

**Table S1. Validated set of GASright designs**

Design ID	Sequence	Computational Score (kcal/mol)	GpA (%)	ΔG (kcal/mol)
G_001	LLLTALLVGLLGGFLLLILI	-24.58	0.29 ± 0.05	NA
G_002	LLLFLLATLGLYLLSILILI	-31.69	0.42 ± 0.04	-2.49 ± 0.23
G_003	LLLLFLLGTLLGALLAYLILI	-31.69	1.15 ± 0.16	-3.85 ± 0.54
G_004	LLLVTLFLSLLGALLSLLILI	-17.19	0.48 ± 0.05	-2.74 ± 0.28
G_005	LLLYTLLGLLLGTLLASLILI	-32.08	0.31 ± 0.04	-0.52 ± 0.07
G_006	LLLVVLLTGLLGFLYLILI	-26.51	0.31 ± 0.08	-0.06 ± 0.01
G_007	LLLFALLSLLGILLLTLLILI	-26.35	0.19 ± 0.04	NA
G_008	LLLTFLLAFLVGLLGGFLILILI	-21.45	0.65 ± 0.11	-3.18 ± 0.53
G_009	LLLSFLLVVLLGLTLLAYLILI	-21.46	0.19 ± 0.07	NA
G_010	LLLYLLGALLGTLLSFLILLI	-32.9	0.53 ± 0.04	-2.9 ± 0.22
G_011	LLTVLFLGLLGLLGFLLILI	-32.92	0.54 ± 0.06	-2.93 ± 0.3
G_012	LLLYFLLGTLLGALLGLLILI	-33.02	0.81 ± 0.07	-3.44 ± 0.3
G_013	LLAVLVLTSLLGGFLFLILLI	-21.13	0.25 ± 0.04	NA
G_014	LLVTFLLLGLLFLFALLSLLILI	-26.16	0.25 ± 0.05	NA
G_015	LLTFLLGLLLGYLLSILILI	-33.27	1.23 ± 0.08	-3.93 ± 0.27
G_016	LLLYVLLGALGFLILLLTLLILI	-33.55	0.95 ± 0.1	-3.62 ± 0.39
G_017	LLLYFLLGVLGLTLLGFLILLI	-33.58	1.07 ± 0.03	-3.76 ± 0.11
G_018	LLYALLALLGLTLLGFLILLI	-16.12	0.19 ± 0.03	NA
G_019	LLYLALLASLLGFLILFLILLI	-34.17	0.15 ± 0.02	NA
G_020	LLYLGLLGALGFLTFLILLI	-34.32	1.12 ± 0.17	-3.82 ± 0.59
G_021	LLLTVLLGLLGFGLLFALLSLLILI	-22.26	0.5 ± 0.05	-2.81 ± 0.3
G_022	LLTVLALLLGLGFLGLSLLILI	-9.61	0.78 ± 0.07	-3.39 ± 0.3
G_023	LLYVLLTLLGLGALLGFLILLI	-22.36	0.26 ± 0.08	NA
G_024	LLYVLLGLLGLTLLFLFALLSLLILI	-34.97	0.32 ± 0.14	-1.25 ± 0.56
G_025	LLYFLLATLGLLGLGVLLILI	-35.12	0.36 ± 0.02	-2.02 ± 0.14
G_026	LLYGLLFALLGFLILLLTLLILI	-33.23	0.36 ± 0.05	-2.08 ± 0.29
G_027	LLTFLLATLGLLGLGVLLILI	-21.01	0.64 ± 0.05	-3.15 ± 0.26
G_028	LLAANALLGLGVLLTLLILI	-17.8	0.39 ± 0.04	-2.33 ± 0.22
G_029	LIAANLFSLLGLLGGFLILLI	-26.92	0.3 ± 0.09	NA
G_030	LLYALLTALLGGFLLLILI	-19.63	0.22 ± 0.06	NA
G_031	LLLITLVLGLFLFALLVGLLILI	-27.85	0.25 ± 0.02	NA
G_032	LLYIPLLGLLGLTLLFLFALLSLLILI	-28.2	0.25 ± 0.09	NA
G_033	LLLVLLATLGLGFLSILILI	-19.93	0.26 ± 0.05	NA
G_034	LLYGLFLALGFLILLLTLLILI	-28.27	0.28 ± 0.01	NA
G_035	LLSTLGLGALGFLFLAVLILI	-28.31	0.91 ± 0.09	-3.58 ± 0.36
G_036	LLYVLLFTLGLGALLGFLILLI	-27.82	0.22 ± 0.03	NA
G_037	LLYVLLATLGLLGLGFLLILI	-28.48	0.3 ± 0.06	NA
G_038	LLYLLGLTLLGFLILFLILLI	-19.35	0.43 ± 0.07	-2.55 ± 0.43
G_039	LLYGLFLFLLGVLVLLATLILI	-27.64	0.4 ± 0.04	-2.39 ± 0.22
G_040	LLYFLLATLGLGVLLFLFALLSLLILI	-19.14	0.34 ± 0.05	-1.8 ± 0.24
G_041	LLYVLLTLLGLAGLFLSLLILI	-20.09	0.17 ± 0.1	NA
G_042	LLTFLLALLLGLGFLSLLILI	-20.12	0.95 ± 0.14	-3.62 ± 0.52
G_043	LLVTLLLTLLGALLGSLLILI	-27.56	0.28 ± 0.03	NA
G_044	LLLTLLVALLAGLFLSLLILI	-20.31	0.31 ± 0.03	NA
G_045	LLYGLFLFLLGVLVLLSLLILI	-28.77	0.32 ± 0.06	-1.31 ± 0.23
G_046	LLYVLLALLLGLTLLGFLILLI	-27.25	0.18 ± 0.03	NA
G_047	LLTALLVGGLLGFLLFLILLI	-18.68	0.27 ± 0.02	NA
G_048	LLYVLLGAGLGVVLSTLLILI	-24.54	0.84 ± 0.22	-3.48 ± 0.9
G_049	LLLIALLFALGFLILLLTLLILI	-18.68	0.25 ± 0.12	NA
G_050	LLYFLLAVLGLLGGFLILLI	-29.4	0.28 ± 0.06	NA
G_051	LLYGLFLALGFLTLLSLLILI	-29.53	0.19 ± 0.01	NA
G_052	LLLVALLALLLGTLLSFLILLI	-27.01	0.28 ± 0.05	NA
G_053	LLYLLGLGALGFLILLLTLLILI	-29.9	0.75 ± 0.08	-3.35 ± 0.34
G_054	LLTFLLAVLGLLGLGSLLILI	-27.01	0.6 ± 0.14	-3.08 ± 0.7
G_055	LLYALLFLLLGTLLSILILI	-15.45	0.17 ± 0.05	NA
G_056	LLYFLLLALLLGTLLGSLILLI	-35.41	0.23 ± 0.02	NA
G_057	LLTALLFLGLGVLLASLILLI	-16.15	0.82 ± 0.11	-3.45 ± 0.45
G_058	LLLAGLFLPLLGVLVLLATLILI	-22.42	0.33 ± 0.01	-1.62 ± 0.03
G_059	LLYVLLATLGLGFLFLILLI	-23.03	0.21 ± 0.06	NA
G_060	LLTALLLALLFLGFLSLLILI	-13.75	0.38 ± 0.03	-2.21 ± 0.2
G_061	LLVVLTTLLGGFLFLFALLSLLILI	-13.73	0.32 ± 0.04	-0.98 ± 0.12
G_062	LLAYLGLTLLGLLGLFLLILI	-45.74	1.14 ± 0.15	-3.83 ± 0.49
G_063	LLVVLATLGLSLLGFLILLI	-13.7	0.31 ± 0.07	-0.17 ± 0.04
G_064	LLALLLGLLGLTLLSFLILLI	-45.31	1.04 ± 0.05	-3.72 ± 0.18
G_065	LLLVLLTLLGLLGLFALLSLLILI	-25.32	0.29 ± 0.04	NA
G_066	LLAYLGLLGLGFLGFLTLLILI	-39.49	1.11 ± 0.11	-3.81 ± 0.37
G_067	LLYTLLATLGLLGLGSLLILI	-44.96	0.24 ± 0.03	NA
G_068	LLTSLLVGLLGLLGLSLLILI	-11.56	0.41 ± 0.02	-2.45 ± 0.09
G_069	LLAYLGLVLLAYLGLLGLSLLILI	-35.55	1.12 ± 0.09	-3.81 ± 0.31
G_070	LLYFLLLAVLGLLGLGSLLILI	-23.94	0.25 ± 0.15	NA
G_071	LLSYLGLVLLGLLGGFLILLI	-44.36	0.95 ± 0.08	-3.62 ± 0.32
G_072	LLALLLGLTLLGFLSLLILI	-43.23	1.26 ± 0.1	-3.96 ± 0.31
G_073	LLTALLAGLFLFLSLLVLLILI	-13.06	0.31 ± 0.02	-0.87 ± 0.05
G_074	LLSYLGLVLLGLLFLATLILI	-41.31	1.03 ± 0.11	-3.71 ± 0.41
G_075	LLSYLGLVLLGLTLLGFLILLI	-42.81	0.79 ± 0.12	-3.4 ± 0.5
G_076	LLSYLGLLGLGFLTLLSFLILLI	-42.79	0.83 ± 0.06	-3.47 ± 0.24
G_077	LLYLLGLGALFLFLSTLLILI	-25.05	0.18 ± 0.01	NA
G_078	LLTYLGLGVLLGLLGLFLLILI	-42.23	0.87 ± 0.19	-3.52 ± 0.76
G_079	LLVVLGLGALGFLSFLILLI	-24.93	0.44 ± 0.07	-2.6 ± 0.39
G_080	LLAYLGLVLLGLLGLGSLLILI	-41.95	1.11 ± 0.12	-3.81 ± 0.41
G_081	LLALLLGVLLGLTLLGFLILLI	-38.02	0.95 ± 0.12	-3.62 ± 0.44
G_082	LLSYLGLLGLGFLSLLILI	-38.42	1.09 ± 0.18	-3.78 ± 0.62
G_083	LLYLLLGLLGLFLSTLLSFLILLI	-48.02	1.11 ± 0.17	-3.8 ± 0.58
G_084	LLYSLLFLALGFLGALTLFLILLI	-24.61	0.36 ± 0.04	-1.99 ± 0.22
G_085	LLFVLLTLLFLGALSLILLI	-15.06	0.25 ± 0.05	NA
G_086	LLYTLLVALLGLLGLLFLILLI	-22.53	0.33 ± 0.05	-1.44 ± 0.22
G_087	LLYSLLALLLGLTLLGFLILLI	-22.59	0.15 ± 0.05	NA
G_088	LLIALLTLVLLGGFLSLLILI	-25.5	0.26 ± 0.04	NA
G_089	LLTSLLLGLLGLFALLYLLILI	-24.73	0.22 ± 0.13	NA
G_090	LLYLLGLLGLTLLFLFALLSLLILI	-36.83	0.53 ± 0.04	-2.9 ± 0.2
G_091	LLVTLLFLGLFLFALLSLLILI	-22.79	0.83 ± 0.23	-3.47 ± 0.95
G_092	LLYIPLLTLGLGALLAFLILLI	-6.71	0.29 ± 0.14	NA
G_093	LLFYLGLGVLLGLLGLSILILI	-47.35	0.92 ± 0.1	-3.58 ± 0.39
G_094	LLYVLLFLLLGFLGALLTFLILLI	-25.05	0.17 ± 0.02	NA
G_095	LLTLLLGLLGLVLLGSLLILI	-37.29	0.91 ± 0.21	-3.57 ± 0.83
G_096	LLALLLGLLGLGVLLGSLLILI	-37.44	1.04 ± 0.21	-3.73 ± 0.74
G_097	LLTVLFLGLLGLFALLYLLILI	-37.57	0.71 ± 0.06	-3.28 ± 0.25
G_098	LLSSLLFLLLGFLVLLTLLILI	-6.06	0.3 ± 0.06	NA
G_099	LLVLLFLGLLGLFALLYLLILI	-14.18	0.25 ± 0.07	NA
G_100	LLAVLFLSLLGLLGLSLLILI	-22.9	0.27 ± 0.04	NA
G_101	LLTALLFLFLGLVLLGSLLILI	-13.97	0.72 ± 0.06	-3.29 ± 0.27
G_102	LLAGLFLPLLGFLFLSYLILLI	-25.42	0.14 ± 0.02	NA
G_103	LLYVLLGLLGLGFLFLLSFLILLI	-52.21	1.04 ± 0.05	-3.72 ± 0.19
G_104	LLAFLGLTLLGVLLGLLGLSLLILI	-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	LLLLLLTALLFVLSLIL	-24.86	0.23 ± 0.09	NA
L_002	LLLLVLIALLTFLFSLIL	-19.91	0.28 ± 0.05	NA
L_003	LLLVALLLTFLASLIL	-19.85	0.35 ± 0.06	-1.97 ± 0.35
L_004	LLLLFVLTILLALLYSLLIL	-27.78	0.19 ± 0.1	NA
L_005	LLLAYLALLFLFLSLLIL	-24.92	0.32 ± 0.07	-1.18 ± 0.27
L_006	LLLYALFVLTALLSLLIL	-20.96	0.49 ± 0.08	-2.78 ± 0.45
L_007	LLLYVLLATLALLSFLIL	-20.52	0.28 ± 0.08	NA
L_008	LLLAIDLTLAVLFSLIL	-25.76	0.61 ± 0.06	-3.09 ± 0.3
L_009	LLLVALLLFLFLTSLLIL	-22.22	0.48 ± 0.23	-2.75 ± 1.31
L_010	LLLYFLAILVTLLSLLIL	-22.59	0.19 ± 0.11	NA
L_011	LLLFLALLAVLTSLLIL	-19.85	0.15 ± 0.05	NA
L_012	LLLAVALFLFLATLISLLIL	-26.1	0.22 ± 0.05	NA
L_013	LLLLLFLFLAVLSTLIL	-26.11	0.16 ± 0.05	NA
L_014	LLLYVLATLFLSLLIL	-21.98	0.41 ± 0.16	-2.44 ± 0.94
L_015	LLLLLVALFLFLTSLLIL	-26.31	0.41 ± 0.26	-2.4 ± 1.54
L_016	LLLYFLALLAVLTSLLIL	-21.69	0.27 ± 0.09	NA
L_017	LLLYLLTVLALLFSLLIL	-21.39	0.23 ± 0.06	NA
L_018	LLLLLALLALIVLFLSLLIL	-21.35	0.47 ± 0.12	-2.7 ± 0.69
L_019	LLLVLLTFLFLSLLIL	-26.56	0.23 ± 0.04	NA
L_020	LLLYLLFLFLAVLSTLIL	-23.39	0.21 ± 0.09	NA
L_021	LLLLFFLATLILLSVLIL	-21.08	0.25 ± 0.05	NA
L_022	LLLYLVALVITALFLSLLIL	-21.06	0.27 ± 0.09	NA
L_023	LLLYVLLALFLFLTSLLIL	-25.06	0.18 ± 0.12	NA
L_024	LLVTILLALLFLSLLIL	-20.94	0.27 ± 0.06	NA
L_025	LLLYALLFLFLATLISLLIL	-26.79	0.45 ± 0.14	-2.61 ± 0.83
L_026	LLLLLFLFLAVLTSLLIL	-26.85	0.23 ± 0.07	NA
L_027	LLLFLLVLLTALLYLIL	-20.71	0.23 ± 0.05	NA
L_028	LLLTILLVLLALLSFLIL	-26.94	0.23 ± 0.19	NA
L_029	LLLFLLIAILVLLSTLIL	-23.7	0.21 ± 0.05	NA
L_030	LLLYVLLALFLFLTSLLIL	-23.75	0.23 ± 0.07	NA
L_031	LLLAVALFLFLALTSLLIL	-27.1	0.41 ± 0.08	-2.45 ± 0.5
L_032	LLLVALLTFLALFTSLLIL	-27.98	0.41 ± 0.15	-2.45 ± 0.88
L_033	LLVSLLILTALLFLSLLIL	-22.28	0.35 ± 0.11	-1.89 ± 0.59
L_034	LLLFALLTFLVALLSLLIL	-28.01	0.36 ± 0.05	-2.09 ± 0.26
L_035	LLLAVALTALLFLSLLIL	-36.08	0.21 ± 0.13	NA
L_036	LLLYVLTALLFLSLLIL	-35.8	0.26 ± 0.1	NA
L_037	LLLVLLTFLFLSLLIL	-34.96	0.21 ± 0.09	NA
L_038	LLLYLVLSSLILTFLSLLIL	-34.36	0.48 ± 0.16	-2.75 ± 0.89
L_039	LLIVSLLILTALLFLSLLIL	-34.32	0.41 ± 0.11	-2.42 ± 0.67
L_040	LLLAYLTVLISLFLSLLIL	-16.04	0.38 ± 0.08	-2.25 ± 0.48
L_041	LLLAAILLALFLSLLIL	-34.1	0.3 ± 0.1	NA
L_042	LLLFVLLLALLATLISLLIL	-36.31	0.27 ± 0.08	NA
L_043	LLLYTFLAVLALLSLLIL	-16.38	0.44 ± 0.09	-2.56 ± 0.52
L_044	LLLFILLAVLFLTSLLIL	-32.64	0.22 ± 0.13	NA
L_045	LLVAFLFLSLLTFLSLLIL	-32.59	0.27 ± 0.08	NA
L_046	LLLVLLAALFTSLLIL	-32.33	0.29 ± 0.07	NA
L_047	LLVALFLFLSLLTFLSLLIL	-27.98	0.21 ± 0.07	NA
L_048	LLLFILLAVLFLSLLIL	-32.17	0.32 ± 0.14	-1.14 ± 0.51
L_049	LLLSYLLAVLFTLIL	-32.13	0.34 ± 0.08	-1.82 ± 0.4
L_050	LLLFLLAALTVLISLIL	-32.09	0.33 ± 0.1	-1.46 ± 0.44
L_051	LLYFLFLAVLITLSSLIL	-33.12	0.18 ± 0.09	NA
L_052	LLLTYYLAIIFVLLSLLIL	-32.09	0.25 ± 0.12	NA
L_053	LLVLLLAIFFLTSLLIL	-36.54	0.24 ± 0.09	NA
L_054	LLLYTFLAVLALLSLLIL	-14.73	0.15 ± 0.05	NA
L_055	LLYALLLTFLIVLFSLLIL	-8.65	0.55 ± 0.3	-2.94 ± 1.59
L_056	LLLLLLAVLTAFLFIL	-44.72	0.28 ± 0.06	NA
L_057	LLLVALLLTSFLFLSLLIL	-44.48	0.48 ± 0.05	-2.72 ± 0.26
L_058	LLYALLLVIITFLSLLIL	-11.73	0.35 ± 0.12	-1.95 ± 0.64
L_059	LLLFALLTFLTALLYLIL	-12.21	0.37 ± 0.12	-2.12 ± 0.69
L_060	LLLFYLTALLFLSLLIL	-12.34	0.28 ± 0.15	NA
L_061	LLLVALLLTTFLFLSLLIL	-41.95	0.43 ± 0.16	-2.53 ± 0.93
L_062	LLLAAILLAVLFLFLSLLIL	-36.63	0.25 ± 0.11	NA
L_063	LLLLLALLFLVLTSLYLIL	-41.84	0.41 ± 0.04	-2.44 ± 0.24
L_064	LLLYVLTALLFLSLLIL	-13.11	0.36 ± 0.29	-2.08 ± 1.65
L_065	LLLYWLTIIFLFLSLLIL	-40.46	0.4 ± 0.13	-2.34 ± 0.77
L_066	LLLYSLTALLFVLLLIL	-39.3	0.27 ± 0.06	NA
L_067	LLLTVLLALLFLSLLIL	-38.49	0.2 ± 0.12	NA
L_068	LLLVALLLTTSLFLSLLIL	-37.95	0.27 ± 0.11	NA
L_069	LLLFVLLAIFLFLSLLIL	-37.79	0.35 ± 0.08	-1.89 ± 0.41
L_070	LLLFALLLTVLFLSLLIL	-36.99	0.29 ± 0.07	NA
L_071	LLLFWFLAVLFLSLLIL	-41.58	0.38 ± 0.06	-2.23 ± 0.37
L_072	LLLVALLLTFLLFLSLLIL	-32.06	0.26 ± 0.03	NA
L_073	LLLVALLLTFLLFLSLLIL	-32.21	0.28 ± 0.08	NA
L_074	LLLSYLVLLAVLFTLIL	-31.72	0.37 ± 0.28	-2.18 ± 1.61
L_075	LLLVLLVLAIFLFLSLLIL	-29.41	0.24 ± 0.1	NA
L_076	LLLYWLTIIFLVALLSFLIL	-29.15	0.42 ± 0.06	-2.5 ± 0.34
L_077	LLLYLLAVLTSFLFLSLLIL	-28.74	0.14 ± 0.1	NA
L_078	LLLAAILLFLVFLSLLIL	-28.66	0.24 ± 0.07	NA
L_079	LLLLFLTALLYLFLSLLIL	-28.61	0.28 ± 0.27	NA
L_080	LLLYVLLAIFLFLSLLIL	-19.09	0.19 ± 0.11	NA
L_081	LLLYLVALLFLVLLSFLIL	-29.49	0.26 ± 0.08	NA
L_082	LLLYFLFLAVLITLSSLIL	-19.2	0.16 ± 0.09	NA
L_083	LLLLALLLFLVFLSLLIL	-28.35	0.32 ± 0.1	-1.29 ± 0.41
L_084	LLLWTIALLVFLSLLIL	-28.25	0.32 ± 0.08	-1.09 ± 0.29
L_085	LLYALLFLFLTSFLSLLIL	-28.21	0.14 ± 0.08	NA
L_086	LLLLFLFLAVLFTLIL	-28.07	0.23 ± 0.04	NA
L_087	LLLYALLLFLVFLSLLIL	-28.03	0.22 ± 0.08	NA
L_088	LLYALFVLLFLTSFLSLLIL	-19.75	0.17 ± 0.07	NA
L_089	LLLAAILLFLVFLSLLIL	-28.43	0.18 ± 0.08	NA
L_090	LLLYLLALFLVFLSLLIL	-30	0.22 ± 0.02	NA
L_091	LLYALLFVLLFLSLLIL	-18.68	0.14 ± 0.05	NA
L_092	LLLAFLFLTSFLVFLSLLIL	-31.34	0.36 ± 0.04	-1.99 ± 0.22
L_093	LLLYWLLTVLFLASLIL	-17.52	0.28 ± 0.03	NA
L_094	LLLYFLFLAVLFLSLLIL	-31.23	0.47 ± 0.13	-2.7 ± 0.73
L_095	LLLAAILLFLVFLSLLIL	-30.54	0.35 ± 0.14	-1.89 ± 0.76
L_096	LLLAAILLFLVFLSLLIL	-17.48	0.53 ± 0.08	-2.89 ± 0.43
L_097	LLLAVALLFLFLTSFLSLLIL	-30.86	0.38 ± 0.2	-2.19 ± 1.14
L_098	LLLTVALLFLFLTSFLSLLIL	-30.91	0.29 ± 0.09	NA
L_099	LLYSLLLFLFLAVLFLSLLIL	-31.39	0.2 ± 0.18	NA
L_100	LLLAVALLFLFLTSFLSLLIL	-31.53	0.2 ± 0.02	NA

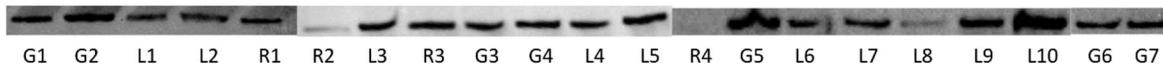
**Table S3. Validated set of Right designs**

Design ID	Sequence	Computational Score (kcal/mol)	GpA (%)	ΔG (kcal/mol)
R_001	LLYTLVLLVLLAFLLSLIL	-26.75	0.3 ± 0.07	NA
R_002	LLYSLLLTLLFVLLSLLIL	-30.22	0.3 ± 0.13	NA
R_003	LLYTLLIALFVLLSLLIL	-26.69	0.28 ± 0.04	NA
R_004	LLYSLLVALLFTLLFLLIL	-26.6	0.23 ± 0.1	NA
R_005	LLLSLFLALLTLLAVLTLIL	-24.71	0.29 ± 0.03	NA
R_006	LLYLLFTLLAVLTSLLIL	-8.79	0.3 ± 0.06	NA
R_007	LLYALLVALLFTLSSLIL	-24.88	0.26 ± 0.05	NA
R_008	LLTYLLFVLLAFLSSLLIL	-24.89	0.29 ± 0.1	NA
R_009	LLYTLISLLVALLEFLIL	-25.05	0.25 ± 0.1	NA
R_010	LLYTLLVSLLALLAFLSLLIL	-25.05	0.31 ± 0.07	0.43 ± 0.1
R_011	LLLYLLVALLSLLFTLIL	-25.89	0.39 ± 0.18	-2.33 ± 1.07
R_012	LLYSLLALFLFVLLTILIL	-27.63	0.3 ± 0.06	NA
R_013	LLLVLLTALLFTLSSLIL	-25.24	0.33 ± 0.04	-1.62 ± 0.21
R_014	LLSYLLVLLLAFLSTLIL	-25.39	0.35 ± 0.08	-1.9 ± 0.43
R_015	LLYTLLISLLFVLLAFLIL	-26.81	0.31 ± 0.08	0.25 ± 0.07
R_016	LLYFLVALLTLLSLLIL	-26.06	0.27 ± 0.09	NA
R_017	LLSYLLFVLLALLLTLIL	-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	LLWTLVLLFVLLAFLSLLIL	-29.79	0.29 ± 0.06	NA
R_020	LLSYLLFTLLAFLLTLLIL	-29.93	0.3 ± 0.09	NA
R_021	LLYSLLIALFVLTLIL	-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	LLYTLLIALFVLLFSLIL	-24.33	0.31 ± 0.18	-0.41 ± 0.24
R_025	LLFYLVLLVALLLSTLIL	-16.37	0.29 ± 0.14	NA
R_026	LLFYLVALLSLLTLLIL	-16.35	0.34 ± 0.05	-1.79 ± 0.24
R_027	LLYIALLATLAFLSLLIL	-16.29	0.27 ± 0.12	NA
R_028	LLFYLVALLFTLSSLIL	-16.26	0.4 ± 0.08	-2.36 ± 0.48
R_029	LLYALLTALLFTLVLIL	-16.15	0.3 ± 0.03	NA
R_030	LLYALLTTLSVLLFLLIL	-16.09	0.44 ± 0.07	-2.58 ± 0.43
R_031	LLTALLTALLFVLLSLLIL	-16.08	0.33 ± 0.01	-1.57 ± 0.04
R_032	LLYSLLTLLVALLFILIL	-15.9	0.24 ± 0.11	NA
R_033	LLYSLLALLATLFLSLLIL	-15.86	0.24 ± 0.07	NA
R_034	LLYVLTLLTLLALLSLLIL	-15.76	0.34 ± 0.13	-1.84 ± 0.72
R_035	LLYLLATLFLVLLSLLIL	-15.7	0.31 ± 0.03	-0.91 ± 0.1
R_036	LLYTLLIALLAVLSSLIL	-15.58	0.37 ± 0.05	-2.1 ± 0.31
R_037	LLYALLVALLTLLFLLIL	-15.3	0.3 ± 0.07	NA
R_038	LLFYLLTLLVALLSLLIL	-15.25	0.34 ± 0.09	-1.79 ± 0.49
R_039	LLYLLLATLFLAILSLLIL	-15.07	0.14 ± 0.06	NA
R_040	LLYLLLATLFLAVLSSLIL	-16.45	0.25 ± 0.07	NA
R_041	LLYSLLTLLLATLAFLIL	-16.53	0.21 ± 0.08	NA
R_042	LLVSLSLTLLTFLAYLIL	-16.54	0.29 ± 0.03	NA
R_043	LLTALLVALLAYLSSLIL	-16.55	0.5 ± 0.04	-2.81 ± 0.24
R_044	LLTYLVTLLAFLSLLIL	-17.5	0.41 ± 0.05	-2.44 ± 0.27
R_045	LLLVLLTLLTFLASSYLLIL	-17.49	0.32 ± 0.06	-1.37 ± 0.27
R_046	LLYLLTLLVALLSLLIL	-17.43	0.44 ± 0.05	-2.58 ± 0.31
R_047	LLYLLVTLTLLAFLSLLIL	-17.35	0.17 ± 0.09	NA
R_048	LLYSLVALLATLFLSLLIL	-17.33	0.26 ± 0.07	NA
R_049	LLAAILLVTLLFTLSSLIL	-17.29	0.36 ± 0.09	-1.99 ± 0.48
R_050	LLYALLTALLSVLLFLLIL	-17.19	0.37 ± 0.03	-2.1 ± 0.18
R_051	LLYIILTALLVALLSLLIL	-15.06	0.31 ± 0.05	-0.94 ± 0.15
R_052	LLFSLLTLLVALLSLLIL	-17.12	0.26 ± 0.08	NA
R_053	LLVYVLTLLTALLSLLIL	-16.69	0.37 ± 0.05	-2.14 ± 0.31
R_054	LLYSLLTLLVALLSLLIL	-16.68	0.29 ± 0.1	NA
R_055	LLYALLVALLTALLSLLIL	-16.67	0.35 ± 0.08	-1.96 ± 0.42
R_056	LLTALLIALLAVLSSLIL	-16.65	0.4 ± 0.06	-2.35 ± 0.38
R_057	LLAVLVLTTLLFALLSLLIL	-16.62	0.26 ± 0.06	NA
R_058	LLYIILTLLAVLSSLIL	-16.59	0.24 ± 0.04	NA
R_059	LLYFLVALLALLFTLIL	-16.58	0.32 ± 0.03	-1.1 ± 0.11
R_060	LLYIILTLLFALLVLLSLLIL	-17.06	0.26 ± 0.06	NA
R_061	LLYVLTLLATLFLSLLIL	-15.04	0.33 ± 0.06	-1.52 ± 0.29
R_062	LLYALLVALLSLLTFLIL	-15.04	0.35 ± 0.03	-1.87 ± 0.14
R_063	LLYSLLTALLVALLFLLIL	-14.78	0.29 ± 0.08	NA
R_064	LLTYLVLVLLATLFLSLLIL	-12.04	0.19 ± 0.12	NA
R_065	LLYVLLTALLFTLSSLIL	-11.97	0.26 ± 0.07	NA
R_066	LLYVLTLLTALLAFLIL	-11.94	0.32 ± 0.09	-1.38 ± 0.4
R_067	LLYLLSTLLAFLFLATLIL	-11.93	0.28 ± 0.04	NA
R_068	LLYVLLVLLAFLSFLIL	-11.69	0.41 ± 0.02	-2.4 ± 0.1
R_069	LLYLLFTLLAALLSLLIL	-11.61	0.12 ± 0.06	NA
R_070	LLYALLFALLSLLTFLIL	-11.25	0.27 ± 0.02	NA
R_071	LLYVLLVALLFLFLIL	-12.11	0.32 ± 0.07	-0.98 ± 0.21
R_072	LLYVLLTLLTFLASSSLLIL	-11.22	0.28 ± 0.08	NA
R_073	LLAALLSLLFTLFLVFLIL	-10.66	0.46 ± 0.05	-2.65 ± 0.27
R_074	LLYIILTLLAVLSSLIL	-10.64	0.24 ± 0.07	NA
R_075	LLYALLSLLTALLFLVFLIL	-10.61	0.28 ± 0.09	NA
R_076	LLTALLIALFLLSVLIL	-10.55	0.4 ± 0.04	-2.36 ± 0.25
R_077	LLYVLLFALLVLLSLLIL	-10.4	0.3 ± 0.02	NA
R_078	LLYSLFVLLAFLITLIL	-10.33	0.25 ± 0.1	NA
R_079	LLAYLVLVLLATLFLSLLIL	-10.19	0.34 ± 0.07	-1.71 ± 0.38
R_080	LLYVLLAFLTLLFLLSLLIL	-10.68	0.27 ± 0.1	NA
R_081	LLYIILTLLVLLFLSFLIL	-17.69	0.25 ± 0.07	NA
R_082	LLYVLLATLFLALLSFLIL	-12.44	0.26 ± 0.03	NA
R_083	LLYALLTLLVALLSFLIL	-12.82	0.25 ± 0.08	NA
R_084	LLYALLTLLSILVFLIL	-14.69	0.22 ± 0.04	NA
R_085	LLYALLIALFSLVTLIL	-14.68	0.3 ± 0.1	NA
R_086	LLLYLLTALLIAFLFVLIL	-14.55	0.27 ± 0.06	NA
R_087	LLLILLSTLLATLFLVFLIL	-14.36	0.23 ± 0.05	NA
R_088	LLYIILTLLVALLSFLIL	-14.33	0.28 ± 0.01	NA
R_089	LLIALLFLALLVSLLTFLIL	-14.2	0.3 ± 0.0	NA
R_090	LLTALLIALFLALLSLLIL	-14.11	0.36 ± 0.06	-2.01 ± 0.32
R_091	LLYVLLTALLLALLSFLIL	-12.66	0.33 ± 0.07	-1.51 ± 0.34
R_092	LLYVLLFTLLAALLSLLIL	-13.95	0.28 ± 0.06	NA
R_093	LLVYLLLALLTSLLFILIL	-13.89	0.39 ± 0.03	-2.3 ± 0.16
R_094	LLYSLLILLAVLFLFILIL	-13.86	0.24 ± 0.07	NA
R_095	LLTYLLVFLVLLALLSLLIL	-13.66	0.34 ± 0.09	-1.68 ± 0.45
R_096	LLYALLTLLSVLFLIL	-13.65	0.3 ± 0.07	NA
R_097	LLIALLVLLTLLAFLSFLIL	-13.32	0.17 ± 0.07	NA
R_098	LLTVLALLLALLAFLSLLIL	-12.94	0.35 ± 0.06	-1.9 ± 0.33
R_099	LLTYLLVALLIALFLFILIL	-12.88	0.37 ± 0.05	-2.12 ± 0.3
R_100	LLYVLLTLLTFLASSSLLIL	-13.89	0.3 ± 0.11	NA

R_101	LLLYWLLVALLISLTLI	-24.44	0.32 ± 0.03	-1.09 ± 0.09
R_102	LLLYLLLVALLATLLSFLILI	-17.7	0.22 ± 0.08	NA
R_103	LLLYFLLTLLAVLLSILILI	-17.85	0.48 ± 0.06	-2.74 ± 0.36
R_104	LLLYLFTLLAVLLSILILI	-22.18	0.36 ± 0.04	-2.01 ± 0.25
R_105	LLLYWLLTALLLSLFVLILI	-22.11	0.21 ± 0.05	NA
R_106	LLLYVLLTALLLSFLFLILI	-21.91	0.22 ± 0.12	NA
R_107	LLLYLVALLAILLSLILI	-21.41	0.28 ± 0.02	NA
R_108	LLLYSLLTLLAVLFLSFLILI	-21.39	0.21 ± 0.1	NA
R_109	LLLYLLITLLFSLVALILILI	-21.29	0.3 ± 0.05	NA
R_110	LLLYSLLALLLFALLTLLILI	-21.29	0.27 ± 0.05	NA
R_111	LLLYVLLVALLTLLFLFLILI	-21.29	0.28 ± 0.12	NA
R_112	LLLFSLLLTLLAALLSFLILI	-21.16	0.21 ± 0.07	NA
R_113	LLLYISSLTLALLAFLFLILI	-21.11	0.21 ± 0.04	NA
R_114	LLYSLLTLLFVLLFLFLILI	-20.93	0.25 ± 0.09	NA
R_115	LLYTLLATLLFLLSVLILI	-20.85	0.27 ± 0.11	NA
R_116	LLLYVLLFLLALLSTLFLILI	-20.83	0.22 ± 0.1	NA
R_117	LLLYLSSVLLALLTFLFLILI	-20.82	0.19 ± 0.08	NA
R_118	LLYTLLVALLFALLSLLILI	-20.72	0.3 ± 0.07	NA
R_119	LLLYYLLIALLFSLTLFLILI	-22.22	0.34 ± 0.04	-1.71 ± 0.23
R_120	LLYVALLTLLTFLSFLFLILI	-22.25	0.28 ± 0.15	NA
R_121	LLYVALLTLLVALFLFLILI	-22.5	0.34 ± 0.02	-1.73 ± 0.08
R_122	LLYSLLALLLFALLTLLFLILI	-22.52	0.45 ± 0.06	-2.6 ± 0.36
R_123	LLYTLLVSLLLTLLFLFLILI	-24.31	0.23 ± 0.06	NA
R_124	LLLYVLLTALLSLLFLFLILI	-24.25	0.37 ± 0.07	-2.17 ± 0.4
R_125	LLLYWLLVLLTALLSFLFLILI	-24.21	0.35 ± 0.07	-1.95 ± 0.39
R_126	LLYSLLTLLATLLFLFLILI	-24.19	0.21 ± 0.08	NA
R_127	LLYVLLATLLTLLSFLFLILI	-24.1	0.21 ± 0.11	NA
R_128	LLLFVLLATLLAYLLSLLILI	-23.75	0.36 ± 0.03	-2.07 ± 0.14
R_129	LLYSLLVALLFALLTLLFLILI	-23.75	0.37 ± 0.07	-2.16 ± 0.4
R_130	LLYLLVALVLAFLTSLLFLILI	-20.67	0.24 ± 0.09	NA
R_131	LLYSLLVFLATLLSLLFLILI	-23.6	0.39 ± 0.06	-2.32 ± 0.34
R_132	LLYSLLTLLALLAFLFLILI	-23.54	0.3 ± 0.08	NA
R_133	LLYSLLTLLFALLVILFLILI	-23.43	0.36 ± 0.02	-2.01 ± 0.12
R_134	LLYVLLATLLAFLSLLFLILI	-23.31	0.29 ± 0.06	NA
R_135	LLLYLVTLLVALFLSLLFLILI	-23.2	0.37 ± 0.07	-2.15 ± 0.4
R_136	LLLATLLISLFTLVLFLFLILI	-23.06	0.43 ± 0.09	-2.51 ± 0.56
R_137	LLYLFLATLLFVLLSLLFLILI	-22.94	0.21 ± 0.12	NA
R_138	LLYALLALLLVSLFLFLILI	-22.59	0.38 ± 0.06	-2.2 ± 0.38
R_139	LLYVLLALLTALLSLLFLILI	-23.55	0.36 ± 0.11	-2.07 ± 0.63
R_140	LLYVLLTALLFALLSLLFLILI	-20.62	0.39 ± 0.03	-2.31 ± 0.17
R_141	LLVYLLTLLFALLSLLFLILI	-20.57	0.43 ± 0.04	-2.51 ± 0.25
R_142	LLYVLLTVLLALLSFLFLILI	-20.38	0.26 ± 0.05	NA
R_143	LLYTLLVALLSTLLFLFLILI	-19.39	0.23 ± 0.09	NA
R_144	LLLTLLATLLVALFLSFLILI	-19.38	0.37 ± 0.03	-2.09 ± 0.16
R_145	LLVYLLALLFTLLSLLFLILI	-19.07	0.47 ± 0.06	-2.68 ± 0.36
R_146	LLYVLLTALLFALLSLLFLILI	-19.06	0.32 ± 0.06	-0.98 ± 0.18
R_147	LLLTLLALLLVALFLSFLILI	-18.94	0.34 ± 0.07	-1.8 ± 0.37
R_148	LLFVLLTLLVALFLSLLFLILI	-18.76	0.22 ± 0.02	NA
R_149	LLYFLLAILLAVLTLFLFLILI	-18.7	0.24 ± 0.06	NA
R_150	LLLTLLALLLFVLLSFLFLILI	-19.44	0.43 ± 0.06	-2.52 ± 0.34
R_151	LLVALLALLFALLSTLFLILI	-18.56	0.36 ± 0.04	-2.01 ± 0.23
R_152	LLVALLTLLAILLFLSFLILI	-18.48	0.28 ± 0.05	NA
R_153	LLYVLLVALLATLLTLLFLILI	-18.48	0.34 ± 0.11	-1.84 ± 0.61
R_154	LLYVLLTVLLAFLSLLFLILI	-18.43	0.27 ± 0.05	NA
R_155	LLTYLVALVALLSLLFLFLILI	-18.14	0.36 ± 0.02	-2.0 ± 0.09
R_156	LLYALLVALVALLSTLFLFLILI	-18.12	0.39 ± 0.06	-2.31 ± 0.37
R_157	LLTYLVALALLAFLFLFLILI	-18.08	0.4 ± 0.01	-2.35 ± 0.05
R_158	LLYSLLVALTLLFLSFLILI	-17.88	0.31 ± 0.13	-0.84 ± 0.34
R_159	LLYALLFALLTLLSLLFLILI	-18.52	0.44 ± 0.02	-2.59 ± 0.13
R_160	LLYVLLALLAFLVLTFLFLILI	-17.72	0.31 ± 0.22	0.32 ± 0.23
R_161	LLAAILLTLFLVLLSLLFLILI	-19.44	0.33 ± 0.06	-1.49 ± 0.26
R_162	LLTYLVALVALLSLLFLFLILI	-19.5	0.59 ± 0.25	-3.04 ± 1.29
R_163	LLAVLLTLLFTFLSLLFLILI	-20.37	0.21 ± 0.11	NA
R_164	LLYVLLVALFLFLVALFLFLILI	-20.33	0.28 ± 0.1	NA
R_165	LLYVLLTLLAALLVFLFLILI	-20.13	0.23 ± 0.08	NA
R_166	LLLYLVALVALLVALFLFLILI	-20.11	0.3 ± 0.05	NA
R_167	LLYTLLVALFLFLSLLFLILI	-20.05	0.27 ± 0.1	NA
R_168	LLYFLLTALLIALLSLLFLILI	-20	0.38 ± 0.03	-2.23 ± 0.15
R_169	LLYVLLVALVALLSLLFLFLILI	-19.98	0.36 ± 0.01	-2.06 ± 0.04
R_170	LLYVLLFTLLVALSLLFLFLILI	-19.46	0.19 ± 0.06	NA
R_171	LLYVLLTLLLAYLLSLLFLILI	-19.95	0.4 ± 0.06	-2.34 ± 0.34
R_172	LLYVLLVALVALLSLLFLFLILI	-19.84	0.27 ± 0.04	NA
R_173	LLYVLLFTLLVALLLFLFLILI	-19.77	0.32 ± 0.1	-1.4 ± 0.42
R_174	LLYVLLVALVALLSTLFLFLILI	-19.77	0.3 ± 0.04	NA
R_175	LLYALLVALFLVLLSLLFLFLILI	-19.62	0.27 ± 0.05	NA
R_176	LLYVLLVSLLAILLTLFLFLILI	-19.61	0.33 ± 0.09	-1.58 ± 0.45
R_177	LLYVLLTALLTLLVFLFLFLILI	-19.54	0.31 ± 0.09	NA
R_178	LLSYVLLVFLALLLATLFLFLILI	-19.53	0.48 ± 0.07	-2.74 ± 0.39
R_179	LLYVLLVALVALLSLLFLFLILI	-19.87	0.47 ± 0.09	-2.68 ± 0.54
R_180	LLYVLLTALLTFLSLLFLFLILI	-9.81	0.29 ± 0.02	NA

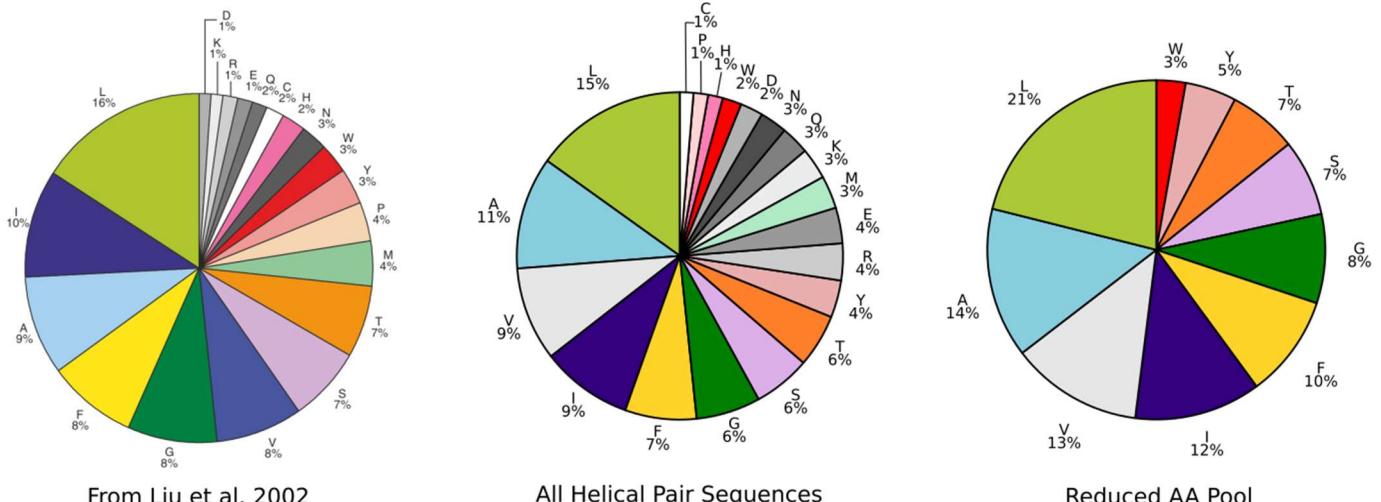
Validated sets of designs where clashing mutations < 35% GpA

Designs where a positive ΔG was calculated are designated NA

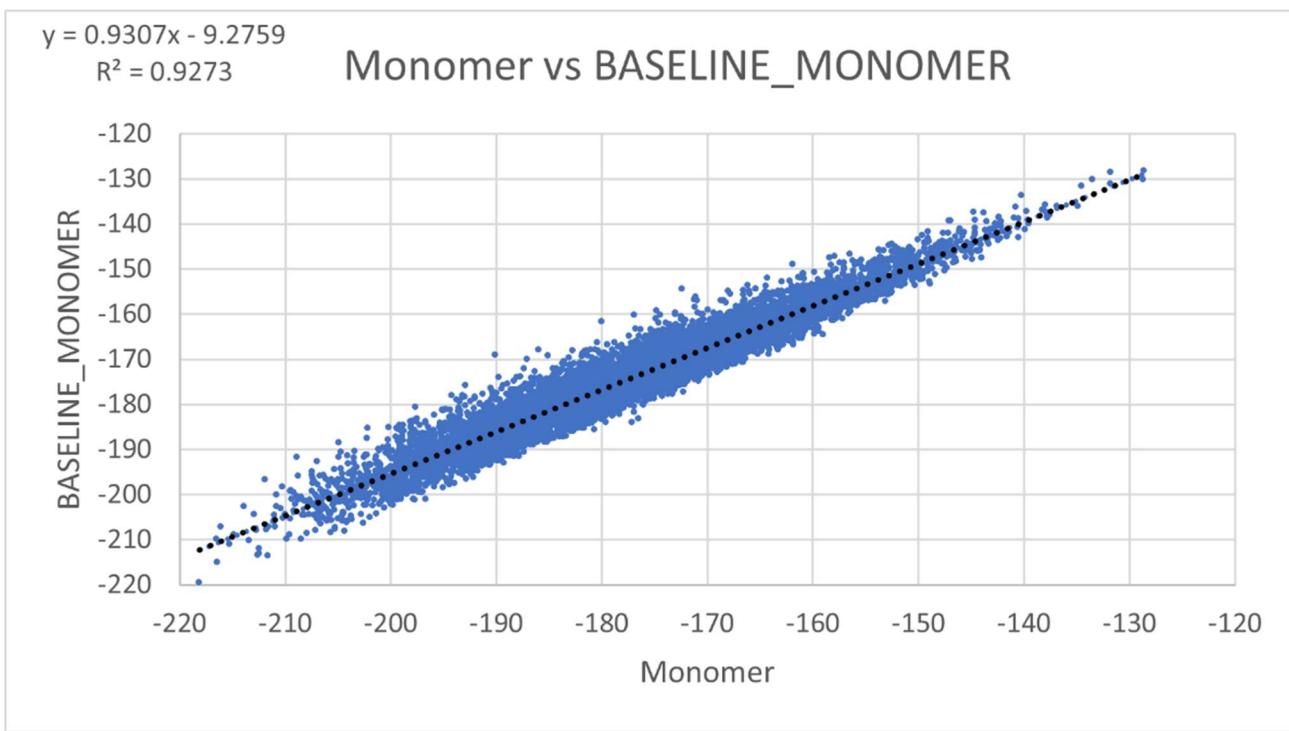


Western ID	Sequence	Design ID
G1	LLLAVLLTLLGGLLFALILI	
G2	LLLYVLLGALLGILLTLLIL	G_016
L1	LLLLLFLLATLILLSVLILI	L_021
L2	LLLFSLLLLLVALLTLLIL	
R1	LLLYILLTALLVALLSLLIL	R_051
R2	LLLFYLLVALLTALLSLLIL	R_140
L3	LLLLAVLLFLLALLTSLLIL	L_031
R3	LLLTVLLLALLFALLSILILI	R_090
G3	LLLTALLLALLFGGLLFSLLIL	G_060
G4	LLLTALLIGLLFGLLVLLIL	
L4	LLLLYLLLAVLTALLFSLLIL	L_022
L5	LLLLLALLLILFVLLSTLILI	
R4	LLLTSLLLALLFVLLLIL	
G5	LLLVALALLLGTLLSFLIL	G_052
L6	LLLLFALLALLYVLTSLLIL	
L7	LLLLAILLAVALFTLLSLLIL	
L8	LLLYALLFVLTALELTSLLIL	L_006
L9	LLLLAVLLFLLALTSLLIL	L_031
L10	LLLFAALLVLITLLYSLLIL	
G6	LLLTVLLALLLGFLLGSLIL	G_022
G7	LLLVALALLLGTLLSFLIL	G_052

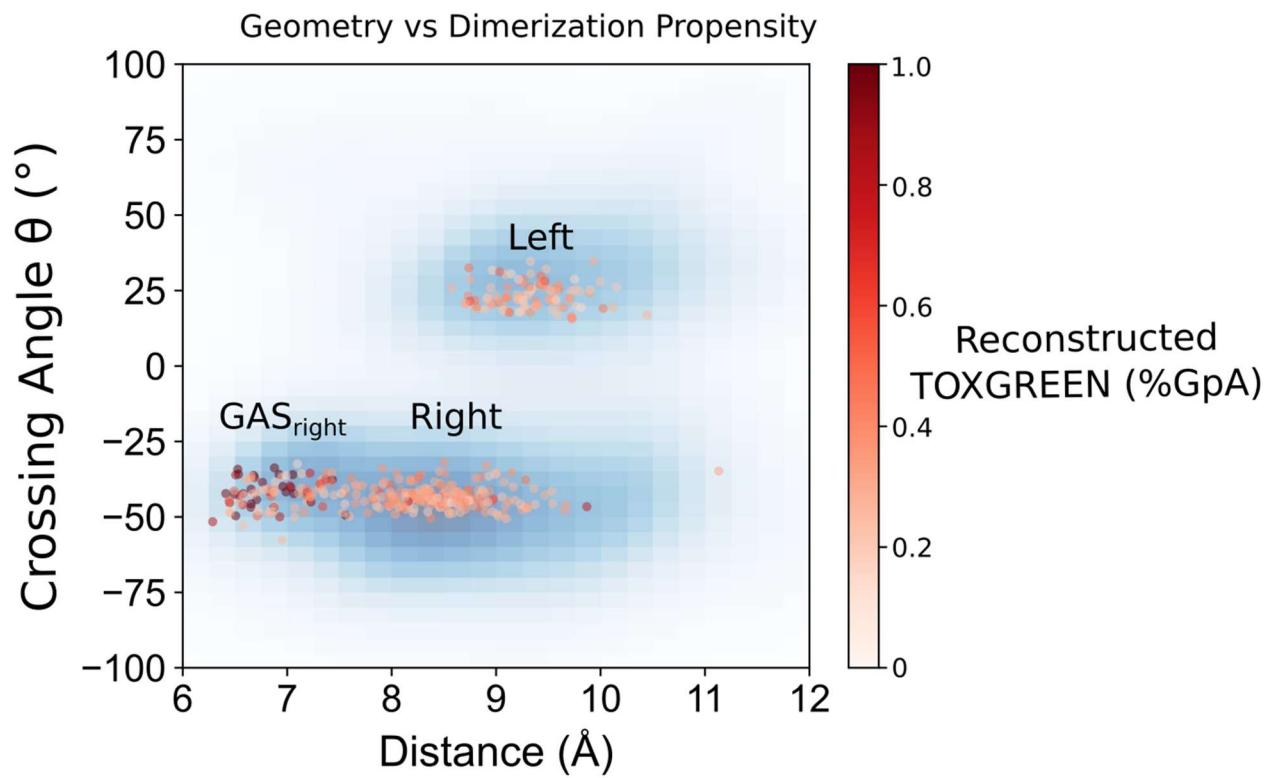
**Figure S1. Immunoblotting of designed constructs.** A subset of designed constructs were verified for their expression levels with western blots. While GAS<sub>right</sub> and Left show similar levels of expression, Right designs often have fainter bands on western blots. Sequences without a Design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



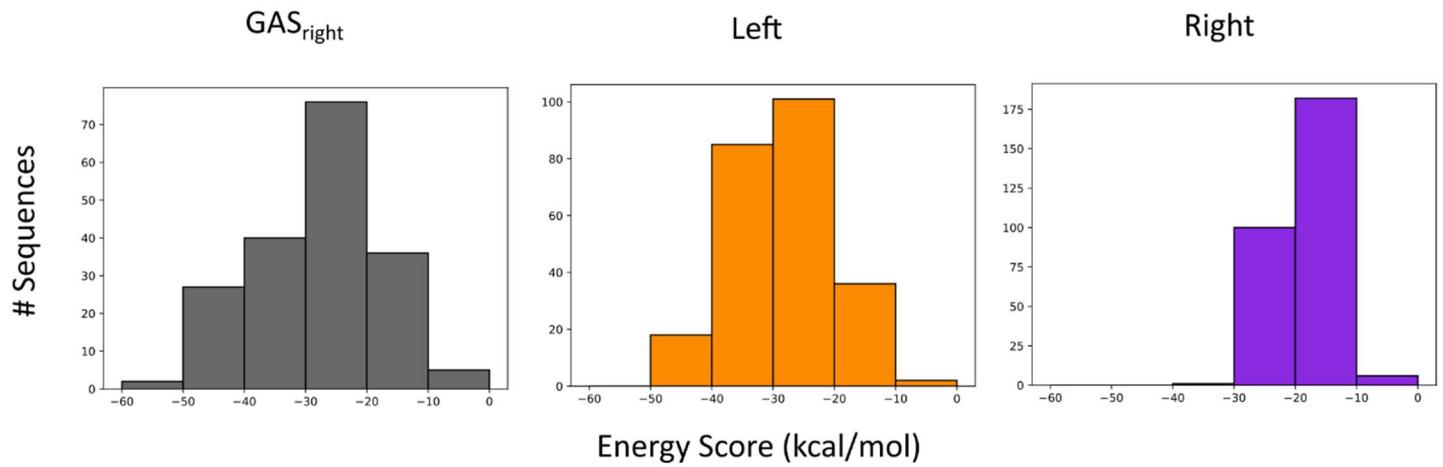
**Figure S2. Amino acid composition.** Frequency of amino acids from all transmembrane helical sequences extracted from OPM (Middle) as compared to membrane proteins from Liu et al. 2002 (Left). The frequency of the reduced pool of amino acids used for design (Right). Sequences were designed with interfaces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



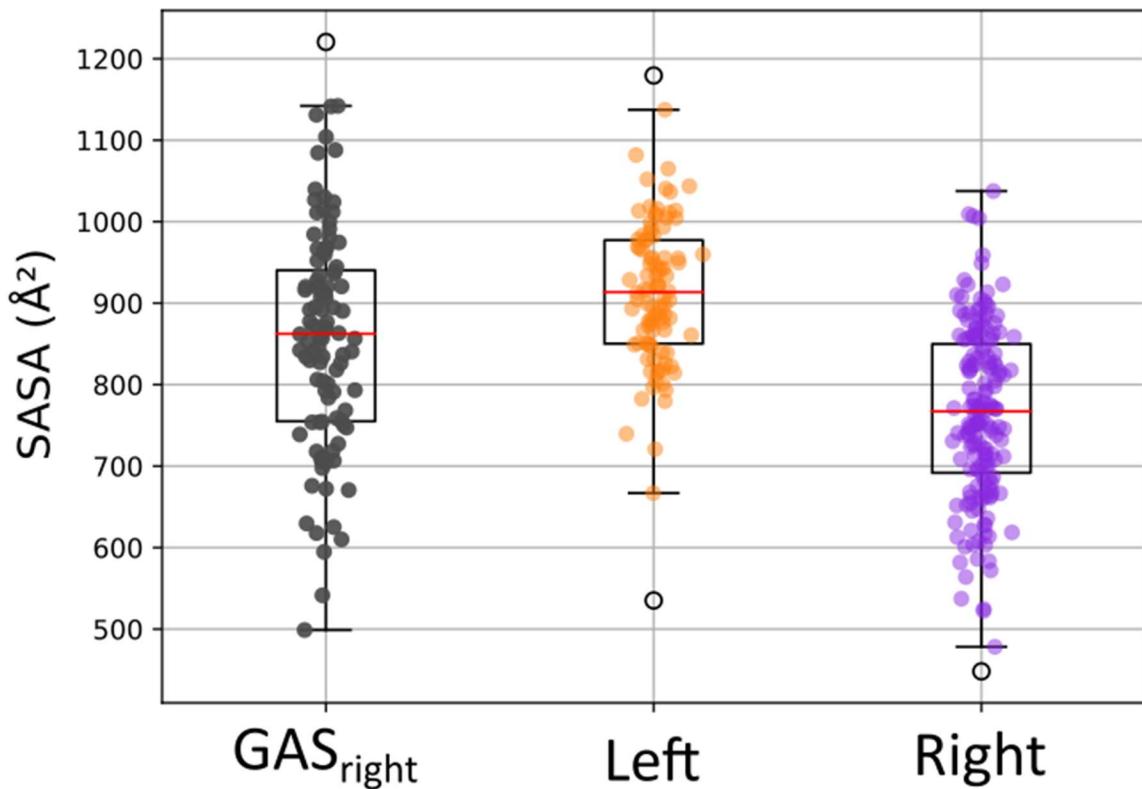
**Figure S3. BASELINE\_MONOMER.** Calculated monomer energy as compared to the estimated term BASELINE\_MONOMER used in the sequence design search.



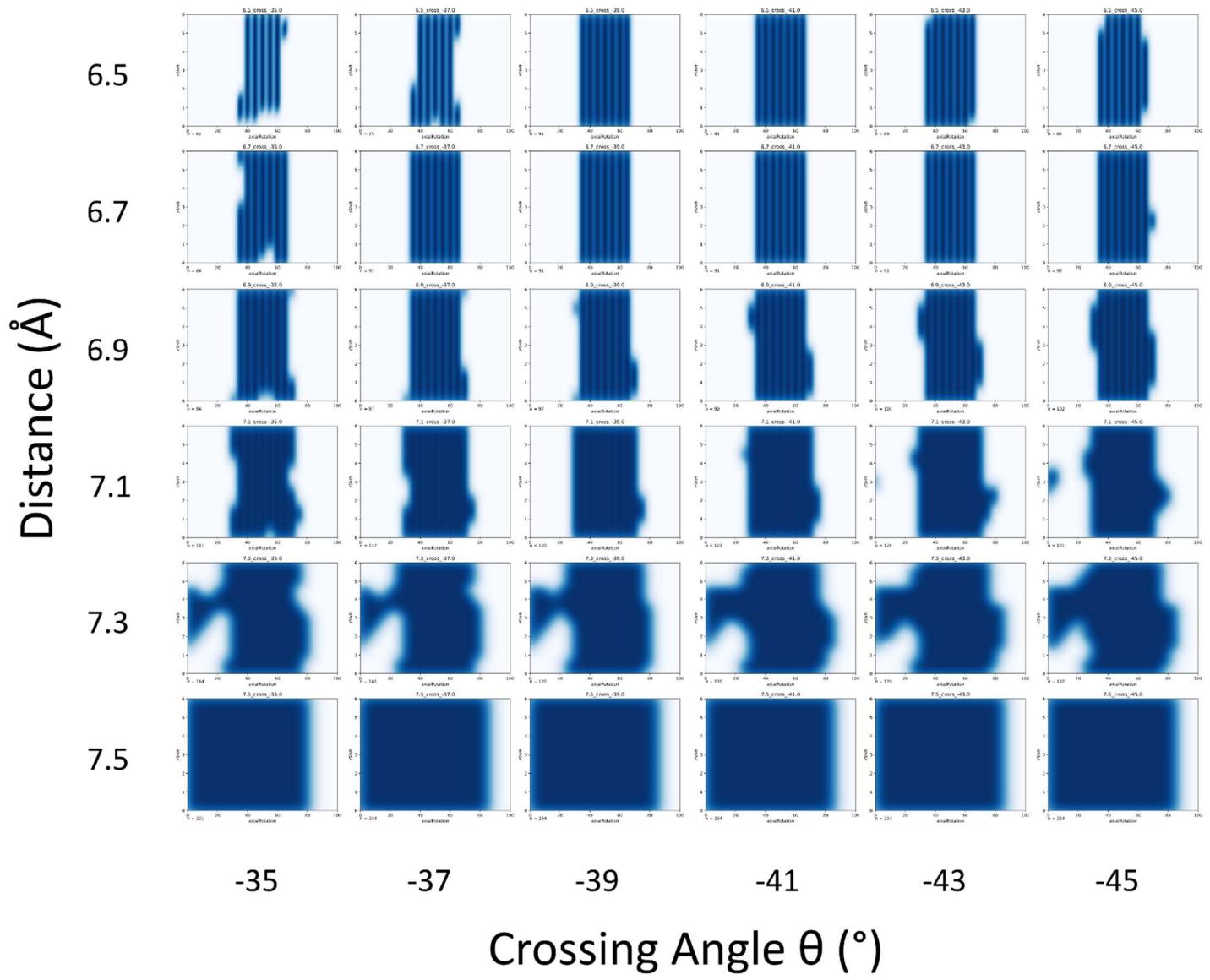
**Figure S4. Output Geometry vs Dimerization Propensity.** Distance and crossing angle of validated designed sequences plotted against %GpA in red. Sequences with highest dimerization propensity are darker red, most often found in GAS<sub>right</sub>.



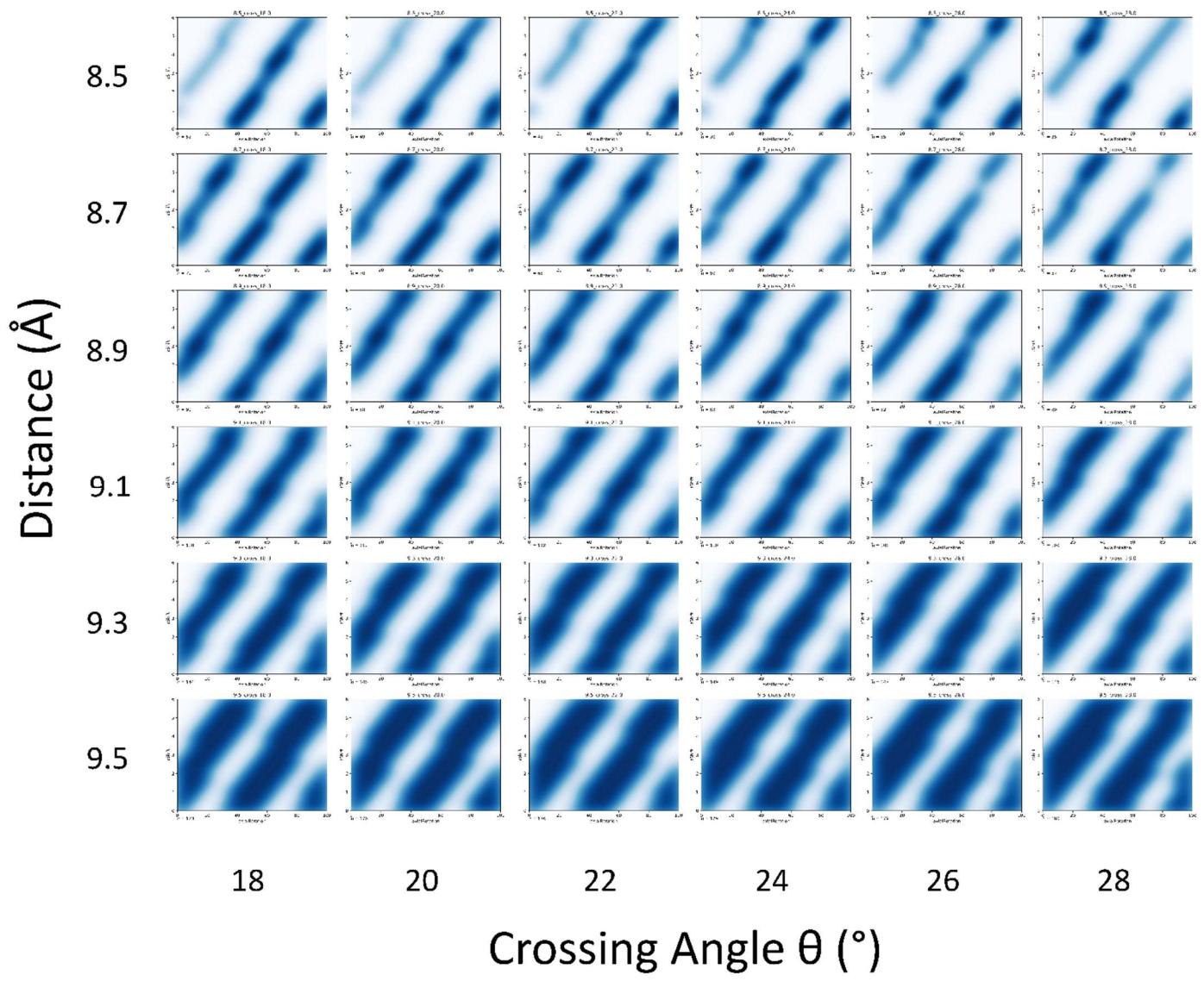
**Figure S5. Frequency of sequences by energy score.** Energy score of sequences present in sort-seq and the frequency for each design region.



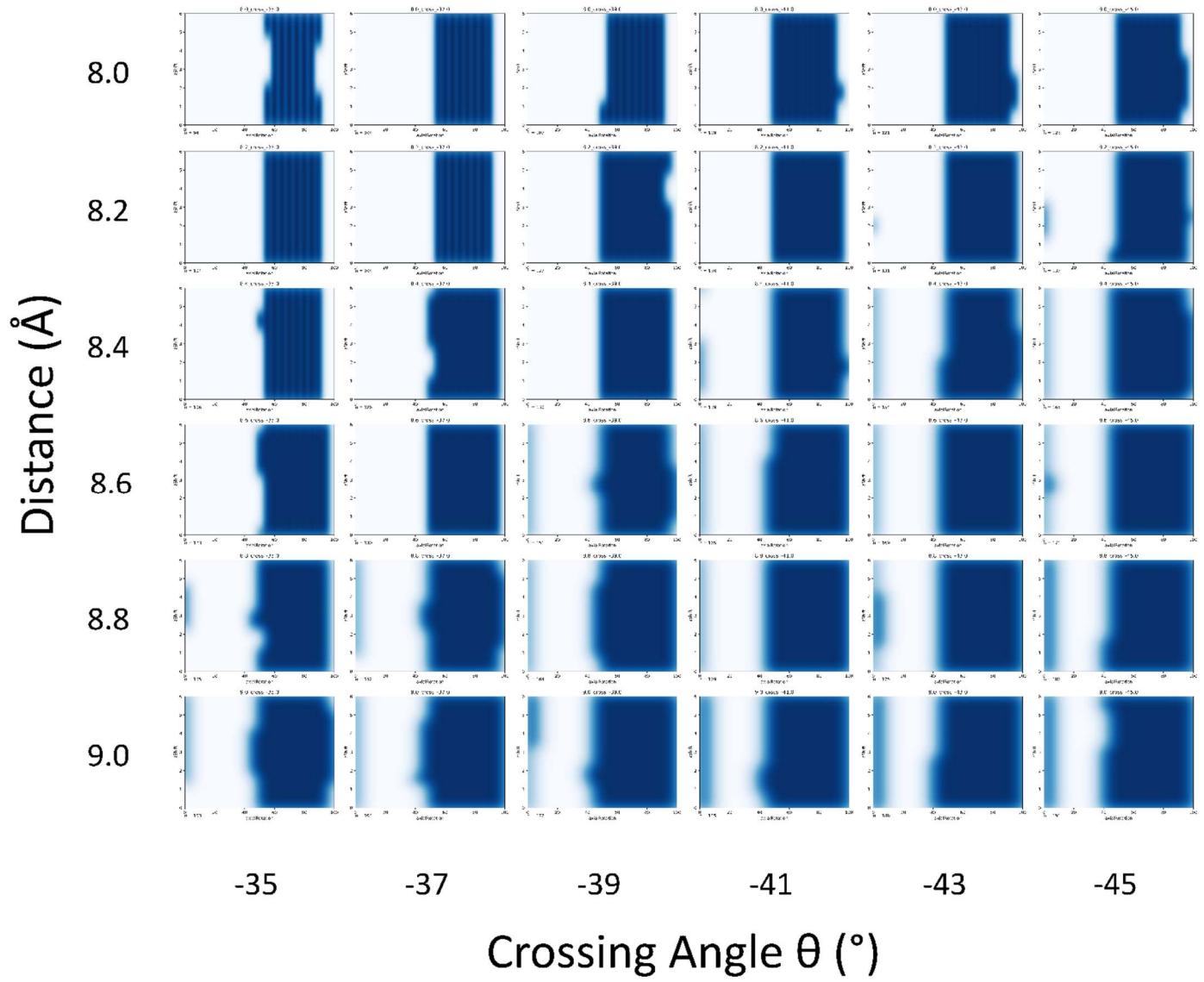
**Figure S6. Interface SASA.** Boxplots of validated sequences of interface SASA. GAS<sub>right</sub> and Left design interfaces are larger than Right, which may contribute to Right designs having a lower computational energy score.



**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.