

**PDB file of KAP8.1 Model**

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REMARK      Accelrys Discovery Studio PDB file
REMARK      Created: 2016-07-01T15:14:01Z
SSBOND      1 CYS A      1      CYS A      28
SSBOND      2 CYS A     13      CYS A     43
ATOM        1  N      MET A    -1          27.440  17.934  11.835  1.00  0.00
N1+
ATOM        2  HT1   MET A    -1          27.384  18.772  12.446  1.00  0.00
H
ATOM        3  HT2   MET A    -1          28.365  17.475  11.936  1.00  0.00
H
ATOM        4  HT3   MET A    -1          26.717  17.236  12.139  1.00  0.00
H
ATOM        5  CA     MET A    -1          27.128  18.212  10.432  1.00  0.00
C
ATOM        6  HA     MET A    -1          26.559  19.143  10.391  1.00  0.00
H
ATOM        7  CB     MET A    -1          28.350  18.270   9.493  1.00  0.00
C
ATOM        8  HB1   MET A    -1          29.077  17.497   9.747  1.00  0.00
H
ATOM        9  HB2   MET A    -1          28.041  18.058   8.467  1.00  0.00
H
ATOM       10  CG     MET A    -1          29.020  19.648   9.471  1.00  0.00
C
ATOM       11  HG1   MET A    -1          28.276  20.420   9.270  1.00  0.00
H
ATOM       12  HG2   MET A    -1          29.478  19.862  10.437  1.00  0.00
H
ATOM       13  SD     MET A    -1          30.292  19.698   8.194  1.00  0.00
S
ATOM       14  CE     MET A    -1          29.813  21.223   7.360  1.00  0.00
C
ATOM       15  HE1   MET A    -1          30.570  21.513   6.630  1.00  0.00
H
ATOM       16  HE2   MET A    -1          29.713  22.029   8.088  1.00  0.00
H
ATOM       17  HE3   MET A    -1          28.848  21.100   6.865  1.00  0.00
H
ATOM       18  C      MET A    -1          26.167  17.100  10.050  1.00  0.00
C
ATOM       19  O      MET A    -1          25.973  16.228  10.887  1.00  0.00
O
ATOM       20  N      LEU A     0          25.577  17.246   8.844  1.00  0.00
N
ATOM       21  HN     LEU A     0          25.973  17.949   8.252  1.00  0.00
H
ATOM       22  CA     LEU A     0          24.200  16.840   8.482  1.00  0.00
C
ATOM       23  HA     LEU A     0          24.212  16.663   7.407  1.00  0.00
H
ATOM       24  CB     LEU A     0          23.629  15.615   9.238  1.00  0.00
C
ATOM       25  HB1   LEU A     0          23.763  15.734  10.315  1.00  0.00
H
ATOM       26  HB2   LEU A     0          22.549  15.557   9.112  1.00  0.00
H
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ATOM C	27	CG	LEU	A	0	24.188	14.265	8.765	1.00	0.00
ATOM H	28	HG	LEU	A	0	25.269	14.352	8.652	1.00	0.00
ATOM C	29	CD1	LEU	A	0	23.932	13.186	9.822	1.00	0.00
ATOM H	30	1HD1	LEU	A	0	24.258	12.205	9.478	1.00	0.00
ATOM H	31	2HD1	LEU	A	0	22.875	13.108	10.074	1.00	0.00
ATOM H	32	3HD1	LEU	A	0	24.471	13.411	10.742	1.00	0.00
ATOM C	33	CD2	LEU	A	0	23.576	13.841	7.420	1.00	0.00
ATOM H	34	1HD2	LEU	A	0	23.985	12.880	7.101	1.00	0.00
ATOM H	35	2HD2	LEU	A	0	23.789	14.562	6.631	1.00	0.00
ATOM H	36	3HD2	LEU	A	0	22.491	13.728	7.488	1.00	0.00
ATOM C	37	C	LEU	A	0	23.374	18.109	8.728	1.00	0.00
ATOM O	38	O	LEU	A	0	23.998	19.155	8.908	1.00	0.00
ATOM N	39	N	CYS	A	1	22.034	17.996	8.789	1.00	0.00
ATOM H	40	HN	CYS	A	1	21.538	17.167	8.525	1.00	0.00
ATOM C	41	CA	CYS	A	1	21.277	19.061	9.420	1.00	0.00
ATOM H	42	HA	CYS	A	1	21.905	19.542	10.176	1.00	0.00
ATOM C	43	CB	CYS	A	1	20.820	20.113	8.404	1.00	0.00
ATOM H	44	HB1	CYS	A	1	19.777	20.387	8.574	1.00	0.00
ATOM H	45	HB2	CYS	A	1	21.406	21.022	8.535	1.00	0.00
ATOM S	46	SG	CYS	A	1	21.021	19.567	6.699	1.00	0.00
ATOM C	47	C	CYS	A	1	20.138	18.363	10.144	1.00	0.00
ATOM O	48	O	CYS	A	1	19.100	18.000	9.578	1.00	0.00
ATOM N	49	N	ASP	A	2	20.428	18.155	11.438	1.00	0.00
ATOM H	50	HN	ASP	A	2	21.322	18.406	11.821	1.00	0.00
ATOM C	51	CA	ASP	A	2	19.490	17.554	12.374	1.00	0.00
ATOM H	52	HA	ASP	A	2	19.068	16.678	11.877	1.00	0.00
ATOM C	53	CB	ASP	A	2	20.220	17.098	13.659	1.00	0.00
ATOM H	54	HB1	ASP	A	2	20.035	17.808	14.469	1.00	0.00
ATOM H	55	HB2	ASP	A	2	19.805	16.150	14.006	1.00	0.00







ATOM H	143	HN	PHE	A	9	5.071	22.758	22.715	1.00	0.00
ATOM C	144	CA	PHE	A	9	3.551	24.207	23.028	1.00	0.00
ATOM H	145	HA	PHE	A	9	3.334	25.177	22.576	1.00	0.00
ATOM C	146	CB	PHE	A	9	2.480	23.130	22.726	1.00	0.00
ATOM H	147	HB1	PHE	A	9	2.618	22.753	21.713	1.00	0.00
ATOM H	148	HB2	PHE	A	9	2.602	22.292	23.402	1.00	0.00
ATOM C	149	CG	PHE	A	9	1.052	23.569	22.871	1.00	0.00
ATOM C	150	CD1	PHE	A	9	0.333	24.021	21.771	1.00	0.00
ATOM H	151	HD1	PHE	A	9	0.799	24.079	20.794	1.00	0.00
ATOM C	152	CD2	PHE	A	9	0.423	23.511	24.111	1.00	0.00
ATOM H	153	HD2	PHE	A	9	0.950	23.103	24.962	1.00	0.00
ATOM C	154	CE1	PHE	A	9	-0.992	24.410	21.919	1.00	0.00
ATOM H	155	HE1	PHE	A	9	-1.550	24.773	21.067	1.00	0.00
ATOM C	156	CE2	PHE	A	9	-0.890	23.932	24.265	1.00	0.00
ATOM H	157	HE2	PHE	A	9	-1.373	23.913	25.235	1.00	0.00
ATOM C	158	CZ	PHE	A	9	-1.600	24.374	23.165	1.00	0.00
ATOM H	159	HZ	PHE	A	9	-2.623	24.705	23.291	1.00	0.00
ATOM C	160	C	PHE	A	9	3.823	24.307	24.533	1.00	0.00
ATOM O	161	O	PHE	A	9	4.635	23.537	25.050	1.00	0.00
ATOM N	162	N	PRO	A	10	3.122	25.215	25.273	1.00	0.00
ATOM C	163	CD	PRO	A	10	2.287	26.304	24.759	1.00	0.00
ATOM H	164	HD1	PRO	A	10	2.933	27.077	24.345	1.00	0.00
ATOM H	165	HD2	PRO	A	10	1.595	25.986	23.981	1.00	0.00
ATOM C	166	CA	PRO	A	10	3.160	25.146	26.736	1.00	0.00
ATOM H	167	HA	PRO	A	10	4.186	25.075	27.104	1.00	0.00
ATOM C	168	CB	PRO	A	10	2.510	26.482	27.152	1.00	0.00
ATOM H	169	HB1	PRO	A	10	2.046	26.527	28.138	1.00	0.00
ATOM H	170	HB2	PRO	A	10	3.297	27.238	27.169	1.00	0.00
ATOM C	171	CG	PRO	A	10	1.558	26.823	26.005	1.00	0.00







ATOM C	230	CA	GLY	A	16	-1.870	20.546	24.466	1.00	0.00
ATOM H	231	HA1	GLY	A	16	-2.854	20.089	24.354	1.00	0.00
ATOM H	232	HA2	GLY	A	16	-2.006	21.619	24.389	1.00	0.00
ATOM C	233	C	GLY	A	16	-0.931	20.047	23.363	1.00	0.00
ATOM O	234	O	GLY	A	16	0.262	19.825	23.538	1.00	0.00
ATOM N	235	N	SER	A	17	-1.558	19.868	22.174	1.00	0.00
ATOM H	236	HN	SER	A	17	-2.471	20.261	22.029	1.00	0.00
ATOM C	237	CA	SER	A	17	-0.841	19.162	21.086	1.00	0.00
ATOM H	238	HA	SER	A	17	-0.633	18.163	21.475	1.00	0.00
ATOM C	239	CB	SER	A	17	-1.767	19.058	19.844	1.00	0.00
ATOM H	240	HB1	SER	A	17	-2.773	18.783	20.161	1.00	0.00
ATOM H	241	HB2	SER	A	17	-1.874	20.053	19.417	1.00	0.00
ATOM O	242	OG	SER	A	17	-1.414	18.143	18.801	1.00	0.00
ATOM H	243	HG	SER	A	17	-0.466	17.923	18.857	1.00	0.00
ATOM C	244	C	SER	A	17	0.504	19.861	20.691	1.00	0.00
ATOM O	245	O	SER	A	17	0.516	21.014	20.252	1.00	0.00
ATOM N	246	N	TYR	A	18	1.599	19.060	20.819	1.00	0.00
ATOM H	247	HN	TYR	A	18	1.470	18.144	21.202	1.00	0.00
ATOM C	248	CA	TYR	A	18	2.959	19.485	20.477	1.00	0.00
ATOM H	249	HA	TYR	A	18	3.078	20.522	20.793	1.00	0.00
ATOM C	250	CB	TYR	A	18	3.995	18.519	21.115	1.00	0.00
ATOM H	251	HB1	TYR	A	18	3.560	17.530	21.275	1.00	0.00
ATOM H	252	HB2	TYR	A	18	4.832	18.355	20.434	1.00	0.00
ATOM C	253	CG	TYR	A	18	4.583	19.014	22.415	1.00	0.00
ATOM C	254	CD1	TYR	A	18	3.979	20.028	23.135	1.00	0.00
ATOM H	255	HD1	TYR	A	18	3.015	20.383	22.820	1.00	0.00
ATOM C	256	CE1	TYR	A	18	4.557	20.540	24.279	1.00	0.00
ATOM H	257	HE1	TYR	A	18	4.024	21.302	24.823	1.00	0.00
ATOM C	258	CD2	TYR	A	18	5.759	18.475	22.921	1.00	0.00



ATOM C	288	CE2	TYR	A	20	3.202	23.238	11.870	1.00	0.00
ATOM H	289	HE2	TYR	A	20	2.348	23.827	12.169	1.00	0.00
ATOM C	290	CZ	TYR	A	20	4.074	23.702	10.886	1.00	0.00
ATOM O	291	OH	TYR	A	20	3.858	24.888	10.180	1.00	0.00
ATOM H	292	HH	TYR	A	20	2.960	25.232	10.131	1.00	0.00
ATOM C	293	C	TYR	A	20	7.025	19.911	13.684	1.00	0.00
ATOM O	294	O	TYR	A	20	7.462	21.062	13.611	1.00	0.00
ATOM N	295	N	PRO	A	21	7.765	18.797	13.376	1.00	0.00
ATOM C	296	CD	PRO	A	21	7.337	17.395	13.467	1.00	0.00
ATOM H	297	HD1	PRO	A	21	7.332	17.086	14.514	1.00	0.00
ATOM H	298	HD2	PRO	A	21	6.349	17.241	13.034	1.00	0.00
ATOM C	299	CA	PRO	A	21	9.049	18.935	12.727	1.00	0.00
ATOM H	300	HA	PRO	A	21	9.680	19.594	13.303	1.00	0.00
ATOM C	301	CB	PRO	A	21	9.592	17.517	12.562	1.00	0.00
ATOM H	302	HB1	PRO	A	21	10.261	17.313	13.388	1.00	0.00
ATOM H	303	HB2	PRO	A	21	10.163	17.355	11.643	1.00	0.00
ATOM C	304	CG	PRO	A	21	8.374	16.605	12.659	1.00	0.00
ATOM H	305	HG1	PRO	A	21	7.999	16.388	11.658	1.00	0.00
ATOM H	306	HG2	PRO	A	21	8.634	15.659	13.126	1.00	0.00
ATOM C	307	C	PRO	A	21	8.747	19.517	11.371	1.00	0.00
ATOM O	308	O	PRO	A	21	7.679	19.219	10.822	1.00	0.00
ATOM N	309	N	LEU	A	22	9.687	20.348	10.898	1.00	0.00
ATOM H	310	HN	LEU	A	22	10.516	20.540	11.431	1.00	0.00
ATOM C	311	CA	LEU	A	22	9.595	20.772	9.519	1.00	0.00
ATOM H	312	HA	LEU	A	22	8.560	21.049	9.313	1.00	0.00
ATOM C	313	CB	LEU	A	22	10.519	21.979	9.249	1.00	0.00
ATOM H	314	HB1	LEU	A	22	10.362	22.337	8.229	1.00	0.00
ATOM H	315	HB2	LEU	A	22	11.562	21.659	9.294	1.00	0.00
ATOM C	316	CG	LEU	A	22	10.315	23.157	10.220	1.00	0.00







ATOM H	404	HA2	GLY	A	29	17.543	14.488	9.369	1.00	0.00
ATOM C	405	C	GLY	A	29	15.581	14.845	8.593	1.00	0.00
ATOM O	406	O	GLY	A	29	14.999	15.927	8.691	1.00	0.00
ATOM N	407	N	TYR	A	30	14.946	13.654	8.708	1.00	0.00
ATOM H	408	HN	TYR	A	30	15.507	12.868	8.424	1.00	0.00
ATOM C	409	CA	TYR	A	30	13.588	13.666	9.212	1.00	0.00
ATOM H	410	HA	TYR	A	30	13.093	14.392	8.569	1.00	0.00
ATOM C	411	CB	TYR	A	30	12.814	12.352	8.984	1.00	0.00
ATOM H	412	HB1	TYR	A	30	12.773	12.192	7.915	1.00	0.00
ATOM H	413	HB2	TYR	A	30	11.783	12.461	9.319	1.00	0.00
ATOM C	414	CG	TYR	A	30	13.362	11.080	9.568	1.00	0.00
ATOM C	415	CD1	TYR	A	30	12.879	10.614	10.781	1.00	0.00
ATOM H	416	HD1	TYR	A	30	12.184	11.234	11.309	1.00	0.00
ATOM C	417	CE1	TYR	A	30	13.283	9.388	11.284	1.00	0.00
ATOM H	418	HE1	TYR	A	30	12.882	9.007	12.216	1.00	0.00
ATOM C	419	CD2	TYR	A	30	14.299	10.315	8.882	1.00	0.00
ATOM H	420	HD2	TYR	A	30	14.722	10.655	7.948	1.00	0.00
ATOM C	421	CE2	TYR	A	30	14.722	9.096	9.383	1.00	0.00
ATOM H	422	HE2	TYR	A	30	15.456	8.521	8.831	1.00	0.00
ATOM C	423	CZ	TYR	A	30	14.206	8.629	10.580	1.00	0.00
ATOM O	424	OH	TYR	A	30	14.607	7.422	11.098	1.00	0.00
ATOM H	425	HH	TYR	A	30	15.064	7.657	11.906	1.00	0.00
ATOM C	426	C	TYR	A	30	13.574	14.243	10.645	1.00	0.00
ATOM O	427	O	TYR	A	30	13.981	13.638	11.637	1.00	0.00
ATOM N	428	N	GLY	A	31	13.097	15.503	10.693	1.00	0.00
ATOM H	429	HN	GLY	A	31	13.261	15.933	9.802	1.00	0.00
ATOM C	430	CA	GLY	A	31	12.975	16.167	11.987	1.00	0.00
ATOM H	431	HA1	GLY	A	31	13.978	16.239	12.417	1.00	0.00
ATOM H	432	HA2	GLY	A	31	12.581	17.167	11.809	1.00	0.00

ATOM C	433	C	GLY	A	31	12.027	15.385	12.912	1.00	0.00
ATOM O	434	O	GLY	A	31	11.132	14.661	12.459	1.00	0.00
ATOM N	435	N	SER	A	32	12.210	15.583	14.234	1.00	0.00
ATOM H	436	HN	SER	A	32	12.910	16.257	14.456	1.00	0.00
ATOM C	437	CA	SER	A	32	11.550	14.769	15.258	1.00	0.00
ATOM H	438	HA	SER	A	32	11.396	13.796	14.810	1.00	0.00
ATOM C	439	CB	SER	A	32	12.428	14.590	16.517	1.00	0.00
ATOM H	440	HB1	SER	A	32	13.310	14.006	16.232	1.00	0.00
ATOM H	441	HB2	SER	A	32	12.818	15.549	16.879	1.00	0.00
ATOM O	442	OG	SER	A	32	11.751	13.861	17.550	1.00	0.00
ATOM H	443	HG	SER	A	32	11.379	14.418	18.249	1.00	0.00
ATOM C	444	C	SER	A	32	10.165	15.278	15.652	1.00	0.00
ATOM O	445	O	SER	A	32	9.757	16.429	15.512	1.00	0.00
ATOM N	446	N	THR	A	33	9.419	14.313	16.238	1.00	0.00
ATOM H	447	HN	THR	A	33	9.923	13.496	16.534	1.00	0.00
ATOM C	448	CA	THR	A	33	8.152	14.624	16.901	1.00	0.00
ATOM H	449	HA	THR	A	33	7.658	15.413	16.334	1.00	0.00
ATOM C	450	CB	THR	A	33	7.293	13.330	16.876	1.00	0.00
ATOM H	451	HB	THR	A	33	7.668	12.765	16.024	1.00	0.00
ATOM O	452	OG1	THR	A	33	5.933	13.623	16.571	1.00	0.00
ATOM H	453	HG1	THR	A	33	5.397	12.826	16.635	1.00	0.00
ATOM C	454	CG2	THR	A	33	7.458	12.409	18.101	1.00	0.00
ATOM H	455	1HG2	THR	A	33	8.512	12.297	18.360	1.00	0.00
ATOM H	456	2HG2	THR	A	33	6.935	12.783	18.981	1.00	0.00
ATOM H	457	3HG2	THR	A	33	7.083	11.407	17.896	1.00	0.00
ATOM C	458	C	THR	A	33	8.570	15.176	18.286	1.00	0.00
ATOM O	459	O	THR	A	33	9.764	15.418	18.487	1.00	0.00
ATOM N	460	N	TYR	A	34	7.610	15.310	19.217	1.00	0.00
ATOM H	461	HN	TYR	A	34	6.642	15.095	19.068	1.00	0.00















ATOM C	636	C	GLY	A	47	1.051	13.857	21.687	1.00	0.00
ATOM O	637	O	GLY	A	47	1.175	15.085	21.675	1.00	0.00
ATOM N	638	N	TYR	A	48	1.711	13.001	20.881	1.00	0.00
ATOM H	639	HN	TYR	A	48	1.547	12.019	20.863	1.00	0.00
ATOM C	640	CA	TYR	A	48	2.732	13.479	19.954	1.00	0.00
ATOM H	641	HA	TYR	A	48	3.108	14.445	20.303	1.00	0.00
ATOM C	642	CB	TYR	A	48	3.891	12.461	19.914	1.00	0.00
ATOM H	643	HB1	TYR	A	48	4.588	12.676	19.106	1.00	0.00
ATOM H	644	HB2	TYR	A	48	4.470	12.570	20.831	1.00	0.00
ATOM C	645	CG	TYR	A	48	3.442	11.023	19.825	1.00	0.00
ATOM C	646	CD1	TYR	A	48	2.804	10.528	18.690	1.00	0.00
ATOM H	647	HD1	TYR	A	48	2.604	11.163	17.846	1.00	0.00
ATOM C	648	CE1	TYR	A	48	2.382	9.210	18.624	1.00	0.00
ATOM H	649	HE1	TYR	A	48	1.899	8.829	17.734	1.00	0.00
ATOM C	650	CD2	TYR	A	48	3.655	10.166	20.901	1.00	0.00
ATOM H	651	HD2	TYR	A	48	4.142	10.509	21.804	1.00	0.00
ATOM C	652	CE2	TYR	A	48	3.225	8.848	20.844	1.00	0.00
ATOM H	653	HE2	TYR	A	48	3.387	8.194	21.684	1.00	0.00
ATOM C	654	CZ	TYR	A	48	2.584	8.375	19.711	1.00	0.00
ATOM O	655	OH	TYR	A	48	2.147	7.071	19.668	1.00	0.00
ATOM H	656	HH	TYR	A	48	2.640	6.610	18.990	1.00	0.00
ATOM C	657	C	TYR	A	48	2.086	13.683	18.579	1.00	0.00
ATOM O	658	O	TYR	A	48	0.922	13.310	18.373	1.00	0.00
ATOM N	659	N	ARG	A	49	2.937	14.273	17.695	1.00	0.00
ATOM H	660	HN	ARG	A	49	3.885	14.463	17.965	1.00	0.00
ATOM C	661	CA	ARG	A	49	2.580	14.476	16.302	1.00	0.00
ATOM H	662	HA	ARG	A	49	1.524	14.224	16.195	1.00	0.00
ATOM C	663	CB	ARG	A	49	2.784	15.976	15.951	1.00	0.00
ATOM H	664	HB1	ARG	A	49	2.668	16.573	16.857	1.00	0.00







ATOM C	723	CZ	TYR	A	51	11.219	10.875	16.501	1.00	0.00
ATOM O	724	OH	TYR	A	51	11.883	10.766	17.716	1.00	0.00
ATOM H	725	HH	TYR	A	51	11.313	10.703	18.495	1.00	0.00
ATOM C	726	C	TYR	A	51	8.094	13.362	11.267	1.00	0.00
ATOM O	727	O	TYR	A	51	6.909	13.660	11.063	1.00	0.00
ATOM N	728	N	SER	A	52	9.126	13.552	10.408	1.00	0.00
ATOM H	729	HN	SER	A	52	10.049	13.193	10.590	1.00	0.00
ATOM C	730	CA	SER	A	52	8.979	14.042	9.035	1.00	0.00
ATOM H	731	HA	SER	A	52	8.017	14.550	8.940	1.00	0.00
ATOM C	732	CB	SER	A	52	10.175	15.005	8.770	1.00	0.00
ATOM H	733	HB1	SER	A	52	10.024	15.914	9.361	1.00	0.00
ATOM H	734	HB2	SER	A	52	11.047	14.511	9.201	1.00	0.00
ATOM O	735	OG	SER	A	52	10.441	15.418	7.420	1.00	0.00
ATOM H	736	HG	SER	A	52	11.374	15.659	7.303	1.00	0.00
ATOM C	737	C	SER	A	52	8.998	12.782	8.144	1.00	0.00
ATOM O	738	O	SER	A	52	9.191	11.653	8.618	1.00	0.00
ATOM N	739	N	PRO	A	53	8.771	12.977	6.814	1.00	0.00
ATOM C	740	CD	PRO	A	53	7.982	14.066	6.239	1.00	0.00
ATOM H	741	HD1	PRO	A	53	8.558	14.990	6.211	1.00	0.00
ATOM H	742	HD2	PRO	A	53	7.071	14.242	6.806	1.00	0.00
ATOM C	743	CA	PRO	A	53	9.331	12.082	5.805	1.00	0.00
ATOM H	744	HA	PRO	A	53	8.950	11.071	5.955	1.00	0.00
ATOM C	745	CB	PRO	A	53	8.845	12.659	4.464	1.00	0.00
ATOM H	746	HB1	PRO	A	53	8.573	11.879	3.750	1.00	0.00
ATOM H	747	HB2	PRO	A	53	9.624	13.263	4.003	1.00	0.00
ATOM C	748	CG	PRO	A	53	7.673	13.576	4.822	1.00	0.00
ATOM H	749	HG1	PRO	A	53	7.529	14.394	4.115	1.00	0.00
ATOM H	750	HG2	PRO	A	53	6.760	12.981	4.834	1.00	0.00
ATOM C	751	C	PRO	A	53	10.870	12.085	5.886	1.00	0.00



ATOM C	781	C	ALA	A	55	15.383	12.048	1.493	1.00	0.00
ATOM O	782	O	ALA	A	55	15.691	12.543	0.412	1.00	0.00
ATOM N	783	N	LEU	A	56	15.595	10.767	1.833	1.00	0.00
ATOM H	784	HN	LEU	A	56	15.056	10.415	2.596	1.00	0.00
ATOM C	785	CA	LEU	A	56	16.723	9.939	1.414	1.00	0.00
ATOM H	786	HA	LEU	A	56	16.296	8.959	1.220	1.00	0.00
ATOM C	787	CB	LEU	A	56	17.514	10.394	0.163	1.00	0.00
ATOM H	788	HB1	LEU	A	56	17.848	11.423	0.298	1.00	0.00
ATOM H	789	HB2	LEU	A	56	18.432	9.809	0.078	1.00	0.00
ATOM C	790	CG	LEU	A	56	16.731	10.242	-1.156	1.00	0.00
ATOM H	791	HG	LEU	A	56	15.709	10.589	-0.996	1.00	0.00
ATOM C	792	CD1	LEU	A	56	17.340	11.124	-2.253	1.00	0.00
ATOM H	793	1HD1	LEU	A	56	17.354	12.172	-1.954	1.00	0.00
ATOM H	794	2HD1	LEU	A	56	18.363	10.823	-2.485	1.00	0.00
ATOM H	795	3HD1	LEU	A	56	16.762	11.057	-3.174	1.00	0.00
ATOM C	796	CD2	LEU	A	56	16.664	8.778	-1.620	1.00	0.00
ATOM H	797	1HD2	LEU	A	56	16.160	8.141	-0.893	1.00	0.00
ATOM H	798	2HD2	LEU	A	56	17.656	8.361	-1.800	1.00	0.00
ATOM H	799	3HD2	LEU	A	56	16.105	8.695	-2.553	1.00	0.00
ATOM C	800	C	LEU	A	56	17.656	9.786	2.626	1.00	0.00
ATOM O	801	O	LEU	A	56	18.488	8.883	2.646	1.00	0.00
ATOM N	802	N	TYR	A	57	17.449	10.678	3.623	1.00	0.00
ATOM H	803	HN	TYR	A	57	16.724	11.365	3.614	1.00	0.00
ATOM C	804	CA	TYR	A	57	18.082	10.521	4.919	1.00	0.00
ATOM H	805	HA	TYR	A	57	18.519	9.521	4.974	1.00	0.00
ATOM C	806	CB	TYR	A	57	19.167	11.590	5.114	1.00	0.00
ATOM H	807	HB1	TYR	A	57	19.741	11.712	4.196	1.00	0.00
ATOM H	808	HB2	TYR	A	57	18.723	12.560	5.352	1.00	0.00
ATOM C	809	CG	TYR	A	57	20.092	11.153	6.213	1.00	0.00

