

Supplemental Table S3

Table S3. TWOW-1 Binding Arranged by Amino Acid Position of Mutation																				
A	B	C	D	E	F	G	H	I	J	K	L	M	N	O						
mys allele	β PS AA Change	β 3 AA	Domain	Relative TWOW-1 Binding	Median	S.E.	Relative TWOW-1	Z score	WT vs Mut	p=	Relative noMn/wMn	Z score	Relative noMn/wMn	Median	S.E.	Relative PS2 Integrin Level	Median	S.E.	Int. with rhea	refs
b41	C40Y	C5	PSI	1.90	0.03	8.7	0.000	12.2	2.80	0.12	0.48	0.04	b41							
b33	I50F	L17	PSI	0.88	0.13	-2.7	0.149	0.7	1.29	0.10	0.63	0.08	b33							
b3	C58S	C26	PSI	1.72	0.52	6.7	0.000	3.6	1.66	0.18	0.30	0.05	b3							
b68	C58Y	C26	PSI	1.82	0.11	7.9	0.000	10.1	2.52	0.08	0.44	0.04	b68							
G4	S196F	S123	MIDAS	0.00	0.01	-12.6	0.000	-9.1	0.00	0.09	0.83	0.08	G4	1,2						
b67	D200N	D127	ADMIDAS	2.15	0.11	11.6	0.000	1.5	1.39	0.04	0.25	0.06	b67	1,3-8						
b38	L224F	I151	ADMIDAS	1.73	0.33	6.9	0.000	4.5	1.79	0.40	0.69	0.08	b38							
b26	G227S	G154	SyMBS	0.35	0.11	-8.6	0.000	-6.4	0.35	0.14	0.34	0.04	b26							
b20	P242L	P170	β -I	1.02	0.06	-1.2	0.295	-2.3	0.89	0.07	0.56	0.07	b20							
b21	L264F	L196	ADMIDAS	1.84	0.30	8.1	0.000	6.2	2.01	0.54	0.32	0.03	b21	9,10						
b69	S272+SVRQ	N204+	MIDAS/SyMBS	0.28	0.15	-9.5	0.000	-5.7	0.44	0.20	0.29	0.04	b69							
b50	S272+Q	N204+	MIDAS/SyMBS	1.65	0.06	5.9	0.000	4.2	1.75	0.13	0.53	0.05	b50							
b13	E274V	E206	MIDAS/SyMBS	0.29	0.03	-9.4	0.000	-6.0	0.40	0.09	0.36	0.06	b13	11						
b47	A293T	A225	MIDAS/SyMBS	0.20	0.24	-10.4	0.000	-6.2	0.38	0.38	0.09	0.00	b47							
b30	I298F	T230	β -I	1.56	0.10	4.9	0.001	0.4	1.25	0.09	0.24	0.03	b30							
b65	A310T	A242	β -I	0.98	0.22	-1.6	0.610	2.8	1.56	0.28	0.53	0.13	b65							
b45	R312Q	H244	ADMIDAS	1.57	0.19	5.0	0.000	3.2	1.62	0.27	0.29	0.09	b45							
b25	S317L	T249	ADMIDAS	1.91	0.12	8.8	0.000	7.8	2.22	0.09	0.49	0.07	b25							
b48	A325T	A257	β -I	1.04	0.15	-0.9	0.432	-0.5	1.13	0.09	0.72	0.08	b48							
b66	P336S	P268	β -I	0.92	0.10	-2.3	0.180	-1.2	1.03	0.06	0.63	0.09	b66							
b57	G339S	G271	β -I	1.28	0.14	1.8	0.106	-1.3	0.81	0.01	0.33	0.05	b57	12,13						
b49	H342Y	H274	β -I	1.45	0.10	3.6	0.003	1.1	1.34	0.11	0.54	0.04	b49							
b42	G347S	N279	β -I	1.09	0.15	-0.3	0.831	1.0	1.33	0.18	0.45	0.02	b42							
ts2	G347D	N279	β -I	1.10	0.11	-0.2	0.595	1.4	1.38	0.12	0.44	0.05	ts2							
b44	I375F	I307	ADMIDAS	1.44	0.09	3.6	0.001	3.2	1.61	0.13	0.38	0.12	b44							
b53	E387V	N319	β -I	1.05	0.08	-0.8	0.205	-2.1	0.91	0.10	0.40	0.05	b53							
b56	G395S	G327	ADMIDAS	1.81	0.11	7.7	0.000	5.4	1.90	0.06	0.50	0.08	b56							
b7	D404N	D336	β -I	1.26	0.15	1.5	0.586	0.4	1.25	0.21	0.61	0.08	b7							
b23	N407Y	N339	ADMIDAS	3.61	0.24	28.0	0.000	14.6	3.11	0.21	0.24	0.03	b23	12,13						
b58	V409D	L341	ADMIDAS	2.07	0.14	10.6	0.000	9.3	2.41	0.17	0.30	0.02	b58							
b27	V423E	V355	Hybrid	2.21	0.16	12.3	0.000	7.0	2.11	0.24	0.77	0.06	b27							
b37	C441Y	C374	Hybrid	1.81	0.24	7.8	0.000	-1.4	0.97	0.14	0.23	0.06	b37	14						
b63	G531D	G458	I-EGF1	1.53	0.08	4.6	0.001	2.0	1.46	0.10	0.39	0.06	b63	15						
b31	G541S	G468	I-EGF1	1.76	0.10	7.2	0.000	8.1	2.25	0.11	1.03	0.07	b31							
b64	C544Y	C471	I-EGF1	2.40	0.26	14.4	0.000	9.1	2.38	0.29	0.48	0.06	b64	16						
b55	R587Q	S511	I-EGF2	1.58	0.10	5.2	0.000	5.9	1.96	0.10	0.91	0.08	b55							
b46	G596S	G518	I-EGF2	1.34	0.08	2.4	0.001	0.7	1.29	0.09	0.55	0.09	b46							
b52	G596R	G518	I-EGF2	1.92	0.24	9.0	0.000	6.8	2.09	0.38	0.36	0.04	b52							
b24	E600K	E522	I-EGF2-3	1.21	0.1	1.0	0.102	-0.4	1.14	0.06	0.61	0.08	b24							
b51	E607K	V529	I-EGF3	3.51	0.17	26.8	0.000	22.3	4.12	0.59	0.35	0.04	b51							
XN101	C629S	C549	I-EGF3	1.94	0.46	9.1	0.000	6.3	2.02	0.50	0.05	0.00	XN101	16,17						
b22	R676C	G592	I-EGF4	1.65	0.12	5.9	0.000	4.2	1.74	0.14	0.34	0.03	b22							
b39	G679D	G595	I-EGF4	1.23	0.08	1.2	0.311	1.1	1.33	0.15	1.03	0.27	b39							
b4	C701Y	C617	β -TD	1.11	0.04	-0.1	0.634	-0.3	1.16	0.04	0.70	0.07	b4							
b34	G707S	G623	β -TD	1.12	0.07	0.0	0.451	-0.2	1.17	0.07	0.96	0.07	b34							
b29	F743I	Y657	β -TD	2.00	0.23	9.9	0.000	4.7	1.81	0.23	0.57	0.03	b29							
b32	V763I	S677	β -TD	1.21	0.11	0.9	0.962	2.1	1.46	0.10	0.51	0.06	b32							
b40	V775D	P691	β -TD	1.51	0.08	4.4	0.001	-0.2	1.16	0.09	0.56	0.08	b40							
b1	G792D	G708	Transmembrane	1.44	0.07	3.5	0.001	-0.9	1.08	0.04	0.50	0.06	b1	18-20						
b70	S836T P841T	S752 I757	Cytoplasmic	1.02	0.14	-1.1	0.390	0.3	1.24	0.11	0.61	0.23	b70	21-27						
G1	delT825>	delT74	Cytoplasmic	0.96	0.12	-1.9	0.503	1.46	1.39	0.07	0.68	0.10	G1							

Table S3. Distribution, based on position, of TWOW-1 binding of mutant β PS integrins expressed together with α PS2C in stably transformed cell lines. Data and shading is the same as in Table S2 but mutants have been sorted according to their position (Column B) in the β PS integrin subunit. As in Table S2, allele identification (Column A) is shaded according to TWOW-1 binding ability (Column G); red, z scores less than -10; dark pink, z scores between -5 and -10; no fill, z scores between -2.9 and 2.4; light green, z scores between 2.4 and 5; dark green z scores between 5 and 10; blue, z scores greater than 10. Columns are the same as in Table S2 except that Column has been added containing references for mutations in other β integrin subunits at the homologous residue (see paper for references).