

**Table S1. Validated set of GAS<sub>right</sub> designs**

Design ID	Sequence	Computational Score (kcal/mol)	GpA (%)	ΔG (kcal/mol)
G_001	LLL <b>TALLVGLLGGLLFLL</b> LILI	-24.58	0.29 ± 0.05	NA
G_002	LLL <b>LFLLATLLGYLLS</b> LILI	-31.69	0.42 ± 0.04	-2.49 ± 0.23
G_003	LLL <b>FLLGTLLGALIAY</b> LILI	-31.69	1.15 ± 0.16	-3.85 ± 0.54
G_004	LLL <b>VTLFSLLGALI</b> ASLILI	-17.19	0.48 ± 0.05	-2.74 ± 0.28
G_005	LLL <b>YILLGLLGTLI</b> ASLILI	-32.08	0.31 ± 0.04	-0.52 ± 0.07
G_006	LLL <b>VLVTGFLYAL</b> IYLILI	-26.51	0.31 ± 0.08	-0.06 ± 0.01
G_007	LLL <b>FALLASILGILITL</b> LILI	-26.35	0.19 ± 0.04	NA
G_008	LLL <b>TFLAVLLGLLG</b> IYLILI	-21.45	0.65 ± 0.11	-3.18 ± 0.53
G_009	LLL <b>SFLVLLGTLIAY</b> LILI	-21.46	0.19 ± 0.07	NA
G_010	LLL <b>YLLLGALLGTLIS</b> LILI	-32.9	0.53 ± 0.04	-2.9 ± 0.22
G_011	LLL <b>TVLLGLLGILIGF</b> LILI	-32.92	0.54 ± 0.06	-2.93 ± 0.3
G_012	LLL <b>YFLLGALIAGLL</b> IYLILI	-33.02	0.81 ± 0.07	-3.44 ± 0.3
G_013	LLL <b>AVLTSLLGGLLF</b> LILI	-21.13	0.25 ± 0.04	NA
G_014	LLL <b>VTLLGLLFALLS</b> LILI	-26.16	0.25 ± 0.05	NA
G_015	LLL <b>TFLLGLLGYLLA</b> SLILI	-33.27	1.23 ± 0.08	-3.93 ± 0.27
G_016	LLL <b>YVLLGALLGILITL</b> LILI	-33.55	0.95 ± 0.1	-3.62 ± 0.39
G_017	LLL <b>YFLGVVLGTLIGL</b> LILI	-33.58	1.07 ± 0.03	-3.76 ± 0.11
G_018	LLL <b>YALLALLGTLIGF</b> LILI	-16.12	0.19 ± 0.03	NA
G_019	LLL <b>YLLLASILGILIAF</b> LILI	-34.17	0.15 ± 0.02	NA
G_020	LLL <b>YLLLGALLGALITF</b> LILI	-34.32	1.12 ± 0.17	-3.82 ± 0.59
G_021	LLL <b>TVLLGLLFGLLF</b> AFLILI	-22.26	0.5 ± 0.05	-2.81 ± 0.3
G_022	LLL <b>TVLLALLGFLIGS</b> LILI	-9.61	0.78 ± 0.07	-3.39 ± 0.3
G_023	LLL <b>YVLLTLLGALLGCF</b> LILI	-22.36	0.26 ± 0.08	NA
G_024	LLL <b>YVLLGALLGTLIAFL</b> LILI	-34.97	0.32 ± 0.14	-1.25 ± 0.56
G_025	LLL <b>YFLLATLLGLLGV</b> LILI	-35.12	0.36 ± 0.02	-2.02 ± 0.14
G_026	LLL <b>VGLLFALLGILITL</b> LILI	-33.23	0.36 ± 0.05	-2.08 ± 0.29
G_027	LLL <b>TFLLAIIIGLLIGV</b> LILI	-21.01	0.64 ± 0.05	-3.15 ± 0.26
G_028	LLL <b>AALLALLGVLLG</b> IYLILI	-17.8	0.39 ± 0.04	-2.33 ± 0.22
G_029	LLL <b>AALFSLLGLLG</b> IYLILI	-26.92	0.3 ± 0.09	NA
G_030	LLL <b>YALLTALLGGLLF</b> LILI	-19.63	0.22 ± 0.06	NA
G_031	LLL <b>LTLLVGLLFALLYG</b> LILI	-27.85	0.25 ± 0.02	NA
G_032	LLL <b>YLLGLLGTLIATL</b> AFLILI	-28.2	0.25 ± 0.09	NA
G_033	LLL <b>LVLLATLGGLLS</b> IYLILI	-19.93	0.26 ± 0.05	NA
G_034	LLL <b>YGULFALLGILITL</b> LILI	-28.27	0.28 ± 0.01	NA
G_035	LLL <b>STLGALLGLLAV</b> LILI	-28.31	0.91 ± 0.09	-3.58 ± 0.36
G_036	LLL <b>YVLLFTLLGALIAGL</b> LILI	-27.82	0.22 ± 0.03	NA
G_037	LLL <b>YVLLATLLGLLIGF</b> LILI	-28.48	0.3 ± 0.06	NA
G_038	LLL <b>YLLGTLLGILIAFL</b> LILI	-19.35	0.43 ± 0.07	-2.55 ± 0.43
G_039	LLL <b>YGULFLLGVLLATL</b> LILI	-27.64	0.4 ± 0.04	-2.39 ± 0.22
G_040	LLL <b>YFLLATLLGVLLG</b> LILI	-19.14	0.34 ± 0.05	-1.8 ± 0.24
G_041	LLL <b>YLLTLLAGLIFSL</b> LILI	-20.09	0.17 ± 0.1	NA
G_042	LLL <b>TFLLAIIIGLYLGS</b> LILI	-20.12	0.95 ± 0.14	-3.62 ± 0.52
G_043	LLL <b>VLLLTLLGALLSAL</b> IYLILI	-27.56	0.28 ± 0.03	NA
G_044	LLL <b>LTLLVALLAGLIFSL</b> LILI	-20.31	0.31 ± 0.03	NA
G_045	LLL <b>YGULFLLGVLLAS</b> LILI	-28.77	0.32 ± 0.06	-1.31 ± 0.23
G_046	LLL <b>YVLLALLGTLIGF</b> LILI	-27.25	0.18 ± 0.03	NA
G_047	LLL <b>TALLVGLLGLLGF</b> LILI	-18.68	0.27 ± 0.02	NA
G_048	LLL <b>YLLGALLGVLLSTL</b> LILI	-24.54	0.84 ± 0.22	-3.48 ± 0.9
G_049	LLL <b>AALLFALLGILISTL</b> LILI	-18.68	0.25 ± 0.12	NA
G_050	LLL <b>YFLAVLLGLLG</b> IYLILI	-29.4	0.28 ± 0.06	NA
G_051	LLL <b>YGULFALLGTLISL</b> LILI	-29.53	0.19 ± 0.01	NA
G_052	LLL <b>VALLALLGTLISF</b> LILI	-27.01	0.28 ± 0.05	NA
G_053	LLL <b>YLLGALLGILISTL</b> LILI	-29.9	0.75 ± 0.08	-3.35 ± 0.34
G_054	LLL <b>TFLAVLLGLLIGS</b> LILI	-27.01	0.6 ± 0.14	-3.08 ± 0.7
G_055	LLL <b>YFLAVLLGTLISL</b> LILI	-15.45	0.17 ± 0.05	NA
G_056	LLL <b>YFLALLGTLIGS</b> LILI	-35.41	0.23 ± 0.02	NA
G_057	LLL <b>TALLFLLGVLLAS</b> LILI	-16.15	0.82 ± 0.11	-3.45 ± 0.45
G_058	LLL <b>AGLIFLLGVLLATL</b> LILI	-22.42	0.33 ± 0.01	-1.62 ± 0.03
G_059	LLL <b>YVLLATLLGGLLF</b> LILI	-23.03	0.21 ± 0.06	NA
G_060	LLL <b>TALLALLFGLLIFSL</b> LILI	-13.75	0.38 ± 0.03	-2.21 ± 0.2
G_061	LLL <b>YVLTLLGGLLFAL</b> LILI	-13.73	0.32 ± 0.04	-0.98 ± 0.12
G_062	LLL <b>AYLLGFLGLLG</b> IYLILI	-45.74	1.14 ± 0.15	-3.83 ± 0.49
G_063	LLL <b>VLLATLLGSLIGT</b> LILI	-13.7	0.31 ± 0.07	-0.17 ± 0.04
G_064	LLL <b>ALLGLLGTLISF</b> LILI	-45.31	1.04 ± 0.05	-3.72 ± 0.18
G_065	LLL <b>LVLLTTLGGLLFAL</b> LILI	-25.32	0.29 ± 0.04	NA
G_066	LLL <b>AYLLGFLGFLG</b> IYLILI	-39.49	1.11 ± 0.11	-3.81 ± 0.37
G_067	LLL <b>YTLIAIIIGLLIGF</b> LILI	-44.96	0.24 ± 0.03	NA
G_068	LLL <b>TSLLVGLIAYLIGL</b> LILI	-11.56	0.41 ± 0.02	-2.45 ± 0.09
G_069	LLL <b>AYLLGVLLGLLIAF</b> LILI	-35.55	1.12 ± 0.09	-3.81 ± 0.31
G_070	LLL <b>YFLAVLLGLLG</b> IYLILI	-23.94	0.25 ± 0.15	NA

G_071	LLL <b>S</b> YLLGVLL <b>G</b> LLL <b>G</b> T <b>L</b> L <b>I</b>	-44.36	0.95 ± 0.08	-3.62 ± 0.32
G_072	LLL <b>A</b> LL <b>G</b> VLL <b>G</b> F <b>L</b> L <b>I</b> <b>S</b> L <b>I</b> <b>L</b> <b>I</b>	-43.23	1.26 ± 0.1	-3.96 ± 0.31
G_073	LLL <b>T</b> ALL <b>A</b> LL <b>G</b> VLL <b>G</b> L <b>I</b> <b>S</b> V <b>L</b> <b>I</b> <b>L</b> <b>I</b>	-13.06	0.31 ± 0.02	-0.87 ± 0.05
G_074	LLL <b>S</b> YLLGVLL <b>G</b> LLI <b>A</b> T <b>L</b> <b>I</b> <b>L</b> <b>I</b>	-41.31	1.03 ± 0.11	-3.71 ± 0.41
G_075	LLL <b>S</b> YLLGVLL <b>G</b> LL <b>G</b> T <b>L</b> <b>I</b> <b>G</b> F <b>L</b> <b>I</b> <b>L</b> <b>I</b>	-42.81	0.79 ± 0.12	-3.4 ± 0.5
G_076	LLL <b>S</b> YLL <b>G</b> LL <b>G</b> T <b>L</b> <b>I</b> <b>G</b> F <b>L</b> <b>I</b> <b>L</b> <b>I</b>	-42.79	0.83 ± 0.06	-3.47 ± 0.24
G_077	LLL <b>Y</b> LL <b>G</b> ALL <b>A</b> FL <b>I</b> <b>S</b> T <b>L</b> <b>I</b> <b>L</b> <b>I</b>	-25.05	0.18 ± 0.01	NA
G_078	LLL <b>T</b> YLLGVLL <b>G</b> LL <b>G</b> F <b>L</b> <b>I</b> <b>S</b> F <b>L</b> <b>I</b> <b>L</b> <b>I</b>	-42.23	0.87 ± 0.19	-3.52 ± 0.76
G_079	LLL <b>L</b> VLL <b>G</b> ALL <b>G</b> F <b>L</b> <b>I</b> <b>S</b> F <b>L</b> <b>I</b> <b>L</b> <b>I</b>	-24.93	0.44 ± 0.07	-2.6 ± 0.39
G_080	LLL <b>A</b> YLLGVLL <b>G</b> LL <b>G</b> S <b>L</b> <b>I</b> <b>L</b> <b>I</b>	-41.95	1.11 ± 0.12	-3.81 ± 0.41
G_081	LLL <b>A</b> LL <b>G</b> VLL <b>G</b> T <b>L</b> <b>I</b> <b>G</b> F <b>L</b> <b>I</b> <b>L</b> <b>I</b>	-38.02	0.95 ± 0.12	-3.62 ± 0.44
G_082	LLL <b>S</b> YLL <b>G</b> LL <b>G</b> F <b>L</b> <b>I</b> <b>S</b> T <b>L</b> <b>I</b> <b>L</b> <b>I</b>	-38.42	1.09 ± 0.18	-3.78 ± 0.62
G_083	LLL <b>Y</b> LL <b>G</b> ALL <b>G</b> F <b>L</b> <b>I</b> <b>S</b> T <b>L</b> <b>I</b> <b>L</b> <b>I</b>	-48.02	1.11 ± 0.17	-3.8 ± 0.58
G_084	LLL <b>Y</b> LL <b>F</b> ALL <b>G</b> ALL <b>T</b> <b>L</b> <b>I</b> <b>L</b> <b>I</b> <b>L</b> <b>I</b>	-24.61	0.36 ± 0.04	-1.99 ± 0.22
G_085	LLL <b>F</b> VLL <b>T</b> IL <b>G</b> ALL <b>S</b> L <b>I</b> <b>L</b> <b>I</b>	-15.06	0.25 ± 0.05	NA
G_086	LLL <b>Y</b> LL <b>V</b> ALL <b>A</b> LL <b>G</b> L <b>I</b> <b>L</b> <b>I</b> <b>L</b> <b>I</b>	-22.53	0.33 ± 0.05	-1.44 ± 0.22
G_087	LLL <b>Y</b> SL <b>A</b> LL <b>G</b> T <b>L</b> <b>I</b> <b>G</b> F <b>L</b> <b>I</b> <b>L</b> <b>I</b>	-22.59	0.15 ± 0.05	NA
G_088	LLL <b>A</b> LL <b>L</b> T <b>V</b> LL <b>G</b> LL <b>F</b> S <b>L</b> <b>I</b> <b>L</b> <b>I</b>	-25.5	0.26 ± 0.04	NA
G_089	LLL <b>T</b> SL <b>L</b> LL <b>G</b> LL <b>F</b> ALL <b>A</b> Y <b>L</b> <b>I</b> <b>L</b> <b>I</b>	-24.73	0.22 ± 0.13	NA
G_090	LLL <b>Y</b> LL <b>G</b> IL <b>G</b> T <b>L</b> <b>I</b> <b>A</b> F <b>L</b> <b>I</b> <b>L</b> <b>I</b>	-36.83	0.53 ± 0.04	-2.9 ± 0.2
G_091	LLL <b>V</b> LL <b>L</b> GL <b>G</b> F <b>L</b> <b>I</b> <b>F</b> ALL <b>I</b> <b>L</b> <b>I</b> <b>L</b> <b>I</b>	-22.79	0.83 ± 0.23	-3.47 ± 0.95
G_092	LLL <b>Y</b> ILL <b>T</b> LL <b>G</b> AL <b>I</b> <b>A</b> F <b>L</b> <b>I</b> <b>L</b> <b>I</b>	-6.71	0.29 ± 0.14	NA
G_093	LLL <b>F</b> YLL <b>G</b> V <b>L</b> <b>G</b> LL <b>A</b> S <b>L</b> <b>I</b> <b>L</b> <b>I</b>	-47.35	0.92 ± 0.1	-3.58 ± 0.39
G_094	LLL <b>Y</b> VLL <b>F</b> LL <b>G</b> AL <b>I</b> <b>G</b> T <b>L</b> <b>I</b> <b>L</b> <b>I</b>	-25.05	0.17 ± 0.02	NA
G_095	LLL <b>T</b> LL <b>G</b> LL <b>G</b> V <b>L</b> <b>G</b> S <b>L</b> <b>I</b> <b>L</b> <b>I</b>	-37.29	0.91 ± 0.21	-3.57 ± 0.83
G_096	LLL <b>A</b> LL <b>G</b> LL <b>G</b> V <b>L</b> <b>G</b> S <b>L</b> <b>I</b> <b>L</b> <b>I</b>	-37.44	1.04 ± 0.21	-3.73 ± 0.74
G_097	LLL <b>T</b> VL <b>G</b> LL <b>G</b> LL <b>A</b> F <b>L</b> <b>I</b> <b>L</b> <b>I</b>	-37.57	0.71 ± 0.06	-3.28 ± 0.25
G_098	LLL <b>S</b> LL <b>F</b> LL <b>G</b> V <b>L</b> <b>G</b> T <b>L</b> <b>I</b> <b>L</b> <b>I</b>	-6.06	0.3 ± 0.06	NA
G_099	LLL <b>V</b> LL <b>T</b> GL <b>G</b> LL <b>F</b> ALL <b>A</b> Y <b>L</b> <b>I</b> <b>L</b> <b>I</b>	-14.18	0.25 ± 0.07	NA
G_100	LLL <b>A</b> V <b>L</b> F <b>S</b> LL <b>G</b> LL <b>G</b> T <b>L</b> <b>I</b> <b>L</b> <b>I</b>	-22.9	0.27 ± 0.04	NA
G_101	LLL <b>T</b> ALL <b>F</b> LL <b>G</b> V <b>L</b> <b>G</b> I <b>L</b> <b>I</b> <b>L</b> <b>I</b>	-13.97	0.72 ± 0.06	-3.29 ± 0.27
G_102	LLL <b>A</b> GL <b>L</b> F <b>L</b> <b>G</b> T <b>L</b> <b>I</b> <b>S</b> Y <b>L</b> <b>I</b> <b>L</b> <b>I</b>	-25.42	0.14 ± 0.02	NA
G_103	LLL <b>Y</b> VLL <b>G</b> LL <b>G</b> F <b>L</b> <b>I</b> <b>S</b> T <b>L</b> <b>I</b> <b>L</b> <b>I</b>	-52.21	1.04 ± 0.05	-3.72 ± 0.19
G_104	LLL <b>A</b> FL <b>L</b> G <b>T</b> LL <b>G</b> V <b>L</b> <b>G</b> L <b>I</b> <b>L</b> <b>I</b>	-37.15	1.33 ± 0.24	-4.02 ± 0.74

**Table S2. Validated set of Left designs**

Design ID	Sequence	Computational Score (kcal/mol)	GpA (%)	ΔG (kcal/mol)
L_001	LLLLLLLLTALLFLVSLLILI	-24.86	0.23 ± 0.09	NA
L_002	LLLLYVLLIAALLTLFLSLLILI	-19.91	0.28 ± 0.05	NA
L_003	LLLVALLLILITFLLLASLLILI	-19.85	0.35 ± 0.06	-1.97 ± 0.35
L_004	LLLLFVLTLLTALLYSLLILI	-27.78	0.19 ± 0.1	NA
L_005	LLLLAYLLAALLFLTSLLILI	-24.92	0.32 ± 0.07	-1.18 ± 0.27
L_006	LLLTYALLFVLTALLLSLLILI	-20.96	0.49 ± 0.08	-2.78 ± 0.45
L_007	LLLLYVLLATLLALLSFLLILI	-20.52	0.28 ± 0.08	NA
L_008	LLLLLAIIITLAVLFSLLILI	-25.76	0.61 ± 0.06	-3.09 ± 0.3
L_009	LLLVALLLILFLLLTSLLILI	-22.22	0.48 ± 0.23	-2.75 ± 1.31
L_010	LLLYFLLAIIITLTSLLILI	-22.59	0.19 ± 0.11	NA
L_011	LLLLFVLLAIIITLTSLLILI	-19.85	0.15 ± 0.05	NA
L_012	LLLLAVLLFLATLISLLILI	-26.1	0.22 ± 0.05	NA
L_013	LLLLLLFLIATLISLLILI	-26.11	0.16 ± 0.05	NA
L_014	LLLLYVLLATLFLSLLILI	-21.98	0.41 ± 0.16	-2.44 ± 0.94
L_015	LLLLTLLVALLLFLISLLILI	-26.31	0.41 ± 0.26	-2.4 ± 1.54
L_016	LLLLYFLLAIIAVLTSLLILI	-21.69	0.27 ± 0.09	NA
L_017	LLLYLLLTVIALLFLSLLILI	-21.39	0.23 ± 0.06	NA
L_018	LLLTLLLAIIIVLFSLLILI	-21.35	0.47 ± 0.12	-2.7 ± 0.69
L_019	LLLLVLLTILFLLSALILI	-26.56	0.23 ± 0.04	NA
L_020	LLLLYLLFLIATLTSLLILI	-23.39	0.21 ± 0.09	NA
L_021	LLLLLFLLATLILLSLLILI	-21.08	0.25 ± 0.05	NA
L_022	LLLLYLLAVLITALLFSLLILI	-21.06	0.27 ± 0.09	NA
L_023	LLLLYVLLAIIIFTLISLLILI	-25.06	0.18 ± 0.12	NA
L_024	LLVTLLLAIIILFLSLLILI	-20.94	0.27 ± 0.06	NA
L_025	LLLLYALLFLTALLFSLLILI	-26.79	0.45 ± 0.14	-2.61 ± 0.83
L_026	LLLLLLFLFLLATLTSLLILI	-26.85	0.23 ± 0.07	NA
L_027	LLLFSLLVLLTALLYLLLILI	-20.71	0.23 ± 0.05	NA
L_028	LLLTTILLVLVLLSFLLILI	-26.94	0.23 ± 0.19	NA
L_029	LLLFLLLAILLVLSTLILI	-23.7	0.21 ± 0.05	NA
L_030	LLLLYVLLAIIFTLTSLLILI	-23.75	0.23 ± 0.07	NA
L_031	LLLLAVLLFLAIIATLTSLLILI	-27.1	0.41 ± 0.08	-2.45 ± 0.5
L_032	LLLVALLTIIIAALLFSLLILI	-27.98	0.41 ± 0.15	-2.45 ± 0.88
L_033	LLLVSSLILITALLFLLLILI	-22.28	0.35 ± 0.11	-1.89 ± 0.59
L_034	LLLFAIIITLVALLTSLLILI	-28.01	0.36 ± 0.05	-2.09 ± 0.26
L_035	LLLLAVIITAIIILFLSLLILI	-36.08	0.21 ± 0.13	NA
L_036	LLLLYVLTAAIIFLLISLLILI	-35.8	0.26 ± 0.1	NA
L_037	LLLVLLLTIIIFLFLSLLILI	-34.96	0.21 ± 0.09	NA
L_038	LLLLWYLVSLILITFLLLILI	-34.36	0.48 ± 0.16	-2.75 ± 0.89
L_039	LLLLVSILILITALLFLLLILI	-34.32	0.41 ± 0.11	-2.42 ± 0.67
L_040	LLLLAYLTIVLSSILFLLLILI	-16.04	0.38 ± 0.08	-2.25 ± 0.48
L_041	LLLLAIIILALFLVLLTSLLILI	-34.1	0.3 ± 0.1	NA
L_042	LLLLFVLLLITATLISLLILI	-36.31	0.27 ± 0.08	NA
L_043	LLYTLLAVIIAALLSLLILI	-16.38	0.44 ± 0.09	-2.56 ± 0.52
L_044	LLLLFILLAVALLTLTSLLILI	-32.64	0.22 ± 0.13	NA
L_045	LLVALLFLSLLTLYTLLILI	-32.59	0.27 ± 0.08	NA
L_046	LLLLVLLLAIIFLTSLLILI	-32.33	0.29 ± 0.07	NA
L_047	LLVALLFLITSLLYLILILI	-27.98	0.21 ± 0.07	NA
L_048	LLLLFLLAVLYLLSTLILI	-32.17	0.32 ± 0.14	-1.14 ± 0.51
L_049	LLLSYLLAVLITFLLLILI	-32.13	0.34 ± 0.08	-1.82 ± 0.4
L_050	LLLFLLLAIIATVLLSLLILI	-32.09	0.33 ± 0.1	-1.46 ± 0.44
L_051	LLYLFLAVIITLTSLLILI	-33.12	0.18 ± 0.09	NA
L_052	LLLLTYLLAIIFLVLLLSLLILI	-32.09	0.25 ± 0.12	NA
L_053	LLLVLLAIIIFLLLTSLLILI	-36.54	0.24 ± 0.09	NA
L_054	LLYTLLAVLILLLASLLILI	-14.73	0.15 ± 0.05	NA
L_055	LLYALLTIIIVLFSLLILI	-8.65	0.55 ± 0.3	-2.94 ± 1.59
L_056	LLLLLLAVIITAIIFLLILI	-44.72	0.28 ± 0.06	NA
L_057	LLLLVALLLITSLLFLLILI	-44.48	0.48 ± 0.05	-2.72 ± 0.26
L_058	LLYALLLVIITLFSLLILI	-11.73	0.35 ± 0.12	-1.95 ± 0.64
L_059	LLLFAIIITALLYVLLILI	-12.21	0.37 ± 0.12	-2.12 ± 0.69
L_060	LLLFLYIITAIIILVSLLILI	-12.34	0.28 ± 0.15	NA
L_061	LLLLVALLLITAIIFLLILI	-41.95	0.43 ± 0.16	-2.53 ± 0.93
L_062	LLLLAIIAVLFLLLTSLLILI	-36.63	0.25 ± 0.11	NA
L_063	LLLLLAIIFLTSLLYLILILI	-41.84	0.41 ± 0.04	-2.44 ± 0.24
L_064	LLLLYVLLAIIALLTSLLILI	-13.11	0.36 ± 0.29	-2.08 ± 1.65
L_065	LLLLYVLLTILAFLTSLLILI	-40.46	0.4 ± 0.13	-2.34 ± 0.77
L_066	LLLYSITAIIFVLLLSLLILI	-39.3	0.27 ± 0.06	NA
L_067	LLLLTVLLAIIFLLISLLILI	-38.49	0.2 ± 0.12	NA
L_068	LLLLVALLLITSLLFLLILI	-37.95	0.27 ± 0.11	NA
L_069	LLLLFVLLAIIYLLSTLILI	-37.79	0.35 ± 0.08	-1.89 ± 0.41
L_070	LLLFAIIITVLLYLLSLLILI	-36.99	0.29 ± 0.07	NA

L_071	LLLLFWLLAVLTALLYLILLI	-41.58	0.38 ± 0.06	-2.23 ± 0.37
L_072	LLLLAVLLTIALLISFLILLI	-32.06	0.26 ± 0.03	NA
L_073	LLLLVALLLILFLLSTLILLI	-32.21	0.28 ± 0.08	NA
L_074	LLLLSYLVALLTTLFLLILLI	-31.72	0.37 ± 0.28	-2.18 ± 1.61
L_075	LLLLLVLLAILLFSLLILLI	-29.41	0.24 ± 0.1	NA
L_076	LLLLYWLLTILVALLSFLILLI	-29.15	0.42 ± 0.06	-2.5 ± 0.34
L_077	LLLYLLLAVLTSLLFLLILLI	-28.74	0.14 ± 0.1	NA
L_078	LLLLALLLFITVLISLILLI	-28.66	0.24 ± 0.07	NA
L_079	LLLLLFITALLYVLISLLILLI	-28.61	0.28 ± 0.27	NA
L_080	LLLLYVLLALTTILLFSLILLI	-19.09	0.19 ± 0.11	NA
L_081	LLLLYLLLAVLSSLFTLILLI	-29.49	0.26 ± 0.08	NA
L_082	LLLYFLLAVLILTLLFSLLILLI	-19.2	0.16 ± 0.09	NA
L_083	LLLLLALLLILVTLISLLILLI	-28.35	0.32 ± 0.1	-1.29 ± 0.41
L_084	LLLLWTLIAALLVLFSLLILLI	-28.25	0.32 ± 0.08	-1.09 ± 0.29
L_085	LLLYALLFITSLLFSLLILLI	-28.21	0.14 ± 0.08	NA
L_086	LLLLLLLAVLYTLLISFLILLI	-28.07	0.23 ± 0.04	NA
L_087	LLLYAALLLIVTLLFSLLILLI	-28.03	0.22 ± 0.08	NA
L_088	LLLYAALLFVULLLTSLLILLI	-19.75	0.17 ± 0.07	NA
L_089	LLLLAILLLLTIVLFSLLILLI	-28.43	0.18 ± 0.08	NA
L_090	LLLLYILLALLFVLSTLILLI	-30	0.22 ± 0.02	NA
L_091	LLLYAALLFVULLLFSLLILLI	-18.68	0.14 ± 0.05	NA
L_092	LLLLAALLFITSLLYVLLILLI	-31.34	0.36 ± 0.04	-1.99 ± 0.22
L_093	LLLYWLLTVLFLLLASLLILLI	-17.52	0.28 ± 0.03	NA
L_094	LLLLYFLIATLVALLLSLLILLI	-31.23	0.47 ± 0.13	-2.7 ± 0.73
L_095	LLLLILLIALLFVLTSLLILLI	-30.54	0.35 ± 0.14	-1.89 ± 0.76
L_096	LLLAAALLLIVTLLFSLLILLI	-17.48	0.53 ± 0.08	-2.89 ± 0.43
L_097	LLLLAVLLILITLLISFLILLI	-30.86	0.38 ± 0.2	-2.19 ± 1.14
L_098	LLLLTVLLAILFLLSSLILLI	-30.91	0.29 ± 0.09	NA
L_099	LLLYSLLLLITFLLAVALLILLI	-31.39	0.2 ± 0.18	NA
L_100	LLLLAVLLAILLILISTLILLI	-31.53	0.2 ± 0.02	NA

**Table S3. Validated set of Right designs**

Design ID	Sequence	Computational Score (kcal/mol)	GpA (%)	ΔG (kcal/mol)
R_001	LLLYTLLVLLAFLLSLIL	-26.75	0.3 ± 0.07	NA
R_002	LLLYSLLTLLFVLLALLIL	-30.22	0.3 ± 0.13	NA
R_003	LLLYTLLIALFVLLSLLIL	-26.69	0.28 ± 0.04	NA
R_004	LLLYSLLVALFTLLFLLIL	-26.6	0.23 ± 0.1	NA
R_005	LLLSLLFALLIALVTLLIL	-24.71	0.29 ± 0.03	NA
R_006	LLLYLLLFTLLAVVLSLIL	-8.79	0.3 ± 0.06	NA
R_007	LLYALLVALFTLLSLLIL	-24.88	0.26 ± 0.05	NA
R_008	LLTYLLFVLLAFLLSLIL	-24.89	0.29 ± 0.1	NA
R_009	LLLYTLLISLVALFLFLIL	-25.05	0.25 ± 0.1	NA
R_010	LLLYTLLVSLLALLLAFLIL	-25.05	0.31 ± 0.07	0.43 ± 0.1
R_011	LLLYLYVALISLISLFTLIL	-25.89	0.39 ± 0.18	-2.33 ± 1.07
R_012	LLYSLLIALFVLLTTLIL	-27.63	0.3 ± 0.06	NA
R_013	LLLVLLIALFTLLSYLIL	-25.24	0.33 ± 0.04	-1.62 ± 0.21
R_014	LLSYLLVLLAFLTTLIL	-25.39	0.35 ± 0.08	-1.9 ± 0.43
R_015	LLLYTLLISLFLVLLTTLIL	-26.81	0.31 ± 0.08	0.25 ± 0.07
R_016	LLYFLLVALTLLSLLIL	-26.06	0.27 ± 0.09	NA
R_017	LLSYLLFVLLALLSLLIL	-26.54	0.39 ± 0.07	-2.28 ± 0.4
R_018	LLSYLLTLLAFLSLLIL	-26.9	0.55 ± 0.08	-2.94 ± 0.45
R_019	LLWTLLVFVLLAFLSLLIL	-29.79	0.29 ± 0.06	NA
R_020	LLSYLLFTLLAFLTLLIL	-29.93	0.3 ± 0.09	NA
R_021	LLYSLLIALFVLLTTLIL	-27.75	0.28 ± 0.1	NA
R_022	LLSYLLFTLLALLIAVLIL	-27.41	0.38 ± 0.03	-2.26 ± 0.15
R_023	LLYALLTLLVALLSLLIL	-10.03	0.33 ± 0.05	-1.61 ± 0.26
R_024	LLYTLLIALVLLFSLIL	-24.33	0.31 ± 0.18	-0.41 ± 0.24
R_025	LLFYLLVLLALLSLLIL	-16.37	0.29 ± 0.14	NA
R_026	LLLFYLLVALSLLTTLIL	-16.35	0.34 ± 0.05	-1.79 ± 0.24
R_027	LLYILLATLLAFLSLLIL	-16.29	0.27 ± 0.12	NA
R_028	LLLFYLLVALTLLSLLIL	-16.26	0.4 ± 0.08	-2.36 ± 0.48
R_029	LLYALLIALFTLLVLLIL	-16.15	0.3 ± 0.03	NA
R_030	LLYALLTLLSVLLFLIL	-16.09	0.44 ± 0.07	-2.58 ± 0.43
R_031	LLTALLIALFVLLSLLIL	-16.08	0.33 ± 0.01	-1.57 ± 0.04
R_032	LLLYSLLTLLVALLIFLIL	-15.9	0.24 ± 0.11	NA
R_033	LLYSLLALATLLVFLIL	-15.86	0.24 ± 0.07	NA
R_034	LLYVLLTLLALLSFLIL	-15.76	0.34 ± 0.13	-1.84 ± 0.72
R_035	LLYILLATLLFVLLSLLIL	-15.7	0.31 ± 0.03	-0.91 ± 0.1
R_036	LLYTLLIALVALLSLLIL	-15.58	0.37 ± 0.05	-2.1 ± 0.31
R_037	LLYALLVALTLLFLLIL	-15.3	0.3 ± 0.07	NA
R_038	LLLFYLLITLLVALLSLLIL	-15.25	0.34 ± 0.09	-1.79 ± 0.49
R_039	LLYILLATLLAFLSFLIL	-15.07	0.14 ± 0.06	NA
R_040	LLYILLATLLAVLFSFLIL	-16.45	0.25 ± 0.07	NA
R_041	LLYSLLTLLATLLAFLIL	-16.53	0.21 ± 0.08	NA
R_042	LLLVSLLLTLLFALLAYLIL	-16.54	0.29 ± 0.03	NA
R_043	LLLTALLVALAYLLSFLIL	-16.55	0.5 ± 0.04	-2.81 ± 0.24
R_044	LLTYLLTLLAFLPSLIL	-17.5	0.41 ± 0.05	-2.44 ± 0.27
R_045	LLLLVLLITLLFALLSYLIL	-17.49	0.32 ± 0.06	-1.37 ± 0.27
R_046	LLYLILLTTLLVALLSFLIL	-17.43	0.44 ± 0.05	-2.58 ± 0.31
R_047	LLLYLLLVTLLAFLSFLIL	-17.35	0.17 ± 0.09	NA
R_048	LLYSLLVALATLLFLLIL	-17.33	0.26 ± 0.07	NA
R_049	LLLAILLVTLLFTLLSLLIL	-17.29	0.36 ± 0.09	-1.99 ± 0.48
R_050	LLYALLTALSVLLFLIL	-17.19	0.37 ± 0.03	-2.1 ± 0.18
R_051	LLYILLTLLVALSLLIL	-15.06	0.31 ± 0.05	-0.94 ± 0.15
R_052	LLFSLLTLLVALSLLIL	-17.12	0.26 ± 0.08	NA
R_053	LLLVYLLTALLIALSLLIL	-16.69	0.37 ± 0.05	-2.14 ± 0.31
R_054	LLYSLLTLLVALLSFLIL	-16.68	0.29 ± 0.1	NA
R_055	LLYALLVALTALSLIL	-16.67	0.35 ± 0.08	-1.96 ± 0.42
R_056	LLLTALLIALVALSFLIL	-16.65	0.4 ± 0.06	-2.35 ± 0.38
R_057	LLLAVALLTLLFALLSYLIL	-16.62	0.26 ± 0.06	NA
R_058	LLYILLLTLLAVLFSFLIL	-16.59	0.24 ± 0.04	NA
R_059	LLYFLLVALALLSLLIL	-16.58	0.32 ± 0.03	-1.1 ± 0.11
R_060	LLYILLFAALTIVLLSLLIL	-17.06	0.26 ± 0.06	NA
R_061	LLYVLLIALATLLSLLIL	-15.04	0.33 ± 0.06	-1.52 ± 0.29
R_062	LLYALLVALSLLFTLIL	-15.04	0.35 ± 0.03	-1.87 ± 0.14
R_063	LLYSLLTALLVALFLLIL	-14.78	0.29 ± 0.08	NA
R_064	LLLTYLLVLLAFLSFLIL	-12.04	0.19 ± 0.12	NA
R_065	LLYVLLIALFTLLSLLIL	-11.97	0.26 ± 0.07	NA
R_066	LLYVLLTILLALLAFLIL	-11.94	0.32 ± 0.09	-1.38 ± 0.4
R_067	LLYLLLSTLLAFLTAFLIL	-11.93	0.28 ± 0.04	NA
R_068	LLTYLLIVLLALLSFLIL	-11.69	0.41 ± 0.02	-2.4 ± 0.1
R_069	LLYLLLFTLLAFLTSLLIL	-11.61	0.12 ± 0.06	NA
R_070	LLYALLFALLSLLVTLIL	-11.25	0.27 ± 0.02	NA

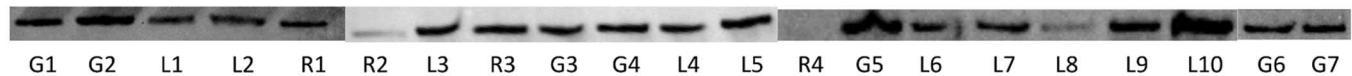
R_071	LLLTYLLAVLLAAILLFLLLIL	-12.11	0.32 ± 0.07	-0.98 ± 0.21
R_072	LLLYVLLTTLFALLSLLIL	-11.22	0.28 ± 0.08	NA
R_073	LLLAALLSLLFLLVFLILI	-10.66	0.46 ± 0.05	-2.65 ± 0.27
R_074	LLLYLLLATLAVLLSLLIL	-10.64	0.24 ± 0.07	NA
R_075	LLLYALLSLLTALLSVFLILI	-10.61	0.28 ± 0.09	NA
R_076	LLLTALLIALFLLSVLIL	-10.55	0.4 ± 0.04	-2.36 ± 0.25
R_077	LLLYVLLFALLTVLSSLIL	-10.4	0.3 ± 0.02	NA
R_078	LLLYSLLFVLLAAILLTLIL	-10.33	0.25 ± 0.1	NA
R_079	LLLAYLLVLLATLLSFLLIL	-10.19	0.34 ± 0.07	-1.71 ± 0.38
R_080	LLLYVLLAAILTLLLSFLIL	-10.68	0.27 ± 0.1	NA
R_081	LLLYTLLATLVLSSFLIL	-17.69	0.25 ± 0.07	NA
R_082	LLLYVLLATLALLSFLLIL	-12.44	0.26 ± 0.03	NA
R_083	LLLYALLSLLVALLSFLLIL	-12.82	0.25 ± 0.08	NA
R_084	LLLYAALLTLSLILVFLIL	-14.69	0.22 ± 0.04	NA
R_085	LLLYAALLLFSLLVTFLIL	-14.68	0.3 ± 0.1	NA
R_086	LLLYLLTALLIAILFVLIL	-14.55	0.27 ± 0.06	NA
R_087	LLLIILLSTLALILVFLIL	-14.36	0.23 ± 0.05	NA
R_088	LLLYILLTLLVALLSFLIL	-14.33	0.28 ± 0.01	NA
R_089	LLLAALLFALLSLLTWLIL	-14.2	0.3 ± 0.0	NA
R_090	LLLTVLLALLFALLSILIL	-14.11	0.36 ± 0.06	-2.01 ± 0.32
R_091	LLLYVLLTALLLALLSFLLIL	-12.66	0.33 ± 0.07	-1.51 ± 0.34
R_092	LLLYVLLFTLALLSLLIL	-13.95	0.28 ± 0.06	NA
R_093	LLLYVLLALLTSLLFLIL	-13.89	0.39 ± 0.03	-2.3 ± 0.16
R_094	LLLYSLLILLAVLLTFLLIL	-13.86	0.24 ± 0.07	NA
R_095	LLLYTLLVFLALLSLLIL	-13.66	0.34 ± 0.09	-1.68 ± 0.45
R_096	LLLYAALLLSSVLLFLLIL	-13.65	0.3 ± 0.07	NA
R_097	LLLAALLVTLAAILLSFLIL	-13.32	0.17 ± 0.07	NA
R_098	LLLTVLLALLAFLLSLIL	-12.94	0.35 ± 0.06	-1.9 ± 0.33
R_099	LLLYTLLVALIAAILLFLIL	-12.88	0.37 ± 0.05	-2.12 ± 0.3
R_100	LLLYVLLTLLVALLSFLIL	-13.89	0.3 ± 0.11	NA
R_101	LLLYVLLVALISLLTLLIL	-24.44	0.32 ± 0.03	-1.09 ± 0.09
R_102	LLLYVLLVALATLSSFLIL	-17.7	0.22 ± 0.08	NA
R_103	LLLGYLLLTLLVALSLLIL	-17.85	0.48 ± 0.06	-2.74 ± 0.36
R_104	LLLYTLLFTLAVLLSLLIL	-22.18	0.36 ± 0.04	-2.01 ± 0.25
R_105	LLLYWLLTALLSLLFVLIL	-22.11	0.21 ± 0.05	NA
R_106	LLLYVLLTLLATLSSFLIL	-21.91	0.22 ± 0.12	NA
R_107	LLLYTLLVALAAILLSLLIL	-21.41	0.28 ± 0.02	NA
R_108	LLLYSLLLTLLAVLFSFLIL	-21.39	0.21 ± 0.1	NA
R_109	LLLYLLITLLFSLLVALIL	-21.29	0.3 ± 0.05	NA
R_110	LLLYSLLALLFALLVTFLIL	-21.29	0.27 ± 0.05	NA
R_111	LLLYSLLVALFTLLLIL	-21.29	0.28 ± 0.12	NA
R_112	LLLFSLLLTLLAALLSYLIL	-21.16	0.21 ± 0.07	NA
R_113	LLLYILLSTLALLIAFLIL	-21.11	0.21 ± 0.04	NA
R_114	LLLYSLLITLLFVLLALIL	-20.93	0.25 ± 0.09	NA
R_115	LLLYTLLATLFLLSVLIL	-20.85	0.27 ± 0.11	NA
R_116	LLLYVLLFIALLLSTLIL	-20.83	0.22 ± 0.1	NA
R_117	LLLYILLSVLLALLTFLLIL	-20.82	0.19 ± 0.08	NA
R_118	LLLYTLLVALFALLSLLIL	-20.72	0.3 ± 0.07	NA
R_119	LLLYVLLIALFSLLTLLIL	-22.22	0.34 ± 0.04	-1.71 ± 0.23
R_120	LLLYALLTLLFTFLSLLIL	-22.25	0.28 ± 0.15	NA
R_121	LLLYALLTSLLVALLSFLIL	-22.5	0.34 ± 0.02	-1.73 ± 0.08
R_122	LLLYSLLALLFALLTIL	-22.52	0.45 ± 0.06	-2.6 ± 0.36
R_123	LLLYTLLVSLLFALLLIL	-24.31	0.23 ± 0.06	NA
R_124	LLLYVLLTALLSLLFLIL	-24.25	0.37 ± 0.07	-2.17 ± 0.4
R_125	LLLYWLLVLLATLSSFLIL	-24.21	0.35 ± 0.07	-1.95 ± 0.39
R_126	LLLYSLLLTLLATLFLIL	-24.19	0.21 ± 0.08	NA
R_127	LLLYILLATLTLSSFLIL	-24.1	0.21 ± 0.11	NA
R_128	LLLFVLLATLAYLLSLLIL	-23.75	0.36 ± 0.03	-2.07 ± 0.14
R_129	LLLYSLLVALFALLTLLIL	-23.75	0.37 ± 0.07	-2.16 ± 0.4
R_130	LLLYLLAVLAPLLTSLLIL	-20.67	0.24 ± 0.09	NA
R_131	LLLSYLLVFLLATLSSLLIL	-23.6	0.39 ± 0.06	-2.32 ± 0.34
R_132	LLLYSLLLTLLAAILFLIL	-23.54	0.3 ± 0.08	NA
R_133	LLLYSLLLTLLFALLVIL	-23.43	0.36 ± 0.02	-2.01 ± 0.12
R_134	LLLYVLLATLAFLLSLLIL	-23.31	0.29 ± 0.06	NA
R_135	LLLYLLVTLLFALLSLLIL	-23.2	0.37 ± 0.07	-2.15 ± 0.4
R_136	LLLATLISLLFTLLVLLIL	-23.06	0.43 ± 0.09	-2.51 ± 0.56
R_137	LLLYLLLATLFLVLLSLLIL	-22.94	0.21 ± 0.12	NA
R_138	LLLYAALLLVSLLFTFLIL	-22.59	0.38 ± 0.06	-2.2 ± 0.38
R_139	LLLYVLLALLTALLSLLIL	-23.55	0.36 ± 0.11	-2.07 ± 0.63
R_140	LLLFYLLVALTALLSLLIL	-20.62	0.39 ± 0.03	-2.31 ± 0.17

R_141	<b>LLLVYLLITLLFALLSLLLILI</b>	-20.57	0.43 ± 0.04	-2.51 ± 0.25
R_142	<b>LLLYIILLTVLLALLLSFLIL</b> I	-20.38	0.26 ± 0.05	NA
R_143	<b>LLLYTLLVALLSTLLFLL</b> LILI	-19.39	0.23 ± 0.09	NA
R_144	<b>LLLTLTLLATLLAVLLSFL</b> LILI	-19.38	0.37 ± 0.03	-2.09 ± 0.16
R_145	<b>LLLVYLLLAFLLLSFL</b> LILI	-19.07	0.47 ± 0.06	-2.68 ± 0.36
R_146	<b>LLLYVILLTAFLFALLSLL</b> LILI	-19.06	0.32 ± 0.06	-0.98 ± 0.18
R_147	<b>LLLLTLLIAALLVALLSFL</b> LILI	-18.94	0.34 ± 0.07	-1.8 ± 0.37
R_148	<b>LLLFVILLTTLAAILLSL</b> LILI	-18.76	0.22 ± 0.02	NA
R_149	<b>LLLYFLLIAALLAVLLT</b> LILI	-18.7	0.24 ± 0.06	NA
R_150	<b>LLLTLTLLIAFLFVLLYS</b> LILI	-19.44	0.43 ± 0.06	-2.52 ± 0.34
R_151	<b>LLLVALLLAFLFALLSFL</b> LILI	-18.56	0.36 ± 0.04	-2.01 ± 0.23
R_152	<b>LLVALLLTLLAAILLSFL</b> LILI	-18.48	0.28 ± 0.05	NA
R_153	<b>LLLYIILLVALLATLLT</b> LILI	-18.48	0.34 ± 0.11	-1.84 ± 0.61
R_154	<b>LLLYLILLTVLLAFLPSL</b> LILI	-18.43	0.27 ± 0.05	NA
R_155	<b>LLLTYLVALVALIAALLS</b> LILI	-18.14	0.36 ± 0.02	-2.0 ± 0.09
R_156	<b>LLLAVALVALSTLLIF</b> LILI	-18.12	0.39 ± 0.06	-2.31 ± 0.37
R_157	<b>LLTYLLIAALLLAFLFV</b> LILI	-18.08	0.4 ± 0.01	-2.35 ± 0.05
R_158	<b>LLYSILLVALTLLLF</b> LILI	-17.88	0.31 ± 0.13	-0.84 ± 0.34
R_159	<b>LLLALLLFALLTVLLS</b> LILI	-18.52	0.44 ± 0.02	-2.59 ± 0.13
R_160	<b>LLYSILLVALAVLLT</b> LILI	-17.72	0.31 ± 0.22	0.32 ± 0.23
R_161	<b>LLLAAILLTLLFVLLS</b> LILI	-19.44	0.33 ± 0.06	-1.49 ± 0.26
R_162	<b>LLTYLLVALTFLLS</b> LILI	-19.5	0.59 ± 0.25	-3.04 ± 1.29
R_163	<b>LLAVILLTLLFTLLS</b> LILI	-20.37	0.21 ± 0.11	NA
R_164	<b>LLYSILLVALFLLAT</b> LILI	-20.33	0.28 ± 0.1	NA
R_165	<b>LLYSILLTLLAALLVF</b> LILI	-20.13	0.23 ± 0.08	NA
R_166	<b>LLLYLILLVALVALS</b> LILI	-20.11	0.3 ± 0.05	NA
R_167	<b>LLYTLLVALFLLS</b> LILI	-20.05	0.27 ± 0.1	NA
R_168	<b>LLLFYLLTALLIAALLS</b> LILI	-20	0.38 ± 0.03	-2.23 ± 0.15
R_169	<b>LLYWILLVALLLALLS</b> LILI	-19.98	0.36 ± 0.01	-2.06 ± 0.04
R_170	<b>LLLYIILLFTLLVALLS</b> LILI	-19.46	0.19 ± 0.06	NA
R_171	<b>LLLFALLTILVALVLL</b> LILI	-19.95	0.4 ± 0.06	-2.34 ± 0.34
R_172	<b>LLLYALLVALLLTLLS</b> LILI	-19.84	0.27 ± 0.04	NA
R_173	<b>LLYSILLFTLLAVLIAL</b> LILI	-19.77	0.32 ± 0.1	-1.4 ± 0.42
R_174	<b>LLLYWILLVALVALS</b> LILI	-19.77	0.3 ± 0.04	NA
R_175	<b>LLLALLLIAFLFVLLS</b> LILI	-19.62	0.27 ± 0.05	NA
R_176	<b>LLLYTLLVSLLAAILT</b> LILI	-19.61	0.33 ± 0.09	-1.58 ± 0.45
R_177	<b>LLLFTYLLTALLTLLV</b> LILI	-19.54	0.31 ± 0.09	NA
R_178	<b>LLLSYLLVFLALLLAT</b> LILI	-19.53	0.48 ± 0.07	-2.74 ± 0.39
R_179	<b>LLLTYLLLAVALVSLLF</b> LILI	-19.87	0.47 ± 0.09	-2.68 ± 0.54
R_180	<b>LLLYVILLATLLTFLLS</b> LILI	-9.81	0.29 ± 0.02	NA

Data for validated sets of designs where clashing mutations < 35% GpA

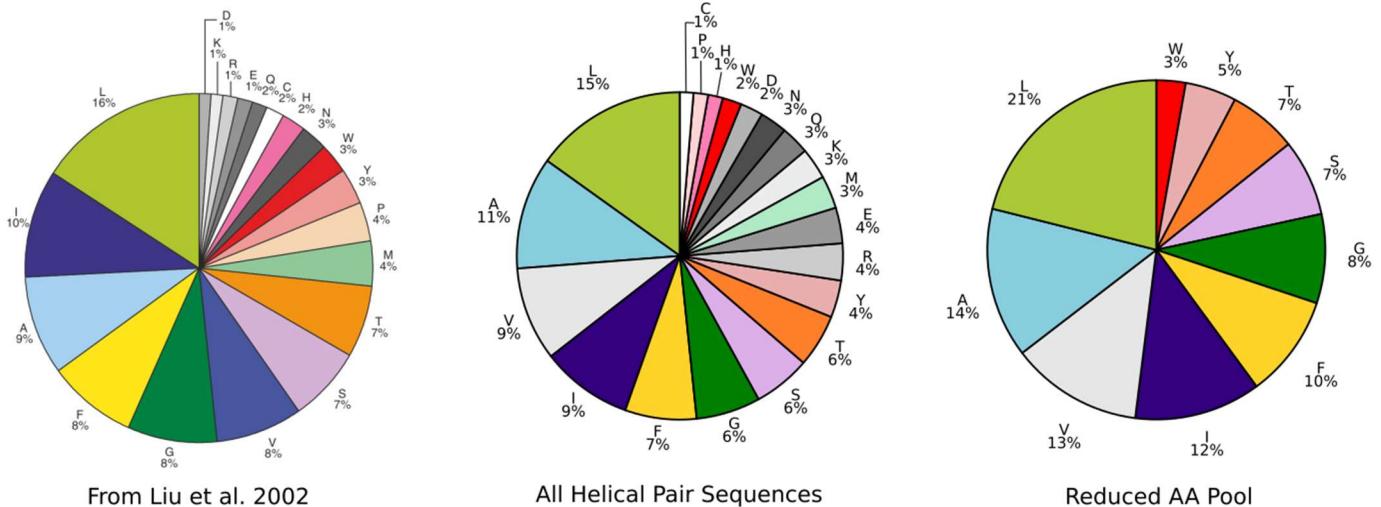
Interfacial designed positions of each sequence in bold

Designs where a positive ΔG was calculated are designated NA



Western ID	Sequence	Design ID
G1	LLL <b>A</b> VLL <b>L</b> T <b>L</b> GG <b>L</b> F <b>A</b> L <b>I</b> L <b>I</b>	
G2	LLL <b>Y</b> V <b>L</b> L <b>G</b> <b>A</b> L <b>G</b> <b>I</b> <b>L</b> <b>T</b> <b>L</b> <b>I</b> <b>I</b>	G_016
L1	LLL <b>L</b> LL <b>F</b> <b>L</b> <b>A</b> <b>T</b> <b>L</b> <b>L</b> <b>I</b> <b>L</b> <b>S</b> <b>V</b> <b>L</b> <b>I</b> <b>I</b>	L_021
L2	LLL <b>F</b> <b>S</b> LLL <b>L</b> LL <b>V</b> <b>A</b> <b>L</b> <b>L</b> <b>T</b> <b>L</b> <b>L</b> <b>I</b> <b>I</b>	
R1	LLL <b>Y</b> <b>I</b> <b>L</b> <b>T</b> <b>A</b> <b>L</b> <b>L</b> <b>V</b> <b>A</b> <b>L</b> <b>S</b> <b>L</b> <b>I</b> <b>I</b>	R_051
R2	LLL <b>F</b> <b>Y</b> <b>L</b> <b>L</b> <b>V</b> <b>A</b> <b>L</b> <b>T</b> <b>A</b> <b>L</b> <b>S</b> <b>L</b> <b>I</b> <b>I</b>	R_140
L3	LLL <b>L</b> LL <b>A</b> <b>V</b> <b>L</b> <b>F</b> <b>L</b> <b>A</b> <b>L</b> <b>T</b> <b>S</b> <b>L</b> <b>I</b> <b>I</b>	L_031
R3	LLL <b>T</b> <b>V</b> <b>L</b> <b>L</b> <b>A</b> <b>L</b> <b>L</b> <b>F</b> <b>A</b> <b>L</b> <b>S</b> <b>I</b> <b>L</b> <b>I</b> <b>I</b>	R_090
G3	LLL <b>T</b> <b>A</b> <b>L</b> <b>L</b> <b>A</b> <b>L</b> <b>L</b> <b>F</b> <b>G</b> <b>L</b> <b>F</b> <b>S</b> <b>L</b> <b>I</b> <b>I</b>	G_060
G4	LLL <b>T</b> <b>A</b> <b>L</b> <b>L</b> <b>I</b> <b>G</b> <b>L</b> <b>F</b> <b>G</b> <b>L</b> <b>I</b> <b>V</b> <b>L</b> <b>L</b> <b>I</b> <b>I</b>	
L4	LLL <b>L</b> <b>L</b> <b>Y</b> <b>L</b> <b>L</b> <b>A</b> <b>V</b> <b>L</b> <b>T</b> <b>A</b> <b>L</b> <b>F</b> <b>S</b> <b>L</b> <b>I</b> <b>I</b>	L_022
L5	LLL <b>L</b> <b>L</b> <b>L</b> <b>A</b> <b>L</b> <b>L</b> <b>I</b> <b>L</b> <b>F</b> <b>V</b> <b>L</b> <b>L</b> <b>S</b> <b>T</b> <b>L</b> <b>I</b> <b>I</b>	
R4	LLL <b>T</b> <b>S</b> <b>L</b> <b>L</b> <b>A</b> <b>L</b> <b>L</b> <b>F</b> <b>V</b> <b>L</b> <b>L</b> <b>I</b> <b>L</b> <b>I</b> <b>I</b>	
G5	LLL <b>V</b> <b>A</b> <b>L</b> <b>L</b> <b>A</b> <b>L</b> <b>L</b> <b>G</b> <b>T</b> <b>L</b> <b>S</b> <b>F</b> <b>L</b> <b>I</b> <b>I</b>	G_052
L6	LLL <b>L</b> <b>L</b> <b>F</b> <b>A</b> <b>L</b> <b>L</b> <b>A</b> <b>L</b> <b>Y</b> <b>V</b> <b>L</b> <b>T</b> <b>S</b> <b>L</b> <b>I</b> <b>I</b>	
L7	LLL <b>L</b> <b>A</b> <b>I</b> <b>L</b> <b>L</b> <b>A</b> <b>V</b> <b>L</b> <b>F</b> <b>T</b> <b>L</b> <b>S</b> <b>L</b> <b>I</b> <b>I</b>	
L8	LLL <b>Y</b> <b>A</b> <b>L</b> <b>L</b> <b>F</b> <b>V</b> <b>L</b> <b>T</b> <b>A</b> <b>L</b> <b>S</b> <b>L</b> <b>I</b> <b>I</b>	L_006
L9	LLL <b>L</b> <b>L</b> <b>A</b> <b>V</b> <b>L</b> <b>F</b> <b>L</b> <b>L</b> <b>A</b> <b>L</b> <b>T</b> <b>S</b> <b>L</b> <b>I</b> <b>I</b>	L_031
L10	LLL <b>F</b> <b>A</b> <b>L</b> <b>L</b> <b>V</b> <b>L</b> <b>I</b> <b>T</b> <b>L</b> <b>L</b> <b>Y</b> <b>S</b> <b>L</b> <b>I</b> <b>I</b>	
G6	LLL <b>T</b> <b>V</b> <b>L</b> <b>L</b> <b>A</b> <b>L</b> <b>L</b> <b>G</b> <b>F</b> <b>L</b> <b>L</b> <b>G</b> <b>S</b> <b>L</b> <b>I</b> <b>I</b>	G_022
G7	LLL <b>V</b> <b>A</b> <b>L</b> <b>L</b> <b>A</b> <b>L</b> <b>L</b> <b>G</b> <b>T</b> <b>L</b> <b>S</b> <b>F</b> <b>L</b> <b>I</b> <b>I</b>	G_052

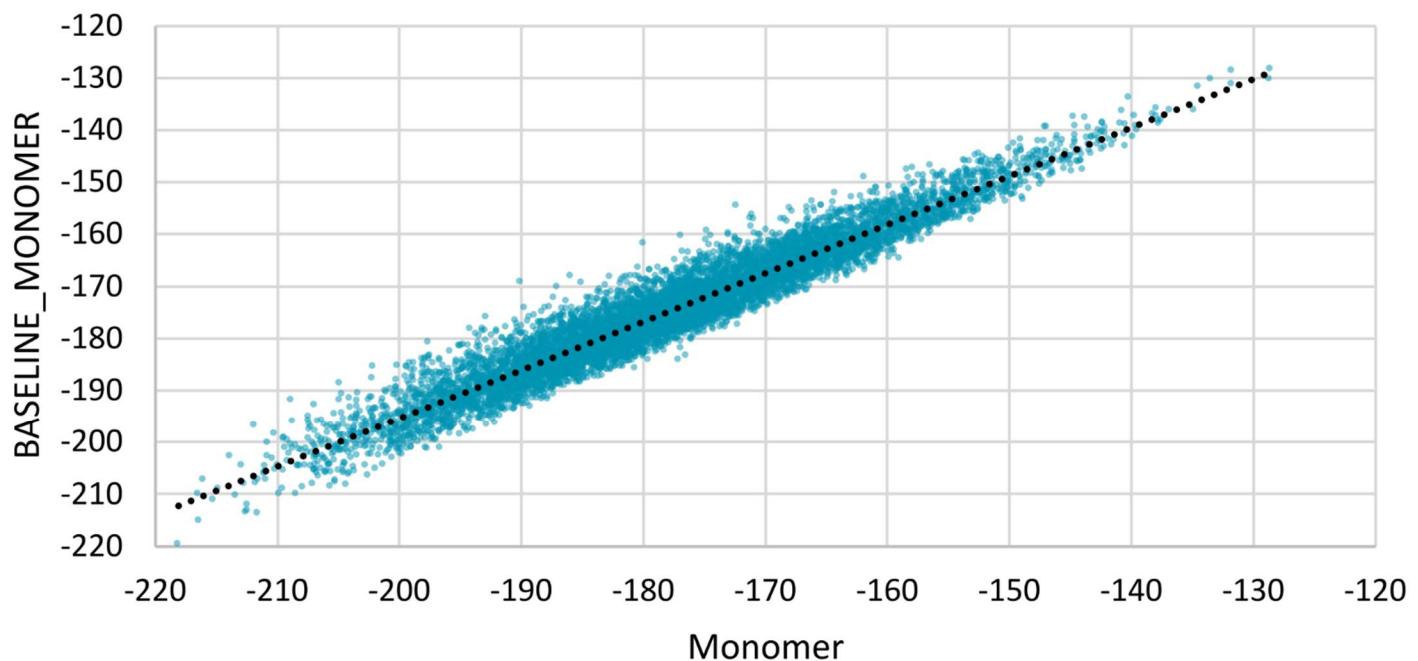
**Figure S1. Immunoblotting of designed constructs.** A subset of designed constructs were verified for their expression levels with western blots. While GAS<sub>right</sub> and Left show similar levels of expression, Right designs often have fainter bands on western blots. Sequences without a Design ID are present in our sort-seq data but not part of our validated set (clashing mutants < 35% GpA)



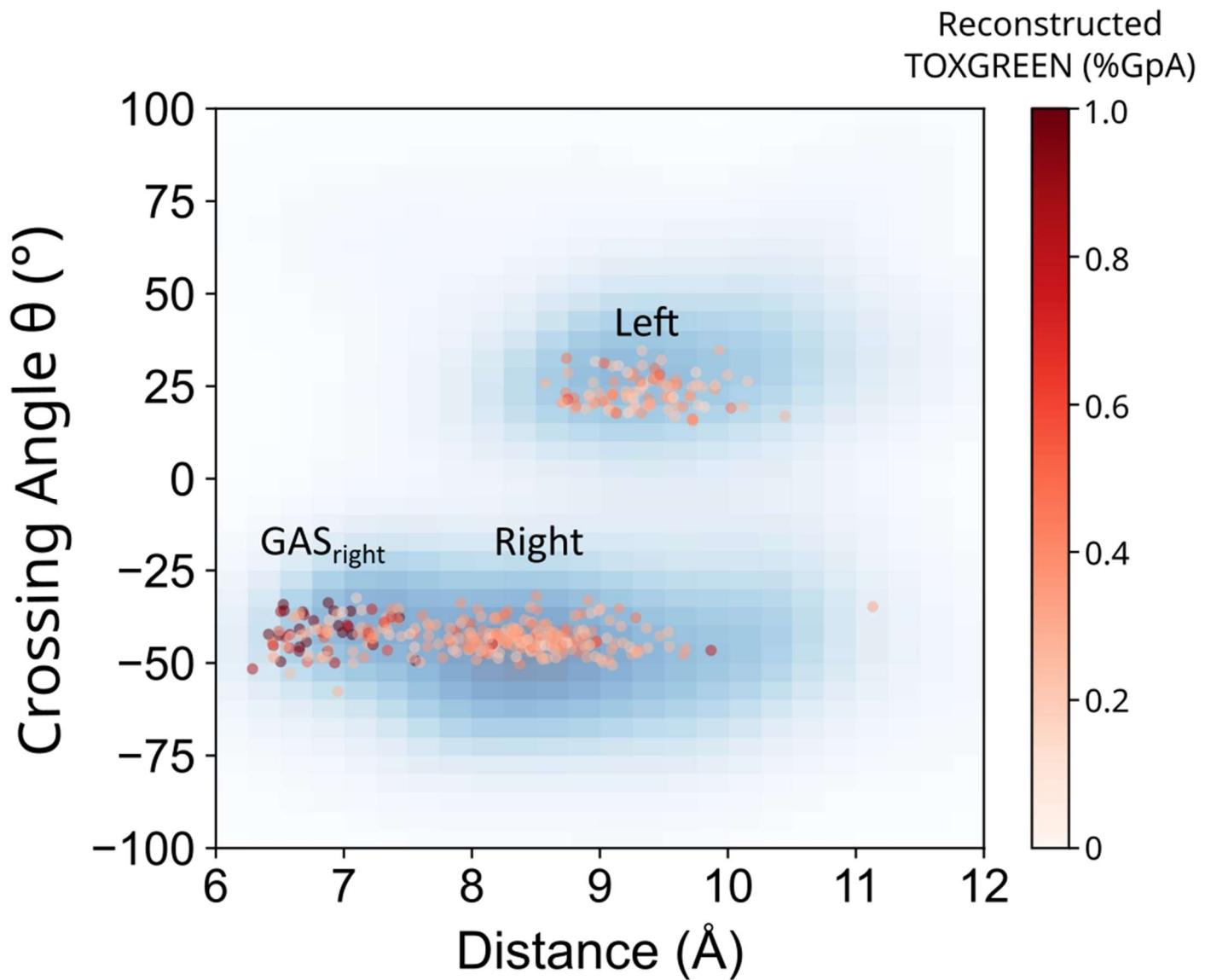
**Figure S2. Amino acid composition.** Frequency of amino acids from all transmembrane helical sequences extracted from OPM (Middle) as compared to membrane proteins from Liu et al. 2002 (Left). The frequency of the reduced pool of amino acids used for design (Right). Sequences were designed with interfaces aiming to match the frequency of the reduced pool of amino acids (SEQUENCE\_ENTROPY).

$$y = 0.9307x - 9.2759$$

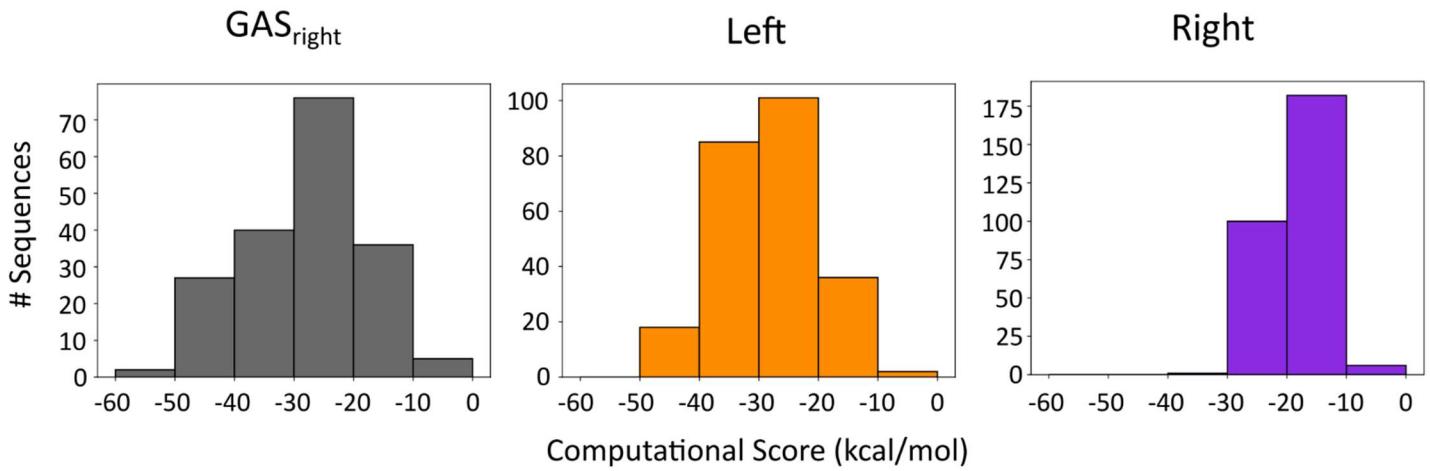
$$R^2 = 0.9273$$



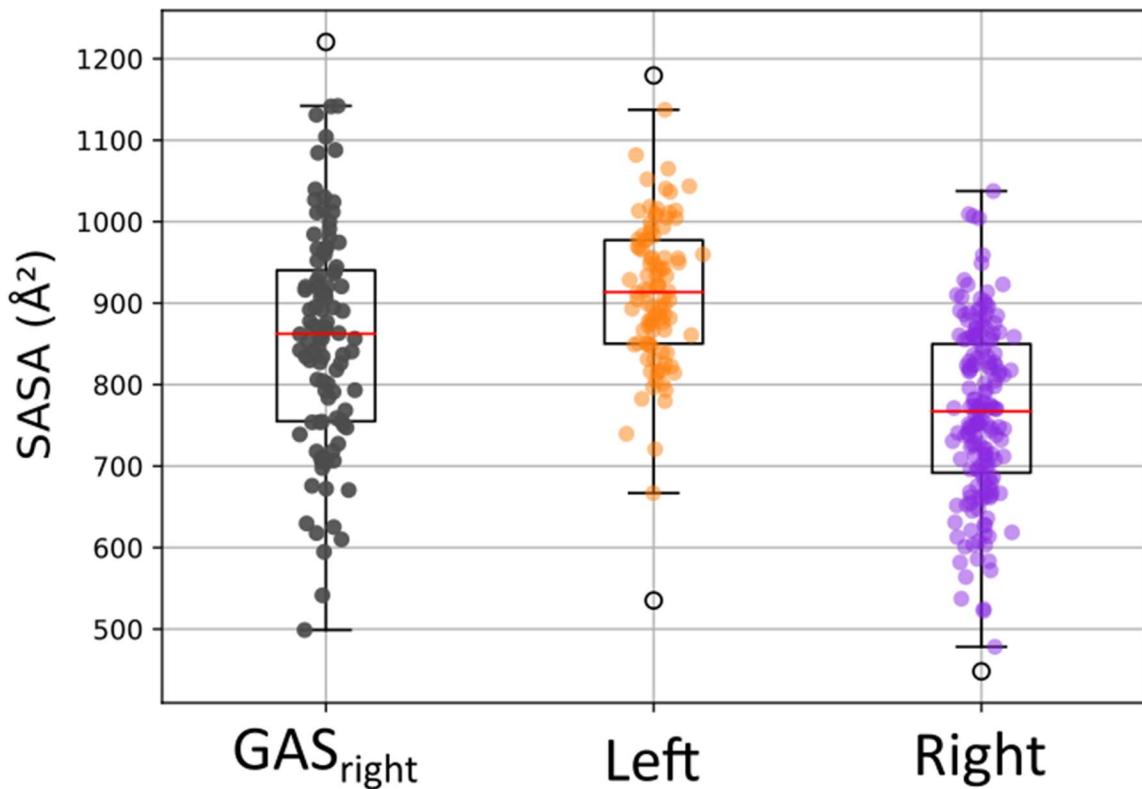
**Figure S3. BASELINE\_MONOMER.** Calculated monomer energy as compared to the estimated term BASELINE\_MONOMER used in the sequence design search.



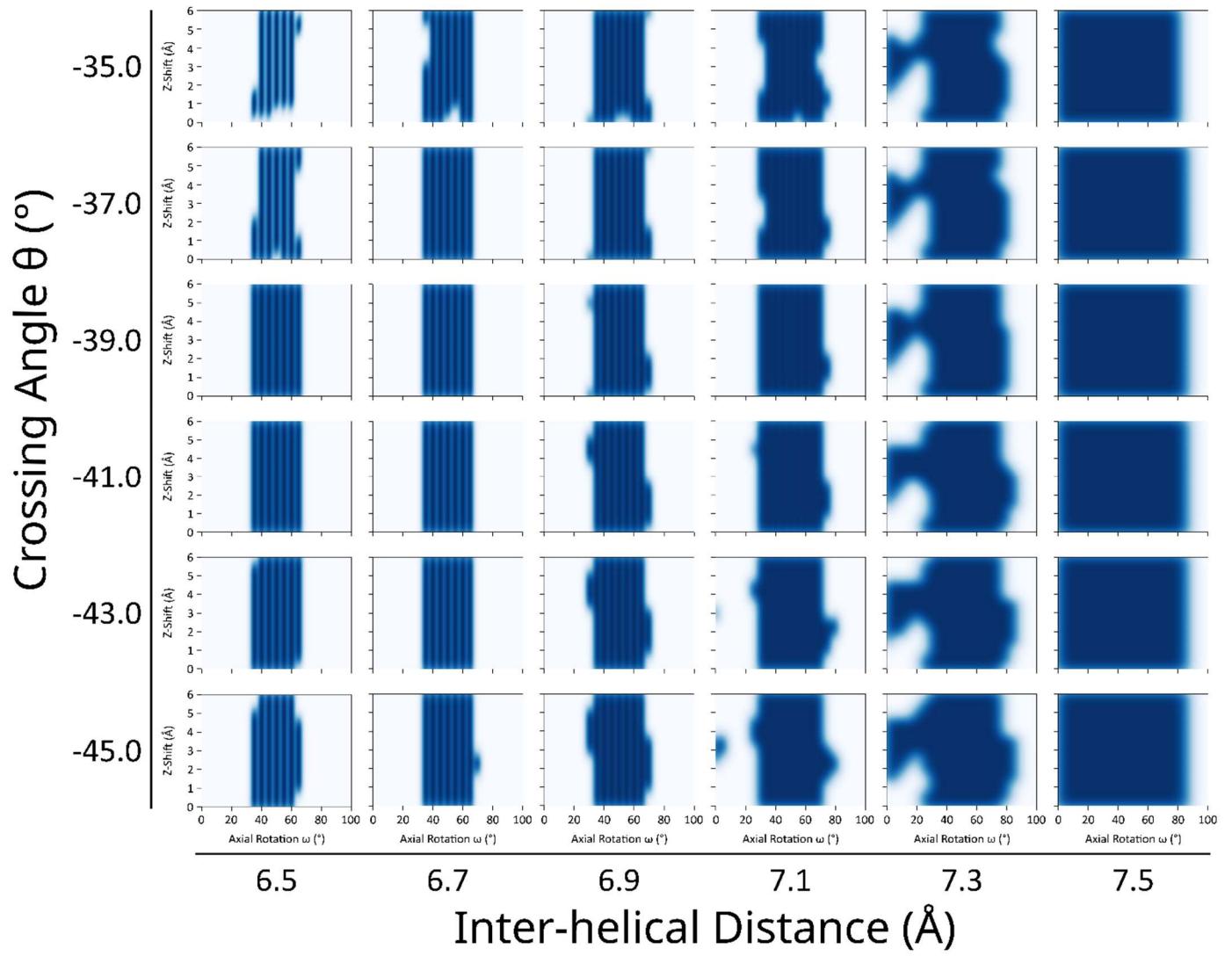
**Figure S4. Output Geometry vs Dimerization Propensity.** Distance and crossing angle of validated designed sequences plotted against %GpA in red. Sequences with highest dimerization propensity are darker red, most often found in GAS<sub>right</sub>.



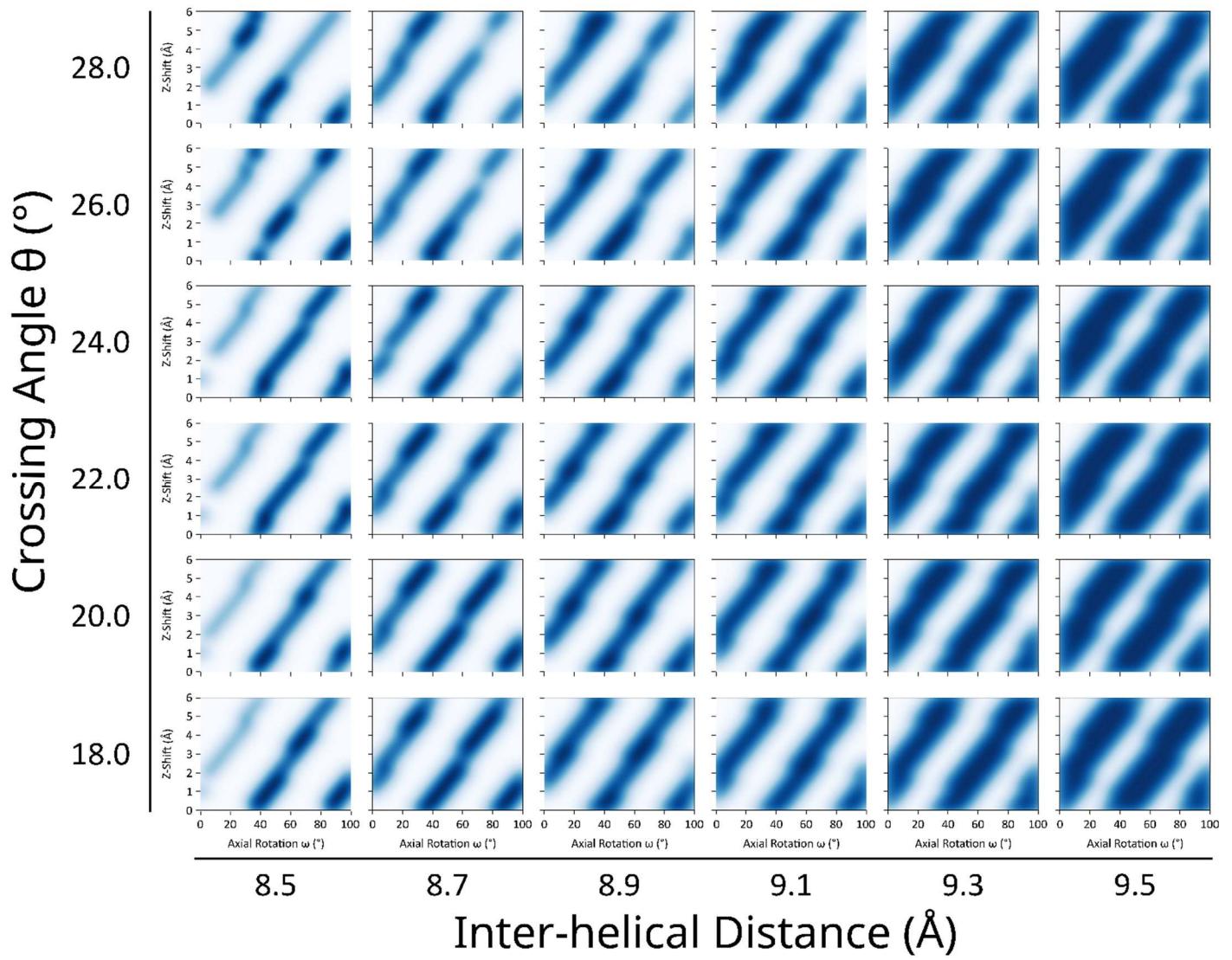
**Figure S5. Frequency of sequences by computational score.** Computational energy score of sequences present in sort-seq and the frequency for each design region.



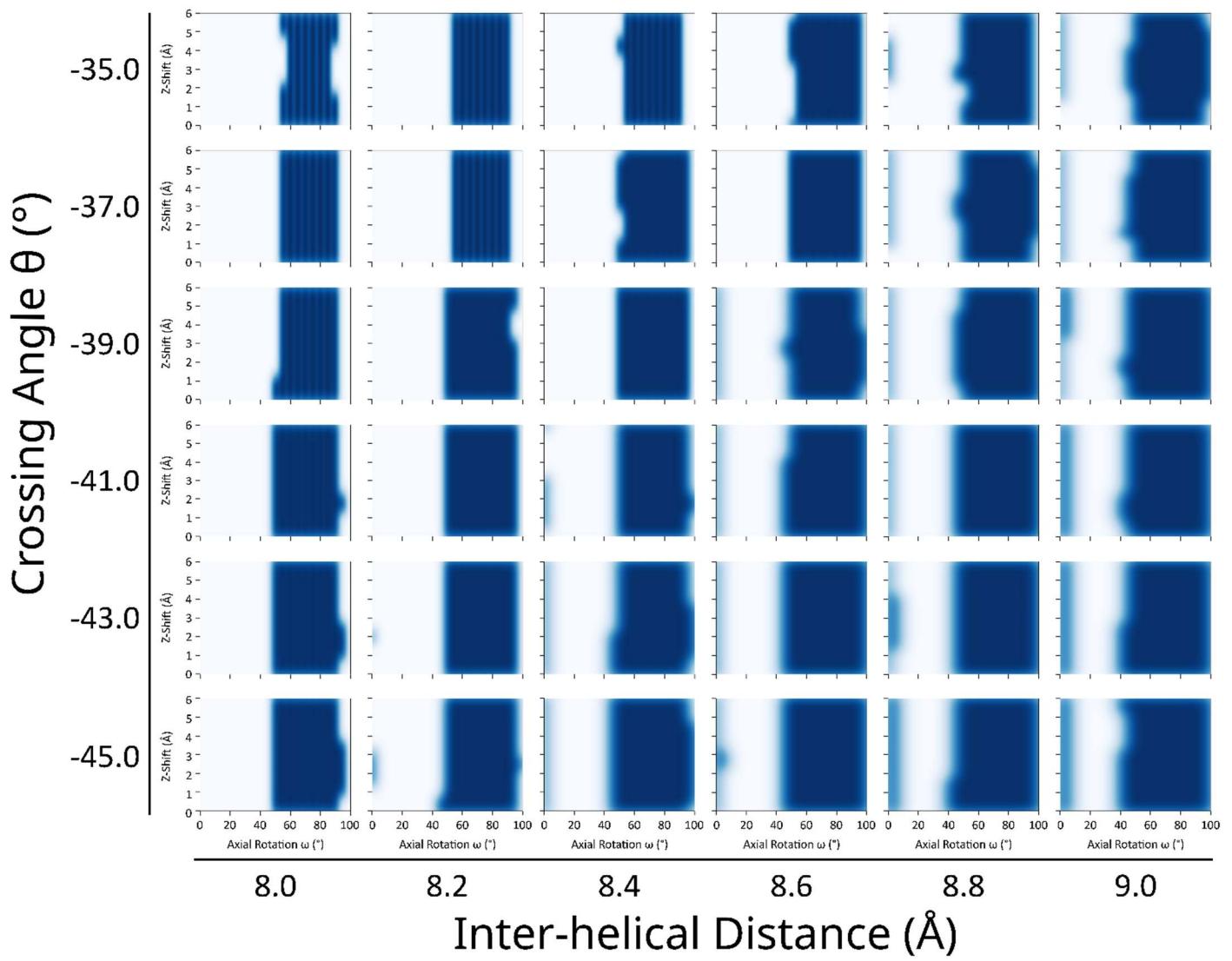
**Figure S6. Interface SASA.** Boxplots of validated sequences of interface SASA. GAS<sub>right</sub> and Left design interfaces are larger than Right, which may contribute to Right designs having a lower computational energy score.



**Figure S7. GAS<sub>right</sub> axial rotations and z-shifts.** Grid of favorable axial rotations and z-shifts for various design distances and crossing angles. Dark blue areas are potential geometries that were randomly chosen for design.



**Figure S8. Left axial rotations and z-shifts.** Grid of favorable axial rotations and z-shifts for various design distances and crossing angles. Dark blue areas are potential geometries that were randomly chosen for design.



**Figure S9. Right axial rotations and z-shifts.** Grid of favorable axial rotations and z-shifts for various design distances and crossing angles. Dark blue areas are potential geometries that were randomly chosen for design.