Design and Directed Evolution of a Dideoxy Purine Nucleoside Phosphorylase

Supplementary Figures & Tables

David P. Nannemann, Kristian W. Kaufmann, Jens Meiler* and Brian O. Bachmann*

Department of Chemistry, Vanderbilt University, Nashville, TN 37235, USA

Corresponding Author: brian.bachmann@vanderbilt.edu

Table S1. Predicted Binding Energies for hPNP-Y88X variants

Variant	Experimental Binding Energy (kJ/mol)[a]		Predicted Binding Energy (REU)[b]		Predicted Binding Energy (kJ/mol)[c]	
	Inosine	ddI	Inosine	ddI	Inosine	ddI
Wild-type	-34.0	-16.8	-7.73	-7.78	-19.82	-23.39
Y88F	-31.9	-24.9	-7.24	-8.46	-29.70	-21.75
Y88H	-28.9	-20.3	-6.71	-7.39	-25.67	-14.08
Y88W	-23.1	-11.2	-5.86	-6.66	-20.40	-18.48
Y88A	-30.5	-18.4	-4.76	-5.78	-22.44	-13.28
Y88V	-18.8	-12.3	-7.01	-7.31	-25.84	-16.30
Y88L	-29.8	-23.9	-7.12	-7.91	-27.03	-15.61
Y88I	-17.0	-11.8	-5.06	-6.83	-21.27	-13.03
Y88M	-26.1	-22.3	-7.57	-8.09	-30.77	-22.41
Y88C	-25.7	-19.9	-5.15	-5.85	-21.81	-9.66
Y88S	-24.6	-16.1	-6.72	-7.44	-27.00	-12.24
Y88T	-18.8	-9.4	-6.62	-7.1	-16.60	-4.15
Y88N	-23.2	-12.5	-6.46	-6.9	-19.99	-13.52
Y88Q	-18.4	-12.8	-5.75	-6.64	-25.41	-16.50
Y88D	-14.1	-1.5	-7.78	-8.73	-20.92	-11.37
Y88E	-12.3	0.3	-8.13	-8.93	-19.12	-12.13
Y88K	n/d[d]	n/d[d]	-9.01	-9.14	n/d[d]	n/d[d]
Y88R	-7.21	n/d[d]	-7.66	-7.26	n/d[d]	n/d[d]

a. Experimental binding energy, $\Delta G^{\ddagger}_{TS} = -RT \ln(k_{cat}/K_M)$

b. Binding energies established using the Protein:Ligand weightset.

c. Binding energies established using the PNP:Nucleoside customized weightset.

d. Values for lysine and arginine mutants were not determined with the reweighted scoring function nor plotted in Fig. 3 of the main text as kinetic data was incomplete for these mutants.

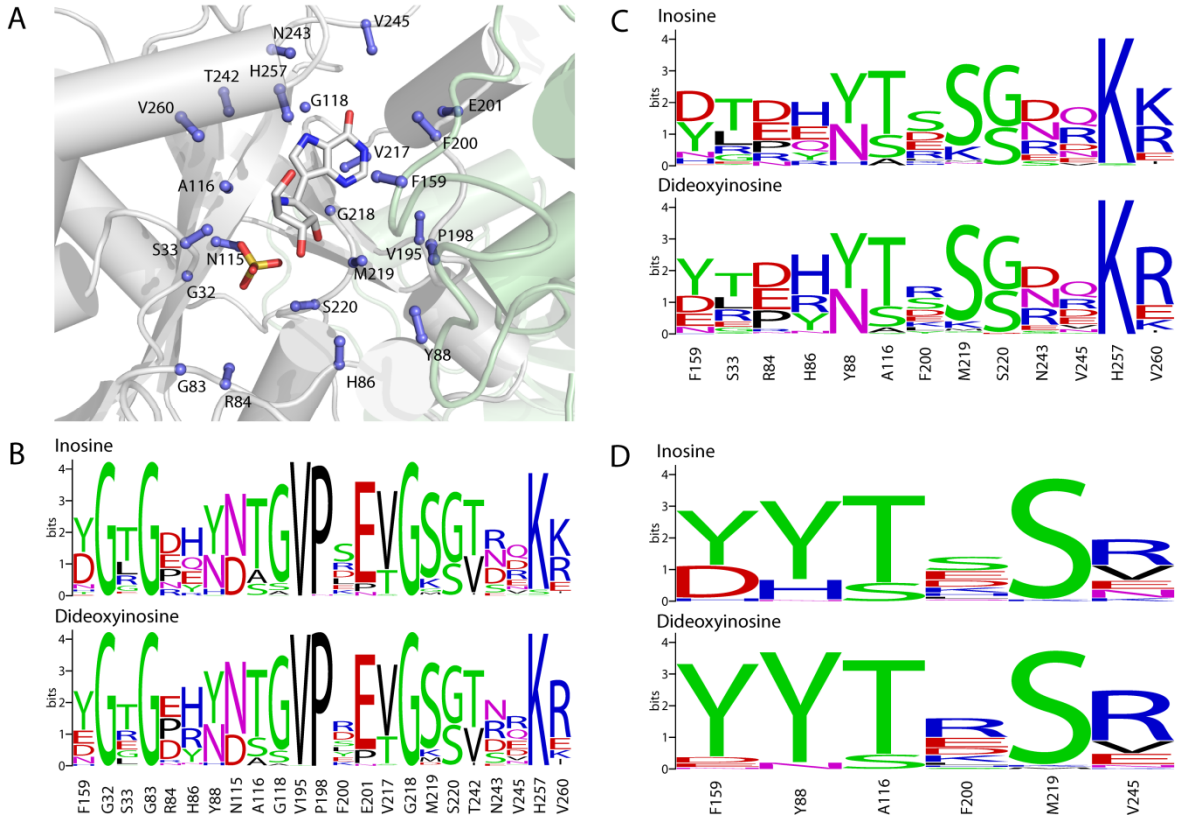

Fig. S1. Cα and Cβ atoms are shown as balls and sticks for residues allowed to design while identifying amino acids involved in substrate selectivity (A). ImmucilinH and sulfate are depicted as sticks (PDB code: 1pf7). 23 residues were designed during the first round (B), 13 during the second round (C) and 6 during the third round (D). Images were generated using the WebLogo server (Crooks *et al.*, 2004) and indicate the frequency of each amino acid at each position with information content plotted on the y-axis.

References

Crooks G.E., Hon G., Chandonia J.M. and Brenner S.E. (2004) *Genome Res,* **14**, 1188-1190.