Supporting Information, Table S1. The free energies for the binding of GPIbα to FLNa domains, calculated by MMGBSA. Estimations of ΔG_{bind} (in kcal/mol) are based on snapshots obtained from trajectories after 6 ns-MD simulations. The results, with standard error, for each individual repeat are shown here. The averages of the repeats are shown in Table 1.

GB-model	Repeat	FLNa9	FLNa12	FLNa17	FLNa19	FLNa21	FLNa23
igb=1	1	-95.4 ± 6.0	-86.2 ± 5.0	-97.1 ± 5.0	-91.5 ± 5.0	-97.4 ± 5.3	-94.6 ± 5.5
	2	-93.3 ± 4.9	-89.8 ± 7.4	-93.0 ± 6.9	-96.3 ± 8.4	-96.3 ± 4.9	-93.5 ± 6.8
	3	-93.7 ± 4.9	-91.3 ± 6.4	-95.9 ± 7.8	-92.1 ± 6.5	-97.8 ± 5.2	-96.4 ± 7.4
igb=2	1	-75.4 ± 5.3	-66.5 ± 4.8	-76.6 ± 4.6	-71.3 ± 4.7	-77.2 ± 4.9	-72.5 ± 5.1
	2	-74.0 ± 4.6	-69.2 ± 6.2	-71.6 ± 6.3	-74.8 ± 6.9	-75.3 ± 4.4	-72.2 ± 5.8
	3	-74.3 ± 4.9	-70.9 ± 5.5	-73.4 ± 6.8	-71.4 ± 6.2	-78.2 ± 4.6	-73.1 ± 6.5
igb=5	1	-69.3 ± 11	-48.1 ± 11	-68.2 ± 11	-52.3 ± 10	-59.3 ± 10	-53.7 ± 12
	2	-62.8 ± 11	-55.8 ± 12	-55.3 ± 13	-66.4 ± 16	-56.6 ± 11	-63.6 ± 11
	3	-58.8 ± 11	-46.4 ± 13	-53.3 ± 14	-47.2 ± 12	-64.0 ± 8.5	-50.3 ± 13

Supporting Information, Table S2. The free energies for the binding of various peptide-ligands to FLNa21, calculated by MMGBSA. Estimations of ΔG_{bind} (in kcal/mol) are based on snapshots obtained from trajectories after 6 ns-MD simulations. The results, with standard error, for each individual repeat are shown here. The averages of the repeats are shown in Table 2.

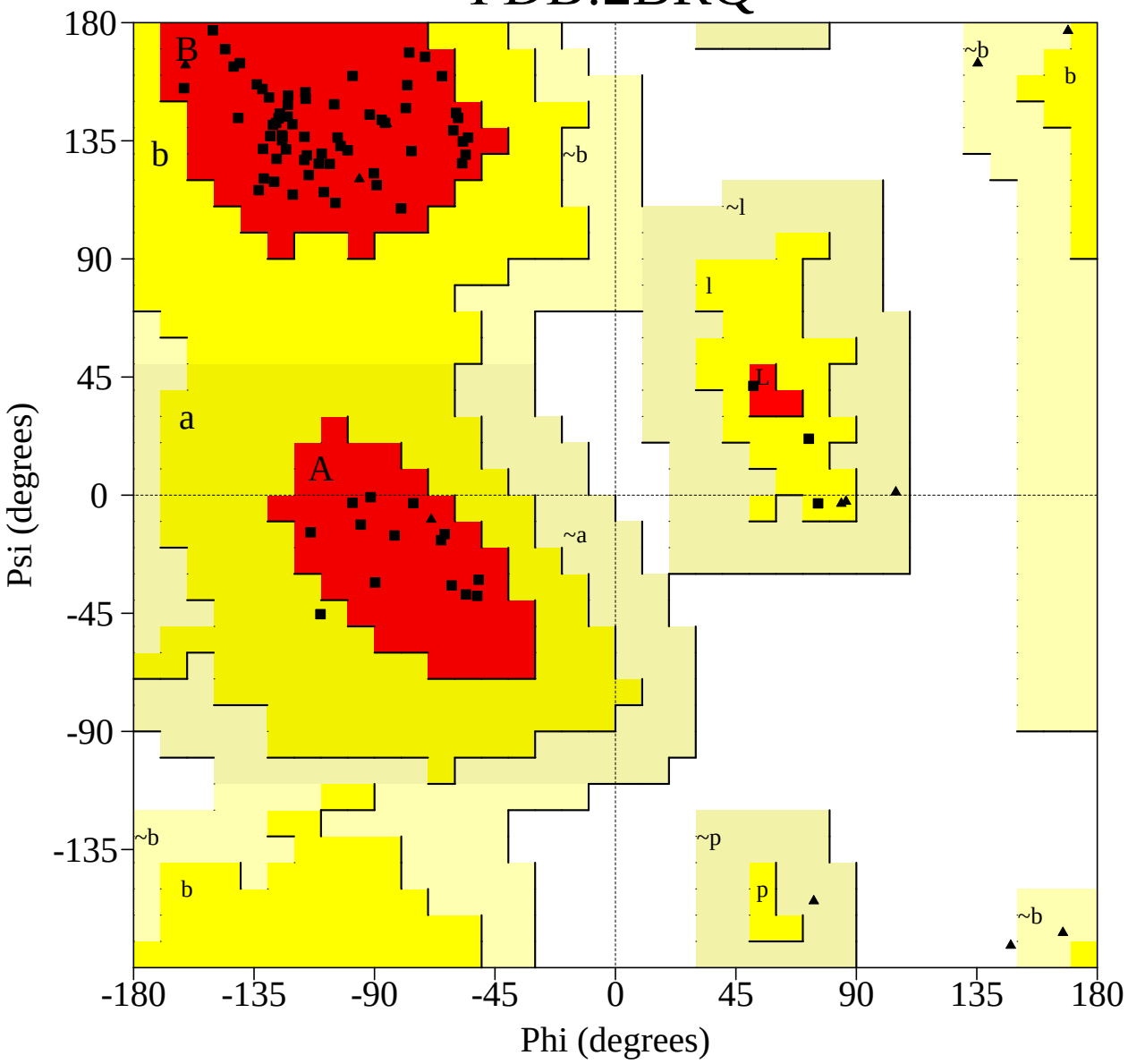
GB-model	Repeat	GPIbα	Migfilin	Integrin β2	Integrin β7
igb=1	1	-97.4 ± 5.3	-98.0 ± 5.8	-80.2 ± 5.8	-81.0 ± 4.2
	2	-96.3 ± 4.9	-95.5 ± 6.3	-79.0 ± 5.6	-86.0 ± 5.2
	3	-97.8 ± 5.2	-88.8 ± 7.1	-80.0 ± 4.9	-81.0 ± 3.9
igb=2	1	-77.2 ± 4.9	-75.7 ± 5.2	-60.8 ± 5.0	-61.8 ± 4.1
	2	-75.3 ± 4.4	-74.1 ± 5.9	-59.7 ± 5.0	-65.4 ± 5.0
	3	-78.2 ± 4.6	-68.2 ± 5.7	-61.1 ± 4.6	-62.5 ± 3.8
igb=5	1	-59.3 ± 10	-59.8 ± 12	-39.7 ± 11	-35.9 ± 11
	2	-56.6 ± 11	-55.3 ± 12	-36.5 ± 13	-41.6 ± 11
	3	-64.0 ± 8.5	-46.2 ± 11	-37.1 ± 11	-45.0 ± 11

Supporting Information, Figure S1. Ramachandran plots of the crystal structure of FLNa21 (PDB: 2BRQ) and homology models of FLNa domains 9, 12, 19, and 23. All the models were built based on the alignment of the crystal structure of FLNa21 and the corresponding sub-section of the human FLNa sequence (Uniprot: FLNA_HUMAN).

PROCHECK

Ramachandran Plot

PDB:2BRQ



Plot statistics

Residues in most favoured regions [A,B,L]	69	95.8%
Residues in additional allowed regions [a,b,l,p]	3	4.2%
Residues in generously allowed regions [~a,~b,~l,~p]	0	0.0%
Residues in disallowed regions	0	0.0%
	----	------
Number of non-glycine and non-proline residues	72	100.0%
Number of end-residues (excl. Gly and Pro)	1	
Number of glycine residues (shown as triangles)	13	
Number of proline residues	8	

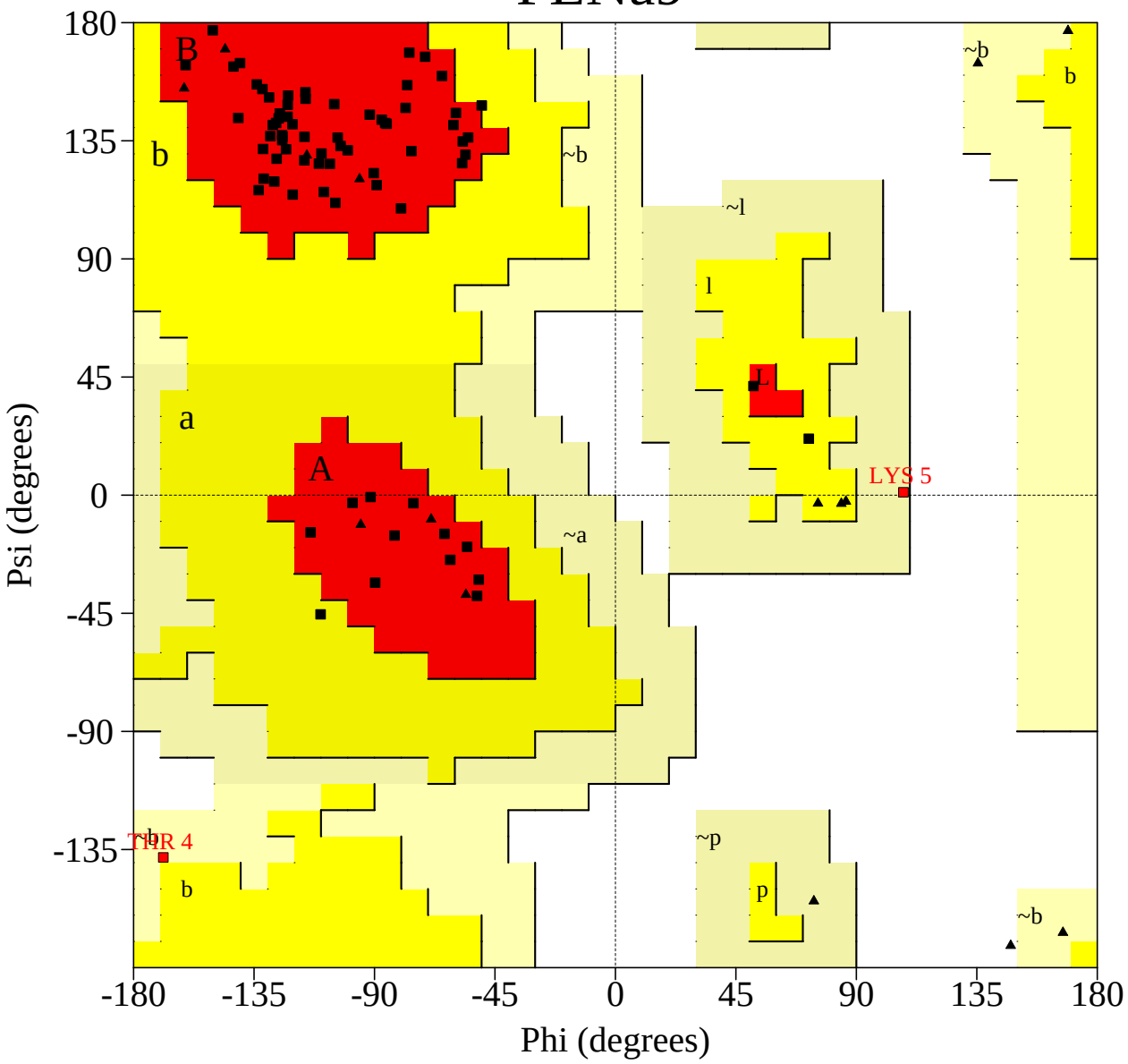
Total number of residues	94	

Based on an analysis of 118 structures of resolution of at least 2.0 Angstroms and R-factor no greater than 20%, a good quality model would be expected to have over 90% in the most favoured regions.

PROCHECK

Ramachandran Plot

FLNa9



Plot statistics

Residues in most favoured regions [A,B,L]	63	94.0%
Residues in additional allowed regions [a,b,l,p]	2	3.0%
Residues in generously allowed regions [~a,~b,~l,~p]	2	3.0%
Residues in disallowed regions	0	0.0%
	----	------
Number of non-glycine and non-proline residues	67	100.0%
Number of end-residues (excl. Gly and Pro)	2	
Number of glycine residues (shown as triangles)	15	
Number of proline residues	9	

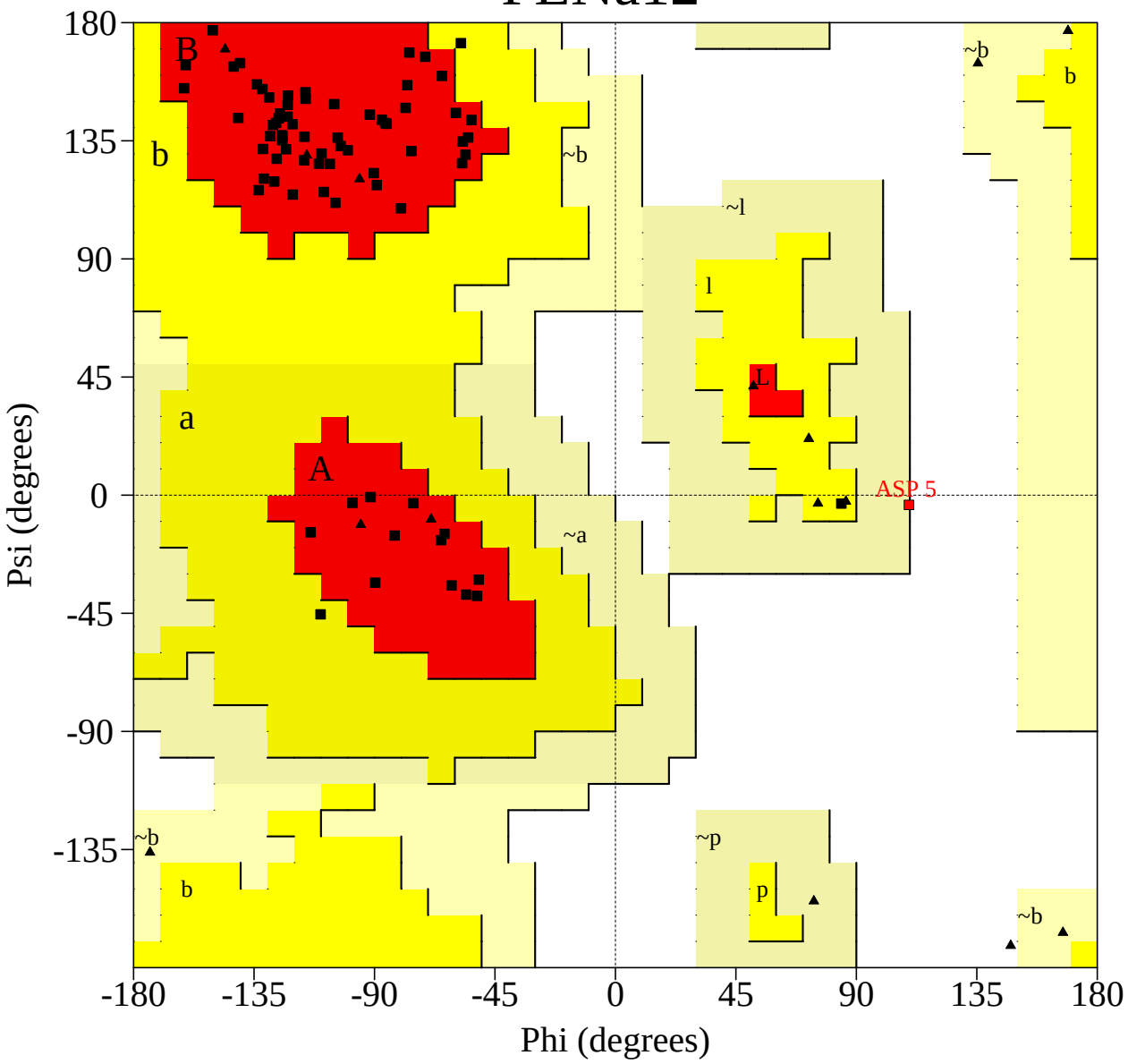
Total number of residues	93	

Based on an analysis of 118 structures of resolution of at least 2.0 Angstroms and R-factor no greater than 20%, a good quality model would be expected to have over 90% in the most favoured regions.

PROCHECK

Ramachandran Plot

FLNa12



Plot statistics

Residues in most favoured regions [A,B,L]	64	94.1%
Residues in additional allowed regions [a,b,l,p]	3	4.4%
Residues in generously allowed regions [~a,~b,~l,~p]	1	1.5%
Residues in disallowed regions	0	0.0%
	----	------
Number of non-glycine and non-proline residues	68	100.0%
Number of end-residues (excl. Gly and Pro)	2	
Number of glycine residues (shown as triangles)	15	
Number of proline residues	8	

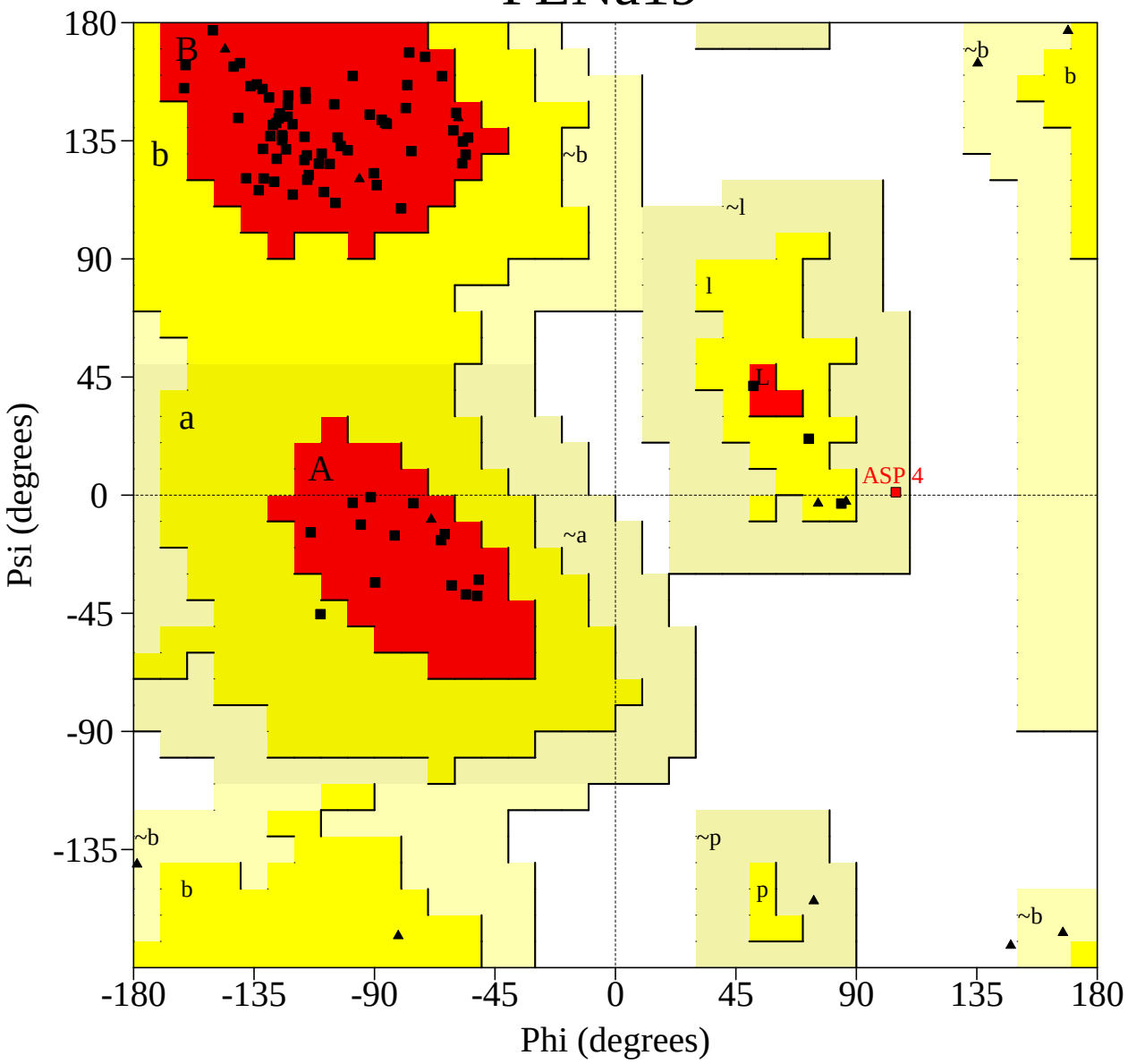
Total number of residues	93	

Based on an analysis of 118 structures of resolution of at least 2.0 Angstroms and R-factor no greater than 20%, a good quality model would be expected to have over 90% in the most favoured regions.

PROCHECK

Ramachandran Plot

FLNa19



Plot statistics

Residues in most favoured regions [A,B,L]	74	94.9%
Residues in additional allowed regions [a,b,l,p]	3	3.8%
Residues in generously allowed regions [~a,~b,~l,~p]	1	1.3%
Residues in disallowed regions	0	0.0%
	----	------
Number of non-glycine and non-proline residues	78	100.0%
Number of end-residues (excl. Gly and Pro)	2	
Number of glycine residues (shown as triangles)	13	
Number of proline residues	6	

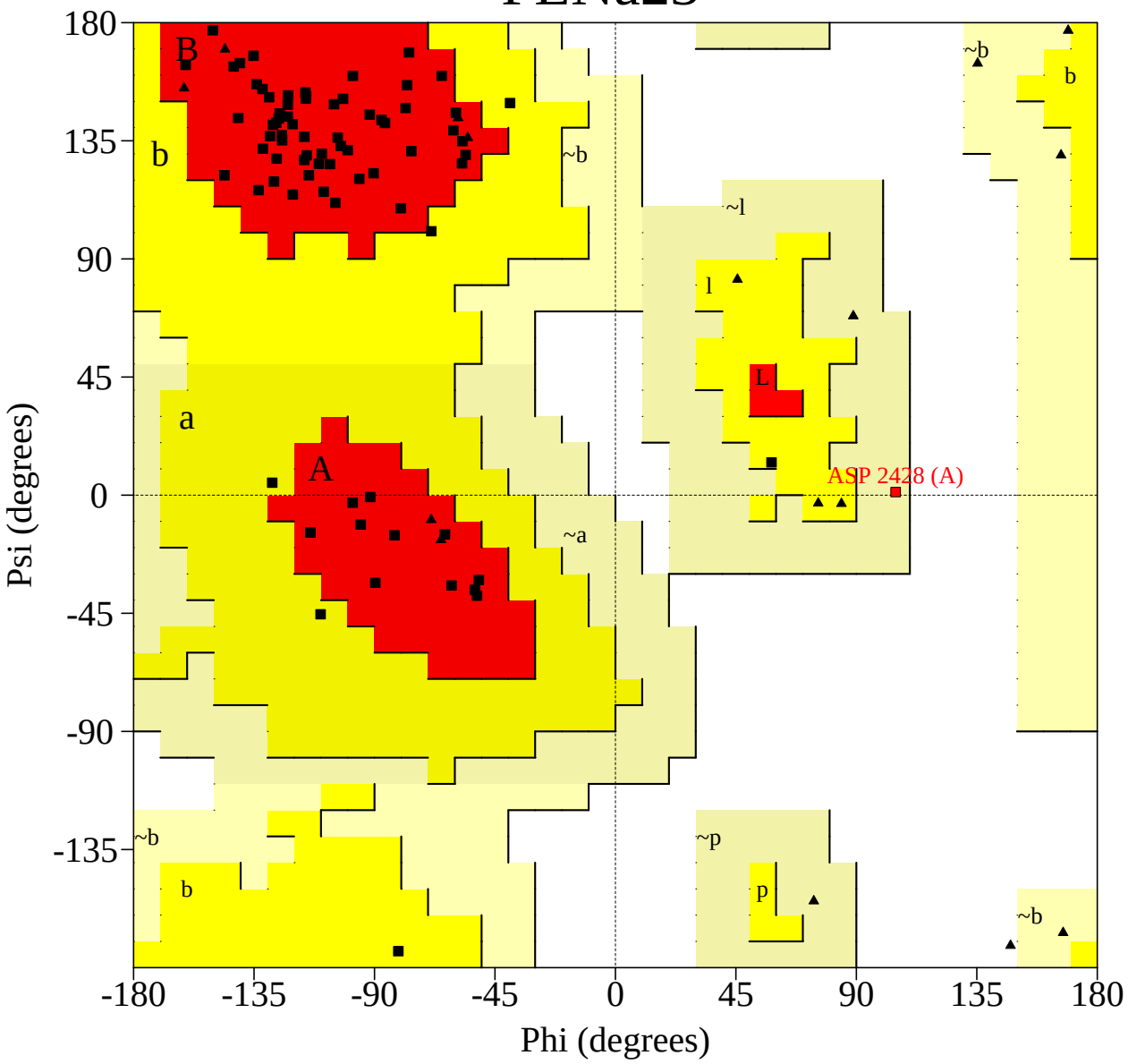
Total number of residues	99	

Based on an analysis of 118 structures of resolution of at least 2.0 Angstroms and R-factor no greater than 20%, a good quality model would be expected to have over 90% in the most favoured regions.

PROCHECK

Ramachandran Plot

FLNa23



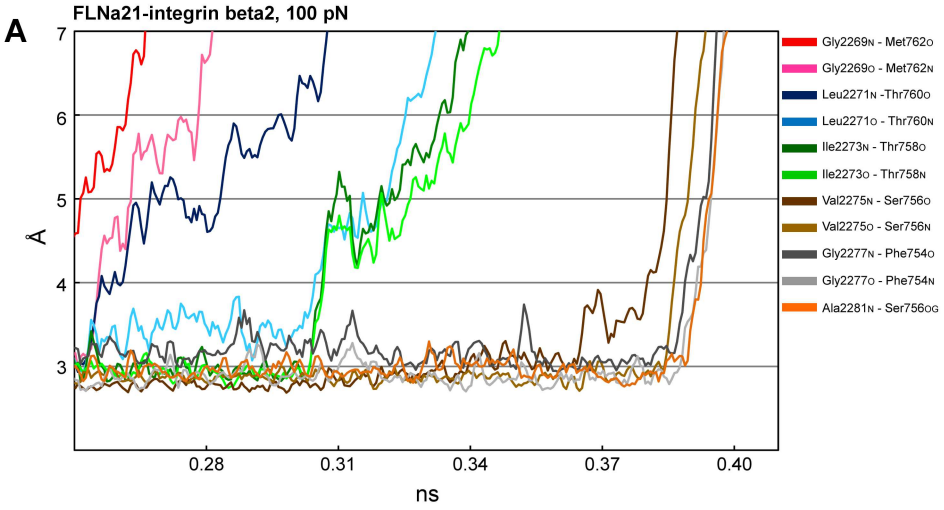
Plot statistics

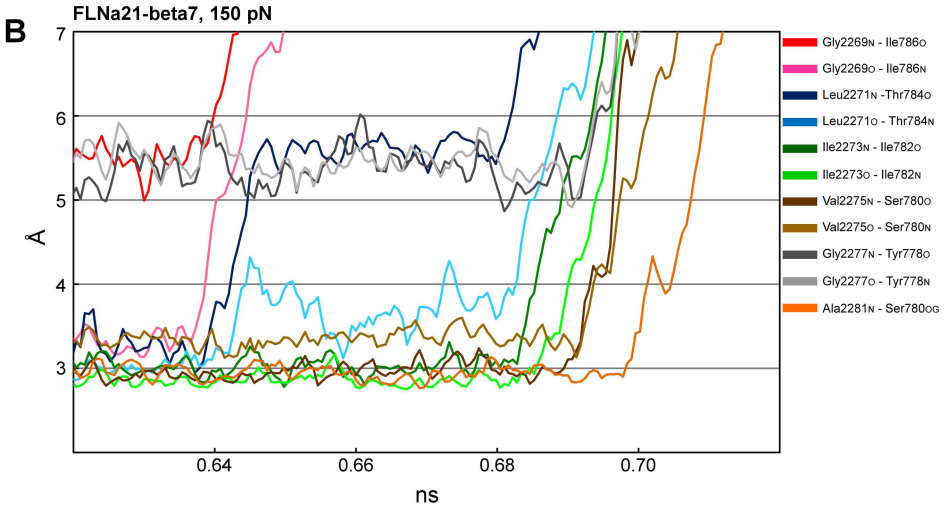
Residues in most favoured regions [A,B,L]	63	91.3%
Residues in additional allowed regions [a,b,l,p]	5	7.2%
Residues in generously allowed regions [~a,~b,~l,~p]	1	1.4%
Residues in disallowed regions	0	0.0%
	----	------
Number of non-glycine and non-proline residues	69	100.0%
Number of end-residues (excl. Gly and Pro)	1	
Number of glycine residues (shown as triangles)	17	
Number of proline residues	9	

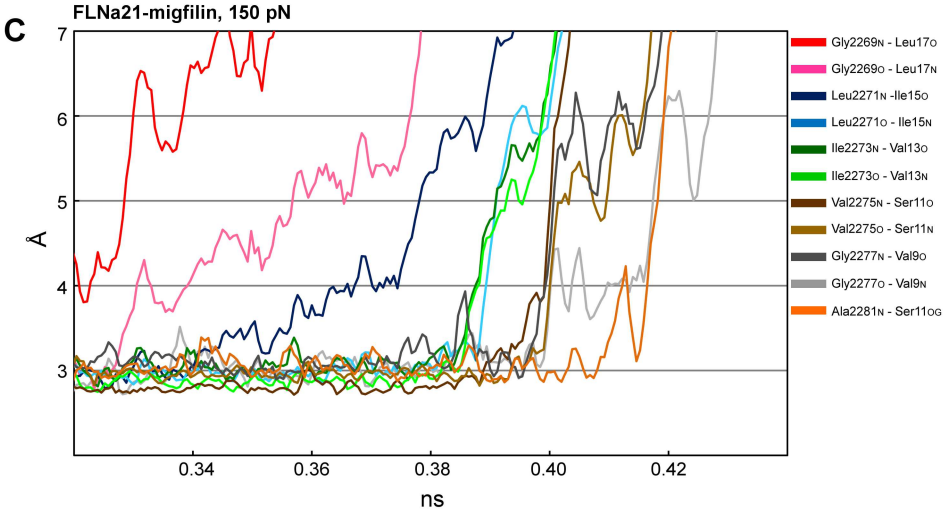
Total number of residues	96	

Based on an analysis of 118 structures of resolution of at least 2.0 Angstroms and R-factor no greater than 20%, a good quality model would be expected to have over 90% in the most favoured regions.

Supporting Information, Figure S3. Atom distances in SMD simulations of FLNa21 in complex with peptide-ligands. Distances (moving averages, period of 3) between atoms from the D-face of FLNa21 and either (A) filamin β2, (B) filamin β7, or (C) migfilin in SMD simulations are shown. In addition to the main chain N or O atoms, the side-chain O(H) of serine in position 4 of the ligands is considered. Distances from the SMD simulation between FLNa21 and GPIbα are shown in Figure 3A.


A
FLNa21-integrin beta2, 100 pN
Å
ns
Gly2269N - Met762O
Gly2269O - Met762N
Leu2271N -Thr760O
Leu2271O - Thr760N
Ile2273N - Thr758O
Ile2273O - Thr758N
Val2275N - Ser756O
Val2275O - Ser756N
Gly2277N - Phe754O
Gly2277O - Phe754N
Ala2281N - Ser756OG


B
FLNa21-beta7, 150 pN
Å
ns
Gly2269N - Ile786O
Gly2269O - Ile786N
Leu2271N -Thr784O
Leu2271O - Thr784N
Ile2273N - Ile782O
Ile2273O - Ile782N
Val2275N - Ser780O
Val2275O - Ser780N
Gly2277N - Tyr778O
Gly2277O - Tyr778N
Ala2281N - Ser780OG


C
FLNa21-migfilin, 150 pN
Å
ns
Gly2269N - Leu17O
Gly2269O - Leu17N
Leu2271N -Ile15O
Leu2271O - Ile15N
Ile2273N - Val13O
Ile2273O - Val13N
Val2275N - Ser11O
Val2275O - Ser11N
Gly2277N - Val9O
Gly2277O - Val9N
Ala2281N - Ser11OG