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Supplemental Information

Structural Insights into Hearing Loss Genetics from Polarizable Protein Repacking

Mallory R. Tollefson, Jacob M. Litman, Guowei Qi, Claire E. O'Connell, Matthew J. Wipfler, Robert J. Marini, Hernan V. Bernabe, William T.A. Tollefson, Terry A. Braun, Thomas L. Casavant, Richard J.H. Smith, and Michael J. Schnieders

Supplementary Information

Table S1. This list includes all genes published in version 8 of the Deafness Variation Database (http://deafnessvariationdatabase.org/).

ACTG1
ADCY1
AIFM1
ALMS1
ATP2B2
ATP6V1B1
BDP1
BSND
CABP2
CACNA1D
CCCP110
CCDC50
CD164
CDC14A
CDH23
CEACAM16
CIB2
CISD2
CLDN14
CLIC5
CLPP
CLRN1
COCH
COL11A1
COL11A2
COL2A1
COL4A3
COL4A4
COL4A5
COL4A6
COL9A1
COL9A2
CRYM
DCDC2
DFNA5 (GSDME)
DFNB31
DFNB59
DIABLO
DIAPH1
DIAPH3
DSPP
EDN3
EDNRB
ELMOD3
EPS8
EPS8L2
ESPN
ESRRB
EYA1
EYA4
FAM65B (RIPOR2)
FGF3
FGFR1
FGFR2
FOXI1
GATA3
GIPC3
GJB2
GJB3
GJB6
GPR98 (ADGRV1)
GPSM2
GRHL2
GRXCR1
GRXCR2
HARS2
HGF
HOMER2
HSD17B4
ILDR1
KARS
KCNE1
KCNJ10
KCNQ1
KCNQ4
KITLG
LARS2
LHFPL5
LOXHD1
LOXL3
LRTOMT
MARVELD2
MCM2
MET
MIR-96
MITF
MSRB3
MT-TL1
MT-TS1
MT-RNR1
MYH14
MYH9
MYO15A
MYO3A
MYO6
MYO7A
NARS2
NLRP3
OPA1
OSBPL2
OTOA
OTOF
OTOG
OTOGL
P2RX2
PAX3
PCDH15
PDZD7
PEX1
PEX6
PJVK
PNPT1
POLR1C
POLR1D
POU3F4
POU4F3
PRPS1
PTPRQ
RDX
ROR1
S1PR2
SCN7A
SERPINB6
SIX1
SIX5
SLC17A8
SLC22A4
SLC26A4
SLC26A5
SLITRK6
SMPX
SNAI2
SOX10
STRC
SYNE4
TBC1D24
TBX1
TCOF1
TECTA
TECTB
TIMM8A
TJP2
TMC1
TMEM132E
TMIE
TMPRSS3
TNC
TPRN
TRIOBP
TSPEAR
TWNK
USH1C
USH1G
USH2A
WFS1
WHRN

Table S2. Related to Table 1. Decomposition of the many-body energy expansion (up to 3-body terms) for COCH domain residues 27-125 as function of generalized Kirkwood (GK) implicit solvent use and residue cutoff. Without GK, the energy expansion decays slowly, and the neglected energy terms sum to hundreds of kcal/mol (i.e. the neglected energy is the known Total AMOEBA/GK potential energy less explicitly calculated terms in the expansion). With GK, the energy expansion decays quickly, and neglected energy is on the order of only a few kcal/mol. The sum of 3-body energy terms when using GK is always less than 1 kcal/mol, but reaches 3.9 kcal/mol without GK.

GK Solvent	Cutoff (Å)	Backbone (kcal/mol)	Self-Energy Sum (kcal/mol)	2-Body Energy Sum (kcal/mol)	3-Body Energy Sum (kcal/mol)	Neglected Sum (kcal/mol)	Total Potential (kcal/mol)
No	2	-953.34	-1215.03	18.17	-0.19	302.76	-1847.63
No	3			-3.59	3.89	320.44	
No	6			163.77	1.77	155.19	
No	9			374.22	0.06	-53.54	
Yes	2	-2039.14	-1508.40	-99.69	-0.06	-11.88	-3659.19
Yes	3			-110.10	-0.13	-1.41	
Yes	6			-112.61	-0.30	1.27	
Yes	9			-110.88	-0.57	-0.19	

Table S3. Related to Table 1. Energy timings for a three-body expansion of the COCH domain residues 27-125.

Term	Number of Energies	% of Total Energies	Seconds
Self	947	0.01	262
Two-body	120,855	1.91	32,940
Three-body*	6,214,642	98.08	1,624,625
Total	6,336,444	100.00	1,657,827

*indicates extrapolation from finishing 3% of 3-body energies

Table S4. Related to Table 1. Residue cutoffs of 2, 3 and 6 Å are examined for three different structures. A comparison of 2 and 3 Å residue cutoffs (applied to residue pair distances from Eq. 7) shows no total potential energy differences greater than 2.5 kcal/mol and MolProbity scores do not vary by more than 0.04 Å.

Residue Cutoff (Å)	Gene and Residue Range	Total Potential	MolProbity
2	ACTG1 2-375	-16919.89	0.71
3	ACTG1 2-375	-16922.21	0.71
6	ACTG1 2-375	-16920.71	0.93
2	COCH 27-125	-3549.42	1.78
3	COCH 27-125	-3549.99	1.78
6	COCH 27-125	-3550.16	1.74
2	LRTOMT 118-287	-7112.79	1.40
3	LRTOMT 118-287	-7112.96	1.40
6	LRTOMT 118-287	-7117.19	1.42

Table S5. Related to Table 2. Energy evaluation timings for global side-chain optimization of residues 27-125 for the COCH domain using a varying number of GPUs (each node contains two Intel Xeon E5-2680v4 CPUs and one or more NVIDIA GTX 1080 TI GPUs) and the AMBER99sb/GB force field.

Computing Unit (# GPUs)	Time For Energies (sec)	Speed-Up (Relative to Using all CPU Cores and no GPU)
0 (CPUs only)	1034.0	1.0x
1	216.5	4.8x
2	124.5	8.3x
4	69.4	14.9x
8	43.5	23.8x
16	28.0	36.9x

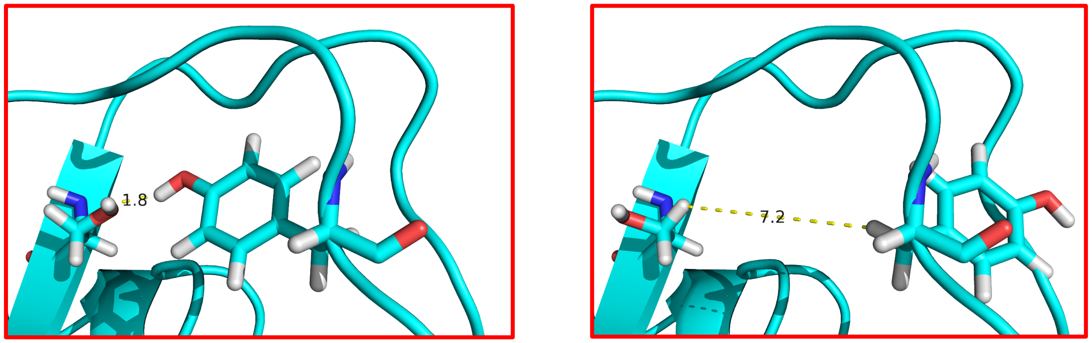

Figure S1. Related to Table 1B. Side-chain repacking distance cutoffs. The distances between two (or more) side-chains can vary widely as a function of the currently applied rotamers. The interaction above shows one rotamer pair with a 7.2 Å separation distance, while those same two side-chains have a separation distance of only 1.8 Å for a 2nd rotamer pair. The minimum distance between the two residues (i.e. from applying Equation 7) in this case is 1.8 Å, which is within a 2 Å cutoff.

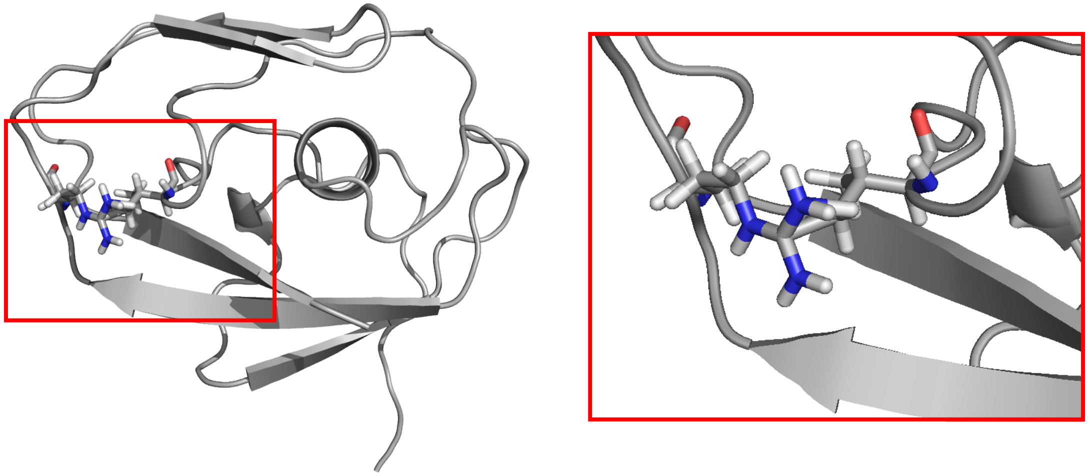

Figure S2. Related to Table 1B. Side-chain repacking clashes. Two interacting residues often have a clash for some rotamer permutations for one or more pairs of atoms. These clashes lead to residue separation distance of ~0 Å when applying Equation 7, which results in 2-body energies being calculated for all rotamer permutations.

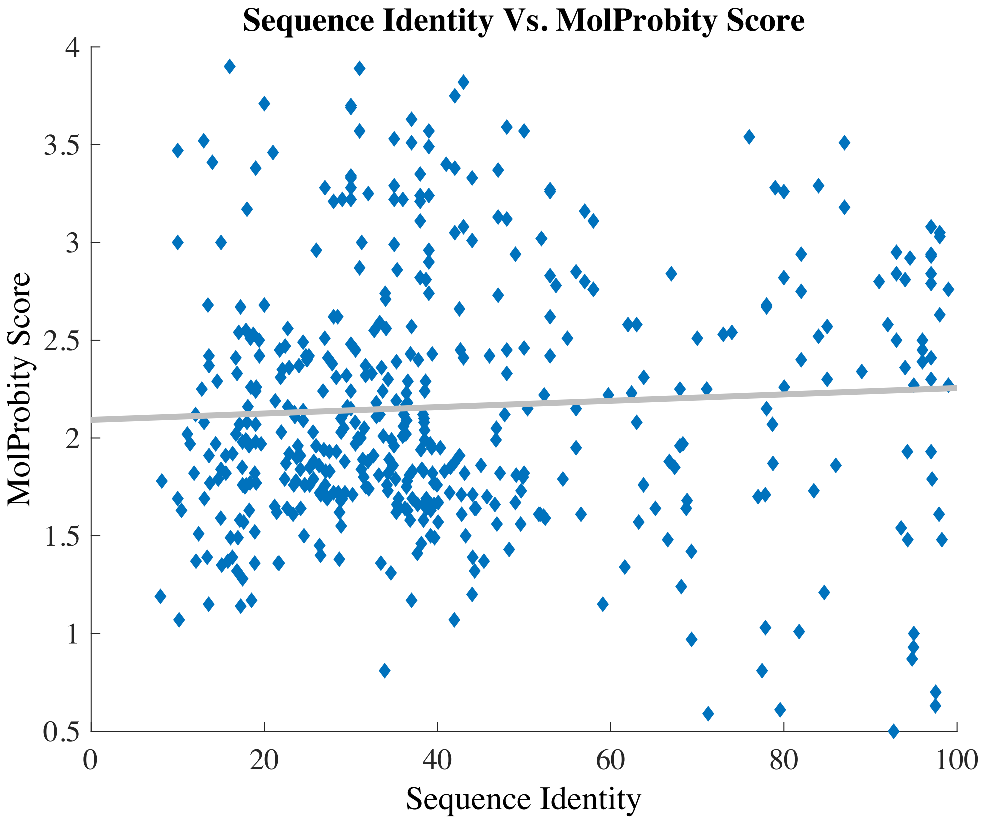

Figure S3. Related to Figure 3. Scatter plot of sequence identity vs MolProbity score for the 473 wildtype protein structures results in a linear regression R^2 of only 0.0035.

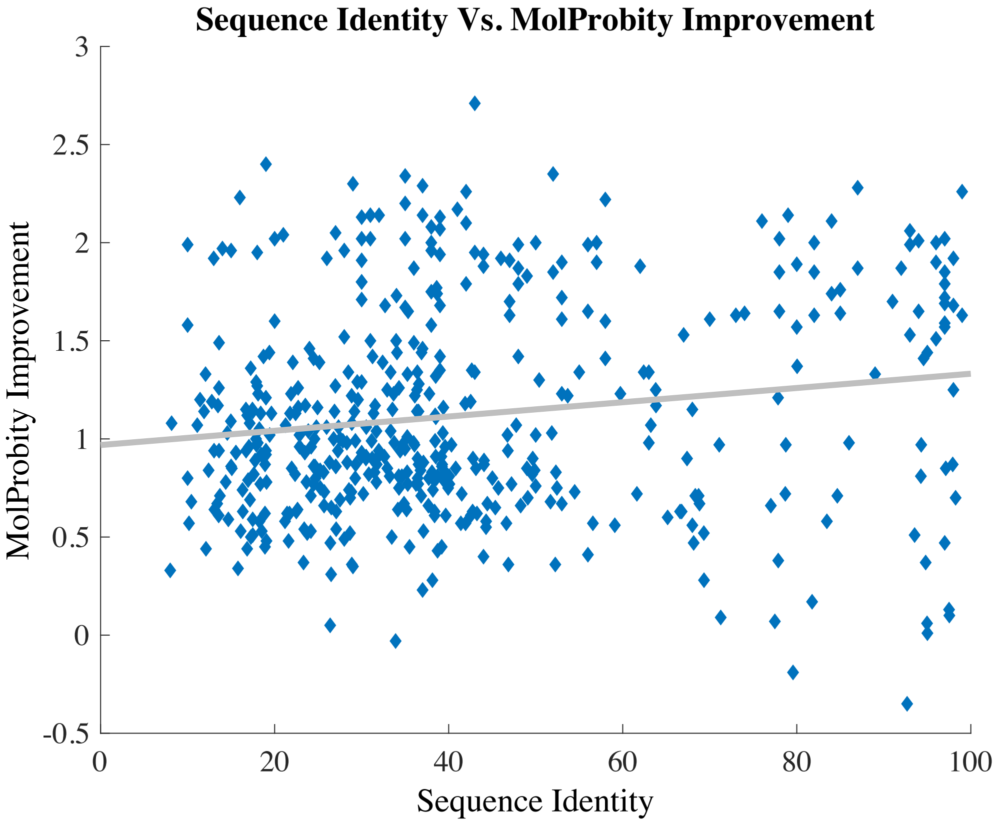

Figure S4. Related to Figure 3. Scatter plot of sequence identity vs. MolProbity improvement (*i.e.* the difference between original homology model MolProbity score compared to after AMOEBA/GK repacking) for the 473 wildtype protein structures results in a linear regression R^2 of only 0.0256.

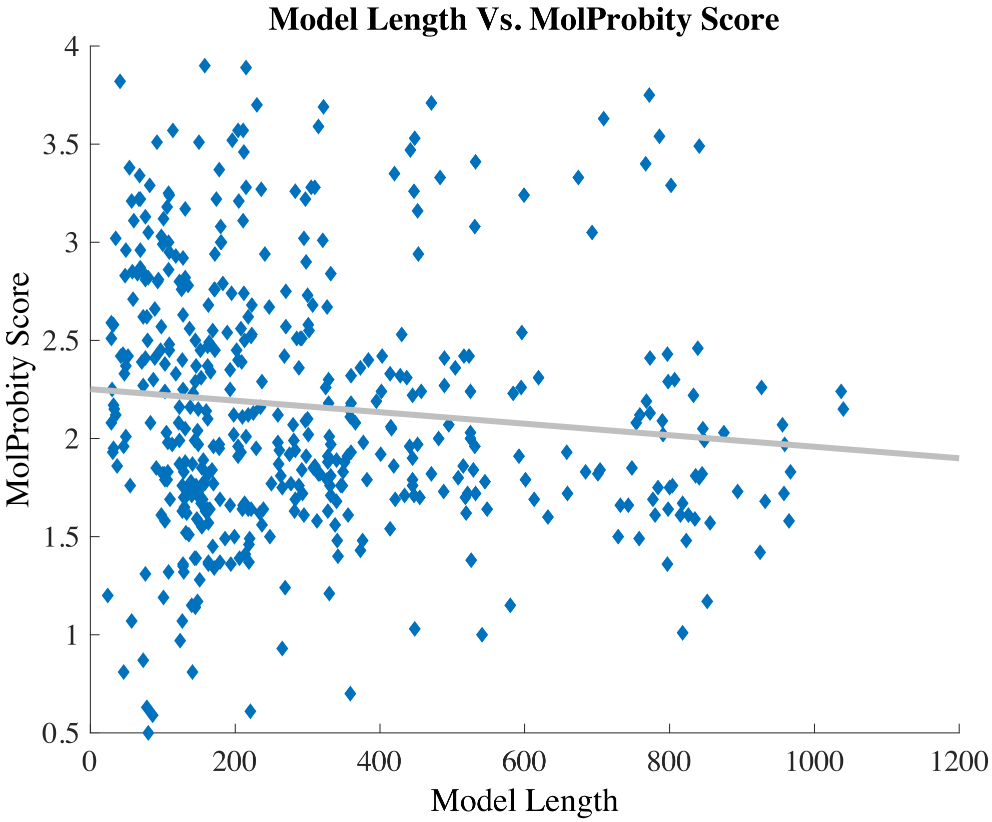

Figure S5. Related to Figure 3. Scatter plot of model length vs. MolProbity score for the 473 wildtype protein structures results in a linear regression R^2 of only 0.0119.

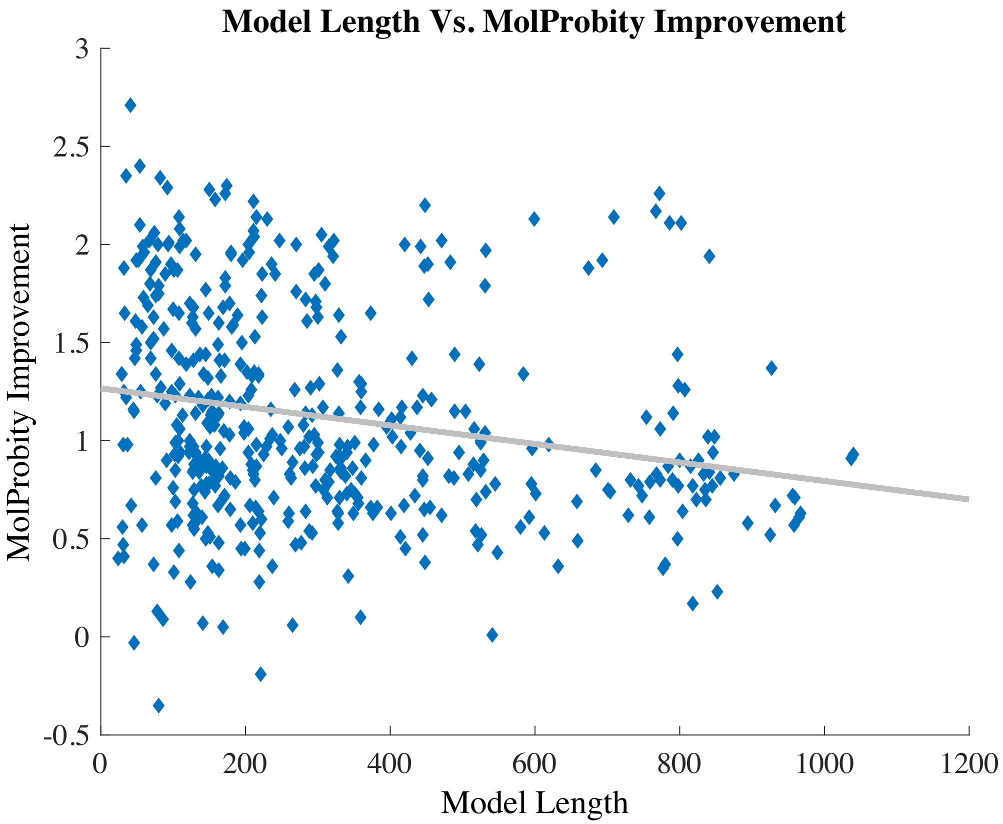

Figure S6. Related to Figure 3. Scatter plot of model length vs. MolProbity improvement for the 473 wildtype protein structures results in a linear regression R^2 of only 0.0449.

Table S6. Refinement statistics for all of the homology models analyzed in this work. The gene and residue ranges being modeled are shown in the two left-most columns, followed by the sequence identity to the template experimental structure the model was based off of, and then output from the MolProbity scoring algorithm. Table S6 is available in CSV format upon request.

Gene	Residue Range	Sequence Identity	Model	% Poor Rotamers	Clash Score	Ramachandran Outliers	Ramachandran Favored	MolProbity Score	Amoeba Energy (Kcal/Mol)
ACTG1	2-375	94.0	Original	2.21	41.67	0.27	99.46	2.36	-16095.87
			FFX	1.89	0.00	0.00	98.92	0.71	-16919.89
ADCY1	288-477	74.0	Original	2.44	55.59	0.53	97.87	2.54	-8160.62
			FFX	1.22	0.00	0.00	95.21	0.90	-8758.46
	855-1057	42.7	Original	4.00	8.13	4.48	90.05	2.45	-8507.87
			FFX	1.71	0.00	1.49	93.53	1.10	-9004.61
AIFM1	122-611	95.0	Original	1.74	40.78	0.20	98.36	2.27	-20925.26
			FFX	0.74	0.00	0.20	95.29	0.83	-22227.11
ALMS1	3992-4150	16.0	Original	6.21	201.82	2.55	90.45	3.90	-7731.67
			FFX	5.52	0.00	2.55	87.90	1.67	-8383.55
ATP2B2	364-948	36.4	Original	2.17	7.71	1.54	89.88	2.23	-23907.04
			FFX	0.39	0.00	0.69	94.17	0.89	-25502.09
	49-1086	30.0	Original	3.42	4.59	3.47	87.84	2.24	-41790.12
			FFX	2.51	0.06	1.25	91.70	1.33	-45041.74
	49-1089	30.0	Original	3.19	4.26	2.41	89.70	2.15	-42612.58
			FFX	1.82	0.00	1.54	90.95	1.22	-45130.05
ATP6V1B1	42-497	77.0	Original	0.52	6.18	0.66	94.71	1.70	-19376.71
			FFX	1.29	0.28	0.44	94.93	1.04	-20325.82
ATP6V1B1	49-501	57.0	Original	3.65	87.65	1.11	95.34	3.16	-19140.93
			FFX	2.60	0.00	1.55	93.13	1.26	-20274.24
BDP1	247-376	37.1	Original	0.85	4.21	2.34	86.72	1.83	-6161.71
			FFX	0.85	0.00	0.00	92.97	0.95	-6439.74
	864-1069	28.0	Original	5.43	124.33	1.47	97.55	3.21	-11302.65
			FFX	3.80	0.00	0.00	95.59	1.25	-12098.05
BSND	240-313	28.0	Original	1.61	71.11	1.39	97.22	2.62	-4105.85
			FFX	1.61	0.00	0.00	93.06	1.10	-4305.94
CABP2	71-220	78.0	Original	0.00	46.55	0.00	98.65	2.15	-7773.50
			FFX	0.78	0.00	0.00	98.65	0.50	-8105.86
	72-220	77.9	Original	6.30	2.99	0.00	97.96	1.71	-7879.95
			FFX	0.00	0.00	0.00	98.64	0.50	-8130.21
	73-218	38.6	Original	8.87	5.22	1.39	95.83	2.29	-7431.79
			FFX	0.81	0.00	0.00	97.92	0.52	-7805.44

Gene	Residue Range	Sequence Identity	Model	% Poor Rotamers	Clash Score	Ramachandran Outliers	Ramachandran Favored	MolProbity Score	Amoeba Energy (Kcal/Mol)
	73-219	44.1	Original	1.60	1.30	1.38	94.48	1.39	-7642.12
			FFX	0.00	0.00	0.00	97.93	0.52	-7839.68
	76-216	44.1	Original	1.68	2.72	2.16	92.09	1.71	-7306.47
			FFX	0.00	0.45	1.44	97.12	0.82	-7534.06
CACNA1D	1548-1622	93.0	Original	3.08	50.75	0.00	95.89	2.84	-3392.78
			FFX	0.00	0.00	0.00	95.89	0.78	-3544.73
	1549-1622	94.8	Original	3.08	0.00	0.00	100.00	0.87	-3418.61
			FFX	0.00	0.00	0.00	100.00	0.50	-3535.79
CCDC50	77-159	35.0	Original	5.48	82.14	0.00	95.06	3.29	-4932.08
			FFX	1.37	0.00	0.00	95.06	0.95	-5165.75
CD164	56-105	26.0	Original	0.00	121.64	2.08	93.75	2.96	-2036.11
			FFX	2.13	0.00	2.08	95.83	1.04	-2159.47
CDC14A	11-343	67.0	Original	2.08	72.05	0.91	96.07	2.84	-14382.76
			FFX	3.82	0.00	0.91	94.56	1.31	-15526.89
	15-343	66.8	Original	2.11	4.29	1.22	93.58	1.88	-14707.84
			FFX	2.81	0.00	0.61	93.88	1.25	-15318.90
CDH23	1107-1626	28.7	Original	0.00	4.16	0.58	93.63	1.62	-24391.45
			FFX	0.45	0.00	0.39	93.63	0.92	-25458.39
	1321-1846	31.1	Original	0.44	7.97	2.48	89.50	2.00	-24475.87
			FFX	0.66	0.00	1.15	91.41	1.01	-25750.00
	1424-1953	31.2	Original	0.65	6.28	0.95	91.86	1.84	-25304.09
			FFX	0.43	0.00	1.52	93.18	0.94	-26868.44
	2211-2699	34.3	Original	0.24	5.37	0.82	93.22	1.73	-22811.90
			FFX	0.24	0.00	0.82	93.63	0.92	-23959.17
	240-772	28.5	Original	0.43	4.51	2.45	91.71	1.72	-23024.64
			FFX	1.07	0.00	1.13	92.66	0.98	-24278.44
	2503-2603	35.0	Original	1.14	91.82	2.02	90.91	2.99	-4297.13
			FFX	2.27	0.00	1.01	89.90	1.32	-4518.60
	2506-3051	23.7	Original	0.42	5.75	1.65	92.65	1.78	-23327.99
			FFX	1.26	0.00	1.29	93.57	1.00	-24699.75
	375-879	33.5	Original	2.68	7.97	2.78	87.87	2.36	-22035.26
			FFX	1.79	0.00	1.19	91.05	1.21	-23748.16
	782-1308	28.7	Original	1.52	1.12	1.14	93.52	1.38	-22585.79
			FFX	1.08	0.00	0.38	95.24	0.86	-23810.21
	887-1408	26.4	Original	3.79	0.50	2.88	87.88	1.72	-21387.14
			FFX	2.23	0.00	1.92	92.12	1.25	-22569.53
	894-1417	25.2	Original	3.33	7.86	3.45	88.12	2.42	-21311.52

Gene	Residue Range	Sequence Identity	Model	% Poor Rotamers	Clash Score	Ramachandran Outliers	Ramachandran Favored	MolProbity Score	Amoeba Energy (Kcal/Mol)
			FFX	0.67	0.00	0.96	90.61	1.03	-22767.11
	905-1413	31.5	Original	0.69	5.52	2.17	91.52	1.80	-22301.54
			FFX	0.92	0.00	0.59	92.50	0.97	-23487.82
	997-1528	23.9	Original	1.10	7.75	3.77	91.32	1.96	-22806.57
			FFX	0.66	0.00	0.94	93.58	0.92	-23896.39
CEACAM16	20-118	37.0	Original	1.22	55.06	0.00	95.88	2.57	-3994.18
			FFX	3.66	0.00	0.00	96.91	1.11	-4163.72
	20-421	16.3	Original	1.47	4.58	3.50	89.50	1.92	-14857.10
			FFX	2.36	0.00	2.50	91.50	1.29	-15858.62
CEACAM16-Dimer	19-422	19.4	Original	1.77	12.57	4.10	87.19	2.42	-29164.80
			FFX	2.95	0.08	1.87	91.42	1.40	-31738.99
	27-422	21.3	Original	1.20	10.73	3.30	88.83	2.19	-28921.58
			FFX	1.35	0.17	1.40	92.77	1.12	-31200.05
CIB2	139-174	52.0	Original	3.33	98.11	0.00	97.06	3.02	-2189.09
			FFX	0.00	0.00	0.00	97.06	0.67	-2239.22
	8-187	38.7	Original	1.22	3.12	3.93	91.01	1.69	-8802.87
			FFX	1.22	0.00	1.69	95.51	0.88	-9158.32
	9-187	39.3	Original	3.07	3.84	1.69	93.79	1.95	-8757.11
			FFX	1.84	0.00	1.13	96.61	0.92	-9142.42
CISD2	68-133	97.0	Original	3.33	29.92	1.56	92.19	2.84	-3208.38
			FFX	1.67	0.00	0.00	92.19	1.15	-3311.94
CLDN14	4-183	45.4	Original	1.36	4.34	1.12	97.75	1.37	-5385.07
			FFX	0.68	0.00	0.56	96.63	0.72	-5711.90
	4-184	43.0	Original	2.70	85.67	3.35	94.97	3.08	-5109.82
			FFX	0.00	0.36	3.35	91.62	1.13	-5632.88
CLIC5	162-409	78.0	Original	1.42	63.67	0.81	95.93	2.67	-11551.14
			FFX	0.94	0.00	0.41	97.15	0.65	-12269.96
CLPP	74-245	58.0	Original	2.76	76.35	0.00	97.65	2.76	-6754.55
			FFX	4.83	0.00	0.00	95.29	1.35	-7103.42
CLRN1	99-213	31.0	Original	4.00	120.43	0.88	89.38	3.57	-3651.63
			FFX	4.00	0.00	0.00	88.50	1.55	-4016.48
COCH	162-387	23.5	Original	0.52	10.24	4.46	87.95	2.13	-9177.87
			FFX	2.09	0.00	1.79	92.86	1.20	-9645.22
	162-544	25.7	Original	1.87	2.37	2.36	89.50	1.79	-15705.36
			FFX	1.56	0.00	1.57	92.13	1.13	-16649.60
	266-503	14.6	Original	2.46	11.51	2.12	93.64	2.29	-9283.22

Gene	Residue Range	Sequence Identity	Model	% Poor Rotamers	Clash Score	Ramachandran Outliers	Ramachandran Favored	MolProbity Score	Amoeba Energy (Kcal/Mol)
			FFX	2.96	0.00	2.54	94.07	1.26	-9764.98
	27-125	98.0	Original	2.50	70.10	1.03	93.81	3.03	-3659.32
			FFX	5.00	0.69	0.00	90.72	1.78	-3868.52
COL11A1	1500-1532	62.0	Original	4.76	38.65	0.00	100.00	2.58	-1222.53
			FFX	0.00	0.00	0.00	96.77	0.70	-1271.96
	67-229	28.9	Original	0.00	10.88	2.48	90.06	2.10	-7224.92
			FFX	0.00	0.00	0.62	94.41	0.88	-7500.58
COL11A1-Trimer	1595-1805	44.3	Original	0.18	3.18	2.72	90.72	1.64	-29011.08
			FFX	1.07	0.00	1.28	90.56	1.06	-30608.28
COL11A2	46-192	31.7	Original	3.31	6.87	5.52	88.28	2.37	-5528.01
			FFX	4.13	0.00	4.83	86.90	1.59	-5783.03
	919-950	63.0	Original	0.00	46.39	0.00	93.33	2.58	-1201.33
			FFX	5.26	0.00	0.00	90.00	1.60	-1284.63
COL11A2-Trimer	1542-1735	46.6	Original	1.00	3.65	2.26	91.49	1.66	-26654.76
			FFX	1.20	0.00	1.56	90.80	1.09	-28017.99
COL2A1	969-1000	97.0	Original	0.00	27.59	0.00	100.00	1.93	-1166.62
			FFX	5.00	0.00	0.00	93.33	1.46	-1247.06
COL2A1-Trimer	1248-1487	68.7	Original	1.78	2.80	0.99	94.51	1.64	-33839.58
			FFX	1.13	0.00	0.70	94.23	0.93	-35383.79
COL4A3	637-674	86.0	Original	0.00	23.31	0.00	100.00	1.86	-1333.20
			FFX	0.00	0.00	0.00	94.44	0.88	-1375.13
COL4A4	1465-1688	73.0	Original	0.53	50.91	0.90	95.05	2.53	-8666.36
			FFX	0.53	0.00	0.90	94.14	0.90	-9175.96
COL4A5	1461-1683	84.0	Original	2.63	38.68	0.45	97.29	2.52	-8494.09
			FFX	0.53	0.00	0.00	95.93	0.78	-9001.87
COL4A6	1466-1689	78.0	Original	2.07	41.50	0.45	95.05	2.68	-8416.80
			FFX	1.04	0.00	0.45	95.50	0.83	-8987.94
COL4A6-Hexamer	1467-1689	65.2	Original	1.04	4.50	0.90	94.12	1.64	-52381.81
			FFX	1.56	0.05	1.28	94.49	1.04	-54965.54
COL9A1	363-392	63.0	Original	5.26	10.26	0.00	100.00	2.08	-1085.20
			FFX	0.00	0.00	0.00	96.43	0.74	-1140.12
COL9A2	33-79	68.0	Original	0.00	26.55	0.00	97.78	1.96	-2055.17
			FFX	0.00	0.00	0.00	95.56	0.81	-2123.72
CRYM	4-314	30.0	Original	2.36	0.00	1.29	93.20	3.28	-12367.56
			FFX	4.33	0.00	0.65	91.59	1.48	-13220.35

Gene	Residue Range	Sequence Identity	Model	% Poor Rotamers	Clash Score	Ramachandran Outliers	Ramachandran Favored	MolProbity Score	Amoeba Energy (Kcal/Mol)
DCDC2	129-226	96.0	Original	1.16	54.04	0.00	96.88	2.45	-4310.76
			FFX	1.16	0.00	0.00	100.00	0.55	-4545.30
	15-123	31.3	Original	5.38	18.22	3.74	83.18	3.00	-4650.71
			FFX	4.30	0.00	3.74	87.85	1.58	-4906.98
DIABLO	67-239	99.0	Original	3.38	44.82	0.58	96.49	2.76	-8041.05
			FFX	0.68	0.00	0.00	98.25	0.50	-8591.04
DIAPH1	762-1215	97.0	Original	4.13	44.35	1.33	94.91	2.94	-22098.48
			FFX	3.64	0.00	0.22	95.80	1.22	-23358.68
	92-452	94.3	Original	10.67	0.68	0.56	93.59	1.93	-16982.34
			FFX	2.44	0.00	0.28	95.26	1.12	-17823.43
DIAPH1-Dimer	142-483	94.3	Original	5.86	0.82	0.15	97.21	1.48	-33400.71
			FFX	0.81	0.00	0.00	97.94	0.51	-34668.15
DIAPH3	122-479	50.4	Original	4.55	4.10	1.69	92.70	2.15	-16786.33
			FFX	1.52	0.00	0.28	96.63	0.85	-17635.74
	633-1078	59.7	Original	4.06	4.69	2.25	91.22	2.22	-21919.74
			FFX	1.43	0.00	0.90	94.59	0.99	-23168.42
	916-1096	15.0	Original	2.99	91.18	0.56	96.65	3.00	-9348.95
			FFX	1.80	0.00	0.56	94.97	1.04	-9999.64
DIAPH3-Dimer	173-511	49.6	Original	2.88	1.18	0.74	94.51	1.56	-32558.65
			FFX	0.80	0.00	0.30	96.44	0.74	-33949.54
	637-1053	31.5	Original	2.27	6.40	1.69	93.37	2.05	-41250.90
			FFX	0.50	0.14	0.48	95.30	0.88	-43599.46
DSPP	88-318	30.0	Original	3.26	140.58	6.11	82.53	3.70	-12328.88
			FFX	2.72	0.00	3.06	79.48	1.57	-13123.69
EDN3	42-91	24.0	Original	0.00	24.19	2.08	91.67	2.37	-2258.58
			FFX	0.00	0.00	0.00	93.75	0.91	-2367.87
	97-121	44.0	Original	0.00	0.00	4.35	82.61	1.20	-1098.66
			FFX	0.00	0.00	0.00	95.65	0.80	-1156.49
EDNRB	105-402	30.0	Original	1.88	130.30	3.04	93.24	3.22	-9457.52
			FFX	4.51	0.00	1.69	91.22	1.51	-10589.24
ELMOD3	277-312	36.1	Original	6.25	1.69	0.00	88.24	2.12	-1423.19
			FFX	0.00	0.00	0.00	94.12	0.90	-1483.05
EPS8	699-788	97.0	Original	0.00	51.58	1.14	96.59	2.41	-3756.63
			FFX	0.00	0.00	0.00	97.73	0.56	-3909.23
EPS8-Dimer	59-188	44.3	Original	0.83	3.40	0.78	96.88	1.32	-12611.43
			FFX	0.00	0.00	0.00	96.09	0.77	-13017.20

Gene	Residue Range	Sequence Identity	Model	% Poor Rotamers	Clash Score	Ramachandran Outliers	Ramachandran Favored	MolProbity Score	Amoeba Energy (Kcal/Mol)
EPS8L2	611-698	97.0	Original	1.28	47.01	0.00	97.67	2.30	-4135.37
			FFX	0.00	0.00	0.00	96.51	0.73	-4343.06
EPS8L2-Dimer	46-175	45.7	Original	3.23	2.16	0.78	95.31	1.70	-12837.81
			FFX	0.81	0.00	0.00	92.97	0.95	-13329.34
	495-550	63.8	Original	5.21	4.36	0.00	99.07	1.76	-5608.72
			FFX	1.04	0.00	0.00	99.07	0.51	-5800.21
ESPN	1-330	85.0	Original	2.00	38.75	0.00	98.17	2.30	-14391.48
			FFX	1.60	0.00	0.00	99.09	0.66	-14931.84
	1-331	84.7	Original	1.20	2.06	0.30	96.96	1.21	-14472.53
			FFX	0.00	0.00	0.00	98.18	0.50	-14916.48
	75-325	39.6	Original	1.03	6.54	0.00	93.98	1.77	-10938.03
			FFX	0.00	0.00	0.00	95.58	0.81	-11336.42
	90-324	35.2	Original	0.55	5.84	2.15	95.71	1.62	-10238.66
			FFX	0.55	0.29	0.43	98.28	0.61	-10659.53
ESRRB	100-429	36.5	Original	2.08	6.33	3.66	88.41	2.18	-14868.95
			FFX	1.04	0.00	1.22	90.85	1.04	-15556.17
	100-432	36.8	Original	1.03	5.71	2.42	91.84	1.81	-14774.04
			FFX	0.69	0.00	0.91	92.45	0.97	-15497.02
	101-431	36.0	Original	1.38	7.62	1.52	92.10	2.01	-14899.18
			FFX	1.04	0.19	1.22	93.01	1.03	-15734.16
	102-429	35.2	Original	1.74	3.00	2.76	91.10	1.79	-14802.81
			FFX	1.74	0.00	1.84	92.64	1.15	-15488.66
	102-430	32.6	Original	0.35	7.11	2.14	91.13	1.91	-14512.62
			FFX	1.39	0.00	0.92	94.19	1.00	-15256.71
	99-430	27.0	Original	1.72	3.33	1.21	92.73	1.76	-14609.35
			FFX	1.03	0.00	0.61	94.24	0.90	-15357.72
	99-431	27.0	Original	0.69	5.91	0.91	94.26	1.71	-14988.56
			FFX	1.03	0.00	1.21	95.17	0.85	-15782.58
ESRRB-Dimer	209-430	79.6	Original	1.02	0.27	0.00	98.64	0.61	-20082.23
			FFX	0.51	0.27	0.00	96.82	0.80	-20615.47
EYA1	322-592	85.0	Original	0.87	58.03	0.74	95.17	2.57	-11383.47
			FFX	0.87	0.00	0.37	95.54	0.81	-12281.43
EYA4	369-639	82.0	Original	2.16	51.02	0.37	95.54	2.75	-11545.13
			FFX	0.43	0.00	0.37	96.28	0.75	-12327.92
FGF3	38-86	53.0	Original	0.00	87.58	0.00	93.62	2.83	-1965.90
			FFX	2.50	0.00	4.26	93.62	1.22	-2085.72
FGF3-Dimer	34-196	44.4	Original	2.56	1.14	1.57	91.54	1.64	-14359.07

Gene	Residue Range	Sequence Identity	Model	% Poor Rotamers	Clash Score	Ramachandran Outliers	Ramachandran Favored	MolProbity Score	Amoeba Energy (Kcal/Mol)
			FFX	1.10	0.00	0.31	93.10	0.97	-15034.82
FGFR1	288-771	30.0	Original	2.59	120.34	2.49	92.32	3.33	-19802.51
			FFX	3.54	0.00	1.66	91.49	1.42	-21460.86
FGFR2	479-801	30.0	Original	3.85	152.48	3.12	87.85	3.69	-13668.07
			FFX	3.85	0.39	1.56	88.79	1.67	-15020.36
FOXI1	121-212	67.4	Original	3.70	1.37	1.11	90.00	1.85	-4245.86
			FFX	1.23	0.00	1.11	94.44	0.95	-4398.66
	122-220	56.6	Original	2.27	0.62	2.06	86.60	1.61	-5186.87
			FFX	1.14	0.00	3.09	91.75	1.04	-5375.18
GIPC3	105-198	57.0	Original	3.75	47.75	0.00	96.74	2.80	-4473.00
			FFX	0.00	0.00	0.00	95.65	0.80	-4679.23
	70-193	18.1	Original	1.90	7.74	2.46	90.98	2.16	-5419.67
			FFX	0.95	0.00	0.00	93.44	0.93	-5653.88
GIPC3-Dimer	37-306	68.2	Original	1.34	1.32	0.56	95.90	1.24	-24916.75
			FFX	0.67	0.00	0.37	96.08	0.77	-25856.15
GJB3	2-213	58.0	Original	2.12	83.69	2.38	92.38	3.11	-7705.75
			FFX	0.53	0.00	0.95	94.29	0.89	-8523.55
GJB6	2-217	79.0	Original	3.06	87.49	1.40	91.59	3.28	-7833.48
			FFX	2.04	0.00	1.87	93.93	1.14	-8699.71
GPR98(ADGRV1)	3254-3579	18.5	Original	0.35	13.47	1.23	87.04	2.26	-12294.56
			FFX	2.43	0.00	0.31	90.12	1.34	-13159.68
	4270-4339	39.0	Original	1.75	69.98	2.94	92.65	2.96	-3093.62
			FFX	3.51	0.00	1.47	86.76	1.54	-3302.16
	5593-5900	13.5	Original	2.58	21.10	3.27	90.20	2.68	-12773.41
			FFX	4.43	0.21	1.31	93.14	1.51	-13419.72
GPSM2	117-648	97.0	Original	5.66	52.45	1.51	95.47	3.08	-23631.57
			FFX	3.49	0.00	0.57	94.53	1.29	-25193.32
	169-509	34.4	Original	2.78	2.42	2.06	90.86	1.89	-15950.79
			FFX	0.69	0.00	0.59	92.92	0.95	-16716.64
GRHL2	248-489	82.0	Original	5.05	47.45	0.83	96.25	2.94	-10926.10
			FFX	2.29	0.00	1.25	95.42	1.09	-11718.01
GRXCR1	231-288	38.0	Original	1.96	68.60	1.79	83.93	3.21	-2450.97
			FFX	3.92	0.00	3.57	83.93	1.63	-2605.75
GRXCR1-Heteromer	91-218	25.2	Original	3.11	1.45	2.39	91.43	1.76	-22461.96
			FFX	0.44	0.00	1.20	93.63	0.92	-23762.37

Gene	Residue Range	Sequence Identity	Model	% Poor Rotamers	Clash Score	Ramachandran Outliers	Ramachandran Favored	MolProbity Score	Amoeba Energy (Kcal/Mol)
GRXCR2	187-247	38.0	Original	3.85	56.37	1.69	93.22	3.11	-2673.31
			FFX	1.92	0.00	0.00	93.22	1.15	-2789.45
	195-240	39.4	Original	0.00	13.43	2.27	75.00	2.43	-2350.18
			FFX	0.00	0.00	2.27	77.27	1.27	-2442.84
GSDME(DFNA5)	17-125	32.0	Original	2.04	80.16	0.93	85.98	3.25	-4572.65
			FFX	1.02	0.00	1.87	87.85	1.11	-4910.86
HARS2	55-502	80.0	Original	5.68	77.41	1.35	95.29	3.26	-19109.03
			FFX	3.10	0.14	0.90	93.05	1.37	-20522.59
HARS2-Dimer	54-502	77.9	Original	0.39	0.90	0.56	96.20	1.03	-41206.82
			FFX	0.64	0.00	0.22	97.20	0.65	-42575.75
HGF	104-723	28.3	Original	1.82	8.42	3.88	85.28	2.31	-26789.58
			FFX	2.37	0.00	1.62	90.13	1.33	-28790.75
	128-720	42.5	Original	2.48	3.38	1.86	92.05	1.91	-26310.95
			FFX	2.10	0.22	0.51	92.39	1.30	-27701.16
	200-725	26.8	Original	1.72	8.72	4.39	88.17	2.24	-22816.06
			FFX	1.72	0.00	1.91	89.50	1.24	-24431.93
	210-288	53.0	Original	1.37	48.45	0.00	94.81	2.62	-4183.65
			FFX	4.11	0.00	0.00	93.51	1.39	-4359.49
	210-469	47.8	Original	2.95	4.99	2.33	91.47	2.12	-12744.38
			FFX	0.84	0.00	0.78	89.92	1.05	-13296.22
	305-720	36.1	Original	1.38	6.38	3.38	87.92	2.06	-17517.62
			FFX	0.55	0.16	0.97	90.82	1.09	-18807.03
	38-722	40.8	Original	1.15	5.90	1.02	92.68	1.83	-30590.94
			FFX	0.82	0.00	0.73	92.24	0.98	-32159.77
HOMER2	1-128	82.0	Original	2.65	32.96	0.79	97.62	2.40	-5558.27
			FFX	1.77	0.00	0.00	97.62	0.77	-5877.25
	1-142	77.5	Original	0.00	0.45	0.00	97.14	0.81	-6322.14
			FFX	0.00	0.00	0.71	96.43	0.74	-6492.85
	173-301	15.1	Original	0.83	5.14	0.00	97.64	1.35	-7330.05
			FFX	0.00	0.00	0.00	98.43	0.50	-7588.77
	178-341	15.8	Original	0.65	1.45	1.85	91.98	1.37	-9254.21
			FFX	0.65	0.00	0.62	90.74	1.03	-9684.81
	179-307	21.7	Original	1.64	0.93	1.57	93.70	1.36	-7472.92
			FFX	1.64	0.00	0.00	97.64	0.74	-7738.62
	179-337	18.4	Original	1.32	4.47	2.55	92.99	1.77	-9071.76
			FFX	0.66	0.00	0.00	91.72	1.00	-9402.83
	182-345	17.6	Original	0.00	5.05	0.62	95.68	1.57	-9688.88

Gene	Residue Range	Sequence Identity	Model	% Poor Rotamers	Clash Score	Ramachandran Outliers	Ramachandran Favored	MolProbity Score	Amoeba Energy (Kcal/Mol)
			FFX	0.00	0.00	0.00	96.30	0.75	-9973.96
	184-320	12.4	Original	1.54	1.74	0.74	93.33	1.51	-8141.61
			FFX	0.77	0.00	0.00	97.04	0.67	-8405.78
	189-316	10.2	Original	0.83	1.41	0.00	96.83	1.07	-7565.58
			FFX	0.83	0.00	0.00	99.21	0.50	-7760.58
	189-333	16.3	Original	2.17	0.82	0.70	94.41	1.39	-8360.12
			FFX	0.72	0.00	0.70	97.20	0.65	-8658.59
	218-350	18.9	Original	0.00	6.22	0.76	96.95	1.52	-8226.06
			FFX	1.56	0.00	0.00	99.24	0.65	-8474.48
HSD17B4	3-304	92.0	Original	3.36	50.82	0.00	98.00	2.58	-12922.94
			FFX	0.84	0.00	0.33	96.67	0.71	-13626.82
HSD17B4-Dimer	5-606	54.5	Original	1.35	3.97	1.92	91.25	1.79	-49290.79
			FFX	1.35	0.16	0.75	94.17	1.06	-52671.92
ILDR1	24-155	18.0	Original	2.54	83.29	0.00	92.31	3.17	-5393.05
			FFX	1.69	0.00	1.54	90.00	1.22	-5888.80
	24-166	22.4	Original	2.33	8.75	7.80	80.85	2.47	-6223.82
			FFX	2.33	0.00	2.13	89.36	1.34	-6551.44
KARS	124-595	20.0	Original	5.30	153.33	2.98	91.28	3.71	-20476.23
			FFX	6.27	0.00	1.06	88.51	1.69	-22024.15
KCNE1	1-129	98.0	Original	3.48	35.44	0.79	96.85	2.63	-5157.13
			FFX	1.74	0.00	0.00	96.06	0.95	-5480.14
KCNJ10	27-348	44.0	Original	2.12	88.16	1.25	95.00	3.01	-11841.26
			FFX	1.77	0.00	0.62	94.38	1.07	-12971.09
KCNJ10-Tetramer	26-343	43.1	Original	0.36	8.48	1.27	94.70	1.82	-49492.06
			FFX	1.08	0.20	0.32	94.62	0.97	-52624.89
	28-338	45.0	Original	2.47	3.42	2.02	93.45	1.86	-47479.16
			FFX	1.56	0.00	0.40	93.69	1.06	-50941.79
KCNQ1	352-535	97.0	Original	7.14	45.66	0.55	98.35	2.79	-7901.49
			FFX	2.98	0.00	0.00	95.05	1.20	-8417.19
KCNQ4	317-369	46.0	Original	2.27	47.03	0.00	98.04	2.42	-2222.05
			FFX	0.00	0.00	0.00	98.04	0.50	-2340.36
	80-328	24.6	Original	0.97	5.46	0.40	96.76	1.50	-8543.28
			FFX	0.00	0.00	0.00	98.79	0.50	-9002.39
KITLG	35-166	80.0	Original	3.15	50.00	0.77	96.15	2.82	-5854.88
			FFX	3.15	0.00	0.00	94.62	1.25	-6186.32
LARS2	50-902	37.0	Original	0.95	0.67	1.53	92.83	1.17	-35950.27

Gene	Residue Range	Sequence Identity	Model	% Poor Rotamers	Clash Score	Ramachandran Outliers	Ramachandran Favored	MolProbity Score	Amoeba Energy (Kcal/Mol)
			FFX	1.09	0.00	0.59	93.89	0.94	-37519.62
	55-835	23.3	Original	2.24	0.89	3.08	89.09	1.61	-32531.02
			FFX	1.79	0.08	1.67	91.14	1.24	-33988.55
	60-901	39.0	Original	3.04	130.50	2.50	90.00	3.49	-32663.97
			FFX	4.28	0.00	1.31	89.29	1.55	-36443.15
LHFPL5	131-190	34.0	Original	2.17	57.21	1.72	96.55	2.71	-2199.09
			FFX	2.17	0.00	0.00	96.55	0.98	-2313.81
LOXHD1	1253-1371	32.4	Original	2.94	10.42	1.71	93.16	2.33	-5715.04
			FFX	0.00	0.00	0.85	93.16	0.94	-5961.18
	1591-1784	12.8	Original	1.16	14.44	3.12	90.62	2.25	-8879.86
			FFX	1.16	0.00	2.60	91.15	1.06	-9306.84
	173-281	35.3	Original	2.25	19.52	1.87	73.83	2.86	-5567.95
			FFX	1.12	0.00	0.93	84.11	1.21	-5837.29
	1861-2065	26.0	Original	2.22	3.63	3.45	90.15	1.96	-9032.35
			FFX	0.00	0.00	0.99	94.09	0.90	-9621.85
	1888-2057	32.7	Original	2.68	12.79	1.79	87.50	2.55	-7601.60
			FFX	0.67	0.00	0.60	94.64	0.87	-8028.69
	275-384	38.0	Original	2.13	82.75	0.93	87.96	3.24	-5388.92
			FFX	0.00	0.00	0.00	85.19	1.16	-5736.96
	297-430	32.1	Original	0.00	5.55	2.27	93.18	1.74	-5506.01
			FFX	0.00	0.00	0.76	95.45	0.82	-5731.04
	554-685	32.0	Original	0.00	6.80	2.31	91.54	1.88	-6692.70
			FFX	0.00	0.00	0.77	93.08	0.94	-6941.61
	781-935	28.9	Original	0.74	2.81	3.27	92.16	1.55	-7237.93
			FFX	2.22	0.00	0.65	93.46	1.19	-7516.26
	816-947	29.2	Original	0.00	9.56	1.54	90.00	2.05	-6291.13
			FFX	0.00	0.00	0.77	93.85	0.91	-6493.64
LOXL3	167-527	32.9	Original	1.41	9.89	2.51	89.97	2.18	-14710.24
			FFX	0.70	0.00	1.67	93.31	0.93	-15690.38
	184-388	37.8	Original	4.40	5.94	3.94	88.67	2.40	-8099.56
			FFX	1.89	0.00	1.48	92.61	1.17	-8609.37
	307-744	63.8	Original	8.31	3.76	1.15	93.12	2.31	-19944.74
			FFX	2.22	0.00	0.69	94.50	1.14	-21472.74
	42-408	30.5	Original	1.71	4.38	4.93	83.56	2.08	-15337.46
			FFX	1.37	0.00	3.29	89.04	1.18	-16396.54
	43-144	48.0	Original	2.47	80.13	4.00	93.00	3.12	-4605.90
			FFX	2.47	0.00	1.00	93.00	1.25	-4830.31

Gene	Residue Range	Sequence Identity	Model	% Poor Rotamers	Clash Score	Ramachandran Outliers	Ramachandran Favored	MolProbity Score	Amoeba Energy (Kcal/Mol)
LRTOMT	118-287	26.4	Original	0.72	2.23	1.79	92.86	1.45	-6833.86
			FFX	3.60	0.00	1.19	92.26	1.40	-7112.79
	75-290	39.3	Original	0.00	5.61	0.00	94.86	1.66	-8886.91
			FFX	0.56	0.00	0.93	95.79	0.79	-9250.56
	76-290	37.7	Original	0.00	2.66	0.47	94.84	1.41	-8725.89
			FFX	1.13	0.00	0.47	96.71	0.75	-9040.89
	77-290	38.6	Original	0.00	4.17	0.47	92.45	1.67	-8760.98
			FFX	1.14	0.00	0.47	95.28	0.87	-9099.92
	79-291	39.0	Original	1.15	86.07	0.95	95.73	2.74	-8470.37
			FFX	4.60	0.00	0.95	94.31	1.39	-9039.09
MARVELD2	442-551	30.0	Original	1.90	62.63	0.93	98.15	2.48	-6246.62
			FFX	3.81	0.00	1.85	96.30	1.19	-6593.96
MCM2	189-821	52.3	Original	0.73	3.02	1.90	91.28	1.60	-27240.82
			FFX	2.20	0.00	1.27	92.23	1.24	-28883.93
	192-805	37.1	Original	3.02	1.04	1.14	90.85	1.69	-27107.95
			FFX	1.89	0.00	0.98	92.97	1.16	-28427.32
	199-798	39.0	Original	4.26	92.25	1.51	95.32	3.24	-25159.52
			FFX	1.55	0.00	1.00	92.64	1.11	-27492.89
MET	1082-1380	39.0	Original	1.13	100.40	2.02	94.28	2.90	-12426.36
			FFX	1.89	0.00	1.68	91.25	1.22	-13390.96
	44-919	25.6	Original	1.77	4.10	4.81	85.47	2.03	-34865.68
			FFX	1.52	0.00	1.26	89.70	1.20	-37452.36
MITF	323-402	96.0	Original	4.11	35.23	0.00	100.00	2.50	-4301.54
			FFX	0.00	0.00	0.00	98.72	0.50	-4477.61
MITF-Dimer	324-402	97.5	Original	0.00	0.37	0.00	99.35	0.63	-8691.33
			FFX	0.00	0.00	0.00	98.70	0.50	-8958.68
MSRB3	36-171	53.7	Original	6.72	7.20	5.97	78.36	2.78	-6116.73
			FFX	3.36	0.00	2.24	85.07	1.56	-6440.73
	41-167	58.0	Original	2.70	47.37	0.00	96.00	2.76	-5823.79
			FFX	2.70	0.00	0.00	95.20	1.16	-6074.23
MYH14	15-863	46.8	Original	6.79	1.54	1.77	92.80	1.99	-36828.72
			FFX	1.39	0.00	1.18	94.69	0.97	-39251.64
	17-863	46.8	Original	6.94	1.84	2.25	92.54	2.05	-36762.29
			FFX	1.94	0.00	1.30	94.20	1.11	-39080.37
	18-863	47.2	Original	5.01	0.96	2.49	91.47	1.82	-37086.67
			FFX	1.53	0.00	0.95	93.84	1.05	-39116.26
	18-983	38.4	Original	1.47	1.16	3.63	86.72	1.58	-42927.11

Gene	Residue Range	Sequence Identity	Model	% Poor Rotamers	Clash Score	Ramachandran Outliers	Ramachandran Favored	MolProbity Score	Amoeba Energy (Kcal/Mol)
			FFX	0.98	0.00	1.97	92.32	0.97	-45619.24
	18-985	38.4	Original	2.32	1.68	3.52	86.44	1.83	-43098.83
			FFX	1.46	0.13	1.86	90.99	1.20	-45878.51
	21-860	50.0	Original	6.44	5.28	2.74	89.62	2.46	-33826.45
			FFX	4.20	0.00	1.43	92.48	1.44	-38511.85
	21-862	49.9	Original	2.37	2.82	1.90	92.98	1.80	-37322.04
			FFX	1.26	0.00	1.07	94.29	0.96	-39078.35
	22-947	69.3	Original	1.28	1.48	1.52	92.86	1.42	-41912.86
			FFX	0.77	0.07	1.08	94.59	0.90	-43756.53
	22-954	68.8	Original	6.20	0.33	1.83	92.91	1.68	-42074.66
			FFX	2.03	0.00	0.75	96.03	1.01	-44297.87
	24-983	68.3	Original	6.39	1.04	2.30	89.67	1.97	-43333.54
			FFX	2.70	0.00	1.25	93.32	1.26	-45836.83
	46-832	76.0	Original	4.91	110.75	2.55	91.46	3.54	-33827.51
			FFX	3.42	0.16	1.27	92.74	1.43	-36806.16
	804-955	17.5	Original	0.00	0.80	4.00	90.67	1.28	-7308.23
			FFX	0.00	0.00	2.00	96.00	0.77	-7614.00
	804-957	17.5	Original	1.56	3.15	1.97	91.45	1.76	-7430.33
			FFX	0.00	0.00	0.66	97.37	0.62	-7775.44
MYH9	1-895	83.5	Original	6.91	0.41	1.34	93.06	1.73	-40874.20
			FFX	2.56	0.00	0.34	95.18	1.15	-43224.10
	3-836	52.3	Original	7.16	2.73	1.92	91.35	2.22	-37113.74
			FFX	3.99	0.00	1.20	93.27	1.39	-39398.78
	3-838	52.4	Original	2.20	1.77	1.68	94.12	1.59	-37995.78
			FFX	0.96	0.00	0.60	95.08	0.84	-39856.15
	3-839	49.1	Original	4.39	1.40	1.44	92.93	1.81	-37891.89
			FFX	2.47	0.00	0.72	95.57	1.11	-39763.09
	3-930	80.0	Original	13.70	1.79	1.30	92.76	2.26	-42488.88
			FFX	1.23	0.00	0.54	95.36	0.89	-45482.92
	3-959	78.7	Original	8.60	1.03	2.30	89.53	2.07	-44553.71
			FFX	3.70	0.00	0.73	93.72	1.35	-46912.41
	3-961	41.4	Original	3.34	0.71	2.40	88.30	1.72	-44363.09
			FFX	1.67	0.00	1.67	92.27	1.15	-47112.65
	4-822	81.8	Original	0.98	0.45	0.73	94.86	1.01	-37633.44
			FFX	0.70	0.00	0.24	95.10	0.84	-39341.73
	6-808	84.0	Original	3.72	81.41	1.50	92.38	3.29	-35717.79
			FFX	2.87	0.00	0.62	95.26	1.18	-38513.52

Gene	Residue Range	Sequence Identity	Model	% Poor Rotamers	Clash Score	Ramachandran Outliers	Ramachandran Favored	MolProbity Score	Amoeba Energy (Kcal/Mol)
MYO15A	1215-1973	39.7	Original	1.20	2.51	1.45	94.06	1.49	-32732.14
			FFX	0.30	0.08	0.40	94.98	0.88	-34414.53
	1217-1946	43.3	Original	0.47	3.30	1.24	94.51	1.50	-31766.64
			FFX	1.25	0.00	0.69	95.60	0.88	-32980.55
	1217-1949	37.7	Original	1.86	2.19	2.05	92.61	1.66	-31584.53
			FFX	0.78	0.00	0.82	94.80	0.86	-33085.18
	1217-1960	35.3	Original	1.98	2.73	1.75	94.47	1.66	-31898.35
			FFX	1.07	0.00	0.81	94.61	0.89	-33583.03
	1217-1971	38.5	Original	3.16	4.39	2.39	92.16	2.08	-32178.53
			FFX	1.05	0.08	1.06	93.76	0.96	-33927.40
	1217-1976	38.3	Original	5.83	1.69	4.49	87.07	2.12	-31936.39
			FFX	2.39	0.08	0.92	91.42	1.33	-34070.24
	1224-1898	44.0	Original	2.69	110.88	3.57	91.68	3.33	-27856.11
			FFX	3.87	0.00	2.08	91.38	1.45	-30070.82
	1224-1972	41.5	Original	3.33	1.80	2.14	91.03	1.85	-31233.69
			FFX	1.82	0.00	0.94	93.44	1.13	-33390.91
MYO3A	293-1084	36.4	Original	1.56	7.09	1.90	92.15	2.02	-34859.62
			FFX	0.71	0.00	1.01	94.43	0.88	-36639.40
	337-1105	35.2	Original	4.54	3.86	2.74	91.00	2.19	-32598.46
			FFX	3.66	0.00	1.04	93.48	1.36	-35047.45
	337-1121	31.7	Original	2.44	1.81	2.81	91.19	1.75	-34283.28
			FFX	1.00	0.00	0.89	94.51	0.88	-36029.26
	337-1134	33.5	Original	1.55	0.93	1.38	93.22	1.36	-35604.20
			FFX	0.84	0.08	0.50	95.23	0.86	-37039.84
	337-1141	34.2	Original	2.23	2.15	2.37	91.41	1.76	-35112.19
			FFX	1.81	0.00	0.62	93.52	1.12	-37088.28
	337-1144	34.3	Original	4.87	4.13	2.73	88.59	2.30	-34309.50
			FFX	1.25	0.00	0.87	92.43	1.04	-37189.39
	341-1141	36.4	Original	1.68	3.01	1.88	91.99	1.75	-34880.48
			FFX	0.98	0.00	0.38	94.99	0.85	-36959.65
	9-292	53.0	Original	4.40	75.40	0.71	93.62	3.26	-12719.88
			FFX	4.80	0.22	0.35	93.26	1.54	-13445.29
MYO6	1-768	41.0	Original	3.55	122.72	1.96	93.34	3.40	-33402.75
			FFX	2.36	0.00	0.91	92.95	1.23	-36924.83
	1166-1294	94.6	Original	26.79	3.72	4.72	84.25	2.92	-5982.26
			FFX	5.36	0.00	0.79	92.91	1.51	-6479.49
	2-825	98.3	Original	7.26	0.45	0.49	97.08	1.48	-38294.58

Gene	Residue Range	Sequence Identity	Model	% Poor Rotamers	Clash Score	Ramachandran Outliers	Ramachandran Favored	MolProbity Score	Amoeba Energy (Kcal/Mol)
			FFX	1.23	0.00	0.49	96.72	0.78	-40215.77
	4-819	97.9	Original	4.16	1.37	0.61	96.07	1.61	-37813.07
			FFX	1.11	0.00	0.25	96.68	0.74	-39722.30
	61-833	42.0	Original	6.55	139.62	3.63	90.79	3.75	-14162.08
			FFX	3.49	0.16	1.69	91.05	1.49	-36786.67
MYO7A	2-792	36.4	Original	5.29	2.74	2.28	92.27	2.09	-34567.67
			FFX	3.15	0.00	0.89	93.79	1.29	-36594.65
	2-800	36.2	Original	1.13	4.10	1.00	93.98	1.64	-35215.32
			FFX	1.42	0.00	0.50	96.24	0.87	-37243.87
	3-800	36.9	Original	6.68	5.35	2.51	91.21	2.43	-34400.84
			FFX	1.14	0.00	1.13	92.96	0.99	-37168.60
	3-801	36.6	Original	6.38	3.64	2.01	90.84	2.29	-34816.36
			FFX	1.42	0.00	0.88	94.10	1.01	-37198.43
	3-859	40.1	Original	1.72	2.15	0.70	94.04	1.57	-38082.79
			FFX	0.80	0.07	0.70	96.49	0.76	-39912.59
	35-861	42.8	Original	1.79	2.15	0.97	93.45	1.61	-36245.95
			FFX	0.69	0.00	0.61	96.73	0.71	-38554.77
	56-874	40.1	Original	3.47	0.74	2.33	90.82	1.67	-36058.68
			FFX	0.69	0.07	0.49	94.61	0.90	-37787.06
	993-1686	98.0	Original	4.49	66.25	0.58	96.10	3.05	-28861.43
			FFX	2.66	0.00	0.14	95.52	1.13	-31460.80
NARS2	28-476	35.0	Original	4.31	109.51	2.46	90.38	3.53	-18930.09
			FFX	2.54	0.00	0.89	91.05	1.33	-20500.29
NARS2-Dimer	24-476	30.5	Original	0.63	8.26	2.00	91.01	1.97	-39334.62
			FFX	1.26	0.07	1.44	92.90	1.06	-41771.93
	3-474	18.9	Original	1.33	3.66	1.49	89.15	1.82	-40516.60
			FFX	1.69	0.00	1.17	90.64	1.20	-43131.52
NLRP3	699-1031	39.2	Original	1.67	8.70	0.00	95.17	1.97	-13151.50
			FFX	2.00	0.00	0.30	95.17	1.06	-13800.50
	725-897	48.0	Original	0.65	65.32	1.75	97.08	2.45	-6555.98
			FFX	1.31	0.00	0.58	97.66	0.66	-7059.46
OPA1	262-707	22.4	Original	0.75	5.48	1.35	91.89	1.79	-20127.19
			FFX	1.00	0.14	1.13	93.69	0.97	-21168.48
	262-709	26.5	Original	0.50	6.44	1.57	94.84	1.71	-20217.92
			FFX	1.73	0.00	0.45	94.39	1.06	-21382.78
	272-577	27.0	Original	2.59	112.97	2.30	93.09	3.28	-12921.66
			FFX	2.59	0.00	0.66	93.75	1.23	-13886.11

Gene	**Residue Range**	**Sequence Identity**	**Model**	**% Poor Rotamers**	**Clash Score**	**Ramachandran Outliers**	**Ramachandran Favored**	**MolProbity Score**	**Amoeba Energy (Kcal/Mol)**
OPA1-Dimer	261-706	24.7	Original	1.00	5.27	2.25	92.22	1.76	-39892.72
			FFX	0.87	0.14	0.79	93.91	0.96	-42168.82
OPA1-Tetramer	262-707	23.7	Original	1.43	5.45	1.91	92.06	1.90	-80139.24
			FFX	0.81	1.76	0.90	93.02	1.38	-83370.60
OSBPL2	59-480	35.5	Original	1.86	2.35	2.14	92.38	1.69	-19582.91
			FFX	2.13	0.00	1.19	91.90	1.24	-20470.55
	60-480	38.0	Original	2.67	105.26	3.58	90.21	3.35	-18445.66
			FFX	1.60	0.29	1.67	88.78	1.35	-20083.10
	84-116	36.4	Original	0.00	7.29	3.23	77.42	2.17	-1363.63
			FFX	0.00	0.00	3.23	93.55	0.92	-1428.61
OTOA	1-533	14.0	Original	3.40	137.94	1.32	93.97	3.41	-20815.35
			FFX	4.26	0.12	0.94	93.79	1.44	-22702.08
OTOF	1-124	91.0	Original	2.65	46.12	0.82	95.08	2.80	-5804.22
			FFX	2.65	0.00	0.00	95.90	1.10	-6024.71
	250-542	18.4	Original	3.05	11.43	2.75	89.35	2.51	-12824.48
			FFX	2.67	0.00	2.06	89.69	1.38	-13566.43
	251-543	24.2	Original	0.00	3.67	4.81	83.85	1.84	-12738.80
			FFX	1.91	0.00	2.41	87.97	1.31	-13388.82
	950-1095	19.4	Original	1.60	16.47	3.47	86.81	2.50	-6301.44
			FFX	0.00	0.00	4.17	89.58	1.06	-6578.52
	951-1226	22.9	Original	0.42	5.25	5.47	86.13	1.92	-11426.39
			FFX	0.00	0.00	1.46	92.70	0.96	-12051.09
OTOG	1244-1398	17.5	Original	1.63	5.42	0.65	94.12	1.85	-6253.09
			FFX	0.81	0.00	0.00	96.73	0.70	-6486.41
	1285-1398	19.6	Original	0.00	8.92	0.89	91.96	1.97	-4760.31
			FFX	1.09	0.00	0.00	95.54	0.84	-4926.79
	1880-2032	21.8	Original	2.61	9.37	3.97	86.09	2.45	-4972.10
			FFX	1.74	0.00	1.99	86.09	1.32	-5309.56
	408-511	33.7	Original	5.68	2.05	2.94	83.33	2.24	-4088.90
			FFX	0.00	0.00	0.98	91.18	1.01	-4371.26
	768-877	30.5	Original	5.43	4.65	7.41	85.19	2.45	-4836.07
			FFX	3.26	0.00	2.78	91.67	1.39	-5066.96
	906-982	47.0	Original	4.48	78.36	0.00	96.00	3.13	-2999.11
			FFX	5.97	0.00	0.00	97.33	1.22	-3184.02
OTOGL	1242-1352	27.3	Original	1.00	5.03	0.92	93.58	1.69	-5058.92
			FFX	1.00	0.00	0.92	96.33	0.75	-5255.68
	394-470	38.7	Original	10.45	7.51	5.33	86.67	2.81	-3138.40

Gene	Residue Range	Sequence Identity	Model	% Poor Rotamers	Clash Score	Ramachandran Outliers	Ramachandran Favored	MolProbity Score	Amoeba Energy (Kcal/Mol)
			FFX	1.49	0.00	1.33	93.33	1.07	-3315.85
	480-602	13.0	Original	0.00	10.20	3.31	90.08	2.08	-4681.90
			FFX	0.93	0.00	1.65	85.95	1.14	-4924.05
	724-827	27.8	Original	5.32	4.61	3.92	88.24	2.38	-4142.00
			FFX	2.13	0.00	1.96	86.27	1.39	-4399.41
	846-935	42.5	Original	10.39	3.11	10.23	76.14	2.66	-3161.11
			FFX	2.60	0.00	1.14	85.23	1.47	-3344.74
P2RX2	120-178	56.0	Original	4.08	82.64	0.00	98.25	2.85	-2370.78
			FFX	0.00	0.00	0.00	94.74	0.86	-2504.03
P2RX2-Trimer	25-381	51.7	Original	0.75	4.84	0.56	94.84	1.61	-43180.54
			FFX	0.54	0.00	0.28	93.43	0.93	-45458.83
PAX3	111-274	21.6	Original	1.36	0.37	3.09	87.04	1.36	-8938.18
			FFX	0.68	0.00	0.00	94.44	0.88	-9344.49
	112-272	24.5	Original	1.39	6.87	2.52	85.53	2.14	-8746.00
			FFX	2.78	0.00	1.89	93.08	1.28	-9164.32
	112-276	24.5	Original	4.73	6.26	4.91	86.50	2.49	-8950.34
			FFX	1.35	0.00	1.23	92.02	1.08	-9401.07
	124-277	21.9	Original	4.38	4.77	4.61	88.82	2.31	-8297.61
			FFX	2.19	0.00	0.00	95.39	1.08	-8708.82
	295-476	10.0	Original	0.61	92.78	3.33	89.44	3.00	-5896.49
			FFX	2.44	0.00	3.33	86.67	1.42	-6548.27
	34-162	71.1	Original	4.39	2.90	3.15	83.46	2.25	-5572.81
			FFX	1.75	0.00	1.57	88.19	1.28	-5797.47
	35-158	78.7	Original	6.36	1.01	1.64	92.62	1.87	-5378.74
			FFX	1.82	0.00	0.82	96.72	0.90	-5637.72
	37-161	69.3	Original	1.79	0.00	0.00	95.93	0.97	-5513.05
			FFX	1.79	0.00	0.00	99.19	0.69	-5738.66
PCDH15	1140-1405	95.0	Original	0.00	0.23	0.00	95.08	0.93	-11351.62
			FFX	1.30	0.00	0.00	95.83	0.87	-11966.15
	1804-1836	56.0	Original	0.00	29.41	0.00	100.00	1.95	-824.47
			FFX	12.90	0.00	0.00	96.77	1.54	-863.96
	380-814	30.2	Original	0.26	4.81	1.62	92.61	1.71	-19590.68
			FFX	0.79	0.15	0.92	93.30	0.99	-20467.96
	398-812	93.5	Original	3.61	0.79	0.48	94.67	1.54	-19582.55
			FFX	1.39	0.00	0.00	93.70	1.03	-20371.44
PCDH15-Dimer	28-387	97.5	Original	0.62	0.62	0.00	98.32	0.70	-36577.40
			FFX	0.77	0.00	0.28	97.49	0.60	-37684.46

Gene	Residue Range	Sequence Identity	Model	% Poor Rotamers	Clash Score	Ramachandran Outliers	Ramachandran Favored	MolProbity Score	Amoeba Energy (Kcal/Mol)
	337-756	34.9	Original	0.96	5.37	3.11	89.00	1.86	-37557.11
			FFX	1.64	0.08	1.32	91.87	1.19	-39943.43
	400-918	27.1	Original	1.77	1.95	2.61	90.04	1.70	-44213.41
			FFX	1.66	0.00	1.45	91.97	1.16	-46932.94
	509-1034	22.0	Original	1.55	5.46	3.24	88.36	2.03	-43488.41
			FFX	1.99	0.00	1.62	92.94	1.18	-46428.23
	545-1026	30.8	Original	0.84	8.18	2.40	89.90	2.00	-39401.63
			FFX	1.57	0.00	1.25	90.62	1.18	-42360.67
	621-1136	26.3	Original	0.34	7.19	1.46	92.70	1.86	-42060.04
			FFX	0.89	0.00	1.36	92.12	0.98	-45169.74
	816-1357	95.0	Original	0.42	0.47	0.56	95.09	1.00	-45197.19
			FFX	1.16	0.12	0.28	94.07	0.99	-48093.70
PCDH15-Heteromer	623-1139	24.8	Original	2.42	9.20	4.52	86.03	2.42	-39595.14
			FFX	2.42	0.00	2.31	89.39	1.36	-42772.42
PDZD7	4-294	27.0	Original	3.32	10.52	3.46	89.27	2.51	-11934.29
			FFX	2.07	0.00	1.38	91.70	1.24	-12704.20
	76-170	94.0	Original	0.00	74.89	1.08	92.47	2.81	-3967.22
			FFX	0.00	0.00	1.08	95.70	0.80	-4269.21
	83-293	33.0	Original	1.14	7.81	3.83	86.12	2.11	-9072.93
			FFX	2.27	0.00	0.00	91.87	1.26	-9474.97
	84-292	28.3	Original	0.00	6.01	4.35	87.92	1.93	-8950.79
			FFX	0.00	0.00	0.97	89.86	1.05	-9429.77
	85-293	22.7	Original	2.87	10.11	5.31	83.57	2.56	-8877.05
			FFX	2.30	0.00	1.93	90.82	1.30	-9456.83
PEX1	13-179	89.0	Original	2.08	33.67	0.00	97.58	2.34	-6813.34
			FFX	1.39	0.00	0.61	93.94	1.01	-7102.25
	405-1063	27.5	Original	2.41	3.25	3.04	91.02	1.93	-27332.24
			FFX	2.59	0.10	0.46	94.37	1.24	-29076.06
PEX1-Hexamer(*used monomer)	405-1064	28.0	Original	2.75	0.76	4.26	86.02	1.72	-26998.71
			FFX	1.55	0.00	1.06	88.45	1.23	-28770.29
PEX6	202-975	29.3	Original	2.20	5.11	3.76	87.82	2.13	-30173.01
			FFX	2.51	0.00	2.07	90.80	1.33	-32131.23
	203-976	27.3	Original	1.72	15.06	3.76	89.90	2.41	-29687.16
			FFX	2.51	0.09	1.94	91.19	1.35	-32408.08

Gene	Residue Range	Sequence Identity	Model	% Poor Rotamers	Clash Score	Ramachandran Outliers	Ramachandran Favored	MolProbity Score	Amoeba Energy (Kcal/Mol)
	757-935	47.0	Original	1.99	111.88	5.65	86.44	3.37	-7146.98
			FFX	5.30	0.00	2.82	87.01	1.67	-7708.58
PEX6-Hexamer(*used monomer)	202-979	29.0	Original	2.50	0.85	3.87	86.86	1.69	-30409.87
			FFX	2.66	0.00	2.58	90.98	1.34	-32276.23
	435-930	19.0	Original	2.49	3.48	4.05	86.44	2.07	-18814.25
			FFX	1.25	0.00	2.63	89.68	1.13	-20024.72
PJVK	1-236	22.7	Original	0.98	12.08	2.14	89.32	2.16	-9790.25
			FFX	0.49	0.27	1.28	94.02	1.00	-10355.57
	27-95	30.0	Original	6.35	61.84	1.49	92.54	3.34	-3121.04
			FFX	3.17	0.00	1.49	85.07	1.54	-3311.64
PNPT1	45-754	37.0	Original	3.80	125.40	3.39	86.86	3.63	-28238.18
			FFX	3.47	0.00	2.82	88.98	1.49	-30994.57
	606-752	17.9	Original	1.57	3.44	2.07	92.41	1.76	-6502.94
			FFX	0.79	0.00	0.69	95.86	0.79	-6744.39
PNPT1-Heteromer	45-749	38.2	Original	1.91	4.05	1.43	93.20	1.84	-85144.13
			FFX	1.85	0.03	0.64	94.28	1.10	-89951.07
PNPT1-Trimer	43-744	34.3	Original	1.51	3.49	2.52	90.10	1.82	-88386.97
			FFX	1.17	0.09	1.57	92.29	1.07	-93356.95
	45-593	38.7	Original	1.36	2.27	2.74	90.49	1.64	-70064.50
			FFX	1.36	0.27	0.91	91.41	1.21	-73893.79
POLR1C	40-340	47.0	Original	1.88	84.54	0.33	97.32	2.73	-13874.72
			FFX	2.63	0.00	0.33	95.99	1.10	-14514.71
	51-332	34.7	Original	0.81	8.46	2.14	90.71	1.99	-12663.51
			FFX	1.21	0.00	2.14	92.86	1.02	-13196.05
POLR1D	20-120	50.0	Original	2.22	2.52	3.03	90.91	1.82	-4829.22
			FFX	1.11	0.00	1.01	90.91	1.06	-5027.74
POU3F4	187-338	63.2	Original	2.96	0.81	0.67	92.67	1.57	-6883.42
			FFX	0.00	0.00	0.00	98.00	0.50	-7156.86
	188-338	87.0	Original	3.73	177.48	2.01	94.63	3.51	-6419.51
			FFX	2.99	0.00	2.01	94.63	1.23	-7009.59
	190-331	41.9	Original	3.20	3.49	0.71	95.00	1.87	-6367.05
			FFX	1.60	0.00	0.00	97.86	0.69	-6623.25
	194-336	62.4	Original	5.56	4.27	2.13	92.91	2.23	-6359.23
			FFX	0.00	0.00	0.71	94.33	0.89	-6638.38
POU4F3	180-333	49.0	Original	0.00	3.58	3.29	90.79	1.67	-7176.66

Gene	Residue Range	Sequence Identity	Model	% Poor Rotamers	Clash Score	Ramachandran Outliers	Ramachandran Favored	MolProbity Score	Amoeba Energy (Kcal/Mol)
			FFX	0.76	0.00	0.66	95.39	0.82	-7467.15
	183-327	38.5	Original	3.28	2.56	2.80	89.51	1.99	-6600.18
			FFX	1.64	0.00	0.70	93.71	1.08	-6925.45
	183-331	38.5	Original	3.17	5.35	0.68	94.56	2.04	-6852.23
			FFX	0.79	0.00	0.68	96.60	0.72	-7176.18
	184-333	49.7	Original	3.15	2.85	1.35	95.95	1.73	-6889.21
			FFX	0.79	0.00	0.00	95.27	0.83	-7128.31
PRPS1	3-318	48.0	Original	4.48	127.69	3.50	90.76	3.59	-12861.62
			FFX	4.85	0.20	2.23	91.72	1.60	-13881.79
PTPRQ	2013-2328	39.4	Original	0.70	6.16	1.59	92.04	1.82	-13981.36
			FFX	1.41	0.00	0.64	93.63	1.03	-14648.04
	614-894	17.1	Original	0.77	8.24	2.15	87.10	2.07	-11639.20
			FFX	1.15	0.00	1.43	93.19	0.99	-12400.27
	711-988	19.1	Original	2.72	1.36	3.26	89.13	1.77	-11167.89
			FFX	2.33	0.00	1.81	91.30	1.29	-11814.13
	714-1091	18.1	Original	0.57	8.04	3.46	90.43	1.98	-14577.67
			FFX	0.86	0.00	1.33	91.76	1.00	-15614.36
	797-993	13.0	Original	3.33	107.52	3.08	86.67	3.52	-7577.96
			FFX	3.33	0.00	1.54	82.05	1.60	-8267.21
	948-1378	18.7	Original	2.53	11.98	2.10	86.71	2.53	-15894.05
			FFX	1.27	0.00	2.10	90.44	1.11	-17136.20
PTPRQ-Dimer	571-898	17.3	Original	3.62	14.17	5.06	88.65	2.67	-25571.82
			FFX	2.14	0.00	1.69	89.57	1.31	-28097.56
	664-992	18.3	Original	0.99	3.19	3.98	91.13	1.63	-26754.80
			FFX	1.32	0.00	1.68	92.66	1.05	-28679.84
RDX	3-583	59.1	Original	0.78	3.01	1.04	97.75	1.15	-31483.40
			FFX	0.58	0.00	0.17	97.58	0.59	-32700.66
	337-445	16.8	Original	0.00	1.10	3.74	91.59	1.32	-6936.13
			FFX	0.00	0.00	0.00	94.39	0.88	-7093.26
	497-583	71.3	Original	1.30	0.00	0.00	100.00	0.59	-4967.98
			FFX	0.00	0.00	0.00	100.00	0.50	-5082.64
RIPOR2 (FAM65B)	1011-1065	19.0	Original	4.26	113.61	1.89	94.34	3.38	-2734.91
			FFX	4.26	0.00	0.00	98.11	0.98	-2850.65
	832-1036	13.6	Original	1.09	7.69	2.46	92.61	1.91	-8316.03
			FFX	1.09	0.00	0.49	93.10	0.97	-8758.21
	883-1032	14.4	Original	0.75	8.36	2.70	91.22	1.97	-6129.71

Gene	**Residue Range**	**Sequence Identity**	**Model**	**% Poor Rotamers**	**Clash Score**	**Ramachandran Outliers**	**Ramachandran Favored**	**MolProbity Score**	**Amoeba Energy (Kcal/Mol)**
			FFX	1.49	0.42	0.68	93.92	1.19	-6490.87
ROR1	442-742	38.4	Original	0.75	8.53	5.69	86.29	2.10	-12934.43
			FFX	1.49	0.00	1.67	92.31	1.11	-13705.75
	464-749	70.0	Original	0.78	52.34	0.70	95.42	2.51	-12451.63
			FFX	0.39	0.00	0.00	94.01	0.90	-13090.59
	467-749	39.2	Original	1.19	3.75	1.42	93.95	1.63	-12334.67
			FFX	0.40	0.00	1.07	96.09	0.77	-12938.67
S1PR2	6-301	52.0	Original	1.97	90.68	0.68	94.56	3.02	-9461.44
			FFX	2.36	0.00	1.36	94.22	1.17	-10159.44
	7-302	51.9	Original	1.18	4.24	0.68	94.90	1.61	-9722.30
			FFX	0.79	0.00	0.34	97.62	0.58	-10288.58
SERPINB6	3-376	48.3	Original	2.45	3.39	0.00	98.39	1.43	-16873.97
			FFX	0.31	0.17	0.27	96.77	0.77	-17578.23
	347-376	55.0	Original	0.00	37.58	3.57	92.86	2.51	-1152.52
			FFX	3.70	0.00	0.00	96.43	1.17	-1229.01
SIX5	129-259	21.2	Original	0.93	2.28	5.43	86.05	1.65	-6175.02
			FFX	0.93	0.00	1.55	89.15	1.07	-6432.00
	222-255	56.0	Original	0.00	46.71	0.00	100.00	2.15	-1675.27
			FFX	0.00	0.00	0.00	100.00	0.50	-1752.58
	86-257	61.6	Original	2.14	1.06	1.18	95.88	1.34	-8061.04
			FFX	1.43	0.00	1.18	98.24	0.62	-8269.43
SLC17A8	78-520	10.0	Original	3.59	163.18	2.27	94.56	3.47	-13946.29
			FFX	3.87	0.00	1.59	90.70	1.48	-15416.53
SLC22A4	150-217	35.0	Original	1.72	101.40	4.55	89.39	3.22	-2027.87
			FFX	1.72	0.00	0.00	90.91	1.20	-2174.70
SLC26A4	516-562	33.9	Original	0.00	0.00	0.00	95.56	0.81	-1945.74
			FFX	2.38	0.00	0.00	97.78	0.84	-2021.96
	516-727	39.0	Original	5.18	110.72	2.38	90.95	3.57	-8510.95
			FFX	4.15	0.00	1.43	90.48	1.50	-9491.82
	655-731	34.6	Original	0.00	3.97	0.00	97.33	1.31	-3452.13
			FFX	0.00	0.00	0.00	98.67	0.50	-3562.96
SLC26A5	505-718	93.0	Original	2.78	40.18	0.00	97.64	2.50	-9148.25
			FFX	2.22	0.00	0.00	96.70	0.97	-9774.35
	638-718	92.7	Original	0.00	0.00	0.00	100.00	0.50	-3457.98
			FFX	0.00	0.00	0.00	94.94	0.85	-3571.74
SLITRK6	31-267	53.0	Original	4.19	70.55	0.85	92.34	3.27	-9795.96
			FFX	3.72	0.00	0.43	93.19	1.37	-10395.82

Gene	Residue Range	Sequence Identity	Model	% Poor Rotamers	Clash Score	Ramachandran Outliers	Ramachandran Favored	MolProbity Score	Amoeba Energy (Kcal/Mol)
	330-567	46.9	Original	1.34	2.09	0.85	91.95	1.56	-10003.81
			FFX	2.23	0.00	2.12	93.22	1.20	-10453.29
SMPX	6-75	31.0	Original	3.45	66.48	1.47	97.06	2.87	-2975.18
			FFX	3.45	0.00	0.00	92.65	1.37	-3157.80
	13-42	33.3	Original	4.35	4.42	21.43	64.29	2.59	-1232.88
			FFX	0.00	0.00	3.57	78.57	1.25	-1313.04
SNAI2	124-263	36.5	Original	3.17	1.79	0.00	92.75	1.78	-7367.52
			FFX	0.00	0.00	0.72	91.30	1.01	-7643.96
	125-263	29.6	Original	4.00	3.16	2.92	88.32	2.16	-6887.70
			FFX	0.80	0.00	2.92	92.70	0.96	-7244.36
	126-263	34.1	Original	7.20	4.09	6.62	81.62	2.56	-6107.16
			FFX	1.60	0.00	2.21	92.65	1.12	-6492.47
	129-262	42.8	Original	0.82	4.66	2.27	92.42	1.71	-7381.13
			FFX	0.00	0.00	3.79	88.64	1.08	-7646.15
	158-264	87.0	Original	8.25	47.51	0.95	95.24	3.18	-4708.72
			FFX	3.09	0.00	0.95	93.33	1.31	-5007.63
SOX10	102-173	96.0	Original	3.12	34.04	0.00	98.57	2.39	-3771.96
			FFX	3.12	0.00	0.00	100.00	0.88	-3907.17
STRC	859-1074	31.0	Original	4.35	176.85	5.14	82.71	3.89	-7392.04
			FFX	4.35	0.30	3.74	85.05	1.75	-8165.92
SYNE4	100-201	8.0	Original	1.28	0.62	3.00	94.00	1.19	-4392.20
			FFX	1.28	0.00	1.00	96.00	0.86	-4539.33
	122-249	10.4	Original	1.00	3.57	1.59	92.06	1.63	-5385.38
			FFX	1.00	0.00	2.38	92.86	0.95	-5588.68
	24-202	11.4	Original	1.44	7.08	1.13	92.66	1.97	-7712.27
			FFX	0.72	0.00	0.56	96.05	0.77	-8075.28
	25-195	13.7	Original	0.76	3.54	4.14	86.98	1.77	-7379.36
			FFX	1.52	0.00	1.18	93.49	1.06	-7692.95
	41-253	21.0	Original	4.76	124.45	1.42	94.31	3.46	-8804.74
			FFX	4.17	0.00	0.47	92.89	1.42	-9519.97
TBC1D24	124-292	15.0	Original	0.68	6.24	1.80	91.62	1.84	-6910.31
			FFX	2.05	0.00	0.60	96.41	0.98	-7245.65
	27-310	26.9	Original	1.22	8.77	0.35	93.97	1.94	-11757.11
			FFX	0.81	0.00	0.00	95.74	0.80	-12335.34
	339-554	33.7	Original	0.55	6.28	5.14	84.58	2.01	-8822.86
			FFX	1.09	0.00	0.00	91.59	1.03	-9293.55
	442-522	38.0	Original	1.56	71.07	1.27	94.94	2.82	-3175.68

Gene	Residue Range	Sequence Identity	Model	% Poor Rotamers	Clash Score	Ramachandran Outliers	Ramachandran Favored	MolProbity Score	Amoeba Energy (Kcal/Mol)
			FFX	1.56	0.00	0.00	93.67	1.07	-3347.27
TBX1	37-79	53.0	Original	0.00	39.86	0.00	95.12	2.42	-1393.20
			FFX	7.14	0.00	2.44	87.80	1.75	-1457.50
TCOF1	302-465	20.0	Original	4.59	49.77	0.00	98.77	2.68	-7143.75
			FFX	2.75	0.00	1.23	96.30	1.08	-7581.41
TECTA	1801-2066	17.8	Original	0.84	9.40	1.52	96.21	1.75	-11250.03
			FFX	0.42	0.00	0.38	94.70	0.86	-11843.56
	584-691	27.6	Original	6.32	0.66	1.89	91.51	1.83	-4183.96
			FFX	0.00	0.00	2.83	95.28	0.83	-4373.30
	973-1078	28.9	Original	3.09	2.60	3.85	87.50	2.03	-4550.77
			FFX	1.03	0.00	0.96	93.27	0.95	-4786.39
	993-1100	19.0	Original	5.26	2.61	1.89	94.34	1.98	-4792.71
			FFX	1.05	0.65	0.94	95.28	1.06	-4991.64
TECTA-Heteromer	1772-2085	36.8	Original	0.37	4.22	1.33	94.52	1.58	-26318.22
			FFX	0.55	0.00	0.17	94.68	0.87	-27657.23
TECTB	188-280	37.0	Original	4.71	85.75	5.49	87.91	3.51	-3739.66
			FFX	1.18	0.00	2.20	84.62	1.22	-4026.46
	27-286	17.5	Original	0.86	7.05	3.10	88.37	1.98	-10322.39
			FFX	3.00	0.00	0.78	90.70	1.39	-10944.05
TECTB-Dimer	27-287	22.5	Original	0.64	6.42	1.54	91.12	1.87	-20632.12
			FFX	2.35	0.00	0.97	92.66	1.24	-22097.80
TIMM8A	27-84	41.9	Original	1.82	0.00	0.00	94.64	1.07	-2827.67
			FFX	0.00	0.00	0.00	100.00	0.50	-2916.38
TJP2	23-132	93.0	Original	2.20	62.02	0.93	93.52	2.95	-4665.02
			FFX	1.10	0.00	0.93	93.52	0.96	-4961.45
	24-127	97.1	Original	2.30	1.25	3.92	84.31	1.79	-4549.09
			FFX	0.00	0.00	0.98	93.14	0.94	-4803.10
	511-887	66.6	Original	1.88	1.34	2.13	93.87	1.48	-17177.87
			FFX	0.62	0.00	0.53	94.93	0.85	-17936.64
TMC1	68-137	36.0	Original	4.92	67.17	2.94	94.12	3.22	-4278.30
			FFX	3.28	0.00	0.00	92.65	1.35	-4505.95
TMEM132E	337-460	17.9	Original	1.82	3.63	3.28	86.07	1.99	-4880.51
			FFX	0.00	0.00	1.64	91.80	0.99	-5098.02
	532-706	29.0	Original	2.68	102.30	1.73	93.64	3.22	-6238.41
			FFX	0.67	0.00	0.00	93.64	0.92	-6809.73
	542-675	21.4	Original	0.87	3.97	2.27	93.18	1.62	-4704.34

Gene	Residue Range	Sequence Identity	Model	% Poor Rotamers	Clash Score	Ramachandran Outliers	Ramachandran Favored	MolProbity Score	Amoeba Energy (Kcal/Mol)
			FFX	0.00	0.00	2.27	91.67	1.00	-4920.92
TMIE	1-48	48.0	Original	0.00	34.74	0.00	95.65	2.33	-1477.67
			FFX	3.03	0.00	0.00	97.83	0.91	-1560.68
TMPRSS3	105-451	39.9	Original	1.03	4.58	1.16	91.01	1.76	-13588.80
			FFX	1.03	0.19	0.87	93.62	1.01	-14260.37
	242-446	50.0	Original	3.53	108.62	5.91	85.22	3.57	-7273.74
			FFX	3.53	0.00	2.96	85.22	1.57	-7949.33
TNC	1043-1340	24.5	Original	2.44	6.18	1.35	92.91	2.09	-12396.62
			FFX	3.66	0.00	1.01	94.26	1.32	-12942.89
	1132-1420	22.9	Original	2.10	11.72	1.74	90.59	2.36	-11402.42
			FFX	2.94	0.00	0.35	91.99	1.34	-12101.86
	1223-1511	23.4	Original	0.81	4.55	0.70	90.59	1.76	-11786.17
			FFX	1.63	0.00	0.70	89.55	1.22	-12298.44
	1254-1603	27.1	Original	3.02	1.50	3.45	89.08	1.83	-13972.21
			FFX	2.01	0.00	1.72	92.53	1.20	-14704.18
	1545-1885	28.8	Original	1.03	4.97	2.06	93.81	1.68	-13941.24
			FFX	1.03	0.00	0.88	93.22	0.95	-14575.78
	1580-1878	15.5	Original	1.18	5.23	3.03	88.89	1.91	-12200.97
			FFX	0.00	0.00	1.01	92.26	0.98	-12768.28
	1585-1886	16.7	Original	0.78	11.04	2.33	92.67	2.02	-12162.46
			FFX	1.17	0.22	1.33	93.00	1.08	-12897.68
	1620-1968	24.6	Original	0.66	5.63	2.02	92.80	1.76	-14168.54
			FFX	1.00	0.00	0.29	93.95	0.90	-14873.07
	1620-1975	24.2	Original	0.98	6.99	3.67	90.96	1.91	-14342.97
			FFX	1.95	0.00	1.69	92.09	1.20	-15032.24
	1625-1797	49.0	Original	3.33	81.93	0.58	97.08	2.94	-6989.31
			FFX	2.67	0.00	0.00	95.91	1.11	-7495.39
	175-374	39.2	Original	1.20	1.48	1.01	89.90	1.50	-9304.26
			FFX	0.00	0.00	0.00	89.90	1.05	-9766.58
	1980-2191	39.6	Original	0.57	5.15	0.95	94.29	1.66	-10212.48
			FFX	0.57	0.00	0.00	95.24	0.83	-10599.75
	206-425	38.1	Original	1.10	1.68	0.92	91.28	1.46	-10407.75
			FFX	1.66	0.00	0.00	91.28	1.18	-10818.11
	237-498	38.1	Original	0.46	5.59	3.85	86.15	1.94	-12678.03
			FFX	0.46	0.00	0.38	87.31	1.11	-13290.20
	297-560	33.2	Original	0.00	3.63	2.67	85.11	1.81	-12970.87
			FFX	0.45	0.00	0.38	91.60	1.00	-13576.63

Gene	Residue Range	Sequence Identity	Model	% Poor Rotamers	Clash Score	Ramachandran Outliers	Ramachandran Favored	MolProbity Score	Amoeba Energy (Kcal/Mol)
	300-529	40.3	Original	1.05	7.35	0.44	90.79	1.95	-11412.66
			FFX	0.00	0.00	0.88	92.11	0.98	-11821.36
	623-974	29.3	Original	0.32	7.06	1.14	92.00	1.88	-16127.06
			FFX	0.32	0.00	0.29	94.29	0.89	-16856.75
	623-983	29.5	Original	0.63	22.15	0.84	92.20	2.32	-16255.07
			FFX	1.58	0.00	0.56	94.43	1.03	-17087.80
	625-893	13.6	Original	0.41	19.47	3.37	86.52	2.42	-11983.81
			FFX	1.65	0.00	1.87	91.76	1.16	-12615.37
	712-1063	25.7	Original	0.65	7.42	1.43	92.29	1.88	-16105.37
			FFX	1.95	0.00	0.86	93.43	1.15	-16762.76
	712-1071	23.5	Original	1.27	10.27	1.12	91.62	2.11	-16260.65
			FFX	0.96	0.00	0.84	93.30	0.94	-17086.75
	766-984	28.5	Original	3.21	11.92	4.15	85.71	2.62	-9507.50
			FFX	2.14	0.00	4.15	90.78	1.28	-10175.25
	854-1147	29.3	Original	1.21	4.40	2.05	93.15	1.72	-12802.49
			FFX	1.21	0.00	1.03	95.89	0.85	-13386.34
	854-1162	25.3	Original	0.77	5.87	2.28	90.55	1.85	-13259.80
			FFX	1.54	0.00	0.98	92.83	1.10	-13919.22
	893-1235	26.5	Original	0.00	1.52	0.88	91.50	1.40	-14380.96
			FFX	1.42	0.00	0.88	92.38	1.09	-15036.88
TPRN	159-189	68.0	Original	0.00	35.26	0.00	96.55	2.25	-873.77
			FFX	9.52	0.00	0.00	93.10	1.69	-913.37
TRIOBP	1807-1887	42.0	Original	1.39	83.96	1.27	89.87	3.05	-3867.36
			FFX	2.78	0.00	1.27	93.67	1.26	-4083.53
	2065-2251	17.0	Original	0.00	2.99	1.62	94.05	1.49	-9877.05
			FFX	0.62	0.00	1.08	96.76	0.70	-10281.07
	2072-2355	13.1	Original	0.00	4.13	1.42	91.84	1.69	-14628.96
			FFX	1.20	0.00	1.42	91.84	1.05	-15173.87
	2113-2332	12.1	Original	2.03	0.56	1.83	93.12	1.37	-11556.28
			FFX	1.02	0.00	0.00	93.58	0.93	-12051.77
	2115-2255	13.6	Original	0.80	2.17	0.00	97.12	1.15	-7853.07
			FFX	0.00	0.00	0.72	97.84	0.54	-8058.03
	2115-2262	15.0	Original	0.00	4.96	0.68	95.21	1.59	-8036.34
			FFX	0.00	0.00	0.00	98.63	0.50	-8299.32
	2115-2263	18.5	Original	0.76	1.23	0.68	95.24	1.17	-8075.60
			FFX	0.76	0.00	0.00	97.28	0.64	-8356.36
	2115-2321	13.4	Original	0.00	3.86	0.49	96.59	1.39	-10939.76

Gene	Residue Range	Sequence Identity	Model	% Poor Rotamers	Clash Score	Ramachandran Outliers	Ramachandran Favored	MolProbity Score	Amoeba Energy (Kcal/Mol)
			FFX	0.00	0.00	0.00	96.59	0.72	-11368.16
	2117-2335	22.6	Original	0.00	3.36	2.76	91.24	1.64	-11507.78
			FFX	0.00	0.00	0.92	91.71	1.00	-11940.14
	2127-2345	12.1	Original	2.54	6.11	2.30	92.17	2.12	-11779.01
			FFX	0.00	0.00	0.46	95.85	0.79	-12283.39
	2129-2349	16.1	Original	1.01	1.37	3.20	87.21	1.49	-11590.46
			FFX	0.51	0.00	1.37	92.69	0.96	-12131.63
	2130-2287	8.2	Original	0.00	7.07	1.28	94.23	1.78	-8328.24
			FFX	0.00	0.00	0.00	96.79	0.70	-8722.64
	2130-2324	18.9	Original	0.00	1.57	2.59	92.75	1.36	-10347.82
			FFX	0.58	0.00	0.00	93.78	0.91	-10727.58
	2137-2335	11.1	Original	2.26	4.32	3.55	90.36	2.02	-10214.41
			FFX	1.13	0.00	1.52	93.91	0.95	-10701.98
	2154-2317	11.9	Original	0.00	7.53	1.85	93.83	1.82	-8474.53
			FFX	0.69	0.00	0.62	96.91	0.68	-8854.40
	2166-2311	17.3	Original	0.00	0.84	0.00	94.44	1.14	-7682.42
			FFX	0.00	0.00	0.69	97.22	0.64	-7998.45
	2188-2350	13.6	Original	2.01	11.86	3.73	90.06	2.37	-8608.91
			FFX	0.67	0.00	0.62	94.41	0.88	-9076.94
	2190-2360	18.2	Original	0.65	7.47	1.78	89.94	1.96	-8924.89
			FFX	1.29	0.00	0.59	95.27	0.91	-9368.68
	2200-2355	10.0	Original	0.71	4.28	2.60	92.21	1.69	-8213.13
			FFX	0.00	0.00	0.00	94.16	0.89	-8548.80
TSPEAR	106-160	42.0	Original	4.26	92.45	1.89	92.45	3.38	-2148.61
			FFX	2.13	0.00	0.00	90.57	1.28	-2283.72
TWNK	174-631	19.0	Original	0.50	14.05	2.85	88.60	2.24	-19079.66
			FFX	1.00	0.00	0.44	90.57	1.03	-20395.36
	404-453	36.0	Original	0.00	31.83	0.00	97.92	2.01	-2036.69
			FFX	0.00	0.00	0.00	97.92	0.52	-2141.70
	57-359	17.9	Original	2.33	15.47	3.32	89.04	2.55	-12491.61
			FFX	2.71	0.00	0.00	93.36	1.26	-13352.53
USH1C	108-301	22.1	Original	2.42	9.86	3.12	90.10	2.35	-7836.33
			FFX	0.61	0.00	1.04	92.71	0.96	-8230.81
	300-383	18.0	Original	1.30	32.06	0.00	100.00	2.08	-5397.15
			FFX	2.60	0.00	0.00	100.00	0.81	-5648.61
	82-291	35.3	Original	1.68	11.24	6.25	85.58	2.39	-8556.78
			FFX	1.12	0.00	1.92	90.87	1.06	-8985.90

Gene	Residue Range	Sequence Identity	Model	% Poor Rotamers	Clash Score	Ramachandran Outliers	Ramachandran Favored	MolProbity Score	Amoeba Energy (Kcal/Mol)
	83-281	33.3	Original	0.59	8.88	3.55	85.79	2.12	-8280.33
			FFX	1.18	0.00	3.05	90.86	1.08	-8686.03
	86-281	34.0	Original	6.59	7.06	4.64	80.41	2.74	-7865.19
			FFX	1.80	0.00	2.06	90.21	1.24	-8398.80
USH1G	1-157	31.4	Original	0.00	9.29	1.94	94.19	1.89	-7572.73
			FFX	0.76	0.00	0.00	96.13	0.76	-7813.57
	1-166	24.2	Original	2.14	2.63	0.61	95.12	1.64	-8160.69
			FFX	0.71	0.00	0.00	96.95	0.68	-8479.82
	2-161	36.5	Original	0.00	3.95	2.53	93.04	1.63	-7839.43
			FFX	0.00	0.00	0.63	96.20	0.76	-8128.72
	388-461	99.0	Original	0.00	31.75	0.00	95.83	2.27	-3532.39
			FFX	1.54	0.00	0.00	98.61	0.64	-3630.99
USH2A	1509-1893	24.9	Original	1.85	13.01	3.13	89.03	2.40	-15049.74
			FFX	1.85	0.00	1.04	90.60	1.24	-16074.76
	2325-2921	17.1	Original	3.35	9.92	4.71	86.89	2.54	-20997.61
			FFX	3.35	0.22	3.36	88.24	1.58	-22643.89
	2326-2921	19.1	Original	2.24	6.81	3.87	87.21	2.26	-20939.33
			FFX	3.36	0.00	3.03	88.72	1.48	-22746.31
	2327-2816	16.7	Original	2.06	10.47	5.33	86.48	2.41	-16756.46
			FFX	1.38	0.13	2.66	88.11	1.26	-18417.38
	2409-2823	16.9	Original	2.16	9.44	4.36	88.86	2.33	-14460.91
			FFX	1.35	0.16	1.94	90.07	1.21	-15647.65
	287-715	31.7	Original	2.36	8.65	2.58	89.23	2.32	-18464.57
			FFX	2.36	0.00	1.87	91.80	1.28	-19742.57
	287-728	35.0	Original	0.76	6.29	1.36	87.27	1.96	-19133.75
			FFX	1.02	0.00	0.23	91.59	1.01	-20375.77
	326-728	38.5	Original	1.39	9.38	2.74	86.28	2.24	-17655.70
			FFX	1.39	0.16	1.50	92.77	1.13	-18658.26
	950-991	43.0	Original	8.57	108.62	2.50	87.50	3.82	-1696.90
			FFX	0.00	0.00	0.00	87.50	1.11	-1814.62
WFS1	759-835	43.0	Original	0.00	36.10	1.33	94.67	2.41	-3422.21
			FFX	0.00	0.00	1.33	89.33	1.07	-3610.99
	82-188	14.7	Original	0.00	5.27	1.90	91.43	1.79	-5440.82
			FFX	2.25	0.00	0.95	93.33	1.20	-5633.96
	83-186	17.2	Original	1.15	1.80	2.94	88.24	1.58	-5226.81
			FFX	1.15	0.00	0.98	95.10	0.89	-5479.67
	86-188	15.6	Original	1.16	3.62	0.00	87.13	1.82	-5160.64

Gene	Residue Range	Sequence Identity	Model	% Poor Rotamers	Clash Score	Ramachandran Outliers	Ramachandran Favored	MolProbity Score	Amoeba Energy (Kcal/Mol)
			FFX	1.16	0.00	0.99	95.05	0.89	-5340.43
WHRN	260-378	97.0	Original	2.06	55.43	2.56	92.31	2.93	-5267.44
			FFX	1.03	0.00	0.85	94.02	0.91	-5615.43
Averages		41.74	Original	2.33	25.00	2.03	91.94	2.16	-15342.08
			FFX	1.60	0.03	0.93	93.48	1.04	-16287.37