

## **Supplementary Information**

**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>YFLLGALI</b> GLLILILI	-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>VTLLGLLFALLST</b> LILI	-26.16	0.25 ± 0.05	NA
G_015	LLL <b>TFLLGLLGYLLAS</b> LILI	-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>YFLGVVLGTLI</b> GLLILILI	-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>TVLLGLLFGLLFAL</b> IILI	-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>YVLLGLLGTLIAFI</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> IYLILI	-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>YVLLFTLLGALIGL</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>YLLGTLLGILIAF</b> LILI	-19.35	0.43 ± 0.07	-2.55 ± 0.43
G_039	LLL <b>YGULFLLGVLIAT</b> LILI	-27.64	0.4 ± 0.04	-2.39 ± 0.22
G_040	LLL <b>YFLLATLLGVLLG</b> IYLILI	-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>TFLLAIIIGYLG</b> IYLILI	-20.12	0.95 ± 0.14	-3.62 ± 0.52
G_043	LLL <b>VTLLTLLGALLSAL</b> IILI	-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>YGULFLLGVLIAS</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>YLLGALLGVLI</b> STLILI	-24.54	0.84 ± 0.22	-3.48 ± 0.9
G_049	LLL <b>AALLFALLGILIST</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>TALLFLLGVLIAS</b> LILI	-16.15	0.82 ± 0.11	-3.45 ± 0.45
G_058	LLL <b>AGLIFLLGVLIAT</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>YVLTLLGGGLFAL</b> IILI	-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>VLLATLLGSLIGF</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>LVLLTTLLGGGLFAL</b> IILI	-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>YTLIATLLGSLIGF</b> LILI	-44.96	0.24 ± 0.03	NA
G_068	LLL <b>TSLLVGLIAYLIG</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>YFLAVLLGLLGS</b> LILI	-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> T <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> GL <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>F</b> GL <b>I</b> <b>F</b> ALL <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>F</b> ALL <b>A</b> Y <b>L</b> <b>I</b> <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> <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> LL <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> VL <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	LLLLYVLIAITLTLFSLLILI	-19.91	0.28 ± 0.05	NA
L_003	LLIVALLLILITFLLLASLLILI	-19.85	0.35 ± 0.06	-1.97 ± 0.35
L_004	LLLLFVLTLLTALLYSLLILI	-27.78	0.19 ± 0.1	NA
L_005	LLLAYLIALLFLTSLLILI	-24.92	0.32 ± 0.07	-1.18 ± 0.27
L_006	LLLYALLFVLTALLLSLLILI	-20.96	0.49 ± 0.08	-2.78 ± 0.45
L_007	LLLYYVLLATLALLSFLLLILI	-20.52	0.28 ± 0.08	NA
L_008	LLLLAIIITLAVLFSLLILI	-25.76	0.61 ± 0.06	-3.09 ± 0.3
L_009	LLIVALLLILFLLTSLLILI	-22.22	0.48 ± 0.23	-2.75 ± 1.31
L_010	LLLYFVLLAIIITLTSLLILI	-22.59	0.19 ± 0.11	NA
L_011	LLLLFVLLALLTTLTSLLILI	-19.85	0.15 ± 0.05	NA
L_012	LLLLAVLLFLATLISLLILI	-26.1	0.22 ± 0.05	NA
L_013	LLLLLFLFLAVLSTLILI	-26.11	0.16 ± 0.05	NA
L_014	LLLYYVLLATLFLSLLILI	-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	LLLYFVLLALAVTSLLILI	-21.69	0.27 ± 0.09	NA
L_017	LLLYLLLTVIALLFSLLILI	-21.39	0.23 ± 0.06	NA
L_018	LLLTLLLAIALVLFSLLLILI	-21.35	0.47 ± 0.12	-2.7 ± 0.69
L_019	LLLLVLLTILFLLSALILI	-26.56	0.23 ± 0.04	NA
L_020	LLLYYLLFLAVLSTLILI	-23.39	0.21 ± 0.09	NA
L_021	LLLLFLFLATLILLSVLLILI	-21.08	0.25 ± 0.05	NA
L_022	LLLYYLLAVLTALLFSLLILI	-21.06	0.27 ± 0.09	NA
L_023	LLLYYVLLAALLFTLISLLILI	-25.06	0.18 ± 0.12	NA
L_024	LLVTLLLAIALLFLSLLILI	-20.94	0.27 ± 0.06	NA
L_025	LLLYYALLFLTALLFSLLILI	-26.79	0.45 ± 0.14	-2.61 ± 0.83
L_026	LLLLLFLFLATLTSLLILI	-26.85	0.23 ± 0.07	NA
L_027	LLLFSLVLLTALLYLLLILI	-20.71	0.23 ± 0.05	NA
L_028	LLLTILLVLLAVLSTLILI	-26.94	0.23 ± 0.19	NA
L_029	LLLFFLLLAAILLFLSLLILI	-23.7	0.21 ± 0.05	NA
L_030	LLLYVLLAIALFLLSLLILI	-23.75	0.23 ± 0.07	NA
L_031	LLLVAVLFLALATSLLILI	-27.1	0.41 ± 0.08	-2.45 ± 0.5
L_032	LLIVALLTIIALFLSLLILI	-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	LLLFALLTIIIVLLSLLILI	-28.01	0.36 ± 0.05	-2.09 ± 0.26
L_035	LLLVAVLTAIPLLFSLLILI	-36.08	0.21 ± 0.13	NA
L_036	LLLYYVLTAAFLLLSLLILI	-35.8	0.26 ± 0.1	NA
L_037	LLLVVLLTIIIFLLSLLILI	-34.96	0.21 ± 0.09	NA
L_038	LLLYWYLVSLILITFLLLILI	-34.36	0.48 ± 0.16	-2.75 ± 0.89
L_039	LLLVVSLLILITALLFLLLILI	-34.32	0.41 ± 0.11	-2.42 ± 0.67
L_040	LLLYAYLTIVLLSIIFLLLILI	-16.04	0.38 ± 0.08	-2.25 ± 0.48
L_041	LLLAIIILALFLVTSLLILI	-34.1	0.3 ± 0.1	NA
L_042	LLLLFVLLLALATLISLLILI	-36.31	0.27 ± 0.08	NA
L_043	LLYTLLAVLIAALLSLLILI	-16.38	0.44 ± 0.09	-2.56 ± 0.52
L_044	LLLLFILLAVLAVLTLSSLLILI	-32.64	0.22 ± 0.13	NA
L_045	LLIVALLFLSLLYTLILILI	-32.59	0.27 ± 0.08	NA
L_046	LLLLVLLLAIALFTLSSLLILI	-32.33	0.29 ± 0.07	NA
L_047	LLIVALLFLITSLLYLILILI	-27.98	0.21 ± 0.07	NA
L_048	LLLLFLLAVLYLLSTLILILI	-32.17	0.32 ± 0.14	-1.14 ± 0.51
L_049	LLLSYFLAVLFTFLLLILILI	-32.13	0.34 ± 0.08	-1.82 ± 0.4
L_050	LLLFFLLLAITALVLLSLLILI	-32.09	0.33 ± 0.1	-1.46 ± 0.44
L_051	LLLYFLAVLITLILSLLILI	-33.12	0.18 ± 0.09	NA
L_052	LLLTYYLLAIALFVLLLSLLILI	-32.09	0.25 ± 0.12	NA
L_053	LLIVLLLAIALFLLLTSLLILI	-36.54	0.24 ± 0.09	NA
L_054	LLLYTLLAVLILLASLLILI	-14.73	0.15 ± 0.05	NA
L_055	LLYALLTIIIVLFSLLILI	-8.65	0.55 ± 0.3	-2.94 ± 1.59
L_056	LLLLLLAVLITALLFLILILI	-44.72	0.28 ± 0.06	NA
L_057	LLLLVALLLITSLLFLILILI	-44.48	0.48 ± 0.05	-2.72 ± 0.26
L_058	LLYALLLVIITLILFSLLILI	-11.73	0.35 ± 0.12	-1.95 ± 0.64
L_059	LLLFALLLITALLYVLLILI	-12.21	0.37 ± 0.12	-2.12 ± 0.69
L_060	LLLFYLTALLLILIVSLLILI	-12.34	0.28 ± 0.15	NA
L_061	LLLLVALLLITAFLSLLILI	-41.95	0.43 ± 0.16	-2.53 ± 0.93
L_062	LLLAIIILAVLFLLSTLILILI	-36.63	0.25 ± 0.11	NA
L_063	LLLLLALLFLTSLLYLILILI	-41.84	0.41 ± 0.04	-2.44 ± 0.24
L_064	LLLYVLIALLLTSLLILI	-13.11	0.36 ± 0.29	-2.08 ± 1.65
L_065	LLLYWLLTILAFLLSLLILI	-40.46	0.4 ± 0.13	-2.34 ± 0.77
L_066	LLLYSITALLFVLLLILILI	-39.3	0.27 ± 0.06	NA
L_067	LLLTTVLLAIALFLSLLILI	-38.49	0.2 ± 0.12	NA
L_068	LLLVALLLLTSLLFLILILI	-37.95	0.27 ± 0.11	NA
L_069	LLLFVLLAIALYLLSTLILILI	-37.79	0.35 ± 0.08	-1.89 ± 0.41
L_070	LLLFALLLLVTLLYSLLILI	-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	LLLLSYLVALLTTLFLLSTLILLI	-31.72	0.37 ± 0.28	-2.18 ± 1.61
L_075	LLLLLVLLAILLFLSTLILLI	-29.41	0.24 ± 0.1	NA
L_076	LLLLYWLLTILVALLSFLILLI	-29.15	0.42 ± 0.06	-2.5 ± 0.34
L_077	LLLYYLLLAVITSLLFLLLILLI	-28.74	0.14 ± 0.1	NA
L_078	LLLALLLFITVLLSILILLI	-28.66	0.24 ± 0.07	NA
L_079	LLLLLFITALLYVLISLLILLI	-28.61	0.28 ± 0.27	NA
L_080	LLLLYVLLLAITLILFSLLILLI	-19.09	0.19 ± 0.11	NA
L_081	LLLLYLLLAVLSSLFLFTLILLI	-29.49	0.26 ± 0.08	NA
L_082	LLLYFLLAIVLITLFLSLLILLI	-19.2	0.16 ± 0.09	NA
L_083	LLLLLALLLILVTLISLLILLI	-28.35	0.32 ± 0.1	-1.29 ± 0.41
L_084	LLLLWTLIAILLLVLFLLILLI	-28.25	0.32 ± 0.08	-1.09 ± 0.29
L_085	LLLYALLFLITSLLFSLLILLI	-28.21	0.14 ± 0.08	NA
L_086	LLLLLLILAVLYTLLISFLILLI	-28.07	0.23 ± 0.04	NA
L_087	LLLYAALLLILVTLISLLILLI	-28.03	0.22 ± 0.08	NA
L_088	LLLYAALLFVULLLTSLLILLI	-19.75	0.17 ± 0.07	NA
L_089	LLLLAILLLILTVLFLLILLI	-28.43	0.18 ± 0.08	NA
L_090	LLLLYILLALLFVLILSTLILLI	-30	0.22 ± 0.02	NA
L_091	LLLYAALLFVULLLFSLLILLI	-18.68	0.14 ± 0.05	NA
L_092	LLLLAALLFLITSLLYVLLILLI	-31.34	0.36 ± 0.04	-1.99 ± 0.22
L_093	LLLYWLLTVLFLLASLLILLI	-17.52	0.28 ± 0.03	NA
L_094	LLLLYFLILATLVALLLSLLILLI	-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	LLLAAALLLILVTLFSLLILLI	-17.48	0.53 ± 0.08	-2.89 ± 0.43
L_097	LLLLAVLLILITLFLSLLILLI	-30.86	0.38 ± 0.2	-2.19 ± 1.14
L_098	LLLLTVLLAILFLLSSLILLI	-30.91	0.29 ± 0.09	NA
L_099	LLLYSLLLILTFLLAVLLILLI	-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	LLLYTLLIAFLVLLSLLIL	-26.69	0.28 ± 0.04	NA
R_004	LLLYSLLVALFTLLFLLIL	-26.6	0.23 ± 0.1	NA
R_005	LLLSLLFALLIAFLVTLIL	-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	LLTYLLFVLAFLSLLIL	-24.89	0.29 ± 0.1	NA
R_009	LLLYTLLISLVALFLFLIL	-25.05	0.25 ± 0.1	NA
R_010	LLLYTLLVSLLALLAFLIL	-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	LLYSLLIAFLFTLLTILIL	-27.63	0.3 ± 0.06	NA
R_013	LLLVLLIAFLFTLLSYLIL	-25.24	0.33 ± 0.04	-1.62 ± 0.21
R_014	LLSYLLVLLAFLFTLILIL	-25.39	0.35 ± 0.08	-1.9 ± 0.43
R_015	LLLYTLLISLFLVLLTILIL	-26.81	0.31 ± 0.08	0.25 ± 0.07
R_016	LLYFLLVALFTLLSLLIL	-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	LLWTLLVFLLAFLSLLIL	-29.79	0.29 ± 0.06	NA
R_020	LLSYLLFTLLAFLFTLIL	-29.93	0.3 ± 0.09	NA
R_021	LLYSLLIAFLFVLLTILIL	-27.75	0.28 ± 0.1	NA
R_022	LLSYLLFTLLAFLAVLIL	-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	LLYTLLIAFLVLLFSLIL	-24.33	0.31 ± 0.18	-0.41 ± 0.24
R_025	LLFYLLVLLALLSLLIL	-16.37	0.29 ± 0.14	NA
R_026	LLLFYLLVALISLTLIL	-16.35	0.34 ± 0.05	-1.79 ± 0.24
R_027	LLYILLATLLAFLSLLIL	-16.29	0.27 ± 0.12	NA
R_028	LLLFYLLVALFTLLSLLIL	-16.26	0.4 ± 0.08	-2.36 ± 0.48
R_029	LLYALLIAFLFTLLVILIL	-16.15	0.3 ± 0.03	NA
R_030	LLYALLTTLSVLLFLIL	-16.09	0.44 ± 0.07	-2.58 ± 0.43
R_031	LLTALLIAFLFVLLSLLIL	-16.08	0.33 ± 0.01	-1.57 ± 0.04
R_032	LLLYSLLTLLVALLIFLIL	-15.9	0.24 ± 0.11	NA
R_033	LLYSLLAFLATLLVFLIL	-15.86	0.24 ± 0.07	NA
R_034	LLYVLLTLLAFLSFLIL	-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	LLYTLLIAFLAVLSSLIL	-15.58	0.37 ± 0.05	-2.1 ± 0.31
R_037	LLYALLVALITLLFLLIL	-15.3	0.3 ± 0.07	NA
R_038	LLFYLLITLLVALLSLLIL	-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	LLVSLLLTLLFALLAYLIL	-16.54	0.29 ± 0.03	NA
R_043	LLTALLVALAYLFLSFLIL	-16.55	0.5 ± 0.04	-2.81 ± 0.24
R_044	LLTYLLTLLAFLPSSFLIL	-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	LLYILLTTLLVALLSFLIL	-17.43	0.44 ± 0.05	-2.58 ± 0.31
R_047	LLYLLLVTLLAFLSFLIL	-17.35	0.17 ± 0.09	NA
R_048	LLYSLLVALATLLFLLIL	-17.33	0.26 ± 0.07	NA
R_049	LLLAFLVLLFTLLSLLIL	-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	LLYILLTALLVALLSLLIL	-15.06	0.31 ± 0.05	-0.94 ± 0.15
R_052	LLFSLLTLLVALLSLLIL	-17.12	0.26 ± 0.08	NA
R_053	LLVYLLTALLIAFLSLLIL	-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	LLTALLIAFLAVLFSFLIL	-16.65	0.4 ± 0.06	-2.35 ± 0.38
R_057	LLAVLLTLLFALLSYLIL	-16.62	0.26 ± 0.06	NA
R_058	LLYILLTLLAVLFSFLIL	-16.59	0.24 ± 0.04	NA
R_059	LLYFLLVALALLSLLIL	-16.58	0.32 ± 0.03	-1.1 ± 0.11
R_060	LLYILLFAFLTVLSSLLIL	-17.06	0.26 ± 0.06	NA
R_061	LLYVLLIAFLATLLSLLIL	-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	LLYSLLTALLVALLFLLIL	-14.78	0.29 ± 0.08	NA
R_064	LLTYLLVLLAFLSLLIL	-12.04	0.19 ± 0.12	NA
R_065	LLYVLLIAFLFTLLSLLIL	-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

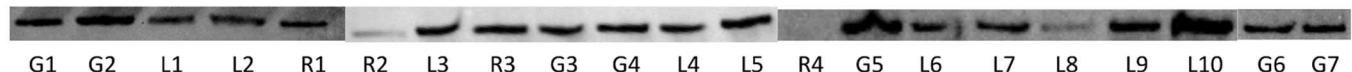
R_071	LLLTYLLAVLLAAILLFLLLIL	-12.11	0.32 ± 0.07	-0.98 ± 0.21
R_072	LLLYVLLTTLFALLSLLIL	-11.22	0.28 ± 0.08	NA
R_073	LLLAALLSLLFLLVFLILI	-10.66	0.46 ± 0.05	-2.65 ± 0.27
R_074	LLLYLLLATLAVLLSLLIL	-10.64	0.24 ± 0.07	NA
R_075	LLLYALLSLLTALLSVFLILI	-10.61	0.28 ± 0.09	NA
R_076	LLLTALLIALFLLSVLIL	-10.55	0.4 ± 0.04	-2.36 ± 0.25
R_077	LLLYVLLFALLTVLLSLLIL	-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	LLLYTLLATLVLVLLSFLIL	-17.69	0.25 ± 0.07	NA
R_082	LLLYVLLATLALLSFLIL	-12.44	0.26 ± 0.03	NA
R_083	LLLYALLLTLLVALLSFLIL	-12.82	0.25 ± 0.08	NA
R_084	LLLYAALLTLSLLVFLIL	-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	LLLIILLSTLATLIVFLIL	-14.36	0.23 ± 0.05	NA
R_088	LLLYILLTLLVALLSFLIL	-14.33	0.28 ± 0.01	NA
R_089	LLLAALLFALLVSLLTWLIL	-14.2	0.3 ± 0.0	NA
R_090	LLLTVLLALLFALLSILIL	-14.11	0.36 ± 0.06	-2.01 ± 0.32
R_091	LLLYVLLTALLSFLIL	-12.66	0.33 ± 0.07	-1.51 ± 0.34
R_092	LLLYVLLFTLALLSLLIL	-13.95	0.28 ± 0.06	NA
R_093	LLLYVLLALTSLLFLIL	-13.89	0.39 ± 0.03	-2.3 ± 0.16
R_094	LLLYSLLLILLAVLLTFIL	-13.86	0.24 ± 0.07	NA
R_095	LLLYTLLVFLALLSILIL	-13.66	0.34 ± 0.09	-1.68 ± 0.45
R_096	LLLYAALLTLLSVLLFIL	-13.65	0.3 ± 0.07	NA
R_097	LLLAALLVTLAAILLSFLIL	-13.32	0.17 ± 0.07	NA
R_098	LLLTVLLALLAFLLSILIL	-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	LLLYVLLTLLFALLSLLIL	-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	LLLGYLLLTLLVALLSILIL	-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	LLYSLLLTLLAVLFLSILIL	-21.39	0.21 ± 0.1	NA
R_109	LLLYLLITLLFSLLVALIL	-21.29	0.3 ± 0.05	NA
R_110	LLYSLLALLFALLVTFLIL	-21.29	0.27 ± 0.05	NA
R_111	LLLYSLLVALFTLLIL	-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	LLYSLLITLLFVLLALIL	-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	LLLYILLSVLLALLTFIL	-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	LLLYALLTSLLVALFLSIL	-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	LLYTLLVSLLFALLLIL	-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	LLLFVLLATLAYLSSLLIL	-23.75	0.36 ± 0.03	-2.07 ± 0.14
R_129	LLLYSLLVALFALLTIL	-23.75	0.37 ± 0.07	-2.16 ± 0.4
R_130	LLLYLLAVLAPLLTSIL	-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	LLLYLLVTLLFALLSIL	-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	LLLYLLATLLFVLLSLLIL	-22.94	0.21 ± 0.12	NA
R_138	LLLYAALLLVSLLEFTLIL	-22.59	0.38 ± 0.06	-2.2 ± 0.38
R_139	LLLYVLLAALLTALLSILIL	-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>LLLYTLLVALSTLLFLL</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>LLLVYLLLAFLLLSLL</b> LILI	-19.07	0.47 ± 0.06	-2.68 ± 0.36
R_146	<b>LLLYVLLTAFLFALLSLL</b> LILI	-19.06	0.32 ± 0.06	-0.98 ± 0.18
R_147	<b>LLLLTLLIAVALLSFL</b> LILI	-18.94	0.34 ± 0.07	-1.8 ± 0.37
R_148	<b>LLLFVLLTTLAAILLSFL</b> LILI	-18.76	0.22 ± 0.02	NA
R_149	<b>LLLYFLLAVALAVLLTLL</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>LLLYIILLVALATLLTLL</b> LILI	-18.48	0.34 ± 0.11	-1.84 ± 0.61
R_154	<b>LLLYLILLTVLAFPLSIL</b> LILI	-18.43	0.27 ± 0.05	NA
R_155	<b>LLLTYLVALVALIAALSL</b> LILI	-18.14	0.36 ± 0.02	-2.0 ± 0.09
R_156	<b>LLLAVALVALSTLLIFL</b> LILI	-18.12	0.39 ± 0.06	-2.31 ± 0.37
R_157	<b>LLTYLLIAVALLAFLFV</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>LLLALLLFALLTVLLSIL</b> LILI	-18.52	0.44 ± 0.02	-2.59 ± 0.13
R_160	<b>LLYSILLVALAVLTL</b> LILI	-17.72	0.31 ± 0.22	0.32 ± 0.23
R_161	<b>LLLAAILLTLLFVLLSFL</b> LILI	-19.44	0.33 ± 0.06	-1.49 ± 0.26
R_162	<b>LLTYLLVALTFPLSFL</b> LILI	-19.5	0.59 ± 0.25	-3.04 ± 1.29
R_163	<b>LLLAVALLTLLFTLSSYL</b> LILI	-20.37	0.21 ± 0.11	NA
R_164	<b>LLLYSILLVALFLLLATL</b> LILI	-20.33	0.28 ± 0.1	NA
R_165	<b>LLLYSILLTLLAAILVF</b> LILI	-20.13	0.23 ± 0.08	NA
R_166	<b>LLLYLILLVALVALSFL</b> LILI	-20.11	0.3 ± 0.05	NA
R_167	<b>LLYTLLVALFLLSFL</b> LILI	-20.05	0.27 ± 0.1	NA
R_168	<b>LLLFYLLTALLIAALSL</b> LILI	-20	0.38 ± 0.03	-2.23 ± 0.15
R_169	<b>LLLYWLLVALLLALLSFL</b> LILI	-19.98	0.36 ± 0.01	-2.06 ± 0.04
R_170	<b>LLLYIILLFTLLVALLSFL</b> LILI	-19.46	0.19 ± 0.06	NA
R_171	<b>LLLFALLTILVALYLLSFL</b> LILI	-19.95	0.4 ± 0.06	-2.34 ± 0.34
R_172	<b>LLLYAVALVALLTLLSFL</b> LILI	-19.84	0.27 ± 0.04	NA
R_173	<b>LLYSILLFTLLAVLIALL</b> LILI	-19.77	0.32 ± 0.1	-1.4 ± 0.42
R_174	<b>LLLYWLLVALVALSFL</b> LILI	-19.77	0.3 ± 0.04	NA
R_175	<b>LLLALLLIAFLFVLLSFL</b> LILI	-19.62	0.27 ± 0.05	NA
R_176	<b>LLLYTLLVSLLAAILTLL</b> LILI	-19.61	0.33 ± 0.09	-1.58 ± 0.45
R_177	<b>LLLFTYLLTALLTLLVL</b> LILI	-19.54	0.31 ± 0.09	NA
R_178	<b>LLLSYLLVFLALLLATL</b> LILI	-19.53	0.48 ± 0.07	-2.74 ± 0.39
R_179	<b>LLLTYLLAVALVSLLFT</b> LILI	-19.87	0.47 ± 0.09	-2.68 ± 0.54
R_180	<b>LLLYVLLATLLTFLLSFL</b> LILI	-9.81	0.29 ± 0.02	NA

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

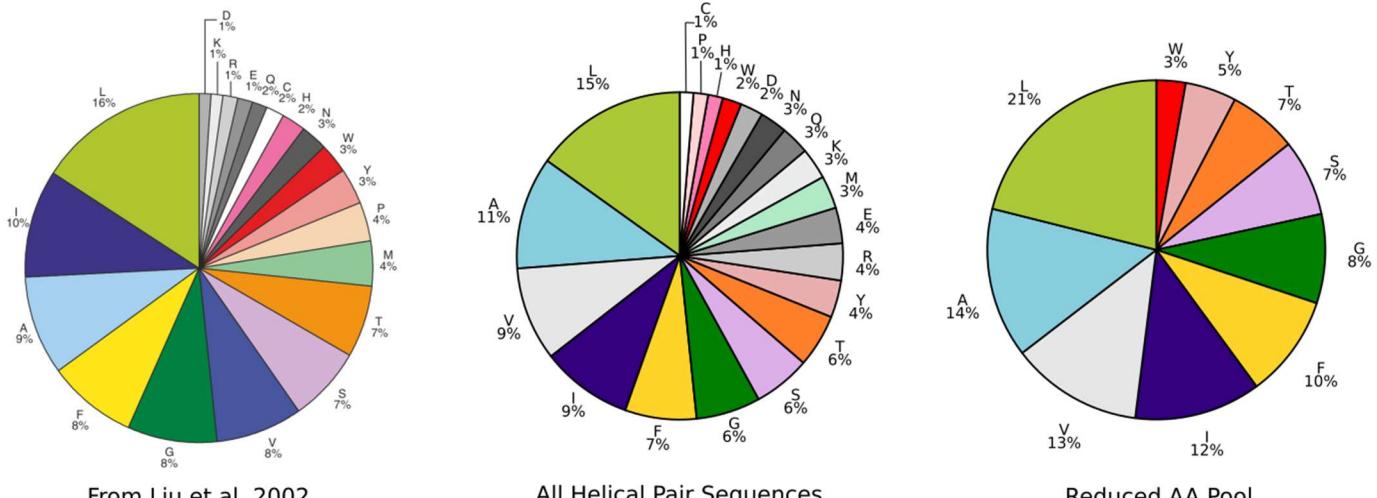
Interfacial designed positions of each sequence in bold

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>I</b> <b>I</b>	
L4	LLL <b>L</b> LL <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> LL <b>L</b> <b>L</b> <b>L</b> <b>A</b> <b>L</b> <b>I</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> LL <b>F</b> <b>A</b> <b>L</b> <b>L</b> <b>A</b> <b>L</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> LL <b>A</b> <b>I</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> LL <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

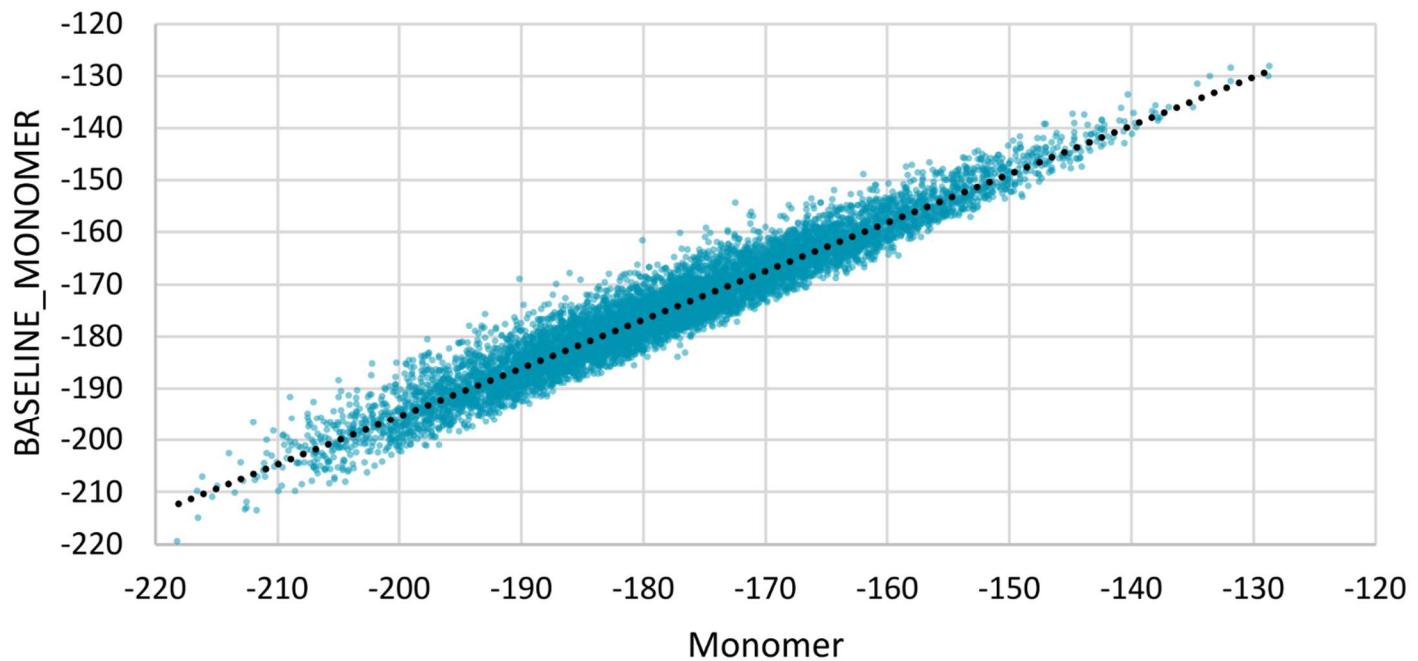
**Figure S1. Immunoblotting of designed constructs.** A subset of designed constructs were verified for their expression levels with western blots. While GAS<sub>right</sub> and Left show similar levels of expression, Right designs often have fainter bands on western blots. Sequences without a Design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



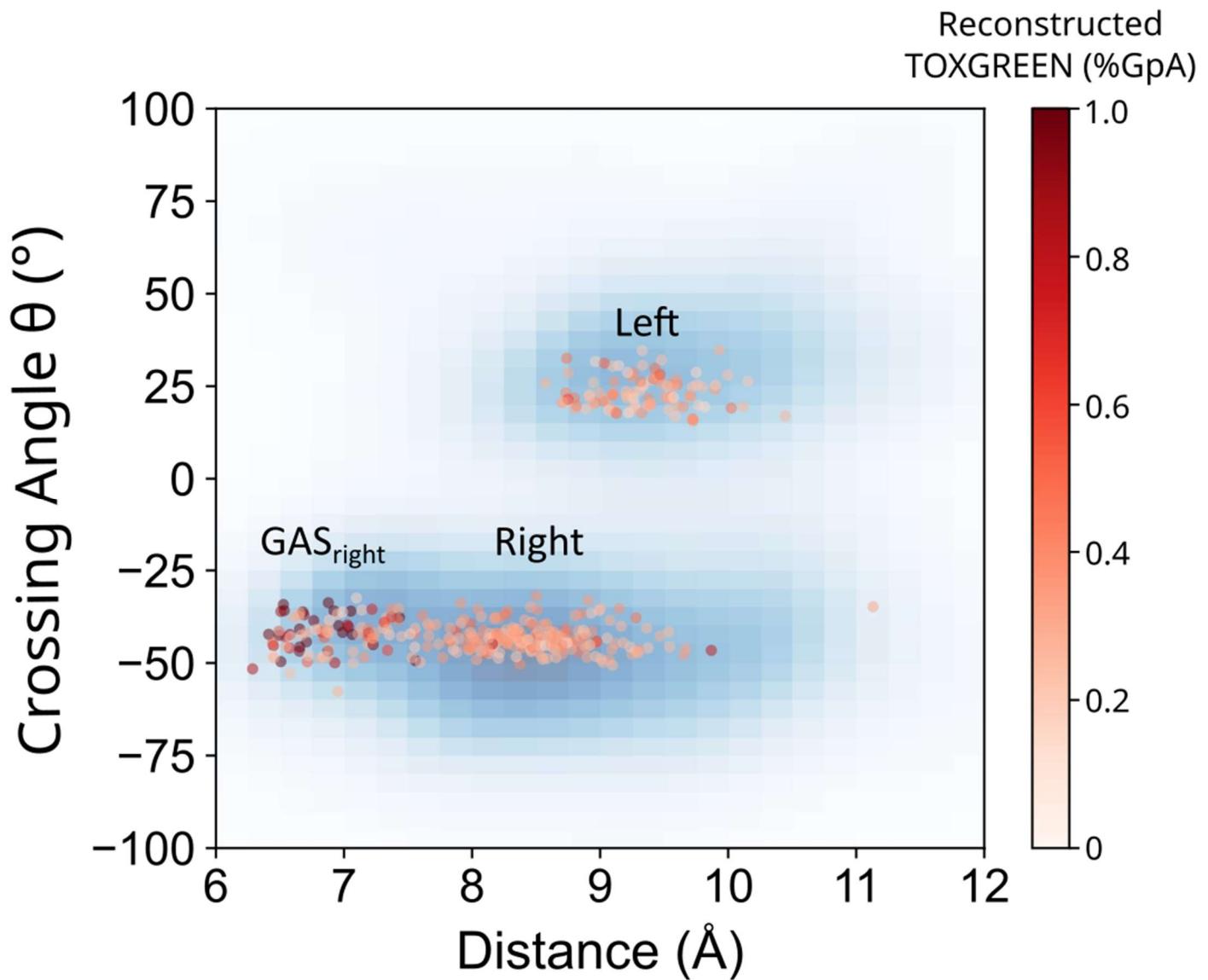
**Figure S2. Amino acid composition.** Frequency of amino acids from all transmembrane helical sequences extracted from OPM (Middle) as compared to membrane proteins from Liu et al. 2002 (Left). The frequency of the reduced pool of amino acids used for design (Right). Sequences were designed with interfaces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

$$y = 0.9307x - 9.2759$$

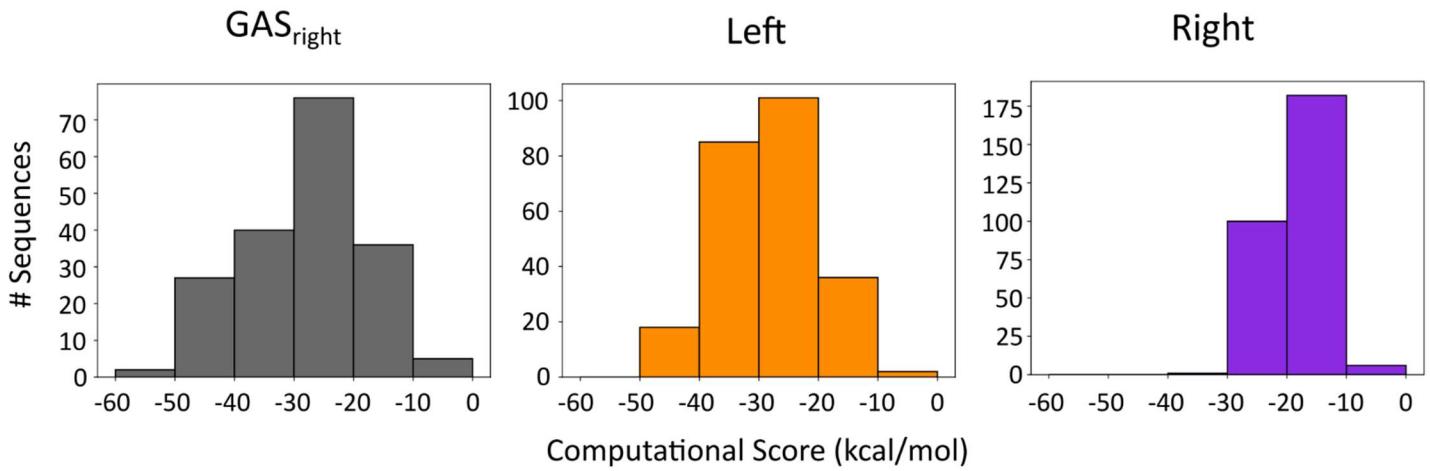
$$R^2 = 0.9273$$



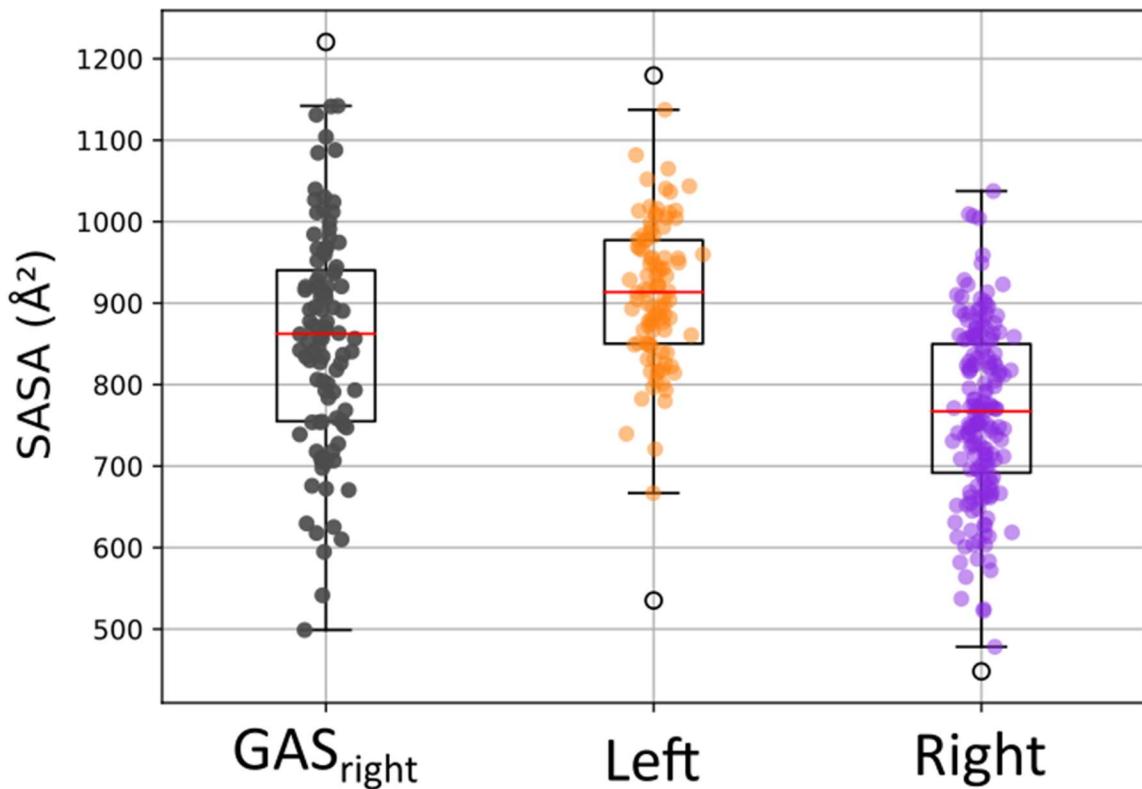
**Figure S3. BASELINE\_MONOMER.** Calculated monomer energy as compared to the estimated term BASELINE\_MONOMER used in the sequence design search.



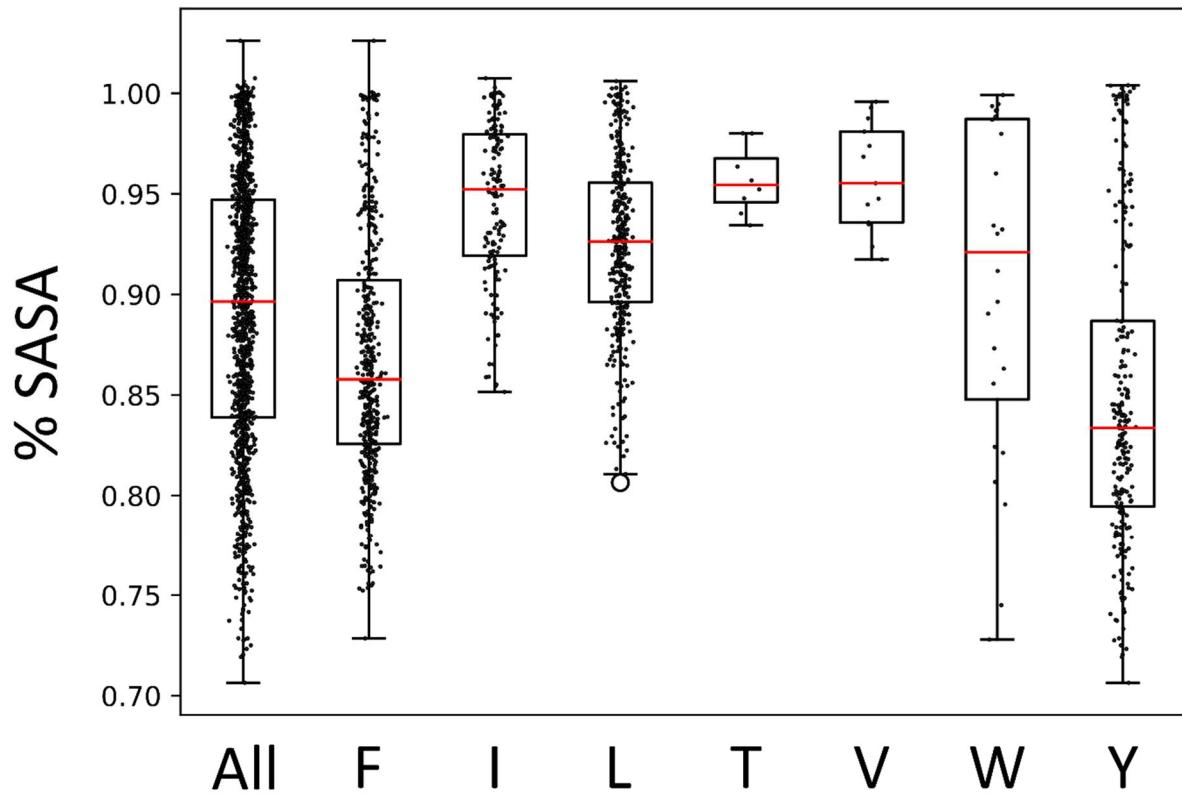
**Figure S4. Output Geometry vs Dimerization Propensity.** Distance and crossing angle of validated designed sequences plotted against %GpA in red. Sequences with highest dimerization propensity are dark red, most often found in GAS<sub>right</sub>.



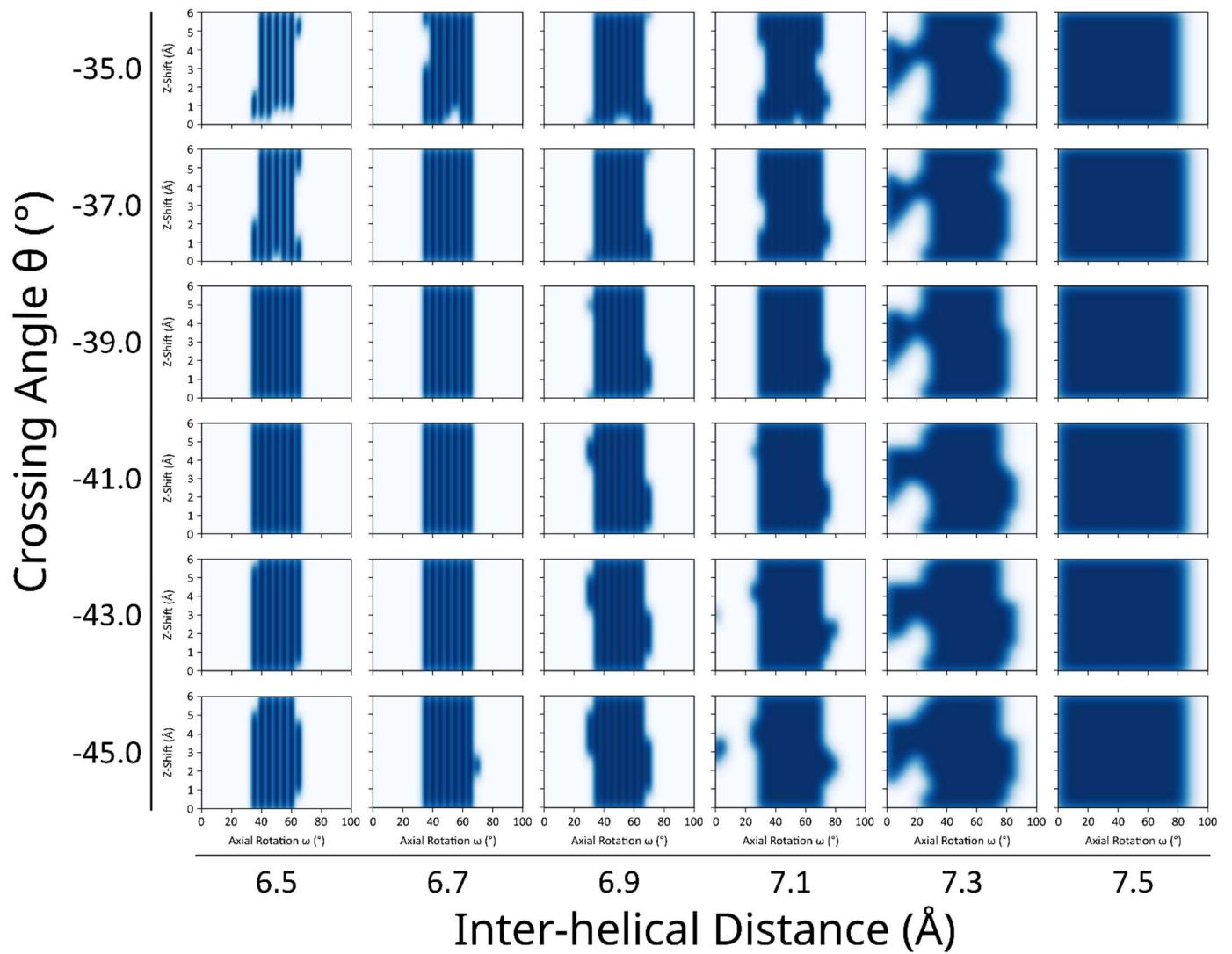
**Figure S5. Frequency of sequences by computational score.** Computational energy score of sequences present in sort-seq and the frequency for each design region.



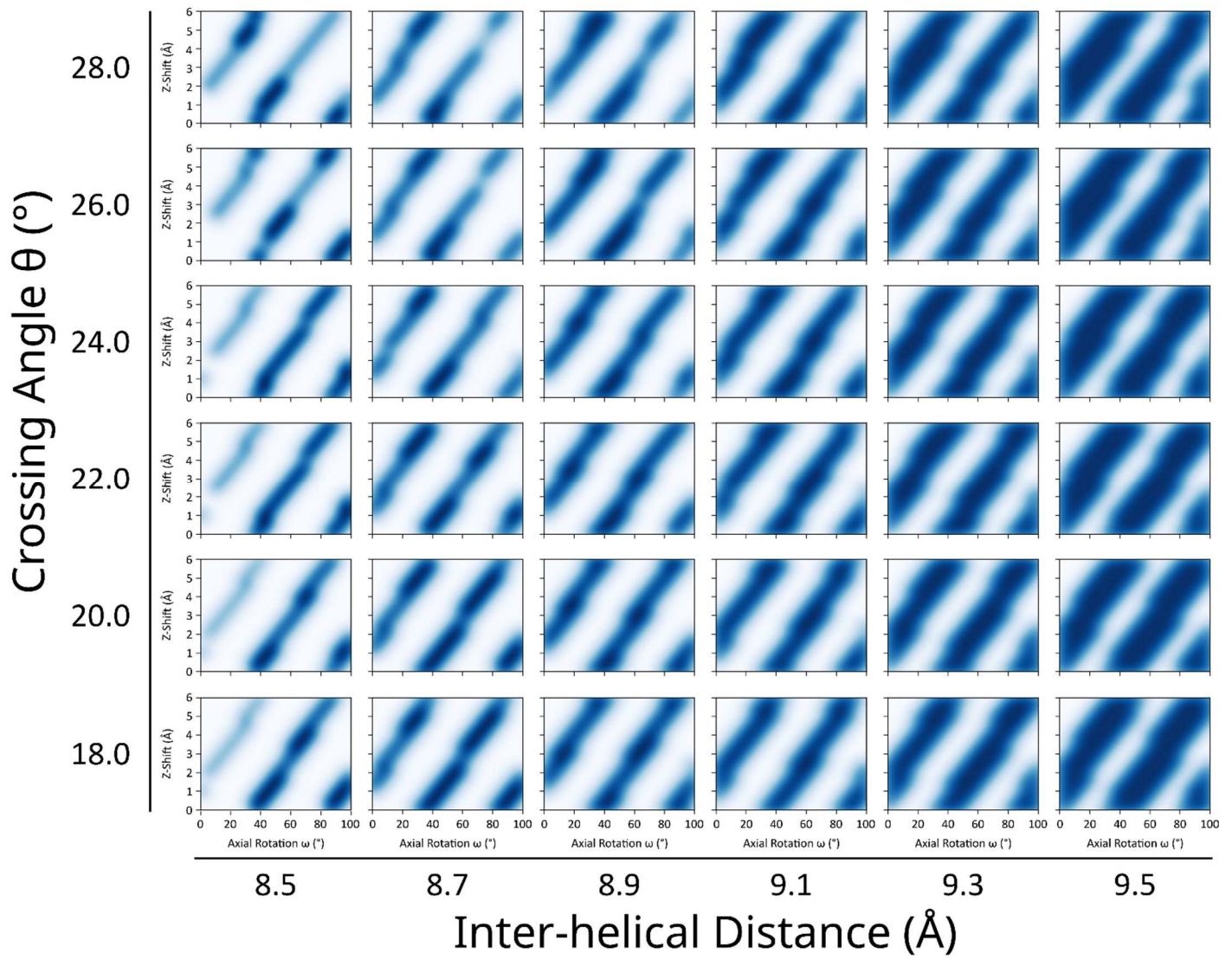
**Figure S6. Interface SASA.** Boxplots of calculated SASA at the interface of design structures of validated sequences. GAS<sub>right</sub> and Left design interfaces are larger than Right, which may contribute to Right designs having a lower computational energy score.



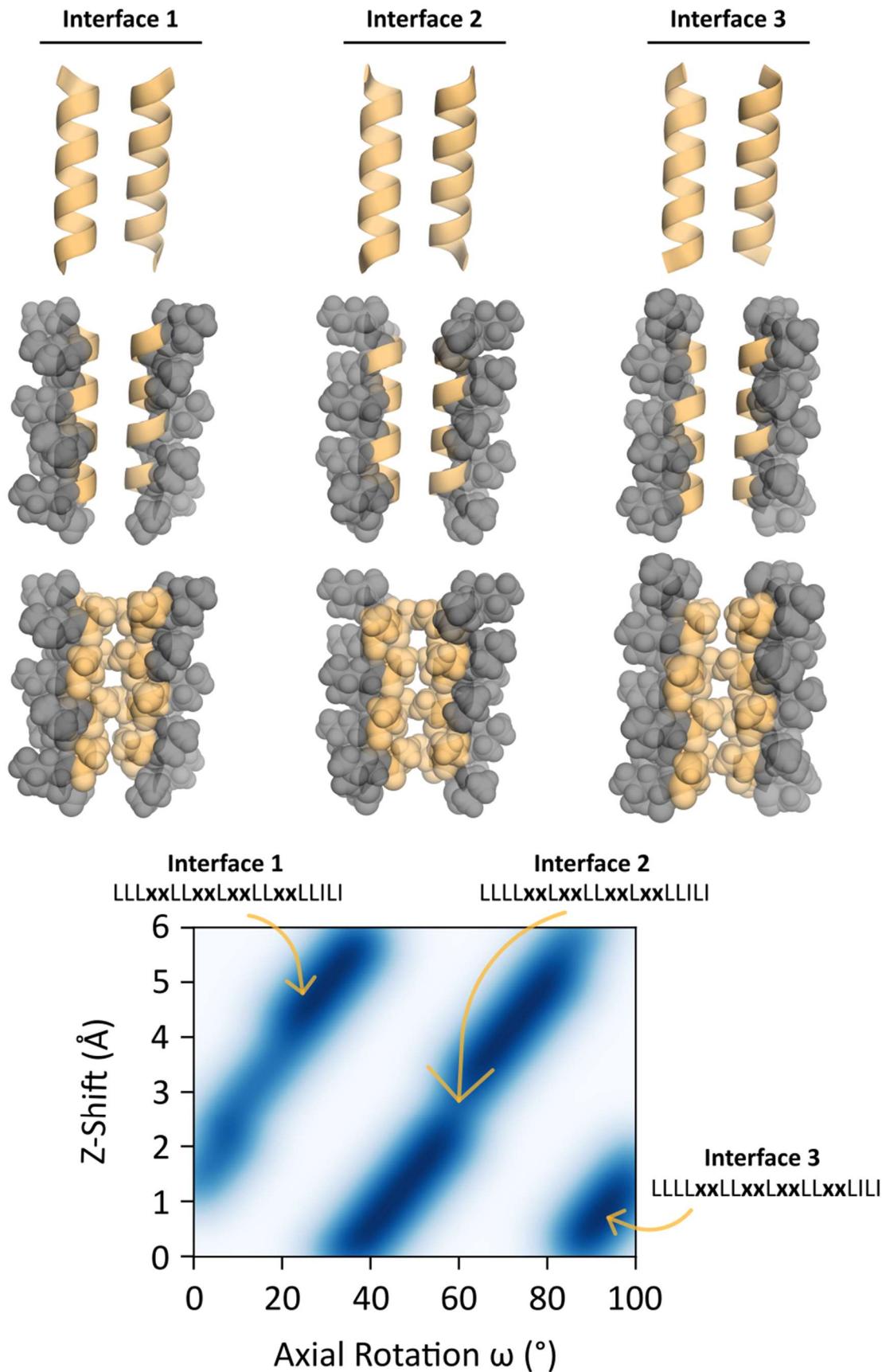
**Figure S7. % SASA of Large→Ala.** Single alanine point mutations were made on all interfacial positions designed structures. Mutants where the interface decreased the most, or the smallest % SASA (Design Interface SASA/Mutant Interface SASA x 100%), were selected.



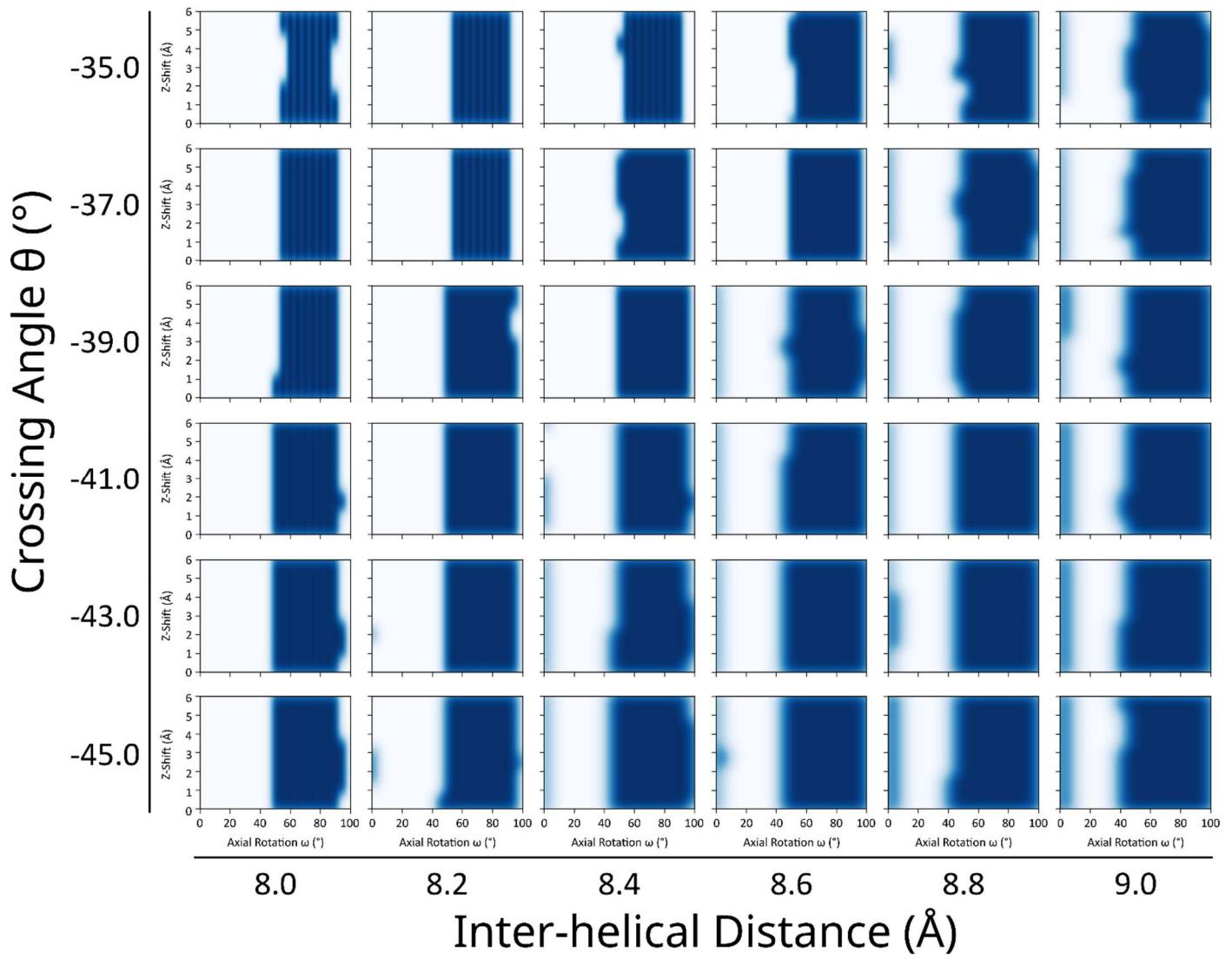
**Figure S8. GAS<sub>right</sub> axial rotations and z-shifts.** A 4-dimensional grid of geometries were randomly generated to determine axial rotations and z-shifts for design. Poly-leucine helices with Ala at the design interface positions were placed at 3000 geometries and computational energy score measured. Geometries where energy score < 10 kcal/mol were plotted on a KDE plot of Z-Shift vs Axial Rotation. Values with KDE > 0.8 were randomly selected for design.



**Figure S9. Left axial rotations and z-shifts.** A 4-dimensional grid of geometries were randomly generated to determine axial rotations and z-shifts for design. Poly-leucine helices with Ala at the design interface positions were placed at 3000 geometries and computational energy score measured. Geometries where energy score < 10 kcal/mol were plotted on a KDE plot of Z-Shift vs Axial Rotation. Values with KDE > 0.8 were randomly selected for design.



**Figure S10. Left interfaces.** Left-handed areas of high density were visually inspected to determine interfacial positions. Each design interface corresponds to a striped region of the axial rotation and z-shift density.



**Figure S11. Right axial rotations and z-shifts.** A 4-dimensional grid of geometries were randomly generated to determine axial rotations and z-shifts for design. Poly-leucine helices with Ala at the design interface positions were placed at 3000 geometries and computational energy score measured. Geometries where energy score < 10 kcal/mol were plotted on a KDE plot of Z-Shift vs Axial Rotation. Values with KDE > 0.8 were randomly selected for design.