A.

Dataset	**All mutations**			$\Delta\Delta G_{exp} \geq 0$		$\Delta\Delta G_{exp} < 0$	
	# of mutations	**# of proteins**	**# of structures**	**# of mutations**	**# of structures**	**# of mutations**	**# of structures**
S2648	2648	129	131	2080	119	568	93
S5296	5296	129	131	2682	131	2614	130
S350	350	66	67	260	57	90	35
S605	605	55	58	467	54	138	34
S1925	1925	53	55	1373	48	552	42
S134	134	1	6	98	6	36	6
p53	42	1	1	31	1	11	1
S^{sym}	684	14	357	350	103	334	262
S250	250	9	134	125	37	125	101
S921	921	54	195	634	82	287	145

One mutation/protein could be mapped to several PDB structures, and the sequences of these structures may be the same or complementary.

B.

Dataset	**Forward mutations**		**Reverse mutations**	
	# of mutations	**# of structures**	**# of mutations**	**# of structures**
S^{sym}	342	15	342	342
S250	125	9	125	125
S2000	1000	710	1000	636

C.

S350	**S605**	**S1925**	**S134**	**p53**	**S^{sym}**	**S250**	**S2000**	**S921**
350 (67)	277 (40)	903 (45)	41 (1)	5 (1)	402 (14)	218 (9)	228 (13)	0(0)
4334 (75)	3694 (56)	3842 (56)	82 (1)	10 (1)	2444 (18)	1342 (13)	3356 (50)	3710 (47)