

**Supplementary Information For:** Flexible CDOCKER: Development and application of a pseudo-explicit structure-based docking method within CHARMM

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**Table 1:**

The PDBIDs and CDOCKER results for CCDC/Astex subset. Included are lowest RMSD conformation found and the RMSD for the lowest energy conformation for the two simulated annealing implementations and the MD+Minimization protocols.

*Rigid CDOCKER results*

PDBID	<i>SA- 1 Grid</i>		<i>SA- 2 Grids</i>		<i>MD+Minimization</i>	
	Lowest RMSD	Lowest Energy	Lowest RMSD	Lowest Energy	Lowest RMSD	Lowest Energy
1a28	0.2	0.3	0.4	0.4	0.2	0.2
1a6w	1.8	2.2	1.5	2.9	1.8	2.1
1abe	1.2	2.9	1.7	2.6	1.1	2.9
1abf	0.9	3.2	2.2	3.4	1.2	3.2
1acj	0.6	0.7	0.3	0.6	0.4	0.5
1acl	2.3	4.2	2.3	5.5	2.5	2.7
1acm	1.1	2.0	1.5	2.3	0.9	1.2
1aco	0.9	3.7	1.7	2.9	0.8	1.4
1aec	1.4	2.5	1.4	1.4	1.6	1.6
1ai5	0.6	1.1	1.0	1.3	0.6	0.6
1aoe	1.9	2.2	1.8	1.9	1.8	2.0
1aqw	0.8	2.5	1.6	2.7	0.7	1.3
1ase	1.6	3.1	1.7	2.9	1.1	3.1
1azm	1.6	5.8	1.7	2.0	1.6	2.0
1b59	0.4	5.3	0.5	6.9	0.5	5.6
1b9v	1.8	2.1	1.9	2.5	1.7	2.0
1baf	1.0	6.1	1.9	4.4	1.1	2.4
1bbp	1.1	8.3	1.2	2.3	1.1	2.7
1bgo	1.8	1.8	1.6	2.1	2.0	2.1
1blh	1.8	1.8	1.4	2.5	1.7	1.8
1bmq	1.6	2.3	1.6	2.0	1.9	1.9
1byg	0.6	2.6	0.5	1.6	0.5	1.7
1c12	1.6	2.3	1.8	2.5	1.7	2.3
1c1e	0.6	4.4	0.7	0.8	0.5	0.6
1c5c	1.7	2.3	1.4	3.4	1.5	2.3
1c5x	1.2	1.3	0.5	0.9	1.2	1.3
1c83	0.6	0.6	1.0	1.0	0.6	0.9

lcbs	0.9	1.1	0.8	1.1	1.0	1.1
lcbx	0.7	1.1	0.9	1.3	0.6	1.1
lcdg	1.8	4.0	1.8	2.9	2.0	2.9
lckp	0.6	2.9	0.6	2.9	0.6	2.9
lcle	2.1	3.1	1.4	1.9	2.3	2.3
lcom	1.7	4.3	0.6	4.3	1.0	1.7
lcoy	0.8	0.9	0.7	1.2	0.8	0.9
lcqp	1.1	1.1	1.0	2.0	1.1	1.2
lcvu	1.1	1.7	1.2	2.3	1.1	2.3
lcx2	1.5	1.8	1.5	1.8	1.5	1.7
ld0l	1.2	1.4	1.2	1.8	1.2	3.0
ld3h	1.5	7.3	0.9	1.1	1.4	7.3
ld4p	1.1	1.6	1.3	2.2	1.1	8.5
ldbb	1.8	5.3	1.4	5.2	1.3	4.6
ldbj	0.7	0.8	0.6	0.7	0.7	0.8
ldd7	3.0	3.9	3.1	6.0	1.1	4.6
ldg5	1.5	5.8	1.5	6.0	1.5	2.5
ldid	1.2	5.5	1.9	2.6	1.2	5.4
ldmp	3.4	3.4	3.5	4.9	3.5	3.9
ldog	0.4	4.1	1.0	3.1	0.3	3.7
ldr1	0.5	2.5	1.0	2.4	0.6	2.4
ldwb	2.0	2.2	0.9	2.1	0.6	2.2
ldwc	0.9	1.3	2.6	5.6	1.0	1.0
ldwd	2.3	6.1	2.5	5.7	1.2	1.3
ldy9	1.4	1.4	1.8	3.1	1.3	1.4
leap	2.2	4.3	2.3	3.6	2.3	3.8
lebg	0.6	3.0	0.9	2.6	0.6	3.0
leil	0.6	0.6	1.9	1.9	0.6	0.6
lejn	1.8	5.5	1.7	4.1	1.6	5.7
leoc	1.5	1.7	1.3	2.5	1.5	1.5
lepb	1.1	2.8	1.1	1.8	1.1	1.2
letr	0.9	0.9	0.9	0.9	1.0	1.0
lets	3.5	4.5	3.2	4.2	3.6	4.6
lf0r	2.0	4.1	1.8	3.8	2.5	3.9
lf0s	1.4	3.9	1.8	4.2	2.4	3.9
lfen	0.6	0.8	0.6	0.6	0.5	0.6
lfgi	0.6	5.7	0.5	0.6	0.7	1.1
lflg	1.4	2.3	1.0	1.8	1.0	2.0
lfl3	0.6	1.2	0.7	0.7	0.7	0.8
lflr	2.3	4.5	2.3	4.5	2.3	4.5
lfrp	1.0	1.0	1.2	2.3	0.7	1.0
lglp	0.9	0.9	1.0	3.0	1.6	1.8
lglq	3.1	4.8	2.7	5.4	3.0	4.5

lhak	1.9	4.0	1.5	7.8	1.8	4.3
lhdc	0.8	1.2	0.8	1.2	0.8	0.9
lhfc	2.3	3.8	2.2	3.5	1.9	3.4
lhiv	1.2	1.7	1.8	1.9	1.9	3.1
lhpv	1.0	1.2	1.1	1.4	1.0	1.1
lhri	0.9	2.0	1.0	1.2	0.9	1.1
lhtf	1.8	1.9	1.5	7.4	1.7	3.5
lhyt	2.4	3.2	2.4	2.9	2.5	2.8
libg	0.7	0.8	0.6	1.5	0.7	0.7
limb	2.7	6.7	3.2	6.6	2.6	7.1
livb	2.0	3.5	2.4	3.3	2.0	4.5
lkel	1.1	1.4	1.4	1.8	1.2	1.4
llah	0.5	1.1	1.1	2.7	0.5	1.1
llcp	0.6	1.0	0.9	1.0	0.5	0.8
llic	1.3	3.9	1.4	2.2	1.5	2.7
llpm	0.9	4.8	0.5	0.5	0.6	0.6
llst	1.1	1.2	1.1	2.2	1.0	2.0
lmcq	0.7	1.1	0.7	1.9	0.7	1.1
lmdr	1.3	2.5	1.5	2.6	1.3	2.5
lmlc	1.3	1.5	1.6	2.6	1.4	1.5
lmsg	1.2	4.8	1.0	3.4	1.2	4.8
lmrk	1.4	1.7	1.4	1.5	1.4	1.5
lmts	0.9	2.1	1.1	2.1	1.1	2.0
lmup	1.2	1.4	1.1	4.3	1.1	1.3
lncp	1.1	3.5	1.1	2.6	1.4	3.5
lngp	1.8	4.1	0.9	4.4	1.2	4.0
lokl	1.7	2.4	1.0	3.0	1.3	2.0
lpdz	1.7	2.2	1.7	4.4	1.4	2.2
lphd	1.8	3.0	2.1	7.0	1.6	3.6
lphg	2.1	4.9	1.3	6.4	1.9	4.9
lpoc	1.0	1.0	1.5	1.5	1.0	1.0
lppc	1.6	3.1	2.3	7.5	1.2	1.2
lpph	4.9	6.2	4.4	6.1	4.9	5.6
lptv	4.3	7.3	3.9	7.2	4.3	8.6
lqcf	1.3	1.4	0.8	0.8	1.3	1.4
lqpe	1.7	2.2	0.7	0.7	1.4	1.5
lqpq	0.7	3.0	1.1	2.4	0.7	3.0
lrnt	0.6	0.6	0.8	1.1	0.5	0.5
lrob	0.9	1.1	0.7	3.3	0.9	1.1
lrt2	0.6	0.6	0.6	0.7	0.5	0.6
lslt	2.2	3.0	2.1	2.8	1.4	4.8
lsnc	1.2	5.3	2.6	5.3	0.7	1.4
lsrj	0.9	3.6	0.9	1.2	0.9	2.8

1tdb	1.6	1.8	1.4	3.5	1.4	2.1
1tmn	1.5	1.8	2.3	2.8	1.7	2.4
1tng	0.4	0.4	4.4	4.4	0.3	0.4
1tnh	1.4	1.5	1.4	1.5	1.4	1.6
1tni	1.3	3.0	1.5	2.1	1.6	1.6
1tpp	5.7	7.1	4.8	6.5	5.7	5.9
1tyl	0.8	0.8	0.6	2.1	0.9	0.9
1ukz	0.6	6.3	0.8	4.5	0.6	0.9
1ulb	0.9	0.9	0.6	3.5	0.7	0.9
1uvs	1.8	2.2	1.7	3.9	1.5	1.7
1uvt	3.2	3.8	3.3	3.4	3.1	3.9
1vgc	1.3	2.0	1.3	5.3	1.3	5.3
1xid	1.3	2.1	1.2	2.6	1.2	1.8
1xie	1.6	1.9	3.9	6.5	1.5	1.9
1ydr	0.9	4.0	0.8	3.5	0.9	0.9
1yee	0.9	1.0	1.1	3.2	0.9	1.1
25c8	1.8	2.6	1.6	1.9	1.7	2.0
2aad	0.8	0.9	0.5	1.0	0.8	0.8
2ada	0.8	1.1	0.7	0.8	0.7	1.0
2cht	1.1	3.9	1.3	4.1	1.0	3.4
2cmd	1.1	1.5	1.6	3.4	1.2	1.8
2cpp	0.3	2.7	1.5	2.8	0.3	2.6
2ctc	2.1	2.5	2.1	2.7	1.1	1.6
2fox	1.4	1.4	1.1	1.3	1.2	1.6
2gbp	0.3	0.7	0.7	3.5	0.3	0.7
2h4n	2.0	5.6	1.7	5.8	1.4	5.6
2ifb	1.0	1.3	0.9	1.6	1.0	1.5
2mcp	1.0	3.0	4.5	4.6	0.9	1.0
2pk4	1.2	2.3	1.0	2.8	1.1	2.2
2r07	0.7	0.7	0.7	0.7	0.7	0.7
2yhx	0.8	2.8	1.6	5.4	1.0	1.4
2ypi	1.1	1.5	1.1	1.3	0.7	1.4
3ert	0.6	1.1	1.1	1.5	0.7	1.1
3gpb	1.3	5.5	0.8	2.3	1.2	5.5
3hvt	0.9	0.9	0.8	0.8	0.9	0.9
4aah	0.7	1.0	1.2	5.9	0.6	5.8
4cox	0.6	0.7	0.4	0.7	0.6	0.7
4cts	1.8	2.1	1.7	2.1	1.3	2.2
4dfr	2.9	4.7	1.7	5.6	2.3	3.8
4est	2.3	2.9	2.2	3.8	2.2	3.4
4fbp	0.6	5.7	1.7	2.2	0.4	1.7
4lbd	1.0	1.0	1.0	1.2	1.0	1.0
4phv	3.2	4.8	2.9	5.4	3.2	5.0

5abp	0.8	0.8	0.8	1.4	0.8	0.8
5cpp	2.0	3.0	1.9	2.2	2.0	3.0
6rnt	1.8	2.4	3.0	4.0	1.3	4.1
6rsa	0.8	1.1	0.9	2.1	0.8	0.8
7tim	0.9	1.6	1.3	1.8	0.8	1.6
<b>Averages</b>	1.4	2.7	1.5	2.9	1.3	2.4

*Flexible CDOCKER results*

PDBID	<i>SA- 1 Grid</i>		<i>SA- 2 Grids</i>		<i>MD+Minimization</i>	
	Lowest RMSD	Lowest Energy	Lowest RMSD	Lowest Energy	Lowest RMSD	Lowest Energy
1a28	0.2	0.2	0.2	0.3	0.2	0.3
1a6w	1.8	3.0	1.8	2.8	1.7	2.2
1abe	1.1	2.9	2.3	2.9	1.3	2.8
1abf	0.8	3.0	3.3	10.6	1.1	3.0
1acj	0.4	0.7	0.6	1.2	0.3	0.4
1acl	2.1	4.3	2.1	4.2	2.1	3.3
1acm	1.4	2.1	3.3	10.0	0.4	2.4
1aco	0.4	2.9	6.2	7.2	0.6	1.1
1aec	1.7	3.2	4.5	6.9	1.5	1.7
1ai5	0.5	1.0	0.6	8.0	0.6	0.9
1aoe	0.9	1.7	2.6	8.0	1.7	1.8
1aqw	1.1	2.5	1.3	6.5	0.7	2.0
1ase	2.4	4.9	3.1	4.7	1.4	2.7
1azm	1.6	2.2	2.5	4.4	1.5	2.0
1b59	0.4	2.7	2.9	4.0	0.4	2.2
1b9v	1.8	1.9	2.6	8.5	1.6	1.9
1baf	2.3	2.5	3.9	7.3	3.3	3.9
1bbp	1.3	8.1	2.2	3.9	1.4	1.8
1bgo	1.9	2.1	2.4	3.8	1.5	2.2
1blh	1.9	1.9	3.8	4.8	1.8	2.0
1bmq	2.0	2.3	5.0	5.0	1.6	1.9
1byg	0.4	1.8	0.4	0.9	0.3	0.3
1c12	1.5	2.3	1.3	2.8	1.3	2.3
1c1e	0.3	0.3	0.4	0.4	0.3	0.4
1c5c	1.6	4.7	2.6	5.2	1.4	3.9
1c5x	0.9	0.9	0.9	0.9	0.9	0.9
1c83	0.6	1.0	5.5	11.1	0.8	1.0
1cbs	0.8	1.1	1.0	3.5	1.1	1.4
1cbx	0.6	1.1	3.7	5.6	0.7	1.3
1cdg	2.0	2.0	2.0	2.5	2.0	2.6

lckp	0.9	1.2	3.2	5.2	0.5	1.0
lcle	3.6	5.1	4.2	4.7	3.0	3.1
lcom	1.6	3.9	4.8	8.3	0.9	1.9
lcoy	0.7	0.8	0.5	0.9	0.6	0.8
lcqp	0.7	1.0	1.1	1.6	1.0	1.5
lcvu	0.9	1.1	1.2	1.7	1.3	1.4
lcx2	1.5	1.7	1.6	1.7	1.5	1.6
ld0l	1.3	1.7	3.3	5.4	1.1	1.5
ld3h	1.5	1.9	1.3	7.6	1.5	1.9
ld4p	1.0	1.3	1.9	7.9	1.0	1.4
ldbb	0.7	4.4	3.0	5.0	0.8	3.5
ldbj	0.4	0.8	0.9	1.3	0.4	0.5
ldd7	2.3	5.1	3.8	6.3	1.8	4.0
ldg5	1.4	2.9	2.5	4.6	0.7	0.9
ldid	1.0	5.7	4.9	7.7	1.0	5.7
ldmp	3.5	5.0	3.4	4.5	3.5	4.2
ldog	1.6	2.2	1.9	8.4	0.2	0.3
ldr1	0.4	2.4	3.6	3.6	0.3	2.3
ldwb	0.5	0.5	0.4	2.0	0.4	0.4
ldwc	0.9	0.9	3.3	5.1	0.9	0.9
ldwd	2.2	3.7	3.6	7.5	1.3	1.9
ldy9	1.6	1.6	3.5	5.6	1.4	1.5
leap	2.0	4.1	2.5	3.7	2.3	4.1
lebg	0.5	2.0	8.7	9.9	0.4	1.6
leil	0.4	0.5	8.2	9.7	0.5	0.5
lejn	1.5	7.0	1.2	4.7	1.7	3.9
leoc	2.0	4.5	5.4	7.2	1.8	2.4
lepb	1.0	1.3	0.9	1.2	1.0	1.2
letr	0.7	0.7	6.1	6.8	0.8	0.9
lets	3.7	3.7	3.7	4.1	4.0	4.2
lf0r	2.2	4.6	2.2	4.0	2.4	3.3
lf0s	2.5	4.9	1.6	3.4	1.9	5.0
lfen	0.6	0.7	0.5	0.6	0.6	0.7
lfgi	0.4	0.6	2.9	4.7	0.5	0.5
lfgk	1.5	1.6	1.7	2.4	1.3	1.3
lfl3	0.5	1.0	0.8	1.4	0.8	1.2
lflr	2.2	4.5	2.8	4.9	2.2	4.5
lfrp	0.4	1.1	5.8	9.8	0.4	0.5
lglp	1.0	5.0	5.3	5.8	1.1	1.4
lglq	2.5	6.7	5.1	6.8	2.0	2.1
lhak	2.2	3.8	2.3	6.2	1.9	3.7
lhdc	0.9	1.2	0.9	1.3	0.8	1.0
lhfc	2.6	3.4	2.4	4.7	2.2	2.4

lhiv	2.2	3.5	1.3	1.3	2.5	2.5
lhpv	1.0	1.4	1.1	1.2	1.3	1.3
lhri	0.9	2.5	0.8	3.8	0.7	0.9
lhtf	1.9	3.9	1.8	3.0	1.5	2.2
lhyt	2.5	2.8	2.4	2.9	2.4	3.2
libg	0.8	1.8	1.8	2.2	0.7	0.7
limb	2.8	6.5	5.4	11.8	2.6	4.2
livb	1.7	3.8	2.4	4.3	1.8	1.8
lkel	1.0	1.3	1.8	1.8	1.4	1.4
llah	0.4	1.1	1.5	2.5	0.5	1.1
llcp	0.8	0.9	1.2	8.2	0.6	0.9
llic	1.7	2.7	2.7	3.9	1.2	2.6
llpm	1.9	2.4	1.6	4.2	1.2	2.3
llst	1.1	1.4	0.9	1.8	1.0	1.6
lmcq	0.7	1.7	0.7	1.2	0.7	2.5
lmdr	1.1	3.0	2.4	4.1	1.2	2.0
lmlD	1.5	1.7	3.6	4.1	1.4	1.8
lmrg	1.2	2.5	5.3	10.5	1.1	1.3
lmrk	0.8	1.1	5.7	10.5	0.8	1.2
lmts	0.9	1.3	1.4	2.2	1.1	1.2
lmup	0.9	1.4	1.2	1.5	0.9	1.2
lneo	1.3	2.2	3.6	3.8	0.9	2.1
lngp	1.1	3.6	2.9	5.0	1.0	3.7
lokI	0.5	2.2	3.4	5.5	1.5	2.2
lpdz	1.4	3.7	2.7	3.2	1.4	2.0
lphd	1.6	4.2	1.5	6.7	1.5	2.6
lphg	2.5	4.2	2.8	6.4	2.4	2.7
lpoc	0.8	1.0	1.3	2.1	0.9	0.9
lppc	2.0	3.3	3.5	7.2	1.2	2.0
lpph	4.9	5.6	5.2	6.1	4.8	5.7
lptv	4.4	8.0	4.1	9.8	4.1	8.5
lqcf	0.8	1.3	3.8	9.5	1.3	1.3
lqpe	0.7	1.2	1.7	1.7	1.1	1.3
lqqq	1.2	1.5	2.6	12.1	0.8	1.2
lrnt	0.8	1.3	3.9	7.0	0.8	0.8
lrob	0.9	0.9	4.6	8.8	0.7	1.1
lrt2	0.6	0.7	0.5	0.6	0.5	1.1
lslt	1.3	4.7	2.1	6.3	1.0	1.8
lsnc	0.9	1.9	4.7	5.8	0.8	4.6
lstrj	0.8	1.9	3.4	3.4	0.7	1.0
ltdb	1.6	3.4	3.8	8.7	1.1	1.6
ltmn	1.8	2.1	2.4	2.7	1.4	3.0
ltng	0.1	0.1	3.5	3.7	0.1	0.2

1tnh	1.4	1.8	1.3	1.6	1.4	1.7
1tni	1.4	2.8	1.4	2.0	1.6	2.6
1tpp	5.6	6.0	6.3	11.2	5.5	5.8
1tyl	0.9	1.5	1.5	3.0	0.7	0.8
1ukz	0.5	2.4	5.1	7.7	0.5	0.7
1ulb	0.5	1.3	2.7	7.8	0.4	1.3
1uvs	1.5	1.9	3.8	6.0	1.7	2.4
1uvt	2.9	3.2	3.1	3.5	3.5	4.7
1vgc	1.1	2.0	1.1	1.5	1.1	1.5
1xid	1.4	2.3	1.3	1.6	1.3	1.4
1xie	1.9	4.3	8.2	12.2	1.1	2.2
1ydr	0.5	0.6	1.0	1.6	0.5	0.6
1yee	1.2	1.2	2.3	3.7	1.0	1.2
25c8	1.7	2.1	2.4	4.3	1.5	1.7
2aad	0.6	0.8	3.8	6.9	0.6	0.8
2ada	0.4	0.5	2.9	11.1	0.5	0.5
2cht	1.4	3.1	2.4	8.7	1.1	1.6
2cmd	1.3	1.8	2.8	4.1	1.3	2.1
2cpp	0.5	2.1	1.9	5.5	0.2	0.3
2ctc	2.3	2.6	2.2	2.7	2.3	2.8
2fox	1.1	1.5	6.1	7.9	0.6	1.5
2gbp	0.5	0.7	2.1	14.6	0.3	0.4
2h4n	1.6	1.7	1.8	3.9	1.6	1.8
2ifb	1.0	1.7	1.8	2.6	1.0	1.8
2mcp	0.9	1.6	4.2	6.5	0.8	1.2
2pk4	1.1	2.1	1.2	2.3	1.3	2.5
2r07	0.6	0.9	0.6	1.3	0.6	0.8
2yhx	0.8	2.9	1.8	6.2	0.7	0.8
2ypi	1.0	1.5	3.0	10.3	0.9	1.5
3ert	1.0	1.2	0.9	1.2	0.9	1.4
3gpb	1.1	2.1	3.0	13.0	1.1	2.0
3hvt	0.5	0.7	0.4	0.8	0.7	0.9
4aah	0.5	0.8	4.0	5.6	0.5	3.8
4cox	0.4	0.6	0.7	0.9	0.5	0.5
4cts	2.1	3.7	3.9	8.2	1.5	1.6
4dfr	2.9	8.4	3.5	5.3	2.4	3.5
4est	2.1	2.9	2.3	2.9	2.3	3.5
4fbp	0.3	0.5	5.7	10.8	0.3	0.4
4lbd	1.0	1.0	1.0	1.1	1.0	1.0
4phv	3.7	5.2	3.4	4.9	3.5	4.2
5abp	0.5	0.5	2.1	11.5	0.4	0.5
5cpp	1.9	1.9	1.9	5.4	1.9	1.9
6rnt	1.5	2.1	6.7	10.8	1.0	1.1



6rsa	0.4	0.8	2.6	10.1	0.4	0.9
7tim	1.1	1.7	3.6	4.0	0.8	1.7
<b>Averages</b>	1.3	2.4	2.8	5.2	1.3	1.9

**Table 2:**

Details of temperatures and molecular dynamics steps for each of the simulated annealing protocols.

<b>Protocol</b>		<b>Phase 1</b>	<b>Phase 2</b>	<b>Phase 3</b>	<b>Phase 4</b>
<i>SA- 1 Grid</i>	Temps	300 → 700	700	700 → 300	300 → 50
	Steps	2,250	10,500	5,250	2,250
<i>SA- 2Grids*</i>	Temps	300 → 700	700 → 300	500 → 300	400 → 300
	Steps	2,250	10,500	5,250	2,250

\*Wu, G. S.; Robertson, D. H.; Brooks, C. L. III; Vieth, M. J. *Comput. Chem.* **2003**, *24*, 1549.

**Table 3:**

Results for HIV Reverse Transcriptase cross-docking trial, totaling 173 unique protein-ligand complexes. The MD+Minimization protocol was the only one used in this trial as it was the most successful docking protocol in the redocking trials. Reported are the lowest RMSD structure sampled and the lowest energy RMSD conformation.

<b>Receptor PDBID</b>	<b>Ligand PDBID</b>	<i>Rigid CDOCKER</i>		<i>Flexible CDOCKER</i>	
		<b>Lowest RMSD</b>	<b>Lowest Energy</b>	<b>Lowest RMSD</b>	<b>Lowest Energy</b>
1clb	1clc	0.9	6.0	1.0	1.6
1clb	1ep4	1.7	7.2	1.5	5.5
1clb	1rth	0.9	6.2	0.9	6.2
1clb	1vru	1.1	2.2	0.9	5.6
1clb	2be2	1.3	1.8	1.4	1.5
1clb	2rf2	2.6	3.4	2.6	2.9
1clb	2rki	1.9	2.2	1.9	5.7
1clb	3dlg	1.2	1.3	2.4	8.9
1clb	3dol	2.5	10.8	3.8	10.6
1clb	3dya	2.9	3.0	2.9	3.7
1clc	1clb	0.8	2.0	0.8	2.1
1clc	1ep4	2.0	7.0	1.7	6.1
1clc	1rt2	0.7	0.7	0.8	1.6
1clc	1rth	1.2	14.6	1.1	6.3
1clc	1vru	1.5	5.2	1.5	5.5

1c1c	2be2	1.0	2.2	1.0	1.3
1c1c	2rf2	2.2	6.3	2.1	6.1
1c1c	2rki	1.8	2.5	1.7	7.8
1ep4	1c1b	0.9	1.3	1.4	2.8
1ep4	1rt2	1.3	2.0	1.4	5.1
1ep4	1rth	1.2	12.4	1.7	4.6
1ep4	1vru	1.6	5.1	2.1	4.9
1ep4	2be2	1.5	1.6	1.3	2.0
1ep4	2rf2	3.2	5.8	3.3	5.8
1ep4	2rki	2.8	5.0	3.0	5.7
likw	1c1b	4.1	5.7	4.3	7.2
likw	1c1c	4.2	5.9	4.7	7.0
likw	1ep4	3.7	6.6	3.9	6.5
likw	1vru	4.9	5.5	4.8	6.5
likw	2be2	7.1	10.4	6.7	10.8
likw	2rf2	4.4	7.3	4.4	6.7
likw	2rki	5.2	8.8	5.2	8.8
likw	3dol	7.9	10.0	7.9	10.6
1rt2	1ep4	2.2	13.6	2.1	2.8
1rt2	1rth	1.5	14.9	4.2	14.7
1rt2	1vru	1.8	14.9	1.6	5.1
1rt2	2be2	1.4	13.1	1.3	2.4
1rt2	2rf2	2.1	15.4	2.1	2.2
1rt2	2rki	1.7	13.2	1.8	2.8
1rt2	3dlg	1.0	12.8	0.8	1.6
1rth	1c1b	0.9	4.1	0.9	2.1
1rth	1c1c	1.3	5.4	1.2	1.7
1rth	1rt2	2.4	7.8	2.8	7.3
1rth	1vru	1.3	4.6	0.8	5.3
1rth	2be2	3.1	6.6	2.6	6.3
1rth	2rki	2.8	7.7	2.8	7.9
1slt	1c1b	0.8	1.2	1.1	1.5
1slt	1c1c	1.0	6.2	1.1	5.5
1slt	1rt2	2.6	7.8	2.5	7.0
1slt	1rth	1.0	13.8	1.1	6.1
1slt	1vru	1.2	2.3	0.9	5.2
1slt	2be2	2.3	6.3	2.2	6.8
1slt	2rf2	1.7	1.9	1.4	4.7
1slt	2rki	1.7	7.6	2.4	7.4
1slt	3dlg	3.8	11.4	4.4	8.5
1vrt	1c1b	1.0	5.1	1.0	5.8
1vrt	1c1c	1.1	3.2	1.1	2.9
1vrt	1rt2	2.7	7.3	3.0	7.3

1vrt	1rth	0.7	14.5	0.6	6.1
1vrt	2be2	2.6	6.5	2.4	6.5
1vrt	2rf2	1.2	4.5	1.5	4.5
1vrt	2rki	2.5	8.2	2.8	6.2
1vru	1c1b	1.0	5.0	1.0	1.9
1vru	1c1c	1.2	3.1	1.2	5.0
1vru	1rt2	3.3	7.9	2.9	7.1
1vru	1rth	0.8	13.0	0.7	1.3
1vru	2be2	3.2	6.3	2.9	6.5
1vru	2rf2	1.5	4.5	1.4	5.8
2be2	1c1b	1.3	1.4	1.2	5.0
2be2	1c1c	1.2	1.2	1.2	1.4
2be2	1rt2	1.2	13.1	1.1	1.6
2be2	1rth	1.9	13.4	2.3	5.9
2be2	2rf2	2.2	5.8	2.3	6.8
2hnd	1c1b	1.3	5.7	1.3	1.3
2hnd	1c1c	1.3	5.5	1.1	5.5
2hnd	1rth	1.3	13.9	0.8	1.7
2hnd	2rf2	1.0	4.4	1.0	4.5
2hny	1c1b	1.3	5.8	1.2	5.5
2hny	1c1c	1.2	3.3	1.2	3.1
2hny	1rth	1.2	4.4	1.0	1.3
2hny	2rf2	0.9	4.3	0.9	4.5
2hny	3dlg	4.6	9.5	4.8	7.8
2hny	3dol	6.9	11.4	6.5	11.2
2ops	1c1c	1.3	5.4	1.1	1.6
2ops	1rt2	2.2	6.2	2.7	6.3
2ops	1rth	1.1	14.3	0.7	6.0
2ops	2be2	2.7	6.5	3.1	6.8
2ops	2rf2	1.6	4.6	1.5	4.5
2ops	3dlg	3.9	8.5	4.1	9.4
2rf2	1c1b	1.5	13.9	1.3	5.4
2rf2	1c1c	1.1	5.5	1.3	5.5
2rf2	1ep4	3.4	9.3	3.2	7.3
2rf2	1rt2	2.8	7.6	3.0	7.9
2rf2	1rth	1.4	16.0	1.6	6.0
2rf2	1vru	1.8	1.8	1.6	5.0
2rf2	2be2	3.8	13.7	3.5	7.2
2rf2	2rki	2.7	14.9	2.6	4.2
2rf2	3dlg	4.2	13.1	4.3	10.2
2rf2	3dol	6.9	13.7	6.2	12.3
2rf2	3dya	3.6	14.2	3.6	7.1
2rki	1c1b	1.6	12.2	1.6	2.5

2rki	1c1c	1.6	5.7	1.3	5.5
2rki	1ep4	2.4	10.9	2.3	7.5
2rki	1rt2	1.5	13.3	1.2	1.6
2rki	1rth	2.3	13.7	2.6	6.0
2rki	1vru	2.1	6.6	3.1	4.3
2rki	2be2	1.7	12.2	2.0	2.1
2rki	2rf2	1.5	12.8	1.2	4.7
2rki	3dlg	1.5	4.8	1.5	1.5
2rki	3dol	2.5	10.8	2.3	2.3
2rki	3dya	1.6	11.6	1.5	8.7
2zd1	1c1b	1.5	2.7	1.5	1.6
2zd1	1c1c	1.8	6.7	1.9	6.6
2zd1	1ep4	3.3	6.8	3.3	6.4
2zd1	1rt2	3.0	7.7	3.0	7.9
2zd1	1rth	1.1	5.4	0.9	6.2
2zd1	1vru	1.6	2.3	1.8	2.4
2zd1	2be2	3.1	7.6	2.4	6.0
2zd1	2rf2	2.5	5.0	2.4	5.1
2zd1	2rki	3.0	8.2	3.0	8.1
2zd1	3dlg	4.6	9.8	4.3	9.2
2zd1	3dol	6.5	11.7	6.6	11.4
2zd1	3dya	3.4	6.7	3.4	6.5
3bgr	1c1b	1.4	3.1	1.4	6.1
3bgr	1c1c	1.9	7.0	1.9	6.7
3bgr	1ep4	2.8	8.7	2.8	6.2
3bgr	1rt2	2.5	9.0	3.0	7.8
3bgr	1rth	1.1	6.1	1.0	1.5
3bgr	1vru	1.5	3.3	1.7	4.0
3bgr	2be2	2.2	5.6	2.0	5.6
3bgr	2rf2	3.0	5.2	2.9	5.1
3bgr	2rki	2.8	10.3	3.1	8.2
3bgr	3dol	6.5	13.0	6.2	9.4
3bgr	3dya	2.3	6.4	2.9	6.4
3dle	1c1b	1.2	14.3	1.3	6.0
3dle	1c1c	1.5	6.0	1.3	4.8
3dle	1ep4	2.3	13.2	2.2	2.7
3dle	1rt2	0.7	12.4	0.5	0.8
3dle	1rth	3.7	14.6	4.8	5.0
3dle	1vru	3.2	5.3	3.8	5.2
3dle	2be2	1.4	1.7	1.3	2.5
3dle	2rf2	2.3	5.0	2.7	7.4
3dle	2rki	2.4	15.4	2.0	2.8
3dle	3dol	1.1	4.4	1.7	2.2

3dle	3dya	2.5	11.9	2.4	2.5
3dlg	1c1b	1.3	13.9	1.7	5.2
3dlg	1c1c	1.2	14.6	1.6	6.3
3dlg	1ep4	2.2	13.7	2.1	5.6
3dlg	1rt2	1.0	13.4	1.0	2.1
3dlg	1rth	1.9	12.4	6.0	12.5
3dlg	1vru	2.7	14.8	3.5	4.5
3dlg	2be2	1.2	1.5	1.0	1.5
3dlg	2rf2	2.3	5.0	3.7	5.6
3dlg	2rki	2.2	11.9	2.2	6.8
3dlg	3dol	1.4	2.4	1.7	2.5
3dlg	3dya	2.5	3.6	2.3	2.5
3dol	1c1b	4.7	13.5	2.6	2.6
3dol	1c1c	4.4	5.5	4.8	5.7
3dol	1ep4	3.0	12.8	4.0	8.4
3dol	1rt2	1.9	11.8	2.2	2.6
3dol	1vru	5.4	15.8	4.8	6.8
3dol	2be2	2.4	2.4	2.3	2.9
3dol	2rki	3.4	13.3	3.2	4.3
3dol	3dlg	1.6	2.7	1.4	1.4
3dol	3dya	3.2	4.1	1.5	1.5
3dya	1c1b	2.3	2.5	2.2	2.2
3dya	1c1c	2.1	6.6	1.9	6.5
3dya	1ep4	2.1	3.0	2.0	2.8
3dya	1rt2	2.3	2.9	2.1	2.4
3dya	1rth	3.0	13.6	3.2	6.7
3dya	1vru	3.3	6.0	3.9	5.8
3dya	2be2	1.3	2.3	1.4	2.3
3dya	2rf2	1.9	2.7	1.9	6.4
3dya	2rki	2.2	2.7	2.0	2.3
<b>Averages</b>		2.3	7.7	2.3	5.2

**Table 4:**

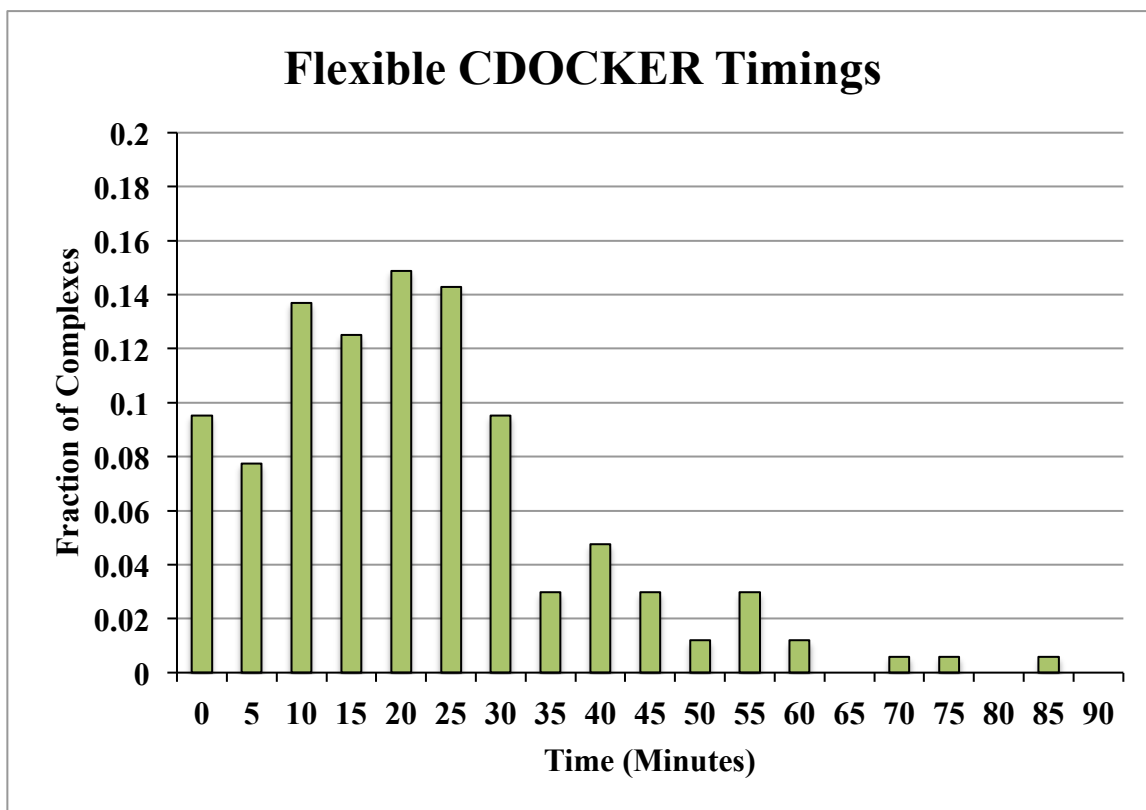
HIV Reverse transcriptase cross-docking results with comparison to results as published by Rizzo et al.

		<b>%Found</b>	<b>%Scored</b>
<b>131 Unique Complexes</b>	Flexible CDOCKER	47.3	19.1
	Rigid CDOCKER	48.1	10.7
<b>61 Overlap Complexes</b>	Flexible CDOCKER	63.9	24.6
	Rigid CDOCKER	65.6	14.8
	DOCK 6*	-	66.7
<b>70 Complexes</b>	Flexible CDOCKER	32.9	14.3
<b>"Non-viable Pairings"</b>	Rigid CDOCKER	32.9	7.1

\* Allen, W. J.; Balius, T. E.; Mukherjee, S.; Brozell, S. R.; Moustakas, D. T.; Lang, P. T.; Case, D. A.; Kuntz, I. D.; Rizzo, R. C. *J. Comput. Chem.* 2015, 36, 1132.

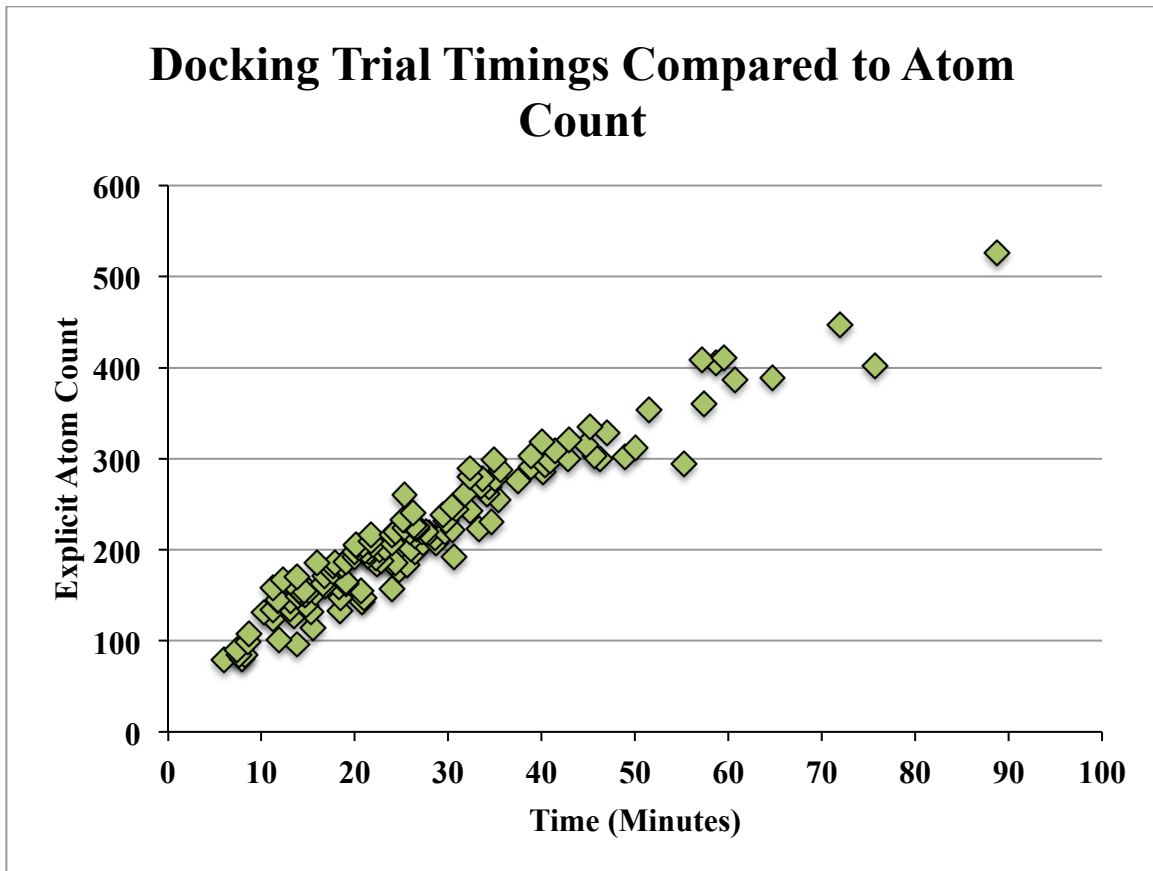
**Figure 1:**

The time taken by Flexible CDOCKER to generate 50 conformations for a single docking trial as distributed over the CCDC/Astex clean-set. All complexes took under 10 minutes for Rigid CDOCKER.



**Figure 2:**

The time taken for a single docking trial scales linearly with the number of explicit atoms included in the flexible receptor docking.





**Figure 3:**

(Supporting information Figure 1 in section “Flexible CDOCKER improves cross-docking accuracy: A case study”)

Overlay of the predicted lowest free energy conformation found with Flexible CDOCKER and crystallographic structures of Alpha MMC. The ligand conformation (gray) has an RMSD of 1.42Å from the crystallographic conformation. The tyrosine residue on the protein from the apo structure (green) clashed with ligand causing a dihedral angle shift of this residue in the holo structure (blue). The tyrosine from the predicted conformation (magenta) remains near the apo dihedral angle, suggesting that this small shift is sufficient to achieve a low energy docked conformation.

