SUPPORTING INFORMATION for

Intrinsic energy landscapes of amino acid sidechains

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* Additional data including QM energies and geometries are available for download at
http://mackerell.umaryland.edu/MacKerell_Lab.html.

Table S1. PDB survey statistics.

Residue	ALL	ALPHAR	BETA	ALPHAL
ala	35,776	22,650	12,424	425
arg	16,918	9,463	6,904	405
asn	16,881	7,886	6,784	1,925
asp	22,833	12,109	9,347	1,076
cys	5,073	2,155	2,758	108
gln	13,235	7,935	4,833	358
glu	20,956	13,578	6,861	362
gly	32,937	7,434	7,712	6,065
his	9,368	4,443	4,432	368
ile	22,286	9,699	12,490	18
leu	36,182	20,651	15,016	275
lys	17,451	10,111	6,699	482
met	6,031	3,366	2,546	88
phe	17,089	7,841	8,866	266
pro	19,468	8,243	11,113	0
ser	21,326	10,184	10,538	361
thr	22,579	10,557	11,854	58
trp	6,517	3,260	3,113	90
tyr	14,984	6,793	7,814	262
val	29,296	11,491	17,669	47
SUM	**387,186**	**189,849**	**169,773**	**13,039**

Data extracted from a total of 2106 non-redundant PDB structures using selection criteria described in Methods.

Table S2. Rotamer populations calculated from 5 random and non-overlapping subsets of the crystallographic survey. Values in parenthesis represent the standard deviations.

	Chi1					
	Full			Average of 5		
Residue	t	m	p	t	m	p
arg	0.32	0.58	0.10	0.32 (0.01)	0.58 (0.01)	0.10 (0.01)
asn	0.29	0.56	0.15	0.29 (0.01)	0.56 (0.01)	0.15 (0.01)
asp	0.32	0.51	0.18	0.32 (0.00)	0.51 (0.01)	0.18 (0.01)
cys	0.26	0.57	0.17	0.26 (0.02)	0.57 (0.01)	0.17 (0.02)
gln	0.31	0.61	0.08	0.31 (0.01)	0.61 (0.01)	0.08 (0.00)
glu	0.33	0.58	0.10	0.33 (0.01)	0.58 (0.01)	0.10 (0.00)
his	0.33	0.54	0.13	0.33 (0.01)	0.54 (0.01)	0.13 (0.01)
ile	0.09	0.77	0.14	0.09 (0.00)	0.77 (0.01)	0.14 (0.01)
leu	0.31	0.67	0.01	0.31 (0.00)	0.67 (0.01)	0.01 (0.00)
lys	0.34	0.59	0.07	0.34 (0.01)	0.59 (0.02)	0.07 (0.00)
met	0.28	0.64	0.08	0.28 (0.01)	0.64 (0.01)	0.08 (0.00)
phe	0.34	0.54	0.11	0.34 (0.01)	0.54 (0.01)	0.11 (0.01)
ser	0.23	0.28	0.49	0.23 (0.01)	0.28 (0.01)	0.49 (0.01)
thr	0.07	0.43	0.49	0.07 (0.00)	0.43 (0.01)	0.49 (0.01)
trp	0.34	0.50	0.16	0.34 (0.01)	0.50 (0.02)	0.16 (0.01)
tyr	0.34	0.54	0.12	0.34 (0.01)	0.54 (0.01)	0.12 (0.00)
val	0.74	0.19	0.07	0.74 (0.01)	0.19 (0.01)	0.07 (0.01)

	Chi2						
arg	0.78		0.13	0.08	0.78 (0.00)	0.13 (0.01)	0.08 (0.00)
asn*	0.52	0.05	0.17	0.26	0.52 (0.01) 0.05 (0.00)	0.17 (0.01)	0.26 (0.00)
asp	0.82		0.18		0.82 (0.00)	0.18 (0.00)	
gln	0.61		0.22	0.16	0.61 (0.01)	0.22 (0.01)	0.16 (0.01)
glu	0.63		0.20	0.17	0.63 (0.01)	0.20 (0.00)	0.17 (0.01)
his	0.08		0.39	0.53	0.08 (0.01)	0.39 (0.01)	0.53 (0.00)
ile	0.79		0.16	0.05	0.79 (0.01)	0.16 (0.01)	0.05 (0.00)
leu	0.66		0.01	0.33	0.66 (0.01)	0.01 (0.00)	0.33 (0.00)
lys	0.78		0.15	0.07	0.78 (0.00)	0.15 (0.00)	0.07 (0.00)
met	0.56		0.32	0.11	0.56 (0.01)	0.33 (0.01)	0.11 (0.01)
phe	0.14		0.86		0.14 (0.00)	0.86 (0.00)	
trp*	0.01	0.17	0.31	0.51	0.01 (0.00) 0.17 (0.01)	0.31 (0.01)	0.51 (0.01)
tyr	0.12		0.88		0.12 (0.01)	0.88 (0.01)	

 * for Asn and Trp Chi2, which involves a sp^2 atom center, the **t** rotamer column includes data for the 'cis' conformation where Chi2=0 (right). Definitions of rotamers are indicated in Methods section of the main text.

Table S3. Sum of normalized Boltzmann factors calculated from QM data offset to global minimum around each rotameric χ_1,χ_2 conformations.

QM					% of all residues of same type								
phi300													
Residue	tt	tc	tm	tp	mt	mc	mm	mp	pt	pc	pm	pp	sum
arg	0.00		22.04	6.74	0.00		0.06	0.00	0.00		0.00	0.00	28.85
asn	0.00	0.50	0.03	0.00	1.04	0.01	6.76	0.01	5.54	0.00	0.01	6.86	20.75
asp	0.00		0.00		0.00		0.00		29.79		0.64		30.43
gln	0.33		1.45	0.20	0.58		20.50	0.45	0.26		0.36	5.65	29.77
glu	0.00		0.00	0.00	0.00		0.00	5.04	0.00		24.36	0.14	29.55
hsd	19.52		0.03	0.19	1.84		0.18	3.94	1.07		15.74	0.04	42.55
hse	0.00		0.01	0.00	1.29		8.37	0.01	6.96		0.01	4.33	20.98
hsp	31.72		0.00	0.00	0.00		0.00	0.00	0.00		0.00	0.00	31.72
ile	5.21		0.36	12.65	9.52		9.45	1.84	2.03		0.20	0.14	41.40
leu	1.48		0.62	18.39	6.45		0.51	0.99	0.27		0.00	0.08	28.79
lys	0.00		1.26	31.56	0.00		0.01	0.00	0.00		0.00	0.00	32.83
met	3.85		0.04	1.14	1.07		0.06	30.87	0.21		0.00	0.02	37.27
phe	0.05		0.73		4.28		26.99		0.00		7.72		39.76
trp	0.00	0.13	0.10	0.14	1.00	0.67	14.44	6.28	0.00	0.00	7.21	10.26	40.24
tyr	0.06		0.84		4.78		27.15		0.01		10.07		42.89
phi-120													
Residue	tt	tc	tm	tp	mt	mc	mm	mp	pt	pc	pm	pp	sum
arg	0.00		0.00	0.00	0.01		12.01	38.50	0.00		0.00	0.02	50.54
asn	12.12	0.03	7.73	0.35	0.05	15.45	0.49	0.26	0.59	4.78	0.00	7.08	48.94
asp	34.59		0.67		0.08		1.32		0.54		0.03		37.23
gln	1.22		14.00	16.27	0.89		0.27	8.78	0.07		0.08	4.01	45.58
glu	0.00		0.09	7.83	0.00		0.29	34.82	0.00		0.18	0.00	43.20
hsd	0.91		0.25	6.09	6.13		0.03	0.05	7.15		11.65	0.00	32.27
hse	11.87		9.83	0.58	0.25		2.68	1.31	1.85		0.01	1.06	29.45
hsp	0.00		0.00	0.00	38.41		0.00	0.00	4.80		0.87	0.00	44.08
ile	1.05		0.09	1.16	10.77		13.22	1.54	0.70		0.07	0.04	28.63
leu	1.46		0.65	10.32	18.29		1.07	1.22	0.11		0.00	0.03	33.15
lys	0.00		0.00	0.00	0.00		36.29	2.56	0.00		0.01	0.02	38.89
met	0.86		0.00	23.05	0.59		0.11	0.17	0.10		0.00	0.01	24.90
phe	0.08		24.93		0.80		2.12		0.00		0.19		28.13
trp	0.03	0.02	15.68	10.11	0.03	0.48	0.79	0.21	0.00	0.00	0.01	0.28	27.64
tyr	0.07		23.60		0.68		1.76		0.00		0.23		26.33
phi63													
Residue	tt	tc	tm	tp	mt	mc	mm	mp	pt	pc	pm	pp	sum
arg	0.00		0.18	0.00	0.00		0.00	0.00	0.02		0.05	20.35	20.61
asn	0.15	0.17	1.88	0.00	21.24	0.00	2.00	1.74	0.01	0.00	0.00	3.11	30.31
asp	0.00		0.00		29.26		3.08		0.00		0.00		32.34
gln	0.08		0.27	0.01	1.81		19.21	2.94	0.00		0.01	0.31	24.65
glu	0.00		0.00	0.00	0.00		1.55	24.85	0.00		0.85	0.00	27.25
hsd	5.95		0.00	5.73	0.03		2.38	0.26	0.24		10.59	0.00	25.18
hse	0.02		0.11	0.00	36.82		9.45	1.77	0.06		0.00	1.34	49.57
hsp	0.94		0.00	0.12	0.00		0.00	0.00	4.00		19.13	0.01	24.20
ile	0.26		0.01	0.32	15.48		7.60	0.52	5.27		0.07	0.45	29.97
leu	0.23		0.09	4.24	27.98		1.70	3.71	0.06		0.00	0.05	38.06
lys	0.01		0.16	0.00	0.00		0.00	0.00	0.02		0.00	28.09	28.28
met	0.77		0.00	3.55	0.86		0.02	32.60	0.03		0.00	0.00	37.83
phe	0.01		0.06		1.09		30.79		0.00		0.17		32.11
trp	0.00	0.00	0.05	0.00	1.23	0.09	15.54	13.12	0.00	0.00	0.01	2.07	32.12
tyr	0.00		0.04		1.19		29.25		0.00		0.29		30.78

Calculated by summing probabilities within a window side of ±60° around exact rotamer definitions. For Asp, Asn, Phe, Trp, and Tyr, window size of ±45° was used around sp3-sp2 rotamer definitions as described in Methods section of the main text.

Table S4. Sum of survey probabilities around rotameric χ_1,χ_2 conformations.

XTAL						% of all residues of same type							
_alphaR													
Residue	tt	tc	tm	tp	mt	mc	mm	mp	pt	pc	pm	pp	sum
arg	18.72		0.72	5.56	28.84		5.00	0.42	2.07		0.02	0.57	61.91
asn	0.86	0.19	4.93	2.71	27.66	1.75	1.45	8.41	1.05	0.07	0.13	0.26	49.46
asp	1.78		8.04		45.32		1.74		2.77		0.29		59.94
gln	11.65		1.23	11.14	27.40		11.25	2.05	1.10		0.33	0.65	66.81
glu	16.48		1.34	8.01	26.24		10.95	5.13	1.14		0.75	0.80	70.85
his	0.45		14.05	7.50	3.06		9.35	14.57	0.30		0.71	1.48	51.46
ile	1.28		0.03	2.04	32.96		6.46	0.23	2.54		0.00	0.14	45.68
leu	1.19		0.23	19.03	39.18		0.37	1.19	0.01		0.00	0.22	61.41
lys	21.47		0.46	5.30	27.88		6.17	0.27	1.75		0.00	0.10	63.38
met	8.12		2.98	6.60	22.88		18.24	1.61	1.17		0.05	0.12	61.75
phe	0.63		26.42	0.00	7.52		12.90	0.00	0.04		0.82	0.00	48.34
trp	0.02	1.98	11.67	14.29	0.54	6.78	0.73	12.14	0.00	0.17	2.62	0.45	51.40
tyr	0.43		25.39		7.35		12.81		0.03		1.33		47.34
_beta													
Residue	tt	tc	tm	tp	mt	mc	mm	mp	pt	pc	pm	pp	sum
arg	10.78		0.44	1.37	12.03		4.64	0.64	3.68		0.26	0.33	34.16
asn	6.32	0.49	2.41	2.99	4.77	1.04	1.73	6.58	1.30	0.06	1.25	0.74	29.68
asp	11.92		3.37		9.56		2.13		1.98		1.04		30.00
gln	9.31		0.55	2.65	8.63		3.80	0.66	2.88		0.29	0.30	29.07
glu	9.77		0.38	1.28	9.03		2.46	0.45	2.62		0.07	0.33	26.39
his	0.87		6.66	7.46	1.32		5.62	13.29	0.04		3.12	3.23	41.61
ile	4.16		0.02	0.56	32.21		9.23	1.26	6.27		0.05	0.31	54.07
leu	1.35		0.23	14.42	18.17		0.24	1.90	0.40		0.01	0.66	37.38
lys	11.07		0.18	1.72	11.30		4.30	0.39	3.15		0.06	0.02	32.18
met	9.63		1.73	2.49	9.79		7.23	0.84	3.40		0.75	0.35	36.22
phe	0.63		11.12	0.00	2.79		24.82	0.00	0.07		9.82	0.00	49.26
trp	0.00	2.69	4.68	3.02	0.05	3.50	3.64	20.39	0.00	0.31	5.01	3.33	46.61
tyr	0.69		11.35		2.43		25.91		0.07		9.51		49.96
_alphaL													
Residue	tt	tc	tm	tp	mt	mc	mm	mp	pt	pc	pm	pp	sum
arg	0.16		0.01	0.08	2.51		0.81	0.22	0.06		0.00	0.06	3.92
asn	2.87	0.25	3.34	0.18	6.16	1.23	1.37	5.25	0.05	0.10	0.02	0.03	20.86
asp	2.00		1.37		5.90		0.60		0.15		0.03		10.06
gln	0.09		0.00	0.06	2.26		1.40	0.27	0.02		0.01	0.01	4.12
glu	0.09		0.01	0.06	1.83		0.62	0.07	0.01		0.02	0.05	2.76
his	0.11		0.22	0.24	0.97		1.61	3.49	0.04		0.15	0.11	6.94
ile	0.00		0.00	0.00	0.17		0.04	0.01	0.04		0.00	0.00	0.26
leu	0.01		0.00	0.11	1.03		0.01	0.03	0.00		0.00	0.00	1.20
lys	0.11		0.00	0.03	2.90		1.25	0.13	0.01		0.00	0.00	4.43
met	0.05		0.02	0.09	0.72		1.07	0.02	0.02		0.00	0.02	2.03
phe	0.02		0.16	0.00	0.51		1.71	0.00	0.00		0.01	0.00	2.40
trp	0.00	0.02	0.17	0.02	0.00	0.45	0.33	0.99	0.00	0.00	0.00	0.00	1.98
tyr	0.01		0.21		0.55		1.89		0.01		0.03		2.71

Calculated by summing probabilities within a window side of ±60° around exact rotamer definitions. For Asp, Asn, Phe, Trp, and Tyr, window size of ±45° was used around sp^3-sp^2 rotamer definitions as described in Methods section of the main text.

Table S5. Secondary structure propensity scale derived from intrinsic energetics.

Residue	alphaR	beta	alphaL
arg	-2.95	-0.60	-0.13
asn	-0.90	-0.51	-0.25
cys	-1.42	-0.07	-0.93
gln	-2.14	-0.04	-1.06
hsd	-2.28	-0.05	-1.00
hse	-0.20	-0.69	-0.80
ile	-2.21	0.00	-3.19
leu	-1.72	-0.01	-2.01
lys	-2.62	-0.85	-0.07
met	-2.01	-0.02	-1.46
phe	-1.82	-0.04	-1.10
ser	-1.57	-0.05	-1.13
thr	-1.89	-0.01	-2.77
trp	-1.70	-0.04	-1.20
tyr	-1.78	-0.04	-1.16
val	-2.17	0.00	-2.91

Lowest value reflects least likelihood.
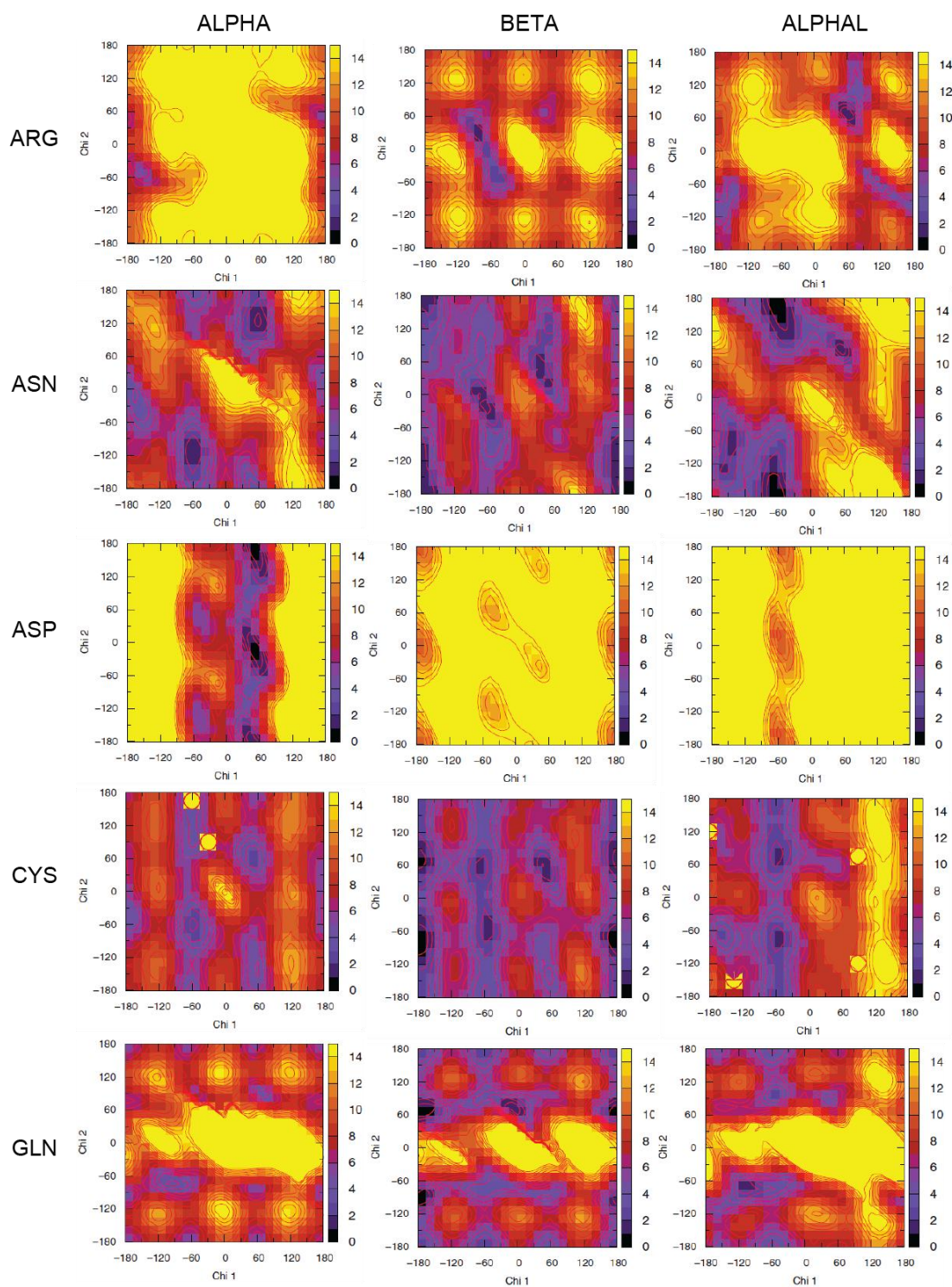
Figure S1. QM energy surfaces for the rotation of χ_1 and χ_2 dihedrals. For Phe/Tyr/Asp, a continuous 360° scan of the side chains is included, although they are symmetric, to show the extent of error in QM calculations. ALPHA = ALPHAR.

Figure S1 cont'd

ALPHA   BETA   ALPHAL

LEU

LYS

MET

PHE

SER
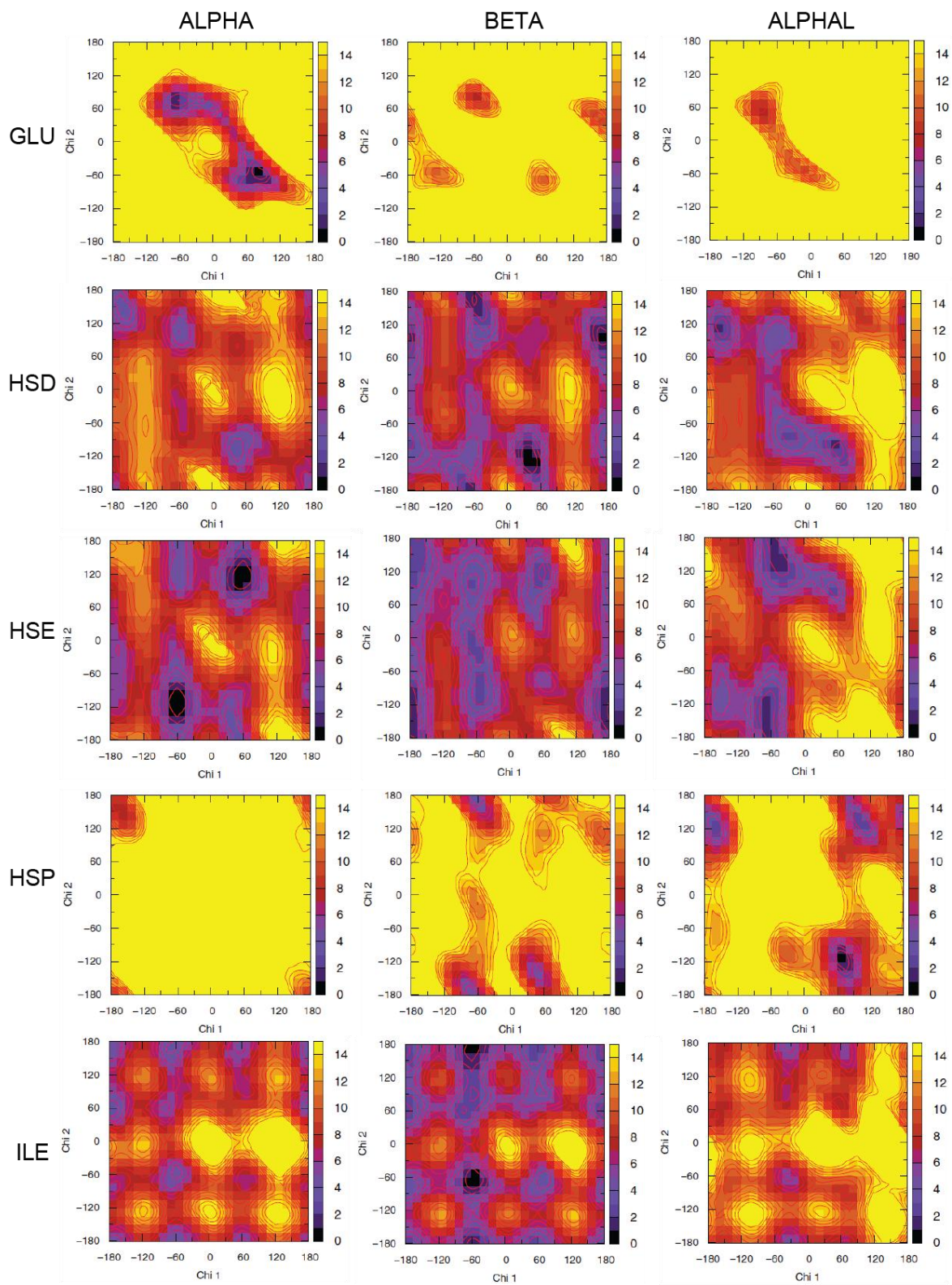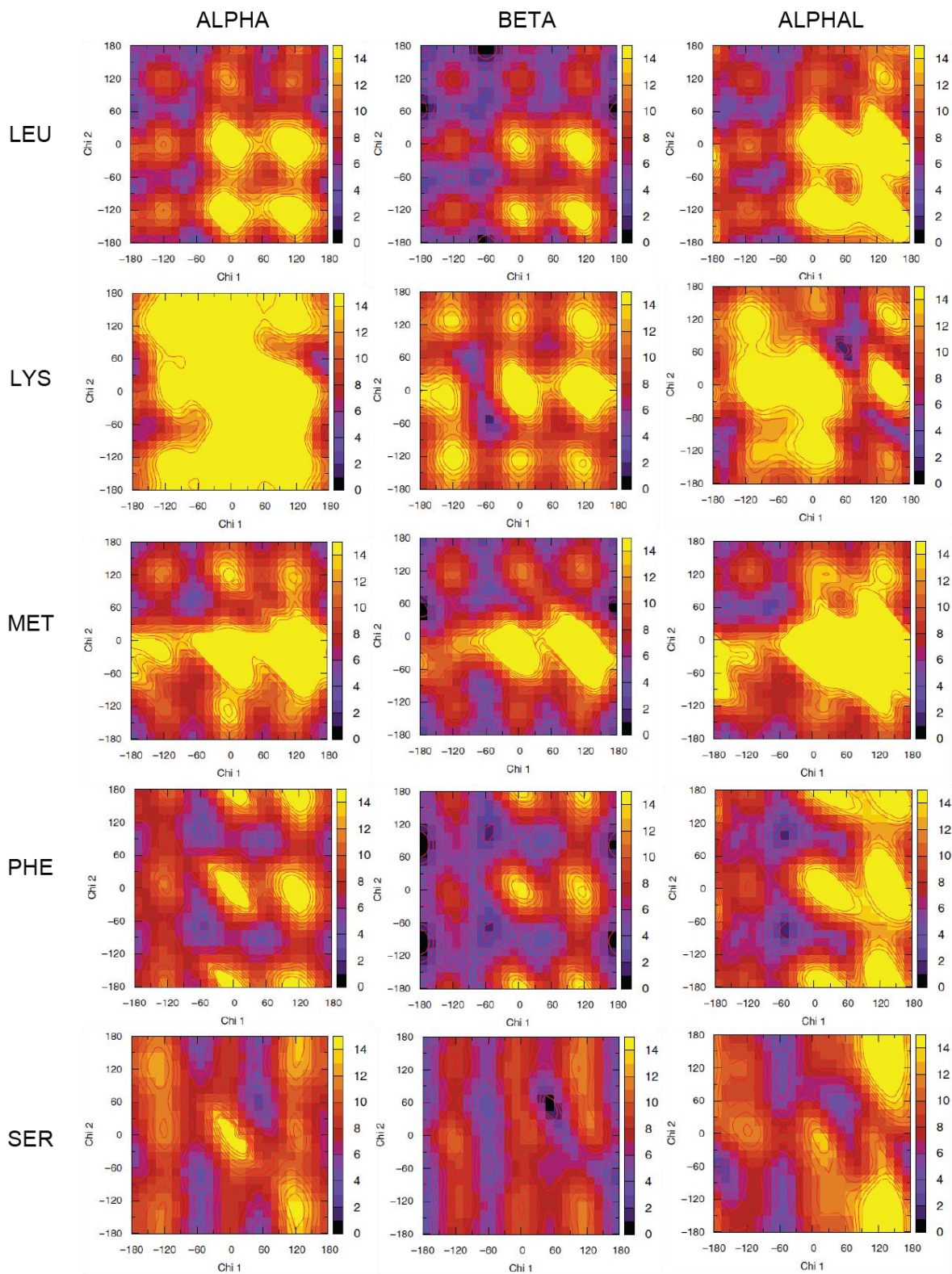
Figure S1 cont'd
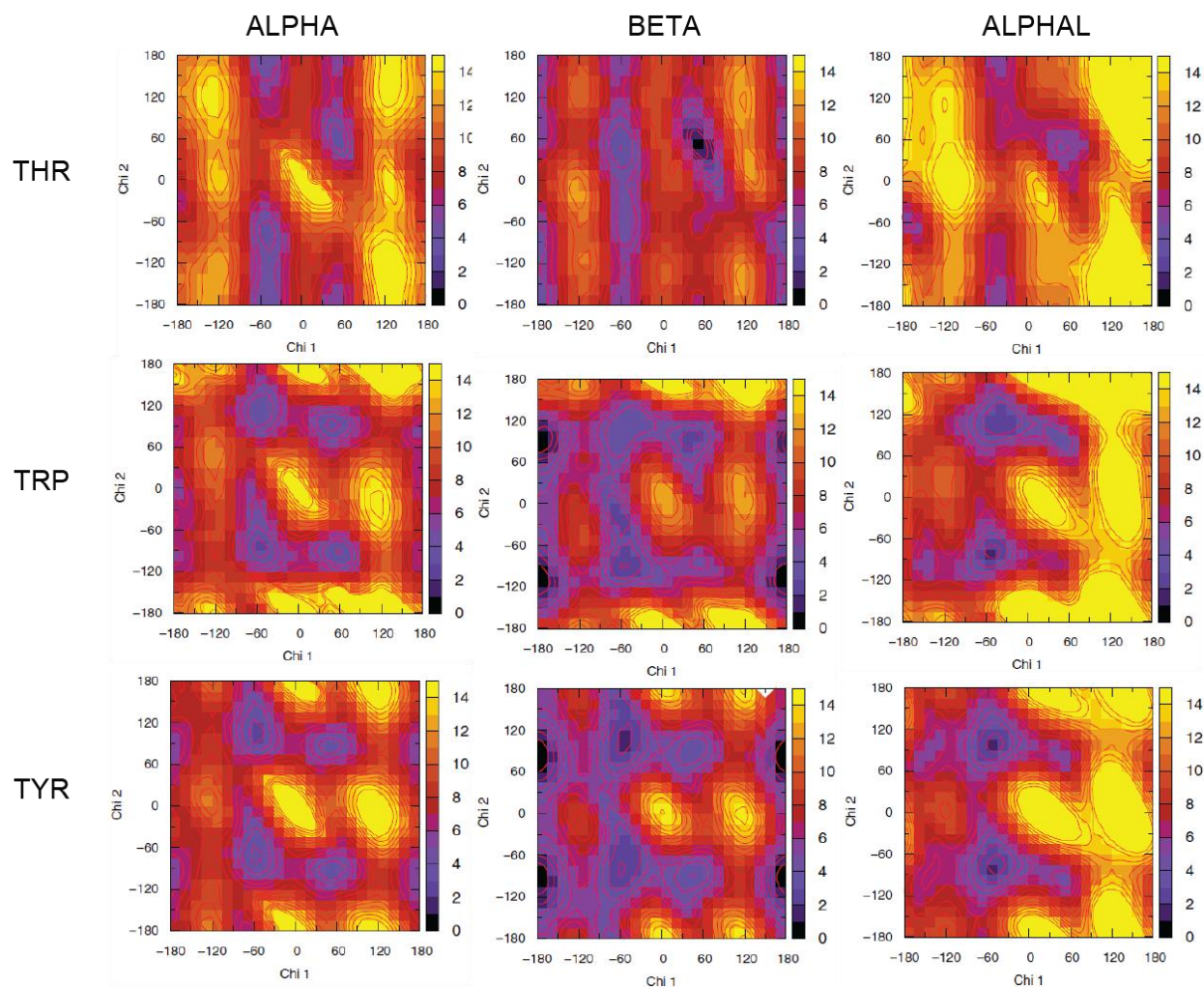
Figure S1 cont'd
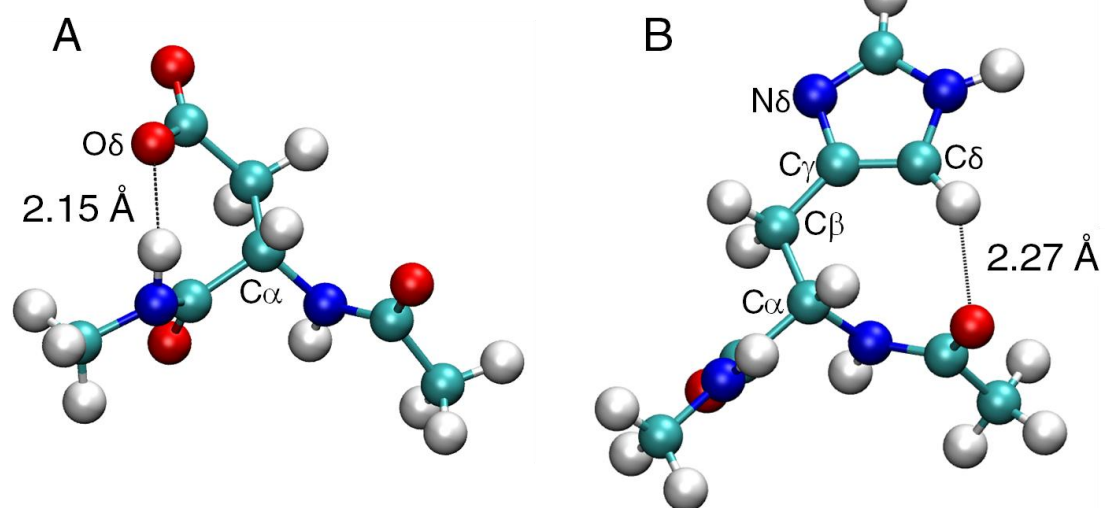
Figure S2. A) Asp and B) Hse dipeptides with Beta backbone and at $(\chi_1,\chi_2) = (-180°,0°)$ and (**m**, 0°) conformations, respectively, showing close interactions with the backbone.
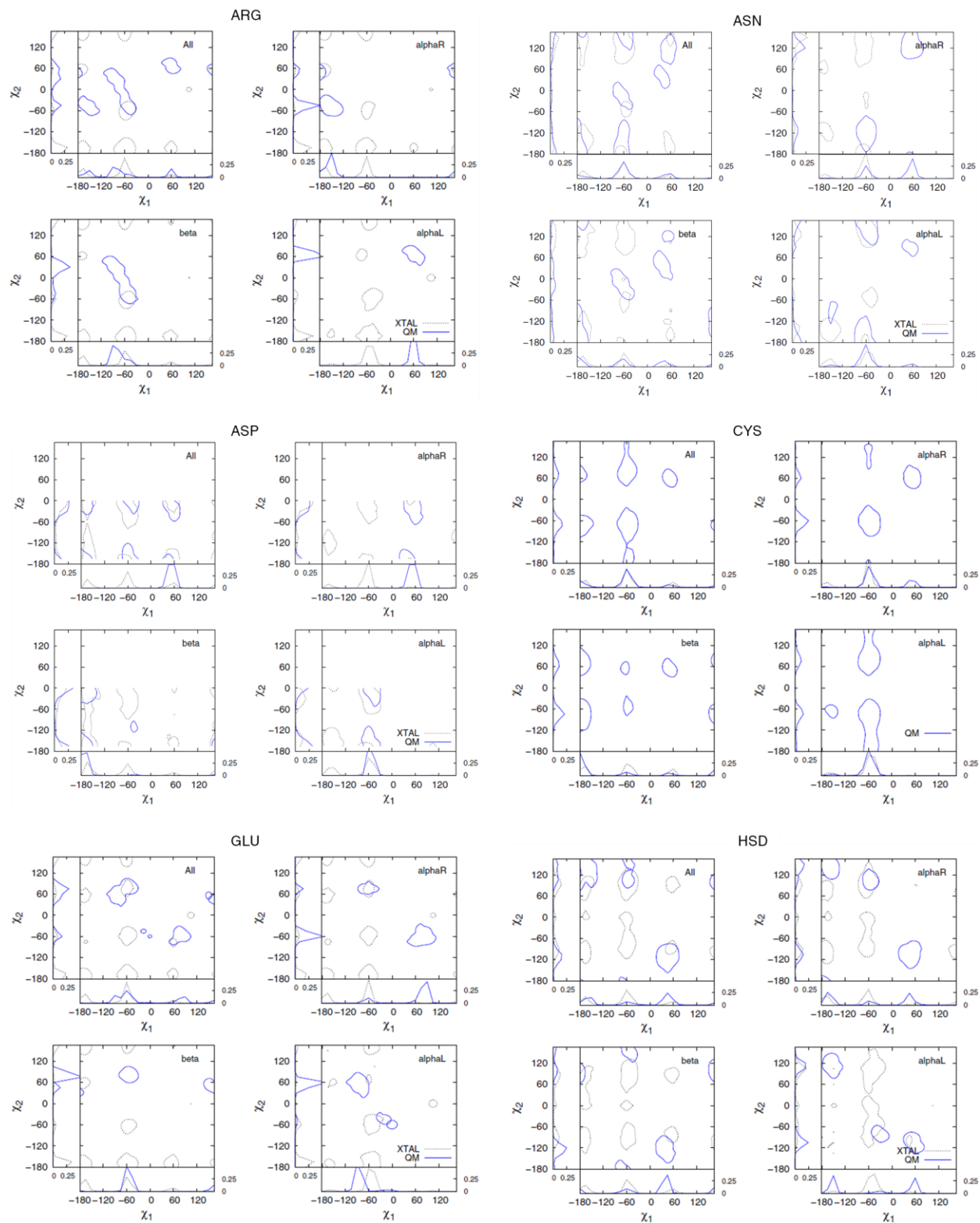
Figure S3. Combined QM (solid) and PDB survey (dashed) probability distributions with a contour level of 0.005. Backbone-dependent data are derived from individually pooled backbone conformations and are not normalized to global population.
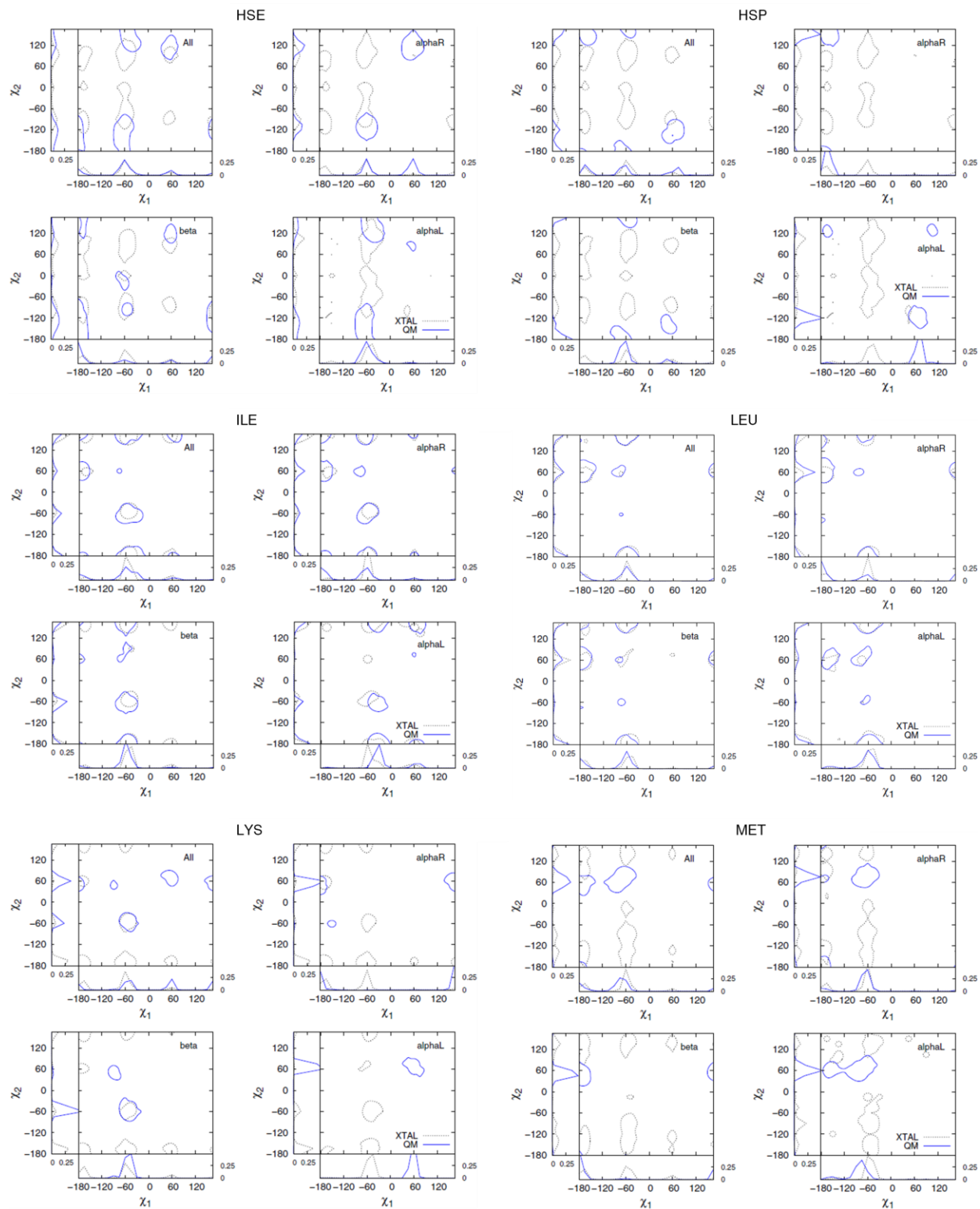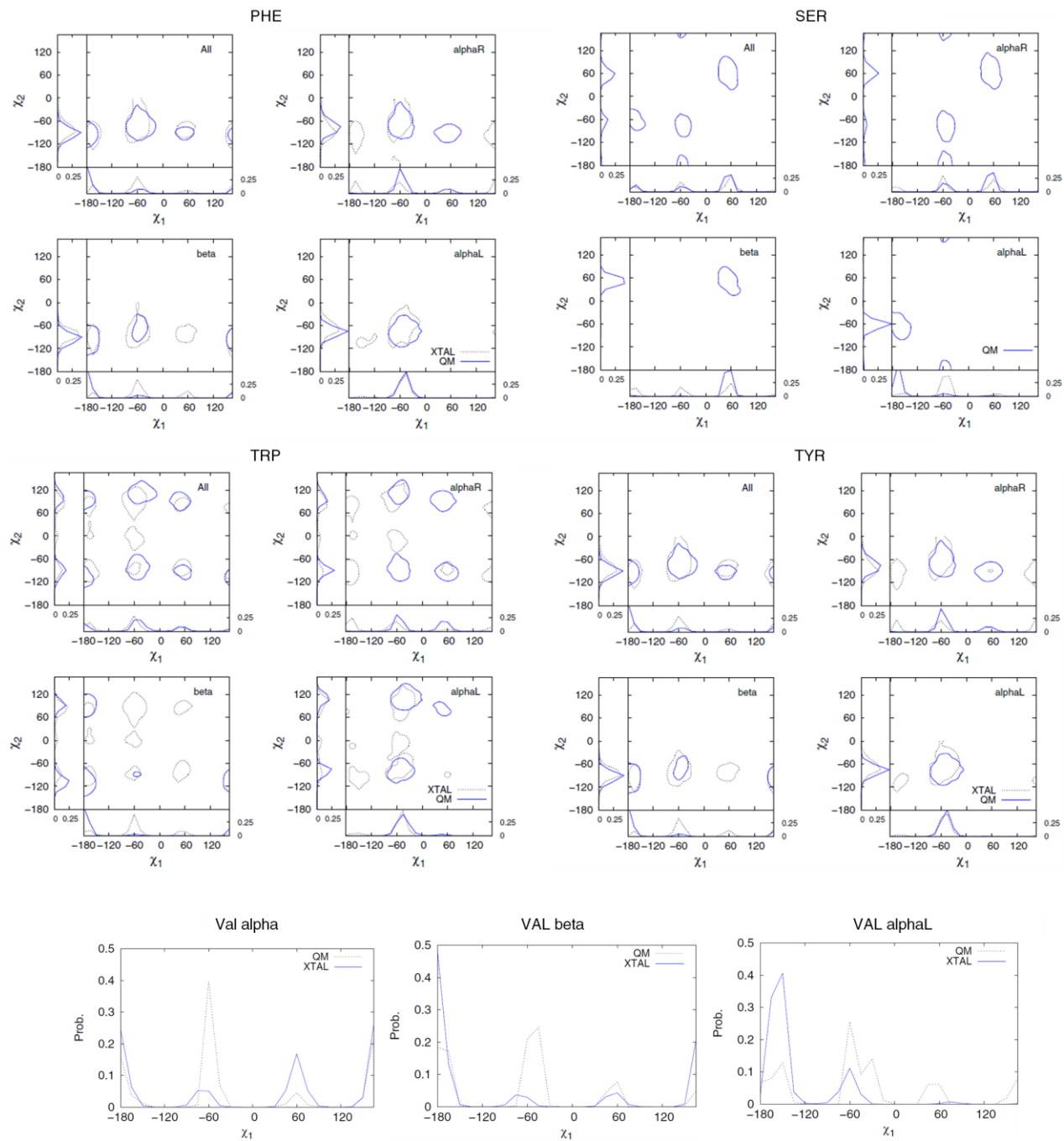
Figure S3 cont'd

Figure S3 cont'd