

[illegible]

[illegible]

LOC	AlphaHelix	VAL	708 A	THR	736 A	3G5U
LOC	AlphaHelix	THR	743 A	ARG	794 A	3G5U
LOC	AlphaHelix	THR	807 A	ILE	848 A	3G5U
LOC	AlphaHelix	THR	854 A	GLU	898 A	3G5U
LOC	AlphaHelix	GLN	910 A	ALA	957 A	3G5U
LOC	AlphaHelix	ASN	969 A	SER	988 A	3G5U
LOC	AlphaHelix	LYS	996 A	GLU	1009 A	3G5U
LOC	AlphaHelix	LYS	1072 A	GLU	1080 A	3G5U
LOC	AlphaHelix	VAL	1102 A	ARG	1106 A	3G5U
LOC	AlphaHelix	ILE	1123 A	ALA	1128 A	3G5U
LOC	AlphaHelix	TYR	1138 A	ALA	1148 A	3G5U
LOC	AlphaHelix	ILE	1150 A	ASP	1155 A	3G5U
LOC	AlphaHelix	GLY	1174 A	ARG	1188 A	3G5U
LOC	AlphaHelix	THR	1204 A	ALA	1217 A	3G5U
LOC	AlphaHelix	HIS	1253 A	ALA	1258 A	3G5U
LOC	AlphaHelix	ILE	1262 A	GLN	1270 A	3G5U
LOC	310Helix	GLU	155 A	GLY	157 A	3G5U
LOC	310Helix	ILE	454 A	THR	456 A	3G5U
LOC	310Helix	LEU	585 A	THR	587 A	3G5U
LOC	310Helix	LYS	1160 A	ASN	1162 A	3G5U
LOC	Strand	LEU	388 A	LYS	391 A	3G5U
LOC	Strand	ILE	393 A	PHE	395 A	3G5U
LOC	Strand	LEU	406 A	LEU	409 A	3G5U
LOC	Strand	LEU	411 A	VAL	413 A	3G5U
LOC	Strand	THR	418 A	VAL	422 A	3G5U
LOC	Strand	MET	446 A	ILE	449 A	3G5U
LOC	Strand	GLN	452 A	ASP	453 A	3G5U
LOC	Strand	ILE	466 A	VAL	469 A	3G5U
LOC	Strand	ILE	547 A	ASP	551 A	3G5U
LOC	Strand	THR	577 A	ILE	581 A	3G5U
LOC	Strand	VAL	593 A	GLY	596 A	3G5U
LOC	Strand	GLU	604 A	GLY	606 A	3G5U
LOC	Strand	VAL	1031 A	SER	1034 A	3G5U
LOC	Strand	VAL	1037 A	PHE	1038 A	3G5U
LOC	Strand	LEU	1049 A	GLN	1050 A	3G5U
LOC	Strand	LEU	1054 A	VAL	1056 A	3G5U
LOC	Strand	THR	1061 A	VAL	1065 A	3G5U
LOC	Strand	SER	1089 A	PHE	1091 A	3G5U
LOC	Strand	GLY	1110 A	SER	1113 A	3G5U
LOC	Strand	LEU	1193 A	ASP	1196 A	3G5U
LOC	Strand	CYS	1223 A	ILE	1226 A	3G5U
LOC	Strand	LEU	1238 A	GLN	1243 A	3G5U
LOC	Strand	LYS	1246 A	GLY	1251 A	3G5U
LOC	TurnIV	MET	152 A	GLU	155 A	3G5U
LOC	TurnIV	PHE	200 A	GLY	203 A	3G5U
LOC	TurnI	ILE	201 A	PHE	204 A	3G5U
LOC	TurnIV	ILE	202 A	THR	205 A	3G5U
LOC	TurnIV	GLY	203 A	ARG	206 A	3G5U
LOC	TurnVIII	PHE	204 A	GLY	207 A	3G5U
LOC	TurnIV	THR	205 A	TRP	208 A	3G5U
LOC	TurnIV	GLY	207 A	LEU	210 A	3G5U
LOC	TurnIV	VAL	249 A	GLU	252 A	3G5U
LOC	TurnIV	LEU	254 A	ILE	257 A	3G5U
LOC	TurnIV	ILE	285 A	ALA	288 A	3G5U
LOC	TurnI	LYS	286 A	ILE	289 A	3G5U
LOC	TurnIV	LYS	320 A	SER	323 A	3G5U
LOC	TurnIV	ILE	364 A	ASN	367 A	3G5U
LOC	TurnIV	SER	370 A	SER	373 A	3G5U
LOC	TurnIV	ILE	371 A	PHE	374 A	3G5U
LOC	TurnI	PRO	381 A	ILE	384 A	3G5U
LOC	TurnIV	PHE	390 A	ILE	393 A	3G5U
LOC	TurnIV	TYR	397 A	ARG	400 A	3G5U
LOC	TurnIV	SER	399 A	GLU	402 A	3G5U
LOC	TurnVIII	GLN	404 A	LYS	407 A	3G5U
LOC	TurnIV	LEU	406 A	LEU	409 A	3G5U
LOC	TurnIV	LYS	414 A	GLN	417 A	3G5U
LOC	TurnIV	GLY	423 A	GLY	426 A	3G5U
LOC	TurnVIII	ARG	438 A	ASP	441 A	3G5U
LOC	TurnVIII	PRO	442 A	GLY	445 A	3G5U
LOC	TurnIV	SER	448 A	GLY	451 A	3G5U
LOC	TurnII'	ILE	449 A	GLN	452 A	3G5U
LOC	TurnIV	SER	470 A	PRO	473 A	3G5U
LOC	TurnIV	ARG	488 A	VAL	491 A	3G5U
LOC	TurnIV	LEU	512 A	GLN	515 A	3G5U

LOC	TurnII'	HIS	514	A	ASP	517	A	3G5U
LOC	TurnI	GLN	515	A	THR	518	A	3G5U
LOC	TurnIV	VAL	520	A	ARG	523	A	3G5U
LOC	TurnIV	GLU	522	A	ALA	525	A	3G5U
LOC	TurnIV	PRO	545	A	LEU	548	A	3G5U
LOC	TurnII	LEU	550	A	ALA	553	A	3G5U
LOC	TurnIV	GLU	552	A	SER	555	A	3G5U
LOC	TurnIV	THR	554	A	LEU	557	A	3G5U
LOC	TurnVIII	GLU	574	A	THR	577	A	3G5U
LOC	TurnIV	THR	587	A	ASN	590	A	3G5U
LOC	TurnIV	VAL	588	A	ALA	591	A	3G5U
LOC	TurnIV	ALA	591	A	ILE	594	A	3G5U
LOC	TurnIV	PHE	597	A	GLY	600	A	3G5U
LOC	TurnIV	ASP	598	A	VAL	601	A	3G5U
LOC	TurnII	SER	692	A	ARG	695	A	3G5U
LOC	TurnII	PRO	740	A	THR	743	A	3G5U
LOC	TurnIV	ASP	796	A	TRP	799	A	3G5U
LOC	TurnIV	VAL	797	A	PHE	800	A	3G5U
LOC	TurnIV	SER	798	A	ASP	801	A	3G5U
LOC	TurnI	TRP	799	A	ASP	802	A	3G5U
LOC	TurnIV	PHE	800	A	PRO	803	A	3G5U
LOC	TurnIV	TRP	851	A	THR	854	A	3G5U
LOC	TurnIV	ASN	899	A	THR	902	A	3G5U
LOC	TurnIV	PHE	900	A	VAL	903	A	3G5U
LOC	TurnIV	ARG	901	A	VAL	904	A	3G5U
LOC	TurnIV	THR	902	A	SER	905	A	3G5U
LOC	TurnI	VAL	903	A	LEU	906	A	3G5U
LOC	TurnIV	LEU	906	A	GLU	909	A	3G5U
LOC	TurnIV	ALA	957	A	VAL	960	A	3G5U
LOC	TurnII	VAL	960	A	GLN	963	A	3G5U
LOC	TurnIV	THR	961	A	LEU	964	A	3G5U
LOC	TurnIV	PRO	1012	A	ASP	1015	A	3G5U
LOC	TurnIV	SER	1018	A	GLY	1021	A	3G5U
LOC	TurnIV	LYS	1023	A	MET	1026	A	3G5U
LOC	TurnIV	ASN	1025	A	GLU	1028	A	3G5U
LOC	TurnIV	PHE	1033	A	VAL	1036	A	3G5U
LOC	TurnIV	ASN	1039	A	THR	1042	A	3G5U
LOC	TurnIV	TYR	1040	A	ARG	1043	A	3G5U
LOC	TurnIV	THR	1042	A	SER	1045	A	3G5U
LOC	TurnI	ARG	1043	A	ILE	1046	A	3G5U
LOC	TurnIV	PRO	1047	A	GLN	1050	A	3G5U
LOC	TurnIV	LEU	1049	A	LEU	1052	A	3G5U
LOC	TurnIV	LYS	1057	A	GLN	1060	A	3G5U
LOC	TurnIV	GLY	1069	A	LYS	1072	A	3G5U
LOC	TurnVIII	ARG	1081	A	ASP	1084	A	3G5U
LOC	TurnIV	PRO	1085	A	GLY	1088	A	3G5U
LOC	TurnIV	PHE	1091	A	GLY	1094	A	3G5U
LOC	TurnIV	GLU	1096	A	GLN	1099	A	3G5U
LOC	TurnIV	ILE	1097	A	LEU	1100	A	3G5U
LOC	TurnVIII	ARG	1106	A	LEU	1109	A	3G5U
LOC	TurnIV	SER	1113	A	PRO	1116	A	3G5U
LOC	TurnIV	ASP	1131	A	ARG	1134	A	3G5U
LOC	TurnII	LEU	1157	A	LYS	1160	A	3G5U
LOC	TurnIV	VAL	1165	A	LYS	1168	A	3G5U
LOC	TurnI'	GLY	1166	A	GLY	1169	A	3G5U
LOC	TurnIV	ASP	1167	A	THR	1170	A	3G5U
LOC	TurnIV	GLY	1169	A	LEU	1172	A	3G5U
LOC	TurnIV	LEU	1195	A	ALA	1198	A	3G5U
LOC	TurnIV	GLU	1197	A	SER	1200	A	3G5U
LOC	TurnIV	THR	1199	A	LEU	1202	A	3G5U
LOC	TurnIV	ALA	1217	A	GLY	1220	A	3G5U
LOC	TurnIV	ARG	1218	A	ARG	1221	A	3G5U
LOC	TurnIV	GLU	1219	A	THR	1222	A	3G5U
LOC	TurnIV	ARG	1229	A	THR	1232	A	3G5U
LOC	TurnI	LEU	1230	A	ILE	1233	A	3G5U
LOC	TurnI	SER	1231	A	GLN	1234	A	3G5U
LOC	TurnIV	THR	1232	A	ASN	1235	A	3G5U
LOC	TurnIV	ILE	1233	A	ALA	1236	A	3G5U
LOC	TurnVIII	ALA	1236	A	ILE	1239	A	3G5U
LOC	TurnIV	GLN	1243	A	LYS	1246	A	3G5U
LOC	GammaClassic	GLN	266	A	LYS	268	A	3G5U
LOC	GammaInv	HIS	583	A	LEU	585	A	3G5U
LOC	GammaInv	LEU	964	A	THR	966	A	3G5U
LOC	GammaInv	PRO	992	A	TYR	994	A	3G5U

LOC	GammaInv	LEU	1109	A	ILE	1111	A		3G5U
LOC	GammaInv	PHE	1119	A	CYS	1121	A		3G5U
LOC	GammaInv	TYR	1129	A	ASP	1131	A		3G5U
LOC	GammaInv	VAL	1135	A	SER	1137	A		3G5U
REM									3G5U
REM	----- Detailed secondary structure assignment-----								3G5U
REM									3G5U
REM	---Residue---		--Structure--		-Phi-	-Psi-	-Area-		3G5U
ASG	VAL A	33	1	C	Coil	360.00	-172.13	113.5	3G5U
ASG	SER A	34	2	C	Coil	1.86	-66.34	67.0	3G5U
ASG	VAL A	35	3	H	AlphaHelix	-50.42	-77.01	26.9	3G5U
ASG	LEU A	36	4	H	AlphaHelix	-73.23	-49.20	72.1	3G5U
ASG	THR A	37	5	H	AlphaHelix	-69.77	-60.54	68.0	3G5U
ASG	MET A	38	6	H	AlphaHelix	-49.23	-42.40	63.8	3G5U
ASG	PHE A	39	7	H	AlphaHelix	-50.98	-39.23	11.4	3G5U
ASG	ARG A	40	8	C	Coil	-116.31	69.88	86.2	3G5U
ASG	TYR A	41	9	C	Coil	-104.85	-159.71	47.3	3G5U
ASG	ALA A	42	10	C	Coil	47.82	93.92	21.0	3G5U
ASG	GLY A	43	11	C	Coil	161.66	99.12	13.2	3G5U
ASG	TRP A	44	12	H	AlphaHelix	-79.84	-95.19	201.1	3G5U
ASG	LEU A	45	13	H	AlphaHelix	-57.53	1.62	111.3	3G5U
ASG	ASP A	46	14	H	AlphaHelix	-82.72	-75.42	12.8	3G5U
ASG	ARG A	47	15	H	AlphaHelix	-42.38	-36.90	127.5	3G5U
ASG	LEU A	48	16	H	AlphaHelix	-73.44	-50.31	97.6	3G5U
ASG	TYR A	49	17	H	AlphaHelix	-57.48	-34.70	50.3	3G5U
ASG	MET A	50	18	H	AlphaHelix	-56.39	-65.83	7.0	3G5U
ASG	LEU A	51	19	H	AlphaHelix	-53.15	-31.98	95.0	3G5U
ASG	VAL A	52	20	H	AlphaHelix	-58.60	-65.96	73.5	3G5U
ASG	GLY A	53	21	H	AlphaHelix	-49.07	-38.97	0.0	3G5U
ASG	THR A	54	22	H	AlphaHelix	-53.19	-56.44	13.8	3G5U
ASG	LEU A	55	23	H	AlphaHelix	-43.01	-56.73	114.7	3G5U
ASG	ALA A	56	24	H	AlphaHelix	-46.58	-45.34	3.4	3G5U
ASG	ALA A	57	25	H	AlphaHelix	-52.23	-53.11	0.0	3G5U
ASG	ILE A	58	26	H	AlphaHelix	-46.23	-72.43	32.5	3G5U
ASG	ILE A	59	27	H	AlphaHelix	-43.56	-43.80	70.4	3G5U
ASG	HIS A	60	28	H	AlphaHelix	-52.98	-52.49	2.6	3G5U
ASG	GLY A	61	29	H	AlphaHelix	-59.02	-44.25	0.0	3G5U
ASG	VAL A	62	30	H	AlphaHelix	-56.03	-31.50	28.1	3G5U
ASG	ALA A	63	31	H	AlphaHelix	-56.53	-54.92	10.3	3G5U
ASG	LEU A	64	32	H	AlphaHelix	-48.86	-49.41	57.5	3G5U
ASG	PRO A	65	33	H	AlphaHelix	-81.27	-23.36	0.4	3G5U
ASG	LEU A	66	34	H	AlphaHelix	-58.00	-46.58	72.8	3G5U
ASG	MET A	67	35	H	AlphaHelix	-49.30	-38.94	6.5	3G5U
ASG	MET A	68	36	H	AlphaHelix	-57.70	-65.52	13.2	3G5U
ASG	LEU A	69	37	H	AlphaHelix	-37.57	-61.00	46.7	3G5U
ASG	ILE A	70	38	H	AlphaHelix	-50.12	-43.19	47.9	3G5U
ASG	PHE A	71	39	H	AlphaHelix	-53.14	-35.34	23.9	3G5U
ASG	GLY A	72	40	H	AlphaHelix	-63.66	-63.32	0.0	3G5U
ASG	ASP A	73	41	H	AlphaHelix	-52.63	-35.66	87.4	3G5U
ASG	MET A	74	42	H	AlphaHelix	-66.08	-42.06	3.8	3G5U
ASG	THR A	75	43	H	AlphaHelix	-64.72	-35.24	20.5	3G5U
ASG	ASP A	76	44	H	AlphaHelix	-65.65	-53.58	39.3	3G5U
ASG	SER A	77	45	H	AlphaHelix	-51.04	-31.68	31.9	3G5U
ASG	PHE A	78	46	H	AlphaHelix	-66.05	-34.53	54.6	3G5U
ASG	ALA A	79	47	H	AlphaHelix	-72.54	-49.95	16.2	3G5U
ASG	SER A	80	48	H	AlphaHelix	-53.05	-44.52	72.6	3G5U
ASG	VAL A	81	49	H	AlphaHelix	-66.83	-34.74	18.7	3G5U
ASG	GLY A	82	50	H	AlphaHelix	-79.07	-22.27	14.3	3G5U
ASG	ASN A	83	51	H	AlphaHelix	-71.66	-51.27	97.4	3G5U
ASG	VAL A	84	52	H	AlphaHelix	-69.80	-24.28	59.6	3G5U
ASG	SER A	85	53	H	AlphaHelix	-65.67	-41.00	29.1	3G5U
ASG	LYS A	86	54	H	AlphaHelix	-60.30	-46.07	124.4	3G5U
ASG	ASN A	87	55	H	AlphaHelix	-59.33	-61.07	79.4	3G5U
ASG	SER A	88	56	C	Coil	31.41	-136.82	31.7	3G5U
ASG	THR A	89	57	C	Coil	46.34	14.85	121.4	3G5U
ASG	ASN A	90	58	C	Coil	-139.72	-157.20	89.5	3G5U
ASG	MET A	91	59	C	Coil	-37.12	92.42	88.7	3G5U
ASG	SER A	92	60	H	AlphaHelix	-56.31	-53.22	50.0	3G5U
ASG	GLU A	93	61	H	AlphaHelix	-53.38	-38.46	104.7	3G5U
ASG	ALA A	94	62	H	AlphaHelix	-71.81	-8.75	24.7	3G5U
ASG	ASP A	95	63	H	AlphaHelix	-90.42	-36.41	4.4	3G5U
ASG	LYS A	96	64	H	AlphaHelix	-66.44	-32.67	74.5	3G5U
ASG	ARG A	97	65	H	AlphaHelix	-81.19	-49.83	183.3	3G5U
ASG	ALA A	98	66	H	AlphaHelix	-57.45	-40.30	37.7	3G5U

ASG	MET	A	99	67	H	AlphaHelix	-71.19	-61.88	4.0	3G5U
ASG	PHE	A	100	68	H	AlphaHelix	-56.05	-19.00	103.2	3G5U
ASG	ALA	A	101	69	H	AlphaHelix	-61.97	-75.07	28.2	3G5U
ASG	LYS	A	102	70	H	AlphaHelix	-60.28	-23.86	77.3	3G5U
ASG	LEU	A	103	71	H	AlphaHelix	-63.53	-76.45	12.9	3G5U
ASG	GLU	A	104	72	H	AlphaHelix	-53.02	-40.43	109.8	3G5U
ASG	GLU	A	105	73	H	AlphaHelix	-54.43	-62.31	69.4	3G5U
ASG	GLU	A	106	74	H	AlphaHelix	-67.91	-14.45	8.6	3G5U
ASG	MET	A	107	75	H	AlphaHelix	-66.81	-31.48	48.9	3G5U
ASG	THR	A	108	76	H	AlphaHelix	-73.78	-46.38	69.1	3G5U
ASG	THR	A	109	77	H	AlphaHelix	-56.43	-42.22	50.7	3G5U
ASG	TYR	A	110	78	H	AlphaHelix	-60.17	-50.59	13.4	3G5U
ASG	ALA	A	111	79	H	AlphaHelix	-47.61	-58.62	30.0	3G5U
ASG	TYR	A	112	80	H	AlphaHelix	-63.12	-16.67	168.2	3G5U
ASG	TYR	A	113	81	H	AlphaHelix	-81.28	-57.34	5.3	3G5U
ASG	TYR	A	114	82	H	AlphaHelix	-56.43	-38.91	89.8	3G5U
ASG	THR	A	115	83	H	AlphaHelix	-55.32	-90.80	53.0	3G5U
ASG	GLY	A	116	84	H	AlphaHelix	-25.15	-59.00	50.2	3G5U
ASG	ILE	A	117	85	H	AlphaHelix	-64.34	-70.48	17.5	3G5U
ASG	GLY	A	118	86	H	AlphaHelix	-34.66	-70.31	0.0	3G5U
ASG	ALA	A	119	87	H	AlphaHelix	-49.73	-46.15	49.7	3G5U
ASG	GLY	A	120	88	H	AlphaHelix	-42.53	-73.31	26.4	3G5U
ASG	VAL	A	121	89	H	AlphaHelix	-46.59	-61.38	1.3	3G5U
ASG	LEU	A	122	90	H	AlphaHelix	-35.18	-60.56	62.0	3G5U
ASG	ILE	A	123	91	H	AlphaHelix	-54.11	-57.77	112.7	3G5U
ASG	VAL	A	124	92	H	AlphaHelix	-74.16	-24.54	15.0	3G5U
ASG	ALA	A	125	93	H	AlphaHelix	-64.54	-58.70	0.0	3G5U
ASG	TYR	A	126	94	H	AlphaHelix	-46.04	-36.12	68.3	3G5U
ASG	ILE	A	127	95	H	AlphaHelix	-68.50	-53.13	46.1	3G5U
ASG	GLN	A	128	96	H	AlphaHelix	-59.88	-24.81	2.0	3G5U
ASG	VAL	A	129	97	H	AlphaHelix	-79.26	-30.19	11.5	3G5U
ASG	SER	A	130	98	H	AlphaHelix	-62.94	-22.07	15.3	3G5U
ASG	PHE	A	131	99	H	AlphaHelix	-63.78	-67.72	0.4	3G5U
ASG	TRP	A	132	100	H	AlphaHelix	-28.87	-81.01	55.3	3G5U
ASG	CYS	A	133	101	H	AlphaHelix	-72.78	-44.96	8.0	3G5U
ASG	LEU	A	134	102	H	AlphaHelix	-43.83	-52.98	52.9	3G5U
ASG	ALA	A	135	103	H	AlphaHelix	-55.30	-98.03	3.5	3G5U
ASG	ALA	A	136	104	H	AlphaHelix	-28.27	-44.13	0.0	3G5U
ASG	GLY	A	137	105	H	AlphaHelix	-49.46	-74.73	20.9	3G5U
ASG	ARG	A	138	106	H	AlphaHelix	-53.47	-40.47	85.4	3G5U
ASG	GLN	A	139	107	H	AlphaHelix	-55.76	-43.10	17.4	3G5U
ASG	ILE	A	140	108	H	AlphaHelix	-73.72	-51.76	3.4	3G5U
ASG	HIS	A	141	109	H	AlphaHelix	-37.86	-57.80	30.7	3G5U
ASG	LYS	A	142	110	H	AlphaHelix	-51.54	-59.44	93.1	3G5U
ASG	ILE	A	143	111	H	AlphaHelix	-45.07	-76.82	9.2	3G5U
ASG	ARG	A	144	112	H	AlphaHelix	-22.51	-64.38	43.3	3G5U
ASG	GLN	A	145	113	H	AlphaHelix	-60.62	-43.31	80.6	3G5U
ASG	LYS	A	146	114	H	AlphaHelix	-57.82	-50.25	93.8	3G5U
ASG	PHE	A	147	115	H	AlphaHelix	-59.50	-49.96	3.8	3G5U
ASG	PHE	A	148	116	H	AlphaHelix	-45.02	-61.01	7.6	3G5U
ASG	HIS	A	149	117	H	AlphaHelix	-64.29	-28.53	61.1	3G5U
ASG	ALA	A	150	118	H	AlphaHelix	-63.36	-63.42	9.3	3G5U
ASG	ILE	A	151	119	H	AlphaHelix	-43.37	-62.97	8.7	3G5U
ASG	MET	A	152	120	H	AlphaHelix	-50.91	0.71	5.3	3G5U
ASG	ASN	A	153	121	T	Turn	-122.43	-11.63	15.6	3G5U
ASG	GLN	A	154	122	T	Turn	-60.08	-3.69	51.3	3G5U
ASG	GLU	A	155	123	G	310Helix	34.64	-135.80	2.1	3G5U
ASG	ILE	A	156	124	G	310Helix	-61.09	23.01	9.5	3G5U
ASG	GLY	A	157	125	G	310Helix	-103.47	-29.56	8.2	3G5U
ASG	TRP	A	158	126	H	AlphaHelix	-63.65	4.47	10.5	3G5U
ASG	PHE	A	159	127	H	AlphaHelix	-133.73	-44.48	119.8	3G5U
ASG	ASP	A	160	128	H	AlphaHelix	-42.43	-42.96	43.9	3G5U
ASG	VAL	A	161	129	C	Coil	-147.63	-147.72	89.8	3G5U
ASG	HIS	A	162	130	C	Coil	62.45	117.91	70.2	3G5U
ASG	ASP	A	163	131	C	Coil	-56.39	-16.36	130.4	3G5U
ASG	VAL	A	164	132	C	Coil	64.50	-24.16	35.3	3G5U
ASG	GLY	A	165	133	H	AlphaHelix	-96.84	-61.06	32.8	3G5U
ASG	GLU	A	166	134	H	AlphaHelix	-48.22	-25.10	72.2	3G5U
ASG	LEU	A	167	135	H	AlphaHelix	-70.86	-76.45	14.2	3G5U
ASG	ASN	A	168	136	H	AlphaHelix	-39.92	-46.28	29.6	3G5U
ASG	THR	A	169	137	H	AlphaHelix	-47.13	-56.11	71.6	3G5U
ASG	ARG	A	170	138	H	AlphaHelix	-63.39	-29.88	54.4	3G5U
ASG	LEU	A	171	139	H	AlphaHelix	-50.24	-60.31	12.4	3G5U
ASG	THR	A	172	140	H	AlphaHelix	-67.79	-59.43	46.3	3G5U

ASG	ASP	A	173	141	H	AlphaHelix	-39.57	-62.32	85.5	3G5U
ASG	ASP	A	174	142	H	AlphaHelix	-62.17	-58.95	19.0	3G5U
ASG	VAL	A	175	143	H	AlphaHelix	-35.40	-52.09	3.8	3G5U
ASG	SER	A	176	144	H	AlphaHelix	-59.97	-49.96	39.7	3G5U
ASG	LYS	A	177	145	H	AlphaHelix	-54.76	-24.43	100.9	3G5U
ASG	ILE	A	178	146	H	AlphaHelix	-67.22	-53.94	6.4	3G5U
ASG	ASN	A	179	147	H	AlphaHelix	-45.17	-61.49	37.7	3G5U
ASG	GLU	A	180	148	H	AlphaHelix	-48.99	-41.02	104.2	3G5U
ASG	GLY	A	181	149	H	AlphaHelix	-50.38	-44.99	0.9	3G5U
ASG	ILE	A	182	150	H	AlphaHelix	-71.65	-59.01	7.6	3G5U
ASG	GLY	A	183	151	H	AlphaHelix	-65.61	-27.73	1.7	3G5U
ASG	ASP	A	184	152	H	AlphaHelix	-73.41	-49.01	43.7	3G5U
ASG	LYS	A	185	153	H	AlphaHelix	-43.45	-39.80	7.2	3G5U
ASG	ILE	A	186	154	H	AlphaHelix	-57.25	-57.17	6.2	3G5U
ASG	GLY	A	187	155	H	AlphaHelix	-39.08	-56.34	14.6	3G5U
ASG	MET	A	188	156	H	AlphaHelix	-47.63	-72.52	29.5	3G5U
ASG	PHE	A	189	157	H	AlphaHelix	-25.33	-65.59	73.4	3G5U
ASG	PHE	A	190	158	H	AlphaHelix	-39.88	-71.90	29.3	3G5U
ASG	GLN	A	191	159	H	AlphaHelix	-55.21	-38.36	39.3	3G5U
ASG	ALA	A	192	160	H	AlphaHelix	-49.98	-34.28	31.6	3G5U
ASG	MET	A	193	161	H	AlphaHelix	-89.51	-26.76	43.7	3G5U
ASG	ALA	A	194	162	H	AlphaHelix	-68.82	-33.66	1.4	3G5U
ASG	THR	A	195	163	H	AlphaHelix	-74.43	-54.35	19.8	3G5U
ASG	PHE	A	196	164	H	AlphaHelix	-51.72	-68.25	141.9	3G5U
ASG	PHE	A	197	165	H	AlphaHelix	-60.95	-37.24	63.9	3G5U
ASG	GLY	A	198	166	H	AlphaHelix	-56.02	-79.17	1.3	3G5U
ASG	GLY	A	199	167	H	AlphaHelix	-37.98	-21.05	19.8	3G5U
ASG	PHE	A	200	168	H	AlphaHelix	-93.85	-91.76	113.0	3G5U
ASG	ILE	A	201	169	T	Turn	-15.77	-69.69	48.3	3G5U
ASG	ILE	A	202	170	T	Turn	-77.16	-46.11	2.2	3G5U
ASG	GLY	A	203	171	T	Turn	-51.88	4.41	0.5	3G5U
ASG	PHE	A	204	172	T	Turn	-147.03	-71.19	107.0	3G5U
ASG	THR	A	205	173	T	Turn	-32.11	-53.28	65.3	3G5U
ASG	ARG	A	206	174	T	Turn	-92.65	107.89	121.7	3G5U
ASG	GLY	A	207	175	T	Turn	132.34	-35.02	11.6	3G5U
ASG	TRP	A	208	176	T	Turn	43.04	77.82	186.4	3G5U
ASG	LYS	A	209	177	T	Turn	85.15	-15.75	137.8	3G5U
ASG	LEU	A	210	178	H	AlphaHelix	-97.32	-43.14	6.6	3G5U
ASG	THR	A	211	179	H	AlphaHelix	-63.71	-15.71	0.0	3G5U
ASG	LEU	A	212	180	H	AlphaHelix	-88.24	-31.55	75.6	3G5U
ASG	VAL	A	213	181	H	AlphaHelix	-53.43	-42.29	28.1	3G5U
ASG	ILE	A	214	182	H	AlphaHelix	-52.72	-85.78	0.0	3G5U
ASG	LEU	A	215	183	H	AlphaHelix	-22.55	-54.45	55.4	3G5U
ASG	ALA	A	216	184	H	AlphaHelix	-57.04	-103.19	44.7	3G5U
ASG	ILE	A	217	185	H	AlphaHelix	-34.77	-62.86	43.3	3G5U
ASG	SER	A	218	186	H	AlphaHelix	-47.97	-88.11	16.3	3G5U
ASG	PRO	A	219	187	H	AlphaHelix	-36.35	-27.83	55.9	3G5U
ASG	VAL	A	220	188	H	AlphaHelix	-73.50	-50.71	81.9	3G5U
ASG	LEU	A	221	189	H	AlphaHelix	-55.11	-53.82	30.7	3G5U
ASG	GLY	A	222	190	H	AlphaHelix	-46.28	-31.05	38.5	3G5U
ASG	LEU	A	223	191	H	AlphaHelix	-67.16	-55.39	108.6	3G5U
ASG	SER	A	224	192	H	AlphaHelix	-53.75	-38.21	51.7	3G5U
ASG	ALA	A	225	193	H	AlphaHelix	-60.72	-64.56	10.3	3G5U
ASG	GLY	A	226	194	H	AlphaHelix	-42.59	-52.32	30.4	3G5U
ASG	ILE	A	227	195	H	AlphaHelix	-63.91	-75.36	104.6	3G5U
ASG	TRP	A	228	196	H	AlphaHelix	-44.69	-56.11	158.1	3G5U
ASG	ALA	A	229	197	H	AlphaHelix	-50.24	-68.12	1.6	3G5U
ASG	LYS	A	230	198	H	AlphaHelix	-51.41	-30.57	120.4	3G5U
ASG	ILE	A	231	199	H	AlphaHelix	-57.17	-64.60	81.8	3G5U
ASG	LEU	A	232	200	H	AlphaHelix	-54.66	-39.16	25.9	3G5U
ASG	SER	A	233	201	H	AlphaHelix	-52.63	-46.60	37.6	3G5U
ASG	SER	A	234	202	H	AlphaHelix	-61.97	-45.79	78.2	3G5U
ASG	PHE	A	235	203	H	AlphaHelix	-47.91	-41.92	94.0	3G5U
ASG	THR	A	236	204	H	AlphaHelix	-60.11	-57.10	13.4	3G5U
ASG	ASP	A	237	205	H	AlphaHelix	-49.12	-52.46	88.2	3G5U
ASG	LYS	A	238	206	H	AlphaHelix	-48.75	-47.83	115.1	3G5U
ASG	GLU	A	239	207	H	AlphaHelix	-52.68	-47.50	38.9	3G5U
ASG	LEU	A	240	208	H	AlphaHelix	-61.00	-39.35	69.9	3G5U
ASG	HIS	A	241	209	H	AlphaHelix	-61.30	-53.17	122.7	3G5U
ASG	ALA	A	242	210	H	AlphaHelix	-55.48	-38.18	23.2	3G5U
ASG	TYR	A	243	211	H	AlphaHelix	-50.39	-65.76	54.9	3G5U
ASG	ALA	A	244	212	H	AlphaHelix	-38.67	-42.78	56.8	3G5U
ASG	LYS	A	245	213	H	AlphaHelix	-61.55	-55.26	138.6	3G5U
ASG	ALA	A	246	214	H	AlphaHelix	-52.31	-34.06	2.4	3G5U

ASG	GLY	A	247	215	H	AlphaHelix	-70.12	-29.37	10.9	3G5U
ASG	ALA	A	248	216	H	AlphaHelix	-73.45	-43.50	56.7	3G5U
ASG	VAL	A	249	217	H	AlphaHelix	-73.34	2.63	69.8	3G5U
ASG	ALA	A	250	218	T	Turn	-101.87	-4.46	3.8	3G5U
ASG	GLU	A	251	219	T	Turn	-97.99	-72.24	52.9	3G5U
ASG	GLU	A	252	220	T	Turn	63.37	-162.01	69.0	3G5U
ASG	VAL	A	253	221	C	Coil	-85.29	161.73	64.4	3G5U
ASG	LEU	A	254	222	T	Turn	-158.71	7.54	52.8	3G5U
ASG	ALA	A	255	223	T	Turn	-109.55	-166.08	28.5	3G5U
ASG	ALA	A	256	224	T	Turn	65.75	0.11	49.2	3G5U
ASG	ILE	A	257	225	H	AlphaHelix	-38.10	-35.13	26.5	3G5U
ASG	ARG	A	258	226	H	AlphaHelix	-53.34	-56.21	127.3	3G5U
ASG	THR	A	259	227	H	AlphaHelix	-55.95	-33.24	49.5	3G5U
ASG	VAL	A	260	228	H	AlphaHelix	-79.94	-15.01	22.5	3G5U
ASG	ILE	A	261	229	H	AlphaHelix	-81.38	-36.43	12.9	3G5U
ASG	ALA	A	262	230	H	AlphaHelix	-79.16	3.29	16.2	3G5U
ASG	PHE	A	263	231	C	Coil	-98.45	-47.58	45.4	3G5U
ASG	GLY	A	264	232	C	Coil	139.48	-68.55	25.9	3G5U
ASG	GLY	A	265	233	C	Coil	156.40	110.65	14.7	3G5U
ASG	GLN	A	266	234	T	Turn	-52.33	-71.61	43.5	3G5U
ASG	LYS	A	267	235	T	Turn	71.53	-28.63	81.6	3G5U
ASG	LYS	A	268	236	H	AlphaHelix	-119.11	-30.46	119.7	3G5U
ASG	GLU	A	269	237	H	AlphaHelix	-69.36	-47.40	98.2	3G5U
ASG	LEU	A	270	238	H	AlphaHelix	-51.01	-66.76	15.1	3G5U
ASG	GLU	A	271	239	H	AlphaHelix	-47.76	-52.05	51.5	3G5U
ASG	ARG	A	272	240	H	AlphaHelix	-42.16	-68.95	123.3	3G5U
ASG	TYR	A	273	241	H	AlphaHelix	-62.32	-40.07	109.8	3G5U
ASG	ASN	A	274	242	H	AlphaHelix	-45.25	-86.18	5.6	3G5U
ASG	ASN	A	275	243	H	AlphaHelix	-48.77	-24.38	29.6	3G5U
ASG	ASN	A	276	244	H	AlphaHelix	-57.87	-85.29	63.9	3G5U
ASG	LEU	A	277	245	H	AlphaHelix	-54.26	-43.35	41.7	3G5U
ASG	GLU	A	278	246	H	AlphaHelix	-52.71	-65.03	0.6	3G5U
ASG	GLU	A	279	247	H	AlphaHelix	-41.99	-55.53	90.0	3G5U
ASG	ALA	A	280	248	H	AlphaHelix	-37.29	-84.43	44.2	3G5U
ASG	LYS	A	281	249	H	AlphaHelix	-65.40	-2.40	43.6	3G5U
ASG	ARG	A	282	250	H	AlphaHelix	-65.62	-88.34	0.2	3G5U
ASG	LEU	A	283	251	H	AlphaHelix	-46.01	-34.13	97.4	3G5U
ASG	GLY	A	284	252	H	AlphaHelix	-61.00	-69.79	20.1	3G5U
ASG	ILE	A	285	253	H	AlphaHelix	-64.89	-4.08	3.5	3G5U
ASG	LYS	A	286	254	T	Turn	-91.36	-11.70	6.3	3G5U
ASG	LYS	A	287	255	T	Turn	-86.14	-43.27	135.9	3G5U
ASG	ALA	A	288	256	T	Turn	-72.33	-23.30	0.0	3G5U
ASG	ILE	A	289	257	H	AlphaHelix	-67.53	-67.18	42.9	3G5U
ASG	THR	A	290	258	H	AlphaHelix	-61.68	6.93	19.8	3G5U
ASG	ALA	A	291	259	H	AlphaHelix	-110.08	-23.31	4.6	3G5U
ASG	ASN	A	292	260	H	AlphaHelix	-75.81	-40.04	85.0	3G5U
ASG	ILE	A	293	261	H	AlphaHelix	-60.57	-65.87	5.6	3G5U
ASG	SER	A	294	262	H	AlphaHelix	-48.99	-18.65	34.1	3G5U
ASG	MET	A	295	263	H	AlphaHelix	-82.41	-43.00	8.8	3G5U
ASG	GLY	A	296	264	H	AlphaHelix	-53.49	-43.31	19.5	3G5U
ASG	ALA	A	297	265	H	AlphaHelix	-56.22	-39.77	0.6	3G5U
ASG	ALA	A	298	266	H	AlphaHelix	-61.15	-89.62	11.3	3G5U
ASG	PHE	A	299	267	H	AlphaHelix	-30.56	-45.21	95.0	3G5U
ASG	LEU	A	300	268	H	AlphaHelix	-74.80	-47.39	57.7	3G5U
ASG	LEU	A	301	269	H	AlphaHelix	-54.00	-53.62	43.1	3G5U
ASG	ILE	A	302	270	H	AlphaHelix	-65.29	-17.45	38.0	3G5U
ASG	TYR	A	303	271	H	AlphaHelix	-66.89	-66.14	59.6	3G5U
ASG	ALA	A	304	272	H	AlphaHelix	-53.81	-22.07	0.8	3G5U
ASG	SER	A	305	273	H	AlphaHelix	-65.61	-43.63	18.4	3G5U
ASG	TYR	A	306	274	H	AlphaHelix	-46.28	-59.47	22.6	3G5U
ASG	ALA	A	307	275	H	AlphaHelix	-45.09	-46.80	0.6	3G5U
ASG	LEU	A	308	276	H	AlphaHelix	-47.17	-93.49	53.5	3G5U
ASG	ALA	A	309	277	H	AlphaHelix	-43.60	-33.61	8.3	3G5U
ASG	PHE	A	310	278	H	AlphaHelix	-46.04	-89.28	2.2	3G5U
ASG	TRP	A	311	279	H	AlphaHelix	-52.53	-40.94	6.6	3G5U
ASG	TYR	A	312	280	H	AlphaHelix	-53.71	-83.68	115.9	3G5U
ASG	GLY	A	313	281	H	AlphaHelix	-40.58	-28.17	16.1	3G5U
ASG	THR	A	314	282	H	AlphaHelix	-68.16	-64.86	7.2	3G5U
ASG	SER	A	315	283	H	AlphaHelix	-47.17	-54.79	1.4	3G5U
ASG	LEU	A	316	284	H	AlphaHelix	-51.23	-55.17	61.9	3G5U
ASG	VAL	A	317	285	H	AlphaHelix	-73.94	24.27	13.1	3G5U
ASG	ILE	A	318	286	H	AlphaHelix	-133.35	-14.42	7.2	3G5U
ASG	SER	A	319	287	H	AlphaHelix	-99.07	-27.03	55.5	3G5U
ASG	LYS	A	320	288	H	AlphaHelix	-88.83	-94.98	149.1	3G5U

ASG	GLU	A	321	289	T	Turn	-89.90	177.10	127.9	3G5U
ASG	TYR	A	322	290	T	Turn	35.27	46.67	80.4	3G5U
ASG	SER	A	323	291	T	Turn	-69.86	93.09	74.2	3G5U
ASG	ILE	A	324	292	C	Coil	-131.76	-20.74	41.0	3G5U
ASG	GLY	A	325	293	C	Coil	64.10	21.78	12.8	3G5U
ASG	GLN	A	326	294	H	AlphaHelix	-124.97	14.66	3.9	3G5U
ASG	VAL	A	327	295	H	AlphaHelix	-71.38	-21.77	2.4	3G5U
ASG	LEU	A	328	296	H	AlphaHelix	-39.28	-82.89	6.4	3G5U
ASG	THR	A	329	297	H	AlphaHelix	-25.80	-59.31	2.2	3G5U
ASG	VAL	A	330	298	H	AlphaHelix	-56.96	-87.43	0.0	3G5U
ASG	PHE	A	331	299	H	AlphaHelix	-37.61	-59.20	0.4	3G5U
ASG	PHE	A	332	300	H	AlphaHelix	-42.74	-47.27	32.7	3G5U
ASG	SER	A	333	301	H	AlphaHelix	-67.24	-44.68	0.3	3G5U
ASG	VAL	A	334	302	H	AlphaHelix	-55.00	-40.58	14.4	3G5U
ASG	LEU	A	335	303	H	AlphaHelix	-52.29	-49.66	26.5	3G5U
ASG	ILE	A	336	304	H	AlphaHelix	-47.07	-38.51	43.5	3G5U
ASG	GLY	A	337	305	H	AlphaHelix	-56.11	-56.55	4.4	3G5U
ASG	ALA	A	338	306	H	AlphaHelix	-48.55	-63.57	59.3	3G5U
ASG	PHE	A	339	307	H	AlphaHelix	-40.56	-48.51	130.5	3G5U
ASG	SER	A	340	308	H	AlphaHelix	-61.20	-34.65	3.0	3G5U
ASG	VAL	A	341	309	H	AlphaHelix	-62.87	-27.92	84.3	3G5U
ASG	GLY	A	342	310	H	AlphaHelix	-63.77	-64.79	32.5	3G5U
ASG	GLN	A	343	311	H	AlphaHelix	-48.58	-43.24	111.9	3G5U
ASG	ALA	A	344	312	H	AlphaHelix	-51.08	-46.28	12.2	3G5U
ASG	SER	A	345	313	H	AlphaHelix	-55.92	-53.30	76.6	3G5U
ASG	PRO	A	346	314	H	AlphaHelix	-60.63	-39.55	70.8	3G5U
ASG	ASN	A	347	315	H	AlphaHelix	-54.96	-45.25	34.7	3G5U
ASG	ILE	A	348	316	H	AlphaHelix	-58.58	-50.28	75.2	3G5U
ASG	GLU	A	349	317	H	AlphaHelix	-43.87	-58.15	125.0	3G5U
ASG	ALA	A	350	318	H	AlphaHelix	-42.73	-56.36	23.7	3G5U
ASG	PHE	A	351	319	H	AlphaHelix	-48.03	-73.13	41.1	3G5U
ASG	ALA	A	352	320	H	AlphaHelix	-38.70	-45.37	47.0	3G5U
ASG	ASN	A	353	321	H	AlphaHelix	-60.00	-57.75	91.4	3G5U
ASG	ALA	A	354	322	H	AlphaHelix	-55.11	-33.82	1.5	3G5U
ASG	ARG	A	355	323	H	AlphaHelix	-63.81	-68.48	70.0	3G5U
ASG	GLY	A	356	324	H	AlphaHelix	-37.07	-57.33	20.7	3G5U
ASG	ALA	A	357	325	H	AlphaHelix	-47.29	-80.88	25.8	3G5U
ASG	ALA	A	358	326	H	AlphaHelix	-47.93	-86.20	1.0	3G5U
ASG	TYR	A	359	327	H	AlphaHelix	-20.84	-59.08	51.6	3G5U
ASG	GLU	A	360	328	H	AlphaHelix	-69.97	-61.47	92.2	3G5U
ASG	VAL	A	361	329	H	AlphaHelix	-79.44	26.86	22.8	3G5U
ASG	PHE	A	362	330	H	AlphaHelix	-109.50	-34.84	6.6	3G5U
ASG	LYS	A	363	331	H	AlphaHelix	-72.08	-17.38	125.6	3G5U
ASG	ILE	A	364	332	H	AlphaHelix	-85.23	-28.83	86.4	3G5U
ASG	ILE	A	365	333	T	Turn	-78.55	-92.89	3.9	3G5U
ASG	ASP	A	366	334	T	Turn	-35.28	-82.22	36.7	3G5U
ASG	ASN	A	367	335	T	Turn	0.67	135.54	56.6	3G5U
ASG	LYS	A	368	336	C	Coil	-116.46	58.32	99.3	3G5U
ASG	PRO	A	369	337	C	Coil	-43.61	-84.04	69.6	3G5U
ASG	SER	A	370	338	T	Turn	48.07	-132.62	22.5	3G5U
ASG	ILE	A	371	339	T	Turn	64.56	-25.25	141.9	3G5U
ASG	ASP	A	372	340	T	Turn	-81.84	16.62	51.0	3G5U
ASG	SER	A	373	341	T	Turn	171.56	-61.27	8.8	3G5U
ASG	PHE	A	374	342	T	Turn	69.29	-169.38	83.1	3G5U
ASG	SER	A	375	343	C	Coil	178.99	59.38	26.6	3G5U
ASG	LYS	A	376	344	C	Coil	-144.66	-175.85	110.4	3G5U
ASG	SER	A	377	345	C	Coil	-7.98	-108.65	86.5	3G5U
ASG	GLY	A	378	346	C	Coil	89.50	-157.69	64.1	3G5U
ASG	HIS	A	379	347	C	Coil	-111.32	146.62	85.1	3G5U
ASG	LYS	A	380	348	C	Coil	-129.91	104.14	109.6	3G5U
ASG	PRO	A	381	349	T	Turn	-90.06	81.56	8.9	3G5U
ASG	ASP	A	382	350	T	Turn	-84.49	6.18	88.1	3G5U
ASG	ASN	A	383	351	T	Turn	-60.91	-16.90	76.5	3G5U
ASG	ILE	A	384	352	T	Turn	62.57	-154.19	90.2	3G5U
ASG	GLN	A	385	353	C	Coil	6.87	150.89	73.4	3G5U
ASG	GLY	A	386	354	C	Coil	161.89	172.14	7.4	3G5U
ASG	ASN	A	387	355	C	Coil	-105.23	151.82	49.5	3G5U
ASG	LEU	A	388	356	E	Strand	-84.44	152.53	2.4	3G5U
ASG	GLU	A	389	357	E	Strand	-142.98	93.78	53.1	3G5U
ASG	PHE	A	390	358	E	Strand	-85.11	107.99	11.2	3G5U
ASG	LYS	A	391	359	E	Strand	-113.95	116.65	124.6	3G5U
ASG	ASN	A	392	360	T	Turn	38.10	66.83	70.2	3G5U
ASG	ILE	A	393	361	E	Strand	-112.77	124.50	1.6	3G5U
ASG	HIS	A	394	362	E	Strand	-102.15	155.00	60.7	3G5U

ASG	PHE	A	395	363	E	Strand	-174.19	142.47	9.8	3G5U
ASG	SER	A	396	364	C	Coil	-125.24	148.44	8.9	3G5U
ASG	TYR	A	397	365	T	Turn	-51.63	168.01	70.7	3G5U
ASG	PRO	A	398	366	T	Turn	-54.49	-28.80	49.9	3G5U
ASG	SER	A	399	367	T	Turn	-67.07	68.88	55.2	3G5U
ASG	ARG	A	400	368	T	Turn	7.79	-32.88	232.0	3G5U
ASG	LYS	A	401	369	T	Turn	-116.17	-19.57	168.1	3G5U
ASG	GLU	A	402	370	T	Turn	-50.65	158.11	89.0	3G5U
ASG	VAL	A	403	371	C	Coil	-57.75	143.54	100.9	3G5U
ASG	GLN	A	404	372	T	Turn	-66.30	82.85	92.6	3G5U
ASG	ILE	A	405	373	T	Turn	-32.48	-56.43	7.4	3G5U
ASG	LEU	A	406	374	E	Strand	-81.09	92.21	5.9	3G5U
ASG	LYS	A	407	375	E	Strand	-85.06	36.06	86.8	3G5U
ASG	GLY	A	408	376	E	Strand	99.16	89.90	22.0	3G5U
ASG	LEU	A	409	377	E	Strand	-128.87	138.61	1.8	3G5U
ASG	ASN	A	410	378	C	Coil	-122.78	142.40	90.5	3G5U
ASG	LEU	A	411	379	E	Strand	-173.99	153.06	20.1	3G5U
ASG	LYS	A	412	380	E	Strand	-142.75	156.43	126.2	3G5U
ASG	VAL	A	413	381	E	Strand	-153.06	116.85	7.0	3G5U
ASG	LYS	A	414	382	T	Turn	-57.73	167.80	104.4	3G5U
ASG	SER	A	415	383	T	Turn	-70.14	175.68	54.6	3G5U
ASG	GLY	A	416	384	T	Turn	40.06	-6.57	22.7	3G5U
ASG	GLN	A	417	385	T	Turn	-74.94	-170.46	43.5	3G5U
ASG	THR	A	418	386	E	Strand	-157.63	119.84	8.0	3G5U
ASG	VAL	A	419	387	E	Strand	-110.06	141.27	3.6	3G5U
ASG	ALA	A	420	388	E	Strand	-104.07	130.06	3.6	3G5U
ASG	LEU	A	421	389	E	Strand	-107.32	133.69	4.2	3G5U
ASG	VAL	A	422	390	E	Strand	-120.67	111.80	13.9	3G5U
ASG	GLY	A	423	391	T	Turn	-143.04	-176.48	8.6	3G5U
ASG	ASN	A	424	392	T	Turn	-157.48	-52.93	84.0	3G5U
ASG	SER	A	425	393	T	Turn	-66.33	20.76	78.6	3G5U
ASG	GLY	A	426	394	T	Turn	56.42	-174.16	25.1	3G5U
ASG	CYS	A	427	395	C	Coil	64.46	33.65	77.5	3G5U
ASG	GLY	A	428	396	C	Coil	-160.19	-77.52	0.8	3G5U
ASG	LYS	A	429	397	H	AlphaHelix	-21.95	-80.32	7.0	3G5U
ASG	SER	A	430	398	H	AlphaHelix	-37.88	-47.78	26.6	3G5U
ASG	THR	A	431	399	H	AlphaHelix	-59.79	-44.13	0.6	3G5U
ASG	THR	A	432	400	H	AlphaHelix	-62.30	-41.30	1.4	3G5U
ASG	VAL	A	433	401	H	AlphaHelix	-59.84	-18.27	4.1	3G5U
ASG	GLN	A	434	402	H	AlphaHelix	-74.64	-82.55	42.9	3G5U
ASG	LEU	A	435	403	H	AlphaHelix	-50.33	-12.50	2.9	3G5U
ASG	MET	A	436	404	H	AlphaHelix	-65.55	9.99	0.4	3G5U
ASG	GLN	A	437	405	C	Coil	-134.00	14.33	8.8	3G5U
ASG	ARG	A	438	406	T	Turn	61.60	5.07	32.1	3G5U
ASG	LEU	A	439	407	T	Turn	-35.98	-43.51	13.8	3G5U
ASG	TYR	A	440	408	T	Turn	-136.23	139.11	19.9	3G5U
ASG	ASP	A	441	409	T	Turn	-72.80	148.74	51.5	3G5U
ASG	PRO	A	442	410	T	Turn	-62.40	135.00	10.2	3G5U
ASG	LEU	A	443	411	T	Turn	-61.03	-46.46	98.6	3G5U
ASG	ASP	A	444	412	B	Bridge	-149.71	159.76	87.5	3G5U
ASG	GLY	A	445	413	T	Turn	79.71	-141.38	17.2	3G5U
ASG	MET	A	446	414	E	Strand	179.55	178.40	89.2	3G5U
ASG	VAL	A	447	415	E	Strand	-139.44	153.43	1.0	3G5U
ASG	SER	A	448	416	E	Strand	-135.76	138.95	14.8	3G5U
ASG	ILE	A	449	417	E	Strand	-102.36	162.68	13.8	3G5U
ASG	ASP	A	450	418	T	Turn	44.87	-120.49	46.7	3G5U
ASG	GLY	A	451	419	T	Turn	-119.19	8.69	55.5	3G5U
ASG	GLN	A	452	420	E	Strand	-103.06	166.50	51.8	3G5U
ASG	ASP	A	453	421	E	Strand	-85.84	126.46	26.6	3G5U
ASG	ILE	A	454	422	G	310Helix	-37.13	-63.33	2.7	3G5U
ASG	ARG	A	455	423	G	310Helix	-42.22	-41.81	89.5	3G5U
ASG	THR	A	456	424	G	310Helix	-63.38	-34.51	67.8	3G5U
ASG	ILE	A	457	425	C	Coil	-80.22	159.96	7.7	3G5U
ASG	ASN	A	458	426	C	Coil	-69.07	147.36	20.0	3G5U
ASG	VAL	A	459	427	H	AlphaHelix	-63.24	-73.45	8.5	3G5U
ASG	ARG	A	460	428	H	AlphaHelix	-32.33	-45.09	130.0	3G5U
ASG	TYR	A	461	429	H	AlphaHelix	-64.85	-53.73	38.5	3G5U
ASG	LEU	A	462	430	H	AlphaHelix	-50.60	-71.89	3.0	3G5U
ASG	ARG	A	463	431	H	AlphaHelix	-37.35	-35.56	1.6	3G5U
ASG	GLU	A	464	432	H	AlphaHelix	-71.61	-53.41	71.9	3G5U
ASG	ILE	A	465	433	H	AlphaHelix	-63.03	4.65	41.9	3G5U
ASG	ILE	A	466	434	E	Strand	-129.96	88.39	2.3	3G5U
ASG	GLY	A	467	435	E	Strand	-62.83	137.46	1.9	3G5U
ASG	VAL	A	468	436	E	Strand	-144.77	127.65	26.4	3G5U

ASG	VAL	A	469	437	E	Strand	-134.05	108.54	11.3	3G5U
ASG	SER	A	470	438	T	Turn	-96.84	-175.27	42.2	3G5U
ASG	GLN	A	471	439	T	Turn	-58.59	-106.07	79.4	3G5U
ASG	GLU	A	472	440	T	Turn	-28.03	101.08	73.8	3G5U
ASG	PRO	A	473	441	T	Turn	-87.49	112.61	21.6	3G5U
ASG	VAL	A	474	442	C	Coil	-100.82	136.94	4.6	3G5U
ASG	LEU	A	475	443	C	Coil	-128.04	127.14	0.4	3G5U
ASG	PHE	A	476	444	C	Coil	-71.42	163.14	7.7	3G5U
ASG	ALA	A	477	445	C	Coil	-71.14	92.91	33.2	3G5U
ASG	THR	A	478	446	C	Coil	-166.55	-167.19	33.7	3G5U
ASG	THR	A	479	447	C	Coil	-75.71	158.64	29.5	3G5U
ASG	ILE	A	480	448	H	AlphaHelix	-57.17	-57.80	0.4	3G5U
ASG	ALA	A	481	449	H	AlphaHelix	-38.29	-66.83	10.4	3G5U
ASG	GLU	A	482	450	H	AlphaHelix	-46.63	-36.72	52.7	3G5U
ASG	ASN	A	483	451	H	AlphaHelix	-66.84	-50.04	0.4	3G5U
ASG	ILE	A	484	452	H	AlphaHelix	-55.69	-41.99	0.0	3G5U
ASG	ARG	A	485	453	H	AlphaHelix	-57.67	-35.95	79.1	3G5U
ASG	TYR	A	486	454	H	AlphaHelix	-57.14	-38.54	20.7	3G5U
ASG	GLY	A	487	455	H	AlphaHelix	-52.84	-43.25	0.9	3G5U
ASG	ARG	A	488	456	T	Turn	-148.32	111.23	67.5	3G5U
ASG	GLU	A	489	457	T	Turn	-40.68	-86.44	80.7	3G5U
ASG	ASP	A	490	458	T	Turn	-69.00	137.22	124.9	3G5U
ASG	VAL	A	491	459	T	Turn	164.36	132.02	11.0	3G5U
ASG	THR	A	492	460	C	Coil	-95.98	142.85	76.3	3G5U
ASG	MET	A	493	461	H	AlphaHelix	-45.75	-13.62	101.1	3G5U
ASG	ASP	A	494	462	H	AlphaHelix	-73.53	-42.45	94.4	3G5U
ASG	GLU	A	495	463	H	AlphaHelix	-70.37	-45.19	68.5	3G5U
ASG	ILE	A	496	464	H	AlphaHelix	-59.24	-49.27	2.4	3G5U
ASG	GLU	A	497	465	H	AlphaHelix	-45.34	-59.26	63.9	3G5U
ASG	LYS	A	498	466	H	AlphaHelix	-50.40	-59.53	95.1	3G5U
ASG	ALA	A	499	467	H	AlphaHelix	-40.60	-63.50	3.7	3G5U
ASG	VAL	A	500	468	H	AlphaHelix	-51.30	-62.88	0.0	3G5U
ASG	LYS	A	501	469	H	AlphaHelix	-43.90	-39.62	88.5	3G5U
ASG	GLU	A	502	470	H	AlphaHelix	-66.76	-35.28	58.6	3G5U
ASG	ALA	A	503	471	H	AlphaHelix	-98.92	39.96	0.8	3G5U
ASG	ASN	A	504	472	C	Coil	30.09	54.03	23.7	3G5U
ASG	ALA	A	505	473	H	AlphaHelix	-113.12	-21.87	0.0	3G5U
ASG	TYR	A	506	474	H	AlphaHelix	-51.84	-28.18	72.8	3G5U
ASG	ASP	A	507	475	H	AlphaHelix	-73.73	-62.48	96.2	3G5U
ASG	PHE	A	508	476	H	AlphaHelix	-60.93	-37.57	14.4	3G5U
ASG	ILE	A	509	477	H	AlphaHelix	-63.24	-25.15	0.0	3G5U
ASG	MET	A	510	478	H	AlphaHelix	-81.40	-48.13	53.6	3G5U
ASG	LYS	A	511	479	H	AlphaHelix	-69.83	-45.12	187.6	3G5U
ASG	LEU	A	512	480	T	Turn	-46.15	143.82	37.0	3G5U
ASG	PRO	A	513	481	T	Turn	-52.98	171.46	82.9	3G5U
ASG	HIS	A	514	482	T	Turn	52.00	-15.89	130.7	3G5U
ASG	GLN	A	515	483	T	Turn	81.36	-142.11	79.6	3G5U
ASG	PHE	A	516	484	T	Turn	-74.43	-22.01	28.1	3G5U
ASG	ASP	A	517	485	T	Turn	-82.25	-0.15	116.9	3G5U
ASG	THR	A	518	486	T	Turn	-61.93	152.29	3.4	3G5U
ASG	LEU	A	519	487	C	Coil	-96.22	-157.38	75.1	3G5U
ASG	VAL	A	520	488	T	Turn	-146.98	70.99	1.6	3G5U
ASG	GLY	A	521	489	T	Turn	-18.53	76.61	28.6	3G5U
ASG	GLU	A	522	490	T	Turn	53.42	103.46	159.5	3G5U
ASG	ARG	A	523	491	T	Turn	71.68	176.40	84.7	3G5U
ASG	GLY	A	524	492	T	Turn	-71.15	43.78	4.2	3G5U
ASG	ALA	A	525	493	T	Turn	-113.75	94.99	60.2	3G5U
ASG	GLN	A	526	494	C	Coil	-174.48	-36.64	111.8	3G5U
ASG	LEU	A	527	495	C	Coil	-126.67	172.81	38.5	3G5U
ASG	SER	A	528	496	C	Coil	-67.42	133.79	58.0	3G5U
ASG	GLY	A	529	497	H	AlphaHelix	-45.24	-32.05	32.7	3G5U
ASG	GLY	A	530	498	H	AlphaHelix	-53.64	-62.68	1.7	3G5U
ASG	GLN	A	531	499	H	AlphaHelix	-62.33	-41.01	41.7	3G5U
ASG	LYS	A	532	500	H	AlphaHelix	-46.69	-66.62	23.5	3G5U
ASG	GLN	A	533	501	H	AlphaHelix	-42.53	-47.78	5.8	3G5U
ASG	ARG	A	534	502	H	AlphaHelix	-56.58	-55.71	23.9	3G5U
ASG	ILE	A	535	503	H	AlphaHelix	-47.00	-47.25	0.0	3G5U
ASG	ALA	A	536	504	H	AlphaHelix	-47.13	-64.98	4.0	3G5U
ASG	ILE	A	537	505	H	AlphaHelix	-40.27	-40.24	4.3	3G5U
ASG	ALA	A	538	506	H	AlphaHelix	-63.13	-52.80	0.0	3G5U
ASG	ARG	A	539	507	H	AlphaHelix	-47.76	-66.04	35.5	3G5U
ASG	ALA	A	540	508	H	AlphaHelix	-54.68	-31.87	18.6	3G5U
ASG	LEU	A	541	509	H	AlphaHelix	-59.19	-38.27	14.6	3G5U
ASG	VAL	A	542	510	H	AlphaHelix	-75.73	-27.98	8.4	3G5U

ASG	ARG	A	543	511	H	AlphaHelix	-58.29	-34.89	28.6	3G5U
ASG	ASN	A	544	512	C	Coil	38.19	74.80	81.7	3G5U
ASG	PRO	A	545	513	T	Turn	-78.01	-161.55	7.7	3G5U
ASG	LYS	A	546	514	T	Turn	-133.90	-5.52	56.5	3G5U
ASG	ILE	A	547	515	E	Strand	-134.18	140.70	3.6	3G5U
ASG	LEU	A	548	516	E	Strand	-136.21	122.98	12.8	3G5U
ASG	LEU	A	549	517	E	Strand	-110.66	129.53	0.2	3G5U
ASG	LEU	A	550	518	E	Strand	-118.67	105.49	1.4	3G5U
ASG	ASP	A	551	519	E	Strand	-86.78	80.57	14.8	3G5U
ASG	GLU	A	552	520	T	Turn	63.02	-2.08	46.3	3G5U
ASG	ALA	A	553	521	T	Turn	-3.19	-98.34	4.2	3G5U
ASG	THR	A	554	522	T	Turn	-28.91	-46.50	3.7	3G5U
ASG	SER	A	555	523	T	Turn	-34.10	171.73	18.1	3G5U
ASG	ALA	A	556	524	T	Turn	41.93	50.59	108.4	3G5U
ASG	LEU	A	557	525	T	Turn	-150.61	154.19	41.8	3G5U
ASG	ASP	A	558	526	C	Coil	-56.45	149.07	86.5	3G5U
ASG	THR	A	559	527	H	AlphaHelix	-50.18	-68.15	114.0	3G5U
ASG	GLU	A	560	528	H	AlphaHelix	-43.57	-49.00	120.6	3G5U
ASG	SER	A	561	529	H	AlphaHelix	-59.71	-55.62	2.4	3G5U
ASG	GLU	A	562	530	H	AlphaHelix	-32.98	-38.29	37.0	3G5U
ASG	ALA	A	563	531	H	AlphaHelix	-64.23	-75.22	58.4	3G5U
ASG	VAL	A	564	532	H	AlphaHelix	-40.58	-46.61	36.0	3G5U
ASG	VAL	A	565	533	H	AlphaHelix	-60.35	-52.42	0.0	3G5U
ASG	GLN	A	566	534	H	AlphaHelix	-60.15	-31.70	24.9	3G5U
ASG	ALA	A	567	535	H	AlphaHelix	-57.89	-49.37	46.4	3G5U
ASG	ALA	A	568	536	H	AlphaHelix	-67.30	-39.42	1.4	3G5U
ASG	LEU	A	569	537	H	AlphaHelix	-56.27	-52.71	3.6	3G5U
ASG	ASP	A	570	538	H	AlphaHelix	-50.72	-61.79	64.2	3G5U
ASG	LYS	A	571	539	H	AlphaHelix	-52.93	-10.69	131.3	3G5U
ASG	ALA	A	572	540	H	AlphaHelix	-91.68	-55.09	3.3	3G5U
ASG	ARG	A	573	541	H	AlphaHelix	-70.50	-36.07	12.6	3G5U
ASG	GLU	A	574	542	H	AlphaHelix	-59.22	-42.46	108.5	3G5U
ASG	GLY	A	575	543	T	Turn	-43.72	-36.99	73.4	3G5U
ASG	ARG	A	576	544	T	Turn	-108.00	147.08	40.5	3G5U
ASG	THR	A	577	545	E	Strand	-73.09	123.95	1.4	3G5U
ASG	THR	A	578	546	E	Strand	-135.24	131.91	2.7	3G5U
ASG	ILE	A	579	547	E	Strand	-97.40	115.83	10.4	3G5U
ASG	VAL	A	580	548	E	Strand	-121.27	133.43	26.4	3G5U
ASG	ILE	A	581	549	E	Strand	-115.17	132.48	1.6	3G5U
ASG	ALA	A	582	550	C	Coil	-170.71	172.42	11.6	3G5U
ASG	HIS	A	583	551	T	Turn	-99.63	-21.19	47.7	3G5U
ASG	ARG	A	584	552	T	Turn	-74.25	75.02	65.5	3G5U
ASG	LEU	A	585	553	G	310Helix	-44.02	-24.55	26.5	3G5U
ASG	SER	A	586	554	G	310Helix	-64.16	-37.31	93.7	3G5U
ASG	THR	A	587	555	G	310Helix	-97.84	10.22	26.1	3G5U
ASG	VAL	A	588	556	T	Turn	-88.58	-56.53	6.8	3G5U
ASG	ARG	A	589	557	T	Turn	-15.48	-70.92	129.5	3G5U
ASG	ASN	A	590	558	T	Turn	-59.46	32.20	77.4	3G5U
ASG	ALA	A	591	559	T	Turn	-90.13	131.38	8.0	3G5U
ASG	ASP	A	592	560	T	Turn	-61.17	-25.53	70.7	3G5U
ASG	VAL	A	593	561	E	Strand	-165.60	155.86	16.2	3G5U
ASG	ILE	A	594	562	E	Strand	-130.32	159.47	0.0	3G5U
ASG	ALA	A	595	563	E	Strand	-141.06	141.41	2.0	3G5U
ASG	GLY	A	596	564	E	Strand	-89.87	109.63	0.2	3G5U
ASG	PHE	A	597	565	T	Turn	-123.31	-177.18	5.9	3G5U
ASG	ASP	A	598	566	T	Turn	155.55	71.07	44.0	3G5U
ASG	GLY	A	599	567	T	Turn	81.88	73.01	25.9	3G5U
ASG	GLY	A	600	568	T	Turn	45.61	69.12	12.2	3G5U
ASG	VAL	A	601	569	T	Turn	-163.54	93.05	55.9	3G5U
ASG	ILE	A	602	570	C	Coil	-76.21	134.68	42.5	3G5U
ASG	VAL	A	603	571	C	Coil	-147.38	-86.55	72.3	3G5U
ASG	GLU	A	604	572	E	Strand	-82.34	111.17	37.6	3G5U
ASG	GLN	A	605	573	E	Strand	-112.22	141.35	95.1	3G5U
ASG	GLY	A	606	574	E	Strand	140.46	-176.23	13.6	3G5U
ASG	ASN	A	607	575	C	Coil	-70.53	160.05	52.6	3G5U
ASG	HIS	A	608	576	H	AlphaHelix	-40.43	-79.51	8.8	3G5U
ASG	ASP	A	609	577	H	AlphaHelix	-47.15	-20.41	96.2	3G5U
ASG	GLU	A	610	578	H	AlphaHelix	-76.42	-45.19	109.8	3G5U
ASG	LEU	A	611	579	H	AlphaHelix	-76.86	-17.46	4.2	3G5U
ASG	MET	A	612	580	H	AlphaHelix	-84.10	-47.10	50.0	3G5U
ASG	ARG	A	613	581	H	AlphaHelix	-57.22	-23.59	199.7	3G5U
ASG	GLU	A	614	582	H	AlphaHelix	-80.52	-31.54	121.8	3G5U
ASG	LYS	A	615	583	C	Coil	65.98	25.97	160.0	3G5U
ASG	GLY	A	616	584	C	Coil	-91.70	-131.80	17.0	3G5U

ASG	ILE	A	617	585	H	AlphaHelix	-65.82	-58.06	58.3	3G5U
ASG	TYR	A	618	586	H	AlphaHelix	-46.81	-68.75	3.6	3G5U
ASG	PHE	A	619	587	H	AlphaHelix	-44.07	-53.15	72.4	3G5U
ASG	LYS	A	620	588	H	AlphaHelix	-48.49	-73.28	112.7	3G5U
ASG	LEU	A	621	589	H	AlphaHelix	-52.84	-31.75	42.5	3G5U
ASG	VAL	A	622	590	H	AlphaHelix	-61.74	-46.88	14.9	3G5U
ASG	MET	A	623	591	H	AlphaHelix	-78.22	-31.23	93.1	3G5U
ASG	THR	A	624	592	H	AlphaHelix	-59.05	-35.36	86.1	3G5U
ASG	GLN	A	625	593	H	AlphaHelix	-84.55	-10.99	77.9	3G5U
ASG	THR	A	626	594	C	Coil	94.12	360.00	140.5	3G5U
ASG	LEU	A	684	595	C	Coil	360.00	72.65	151.2	3G5U
ASG	ASP	A	685	596	C	Coil	-82.09	163.84	147.9	3G5U
ASG	GLU	A	686	597	C	Coil	179.52	-50.68	94.0	3G5U
ASG	ASP	A	687	598	C	Coil	0.30	121.77	121.3	3G5U
ASG	VAL	A	688	599	C	Coil	-110.36	143.67	63.1	3G5U
ASG	PRO	A	689	600	C	Coil	-58.16	-47.37	119.8	3G5U
ASG	PRO	A	690	601	C	Coil	-52.58	124.59	67.8	3G5U
ASG	ALA	A	691	602	C	Coil	-96.58	-129.26	67.7	3G5U
ASG	SER	A	692	603	T	Turn	177.90	52.07	9.0	3G5U
ASG	PHE	A	693	604	T	Turn	-41.21	109.28	150.8	3G5U
ASG	TRP	A	694	605	T	Turn	57.90	-3.40	152.2	3G5U
ASG	ARG	A	695	606	H	AlphaHelix	-71.47	-49.08	97.4	3G5U
ASG	ILE	A	696	607	H	AlphaHelix	-68.49	-1.79	2.0	3G5U
ASG	LEU	A	697	608	H	AlphaHelix	-84.44	-52.43	45.7	3G5U
ASG	LYS	A	698	609	H	AlphaHelix	-54.86	-65.02	123.9	3G5U
ASG	LEU	A	699	610	H	AlphaHelix	-56.78	-29.49	46.7	3G5U
ASG	ASN	A	700	611	H	AlphaHelix	-44.45	-79.78	9.6	3G5U
ASG	SER	A	701	612	H	AlphaHelix	-42.18	-34.30	63.6	3G5U
ASG	THR	A	702	613	H	AlphaHelix	-55.35	-55.51	94.3	3G5U
ASG	GLU	A	703	614	C	Coil	-70.94	43.61	24.5	3G5U
ASG	TRP	A	704	615	C	Coil	-156.03	144.36	83.2	3G5U
ASG	PRO	A	705	616	C	Coil	-96.44	-60.22	70.0	3G5U
ASG	TYR	A	706	617	C	Coil	162.18	146.73	149.3	3G5U
ASG	PHE	A	707	618	C	Coil	-172.67	56.38	25.8	3G5U
ASG	VAL	A	708	619	H	AlphaHelix	-63.94	-31.25	87.8	3G5U
ASG	VAL	A	709	620	H	AlphaHelix	-48.11	-58.16	52.1	3G5U
ASG	GLY	A	710	621	H	AlphaHelix	-50.04	-70.24	2.0	3G5U
ASG	ILE	A	711	622	H	AlphaHelix	-45.15	-27.08	38.5	3G5U
ASG	PHE	A	712	623	H	AlphaHelix	-58.70	-66.08	140.5	3G5U
ASG	CYS	A	713	624	H	AlphaHelix	-60.10	-21.53	5.2	3G5U
ASG	ALA	A	714	625	H	AlphaHelix	-53.60	-56.26	7.2	3G5U
ASG	ILE	A	715	626	H	AlphaHelix	-51.22	-47.95	51.7	3G5U
ASG	ILE	A	716	627	H	AlphaHelix	-60.04	-48.99	66.2	3G5U
ASG	ASN	A	717	628	H	AlphaHelix	-45.60	-49.86	16.4	3G5U
ASG	GLY	A	718	629	H	AlphaHelix	-52.80	-58.94	0.0	3G5U
ASG	GLY	A	719	630	H	AlphaHelix	-52.06	-45.02	21.4	3G5U
ASG	LEU	A	720	631	H	AlphaHelix	-39.45	-49.99	11.9	3G5U
ASG	GLN	A	721	632	H	AlphaHelix	-61.83	-64.77	55.3	3G5U
ASG	PRO	A	722	633	H	AlphaHelix	-53.07	-29.03	0.4	3G5U
ASG	ALA	A	723	634	H	AlphaHelix	-51.28	-50.18	39.0	3G5U
ASG	PHE	A	724	635	H	AlphaHelix	-56.18	-50.38	14.1	3G5U
ASG	SER	A	725	636	H	AlphaHelix	-41.47	-47.33	0.0	3G5U
ASG	VAL	A	726	637	H	AlphaHelix	-78.17	-45.02	47.5	3G5U
ASG	ILE	A	727	638	H	AlphaHelix	-52.11	-41.66	15.9	3G5U
ASG	PHE	A	728	639	H	AlphaHelix	-69.35	-60.36	4.8	3G5U
ASG	SER	A	729	640	H	AlphaHelix	-46.63	-32.25	1.2	3G5U
ASG	LYS	A	730	641	H	AlphaHelix	-67.25	-57.09	102.4	3G5U
ASG	VAL	A	731	642	H	AlphaHelix	-43.22	-73.75	5.6	3G5U
ASG	VAL	A	732	643	H	AlphaHelix	-42.36	-58.31	14.6	3G5U
ASG	GLY	A	733	644	H	AlphaHelix	-46.00	-66.55	3.7	3G5U
ASG	VAL	A	734	645	H	AlphaHelix	-66.62	24.73	35.6	3G5U
ASG	PHE	A	735	646	H	AlphaHelix	-151.70	-7.57	41.8	3G5U
ASG	THR	A	736	647	H	AlphaHelix	-99.57	-10.23	23.0	3G5U
ASG	ASN	A	737	648	C	Coil	-168.01	108.18	50.1	3G5U
ASG	GLY	A	738	649	C	Coil	173.79	-165.71	23.4	3G5U
ASG	GLY	A	739	650	C	Coil	-79.26	121.64	45.6	3G5U
ASG	PRO	A	740	651	T	Turn	-42.43	-59.05	104.0	3G5U
ASG	PRO	A	741	652	T	Turn	-76.99	159.60	92.5	3G5U
ASG	GLU	A	742	653	T	Turn	81.15	-18.07	124.8	3G5U
ASG	THR	A	743	654	H	AlphaHelix	-56.63	-25.96	27.1	3G5U
ASG	GLN	A	744	655	H	AlphaHelix	-68.24	-50.87	88.0	3G5U
ASG	ARG	A	745	656	H	AlphaHelix	-66.08	-42.29	161.0	3G5U
ASG	GLN	A	746	657	H	AlphaHelix	-56.74	-52.36	71.6	3G5U
ASG	ASN	A	747	658	H	AlphaHelix	-56.62	-90.29	4.2	3G5U

ASG	SER	A	748	659	H	AlphaHelix	-22.70	-48.40	33.1	3G5U
ASG	ASN	A	749	660	H	AlphaHelix	-59.85	-78.26	59.6	3G5U
ASG	LEU	A	750	661	H	AlphaHelix	-38.91	-39.54	1.0	3G5U
ASG	PHE	A	751	662	H	AlphaHelix	-54.16	-73.30	23.3	3G5U
ASG	SER	A	752	663	H	AlphaHelix	-45.67	-47.87	43.7	3G5U
ASG	LEU	A	753	664	H	AlphaHelix	-47.56	-54.18	48.7	3G5U
ASG	LEU	A	754	665	H	AlphaHelix	-52.21	-46.51	2.2	3G5U
ASG	PHE	A	755	666	H	AlphaHelix	-65.88	-83.29	57.7	3G5U
ASG	LEU	A	756	667	H	AlphaHelix	-32.12	-51.77	72.5	3G5U
ASG	ILE	A	757	668	H	AlphaHelix	-56.02	-87.07	46.5	3G5U
ASG	LEU	A	758	669	H	AlphaHelix	-43.34	-80.27	12.0	3G5U
ASG	GLY	A	759	670	H	AlphaHelix	-23.65	-69.86	0.0	3G5U
ASG	ILE	A	760	671	H	AlphaHelix	-62.94	-81.18	74.6	3G5U
ASG	ILE	A	761	672	H	AlphaHelix	-20.87	-56.70	57.3	3G5U
ASG	SER	A	762	673	H	AlphaHelix	-63.90	-61.65	3.6	3G5U
ASG	PHE	A	763	674	H	AlphaHelix	-33.30	-48.72	88.8	3G5U
ASG	ILE	A	764	675	H	AlphaHelix	-58.62	-74.99	85.2	3G5U
ASG	THR	A	765	676	H	AlphaHelix	-22.85	-58.04	0.2	3G5U
ASG	PHE	A	766	677	H	AlphaHelix	-58.15	-74.93	28.3	3G5U
ASG	PHE	A	767	678	H	AlphaHelix	-25.65	-64.93	102.6	3G5U
ASG	LEU	A	768	679	H	AlphaHelix	-57.50	-64.99	51.7	3G5U
ASG	GLN	A	769	680	H	AlphaHelix	-52.06	-45.83	15.4	3G5U
ASG	GLY	A	770	681	H	AlphaHelix	-59.27	-33.96	0.0	3G5U
ASG	PHE	A	771	682	H	AlphaHelix	-63.65	-62.85	117.0	3G5U
ASG	THR	A	772	683	H	AlphaHelix	-59.36	-64.12	18.0	3G5U
ASG	PHE	A	773	684	H	AlphaHelix	-59.43	-38.36	37.5	3G5U
ASG	GLY	A	774	685	H	AlphaHelix	-60.61	-46.52	2.3	3G5U
ASG	LYS	A	775	686	H	AlphaHelix	-58.35	-26.96	66.7	3G5U
ASG	ALA	A	776	687	H	AlphaHelix	-69.10	-35.33	2.6	3G5U
ASG	GLY	A	777	688	H	AlphaHelix	-69.25	-43.81	2.2	3G5U
ASG	GLU	A	778	689	H	AlphaHelix	-52.57	-82.43	9.8	3G5U
ASG	ILE	A	779	690	H	AlphaHelix	-39.48	-60.24	43.4	3G5U
ASG	LEU	A	780	691	H	AlphaHelix	-41.03	-50.49	0.8	3G5U
ASG	THR	A	781	692	H	AlphaHelix	-63.67	-41.27	4.6	3G5U
ASG	LYS	A	782	693	H	AlphaHelix	-70.31	-67.46	9.2	3G5U
ASG	ARG	A	783	694	H	AlphaHelix	-49.69	-16.46	91.4	3G5U
ASG	LEU	A	784	695	H	AlphaHelix	-84.21	-57.67	5.2	3G5U
ASG	ARG	A	785	696	H	AlphaHelix	-46.88	-42.27	8.7	3G5U
ASG	TYR	A	786	697	H	AlphaHelix	-59.15	-74.88	92.8	3G5U
ASG	MET	A	787	698	H	AlphaHelix	-30.65	-56.53	92.2	3G5U
ASG	VAL	A	788	699	H	AlphaHelix	-59.04	-51.59	6.8	3G5U
ASG	PHE	A	789	700	H	AlphaHelix	-55.37	-55.08	25.3	3G5U
ASG	LYS	A	790	701	H	AlphaHelix	-57.43	-32.22	24.1	3G5U
ASG	SER	A	791	702	H	AlphaHelix	-53.89	-42.16	0.4	3G5U
ASG	MET	A	792	703	H	AlphaHelix	-69.38	-56.18	16.8	3G5U
ASG	LEU	A	793	704	H	AlphaHelix	-47.03	-51.73	15.6	3G5U
ASG	ARG	A	794	705	H	AlphaHelix	-67.64	-41.76	82.8	3G5U
ASG	GLN	A	795	706	C	Coil	-56.14	-177.56	22.6	3G5U
ASG	ASP	A	796	707	T	Turn	151.22	-154.01	6.3	3G5U
ASG	VAL	A	797	708	T	Turn	74.58	-167.60	40.5	3G5U
ASG	SER	A	798	709	T	Turn	-46.85	7.41	22.3	3G5U
ASG	TRP	A	799	710	T	Turn	-58.66	-80.71	65.3	3G5U
ASG	PHE	A	800	711	T	Turn	-87.05	-16.42	46.5	3G5U
ASG	ASP	A	801	712	T	Turn	-58.96	-23.04	19.6	3G5U
ASG	ASP	A	802	713	T	Turn	-169.69	81.36	42.4	3G5U
ASG	PRO	A	803	714	T	Turn	-101.84	-153.96	57.9	3G5U
ASG	LYS	A	804	715	C	Coil	171.21	29.22	151.5	3G5U
ASG	ASN	A	805	716	C	Coil	-126.04	72.42	44.0	3G5U
ASG	THR	A	806	717	C	Coil	-51.95	159.93	71.6	3G5U
ASG	THR	A	807	718	H	AlphaHelix	-47.63	-49.01	60.3	3G5U
ASG	GLY	A	808	719	H	AlphaHelix	-52.10	-68.15	22.9	3G5U
ASG	ALA	A	809	720	H	AlphaHelix	-32.82	-34.07	23.2	3G5U
ASG	LEU	A	810	721	H	AlphaHelix	-86.05	-47.06	18.8	3G5U
ASG	THR	A	811	722	H	AlphaHelix	-56.48	-45.69	23.9	3G5U
ASG	THR	A	812	723	H	AlphaHelix	-44.16	-74.16	61.2	3G5U
ASG	ARG	A	813	724	H	AlphaHelix	-33.33	-58.48	45.2	3G5U
ASG	LEU	A	814	725	H	AlphaHelix	-45.36	-73.87	18.4	3G5U
ASG	ALA	A	815	726	H	AlphaHelix	-54.42	-72.30	31.5	3G5U
ASG	ASN	A	816	727	H	AlphaHelix	-44.30	-60.41	45.0	3G5U
ASG	ASP	A	817	728	H	AlphaHelix	-51.56	-47.39	2.4	3G5U
ASG	ALA	A	818	729	H	AlphaHelix	-53.29	-53.15	2.7	3G5U
ASG	ALA	A	819	730	H	AlphaHelix	-44.43	-71.60	33.1	3G5U
ASG	GLN	A	820	731	H	AlphaHelix	-34.58	-57.49	56.9	3G5U
ASG	VAL	A	821	732	H	AlphaHelix	-52.54	-47.74	8.2	3G5U

ASG	LYS	A	822	733	H	AlphaHelix	-43.21	-40.26	55.9	3G5U
ASG	GLY	A	823	734	H	AlphaHelix	-58.43	-46.38	8.1	3G5U
ASG	ALA	A	824	735	H	AlphaHelix	-57.80	-31.40	0.4	3G5U
ASG	THR	A	825	736	H	AlphaHelix	-78.43	-53.02	12.1	3G5U
ASG	GLY	A	826	737	H	AlphaHelix	-54.87	-27.57	16.3	3G5U
ASG	SER	A	827	738	H	AlphaHelix	-67.67	-51.25	19.7	3G5U
ASG	ARG	A	828	739	H	AlphaHelix	-50.52	-29.49	60.7	3G5U
ASG	LEU	A	829	740	H	AlphaHelix	-68.26	-58.45	28.6	3G5U
ASG	ALA	A	830	741	H	AlphaHelix	-64.29	-0.52	22.7	3G5U
ASG	VAL	A	831	742	H	AlphaHelix	-86.66	-74.30	73.4	3G5U
ASG	ILE	A	832	743	H	AlphaHelix	-42.42	-44.15	67.9	3G5U
ASG	PHE	A	833	744	H	AlphaHelix	-57.66	-84.05	18.2	3G5U
ASG	GLN	A	834	745	H	AlphaHelix	-36.33	-45.04	61.5	3G5U
ASG	ASN	A	835	746	H	AlphaHelix	-42.13	-76.82	68.9	3G5U
ASG	ILE	A	836	747	H	AlphaHelix	-44.15	-61.64	60.9	3G5U
ASG	ALA	A	837	748	H	AlphaHelix	-33.57	-91.67	0.0	3G5U
ASG	ASN	A	838	749	H	AlphaHelix	-38.56	-72.89	42.7	3G5U
ASG	LEU	A	839	750	H	AlphaHelix	-63.62	-88.59	91.8	3G5U
ASG	GLY	A	840	751	H	AlphaHelix	-17.59	-67.60	24.2	3G5U
ASG	THR	A	841	752	H	AlphaHelix	-63.31	-41.22	33.0	3G5U
ASG	GLY	A	842	753	H	AlphaHelix	-64.85	-44.61	2.1	3G5U
ASG	ILE	A	843	754	H	AlphaHelix	-60.74	-48.20	79.0	3G5U
ASG	ILE	A	844	755	H	AlphaHelix	-52.54	-59.39	99.0	3G5U
ASG	ILE	A	845	756	H	AlphaHelix	-61.77	-10.33	33.9	3G5U
ASG	SER	A	846	757	H	AlphaHelix	-81.13	-23.14	21.2	3G5U
ASG	LEU	A	847	758	H	AlphaHelix	-70.23	-59.58	120.5	3G5U
ASG	ILE	A	848	759	H	AlphaHelix	-52.93	-17.19	99.0	3G5U
ASG	TYR	A	849	760	C	Coil	-70.27	138.08	7.9	3G5U
ASG	GLY	A	850	761	C	Coil	-93.22	61.35	34.7	3G5U
ASG	TRP	A	851	762	T	Turn	29.37	73.07	200.8	3G5U
ASG	GLN	A	852	763	T	Turn	-166.52	10.51	116.1	3G5U
ASG	LEU	A	853	764	T	Turn	-148.76	-67.50	13.2	3G5U
ASG	THR	A	854	765	H	AlphaHelix	-23.12	-60.58	28.8	3G5U
ASG	LEU	A	855	766	H	AlphaHelix	-71.19	-41.86	102.8	3G5U
ASG	LEU	A	856	767	H	AlphaHelix	-43.76	-38.29	22.5	3G5U
ASG	LEU	A	857	768	H	AlphaHelix	-96.63	-59.12	12.5	3G5U
ASG	LEU	A	858	769	H	AlphaHelix	-40.63	-27.75	92.9	3G5U
ASG	ALA	A	859	770	H	AlphaHelix	-67.55	-51.92	40.9	3G5U
ASG	ILE	A	860	771	H	AlphaHelix	-55.97	-58.73	44.7	3G5U
ASG	VAL	A	861	772	H	AlphaHelix	-48.52	-59.61	28.1	3G5U
ASG	PRO	A	862	773	H	AlphaHelix	-47.39	-45.78	62.4	3G5U
ASG	ILE	A	863	774	H	AlphaHelix	-63.43	-50.07	76.8	3G5U
ASG	ILE	A	864	775	H	AlphaHelix	-65.01	-40.40	55.7	3G5U
ASG	ALA	A	865	776	H	AlphaHelix	-56.43	-56.74	49.7	3G5U
ASG	ILE	A	866	777	H	AlphaHelix	-44.88	-33.72	104.3	3G5U
ASG	ALA	A	867	778	H	AlphaHelix	-66.18	-62.45	5.9	3G5U
ASG	GLY	A	868	779	H	AlphaHelix	-29.04	-56.05	41.3	3G5U
ASG	VAL	A	869	780	H	AlphaHelix	-61.20	-71.36	102.2	3G5U
ASG	VAL	A	870	781	H	AlphaHelix	-41.23	-45.65	77.7	3G5U
ASG	GLU	A	871	782	H	AlphaHelix	-58.32	-64.45	62.1	3G5U
ASG	MET	A	872	783	H	AlphaHelix	-47.43	-41.16	88.6	3G5U
ASG	LYS	A	873	784	H	AlphaHelix	-54.12	-63.79	125.9	3G5U
ASG	MET	A	874	785	H	AlphaHelix	-56.31	-38.56	100.4	3G5U
ASG	LEU	A	875	786	H	AlphaHelix	-55.96	-38.84	73.4	3G5U
ASG	SER	A	876	787	H	AlphaHelix	-68.58	-51.17	49.6	3G5U
ASG	GLY	A	877	788	H	AlphaHelix	-46.03	-54.91	31.0	3G5U
ASG	GLN	A	878	789	H	AlphaHelix	-60.18	-44.17	35.6	3G5U
ASG	ALA	A	879	790	H	AlphaHelix	-54.73	-53.36	34.0	3G5U
ASG	LEU	A	880	791	H	AlphaHelix	-63.40	-53.35	114.2	3G5U
ASG	LYS	A	881	792	H	AlphaHelix	-49.19	-46.39	69.0	3G5U
ASG	ASP	A	882	793	H	AlphaHelix	-59.71	-45.10	29.5	3G5U
ASG	LYS	A	883	794	H	AlphaHelix	-49.32	-28.97	101.0	3G5U
ASG	LYS	A	884	795	H	AlphaHelix	-72.68	-66.13	106.5	3G5U
ASG	GLU	A	885	796	H	AlphaHelix	-43.70	-55.10	49.4	3G5U
ASG	LEU	A	886	797	H	AlphaHelix	-55.25	-34.47	46.0	3G5U
ASG	GLU	A	887	798	H	AlphaHelix	-60.74	-39.81	68.6	3G5U
ASG	GLY	A	888	799	H	AlphaHelix	-58.96	-56.15	34.4	3G5U
ASG	SER	A	889	800	H	AlphaHelix	-53.00	-74.34	5.1	3G5U
ASG	GLY	A	890	801	H	AlphaHelix	-41.65	-39.22	13.1	3G5U
ASG	LYS	A	891	802	H	AlphaHelix	-57.08	-46.01	142.8	3G5U
ASG	ILE	A	892	803	H	AlphaHelix	-76.77	-24.97	57.5	3G5U
ASG	ALA	A	893	804	H	AlphaHelix	-71.49	-22.62	5.1	3G5U
ASG	THR	A	894	805	H	AlphaHelix	-81.81	-42.31	29.5	3G5U
ASG	GLU	A	895	806	H	AlphaHelix	-41.49	-53.86	37.0	3G5U

ASG	ALA	A	896	807	H	AlphaHelix	-66.65	-64.40	0.6	3G5U
ASG	ILE	A	897	808	H	AlphaHelix	-52.03	-41.80	7.1	3G5U
ASG	GLU	A	898	809	H	AlphaHelix	-66.71	-16.31	95.9	3G5U
ASG	ASN	A	899	810	T	Turn	-117.45	30.34	9.7	3G5U
ASG	PHE	A	900	811	T	Turn	-10.83	-29.27	61.9	3G5U
ASG	ARG	A	901	812	T	Turn	-59.61	33.71	80.6	3G5U
ASG	THR	A	902	813	T	Turn	-119.73	-49.77	0.0	3G5U
ASG	VAL	A	903	814	T	Turn	-54.51	-17.45	9.8	3G5U
ASG	VAL	A	904	815	T	Turn	-50.39	-44.45	35.9	3G5U
ASG	SER	A	905	816	T	Turn	-111.51	-28.84	18.7	3G5U
ASG	LEU	A	906	817	T	Turn	56.50	3.52	1.5	3G5U
ASG	THR	A	907	818	T	Turn	-80.60	59.66	8.8	3G5U
ASG	ARG	A	908	819	T	Turn	-173.94	-41.58	8.1	3G5U
ASG	GLU	A	909	820	T	Turn	2.41	-102.54	17.2	3G5U
ASG	GLN	A	910	821	H	AlphaHelix	-55.61	-56.78	87.8	3G5U
ASG	LYS	A	911	822	H	AlphaHelix	-26.66	-46.59	78.8	3G5U
ASG	PHE	A	912	823	H	AlphaHelix	-63.04	-86.62	0.0	3G5U
ASG	GLU	A	913	824	H	AlphaHelix	-42.74	-20.73	5.6	3G5U
ASG	THR	A	914	825	H	AlphaHelix	-64.77	-54.65	51.3	3G5U
ASG	MET	A	915	826	H	AlphaHelix	-51.00	-35.67	59.3	3G5U
ASG	TYR	A	916	827	H	AlphaHelix	-75.57	-20.97	8.8	3G5U
ASG	ALA	A	917	828	H	AlphaHelix	-65.39	-34.18	25.6	3G5U
ASG	GLN	A	918	829	H	AlphaHelix	-68.10	-62.22	100.4	3G5U
ASG	SER	A	919	830	H	AlphaHelix	-38.07	-64.20	32.3	3G5U
ASG	LEU	A	920	831	H	AlphaHelix	-38.94	-67.87	13.7	3G5U
ASG	GLN	A	921	832	H	AlphaHelix	-21.28	-59.78	67.2	3G5U
ASG	ILE	A	922	833	H	AlphaHelix	-61.18	-58.75	83.7	3G5U
ASG	PRO	A	923	834	H	AlphaHelix	-56.83	-11.69	17.9	3G5U
ASG	TYR	A	924	835	H	AlphaHelix	-78.04	-52.71	47.2	3G5U
ASG	ARG	A	925	836	H	AlphaHelix	-56.78	-51.11	147.5	3G5U
ASG	ASN	A	926	837	H	AlphaHelix	-50.48	-35.34	40.7	3G5U
ASG	ALA	A	927	838	H	AlphaHelix	-64.00	-49.01	14.6	3G5U
ASG	MET	A	928	839	H	AlphaHelix	-51.59	-47.73	67.2	3G5U
ASG	LYS	A	929	840	H	AlphaHelix	-55.28	-68.03	144.3	3G5U
ASG	LYS	A	930	841	H	AlphaHelix	-44.78	-23.69	33.1	3G5U
ASG	ALA	A	931	842	H	AlphaHelix	-60.74	-66.36	5.8	3G5U
ASG	HIS	A	932	843	H	AlphaHelix	-41.48	-55.12	92.8	3G5U
ASG	VAL	A	933	844	H	AlphaHelix	-44.25	-54.44	28.9	3G5U
ASG	PHE	A	934	845	H	AlphaHelix	-52.48	-40.01	44.8	3G5U
ASG	GLY	A	935	846	H	AlphaHelix	-59.62	-72.48	0.0	3G5U
ASG	ILE	A	936	847	H	AlphaHelix	-39.52	-54.64	83.6	3G5U
ASG	THR	A	937	848	H	AlphaHelix	-48.58	-75.44	43.7	3G5U
ASG	PHE	A	938	849	H	AlphaHelix	-33.02	-58.35	46.7	3G5U
ASG	SER	A	939	850	H	AlphaHelix	-46.60	-72.60	5.2	3G5U
ASG	PHE	A	940	851	H	AlphaHelix	-34.03	-33.64	114.0	3G5U
ASG	THR	A	941	852	H	AlphaHelix	-69.15	-43.64	28.8	3G5U
ASG	GLN	A	942	853	H	AlphaHelix	-70.12	-32.34	49.9	3G5U
ASG	ALA	A	943	854	H	AlphaHelix	-59.81	-48.28	3.4	3G5U
ASG	MET	A	944	855	H	AlphaHelix	-48.63	-39.98	36.7	3G5U
ASG	MET	A	945	856	H	AlphaHelix	-42.04	-71.69	34.1	3G5U
ASG	TYR	A	946	857	H	AlphaHelix	-56.55	-53.26	24.6	3G5U
ASG	PHE	A	947	858	H	AlphaHelix	-41.29	-62.43	94.5	3G5U
ASG	SER	A	948	859	H	AlphaHelix	-42.34	-78.78	14.2	3G5U
ASG	TYR	A	949	860	H	AlphaHelix	-36.67	-72.25	103.9	3G5U
ASG	ALA	A	950	861	H	AlphaHelix	-34.48	-73.62	8.0	3G5U
ASG	ALA	A	951	862	H	AlphaHelix	-41.51	-51.94	43.3	3G5U
ASG	ALA	A	952	863	H	AlphaHelix	-47.55	-77.65	12.0	3G5U
ASG	PHE	A	953	864	H	AlphaHelix	-48.25	-39.10	38.9	3G5U
ASG	ARG	A	954	865	H	AlphaHelix	-60.71	-67.67	92.4	3G5U
ASG	PHE	A	955	866	H	AlphaHelix	-47.31	-52.02	64.0	3G5U
ASG	GLY	A	956	867	H	AlphaHelix	-46.97	-70.71	5.9	3G5U
ASG	ALA	A	957	868	H	AlphaHelix	-33.65	-39.58	4.8	3G5U
ASG	TYR	A	958	869	T	Turn	-18.18	112.81	135.9	3G5U
ASG	LEU	A	959	870	T	Turn	72.38	83.75	55.2	3G5U
ASG	VAL	A	960	871	T	Turn	-123.50	41.76	14.8	3G5U
ASG	THR	A	961	872	T	Turn	-82.88	88.12	41.8	3G5U
ASG	GLN	A	962	873	T	Turn	91.83	9.51	76.8	3G5U
ASG	GLN	A	963	874	T	Turn	85.01	82.95	66.3	3G5U
ASG	LEU	A	964	875	T	Turn	-115.91	177.59	77.0	3G5U
ASG	MET	A	965	876	T	Turn	-43.16	8.71	137.2	3G5U
ASG	THR	A	966	877	T	Turn	-110.52	105.79	20.1	3G5U
ASG	PHE	A	967	878	C	Coil	-160.72	-140.96	88.2	3G5U
ASG	GLU	A	968	879	C	Coil	-45.09	-46.95	33.8	3G5U
ASG	ASN	A	969	880	H	AlphaHelix	-30.35	-31.84	20.7	3G5U

ASG	VAL	A	970	881	H	AlphaHelix	-47.97	-25.95	20.2	3G5U
ASG	LEU	A	971	882	H	AlphaHelix	-68.57	-30.47	25.5	3G5U
ASG	LEU	A	972	883	H	AlphaHelix	-75.94	-23.10	15.2	3G5U
ASG	VAL	A	973	884	H	AlphaHelix	-61.91	-46.33	9.0	3G5U
ASG	PHE	A	974	885	H	AlphaHelix	-53.97	-38.01	40.8	3G5U
ASG	SER	A	975	886	H	AlphaHelix	-54.63	-46.91	0.2	3G5U
ASG	ALA	A	976	887	H	AlphaHelix	-75.40	-25.17	15.4	3G5U
ASG	ILE	A	977	888	H	AlphaHelix	-71.61	-52.74	42.6	3G5U
ASG	VAL	A	978	889	H	AlphaHelix	-63.00	-20.14	30.7	3G5U
ASG	PHE	A	979	890	H	AlphaHelix	-67.02	-59.75	2.8	3G5U
ASG	GLY	A	980	891	H	AlphaHelix	-46.56	-47.99	11.0	3G5U
ASG	ALA	A	981	892	H	AlphaHelix	-60.65	-28.06	56.0	3G5U
ASG	MET	A	982	893	H	AlphaHelix	-65.00	-51.72	13.2	3G5U
ASG	ALA	A	983	894	H	AlphaHelix	-59.38	-33.70	17.3	3G5U
ASG	VAL	A	984	895	H	AlphaHelix	-56.21	-48.31	77.8	3G5U
ASG	GLY	A	985	896	H	AlphaHelix	-49.20	-46.58	31.5	3G5U
ASG	GLN	A	986	897	H	AlphaHelix	-58.09	-52.61	50.8	3G5U
ASG	VAL	A	987	898	H	AlphaHelix	-58.73	-47.68	76.3	3G5U
ASG	SER	A	988	899	H	AlphaHelix	-83.75	23.24	92.5	3G5U
ASG	SER	A	989	900	C	Coil	-147.38	175.72	66.3	3G5U
ASG	PHE	A	990	901	C	Coil	63.03	-149.60	110.8	3G5U
ASG	ALA	A	991	902	C	Coil	-45.51	168.78	41.1	3G5U
ASG	PRO	A	992	903	T	Turn	-58.70	140.86	56.5	3G5U
ASG	ASP	A	993	904	T	Turn	-46.82	50.90	99.6	3G5U
ASG	TYR	A	994	905	T	Turn	51.88	-132.62	68.9	3G5U
ASG	ALA	A	995	906	C	Coil	52.46	-131.46	45.2	3G5U
ASG	LYS	A	996	907	H	AlphaHelix	-17.83	-38.03	84.9	3G5U
ASG	ALA	A	997	908	H	AlphaHelix	-69.78	-51.92	0.2	3G5U
ASG	THR	A	998	909	H	AlphaHelix	-56.98	-47.26	23.5	3G5U
ASG	VAL	A	999	910	H	AlphaHelix	-54.67	-57.14	78.4	3G5U
ASG	SER	A	1000	911	H	AlphaHelix	-53.27	-36.94	9.4	3G5U
ASG	ALA	A	1001	912	H	AlphaHelix	-63.12	-56.89	2.0	3G5U
ASG	SER	A	1002	913	H	AlphaHelix	-45.43	-53.32	9.0	3G5U
ASG	HIS	A	1003	914	H	AlphaHelix	-49.48	-65.54	13.4	3G5U
ASG	ILE	A	1004	915	H	AlphaHelix	-59.63	-19.58	6.2	3G5U
ASG	ILE	A	1005	916	H	AlphaHelix	-77.67	-49.21	8.4	3G5U
ASG	ARG	A	1006	917	H	AlphaHelix	-54.74	-41.64	77.4	3G5U
ASG	ILE	A	1007	918	H	AlphaHelix	-67.36	-32.67	22.5	3G5U
ASG	ILE	A	1008	919	H	AlphaHelix	-82.33	-19.22	22.9	3G5U
ASG	GLU	A	1009	920	H	AlphaHelix	-71.44	-65.24	95.5	3G5U
ASG	LYS	A	1010	921	C	Coil	39.01	-155.03	51.9	3G5U
ASG	THR	A	1011	922	C	Coil	-151.52	79.50	81.1	3G5U
ASG	PRO	A	1012	923	T	Turn	-17.87	-43.77	52.9	3G5U
ASG	GLU	A	1013	924	T	Turn	62.67	-23.85	70.5	3G5U
ASG	ILE	A	1014	925	T	Turn	-177.15	71.37	14.0	3G5U
ASG	ASP	A	1015	926	T	Turn	-94.72	-91.57	94.5	3G5U
ASG	SER	A	1016	927	C	Coil	-106.40	-164.19	76.2	3G5U
ASG	TYR	A	1017	928	C	Coil	146.74	172.55	111.1	3G5U
ASG	SER	A	1018	929	T	Turn	-112.66	-58.43	81.5	3G5U
ASG	THR	A	1019	930	T	Turn	23.56	39.81	44.4	3G5U
ASG	GLN	A	1020	931	T	Turn	138.14	175.85	30.0	3G5U
ASG	GLY	A	1021	932	T	Turn	-137.84	30.88	45.3	3G5U
ASG	LEU	A	1022	933	C	Coil	57.10	32.73	86.2	3G5U
ASG	LYS	A	1023	934	T	Turn	-27.71	131.46	100.8	3G5U
ASG	PRO	A	1024	935	T	Turn	-67.56	41.91	124.6	3G5U
ASG	ASN	A	1025	936	T	Turn	-153.60	-18.50	102.0	3G5U
ASG	MET	A	1026	937	T	Turn	-62.82	17.14	4.4	3G5U
ASG	LEU	A	1027	938	T	Turn	-82.89	-13.38	82.4	3G5U
ASG	GLU	A	1028	939	T	Turn	-46.93	-75.61	91.1	3G5U
ASG	GLY	A	1029	940	C	Coil	101.72	37.10	6.3	3G5U
ASG	ASN	A	1030	941	C	Coil	-93.48	117.25	42.7	3G5U
ASG	VAL	A	1031	942	E	Strand	-89.72	130.87	5.2	3G5U
ASG	GLN	A	1032	943	E	Strand	-115.72	120.84	72.0	3G5U
ASG	PHE	A	1033	944	E	Strand	-122.31	112.33	9.2	3G5U
ASG	SER	A	1034	945	E	Strand	-126.21	136.79	66.5	3G5U
ASG	GLY	A	1035	946	T	Turn	73.47	-51.69	24.3	3G5U
ASG	VAL	A	1036	947	T	Turn	15.61	92.23	0.8	3G5U
ASG	VAL	A	1037	948	E	Strand	-125.50	133.04	37.1	3G5U
ASG	PHE	A	1038	949	E	Strand	-176.53	147.50	6.0	3G5U
ASG	ASN	A	1039	950	T	Turn	-141.95	115.30	1.7	3G5U
ASG	TYR	A	1040	951	T	Turn	-44.85	121.64	74.2	3G5U
ASG	PRO	A	1041	952	T	Turn	-22.40	102.00	69.3	3G5U
ASG	THR	A	1042	953	T	Turn	157.00	12.22	60.1	3G5U
ASG	ARG	A	1043	954	T	Turn	-25.51	-31.47	137.6	3G5U

ASG	PRO	A	1044	955	T	Turn	-49.07	-36.65	118.2	3G5U
ASG	SER	A	1045	956	T	Turn	-76.65	35.21	75.1	3G5U
ASG	ILE	A	1046	957	T	Turn	42.09	175.09	105.6	3G5U
ASG	PRO	A	1047	958	T	Turn	-91.05	164.01	23.6	3G5U
ASG	VAL	A	1048	959	T	Turn	-97.08	0.64	25.2	3G5U
ASG	LEU	A	1049	960	E	Strand	-128.82	102.82	1.2	3G5U
ASG	GLN	A	1050	961	E	Strand	-120.71	83.89	105.2	3G5U
ASG	GLY	A	1051	962	T	Turn	85.12	49.26	45.9	3G5U
ASG	LEU	A	1052	963	T	Turn	-94.19	146.77	1.6	3G5U
ASG	SER	A	1053	964	C	Coil	-158.92	115.80	54.6	3G5U
ASG	LEU	A	1054	965	E	Strand	-143.02	-163.92	33.1	3G5U
ASG	GLU	A	1055	966	E	Strand	-179.43	171.14	60.0	3G5U
ASG	VAL	A	1056	967	E	Strand	-151.10	124.25	1.0	3G5U
ASG	LYS	A	1057	968	B	Bridge	-53.58	-159.29	89.4	3G5U
ASG	LYS	A	1058	969	T	Turn	-110.98	169.17	97.4	3G5U
ASG	GLY	A	1059	970	T	Turn	36.20	28.39	11.7	3G5U
ASG	GLN	A	1060	971	T	Turn	-126.20	-137.54	14.6	3G5U
ASG	THR	A	1061	972	E	Strand	-152.69	102.61	2.2	3G5U
ASG	LEU	A	1062	973	E	Strand	-79.45	113.73	6.0	3G5U
ASG	ALA	A	1063	974	E	Strand	-88.98	124.52	0.0	3G5U
ASG	LEU	A	1064	975	E	Strand	-117.92	124.22	7.2	3G5U
ASG	VAL	A	1065	976	E	Strand	-131.12	106.58	10.8	3G5U
ASG	GLY	A	1066	977	C	Coil	-111.54	-160.62	5.9	3G5U
ASG	SER	A	1067	978	C	Coil	-76.68	-72.16	40.0	3G5U
ASG	SER	A	1068	979	C	Coil	-175.40	153.08	81.2	3G5U
ASG	GLY	A	1069	980	T	Turn	53.66	-114.92	47.0	3G5U
ASG	CYS	A	1070	981	T	Turn	-48.99	168.00	49.8	3G5U
ASG	GLY	A	1071	982	T	Turn	99.58	-71.99	4.7	3G5U
ASG	LYS	A	1072	983	H	AlphaHelix	-62.46	-43.81	3.6	3G5U
ASG	SER	A	1073	984	H	AlphaHelix	-62.25	-58.22	29.8	3G5U
ASG	THR	A	1074	985	H	AlphaHelix	-49.02	-46.83	4.8	3G5U
ASG	VAL	A	1075	986	H	AlphaHelix	-51.15	-68.84	12.4	3G5U
ASG	VAL	A	1076	987	H	AlphaHelix	-37.76	-67.89	6.8	3G5U
ASG	GLN	A	1077	988	H	AlphaHelix	-37.90	-63.89	24.7	3G5U
ASG	LEU	A	1078	989	H	AlphaHelix	-39.27	-42.77	1.3	3G5U
ASG	LEU	A	1079	990	H	AlphaHelix	-65.43	-39.19	5.6	3G5U
ASG	GLU	A	1080	991	H	AlphaHelix	-73.26	2.82	2.8	3G5U
ASG	ARG	A	1081	992	T	Turn	37.33	56.80	31.4	3G5U
ASG	PHE	A	1082	993	T	Turn	-84.18	-50.33	19.4	3G5U
ASG	TYR	A	1083	994	T	Turn	-115.25	137.05	17.0	3G5U
ASG	ASP	A	1084	995	T	Turn	-92.59	130.68	61.6	3G5U
ASG	PRO	A	1085	996	T	Turn	-43.40	137.64	14.6	3G5U
ASG	MET	A	1086	997	T	Turn	-71.02	-16.58	60.0	3G5U
ASG	ALA	A	1087	998	B	Bridge	-166.42	141.43	44.9	3G5U
ASG	GLY	A	1088	999	T	Turn	101.30	-168.46	40.5	3G5U
ASG	SER	A	1089	1000	E	Strand	-157.52	-175.90	18.9	3G5U
ASG	VAL	A	1090	1001	E	Strand	-147.93	160.74	2.5	3G5U
ASG	PHE	A	1091	1002	E	Strand	-145.31	102.71	69.6	3G5U
ASG	LEU	A	1092	1003	T	Turn	-59.89	-3.58	15.6	3G5U
ASG	ASP	A	1093	1004	T	Turn	176.87	-59.89	37.4	3G5U
ASG	GLY	A	1094	1005	T	Turn	-135.66	-1.89	31.9	3G5U
ASG	LYS	A	1095	1006	C	Coil	-173.39	129.34	70.2	3G5U
ASG	GLU	A	1096	1007	T	Turn	6.72	89.93	70.6	3G5U
ASG	ILE	A	1097	1008	B	Bridge	-83.39	78.21	0.6	3G5U
ASG	LYS	A	1098	1009	T	Turn	-163.24	-66.03	105.3	3G5U
ASG	GLN	A	1099	1010	T	Turn	-123.06	93.91	87.0	3G5U
ASG	LEU	A	1100	1011	T	Turn	-146.57	146.61	0.3	3G5U
ASG	ASN	A	1101	1012	C	Coil	-65.42	105.52	13.2	3G5U
ASG	VAL	A	1102	1013	H	AlphaHelix	-35.39	-56.62	0.6	3G5U
ASG	GLN	A	1103	1014	H	AlphaHelix	-51.46	-39.47	92.5	3G5U
ASG	TRP	A	1104	1015	H	AlphaHelix	-76.72	-51.22	23.9	3G5U
ASG	LEU	A	1105	1016	H	AlphaHelix	-42.20	-48.89	2.9	3G5U
ASG	ARG	A	1106	1017	H	AlphaHelix	-80.42	-2.46	13.4	3G5U
ASG	ALA	A	1107	1018	T	Turn	-59.27	-46.07	29.1	3G5U
ASG	GLN	A	1108	1019	T	Turn	-97.89	112.28	32.3	3G5U
ASG	LEU	A	1109	1020	T	Turn	-173.24	88.59	2.3	3G5U
ASG	GLY	A	1110	1021	E	Strand	-78.82	78.71	0.2	3G5U
ASG	ILE	A	1111	1022	E	Strand	-95.33	139.95	33.4	3G5U
ASG	VAL	A	1112	1023	E	Strand	-162.16	125.29	6.1	3G5U
ASG	SER	A	1113	1024	E	Strand	-124.42	178.46	18.8	3G5U
ASG	GLN	A	1114	1025	T	Turn	-31.38	-84.97	72.3	3G5U
ASG	GLU	A	1115	1026	T	Turn	-82.09	104.04	147.3	3G5U
ASG	PRO	A	1116	1027	T	Turn	-69.36	-139.89	14.1	3G5U
ASG	ILE	A	1117	1028	C	Coil	145.38	155.91	46.0	3G5U

ASG	LEU	A	1118	1029	C	Coil	-158.88	135.69	10.1	3G5U
ASG	PHE	A	1119	1030	T	Turn	-80.72	149.31	60.5	3G5U
ASG	ASP	A	1120	1031	T	Turn	-55.03	55.82	22.8	3G5U
ASG	CYS	A	1121	1032	T	Turn	-100.74	171.51	43.3	3G5U
ASG	SER	A	1122	1033	B	Bridge	-63.36	156.35	24.4	3G5U
ASG	ILE	A	1123	1034	H	AlphaHelix	-60.38	-27.94	18.2	3G5U
ASG	ALA	A	1124	1035	H	AlphaHelix	-57.23	-38.98	9.8	3G5U
ASG	GLU	A	1125	1036	H	AlphaHelix	-74.92	-49.01	83.2	3G5U
ASG	ASN	A	1126	1037	H	AlphaHelix	-50.29	-69.44	5.2	3G5U
ASG	ILE	A	1127	1038	H	AlphaHelix	-29.78	-56.93	0.2	3G5U
ASG	ALA	A	1128	1039	H	AlphaHelix	-64.64	17.52	10.5	3G5U
ASG	TYR	A	1129	1040	T	Turn	-26.35	101.40	11.9	3G5U
ASG	GLY	A	1130	1041	T	Turn	-52.45	51.70	40.5	3G5U
ASG	ASP	A	1131	1042	T	Turn	-37.86	-34.04	19.1	3G5U
ASG	ASN	A	1132	1043	T	Turn	174.60	-152.82	80.2	3G5U
ASG	SER	A	1133	1044	T	Turn	-41.94	-26.58	117.6	3G5U
ASG	ARG	A	1134	1045	T	Turn	-38.06	107.81	112.8	3G5U
ASG	VAL	A	1135	1046	T	Turn	-75.52	155.89	110.9	3G5U
ASG	VAL	A	1136	1047	T	Turn	-61.14	60.09	63.5	3G5U
ASG	SER	A	1137	1048	T	Turn	-54.90	98.72	29.6	3G5U
ASG	TYR	A	1138	1049	H	AlphaHelix	-45.33	-80.40	133.9	3G5U
ASG	GLU	A	1139	1050	H	AlphaHelix	-42.56	-27.08	117.3	3G5U
ASG	GLU	A	1140	1051	H	AlphaHelix	-67.55	-60.13	21.9	3G5U
ASG	ILE	A	1141	1052	H	AlphaHelix	-50.95	-24.24	3.8	3G5U
ASG	VAL	A	1142	1053	H	AlphaHelix	-77.65	-41.73	23.1	3G5U
ASG	ARG	A	1143	1054	H	AlphaHelix	-55.41	-48.07	130.3	3G5U
ASG	ALA	A	1144	1055	H	AlphaHelix	-56.38	-72.45	0.0	3G5U
ASG	ALA	A	1145	1056	H	AlphaHelix	-37.27	-35.73	0.0	3G5U
ASG	LYS	A	1146	1057	H	AlphaHelix	-61.42	-82.58	108.3	3G5U
ASG	GLU	A	1147	1058	H	AlphaHelix	-60.37	-15.38	55.8	3G5U
ASG	ALA	A	1148	1059	H	AlphaHelix	-68.23	-42.46	0.6	3G5U
ASG	ASN	A	1149	1060	C	Coil	78.46	23.63	26.7	3G5U
ASG	ILE	A	1150	1061	H	AlphaHelix	-96.98	-8.23	4.0	3G5U
ASG	HIS	A	1151	1062	H	AlphaHelix	-55.73	-28.85	33.7	3G5U
ASG	GLN	A	1152	1063	H	AlphaHelix	-54.34	-29.26	85.0	3G5U
ASG	PHE	A	1153	1064	H	AlphaHelix	-92.71	-29.97	50.5	3G5U
ASG	ILE	A	1154	1065	H	AlphaHelix	-69.67	-37.35	6.8	3G5U
ASG	ASP	A	1155	1066	H	AlphaHelix	-50.68	-55.61	90.2	3G5U
ASG	SER	A	1156	1067	C	Coil	-113.12	-80.72	81.5	3G5U
ASG	LEU	A	1157	1068	T	Turn	3.60	110.14	71.3	3G5U
ASG	PRO	A	1158	1069	T	Turn	-16.07	138.43	108.7	3G5U
ASG	ASP	A	1159	1070	T	Turn	53.12	2.97	117.7	3G5U
ASG	LYS	A	1160	1071	G	310Helix	40.72	-140.93	99.7	3G5U
ASG	TYR	A	1161	1072	G	310Helix	-41.67	-36.84	9.2	3G5U
ASG	ASN	A	1162	1073	G	310Helix	-61.11	-24.77	109.2	3G5U
ASG	THR	A	1163	1074	C	Coil	-56.17	113.05	43.8	3G5U
ASG	ARG	A	1164	1075	B	Bridge	-61.74	157.94	129.8	3G5U
ASG	VAL	A	1165	1076	T	Turn	-55.14	-11.97	6.2	3G5U
ASG	GLY	A	1166	1077	T	Turn	56.58	97.02	15.4	3G5U
ASG	ASP	A	1167	1078	T	Turn	74.14	32.85	109.2	3G5U
ASG	LYS	A	1168	1079	T	Turn	75.26	3.76	90.8	3G5U
ASG	GLY	A	1169	1080	T	Turn	144.09	-71.47	4.0	3G5U
ASG	THR	A	1170	1081	T	Turn	-32.95	91.78	120.7	3G5U
ASG	GLN	A	1171	1082	T	Turn	172.48	12.49	94.8	3G5U
ASG	LEU	A	1172	1083	T	Turn	-162.15	134.02	58.3	3G5U
ASG	SER	A	1173	1084	C	Coil	-58.02	150.54	57.7	3G5U
ASG	GLY	A	1174	1085	H	AlphaHelix	-55.66	-29.07	31.4	3G5U
ASG	GLY	A	1175	1086	H	AlphaHelix	-54.55	-57.84	0.0	3G5U
ASG	GLN	A	1176	1087	H	AlphaHelix	-58.13	-44.16	19.8	3G5U
ASG	LYS	A	1177	1088	H	AlphaHelix	-49.21	-57.12	30.4	3G5U
ASG	GLN	A	1178	1089	H	AlphaHelix	-54.66	-33.93	6.0	3G5U
ASG	ARG	A	1179	1090	H	AlphaHelix	-58.14	-45.96	15.7	3G5U
ASG	ILE	A	1180	1091	H	AlphaHelix	-64.15	-52.65	3.8	3G5U
ASG	ALA	A	1181	1092	H	AlphaHelix	-45.12	-53.11	4.2	3G5U
ASG	ILE	A	1182	1093	H	AlphaHelix	-55.42	-41.61	19.2	3G5U
ASG	ALA	A	1183	1094	H	AlphaHelix	-53.97	-80.97	0.0	3G5U
ASG	ARG	A	1184	1095	H	AlphaHelix	-13.77	-61.03	26.5	3G5U
ASG	ALA	A	1185	1096	H	AlphaHelix	-59.28	-74.26	8.5	3G5U
ASG	LEU	A	1186	1097	H	AlphaHelix	-55.97	-1.99	11.9	3G5U
ASG	VAL	A	1187	1098	H	AlphaHelix	-84.25	-32.43	6.7	3G5U
ASG	ARG	A	1188	1099	H	AlphaHelix	-71.90	-20.36	40.4	3G5U
ASG	GLN	A	1189	1100	C	Coil	55.62	59.81	103.3	3G5U
ASG	PRO	A	1190	1101	C	Coil	-63.77	-144.88	7.1	3G5U
ASG	HIS	A	1191	1102	C	Coil	-158.39	-29.84	51.9	3G5U

ASG	ILE	A	1192	1103	C	Coil	-122.03	162.84	10.0	3G5U
ASG	LEU	A	1193	1104	E	Strand	-143.47	138.79	10.4	3G5U
ASG	LEU	A	1194	1105	E	Strand	-113.48	93.23	1.6	3G5U
ASG	LEU	A	1195	1106	E	Strand	-96.25	83.59	10.2	3G5U
ASG	ASP	A	1196	1107	E	Strand	-77.00	86.55	13.0	3G5U
ASG	GLU	A	1197	1108	T	Turn	44.71	21.61	29.1	3G5U
ASG	ALA	A	1198	1109	T	Turn	-18.96	-91.00	12.9	3G5U
ASG	THR	A	1199	1110	T	Turn	-74.67	99.09	12.1	3G5U
ASG	SER	A	1200	1111	T	Turn	-140.21	23.53	46.6	3G5U
ASG	ALA	A	1201	1112	T	Turn	-175.10	93.43	82.7	3G5U
ASG	LEU	A	1202	1113	T	Turn	-169.02	-143.88	39.5	3G5U
ASG	ASP	A	1203	1114	C	Coil	-173.68	-176.04	83.7	3G5U
ASG	THR	A	1204	1115	H	AlphaHelix	0.14	-98.97	97.9	3G5U
ASG	GLU	A	1205	1116	H	AlphaHelix	-83.74	0.38	118.1	3G5U
ASG	SER	A	1206	1117	H	AlphaHelix	-93.36	-59.45	17.0	3G5U
ASG	GLU	A	1207	1118	H	AlphaHelix	-48.55	-77.07	53.7	3G5U
ASG	LYS	A	1208	1119	H	AlphaHelix	-40.49	-68.60	108.7	3G5U
ASG	VAL	A	1209	1120	H	AlphaHelix	-44.64	-39.08	6.6	3G5U
ASG	VAL	A	1210	1121	H	AlphaHelix	-66.49	-35.14	6.0	3G5U
ASG	GLN	A	1211	1122	H	AlphaHelix	-67.52	-23.86	41.3	3G5U
ASG	GLU	A	1212	1123	H	AlphaHelix	-77.57	-39.08	69.5	3G5U
ASG	ALA	A	1213	1124	H	AlphaHelix	-65.48	-77.62	2.0	3G5U
ASG	LEU	A	1214	1125	H	AlphaHelix	-36.39	-30.87	14.3	3G5U
ASG	ASP	A	1215	1126	H	AlphaHelix	-63.21	-81.80	62.0	3G5U
ASG	LYS	A	1216	1127	H	AlphaHelix	-56.87	-14.53	131.3	3G5U
ASG	ALA	A	1217	1128	H	AlphaHelix	-71.73	-32.17	6.5	3G5U
ASG	ARG	A	1218	1129	T	Turn	-97.60	-164.88	25.5	3G5U
ASG	GLU	A	1219	1130	T	Turn	66.52	-22.27	125.8	3G5U
ASG	GLY	A	1220	1131	T	Turn	-88.96	-16.66	63.9	3G5U
ASG	ARG	A	1221	1132	T	Turn	-155.99	160.93	31.8	3G5U
ASG	THR	A	1222	1133	T	Turn	-69.16	141.55	0.6	3G5U
ASG	CYS	A	1223	1134	E	Strand	-158.65	126.95	0.4	3G5U
ASG	ILE	A	1224	1135	E	Strand	-91.21	102.93	11.9	3G5U
ASG	VAL	A	1225	1136	E	Strand	-93.59	111.01	23.7	3G5U
ASG	ILE	A	1226	1137	E	Strand	-116.20	145.51	2.1	3G5U
ASG	ALA	A	1227	1138	C	Coil	-171.21	176.86	16.6	3G5U
ASG	HIS	A	1228	1139	C	Coil	-112.37	13.32	94.6	3G5U
ASG	ARG	A	1229	1140	T	Turn	-88.88	61.88	60.2	3G5U
ASG	LEU	A	1230	1141	T	Turn	-42.83	-25.32	39.9	3G5U
ASG	SER	A	1231	1142	T	Turn	-78.69	-69.75	50.9	3G5U
ASG	THR	A	1232	1143	T	Turn	-70.84	8.22	54.2	3G5U
ASG	ILE	A	1233	1144	T	Turn	-79.12	-14.60	12.5	3G5U
ASG	GLN	A	1234	1145	T	Turn	-47.23	-36.35	123.6	3G5U
ASG	ASN	A	1235	1146	T	Turn	-76.82	48.78	75.3	3G5U
ASG	ALA	A	1236	1147	T	Turn	-108.15	150.72	15.1	3G5U
ASG	ASP	A	1237	1148	T	Turn	-79.30	-63.57	75.2	3G5U
ASG	LEU	A	1238	1149	E	Strand	-124.25	108.51	32.5	3G5U
ASG	ILE	A	1239	1150	E	Strand	-93.37	112.55	0.6	3G5U
ASG	VAL	A	1240	1151	E	Strand	-105.18	133.87	3.2	3G5U
ASG	VAL	A	1241	1152	E	Strand	-105.82	105.37	4.4	3G5U
ASG	ILE	A	1242	1153	E	Strand	-100.05	140.05	9.2	3G5U
ASG	GLN	A	1243	1154	E	Strand	-112.58	90.43	79.2	3G5U
ASG	ASN	A	1244	1155	T	Turn	9.69	101.60	44.9	3G5U
ASG	GLY	A	1245	1156	T	Turn	100.35	-35.11	0.2	3G5U
ASG	LYS	A	1246	1157	E	Strand	-136.45	131.66	86.6	3G5U
ASG	VAL	A	1247	1158	E	Strand	-82.92	120.77	46.8	3G5U
ASG	LYS	A	1248	1159	E	Strand	-109.03	-31.98	147.6	3G5U
ASG	GLU	A	1249	1160	E	Strand	-130.46	172.57	17.7	3G5U
ASG	HIS	A	1250	1161	E	Strand	167.54	158.92	99.9	3G5U
ASG	GLY	A	1251	1162	E	Strand	136.42	-152.36	6.0	3G5U
ASG	THR	A	1252	1163	C	Coil	-89.30	160.66	43.9	3G5U
ASG	HIS	A	1253	1164	H	AlphaHelix	-45.58	-71.87	30.8	3G5U
ASG	GLN	A	1254	1165	H	AlphaHelix	-56.09	-29.65	122.1	3G5U
ASG	GLN	A	1255	1166	H	AlphaHelix	-68.51	-37.10	92.3	3G5U
ASG	LEU	A	1256	1167	H	AlphaHelix	-68.70	-44.64	0.0	3G5U
ASG	LEU	A	1257	1168	H	AlphaHelix	-63.37	-39.11	66.5	3G5U
ASG	ALA	A	1258	1169	H	AlphaHelix	-49.22	-44.13	46.4	3G5U
ASG	GLN	A	1259	1170	C	Coil	-79.00	62.10	89.6	3G5U
ASG	LYS	A	1260	1171	C	Coil	-48.31	124.46	134.0	3G5U
ASG	GLY	A	1261	1172	C	Coil	162.56	-116.56	33.8	3G5U
ASG	ILE	A	1262	1173	H	AlphaHelix	-57.25	-77.65	69.6	3G5U
ASG	TYR	A	1263	1174	H	AlphaHelix	-45.66	-33.88	5.6	3G5U
ASG	PHE	A	1264	1175	H	AlphaHelix	-59.76	-64.00	74.4	3G5U
ASG	SER	A	1265	1176	H	AlphaHelix	-45.90	-38.20	70.2	3G5U

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ASG MET A 1266 1177 H AlphaHelix -61.46 -41.66 63.6 3G5U
ASG VAL A 1267 1178 H AlphaHelix -78.27 -30.69 28.1 3G5U
ASG SER A 1268 1179 H AlphaHelix -74.56 -19.04 65.6 3G5U
ASG VAL A 1269 1180 H AlphaHelix -90.86 -33.43 101.7 3G5U
ASG GLN A 1270 1181 H AlphaHelix -56.64 -34.74 64.6 3G5U
ASG ALA A 1271 1182 C Coil 56.92 360.00 117.8 3G5U
REM
REM ----- Mainchain hydrogen bonds ----- 3G5U
REM
REM Definition of Stickle et al., J.Mol.Biol. 226:1143-1159, 1992 3G5U
REM A1 is the angle between the planes of donor complex and O..N-C 3G5U
REM A2 is the angle between the planes of acceptor complex and N..O=C 3G5U
REM 3G5U
HBT 995 3G5U
HBI 0 3G5U
HBC 995 3g5u.pdb A 1182 3G5U
REM
REM |--Residue 1--| |--Residue 2--| N-O N..O=C O..N-C A1 A2 3G5U
ACC VAL A 33 0 -> LEU A 36 3 3.0 172.5 95.5 59.5 65.9 3G5U
ACC VAL A 33 0 -> THR A 37 4 3.0 108.5 114.5 29.1 71.1 3G5U
ACC SER A 34 1 -> PHE A 39 6 3.0 150.0 104.6 27.3 76.6 3G5U
ACC VAL A 35 2 -> PHE A 39 6 3.1 127.8 154.7 27.8 75.5 3G5U
DNR LEU A 36 3 -> VAL A 33 0 3.0 172.5 95.5 59.5 65.9 3G5U
ACC LEU A 36 3 -> ARG A 40 7 3.0 143.3 108.9 37.9 51.9 3G5U
DNR THR A 37 4 -> VAL A 33 0 3.0 108.5 114.5 29.1 71.1 3G5U
ACC THR A 37 4 -> ARG A 40 7 3.0 124.0 124.2 49.3 81.3 3G5U
ACC MET A 38 5 -> TYR A 41 8 3.0 121.5 106.5 50.0 82.1 3G5U
DNR PHE A 39 6 -> SER A 34 1 3.0 150.0 104.6 27.3 76.6 3G5U
DNR PHE A 39 6 -> VAL A 35 2 3.1 127.8 154.7 27.8 75.5 3G5U
DNR ARG A 40 7 -> LEU A 36 3 3.0 143.3 108.9 37.9 51.9 3G5U
DNR ARG A 40 7 -> THR A 37 4 3.0 124.0 124.2 49.3 81.3 3G5U
DNR TYR A 41 8 -> MET A 38 5 3.0 121.5 106.5 50.0 82.1 3G5U
ACC GLY A 43 10 -> ARG A 47 14 3.1 107.1 135.8 19.3 78.5 3G5U
ACC TRP A 44 11 -> LEU A 48 15 3.1 162.2 113.5 10.2 22.6 3G5U
ACC LEU A 45 12 -> TYR A 49 16 3.2 116.5 137.3 12.6 80.7 3G5U
ACC ASP A 46 13 -> MET A 50 17 3.0 167.3 119.0 13.3 10.6 3G5U
DNR ARG A 47 14 -> GLY A 43 10 3.1 107.1 135.8 19.3 78.5 3G5U
ACC ARG A 47 14 -> LEU A 51 18 3.0 150.4 115.4 0.4 74.6 3G5U
DNR LEU A 48 15 -> TRP A 44 11 3.1 162.2 113.5 10.2 22.6 3G5U
ACC LEU A 48 15 -> VAL A 52 19 3.1 159.3 127.3 15.6 74.8 3G5U
DNR TYR A 49 16 -> LEU A 45 12 3.2 116.5 137.3 12.6 80.7 3G5U
ACC TYR A 49 16 -> GLY A 53 20 3.0 161.1 117.0 4.9 64.8 3G5U
DNR MET A 50 17 -> ASP A 46 13 3.0 167.3 119.0 13.3 10.6 3G5U
ACC MET A 50 17 -> THR A 54 21 3.0 165.4 114.5 11.6 3.5 3G5U
DNR LEU A 51 18 -> ARG A 47 14 3.0 150.4 115.4 0.4 74.6 3G5U
ACC LEU A 51 18 -> LEU A 55 22 3.1 149.0 120.0 3.5 72.3 3G5U
DNR VAL A 52 19 -> LEU A 48 15 3.1 159.3 127.3 15.6 74.8 3G5U
ACC VAL A 52 19 -> ALA A 56 23 3.2 155.5 103.6 0.5 18.3 3G5U
DNR GLY A 53 20 -> TYR A 49 16 3.0 161.1 117.0 4.9 64.8 3G5U
ACC GLY A 53 20 -> ALA A 57 24 3.0 158.7 116.5 10.9 58.9 3G5U
DNR THR A 54 21 -> MET A 50 17 3.0 165.4 114.5 11.6 3.5 3G5U
ACC THR A 54 21 -> ALA A 57 24 3.0 130.2 125.5 58.7 80.5 3G5U
ACC THR A 54 21 -> ILE A 58 25 3.0 156.0 103.1 5.0 25.9 3G5U
DNR LEU A 55 22 -> LEU A 51 18 3.1 149.0 120.0 3.5 72.3 3G5U
ACC LEU A 55 22 -> ILE A 59 26 3.1 169.1 103.1 17.1 32.0 3G5U
DNR ALA A 56 23 -> VAL A 52 19 3.2 155.5 103.6 0.5 18.3 3G5U
ACC ALA A 56 23 -> HIS A 60 27 3.0 163.0 124.5 7.9 60.0 3G5U
DNR ALA A 57 24 -> GLY A 53 20 3.0 158.7 116.5 10.9 58.9 3G5U
DNR ALA A 57 24 -> THR A 54 21 3.0 130.2 125.5 58.7 80.5 3G5U
ACC ALA A 57 24 -> GLY A 61 28 3.1 167.6 113.0 9.7 54.0 3G5U
DNR ILE A 58 25 -> THR A 54 21 3.0 156.0 103.1 5.0 25.9 3G5U
ACC ILE A 58 25 -> GLY A 61 28 3.0 137.4 115.0 48.6 80.9 3G5U
ACC ILE A 58 25 -> VAL A 62 29 3.2 158.2 115.3 2.4 27.0 3G5U
DNR ILE A 59 26 -> LEU A 55 22 3.1 169.1 103.1 17.1 32.0 3G5U
ACC ILE A 59 26 -> ALA A 63 30 3.0 150.7 107.9 37.6 39.3 3G5U
DNR HIS A 60 27 -> ALA A 56 23 3.0 163.0 124.5 7.9 60.0 3G5U
ACC HIS A 60 27 -> ALA A 63 30 3.0 109.1 133.2 47.8 84.9 3G5U
ACC HIS A 60 27 -> LEU A 64 31 3.3 157.8 98.4 5.2 39.7 3G5U
DNR GLY A 61 28 -> ALA A 57 24 3.1 167.6 113.0 9.7 54.0 3G5U
DNR GLY A 61 28 -> ILE A 58 25 3.0 137.4 115.0 48.6 80.9 3G5U
ACC GLY A 61 28 -> LEU A 64 31 3.0 121.7 112.4 56.8 89.2 3G5U
DNR VAL A 62 29 -> ILE A 58 25 3.2 158.2 115.3 2.4 27.0 3G5U
ACC VAL A 62 29 -> LEU A 66 33 3.0 161.4 128.6 13.8 54.5 3G5U
DNR ALA A 63 30 -> ILE A 59 26 3.0 150.7 107.9 37.6 39.3 3G5U

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DNR	ALA	A	63	30	->	HIS	A	60	27	3.0	109.1	133.2	47.8	84.9	3G5U
ACC	ALA	A	63	30	->	LEU	A	66	33	3.0	118.0	114.6	59.4	85.2	3G5U
ACC	ALA	A	63	30	->	MET	A	67	34	3.0	169.5	123.6	5.7	60.7	3G5U
DNR	LEU	A	64	31	->	HIS	A	60	27	3.3	157.8	98.4	5.2	39.7	3G5U
DNR	LEU	A	64	31	->	GLY	A	61	28	3.0	121.7	112.4	56.8	89.2	3G5U
ACC	LEU	A	64	31	->	MET	A	68	35	3.2	141.5	109.6	28.2	48.6	3G5U
ACC	PRO	A	65	32	->	MET	A	68	35	3.0	105.3	127.4	55.9	88.2	3G5U
ACC	PRO	A	65	32	->	LEU	A	69	36	3.1	159.6	104.9	10.3	47.4	3G5U
DNR	LEU	A	66	33	->	VAL	A	62	29	3.0	161.4	128.6	13.8	54.5	3G5U
DNR	LEU	A	66	33	->	ALA	A	63	30	3.0	118.0	114.6	59.4	85.2	3G5U
ACC	LEU	A	66	33	->	ILE	A	70	37	3.0	169.9	110.8	9.8	9.1	3G5U
DNR	MET	A	67	34	->	ALA	A	63	30	3.0	169.5	123.6	5.7	60.7	3G5U
ACC	MET	A	67	34	->	PHE	A	71	38	3.1	150.9	124.0	15.3	65.3	3G5U
DNR	MET	A	68	35	->	LEU	A	64	31	3.2	141.5	109.6	28.2	48.6	3G5U
DNR	MET	A	68	35	->	PRO	A	65	32	3.0	105.3	127.4	55.9	88.2	3G5U
ACC	MET	A	68	35	->	PHE	A	71	38	3.0	133.5	119.4	57.8	86.6	3G5U
ACC	MET	A	68	35	->	GLY	A	72	39	3.0	157.8	103.7	16.3	19.8	3G5U
DNR	LEU	A	69	36	->	PRO	A	65	32	3.1	159.6	104.9	10.3	47.4	3G5U
ACC	LEU	A	69	36	->	GLY	A	72	39	3.0	126.9	132.3	49.5	81.9	3G5U
ACC	LEU	A	69	36	->	ASP	A	73	40	3.1	158.5	96.1	7.3	37.9	3G5U
DNR	ILE	A	70	37	->	LEU	A	66	33	3.0	169.9	110.8	9.8	9.1	3G5U
ACC	ILE	A	70	37	->	MET	A	74	41	3.0	166.5	124.3	7.0	82.1	3G5U
DNR	PHE	A	71	38	->	MET	A	67	34	3.1	150.9	124.0	15.3	65.3	3G5U
DNR	PHE	A	71	38	->	MET	A	68	35	3.0	133.5	119.4	57.8	86.6	3G5U
ACC	PHE	A	71	38	->	THR	A	75	42	3.0	144.2	129.4	24.8	62.4	3G5U
DNR	GLY	A	72	39	->	MET	A	68	35	3.0	157.8	103.7	16.3	19.8	3G5U
DNR	GLY	A	72	39	->	LEU	A	69	36	3.0	126.9	132.3	49.5	81.9	3G5U
ACC	GLY	A	72	39	->	ASP	A	76	43	3.0	163.4	106.1	21.3	11.8	3G5U
DNR	ASP	A	73	40	->	LEU	A	69	36	3.1	158.5	96.1	7.3	37.9	3G5U
ACC	ASP	A	73	40	->	ASP	A	76	43	3.3	96.4	119.0	55.4	87.6	3G5U
ACC	ASP	A	73	40	->	SER	A	77	44	3.1	149.9	119.5	5.4	89.5	3G5U
DNR	MET	A	74	41	->	ILE	A	70	37	3.0	166.5	124.3	7.0	82.1	3G5U
ACC	MET	A	74	41	->	PHE	A	78	45	3.1	150.8	121.8	31.2	49.0	3G5U
DNR	THR	A	75	42	->	PHE	A	71	38	3.0	144.2	129.4	24.8	62.4	3G5U
ACC	THR	A	75	42	->	PHE	A	78	45	3.2	101.2	132.5	59.0	80.2	3G5U
ACC	THR	A	75	42	->	ALA	A	79	46	3.0	151.6	104.9	34.0	54.4	3G5U
DNR	ASP	A	76	43	->	GLY	A	72	39	3.0	163.4	106.1	21.3	11.8	3G5U
DNR	ASP	A	76	43	->	ASP	A	73	40	3.3	96.4	119.0	55.4	87.6	3G5U
ACC	ASP	A	76	43	->	ALA	A	79	46	3.0	124.2	124.0	37.8	85.4	3G5U
ACC	ASP	A	76	43	->	SER	A	80	47	3.1	168.5	108.1	2.0	1.7	3G5U
DNR	SER	A	77	44	->	ASP	A	73	40	3.1	149.9	119.5	5.4	89.5	3G5U
ACC	SER	A	77	44	->	VAL	A	81	48	3.1	150.0	121.3	16.2	63.0	3G5U
DNR	PHE	A	78	45	->	MET	A	74	41	3.1	150.8	121.8	31.2	49.0	3G5U
DNR	PHE	A	78	45	->	THR	A	75	42	3.2	101.2	132.5	59.0	80.2	3G5U
ACC	PHE	A	78	45	->	GLY	A	82	49	3.1	137.1	125.4	32.7	64.8	3G5U
DNR	ALA	A	79	46	->	THR	A	75	42	3.0	151.6	104.9	34.0	54.4	3G5U
DNR	ALA	A	79	46	->	ASP	A	76	43	3.0	124.2	124.0	37.8	85.4	3G5U
ACC	ALA	A	79	46	->	GLY	A	82	49	3.0	114.5	124.4	56.0	87.0	3G5U
ACC	ALA	A	79	46	->	ASN	A	83	50	3.0	167.0	114.3	34.8	34.1	3G5U
DNR	SER	A	80	47	->	ASP	A	76	43	3.1	168.5	108.1	2.0	1.7	3G5U
ACC	SER	A	80	47	->	ASN	A	83	50	3.2	99.8	129.4	48.0	85.9	3G5U
ACC	SER	A	80	47	->	VAL	A	84	51	3.1	152.7	116.6	6.7	77.3	3G5U
DNR	VAL	A	81	48	->	SER	A	77	44	3.1	150.0	121.3	16.2	63.0	3G5U
ACC	VAL	A	81	48	->	SER	A	85	52	3.0	138.2	129.2	38.2	64.0	3G5U
DNR	GLY	A	82	49	->	PHE	A	78	45	3.1	137.1	125.4	32.7	64.8	3G5U
DNR	GLY	A	82	49	->	ALA	A	79	46	3.0	114.5	124.4	56.0	87.0	3G5U
ACC	GLY	A	82	49	->	LYS	A	86	53	3.0	134.9	120.7	29.8	74.9	3G5U
DNR	ASN	A	83	50	->	ALA	A	79	46	3.0	167.0	114.3	34.8	34.1	3G5U
DNR	ASN	A	83	50	->	SER	A	80	47	3.2	99.8	129.4	48.0	85.9	3G5U
ACC	ASN	A	83	50	->	LYS	A	86	53	3.0	107.5	127.7	57.8	83.9	3G5U
ACC	ASN	A	83	50	->	ASN	A	87	54	3.0	151.2	108.4	16.2	33.8	3G5U
DNR	VAL	A	84	51	->	SER	A	80	47	3.1	152.7	116.6	6.7	77.3	3G5U
ACC	VAL	A	84	51	->	SER	A	88	55	3.0	150.8	122.5	5.8	80.3	3G5U
DNR	SER	A	85	52	->	VAL	A	81	48	3.0	138.2	129.2	38.2	64.0	3G5U
DNR	LYS	A	86	53	->	GLY	A	82	49	3.0	134.9	120.7	29.8	74.9	3G5U
DNR	LYS	A	86	53	->	ASN	A	83	50	3.0	107.5	127.7	57.8	83.9	3G5U
DNR	ASN	A	87	54	->	ASN	A	83	50	3.0	151.2	108.4	16.2	33.8	3G5U
DNR	SER	A	88	55	->	VAL	A	84	51	3.0	150.8	122.5	5.8	80.3	3G5U
ACC	MET	A	91	58	->	ALA	A	94	61	3.3	114.3	122.7	49.4	77.0	3G5U
ACC	SER	A	92	59	->	ASP	A	95	62	3.0	125.3	139.6	13.0	77.7	3G5U
ACC	SER	A	92	59	->	LYS	A	96	63	3.1	158.0	104.4	20.2	0.2	3G5U
ACC	GLU	A	93	60	->	LYS	A	96	63	3.0	107.1	124.0	53.4	88.3	3G5U
ACC	GLU	A	93	60	->	ARG	A	97	64	3.0	151.5	112.6	27.6	49.8	3G5U
DNR	ALA	A	94	61	->	MET	A	91	58	3.3	114.3	122.7	49.4	77.0	3G5U

ACC	ALA	A	94	61	->	ALA	A	98	65	3.0	126.4	133.1	9.9	77.5	3G5U
DNR	ASP	A	95	62	->	SER	A	92	59	3.0	125.3	139.6	13.0	77.7	3G5U
ACC	ASP	A	95	62	->	MET	A	99	66	3.0	140.9	137.1	11.2	78.3	3G5U
DNR	LYS	A	96	63	->	SER	A	92	59	3.1	158.0	104.4	20.2	0.2	3G5U
DNR	LYS	A	96	63	->	GLU	A	93	60	3.0	107.1	124.0	53.4	88.3	3G5U
ACC	LYS	A	96	63	->	PHE	A	100	67	3.1	137.1	131.0	11.6	85.2	3G5U
DNR	ARG	A	97	64	->	GLU	A	93	60	3.0	151.5	112.6	27.6	49.8	3G5U
ACC	ARG	A	97	64	->	ALA	A	101	68	3.0	146.8	135.0	40.1	84.7	3G5U
DNR	ALA	A	98	65	->	ALA	A	94	61	3.0	126.4	133.1	9.9	77.5	3G5U
ACC	ALA	A	98	65	->	LYS	A	102	69	3.1	150.5	112.1	1.3	53.8	3G5U
DNR	MET	A	99	66	->	ASP	A	95	62	3.0	140.9	137.1	11.2	78.3	3G5U
ACC	MET	A	99	66	->	LEU	A	103	70	3.0	171.9	127.6	17.9	25.3	3G5U
DNR	PHE	A	100	67	->	LYS	A	96	63	3.1	137.1	131.0	11.6	85.2	3G5U
ACC	PHE	A	100	67	->	GLU	A	104	71	3.0	137.5	122.2	26.1	71.7	3G5U
DNR	ALA	A	101	68	->	ARG	A	97	64	3.0	146.8	135.0	40.1	84.7	3G5U
ACC	ALA	A	101	68	->	GLU	A	105	72	3.0	163.6	137.7	2.6	49.5	3G5U
DNR	LYS	A	102	69	->	ALA	A	98	65	3.1	150.5	112.1	1.3	53.8	3G5U
ACC	LYS	A	102	69	->	GLU	A	106	73	3.0	138.3	126.1	8.8	72.6	3G5U
DNR	LEU	A	103	70	->	MET	A	99	66	3.0	171.9	127.6	17.9	25.3	3G5U
ACC	LEU	A	103	70	->	MET	A	107	74	3.0	160.9	128.1	37.9	41.1	3G5U
DNR	GLU	A	104	71	->	PHE	A	100	67	3.0	137.5	122.2	26.1	71.7	3G5U
ACC	GLU	A	104	71	->	MET	A	107	74	3.0	107.5	136.8	56.5	77.0	3G5U
ACC	GLU	A	104	71	->	THR	A	108	75	3.0	157.0	101.2	34.4	50.0	3G5U
DNR	GLU	A	105	72	->	ALA	A	101	68	3.0	163.6	137.7	2.6	49.5	3G5U
ACC	GLU	A	105	72	->	THR	A	108	75	3.0	117.8	130.3	33.6	83.6	3G5U
ACC	GLU	A	105	72	->	THR	A	109	76	3.1	149.1	112.2	6.6	22.1	3G5U
DNR	GLU	A	106	73	->	LYS	A	102	69	3.0	138.3	126.1	8.8	72.6	3G5U
ACC	GLU	A	106	73	->	TYR	A	110	77	3.0	156.7	113.9	18.3	73.8	3G5U
DNR	MET	A	107	74	->	LEU	A	103	70	3.0	160.9	128.1	37.9	41.1	3G5U
DNR	MET	A	107	74	->	GLU	A	104	71	3.0	107.5	136.8	56.5	77.0	3G5U
ACC	MET	A	107	74	->	ALA	A	111	78	3.1	137.4	124.6	8.1	72.8	3G5U
DNR	THR	A	108	75	->	GLU	A	104	71	3.0	157.0	101.2	34.4	50.0	3G5U
DNR	THR	A	108	75	->	GLU	A	105	72	3.0	117.8	130.3	33.6	83.6	3G5U
ACC	THR	A	108	75	->	TYR	A	112	79	3.0	168.5	112.5	1.0	31.6	3G5U
DNR	THR	A	109	76	->	GLU	A	105	72	3.1	149.1	112.2	6.6	22.1	3G5U
ACC	THR	A	109	76	->	TYR	A	113	80	3.0	151.6	117.6	43.9	64.0	3G5U
DNR	TYR	A	110	77	->	GLU	A	106	73	3.0	156.7	113.9	18.3	73.8	3G5U
ACC	TYR	A	110	77	->	TYR	A	113	80	3.0	118.7	134.9	37.2	82.4	3G5U
ACC	TYR	A	110	77	->	TYR	A	114	81	3.0	179.1	107.4	6.4	66.3	3G5U
DNR	ALA	A	111	78	->	MET	A	107	74	3.1	137.4	124.6	8.1	72.8	3G5U
ACC	ALA	A	111	78	->	THR	A	115	82	3.0	159.9	133.9	9.9	59.6	3G5U
DNR	TYR	A	112	79	->	THR	A	108	75	3.0	168.5	112.5	1.0	31.6	3G5U
ACC	TYR	A	112	79	->	GLY	A	116	83	3.1	134.2	121.7	37.6	88.2	3G5U
DNR	TYR	A	113	80	->	THR	A	109	76	3.0	151.6	117.6	43.9	64.0	3G5U
DNR	TYR	A	113	80	->	TYR	A	110	77	3.0	118.7	134.9	37.2	82.4	3G5U
ACC	TYR	A	113	80	->	ILE	A	117	84	3.1	159.6	129.4	16.8	76.9	3G5U
DNR	TYR	A	114	81	->	TYR	A	110	77	3.0	179.1	107.4	6.4	66.3	3G5U
ACC	TYR	A	114	81	->	GLY	A	118	85	3.0	150.2	136.1	45.5	73.8	3G5U
DNR	THR	A	115	82	->	ALA	A	111	78	3.0	159.9	133.9	9.9	59.6	3G5U
ACC	THR	A	115	82	->	ALA	A	119	86	3.0	152.0	109.1	30.8	47.7	3G5U
DNR	GLY	A	116	83	->	TYR	A	112	79	3.1	134.2	121.7	37.6	88.2	3G5U
ACC	GLY	A	116	83	->	GLY	A	120	87	3.0	138.7	149.4	15.0	69.2	3G5U
DNR	ILE	A	117	84	->	TYR	A	113	80	3.1	159.6	129.4	16.8	76.9	3G5U
ACC	ILE	A	117	84	->	VAL	A	121	88	3.0	157.9	95.6	8.8	76.9	3G5U
DNR	GLY	A	118	85	->	TYR	A	114	81	3.0	150.2	136.1	45.5	73.8	3G5U
ACC	GLY	A	118	85	->	LEU	A	122	89	3.1	174.2	115.3	22.6	48.5	3G5U
DNR	ALA	A	119	86	->	THR	A	115	82	3.0	152.0	109.1	30.8	47.7	3G5U
ACC	ALA	A	119	86	->	ILE	A	123	90	3.1	173.7	120.0	7.8	81.3	3G5U
DNR	GLY	A	120	87	->	GLY	A	116	83	3.0	138.7	149.4	15.0	69.2	3G5U
ACC	GLY	A	120	87	->	VAL	A	124	91	3.1	162.6	115.6	2.5	27.0	3G5U
DNR	VAL	A	121	88	->	ILE	A	117	84	3.0	157.9	95.6	8.8	76.9	3G5U
ACC	VAL	A	121	88	->	ALA	A	125	92	3.0	160.4	119.5	7.8	55.3	3G5U
DNR	LEU	A	122	89	->	GLY	A	118	85	3.1	174.2	115.3	22.6	48.5	3G5U
ACC	LEU	A	122	89	->	TYR	A	126	93	3.2	154.5	128.2	13.8	86.1	3G5U
DNR	ILE	A	123	90	->	ALA	A	119	86	3.1	173.7	120.0	7.8	81.3	3G5U
ACC	ILE	A	123	90	->	ILE	A	127	94	3.2	147.2	118.5	32.0	35.1	3G5U
DNR	VAL	A	124	91	->	GLY	A	120	87	3.1	162.6	115.6	2.5	27.0	3G5U
ACC	VAL	A	124	91	->	GLN	A	128	95	3.0	150.1	114.2	10.3	67.4	3G5U
DNR	ALA	A	125	92	->	VAL	A	121	88	3.0	160.4	119.5	7.8	55.3	3G5U
ACC	ALA	A	125	92	->	GLN	A	128	95	3.0	128.0	105.7	58.5	83.9	3G5U
ACC	ALA	A	125	92	->	VAL	A	129	96	3.1	168.4	110.3	17.3	17.0	3G5U
DNR	TYR	A	126	93	->	LEU	A	122	89	3.2	154.5	128.2	13.8	86.1	3G5U
ACC	TYR	A	126	93	->	SER	A	130	97	3.1	144.2	123.3	29.0	60.6	3G5U
DNR	ILE	A	127	94	->	ILE	A	123	90	3.2	147.2	118.5	32.0	35.1	3G5U

ACC	ILE	A	127	94	->	SER	A	130	97	3.0	121.3	122.5	52.5	89.3	3G5U
ACC	ILE	A	127	94	->	PHE	A	131	98	3.1	160.1	104.5	29.9	29.3	3G5U
DNR	GLN	A	128	95	->	VAL	A	124	91	3.0	150.1	114.2	10.3	67.4	3G5U
DNR	GLN	A	128	95	->	ALA	A	125	92	3.0	128.0	105.7	58.5	83.9	3G5U
ACC	GLN	A	128	95	->	PHE	A	131	98	3.1	98.3	141.5	43.6	80.5	3G5U
ACC	GLN	A	128	95	->	TRP	A	132	99	3.2	144.4	108.3	2.1	47.7	3G5U
DNR	VAL	A	129	96	->	ALA	A	125	92	3.1	168.4	110.3	17.3	17.0	3G5U
ACC	VAL	A	129	96	->	CYS	A	133	100	3.3	162.3	102.3	14.0	71.1	3G5U
DNR	SER	A	130	97	->	TYR	A	126	93	3.1	144.2	123.3	29.0	60.6	3G5U
DNR	SER	A	130	97	->	ILE	A	127	94	3.0	121.3	122.5	52.5	89.3	3G5U
ACC	SER	A	130	97	->	LEU	A	134	101	3.2	138.8	140.4	33.1	86.1	3G5U
DNR	PHE	A	131	98	->	ILE	A	127	94	3.1	160.1	104.5	29.9	29.3	3G5U
DNR	PHE	A	131	98	->	GLN	A	128	95	3.1	98.3	141.5	43.6	80.5	3G5U
ACC	PHE	A	131	98	->	ALA	A	135	102	3.0	165.1	133.9	20.3	43.9	3G5U
DNR	TRP	A	132	99	->	GLN	A	128	95	3.2	144.4	108.3	2.1	47.7	3G5U
ACC	TRP	A	132	99	->	ALA	A	136	103	3.1	168.5	108.0	46.9	5.3	3G5U
DNR	CYS	A	133	100	->	VAL	A	129	96	3.3	162.3	102.3	14.0	71.1	3G5U
ACC	CYS	A	133	100	->	GLY	A	137	104	3.0	147.4	141.7	22.0	23.5	3G5U
DNR	LEU	A	134	101	->	SER	A	130	97	3.2	138.8	140.4	33.1	86.1	3G5U
ACC	LEU	A	134	101	->	ARG	A	138	105	3.1	158.3	118.4	13.0	84.6	3G5U
DNR	ALA	A	135	102	->	PHE	A	131	98	3.0	165.1	133.9	20.3	43.9	3G5U
ACC	ALA	A	135	102	->	ARG	A	138	105	3.0	155.9	94.3	57.4	88.4	3G5U
ACC	ALA	A	135	102	->	GLN	A	139	106	3.1	146.4	118.6	4.8	66.4	3G5U
DNR	ALA	A	136	103	->	TRP	A	132	99	3.1	168.5	108.0	46.9	5.3	3G5U
ACC	ALA	A	136	103	->	ILE	A	140	107	3.0	157.2	121.3	19.7	75.6	3G5U
DNR	GLY	A	137	104	->	CYS	A	133	100	3.0	147.4	141.7	22.0	23.5	3G5U
ACC	GLY	A	137	104	->	ILE	A	140	107	3.0	125.5	120.7	44.2	81.5	3G5U
ACC	GLY	A	137	104	->	HIS	A	141	108	3.0	166.2	115.8	7.6	11.8	3G5U
DNR	ARG	A	138	105	->	LEU	A	134	101	3.1	158.3	118.4	13.0	84.6	3G5U
DNR	ARG	A	138	105	->	ALA	A	135	102	3.0	155.9	94.3	57.4	88.4	3G5U
ACC	ARG	A	138	105	->	LYS	A	142	109	3.0	157.4	121.5	1.8	82.1	3G5U
DNR	GLN	A	139	106	->	ALA	A	135	102	3.1	146.4	118.6	4.8	66.4	3G5U
ACC	GLN	A	139	106	->	ILE	A	143	110	3.0	140.7	125.3	7.0	46.6	3G5U
DNR	ILE	A	140	107	->	ALA	A	136	103	3.0	157.2	121.3	19.7	75.6	3G5U
DNR	ILE	A	140	107	->	GLY	A	137	104	3.0	125.5	120.7	44.2	81.5	3G5U
ACC	ILE	A	140	107	->	ARG	A	144	111	3.0	162.0	104.7	32.8	69.9	3G5U
DNR	HIS	A	141	108	->	GLY	A	137	104	3.0	166.2	115.8	7.6	11.8	3G5U
ACC	HIS	A	141	108	->	GLN	A	145	112	3.0	163.2	117.1	1.4	79.5	3G5U
DNR	LYS	A	142	109	->	ARG	A	138	105	3.0	157.4	121.5	1.8	82.1	3G5U
ACC	LYS	A	142	109	->	LYS	A	146	113	3.0	169.5	120.1	5.1	17.9	3G5U
DNR	ILE	A	143	110	->	GLN	A	139	106	3.0	140.7	125.3	7.0	46.6	3G5U
ACC	ILE	A	143	110	->	LYS	A	146	113	3.0	147.2	113.8	53.1	84.5	3G5U
ACC	ILE	A	143	110	->	PHE	A	147	114	3.0	152.5	107.7	4.2	74.4	3G5U
DNR	ARG	A	144	111	->	ILE	A	140	107	3.0	162.0	104.7	32.8	69.9	3G5U
ACC	ARG	A	144	111	->	PHE	A	148	115	3.0	164.3	119.3	4.0	28.7	3G5U
DNR	GLN	A	145	112	->	HIS	A	141	108	3.0	163.2	117.1	1.4	79.5	3G5U
ACC	GLN	A	145	112	->	HIS	A	149	116	3.1	159.0	119.9	7.9	84.6	3G5U
DNR	LYS	A	146	113	->	LYS	A	142	109	3.0	169.5	120.1	5.1	17.9	3G5U
DNR	LYS	A	146	113	->	ILE	A	143	110	3.0	147.2	113.8	53.1	84.5	3G5U
ACC	LYS	A	146	113	->	ALA	A	150	117	3.0	154.2	124.0	38.7	31.8	3G5U
DNR	PHE	A	147	114	->	ILE	A	143	110	3.0	152.5	107.7	4.2	74.4	3G5U
ACC	PHE	A	147	114	->	ALA	A	150	117	3.0	108.8	126.2	58.5	89.2	3G5U
ACC	PHE	A	147	114	->	ILE	A	151	118	3.0	170.7	111.1	10.3	61.2	3G5U
DNR	PHE	A	148	115	->	ARG	A	144	111	3.0	164.3	119.3	4.0	28.7	3G5U
ACC	PHE	A	148	115	->	MET	A	152	119	3.1	153.2	122.2	9.2	41.3	3G5U
DNR	HIS	A	149	116	->	GLN	A	145	112	3.1	159.0	119.9	7.9	84.6	3G5U
DNR	ALA	A	150	117	->	LYS	A	146	113	3.0	154.2	124.0	38.7	31.8	3G5U
DNR	ALA	A	150	117	->	PHE	A	147	114	3.0	108.8	126.2	58.5	89.2	3G5U
ACC	ALA	A	150	117	->	ASN	A	153	120	3.0	129.1	137.4	10.9	77.3	3G5U
ACC	ALA	A	150	117	->	GLN	A	154	121	3.0	162.0	97.2	36.2	28.5	3G5U
DNR	ILE	A	151	118	->	PHE	A	147	114	3.0	170.7	111.1	10.3	61.2	3G5U
ACC	ILE	A	151	118	->	ASN	A	153	120	3.0	91.3	93.1	44.9	48.5	3G5U
ACC	ILE	A	151	118	->	GLN	A	154	121	3.0	137.4	116.2	18.3	82.7	3G5U
DNR	MET	A	152	119	->	PHE	A	148	115	3.1	153.2	122.2	9.2	41.3	3G5U
DNR	ASN	A	153	120	->	ALA	A	150	117	3.0	129.1	137.4	10.9	77.3	3G5U
DNR	ASN	A	153	120	->	ILE	A	151	118	3.0	91.3	93.1	44.9	48.5	3G5U
DNR	GLN	A	154	121	->	ALA	A	150	117	3.0	162.0	97.2	36.2	28.5	3G5U
DNR	GLN	A	154	121	->	ILE	A	151	118	3.0	137.4	116.2	18.3	82.7	3G5U
ACC	GLN	A	154	121	->	GLY	A	157	124	3.5	129.0	131.9	31.2	50.4	3G5U
ACC	GLU	A	155	122	->	GLY	A	157	124	3.0	101.3	97.6	24.8	44.2	3G5U
ACC	GLU	A	155	122	->	TRP	A	158	125	3.0	153.5	123.2	20.4	57.9	3G5U
ACC	ILE	A	156	123	->	ASP	A	160	127	3.2	115.7	144.5	20.6	61.5	3G5U
DNR	GLY	A	157	124	->	GLN	A	154	121	3.5	129.0	131.9	31.2	50.4	3G5U
DNR	GLY	A	157	124	->	GLU	A	155	122	3.0	101.3	97.6	24.8	44.2	3G5U

ACC	GLY	A	157	124	->	VAL	A	161	128	3.0	166.0	106.7	10.0	52.5	3G5U
DNR	TRP	A	158	125	->	GLU	A	155	122	3.0	153.5	123.2	20.4	57.9	3G5U
DNR	ASP	A	160	127	->	ILE	A	156	123	3.2	115.7	144.5	20.6	61.5	3G5U
DNR	VAL	A	161	128	->	GLY	A	157	124	3.0	166.0	106.7	10.0	52.5	3G5U
ACC	VAL	A	164	131	->	ASN	A	168	135	3.2	135.3	112.3	12.4	81.3	3G5U
ACC	GLY	A	165	132	->	THR	A	169	136	3.1	173.5	129.2	11.0	33.2	3G5U
ACC	GLU	A	166	133	->	ARG	A	170	137	3.0	138.2	123.8	21.2	58.9	3G5U
ACC	LEU	A	167	134	->	ARG	A	170	137	3.0	137.4	110.9	57.9	80.3	3G5U
ACC	LEU	A	167	134	->	LEU	A	171	138	3.0	154.5	104.5	11.4	50.7	3G5U
DNR	ASN	A	168	135	->	VAL	A	164	131	3.2	135.3	112.3	12.4	81.3	3G5U
ACC	ASN	A	168	135	->	LEU	A	171	138	3.0	115.8	119.6	56.5	83.5	3G5U
ACC	ASN	A	168	135	->	THR	A	172	139	3.1	173.8	104.4	6.9	76.0	3G5U
DNR	THR	A	169	136	->	GLY	A	165	132	3.1	173.5	129.2	11.0	33.2	3G5U
ACC	THR	A	169	136	->	ASP	A	173	140	3.0	164.5	120.1	23.6	12.4	3G5U
DNR	ARG	A	170	137	->	GLU	A	166	133	3.0	138.2	123.8	21.2	58.9	3G5U
DNR	ARG	A	170	137	->	LEU	A	167	134	3.0	137.4	110.9	57.9	80.3	3G5U
ACC	ARG	A	170	137	->	ASP	A	174	141	3.0	141.4	129.8	28.3	43.7	3G5U
DNR	LEU	A	171	138	->	LEU	A	167	134	3.0	154.5	104.5	11.4	50.7	3G5U
DNR	LEU	A	171	138	->	ASN	A	168	135	3.0	115.8	119.6	56.5	83.5	3G5U
ACC	LEU	A	171	138	->	VAL	A	175	142	3.1	151.6	135.4	24.9	86.0	3G5U
DNR	THR	A	172	139	->	ASN	A	168	135	3.1	173.8	104.4	6.9	76.0	3G5U
ACC	THR	A	172	139	->	SER	A	176	143	3.1	172.4	121.4	0.1	81.3	3G5U
DNR	ASP	A	173	140	->	THR	A	169	136	3.0	164.5	120.1	23.6	12.4	3G5U
ACC	ASP	A	173	140	->	LYS	A	177	144	3.1	155.9	118.2	11.4	24.0	3G5U
DNR	ASP	A	174	141	->	ARG	A	170	137	3.0	141.4	129.8	28.3	43.7	3G5U
ACC	ASP	A	174	141	->	LYS	A	177	144	3.0	131.7	106.3	58.3	77.0	3G5U
ACC	ASP	A	174	141	->	ILE	A	178	145	3.1	171.8	108.6	19.4	49.0	3G5U
DNR	VAL	A	175	142	->	LEU	A	171	138	3.1	151.6	135.4	24.9	86.0	3G5U
ACC	VAL	A	175	142	->	ILE	A	178	145	3.1	116.8	136.3	40.1	74.0	3G5U
ACC	VAL	A	175	142	->	ASN	A	179	146	3.2	152.0	110.1	9.2	18.5	3G5U
DNR	SER	A	176	143	->	THR	A	172	139	3.1	172.4	121.4	0.1	81.3	3G5U
ACC	SER	A	176	143	->	GLU	A	180	147	3.0	166.7	104.4	7.2	19.9	3G5U
DNR	LYS	A	177	144	->	ASP	A	173	140	3.1	155.9	118.2	11.4	24.0	3G5U
DNR	LYS	A	177	144	->	ASP	A	174	141	3.0	131.7	106.3	58.3	77.0	3G5U
ACC	LYS	A	177	144	->	GLY	A	181	148	3.1	140.0	127.0	21.9	68.3	3G5U
DNR	ILE	A	178	145	->	ASP	A	174	141	3.1	171.8	108.6	19.4	49.0	3G5U
DNR	ILE	A	178	145	->	VAL	A	175	142	3.1	116.8	136.3	40.1	74.0	3G5U
ACC	ILE	A	178	145	->	ILE	A	182	149	3.1	166.0	99.7	16.1	1.4	3G5U
DNR	ASN	A	179	146	->	VAL	A	175	142	3.2	152.0	110.1	9.2	18.5	3G5U
ACC	ASN	A	179	146	->	ILE	A	182	149	3.0	128.9	119.2	43.4	86.5	3G5U
ACC	ASN	A	179	146	->	GLY	A	183	150	3.5	168.2	102.6	15.6	51.3	3G5U
DNR	GLU	A	180	147	->	SER	A	176	143	3.0	166.7	104.4	7.2	19.9	3G5U
ACC	GLU	A	180	147	->	ASP	A	184	151	3.2	160.2	137.4	4.4	70.4	3G5U
DNR	GLY	A	181	148	->	LYS	A	177	144	3.1	140.0	127.0	21.9	68.3	3G5U
ACC	GLY	A	181	148	->	LYS	A	185	152	3.2	137.9	141.2	11.2	74.7	3G5U
DNR	ILE	A	182	149	->	ILE	A	178	145	3.1	166.0	99.7	16.1	1.4	3G5U
DNR	ILE	A	182	149	->	ASN	A	179	146	3.0	128.9	119.2	43.4	86.5	3G5U
ACC	ILE	A	182	149	->	ILE	A	186	153	3.3	149.5	113.2	22.3	55.6	3G5U
DNR	GLY	A	183	150	->	ASN	A	179	146	3.5	168.2	102.6	15.6	51.3	3G5U
ACC	GLY	A	183	150	->	GLY	A	187	154	3.3	137.1	112.2	7.1	45.8	3G5U
DNR	ASP	A	184	151	->	GLU	A	180	147	3.2	160.2	137.4	4.4	70.4	3G5U
ACC	ASP	A	184	151	->	MET	A	188	155	3.0	162.3	100.6	6.1	40.4	3G5U
DNR	LYS	A	185	152	->	GLY	A	181	148	3.2	137.9	141.2	11.2	74.7	3G5U
ACC	LYS	A	185	152	->	PHE	A	189	156	3.1	164.2	113.4	19.7	62.5	3G5U
DNR	ILE	A	186	153	->	ILE	A	182	149	3.3	149.5	113.2	22.3	55.6	3G5U
ACC	ILE	A	186	153	->	PHE	A	190	157	3.1	174.5	114.5	15.6	13.1	3G5U
DNR	GLY	A	187	154	->	GLY	A	183	150	3.3	137.1	112.2	7.1	45.8	3G5U
ACC	GLY	A	187	154	->	GLN	A	191	158	3.1	160.4	108.7	9.0	5.1	3G5U
DNR	MET	A	188	155	->	ASP	A	184	151	3.0	162.3	100.6	6.1	40.4	3G5U
ACC	MET	A	188	155	->	ALA	A	192	159	3.0	149.3	113.1	0.8	81.8	3G5U
DNR	PHE	A	189	156	->	LYS	A	185	152	3.1	164.2	113.4	19.7	62.5	3G5U
ACC	PHE	A	189	156	->	MET	A	193	160	3.0	169.4	106.9	24.7	36.5	3G5U
DNR	PHE	A	190	157	->	ILE	A	186	153	3.1	174.5	114.5	15.6	13.1	3G5U
ACC	PHE	A	190	157	->	MET	A	193	160	3.0	130.9	131.4	33.1	72.8	3G5U
ACC	PHE	A	190	157	->	ALA	A	194	161	3.1	152.5	104.3	20.5	25.4	3G5U
DNR	GLN	A	191	158	->	GLY	A	187	154	3.1	160.4	108.7	9.0	5.1	3G5U
ACC	GLN	A	191	158	->	ALA	A	194	161	3.0	112.0	109.7	49.4	75.7	3G5U
ACC	GLN	A	191	158	->	THR	A	195	162	3.0	164.2	121.9	7.3	60.4	3G5U
DNR	ALA	A	192	159	->	MET	A	188	155	3.0	149.3	113.1	0.8	81.8	3G5U
ACC	ALA	A	192	159	->	PHE	A	196	163	3.0	139.3	134.7	9.0	54.3	3G5U
DNR	MET	A	193	160	->	PHE	A	189	156	3.0	169.4	106.9	24.7	36.5	3G5U
DNR	MET	A	193	160	->	PHE	A	190	157	3.0	130.9	131.4	33.1	72.8	3G5U
ACC	MET	A	193	160	->	PHE	A	197	164	3.0	138.9	126.0	31.4	60.5	3G5U
DNR	ALA	A	194	161	->	PHE	A	190	157	3.1	152.5	104.3	20.5	25.4	3G5U

DNR	ALA	A	194	161	->	GLN	A	191	158	3.0	112.0	109.7	49.4	75.7	3G5U
ACC	ALA	A	194	161	->	GLY	A	198	165	3.0	128.1	152.7	8.4	88.9	3G5U
DNR	THR	A	195	162	->	GLN	A	191	158	3.0	164.2	121.9	7.3	60.4	3G5U
ACC	THR	A	195	162	->	GLY	A	199	166	3.0	155.5	118.6	38.2	61.6	3G5U
DNR	PHE	A	196	163	->	ALA	A	192	159	3.0	139.3	134.7	9.0	54.3	3G5U
ACC	PHE	A	196	163	->	PHE	A	200	167	3.0	152.5	118.2	47.6	37.7	3G5U
DNR	PHE	A	197	164	->	MET	A	193	160	3.0	138.9	126.0	31.4	60.5	3G5U
ACC	PHE	A	197	164	->	PHE	A	200	167	3.0	102.0	139.8	47.0	81.4	3G5U
ACC	PHE	A	197	164	->	ILE	A	201	168	3.0	157.2	108.3	53.0	37.0	3G5U
DNR	GLY	A	198	165	->	ALA	A	194	161	3.0	128.1	152.7	8.4	88.9	3G5U
ACC	GLY	A	198	165	->	ILE	A	202	169	3.0	160.6	116.9	35.4	35.7	3G5U
DNR	GLY	A	199	166	->	THR	A	195	162	3.0	155.5	118.6	38.2	61.6	3G5U
DNR	PHE	A	200	167	->	PHE	A	196	163	3.0	152.5	118.2	47.6	37.7	3G5U
DNR	PHE	A	200	167	->	PHE	A	197	164	3.0	102.0	139.8	47.0	81.4	3G5U
ACC	PHE	A	200	167	->	PHE	A	204	171	3.0	154.2	97.7	42.0	38.7	3G5U
DNR	ILE	A	201	168	->	PHE	A	197	164	3.0	157.2	108.3	53.0	37.0	3G5U
ACC	ILE	A	201	168	->	THR	A	205	172	3.0	154.1	129.6	58.2	82.9	3G5U
DNR	ILE	A	202	169	->	GLY	A	198	165	3.0	160.6	116.9	35.4	35.7	3G5U
ACC	ILE	A	202	169	->	PHE	A	204	171	3.0	91.2	98.2	42.4	46.0	3G5U
ACC	ILE	A	202	169	->	ARG	A	206	173	3.1	134.8	129.6	29.9	28.2	3G5U
DNR	PHE	A	204	171	->	PHE	A	200	167	3.0	154.2	97.7	42.0	38.7	3G5U
DNR	PHE	A	204	171	->	ILE	A	202	169	3.0	91.2	98.2	42.4	46.0	3G5U
ACC	PHE	A	204	171	->	TRP	A	208	175	3.5	161.5	122.3	20.1	77.2	3G5U
DNR	THR	A	205	172	->	ILE	A	201	168	3.0	154.1	129.6	58.2	82.9	3G5U
DNR	ARG	A	206	173	->	ILE	A	202	169	3.1	134.8	129.6	29.9	28.2	3G5U
ACC	GLY	A	207	174	->	LEU	A	210	177	3.0	93.6	128.0	29.8	84.0	3G5U
DNR	TRP	A	208	175	->	PHE	A	204	171	3.5	161.5	122.3	20.1	77.2	3G5U
ACC	LYS	A	209	176	->	VAL	A	213	180	3.0	112.2	104.2	47.7	60.0	3G5U
DNR	LEU	A	210	177	->	GLY	A	207	174	3.0	93.6	128.0	29.8	84.0	3G5U
ACC	LEU	A	210	177	->	VAL	A	213	180	3.0	104.9	124.1	52.6	74.2	3G5U
ACC	LEU	A	210	177	->	ILE	A	214	181	3.0	148.5	106.9	8.5	61.6	3G5U
ACC	THR	A	211	178	->	LEU	A	215	182	3.0	133.2	113.2	11.1	39.3	3G5U
ACC	LEU	A	212	179	->	ALA	A	216	183	3.0	158.5	125.0	3.0	62.8	3G5U
DNR	VAL	A	213	180	->	LYS	A	209	176	3.0	112.2	104.2	47.7	60.0	3G5U
DNR	VAL	A	213	180	->	LEU	A	210	177	3.0	104.9	124.1	52.6	74.2	3G5U
ACC	VAL	A	213	180	->	ILE	A	217	184	3.0	163.8	102.2	49.5	70.7	3G5U
DNR	ILE	A	214	181	->	LEU	A	210	177	3.0	148.5	106.9	8.5	61.6	3G5U
ACC	ILE	A	214	181	->	SER	A	218	185	3.0	150.3	120.3	48.2	50.1	3G5U
DNR	LEU	A	215	182	->	THR	A	211	178	3.0	133.2	113.2	11.1	39.3	3G5U
DNR	ALA	A	216	183	->	LEU	A	212	179	3.0	158.5	125.0	3.0	62.8	3G5U
ACC	ALA	A	216	183	->	VAL	A	220	187	3.0	169.0	123.8	20.8	53.0	3G5U
DNR	ILE	A	217	184	->	VAL	A	213	180	3.0	163.8	102.2	49.5	70.7	3G5U
ACC	ILE	A	217	184	->	VAL	A	220	187	3.0	118.8	129.6	53.8	77.3	3G5U
ACC	ILE	A	217	184	->	LEU	A	221	188	3.0	176.0	117.7	2.7	17.7	3G5U
DNR	SER	A	218	185	->	ILE	A	214	181	3.0	150.3	120.3	48.2	50.1	3G5U
ACC	SER	A	218	185	->	LEU	A	221	188	3.0	150.9	106.5	52.6	78.0	3G5U
ACC	SER	A	218	185	->	GLY	A	222	189	3.0	152.4	113.9	14.4	72.7	3G5U
ACC	PRO	A	219	186	->	LEU	A	223	190	3.0	135.7	113.9	44.2	66.3	3G5U
DNR	VAL	A	220	187	->	ALA	A	216	183	3.0	169.0	123.8	20.8	53.0	3G5U
DNR	VAL	A	220	187	->	ILE	A	217	184	3.0	118.8	129.6	53.8	77.3	3G5U
ACC	VAL	A	220	187	->	LEU	A	223	190	3.0	108.7	134.4	44.9	85.6	3G5U
ACC	VAL	A	220	187	->	SER	A	224	191	3.1	157.4	104.1	3.1	36.5	3G5U
DNR	LEU	A	221	188	->	ILE	A	217	184	3.0	176.0	117.7	2.7	17.7	3G5U
DNR	LEU	A	221	188	->	SER	A	218	185	3.0	150.9	106.5	52.6	78.0	3G5U
ACC	LEU	A	221	188	->	ALA	A	225	192	3.0	161.6	110.5	7.8	25.0	3G5U
DNR	GLY	A	222	189	->	SER	A	218	185	3.0	152.4	113.9	14.4	72.7	3G5U
ACC	GLY	A	222	189	->	GLY	A	226	193	3.0	150.3	123.0	7.5	75.5	3G5U
DNR	LEU	A	223	190	->	PRO	A	219	186	3.0	135.7	113.9	44.2	66.3	3G5U
DNR	LEU	A	223	190	->	VAL	A	220	187	3.0	108.7	134.4	44.9	85.6	3G5U
ACC	LEU	A	223	190	->	ILE	A	227	194	3.1	172.8	118.0	1.3	60.6	3G5U
DNR	SER	A	224	191	->	VAL	A	220	187	3.1	157.4	104.1	3.1	36.5	3G5U
ACC	SER	A	224	191	->	TRP	A	228	195	3.1	155.0	121.0	35.7	78.6	3G5U
DNR	ALA	A	225	192	->	LEU	A	221	188	3.0	161.6	110.5	7.8	25.0	3G5U
ACC	ALA	A	225	192	->	ALA	A	229	196	3.0	163.5	131.7	31.1	32.8	3G5U
DNR	GLY	A	226	193	->	GLY	A	222	189	3.0	150.3	123.0	7.5	75.5	3G5U
ACC	GLY	A	226	193	->	LYS	A	230	197	3.1	142.6	138.0	23.2	82.6	3G5U
DNR	ILE	A	227	194	->	LEU	A	223	190	3.1	172.8	118.0	1.3	60.6	3G5U
ACC	ILE	A	227	194	->	ILE	A	231	198	3.0	171.3	121.6	23.2	17.7	3G5U
DNR	TRP	A	228	195	->	SER	A	224	191	3.1	155.0	121.0	35.7	78.6	3G5U
ACC	TRP	A	228	195	->	ILE	A	231	198	3.0	108.8	125.7	58.2	86.1	3G5U
ACC	TRP	A	228	195	->	LEU	A	232	199	3.0	165.0	111.9	6.6	75.1	3G5U
DNR	ALA	A	229	196	->	ALA	A	225	192	3.0	163.5	131.7	31.1	32.8	3G5U
ACC	ALA	A	229	196	->	SER	A	233	200	3.0	157.3	116.3	11.0	18.5	3G5U
DNR	LYS	A	230	197	->	GLY	A	226	193	3.1	142.6	138.0	23.2	82.6	3G5U

ACC	LYS	A	230	197	->	SER	A	234	201	3.0	152.0	113.9	12.3	87.1	3G5U
DNR	ILE	A	231	198	->	ILE	A	227	194	3.0	171.3	121.6	23.2	17.7	3G5U
DNR	ILE	A	231	198	->	TRP	A	228	195	3.0	108.8	125.7	58.2	86.1	3G5U
ACC	ILE	A	231	198	->	SER	A	234	201	3.0	125.8	118.5	51.3	81.3	3G5U
ACC	ILE	A	231	198	->	PHE	A	235	202	3.1	152.8	116.7	4.0	4.6	3G5U
DNR	LEU	A	232	199	->	TRP	A	228	195	3.0	165.0	111.9	6.6	75.1	3G5U
ACC	LEU	A	232	199	->	THR	A	236	203	3.0	169.4	106.7	20.1	22.0	3G5U
DNR	SER	A	233	200	->	ALA	A	229	196	3.0	157.3	116.3	11.0	18.5	3G5U
ACC	SER	A	233	200	->	THR	A	236	203	3.1	104.8	124.8	54.8	89.8	3G5U
ACC	SER	A	233	200	->	ASP	A	237	204	3.1	157.3	112.0	2.0	61.0	3G5U
DNR	SER	A	234	201	->	LYS	A	230	197	3.0	152.0	113.9	12.3	87.1	3G5U
DNR	SER	A	234	201	->	ILE	A	231	198	3.0	125.8	118.5	51.3	81.3	3G5U
ACC	SER	A	234	201	->	LYS	A	238	205	3.0	170.2	113.1	1.8	14.3	3G5U
DNR	PHE	A	235	202	->	ILE	A	231	198	3.1	152.8	116.7	4.0	4.6	3G5U
ACC	PHE	A	235	202	->	GLU	A	239	206	3.1	147.0	120.6	15.8	51.1	3G5U
DNR	THR	A	236	203	->	LEU	A	232	199	3.0	169.4	106.7	20.1	22.0	3G5U
DNR	THR	A	236	203	->	SER	A	233	200	3.1	104.8	124.8	54.8	89.8	3G5U
ACC	THR	A	236	203	->	LEU	A	240	207	3.0	159.0	103.5	11.4	6.4	3G5U
DNR	ASP	A	237	204	->	SER	A	233	200	3.1	157.3	112.0	2.0	61.0	3G5U
ACC	ASP	A	237	204	->	LEU	A	240	207	3.0	120.6	116.4	58.7	86.5	3G5U
ACC	ASP	A	237	204	->	HIS	A	241	208	3.0	170.0	107.1	9.8	5.5	3G5U
DNR	LYS	A	238	205	->	SER	A	234	201	3.0	170.2	113.1	1.8	14.3	3G5U
ACC	LYS	A	238	205	->	HIS	A	241	208	3.1	116.8	117.2	53.8	88.9	3G5U
ACC	LYS	A	238	205	->	ALA	A	242	209	3.2	169.6	116.1	3.2	58.1	3G5U
DNR	GLU	A	239	206	->	PHE	A	235	202	3.1	147.0	120.6	15.8	51.1	3G5U
ACC	GLU	A	239	206	->	TYR	A	243	210	3.1	151.3	123.3	21.4	42.7	3G5U
DNR	LEU	A	240	207	->	THR	A	236	203	3.0	159.0	103.5	11.4	6.4	3G5U
DNR	LEU	A	240	207	->	ASP	A	237	204	3.0	120.6	116.4	58.7	86.5	3G5U
ACC	LEU	A	240	207	->	ALA	A	244	211	3.0	153.0	108.2	2.6	43.2	3G5U
DNR	HIS	A	241	208	->	ASP	A	237	204	3.0	170.0	107.1	9.8	5.5	3G5U
DNR	HIS	A	241	208	->	LYS	A	238	205	3.1	116.8	117.2	53.8	88.9	3G5U
ACC	HIS	A	241	208	->	LYS	A	245	212	3.2	163.1	107.1	13.1	31.1	3G5U
DNR	ALA	A	242	209	->	LYS	A	238	205	3.2	169.6	116.1	3.2	58.1	3G5U
ACC	ALA	A	242	209	->	LYS	A	245	212	3.2	113.4	120.7	53.5	89.3	3G5U
ACC	ALA	A	242	209	->	ALA	A	246	213	3.2	163.2	117.5	2.9	56.4	3G5U
DNR	TYR	A	243	210	->	GLU	A	239	206	3.1	151.3	123.3	21.4	42.7	3G5U
ACC	TYR	A	243	210	->	GLY	A	247	214	3.1	152.9	104.3	19.2	43.5	3G5U
DNR	ALA	A	244	211	->	LEU	A	240	207	3.0	153.0	108.2	2.6	43.2	3G5U
ACC	ALA	A	244	211	->	GLY	A	247	214	3.3	100.5	125.6	52.4	84.4	3G5U
ACC	ALA	A	244	211	->	ALA	A	248	215	3.2	150.6	109.0	28.3	67.8	3G5U
DNR	LYS	A	245	212	->	HIS	A	241	208	3.2	163.1	107.1	13.1	31.1	3G5U
DNR	LYS	A	245	212	->	ALA	A	242	209	3.2	113.4	120.7	53.5	89.3	3G5U
ACC	LYS	A	245	212	->	ALA	A	248	215	3.1	123.7	123.9	37.5	85.7	3G5U
ACC	LYS	A	245	212	->	VAL	A	249	216	3.3	164.3	115.7	4.4	18.0	3G5U
DNR	ALA	A	246	213	->	ALA	A	242	209	3.2	163.2	117.5	2.9	56.4	3G5U
DNR	GLY	A	247	214	->	TYR	A	243	210	3.1	152.9	104.3	19.2	43.5	3G5U
DNR	GLY	A	247	214	->	ALA	A	244	211	3.3	100.5	125.6	52.4	84.4	3G5U
DNR	ALA	A	248	215	->	ALA	A	244	211	3.2	150.6	109.0	28.3	67.8	3G5U
DNR	ALA	A	248	215	->	LYS	A	245	212	3.1	123.7	123.9	37.5	85.7	3G5U
ACC	ALA	A	248	215	->	GLU	A	251	218	3.0	108.7	137.2	0.8	89.6	3G5U
ACC	ALA	A	248	215	->	GLU	A	252	219	3.4	170.3	98.8	13.1	74.9	3G5U
DNR	VAL	A	249	216	->	LYS	A	245	212	3.3	164.3	115.7	4.4	18.0	3G5U
DNR	GLU	A	251	218	->	ALA	A	248	215	3.0	108.7	137.2	0.8	89.6	3G5U
DNR	GLU	A	252	219	->	ALA	A	248	215	3.4	170.3	98.8	13.1	74.9	3G5U
ACC	ALA	A	256	223	->	THR	A	259	226	3.0	156.5	113.1	50.0	61.0	3G5U
ACC	ALA	A	256	223	->	VAL	A	260	227	3.2	134.1	106.4	13.8	41.7	3G5U
ACC	ILE	A	257	224	->	ILE	A	261	228	3.0	169.9	105.3	36.4	83.0	3G5U
ACC	ARG	A	258	225	->	ILE	A	261	228	3.0	118.8	125.8	28.9	86.9	3G5U
ACC	ARG	A	258	225	->	ALA	A	262	229	3.2	166.8	111.1	9.1	50.1	3G5U
DNR	THR	A	259	226	->	ALA	A	256	223	3.0	156.5	113.1	50.0	61.0	3G5U
DNR	VAL	A	260	227	->	ALA	A	256	223	3.2	134.1	106.4	13.8	41.7	3G5U
ACC	VAL	A	260	227	->	GLY	A	264	231	3.0	141.1	114.0	19.5	77.1	3G5U
DNR	ILE	A	261	228	->	ILE	A	257	224	3.0	169.9	105.3	36.4	83.0	3G5U
DNR	ILE	A	261	228	->	ARG	A	258	225	3.0	118.8	125.8	28.9	86.9	3G5U
DNR	ALA	A	262	229	->	ARG	A	258	225	3.2	166.8	111.1	9.1	50.1	3G5U
DNR	GLY	A	264	231	->	VAL	A	260	227	3.0	141.1	114.0	19.5	77.1	3G5U
ACC	GLN	A	266	233	->	LYS	A	268	235	3.0	96.3	96.5	28.1	38.4	3G5U
DNR	LYS	A	268	235	->	GLN	A	266	233	3.0	96.3	96.5	28.1	38.4	3G5U
ACC	LYS	A	268	235	->	ARG	A	272	239	3.0	138.5	134.2	0.4	88.9	3G5U
ACC	GLU	A	269	236	->	TYR	A	273	240	3.1	163.4	113.0	9.3	74.3	3G5U
ACC	LEU	A	270	237	->	ASN	A	274	241	3.0	169.9	131.3	2.9	13.3	3G5U
ACC	GLU	A	271	238	->	ASN	A	275	242	3.0	167.4	104.6	32.7	10.6	3G5U
DNR	ARG	A	272	239	->	LYS	A	268	235	3.0	138.5	134.2	0.4	88.9	3G5U
ACC	ARG	A	272	239	->	ASN	A	276	243	3.1	157.8	135.7	30.0	62.8	3G5U

DNR	TYR	A	273	240	->	GLU	A	269	236	3.1	163.4	113.0	9.3	74.3	3G5U
ACC	TYR	A	273	240	->	ASN	A	276	243	3.1	109.3	126.3	58.1	83.4	3G5U
ACC	TYR	A	273	240	->	LEU	A	277	244	3.2	161.6	107.5	27.0	51.6	3G5U
DNR	ASN	A	274	241	->	LEU	A	270	237	3.0	169.9	131.3	2.9	13.3	3G5U
ACC	ASN	A	274	241	->	GLU	A	278	245	3.0	164.8	131.0	12.1	38.1	3G5U
DNR	ASN	A	275	242	->	GLU	A	271	238	3.0	167.4	104.6	32.7	10.6	3G5U
ACC	ASN	A	275	242	->	GLU	A	279	246	3.0	128.8	135.3	24.7	71.4	3G5U
DNR	ASN	A	276	243	->	ARG	A	272	239	3.1	157.8	135.7	30.0	62.8	3G5U
DNR	ASN	A	276	243	->	TYR	A	273	240	3.1	109.3	126.3	58.1	83.4	3G5U
ACC	ASN	A	276	243	->	ALA	A	280	247	3.1	162.3	121.2	3.3	9.4	3G5U
DNR	LEU	A	277	244	->	TYR	A	273	240	3.2	161.6	107.5	27.0	51.6	3G5U
ACC	LEU	A	277	244	->	LYS	A	281	248	3.1	173.0	104.8	24.8	74.4	3G5U
DNR	GLU	A	278	245	->	ASN	A	274	241	3.0	164.8	131.0	12.1	38.1	3G5U
ACC	GLU	A	278	245	->	ARG	A	282	249	3.0	169.4	128.6	52.9	27.4	3G5U
DNR	GLU	A	279	246	->	ASN	A	275	242	3.0	128.8	135.3	24.7	71.4	3G5U
ACC	GLU	A	279	246	->	ARG	A	282	249	3.0	114.2	139.2	45.9	79.2	3G5U
ACC	GLU	A	279	246	->	LEU	A	283	250	3.1	167.6	95.9	31.3	24.6	3G5U
DNR	ALA	A	280	247	->	ASN	A	276	243	3.1	162.3	121.2	3.3	9.4	3G5U
ACC	ALA	A	280	247	->	GLY	A	284	251	3.0	149.7	135.2	15.8	9.9	3G5U
DNR	LYS	A	281	248	->	LEU	A	277	244	3.1	173.0	104.8	24.8	74.4	3G5U
ACC	LYS	A	281	248	->	ILE	A	285	252	3.0	118.5	129.4	28.7	58.2	3G5U
DNR	ARG	A	282	249	->	GLU	A	278	245	3.0	169.4	128.6	52.9	27.4	3G5U
DNR	ARG	A	282	249	->	GLU	A	279	246	3.0	114.2	139.2	45.9	79.2	3G5U
ACC	ARG	A	282	249	->	LYS	A	286	253	3.0	165.8	125.2	56.7	21.6	3G5U
DNR	LEU	A	283	250	->	GLU	A	279	246	3.1	167.6	95.9	31.3	24.6	3G5U
ACC	LEU	A	283	250	->	LYS	A	286	253	3.0	95.1	149.1	57.9	75.4	3G5U
DNR	GLY	A	284	251	->	ALA	A	280	247	3.0	149.7	135.2	15.8	9.9	3G5U
ACC	GLY	A	284	251	->	LYS	A	287	254	3.0	120.3	129.6	8.3	87.8	3G5U
ACC	GLY	A	284	251	->	ALA	A	288	255	3.1	152.9	106.0	0.7	26.9	3G5U
DNR	ILE	A	285	252	->	LYS	A	281	248	3.0	118.5	129.4	28.7	58.2	3G5U
DNR	LYS	A	286	253	->	ARG	A	282	249	3.0	165.8	125.2	56.7	21.6	3G5U
DNR	LYS	A	286	253	->	LEU	A	283	250	3.0	95.1	149.1	57.9	75.4	3G5U
ACC	LYS	A	286	253	->	THR	A	290	257	3.0	121.0	127.7	0.7	87.1	3G5U
DNR	LYS	A	287	254	->	GLY	A	284	251	3.0	120.3	129.6	8.3	87.8	3G5U
DNR	ALA	A	288	255	->	GLY	A	284	251	3.1	152.9	106.0	0.7	26.9	3G5U
ACC	ALA	A	288	255	->	ASN	A	292	259	3.0	142.5	100.7	47.2	73.1	3G5U
ACC	ILE	A	289	256	->	ASN	A	292	259	3.0	127.7	124.2	28.7	79.8	3G5U
ACC	ILE	A	289	256	->	ILE	A	293	260	3.0	159.6	116.8	4.3	13.5	3G5U
DNR	THR	A	290	257	->	LYS	A	286	253	3.0	121.0	127.7	0.7	87.1	3G5U
ACC	THR	A	290	257	->	SER	A	294	261	3.0	107.7	132.6	23.3	62.8	3G5U
ACC	ALA	A	291	258	->	MET	A	295	262	3.0	119.3	115.1	58.1	85.1	3G5U
DNR	ASN	A	292	259	->	ALA	A	288	255	3.0	142.5	100.7	47.2	73.1	3G5U
DNR	ASN	A	292	259	->	ILE	A	289	256	3.0	127.7	124.2	28.7	79.8	3G5U
ACC	ASN	A	292	259	->	MET	A	295	262	3.0	99.6	145.3	48.2	82.5	3G5U
ACC	ASN	A	292	259	->	GLY	A	296	263	3.0	158.0	104.0	19.7	44.3	3G5U
DNR	ILE	A	293	260	->	ILE	A	289	256	3.0	159.6	116.8	4.3	13.5	3G5U
ACC	ILE	A	293	260	->	GLY	A	296	263	3.0	128.1	110.1	52.2	74.3	3G5U
ACC	ILE	A	293	260	->	ALA	A	297	264	3.0	166.3	115.4	0.4	9.1	3G5U
DNR	SER	A	294	261	->	THR	A	290	257	3.0	107.7	132.6	23.3	62.8	3G5U
ACC	SER	A	294	261	->	ALA	A	298	265	3.0	131.3	106.9	40.5	45.3	3G5U
DNR	MET	A	295	262	->	ALA	A	291	258	3.0	119.3	115.1	58.1	85.1	3G5U
DNR	MET	A	295	262	->	ASN	A	292	259	3.0	99.6	145.3	48.2	82.5	3G5U
ACC	MET	A	295	262	->	ALA	A	298	265	3.0	105.8	122.6	58.1	77.4	3G5U
ACC	MET	A	295	262	->	PHE	A	299	266	3.0	174.2	93.3	38.5	42.5	3G5U
DNR	GLY	A	296	263	->	ASN	A	292	259	3.0	158.0	104.0	19.7	44.3	3G5U
DNR	GLY	A	296	263	->	ILE	A	293	260	3.0	128.1	110.1	52.2	74.3	3G5U
ACC	GLY	A	296	263	->	LEU	A	300	267	3.0	163.8	135.9	4.2	85.8	3G5U
DNR	ALA	A	297	264	->	ILE	A	293	260	3.0	166.3	115.4	0.4	9.1	3G5U
ACC	ALA	A	297	264	->	LEU	A	301	268	3.0	144.2	138.8	1.4	77.4	3G5U
DNR	ALA	A	298	265	->	SER	A	294	261	3.0	131.3	106.9	40.5	45.3	3G5U
DNR	ALA	A	298	265	->	MET	A	295	262	3.0	105.8	122.6	58.1	77.4	3G5U
ACC	ALA	A	298	265	->	LEU	A	301	268	3.0	139.5	104.7	56.5	79.9	3G5U
ACC	ALA	A	298	265	->	ILE	A	302	269	3.0	163.8	118.6	14.7	88.9	3G5U
DNR	PHE	A	299	266	->	MET	A	295	262	3.0	174.2	93.3	38.5	42.5	3G5U
DNR	LEU	A	300	267	->	GLY	A	296	263	3.0	163.8	135.9	4.2	85.8	3G5U
ACC	LEU	A	300	267	->	TYR	A	303	270	3.0	98.8	132.0	46.0	83.2	3G5U
ACC	LEU	A	300	267	->	ALA	A	304	271	3.0	158.5	107.5	10.9	83.4	3G5U
DNR	LEU	A	301	268	->	ALA	A	297	264	3.0	144.2	138.8	1.4	77.4	3G5U
DNR	LEU	A	301	268	->	ALA	A	298	265	3.0	139.5	104.7	56.5	79.9	3G5U
ACC	LEU	A	301	268	->	SER	A	305	272	3.0	148.8	112.0	34.8	21.4	3G5U
DNR	ILE	A	302	269	->	ALA	A	298	265	3.0	163.8	118.6	14.7	88.9	3G5U
ACC	ILE	A	302	269	->	TYR	A	306	273	3.0	134.5	115.9	22.7	75.7	3G5U
DNR	TYR	A	303	270	->	LEU	A	300	267	3.0	98.8	132.0	46.0	83.2	3G5U
ACC	TYR	A	303	270	->	TYR	A	306	273	3.0	133.8	126.2	52.6	84.4	3G5U

ACC	TYR	A	303	270	->	ALA	A	307	274	3.1	147.8	98.4	2.0	12.1	3G5U
DNR	ALA	A	304	271	->	LEU	A	300	267	3.0	158.5	107.5	10.9	83.4	3G5U
ACC	ALA	A	304	271	->	LEU	A	308	275	3.0	146.6	111.0	17.9	54.9	3G5U
DNR	SER	A	305	272	->	LEU	A	301	268	3.0	148.8	112.0	34.8	21.4	3G5U
ACC	SER	A	305	272	->	ALA	A	309	276	3.2	175.7	94.7	30.7	54.1	3G5U
DNR	TYR	A	306	273	->	ILE	A	302	269	3.0	134.5	115.9	22.7	75.7	3G5U
DNR	TYR	A	306	273	->	TYR	A	303	270	3.0	133.8	126.2	52.6	84.4	3G5U
ACC	TYR	A	306	273	->	PHE	A	310	277	3.0	168.8	138.5	12.6	5.7	3G5U
DNR	ALA	A	307	274	->	TYR	A	303	270	3.1	147.8	98.4	2.0	12.1	3G5U
ACC	ALA	A	307	274	->	TRP	A	311	278	3.0	156.1	111.7	26.9	62.9	3G5U
DNR	LEU	A	308	275	->	ALA	A	304	271	3.0	146.6	111.0	17.9	54.9	3G5U
ACC	LEU	A	308	275	->	TYR	A	312	279	3.0	158.6	124.0	11.1	76.1	3G5U
DNR	ALA	A	309	276	->	SER	A	305	272	3.2	175.7	94.7	30.7	54.1	3G5U
ACC	ALA	A	309	276	->	GLY	A	313	280	3.0	139.7	117.6	48.5	47.8	3G5U
DNR	PHE	A	310	277	->	TYR	A	306	273	3.0	168.8	138.5	12.6	5.7	3G5U
ACC	PHE	A	310	277	->	THR	A	314	281	3.0	159.3	130.0	34.4	22.4	3G5U
DNR	TRP	A	311	278	->	ALA	A	307	274	3.0	156.1	111.7	26.9	62.9	3G5U
ACC	TRP	A	311	278	->	SER	A	315	282	3.0	161.9	119.8	5.5	80.7	3G5U
DNR	TYR	A	312	279	->	LEU	A	308	275	3.0	158.6	124.0	11.1	76.1	3G5U
ACC	TYR	A	312	279	->	LEU	A	316	283	3.1	161.9	109.9	12.1	65.6	3G5U
DNR	GLY	A	313	280	->	ALA	A	309	276	3.0	139.7	117.6	48.5	47.8	3G5U
ACC	GLY	A	313	280	->	VAL	A	317	284	3.1	138.3	134.2	4.8	72.0	3G5U
DNR	THR	A	314	281	->	PHE	A	310	277	3.0	159.3	130.0	34.4	22.4	3G5U
DNR	SER	A	315	282	->	TRP	A	311	278	3.0	161.9	119.8	5.5	80.7	3G5U
ACC	SER	A	315	282	->	ILE	A	318	285	3.0	119.7	135.8	28.1	84.9	3G5U
ACC	SER	A	315	282	->	SER	A	319	286	3.0	173.5	101.7	36.9	54.5	3G5U
DNR	LEU	A	316	283	->	TYR	A	312	279	3.1	161.9	109.9	12.1	65.6	3G5U
ACC	LEU	A	316	283	->	SER	A	319	286	3.1	121.9	123.2	21.3	88.1	3G5U
ACC	LEU	A	316	283	->	LYS	A	320	287	3.2	169.4	121.2	16.4	59.5	3G5U
DNR	VAL	A	317	284	->	GLY	A	313	280	3.1	138.3	134.2	4.8	72.0	3G5U
DNR	ILE	A	318	285	->	SER	A	315	282	3.0	119.7	135.8	28.1	84.9	3G5U
DNR	SER	A	319	286	->	SER	A	315	282	3.0	173.5	101.7	36.9	54.5	3G5U
DNR	SER	A	319	286	->	LEU	A	316	283	3.1	121.9	123.2	21.3	88.1	3G5U
DNR	LYS	A	320	287	->	LEU	A	316	283	3.2	169.4	121.2	16.4	59.5	3G5U
ACC	VAL	A	327	294	->	PHE	A	331	298	3.0	175.8	104.7	39.2	12.6	3G5U
ACC	LEU	A	328	295	->	PHE	A	332	299	3.0	161.6	123.4	33.7	61.0	3G5U
ACC	THR	A	329	296	->	SER	A	333	300	3.0	145.7	136.3	24.3	77.6	3G5U
ACC	VAL	A	330	297	->	SER	A	333	300	3.0	136.7	123.9	51.2	80.5	3G5U
ACC	VAL	A	330	297	->	VAL	A	334	301	3.0	155.9	105.0	5.9	51.8	3G5U
DNR	PHE	A	331	298	->	VAL	A	327	294	3.0	175.8	104.7	39.2	12.6	3G5U
ACC	PHE	A	331	298	->	VAL	A	334	301	3.0	119.9	113.7	59.5	87.2	3G5U
ACC	PHE	A	331	298	->	LEU	A	335	302	3.0	165.5	114.7	11.9	30.5	3G5U
DNR	PHE	A	332	299	->	LEU	A	328	295	3.0	161.6	123.4	33.7	61.0	3G5U
ACC	PHE	A	332	299	->	ILE	A	336	303	3.2	144.9	108.2	16.4	34.4	3G5U
DNR	SER	A	333	300	->	THR	A	329	296	3.0	145.7	136.3	24.3	77.6	3G5U
DNR	SER	A	333	300	->	VAL	A	330	297	3.0	136.7	123.9	51.2	80.5	3G5U
ACC	SER	A	333	300	->	GLY	A	337	304	3.1	153.5	105.9	19.9	40.7	3G5U
DNR	VAL	A	334	301	->	VAL	A	330	297	3.0	155.9	105.0	5.9	51.8	3G5U
DNR	VAL	A	334	301	->	PHE	A	331	298	3.0	119.9	113.7	59.5	87.2	3G5U
ACC	VAL	A	334	301	->	GLY	A	337	304	3.0	119.8	132.2	52.1	85.6	3G5U
ACC	VAL	A	334	301	->	ALA	A	338	305	3.2	161.5	96.8	1.9	0.7	3G5U
DNR	LEU	A	335	302	->	PHE	A	331	298	3.0	165.5	114.7	11.9	30.5	3G5U
ACC	LEU	A	335	302	->	ALA	A	338	305	3.0	125.4	108.7	59.5	84.4	3G5U
ACC	LEU	A	335	302	->	PHE	A	339	306	3.2	168.4	108.6	17.0	7.6	3G5U
DNR	ILE	A	336	303	->	PHE	A	332	299	3.2	144.9	108.2	16.4	34.4	3G5U
ACC	ILE	A	336	303	->	SER	A	340	307	3.0	157.6	121.0	13.4	49.4	3G5U
DNR	GLY	A	337	304	->	SER	A	333	300	3.1	153.5	105.9	19.9	40.7	3G5U
DNR	GLY	A	337	304	->	VAL	A	334	301	3.0	119.8	132.2	52.1	85.6	3G5U
ACC	GLY	A	337	304	->	VAL	A	341	308	3.0	162.9	108.1	20.7	20.4	3G5U
DNR	ALA	A	338	305	->	VAL	A	334	301	3.2	161.5	96.8	1.9	0.7	3G5U
DNR	ALA	A	338	305	->	LEU	A	335	302	3.0	125.4	108.7	59.5	84.4	3G5U
ACC	ALA	A	338	305	->	VAL	A	341	308	3.0	134.7	119.4	44.7	87.7	3G5U
ACC	ALA	A	338	305	->	GLY	A	342	309	3.2	162.1	105.3	18.6	12.6	3G5U
DNR	PHE	A	339	306	->	LEU	A	335	302	3.2	168.4	108.6	17.0	7.6	3G5U
ACC	PHE	A	339	306	->	GLY	A	342	309	3.0	118.2	136.4	46.0	77.0	3G5U
ACC	PHE	A	339	306	->	GLN	A	343	310	3.2	158.8	103.1	3.6	3.1	3G5U
DNR	SER	A	340	307	->	ILE	A	336	303	3.0	157.6	121.0	13.4	49.4	3G5U
ACC	SER	A	340	307	->	ALA	A	344	311	3.0	158.4	127.6	5.5	76.5	3G5U
DNR	VAL	A	341	308	->	GLY	A	337	304	3.0	162.9	108.1	20.7	20.4	3G5U
DNR	VAL	A	341	308	->	ALA	A	338	305	3.0	134.7	119.4	44.7	87.7	3G5U
ACC	VAL	A	341	308	->	SER	A	345	312	3.1	143.7	118.0	24.1	67.5	3G5U
DNR	GLY	A	342	309	->	ALA	A	338	305	3.2	162.1	105.3	18.6	12.6	3G5U
DNR	GLY	A	342	309	->	PHE	A	339	306	3.0	118.2	136.4	46.0	77.0	3G5U
ACC	GLY	A	342	309	->	SER	A	345	312	3.0	129.9	121.2	50.3	86.5	3G5U

DNR	GLN	A	343	310	->	PHE	A	339	306	3.2	158.8	103.1	3.6	3.1	3G5U
ACC	GLN	A	343	310	->	ASN	A	347	314	3.2	166.3	121.3	0.3	40.6	3G5U
DNR	ALA	A	344	311	->	SER	A	340	307	3.0	158.4	127.6	5.5	76.5	3G5U
ACC	ALA	A	344	311	->	ILE	A	348	315	3.0	166.4	117.9	12.0	29.5	3G5U
DNR	SER	A	345	312	->	VAL	A	341	308	3.1	143.7	118.0	24.1	67.5	3G5U
DNR	SER	A	345	312	->	GLY	A	342	309	3.0	129.9	121.2	50.3	86.5	3G5U
ACC	SER	A	345	312	->	GLU	A	349	316	3.0	165.5	119.6	1.4	66.9	3G5U
ACC	PRO	A	346	313	->	ALA	A	350	317	3.0	164.3	112.4	1.0	45.0	3G5U
DNR	ASN	A	347	314	->	GLN	A	343	310	3.2	166.3	121.3	0.3	40.6	3G5U
ACC	ASN	A	347	314	->	PHE	A	351	318	3.1	156.6	111.5	5.2	28.1	3G5U
DNR	ILE	A	348	315	->	ALA	A	344	311	3.0	166.4	117.9	12.0	29.5	3G5U
ACC	ILE	A	348	315	->	ALA	A	352	319	3.0	175.2	108.0	22.7	0.3	3G5U
DNR	GLU	A	349	316	->	SER	A	345	312	3.0	165.5	119.6	1.4	66.9	3G5U
ACC	GLU	A	349	316	->	ASN	A	353	320	3.0	169.5	114.6	8.1	28.6	3G5U
DNR	ALA	A	350	317	->	PRO	A	346	313	3.0	164.3	112.4	1.0	45.0	3G5U
ACC	ALA	A	350	317	->	ASN	A	353	320	3.1	115.0	117.2	59.2	83.0	3G5U
ACC	ALA	A	350	317	->	ALA	A	354	321	3.0	170.3	117.8	7.1	61.7	3G5U
DNR	PHE	A	351	318	->	ASN	A	347	314	3.1	156.6	111.5	5.2	28.1	3G5U
ACC	PHE	A	351	318	->	ARG	A	355	322	3.0	164.3	116.7	16.5	38.9	3G5U
DNR	ALA	A	352	319	->	ILE	A	348	315	3.0	175.2	108.0	22.7	0.3	3G5U
ACC	ALA	A	352	319	->	GLY	A	356	323	3.0	161.2	117.1	11.0	67.0	3G5U
DNR	ASN	A	353	320	->	GLU	A	349	316	3.0	169.5	114.6	8.1	28.6	3G5U
DNR	ASN	A	353	320	->	ALA	A	350	317	3.1	115.0	117.2	59.2	83.0	3G5U
ACC	ASN	A	353	320	->	ALA	A	357	324	3.0	165.9	119.9	4.4	48.0	3G5U
DNR	ALA	A	354	321	->	ALA	A	350	317	3.0	170.3	117.8	7.1	61.7	3G5U
ACC	ALA	A	354	321	->	ALA	A	358	325	3.0	151.4	119.7	27.3	86.2	3G5U
DNR	ARG	A	355	322	->	PHE	A	351	318	3.0	164.3	116.7	16.5	38.9	3G5U
DNR	GLY	A	356	323	->	ALA	A	352	319	3.0	161.2	117.1	11.0	67.0	3G5U
ACC	GLY	A	356	323	->	GLU	A	360	327	3.1	149.5	133.6	11.6	68.2	3G5U
DNR	ALA	A	357	324	->	ASN	A	353	320	3.0	165.9	119.9	4.4	48.0	3G5U
ACC	ALA	A	357	324	->	VAL	A	361	328	3.1	167.9	129.4	30.9	73.8	3G5U
DNR	ALA	A	358	325	->	ALA	A	354	321	3.0	151.4	119.7	27.3	86.2	3G5U
ACC	TYR	A	359	326	->	PHE	A	362	329	3.3	93.4	146.7	10.5	79.2	3G5U
ACC	TYR	A	359	326	->	LYS	A	363	330	3.0	139.3	109.2	35.1	79.0	3G5U
DNR	GLU	A	360	327	->	GLY	A	356	323	3.1	149.5	133.6	11.6	68.2	3G5U
ACC	GLU	A	360	327	->	LYS	A	363	330	3.0	121.6	126.4	37.4	88.8	3G5U
ACC	GLU	A	360	327	->	ILE	A	364	331	3.2	141.0	104.4	34.7	32.3	3G5U
DNR	VAL	A	361	328	->	ALA	A	357	324	3.1	167.9	129.4	30.9	73.8	3G5U
ACC	VAL	A	361	328	->	ILE	A	365	332	3.0	102.5	107.9	58.0	56.9	3G5U
DNR	PHE	A	362	329	->	TYR	A	359	326	3.3	93.4	146.7	10.5	79.2	3G5U
ACC	PHE	A	362	329	->	ASP	A	366	333	3.0	151.6	96.7	49.1	23.7	3G5U
DNR	LYS	A	363	330	->	TYR	A	359	326	3.0	139.3	109.2	35.1	79.0	3G5U
DNR	LYS	A	363	330	->	GLU	A	360	327	3.0	121.6	126.4	37.4	88.8	3G5U
DNR	ILE	A	364	331	->	GLU	A	360	327	3.2	141.0	104.4	34.7	32.3	3G5U
DNR	ILE	A	365	332	->	VAL	A	361	328	3.0	102.5	107.9	58.0	56.9	3G5U
DNR	ASP	A	366	333	->	PHE	A	362	329	3.0	151.6	96.7	49.1	23.7	3G5U
ACC	HIS	A	379	346	->	ASN	A	458	425	3.0	128.6	127.2	3.6	26.2	3G5U
ACC	LYS	A	380	347	->	ASP	A	382	349	3.1	90.3	90.7	26.4	41.3	3G5U
DNR	ASP	A	382	349	->	LYS	A	380	347	3.1	90.3	90.7	26.4	41.3	3G5U
DNR	ASN	A	387	354	->	ASP	A	450	417	3.3	101.8	128.7	44.0	25.5	3G5U
DNR	LEU	A	388	355	->	VAL	A	413	380	3.1	155.5	109.4	31.6	25.9	3G5U
ACC	LEU	A	388	355	->	VAL	A	413	380	3.1	141.9	118.3	15.5	77.4	3G5U
DNR	GLU	A	389	356	->	SER	A	448	415	3.0	157.6	110.0	41.6	10.4	3G5U
ACC	GLU	A	389	356	->	SER	A	448	415	3.0	137.6	106.3	18.9	44.7	3G5U
DNR	PHE	A	390	357	->	LEU	A	411	378	3.0	151.0	122.7	50.9	89.3	3G5U
ACC	PHE	A	390	357	->	LEU	A	411	378	3.0	156.2	116.0	21.6	16.6	3G5U
DNR	LYS	A	391	358	->	MET	A	446	413	3.0	158.0	133.1	26.0	48.0	3G5U
ACC	LYS	A	391	358	->	MET	A	446	413	3.1	164.7	119.0	21.6	49.0	3G5U
DNR	ILE	A	393	360	->	LEU	A	409	376	3.0	137.1	108.5	0.6	39.2	3G5U
ACC	ILE	A	393	360	->	LEU	A	409	376	3.0	116.8	114.3	27.0	67.9	3G5U
DNR	HIS	A	394	361	->	ASP	A	444	411	3.0	121.5	98.2	21.8	64.7	3G5U
ACC	HIS	A	394	361	->	ASP	A	444	411	3.0	137.7	112.1	22.4	61.6	3G5U
DNR	PHE	A	395	362	->	LEU	A	406	373	3.0	145.4	98.5	20.2	16.4	3G5U
ACC	PHE	A	395	362	->	LEU	A	406	373	3.1	149.4	115.8	35.1	21.3	3G5U
ACC	PRO	A	398	365	->	ARG	A	400	367	3.0	99.8	100.3	23.2	34.7	3G5U
ACC	SER	A	399	366	->	LYS	A	401	368	3.0	113.3	101.6	31.2	8.8	3G5U
ACC	SER	A	399	366	->	GLU	A	402	369	3.3	161.0	105.0	8.4	62.6	3G5U
DNR	ARG	A	400	367	->	PRO	A	398	365	3.0	99.8	100.3	23.2	34.7	3G5U
DNR	LYS	A	401	368	->	SER	A	399	366	3.0	113.3	101.6	31.2	8.8	3G5U
DNR	GLU	A	402	369	->	SER	A	399	366	3.3	161.0	105.0	8.4	62.6	3G5U
ACC	VAL	A	403	370	->	ILE	A	405	372	3.0	104.1	96.2	34.0	39.7	3G5U
DNR	ILE	A	405	372	->	VAL	A	403	370	3.0	104.1	96.2	34.0	39.7	3G5U
DNR	LEU	A	406	373	->	PHE	A	395	362	3.1	149.4	115.8	35.1	21.3	3G5U
ACC	LEU	A	406	373	->	PHE	A	395	362	3.0	145.4	98.5	20.2	16.4	3G5U

DNR	LEU	A	409	376	->	ILE	A	393	360	3.0	116.8	114.3	27.0	67.9	3G5U
ACC	LEU	A	409	376	->	ILE	A	393	360	3.0	137.1	108.5	0.6	39.2	3G5U
DNR	LEU	A	411	378	->	PHE	A	390	357	3.0	156.2	116.0	21.6	16.6	3G5U
ACC	LEU	A	411	378	->	PHE	A	390	357	3.0	151.0	122.7	50.9	89.3	3G5U
DNR	VAL	A	413	380	->	LEU	A	388	355	3.1	141.9	118.3	15.5	77.4	3G5U
ACC	VAL	A	413	380	->	LEU	A	388	355	3.1	155.5	109.4	31.6	25.9	3G5U
ACC	SER	A	415	382	->	GLN	A	417	384	3.0	99.0	104.2	34.3	42.3	3G5U
DNR	GLN	A	417	384	->	SER	A	415	382	3.0	99.0	104.2	34.3	42.3	3G5U
ACC	GLN	A	417	384	->	THR	A	578	545	3.0	135.0	107.7	8.2	53.2	3G5U
ACC	THR	A	418	385	->	ASP	A	592	559	3.1	173.2	128.1	33.4	48.4	3G5U
DNR	VAL	A	419	386	->	THR	A	578	545	3.0	155.0	102.8	18.5	69.8	3G5U
ACC	VAL	A	419	386	->	VAL	A	580	547	3.0	173.7	121.8	7.5	83.3	3G5U
DNR	ALA	A	420	387	->	VAL	A	593	560	3.0	155.5	120.1	5.7	47.7	3G5U
ACC	ALA	A	420	387	->	ALA	A	595	562	3.0	170.0	98.2	29.0	32.8	3G5U
DNR	LEU	A	421	388	->	VAL	A	580	547	3.0	150.4	108.2	8.2	44.3	3G5U
ACC	LEU	A	421	388	->	ALA	A	582	549	3.3	169.0	105.8	3.7	24.0	3G5U
DNR	VAL	A	422	389	->	ALA	A	595	562	3.0	169.5	129.7	11.2	8.2	3G5U
ACC	VAL	A	422	389	->	PHE	A	597	564	3.0	153.0	136.9	4.7	83.4	3G5U
ACC	GLY	A	426	393	->	GLY	A	599	566	3.3	130.1	156.9	56.1	39.1	3G5U
ACC	CYS	A	427	394	->	GLY	A	600	567	3.2	109.2	116.0	54.5	71.5	3G5U
ACC	GLY	A	428	395	->	THR	A	431	398	3.0	144.3	116.5	53.4	86.6	3G5U
ACC	GLY	A	428	395	->	THR	A	432	399	3.1	152.3	100.6	1.2	86.8	3G5U
ACC	LYS	A	429	396	->	THR	A	432	399	3.0	138.9	114.6	46.4	82.4	3G5U
ACC	LYS	A	429	396	->	VAL	A	433	400	3.1	156.5	117.1	2.3	21.1	3G5U
ACC	SER	A	430	397	->	GLN	A	434	401	3.0	144.6	95.2	51.8	16.1	3G5U
DNR	THR	A	431	398	->	GLY	A	428	395	3.0	144.3	116.5	53.4	86.6	3G5U
ACC	THR	A	431	398	->	GLN	A	434	401	3.0	100.4	143.2	38.7	89.6	3G5U
ACC	THR	A	431	398	->	LEU	A	435	402	3.0	168.0	95.5	20.2	86.3	3G5U
DNR	THR	A	432	399	->	GLY	A	428	395	3.1	152.3	100.6	1.2	86.8	3G5U
DNR	THR	A	432	399	->	LYS	A	429	396	3.0	138.9	114.6	46.4	82.4	3G5U
ACC	THR	A	432	399	->	MET	A	436	403	3.0	160.1	128.7	34.6	85.9	3G5U
DNR	VAL	A	433	400	->	LYS	A	429	396	3.1	156.5	117.1	2.3	21.1	3G5U
DNR	GLN	A	434	401	->	SER	A	430	397	3.0	144.6	95.2	51.8	16.1	3G5U
DNR	GLN	A	434	401	->	THR	A	431	398	3.0	100.4	143.2	38.7	89.6	3G5U
ACC	GLN	A	434	401	->	GLN	A	437	404	3.0	140.9	112.6	45.2	29.1	3G5U
DNR	LEU	A	435	402	->	THR	A	431	398	3.0	168.0	95.5	20.2	86.3	3G5U
ACC	LEU	A	435	402	->	ARG	A	438	405	3.0	114.3	131.1	11.5	71.7	3G5U
DNR	MET	A	436	403	->	THR	A	432	399	3.0	160.1	128.7	34.6	85.9	3G5U
DNR	GLN	A	437	404	->	GLN	A	434	401	3.0	140.9	112.6	45.2	29.1	3G5U
DNR	ARG	A	438	405	->	LEU	A	435	402	3.0	114.3	131.1	11.5	71.7	3G5U
DNR	ASP	A	444	411	->	HIS	A	394	361	3.0	137.7	112.1	22.4	61.6	3G5U
ACC	ASP	A	444	411	->	HIS	A	394	361	3.0	121.5	98.2	21.8	64.7	3G5U
DNR	MET	A	446	413	->	LYS	A	391	358	3.1	164.7	119.0	21.6	49.0	3G5U
ACC	MET	A	446	413	->	LYS	A	391	358	3.0	158.0	133.1	26.0	48.0	3G5U
ACC	VAL	A	447	414	->	ILE	A	454	421	3.0	130.1	103.6	26.4	47.9	3G5U
DNR	SER	A	448	415	->	GLU	A	389	356	3.0	137.6	106.3	18.9	44.7	3G5U
ACC	SER	A	448	415	->	GLU	A	389	356	3.0	157.6	110.0	41.6	10.4	3G5U
DNR	ILE	A	449	416	->	GLN	A	452	419	3.0	167.2	96.7	31.0	74.1	3G5U
ACC	ILE	A	449	416	->	GLN	A	452	419	3.0	176.9	105.1	32.7	86.3	3G5U
ACC	ASP	A	450	417	->	ASN	A	387	354	3.3	101.8	128.7	44.0	25.5	3G5U
DNR	GLN	A	452	419	->	ILE	A	449	416	3.0	176.9	105.1	32.7	86.3	3G5U
ACC	GLN	A	452	419	->	ILE	A	449	416	3.0	167.2	96.7	31.0	74.1	3G5U
ACC	ASP	A	453	420	->	THR	A	456	423	3.0	137.5	125.2	39.7	70.8	3G5U
DNR	ILE	A	454	421	->	VAL	A	447	414	3.0	130.1	103.6	26.4	47.9	3G5U
ACC	ILE	A	454	421	->	ILE	A	457	424	3.0	135.8	116.6	34.7	82.8	3G5U
DNR	THR	A	456	423	->	ASP	A	453	420	3.0	137.5	125.2	39.7	70.8	3G5U
DNR	ILE	A	457	424	->	ILE	A	454	421	3.0	135.8	116.6	34.7	82.8	3G5U
DNR	ASN	A	458	425	->	HIS	A	379	346	3.0	128.6	127.2	3.6	26.2	3G5U
ACC	ASN	A	458	425	->	LEU	A	462	429	3.0	149.3	121.4	16.4	25.7	3G5U
ACC	VAL	A	459	426	->	LEU	A	462	429	3.0	137.3	101.2	59.5	67.1	3G5U
ACC	VAL	A	459	426	->	ARG	A	463	430	3.0	150.0	101.7	36.3	68.6	3G5U
ACC	ARG	A	460	427	->	GLU	A	464	431	3.1	145.6	124.7	36.3	68.0	3G5U
ACC	TYR	A	461	428	->	GLU	A	464	431	3.0	113.6	130.3	49.0	79.9	3G5U
ACC	TYR	A	461	428	->	ILE	A	465	432	3.0	165.9	116.0	2.5	31.2	3G5U
DNR	LEU	A	462	429	->	ASN	A	458	425	3.0	149.3	121.4	16.4	25.7	3G5U
DNR	LEU	A	462	429	->	VAL	A	459	426	3.0	137.3	101.2	59.5	67.1	3G5U
ACC	LEU	A	462	429	->	ILE	A	466	433	3.1	164.0	92.5	52.9	39.7	3G5U
DNR	ARG	A	463	430	->	VAL	A	459	426	3.0	150.0	101.7	36.3	68.6	3G5U
DNR	GLU	A	464	431	->	ARG	A	460	427	3.1	145.6	124.7	36.3	68.0	3G5U
DNR	GLU	A	464	431	->	TYR	A	461	428	3.0	113.6	130.3	49.0	79.9	3G5U
DNR	ILE	A	465	432	->	TYR	A	461	428	3.0	165.9	116.0	2.5	31.2	3G5U
ACC	ILE	A	465	432	->	LYS	A	546	513	3.4	125.2	120.6	14.1	71.5	3G5U
DNR	ILE	A	466	433	->	LEU	A	462	429	3.1	164.0	92.5	52.9	39.7	3G5U
DNR	GLY	A	467	434	->	ILE	A	547	514	3.0	161.1	114.6	45.6	90.0	3G5U

ACC	GLY	A	467	434	->	LEU	A	549	516	3.0	151.1	104.0	7.5	45.0	3G5U
DNR	VAL	A	469	436	->	LEU	A	549	516	3.0	175.6	118.9	3.8	87.6	3G5U
ACC	VAL	A	469	436	->	ASP	A	551	518	3.1	136.3	106.6	21.4	52.5	3G5U
DNR	GLN	A	471	438	->	ASP	A	551	518	3.5	149.1	98.6	60.0	44.3	3G5U
ACC	THR	A	479	446	->	ASN	A	483	450	3.1	148.3	116.2	23.3	63.9	3G5U
DNR	ILE	A	480	447	->	PHE	A	516	483	3.1	152.7	114.8	52.7	67.0	3G5U
DNR	ILE	A	480	447	->	THR	A	518	485	3.1	164.2	93.6	15.2	83.7	3G5U
ACC	ILE	A	480	447	->	ASN	A	483	450	3.0	128.2	126.0	48.5	80.4	3G5U
ACC	ILE	A	480	447	->	ILE	A	484	451	3.1	161.9	107.4	0.9	24.1	3G5U
DNR	ALA	A	481	448	->	PHE	A	516	483	3.1	138.2	118.6	10.9	32.4	3G5U
ACC	ALA	A	481	448	->	ARG	A	485	452	3.0	160.3	117.4	9.5	23.5	3G5U
ACC	GLU	A	482	449	->	TYR	A	486	453	3.0	148.6	111.5	30.3	64.4	3G5U
DNR	ASN	A	483	450	->	THR	A	479	446	3.1	148.3	116.2	23.3	63.9	3G5U
DNR	ASN	A	483	450	->	ILE	A	480	447	3.0	128.2	126.0	48.5	80.4	3G5U
ACC	ASN	A	483	450	->	TYR	A	486	453	3.0	115.3	124.1	50.9	87.0	3G5U
ACC	ASN	A	483	450	->	GLY	A	487	454	3.1	155.1	105.6	14.8	38.9	3G5U
DNR	ILE	A	484	451	->	ILE	A	480	447	3.1	161.9	107.4	0.9	24.1	3G5U
ACC	ILE	A	484	451	->	GLY	A	487	454	3.0	120.8	130.0	55.7	84.4	3G5U
ACC	ILE	A	484	451	->	ARG	A	488	455	3.2	152.0	98.5	14.6	10.9	3G5U
DNR	ARG	A	485	452	->	ALA	A	481	448	3.0	160.3	117.4	9.5	23.5	3G5U
ACC	ARG	A	485	452	->	ARG	A	488	455	3.0	114.3	125.0	55.8	89.9	3G5U
DNR	TYR	A	486	453	->	GLU	A	482	449	3.0	148.6	111.5	30.3	64.4	3G5U
DNR	TYR	A	486	453	->	ASN	A	483	450	3.0	115.3	124.1	50.9	87.0	3G5U
DNR	GLY	A	487	454	->	ASN	A	483	450	3.1	155.1	105.6	14.8	38.9	3G5U
DNR	GLY	A	487	454	->	ILE	A	484	451	3.0	120.8	130.0	55.7	84.4	3G5U
DNR	ARG	A	488	455	->	ILE	A	484	451	3.2	152.0	98.5	14.6	10.9	3G5U
DNR	ARG	A	488	455	->	ARG	A	485	452	3.0	114.3	125.0	55.8	89.9	3G5U
ACC	THR	A	492	459	->	GLU	A	495	462	3.0	147.9	123.8	37.9	73.8	3G5U
ACC	THR	A	492	459	->	ILE	A	496	463	3.1	137.7	100.3	0.9	39.7	3G5U
ACC	MET	A	493	460	->	GLU	A	497	464	3.0	133.0	137.7	4.6	82.5	3G5U
ACC	ASP	A	494	461	->	LYS	A	498	465	3.0	145.4	122.2	5.9	66.9	3G5U
DNR	GLU	A	495	462	->	THR	A	492	459	3.0	147.9	123.8	37.9	73.8	3G5U
ACC	GLU	A	495	462	->	ALA	A	499	466	3.0	160.7	117.7	1.6	31.5	3G5U
DNR	ILE	A	496	463	->	THR	A	492	459	3.1	137.7	100.3	0.9	39.7	3G5U
ACC	ILE	A	496	463	->	VAL	A	500	467	3.0	176.4	109.9	9.4	21.8	3G5U
DNR	GLU	A	497	464	->	MET	A	493	460	3.0	133.0	137.7	4.6	82.5	3G5U
ACC	GLU	A	497	464	->	LYS	A	501	468	3.0	171.8	121.9	20.4	66.5	3G5U
DNR	LYS	A	498	465	->	ASP	A	494	461	3.0	145.4	122.2	5.9	66.9	3G5U
ACC	LYS	A	498	465	->	GLU	A	502	469	3.0	171.4	119.3	20.9	3.7	3G5U
DNR	ALA	A	499	466	->	GLU	A	495	462	3.0	160.7	117.7	1.6	31.5	3G5U
ACC	ALA	A	499	466	->	GLU	A	502	469	3.0	117.9	128.1	55.5	78.6	3G5U
ACC	ALA	A	499	466	->	ALA	A	503	470	3.0	160.6	106.8	23.6	7.9	3G5U
DNR	VAL	A	500	467	->	ILE	A	496	463	3.0	176.4	109.9	9.4	21.8	3G5U
ACC	VAL	A	500	467	->	ALA	A	503	470	3.0	130.2	122.2	47.3	86.3	3G5U
ACC	VAL	A	500	467	->	ALA	A	505	472	3.0	117.8	119.2	21.9	89.4	3G5U
DNR	LYS	A	501	468	->	GLU	A	497	464	3.0	171.8	121.9	20.4	66.5	3G5U
ACC	LYS	A	501	468	->	ASN	A	504	471	3.1	109.1	129.9	44.0	81.0	3G5U
DNR	GLU	A	502	469	->	LYS	A	498	465	3.0	171.4	119.3	20.9	3.7	3G5U
DNR	GLU	A	502	469	->	ALA	A	499	466	3.0	117.9	128.1	55.5	78.6	3G5U
DNR	ALA	A	503	470	->	ALA	A	499	466	3.0	160.6	106.8	23.6	7.9	3G5U
DNR	ALA	A	503	470	->	VAL	A	500	467	3.0	130.2	122.2	47.3	86.3	3G5U
DNR	ASN	A	504	471	->	LYS	A	501	468	3.1	109.1	129.9	44.0	81.0	3G5U
DNR	ALA	A	505	472	->	VAL	A	500	467	3.0	117.8	119.2	21.9	89.4	3G5U
ACC	ALA	A	505	472	->	ILE	A	509	476	3.3	168.3	131.3	2.9	13.3	3G5U
ACC	TYR	A	506	473	->	MET	A	510	477	3.3	129.1	126.2	48.3	73.3	3G5U
ACC	ASP	A	507	474	->	MET	A	510	477	3.0	118.7	136.1	39.1	78.1	3G5U
ACC	ASP	A	507	474	->	LYS	A	511	478	3.0	163.0	106.3	6.0	7.8	3G5U
ACC	PHE	A	508	475	->	LEU	A	512	479	3.0	158.1	134.6	14.1	63.7	3G5U
DNR	ILE	A	509	476	->	ALA	A	505	472	3.3	168.3	131.3	2.9	13.3	3G5U
DNR	MET	A	510	477	->	TYR	A	506	473	3.3	129.1	126.2	48.3	73.3	3G5U
DNR	MET	A	510	477	->	ASP	A	507	474	3.0	118.7	136.1	39.1	78.1	3G5U
DNR	LYS	A	511	478	->	ASP	A	507	474	3.0	163.0	106.3	6.0	7.8	3G5U
DNR	LEU	A	512	479	->	PHE	A	508	475	3.0	158.1	134.6	14.1	63.7	3G5U
ACC	PRO	A	513	480	->	GLN	A	515	482	3.0	99.8	99.2	25.2	38.4	3G5U
DNR	GLN	A	515	482	->	PRO	A	513	480	3.0	99.8	99.2	25.2	38.4	3G5U
ACC	GLN	A	515	482	->	THR	A	518	485	3.1	106.8	141.6	5.5	72.2	3G5U
ACC	PHE	A	516	483	->	ILE	A	480	447	3.1	152.7	114.8	52.7	67.0	3G5U
ACC	PHE	A	516	483	->	ALA	A	481	448	3.1	138.2	118.6	10.9	32.4	3G5U
DNR	THR	A	518	485	->	GLN	A	515	482	3.1	106.8	141.6	5.5	72.2	3G5U
ACC	THR	A	518	485	->	ILE	A	480	447	3.1	164.2	93.6	15.2	83.7	3G5U
ACC	SER	A	528	495	->	GLN	A	531	498	3.0	139.7	108.1	55.4	86.7	3G5U
ACC	SER	A	528	495	->	LYS	A	532	499	3.0	151.0	114.1	0.7	35.8	3G5U
ACC	GLY	A	529	496	->	GLN	A	533	500	3.0	152.9	123.7	12.8	77.4	3G5U
ACC	GLY	A	530	497	->	ARG	A	534	501	3.0	151.2	116.7	17.5	25.0	3G5U

DNR	GLN	A	531	498	->	SER	A	528	495	3.0	139.7	108.1	55.4	86.7	3G5U
ACC	GLN	A	531	498	->	ILE	A	535	502	3.0	176.5	112.8	2.0	74.6	3G5U
DNR	LYS	A	532	499	->	SER	A	528	495	3.0	151.0	114.1	0.7	35.8	3G5U
ACC	LYS	A	532	499	->	ALA	A	536	503	3.0	165.6	112.5	3.2	24.3	3G5U
DNR	GLN	A	533	500	->	GLY	A	529	496	3.0	152.9	123.7	12.8	77.4	3G5U
ACC	GLN	A	533	500	->	ILE	A	537	504	3.0	162.7	111.6	2.3	29.9	3G5U
DNR	ARG	A	534	501	->	GLY	A	530	497	3.0	151.2	116.7	17.5	25.0	3G5U
ACC	ARG	A	534	501	->	ALA	A	538	505	3.0	164.6	109.1	15.0	0.6	3G5U
DNR	ILE	A	535	502	->	GLN	A	531	498	3.0	176.5	112.8	2.0	74.6	3G5U
ACC	ILE	A	535	502	->	ALA	A	538	505	3.0	118.3	130.2	53.4	79.8	3G5U
ACC	ILE	A	535	502	->	ARG	A	539	506	3.0	157.3	109.8	8.2	8.3	3G5U
DNR	ALA	A	536	503	->	LYS	A	532	499	3.0	165.6	112.5	3.2	24.3	3G5U
ACC	ALA	A	536	503	->	ALA	A	540	507	3.0	158.3	102.2	14.0	59.5	3G5U
DNR	ILE	A	537	504	->	GLN	A	533	500	3.0	162.7	111.6	2.3	29.9	3G5U
ACC	ILE	A	537	504	->	LEU	A	541	508	3.0	145.3	131.2	38.3	68.9	3G5U
DNR	ALA	A	538	505	->	ARG	A	534	501	3.0	164.6	109.1	15.0	0.6	3G5U
DNR	ALA	A	538	505	->	ILE	A	535	502	3.0	118.3	130.2	53.4	79.8	3G5U
ACC	ALA	A	538	505	->	VAL	A	542	509	3.0	170.8	100.2	20.6	54.0	3G5U
DNR	ARG	A	539	506	->	ILE	A	535	502	3.0	157.3	109.8	8.2	8.3	3G5U
ACC	ARG	A	539	506	->	VAL	A	542	509	3.0	127.9	119.8	36.6	84.8	3G5U
ACC	ARG	A	539	506	->	ARG	A	543	510	3.2	155.9	111.6	19.5	8.6	3G5U
DNR	ALA	A	540	507	->	ALA	A	536	503	3.0	158.3	102.2	14.0	59.5	3G5U
ACC	ALA	A	540	507	->	ARG	A	543	510	3.0	110.5	129.7	55.6	83.6	3G5U
ACC	ALA	A	540	507	->	ASN	A	544	511	3.1	153.9	104.4	29.4	44.8	3G5U
DNR	LEU	A	541	508	->	ILE	A	537	504	3.0	145.3	131.2	38.3	68.9	3G5U
ACC	LEU	A	541	508	->	ASN	A	544	511	3.2	100.1	137.6	44.8	77.2	3G5U
DNR	VAL	A	542	509	->	ALA	A	538	505	3.0	170.8	100.2	20.6	54.0	3G5U
DNR	VAL	A	542	509	->	ARG	A	539	506	3.0	127.9	119.8	36.6	84.8	3G5U
DNR	ARG	A	543	510	->	ARG	A	539	506	3.2	155.9	111.6	19.5	8.6	3G5U
DNR	ARG	A	543	510	->	ALA	A	540	507	3.0	110.5	129.7	55.6	83.6	3G5U
DNR	ASN	A	544	511	->	ALA	A	540	507	3.1	153.9	104.4	29.4	44.8	3G5U
DNR	ASN	A	544	511	->	LEU	A	541	508	3.2	100.1	137.6	44.8	77.2	3G5U
DNR	LYS	A	546	513	->	ILE	A	465	432	3.4	125.2	120.6	14.1	71.5	3G5U
ACC	LYS	A	546	513	->	THR	A	577	544	3.3	129.8	125.9	38.9	83.5	3G5U
ACC	ILE	A	547	514	->	GLY	A	467	434	3.0	161.1	114.6	45.6	90.0	3G5U
DNR	LEU	A	548	515	->	THR	A	577	544	3.1	144.8	99.1	20.5	41.6	3G5U
ACC	LEU	A	548	515	->	ILE	A	579	546	3.0	156.9	99.8	37.2	75.0	3G5U
DNR	LEU	A	549	516	->	GLY	A	467	434	3.0	151.1	104.0	7.5	45.0	3G5U
ACC	LEU	A	549	516	->	VAL	A	469	436	3.0	175.6	118.9	3.8	87.6	3G5U
DNR	LEU	A	550	517	->	ILE	A	579	546	3.1	149.1	100.9	3.1	36.2	3G5U
ACC	LEU	A	550	517	->	ILE	A	581	548	3.1	157.4	115.9	14.2	83.6	3G5U
DNR	ASP	A	551	518	->	VAL	A	469	436	3.1	136.3	106.6	21.4	52.5	3G5U
ACC	ASP	A	551	518	->	GLN	A	471	438	3.5	149.1	98.6	60.0	44.3	3G5U
DNR	GLU	A	552	519	->	ILE	A	581	548	3.0	164.5	135.5	28.1	81.6	3G5U
ACC	GLU	A	552	519	->	SER	A	555	522	3.0	166.3	120.3	39.9	48.1	3G5U
DNR	SER	A	555	522	->	GLU	A	552	519	3.0	166.3	120.3	39.9	48.1	3G5U
ACC	ASP	A	558	525	->	GLU	A	562	529	3.0	162.6	127.1	2.4	43.3	3G5U
ACC	THR	A	559	526	->	ALA	A	563	530	3.1	161.5	101.9	22.6	1.3	3G5U
ACC	GLU	A	560	527	->	ALA	A	563	530	3.0	109.6	138.7	44.8	76.5	3G5U
ACC	GLU	A	560	527	->	VAL	A	564	531	3.1	152.0	106.3	12.3	20.8	3G5U
ACC	SER	A	561	528	->	VAL	A	565	532	3.0	154.6	112.2	5.0	88.2	3G5U
DNR	GLU	A	562	529	->	ASP	A	558	525	3.0	162.6	127.1	2.4	43.3	3G5U
ACC	GLU	A	562	529	->	GLN	A	566	533	3.0	140.2	131.1	6.1	89.2	3G5U
DNR	ALA	A	563	530	->	THR	A	559	526	3.1	161.5	101.9	22.6	1.3	3G5U
DNR	ALA	A	563	530	->	GLU	A	560	527	3.0	109.6	138.7	44.8	76.5	3G5U
ACC	ALA	A	563	530	->	GLN	A	566	533	3.0	132.1	111.6	58.4	86.0	3G5U
ACC	ALA	A	563	530	->	ALA	A	567	534	3.0	161.5	115.7	21.0	20.0	3G5U
DNR	VAL	A	564	531	->	GLU	A	560	527	3.1	152.0	106.3	12.3	20.8	3G5U
ACC	VAL	A	564	531	->	ALA	A	568	535	3.1	153.8	107.3	18.3	49.0	3G5U
DNR	VAL	A	565	532	->	SER	A	561	528	3.0	154.6	112.2	5.0	88.2	3G5U
ACC	VAL	A	565	532	->	ALA	A	568	535	3.1	114.2	117.5	53.6	87.9	3G5U
ACC	VAL	A	565	532	->	LEU	A	569	536	3.0	157.9	119.7	13.4	37.3	3G5U
DNR	GLN	A	566	533	->	GLU	A	562	529	3.0	140.2	131.1	6.1	89.2	3G5U
DNR	GLN	A	566	533	->	ALA	A	563	530	3.0	132.1	111.6	58.4	86.0	3G5U
ACC	GLN	A	566	533	->	ASP	A	570	537	3.0	157.6	118.5	8.6	66.3	3G5U
DNR	ALA	A	567	534	->	ALA	A	563	530	3.0	161.5	115.7	21.0	20.0	3G5U
ACC	ALA	A	567	534	->	LYS	A	571	538	3.0	154.1	115.8	3.1	49.9	3G5U
DNR	ALA	A	568	535	->	VAL	A	564	531	3.1	153.8	107.3	18.3	49.0	3G5U
DNR	ALA	A	568	535	->	VAL	A	565	532	3.1	114.2	117.5	53.6	87.9	3G5U
ACC	ALA	A	568	535	->	ALA	A	572	539	3.0	147.2	110.7	55.7	63.0	3G5U
DNR	LEU	A	569	536	->	VAL	A	565	532	3.0	157.9	119.7	13.4	37.3	3G5U
ACC	LEU	A	569	536	->	ALA	A	572	539	3.0	119.6	148.2	17.7	72.3	3G5U
ACC	LEU	A	569	536	->	ARG	A	573	540	3.0	167.3	102.5	13.8	32.5	3G5U
DNR	ASP	A	570	537	->	GLN	A	566	533	3.0	157.6	118.5	8.6	66.3	3G5U

ACC	ASP	A	570	537	->	ARG	A	573	540	3.2	122.9	96.5	45.9	77.6	3G5U
DNR	LYS	A	571	538	->	ALA	A	567	534	3.0	154.1	115.8	3.1	49.9	3G5U
DNR	ALA	A	572	539	->	ALA	A	568	535	3.0	147.2	110.7	55.7	63.0	3G5U
DNR	ALA	A	572	539	->	LEU	A	569	536	3.0	119.6	148.2	17.7	72.3	3G5U
DNR	ARG	A	573	540	->	LEU	A	569	536	3.0	167.3	102.5	13.8	32.5	3G5U
DNR	ARG	A	573	540	->	ASP	A	570	537	3.2	122.9	96.5	45.9	77.6	3G5U
ACC	ARG	A	573	540	->	ARG	A	576	543	3.0	127.4	135.2	41.2	76.7	3G5U
DNR	ARG	A	576	543	->	ARG	A	573	540	3.0	127.4	135.2	41.2	76.7	3G5U
DNR	THR	A	577	544	->	LYS	A	546	513	3.3	129.8	125.9	38.9	83.5	3G5U
ACC	THR	A	577	544	->	LEU	A	548	515	3.1	144.8	99.1	20.5	41.6	3G5U
DNR	THR	A	578	545	->	GLN	A	417	384	3.0	135.0	107.7	8.2	53.2	3G5U
ACC	THR	A	578	545	->	VAL	A	419	386	3.0	155.0	102.8	18.5	69.8	3G5U
DNR	ILE	A	579	546	->	LEU	A	548	515	3.0	156.9	99.8	37.2	75.0	3G5U
ACC	ILE	A	579	546	->	LEU	A	550	517	3.1	149.1	100.9	3.1	36.2	3G5U
DNR	VAL	A	580	547	->	VAL	A	419	386	3.0	173.7	121.8	7.5	83.3	3G5U
ACC	VAL	A	580	547	->	LEU	A	421	388	3.0	150.4	108.2	8.2	44.3	3G5U
DNR	ILE	A	581	548	->	LEU	A	550	517	3.1	157.4	115.9	14.2	83.6	3G5U
ACC	ILE	A	581	548	->	GLU	A	552	519	3.0	164.5	135.5	28.1	81.6	3G5U
DNR	ALA	A	582	549	->	LEU	A	421	388	3.3	169.0	105.8	3.7	24.0	3G5U
ACC	HIS	A	583	550	->	LEU	A	585	552	3.0	99.3	95.1	23.6	36.7	3G5U
ACC	ARG	A	584	551	->	THR	A	587	554	3.0	144.4	120.3	30.0	89.8	3G5U
ACC	ARG	A	584	551	->	VAL	A	588	555	3.1	150.4	95.9	47.2	29.0	3G5U
DNR	LEU	A	585	552	->	HIS	A	583	550	3.0	99.3	95.1	23.6	36.7	3G5U
ACC	LEU	A	585	552	->	VAL	A	588	555	3.0	98.8	140.3	15.2	89.0	3G5U
ACC	LEU	A	585	552	->	ARG	A	589	556	3.1	152.0	111.4	2.8	79.2	3G5U
DNR	THR	A	587	554	->	ARG	A	584	551	3.0	144.4	120.3	30.0	89.8	3G5U
DNR	VAL	A	588	555	->	ARG	A	584	551	3.1	150.4	95.9	47.2	29.0	3G5U
DNR	VAL	A	588	555	->	LEU	A	585	552	3.0	98.8	140.3	15.2	89.0	3G5U
ACC	VAL	A	588	555	->	ALA	A	591	558	3.0	157.1	107.7	58.2	14.9	3G5U
DNR	ARG	A	589	556	->	LEU	A	585	552	3.1	152.0	111.4	2.8	79.2	3G5U
ACC	ARG	A	589	556	->	ALA	A	591	558	3.0	96.3	103.7	14.7	44.0	3G5U
DNR	ALA	A	591	558	->	VAL	A	588	555	3.0	157.1	107.7	58.2	14.9	3G5U
DNR	ALA	A	591	558	->	ARG	A	589	556	3.0	96.3	103.7	14.7	44.0	3G5U
DNR	ASP	A	592	559	->	THR	A	418	385	3.1	173.2	128.1	33.4	48.4	3G5U
ACC	VAL	A	593	560	->	ALA	A	420	387	3.0	155.5	120.1	5.7	47.7	3G5U
DNR	ILE	A	594	561	->	GLY	A	606	573	3.0	134.5	122.0	27.4	68.0	3G5U
ACC	ILE	A	594	561	->	GLY	A	606	573	3.0	151.5	107.6	10.6	46.2	3G5U
DNR	ALA	A	595	562	->	ALA	A	420	387	3.0	170.0	98.2	29.0	32.8	3G5U
ACC	ALA	A	595	562	->	VAL	A	422	389	3.0	169.5	129.7	11.2	8.2	3G5U
DNR	GLY	A	596	563	->	GLU	A	604	571	3.1	131.8	102.4	42.1	64.1	3G5U
ACC	GLY	A	596	563	->	VAL	A	603	570	3.1	135.1	92.2	38.6	3.3	3G5U
DNR	PHE	A	597	564	->	VAL	A	422	389	3.0	153.0	136.9	4.7	83.4	3G5U
DNR	GLY	A	599	566	->	GLY	A	426	393	3.3	130.1	156.9	56.1	39.1	3G5U
DNR	GLY	A	600	567	->	CYS	A	427	394	3.2	109.2	116.0	54.5	71.5	3G5U
DNR	VAL	A	603	570	->	GLY	A	596	563	3.1	135.1	92.2	38.6	3.3	3G5U
ACC	GLU	A	604	571	->	GLY	A	596	563	3.1	131.8	102.4	42.1	64.1	3G5U
DNR	GLY	A	606	573	->	ILE	A	594	561	3.0	151.5	107.6	10.6	46.2	3G5U
ACC	GLY	A	606	573	->	ILE	A	594	561	3.0	134.5	122.0	27.4	68.0	3G5U
ACC	ASN	A	607	574	->	GLU	A	610	577	3.0	121.3	140.4	40.6	70.7	3G5U
ACC	ASN	A	607	574	->	LEU	A	611	578	3.0	165.9	104.2	16.4	12.6	3G5U
ACC	HIS	A	608	575	->	LEU	A	611	578	3.0	135.5	113.3	45.2	89.6	3G5U
ACC	HIS	A	608	575	->	MET	A	612	579	3.0	160.8	111.5	24.6	26.9	3G5U
ACC	ASP	A	609	576	->	ARG	A	613	580	3.0	132.1	137.0	21.2	78.3	3G5U
DNR	GLU	A	610	577	->	ASN	A	607	574	3.0	121.3	140.4	40.6	70.7	3G5U
ACC	GLU	A	610	577	->	GLU	A	614	581	3.0	139.6	110.1	48.9	66.2	3G5U
DNR	LEU	A	611	578	->	ASN	A	607	574	3.0	165.9	104.2	16.4	12.6	3G5U
DNR	LEU	A	611	578	->	HIS	A	608	575	3.0	135.5	113.3	45.2	89.6	3G5U
ACC	LEU	A	611	578	->	LYS	A	615	582	3.4	120.0	111.4	41.4	64.5	3G5U
ACC	LEU	A	611	578	->	PHE	A	619	586	3.5	120.5	137.4	16.5	75.7	3G5U
DNR	MET	A	612	579	->	HIS	A	608	575	3.0	160.8	111.5	24.6	26.9	3G5U
ACC	MET	A	612	579	->	LYS	A	615	582	3.0	116.4	128.6	44.4	88.6	3G5U
DNR	ARG	A	613	580	->	ASP	A	609	576	3.0	132.1	137.0	21.2	78.3	3G5U
DNR	GLU	A	614	581	->	GLU	A	610	577	3.0	139.6	110.1	48.9	66.2	3G5U
DNR	LYS	A	615	582	->	LEU	A	611	578	3.4	120.0	111.4	41.4	64.5	3G5U
DNR	LYS	A	615	582	->	MET	A	612	579	3.0	116.4	128.6	44.4	88.6	3G5U
ACC	GLY	A	616	583	->	LYS	A	620	587	3.0	145.2	138.6	12.4	69.6	3G5U
ACC	ILE	A	617	584	->	LEU	A	621	588	3.0	173.6	112.1	21.8	37.1	3G5U
ACC	TYR	A	618	585	->	VAL	A	622	589	3.0	168.1	125.9	21.5	12.3	3G5U
DNR	PHE	A	619	586	->	LEU	A	611	578	3.5	120.5	137.4	16.5	75.7	3G5U
ACC	PHE	A	619	586	->	MET	A	623	590	3.0	166.3	114.4	13.9	79.2	3G5U
DNR	LYS	A	620	587	->	GLY	A	616	583	3.0	145.2	138.6	12.4	69.6	3G5U
ACC	LYS	A	620	587	->	MET	A	623	590	3.0	127.9	118.0	50.6	84.9	3G5U
ACC	LYS	A	620	587	->	THR	A	624	591	3.0	163.5	118.8	15.5	17.4	3G5U
DNR	LEU	A	621	588	->	ILE	A	617	584	3.0	173.6	112.1	21.8	37.1	3G5U

ACC	LEU	A	621	588	->	GLN	A	625	592	3.0	143.0	118.8	27.3	83.5	3G5U
DNR	VAL	A	622	589	->	TYR	A	618	585	3.0	168.1	125.9	21.5	12.3	3G5U
ACC	VAL	A	622	589	->	GLN	A	625	592	3.4	99.3	131.8	51.0	74.2	3G5U
ACC	VAL	A	622	589	->	THR	A	626	593	3.1	135.8	105.2	55.6	37.5	3G5U
DNR	MET	A	623	590	->	PHE	A	619	586	3.0	166.3	114.4	13.9	79.2	3G5U
DNR	MET	A	623	590	->	LYS	A	620	587	3.0	127.9	118.0	50.6	84.9	3G5U
ACC	MET	A	623	590	->	THR	A	626	593	3.0	103.6	132.2	36.3	83.0	3G5U
DNR	THR	A	624	591	->	LYS	A	620	587	3.0	163.5	118.8	15.5	17.4	3G5U
DNR	GLN	A	625	592	->	LEU	A	621	588	3.0	143.0	118.8	27.3	83.5	3G5U
DNR	GLN	A	625	592	->	VAL	A	622	589	3.4	99.3	131.8	51.0	74.2	3G5U
DNR	THR	A	626	593	->	VAL	A	622	589	3.1	135.8	105.2	55.6	37.5	3G5U
DNR	THR	A	626	593	->	MET	A	623	590	3.0	103.6	132.2	36.3	83.0	3G5U
ACC	SER	A	692	602	->	ARG	A	695	605	3.0	119.1	120.9	25.8	73.9	3G5U
ACC	PHE	A	693	603	->	ARG	A	695	605	3.0	92.0	93.0	48.0	47.3	3G5U
ACC	TRP	A	694	604	->	LEU	A	697	607	3.0	100.6	146.8	24.5	74.6	3G5U
ACC	TRP	A	694	604	->	LYS	A	698	608	3.0	151.1	113.3	12.8	60.2	3G5U
DNR	ARG	A	695	605	->	SER	A	692	602	3.0	119.1	120.9	25.8	73.9	3G5U
DNR	ARG	A	695	605	->	PHE	A	693	603	3.0	92.0	93.0	48.0	47.3	3G5U
ACC	ARG	A	695	605	->	LEU	A	699	609	3.0	166.5	115.1	18.2	15.7	3G5U
DNR	LEU	A	697	607	->	TRP	A	694	604	3.0	100.6	146.8	24.5	74.6	3G5U
ACC	LEU	A	697	607	->	SER	A	701	611	3.0	159.4	101.7	15.2	85.3	3G5U
DNR	LYS	A	698	608	->	TRP	A	694	604	3.0	151.1	113.3	12.8	60.2	3G5U
ACC	LYS	A	698	608	->	THR	A	702	612	3.1	148.7	116.6	19.9	15.4	3G5U
DNR	LEU	A	699	609	->	ARG	A	695	605	3.0	166.5	115.1	18.2	15.7	3G5U
ACC	LEU	A	699	609	->	GLU	A	703	613	3.0	170.1	109.1	0.8	43.3	3G5U
DNR	SER	A	701	611	->	LEU	A	697	607	3.0	159.4	101.7	15.2	85.3	3G5U
DNR	THR	A	702	612	->	LYS	A	698	608	3.1	148.7	116.6	19.9	15.4	3G5U
DNR	GLU	A	703	613	->	LEU	A	699	609	3.0	170.1	109.1	0.8	43.3	3G5U
ACC	PHE	A	707	617	->	GLY	A	710	620	3.1	110.3	116.9	57.0	85.4	3G5U
ACC	PHE	A	707	617	->	ILE	A	711	621	3.4	149.4	108.1	15.6	32.5	3G5U
ACC	VAL	A	708	618	->	PHE	A	712	622	3.0	158.7	119.6	36.7	45.2	3G5U
ACC	VAL	A	709	619	->	PHE	A	712	622	3.0	111.9	132.4	54.9	85.3	3G5U
ACC	VAL	A	709	619	->	CYS	A	713	623	3.0	172.0	102.8	3.1	51.0	3G5U
DNR	GLY	A	710	620	->	PHE	A	707	617	3.1	110.3	116.9	57.0	85.4	3G5U
ACC	GLY	A	710	620	->	CYS	A	713	623	3.0	145.8	100.1	54.7	84.6	3G5U
ACC	GLY	A	710	620	->	ALA	A	714	624	3.0	155.0	115.9	18.0	36.9	3G5U
DNR	ILE	A	711	621	->	PHE	A	707	617	3.4	149.4	108.1	15.6	32.5	3G5U
ACC	ILE	A	711	621	->	ILE	A	715	625	3.1	151.0	109.4	10.4	68.5	3G5U
DNR	PHE	A	712	622	->	VAL	A	708	618	3.0	158.7	119.6	36.7	45.2	3G5U
DNR	PHE	A	712	622	->	VAL	A	709	619	3.0	111.9	132.4	54.9	85.3	3G5U
ACC	PHE	A	712	622	->	ILE	A	715	625	3.0	128.2	115.2	55.1	85.1	3G5U
ACC	PHE	A	712	622	->	ILE	A	716	626	3.2	151.4	107.5	4.5	1.4	3G5U
DNR	CYS	A	713	623	->	VAL	A	709	619	3.0	172.0	102.8	3.1	51.0	3G5U
DNR	CYS	A	713	623	->	GLY	A	710	620	3.0	145.8	100.1	54.7	84.6	3G5U
ACC	CYS	A	713	623	->	ASN	A	717	627	3.0	173.7	114.1	1.2	59.9	3G5U
DNR	ALA	A	714	624	->	GLY	A	710	620	3.0	155.0	115.9	18.0	36.9	3G5U
ACC	ALA	A	714	624	->	GLY	A	718	628	3.1	163.7	117.6	6.3	48.7	3G5U
DNR	ILE	A	715	625	->	ILE	A	711	621	3.1	151.0	109.4	10.4	68.5	3G5U
DNR	ILE	A	715	625	->	PHE	A	712	622	3.0	128.2	115.2	55.1	85.1	3G5U
ACC	ILE	A	715	625	->	GLY	A	719	629	3.1	159.7	112.6	2.3	23.3	3G5U
DNR	ILE	A	716	626	->	PHE	A	712	622	3.2	151.4	107.5	4.5	1.4	3G5U
ACC	ILE	A	716	626	->	LEU	A	720	630	3.0	170.6	121.3	4.8	32.7	3G5U
DNR	ASN	A	717	627	->	CYS	A	713	623	3.0	173.7	114.1	1.2	59.9	3G5U
ACC	ASN	A	717	627	->	GLN	A	721	631	3.1	161.1	102.1	15.2	36.3	3G5U
DNR	GLY	A	718	628	->	ALA	A	714	624	3.1	163.7	117.6	6.3	48.7	3G5U
ACC	GLY	A	718	628	->	GLN	A	721	631	3.0	122.0	121.6	49.1	83.6	3G5U
DNR	GLY	A	719	629	->	ILE	A	715	625	3.1	159.7	112.6	2.3	23.3	3G5U
ACC	GLY	A	719	629	->	ALA	A	723	633	3.0	174.6	125.9	12.3	9.9	3G5U
DNR	LEU	A	720	630	->	ILE	A	716	626	3.0	170.6	121.3	4.8	32.7	3G5U
ACC	LEU	A	720	630	->	PHE	A	724	634	3.1	151.1	110.6	21.7	49.3	3G5U
DNR	GLN	A	721	631	->	ASN	A	717	627	3.1	161.1	102.1	15.2	36.3	3G5U
DNR	GLN	A	721	631	->	GLY	A	718	628	3.0	122.0	121.6	49.1	83.6	3G5U
ACC	GLN	A	721	631	->	PHE	A	724	634	3.0	127.8	118.0	51.5	86.9	3G5U
ACC	GLN	A	721	631	->	SER	A	725	635	3.1	162.5	110.1	1.1	0.5	3G5U
ACC	PRO	A	722	632	->	VAL	A	726	636	3.1	157.4	103.7	15.9	35.5	3G5U
DNR	ALA	A	723	633	->	GLY	A	719	629	3.0	174.6	125.9	12.3	9.9	3G5U
ACC	ALA	A	723	633	->	VAL	A	726	636	3.0	116.0	124.0	52.2	78.9	3G5U
ACC	ALA	A	723	633	->	ILE	A	727	637	3.0	165.9	117.0	3.2	3.9	3G5U
DNR	PHE	A	724	634	->	LEU	A	720	630	3.1	151.1	110.6	21.7	49.3	3G5U
DNR	PHE	A	724	634	->	GLN	A	721	631	3.0	127.8	118.0	51.5	86.9	3G5U
ACC	PHE	A	724	634	->	PHE	A	728	638	3.1	161.9	124.0	3.2	52.0	3G5U
DNR	SER	A	725	635	->	GLN	A	721	631	3.1	162.5	110.1	1.1	0.5	3G5U
ACC	SER	A	725	635	->	SER	A	729	639	3.1	145.8	133.3	3.1	52.1	3G5U
DNR	VAL	A	726	636	->	PRO	A	722	632	3.1	157.4	103.7	15.9	35.5	3G5U

DNR	VAL	A	726	636	->	ALA	A	723	633	3.0	116.0	124.0	52.2	78.9	3G5U
ACC	VAL	A	726	636	->	LYS	A	730	640	3.0	159.6	123.6	28.2	89.8	3G5U
DNR	ILE	A	727	637	->	ALA	A	723	633	3.0	165.9	117.0	3.2	3.9	3G5U
ACC	ILE	A	727	637	->	LYS	A	730	640	3.3	97.6	134.4	56.5	76.7	3G5U
ACC	ILE	A	727	637	->	VAL	A	731	641	3.0	147.8	115.8	9.3	53.0	3G5U
DNR	PHE	A	728	638	->	PHE	A	724	634	3.1	161.9	124.0	3.2	52.0	3G5U
ACC	PHE	A	728	638	->	VAL	A	732	642	3.1	170.3	105.0	29.1	86.6	3G5U
DNR	SER	A	729	639	->	SER	A	725	635	3.1	145.8	133.3	3.1	52.1	3G5U
ACC	SER	A	729	639	->	GLY	A	733	643	3.0	143.4	141.3	5.8	76.6	3G5U
DNR	LYS	A	730	640	->	VAL	A	726	636	3.0	159.6	123.6	28.2	89.8	3G5U
DNR	LYS	A	730	640	->	ILE	A	727	637	3.3	97.6	134.4	56.5	76.7	3G5U
ACC	LYS	A	730	640	->	VAL	A	734	644	3.0	175.9	116.9	14.6	32.8	3G5U
DNR	VAL	A	731	641	->	ILE	A	727	637	3.0	147.8	115.8	9.3	53.0	3G5U
DNR	VAL	A	732	642	->	PHE	A	728	638	3.1	170.3	105.0	29.1	86.6	3G5U
ACC	VAL	A	732	642	->	PHE	A	735	645	3.0	126.1	135.7	33.8	74.4	3G5U
ACC	VAL	A	732	642	->	THR	A	736	646	3.0	174.2	108.8	47.5	39.6	3G5U
DNR	GLY	A	733	643	->	SER	A	729	639	3.0	143.4	141.3	5.8	76.6	3G5U
ACC	GLY	A	733	643	->	THR	A	736	646	3.0	121.6	122.1	20.6	85.3	3G5U
ACC	GLY	A	733	643	->	ASN	A	737	647	3.1	171.1	110.6	35.1	70.2	3G5U
DNR	VAL	A	734	644	->	LYS	A	730	640	3.0	175.9	116.9	14.6	32.8	3G5U
DNR	PHE	A	735	645	->	VAL	A	732	642	3.0	126.1	135.7	33.8	74.4	3G5U
DNR	THR	A	736	646	->	VAL	A	732	642	3.0	174.2	108.8	47.5	39.6	3G5U
DNR	THR	A	736	646	->	GLY	A	733	643	3.0	121.6	122.1	20.6	85.3	3G5U
DNR	ASN	A	737	647	->	GLY	A	733	643	3.1	171.1	110.6	35.1	70.2	3G5U
ACC	GLU	A	742	652	->	GLN	A	746	656	3.0	171.3	119.3	4.5	19.2	3G5U
ACC	THR	A	743	653	->	ASN	A	747	657	3.0	139.0	132.2	11.8	84.5	3G5U
ACC	GLN	A	744	654	->	SER	A	748	658	3.0	161.7	115.9	42.3	75.6	3G5U
ACC	ARG	A	745	655	->	ASN	A	749	659	3.0	147.5	138.1	11.0	76.7	3G5U
DNR	GLN	A	746	656	->	GLU	A	742	652	3.0	171.3	119.3	4.5	19.2	3G5U
ACC	GLN	A	746	656	->	LEU	A	750	660	3.0	154.4	120.4	29.0	82.9	3G5U
DNR	ASN	A	747	657	->	THR	A	743	653	3.0	139.0	132.2	11.8	84.5	3G5U
ACC	ASN	A	747	657	->	PHE	A	751	661	3.0	140.9	112.5	1.6	81.3	3G5U
DNR	SER	A	748	658	->	GLN	A	744	654	3.0	161.7	115.9	42.3	75.6	3G5U
ACC	SER	A	748	658	->	SER	A	752	662	3.0	155.5	117.6	18.8	89.9	3G5U
DNR	ASN	A	749	659	->	ARG	A	745	655	3.0	147.5	138.1	11.0	76.7	3G5U
ACC	ASN	A	749	659	->	LEU	A	753	663	3.0	158.8	121.2	4.5	54.4	3G5U
DNR	LEU	A	750	660	->	GLN	A	746	656	3.0	154.4	120.4	29.0	82.9	3G5U
ACC	LEU	A	750	660	->	LEU	A	754	664	3.0	155.5	120.2	11.9	85.1	3G5U
DNR	PHE	A	751	661	->	ASN	A	747	657	3.0	140.9	112.5	1.6	81.3	3G5U
ACC	PHE	A	751	661	->	LEU	A	754	664	3.0	128.0	117.7	59.1	86.2	3G5U
ACC	PHE	A	751	661	->	PHE	A	755	665	3.1	156.3	107.0	8.1	9.0	3G5U
DNR	SER	A	752	662	->	SER	A	748	658	3.0	155.5	117.6	18.8	89.9	3G5U
ACC	SER	A	752	662	->	LEU	A	756	666	3.0	168.1	101.9	39.3	47.6	3G5U
DNR	LEU	A	753	663	->	ASN	A	749	659	3.0	158.8	121.2	4.5	54.4	3G5U
ACC	LEU	A	753	663	->	ILE	A	757	667	3.0	151.5	141.0	16.4	64.8	3G5U
DNR	LEU	A	754	664	->	LEU	A	750	660	3.0	155.5	120.2	11.9	85.1	3G5U
DNR	LEU	A	754	664	->	PHE	A	751	661	3.0	128.0	117.7	59.1	86.2	3G5U
ACC	LEU	A	754	664	->	LEU	A	758	668	3.0	146.4	122.9	41.7	88.9	3G5U
DNR	PHE	A	755	665	->	PHE	A	751	661	3.1	156.3	107.0	8.1	9.0	3G5U
DNR	LEU	A	756	666	->	SER	A	752	662	3.0	168.1	101.9	39.3	47.6	3G5U
ACC	LEU	A	756	666	->	ILE	A	760	670	3.0	134.8	139.5	35.4	66.1	3G5U
DNR	ILE	A	757	667	->	LEU	A	753	663	3.0	151.5	141.0	16.4	64.8	3G5U
ACC	ILE	A	757	667	->	ILE	A	761	671	3.0	168.2	111.7	55.1	4.2	3G5U
DNR	LEU	A	758	668	->	LEU	A	754	664	3.0	146.4	122.9	41.7	88.9	3G5U
ACC	LEU	A	758	668	->	SER	A	762	672	3.0	165.6	124.3	10.4	40.3	3G5U
ACC	GLY	A	759	669	->	PHE	A	763	673	3.1	154.5	130.6	12.2	58.2	3G5U
DNR	ILE	A	760	670	->	LEU	A	756	666	3.0	134.8	139.5	35.4	66.1	3G5U
ACC	ILE	A	760	670	->	ILE	A	764	674	3.0	154.0	112.7	6.5	79.9	3G5U
DNR	ILE	A	761	671	->	ILE	A	757	667	3.0	168.2	111.7	55.1	4.2	3G5U
ACC	ILE	A	761	671	->	THR	A	765	675	3.0	156.3	117.9	8.3	16.8	3G5U
DNR	SER	A	762	672	->	LEU	A	758	668	3.0	165.6	124.3	10.4	40.3	3G5U
ACC	SER	A	762	672	->	PHE	A	766	676	3.0	162.2	105.1	12.1	63.3	3G5U
DNR	PHE	A	763	673	->	GLY	A	759	669	3.1	154.5	130.6	12.2	58.2	3G5U
ACC	PHE	A	763	673	->	PHE	A	767	677	3.1	157.4	123.7	26.6	60.2	3G5U
DNR	ILE	A	764	674	->	ILE	A	760	670	3.0	154.0	112.7	6.5	79.9	3G5U
ACC	ILE	A	764	674	->	LEU	A	768	678	3.1	155.8	109.1	16.7	88.1	3G5U
DNR	THR	A	765	675	->	ILE	A	761	671	3.0	156.3	117.9	8.3	16.8	3G5U
ACC	THR	A	765	675	->	GLN	A	769	679	3.0	158.2	128.5	13.3	53.7	3G5U
DNR	PHE	A	766	676	->	SER	A	762	672	3.0	162.2	105.1	12.1	63.3	3G5U
ACC	PHE	A	766	676	->	GLY	A	770	680	3.0	158.7	122.1	13.5	46.5	3G5U
DNR	PHE	A	767	677	->	PHE	A	763	673	3.1	157.4	123.7	26.6	60.2	3G5U
ACC	PHE	A	767	677	->	PHE	A	771	681	3.0	151.8	122.8	33.2	54.6	3G5U
DNR	LEU	A	768	678	->	ILE	A	764	674	3.1	155.8	109.1	16.7	88.1	3G5U
ACC	LEU	A	768	678	->	PHE	A	771	681	3.0	121.1	128.3	49.8	81.7	3G5U

ACC	LEU	A	768	678	->	THR	A	772	682	3.1	169.0	105.8	8.4	14.6	3G5U
DNR	GLN	A	769	679	->	THR	A	765	675	3.0	158.2	128.5	13.3	53.7	3G5U
ACC	GLN	A	769	679	->	PHE	A	773	683	3.0	165.7	122.1	30.1	59.0	3G5U
DNR	GLY	A	770	680	->	PHE	A	766	676	3.0	158.7	122.1	13.5	46.5	3G5U
ACC	GLY	A	770	680	->	GLY	A	774	684	3.1	126.8	154.1	4.3	73.9	3G5U
DNR	PHE	A	771	681	->	PHE	A	767	677	3.0	151.8	122.8	33.2	54.6	3G5U
DNR	PHE	A	771	681	->	LEU	A	768	678	3.0	121.1	128.3	49.8	81.7	3G5U
ACC	PHE	A	771	681	->	LYS	A	775	685	3.1	145.3	129.1	18.9	68.8	3G5U
DNR	THR	A	772	682	->	LEU	A	768	678	3.1	169.0	105.8	8.4	14.6	3G5U
ACC	THR	A	772	682	->	ALA	A	776	686	3.1	152.1	105.0	32.2	22.6	3G5U
DNR	PHE	A	773	683	->	GLN	A	769	679	3.0	165.7	122.1	30.1	59.0	3G5U
ACC	PHE	A	773	683	->	ALA	A	776	686	3.0	105.9	133.3	47.7	86.7	3G5U
ACC	PHE	A	773	683	->	GLY	A	777	687	3.1	150.3	105.6	27.7	48.5	3G5U
DNR	GLY	A	774	684	->	GLY	A	770	680	3.1	126.8	154.1	4.3	73.9	3G5U
ACC	GLY	A	774	684	->	GLY	A	777	687	3.0	121.2	132.0	43.5	81.2	3G5U
ACC	GLY	A	774	684	->	GLU	A	778	688	3.0	154.9	105.8	9.7	1.2	3G5U
DNR	LYS	A	775	685	->	PHE	A	771	681	3.1	145.3	129.1	18.9	68.8	3G5U
ACC	LYS	A	775	685	->	ILE	A	779	689	3.1	150.5	114.0	24.9	79.5	3G5U
DNR	ALA	A	776	686	->	THR	A	772	682	3.1	152.1	105.0	32.2	22.6	3G5U
DNR	ALA	A	776	686	->	PHE	A	773	683	3.0	105.9	133.3	47.7	86.7	3G5U
ACC	ALA	A	776	686	->	LEU	A	780	690	3.0	144.9	137.0	19.3	87.1	3G5U
DNR	GLY	A	777	687	->	PHE	A	773	683	3.1	150.3	105.6	27.7	48.5	3G5U
DNR	GLY	A	777	687	->	GLY	A	774	684	3.0	121.2	132.0	43.5	81.2	3G5U
ACC	GLY	A	777	687	->	THR	A	781	691	3.0	147.1	130.8	9.4	87.0	3G5U
DNR	GLU	A	778	688	->	GLY	A	774	684	3.0	154.9	105.8	9.7	1.2	3G5U
ACC	GLU	A	778	688	->	THR	A	781	691	3.0	139.8	121.1	51.8	71.4	3G5U
ACC	GLU	A	778	688	->	LYS	A	782	692	3.1	150.7	107.1	11.0	43.3	3G5U
DNR	ILE	A	779	689	->	LYS	A	775	685	3.1	150.5	114.0	24.9	79.5	3G5U
ACC	ILE	A	779	689	->	LYS	A	782	692	3.0	127.8	115.7	55.0	88.6	3G5U
ACC	ILE	A	779	689	->	ARG	A	783	693	3.0	162.8	108.6	31.0	52.2	3G5U
DNR	LEU	A	780	690	->	ALA	A	776	686	3.0	144.9	137.0	19.3	87.1	3G5U
ACC	LEU	A	780	690	->	LEU	A	784	694	3.1	141.3	129.8	58.2	74.7	3G5U
DNR	THR	A	781	691	->	GLY	A	777	687	3.0	147.1	130.8	9.4	87.0	3G5U
DNR	THR	A	781	691	->	GLU	A	778	688	3.0	139.8	121.1	51.8	71.4	3G5U
ACC	THR	A	781	691	->	LEU	A	784	694	3.3	94.0	144.1	47.1	70.9	3G5U
ACC	THR	A	781	691	->	ARG	A	785	695	3.0	151.1	118.0	8.1	65.8	3G5U
DNR	LYS	A	782	692	->	GLU	A	778	688	3.1	150.7	107.1	11.0	43.3	3G5U
DNR	LYS	A	782	692	->	ILE	A	779	689	3.0	127.8	115.7	55.0	88.6	3G5U
ACC	LYS	A	782	692	->	TYR	A	786	696	3.0	175.8	120.8	0.9	72.4	3G5U
DNR	ARG	A	783	693	->	ILE	A	779	689	3.0	162.8	108.6	31.0	52.2	3G5U
ACC	ARG	A	783	693	->	MET	A	787	697	3.1	133.5	130.6	12.8	68.4	3G5U
DNR	LEU	A	784	694	->	LEU	A	780	690	3.1	141.3	129.8	58.2	74.7	3G5U
DNR	LEU	A	784	694	->	THR	A	781	691	3.3	94.0	144.1	47.1	70.9	3G5U
ACC	LEU	A	784	694	->	VAL	A	788	698	3.0	176.4	116.8	5.6	77.5	3G5U
DNR	ARG	A	785	695	->	THR	A	781	691	3.0	151.1	118.0	8.1	65.8	3G5U
ACC	ARG	A	785	695	->	PHE	A	789	699	3.0	156.1	128.4	7.6	70.6	3G5U
DNR	TYR	A	786	696	->	LYS	A	782	692	3.0	175.8	120.8	0.9	72.4	3G5U
ACC	TYR	A	786	696	->	PHE	A	789	699	3.0	137.5	108.1	57.6	85.2	3G5U
ACC	TYR	A	786	696	->	LYS	A	790	700	3.0	162.6	109.4	13.5	86.8	3G5U
DNR	MET	A	787	697	->	ARG	A	783	693	3.1	133.5	130.6	12.8	68.4	3G5U
ACC	MET	A	787	697	->	SER	A	791	701	3.0	152.0	123.5	27.3	40.0	3G5U
DNR	VAL	A	788	698	->	LEU	A	784	694	3.0	176.4	116.8	5.6	77.5	3G5U
ACC	VAL	A	788	698	->	MET	A	792	702	3.1	159.3	104.5	18.9	33.9	3G5U
DNR	PHE	A	789	699	->	ARG	A	785	695	3.0	156.1	128.4	7.6	70.6	3G5U
DNR	PHE	A	789	699	->	TYR	A	786	696	3.0	137.5	108.1	57.6	85.2	3G5U
ACC	PHE	A	789	699	->	MET	A	792	702	3.0	124.2	123.6	47.7	86.6	3G5U
ACC	PHE	A	789	699	->	LEU	A	793	703	3.0	165.2	111.4	6.6	18.0	3G5U
DNR	LYS	A	790	700	->	TYR	A	786	696	3.0	162.6	109.4	13.5	86.8	3G5U
ACC	LYS	A	790	700	->	ARG	A	794	704	3.0	157.7	127.9	0.1	73.7	3G5U
DNR	SER	A	791	701	->	MET	A	787	697	3.0	152.0	123.5	27.3	40.0	3G5U
ACC	SER	A	791	701	->	GLN	A	795	705	3.0	142.2	132.1	28.0	52.9	3G5U
DNR	MET	A	792	702	->	VAL	A	788	698	3.1	159.3	104.5	18.9	33.9	3G5U
DNR	MET	A	792	702	->	PHE	A	789	699	3.0	124.2	123.6	47.7	86.6	3G5U
DNR	LEU	A	793	703	->	PHE	A	789	699	3.0	165.2	111.4	6.6	18.0	3G5U
DNR	ARG	A	794	704	->	LYS	A	790	700	3.0	157.7	127.9	0.1	73.7	3G5U
DNR	GLN	A	795	705	->	SER	A	791	701	3.0	142.2	132.1	28.0	52.9	3G5U
ACC	VAL	A	797	707	->	TRP	A	799	709	3.0	98.4	96.9	39.2	47.3	3G5U
ACC	VAL	A	797	707	->	ASP	A	801	711	3.0	135.8	143.7	3.2	46.3	3G5U
ACC	SER	A	798	708	->	ASP	A	802	712	3.1	97.7	130.7	40.1	62.9	3G5U
DNR	TRP	A	799	709	->	VAL	A	797	707	3.0	98.4	96.9	39.2	47.3	3G5U
DNR	ASP	A	801	711	->	VAL	A	797	707	3.0	135.8	143.7	3.2	46.3	3G5U
DNR	ASP	A	802	712	->	SER	A	798	708	3.1	97.7	130.7	40.1	62.9	3G5U
ACC	THR	A	806	716	->	LEU	A	810	720	3.1	164.4	109.4	24.4	42.6	3G5U
ACC	THR	A	807	717	->	LEU	A	810	720	3.0	116.4	134.6	41.9	76.7	3G5U

ACC	THR	A	807	717	->	THR	A	811	721	3.0	166.4	114.0	6.0	6.5	3G5U
ACC	GLY	A	808	718	->	THR	A	811	721	3.0	139.5	101.7	55.4	73.0	3G5U
ACC	GLY	A	808	718	->	THR	A	812	722	3.0	160.3	118.9	12.4	87.9	3G5U
ACC	ALA	A	809	719	->	ARG	A	813	723	3.1	131.6	129.1	1.7	64.7	3G5U
DNR	LEU	A	810	720	->	THR	A	806	716	3.1	164.4	109.4	24.4	42.6	3G5U
DNR	LEU	A	810	720	->	THR	A	807	717	3.0	116.4	134.6	41.9	76.7	3G5U
ACC	LEU	A	810	720	->	LEU	A	814	724	3.0	159.0	119.2	2.1	81.8	3G5U
DNR	THR	A	811	721	->	THR	A	807	717	3.0	166.4	114.0	6.0	6.5	3G5U
DNR	THR	A	811	721	->	GLY	A	808	718	3.0	139.5	101.7	55.4	73.0	3G5U
ACC	THR	A	811	721	->	ALA	A	815	725	3.1	169.0	108.5	15.6	28.5	3G5U
DNR	THR	A	812	722	->	GLY	A	808	718	3.0	160.3	118.9	12.4	87.9	3G5U
ACC	THR	A	812	722	->	ASN	A	816	726	3.1	158.5	108.1	40.5	70.8	3G5U
DNR	ARG	A	813	723	->	ALA	A	809	719	3.1	131.6	129.1	1.7	64.7	3G5U
ACC	ARG	A	813	723	->	ASP	A	817	727	3.1	147.5	134.9	37.2	53.5	3G5U
DNR	LEU	A	814	724	->	LEU	A	810	720	3.0	159.0	119.2	2.1	81.8	3G5U
ACC	LEU	A	814	724	->	ALA	A	818	728	3.3	161.3	127.6	1.4	81.7	3G5U
DNR	ALA	A	815	725	->	THR	A	811	721	3.1	169.0	108.5	15.6	28.5	3G5U
ACC	ALA	A	815	725	->	ALA	A	818	728	3.4	121.4	109.3	58.9	85.4	3G5U
ACC	ALA	A	815	725	->	ALA	A	819	729	3.3	165.5	123.4	7.0	42.2	3G5U
DNR	ASN	A	816	726	->	THR	A	812	722	3.1	158.5	108.1	40.5	70.8	3G5U
ACC	ASN	A	816	726	->	GLN	A	820	730	3.1	155.7	107.8	11.4	32.3	3G5U
DNR	ASP	A	817	727	->	ARG	A	813	723	3.1	147.5	134.9	37.2	53.5	3G5U
ACC	ASP	A	817	727	->	VAL	A	821	731	3.0	160.1	121.1	2.1	84.9	3G5U
DNR	ALA	A	818	728	->	LEU	A	814	724	3.3	161.3	127.6	1.4	81.7	3G5U
DNR	ALA	A	818	728	->	ALA	A	815	725	3.4	121.4	109.3	58.9	85.4	3G5U
ACC	ALA	A	818	728	->	LYS	A	822	732	3.2	168.4	118.8	2.9	34.2	3G5U
DNR	ALA	A	819	729	->	ALA	A	815	725	3.3	165.5	123.4	7.0	42.2	3G5U
ACC	ALA	A	819	729	->	LYS	A	822	732	3.0	135.2	117.2	59.5	81.7	3G5U
ACC	ALA	A	819	729	->	GLY	A	823	733	3.2	155.1	106.9	16.4	8.4	3G5U
DNR	GLN	A	820	730	->	ASN	A	816	726	3.1	155.7	107.8	11.4	32.3	3G5U
ACC	GLN	A	820	730	->	GLY	A	823	733	3.0	122.3	139.6	53.5	73.5	3G5U
ACC	GLN	A	820	730	->	ALA	A	824	734	3.2	149.0	90.8	16.0	11.2	3G5U
DNR	VAL	A	821	731	->	ASP	A	817	727	3.0	160.1	121.1	2.1	84.9	3G5U
ACC	VAL	A	821	731	->	ALA	A	824	734	3.0	124.9	110.4	50.7	71.9	3G5U
ACC	VAL	A	821	731	->	THR	A	825	735	3.2	172.0	102.9	8.5	1.5	3G5U
DNR	LYS	A	822	732	->	ALA	A	818	728	3.2	168.4	118.8	2.9	34.2	3G5U
DNR	LYS	A	822	732	->	ALA	A	819	729	3.0	135.2	117.2	59.5	81.7	3G5U
ACC	LYS	A	822	732	->	THR	A	825	735	3.3	115.5	126.4	45.6	78.2	3G5U
ACC	LYS	A	822	732	->	GLY	A	826	736	3.2	167.0	118.5	4.3	33.5	3G5U
DNR	GLY	A	823	733	->	ALA	A	819	729	3.2	155.1	106.9	16.4	8.4	3G5U
DNR	GLY	A	823	733	->	GLN	A	820	730	3.0	122.3	139.6	53.5	73.5	3G5U
ACC	GLY	A	823	733	->	SER	A	827	737	3.1	156.3	126.1	30.7	75.1	3G5U
DNR	ALA	A	824	734	->	GLN	A	820	730	3.2	149.0	90.8	16.0	11.2	3G5U
DNR	ALA	A	824	734	->	VAL	A	821	731	3.0	124.9	110.4	50.7	71.9	3G5U
ACC	ALA	A	824	734	->	ARG	A	828	738	3.4	132.4	118.0	23.4	59.4	3G5U
DNR	THR	A	825	735	->	VAL	A	821	731	3.2	172.0	102.9	8.5	1.5	3G5U
DNR	THR	A	825	735	->	LYS	A	822	732	3.3	115.5	126.4	45.6	78.2	3G5U
ACC	THR	A	825	735	->	ARG	A	828	738	3.0	114.8	113.3	59.9	84.5	3G5U
ACC	THR	A	825	735	->	LEU	A	829	739	3.2	153.4	109.8	23.9	42.9	3G5U
DNR	GLY	A	826	736	->	LYS	A	822	732	3.2	167.0	118.5	4.3	33.5	3G5U
ACC	GLY	A	826	736	->	LEU	A	829	739	3.2	100.4	140.5	53.2	74.0	3G5U
ACC	GLY	A	826	736	->	ALA	A	830	740	3.1	150.5	106.9	9.5	37.2	3G5U
DNR	SER	A	827	737	->	GLY	A	823	733	3.1	156.3	126.1	30.7	75.1	3G5U
ACC	SER	A	827	737	->	VAL	A	831	741	3.1	165.4	111.6	47.5	75.3	3G5U
DNR	ARG	A	828	738	->	ALA	A	824	734	3.4	132.4	118.0	23.4	59.4	3G5U
DNR	ARG	A	828	738	->	THR	A	825	735	3.0	114.8	113.3	59.9	84.5	3G5U
ACC	ARG	A	828	738	->	VAL	A	831	741	3.4	98.4	147.4	21.0	73.3	3G5U
ACC	ARG	A	828	738	->	ILE	A	832	742	3.2	152.5	111.6	7.2	69.4	3G5U
DNR	LEU	A	829	739	->	THR	A	825	735	3.2	153.4	109.8	23.9	42.9	3G5U
DNR	LEU	A	829	739	->	GLY	A	826	736	3.2	100.4	140.5	53.2	74.0	3G5U
ACC	LEU	A	829	739	->	PHE	A	833	743	3.1	159.8	127.3	3.2	41.8	3G5U
DNR	ALA	A	830	740	->	GLY	A	826	736	3.1	150.5	106.9	9.5	37.2	3G5U
ACC	ALA	A	830	740	->	GLN	A	834	744	3.2	118.9	128.1	31.7	89.8	3G5U
DNR	VAL	A	831	741	->	SER	A	827	737	3.1	165.4	111.6	47.5	75.3	3G5U
DNR	VAL	A	831	741	->	ARG	A	828	738	3.4	98.4	147.4	21.0	73.3	3G5U
ACC	VAL	A	831	741	->	ASN	A	835	745	3.0	171.9	133.4	12.6	45.4	3G5U
DNR	ILE	A	832	742	->	ARG	A	828	738	3.2	152.5	111.6	7.2	69.4	3G5U
ACC	ILE	A	832	742	->	ILE	A	836	746	3.1	167.8	113.3	10.4	67.2	3G5U
DNR	PHE	A	833	743	->	LEU	A	829	739	3.1	159.8	127.3	3.2	41.8	3G5U
ACC	PHE	A	833	743	->	ALA	A	837	747	3.2	163.4	113.8	26.1	66.1	3G5U
DNR	GLN	A	834	744	->	ALA	A	830	740	3.2	118.9	128.1	31.7	89.8	3G5U
ACC	GLN	A	834	744	->	ASN	A	838	748	3.0	171.9	109.0	39.1	26.5	3G5U
DNR	ASN	A	835	745	->	VAL	A	831	741	3.0	171.9	133.4	12.6	45.4	3G5U
ACC	ASN	A	835	745	->	LEU	A	839	749	3.0	171.1	122.9	42.1	47.8	3G5U

DNR	ILE	A	836	746	->	ILE	A	832	742	3.1	167.8	113.3	10.4	67.2	3G5U
ACC	ILE	A	836	746	->	THR	A	841	751	3.1	151.9	103.7	0.5	81.2	3G5U
DNR	ALA	A	837	747	->	PHE	A	833	743	3.2	163.4	113.8	26.1	66.1	3G5U
ACC	ALA	A	837	747	->	THR	A	841	751	3.1	148.7	136.1	39.7	53.7	3G5U
DNR	ASN	A	838	748	->	GLN	A	834	744	3.0	171.9	109.0	39.1	26.5	3G5U
ACC	ASN	A	838	748	->	GLY	A	842	752	3.0	141.0	151.4	13.5	78.3	3G5U
DNR	LEU	A	839	749	->	ASN	A	835	745	3.0	171.1	122.9	42.1	47.8	3G5U
ACC	LEU	A	839	749	->	GLY	A	842	752	3.0	148.5	115.4	55.2	87.8	3G5U
ACC	LEU	A	839	749	->	ILE	A	843	753	3.0	144.4	108.9	1.3	81.4	3G5U
ACC	GLY	A	840	750	->	ILE	A	844	754	3.0	159.9	119.2	5.7	60.6	3G5U
DNR	THR	A	841	751	->	ILE	A	836	746	3.1	151.9	103.7	0.5	81.2	3G5U
DNR	THR	A	841	751	->	ALA	A	837	747	3.1	148.7	136.1	39.7	53.7	3G5U
ACC	THR	A	841	751	->	ILE	A	845	755	3.1	153.2	126.4	7.9	69.0	3G5U
DNR	GLY	A	842	752	->	ASN	A	838	748	3.0	141.0	151.4	13.5	78.3	3G5U
DNR	GLY	A	842	752	->	LEU	A	839	749	3.0	148.5	115.4	55.2	87.8	3G5U
DNR	ILE	A	843	753	->	LEU	A	839	749	3.0	144.4	108.9	1.3	81.4	3G5U
ACC	ILE	A	843	753	->	SER	A	846	756	3.0	106.3	142.7	39.2	89.1	3G5U
ACC	ILE	A	843	753	->	LEU	A	847	757	3.0	158.8	94.7	35.5	54.3	3G5U
DNR	ILE	A	844	754	->	GLY	A	840	750	3.0	159.9	119.2	5.7	60.6	3G5U
ACC	ILE	A	844	754	->	LEU	A	847	757	3.0	124.8	134.2	26.0	88.1	3G5U
ACC	ILE	A	844	754	->	ILE	A	848	758	3.2	155.6	98.8	9.1	5.3	3G5U
DNR	ILE	A	845	755	->	THR	A	841	751	3.1	153.2	126.4	7.9	69.0	3G5U
ACC	ILE	A	845	755	->	TYR	A	849	759	3.1	127.8	110.0	50.8	55.3	3G5U
DNR	SER	A	846	756	->	ILE	A	843	753	3.0	106.3	142.7	39.2	89.1	3G5U
DNR	LEU	A	847	757	->	ILE	A	843	753	3.0	158.8	94.7	35.5	54.3	3G5U
DNR	LEU	A	847	757	->	ILE	A	844	754	3.0	124.8	134.2	26.0	88.1	3G5U
DNR	ILE	A	848	758	->	ILE	A	844	754	3.2	155.6	98.8	9.1	5.3	3G5U
DNR	TYR	A	849	759	->	ILE	A	845	755	3.1	127.8	110.0	50.8	55.3	3G5U
ACC	LEU	A	853	763	->	LEU	A	857	767	3.0	158.7	96.6	17.2	59.9	3G5U
ACC	THR	A	854	764	->	LEU	A	857	767	3.3	104.7	128.4	31.4	77.4	3G5U
ACC	THR	A	854	764	->	LEU	A	858	768	3.1	157.3	124.1	12.0	56.6	3G5U
DNR	LEU	A	857	767	->	LEU	A	853	763	3.0	158.7	96.6	17.2	59.9	3G5U
DNR	LEU	A	857	767	->	THR	A	854	764	3.3	104.7	128.4	31.4	77.4	3G5U
ACC	LEU	A	857	767	->	ILE	A	860	770	3.0	152.3	108.6	53.7	73.6	3G5U
ACC	LEU	A	857	767	->	VAL	A	861	771	3.0	138.4	95.8	18.6	85.5	3G5U
DNR	LEU	A	858	768	->	THR	A	854	764	3.1	157.3	124.1	12.0	56.6	3G5U
ACC	ALA	A	859	769	->	ILE	A	863	773	3.2	156.7	119.8	8.0	35.6	3G5U
DNR	ILE	A	860	770	->	LEU	A	857	767	3.0	152.3	108.6	53.7	73.6	3G5U
ACC	ILE	A	860	770	->	ILE	A	864	774	3.0	173.9	117.0	3.9	39.6	3G5U
DNR	VAL	A	861	771	->	LEU	A	857	767	3.0	138.4	95.8	18.6	85.5	3G5U
ACC	VAL	A	861	771	->	ALA	A	865	775	3.0	168.4	131.5	0.8	36.2	3G5U
ACC	PRO	A	862	772	->	ILE	A	866	776	3.0	152.6	129.3	1.9	71.6	3G5U
DNR	ILE	A	863	773	->	ALA	A	859	769	3.2	156.7	119.8	8.0	35.6	3G5U
ACC	ILE	A	863	773	->	ALA	A	867	777	3.0	148.0	111.9	33.9	58.8	3G5U
DNR	ILE	A	864	774	->	ILE	A	860	770	3.0	173.9	117.0	3.9	39.6	3G5U
ACC	ILE	A	864	774	->	ALA	A	867	777	3.0	107.9	132.5	49.1	85.7	3G5U
ACC	ILE	A	864	774	->	GLY	A	868	778	3.1	160.5	106.6	5.3	42.8	3G5U
DNR	ALA	A	865	775	->	VAL	A	861	771	3.0	168.4	131.5	0.8	36.2	3G5U
ACC	ALA	A	865	775	->	VAL	A	869	779	3.2	162.6	106.5	3.5	12.7	3G5U
DNR	ILE	A	866	776	->	PRO	A	862	772	3.0	152.6	129.3	1.9	71.6	3G5U
ACC	ILE	A	866	776	->	VAL	A	870	780	3.0	156.1	121.4	19.3	63.3	3G5U
DNR	ALA	A	867	777	->	ILE	A	863	773	3.0	148.0	111.9	33.9	58.8	3G5U
DNR	ALA	A	867	777	->	ILE	A	864	774	3.0	107.9	132.5	49.1	85.7	3G5U
ACC	ALA	A	867	777	->	GLU	A	871	781	3.0	161.3	119.3	7.6	47.7	3G5U
DNR	GLY	A	868	778	->	ILE	A	864	774	3.1	160.5	106.6	5.3	42.8	3G5U
ACC	GLY	A	868	778	->	MET	A	872	782	3.2	155.0	126.4	10.2	67.9	3G5U
DNR	VAL	A	869	779	->	ALA	A	865	775	3.2	162.6	106.5	3.5	12.7	3G5U
ACC	VAL	A	869	779	->	LYS	A	873	783	3.0	168.3	118.5	9.3	28.9	3G5U
DNR	VAL	A	870	780	->	ILE	A	866	776	3.0	156.1	121.4	19.3	63.3	3G5U
ACC	VAL	A	870	780	->	MET	A	874	784	3.1	162.4	114.8	3.3	77.6	3G5U
DNR	GLU	A	871	781	->	ALA	A	867	777	3.0	161.3	119.3	7.6	47.7	3G5U
ACC	GLU	A	871	781	->	LEU	A	875	785	3.0	167.4	123.2	9.3	9.0	3G5U
DNR	MET	A	872	782	->	GLY	A	868	778	3.2	155.0	126.4	10.2	67.9	3G5U
ACC	MET	A	872	782	->	SER	A	876	786	3.0	155.3	111.4	27.2	56.1	3G5U
DNR	LYS	A	873	783	->	VAL	A	869	779	3.0	168.3	118.5	9.3	28.9	3G5U
ACC	LYS	A	873	783	->	SER	A	876	786	3.0	120.7	128.0	45.9	80.6	3G5U
ACC	LYS	A	873	783	->	GLY	A	877	787	3.1	157.8	109.4	2.8	2.5	3G5U
DNR	MET	A	874	784	->	VAL	A	870	780	3.1	162.4	114.8	3.3	77.6	3G5U
ACC	MET	A	874	784	->	GLN	A	878	788	3.1	164.5	114.9	0.6	75.5	3G5U
DNR	LEU	A	875	785	->	GLU	A	871	781	3.0	167.4	123.2	9.3	9.0	3G5U
ACC	LEU	A	875	785	->	ALA	A	879	789	3.1	145.0	129.0	15.3	59.3	3G5U
DNR	SER	A	876	786	->	MET	A	872	782	3.0	155.3	111.4	27.2	56.1	3G5U
DNR	SER	A	876	786	->	LYS	A	873	783	3.0	120.7	128.0	45.9	80.6	3G5U
ACC	SER	A	876	786	->	LEU	A	880	790	3.0	177.6	112.3	1.6	15.3	3G5U

DNR	GLY	A	877	787	->	LYS	A	873	783	3.1	157.8	109.4	2.8	2.5	3G5U
ACC	GLY	A	877	787	->	LYS	A	881	791	3.0	165.1	125.1	8.9	73.4	3G5U
DNR	GLN	A	878	788	->	MET	A	874	784	3.1	164.5	114.9	0.6	75.5	3G5U
ACC	GLN	A	878	788	->	ASP	A	882	792	3.1	158.8	126.4	5.1	87.2	3G5U
DNR	ALA	A	879	789	->	LEU	A	875	785	3.1	145.0	129.0	15.3	59.3	3G5U
ACC	ALA	A	879	789	->	LYS	A	883	793	3.1	150.1	122.7	14.8	44.4	3G5U
DNR	LEU	A	880	790	->	SER	A	876	786	3.0	177.6	112.3	1.6	15.3	3G5U
ACC	LEU	A	880	790	->	LYS	A	884	794	3.0	159.5	100.9	28.3	12.4	3G5U
DNR	LYS	A	881	791	->	GLY	A	877	787	3.0	165.1	125.1	8.9	73.4	3G5U
ACC	LYS	A	881	791	->	LYS	A	884	794	3.0	114.9	137.7	39.6	81.5	3G5U
ACC	LYS	A	881	791	->	GLU	A	885	795	3.1	163.1	101.1	8.0	5.9	3G5U
DNR	ASP	A	882	792	->	GLN	A	878	788	3.1	158.8	126.4	5.1	87.2	3G5U
ACC	ASP	A	882	792	->	LEU	A	886	796	3.0	175.3	121.4	18.2	13.5	3G5U
DNR	LYS	A	883	793	->	ALA	A	879	789	3.1	150.1	122.7	14.8	44.4	3G5U
ACC	LYS	A	883	793	->	GLU	A	887	797	3.0	132.2	130.8	46.4	68.5	3G5U
DNR	LYS	A	884	794	->	LEU	A	880	790	3.0	159.5	100.9	28.3	12.4	3G5U
DNR	LYS	A	884	794	->	LYS	A	881	791	3.0	114.9	137.7	39.6	81.5	3G5U
ACC	LYS	A	884	794	->	GLU	A	887	797	3.0	122.0	130.7	51.5	86.7	3G5U
ACC	LYS	A	884	794	->	GLY	A	888	798	3.0	165.0	97.6	15.9	1.1	3G5U
DNR	GLU	A	885	795	->	LYS	A	881	791	3.1	163.1	101.1	8.0	5.9	3G5U
ACC	GLU	A	885	795	->	GLY	A	888	798	3.0	119.7	125.0	46.5	84.4	3G5U
ACC	GLU	A	885	795	->	SER	A	889	799	3.2	153.6	108.7	3.9	16.4	3G5U
DNR	LEU	A	886	796	->	ASP	A	882	792	3.0	175.3	121.4	18.2	13.5	3G5U
ACC	LEU	A	886	796	->	GLY	A	890	800	3.0	172.8	115.5	26.5	52.8	3G5U
DNR	GLU	A	887	797	->	LYS	A	883	793	3.0	132.2	130.8	46.4	68.5	3G5U
DNR	GLU	A	887	797	->	LYS	A	884	794	3.0	122.0	130.7	51.5	86.7	3G5U
ACC	GLU	A	887	797	->	LYS	A	891	801	3.0	142.9	137.8	15.4	77.6	3G5U
DNR	GLY	A	888	798	->	LYS	A	884	794	3.0	165.0	97.6	15.9	1.1	3G5U
DNR	GLY	A	888	798	->	GLU	A	885	795	3.0	119.7	125.0	46.5	84.4	3G5U
ACC	GLY	A	888	798	->	LYS	A	891	801	3.3	110.0	122.0	59.0	79.3	3G5U
ACC	GLY	A	888	798	->	ILE	A	892	802	3.2	157.5	116.9	17.9	57.9	3G5U
DNR	SER	A	889	799	->	GLU	A	885	795	3.2	153.6	108.7	3.9	16.4	3G5U
ACC	SER	A	889	799	->	ILE	A	892	802	3.0	137.8	122.2	47.3	79.4	3G5U
ACC	SER	A	889	799	->	ALA	A	893	803	3.0	153.0	108.1	19.6	38.1	3G5U
DNR	GLY	A	890	800	->	LEU	A	886	796	3.0	172.8	115.5	26.5	52.8	3G5U
ACC	GLY	A	890	800	->	ALA	A	893	803	3.1	104.0	122.0	53.3	89.3	3G5U
ACC	GLY	A	890	800	->	THR	A	894	804	3.0	154.2	112.2	35.4	75.7	3G5U
DNR	LYS	A	891	801	->	GLU	A	887	797	3.0	142.9	137.8	15.4	77.6	3G5U
DNR	LYS	A	891	801	->	GLY	A	888	798	3.3	110.0	122.0	59.0	79.3	3G5U
ACC	LYS	A	891	801	->	THR	A	894	804	3.4	102.6	136.8	36.3	74.4	3G5U
ACC	LYS	A	891	801	->	GLU	A	895	805	3.2	140.0	117.7	22.1	40.2	3G5U
DNR	ILE	A	892	802	->	GLY	A	888	798	3.2	157.5	116.9	17.9	57.9	3G5U
DNR	ILE	A	892	802	->	SER	A	889	799	3.0	137.8	122.2	47.3	79.4	3G5U
ACC	ILE	A	892	802	->	ALA	A	896	806	3.2	145.5	108.9	11.1	68.8	3G5U
DNR	ALA	A	893	803	->	SER	A	889	799	3.0	153.0	108.1	19.6	38.1	3G5U
DNR	ALA	A	893	803	->	GLY	A	890	800	3.1	104.0	122.0	53.3	89.3	3G5U
ACC	ALA	A	893	803	->	ILE	A	897	807	3.2	140.5	128.3	16.2	71.0	3G5U
DNR	THR	A	894	804	->	GLY	A	890	800	3.0	154.2	112.2	35.4	75.7	3G5U
DNR	THR	A	894	804	->	LYS	A	891	801	3.4	102.6	136.8	36.3	74.4	3G5U
ACC	THR	A	894	804	->	GLU	A	898	808	3.0	154.7	140.3	10.7	26.2	3G5U
DNR	GLU	A	895	805	->	LYS	A	891	801	3.2	140.0	117.7	22.1	40.2	3G5U
ACC	GLU	A	895	805	->	ASN	A	899	809	3.0	142.3	109.0	59.5	50.7	3G5U
DNR	ALA	A	896	806	->	ILE	A	892	802	3.2	145.5	108.9	11.1	68.8	3G5U
ACC	ALA	A	896	806	->	ASN	A	899	809	3.0	118.2	134.8	26.7	88.3	3G5U
DNR	ILE	A	897	807	->	ALA	A	893	803	3.2	140.5	128.3	16.2	71.0	3G5U
ACC	ILE	A	897	807	->	PHE	A	900	810	3.5	115.3	116.3	15.1	89.6	3G5U
DNR	GLU	A	898	808	->	THR	A	894	804	3.0	154.7	140.3	10.7	26.2	3G5U
DNR	ASN	A	899	809	->	GLU	A	895	805	3.0	142.3	109.0	59.5	50.7	3G5U
DNR	ASN	A	899	809	->	ALA	A	896	806	3.0	118.2	134.8	26.7	88.3	3G5U
ACC	ASN	A	899	809	->	ARG	A	901	811	3.0	108.2	93.4	50.3	37.0	3G5U
DNR	PHE	A	900	810	->	ILE	A	897	807	3.5	115.3	116.3	15.1	89.6	3G5U
ACC	PHE	A	900	810	->	VAL	A	903	813	3.0	143.5	107.1	29.1	88.6	3G5U
DNR	ARG	A	901	811	->	ASN	A	899	809	3.0	108.2	93.4	50.3	37.0	3G5U
ACC	THR	A	902	812	->	SER	A	905	815	3.0	133.1	122.4	21.3	74.2	3G5U
ACC	THR	A	902	812	->	LEU	A	906	816	3.0	146.5	120.1	6.3	31.2	3G5U
DNR	VAL	A	903	813	->	PHE	A	900	810	3.0	143.5	107.1	29.1	88.6	3G5U
DNR	SER	A	905	815	->	THR	A	902	812	3.0	133.1	122.4	21.3	74.2	3G5U
DNR	LEU	A	906	816	->	THR	A	902	812	3.0	146.5	120.1	6.3	31.2	3G5U
ACC	LEU	A	906	816	->	GLU	A	909	819	3.5	113.5	113.3	42.7	88.4	3G5U
ACC	ARG	A	908	818	->	PHE	A	912	822	3.0	137.7	102.0	15.4	83.4	3G5U
DNR	GLU	A	909	819	->	LEU	A	906	816	3.5	113.5	113.3	42.7	88.4	3G5U
ACC	GLU	A	909	819	->	PHE	A	912	822	3.0	115.4	132.0	50.4	81.1	3G5U
ACC	GLU	A	909	819	->	GLU	A	913	823	3.1	165.2	100.4	25.8	6.7	3G5U
ACC	GLN	A	910	820	->	THR	A	914	824	3.0	162.4	129.5	22.6	73.4	3G5U

ACC	SER	A	1265	1175	->	VAL	A	1269	1179	3.0	152.1	115.1	41.0	88.6	3G5U
DNR	MET	A	1266	1176	->	ILE	A	1262	1172	3.0	160.8	109.6	11.9	24.2	3G5U
ACC	MET	A	1266	1176	->	GLN	A	1270	1180	3.1	139.0	125.5	30.0	59.5	3G5U
DNR	VAL	A	1267	1177	->	TYR	A	1263	1173	3.0	147.6	110.2	25.1	49.7	3G5U
DNR	VAL	A	1267	1177	->	PHE	A	1264	1174	3.0	132.6	120.3	47.7	89.8	3G5U
ACC	VAL	A	1267	1177	->	ALA	A	1271	1181	3.1	142.2	109.4	34.7	68.1	3G5U
DNR	SER	A	1268	1178	->	PHE	A	1264	1174	3.0	159.2	112.6	14.5	44.3	3G5U
DNR	VAL	A	1269	1179	->	SER	A	1265	1175	3.0	152.1	115.1	41.0	88.6	3G5U
DNR	GLN	A	1270	1180	->	MET	A	1266	1176	3.1	139.0	125.5	30.0	59.5	3G5U
DNR	ALA	A	1271	1181	->	VAL	A	1267	1177	3.1	142.2	109.4	34.7	68.1	3G5U