

Arginine

Arginine

o-label		Arginine																		
seq #	label	Name	#	%	alpha	beta	other	χ^1		χ^2		χ^3		χ^4		$\frac{1}{2}$ width at $\frac{1}{2}$ height				
								mode	comm. ^a	mode	comm.	mode	comm.	mode	comm.	χ^1	χ^2	χ^3	χ^4	
1	mmmm_2	mmm-85°	22	2%	2%	3%	3%	-62	-62	-64	-68	-61	-65	-82	-85	14	13	15	13	
2	mmmt_1	mmm180°	11	1%	<1% ^c	2%	2%	-64	-62	-74	-68	-67	-65	172	175	14	15	10	13	
3	mmmt_2	mmt-85°	22	2%	<1%	4%	3%	-60	-62	-72	-68	-178	180	-92	-85	14	13	15	13	
4	mmtt_2	mmt180°	18	2%	1%	3%	2%	-63	-62	-66	-68	-179	180	-168	180	13	13	10	29	
5	mmtp_1	mmt85° ^b	7	1%	1%	1%	1%		-62		-68		180		85					
6	mtmm_6	mtm-85°	54	6%	13%	2%	3%	-69	-67	-167	-167	-63	-65	-86	-85	14	13	13	13	
7	mtmt_5	mtm180°	48	5%	1%	4%	8%	-68	-67	173	180	-64	-65	180	175	14	17	13	30	
8	mtmp_2	mtm105°	15	2%	1%	1%	2%	-68	-67	-179	180	-65	-65	103	105	12	13	13	15	
9	mttm_6	mtt-85°	53	6%	4%	7%	6%	-66	-67	-177	180	-179	180	-83	-85	13	13	13	13	
10	mttt_9	mtt180°	89	9%	9%	5%	12%	-67	-67	-178	180	-177	180	174	180	14	13	13	21	
11	mttp_4	mtt85°	34	4%	4%	4%	3%	-67	-67	178	180	179	180	83	85	12	19	13	19	
12	mtpm_1	mtp-105°	7	1%	0%	2%	1%	-62	-67	179	180	67	65	-113	-105	11	15	13	15	
13	mtpt_5	mtp180°	45	5%	4%	3%	6%	-65	-67	176	180	64	65	-174	-175	12	19	13	19	
14	mtpp_2	mtp85°	22	2%	2%	3%	2%	-69	-67	177	180	64	65	84	85	13	17	13	13	
15	ttmm_3	tmm-85°	28	3%	3%	3%	3%	-175	-177	-178	180	-65	-65	-84	-85	14	16	15	14	
16	ttmt_1	tmm180°	13	1%	<1%	4%	1%	180	-177	-178	180	-67	-65	176	175	12	11	15	15	
17	ttmp_1	tmm105°	10	1%	2%	1%	<1%	-178	-177	170	180	-66	-65	107	105	15	16	15	15	
18	tttm_3	ttt-85°	26	3%	3%	3%	2%	-179	-177	179	180	180	180	-86	-85	15	14	14	15	
19	tttt_4	ttt180°	33	4%	3%	7%	3%	-179	-177	177	180	-179	180	170	180	15	13	12	27	
20	tttt_2	ttt85°	19	2%	2%	2%	2%	-175	-177	176	180	179	180	83	85	14	14	13	14	
21	ttpm_1	ttp-105°	9	1%	1%	1%	1%		-177		180		65		-105					
22	ttpt_3	ttp180°	25	3%	5%	3%	1%	-178	-177	-178	180	65	65	-162	-175	14	16	14	26	
23	ttpp_4	ttp85°	33	4%	5%	3%	3%	-179	-177	177	180	65	65	83	85	14	17	13	15	
24	tpmt_2	tpm180°	15	2%	3%	1%	1%	179	-177	60	65	178	180	163	180	13	17	14	17	
25	tppt_2	tpm85°	20	2%	3%	2%	2%	177	-177	64	65	180	180	86	85	14	13	15	14	
26	tppt_1	tpm180°	8	1%	1%	0%	1%		-177		65		65		-175					
27	tppp_1	tpm85°	11	1%	3%	1%	<1%	-178	-177	57	65	57	65	85	85	13	13	12	15	
28	ptmm_1	ptm-85°	5	1%	0%	0%	1%		62		180		-65		-85					
29	ptmt_1	ptm180°	6	1%	0%	1%	1%		62		180		-65		175					
30	pttm_2	ptt-85°	15	2%	1%	2%	2%	66	62	-176	180	-178	180	-83	-85	15	14	12	14	
31	pttt_2	ptt180°	16	2%	1%	2%	2%	59	62	176	180	-178	180	-177	180	15	13	15	19	
32	pttp_2	ptt85°	16	2%	1%	2%	2%	65	62	-178	180	-179	180	88	85	13	14	13	17	
33	ptpt_1	ptp180°	11	1%	0%	2%	2%	71	62	171	180	65	65	-161	-175	14	17	10	13	
34	ptpp<1	ptp85°	3	<1%	0%	1%	<1%		62		180		65		85					
			769/938 ^d	82%	79%	81%	84%													
			234	146	389															

Lysine

Lysine

o-label		Lysine																		
seq #	label	Name	#	%	alpha	beta	other	χ^1		χ^2		χ^3		χ^4		$\frac{1}{2}$ width at $\frac{1}{2}$ height				
								mode	comm.	mode	comm.	mode	comm.	mode	comm.	χ^1	χ^2	χ^3	χ^4	
1	mmmt_1	mmmt	10	1%	<1%	1%	1%	-59	-62	-58	-68	-75	-68	-174	180	12	13	10	15	
2	mmtm_1	mmtm	18	1%	1%	1%	2%	-59	-62	-69	-68	-176	180	-70	-65	14	12	10	15	
3	mmtt_6	mmtt	77	6%	3%	5%	8%	-58	-62	-61	-68	-177	180	-179	180	12	13	13	13	
4	mmtp_1	mmtp	9	1%	<1%	0%	1%		-62		-68		180		65					
5	mtmm_1	mtmm	12	1%	0%	1%	1%	-70	-67	-179	180	-66	-68	-64	-65	12	12	12	11	
6	mtmt_3	mtmt	40	3%	6%	2%	3%	-70	-67	-170	180	-66	-68	-175	180	12	13	14	13	
7	mttm_5	mttm	56	5%	3%	5%	6%	-67	-67	-179	180	-179	180	-63	-65	13	12	13	14	
8	mttt20	mttt	244	20%	23%	14%	21%	-67	-67	176	180	179	180	177	180	14	13	12	14	
9	mttp_3	mttp	42	3%	2%	4%	4%	-67	-67	-176	180	174	180	76	65	13	13	14	14	
10	mtpt_3	mtpt	38	3%	4%	2%	3%	-69	-67	164	180	62	68	-179	180	12	13	11	9	
11	mtpp_1	mtpp	12	1%	1%	1%	1%	-69	-67	-179	180	70	68	67	65	10	9	10	13	
12	mptt<1	mptt	4	<1%	0%	0%	1%		-90		68		180		180					
13	ttmm<1	ttmm	5	<1%	1%	0%	<1%		-177		180		-68		-65					
14	ttmt_2	ttmt	20	2%	2%	4%	1%	-175	-177	-174	180	-69	-68	179	180	14	14	10	15	
15	tttm_3	tttm	37	3%	4%	2%	3%	-177	-177	172	180	178	180	-72	-65	12	13	15	13	
16	tttt13	tttt	162	13%	17%	19%	10%	-177	-177	178	180	179	180	180	180	13	13	15	13	
17	tttp_4	tttp	49	4%	5%	5%	3%	-177	-177	180	180	171	180	63	65	14	13	12	12	
18	ttpt_2	ttpt	25	2%	2%	5%	1%	180	-177	179	180	78	68	179	180	14	12	14	14	
19	ttpp_1	ttpp	12	1%	1%	<1%	1%		-177		180		68		65					
20	tptm_1	tptm	7	1%	1%	1%	<1%		-177		68		180		-65	14	9	12	10	
21	tptt_3	tptt	32	3%	5%	1%	2%	179	-177	62	68	173	180	171	180	10	10	13	14	
22	tptp_1	tptp	11	1%	1%	1%	1%	179	-177	59	68	163	180	60	65	13	12	10	11	
23	ptmt<1	ptmt	5	<1%	0%	1%	<1%		62		180		-68		180					
24	pttm_1	pttm	8	1%	0%	1%	1%		62		180		180		-65					
25	pttt_2	pttt	29	2%	0%	4%	3%	63	62	-178	180	178	180	-179	180	13	13	13	10	
26	pttp_1	pttp	13	1%	0%	1%	2%	63	62	-170	180	-177	180	72	65	13	14	14	11	
27	ptpt_1	ptpt	7	1%	0%	2%	<1%		62		180		68		180					
			984/1209	81%	82%	80%	82%													
			261	194	529															

^a"mode" indicates the peak of the smoothed distribution, "comm." indicates the common-atom value (given in bold face).

^bMode and 1/2 width at 1/2 height values are not given for minor rotamers.

^c<1% indicates a value between 0.5% and 0%. 0% indicates no observations.

^dTotal number of rotameric side chains / Total number that pass all data filters.

Reference:

Simon C. Lovell, J. Michael Word, Jane S. Richardson, and David C. Richardson. "The Penultimate Rotamer Library", *PROTEINS: Structure, Function, and Genetics*. 40: 389-408 (2000).

Methionine

o-label							Methionine						½ width			
seq #	label	Name	#	%	alpha	beta	other	χ ¹		χ ²		χ ³		χ ¹	χ ²	
								mode	comm. ^a	mode	comm.	mode	comm.			
1	mmm_19	mmm	105	19%	21%	16%	19%	-66	-65	-60	-65	-67	-70	11	13	
2	mnt_2	mnt	10	2%	0%	2%	3%	-63	-65	-64	-65	180	180	12	14	
3	mmp_3	mmp	15	3%	3%	1%	4%	-64	-65	-63	-65	103	103	9	10	
4	mtm_11	mtm	58	11%	12%	11%	9%	-67	-67	-177	180	-76	-75	12	11	
5	mtt_8	mtt	43	8%	9%	8%	7%	-67	-67	177	180	-178	180	10	13	
6	mtp_17	mtp	92	17%	22%	10%	17%	-68	-67	177	180	72	75	10	12	
7	ttm_7	ttm	36	7%	3%	10%	8%	-177	-177	176	180	-78	-75	10	10	
8	ttt_3	ttt	17	3%	5%	2%	2%	180	-177	171	180	174	180	9	9	
9	ttp_5	ttp	28	5%	7%	7%	2%	176	-177	178	180	73	75	10	11	
10	tpt_2	tpt	9	2%	1%	4%	1%	179	-177	67	65	-179	180	9	8	
11	tpp_5	tpp	30	5%	8%	2%	5%	-177	-177	66	65	75	75	10	15	
12	ptm_3	ptm	17	3%	1%	6%	4%	67	62	174	180	-78	-75	9	10	
13	ptp_2	ptp	12	2%	1%	3%	3%	68	62	-167	180	88	75	11	17	
			86%	91%	84%	83%										
			472/550 ^d	175	112	185										

Glutamate

o-label							Glutamate						½ width			
seq #	label	Name	#	%	alpha	beta	other	χ ¹		χ ²		χ ³		χ ³ range ^e	χ ¹	χ ²
								mode	comm.	mode	comm.	mode	comm.			
1	mm-40*	mm-40°	197	13%	19%	7%	12%	-65	-65	-58	-65	-40	-40	-90 to 30	14	14
2	Smm0_	Smm0°							-65			-75	0			
3	Smt-60	Smt-60°							-67			180	-60			
4	mt-10*	mt-10°	484	33%	36%	29%	32%	-67	-67	177	180	-10	-10	-90 to 90	13	16
5	Smt60_	Smt60°							-67			180	60			
6	mp0_6	mp0°	88	6%	<1%	2%	10%	-65	-65	85	85	-3	0	-60 to 60	14	13
7	tm-20*	tm-20°	17	1%	1%	1%	1%		-177			-80	0	-50 to 10	13	13
8	Stt-60	Stt-60°							-177			180	-60			
9	tt0_24	tt0°	350	24%	25%	42%	18%	-177	-177	178	180	2	0	-90 to 90	14	14
10	Stt60_	Stt60°							-177			180	60			
11	tp10_6	tp10°	91	6%	10%	2%	6%	-177	-177	65	65	13	10	-10 to 90	14	13
12	pm0_2	pm0°	32	2%	0%	0%	4%	71	70	-79	-80	5	0	-50 to 50	14	13
13	Spt-60	Spt-60°							62			180	-60			
14	pt-20*	pt-20°	80	5%	1%	9%	7%	63	62	-175	180	-18	-20	-90 to 90	14	13
15	Spt60_	Spt60°							62			180	60			
			91%	92%	92%	90%										
			1339/1470	394	225	720										

Glutamine

o-label							Glutamine						½ width			
seq #	label	Name	#	%	alpha	beta	other	χ ¹		χ ²		χ ³		χ ³ range ^e	χ ¹	χ ²
								mode	comm.	mode	comm.	mode	comm.			
1	mm-40*	mm-40°	127	15%	12%	13%	17%	-66	-65	-60	-65	-40	-40	-95 to 0	16	18
2	mm100*	mm100°	22	3%	4%	1%	2%		-65			100	0	0 to 150		
3	Smt-60	Smt-60°							-67			180	-60			
4	mt-30*	mt-30°	304	35%	40%	26%	36%	-67	-67	177	180	-25	-25	-90 to 90	16	15
5	Smt60_	Smt60°							-67			180	60			
6	mp0_3	mp0°	24	3%	<1%	1%	5%		-65			85	0	-60 to 60		
7	Stt-60	Stt-60°							-177			180	-60			
8	tt0_16	tt0°	140	16%	16%	29%	12%	-174	-177	173	180	-5	0	-90 to 90	14	13
9	Stt60_	Stt60°							-177			180	60			
10	tp-100	tp-100°	14	2%	4%	2%	<1%		-177			65	-100	-150 to 0		
11	tp60_9	tp60°	78	9%	13%	9%	7%	-175	-177	64	65	60	60	0 to 90	14	15
12	pm0_2	pm0°	15	2%	0%	1%	3%		70			-75	0	-60 to 60		
13	Spt-60	Spt-60°							62			180	-60			
14	pt20_4	pt20°	37	4%	1%	5%	6%	64	62	180	180	20	20	-90 to 90	13	14
15	Spt60_	Spt60°							62			180	60			
			88%	89%	86%	88%										
			761/863	229	137	395										

Aspartate

o-label							Aspartate						½ width at ½ height			
seq #	label	Name	#	%	alpha	beta	other	χ ¹		χ ²		χ ³		χ ² range	χ ¹	χ ²
								mode	comm.	mode	comm.	mode	comm.			
1	m-20**	m-20°	1088	51%	77%	38%	47%	-71	-70	-15	-15			-90 to 20	10	16
2	Sm-60_	Sm-60°							-65			-60	-60			
3	St-30_	St-30°							-170			-30	-30			
4	t0_21	t0°	438	21%	8%	44%	20%	-176	-177	1	0			-50 to 50	12	30
5	t70_6	t70°	118	6%	11%	7%	4%	-179	-177	65	65			50 to 90	12	18
6	Sp-50_	Sp-50°							62			-50	-50			
7	p-10**	p-10°	203	10%	1%	2%	13%	61	62	-4	-10			-90 to 0	9	19
8	p30_9	p30°	194	9%	1%	5%	12%	65	62	9	30			0 to 90	8	14
			96%	97%	95%	96%										
			2041/2124	365	232	1444										

Asparagine

o-label							Asparagine						½ width			
seq #	label	Name	#	%	alpha	beta	other	χ ¹		χ ²		χ ³		χ ³ range ^e	χ ¹	χ ²
								mode	comm.	mode	comm.	mode	comm.			
1	m-80_8	m-80°	118	8%	8%	9%	8%	-71	-65	-76	-75			-100 to -60	9	9
2	m-20**	m-20°	580	39%	65%	28%	33%	-71	-65	-23	-20			-60 to 10	10	20
3	m120_4	m120°	58	4%	3%	3%	4%	-64	-65	132	120			60 to 160	9	18
4	St-80_	St-80°							-174			-80	-80			
5	t-20**	t-20°	177	12%	5%	21%	12%	-174	-174	-20	-20			-120 to 0	5	21
6	t30_15	t30°	228	15%	13%	18%	15%	-168	-177	31	30			0 to 80	14	22
7	Sp-50_	Sp-50°							62			-50	-50			
8	p-10_7	p-10°	103	7%	0%	1%	10%	63	62	-13	-10			-90 to 0	8	9
9	p30_9	p30°	132	9%	<1%	7%	12%	64	62	34	30			0 to 90	6	7
			94%	95%	88%	95%										
			1396/1490	293	179	924										

^a"mode" indicates the peak of the smoothed distribution, "comm." indicates the common-atom value (given in bold face).

^bMode and 1/2 width at 1/2 height values are not given for minor rotamers.

^c<1% indicates a value between 0.5% and 0%. 0% indicates no observations.

^dTotal number of rotameric side chains / Total number that pass all data filters.

^eRanges used in determining frequencies are normally common-atom values ±30°. Exceptions (always in the terminal χ value) are listed here.

^fEntries beginning with capital S, "S", are additional sample points in torsion space.

Reference:

Simon C. Lovell, J. Michael Word, Jane S. Richardson, and David C. Richardson. "The Penultimate Rotamer Library", *PROTEINS: Structure, Function, and Genetics*. 40: 389-408 (2000).

Isoleucine

o-label								Isoleucine				½ width at ½ height	
seq #	label	Name	#	%	alpha	beta	other	χ ¹		χ ²		χ ¹	χ ²
								mode	comm. ^a	mode	comm.		
1	mm__15	mm	242	15%	10%	16%	17%	-57	-57	-59	-60	10	10
2	mt__60	mt	993	60%	81%	58%	41%	-66	-65	169	170	10	10
3	mp__1	mp ^b	19	1%	0% ^c	2%	1%		-65		100		
4	tt__8	tt	127	8%	1%	8%	14%	-174	-177	167	165	13	11
5	tp__2	tp	36	2%	2%	1%	4%	-169	-177	66	66	13	11
6	pt__13	pt	216	13%	4%	13%	22%	61	62	171	170	10	10
7	pp__1	pp	10	1%	<1%	1%	<1%		62		100		
				99%	99%	98%	99%						
			1643/1667 ^d		496	629	518						

Leucine

								Leucine				χ ² range ^e	
seq #	label	Name	#	%	alpha	beta	other	mode	comm.	mode	comm.	χ ¹	χ ²
1	mt__59	mt	1548	59%	62%	46%	66%	-65	-65	174	175	11	11
2	mp__2	mp	63	2%	1%	5%	2%	-85	-85	66	65	45 to 105	11 14
3	tt__2	tt	49	2%	1%	3%	1%	-172	-172	147	145	120 to 180	9 9
4	tp__29	tp	750	29%	30%	36%	23%	177	-177	63	65		10 10
5	pp__1	pp	21	1%	<1%	2%	1%		62		80		
				93%	95%	93%	93%						
			2431/2602		836	644	951						

Histidine

								Histidine					
seq #	label	Name	#	%	alpha	beta	other	mode	comm.	mode	comm.	χ ¹	χ ²
1	m-70**	m-70°	174	29%	26%	30%	30%	-60	-65	-69	-70	-120 to -30	11 23
2	m170_7	m170°	44	7%	9%	3%	9%	-63	-65	165	165	120 to -160	10 16
3	m80_13	m80°	78	13%	14%	10%	14%	-66	-65	83	80	50 to 120	11 18
4	t-80**	t-80°	64	11%	17%	9%	9%	-173	-177	-81	-80	-120 to -50	10 22
5	t-160*	t-160°	31	5%	5%	14%	1%	-178	-177	-163	-165	150 to -120	12 20
6	t60_16	t60°	94	16%	24%	17%	12%	-178	-177	62	60	50 to 120	13 19
7	p-80_9	p-80°	51	9%	0%	6%	13%	60	62	-75	-75	-120 to -50	10 12
8	p80_4	p80°	26	4%	0%	4%	6%	61	62	78	80	50 to 120	13 10
				94%	94%	92%	95%						
			562/598		124	143	295						

Tryptophan

o-label								Tryptophan				½ width at ½ height	
seq #	label	Name	#	%	alpha	beta	other	χ ¹		χ ²		χ ¹	χ ²
								mode	comm.	mode	comm.		
1	m-90_5	m-90°	31	5%	0%	7%	7%	-70	-65	-87	-90	-130 to -60	9 12
2	m0__8	m0°	48	8%	15%	2%	8%	-66	-65	-4	-5	-40 to 20	9 20
3	m95_32	m95°	195	32%	22%	43%	29%	-69	-65	95	95	60 to 130	11 19
4	t-105*	t-105°	100	16%	27%	10%	14%	178	-177	-105	-105	-130 to -60	16 14
5	t90_18	t90°	109	18%	28%	14%	15%	-178	-177	88	90	0 to 100	10 11
6	p-90**	p-90°	67	11%	2%	13%	14%	58	62	-87	-90	-130 to -60	12 10
7	p90_6	p90°	34	6%	1%	9%	6%	60	62	92	90	60 to 130	12 8
				94%	95%	98%	92%						
			584/618		140	175	269						

(for Tyr, Phe 90°=-90°)

Tyrosine

								Tyrosine					
seq #	label	Name	#	%	alpha	beta	other	mode	comm.	mode	comm.	χ ¹	χ ²
1	m-85**	m-85°	618	43%	26%	50%	45%	-65	-65	-87	-85	50 to 90, -90 to -50	11 21
2	m-30_9	m-30°	124	9%	15%	4%	9%	-64	-65	-42	-30	-50 to 0, 0 to 50	11 18
3	Sm30_f	Sm30°							-85		30		
4	t80_34	t80°	486	34%	55%	25%	30%	176	-177	77	80	20 to 90, -90 to -75	11 14
5	p90_13	p90°	182	13%	1%	21%	12%	63	62	89	90	60 to 90, -90 to -60	13 13
				98%	97%	99%	97%						
			1410/1443		290	468	652						

Phenylalanine

								Phenylalanine					
seq #	label	Name	#	%	alpha	beta	other	mode	comm.	mode	comm.	χ ¹	χ ²
1	m-85**	m-85°	697	44%	29%	51%	47%	-64	-65	-83	-85	50 to 90, -90 to -50	12 17
2	m-30_9	m-30°	149	9%	12%	5%	11%	-64	-65	-19	-30	-50 to 0, 0 to 50	9 20
3	Sm30_	Sm30°							-85		30		
4	t80_33	t80°	522	33%	57%	18%	29%	177	-177	80	80	20 to 90, -90 to -75	13 17
5	p90_13	p90°	202	13%	1%	24%	11%	59	62	88	90	60 to 90, -90 to -60	11 11
				98%	97%	99%	98%						
			1570/1599		389	514	667						

^a"mode" indicates the peak of the smoothed distribution, "comm." indicates the common-atom value (given in bold face).

^bMode and 1/2 width at 1/2 height values are not given for minor rotamers.

^c<1% indicates a value between 0.5% and 0%. 0% indicates no observations.

^dTotal number of rotameric side chains / Total number that pass all data filters.

^eRanges used in determining frequencies are normally common-atom values ±30°. Exceptions (always in the terminal χ value) are listed.

^fEntries beginning with capital S, "S", are additional sample points in torsion space.

Reference:

Simon C. Lovell, J. Michael Word, Jane S. Richardson, and David C. Richardson. "The Penultimate Rotamer Library", *PROTEINS: Structure, Function, and Genetics*. 40: 389-408 (2000).

Proline

o-label									χ^1		$\frac{1}{2}$ width at $\frac{1}{2}$ height
seq #	label	Name	#	%	alpha	beta	other	mode	comm. ^a	χ^1 range ^e	χ^1
1	exo_43	Cγ exo	372	43%	68%	28%	44%	-29	-30	-60 to -15	6
2	endo44	Cγ endo	379	44%	23%	54%	43%	30	30	15 to 60	7
		cis, Cγ endo	56	6%	0% ^c	1%	7%	31	30	15 to 60	5
				93%	91%	84%	94%				
			807/928 ^d		20	57	730				

Threonine

1	m___43	m	1062	43%	74%	55%	29%	-61	-65		7
2	t___7	t	169	7%	0%	13%	6%	-171	-175		6
3	p___49	p	1200	49%	25%	31%	65%	59	62		10
				99%	100%	99%	99%				
			2431/2447		395	672	1364				

Valine

1	m___20	m	526	20%	7%	20%	28%	-64	-60	="60" ^b	7
2	t___73	t	1931	73%	90%	72%	63%	175	175	="65"	8
3	p___6	p	169	6%	2%	8%	8%	63	63	="177"	8
				99%	100%	99%	99%				
			2626/2649		622	1080	924				

Serine

1	m___29	m	714	29%	44%	29%	25%	-65	-65		9
2	t___22	t	541	22%	22%	34%	18%	178	-177		11
3	p___48	p	1201	48%	33%	36%	55%	64	62		10
				98%	98%	100%	98%				
			2456/2498		350	485	1621				

Cysteine

1	m___50	m	142	50%	75%	32%	43%	-65	-65		11
2	t___26	t	74	26%	20%	45%	21%	-177	-177		10
3	p___23	p	64	23%	5%	23%	34%	55	62		14
				99%	100%	100%	98%				
			280/285		85	65	130				

^a"mode" indicates the peak of the smoothed distribution, "comm." indicates the common-atom value (given in bold face).

^b Standard conventions result in χ angles being named differently for Val than for Thr and Ile. These figures indicate the equivalent angles.

^c <1% indicates a value between 0.5% and 0%. 0% indicates no observations.

^d Total number of rotameric side chains / Total number that pass all data filters.

^e Ranges used in determining frequencies are normally common-atom values $\pm 30^\circ$. Exceptions (always in the terminal χ value) are listed here.

Reference:

Simon C. Lovell, J. Michael Word, Jane S. Richardson, and David C. Richardson. "The Penultimate Rotamer Library", *PROTEINS: Structure, Function, and Genetics*. **40**: 389-408 (2000).