Supplementary Table I: Template structures used for modeling of the HuCAL domains

	Resolution	% Identity	% Similarity	RMS value
HuCAL Vκ1	*	*	*	*
1FVC VL	2.2 Å	90	91	0.46
1FVC VL	1.9 Å	90	93	0.35
1DFB VL	2.7 Å	89	93	0.53
1VGE VL	2.0 Å	88	91	0.44
1IGM VL	2.3 Å	87	91	0.54
1BRE VL	2.0 Å	86	91	0.57
1REI VL	2.0 Å	85	90	0.50
1WTL VL	1.9 Å	83	90	0.55
1AD9 VL	2.8 Å	81	87	0.52

	Resolution	% Identity	% Similarity	RMS value
HuCAL VH1A	*	*	*	*
1AD9 VH	2.8 Å	76	81	0.55
1VGE VH	2.0 Å	73	76	0.52
1MRC VH	2.4 Å	71	76	0.56
1MRE VH	2.3 Å	69	73	0.60
1FBI VH	3.0 Å	69	73	0.66
1MLB VH	2.1 Å	68	74	0.48
1AXS VH	2.6 Å	68	75	0.56

HuCAL Vκ2	*	*	*	*
2H1P VL	2.4 Å	82	86	0.39
1RMF VL	2.8 Å	82	86	0.55
1NQB VL	2.0 Å	81	85	0.39
1NBV VL	2.0 Å	81	86	0.43
1A4J VL	2.1 Å	81	86	0.40
1FLR VL	1.85 Å	81	86	0.33
1MPA VL	2.6 Å	81	86	0.44
1HYX VL	1.8 Å	80	85	0.36
1IGJ VL	2.5 Å	80	86	0.45

HuCAL VH1B	*	*	*	*
1AD9 VH	2.8 Å	80	87	0.53
1VGE VH	2.0 Å	81	83	0.52
1NQB VH	2.0 Å	75	82	0.49
1NGP VH	2.4 Å	73	81	0.60
1MRC VH	2.4 Å	76	81	0.60
1AE6 VH	3.0 Å	72	81	0.55
1PLG VH	2.8 Å	72	80	0.54
1MRE VH	2.3 Å	74	80	0.62

HuCAL Vκ3	*	*	*	*
1LVE VL	1.95 Å	76	82	0.46
1NSN VL	2.9 Å	73	78	0.56
2IMM VL	2.0 Å	72	83	0.29
2IMN VL	1.97 Å	72	83	0.29
1IBG VL	2.7 Å	71	77	0.59
1GGB VL	2.8 Å	68	77	0.49
1AI1 VL	2.8 Å	68	78	0.45
2HRP VL	2.2 Å	67	78	0.54

HuCAL VH2	*	*	*	*
1JRH VH	2.8 Å	72	78	0.47
1GGB VH	2.8 Å	72	77	0.40
1A2Y VH	1.5 Å	63	71	0.48
1A7Q VH	2.0 Å	63	70	0.52
1GIG VH	2.3 Å	61	68	0.50
1IBG VH	2.7 Å	60	67	0.52
1NLD VH	2.9 Å	57	67	0.70

HuCAL Vκ4	*	*	*	*
1LVE VL	1.95 Å	96	98	0.45
2IMM VL	2.0 Å	82	88	0.43
2IMN VL	1.97 Å	82	88	0.44
1AP2 VL	2.4 Å	80	85	0.45
1HIL VL	2.0 Å	78	85	0.40
1A3R VL	2.1 Å	77	84	0.40
1FRG VL	2.8 Å	76	85	0.45
1NSN VL	2.9 Å	74	79	0.37

HuCAL VH3	*	*	*	*
1IGM VH	2.3 Å	86	90	0.40
1DFB VH	2.7 Å	84	87	0.50
1FGV VH	1.9 Å	84	88	0.40
1AQK VH	1.84 Å	84	88	0.48
1FVC VH	2.2 Å	81	82	0.47
1HIL VH	2.0 Å	81	86	0.60
8FAB VH	1.8 Å	80	84	0.44
1IGT VH	2.8 Å	79	82	0.55
1AR1 VH	2.7 Å	79	84	0.49

HuCAL Vλ1	*	*	*	*
1AQK VL	1.84 Å	86	89	0.64
7FAB VL	2.0 Å	84	86	1.31
2FB4 VL	1.9 Å	83	86	0.53
1BJM VL	2.2 Å	81	86	0.62
2RHE VL	1.6 Å	80	84	0.74
1MCB VL	2.0 Å	72	79	0.69

HuCAL VH4	*	*	*	*
7FAB VH	2.0 Å	76	84	0.47
1AY1 VH	2.2 Å	73	77	0.61
3HFM VH	3.0 Å	73	79	0.46
1NSN VH	2.9 Å	72	78	0.86
1BAF VH	2.9 Å	71	76	0.34
1GPO VH	1.95 Å	71	78	0.43

Sequences of the HuCAL fragments were aligned to the sequences of 100 nonredundant V_L and V_H structures (mouse and human) taken from the the Brookhaven protein structure database (http://www.pdb.bnl.gov/) and sorted according to sequence similarity to identify the most suitable modeling templates. For each of the template structures the resolution, percent sequence identity, percent sequence similarity and the RMS deviation of the Cα position used for superposition (see legend for Figure 3) is listed.