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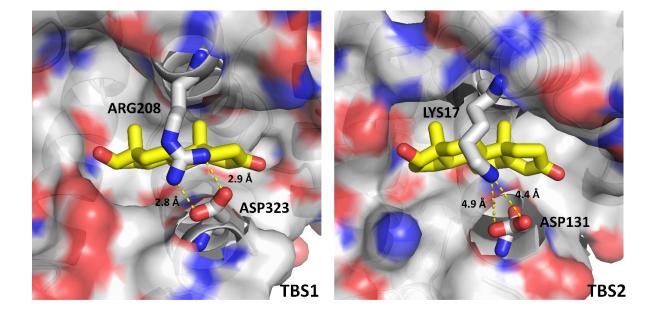
## 1. Supplemental Data

**Table S1.** Retention factors for testosterone on immobilized HSA and control columns in the presence of various mobile phases<sup>a</sup>.

Mobile phase	Retention factor on HSA column <sup>b</sup>	Retention factor on control column <sup>b</sup>	Retention factor due to HSA <sup>c</sup>
67 mM phosphate buffer (KPB, pH 7.4)	26.6 (± 4.0)	4.4 (± 0.7)	22.2 (± 4.1)
KPB (pH 7.4) + 40 μM citrate	16.7 (± 0.9)	5.9 (± 0.1)	10.8 (± 1.1)
KPB (pH 7.4) + 20% DMSO	14.2 (± 1.2)	4.0 (± 0.3)	10.2 (± 1.2)

<sup>&</sup>lt;sup>a</sup>All values in parentheses are a range of  $\pm$  1 S.D. (n = 3-4).

<sup>c</sup>The retention factor for testosterone due to only HSA was found by calculating the difference between the retention factors that were measured on the HSA column and the control column.

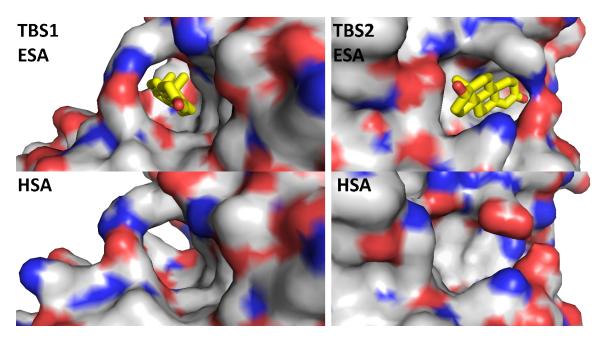


**Figure S1.** Testosterone binding sites are protected by non-covalent interactions between Arg208 and Asp323 in TBS1 and Lys17 and Asp131 in TBS2. The color of the protein surface indicates the character of the environment, and the color scheme is as follows: gray for carbon atoms in ESA, red for oxygen atoms, and blue for nitrogen atoms. Testosterone's carbon atoms are shown in yellow.

<sup>&</sup>lt;sup>b</sup>The retention factor (k) on the HSA column or control column was calculated by using the relationship  $k = (t_R - t_M)/t_M$ , where  $t_R$  is the retention time for testosterone on the column and  $t_M$  is the column void time (e.g., as measured by using sodium nitrate).

ESA HSA	1	DTHKSEIAHRFNDLGEKHFKGLVLVAFSQYLQQCPFEDHVKLVNEVTEFAKKCAADESAE DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAE *:****:******************************	60 60
ESA HSA	61 61	NCDKSLHTLFGDKLCTVATLRATYGELADCCEKQEPERNECFLTHKDDHPNLPKL-KPEP NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEV ************************************	119 120
ESA HSA	120 121	DAQCAAFQEDPDKFLGKYLYEVARRHPYFYGPELLFHAFEYKADFTECCPADDKLACLIP DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLP *. *:**:::::** ************************	179 180
ESA HSA		KLDALKERILLSSAKERLKCSSFQNFGERAVKAWSVARLSQKFPKADFAEVSKIVTDLTK KLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK *** *:: ****:*************************	239 240
ESA HSA	240 241	VHKECCHGDLLECADDRADLAKYICEHQDSISGKLKACCDKPLLQKSHCIAEVKEDDLPS VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPA **.**********************************	299 300
ESA HSA	300 301	DLPALAADFAEDKEICKHYKDAKDVFLGTFLYEYSRRHPDYSVSLLLRIAKTYEATLEKC DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKC ***:***** ****************************	359 360
ESA HSA	360 361	CAEADPPACYRTVFDQFTPLVEEPKSLVKKNCDLFEEVGEYDFQNALIVRYTKKAPQVST CAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST ** *** ** .***:************************	419 420
ESA HSA	420 421	PTLVEIGRTLGKVGSRCCKLPESERLPCSENHLALALNRLCVLHEKTPVSEKITKCCTDS PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES *****: * * * * * * * * * * * * * * * *	479 480
ESA HSA	480 481	LAERRPCFSALELDEGYVPKEFKAETFTFHADICTLPEDEKQIKKQSALAELVKHKPKAT LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKAT *:***********************************	539 540
ESA HSA	540 541	KEQLKTVLGNFSAFVAKCCGREDKEACFAEEGPKLVASSQLALA- KEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGL ****:*::*:*** *** :***:*** ***.	583 585

**Figure S2.** Alignment of ESA and HSA sequences. Residues involved in binding of testosterone molecules in ESA (according to PISA server calculations) and analogous residues inferred for HSA are marked in red (TBS1) and blue (TBS2).



**Figure S3.** Comparison of environment's character of TBS1 and TBS2 in ESA and HSA. The color of the protein surface indicates the character of the environment, and the color scheme is as follows: gray for carbon atoms in ESA and HSA, red for oxygen atoms, and blue for nitrogen atoms. Testosterone's carbon atoms are shown in yellow.