Supplementary Table 1—Hide-and-seek test using inter-subunit Cβ distance as simulated experimental data

Model	RMSD(Å)	ΔTx (Å)	Δθ (deg)	Δϕ (deg)	ΔTz (Å)
1	0.3	0.3	0.6	1.6	0.1
2	0.0	0.0	0.0	0.0	0.0
3	0.0	0.0	0.0	0.0	0.0
4	0.0	0.0	0.0	0.0	0.0
5	0.0	0.0	0.0	0.0	0.0
6	0.0	0.0	0.0	0.9	0.0
7	0.0	0.0	0.0	0.8	0.0
8	0.0	0.0	0.0	0.0	0.0
9	0.6	0.6	1.8	2.8	0.2
10	0.5	0.0	1.4	1.1	0.2

"Δ" indicates the difference between the values of the actual parameters and those obtained after the rigid-body search

Supplementary Table 2—GpA disruption data obtained from Figure 5 of Lemmon et al.[1]

Residue	SeqNumber	Chain	Atom	Dimer Disruption	Flag
ILE	73	A	CB	0.30	1.0
THR	74	A	CB	0.00	1.0
LEU	75	A	CB	1.80	1.0
ILE	76	A	CB	2.00	1.0
ILE	77	A	CB	0.25	1.0
PHE	78	A	CB	0.00	1.0
GLY	79	A	CA	2.30	1.0
VAL	80	A	CB	1.00	1.0
MET	81	A	CB	0.00	1.0
ALA	82	A	CB	0.00	1.0
GLY	83	A	CA	3.00	1.0
VAL	84	A	CB	2.50	1.0
ILE	85	A	CB	0.00	1.0
GLY	86	A	CA	0.20	1.0
THR	87	A	CB	2.00	1.0
ILE	88	A	CB	0.75	1.0
LEU	89	A	CB	0.65	1.0
LEU	90	A	CB	0.40	1.0
ILE	91	A	CB	0.65	1.0
SER	92	A	CB	0.00	1.0
TYR	93	A	CB	0.30	1.0
GLY	94	A	CA	0.00	1.0
ILE	95	A	CB	0.40	1.0

A Flag value of ‘1.0’ indicates that the data value was used

Supplementary Table 3—GpA disulfide cross-linking data obtained from Supplementary Information of Zhu et al.[2]

Residue	SeqNumber	Chain	Atom	%Crosslinking	Flag
ILE	73	A	CB	0.00	1.0
THR	74	A	CB	1.00	1.0
LEU	75	A	CB	44.50	1.0
ILE	76	A	CB	29.25	1.0
ILE	77	A	CB	6.75	1.0
PHE	78	A	CB	1.25	1.0
GLY	79	A	CA	87.25	1.0
VAL	80	A	CB	66.67	1.0
MET	81	A	CB	1.67	1.0
ALA	82	A	CB	0.00	1.0
GLY	83	A	CA	83.00	1.0
VAL	84	A	CB	38.00	1.0
ILE	85	A	CB	1.17	1.0
GLY	86	A	CA	28.00	1.0
THR	87	A	CB	59.67	1.0
ILE	88	A	CB	38.00	1.0
LEU	89	A	CB	6.83	1.0
LEU	90	A	CB	38.00	1.0
ILE	91	A	CB	53.00	1.0
SER	92	A	CB	1.50	1.0
TYR	93	A	CB	5.00	1.0
GLY	94	A	CA	15.50	1.0
ILE	95	A	CB	3.00	1.0

A Flag value of ‘1.0’ indicates that the data value was used

Supplementary Table 4—Pentamer disruption data obtained from Table 1 of Simmermann et al.[3]

Residue	SeqNumber	Chain	Atom	Pentamer Disruption	Flag
LEU	37	A	CB	0.7	1.0
ILE	38	A	CB	43.8	1.0
LEU	39	A	CB	27.3	1.0
ILE	40	A	CB	1.6	1.0
CYS	41	A	CB	28.3	1.0
LEU	42	A	CB	44.6	1.0
LEU	43	A	CB	34.8	1.0
LEU	44	A	CB	2.5	1.0
ILE	45	A	CB	43.2	1.0
CYS	46	A	CB	42.1	1.0
ILE	47	A	CB	2.0	1.0
ILE	48	A	CB	38.1	1.0
VAL	49	A	CB	44.3	1.0
MET	50	A	CB	35.6	1.0
LEU	51	A	CB	14.4	1.0
LEU	52	A	CB	49.1	1.0

A Flag value of ‘1.0’ indicates that the data value was used

Supplementary Table 5—EphA1 TOXR data taken from Table 2 of Volynsky et al.[4]

Residue	SeqNumber	Chain	Atom	TOXR	Flag
VAL	549	A	CB	102.0	0.0
ALA	550	A	CB	50.0	1.0
VAL	551	A	CB	94.0	0.0
ILE	552	A	CB	113.0	1.0
PHE	553	A	CB	82.0	1.0
GLY	554	A	CA	4.0	1.0
LEU	555	A	CB	74.0	1.0
LEU	556	A	CB	116.0	1.0
LEU	557	A	CB	116.0	1.0
GLY	558	A	CA	17.0	1.0
ALA	559	A	CB	95.0	1.0
ALA	560	A	CB	103.0	1.0

A Flag value of '1.0' indicates that the data value was used. Only mutations to hydrophobic residues were considered.

Supplementary Table 6—BNIP3 unified mutagenesis score values for alanine were taken from Figure 7 of Lawrie et al[5]

Residue	SeqNumber	Chain	Atom	UnifiedScore	Flag
LEU	170	A	CB	3.0	1.0
LEU	171	A	CB	2.0	1.0
SER	172	A	CB	4.0	1.0
HIS	173	A	CB	9.0	1.0
LEU	174	A	CB	2.0	1.0
LEU	175	A	CB	ND	ND
ALA	176	A	CB	0.0	1.0
ILE	177	A	CB	4.0	1.0
GLY	178	A	CA	1.0	1.0
LEU	179	A	CB	3.0	1.0
GLY	180	A	CA	10.0	1.0
ILE	181	A	CB	5.0	1.0
TYR	182	A	CB	1.0	1.0
ILE	183	A	CB	5.0	1.0
GLY	184	A	CA	7.0	1.0

'ND' indicates that there was no data for this residue. A Flag value of '1.0' indicates that the data value was used.

Supplementary Table 7—M2 perturbility index (PI) data taken from Figure 2 of Pinto et al.[6]

Residue	SeqNumber	Chain	Atom	PI (Avg)	Flag
LEU	26	A	CB	0.70	1.0
VAL	27	A	CB	1.00	1.0
VAL	28	A	CB	0.50	1.0
ALA	29	A	CB	0.07	1.0
ALA	30	A	CB	0.95	1.0
SER	31	A	CB	0.50	1.0
ILE	32	A	CB	0.25	1.0
ILE	33	A	CB	0.20	1.0
GLY	34	A	CA	0.65	1.0
ILE	35	A	CB	0.35	1.0
LEU	36	A	CB	0.37	1.0
HIS	37	A	CB	0.95	1.0
LEU	38	A	CB	0.00	1.0
ILE	39	A	CB	0.17	1.0
LEU	40	A	CB	0.07	1.0
TRP	41	A	CB	0.57	1.0
ILE	42	A	CB	0.10	1.0
LEU	43	A	CB	0.17	1.0

A Flag value of ‘1.0’ indicates that the data value was used

Supplementary Table 8—BM2 perturbility index (PI) data taken from Figure 3 of Ma et al.[7]

Residue	SeqNumber	Chain	Atom	PI (Avg)	Flag
ILE	7	A	CB	0.30	1.0
LEU	8	A	CB	0.23	1.0
SER	9	A	CB	0.52	1.0
ILE	10	A	CB	0.45	1.0
CYS	11	A	CB	0.09	1.0
SER	12	A	CB	0.34	1.0
PHE	13	A	CB	0.65	1.0
ILE	14	A	CB	0.29	1.0
LEU	15	A	CB	0.48	1.0
SER	16	A	CB	0.33	1.0
ALA	17	A	CB	0.23	1.0
LEU	18	A	CB	0.14	1.0
HIS	19	A	CB	0.99	1.0
PHE	20	A	CB	0.39	1.0
MET	21	A	CB	0.06	1.0
ALA	22	A	CB	0.17	1.0
TRP	23	A	CB	0.77	1.0
THR	24	A	CB	0.06	1.0
ILE	25	A	CB	0.00	1.0

A Flag value of ‘1.0’ indicates that the data value was used

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