Electronic Supplementary Information (ESI)

In silico design of RORγ inverse agonists based on 3D-QSAR and molecular docking

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Table S1 Statistical parameters of the constructed CoMFA and CoMSIA models

							Field contributions (%)				
Model	q^2	ONC	SEE	R^2	F	r_{pred}^2	S	E	H	D	A
S[a]	0.773	3	0.285	0.926	208.001	0.833	1	-	-	-	-
E[a]	0.747	6	0.246	0.948	142.642	0.801	-	1	-	-	-
S+E[a]	0.846	9	0.069	0.996	1281.335	0.923	0.610	0.390	-	-	-
S+E[b]	0.791	4	0.259	0.940	191.510	0.909	0.498	0.502	-	-	-
S+D[b]	0.740	6	0.234	0.953	158.337	0.822	0.622	-	-	0.378	-
E+H[b]	0.737	5	0.212	0.961	233.479	0.902	-	0.502	0.498	-	-
S+H[b]	0.799	7	0.092	0.993	921.010	0.925	0.453	-	0.547	-	-
S+E+D[b]	0.782	8	0.133	0.986	383.508	0.908	0.357	0.401	-	0.242	-
S+E+H[b]	0.786	4	0.211	0.960	293.817	0.936	0.331	0.355	0.314	-	-
S+E+A[b]	0.825	6	0.155	0.979	372.186	0.925	0.224	0.297	-	-	0.479
S+D+A[b]	0.786	5	0.187	0.969	304.587	0.789	0.234	-	-	0.233	0.532
E+D+A[b]	0.818	8	0.121	0.988	462.524	0.905	-	0.283	-	0.219	0.499
S+H+A[b]	0.806	4	0.176	0.972	429.228	0.902	0.208	-	0.297	-	0.495
S+E+H+D[b]	0.775	8	0.104	0.991	628.147	0.928	0.249	0.284	0.263	0.203	-
S+E+H+A[b]	0.827	4	0.169	0.974	467.494	0.939	0.173	0.222	0.217	-	0.387
S+E+D+A[b]	0.818	8	0.106	0.991	609.228	0.908	0.178	0.243	-	0.185	0.394
E+H+D+A[b]	0.794	5	0.154	0.979	453.465	0.940	-	0.220	0.219	0.176	0.385
S+H+D+A[b]	0.781	4	0.195	0.966	349.352	0.900	0.176	-	0.236	0.185	0.404
S+E+H+D+A[b]	0.807	5	0.143	0.982	524.909	0.942	0.139	0.196	0.187	0.156	0.322
Constraints	> 0.5	< 10	< < 1	> 0.9	> 100	> 0.5	-	-	-	-	-

[a] CoMFA model, [b]CoMSIA model; q^2: cross-validated correlation coefficient using the leave-one-out methods; ONC: optimal number of principal components; SEE: standard error of estimate; R^2: non-cross-validated correlation coefficient; F: Fischer F-ratio; r_{pred}^2: external validation correlation coefficient; S: steric; E: electrostatic; H: hydrophobic, D: H-bond donor; A: H-bond acceptor.

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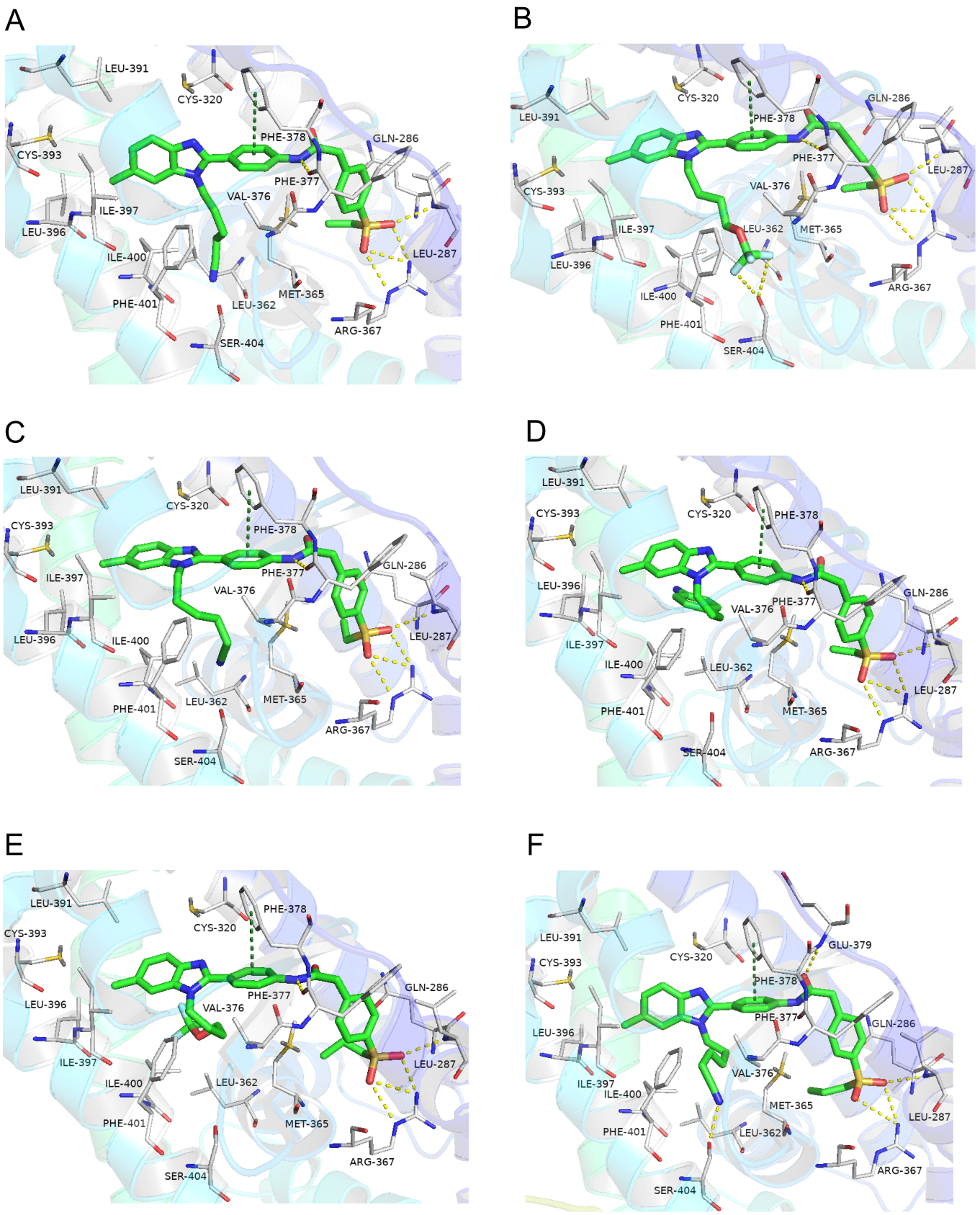

Fig. S1 Docking results of the designed compounds **D01** (A), **D02** (B), **D03** (C), **D04** (D), **D05** (E) and **D06** (F) in the binding site of the protein (PDB code: 6J1L). The ligands and important residues are shown as sticks. The hydrogen bonds and π-π interactions are shown as yellow and green dashed lines, respectively.

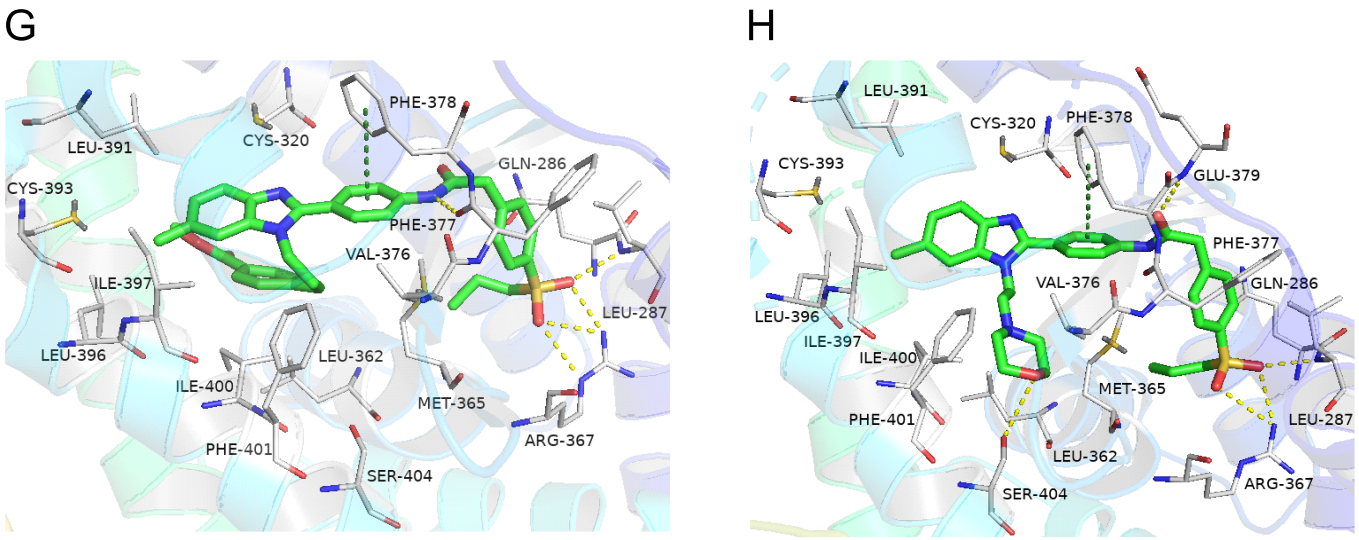

Fig. S2 Docking results of the designed compounds **D08** (G) and **D10** (H) in the binding site of the protein (PDB code: 6J1L). The ligands and important residues are shown as sticks. The hydrogen bonds and π-π interactions are shown as yellow and green dashed lines, respectively.

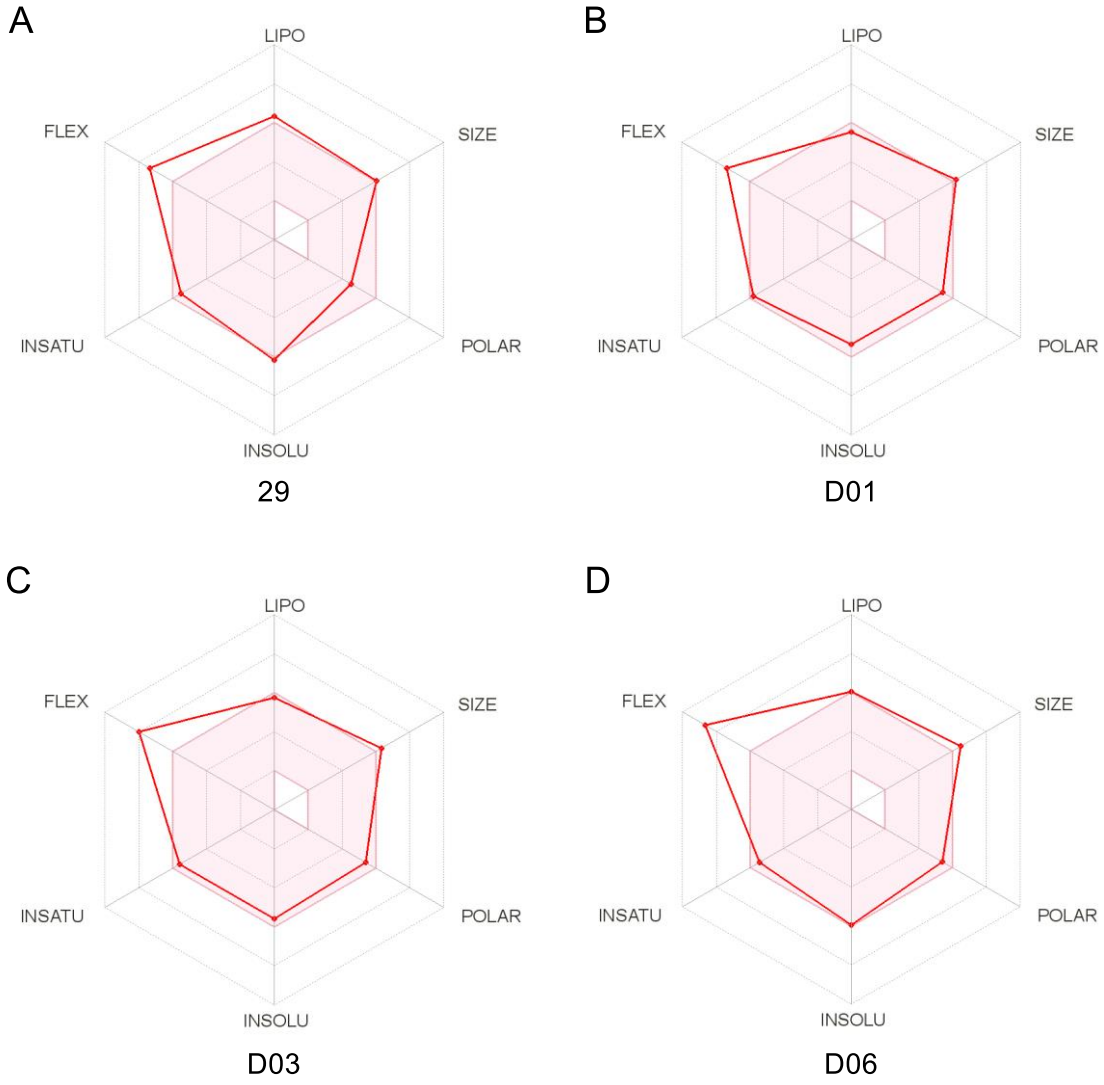

Fig. S3 The bioavailability radars for compounds **29** (A), **D01** (B), **D03** (C) and **D06** (D).