Table S2. *In silico* docking scores for compounds to the HBV RNaseH homology model

		No constraints[a]			Constrained to predicted binding pose[a]	
Compound number	Name	(pH 4-6)	(pH 6-8)	(pH 8-10)	(pH 6-8)	(pH 8-10)
384	AB-2-60	-2.871	-2.22	-6.031	[b]	-6.06
388	RA-1-30	-3.608	-5.293	-6.148	-3.56	-5.544
389	AB-2-66	-3.787	-4.155	-6.145	-4.152	-6.169
390	AB-2-70	-3.331	-6.009	-8.024	-5.178	-6.123
391	AB-2-72	-3.09	-3.863	-7.224	-5.68	-7.224
404	MD-5-75A	-2.477	-5.619	-6.431	-3.444	-5.505
539	AB-2-91	-3.148	-4.849	-5.673	-2.95	-5.539
707	JS-117	-3.704	-4.194	-5.958	-4.193	-5.743
708	AB-3-45	-3.286	-4.274	-6.814	-3.349	-6.625
709	JS-124	-3.761	-4.814	-7.397	-4.358	-7.083
710	JS-112	-2.592	-4.069	-6.565	-2.363	-6.542
711	JS-116	-3.604	-4.193	-5.532	-3.501	-6.202
712	JS-108	-3.546	-5.386	-6.971	-5.147	-6.468
793	AJF-1.020	-3.578	-4.774	-5.61	-4.927	-5.599
794	AJF-1.022	-3.169	-4.46	-5.301	-5.303	-6.031
795	AJF-1.021	-3.457	-7.049	-7.685	-4.321	-6.486
796	AJF-1.027	-2.276	-4.646	-6.159	-3.707	-6.084
797	AJF-1.029	-3.296	-5.383	-6.791	-6.036	-6.677
798	AJF-1.031	-3.198	-3.876	-6.732	-1.963	-5.675
799	AJF-1.033	-3.116	-3.766	-6.076	-0.75	-6.374
800	JS-127	-1.463	-4.526	-5.859	-4.121	-6.209
801	JS-140	-3.807	-3.678	-6.543	-3.676	-6.127
802	JS-136	-1.79	-4.071	-7.088	-4.381	-6.385
803	JS-155	-1.866	-4.86	-6.281	-3.517	-6.437
804	RA-1-62	-3.314	-4.754	-5.605	-3.412	-4.603
805	RA-1-70	-2.77	-2.153	-5.67		-5.682
806	RA-1-66	-3.653	-4.033	-5.82	-3.196	-5.797
807	RA-1-72	-3.033	-5.186	-6.009	-1.136	-5.233
808	RA-1-74	-3.112	-3.257	-5.897	-3.299	-5.942
809	RA-1-82	-3.232	-4.917	-6.348	-3.359	-6.491
810	RA-1-76	-2.661	-3.31	-5.542	-4.625	-5.512
834	AB-2-169	-2.373	-4.369	-6.609		-6.66

835	RA-1-84	-2.602	-4.617	-6.038		-4.726
836	RA-1-86	-3.471	-3.554	-6.237	-4.261	-5.475
837	RA-1-88	-3.691	-3.615	-4.865	-3.14	-5.271
867	DS-1-124	-2.775	-4.259	-5.88	-3.143	-5.73
868	DS-1-133	-6.594	-6.251	-7.106		
869	DS-1-132	-2.774	-3.566	-5.12	0.595	-4.326
870	DS-1-134	-3.057	-4.449	-5.27	-3.107	-5.462
871	RA-1-96	-2.873	-4.755	-6.566	-5.031	-5.941
872	RA-1-94	-2.711	-4.178	-6.348	-3.955	-5.934
873	RA-1-32	-2.508	-4.669	-5.439	-4.277	-5.467
874	JS-164	-2.308	-2.785	-5.546	-0.157	-5.236
875	JS-165	-2.429	-4.058	-6.393	-3.467	-5.892
876	JS-166	-2.472	-4.68	-6.913	-3.747	-5.781
877	RA-1-167	-2.377	-4.294	-6.316	-3.37	-5.468
917	JS-1-173	-2.349	-3.364	-6.24	-3.413	-6.239
918	JS-174	-1.404	-3.597	-6.259	-3.741	-6.108
919	JS-170	-1.989	-2.39	-2.582	-1.422	-2.364
920	RA-1-104	-2.084	-3.891	-6.074	-3.032	-2.546
1016	AL-20	-2.082	-2.412	-2.699	-1.457	-1.855
1017	AL-23	-1.59	-3.794	-1.677	-2.867	-1.689
1018	AL-17	-4.588	-5.75	-6.605		-6.809
1019	AL-22	-3.281	-4.904	-6.052	-3.069	-5.599
1020	JS-1-191					
1021	JS-2-9	-2.074	-5.258	-6.355	-3.448	-5.342
1039	AB-3-45	-3.426	-2.814	-5.447		-5.793

[a] Values are in kcal/mol

[b] Missing values indicate positive docking scores

Docking strategy

The active site of the HBV RNaseH model contains two Mn^{++} ions placed in positions analogous to where they are found in HIV RNaseH crystal structures. α-Hydroxytropolones are known to chelate metal ions in other enzyme actives using the oxygen triad, and this effect is expected to play a key role in the compounds' inhibition of the enzyme. For this reason, binding poses that involved cation coordination were explicitly explored.

"Constrained" poses were obtained with docking parameters that designated spherical coordinate spaces for the metal centers to be used for octahedral coordination rather than simply being cations. This returned primarily poses that placed the appropriate atom types in these spaces. This approach did not return poses that stray significantly from the expected chelation-mediated binding pattern.

"Unconstrained" poses were those with the best docking score without requiring that the compound contact the Mn^{++} ions. This was done to identify binding poses that are energetically favorable but may not fit the expected double cation chelation pose.