Figure S1

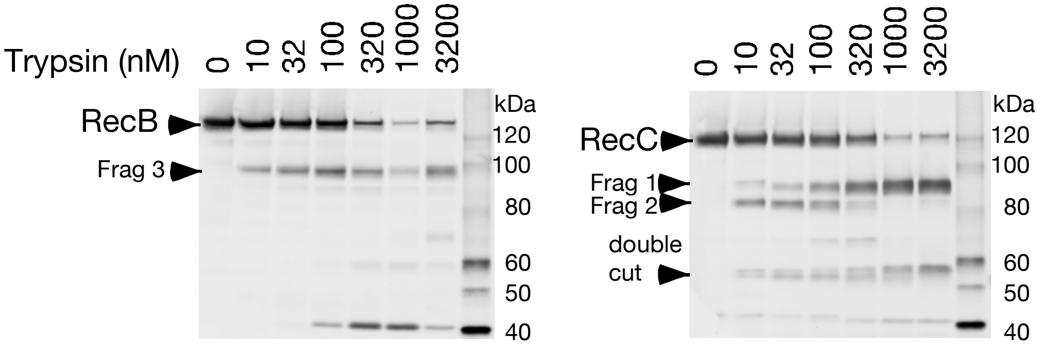


Figure S2

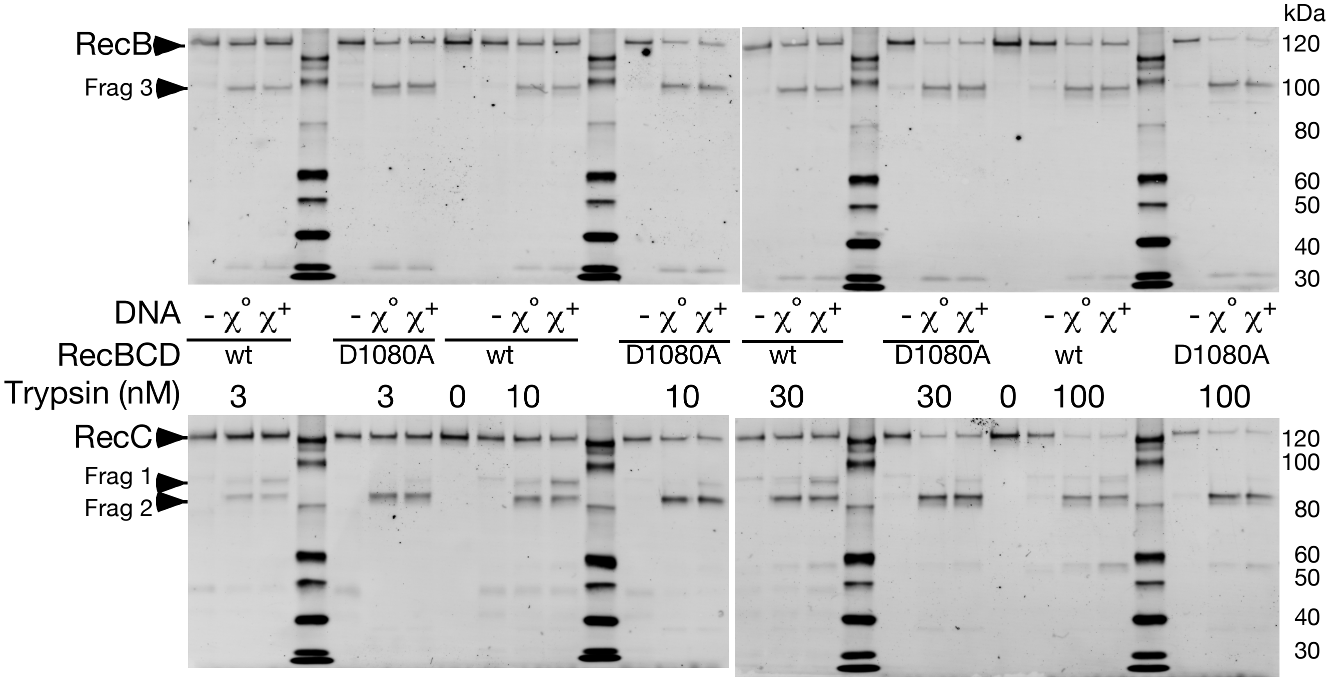


Figure S3

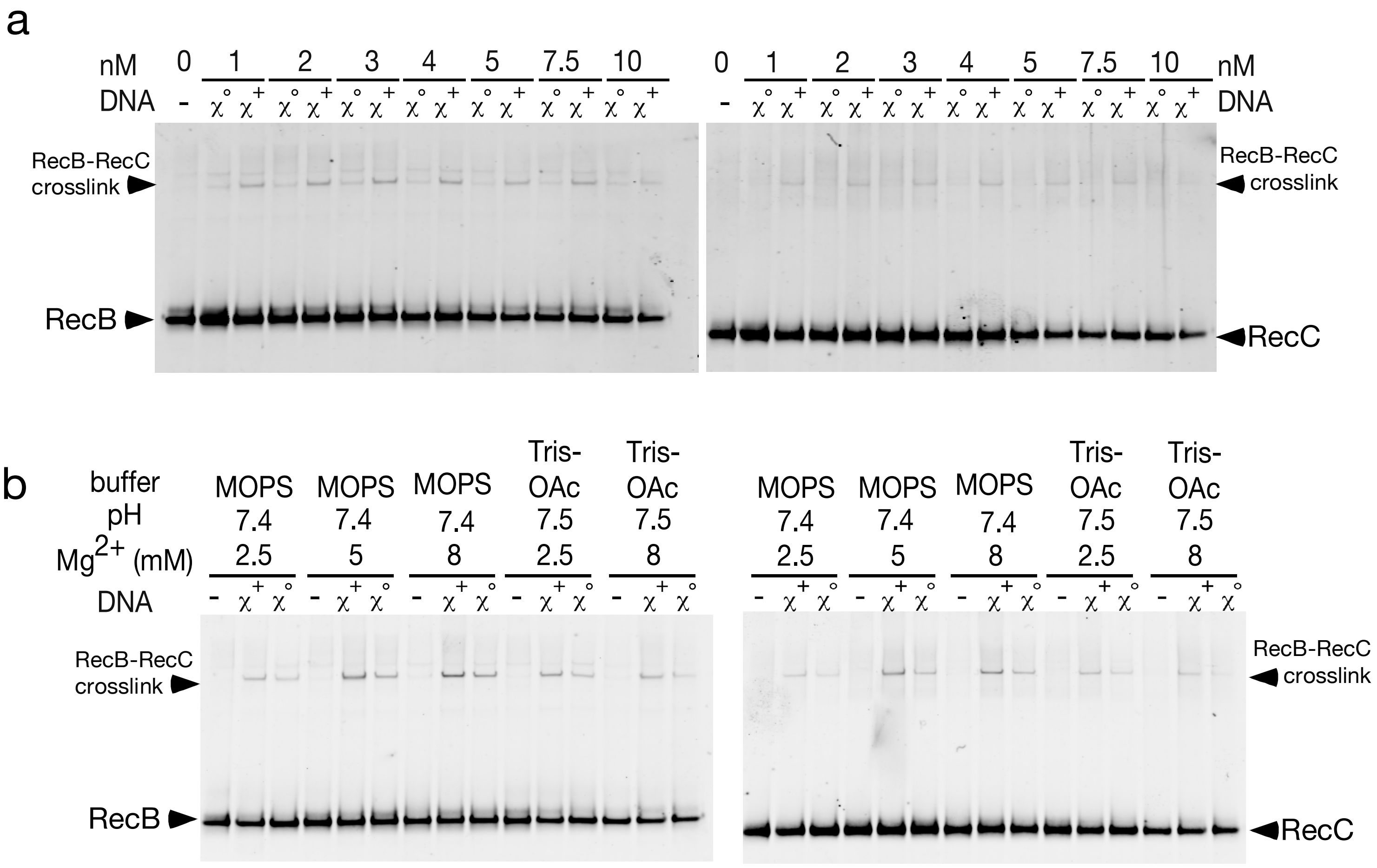

a
nM
0
1
2
3
4
5
7.5
10
DNA
-
χ° χ+
RecB-RecC crosslink
RecB
RecC
b
buffer
pH
Mg2+ (mM)
MOPS 7.4 2.5
MOPS 7.4 5
MOPS 7.4 8
Tris-OAc 7.5 2.5
Tris-OAc 7.5 8
DNA
- χ+ χ°
RecB-RecC crosslink
RecB
RecC

Figure S4a

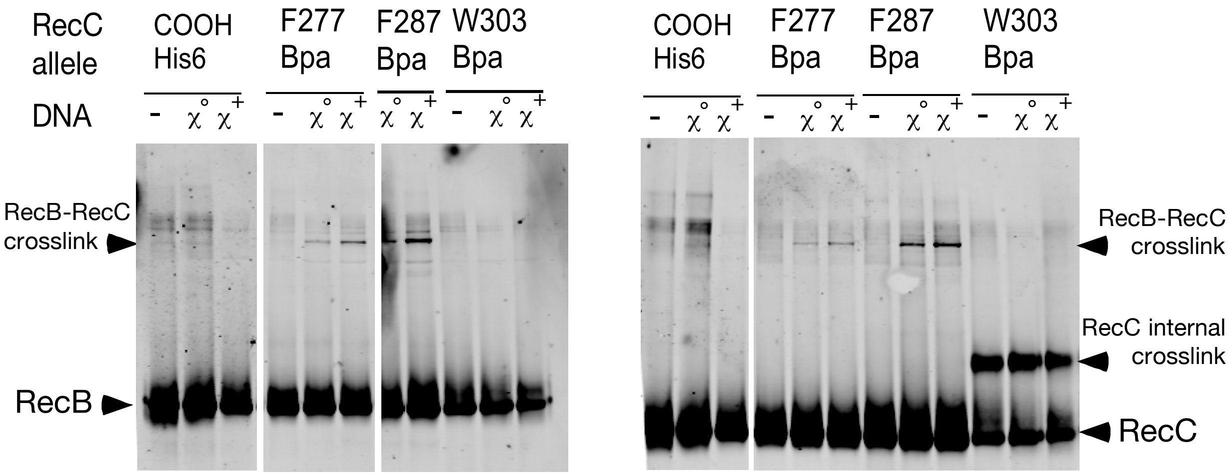
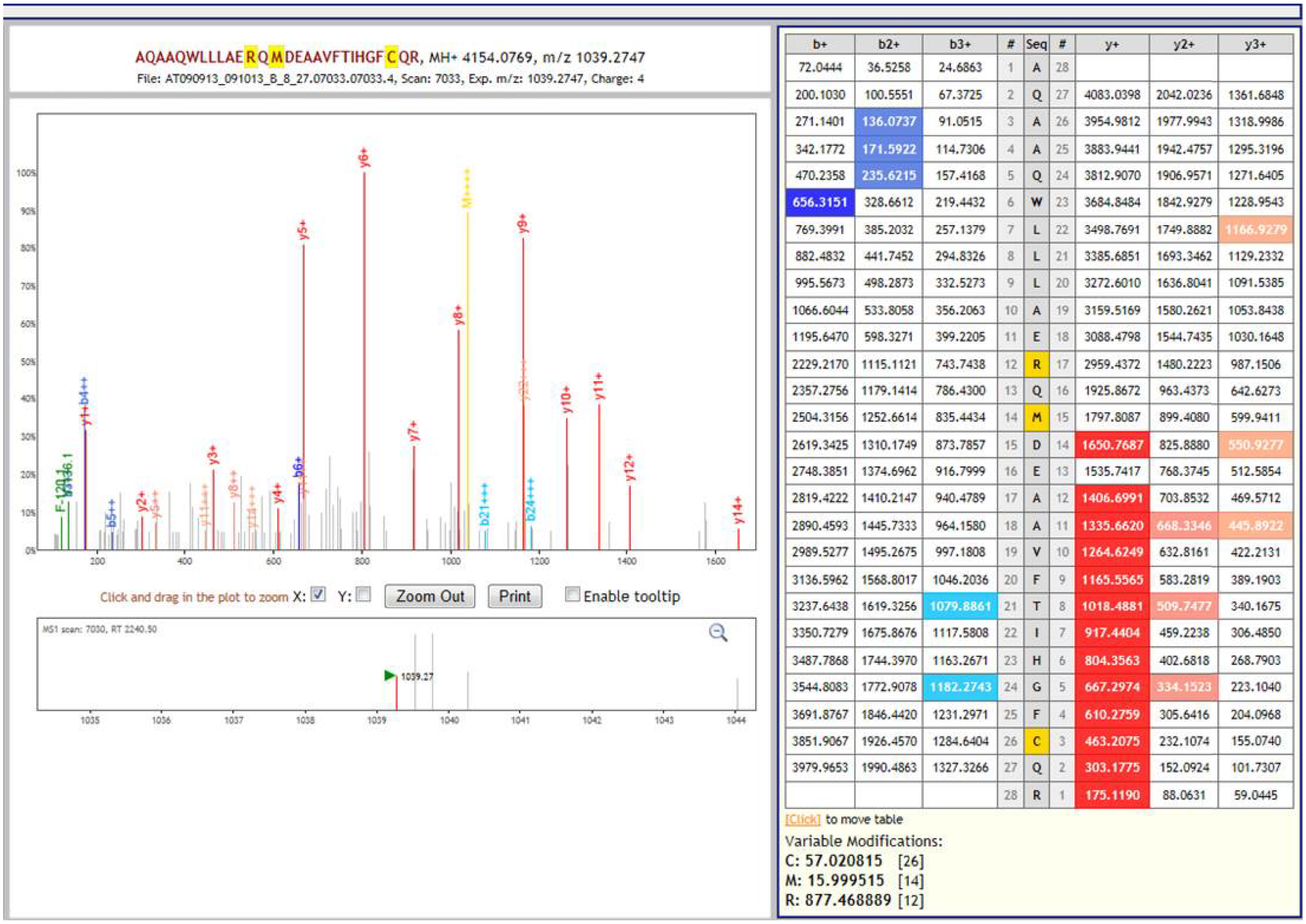


Figure S4b



AQAAQWLLLAERQMDEAAVFTIHGFCQR, MH+ 4154.0769, m/z 1039.2747

File: AT090913_091013_B_8_27.07033.07033.4, Scan: 7033, Exp. m/z: 1039.2747, Charge: 4

Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	b3+	#	Seq	#	y+	y2+	y3+
72.0444	36.5258	24.6863	1	A	28			
200.1030	100.5551	67.3725	2	Q	27	4083.0398	2042.0236	1361.6848
271.1401	136.0737	91.0515	3	A	26	3954.9812	1977.9943	1318.9986
342.1772	171.5922	114.7306	4	A	25	3883.9441	1942.4757	1295.3196
470.2358	235.6215	157.4168	5	Q	24	3812.9070	1906.9571	1271.6405
656.3151	328.6612	219.4432	6	W	23	3684.8484	1842.9279	1228.9543
769.3991	385.2032	257.1379	7	L	22	3498.7691	1749.8882	1166.9279
882.4832	441.7452	294.8326	8	L	21	3385.6851	1693.3462	1129.2332
995.5673	498.2873	332.5273	9	L	20	3272.6010	1636.8041	1091.5385
1066.6044	533.8058	356.2063	10	A	19	3159.5169	1580.2621	1053.8438
1195.6470	598.3271	399.2205	11	E	18	3088.4798	1544.7435	1030.1648
2229.2170	1115.1121	743.7438	12	R	17	2959.4372	1480.2223	987.1506
2357.2756	1179.1414	786.4300	13	Q	16	1925.8672	963.4373	642.6273
2504.3156	1252.6614	835.4434	14	M	15	1797.8087	899.4080	599.9411
2619.3425	1310.1749	873.7857	15	D	14	1650.7687	825.8880	550.9277
2748.3851	1374.6962	916.7999	16	E	13	1535.7417	768.3745	512.5854
2819.4222	1410.2147	940.4789	17	A	12	1406.6991	703.8532	469.5712
2890.4593	1445.7333	964.1580	18	A	11	1335.6620	668.3346	445.8922
2989.5277	1495.2675	997.1808	19	V	10	1264.6249	632.8161	422.2131
3136.5962	1568.8017	1046.2036	20	F	9	1165.5565	583.2819	389.1903
3237.6438	1619.3256	1079.8861	21	T	8	1018.4881	509.7477	340.1675
3350.7279	1675.8676	1117.5808	22	I	7	917.4404	459.2238	306.4850
3487.7868	1744.3970	1163.2671	23	H	6	804.3563	402.6818	268.7903
3544.8083	1772.9078	1182.2743	24	G	5	667.2974	334.1523	223.1040
3691.8767	1846.4420	1231.2971	25	F	4	610.2759	305.6416	204.0968
3851.9067	1926.4570	1284.6404	26	C	3	463.2075	232.1074	155.0740
3979.9653	1990.4863	1327.3266	27	Q	2	303.1775	152.0924	101.7307
			28	R	1	175.1190	88.0631	59.0445

[Click] to move table

Variable Modifications:
C: 57.020815 [26]
M: 15.999515 [14]
R: 877.468889 [12]

Figure S5

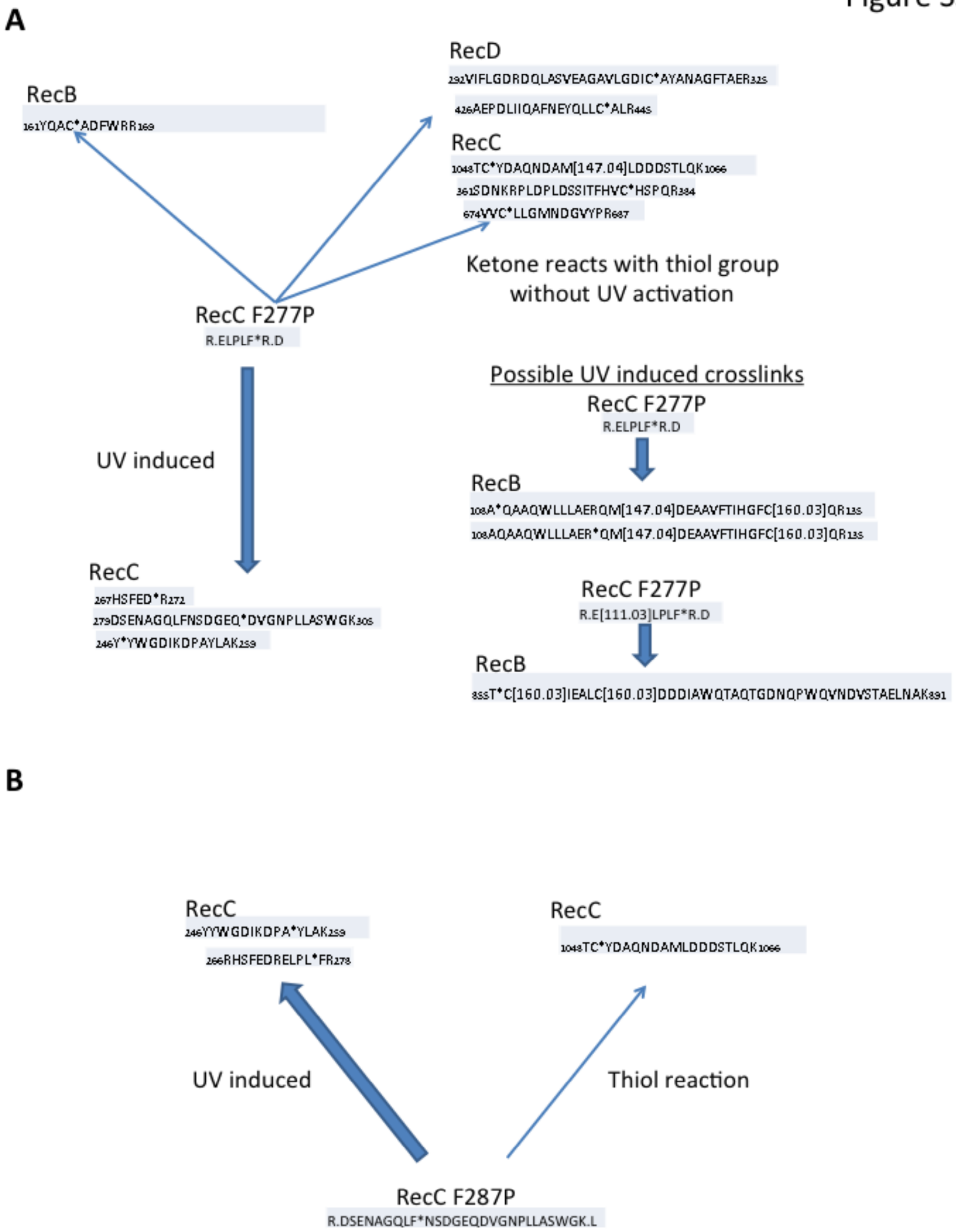
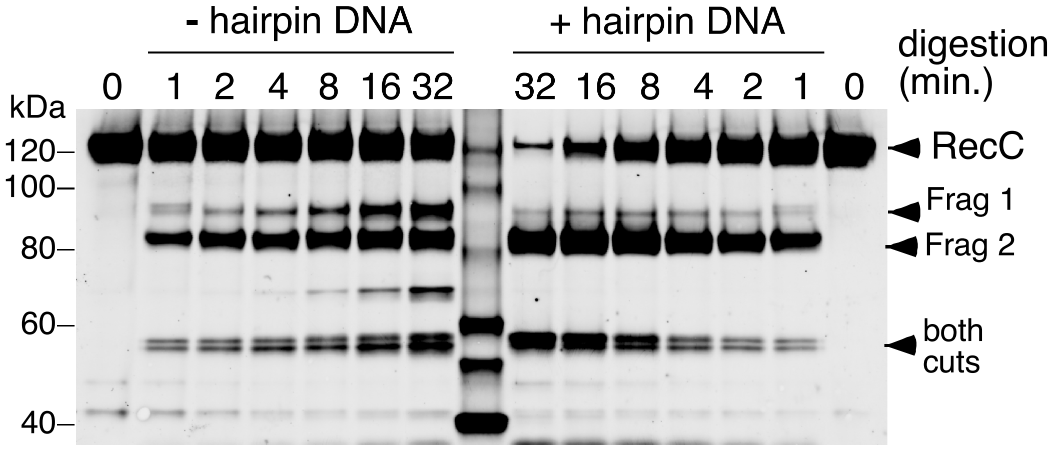
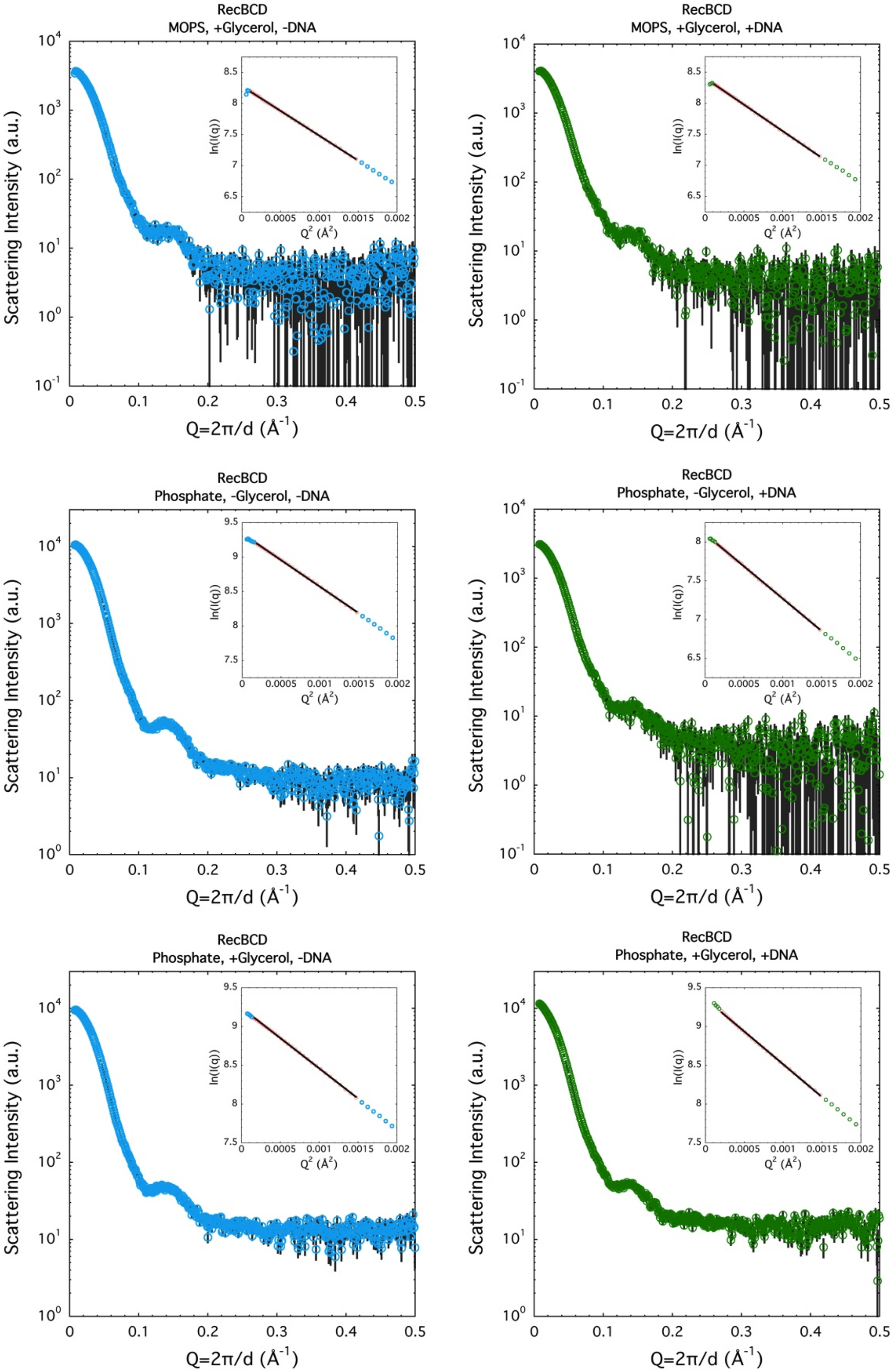
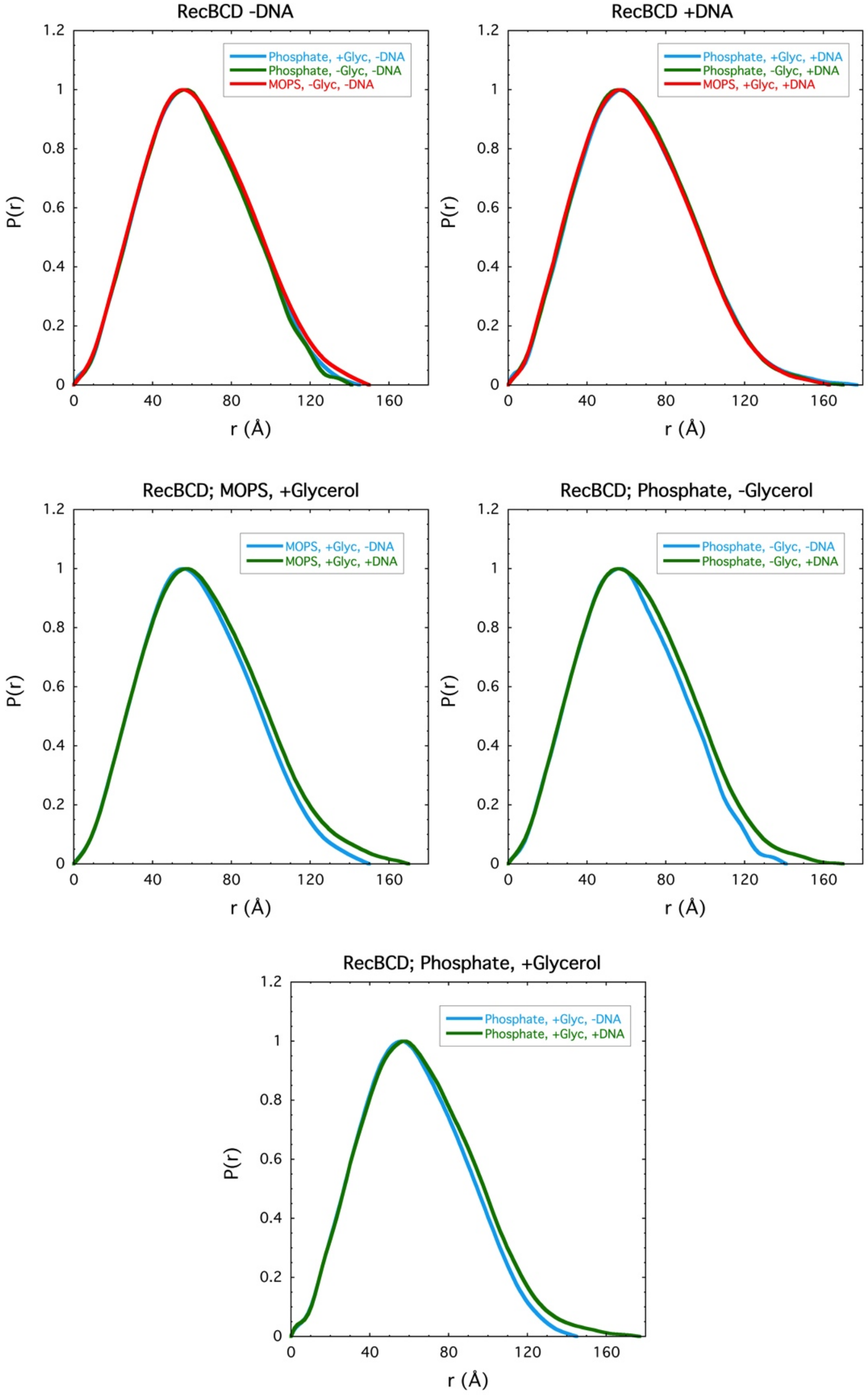

A
RecB
$_{161}$YQAC*ADFWRR$_{169}$
RecD
$_{292}$VIFLGDRDQLASVEAGAVLGDIC*AYANAGFTAER$_{325}$
$_{426}$AEPDLIIQAFNEYQLLC*ALR$_{445}$
RecC
$_{1048}$TC*YDAQNDAM[147.04]LDDDSTLQK$_{1066}$
$_{361}$SDNKRPLDPLDSSITFHVC*HSPQR$_{384}$
$_{674}$VVC*LLGMNDGVYPR$_{687}$
Ketone reacts with thiol group without UV activation
RecC F277P
R.ELPLF*R.D
UV induced
RecC
$_{267}$HSFED*R$_{272}$
$_{279}$DSENAGQLFNSDGEQ*DVGNPLLASWGK$_{305}$
$_{246}$Y*YWGDIKDPAYLAK$_{259}$
Possible UV induced crosslinks
RecC F277P
R.ELPLF*R.D
RecB
$_{108}$A*QAAQWLLLAERQM[147.04]DEAAVFTIHGFC[160.03]QR$_{135}$
$_{108}$AQAAQWLLLAER*QM[147.04]DEAAVFTIHGFC[160.03]QR$_{135}$
RecC F277P
R.E[111.03]LPLF*R.D
RecB
$_{855}$T*C[160.03]IEALC[160.03]DDDIAWQTAQTGDNQPWQVNDVSTAELNAK$_{891}$
B
RecC
$_{246}$YYWGDIKDPA*YLAK$_{259}$
$_{266}$RHSFEDRELPL*FR$_{278}$
RecC
$_{1048}$TC*YDAQNDAMLDDDSTLQK$_{1066}$
UV induced
Thiol reaction
RecC F287P
R.DSENAGQLF*NSDGEQDVGNPLLASWGK.L

Figure S6


- hairpin DNA
+ hairpin DNA
digestion
(min.)
0
1
2
4
8
16
32
32
16
8
4
2
1
0
kDa
120
100
80
60
40
RecC
Frag 1
Frag 2
both
cuts

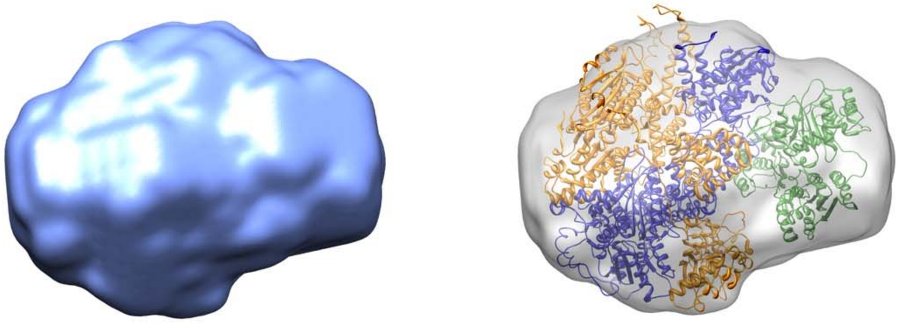


Supplementary Figure S7. SAXS patterns and Guinier plots (inset) for RecBCD in MOPS or K-PO$_4$ buffer, with or without glycerol and with or without hairpin DNA.

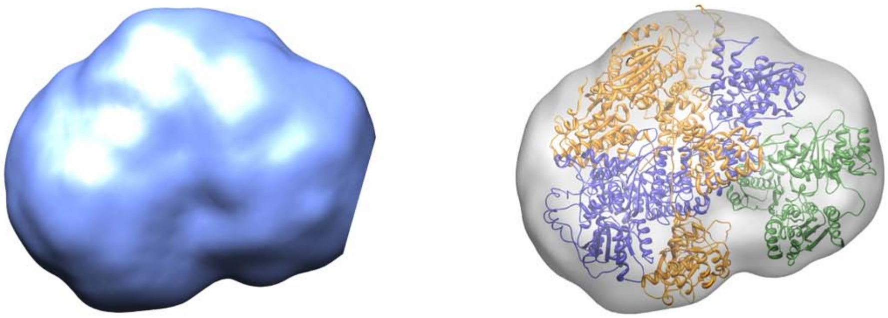


Supplementary Figure S8. Pairwise distance distribution plots, P(r), obtained from SAXS patterns for RecBCD in MOPS or K-PO_4 buffer, with or without glycerol and with or without hairpin DNA.

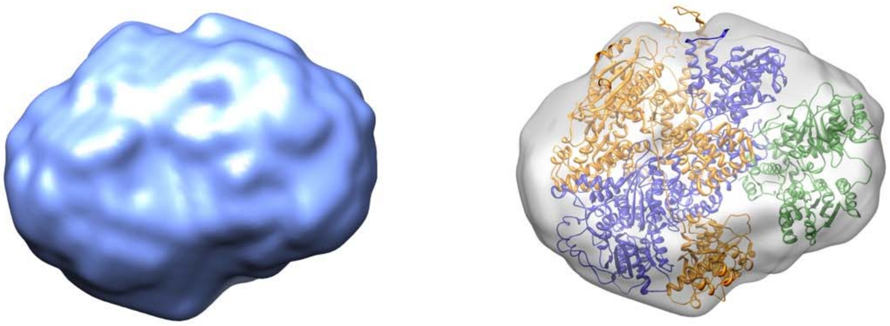
MOPS +Glycerol -DNA



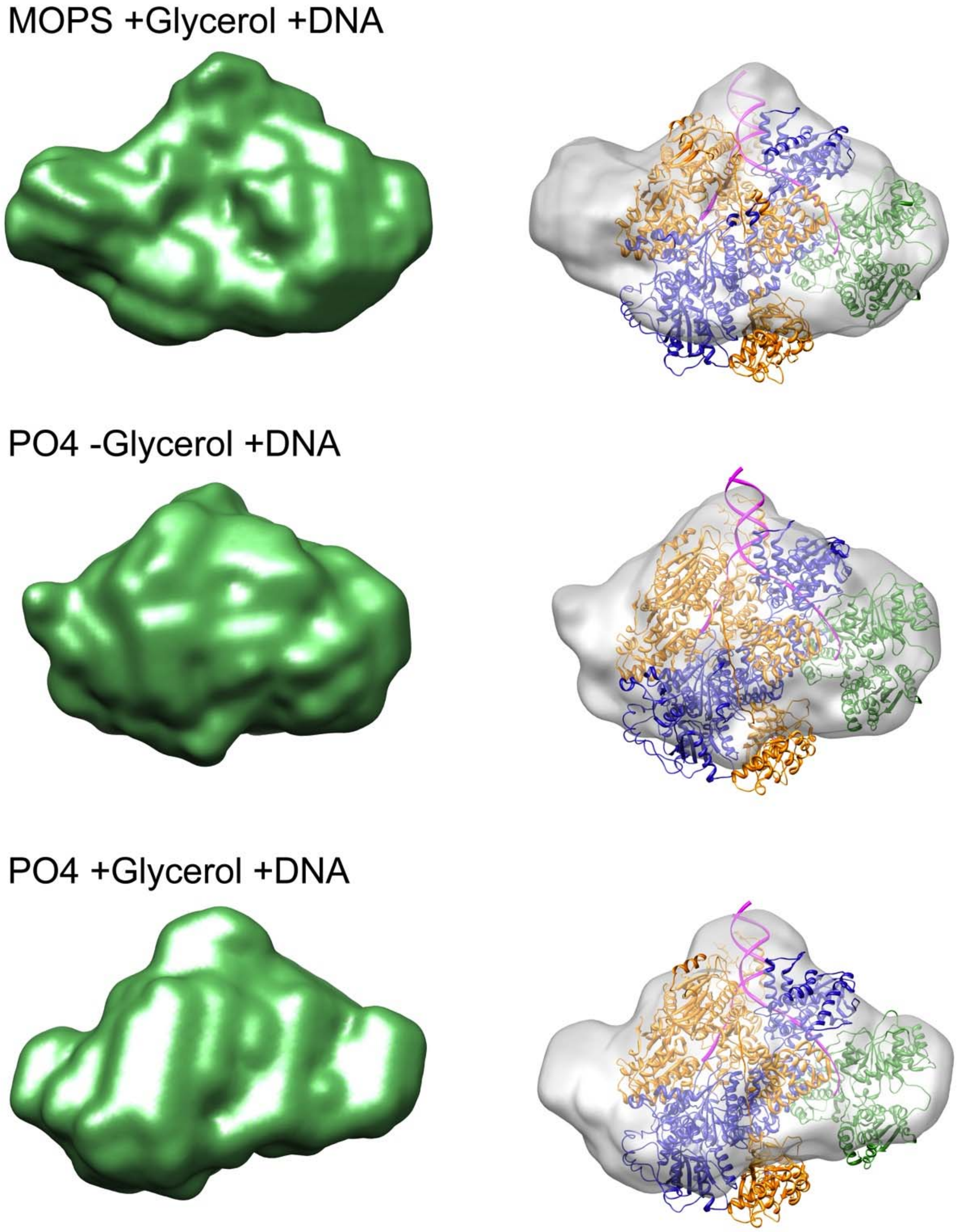
PO4 -Glycerol -DNA



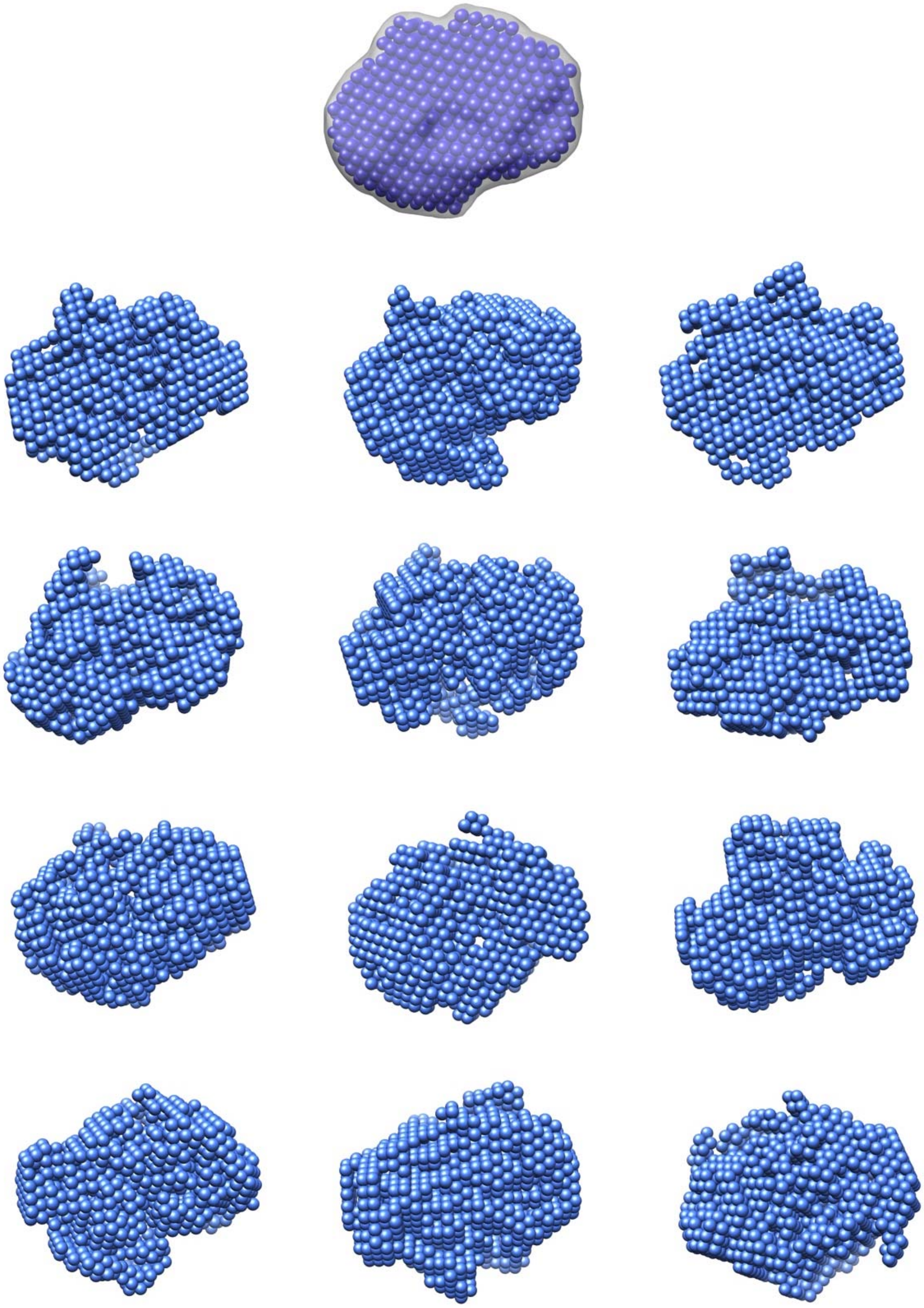
PO4 +Glycerol -DNA



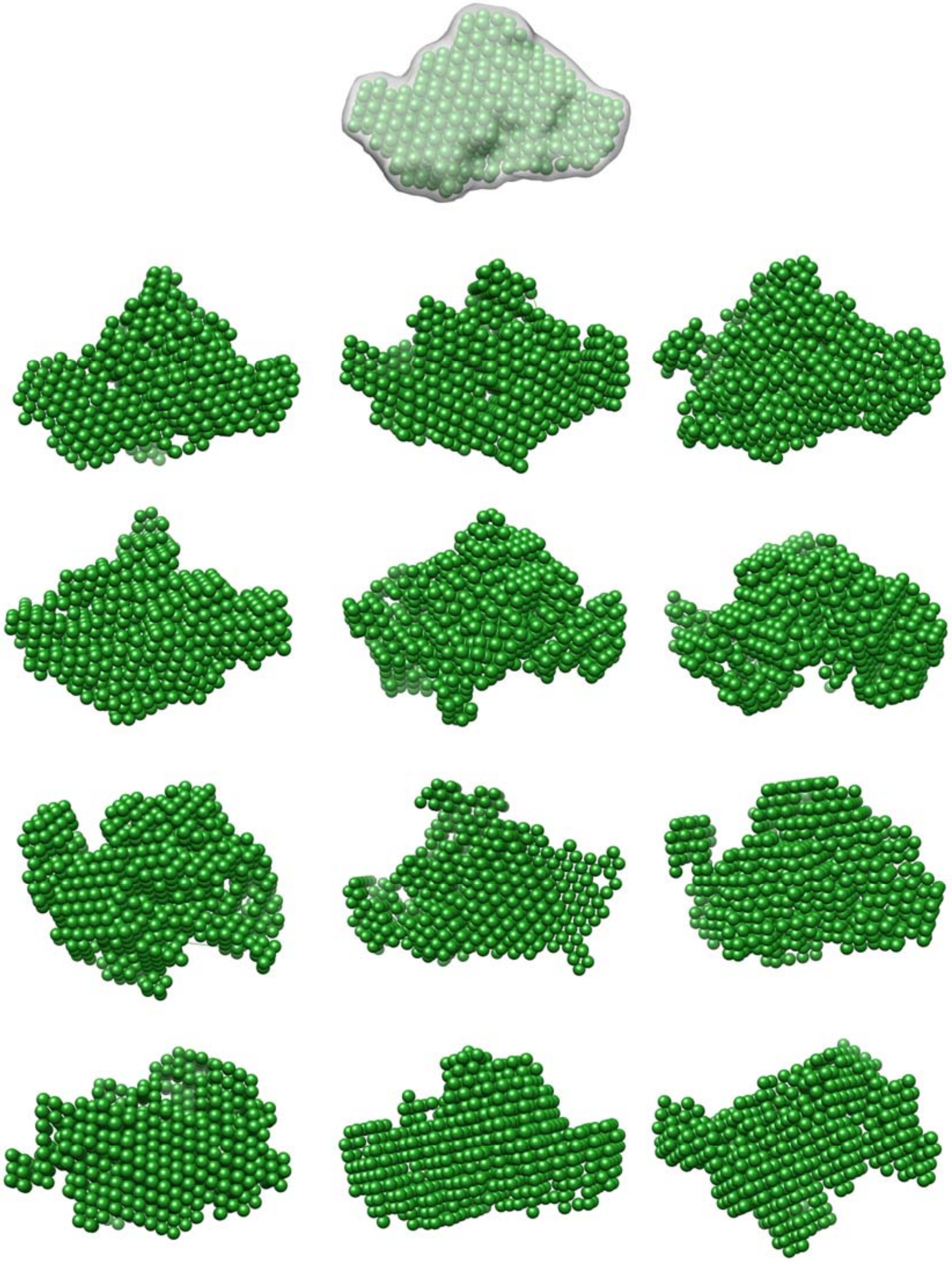
Supplementary Figure S9. SAXS reconstructions for RecBCD in MOPS or K-PO_4 buffer, with or without glycerol and without hairpin DNA. Images on the right have the crystal structure (PDB 3K70), minus the DNA, docked using the automated fit-in-map function in Chimera.



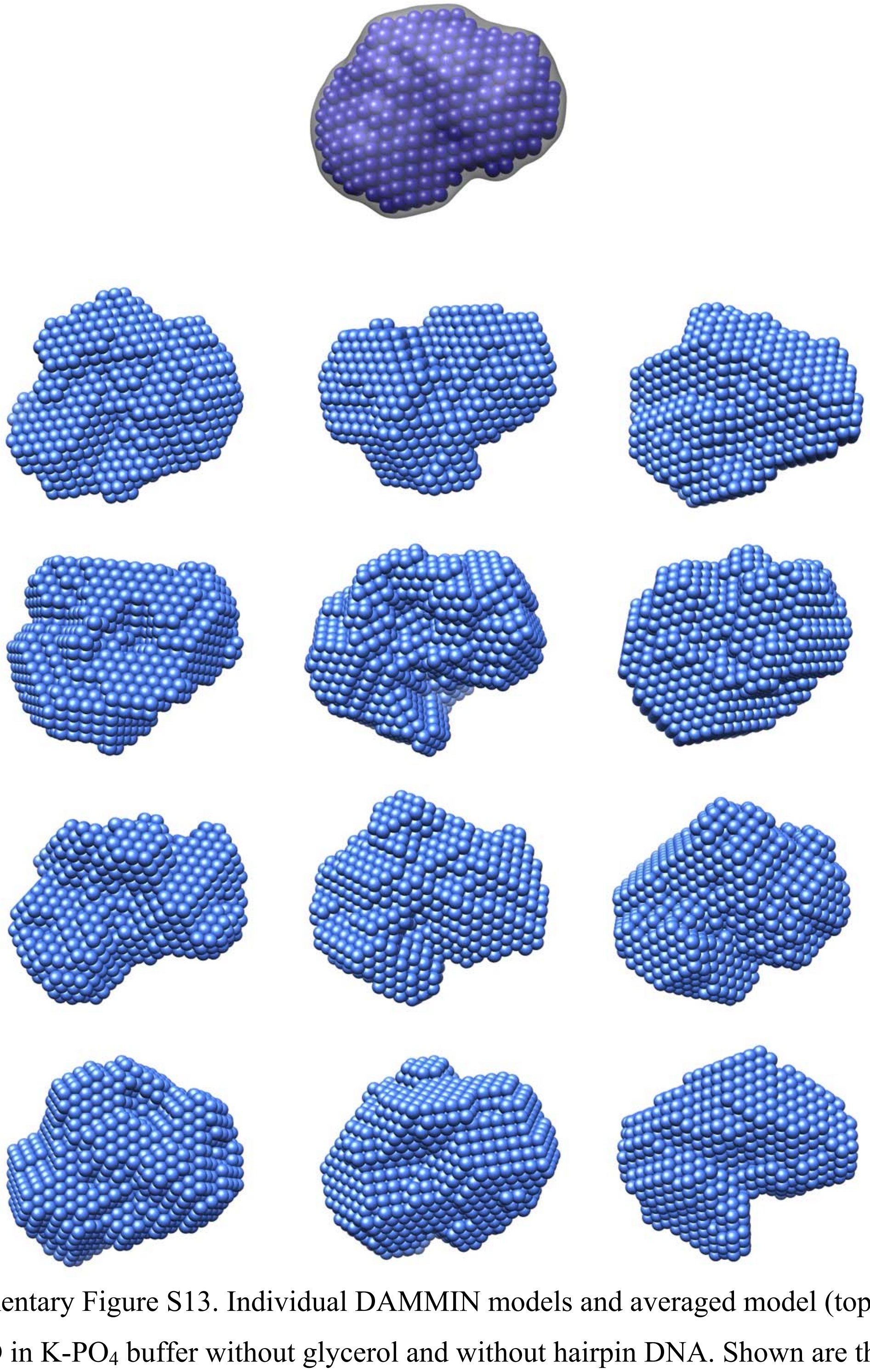
Supplementary Figure S10. SAXS reconstructions for RecBCD in MOPS or K-PO_4 buffer, with or without glycerol and with hairpin DNA bound. Images on the right have the crystal structure (PDB 3K70) docked using the automated fit-in-map function in Chimera.



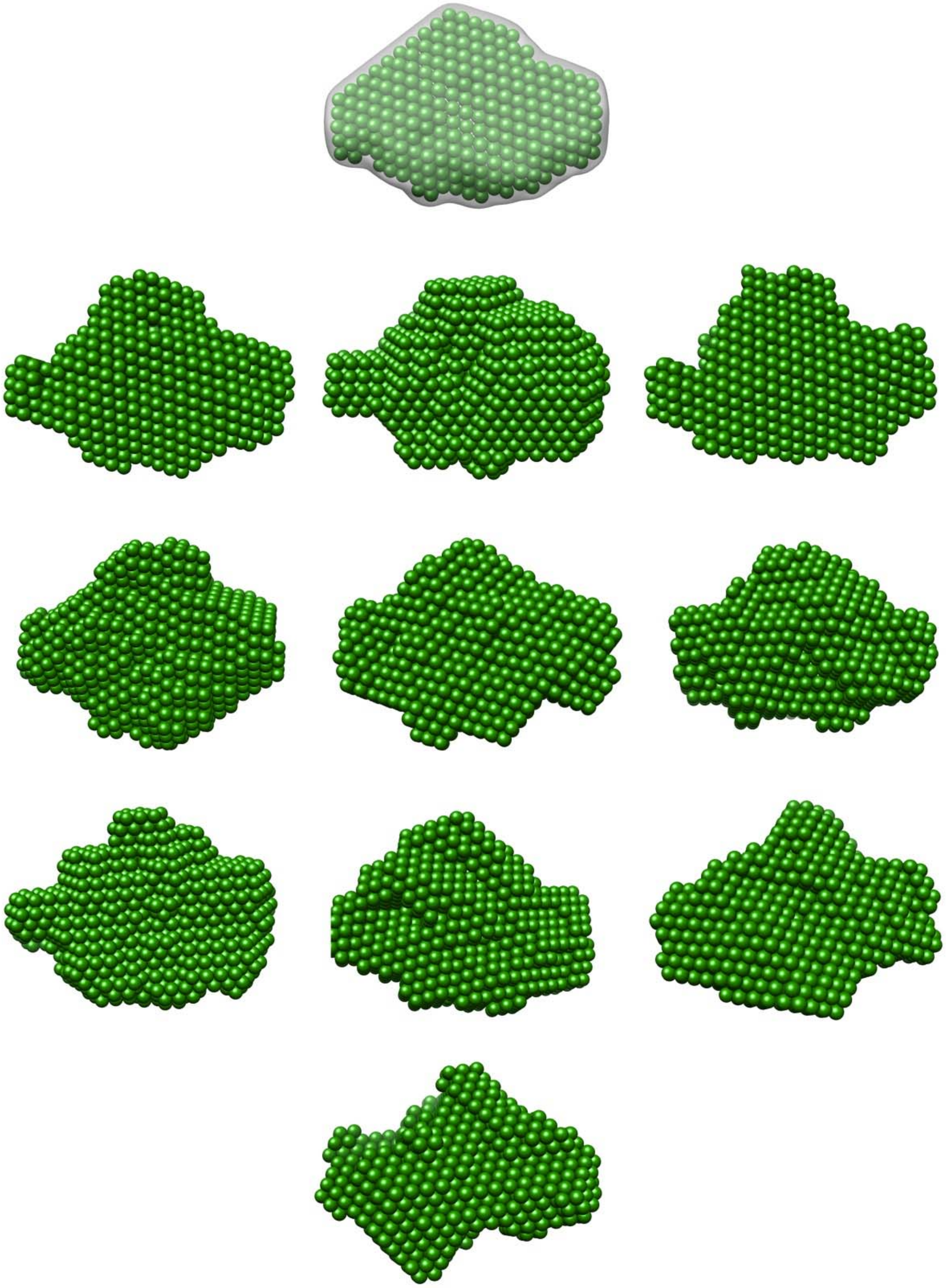
Supplementary Figure S11. Individual DAMMIN models and averaged model (top) for RecBCD in K-PO_4 buffer with glycerol and without hairpin DNA. Shown are the 12 DAMMIN models generated and used to produce the final model.



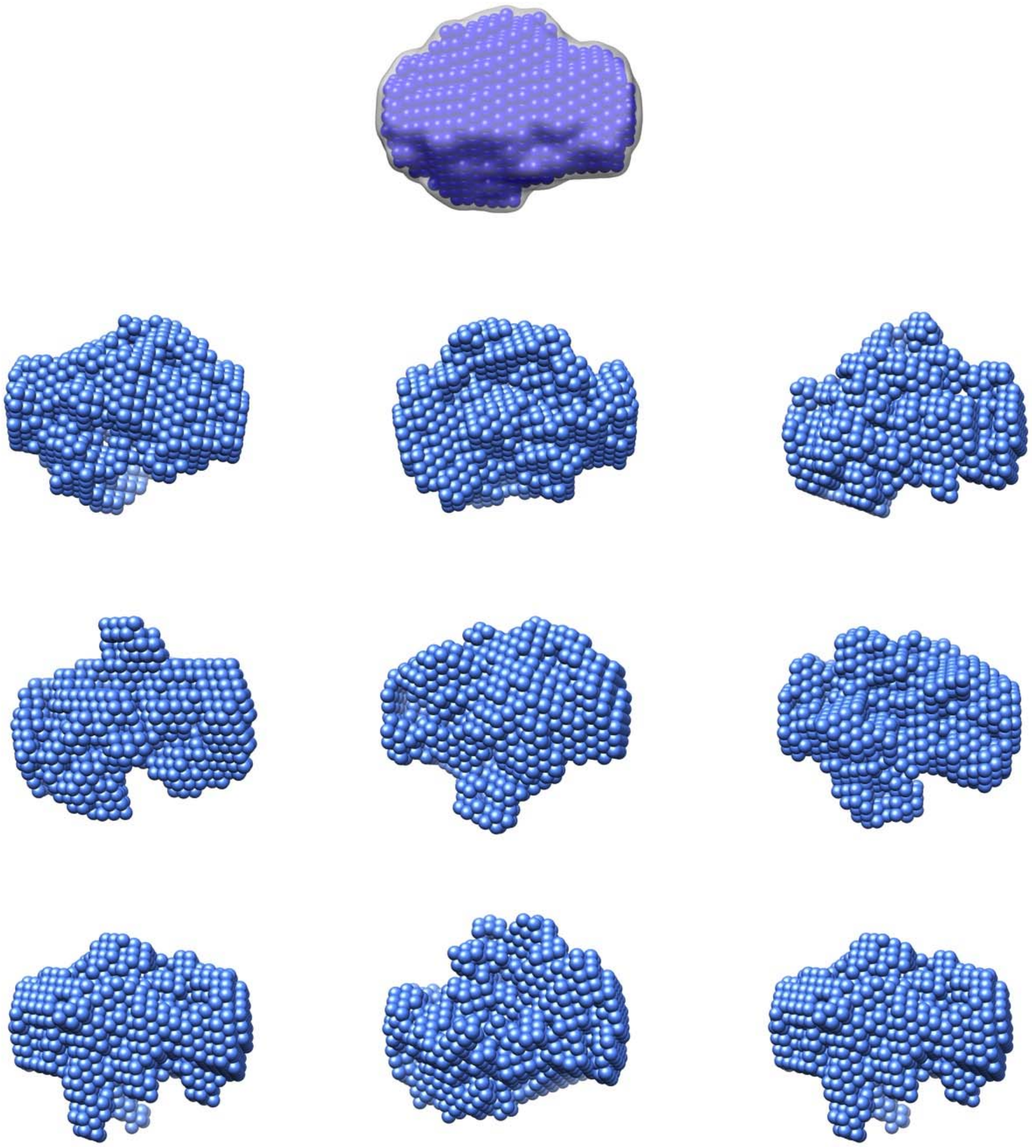
Supplementary Figure S12. Individual DAMMIN models and averaged model (top) for RecBCD in K-PO_4 buffer with glycerol and with hairpin DNA bound. Shown are the 12 DAMMIN models generated and used to produce the final model.



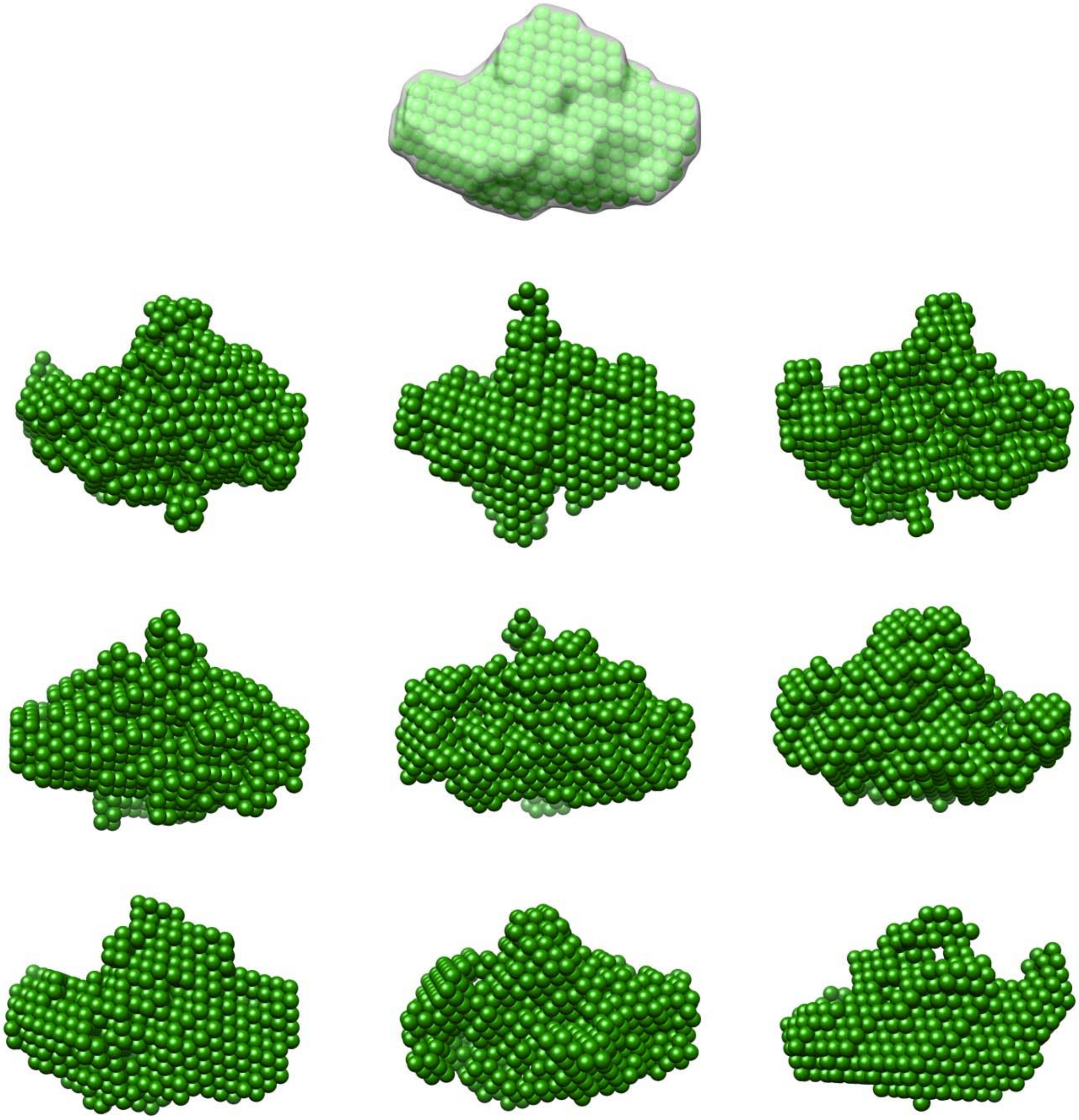
Supplementary Figure S13. Individual DAMMIN models and averaged model (top) for RecBCD in K-PO_4 buffer without glycerol and without hairpin DNA. Shown are the 12 DAMMIN models generated and used to produce the final model.



Supplementary Figure S14. Individual DAMMIN models and averaged model (top) for RecBCD in K-PO$_4$ buffer without glycerol and with hairpin DNA bound. Only the ten models, of the 12 generated, that fall within the ΔNSD < 2(standard deviation) relative to the average NSD among the cohort were used to produce the final model.



Supplementary Figure S15. Individual DAMMIN models and averaged model (top) for RecBCD in MOPS buffer with glycerol and without hairpin DNA. Only the nine models, of the 12 generated, that fall within the ΔNSD < 2(standard deviation) relative to the average NSD among the cohort were used to produce the final model.



Supplementary Figure S16. Individual DAMMIN models and averaged model (top) for RecBCD in MOPS buffer with glycerol and with hairpin DNA bound. Only the nine models, of the 12 generated, that fall within the ΔNSD < 2(standard deviation) relative to the average NSD among the cohort were used to produce the final model.