S6 Table: X-ray data collection and refinement statistics for Bess and ElsE Fabs.

	Fab ElsE1	Fab ElsE2	Fab ElsE5	Fab ElsE6	Fab ElsE7	Fab ElsE8	Fab ElsE9	Fab ElsE11	Fab Bess4	Fab Bess7
PDB code	8V4I	8VBJ	8VBK	8VBL	8VBM	8VBN	8VBO	8VBR	8VBP	8VBQ
Crystallization condition	40% ethylene glycol, 0.1M HEPES, pH 7.5, 5% Peg3000, 20°	0.1M Tris, pH 8.5, 1.5M ammonium sulfate, 12% glycerol, 4°	0.1M sodium cacodylate, pH 6.5, 40% MPD, 5% Peg8000, 20°	0.1M Ches, pH 9.5, 50% Peg200, 20°	0.1M Ches, pH 9.5, 20% Peg 8000, 4°	20% Peg3350, 0.2M KCl, 4°	0.1M sodium cacodylate, pH 6.5, 40% MPD, 5% Peg 8000, 20°	0.1M Ches, pH 9.5, 50% Peg200, 4°	70% MPD, 0.1M Hepes, pH 7.5, 20°	0.095M sodium citrate, pH 5.6, 19% 2-propanol, 5% glycerol, 19% Peg4000, 20°
Wavelength	0.97946	0.97946	1.03317	0.97946	0.97946	0.97741	0.97946	0.97741	0.97946	0.97741
Beamline	SSRL 12-1	SSRL 12-2	APS 23-ID-B	SSRL 12-2	SSRL 12-2	ALS 5.0.1	SSRL 12-1	ALS 5.0.1	SSRL 12-1	ALS 5.0.1
Resolution range	37.89 - 1.81 (1.88 - 1.81)	45.48 - 1.90 (1.97 - 1.90)	43.86 - 1.89 (1.96 - 1.89)	46.80 - 2.35 (2.43 - 2.35)	42.23 - 2.54 (2.63 - 2.54)	46.95 - 1.83 (1.90 - 1.83)	36.30 - 2.30 (2.38 - 2.30)	49.58 - 2.65 (2.75 - 2.65)	29.94 - 2.80 (2.90 - 2.80)	48.29 - 2.10 (2.18 - 2.10)
Space group/twin law	C 2 2 2_1	C 2 2 2_1	P $2_12_12_1$	P 2_1 2_1 2	P 2_1 2_1 2_1	P 2_1 2_1 2_1	P 2_1 2_1 2	P 2_1 2_1 2_1 l,h,-k	P 2_1 2_1 2_1	C 2
Unit cell (Å,°)	69.79, 84.12, 174.58, 90, 90, 90	69.96, 178.59, 105.71, 90, 90, 90	56.26, 70.02, 109.08, 90, 90, 90	117.59, 69.98, 77.32, 90, 90, 90	58.22, 70.61, 123.97, 90, 90, 90	59.22, 120.27, 150.30, 90, 90, 90	70.11, 150.89, 51.32, 90, 90, 90	70.05, 70.19, 241.83, 90, 90, 90	66.61, 70.28, 111.46, 90, 90, 90	83.00, 69.78, 87.52, 90, 103.52, 90
Total reflections	460,645 (32,773)	442,490 (44,977)	423,944 (39,845)	168,777 (17,085)	76,645 (6407)	1,219,769 (90,327)	81,165 (7982)	378,268 (10,647)	44,117 (4130)	98,588 (7823)
Unique reflections	45,028 (3292)	51,939 (5160)	34,653 (3286)	27,185 (2649)	16,971 (1511)	95,768 (9306)	24,379 (2325)	33,457 (1618)	12,710 (1143)	28,113 (2607)
Multiplicity	10.2 (10.0)	8.5 (8.7)	12.2 (12.1)	6.2 (6.4)	4.5 (4.2)	12.8 (9.8)	3.3 (3.4)	11.3 (6.6)	3.5 (3.3)	3.5 (3.0)
Completeness (%)	95.6 (70.1)	98.8 (99.2)	98.7 (94.9)	99.7 (98.8)	96.8 (84.6)	99.8 (98.2)	97.8 (95.3)	94.0 (63.9)	93.8 (87.2)	98.8 (92.4)
Mean I/sigma(I)	10.5 (0.9)	8.4 (1.4)	13.8 (2.4)	9.1 (2.4)	7.5 (1.5)	15.9 (1.3)	9.3 (2.5)	11.3 (6.6)	7.0 (3.0)	8.7 (1.2)
Wilson B-factor	34	23	27	34	44	26	44	51	38	32
R-merge (%)	15.5 (251)	22.4 (224)	11.8 (109)	19.8 (140)	16.4 (135)	11.6 (173)	9.2 (77.8)	9.0 (84.8)	19.1 (80.5)	15.2 (107)
R-meas (%)	16.2 (264)	23.8 (238)	12.3 (114)	21.7 (152)	18.6 (155)	12.0 (183)	10.8 (90.9)	9.4 (91.4)	22.4 (95.9)	17.9 (128)
R-pim (%)	4.6 (77.2)	7.9 (77.6)	3.5 (32.3)	8.6 (59.4)	8.6 (74.2)	3.3 (57.5)	5.6 (46.2)	2.7 (32.0)	11.5 (51.0)	9.3 (70.3)
CC1/2 (%)	99.6 (41.0)	99.5 (41.3)	99.8 (86.7)	99.3 (49.7)	99.0 (40.0)	99.9 (50.8)	99.5 (61.1)	99.0 (77.4)	97.3 (49.8)	99.2 (37.6)
Reflections used in refinement	44,983 (3264)	51,917 (5148)	34,637 (3277)	27,183 (2649)	16,886 (1437)	95,655 (9237)	24,379 (2325)	33,316 (2271)	12,577 (1141)	28,099 (2601)
Reflections used for R-free	2273 (190)	2580 (266)	1773 (159)	1331 (141)	783 (77)	1970 (191)	1175 (117)	1993 (138)	620 (62)	1348 (114)
R-work (%)	22.1 (41.1)	19.5 (35.0)	20.4 (33.9)	19.7 (27.7)	23.5 (37.8)	22.4 (37.5)	24.8 (34.1)	24.7 (49.7)	19.6 (26.2)	23.0 (32.5)
R-free (%)	25.7 (55.6)	22.9 (37.2)	24.5 (39.3)	24.4 (34.5)	29.0 (46.8)	25.8 (39.6)	28.0 (38.9)	26.0 (56.4)	23.2 (30.9)	26.7 (30.7)
Number of non-hydrogen atoms	3750	3889	3707	3593	3463	7146	3535	7026	3257	3715
macromolecules	3563	3555	3496	3477	3463	6755	3465	7026	3257	3569
solvent	191	334	211	116	0	681	70	0	0	142
Protein residues	479	477	473	475	472	915	469	956	441	486
RMS(bonds)	0.003	0.013	0.003	0.002	0.002	0.008	0.002	0.003	0.003	0.003

RMS(angles)	0.66	1.05	0.64	0.56	0.51	0.98	0.53	0.56	0.58	0.56
Ramachandran favored, allowed, outliers (%)	94.3, 5.3, 0.4	97.5, 2.5, 0.0	96.8, 3.2, 0.0	96.2,3.4, 0.4	94.6, 4.7, 0.6	96.56, 3.33, 0.11	94.58, 4.34, 1.08	95.25, 4.11, 0.63	95.17, 4.37, 0.46	95.23, 4.77, 0.00
Rotamer outliers (%)	1.94	2.18	0.99	1.23	1.75	1.79	1.76	1.84	1.58	0.73
Clashscore	3.3	1.9	1.3	3.2	4.6	2.4	3.7	2.9	2.2	1.7
Average B-factor	45	31	35	43	65	35	63	59	36	47
macromolecules	45	31	35	43	65	35	63	59	36	48
solvent	44	35	36	41	NA	37	72	NA	NA	37

Statistics for the highest-resolution shell are shown in parentheses.