Supporting Information

1 Results

Table S1: The Binding Affinity Substitution Matrix (BASM) R score values of the amylin amyloid

Res.	A	R	N	D	C	Q	E	G	H	I	L	K	M	F	P	S	T	W	Y	V
1	100.0	7.2	55.9	183.5	113.7	150.7	196.1	94.1	116.2	101.1	49.3	-4.2	81.0	60.6	32.6	115.8	121.5	42.8	82.6	126.6
2	6.2	-26.8	-0.6	116.3	5.9	61.0	124.6	-8.1	111.2	48.4	38.5	-111.8	25.5	68.3	50.1	163.7	141.8	53.7	55.2	46.0
3	-115.7	93.2	12.9	89.3	50.3	-11.1	101.8	-123.9	-93.8	226.1	-104.6	-160.2	-0.7	-69.3	-150.7	-108.7	111.2	-108.2	-80.1	50.4
4	91.7	28.1	-10.9	85.8	81.5	87.7	82.0	43.2	84.3	56.0	-19.7	-61.4	64.6	-55.8	49.8	87.6	131.3	128.7	48.5	110.0
5	38.1	10.1	55.5	184.5	107.0	66.9	92.8	90.2	28.3	58.0	62.9	36.8	-21.0	-1.1	-3.4	100.1	59.4	36.1	68.2	99.2
6	-53.8	-69.2	-4.9	-96.5	-71.6	-135.9	-127.0	51.9	-169.2	-142.9	12.2	-197.0	-70.8	44.4	39.5	7.3	-99.3	-108.7	14.4	-124.9
7	-79.8	-92.8	-128.1	-19.4	-87.1	-84.4	-4.1	-75.7	-92.0	-67.2	-68.2	-173.4	-93.5	-83.3	-114.0	-70.9	-52.7	-75.7	-72.0	-56.1
8	46.9	-113.9	-28.3	-122.5	-24.6	-138.7	36.2	44.8	47.3	36.9	-90.0	-3.8	-123.1	-11.8	-7.3	79.8	-105.2	12.6	26.6	-49.1
9	13.1	-7.5	-1.2	128.5	18.4	30.1	76.6	20.6	3.7	24.7	19.1	-113.1	-122.4	13.2	-130.3	23.1	46.8	77.2	41.3	30.5
10	-125.0	-131.1	-27.8	78.9	-128.9	-112.6	-60.3	-125.9	-49.7	25.1	-26.7	-161.3	-148.1	-104.8	-105.1	-132.1	-104.9	-97.7	-102.9	-106.1
11	-106.7	-147.3	-165.8	-46.5	-115.0	-110.2	-68.3	-120.4	-132.6	-114.4	-119.1	-212.2	-143.8	-121.7	-139.1	-86.1	-64.3	-138.5	11.0	-99.1
12	16.6	144.1	-173.6	-92.5	25.4	-4.2	51.6	1.8	-22.5	-103.6	79.6	-205.1	-78.1	-27.9	13.7	33.1	46.6	16.0	115.4	50.5
13	-166.7	-188.2	-238.5	-171.9	-164.8	-165.9	-123.9	-166.1	-194.1	-182.0	-186.0	-238.7	-209.6	-181.4	47.0	-156.3	-155.6	20.7	-175.9	-175.5
14	-82.7	-17.3	-218.9	-95.5	-63.4	-167.7	-57.0	-60.5	-192.0	-38.2	50.9	-22.2	-220.4	-175.0	-62.1	-60.4	-20.6	-166.9	-160.5	-162.6
15	-132.6	-136.4	-179.7	-122.3	-131.5	-105.8	-129.6	-138.9	-153.3	-21.6	-133.4	-194.2	-166.3	-142.3	-153.8	-99.5	-70.9	-186.6	-123.6	-109.1
16	11.2	19.6	-171.0	-78.3	66.8	-147.1	-5.5	14.5	-49.8	-42.0	-147.3	-50.9	-143.8	-131.8	57.5	-7.9	139.9	21.9	-122.8	-94.8
17	10.0	34.9	-181.5	2.4	-3.3	102.5	-151.2	11.8	-31.1	-26.8	-99.9	-95.5	-65.1	27.4	-118.0	25.6	55.9	13.6	100.5	-9.6
18	-134.6	20.2	-3.8	63.0	-131.6	148.1	18.2	-127.8	-111.0	-113.8	-22.5	-25.6	7.1	-112.4	-71.2	-116.6	-85.4	-133.4	-154.1	70.4
19	-78.0	-50.4	-102.6	-67.8	-82.6	-85.5	-75.4	-86.7	-121.6	-77.9	-89.1	-36.1	19.8	-109.9	20.3	-67.4	74.0	-83.1	-121.2	-52.9
20	116.0	109.6	3.3	69.2	22.1	63.7	56.1	-55.2	42.5	-76.4	-65.3	-82.9	-22.4	48.9	6.2	67.9	154.5	33.7	-6.3	111.2
21	28.8	90.1	-48.1	41.4	21.2	31.4	36.4	95.7	37.7	-43.0	30.8	-51.6	38.3	60.6	137.2	54.7	122.1	42.2	-37.2	87.5
22	-1.2	67.0	-85.8	-55.6	-1.7	-6.0	10.8	-7.5	-15.5	-80.7	-100.6	-6.5	56.1	-56.3	-99.4	11.7	36.0	-7.4	-102.9	26.3
23	28.8	28.0	-142.5	12.4	46.9	15.7	-48.6	-77.5	-119.2	-151.3	-156.7	40.0	-130.2	-174.1	-117.8	-59.8	138.0	-51.0	-146.7	-28.9
24	-107.9	69.3	-147.6	-30.2	36.5	-112.6	15.3	32.7	-189.8	-62.6	17.0	-52.6	-155.4	102.6	-29.9	-114.5	36.2	25.7	54.1	99.8
25	-75.5	-101.7	-221.3	-178.7	-108.1	-166.7	-183.7	-126.1	-169.4	-189.6	-123.3	-221.3	-195.6	-100.5	-177.2	-126.2	-89.9	-14.9	-117.1	-154.9
26	14.0	9.2	-13.0	38.3	-3.6	-120.7	-46.5	17.9	-119.9	87.6	-107.0	-129.4	-104.6	-79.3	11.2	17.2	-23.0	-78.9	-53.5	-20.8
27	-57.1	-74.7	-96.7	-58.4	-51.5	-78.7	-83.9	-34.8	-93.1	-50.0	-81.7	-139.6	-108.4	54.0	-151.8	-54.3	16.1	-92.0	-77.0	-53.6
28	74.2	1.4	56.7	121.9	53.3	14.7	85.8	101.0	-93.6	-4.1	-129.7	-29.5	34.5	-9.1	86.4	56.0	213.1	77.1	-26.5	27.7
29	-19.6	-89.5	-67.4	-55.5	-38.3	-62.9	-40.6	-32.6	-65.3	-47.2	-90.3	-121.0	-120.4	-81.4	-55.5	-74.2	-53.5	-70.3	-58.3	-47.4
30	89.4	-137.3	-118.8	91.8	78.0	-79.6	99.9	77.3	68.2	-98.7	-98.2	-153.3	33.3	-6.1	66.2	73.0	117.0	73.9	88.0	47.1
31	-133.4	-85.3	-172.3	-59.5	-122.1	-90.2	-144.1	-126.6	-116.5	-138.6	-156.7	-124.8	-164.7	-133.7	-67.0	-98.0	-116.6	-92.7	-142.4	-155.8
32	-55.5	124.3	76.1	110.7	-69.3	-47.5	181.6	-0.4	-2.8	-65.2	6.9	-31.1	-91.2	-66.1	-8.8	-27.7	-14.4	-90.4	-73.1	-69.3
33	-143.4	-142.1	-141.9	-112.0	-126.8	-171.8	-92.3	-108.1	-108.4	-131.5	-142.7	-198.9	-4.4	-129.6	8.8	-139.5	-100.7	-90.8	-103.3	-94.2
34	-5.7	96.2	-141.1	-10.4	-9.4	-125.4	72.8	-15.8	101.0	-97.6	-20.7	-28.1	-98.5	23.4	-4.1	-5.8	-37.0	-35.3	9.1	-10.9
35	-129.9	-104.1	-169.9	-100.9	-151.5	-118.3	-102.0	-140.3	-146.1	-162.0	-106.5	-208.0	-182.4	-70.4	-140.8	-118.2	-98.0	-127.5	-54.3	-114.0
36	52.0	42.6	-4.4	74.9	51.3	-86.5	98.1	44.0	-45.7	49.2	-9.7	6.7	24.4	-86.3	34.9	51.5	67.4	-65.0	-25.2	55.1
37	-156.2	-141.3	-160.9	-157.4	-156.3	-167.6	-154.3	-23.0	-156.6	-170.1	-5.2	-219.5	-165.4	-157.0	8.8	-159.6	14.2	-22.2	-61.5	-151.6

The first column represents the amino acid residue positions 1-37 of the amylin amyloid. The rest of the columns show the R-scores of the 20 amino acids interacting with every residue position of amylin.

Table S2: The Binding Affinity Substitution Matrix (BASM) R score values of the Pramlintide amyloid

Res.	A	R	N	D	C	Q	E	G	H	I	L	K	M	F	P	S	T	W	Y	V
1	132.5	25.4	83.9	213.6	128.2	154.3	224.0	126.2	130.9	135.0	76.9	67.1	113.4	82.2	68.0	-26.8	122.1	65.3	100.4	149.8
2	52.1	34.5	43.6	165.4	39.9	104.6	170.5	37.9	163.1	96.1	85.2	-49.6	72.4	117.5	81.1	164.5	217.2	99.4	100.4	90.4
3	-85.1	109.2	36.3	119.7	42.0	25.7	109.6	-95.1	-67.0	247.3	-107.4	-86.9	27.0	-43.6	-128.6	-77.9	125.4	-100.9	-71.0	96.9
4	93.5	43.3	38.9	145.7	100.9	43.0	81.4	62.7	103.5	107.6	8.0	11.3	56.5	-22.0	69.4	102.4	151.8	190.7	81.2	134.8
5	85.8	52.4	99.2	231.3	147.4	112.8	122.3	139.5	59.2	105.7	109.2	132.0	22.5	45.7	41.4	145.8	107.0	82.5	114.2	147.5
6	-21.5	-50.4	8.7	-60.5	-41.9	-108.4	-94.5	93.4	-139.7	-111.1	21.7	-115.2	-38.2	32.7	78.2	17.8	-65.4	-89.0	4.3	-86.6
7	-47.2	-60.9	-93.9	11.1	-54.1	-49.1	24.8	-49.0	-63.9	-20.7	-34.7	-89.9	-59.0	-51.4	-82.2	-41.3	-13.7	-43.9	-40.7	-22.1
8	97.0	-97.8	-3.4	-82.7	19.9	-94.5	52.9	94.1	96.3	47.5	-52.1	101.2	-94.3	27.4	41.2	102.5	-59.1	18.3	55.2	-14.8
9	31.9	14.4	14.2	150.6	37.9	51.2	92.6	39.0	24.6	44.3	39.3	-45.9	-84.7	35.9	-81.2	43.3	68.3	69.0	58.2	48.6
10	-89.8	-94.2	18.5	65.9	-92.5	-77.0	-33.4	-93.5	-14.2	65.5	-9.7	-79.3	-120.9	-66.8	-61.8	-98.8	-69.1	-60.6	-70.9	-78.5
11	-77.7	-124.4	-144.9	-18.3	-79.1	-85.7	-21.8	-94.1	-110.6	-76.6	-99.9	-139.7	-111.3	-114.8	-109.3	-54.9	-26.3	-114.5	25.4	-64.2
12	52.5	139.5	-149.1	-76.5	59.3	4.4	39.6	40.3	43.9	-82.8	66.7	-97.6	-61.2	5.4	62.2	66.9	81.7	57.4	110.2	90.8
13	-139.7	-157.0	-211.4	-145.1	-146.6	-135.0	-84.3	-134.1	-161.0	-140.0	-150.2	-167.7	-174.8	-150.2	7.9	-114.0	-121.8	1.9	-140.7	-139.6
14	-28.7	10.1	-186.3	-56.0	-44.7	-135.3	11.2	-14.8	-148.2	20.7	69.7	31.9	-177.0	-135.0	-31.8	-56.4	18.8	-115.4	-123.7	-116.2
15	-108.3	-111.2	-154.7	-99.6	-107.1	-96.2	-100.9	-117.4	-124.6	-16.2	-107.9	-111.7	-136.8	-108.6	-121.4	-66.4	8.5	-149.5	-94.3	-91.3
16	27.7	42.4	-149.4	-130.2	60.0	-128.4	25.6	34.0	-20.4	63.9	-111.6	18.8	-125.1	-103.7	79.2	2.5	162.7	-35.3	-92.2	-59.8
17	26.0	51.0	-155.8	54.9	32.8	57.0	-93.1	33.4	-5.5	9.8	-80.0	-23.0	-35.4	22.4	-110.1	58.3	88.3	62.1	86.8	-0.3
18	-106.2	65.5	-4.0	74.2	-112.5	136.2	1.8	-90.1	-84.0	-81.4	0.8	29.2	20.8	-79.6	-37.8	-89.9	-42.4	-86.5	-124.8	69.1
19	-60.1	-39.6	-88.6	-45.3	-64.9	-77.3	-51.9	-75.4	-95.6	-64.0	-58.1	52.0	46.9	-86.6	35.0	-30.5	20.8	-46.6	-84.2	-43.7
20	100.8	112.2	-0.8	96.5	36.1	106.7	90.9	-32.1	48.6	-31.6	-91.4	43.9	-5.6	79.3	9.8	63.3	180.2	55.3	-37.7	128.1
21	58.8	74.8	6.8	59.3	53.6	57.8	73.2	100.9	13.5	-39.6	89.1	7.3	67.2	124.9	81.6	85.5	77.5	68.1	-18.1	99.1
22	20.1	97.4	-44.6	-38.5	32.5	36.3	87.4	32.1	1.3	-44.9	-71.5	53.1	96.4	-7.0	-73.9	36.2	133.7	11.9	-75.1	65.3
23	36.1	80.4	-123.9	18.6	19.7	36.5	-32.8	-38.7	-117.8	-109.1	-132.6	118.1	-87.4	-126.9	-72.6	-39.8	129.0	-79.6	-93.2	13.1
24	-94.4	106.7	-161.0	0.5	27.0	-84.7	11.9	32.9	-147.8	-48.3	0.5	-10.7	-138.3	108.5	21.1	-76.9	76.0	47.1	52.6	66.3
25	-51.2	-77.3	-87.5	-127.1	-55.6	-123.7	-155.3	-96.9	-138.9	-162.9	-138.5	-149.6	-187.2	5.1	-160.6	-108.9	-61.7	36.6	-66.3	-134.6
26	41.8	-0.3	42.8	74.0	41.0	-110.1	-11.7	47.6	-77.5	24.1	-118.0	-60.7	-68.2	-54.8	10.1	62.2	-10.1	-55.4	-26.5	-7.6
27	-54.8	-52.6	-78.9	-29.2	-17.9	-44.4	-54.6	-9.6	25.0	-32.1	-50.0	-61.7	-73.7	69.2	-113.4	-31.6	10.3	-72.0	-56.7	-48.8
28	122.1	129.6	92.4	139.4	97.0	97.9	279.7	162.3	84.6	18.0	-104.1	62.9	72.1	1.8	113.9	98.6	259.6	64.8	-22.2	61.0
29	-26.4	-69.2	-57.6	-39.4	-50.3	-40.0	-19.9	-25.5	-70.9	-39.2	-76.5	-83.3	-87.2	-66.7	-45.2	-36.0	-35.9	-68.9	-43.6	-35.4
30	118.2	-111.7	-124.3	131.5	100.2	-73.5	81.1	121.1	-97.7	-70.6	-106.2	-65.9	88.0	49.6	116.5	133.8	114.6	99.5	132.7	53.5
31	-56.7	-64.3	-136.2	-70.8	-109.1	-91.7	-100.6	-87.5	-94.2	-89.3	-92.1	-21.1	-106.1	-104.4	-72.7	-57.7	-109.4	-37.1	-94.1	-107.6
32	-23.1	175.9	74.9	105.0	-42.3	-25.7	163.7	27.2	-3.9	-12.6	46.4	32.4	-58.1	-11.8	14.5	-12.6	19.9	-51.8	-20.2	5.3
33	-81.9	-102.2	-61.5	-69.1	-97.1	-116.1	-68.5	-91.7	-121.9	-95.6	-106.4	-119.5	15.4	-66.9	25.7	-105.9	-71.2	-56.2	-111.5	-60.6
34	30.2	117.4	-113.7	20.2	37.3	-75.9	131.4	17.9	94.3	-62.8	11.3	45.6	-68.2	74.7	20.5	30.1	3.6	1.4	46.0	13.3
35	-102.5	-78.1	-145.7	-72.3	-125.1	-91.7	-76.3	-112.8	-63.2	-124.2	-81.2	-133.9	-149.0	-104.4	-124.9	-101.3	-77.0	-121.7	-29.3	-92.1
36	82.0	65.1	21.0	82.8	62.0	-78.1	134.1	50.7	-5.9	76.9	16.8	75.2	53.0	-37.4	56.8	81.9	86.6	-23.5	8.5	83.2
37	-120.5	-106.7	-124.3	-111.8	-119.6	-124.3	-107.3	-12.8	-111.1	-142.7	-19.3	-130.1	-132.4	-130.4	18.6	-122.2	39.6	8.3	-58.9	-112.9

The first column represents the amino acid residue positions 1-37 of the Pramlintide amyloid. The rest of the columns show the R-scores of the 20 amino acids interacting with every residue position of Pramlintide.

Table S3: Exploring aggregation properties of top 10 results with TANGO

Mutant	**AGG**	**AMYLO**	**TURN**	**HELIX**	**HELAGG**	**BETA**
M7	20.366	0.0755151	31.0521	16.326	0	52.5555
M4	20.3613	0.000988828	31.1604	20.7997	0	39.2829
M9	20.3598	0.0213931	31.3389	29.4205	0	39.2994
M3	19.6618	0.0699662	28.7727	21.8182	0	42.3278
M8	1.85245	0.141604	36.4188	19.4214	0	43.4389
M2	1.84561	0.0589466	39.0022	18.7469	0	39.0683
M1	0.94131	0.0589388	31.2728	26.4465	0	39.4491
M5	0.94131	0.059078	28.3981	18.7469	0	47.8042
M6	0.94131	0.0589388	37.8203	19.8651	0	38.7392
M10	0.94131	0.0589369	29.2805	21.189	0	45.6678

The AGG column ranks the beta-sheet aggregation propensity of each sequence. TANGO suggests that the top 6 sequences are highly amyloidogenic. All the sequences possess a HELAGG (helix-aggregation propensity) of 0. Although TANGO predicts the aggregation propensity of proteins from sequence alone, the dipolar solvent model provides much more accurate results since it calculates precisely the solvation and enthalpy terms based on the full 3D atomic structure of proteins. It is supportive however to find that the results from TANGO are in-line with our predictions.

Table S4: Exploring aggregation properties of top 10 results with FoldX

Mutant	**Native Energy**	**Amyloid Energy**	ΔG
native (none)	58.7938	35.6609	-23.1329
M1	59.5595	36.6347	-22.9248
M2	59.2388	35.4606	-23.7782
M3	58.265	35.2662	-22.9988
M4	56.0508	35.4992	-20.5516
M5	59.5462	35.809	-23.7372
M6	59.2382	36.2025	-23.0357
M7	58.8138	35.8046	-23.0092
M8	57.6856	35.851	-21.8346
M9	58.5353	35.5489	-22.9864
M10	58.4793	37.0252	-21.4541

The Native and Amyloid Energies are in Kcal/mol and describe the stability of a structure. High energies are less stable than low energies. ΔG is the difference in energies between Amyloid and Native structures. FoldX suggests that the aggregation of all these sequences is highly favourable and the reactions are exothermic. Although we believe that the aggregations are favourable, they are not exothermic in nature as widely known experimentally. FoldX predicts that the 10 mutant structures are all as stable as the native non-mutant structure. These results of high amyloidogenicity and high native stability compare well with our findings.

Table S5: Exploring aggregation properties of top 10 results with Zyggregator

Mutant	**Hydrophbicity**	**Charge**	**Beta sheet propensity**	**alpha helical propensity**	**intrinsic aggregation propensity**
native (none)	13.37	2	152.329	149.633	-4.39989
M1	23.72	5	151.845	150.19	-5.67235
M2	21.43	4	152.236	149.987	-5.23438
M3	20.66	5	152.202	150.518	-5.62767
M4	20.9	5	151.996	150.772	-5.69782
M5	19.77	4	156.566	153.971	-5.26634
M6	26.62	5	151.763	149.718	-5.65616
M7	20.82	4	152.279	150.233	-5.25724
M8	23.56	5	152.12	150.045	-5.61148
M9	20.9	5	151.996	150.772	-5.69782
M10	24.96	5	156.094	153.702	-5.68812

The results returned by Zyggregator suggest that all the 10 mutants possess a high beta-sheet propensity and aggregation potential. The aggregation potential of all 10 mutants are more negative (more favourable) than the native non-mutant structure. The alpha helical propensities of all mutants are roughly equal to the native non-mutant, suggesting that the mutant structures are stable in native form and contain many alpha helices. These results compare well with our findings but do not provide detailed differences between the mutant structures.

Table S6: Exploring aggregation properties of top 10 results with PASTA

Mutant	**length**	**# amyloids**	**best energy**	**% disorder**	**% α-helix**	**% β-strand**	**% coil**
m5	37	6	-5.226754	27.02	0	32.43	67.57
native (none)	37	0	-4.939862	37.83	48.65	0	51.35
m2	37	0	-4.453145	27.02	0	24.32	75.68
m4	37	0	-3.974559	32.43	0	21.62	78.38
m7	37	0	-3.974559	29.72	0	27.03	72.97
m9	37	0	-3.974559	29.72	13.51	21.62	64.86
m8	37	0	-3.779929	37.83	0	16.22	83.78
m1	37	0	-3.62816	32.43	0	24.32	75.68
m3	37	0	-3.62816	27.02	0	32.43	67.57
m6	37	0	-3.62816	64.86	0	13.51	86.49
m10	37	0	-3.62816	48.64	0	29.73	70.27

Description of the columns are as follows: **length** : Protein length, **#amyloids** : the number of amyloid fibril regions predicted by PASTA, **best energy** : the top ranked amyloid region by energy. This column is sorted in order to quickly see the more amyloidogenic sequences. **% disorder** : the percentage of residues predicted to be in a disordered state, **% α-helix** : the percentage of residues predicted to be in a helix state, **% β-strand** : the percentage of residues predicted to be in a strand state, **% coil** : the percentage of residues predicted to be in a coil state.

The results in this table predict that all the mutants (except m9) have high amyloidogenicity and will fold into an amyloid structure. Moreover, all the structures are stable and have low energies. It is highly interesting that PASTA predicts m9 to have fewer α-helices than the native non-mutant and simultaneously suggests that it can contain β-strands. We view this result to be inline with our finding that m9 is a mutant structure that is both extremely stable in native form, yet highly amyloidogenic.

Table S7: Top results solving the 4-residue parsimonious sequences for S^{P_4} with $\alpha = 2$ and $\beta = 1$

No.	**Sequence S^{P_4}**	$F(S^{P_4})$	**Mutations**
1	----------K----------K-H-K-------	-3013.5	L12K I26K S28H T30K
2	----------K----------N--H-K-------	-3007.5	L12K A25N S28H T30K
3	----------K-------K-------H-K-------	-3005.4	L12K S20K S28H T30K
4	---K-------K----------H-K-------	-2993.3	T4K L12K S28H T30K
5	----------K----------H---H-K-------	-2992.3	L12K G24H S28H T30K
6	----------K----------H-K------K	-2975.3	L12K S28H T30K Y37K
7	--K--------K----------H-K-------	-2974.2	N3K L12K S28H T30K
8	----------K----------NK---K-------	-2965.3	L12K A25N I26K T30K
9	----------K-------K-----K---K-------	-2963.2	L12K S20K I26K T30K
10	-------Q---K----------H-K-------	-2957.7	A8Q L12K S28H T30K
11	----------K-------K----N----K-------	-2957.2	L12K S20K A25N T30K
12	--------K--K----------H-K-------	-2954.9	T9K L12K S28H T30K
13	---K-------K----------K---K-------	-2951.1	T4K L12K I26K T30K
14	----------K----------H-K---K-------	-2950.1	L12K G24H I26K T30K
15	---K-------K----------N----K-------	-2945.0	T4K L12K A25N T30K
16	----------K----------HN----K-------	-2944.0	L12K G24H A25N T30K
17	---K-------K-------K---------K-------	-2943.0	T4K L12K S20K T30K
18	----------K-------K---H-----K-------	-2942.0	L12K S20K G24H T30K
19	----------K----------NK-H---------	-2935.3	L12K A25N I26K S28H
20	----------K-------K-----K-H---------	-2933.3	L12K S20K I26K S28H
21	----------K----------K---K------K	-2933.1	L12K I26K T30K Y37K
22	--K--------K----------K---K-------	-2932.0	N3K L12K I26K T30K
23	----------K----------H-K-----F-	-2930.6	L12K S28H T30K T36F
24	---K-------K----------H-----K-------	-2929.8	T4K L12K G24H T30K
25	----------K----E----------H-K-------	-2927.5	L12K V17E S28H T30K
26	----------K-------K----N--H---------	-2927.2	L12K S20K A25N S28H
27	----------K----------N----K------K	-2927.1	L12K A25N T30K Y37K
28	--K--------K----------N----K-------	-2926.0	N3K L12K A25N T30K
29	----------K-------K---------K------K	-2925.0	L12K S20K T30K Y37K
30	--K--------K-------K---------K-------	-2923.9	N3K L12K S20K T30K
31	---K-------K----------K-H---------	-2921.1	T4K L12K I26K S28H
32	----------K----------H-K-H---------	-2920.1	L12K G24H I26K S28H
33	-------Q---K----------K---K-------	-2915.5	A8Q L12K I26K T30K
34	---K-------K----------N--H---------	-2915.1	T4K L12K A25N S28H
35	----------K----------HN--H---------	-2914.1	L12K G24H A25N S28H
36	---K-------K-------K-------H---------	-2913.0	T4K L12K S20K S28H
37	---K-------K----------K------K	-2912.9	T4K L12K T30K Y37K
38	--------K--K----------K---K-------	-2912.7	T9K L12K I26K T30K
39	----------K-------K---H---H---------	-2912.0	L12K S20K G24H S28H
40	----------K----------H-----K------K	-2911.9	L12K G24H T30K Y37K
41	--KK-------K----------K-------	-2911.8	N3K T4K L12K T30K
42	--K--------K----------H-----K-------	-2910.8	N3K L12K G24H T30K
43	-------Q---K----------N----K-------	-2909.5	A8Q L12K A25N T30K
44	-K---------K----------H-K-------	-2907.6	C2K L12K S28H T30K
45	-------Q---K-------K---------K-------	-2907.4	A8Q L12K S20K T30K
46	-----K-----K----------H-K-------	-2907.4	T6K L12K S28H T30K
47	--------K--K----------N----K-------	-2906.7	T9K L12K A25N T30K
48	--------K--K-------K---------K-------	-2904.6	T9K L12K S20K T30K
49	----------K----------K-H--------K	-2903.1	L12K I26K S28H Y37K
50	--K--------K----------K-H---------	-2902.0	N3K L12K I26K S28H

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Table S7 – continued from previous page

No.	Sequence S^{P_4}	$F(S^{P_4})$	Mutations
51	----------NK-H-K-------	-2901.0	A25N I26K S28H T30K
52	---K-------K----------H---H---------	-2899.9	T4K L12K G24H S28H
53	----------K-----K-H-K-------	-2898.9	S20K I26K S28H T30K
54	----------K----------H-K--K----	-2897.9	L12K S28H T30K G33K
55	------K----K----------H-K-------	-2897.8	C7K L12K S28H T30K
56	----------K----------N--H--------K	-2897.1	L12K A25N S28H Y37K
57	----------K----------H-K---Q---	-2897.0	L12K S28H T30K S34Q
58	--K--------K----------N--H---------	-2896.0	N3K L12K A25N S28H
59	---K---Q---K----------K-------	-2895.3	T4K A8Q L12K T30K
60	----------K-------K-------H--------K	-2895.1	L12K S20K S28H Y37K
61	-------Q---K----------H-----K-------	-2894.3	A8Q L12K G24H T30K
62	--K--------K-------K-------H---------	-2894.0	N3K L12K S20K S28H
63	--K--------K----------K------K	-2893.8	N3K L12K T30K Y37K
64	----------K----N--H-K-------	-2892.9	S20K A25N S28H T30K
65	---K----K--K----------K-------	-2892.5	T4K T9K L12K T30K
66	--------K--K----------H-----K-------	-2891.5	T9K L12K G24H T30K
67	----------K----------K---K-----F-	-2888.4	L12K I26K T30K T36F
68	---K----------K-H-K-------	-2886.8	T4K I26K S28H T30K
69	----------H-K-H-K-------	-2885.8	G24H I26K S28H T30K
70	-------Q---K----------K-H---------	-2885.5	A8Q L12K I26K S28H
71	----------K----E--------K---K-------	-2885.2	L12K V17E I26K T30K
72	----------K-------K----NK----------	-2885.0	L12K S20K A25N I26K
73	---K-------K----------H--------K	-2882.9	T4K L12K S28H Y37K
74	--------K--K----------K-H---------	-2882.7	T9K L12K I26K S28H
75	----------K----------N----K-----F-	-2882.4	L12K A25N T30K T36F
76	----------K----------H---H--------K	-2881.9	L12K G24H S28H Y37K
77	--KK-------K----------H---------	-2881.8	N3K T4K L12K S28H
78	--K--------K----------H---H---------	-2880.8	N3K L12K G24H S28H
79	---K----------N--H-K-------	-2880.8	T4K A25N S28H T30K
80	----------K-------K---------K-----F-	-2880.3	L12K S20K T30K T36F
81	----------HN--H-K-------	-2879.8	G24H A25N S28H T30K
82	-------Q---K----------N--H---------	-2879.5	A8Q L12K A25N S28H
83	----------K----E-------N----K-------	-2879.2	L12K V17E A25N T30K
84	---K----------K-------H-K-------	-2878.7	T4K S20K S28H T30K
85	----------K---H---H-K-------	-2877.7	S20K G24H S28H T30K
86	-------Q---K-------K-------H---------	-2877.5	A8Q L12K S20K S28H
87	-------Q---K----------K------K	-2877.3	A8Q L12K T30K Y37K
88	----------K----E--K---------K-------	-2877.2	L12K V17E S20K T30K
89	--------K--K----------N--H---------	-2876.7	T9K L12K A25N S28H
90	--K----Q---K----------K-------	-2876.2	N3K A8Q L12K T30K
91	--------K--K-------K-------H---------	-2874.7	T9K L12K S20K S28H
92	--------K--K----------K------K	-2874.5	T9K L12K T30K Y37K
93	--K-----K--K----------K-------	-2873.4	N3K T9K L12K T30K
94	---K-------K----------NK----------	-2872.9	T4K L12K A25N I26K
95	----------K----------HNK----------	-2871.9	L12K G24H A25N I26K
96	----------KK----------H-K-------	-2871.0	L12K A13K S28H T30K
97	---K-------K-------K-----K----------	-2870.8	T4K L12K S20K I26K
98	----------K-------K---H-K----------	-2869.8	L12K S20K G24H I26K
99	----------K-H-K------K	-2868.8	I26K S28H T30K Y37K
100	---K-------K----------K-----F-	-2868.1	T4K L12K T30K T36F
101	--K----------K-H-K-------	-2867.7	N3K I26K S28H T30K
102	----------K----------H-----K-----F-	-2867.2	L12K G24H T30K T36F

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Table S7 – continued from previous page

No.	Sequence S^{P_4}	$F(S^{P_4})$	Mutations
103	---K-------------------H---H-K-------	-2865.6	T4K G24H S28H T30K
104	-K---------K-------------K---K-------	-2865.4	C2K L12K I26K T30K
105	----------KK---------------H-K-------	-2865.3	R11K L12K S28H T30K
106	---K---Q---K---------------H---------	-2865.3	T4K A8Q L12K S28H
107	-----K-----K-------------K---K-------	-2865.1	T6K L12K I26K T30K
108	---K-------K----E------------K-------	-2865.0	T4K L12K V17E T30K
109	---K-------K-------K----N------------	-2864.8	T4K L12K S20K A25N
110	-------Q---K-----------H---H---------	-2864.3	A8Q L12K G24H S28H
111	-----------K----E------H-----K-------	-2864.0	L12K V17E G24H T30K
112	--K--------K---------------H--------K	-2863.8	N3K L12K S28H Y37K
113	-----------K-------K---HN------------	-2863.8	L12K S20K G24H A25N
114	-----------K--------------KH-K-------	-2863.7	L12K L27K S28H T30K
115	------------------------N--H-K------K	-2862.8	A25N S28H T30K Y37K
116	---K----K--K---------------H---------	-2862.5	T4K T9K L12K S28H
117	-----------K--K------------H-K-------	-2862.3	L12K F15K S28H T30K
118	--K--------------------N--H-K-------	-2861.7	N3K A25N S28H T30K
119	--------K--K-----------H---H---------	-2861.5	T9K L12K G24H S28H
120	-------------------K-------H-K------K	-2860.7	S20K S28H T30K Y37K
121	--K----------------K-------H-K-------	-2859.6	N3K S20K S28H T30K
122	-K---------K------------N----K-------	-2859.4	C2K L12K A25N T30K
123	-----K-----K------------N----K-------	-2859.1	T6K L12K A25N T30K
124	---------K-K---------------H-K-------	-2858.6	Q10K L12K S28H T30K
125	-----------K-------------K-H-------F-	-2858.4	L12K I26K S28H T36F
126	---K-------K-----------H-K-----------	-2857.7	T4K L12K G24H I26K
127	-K---------K-------K---------K-------	-2857.4	C2K L12K S20K T30K
128	-----K-----K-------K---------K-------	-2857.1	T6K L12K S20K T30K
129	-------QK--K-----------------K-------	-2856.9	A8Q T9K L12K T30K
130	-----------K-------------K---K--K----	-2855.7	L12K I26K T30K G33K
131	------K----K-------------K---K-------	-2855.6	C7K L12K I26K T30K
132	-----------K----E--------K-H---------	-2855.3	L12K V17E I26K S28H
133	-----------K------------NK----------K	-2854.9	L12K A25N I26K Y37K
134	-----------K-------------K---K---Q---	-2854.8	L12K I26K T30K S34Q
135	--K--------K------------NK-----------	-2853.8	N3K L12K A25N I26K
136	-----------K-------K-----K----------K	-2852.9	L12K S20K I26K Y37K
137	-----------K------------N--H-------F-	-2852.4	L12K A25N S28H T36F
138	--K--------K-------K-----K-----------	-2851.7	N3K L12K S20K I26K
139	---K-------K-----------HN------------	-2851.6	T4K L12K G24H A25N
140	-------Q----------------K-H-K-------	-2851.2	A8Q I26K S28H T30K
141	-------------------K----NK---K-------	-2850.7	S20K A25N I26K T30K
142	-----------K-------K-------H-------F-	-2850.4	L12K S20K S28H T36F
143	-----------K-----------------K-----FK	-2850.2	L12K T30K T36F Y37K
144	-----------K------------N----K--K----	-2849.7	L12K A25N T30K G33K
145	---K-------K-------K---H-------------	-2849.6	T4K L12K S20K G24H
146	------K----K------------N----K-------	-2849.5	C7K L12K A25N T30K
147	-----------K----E-------N--H---------	-2849.3	L12K V17E A25N S28H
148	--K--------K-----------------K-----F-	-2849.1	N3K L12K T30K T36F
149	-----------K------------N----K---Q---	-2848.7	L12K A25N T30K S34Q
150	---K----------------------H-K------K	-2848.6	T4K S28H T30K Y37K
151	--------K----------------K-H-K-------	-2848.4	T9K I26K S28H T30K
152	-----------K-------K---------K--K----	-2847.7	L12K S20K T30K G33K
153	----------------------H---H-K------K	-2847.6	G24H S28H T30K Y37K
154	------K----K-------K---------K-------	-2847.5	C7K L12K S20K T30K

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Table S7 – continued from previous page

No.	Sequence S^{P_4}	$F(S^{P_4})$	Mutations
155	--KK----------H-K-------	-2847.5	N3K T4K S28H T30K
156	-------Q---K----------H--------K	-2847.3	A8Q L12K S28H Y37K
157	----------K----E--K-------H---------	-2847.2	L12K V17E S20K S28H
158	----------K----E----------K------K	-2847.1	L12K V17E T30K Y37K
159	----------K-------K----N----------K	-2846.8	L12K S20K A25N Y37K
160	----------K-------K---------K---Q---	-2846.7	L12K S20K T30K S34Q
161	--K----------H---H-K-------	-2846.5	N3K G24H S28H T30K
162	--K----Q---K----------H---------	-2846.2	N3K A8Q L12K S28H
163	--K--------K----E----------K-------	-2845.9	N3K L12K V17E T30K
164	--K--------K-------K----N----------	-2845.7	N3K L12K S20K A25N
165	-K-K-------K----------K-------	-2845.2	C2K T4K L12K T30K
166	-------Q----------N--H-K-------	-2845.2	A8Q A25N S28H T30K
167	---K-K-----K----------K-------	-2844.9	T4K T6K L12K T30K
168	--------K--K----------H--------K	-2844.5	T9K L12K S28H Y37K
169	-K---------K----------H-----K-------	-2844.2	C2K L12K G24H T30K
170	-----K-----K----------H-----K-------	-2843.9	T6K L12K G24H T30K
171	--K-----K--K----------H---------	-2843.4	N3K T9K L12K S28H
172	-------Q----------K-------H-K-------	-2843.1	A8Q S20K S28H T30K
173	--------K----------N--H-K-------	-2842.4	T9K A25N S28H T30K
174	---K-------K----------K----------K	-2840.7	T4K L12K I26K Y37K
175	--------K----------K-------H-K-------	-2840.3	T9K S20K S28H T30K
176	----------K----------H-K----K--	-2840.1	L12K S28H T30K N35K
177	----------K----------H-K----------K	-2839.7	L12K G24H I26K Y37K
178	--KK-------K----------K----------	-2839.6	N3K T4K L12K I26K
179	--K--------K----------H-K----------	-2838.6	N3K L12K G24H I26K
180	---K----------NK---K-------	-2838.5	T4K A25N I26K T30K
181	---K-------K----------H-------F-	-2838.2	T4K L12K S28H T36F
182	----------HNK---K-------	-2837.5	G24H A25N I26K T30K
183	-------Q---K----------NK----------	-2837.3	A8Q L12K A25N I26K
184	----------K----------H---H-------F-	-2837.2	L12K G24H S28H T36F
185	---K----------K-----K---K-------	-2836.5	T4K S20K I26K T30K
186	----------K---H-K---K-------	-2835.5	S20K G24H I26K T30K
187	---K-------K----------K--K----	-2835.5	T4K L12K T30K G33K
188	-K---------K----------K-H---------	-2835.5	C2K L12K I26K S28H
189	---K--K----K----------K-------	-2835.3	T4K C7K L12K T30K
190	-------Q---K-------K-----K----------	-2835.2	A8Q L12K S20K I26K
191	-----K-----K----------K-H---------	-2835.2	T6K L12K I26K S28H
192	---K-------K----E----------H---------	-2835.1	T4K L12K V17E S28H
193	---K-------K----------N----------K	-2834.7	T4K L12K A25N Y37K
194	---K-------K----------K---Q---	-2834.5	T4K L12K T30K S34Q
195	----------K----------H-----K--K----	-2834.5	L12K G24H T30K G33K
196	--------K--K----------NK----------	-2834.5	T9K L12K A25N I26K
197	------K----K----------H-----K-------	-2834.3	C7K L12K G24H T30K
198	----------K----E------H---H---------	-2834.1	L12K V17E G24H S28H
199	----------K----------HN----------K	-2833.7	L12K G24H A25N Y37K
200	--KK-------K----------N----------	-2833.6	N3K T4K L12K A25N
201	----------K----------H-----K---Q---	-2833.5	L12K G24H T30K S34Q
202	---K-------K-------K----------K	-2832.6	T4K L12K S20K Y37K
203	-------Q---K----------K-----F-	-2832.6	A8Q L12K T30K T36F
204	--K--------K----------HN----------	-2832.6	N3K L12K G24H A25N
205	--------K--K-------K-----K----------	-2832.5	T9K L12K S20K I26K
206	----------K-------K---H----------K	-2831.6	L12K S20K G24H Y37K

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Table S7 – continued from previous page

No.	Sequence S^{P_4}	$F(S^{P_4})$	Mutations
207	--KK-------K-------K----------	-2831.5	N3K T4K L12K S20K
208	---K---Q----------H-K-------	-2831.0	T4K A8Q S28H T30K
209	--K--------K-------K---H----------	-2830.5	N3K L12K S20K G24H
210	----M------K----------H-K-------	-2830.5	A5M L12K S28H T30K
211	---K----------K----N----K-------	-2830.5	T4K S20K A25N T30K
212	-------Q----------H---H-K-------	-2830.0	A8Q G24H S28H T30K
213	--------K--K----------K-----F-	-2829.8	T9K L12K T30K T36F
214	--K----------H-K------K	-2829.5	N3K S28H T30K Y37K
215	----------K---HN----K-------	-2829.5	S20K G24H A25N T30K
216	-K---------K----------N--H---------	-2829.5	C2K L12K A25N S28H
217	-------Q---K----E----------K-------	-2829.4	A8Q L12K V17E T30K
218	-------Q---K-------K----N----------	-2829.2	A8Q L12K S20K A25N
219	-----K-----K----------N--H---------	-2829.2	T6K L12K A25N S28H
220	----------KK----------K---K-------	-2828.7	L12K A13K I26K T30K
221	---K----K----------H-K-------	-2828.2	T4K T9K S28H T30K
222	-K---------K-------K-------H---------	-2827.4	C2K L12K S20K S28H
223	-K---------K----------K------K	-2827.2	C2K L12K T30K Y37K
224	--------K----------H---H-K-------	-2827.2	T9K G24H S28H T30K
225	-----K-----K-------K-------H---------	-2827.1	T6K L12K S20K S28H
226	-----K-----K----------K------K	-2827.0	T6K L12K T30K Y37K
227	-------QK--K----------H---------	-2826.9	A8Q T9K L12K S28H
228	--------K--K----E----------K-------	-2826.6	T9K L12K V17E T30K
229	--------K--K-------K----N----------	-2826.4	T9K L12K S20K A25N
230	-KK--------K----------K-------	-2826.1	C2K N3K L12K T30K
231	--K--K-----K----------K-------	-2825.8	N3K T6K L12K T30K
232	----------K----------K-H----K----	-2825.8	L12K I26K S28H G33K
233	------K----K----------K-H---------	-2825.6	C7K L12K I26K S28H
234	----------K----------K-H-----Q---	-2824.8	L12K I26K S28H S34Q
235	----------K-H-K-----F-	-2824.1	I26K S28H T30K T36F
236	---K----------H-K---K-------	-2823.3	T4K G24H I26K T30K
237	----------KK----------K---K-------	-2823.1	R11K L12K I26K T30K
238	---K---Q---K----------K----------	-2823.1	T4K A8Q L12K I26K
239	----------KK----------N----K-------	-2822.7	L12K A13K A25N T30K
240	-------Q---K----------H-K----------	-2822.1	A8Q L12K G24H I26K
241	--K--------K----------K----------K	-2821.6	N3K L12K I26K Y37K
242	----------K----------KK--K-------	-2821.5	L12K I26K L27K T30K
243	----------E--------K-H-K-------	-2821.0	V17E I26K S28H T30K
244	----------K----NK-H---------	-2820.7	S20K A25N I26K S28H
245	----------KK------K---------K-------	-2820.7	L12K A13K S20K T30K
246	----------NK---K------K	-2820.6	A25N I26K T30K Y37K
247	---K----K--K----------K----------	-2820.3	T4K T9K L12K I26K
248	----------K----------H-------FK	-2820.2	L12K S28H T36F Y37K
249	----------K--K----------K---K-------	-2820.0	L12K F15K I26K T30K
250	----------K----------N--H----K----	-2819.7	L12K A25N S28H G33K
251	------K----K----------N--H---------	-2819.6	C7K L12K A25N S28H
252	---K-------K----------H----------K	-2819.5	T4K L12K G24H Y37K
253	--K----------NK---K-------	-2819.5	N3K A25N I26K T30K
254	--------K--K----------H-K----------	-2819.3	T9K L12K G24H I26K
255	--K--------K----------H-------F-	-2819.1	N3K L12K S28H T36F
256	----------K----------N--H-----Q---	-2818.8	L12K A25N S28H S34Q
257	----------K------Y--------H-K-------	-2818.7	L12K S19Y S28H T30K
258	----------K-----K---K------K	-2818.5	S20K I26K T30K Y37K

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Table S7 – continued from previous page

No.	Sequence S^{P_4}	$F(S^{P_4})$	Mutations
259	--KK-------K-----------H----------	-2818.4	N3K T4K L12K G24H
260	----------N--H-K-----F-	-2818.1	A25N S28H T30K T36F
261	-----------K-------K-------H----K----	-2817.7	L12K S20K S28H G33K
262	------K----K-------K-------H---------	-2817.5	C7K L12K S20K S28H
263	-----------K----------K--K---K	-2817.5	L12K T30K G33K Y37K
264	--K----------K-----K---K-------	-2817.4	N3K S20K I26K T30K
265	------K----K----------K------K	-2817.4	C7K L12K T30K Y37K
266	---K----------HN----K-------	-2817.3	T4K G24H A25N T30K
267	-----------K----E----------H--------K	-2817.1	L12K V17E S28H Y37K
268	----------KK----------N----K-------	-2817.1	R11K L12K A25N T30K
269	---K---Q---K----------N----------	-2817.1	T4K A8Q L12K A25N
270	-----------K-------K-------H-----Q---	-2816.7	L12K S20K S28H S34Q
271	-----------K----------K---Q--K	-2816.6	L12K T30K S34Q Y37K
272	--K--------K----------K--K----	-2816.4	N3K L12K T30K G33K
273	---------K-K----------K---K-------	-2816.3	Q10K L12K I26K T30K
274	--K---K----K----------K-------	-2816.3	N3K C7K L12K T30K
275	-------Q---K----------HN----------	-2816.1	A8Q L12K G24H A25N
276	----------K-------H-K-----F-	-2816.0	S20K S28H T30K T36F
277	--K--------K----E----------H---------	-2816.0	N3K L12K V17E S28H
278	--K--------K----------N----------K	-2815.6	N3K L12K A25N Y37K
279	-----------K----------N-K--K-------	-2815.5	L12K A25N L27K T30K
280	--K--------K----------K---Q---	-2815.5	N3K L12K T30K S34Q
281	---K----------K---H-----K-------	-2815.3	T4K S20K G24H T30K
282	-K-K-------K----------H---------	-2815.2	C2K T4K L12K S28H
283	----------KK-------K---------K-------	-2815.0	R11K L12K S20K T30K
284	---K---Q---K-------K----------	-2815.0	T4K A8Q L12K S20K
285	---K-K-----K----------H---------	-2815.0	T4K T6K L12K S28H
286	----------E-------N--H-K-------	-2814.9	V17E A25N S28H T30K
287	---K----K--K----------N----------	-2814.3	T4K T9K L12K A25N
288	-K---------K----------H---H---------	-2814.3	C2K L12K G24H S28H
289	-----------K--K---------N----K-------	-2814.0	L12K F15K A25N T30K
290	-------Q---K-------K---H----------	-2814.0	A8Q L12K S20K G24H
291	-----K-----K----------H---H---------	-2814.0	T6K L12K G24H S28H
292	--K--------K-------K----------K	-2813.5	N3K L12K S20K Y37K
293	-----------K-------K------K--K-------	-2813.4	L12K S20K L27K T30K
294	--------K--K----------HN----------	-2813.3	T9K L12K G24H A25N
295	-------Q----------H-K------K	-2813.0	A8Q S28H T30K Y37K
296	----------E--K-------H-K-------	-2812.9	V17E S20K S28H T30K
297	----------K----N----K------K	-2812.5	S20K A25N T30K Y37K
298	-----------K----------HKK-------	-2812.2	L12K S28H S29K T30K
299	---K----K--K-------K----------	-2812.2	T4K T9K L12K S20K
300	-----------K--K----K---------K-------	-2812.0	L12K F15K S20K T30K
301	--K----Q----------H-K-------	-2811.9	N3K A8Q S28H T30K
302	--K----------K----N----K-------	-2811.4	N3K S20K A25N T30K
303	--------K--K-------K---H----------	-2811.2	T9K L12K S20K G24H
304	---------K-K----------N----K-------	-2810.3	Q10K L12K A25N T30K
305	--------K----------H-K------K	-2810.2	T9K S28H T30K Y37K
306	-----------K----------NK---------F-	-2810.2	L12K A25N I26K T36F
307	-K-----Q---K----------K-------	-2809.6	C2K A8Q L12K T30K
308	-----K-Q---K----------K-------	-2809.3	T6K A8Q L12K T30K
309	--K-----K----------H-K-------	-2809.1	N3K T9K S28H T30K
310	---K----------NK-H---------	-2808.6	T4K A25N I26K S28H

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No.	Sequence S^{P_4}	$F(S^{P_4})$	Mutations
311	---K-------KK----------K-------	-2808.5	T4K L12K A13K T30K
312	---------K-K-------K---------K-------	-2808.3	Q10K L12K S20K T30K
313	----------K-------K-----K---------F-	-2808.1	L12K S20K I26K T36F
314	----------HNK-H---------	-2807.6	G24H A25N I26K S28H
315	----------KK----------H-----K-------	-2807.5	L12K A13K G24H T30K
316	----------K----E-------NK----------	-2807.0	L12K V17E A25N I26K
317	-K------K--K----------K-------	-2806.8	C2K T9K L12K T30K
318	-----K--K--K----------K-------	-2806.5	T6K T9K L12K T30K
319	---K----------K-----K-H---------	-2806.5	T4K S20K I26K S28H
320	---K----------K---K------K	-2806.4	T4K I26K T30K Y37K
321	----------K---H-K-H---------	-2805.5	S20K G24H I26K S28H
322	---K-------K----------H----K----	-2805.5	T4K L12K S28H G33K
323	---K--K----K----------H---------	-2805.4	T4K C7K L12K S28H
324	----------H-K---K------K	-2805.4	G24H I26K T30K Y37K
325	--KK----------K---K-------	-2805.2	N3K T4K I26K T30K
326	-------Q---K----------K----------K	-2805.1	A8Q L12K I26K Y37K
327	----------K----E--K-----K----------	-2805.0	L12K V17E S20K I26K
328	---K-------K----------H-----Q---	-2804.6	T4K L12K S28H S34Q
329	----------K----------H---H----K----	-2804.5	L12K G24H S28H G33K
330	------K----K----------H---H---------	-2804.4	C7K L12K G24H S28H
331	--K----------H-K---K-------	-2804.2	N3K G24H I26K T30K
332	--K----Q---K----------K----------	-2804.0	N3K A8Q L12K I26K
333	---K----------H-K-----F-	-2803.9	T4K S28H T30K T36F
334	----------K----------H---H-----Q---	-2803.6	L12K G24H S28H S34Q
335	-------Q----------NK---K-------	-2803.0	A8Q A25N I26K T30K
336	---K------KK----------K-------	-2802.9	T4K R11K L12K T30K
337	----------H---H-K-----F-	-2802.9	G24H S28H T30K T36F
338	-------Q---K----------H-------F-	-2802.6	A8Q L12K S28H T36F
339	----------K----------H-K-V-----	-2802.5	L12K S28H T30K V32V
340	----------K----E----------K-----F-	-2802.3	L12K V17E T30K T36F
341	--------K--K----------K----------K	-2802.3	T9K L12K I26K Y37K
342	----------K-------K----N----------F-	-2802.1	L12K S20K A25N T36F
343	----------KK----------H-----K-------	-2801.9	R11K L12K G24H T30K
344	---K---Q---K----------H----------	-2801.9	T4K A8Q L12K G24H
345	--KK-------K----------K	-2801.4	N3K T4K L12K Y37K
346	---K-------K----------K--K-------	-2801.3	T4K L12K L27K T30K
347	--K-----K--K----------K----------	-2801.2	N3K T9K L12K I26K
348	-K----------K-H-K-------	-2801.1	C2K I26K S28H T30K
349	-------Q----------K-----K---K-------	-2800.9	A8Q S20K I26K T30K
350	-----K----------K-H-K-------	-2800.9	T6K I26K S28H T30K
351	---K----------E----------H-K-------	-2800.7	T4K V17E S28H T30K
352	---K----------K----N--H---------	-2800.5	T4K S20K A25N S28H
353	--K--------K----------H----------K	-2800.4	N3K L12K G24H Y37K
354	---K----------N----K------K	-2800.3	T4K A25N T30K Y37K
355	----------K-----Y---------H-K-------	-2800.3	L12K H18Y S28H T30K
356	----------K----------H--K--K-------	-2800.3	L12K G24H L27K T30K
357	--------K----------NK---K-------	-2800.2	T9K A25N I26K T30K
358	-------Q---K----------K--K----	-2799.9	A8Q L12K T30K G33K
359	--------K--K----------H-------F-	-2799.8	T9K L12K S28H T36F
360	---K-------K--K----------K-------	-2799.8	T4K L12K F15K T30K
361	------KQ---K----------K-------	-2799.8	C7K A8Q L12K T30K
362	----------E------H---H-K-------	-2799.7	V17E G24H S28H T30K

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No.	Sequence S^{P_4}	$F(S^{P_4})$	Mutations
363	----------K---HN--H---------	-2799.5	S20K G24H A25N S28H
364	-------Q---K----E----------H---------	-2799.5	A8Q L12K V17E S28H
365	----------HN----K------K	-2799.4	G24H A25N T30K Y37K
366	--KK----------N----K-------	-2799.2	N3K T4K A25N T30K
367	K----------K----------H-K-------	-2799.2	K1K L12K S28H T30K
368	-------Q---K----------N----------K	-2799.1	A8Q L12K A25N Y37K
369	---K----K--K----------H----------	-2799.1	T4K T9K L12K G24H
370	----------K----E--K----N----------	-2799.0	L12K V17E S20K A25N
371	-------Q---K----------K---Q---	-2799.0	A8Q L12K T30K S34Q
372	----------K--K--------H-----K-------	-2798.8	L12K F15K G24H T30K
373	----------KK----------K-H---------	-2798.8	L12K A13K I26K S28H
374	---K----------K---------K------K	-2798.3	T4K S20K T30K Y37K
375	--K----------HN----K-------	-2798.2	N3K G24H A25N T30K
376	--------K----------K-----K---K-------	-2798.1	T9K S20K I26K T30K
377	--K----Q---K----------N----------	-2798.0	N3K A8Q L12K A25N
378	----------K----------K---K----K--	-2797.8	L12K I26K T30K N35K
379	----------K---H-----K------K	-2797.3	S20K G24H T30K Y37K
380	-K---------K----------H--------K	-2797.3	C2K L12K S28H Y37K
381	--KK----------K---------K-------	-2797.2	N3K T4K S20K T30K
382	--------K--K----------K--K----	-2797.1	T9K L12K T30K G33K
383	-------Q---K-------K----------K	-2797.0	A8Q L12K S20K Y37K
384	-----K-----K----------H--------K	-2797.0	T6K L12K S28H Y37K
385	------K-K--K----------K-------	-2797.0	C7K T9K L12K T30K
386	--------K--K----E----------H---------	-2796.7	T9K L12K V17E S28H
387	--------K--K----------N----------K	-2796.3	T9K L12K A25N Y37K
388	--K----------K---H-----K-------	-2796.2	N3K S20K G24H T30K
389	--------K--K----------K---Q---	-2796.2	T9K L12K T30K S34Q
390	-KK--------K----------H---------	-2796.2	C2K N3K L12K S28H
391	---K-----K-K----------K-------	-2796.1	T4K Q10K L12K T30K
392	---K-------K----------K---------F-	-2796.0	T4K L12K I26K T36F
393	--K----Q---K-------K----------	-2795.9	N3K A8Q L12K S20K
394	--K--K-----K----------H---------	-2795.9	N3K T6K L12K S28H
395	--K-----K--K----------N----------	-2795.2	N3K T9K L12K A25N
396	-K----------N--H-K-------	-2795.1	C2K A25N S28H T30K
397	---------K-K----------H-----K-------	-2795.1	Q10K L12K G24H T30K
398	----------K----------H-K---------F-	-2795.0	L12K G24H I26K T36F
399	-------Q----------K----N----K-------	-2794.9	A8Q S20K A25N T30K
400	-----K----------N--H-K-------	-2794.8	T6K A25N S28H T30K
401	--------K--K-------K----------K	-2794.3	T9K L12K S20K Y37K
402	---K----------H-K-H---------	-2793.4	T4K G24H I26K S28H
403	--K-----K--K-------K----------	-2793.1	N3K T9K L12K S20K
404	----------KK----------K-H---------	-2793.1	R11K L12K I26K S28H
405	-K----------K-------H-K-------	-2793.1	C2K S20K S28H T30K
406	---K-------K----E--------K----------	-2792.8	T4K L12K V17E I26K
407	-----K----------K-------H-K-------	-2792.8	T6K S20K S28H T30K
408	----------KK----------N--H---------	-2792.8	L12K A13K A25N S28H
409	-------QK----------H-K-------	-2792.6	A8Q T9K S28H T30K
410	--------K----------K----N----K-------	-2792.1	T9K S20K A25N T30K
411	----------K----E------H-K----------	-2791.8	L12K V17E G24H I26K
412	----------K----------N----K----K--	-2791.8	L12K A25N T30K N35K
413	----------K----------KKH---------	-2791.5	L12K I26K L27K S28H
414	----------K-H-K--K----	-2791.4	I26K S28H T30K G33K

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No.	Sequence S^{P_4}	$F(S^{P_4})$	Mutations
415	------K------K-H-K-------	-2791.3	C7K I26K S28H T30K
416	----------KK------K-------H---------	-2790.7	L12K A13K S20K S28H
417	----------NK-H--------K	-2790.6	A25N I26K S28H Y37K
418	----------KK----------K------K	-2790.6	L12K A13K T30K Y37K
419	----------K-H-K---Q---	-2790.5	I26K S28H T30K S34Q
420	----------K--------K------H-K-------	-2790.2	L12K N21K S28H T30K
421	----------K--K----------K-H---------	-2790.1	L12K F15K I26K S28H
422	---K-------K----------N----------F-	-2790.0	T4K L12K A25N T36F
423	----------K-------K---------K----K--	-2789.8	L12K S20K T30K N35K
424	--K----------NK-H---------	-2789.5	N3K A25N I26K S28H
425	--K--------KK----------K-------	-2789.4	N3K L12K A13K T30K
426	----------K----------HN----------F-	-2789.0	L12K G24H A25N T36F
427	---K---Q----------K---K-------	-2788.7	T4K A8Q I26K T30K
428	----------K-----K-H--------K	-2788.6	S20K I26K S28H Y37K
429	----M------K----------K---K-------	-2788.3	A5M L12K I26K T30K
430	---K-------K-------K----------F-	-2787.9	T4K L12K S20K T36F
431	-------Q----------H-K---K-------	-2787.7	A8Q G24H I26K T30K
432	----------K----------H----K---K	-2787.6	L12K S28H G33K Y37K
433	--K----------K-----K-H---------	-2787.4	N3K S20K I26K S28H
434	------K----K----------H--------K	-2787.4	C7K L12K S28H Y37K
435	---K----------HN--H---------	-2787.4	T4K G24H A25N S28H
436	--K----------K---K------K	-2787.3	N3K I26K T30K Y37K
437	-K---------K----------NK----------	-2787.2	C2K L12K A25N I26K
438	----------KK----------N--H---------	-2787.1	R11K L12K A25N S28H
439	-----K-----K----------NK----------	-2786.9	T6K L12K A25N I26K
440	----------K-------K---H----------F-	-2786.9	L12K S20K G24H T36F
441	---K-------K----E-------N----------	-2786.8	T4K L12K V17E A25N
442	----------K----------H-----Q--K	-2786.6	L12K S28H S34Q Y37K
443	--K--------K----------H----K----	-2786.5	N3K L12K S28H G33K
444	---------K-K----------K-H---------	-2786.4	Q10K L12K I26K S28H
445	--K---K----K----------H---------	-2786.3	N3K C7K L12K S28H
446	---K----K----------K---K-------	-2786.0	T4K T9K I26K T30K
447	----------H-K-----FK	-2785.9	S28H T30K T36F Y37K
448	----------K----E------HN----------	-2785.8	L12K V17E G24H A25N
449	----------K----------N-KH---------	-2785.5	L12K A25N L27K S28H
450	--K--------K----------H-----Q---	-2785.5	N3K L12K S28H S34Q
451	----------N--H-K--K----	-2785.4	A25N S28H T30K G33K
452	---K----------K---H---H---------	-2785.3	T4K S20K G24H S28H
453	------K----------N--H-K-------	-2785.3	C7K A25N S28H T30K
454	-K---------K-------K-----K----------	-2785.2	C2K L12K S20K I26K
455	---K----------H-----K------K	-2785.1	T4K G24H T30K Y37K
456	----------KK-------K-------H---------	-2785.1	R11K L12K S20K S28H
457	--------K----------H-K---K-------	-2785.0	T9K G24H I26K T30K
458	----------KK----------K------K	-2784.9	R11K L12K T30K Y37K
459	-----K-----K-------K-----K----------	-2784.9	T6K L12K S20K I26K
460	---K---Q---K----------K	-2784.9	T4K A8Q L12K Y37K
461	---K-------K----E--K----------	-2784.8	T4K L12K V17E S20K
462	--K----------H-K-----F-	-2784.8	N3K S28H T30K T36F
463	-------QK--K----------K----------	-2784.7	A8Q T9K L12K I26K
464	----------N--H-K---Q---	-2784.5	A25N S28H T30K S34Q
465	----------K--K---------N--H---------	-2784.1	L12K F15K A25N S28H
466	----------K----------H-KK------	-2784.0	L12K S28H T30K N31K

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No.	Sequence S^{P_4}	$F(S^{P_4})$	Mutations
467	--KK----------H-----K-------	-2784.0	N3K T4K G24H T30K
468	-------Q---K----------H----------K	-2783.9	A8Q L12K G24H Y37K
469	--K-------KK----------K-------	-2783.8	N3K R11K L12K T30K
470	----------K----E--K---H----------	-2783.8	L12K V17E S20K G24H
471	--KK---Q---K----------	-2783.8	N3K T4K A8Q L12K
472	----------K-------K------KH---------	-2783.5	L12K S20K L27K S28H
473	----------K-------H-K--K----	-2783.4	S20K S28H T30K G33K
474	----------K----------K--K------K	-2783.3	L12K L27K T30K Y37K
475	------K----------K-------H-K-------	-2783.2	C7K S20K S28H T30K
476	--K----Q---K----------H----------	-2782.8	N3K A8Q L12K G24H
477	----------E----------H-K------K	-2782.8	V17E S28H T30K Y37K
478	---K---Q----------N----K-------	-2782.7	T4K A8Q A25N T30K
479	----------K----N--H--------K	-2782.6	S20K A25N S28H Y37K
480	-K---------K----------K-----F-	-2782.5	C2K L12K T30K T36F
481	----------K-------H-K---Q---	-2782.4	S20K S28H T30K S34Q
482	----M------K----------N----K-------	-2782.3	A5M L12K A25N T30K
483	-----K-----K----------K-----F-	-2782.2	T6K L12K T30K T36F
484	--K--------K----------K--K-------	-2782.2	N3K L12K L27K T30K
485	---K----K--K----------K	-2782.1	T4K T9K L12K Y37K
486	----------K--K----K-------H---------	-2782.0	L12K F15K S20K S28H
487	----------K--K----------K------K	-2781.9	L12K F15K T30K Y37K
488	-------Q----------HN----K-------	-2781.7	A8Q G24H A25N T30K
489	--K----------E----------H-K-------	-2781.6	N3K V17E S28H T30K
490	--K----------K----N--H---------	-2781.4	N3K S20K A25N S28H
491	--K----------N----K------K	-2781.3	N3K A25N T30K Y37K
492	--------K--K----------H----------K	-2781.1	T9K L12K G24H Y37K
493	--KK----K--K----------	-2781.0	N3K T4K T9K L12K
494	-K-K----------H-K-------	-2780.9	C2K T4K S28H T30K
495	--K--------K--K----------K-------	-2780.7	N3K L12K F15K T30K
496	---K---Q----------K---------K-------	-2780.7	T4K A8Q S20K T30K
497	---K-K----------H-K-------	-2780.6	T4K T6K S28H T30K
498	---------K-K----------N--H---------	-2780.4	Q10K L12K A25N S28H
499	----M------K-------K---------K-------	-2780.2	A5M L12K S20K T30K
500	--K-----K--K----------H----------	-2780.0	N3K T9K L12K G24H
501	---K----K----------N----K-------	-2779.9	T4K T9K A25N T30K
502	-K----------H---H-K-------	-2779.9	C2K G24H S28H T30K
503	-------Q----------K---H-----K-------	-2779.7	A8Q S20K G24H T30K
504	-K-----Q---K----------H---------	-2779.7	C2K A8Q L12K S28H
505	-----K----------H---H-K-------	-2779.6	T6K G24H S28H T30K
506	-K---------K----E----------K-------	-2779.4	C2K L12K V17E T30K
507	-----K-Q---K----------H---------	-2779.4	T6K A8Q L12K S28H
508	--K----------K---------K------K	-2779.2	N3K S20K T30K Y37K
509	-K---------K-------K----N----------	-2779.2	C2K L12K S20K A25N
510	-----K-----K----E----------K-------	-2779.1	T6K L12K V17E T30K
511	--------K----------HN----K-------	-2778.9	T9K G24H A25N T30K
512	-----K-----K-------K----N----------	-2778.9	T6K L12K S20K A25N
513	-------QK--K----------N----------	-2778.7	A8Q T9K L12K A25N
514	---K-------KK----------H---------	-2778.6	T4K L12K A13K S28H
515	---------K-K-------K-------H---------	-2778.3	Q10K L12K S20K S28H
516	---------K-K----------K------K	-2778.2	Q10K L12K T30K Y37K
517	----------K----------K---------FK	-2778.0	L12K I26K T36F Y37K
518	---K----K----------K---------K-------	-2777.9	T4K T9K S20K T30K

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No.	Sequence S^{P_4}	$F(S^{P_4})$	Mutations
519	---K-------K----------K----K--	-2777.6	T4K L12K T30K N35K
520	----------KK----------H---H---------	-2777.6	L12K A13K G24H S28H
521	----------K----------NK------K----	-2777.5	L12K A25N I26K G33K
522	------K----K----------NK----------	-2777.4	C7K L12K A25N I26K
523	--K------K-K----------K-------	-2777.0	N3K Q10K L12K T30K
524	--------K----------K---H-----K-------	-2776.9	T9K S20K G24H T30K
525	--K--------K----------K---------F-	-2776.9	N3K L12K I26K T36F
526	-K------K--K----------H---------	-2776.9	C2K T9K L12K S28H
527	-------QK--K-------K----------	-2776.6	A8Q T9K L12K S20K
528	----------K----------H-----K----K--	-2776.6	L12K G24H T30K N35K
529	-----K--K--K----------H---------	-2776.6	T6K T9K L12K S28H
530	----------K----------NK-------Q---	-2776.6	L12K A25N I26K S34Q
531	----------K------Y------K---K-------	-2776.5	L12K S19Y I26K T30K
532	---K----------K-H--------K	-2776.4	T4K I26K S28H Y37K
533	----------NK---K-----F-	-2775.9	A25N I26K T30K T36F
534	----------K-------K-----K------K----	-2775.5	L12K S20K I26K G33K
535	----------H-K-H--------K	-2775.4	G24H I26K S28H Y37K
536	------K----K-------K-----K----------	-2775.3	C7K L12K S20K I26K
537	--KK----------K-H---------	-2775.3	N3K T4K I26K S28H
538	----------K----------F----H-K-------	-2775.1	L12K F23F S28H T30K
539	----------K----E--------K----------K	-2774.9	L12K V17E I26K Y37K
540	---K-------K----------H----------F-	-2774.8	T4K L12K G24H T36F
541	----------K-------K-----K-------Q---	-2774.5	L12K S20K I26K S34Q
542	--K----------H-K-H---------	-2774.3	N3K G24H I26K S28H
543	----------K-----K---K-----F-	-2773.8	S20K I26K T30K T36F
544	--K--------K----E--------K----------	-2773.8	N3K L12K V17E I26K
545	----------K---N----------H-K-------	-2773.3	L12K L16N S28H T30K
546	-K-K-------K----------K----------	-2773.0	C2K T4K L12K I26K
547	-------Q----------NK-H---------	-2773.0	A8Q A25N I26K S28H
548	-------Q---KK----------K-------	-2772.9	A8Q L12K A13K T30K
549	---K------KK----------H---------	-2772.9	T4K R11K L12K S28H
550	----------K---------Y-----H-K-------	-2772.8	L12K N22Y S28H T30K
551	----------K----------K--K--F-	-2772.8	L12K T30K G33K T36F
552	----------K-M----------H-K-------	-2772.8	L12K N14M S28H T30K
553	---K-K-----K----------K----------	-2772.7	T4K T6K L12K I26K
554	----------E-------NK---K-------	-2772.7	V17E A25N I26K T30K
555	------K----K----------K-----F-	-2772.7	C7K L12K T30K T36F
556	----------K----E----------H-------F-	-2772.4	L12K V17E S28H T36F
557	-K---------K----------H-K----------	-2772.0	C2K L12K G24H I26K
558	----------K----------N----------FK	-2772.0	L12K A25N T36F Y37K
559	----------KK----------H---H---------	-2771.9	R11K L12K G24H S28H
560	----------K----------K---Q-F-	-2771.9	L12K T30K S34Q T36F
561	-----K-----K----------H-K----------	-2771.7	T6K L12K G24H I26K
562	---K-------K----E------H----------	-2771.6	T4K L12K V17E G24H
563	---K-------K----------KH---------	-2771.3	T4K L12K L27K S28H
564	---K----------H-K--K----	-2771.2	T4K S28H T30K G33K
565	---K--K----------H-K-------	-2771.0	T4K C7K S28H T30K
566	-------Q----------K-----K-H---------	-2770.9	A8Q S20K I26K S28H
567	--K--------K----------N----------F-	-2770.9	N3K L12K A25N T36F
568	-------Q----------K---K------K	-2770.8	A8Q I26K T30K Y37K
569	----------E--K-----K---K-------	-2770.7	V17E S20K I26K T30K
570	----------K------Y-----N----K-------	-2770.5	L12K S19Y A25N T30K

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No.	Sequence S^{P_4}	$F(S^{P_4})$	Mutations
571	---K----------N--H--------K	-2770.4	T4K A25N S28H Y37K
572	----------K----------H--KH---------	-2770.3	L12K G24H L27K S28H
573	---K----------H-K---Q---	-2770.3	T4K S28H T30K S34Q
574	----------H---H-K--K----	-2770.2	G24H S28H T30K G33K
575	--------K----------NK-H---------	-2770.2	T9K A25N I26K S28H
576	--------K--KK----------K-------	-2770.2	T9K L12K A13K T30K
577	------K----------H---H-K-------	-2770.1	C7K G24H S28H T30K
578	----------K----------K--KK-------	-2770.0	L12K I26K S29K T30K
579	-------Q---K----------H----K----	-2770.0	A8Q L12K S28H G33K
580	----------K-------K----------FK	-2769.9	L12K S20K T36F Y37K
581	---K-------K--K----------H---------	-2769.9	T4K L12K F15K S28H
582	------KQ---K----------H---------	-2769.8	C7K A8Q L12K S28H
583	----------K----E----------K--K----	-2769.7	L12K V17E T30K G33K
584	--K----Q----------K---K-------	-2769.7	N3K A8Q I26K T30K
585	------K----K----E----------K-------	-2769.5	C7K L12K V17E T30K
586	----------K-------K----N-------K----	-2769.5	L12K S20K A25N G33K
587	----------HN--H--------K	-2769.4	G24H A25N S28H Y37K
588	------K----K-------K----N----------	-2769.3	C7K L12K S20K A25N
589	--KK----------N--H---------	-2769.3	N3K T4K A25N S28H
590	----------H---H-K---Q---	-2769.3	G24H S28H T30K S34Q
591	-------Q---K----------H-----Q---	-2769.0	A8Q L12K S28H S34Q
592	----------K--K--------H---H---------	-2768.9	L12K F15K G24H S28H
593	----------K----E-------N----------K	-2768.9	L12K V17E A25N Y37K
594	--K--------K-------K----------F-	-2768.8	N3K L12K S20K T36F
595	----------K----E----------K---Q---	-2768.7	L12K V17E T30K S34Q
596	----------K-------K----N--------Q---	-2768.5	L12K S20K A25N S34Q
597	----------K------YK---------K-------	-2768.4	L12K S19Y S20K T30K
598	---K----------K-------H--------K	-2768.3	T4K S20K S28H Y37K
599	-------Q----------H-K-----F-	-2768.3	A8Q S28H T30K T36F
600	--K----------HN--H---------	-2768.3	N3K G24H A25N S28H
601	--------K----------K-----K-H---------	-2768.2	T9K S20K I26K S28H
602	---KM------K----------K-------	-2768.1	T4K A5M L12K T30K
603	--------K----------K---K------K	-2768.0	T9K I26K T30K Y37K
604	----------K----------K-H------K--	-2767.9	L12K I26K S28H N35K
605	----------K----N----K-----F-	-2767.8	S20K A25N T30K T36F
606	--K--------K----E-------N----------	-2767.7	N3K L12K V17E A25N
607	---K---Q----------H-----K-------	-2767.5	T4K A8Q G24H T30K
608	----------K---H---H--------K	-2767.3	S20K G24H S28H Y37K
609	-------Q--KK----------K-------	-2767.3	A8Q R11K L12K T30K
610	--KK----------K-------H---------	-2767.2	N3K T4K S20K S28H
611	--------K--K----------H----K----	-2767.2	T9K L12K S28H G33K
612	----M------K----------H-----K-------	-2767.1	A5M L12K G24H T30K
613	--KK----------K------K	-2767.1	N3K T4K T30K Y37K
614	-K-K-------K----------N----------	-2767.0	C2K T4K L12K A25N
615	------K-K--K----------H---------	-2767.0	C7K T9K L12K S28H
616	--K-----K----------K---K-------	-2766.9	N3K T9K I26K T30K
617	----------K----E--K----------K	-2766.8	L12K V17E S20K Y37K
618	---K-K-----K----------N----------	-2766.7	T4K T6K L12K A25N
619	--K----------K---H---H---------	-2766.2	N3K S20K G24H S28H
620	--------K--K----------H-----Q---	-2766.2	T9K L12K S28H S34Q
621	---K-----K-K----------H---------	-2766.2	T4K Q10K L12K S28H
622	--K----------H-----K------K	-2766.1	N3K G24H T30K Y37K

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No.	Sequence S^{P_4}	$F(S^{P_4})$	Mutations
623	-K---------K-----------HN----------	-2766.0	C2K L12K G24H A25N
624	--K----Q---K-----------------------K	-2765.8	N3K A8Q L12K Y37K
625	-----K-----K-----------HN----------	-2765.7	T6K L12K G24H A25N
626	--K--------K----E--K----------	-2765.7	N3K L12K V17E S20K
627	-------Q---K----------K--K-------	-2765.7	A8Q L12K L27K T30K
628	--------K----------H-K-----F-	-2765.5	T9K S28H T30K T36F
629	---------K-K-----------H---H---------	-2765.2	Q10K L12K G24H S28H
630	-------Q--------E----------H-K-------	-2765.1	A8Q V17E S28H T30K
631	-K-K-------K-------K----------	-2765.0	C2K T4K L12K S20K
632	-------Q-----------K----N--H---------	-2764.9	A8Q S20K A25N S28H
633	-------Q----------N----K------K	-2764.8	A8Q A25N T30K Y37K
634	---K----K----------H-----K-------	-2764.7	T4K T9K G24H T30K
635	---K-K-----K-------K----------	-2764.7	T4K T6K L12K S20K
636	----------E--K----N----K-------	-2764.7	V17E S20K A25N T30K
637	--------K-KK----------K-------	-2764.5	T9K R11K L12K T30K
638	---K---QK--K------------------------	-2764.5	T4K A8Q T9K L12K
639	----------K----------K-H-K-------	-2764.5	A13K I26K S28H T30K
640	-------Q---K--K----------K-------	-2764.2	A8Q L12K F15K T30K
641	-----------K----------N---KK-------	-2764.0	L12K A25N S29K T30K
642	-K---------K-------K---H----------	-2764.0	C2K L12K S20K G24H
643	-----K-----K-------K---H----------	-2763.7	T6K L12K S20K G24H
644	--K----Q----------N----K-------	-2763.6	N3K A8Q A25N T30K
645	-------QK--K-----------H----------	-2763.5	A8Q T9K L12K G24H
646	---K-------K----------K------K----	-2763.3	T4K L12K I26K G33K
647	---K--K----K----------K-----------	-2763.2	T4K C7K L12K I26K
648	--K-----K--K-----------------------K	-2763.0	N3K T9K L12K Y37K
649	-K----------H-K------K	-2763.0	C2K S28H T30K Y37K
650	--------K--K----------K--K-------	-2762.9	T9K L12K L27K T30K
651	-------Q-----------K---------K------K	-2762.7	A8Q S20K T30K Y37K
652	-----K----------H-K------K	-2762.7	T6K S28H T30K Y37K
653	--------K-------E----------H-K-------	-2762.4	T9K V17E S28H T30K
654	---K-------K----------K-------Q---	-2762.4	T4K L12K I26K S34Q
655	-----------K-----------H-K------K----	-2762.3	L12K G24H I26K G33K
656	------K----K-----------H-K-----------	-2762.2	C7K L12K G24H I26K
657	--------K----------K----N--H---------	-2762.2	T9K S20K A25N S28H
658	--------K----------N----K------K	-2762.0	T9K A25N T30K Y37K
659	-----------K-------K--------KK-------	-2762.0	L12K S20K S29K T30K
660	-----------K----------N--H------K--	-2761.9	L12K A25N S28H N35K
661	-KK----------H-K-------	-2761.8	C2K N3K S28H T30K
662	---K----------K---K-----F-	-2761.6	T4K I26K T30K T36F
663	--K----Q-----------K---------K-------	-2761.6	N3K A8Q S20K T30K
664	--K--K----------H-K-------	-2761.5	N3K T6K S28H T30K
665	--------K--K--K----------K-------	-2761.5	T9K L12K F15K T30K
666	-----------K-----------H-K-------Q---	-2761.4	L12K G24H I26K S34Q
667	--K-----K----------N----K-------	-2760.9	N3K T9K A25N T30K
668	----------H-K---K-----F-	-2760.6	G24H I26K T30K T36F
669	-----------KK----------H--------K	-2760.6	L12K A13K S28H Y37K
670	-------Q-K-K----------K-------	-2760.5	A8Q Q10K L12K T30K
671	-------Q---K----------K---------F-	-2760.4	A8Q L12K I26K T36F
672	-----------K----------K---K-V-----	-2760.3	L12K I26K T30K V32V
673	--------K----------K---------K------K	-2759.9	T9K S20K T30K Y37K
674	-----------K-------K-------H------K--	-2759.8	L12K S20K S28H N35K

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No.	Sequence S^{P_4}	$F(S^{P_4})$	Mutations
675	----------K----------K----K-K	-2759.7	L12K T30K N35K Y37K
676	--K--------KK----------H---------	-2759.5	N3K L12K A13K S28H
677	-K---K-----K----------K-------	-2759.3	C2K T6K L12K T30K
678	--K-----K----------K---------K-------	-2758.8	N3K T9K S20K T30K
679	----------K----------K-H-K-------	-2758.8	R11K I26K S28H T30K
680	---K---Q----------K-H---------	-2758.8	T4K A8Q I26K S28H
681	--K--------K----------K----K--	-2758.5	N3K L12K T30K N35K
682	---K----------E--------K---K-------	-2758.5	T4K V17E I26K T30K
683	----------K----------N--H-K-------	-2758.4	A13K A25N S28H T30K
684	----M------K----------K-H---------	-2758.3	A5M L12K I26K S28H
685	---K----------K----NK----------	-2758.3	T4K S20K A25N I26K
686	----------K-----Y-------K---K-------	-2758.1	L12K H18Y I26K T30K
687	-------Q----------H-K-H---------	-2757.8	A8Q G24H I26K S28H
688	---K-------K----------FK	-2757.8	T4K L12K T36F Y37K
689	--------KK-K----------K-------	-2757.8	T9K Q10K L12K T30K
690	--------K--K----------K---------F-	-2757.6	T9K L12K I26K T36F
691	----------E------H-K---K-------	-2757.5	V17E G24H I26K T30K
692	--K----------K-H--------K	-2757.3	N3K I26K S28H Y37K
693	----------K---HNK----------	-2757.3	S20K G24H A25N I26K
694	---K-------K----------N-------K----	-2757.3	T4K L12K A25N G33K
695	-------Q---K----E--------K----------	-2757.3	A8Q L12K V17E I26K
696	----------KKH-K-------	-2757.2	I26K L27K S28H T30K
697	---K--K----K----------N----------	-2757.1	T4K C7K L12K A25N
698	K----------K----------K---K-------	-2756.9	K1K L12K I26K T30K
699	----------K----------H----------FK	-2756.8	L12K G24H T36F Y37K
700	--KK-------K----------F-	-2756.7	N3K T4K L12K T36F
701	----------K------K-------H-K-------	-2756.4	A13K S20K S28H T30K
702	---K-------K----------N--------Q---	-2756.3	T4K L12K A25N S34Q
703	----------K----------HN-------K----	-2756.3	L12K G24H A25N G33K
704	---K-------K------Y----------K-------	-2756.2	T4K L12K S19Y T30K
705	------K----K----------HN----------	-2756.1	C7K L12K G24H A25N
706	---K----K----------K-H---------	-2756.0	T4K T9K I26K S28H
707	----------K----------K-H-K-------	-2755.8	F15K I26K S28H T30K
708	--K--------K----------H----------F-	-2755.7	N3K L12K G24H T36F
709	---K----------N----K-----F-	-2755.6	T4K A25N T30K T36F
710	----------K----------HN--------Q---	-2755.4	L12K G24H A25N S34Q
711	---K-------K-------K----------K----	-2755.3	T4K L12K S20K G33K
712	----------K------Y----H-----K-------	-2755.3	L12K S19Y G24H T30K
713	---K----------H---H--------K	-2755.2	T4K G24H S28H Y37K
714	---K--K----K-------K----------	-2755.1	T4K C7K L12K S20K
715	-K---------K----------K----------K	-2755.1	C2K L12K I26K Y37K
716	--------K----------H-K-H---------	-2755.0	T9K G24H I26K S28H
717	----------KK----------H--------K	-2755.0	R11K L12K S28H Y37K
718	-----K-----K----------K----------K	-2754.8	T6K L12K I26K Y37K
719	---K-------K----E----------K	-2754.7	T4K L12K V17E Y37K
720	----------HN----K-----F-	-2754.6	G24H A25N T30K T36F
721	--------K--K----E--------K----------	-2754.5	T9K L12K V17E I26K
722	-------Q---K----------N----------F-	-2754.4	A8Q L12K A25N T36F
723	---K-------K-------K----------Q---	-2754.3	T4K L12K S20K S34Q
724	----------K-------K---H--------K----	-2754.3	L12K S20K G24H G33K
725	----------K----------N----K-V-----	-2754.2	L12K A25N T30K V32V
726	------K----K-------K---H----------	-2754.1	C7K L12K S20K G24H

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Table S7 – continued from previous page

No.	Sequence S^{P_4}	$F(S^{P_4})$	Mutations
727	--KK----------H---H---------	-2754.1	N3K T4K G24H S28H
728	-KK--------K----------K----------	-2753.9	C2K N3K L12K I26K
729	--K-------KK----------H---------	-2753.8	N3K R11K L12K S28H
730	----------K----E------H----------K	-2753.7	L12K V17E G24H Y37K
731	--K--K-----K----------K----------	-2753.7	N3K T6K L12K I26K
732	---K----------K---------K-----F-	-2753.6	T4K S20K T30K T36F
733	--KK-------K----E----------	-2753.5	N3K T4K L12K V17E
734	----------K----------KH--------K	-2753.3	L12K L27K S28H Y37K
735	----------K-------K---H---------Q---	-2753.3	L12K S20K G24H S34Q
736	----------H-K--K---K	-2753.2	S28H T30K G33K Y37K
737	------K----------H-K------K	-2753.1	C7K S28H T30K Y37K
738	-K----------NK---K-------	-2752.9	C2K A25N I26K T30K
739	----------K----------N--H-K-------	-2752.8	R11K A25N S28H T30K
740	---K---Q----------N--H---------	-2752.8	T4K A8Q A25N S28H
741	-----K----------NK---K-------	-2752.6	T6K A25N I26K T30K
742	----------K---H-----K-----F-	-2752.6	S20K G24H T30K T36F
743	-K---------K----------H-------F-	-2752.6	C2K L12K S28H T36F
744	--K--------K----E------H----------	-2752.5	N3K L12K V17E G24H
745	---K----------E-------N----K-------	-2752.5	T4K V17E A25N T30K
746	-------Q---K-------K----------F-	-2752.3	A8Q L12K S20K T36F
747	----M------K----------N--H---------	-2752.3	A5M L12K A25N S28H
748	----------H-K---Q--K	-2752.3	S28H T30K S34Q Y37K
749	-----K-----K----------H-------F-	-2752.3	T6K L12K S28H T36F
750	--K--------K----------KH---------	-2752.2	N3K L12K L27K S28H
751	----------K-------K---------K-V-----	-2752.2	L12K S20K T30K V32V
752	--K----------H-K--K----	-2752.1	N3K S28H T30K G33K
753	----------K-----Y------N----K-------	-2752.1	L12K H18Y A25N T30K
754	---------K----------K-H-K-------	-2752.1	Q10K I26K S28H T30K
755	--K---K----------H-K-------	-2752.0	N3K C7K S28H T30K
756	----------K--K----------H--------K	-2751.9	L12K F15K S28H Y37K
757	-K-K-------K----------H----------	-2751.8	C2K T4K L12K G24H
758	-------Q----------HN--H---------	-2751.8	A8Q G24H A25N S28H
759	--------K--K----------N----------F-	-2751.6	T9K L12K A25N T36F
760	---K-K-----K----------H----------	-2751.5	T4K T6K L12K G24H
761	----------E------HN----K-------	-2751.5	V17E G24H A25N T30K
762	--K----------N--H--------K	-2751.3	N3K A25N S28H Y37K
763	-------Q---K----E-------N----------	-2751.2	A8Q L12K V17E A25N
764	----------N-KH-K-------	-2751.2	A25N L27K S28H T30K
765	--K----------H-K---Q---	-2751.2	N3K S28H T30K S34Q
766	K----------K----------N----K-------	-2750.9	K1K L12K A25N T30K
767	-K----------K-----K---K-------	-2750.9	C2K S20K I26K T30K
768	--K--------K--K----------H---------	-2750.8	N3K L12K F15K S28H
769	----------K--------K-------H-K-------	-2750.8	R11K S20K S28H T30K
770	---K---Q----------K-------H---------	-2750.7	T4K A8Q S20K S28H
771	-----K----------K-----K---K-------	-2750.6	T6K S20K I26K T30K
772	---K---Q----------K------K	-2750.6	T4K A8Q T30K Y37K
773	----------KK----------NK----------	-2750.6	L12K A13K A25N I26K
774	---K----------E--K---------K-------	-2750.5	T4K V17E S20K T30K
775	-------QK----------K---K-------	-2750.4	A8Q T9K I26K T30K
776	----M------K-------K-------H---------	-2750.3	A5M L12K S20K S28H
777	----M------K----------K------K	-2750.1	A5M L12K T30K Y37K
778	----------K-----Y-K---------K-------	-2750.0	L12K H18Y S20K T30K

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No.	Sequence S^{P_4}	$F(S^{P_4})$	Mutations
779	---K----K----------N--H---------	-2750.0	T4K T9K A25N S28H
780	-K---------K----------K--K----	-2749.9	C2K L12K T30K G33K
781	---K-------K----------KK-------	-2749.8	T4K L12K S29K T30K
782	----------K---------N--H-K-------	-2749.7	F15K A25N S28H T30K
783	-------Q----------K---H---H---------	-2749.7	A8Q S20K G24H S28H
784	-K----K----K----------K-------	-2749.7	C2K C7K L12K T30K
785	-----K-----K----------K--K----	-2749.6	T6K L12K T30K G33K
786	-------Q----------H-----K------K	-2749.6	A8Q G24H T30K Y37K
787	--------K--K-------K----------F-	-2749.5	T9K L12K S20K T36F
788	----------E--K---H-----K-------	-2749.5	V17E S20K G24H T30K
789	--KK---Q----------K-------	-2749.4	N3K T4K A8Q T30K
790	-K---------K----E----------H---------	-2749.4	C2K L12K V17E S28H
791	-----KK----K----------K-------	-2749.4	T6K C7K L12K T30K
792	--K----------K-------H--------K	-2749.3	N3K S20K S28H Y37K
793	-------Q---K----E--K----------	-2749.2	A8Q L12K V17E S20K
794	-----K-----K----E----------H---------	-2749.1	T6K L12K V17E S28H
795	----------K------KH-K-------	-2749.1	S20K L27K S28H T30K
796	-K---------K----------N----------K	-2749.0	C2K L12K A25N Y37K
797	--------K----------HN--H---------	-2749.0	T9K G24H A25N S28H
798	--K-M------K----------K-------	-2749.0	N3K A5M L12K T30K
799	-K---------K----------K---Q---	-2748.9	C2K L12K T30K S34Q
800	K----------K-------K---------K-------	-2748.9	K1K L12K S20K T30K
801	----------K----------H----KK-------	-2748.8	L12K G24H S29K T30K
802	-----K-----K----------N----------K	-2748.8	T6K L12K A25N Y37K
803	-----K-----K----------K---Q---	-2748.6	T6K L12K T30K S34Q
804	----------KK------K-----K----------	-2748.5	L12K A13K S20K I26K
805	--------K--K----E-------N----------	-2748.5	T9K L12K V17E A25N
806	--K----Q----------H-----K-------	-2748.4	N3K A8Q G24H T30K
807	---------K-K----------H--------K	-2748.2	Q10K L12K S28H Y37K
808	---K----K----------K-------H---------	-2747.9	T4K T9K S20K S28H
809	----------K--------K----K---K-------	-2747.9	L12K N21K I26K T30K
810	-KK--------K----------N----------	-2747.9	C2K N3K L12K A25N
811	---K----K----------K------K	-2747.8	T4K T9K T30K Y37K
812	----------K----K-------H-K-------	-2747.7	F15K S20K S28H T30K
813	---K-------K----------H------K--	-2747.7	T4K L12K S28H N35K
814	--K--K-----K----------N----------	-2747.6	N3K T6K L12K A25N
815	--K------K-K----------H---------	-2747.1	N3K Q10K L12K S28H
816	-K---------K-------K----------K	-2747.0	C2K L12K S20K Y37K
817	--------K----------K---H---H---------	-2746.9	T9K S20K G24H S28H
818	--------K----------H-----K------K	-2746.8	T9K G24H T30K Y37K
819	-----K-----K-------K----------K	-2746.7	T6K L12K S20K Y37K
820	----------K----------H---H------K--	-2746.7	L12K G24H S28H N35K
821	--KK----K----------K-------	-2746.7	N3K T4K T9K T30K
822	-------QK--K----------K	-2746.5	A8Q T9K L12K Y37K
823	----------K------Y------K-H---------	-2746.5	L12K S19Y I26K S28H
824	--------K--K----E--K----------	-2746.4	T9K L12K V17E S20K
825	---------K----------N--H-K-------	-2746.0	Q10K A25N S28H T30K
826	----------NK-H-------F-	-2745.9	A25N I26K S28H T36F
827	-KK--------K-------K----------	-2745.9	C2K N3K L12K S20K
828	----------KK----------K-----F-	-2745.8	L12K A13K T30K T36F
829	--K-----K----------H-----K-------	-2745.7	N3K T9K G24H T30K
830	--K--K-----K-------K----------	-2745.6	N3K T6K L12K S20K

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No.	Sequence S^{P_4}	$F(S^{P_4})$	Mutations
831	--K----QK--K----------	-2745.4	N3K A8Q T9K L12K
832	----------K----------K------K---K	-2745.4	L12K I26K G33K Y37K
833	-K-----Q----------H-K-------	-2745.3	C2K A8Q S28H T30K
834	------K----K----------K----------K	-2745.2	C7K L12K I26K Y37K
835	---K----------HNK----------	-2745.1	T4K G24H A25N I26K
836	-----K-Q----------H-K-------	-2745.0	T6K A8Q S28H T30K
837	----------KK----------NK----------	-2744.9	R11K L12K A25N I26K
838	-K----------K----N----K-------	-2744.8	C2K S20K A25N T30K
839	-----K----------K----N----K-------	-2744.6	T6K S20K A25N T30K
840	----------K----------K-------Q--K	-2744.4	L12K I26K S34Q Y37K
841	-------QK----------N----K-------	-2744.4	A8Q T9K A25N T30K
842	---K--------K----------H-K-------	-2744.2	T4K A13K S28H T30K
843	--K--------K----------K------K----	-2744.2	N3K L12K I26K G33K
844	--K---K----K----------K----------	-2744.1	N3K C7K L12K I26K
845	---------K---------K-------H-K-------	-2744.0	Q10K S20K S28H T30K
846	----------K-----K-H-------F-	-2743.8	S20K I26K S28H T36F
847	----------K---K-----FK	-2743.7	I26K T30K T36F Y37K
848	----------K----------NKK----------	-2743.3	L12K A25N I26K L27K
849	--K--------K----------K-------Q---	-2743.3	N3K L12K I26K S34Q
850	----------K----------H---H-K-------	-2743.2	A13K G24H S28H T30K
851	----------NK---K--K----	-2743.2	A25N I26K T30K G33K
852	---K----------K---H-K----------	-2743.1	T4K S20K G24H I26K
853	------K----------NK---K-------	-2743.0	C7K A25N I26K T30K
854	-------Q---KK----------H---------	-2743.0	A8Q L12K A13K S28H
855	----------KK-------K-----K----------	-2742.9	R11K L12K S20K I26K
856	----------K----------H----K--F-	-2742.9	L12K S28H G33K T36F
857	----------E-------NK-H---------	-2742.8	V17E A25N I26K S28H
858	----------KK---E----------K-------	-2742.7	L12K A13K V17E T30K
859	------K----K----------H-------F-	-2742.7	C7K L12K S28H T36F
860	--K----------K---K-----F-	-2742.6	N3K I26K T30K T36F
861	-K------K----------H-K-------	-2742.6	C2K T9K S28H T30K
862	----------KK------K----N----------	-2742.5	L12K A13K S20K A25N
863	-------QK----------K---------K-------	-2742.3	A8Q T9K S20K T30K
864	-----K--K----------H-K-------	-2742.3	T6K T9K S28H T30K
865	----------NK---K---Q---	-2742.2	A25N I26K T30K S34Q
866	---K-------K----------H--------K----	-2742.1	T4K L12K G24H G33K
867	-------Q---K----------K----K--	-2742.0	A8Q L12K T30K N35K
868	---K--K----K----------H----------	-2741.9	T4K C7K L12K G24H
869	----------K--------K---N----K-------	-2741.9	L12K N21K A25N T30K
870	----------K----------H-----Q-F-	-2741.9	L12K S28H S34Q T36F
871	----------K--K---------NK----------	-2741.8	L12K F15K A25N I26K
872	----------K----------K---KK------	-2741.8	L12K I26K T30K N31K
873	----------K-------K-----KK----------	-2741.2	L12K S20K I26K L27K
874	----------K-----K---K--K----	-2741.2	S20K I26K T30K G33K
875	---K-------K----------H---------Q---	-2741.1	T4K L12K G24H S34Q
876	------K----------K-----K---K-------	-2741.0	C7K S20K I26K T30K
877	-------Q----------K-H--------K	-2740.8	A8Q I26K S28H Y37K
878	----------E--K-----K-H---------	-2740.7	V17E S20K I26K S28H
879	----------E--------K---K------K	-2740.5	V17E I26K T30K Y37K
880	----------K------Y-----N--H---------	-2740.5	L12K S19Y A25N S28H
881	---K----------H-----K-----F-	-2740.4	T4K G24H T30K T36F
882	----------K----NK----------K	-2740.3	S20K A25N I26K Y37K

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No.	Sequence S^{P_4}	$F(S^{P_4})$	Mutations
883	----------KK----------K-----F-	-2740.2	R11K L12K T30K T36F
884	----------K-----K---K---Q---	-2740.2	S20K I26K T30K S34Q
885	--------K--KK----------H---------	-2740.2	T9K L12K A13K S28H
886	---K---Q---K----------F-	-2740.2	T4K A8Q L12K T36F
887	----------K----------K-HK--------	-2740.1	L12K I26K S28H S29K
888	---K-------K----------K-V-----	-2740.0	T4K L12K T30K V32V
889	------K----K----------K--K----	-2740.0	C7K L12K T30K G33K
890	----------K-------KK--------K-------	-2739.9	L12K S20K N21K T30K
891	----------K--K----K-----K----------	-2739.8	L12K F15K S20K I26K
892	----------K----E----------H----K----	-2739.7	L12K V17E S28H G33K
893	--K----Q----------K-H---------	-2739.7	N3K A8Q I26K S28H
894	------K----K----E----------H---------	-2739.6	C7K L12K V17E S28H
895	--K----------E--------K---K-------	-2739.4	N3K V17E I26K T30K
896	----------K----------N-------K---K	-2739.3	L12K A25N G33K Y37K
897	--------K--K----------K----K--	-2739.2	T9K L12K T30K N35K
898	--K----------K----NK----------	-2739.2	N3K S20K A25N I26K
899	----------K----------K--KQ---	-2739.2	L12K T30K G33K S34Q
900	------K----K----------N----------K	-2739.2	C7K L12K A25N Y37K
901	-------Q---K----------H----------F-	-2739.2	A8Q L12K G24H T36F
902	----------K----------H-----K-V-----	-2739.0	L12K G24H T30K V32V
903	------K----K----------K---Q---	-2739.0	C7K L12K T30K S34Q
904	----------K----E----------H-----Q---	-2738.8	L12K V17E S28H S34Q
905	--K--------K----------FK	-2738.7	N3K L12K T36F Y37K
906	-K-K----------K---K-------	-2738.7	C2K T4K I26K T30K
907	---K------K----------H-K-------	-2738.6	T4K R11K S28H T30K
908	----------K----------K--K-----F-	-2738.6	L12K L27K T30K T36F
909	----------K------YK-------H---------	-2738.5	L12K S19Y S20K S28H
910	---K-K----------K---K-------	-2738.4	T4K T6K I26K T30K
911	----------K----------N--------Q--K	-2738.4	L12K A25N S34Q Y37K
912	----------K------Y----------K------K	-2738.3	L12K S19Y T30K Y37K
913	--K--------K----------N-------K----	-2738.2	N3K L12K A25N G33K
914	---------K-K----------NK----------	-2738.1	Q10K L12K A25N I26K
915	---KM------K----------H---------	-2738.1	T4K A5M L12K S28H
916	--K---K----K----------N----------	-2738.1	N3K C7K L12K A25N
917	----------E----------H-K-----F-	-2738.0	V17E S28H T30K T36F
918	--------K----------K-H--------K	-2738.0	T9K I26K S28H Y37K
919	---K-------K-----Y----------K-------	-2737.9	T4K L12K H18Y T30K
920	----------K----N--H-------F-	-2737.8	S20K A25N S28H T36F
921	-K----------H-K---K-------	-2737.7	C2K G24H I26K T30K
922	----------N----K-----FK	-2737.7	A25N T30K T36F Y37K
923	----------K----------H---H-K-------	-2737.6	R11K G24H S28H T30K
924	---K---Q----------H---H---------	-2737.6	T4K A8Q G24H S28H
925	-K-----Q---K----------K----------	-2737.4	C2K A8Q L12K I26K
926	-----K----------H-K---K-------	-2737.4	T6K G24H I26K T30K
927	---K----K--K----------F-	-2737.4	T4K T9K L12K T36F
928	-------Q--KK----------H---------	-2737.3	A8Q R11K L12K S28H
929	----------K-------K----------K---K	-2737.3	L12K S20K G33K Y37K
930	---K----------E------H-----K-------	-2737.3	T4K V17E G24H T30K
931	--K--------K----------N--------Q---	-2737.3	N3K L12K A25N S34Q
932	--K--------K------Y----------K-------	-2737.2	N3K L12K S19Y T30K
933	-----K-Q---K----------K----------	-2737.2	T6K A8Q L12K I26K
934	----------K--K----------K-----F-	-2737.1	L12K F15K T30K T36F

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No.	Sequence S^{P_4}	$F(S^{P_4})$	Mutations
935	------K----K-------K----------K	-2737.1	C7K L12K S20K Y37K
936	----M------K----------H---H---------	-2737.1	A5M L12K G24H S28H
937	--KK----------H--------K	-2737.1	N3K T4K S28H Y37K
938	---K----------K---HN----------	-2737.1	T4K S20K G24H A25N
939	----------KK----E----------K-------	-2737.1	R11K L12K V17E T30K
940	---K---Q---K----E----------	-2737.0	T4K A8Q L12K V17E
941	---K----------KH-K-------	-2737.0	T4K L27K S28H T30K
942	--K-----K----------K-H---------	-2736.9	N3K T9K I26K S28H
943	----------K-----Y-----H-----K-------	-2736.9	L12K H18Y G24H T30K
944	----------KK-------K----N----------	-2736.9	R11K L12K S20K A25N
945	K--K-------K----------K-------	-2736.7	K1K T4K L12K T30K
946	--K----------N----K-----F-	-2736.5	N3K A25N T30K T36F
947	--------K--K----------H----------F-	-2736.4	T9K L12K G24H T36F
948	---K-------KK----------K----------	-2736.3	T4K L12K A13K I26K
949	----------K-------K----------Q--K	-2736.3	L12K S20K S34Q Y37K
950	--K--------K-------K----------K----	-2736.2	N3K L12K S20K G33K
951	---------K-K-------K-----K----------	-2736.1	Q10K L12K S20K I26K
952	--K----------H---H--------K	-2736.1	N3K G24H S28H Y37K
953	-------Q---K----E------H----------	-2736.0	A8Q L12K V17E G24H
954	--K---K----K-------K----------	-2736.0	N3K C7K L12K S20K
955	----------H--KH-K-------	-2736.0	G24H L27K S28H T30K
956	----------K----------N----KK------	-2735.8	L12K A25N T30K N31K
957	K----------K----------H-----K-------	-2735.7	K1K L12K G24H T30K
958	-------Q---K----------KH---------	-2735.7	A8Q L12K L27K S28H
959	-------Q----------H-K--K----	-2735.6	A8Q S28H T30K G33K
960	----------K---------K-----FK	-2735.6	S20K T30K T36F Y37K
961	--K--------K----E----------K	-2735.6	N3K L12K V17E Y37K
962	---K----------K----------H-K-------	-2735.5	T4K F15K S28H T30K
963	------KQ----------H-K-------	-2735.5	C7K A8Q S28H T30K
964	----------K----E---------K--K-------	-2735.4	L12K V17E L27K T30K
965	----------KK----------H-K----------	-2735.3	L12K A13K G24H I26K
966	----------K-------K----N-K----------	-2735.2	L12K S20K A25N L27K
967	--K--------K-------K----------Q---	-2735.2	N3K L12K S20K S34Q
968	----------K----N----K--K----	-2735.1	S20K A25N T30K G33K
969	------K----------K----N----K-------	-2735.0	C7K S20K A25N T30K
970	-K-K-------K----------K	-2734.8	C2K T4K L12K Y37K
971	-------Q----------N--H--------K	-2734.8	A8Q A25N S28H Y37K
972	---K----K----------H---H---------	-2734.8	T4K T9K G24H S28H
973	----------E--K----N--H---------	-2734.7	V17E S20K A25N S28H
974	-------Q----------H-K---Q---	-2734.7	A8Q S28H T30K S34Q
975	-K------K--K----------K----------	-2734.7	C2K T9K L12K I26K
976	--------K-KK----------H---------	-2734.6	T9K R11K L12K S28H
977	---K-K-----K----------K	-2734.6	T4K T6K L12K Y37K
978	----------K--------H---H-K-------	-2734.5	F15K G24H S28H T30K
979	----------E-------N----K------K	-2734.5	V17E A25N T30K Y37K
980	--K----------K---------K-----F-	-2734.5	N3K S20K T30K T36F
981	-----K--K--K----------K----------	-2734.4	T6K T9K L12K I26K
982	-------Q---K--K----------H---------	-2734.3	A8Q L12K F15K S28H
983	---K----K--K----E----------	-2734.2	T4K T9K L12K V17E
984	----------K----N----K---Q---	-2734.2	S20K A25N T30K S34Q
985	----------K----------N--HK--------	-2734.0	L12K A25N S28H S29K
986	----------K--K-E----------K-------	-2734.0	L12K F15K V17E T30K

Continued on next page

Table S7 – continued from previous page

No.	Sequence S^{P_4}	$F(S^{P_4})$	Mutations
987	-K---------K----------H----------K	-2733.8	C2K L12K G24H Y37K
988	----------K--K----K----N----------	-2733.8	L12K F15K S20K A25N
989	----------K-------K---------KK------	-2733.8	L12K S20K T30K N31K
990	-KKK-------K----------	-2733.7	C2K N3K T4K L12K
991	--K----Q----------N--H---------	-2733.7	N3K A8Q A25N S28H
992	-----K-----K----------H----------K	-2733.6	T6K L12K G24H Y37K
993	----------K-H-K----K--	-2733.6	I26K S28H T30K N35K
994	---------K-K----------K-----F-	-2733.4	Q10K L12K T30K T36F
995	--KK-K-----K----------	-2733.4	N3K T4K T6K L12K
996	--K----------E-------N----K-------	-2733.4	N3K V17E A25N T30K
997	--------K--K----E------H----------	-2733.3	T9K L12K V17E G24H
998	--------K--K----------KH---------	-2732.9	T9K L12K L27K S28H
999	----------K----------F--K---K-------	-2732.9	L12K F23F I26K T30K
1000	--------K----------H-K--K----	-2732.8	T9K S28H T30K G33K

The rest of the 65,045 records can be found at the following link: http://amyloid.cs.mcgill.ca/SEMBA

At the same link is an executable file called "GetRank.py" that can be used to find the specific ranking and affinity of any of the 4-point mutations.