Computational and Kinetics Analyses of an Aminomutase using Ring-substituted Arylalanines Reveal that Sterics and Substituent Effects Dictate Substrate Specificity

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Figure S40. Relationship between protein-ligand interaction energy $E_{(p-l)}$ and experimental $K_{\rm M}$. Substrates were placed in the active site in *NH*₂-*cis* and *NH*₂-*trans* orientations overlaid with the crystallographic orientation of α -phenylalanine from PDB entry 3UNV, and the lower energy orientation was kept. Left panel: (•) Binding site residues of *Pa*PAM were maintained in their crystallographic orientation, yielding a linear correlation coefficient of 0.48 between $E_{(p-l)}$ and experimental $K_{\rm M}$. Right panel: (•) Energy minimization was used to reduce any repulsive interactions, leading to lower correlation between the resulting protein-ligand interaction energy and $K_{\rm M}$ value (correlation coefficient = 0.35).

Figure S41. Relationship between the electrostatic (Coulombic) component of the protein-ligand interaction energy $E_{C(p-l)}$ and experimental K_M . Substrates were placed in the active site in NH_2 -*cis* and NH_2 -*trans* configurations overlaid with the crystallographic orientation of α -phenylalanine, and the lower energy orientation was kept. Left panel: (•) Binding site of *Pa*PAM was kept in the crystallographic orientation (correlation coefficient = 0.33). Right panel: (•) Energy minimization was used to reduce any protein-ligand repulsive interactions (correlation coefficient = 0.011).

Figure S42. Relationship between the van der Waals energy component of the protein-ligand energy $E_{V(p-l)}$ and experimental K_M . Substrates were again placed in NH_2 -cis and NH_2 -trans orientations overlaid with the crystallographic orientation of α -phenylalanine from PDB entry 3UNV, and the lower energy orientation was kept. Left panel: (•) Binding site residues of PaPAM were kept in the crystallographic orientation (correlation coefficient = 0.54). Right panel: (•) Energy minimization was used to reduce any protein-ligand repulsive interactions (correlation coefficient = 0.42). These results indicate that the van der Waals interaction energy between the protein and each substrate overlaid with the α -phenylalanine-bound crystal structure is most predictive of the relative K_M values of the substrates. 43S

Table S1. Comparison of the experimental $K_{\rm M}$ and predicted energetic order of each substituentat *ortho-*, *meta-*, *para-*positions.37

Table S2. Comparison of the experimental $K_{\rm M}$ and predicted energetic order of each substituentat ortho-, meta-, para-positions. This data is the same as presented in Table 1S; here, it isorganized according to substituent position rather than type.38

Table S3. Evaluation of protein-ligand and ligand internal energy values and preference for *NH2-cis versus* NH2-trans *configuration*.

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Substrates, Authentic Standards and Reagents

(*S*)-α-, *p*-Methoxy-(*S*)-α-, *p*-nitro-(*S*)-α-, and *p*-chloro-(*R*/*S*)-β-phenylalanine and (*E*)-*o*methyl-, (*E*)-*p*-methyl-, (*E*)-*p*-methoxy- and (*E*)-*p*-nitro-cinnamic acid, (*E*)-*o*-furyl-acrylate and (trimethylsilyl)diazomethane (2.0 M in diethyl ether) were purchased from Sigma-Aldrich-Fluka (St. Louis, MO). Racemic *p*-nitro-β-phenylalanine was purchased from Oakwood Products, Inc. (West Columbia, SC), and *o*-methoxy-(*S*)-α-, *m*-methoxy-(*S*)-α-, *o*-nitro-(*S*)-α-, *m*-nitro-(*S*)-α-, *o*methoxy-(*S*)-β-, *m*-methoxy-(*S*)-β-, *o*-nitro-(*S*)-β-, and *m*-nitro-(*S*)-β-phenylalanine were purchased from Chem-Impex International, Inc. (Wood Dale, IL). 2-Amino-5-phenylpentanoic acid was purchased from Acros Organics (New Jersey). All other (*S*)-α- and β-amino acids were purchased from PepTech Corporation (Burlington, MA) and the other (*E*)-cinnamic acids were purchased from Alfa Aesar (Ward, Hill, MA). All chemicals were used without further purification, unless noted.

General Instrumentation

GC-MS analysis was performed with an Agilent 6890N gas chromatograph equipped with a capillary GC column (30 m × 0.25 mm × 0.25 μ M; HP-5MS; J&W Scientific) with helium as the carrier gas (flow rate, 1 mL/min). The injector port (at 250 °C) was set to splitless injection mode. A 1- μ L aliquot of each sample was injected using an Agilent 7683 auto-sampler (Agilent, Atlanta; GA). The column temperature was increased from 50 – 110 °C at 30 °C/min, then increased by 10 °C/min to 250 °C (total run time of 16 min), and returned to 50 °C over 5 min, with a 5 min hold. The gas chromatograph was coupled to a mass selective detector (Agilent, 5973 *inert*) operated in electron impact mode (70 eV ionization voltage). All spectra were recorded in the mass range of 50 – 400 *m/z*.



Figure S1. EI-MS spectra of the *N*-(ethoxycarbonyl) methyl ester derivatives of biosynthetic β -phenylalanine made from *Pa*PAM catalysis (top) and authentic β -phenylalanine (bottom). GC retention times (GC R_t) are shown.



Figure S2. EI-MS spectra of the *N*-(ethoxycarbonyl) methyl ester derivatives of biosynthetic *m*-bromo- β -phenylalanine made from *Pa*PAM catalysis (top) and authentic *m*-bromo- β -phenylalanine (bottom). GC retention times (GC R_i) are shown.



Figure S3. EI-MS spectra of the *N*-(ethoxycarbonyl) methyl ester derivatives of biosynthetic *m*-fluoro- β -phenylalanine made from *Pa*PAM catalysis (top) and authentic *m*-fluoro- β -phenylalanine (bottom). GC retention times (GC R_t) are shown.



Figure S4. EI-MS spectra of the *N*-(ethoxycarbonyl) methyl ester derivatives of biosynthetic *m*-chloro- β -phenylalanine made from *Pa*PAM catalysis (top) and authentic *p*-chloro- β -phenylalanine (bottom). GC retention times (GC R_t) are shown. Note, *p*-chloro- β -phenylalanine was on-hand and used as the authentic standard.



Figure S5. EI-MS spectra of the *N*-(ethoxycarbonyl) methyl ester derivatives of biosynthetic *p*-fluoro- β -phenylalanine made from *Pa*PAM catalysis (top) and authentic *p*-fluoro- β -phenylalanine (bottom). GC retention times (GC R_t) are shown.



Figure S6. EI-MS spectra of the *N*-(ethoxycarbonyl) methyl ester derivatives of biosynthetic *o*-methyl- β -phenylalanine made from *Pa*PAM catalysis (top) and authentic *o*-methyl- β -phenylalanine (bottom). GC retention times (GC R_i) are shown.



Figure S7. EI-MS spectra of the *N*-(ethoxycarbonyl) methyl ester derivatives of biosynthetic 2-furyl- β -alanine made from *Pa*PAM catalysis (top) and authentic 2-furyl- β -alanine (bottom). GC retention times (GC R_t) are shown.



Figure S8. EI-MS spectra of the *N*-(ethoxycarbonyl) methyl ester derivatives of biosynthetic 3-thienyl- β -alanine made from *Pa*PAM catalysis (top) and authentic 3-thienyl- β -alanine (bottom). GC retention times (GC R_t) are shown.



Figure S9. EI-MS spectra of the *N*-(ethoxycarbonyl) methyl ester derivatives of biosynthetic *m*-nitro- β -phenylalanine made from *Pa*PAM catalysis (top) and authentic *m*-nitro- β -phenylalanine (bottom). GC retention times (GC R_t) are shown.



Figure S10. EI-MS spectra of the *N*-(ethoxycarbonyl) methyl ester derivatives of biosynthetic *o*-fluoro- β -phenylalanine made from *Pa*PAM catalysis (top) and authentic *o*-fluoro- β -phenylalanine (bottom). GC retention times (GC R_i) are shown.



Figure S11. EI-MS spectra of the *N*-(ethoxycarbonyl) methyl ester derivatives of biosynthetic *m*-methoxy- β -phenylalanine made from *Pa*PAM catalysis (top) and authentic *m*-methoxy- β -phenylalanine (bottom). GC retention times (GC R_t) are shown.



Figure S12. EI-MS spectra of the *N*-(ethoxycarbonyl) methyl ester derivatives of biosynthetic 2-thienyl- β -alanine made from *Pa*PAM catalysis (top) and authentic 2-thienyl- β -alanine (bottom). GC retention times (GC R_t) are shown.



Figure S13. EI-MS spectra of the *N*-(ethoxycarbonyl) methyl ester derivatives of biosynthetic *m*-methyl- β -phenylalanine made from *Pa*PAM catalysis (top) and authentic *m*-methyl- β -phenylalanine (bottom). GC retention times (GC R₁) are shown.



Figure S14. EI-MS spectra of the *N*-(ethoxycarbonyl) methyl ester derivatives of biosynthetic *p*-chloro- β -phenylalanine made from *Pa*PAM catalysis (top) and authentic *p*-chloro- β -phenylalanine (bottom). GC retention times (GC R_i) are shown.



Figure S15. EI-MS spectra of the *N*-(ethoxycarbonyl) methyl ester derivatives of biosynthetic *p*-bromo- β -phenylalanine made from *Pa*PAM catalysis (top) and authentic *p*-bromo- β -phenylalanine (bottom). GC retention times (GC R_i) are shown.



Figure S16. EI-MS spectra of the *N*-(ethoxycarbonyl) methyl ester derivatives of biosynthetic *p*-methyl- β -phenylalanine made from *Pa*PAM catalysis (top) and authentic *p*-methyl- β -phenylalanine (bottom). GC retention times (GC R_t) are shown.



Figure S17. EI-MS spectra of the *N*-(ethoxycarbonyl) methyl ester derivatives of biosynthetic *p*-nitro- β -phenylalanine made from *Pa*PAM catalysis (top) and authentic *p*-nitro- β -phenylalanine (bottom). GC retention times (GC R_t) are shown.



Figure S18. EI-MS spectra of the *N*-(ethoxycarbonyl) methyl ester derivatives of biosynthetic *p*-methoxy- β -phenylalanine made from *Pa*PAM catalysis (top) and authentic *p*-methoxy- β -phenylalanine (bottom). GC retention times (GC R_i) are shown.



Figure S19. EI-MS spectra of the *N*-(ethoxycarbonyl) methyl ester derivatives of biosynthetic *o*-methoxy- β -phenylalanine made from *Pa*PAM catalysis (top) and authentic *o*-methoxy- β -phenylalanine (bottom). GC retention times (GC R₁) are shown.



Figure S20. Hanes-Woolf plot of biosynthetic β -phenylalanine (designated as velocity, *v*) catalyzed by *Pa*PAM from α -phenylalanine (S).



Figure S21. Hanes-Woolf plot of biosynthetic *m*-bromo- β -phenylalanine (designated as velocity, *v*) catalyzed by *Pa*PAM from *m*-bromo- α -phenylalanine (S).



Figure S22. Hanes-Woolf plots of biosynthetic *m*-fluoro- β -phenylalanine (designated as velocity, *v*) catalyzed by *Pa*PAM from *m*-fluoro- α -phenylalanine (S).



Figure S23. Hanes-Woolf plots of biosynthetic *m*-chloro- β -phenylalanine (designated as velocity, *v*) catalyzed by *Pa*PAM from *m*-chloro- α -phenylalanine (S).



Figure S24. Hanes-Woolf plots of biosynthetic *p*-fluoro- β -phenylalanine (designated as velocity, *v*) catalyzed by *Pa*PAM from *p*-fluoro- α -phenylalanine (S).



Figure S25. Hanes-Woolf plots of biosynthetic *o*-methyl- β -phenylalanine (designated as velocity, *v*) catalyzed by *Pa*PAM from *o*-methyl- α -phenylalanine (S).



Figure S26. Hanes-Woolf plots of biosynthetic 2-furyl- β -alanine (designated as velocity, *v*) catalyzed by *Pa*PAM from 2-furyl- α -alanine (S).



Figure S27. Hanes-Woolf plots of biosynthetic 3-thiophenyl- β -alanine (designated as velocity, *v*) catalyzed by *Pa*PAM from 3-thiophenyl- α -alanine (S).



Figure S28. Hanes-Woolf plots of biosynthetic *m*-nitro- β -phenylalanine (designated as velocity, *v*) catalyzed by *Pa*PAM from *m*-nitro- α -phenylalanine (S).



Figure S29. Hanes-Woolf plots of biosynthetic *o*-fluoro- β -phenylalanine (designated as velocity, *v*) catalyzed by *Pa*PAM from *o*-fluoro- α -phenylalanine (S).



Figure S30. Hanes-Woolf plots of biosynthetic *m*-methoxy- β -phenylalanine (designated as velocity, *v*) catalyzed by *Pa*PAM from *m*-methoxy- α -phenylalanine (S).



Figure S31. Hanes-Woolf plots of biosynthetic 2-thiophenyl- β -alanine (designated as velocity, *v*) catalyzed by *Pa*PAM from 2-thiophenyl- α -alanine (S).



Figure S32. Hanes-Woolf plots of biosynthetic *m*-methyl- β -phenylalanine (designated as velocity, *v*) catalyzed by *Pa*PAM from *m*-methyl- α -phenylalanine (S).



Figure S33. Hanes-Woolf plots of biosynthetic *p*-chloro- β -phenylalanine (designated as velocity, *v*) catalyzed by *Pa*PAM from *p*-chloro- α -phenylalanine (S).



Figure S34. Hanes-Woolf plots of biosynthetic *p*-bromo- β -phenylalanine (designated as velocity, *v*) catalyzed by *Pa*PAM from *p*-bromo- α -phenylalanine (S).



Figure S35. Hanes-Woolf plots of biosynthetic *p*-methyl- β -phenylalanine (designated as velocity, *v*) catalyzed by *Pa*PAM from *p*-methyl- α -phenylalanine (S).



Figure S36. Hanes-Woolf plots of biosynthetic *p*-nitro- β -phenylalanine (designated as velocity, *v*) catalyzed by *Pa*PAM from *p*-nitro- α -phenylalanine (S).



Figure S37. Hanes-Woolf plots of biosynthetic *p*-methoxy- β -phenylalanine (designated as velocity, *v*) catalyzed by *Pa*PAM from *p*-methoxy- α -phenylalanine (S).



Figure S38. Hanes-Woolf plots of biosynthetic *o*-methoxy- β -phenylalanine (designated as velocity, *v*) catalyzed by *Pa*PAM from *o*-methoxy- α -phenylalanine (S).

	Fluoro-Substituents ^a		Chloro-Substituents ^a			Bromo-Substituents ^a			
	<i>meta-</i> (3)	<i>para-</i> (5)	<i>ortho</i> -(10)	<i>meta-</i> (4)	<i>para-</i> (14)	ortho- (21)	<i>meta-</i> (2)	<i>para-</i> (15)	ortho- (20)
$K_{\rm M}(\mu{ m M})$	27	29	73	432	491	_ ^c	339	525	-
E _{V(p-l)} (kcal/mol)	19	19	21	33	37	93	55	60	204
$(\mathbf{E}_{(p-l)} + \mathbf{E}_{(l)})$ (kcal/mol)	148	150	149	166	170	226	188	193	338
	Nitro-Substituents ^a		Methyl-Substituents ^b			Methoxy-Substituents ^b			
	<i>meta-</i> (9)	<i>para-</i> (17)	<i>ortho</i> -(22)	ortho- (6)	<i>para-</i> (16)	<i>meta-</i> (13)	<i>ortho-</i> (19)	<i>meta-</i> (11)	<i>para-</i> (18)
$K_{\rm M}(\mu{ m M})$	430	752	-	88 (I)	163 (II)	204 (III)	164 (I)	990 (II)	1187 (III)
E _{V(p-l)} (kcal/mol)	48	186	205	55 (III)	46 (II)	40 (I)	108 (III)	86 (II)	81 (I)
$\frac{(\mathbf{E}_{(p-l)} + \mathbf{E}_{(l)})}{(\mathbf{kcal/mol})}$	236	360	393	190 (III)	179 (II)	174 (I)	292 (III)	240 (II)	219 (I)

Table S1. Comparison of the experimental $K_{\rm M}$ and predicted energetic order of each substituent at *ortho-*, *meta-*, *para-*positions.

^{*a*}Computational approach correctly explained the trends in $K_{\rm M}$ values of substrate analogs.

^bTrends in $K_{\rm M}$ did not correlate well with computationally predicted energy values, which fell within a relatively narrow range. Trends from most (I) to least (III) favorable are shown in (Roman numerals). ^cHyphens indicate non-productive substrates.

Table S2. Comparison of the experimental $K_{\rm M}$ and predicted energetic order of each substituent at *ortho-*, *meta-*, *para-*positions. This data is the same as presented in Table 1S; here, it is organized according to substituent position rather than type.

	ortho-Substituents						
<i>K</i> (M)	Fluoro	Methyl	Methoxy	Bromo	Chloro	Nitro	
Λ _Μ (μΝΙ)	73	88	164	- <i>a</i>	-	-	
$\mathbf{E}_{V(p-l)}$	Fluoro	Methyl	Chloro	Methoxy	Bromo	Nitro	
(kcal/mol)	21	55	93	108	204	205	
$(E_{(p-l)} + E_{(l)})$	Fluoro	Methyl	Chloro	Methoxy	Bromo	Nitro	
(kcal/mol)	149	190	226	292	338	393	
			<i>meta-</i> Sub	stituents			
<i>K</i> _M (μM)	Fluoro	Methyl	Bromo	Nitro	Chloro	Methoxy	
	27	204	339	430	432	990	
$\mathbf{E}_{V(p-l)}$	Fluoro	Chloro	Methyl	Nitro	Bromo	Methoxy	
(kcal/mol)	19	33	40	48	55	86	
$(E_{(p-l)} + E_{(l)})$	Fluoro	Chloro	Methyl	Bromo	Nitro	Methoxy	
(kcal/mol)	148	166	174	188	236	240	
	para-Substituents						
<i>K</i> (M)	Fluoro	Methyl	Chloro	Bromo	Nitro	Methoxy	
$\Lambda_{\rm M}(\mu {\rm WI})$	29	163	491	525	752	1187	
$\mathbf{E}_{V(p-l)}$	Fluoro	Chloro	Methyl	Bromo	Methoxy	Nitro	
(kcal/mol)	19	37	46	60	81	186	
$(E_{(p-l)} + E_{(l)})$	Fluoro	Chloro	Methyl	Bromo	Methoxy	Nitro	
(kcal/mol)	150	170	179	193	219	360	

^{*a*}Non-productive substrates are indicated by hyphens.

	Substrate	$\frac{NH_2\text{-trans}}{\left(\mathbf{E}_{(p-l)} + \mathbf{E}_{(l)}\right)^a}$ (kcal/mol)	$\frac{NH_2\text{-}cis}{\left(\mathbf{E}_{(p-l)}+\mathbf{E}_{(l)}\right)^a}$ (kcal/mol)	E _{V(p-l)} ^b (kcal/mol)	<i>K</i> _M (μM)	Preferred Orientation ^c
1	€ NH ₃	149	149	19	168	Symmetrical ^d
2	Br CO ₂ ⊕NH ₃	429	188	55	339	NH ₂ -cis
3	F → CO ₂ [⊖] ⊕ _{NH3}	153	148	19	27	NSD ^e
4	CI CI CO2 [©] NH ₃	273	166	33	432	NH ₂ -cis
5	F → ^{CO2}	150	150	19	29	Symmetrical
6	€ CO ₂ ⊕NH ₃	190	489	55	88	NH ₂ -trans
7	O → CO ₂ ^O ⊕ _{NH3}	133	115	21	415	NSD
8	S ⊕NH ₃	156	154	21	337	NSD
9		1640	236	48	430	NH ₂ -cis
10	€NH ₃	149	165	21	73	NSD
11	H ₃ C ^O ^(CO2^O) ^(CO2^O) ^(CO2^O)	265	240	86	990	NSD
12	S € CO2 [⊖] WH ₃	132	139	20	132	NSD
13	H ₃ C () () () () () () () () () ()	245	174	40	204	NH ₂ -cis

Table S3. Evaluation of protein-ligand and ligand internal energy values and preference for NH_2 cis versus NH_2 -trans configuration.

Table S3S continued on next page

14	CI BNH3	170	170	37	491	Symmetrical
15	Br CO ₂	193	193	60	525	Symmetrical
16	H ₃ C	179	179	46	163	Symmetrical
17	$O_{\mathbb{C}} \oplus H_3 \\ O_{\mathbb{C}} \otimes O_{\mathbb{C}} \\ O_{\mathbb{C}} \\ O_{\mathbb{C}} \otimes O_{\mathbb{C}} \\ O_{\mathbb{C}} \otimes O_{\mathbb{C}} \\ O_{\mathbb{C}} \otimes O_{\mathbb{C}} \\ O_{\mathbb{C}} \otimes O_{\mathbb{C}} \\ O_{\mathbb{C}} \\ O_{\mathbb{C}} \\ O_{\mathbb{C}} \otimes O_{\mathbb{C}} \\ O_{$	360	360	186	752	Symmetrical
18	H ₃ C _O ⁽¹⁾ ⁽²⁾ ⁽	219	947	81	1187	NH ₂ -trans
19	⊕NH ₃ ⊖ CO2 O CH ₃	409	292	108	164	NH ₂ -cis
20	⊕NH ₃ ⊕NH ₃	338	525	204	<u>_f</u>	NH ₂ -trans
21	€ CI CI	226	401	93	-	NH ₂ -trans
22	€	393	2065	205	-	NH ₂ -trans

^{*a*}($E_{(p-l)} + E_{(l)}$) is the sum of protein-ligand and ligand internal energy, where $E_{(p-l)}$ is the proteinligand interaction energy and $E_{(l)}$ is the ligand internal energy. ^{*b*} $E_{V(p-l)}$ is the vdW energy of protein-ligand interaction, one of the terms contributing to $E_{(p-l)}$. The vdW energy is given for whichever orientation (NH_2 -cis or NH_2 -trans) had the lower, more favorable ($E_{(p-l)} + E_{(l)}$) value. ^{*c*}Substrates were categorized as preferring an NH_2 -cis or NH_2 -trans configuration if the given orientation was at least 25 kcal/mol lower in ($E_{(p-l)} + E_{(l)}$) value. ^{*d*} α -Phenylalanine and *para*substituted substrates have symmetrical aryl rings with equal interaction energies for the NH_2 -cis and NH_2 -trans configurations. ^{*e*}Substrates observed to have no significant difference (NSD) in energy for the NH_2 -cis or NH_2 -trans configuration. ^{*f*}Non-productive substrates are indicated by hyphens. Note, all energies reported should be considered relative rather than absolute.



Figure S39. H-bonding interaction of *ortho*-methoxy- α -phenylalanine (**19**) and active site Tyr320. *o*-Methoxy- α -phenylalanine atoms are colored as C, green; N, blue; O, red and Tyr320 atoms are colored as C, light blue; O, red; H, white.



Figure S40. Relationship between protein-ligand interaction energy $E_{(p-l)}$ and experimental K_M . Substrates were placed in the active site in *NH*₂-*cis* and *NH*₂-*trans* orientations overlaid with the crystallographic orientation of α -phenylalanine from PDB entry 3UNV, and the lower energy orientation was kept. Left panel: (•) Binding site residues of *Pa*PAM were maintained in their crystallographic orientation, yielding a linear correlation coefficient of 0.48 between $E_{(p-l)}$ and experimental K_M . Right panel: (•) Energy minimization was used to reduce any repulsive interactions, leading to lower correlation between the resulting protein-ligand interaction energy and K_M value (correlation coefficient = 0.35).



Figure S41. Relationship between the electrostatic (Coulombic) component of the protein-ligand interaction energy $E_{C(p-l)}$ and experimental K_M . Substrates were placed in the active site in NH_2 -*cis* and NH_2 -*trans* configurations overlaid with the crystallographic orientation of α -phenylalanine, and the lower energy orientation was kept. Left panel: (•) Binding site of *Pa*PAM was kept in the crystallographic orientation (correlation coefficient = 0.33). Right panel: (•) Energy minimization was used to reduce any protein-ligand repulsive interactions (correlation coefficient = 0.011).



Figure S42. Relationship between the van der Waals energy component of the protein-ligand energy $E_{V(p-l)}$ and experimental K_M . Substrates were again placed in NH_2 -cis and NH_2 -trans orientations overlaid with the crystallographic orientation of α -phenylalanine from PDB entry 3UNV, and the lower energy orientation was kept. Left panel: (•) Binding site residues of PaPAM were kept in the crystallographic orientation (correlation coefficient = 0.54). Right panel: (•) Energy minimization was used to reduce any protein-ligand repulsive interactions (correlation coefficient = 0.42). These results indicate that the van der Waals interaction energy between the protein and each substrate overlaid with the α -phenylalanine-bound crystal structure is most predictive of the relative K_M values of the substrates.