / -58.2,105.0	62.3% ( <i>mt</i> ) chi angles: 304.9,175.2	0.02Å	-	-
D 523	ASN	50	0.485Å HA with D 476 THR HB	Favored (20.01%) General / -76.9,-47.8	48.4% ( <i>t30</i> ) chi angles: 182.1,60.4	0.01Å	-	-
D 524	GLU	50	-	Favored (6.4%) General / -157.0,127.2 Favored	11.3% ( <i>tm-20</i> ) chi angles: 179.9,288.5,328.5	0.08Å	-	-

D 525	GLY	50	-	(13.05%) Glycine / 132.8,172.6	-	-	-	-
D 526	LYS	99.99	0.979Å HG3 with D 540 VAL HG13	Favored (51.03%) General / -122.2,128.3	66.7% (tttt) chi angles: 165.7,169.7,180.8,162.5	0.107Å	-	-
D 527	LEU	50	0.906Å HB3 with D 568 ILE HD11	Favored (29.48%) General / -119.4,156.8	9.5% ( <i>mp</i> ) chi angles: 281.9,69.5	0.069Å	-	OUTLIER(S) worst is CD1- CG-CD2: 4.488 o
# Alt	Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
		Avg: 61.33	Clashscore: 65.92	Outliers: 16 of 764	Poor rotamers: 12 of 676	Outliers: 4 of 728	Outliers: 12 of 772	Outliers: 64 of 772
D 528	ALA	50	0.492Å O with D 568 ILE HD12	Favored (54.91%) General / -118.4,128.8	-	0.07Å	-	-
D 529	VAL	50	0.696Å HG22 with D 568 ILE HD13	Favored (70.26%) Isoleucine or valine / -113.0,127.5	22.5% ( <i>t</i> ) chi angles: 187.4	0.056Å	-	-
D 530	VAL	50	-	Favored (3.12%) Isoleucine or valine / -130.1,97.0	7.3% (p) chi angles: 58.8	0.101Å	-	-
D 531	ALA	99.99	0.85Å HB2 with D 566 ALA HB2	Allowed (1.95%) General / -130.4,80.3	-	0.137Å	-	-
D 532	ASP	99.99	-	Favored (11.65%) General / 53.0,31.7	29.4% ( <i>t70</i> ) chi angles: 178.9,77	0.068Å	-	-
D 533	ASP	99.99	-	Favored (31.44%) General / -160.3,165.4	26.1% ( <i>p30</i> ) chi angles: 61.8,29.5	0.02Å	-	-
D 534	GLY	99.99	-	Allowed (0.82%) Glycine / -61.8,105.1	-	-	-	-
D			0.6Å	OUTLIER (0%)	7 1% (n)	. •		

535	VAL 50	11022 willi D 536 THR HG22	rsoreucine or valine / -10.6,108.9	7.170 (ρ) chi angles: 58.4	0.01A	-	-
D 536	THR 99.99	0.6Å HG22 with D 535 VAL HG22	Allowed (1.5%) General / 55.6,15.4	9.9% ( <i>t</i> ) chi angles: 184	0.055Å	-	-
D 537	GLN 99.99	0.524Å HG2 with D 536 THR O	Favored (14.51%) General / 47.9,51.3	18.5% ( <i>pt20</i> ) chi angles: 64.8,180.9,57	0.097Å	-	-
D 538	PHE 99.99	0.489Å CD2 with D 538 PHE O	Favored (14.34%) General / 63.5,32.4	85.3% ( <i>t80</i> ) chi angles: 180.7,81.9	0.055Å	-	-
D 539	VAL 99.99	0.8Å HG12 with D 540 VAL H	Allowed (0.48%) Isoleucine or valine / -119.6,-168.6	63.1% ( <i>t</i> ) chi angles: 180	0.087Å	-	OUTLIER(S) worst is CA- CB-CG1: 4.474 σ
D 540	VAL 99.99	0.979Å HG13 with D 526 LYS HG3	OUTLIER (0.06%) Isoleucine or valine / -158.5,97.4	26.7% (t) chi angles: 164.6	0.381Å	-	OUTLIER(S) worst is N-CA- CB: 5.587 σ
D 541	LEU 50	-	Allowed (1.63%) General / -59.4,112.1	18.6% ( <i>mt</i> ) chi angles: 292,193.2	0.076Å	-	-
D 542	SER 50	-	Allowed (1.05%) General / -124.4,-162.1	20.8% (t) chi angles: 188.4	0.068Å	-	-
D 543	ASP 50	-	Favored (20.24%) General / -50.1,135.9	0.3% chi angles: 313.8,44.5	0.116Å	-	-
D 544	GLY 50	-	Favored (73.87%) Glycine / 79.3,18.6	-	-	-	-
D 545	SER 50	-	Favored (28.28%) General / -124.4,160.4	72.6% ( <i>m</i> ) chi angles: 295.6	0.026Å	-	-
D 546	TYR 50	0.621Å CE1 with D 482 ILE HD13	Favored (7.79%) General / -134.8.177.4	45.9% ( <i>p90</i> ) chi angles: 59,275.2	0.048Å	-	-

D 547	F	PHE	50	0.514Å CE2 with D 527 LEU HD22	Favored (4.1%) General / -173.7,162.6	43.6% ( <i>p90</i> ) chi angles: 60.5,83.6	0.022Å	-	-
#	Alt	Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
			Avg: 61.33	Clashscore: 65.92	Outliers: 16 of 764	Poor rotamers: 12 of 676	Outliers: 4 of 728	Outliers: 12 of 772	Outliers: 64 of 772
D 548	(	GLY	50	-	Favored (62.81%) Glycine / 75.1,28.1	-	-	-	-
D 549	(	GLU	50	-	Favored (29.19%) General / -86.9,-19.2	6.4% (pm0) chi angles: 70.4,293.3,339.2	0.053Å	-	-
D 550		ILE	50	-	Favored (97.65%) Isoleucine or valine / -62.3,-43.1	76.9% ( <i>mt</i> ) chi angles: 298.8,177	0.063Å	-	-
D 551	!	SER	50	-	Favored (66.23%) General / -68.4,-27.5	73.4% ( <i>m</i> ) chi angles: 295.3	0.038Å	-	-
D 552		ILE	99.99	0.808Å HG21 with D 584 LEU HD13	Favored (58.47%) Isoleucine or valine / -73.2,-42.2	65.2% ( <i>mt</i> ) chi angles: 302.9,177.3	0.083Å	-	-
D 553	I	LEU	99.99	0.479Å HD23 with D 554 ASN N	Favored (52.8%) General / -70.0,139.6	6.7% ( <i>tt</i> ) chi angles: 182.7,164	0.065Å	-	-
D 554	ŀ	ASN	99.99	0.479Å N with D 553 LEU HD23	Favored (24.51%) General / -118.8,115.5	41% ( <i>p30</i> ) chi angles: 60.9,25.7	0.036Å	-	OUTLIER(S) worst is OD1- CG-ND2: 6.181 σ
D 555		ILE	99.99	0.855Å H with D 560 SER HB3	Favored (28.01%) Isoleucine or valine / -62.8,134.6	37.2% ( <i>pt</i> ) chi angles: 64,176.5	0.065Å	-	-
D 556		LYS	99.99	-	Favored (50.62%) General / -65.7,133.2	22.7% (pttp) chi angles: 61.9,180,182,64.6	0.024Å	-	-

D 557	GLY	99.99	-	Favored (33.75%) Glycine / 106.2,-21.2	-	-	-	-
D 558	SER	99.99	-	Favored (2.7%) General / -151.6,-167.1	32.1% ( <i>t</i> ) chi angles: 184.5	0.087Å	-	-
D 559	LYS	99.99	-	Favored (30.42%) General / -115.6,117.5	22.6% ( <i>pttp</i> ) chi angles: 59.8,180.7,181.7,66.3	0.056Å	-	-
D 560	SER	99.99	0.855Å HB3 with D 555 ILE H	Favored (5.02%) General / -130.5,27.4	45.1% ( <i>t</i> ) chi angles: 178.7	0.049Å	-	OUTLIER(S) worst is O-C- N: 4.559 σ
D 561	GLY	50	-	Allowed (0.75%) Glycine / 48.6,17.4	-	-	-	-
D 562	ASN	50	0.645Å ND2 with D 563 ARG H	Allowed (0.31%) General / -125.8,-144.1	59% ( <i>t30</i> ) chi angles: 188.9,50.1	0.12Å	-	-
D 563	ARG	50	0.645Å H with D 562 ASN ND2	Favored (22.72%) General / -101.8,150.9	12.2% ( <i>mmt180</i> ) chi angles: 305,301.9,193.1,133.1	0.097Å	-	-
D 564	ARG	50	0.475Å HG2 with D 514 ASP O	,	28.1% (mmt180) chi angles: 296.1,296.9,204.3,186.3	0.057Å	-	-
D 565	THR	50	-	Allowed (0.75%) General / -71.9,10.2	63.3% (p) chi angles: 64.8	0.021Å	-	-
D 566	ALA	50	0.85Å HB2 with D 531 ALA HB2	Allowed (0.63%) General / -173.3,-170.6	-	0.204Å	-	-
D 567	ASN	50	-	Favored (54.23%) General / -121.7,138.7	28.5% ( <i>t-20</i> ) chi angles: 187.7,301.4	0.124Å	-	-
# /	Alt Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
		Avg: 61.33	Clashscore: 65.92	Outliers: 16 of 764	Poor rotamers: 12 of 676	Outliers: 0	Outliers: 12 of 772	Outliers: 64 of 772
_		01.55	1 N25 Å	Favored	0, 0	. 0. 720	J. 7, 2	0.772

D 568	ILE	50	1.033A HG22 with D 510 CYS HB3	(/ 4.3 %) Isoleucine or valine / -117.4,125.9	8.6% ( <i>tp</i> ) chi angles: 183.2,64.9	0.129Å	-	-
D 569	ARG	50	-	Favored (46.23%) General / -124.8,126.9	50.3% (ttp180) chi angles: 184.2,189.1,74.3,213.1	0.114Å	-	-
D 570	SER	50	-	Favored (53%) General / -69.3,137.4	34.4% ( <i>t</i> ) chi angles: 183.1	0.109Å	-	-
D 571	ILE	50	0.956Å HG12 with D 526 LYS HG2	Favored (3.98%) Isoleucine or valine / -101.1,-34.6	0.8% chi angles: 77.1,123.2	0.071Å	-	-
D 572	GLY	50	0.619Å N with D 571 ILE HG13	Favored (14.7%) Glycine / -118.8,172.9	-	-	-	-
D 573	TYR	50	0.55Å CZ with D 443 TYR CE2	OUTLIER (0.02%) General / -60.3,90.5	22.6% ( <i>m</i> -85) chi angles: 274.5,272.2	0.028Å	-	-
D 574	SER	50	-	Favored (40.49%) General / -76.0,145.1	53.7% ( <i>m</i> ) chi angles: 299.9	0.062Å	-	-
D 575	ASP	50	0.484Å O with D 523 ASN HB3	Favored (6.37%) General / -125.7,100.3	90% ( <i>m-20</i> ) chi angles: 294.2,344	0.005Å	-	-
D 576	LEU	50	-	Favored (9.84%) General / -109.0,167.8	37.2% ( <i>mt</i> ) chi angles: 310.5,176.1	0.111Å	-	-
D 577	PHE	50	0.645Å HB2 with D 521 ILE CG1	Favored (51.56%) General / -126.1,133.8	88.9% ( <i>m-85</i> ) chi angles: 300.1,90	0.044Å	-	-
D 578	CYS 9	99.99	) -	Favored (31.6%) General / -104.5,144.5	52.3% ( <i>t</i> ) chi angles: 180	0.035Å	-	-
D 579	LEU	50	0.549Å HD22 with D 494 LEU HD11	Favored (44.24%) General / -129.0,128.7	30.8% ( <i>tp</i> ) chi angles: 188.6,66.7	0.096Å	-	-

D 580	SER	50	-	Favored (21.27%) General / -83.9,159.8	84% ( <i>p</i> ) chi angles: 68.6	0.017Å	-	-
D 581	LYS	50	0.714Å HG3 with D 552 ILE HG23	Favored (79.78%) General / -60.1,-37.4	39.2% ( <i>ttpt</i> ) chi angles: 187,179.1,66.9,179.8	0.066Å	-	-
D 582	ASP	50	-	Allowed (0.83%) General / -52.3,-64.4	5.6% ( <i>m-20</i> ) chi angles: 306.4,84.2	0.075Å	-	-
D 583	ASP	50	-	Favored (78.54%) General / -63.6,-34.8	62% ( <i>m</i> -20) chi angles: 294.3,302.8	0.03Å	-	-
D 584	LEU	99.99	0.808Å HD13 with D 552 ILE HG21	Favored (73.82%) General / -61.0,-50.3	10.3% (tt) chi angles: 183.9,150	0.045Å	-	-
D 585	MET	50	0.625Å O with D 589 THR HG23	Favored (69.05%) General / -69.1,-30.7	60.7% ( <i>mtt</i> ) chi angles: 292.3,183.8,173.7	0.026Å	-	-
D 586	GLU	50	-	Favored (45.07%) General / -66.7,-52.4	62.4% ( <i>tt0</i> ) chi angles: 185.1,189.7,338.7	0.069Å	-	-
D 587	ALA	50	-	Favored (70.58%) General / -61.5,-30.4	-	0.091Å	-	-
# Al	t Res	High B	Clash > 0.4Å	Ramachandran	Rotamer	Cβ deviation	Bond lengths	Bond angles
		Avg: 61.33		Outliers: 16 of 764	Poor rotamers: 12 of 676	Outliers: 4 of 728	Outliers: 12 of 772	Outliers: 64 of 772
D 588	LEU	50	-	Favored (26.72%) General / -86.3,-22.5	48.9% ( <i>mt</i> ) chi angles: 293.2,185.6	0.112Å	-	-
D 589	THR	50	0.625Å HG23 with D 585 MET O	Favored (65.07%) General /	77.8% (p) chi angles: 60.2	0.017Å	-	-
D 590	GLU	50	-	-72.8,-31.9 Favored (57.13%) General /	80.4% ( <i>tt0</i> ) chi angles:	0.094Å	-	-

				-77.0,-32.5	100.2,1//.5,15.0			
D 591	TYR	50	0.748Å CD1 with D 490 LEU HD13	Favored (65.41%) Pre-proline / -133.8,76.7	90.7% ( <i>m-85</i> ) chi angles: 301.5,99.4	0.05Å	-	-
D 592	PRO	50	-	Favored (32.53%) Trans-proline / -60.1,-43.9	82.1% ( <i>Cg_exo</i> ) chi angles: 331.9	0.085Å	-	-
D 593	GLU	50	-	Allowed (0.79%) General / -42.2,-34.6	52.3% ( <i>mm-40</i> ) chi angles: 290.9,289.4,0.6	0.08Å	-	-
D 594	ALA	50	-	Favored (60.22%) General / -74.2,-20.4	-	0.035Å	-	-
D 595	LYS	50	0.411Å O with D 599 GLU HG3	Favored (83.92%) General / -59.5,-39.5	63.6% (tttp) chi angles: 183.3,182.1,179.2,63.2	0.022Å	-	-
D 596	LYS	50	-	Favored (80.88%) General / -64.0,-35.5	64% (tttp) chi angles: 184.1,180.4,179.1,62.3	0.017Å	-	-
D 597	ALA	50	-	Favored (64.25%) General / -56.5,-52.6	-	0.031Å	-	-
D 598	LEU	50	-	Favored (92.89%) General / -64.8,-39.0	10.5% ( <i>mp</i> ) chi angles: 280.6,63.7	0.026Å	-	-
D 599	GLU	99.99	0.411Å HG3 with D 595 LYS O	-	74.9% ( <i>mt-10</i> ) chi angles: 293.7,191.7,332	0.049Å	-	-

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