

SUPPLEMENTARY TABLE S1(A) | RMS deviations of *EcEIIB^{fruc}* with the GOT model, 2R48 and 2R4Q

Superpose Molecules Fixed : Moving Aligned pairs	Fit atoms	Number of atom pairs	RMS XYZ Displacement	Average XYZ Displacement	Maximum XYZ Displacement
<i>EcEIIB^{fruc}</i> : Model 1-107	all	819	2.799	1.762	14.254
	CA	107	2.040	1.161	11.460
	Main chain	428	2.079	1.202	12.225
	Side chain	391	3.390	2.417	14.551
<i>EcEIIB^{fruc}</i> : Model 1-98	all	749	1.880	1.227	10.064
	CA	98	0.660	0.551	2.707
	Main chain	392	0.723	0.579	3.690
	Side chain	357	2.603	1.931	9.976
<i>EcEIIB^{fruc}</i> : 2R48 1-105 : 0-104	all	641	3.529	2.479	17.942
	CA	104	3.290	2.312	13.774
	Main chain	419	3.169	2.236	13.735
	Side chain	222	4.115	2.969	18.112
<i>EcEIIB^{fruc}</i> : 2R48 1-98 : 0-97	all	604	2.846	2.086	9.484
	CA	97	2.501	1.859	6.678
	Main chain	391	2.381	1.779	7.086
	Side chain	213	3.536	2.663	9.682
<i>EcEIIB^{fruc}</i> : 2R4Q 2-105 : 170-273	all	561	3.787	2.741	18.588
	CA	92	3.392	2.452	14.469
	Main chain	377	3.269	2.397	14.490
	Side chain	184	4.641	3.428	18.757
<i>EcEIIB^{fruc}</i> : 2R4Q 2-99 : 170-267	all	533	3.111	2.369	11.099
	CA	87	2.668	2.094	6.697
	Main chain	357	2.571	2.047	7.488
	Side chain	176	3.967	3.011	10.719

SUPPLEMENTARY TABLE S1(B) | RMS deviations of *BtGmhB* with the GOT model, *BbGmhB* and *EcGmhB*

Superpose Molecules Fixed : Moving Aligned pairs	Fit atoms	Number of atom pairs	RMS XYZ Displacement	Average XYZ Displacement	Maximum XYZ Displacement
	all	1188	2.458	1.796	10.750
<i>BtGmhB</i> : Model 7-184	CA	158	1.727	1.257	7.140
	Main chain	632	1.738	1.272	8.009
	Side chain	556	3.061	2.379	10.937
<i>BtGmhB</i> : Model 7-20 38-58 68-94 128-151 168-183	all	778	1.956	1.421	9.299
	CA	102	1.062	0.899	2.875
	Main chain	408	1.060	0.894	3.391
	Side chain	370	2.597	1.993	9.347
<i>BtGmhB</i> : <i>BbGmhB</i> 7-184 : 2-179	all	839	4.667	4.382	13.567
	CA	158	4.125	4.031	8.909
	Main chain	632	7.792	6.412	20.370
	Side chain	253	8.584	7.294	22.314
<i>BtGmhB</i> : <i>BbGmhB</i> 7-20 : 1-14 38-58 : 32-52 68-94 : 62-88 128-151 : 122-145 168-183 : 162-177	all	683	1.636	1.236	8.662
	CA	102	1.063	0.911	2.636
	Main chain	408	1.069	0.909	3.394
	Side chain	275	2.216	1.715	8.572
<i>BtGmhB</i> : <i>EcGmhB</i> 7-184 : 25-202	all	885	8.036	6.661	22.215
	CA	158	7.862	6.517	20.103
	Main chain	632	7.792	6.412	20.370
	Side chain	253	8.584	7.294	22.314
<i>BtGmhB</i> : <i>EcGmhB</i> 7-20 : 25-38 38-58 : 55-75 68-94 : 85-111 128-151 : 152-175 168-183 : 190-205	all	625	1.962	1.542	8.691
	CA	102	1.636	1.341	4.168
	Main chain	408	1.619	1.322	4.655
	Side chain	217	2.463	1.951	8.476