



## Full wwPDB EM Validation Report ⓘ

Jun 10, 2025 – 04:17 PM JST

PDB ID : 5H0S / pdb\_00005h0s  
EMDB ID : EMD-9565  
Title : EM Structure of VP1A and VP1B  
Authors : Li, X.; Zhou, N.; Xu, B.; Chen, W.; Zhu, B.; Wang, X.; Wang, J.; Liu, H.;  
Cheng, L.  
Deposited on : 2016-10-06  
Resolution : 3.30 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

---

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev118  
MolProbity : 4-5-2 with Phenix2.0rc1  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.43.1

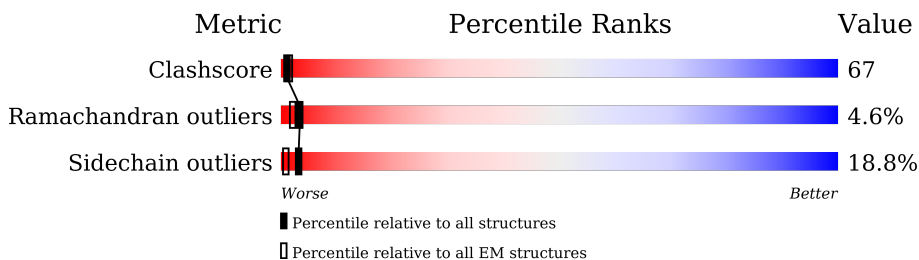
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.30 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	B	1333	<div> <div>21%</div> <div>46%</div> <div>38%</div> <div>•</div> <div>14%</div> </div>
1	C	1333	<div> <div>25%</div> <div>11%</div> <div>31%</div> <div>35%</div> <div>17%</div> <div>6%</div> </div>

## 2 Entry composition

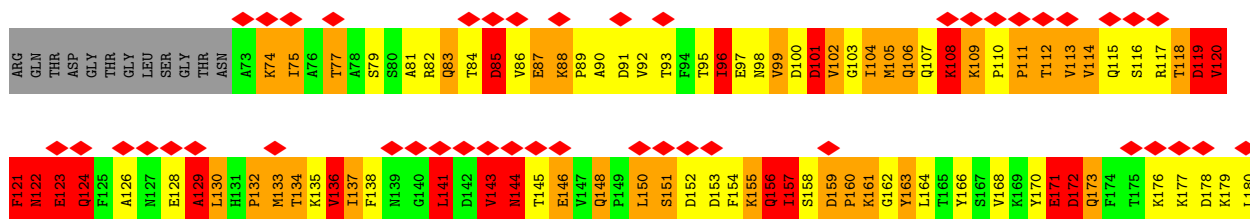
There is only 1 type of molecule in this entry. The entry contains 18885 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called VP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	1148	Total	C	N	O	S	0	0
			9058	5731	1574	1718	35		
1	C	1247	Total	C	N	O	S	0	0
			9827	6202	1709	1878	38		







G1274	D1275	L1276	L1277	Y1278	S1279	P1280	V1281	A1282	N1283	G1284	Q1285	V1286	G1287	I1288	P1289	K1290	L1291	E1292	V1293	D1294	H1295	I1296	S1297	P1298	S1299	N1300	V1301	V1302	S1303	M1304	M1305	T1306	A1307	N1308	I1309	R1310	T1311	G1312	D1313	D1314	M1315	A1316	V1317	E1318	R1319	V1320	M1321	P1322	D1323	G1324	V1325	R1326	A1327	I1328	N1329	I1330	R1331	M1332	A1333
L1211	R1212	P1213	E1214	P1215	D1219	P1220	P1221	A1222	S1223	G1224	E1225	D1226	M1227	R1228	L1229	T1230	Y1231	P1232	L1233	Q1234	P1235	T1236	S1237	V1238	A1239	R1240	S1241	M1242	R1243	A1244	I1245	V1246	M1247	H1248	N1249	E1250	V1251	D1252	R1253	P1254	A1257	V1258	A1259	P1260	S1261	S1262	Y1263	E1264	M1265	D1266	T1267	G1268	L1269	L1270	S1271	R1272	N1273		
L1150	V1151	A1152	D1153	M1154	I1155	I1156	A1157	S1158	V1159	L1160	K1161	S1162	N1163	W1164	V1165	V1166	D1167	I1168	H1169	D1170	I1171	E1172	Y1173	T1174	A1175	E1176	V1177	M1178	T1179	P1180	S1181	E1182	G1183	Y1184	T1185	Q1186	H1187	V1188	D1189	A1190	E1191	S1192	I1193	M1194	T1195	K1198	G1199	K1200	L1201	F1202	H1203	L1204	Q1205	F1206	M1207	D1208	G1209	L1210	
P1090	D1091	V1092	P1093	E1094	G1095	Y1096	V1097	A1098	V1099	Q1100	Y1101	A1102	H1103	R1104	L1105	F1106	S1107	S1108	S1109	L1110	A1111	N1112	K1113	R1114	N1115	R1116	V1117	T1118	Y1119	T1120	H1121	P1122	P1123	T1124	G1125	M1126	A1127	Y1128	P1129	S1130	P1131	T1132	G1133	R1134	P1135	H1136	V1137	H1138	M1139	T1140	I1141	N1142	E1143	R1144	A1145	G1146	M1147	S1148	K1149
L1029	L1030	Y1031	D1032	D1033	Q1034	I1035	D1036	I1037	E1038	A1039	F1040	R1041	W1042	S1043	R1044	Y1045	F1046	L1047	D1048	E1049	L1050	R1051	L1052	R1053	R1054	L1055	G1058	L1059	R1060	L1061	I1062	T1063	N1064	P1065	R1066	I1067	A1068	R1069	R1070	F1071	D1072	G1073	V1074	R1075	I1076	R1077	Y1078	L1079	T1080	D1081	D1082	P1083	P1084	D1085	P1086	D1087	F1088	V1089	

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	27000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	20	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	53.433	Depositor
Minimum map value	-40.259	Depositor
Average map value	0.625	Depositor
Map value standard deviation	5.607	Depositor
Recommended contour level	17	Depositor
Map size (Å)	652.39996, 652.39996, 652.39996	wwPDB
Map dimensions	700, 700, 700	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.9319999, 0.9319999, 0.9319999	Depositor



## 5 Model quality

### 5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	B	0.46	3/9244 (0.0%)	0.70	16/12582 (0.1%)
1	C	2.63	731/10028 (7.3%)	2.23	556/13653 (4.1%)
All	All	1.92	734/19272 (3.8%)	1.68	572/26235 (2.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	9
1	C	0	30
All	All	0	39

All (734) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	278	LEU	C-N	16.35	1.57	1.33
1	C	227	LEU	C-N	14.79	1.53	1.33
1	C	585	PHE	C-O	13.48	1.34	1.24
1	C	244	SER	C-N	13.37	1.52	1.33
1	C	521	PHE	C-O	-12.05	1.11	1.24
1	C	855	TYR	C-O	-11.63	1.10	1.24
1	C	975	SER	CA-C	-11.59	1.47	1.53
1	C	548	TYR	C-O	-11.24	1.10	1.24
1	C	88	LYS	C-O	-11.13	1.14	1.24
1	C	1101	TYR	CA-C	-11.07	1.38	1.52
1	C	735	THR	CA-C	-11.00	1.39	1.52
1	C	1201	LEU	CA-C	-10.93	1.39	1.52
1	C	327	LEU	C-O	-10.83	1.11	1.23
1	C	631	PRO	C-O	-10.73	1.11	1.23
1	C	102	VAL	N-CA	-10.42	1.35	1.46
1	C	354	ALA	C-O	-10.37	1.11	1.24

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	1298	PHE	CA-C	10.15	1.65	1.53
1	C	460	ALA	CA-C	-10.04	1.40	1.52
1	C	1076	ILE	C-O	-9.98	1.13	1.24
1	C	479	HIS	C-O	-9.95	1.12	1.24
1	C	547	GLU	CA-C	-9.81	1.40	1.52
1	C	101	ASP	CA-C	-9.80	1.40	1.52
1	C	1304	MET	C-O	-9.75	1.17	1.24
1	C	525	PHE	C-O	-9.73	1.12	1.24
1	C	1078	TYR	CA-C	-9.73	1.40	1.52
1	C	447	ARG	C-N	9.64	1.47	1.33
1	C	1000	LEU	CA-C	-9.61	1.41	1.52
1	C	1117	VAL	C-O	-9.56	1.13	1.24
1	C	533	GLN	C-O	-9.53	1.12	1.24
1	C	1299	SER	C-O	-9.49	1.14	1.23
1	C	524	GLU	C-O	-9.47	1.13	1.24
1	C	1231	TYR	C-O	-9.47	1.14	1.24
1	C	356	SER	C-O	-9.46	1.13	1.24
1	C	1077	MET	C-O	-9.44	1.13	1.23
1	C	795	ASP	CA-C	-9.41	1.43	1.53
1	C	1064	ASN	CA-C	-9.37	1.42	1.52
1	C	1241	SER	C-O	-9.36	1.15	1.24
1	C	614	ARG	CA-C	-9.29	1.41	1.52
1	C	1198	LYS	CA-C	-9.23	1.40	1.52
1	C	1038	GLU	CA-C	-9.19	1.41	1.52
1	C	463	VAL	C-O	-9.10	1.13	1.24
1	C	691	PHE	C-O	-9.06	1.13	1.24
1	C	1301	VAL	CA-C	-9.01	1.42	1.52
1	C	1301	VAL	C-O	-9.01	1.12	1.24
1	C	683	TRP	C-O	-8.99	1.13	1.24
1	C	1303	SER	C-O	-8.98	1.12	1.24
1	C	350	ILE	C-O	-8.97	1.14	1.24
1	C	346	HIS	N-CA	-8.91	1.35	1.46
1	C	75	ILE	C-O	8.89	1.34	1.24
1	C	378	ALA	C-O	-8.86	1.13	1.24
1	C	1242	MET	C-O	-8.82	1.12	1.23
1	C	742	LYS	C-O	-8.81	1.16	1.24
1	C	426	ILE	C-O	-8.76	1.13	1.24
1	C	1165	VAL	C-O	-8.76	1.13	1.24
1	C	493	HIS	C-O	-8.74	1.12	1.23
1	C	741	TYR	C-O	-8.74	1.13	1.23
1	C	632	GLN	CA-C	8.72	1.63	1.52
1	C	859	ILE	CA-C	-8.69	1.40	1.52

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	999	LYS	CA-C	-8.69	1.41	1.53
1	C	1175	ALA	CA-C	-8.68	1.42	1.52
1	C	1157	ALA	C-O	-8.66	1.14	1.24
1	C	1178	MET	C-O	-8.62	1.13	1.24
1	C	436	SER	C-O	-8.60	1.13	1.24
1	C	662	VAL	C-N	8.55	1.44	1.33
1	C	1051	ARG	C-O	-8.52	1.14	1.24
1	C	359	ASN	C-O	-8.51	1.14	1.24
1	C	707	ALA	CA-C	-8.50	1.41	1.52
1	C	385	ILE	C-O	-8.50	1.15	1.24
1	C	525	PHE	CA-C	-8.48	1.41	1.52
1	C	695	ALA	CA-C	-8.46	1.41	1.52
1	C	720	PHE	CA-C	-8.44	1.40	1.52
1	C	185	ALA	C-N	8.42	1.45	1.33
1	C	530	GLY	C-O	-8.42	1.13	1.23
1	C	390	HIS	C-O	-8.41	1.13	1.23
1	C	1306	THR	CA-C	-8.41	1.41	1.53
1	C	548	TYR	CA-C	-8.40	1.42	1.52
1	C	741	TYR	CA-C	-8.38	1.44	1.53
1	C	625	PRO	C-O	-8.37	1.17	1.24
1	C	494	GLU	C-O	-8.37	1.13	1.23
1	C	1071	PHE	C-O	-8.36	1.13	1.23
1	C	750	GLU	C-O	-8.35	1.13	1.23
1	C	365	LEU	CA-C	-8.31	1.41	1.52
1	C	310	LEU	C-O	-8.30	1.14	1.24
1	C	436	SER	CA-C	-8.27	1.42	1.52
1	C	856	LEU	CA-C	-8.27	1.42	1.52
1	C	667	ALA	CA-C	-8.24	1.42	1.52
1	C	346	HIS	CA-C	-8.23	1.42	1.52
1	C	410	ARG	C-O	-8.22	1.14	1.24
1	C	1275	ASP	CA-C	-8.21	1.42	1.52
1	C	1230	ILE	C-O	-8.17	1.14	1.24
1	C	434	VAL	C-O	-8.16	1.14	1.24
1	C	449	PHE	C-N	8.14	1.52	1.33
1	C	852	TYR	C-O	-8.13	1.14	1.24
1	C	466	VAL	C-O	-8.12	1.14	1.24
1	C	1100	GLN	CA-C	-8.12	1.43	1.52
1	C	1075	ARG	CA-C	-8.12	1.42	1.52
1	C	1202	PHE	C-O	-8.11	1.13	1.23
1	C	979	ILE	C-O	-8.11	1.14	1.24
1	C	393	ASN	C-O	-8.10	1.14	1.23
1	C	490	PHE	C-O	-8.10	1.13	1.24

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	375	ARG	C-O	-8.08	1.14	1.24
1	C	77	THR	C-O	8.08	1.34	1.23
1	C	121	PHE	C-O	-8.07	1.13	1.24
1	C	512	LEU	C-O	-8.07	1.14	1.24
1	C	698	HIS	CA-C	-8.04	1.42	1.52
1	C	559	THR	CA-C	-8.01	1.43	1.52
1	C	1009	THR	C-O	-7.99	1.14	1.24
1	C	383	SER	CA-C	-7.98	1.43	1.52
1	C	456	ASN	C-O	-7.96	1.14	1.23
1	C	680	THR	CB-CG2	-7.95	1.26	1.52
1	C	725	ALA	C-O	-7.93	1.14	1.24
1	C	433	TYR	C-O	-7.90	1.14	1.24
1	C	996	ASP	C-O	-7.90	1.15	1.24
1	C	1139	MET	CA-C	-7.90	1.42	1.52
1	C	1179	THR	C-O	-7.90	1.14	1.24
1	C	1167	ASP	CB-CG	-7.89	1.32	1.52
1	C	587	ALA	CA-C	-7.89	1.42	1.52
1	C	671	ASP	CA-C	-7.88	1.42	1.52
1	C	652	PHE	C-O	-7.86	1.15	1.24
1	C	1176	GLU	CA-C	-7.85	1.43	1.52
1	C	744	ILE	C-O	-7.83	1.15	1.24
1	C	1266	ASP	CA-C	-7.83	1.44	1.53
1	C	427	VAL	C-O	-7.83	1.14	1.24
1	C	493	HIS	CA-C	-7.80	1.43	1.52
1	C	757	ILE	CA-C	-7.78	1.43	1.52
1	C	318	LEU	C-O	-7.76	1.14	1.24
1	C	747	ARG	CA-C	-7.76	1.42	1.52
1	C	531	ASP	CA-C	-7.75	1.42	1.52
1	C	1158	SER	C-O	-7.73	1.14	1.24
1	C	860	ARG	CA-C	-7.71	1.42	1.52
1	C	1220	PRO	C-O	-7.70	1.15	1.24
1	C	1304	MET	CA-CB	-7.70	1.44	1.54
1	C	396	ALA	C-O	-7.69	1.14	1.24
1	C	540	PHE	CA-C	-7.68	1.42	1.52
1	C	361	ASN	C-O	-7.67	1.14	1.24
1	C	747	ARG	C-O	-7.63	1.14	1.23
1	C	637	TYR	C-O	-7.60	1.14	1.24
1	C	422	LEU	CA-C	-7.58	1.43	1.52
1	C	605	ARG	C-O	-7.58	1.14	1.24
1	C	163	TYR	C-O	-7.57	1.15	1.24
1	C	978	GLN	C-O	-7.57	1.14	1.24
1	C	590	SER	CA-C	-7.57	1.43	1.52

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	1099	VAL	C-O	-7.55	1.16	1.24
1	C	1305	MET	C-O	-7.54	1.16	1.24
1	C	1258	VAL	C-O	-7.54	1.16	1.24
1	C	696	VAL	C-O	-7.54	1.15	1.24
1	C	938	ASN	N-CA	-7.53	1.36	1.46
1	C	437	ALA	CA-C	-7.52	1.42	1.52
1	C	1159	VAL	C-O	-7.52	1.15	1.24
1	C	704	VAL	C-O	-7.51	1.15	1.24
1	C	408	ILE	C-O	-7.51	1.15	1.24
1	C	335	ASP	CA-C	-7.51	1.43	1.52
1	C	1229	LEU	C-O	-7.50	1.15	1.24
1	C	1277	LEU	C-O	-7.47	1.14	1.23
1	C	300	LEU	C-O	-7.45	1.14	1.24
1	C	317	MET	C-O	-7.44	1.14	1.24
1	C	157	ILE	CA-C	-7.44	1.42	1.52
1	C	1139	MET	C-O	-7.43	1.15	1.23
1	C	95	THR	C-O	-7.41	1.15	1.24
1	C	967	LEU	C-O	-7.40	1.15	1.24
1	C	815	LEU	CA-C	-7.39	1.43	1.52
1	C	375	ARG	CA-C	-7.39	1.43	1.52
1	C	1000	LEU	C-O	-7.39	1.15	1.24
1	C	703	SER	C-O	-7.38	1.15	1.24
1	C	148	GLN	N-CA	-7.37	1.37	1.46
1	C	310	LEU	CA-C	-7.37	1.43	1.52
1	C	484	ARG	C-O	-7.37	1.14	1.24
1	C	536	LEU	C-O	-7.36	1.15	1.24
1	C	645	THR	CA-C	-7.36	1.42	1.52
1	C	816	PRO	CA-C	-7.35	1.42	1.52
1	C	360	ILE	C-O	-7.34	1.15	1.24
1	C	1140	THR	C-O	-7.33	1.15	1.24
1	C	1051	ARG	CA-C	-7.33	1.43	1.52
1	C	1247	ASN	C-O	-7.33	1.14	1.24
1	C	707	ALA	C-O	-7.33	1.15	1.24
1	C	855	TYR	CA-C	-7.32	1.43	1.52
1	C	1150	LEU	C-O	-7.31	1.14	1.24
1	C	617	ASP	CA-C	-7.30	1.42	1.52
1	C	614	ARG	C-O	-7.29	1.15	1.24
1	C	1320	VAL	C-O	-7.29	1.17	1.24
1	C	1193	ILE	C-O	-7.27	1.16	1.24
1	C	1137	VAL	C-O	-7.26	1.15	1.24
1	C	325	TYR	C-O	-7.26	1.15	1.24
1	C	445	GLU	C-O	-7.26	1.15	1.23

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	1302	VAL	C-O	-7.25	1.16	1.24
1	C	459	ALA	N-CA	-7.24	1.37	1.46
1	C	1253	ARG	CA-C	-7.24	1.43	1.52
1	C	74	LYS	C-O	7.23	1.33	1.24
1	C	119	ASP	CB-CG	7.23	1.70	1.52
1	C	491	ASN	C-O	-7.19	1.15	1.24
1	C	150	LEU	CA-C	-7.16	1.43	1.52
1	C	852	TYR	CA-C	-7.16	1.43	1.52
1	C	1296	ILE	C-O	-7.15	1.15	1.24
1	C	529	LYS	C-O	-7.14	1.14	1.24
1	C	604	MET	C-O	-7.13	1.15	1.24
1	C	305	THR	CA-C	-7.13	1.43	1.52
1	C	120	VAL	C-O	-7.11	1.15	1.24
1	C	800	LEU	CA-C	-7.11	1.43	1.52
1	C	592	VAL	C-O	-7.10	1.16	1.25
1	C	1162	SER	C-O	-7.09	1.14	1.24
1	C	1178	MET	CA-C	-7.08	1.44	1.52
1	C	424	GLY	C-O	-7.07	1.15	1.23
1	C	355	ALA	C-O	-7.07	1.15	1.24
1	C	915	VAL	C-O	-7.07	1.16	1.24
1	C	408	ILE	CA-C	-7.06	1.43	1.52
1	C	543	TRP	CB-CG	-7.06	1.28	1.50
1	C	708	THR	CA-C	-7.06	1.44	1.52
1	C	106	GLN	C-O	-7.06	1.15	1.24
1	C	820	ILE	CA-C	-7.03	1.43	1.52
1	C	697	ALA	C-O	-7.02	1.15	1.24
1	C	758	ILE	CA-C	-7.00	1.43	1.52
1	C	676	THR	C-O	-7.00	1.15	1.24
1	C	719	ASN	CA-C	-6.99	1.42	1.52
1	C	115	GLN	C-O	6.99	1.32	1.23
1	C	699	THR	C-O	-6.99	1.14	1.24
1	C	102	VAL	CA-C	-6.98	1.45	1.53
1	C	713	MET	C-O	-6.98	1.15	1.24
1	C	492	VAL	CA-CB	-6.97	1.47	1.54
1	C	721	SER	N-CA	-6.97	1.37	1.46
1	C	770	CYS	N-CA	-6.97	1.37	1.46
1	C	499	ALA	CA-C	-6.96	1.44	1.53
1	C	1101	TYR	C-O	-6.96	1.15	1.24
1	C	435	ALA	C-O	-6.95	1.15	1.24
1	C	547	GLU	C-O	-6.94	1.16	1.24
1	C	416	ALA	C-O	-6.93	1.16	1.24
1	C	545	PRO	CA-C	-6.93	1.42	1.52

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	575	TRP	C-O	-6.93	1.16	1.24
1	C	1261	SER	C-O	-6.92	1.15	1.24
1	C	151	SER	C-O	-6.92	1.15	1.24
1	C	769	GLN	N-CA	-6.92	1.36	1.46
1	C	354	ALA	CA-C	-6.91	1.43	1.52
1	C	532	ILE	C-O	-6.90	1.16	1.24
1	C	977	SER	N-CA	-6.89	1.37	1.46
1	C	1272	ARG	C-O	-6.89	1.15	1.24
1	C	768	CYS	N-CA	6.89	1.55	1.45
1	C	328	GLY	C-O	-6.88	1.14	1.23
1	C	490	PHE	CA-C	-6.88	1.43	1.52
1	C	428	GLN	C-O	-6.86	1.16	1.24
1	C	1292	GLU	C-O	-6.85	1.15	1.24
1	C	857	SER	C-O	6.84	1.32	1.24
1	C	411	CYS	C-O	-6.83	1.16	1.24
1	C	822	MET	C-O	-6.83	1.16	1.24
1	C	418	ASN	C-O	-6.83	1.15	1.24
1	C	1266	ASP	N-CA	-6.81	1.38	1.46
1	C	1070	ARG	CA-C	-6.80	1.44	1.53
1	C	1297	SER	C-O	-6.79	1.15	1.23
1	C	724	HIS	C-O	-6.79	1.16	1.24
1	C	947	GLU	CA-C	-6.78	1.44	1.52
1	C	766	ILE	C-O	-6.77	1.15	1.24
1	C	467	LYS	C-O	-6.77	1.15	1.24
1	C	1138	HIS	C-O	-6.76	1.15	1.24
1	C	872	ILE	C-O	-6.75	1.16	1.24
1	C	698	HIS	C-O	-6.75	1.16	1.24
1	C	708	THR	C-O	-6.75	1.16	1.24
1	C	731	GLN	C-O	-6.75	1.15	1.24
1	C	1108	SER	C-O	-6.74	1.16	1.23
1	C	798	THR	CA-C	-6.72	1.44	1.52
1	C	1330	ILE	C-O	-6.72	1.16	1.24
1	C	537	LEU	CA-C	-6.72	1.44	1.52
1	C	792	VAL	C-O	-6.71	1.16	1.24
1	C	851	THR	C-O	-6.70	1.15	1.23
1	C	554	ARG	C-O	-6.70	1.15	1.24
1	C	655	ILE	C-O	-6.70	1.16	1.24
1	C	1090	PRO	CA-C	-6.68	1.44	1.52
1	C	638	THR	C-O	-6.67	1.16	1.24
1	C	439	VAL	C-O	-6.67	1.14	1.24
1	C	862	ARG	C-O	-6.66	1.16	1.24
1	C	1100	GLN	C-O	-6.66	1.15	1.24

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	294	VAL	C-O	-6.66	1.16	1.24
1	C	85	ASP	CA-C	-6.66	1.44	1.52
1	C	765	PRO	C-O	-6.65	1.15	1.24
1	C	977	SER	C-O	-6.65	1.15	1.24
1	C	812	LYS	C-O	-6.64	1.16	1.24
1	C	75	ILE	CA-C	-6.64	1.45	1.52
1	C	670	ASP	CA-C	-6.63	1.43	1.52
1	C	156	GLN	CA-C	-6.62	1.43	1.52
1	C	488	PRO	C-O	-6.62	1.16	1.23
1	C	575	TRP	CA-C	-6.62	1.44	1.52
1	C	701	HIS	CA-C	-6.62	1.44	1.53
1	C	1288	ILE	CA-C	-6.61	1.46	1.52
1	C	143	VAL	N-CA	-6.61	1.38	1.46
1	C	533	GLN	CA-C	-6.60	1.44	1.52
1	C	551	PHE	C-O	-6.60	1.16	1.24
1	C	522	PRO	CA-C	-6.59	1.43	1.52
1	C	556	ALA	C-O	-6.59	1.15	1.24
1	C	364	ALA	C-O	-6.58	1.16	1.24
1	C	343	ILE	C-O	-6.58	1.16	1.24
1	C	683	TRP	CB-CG	-6.58	1.29	1.50
1	C	130	LEU	C-O	-6.57	1.15	1.24
1	C	151	SER	CA-C	-6.57	1.43	1.52
1	C	511	VAL	CA-C	-6.57	1.44	1.52
1	C	806	VAL	C-O	-6.57	1.16	1.24
1	C	226	PRO	C-N	-6.57	1.24	1.33
1	C	327	LEU	CA-C	-6.56	1.44	1.52
1	C	863	LEU	C-O	-6.56	1.16	1.24
1	C	1267	THR	CA-C	-6.55	1.44	1.52
1	C	526	ASN	C-O	-6.54	1.15	1.24
1	C	705	VAL	CA-CB	-6.54	1.46	1.54
1	C	811	SER	CA-C	-6.54	1.44	1.52
1	C	580	TYR	C-O	-6.54	1.16	1.24
1	C	358	LEU	C-O	-6.54	1.16	1.24
1	C	1180	PRO	C-O	-6.54	1.15	1.24
1	C	1191	GLU	CA-C	-6.53	1.44	1.52
1	C	1242	MET	CA-C	-6.52	1.44	1.52
1	C	543	TRP	C-O	-6.52	1.15	1.24
1	C	1141	ILE	C-O	-6.52	1.16	1.24
1	C	1151	VAL	C-O	-6.51	1.16	1.24
1	C	613	LEU	C-O	-6.51	1.16	1.24
1	C	800	LEU	C-O	-6.51	1.16	1.24
1	C	75	ILE	N-CA	-6.50	1.38	1.46

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	1016	ASN	CA-C	-6.49	1.45	1.52
1	C	365	LEU	C-O	-6.48	1.15	1.24
1	C	302	ARG	CA-C	-6.48	1.44	1.52
1	C	482	ILE	C-O	-6.48	1.16	1.24
1	C	1176	GLU	C-O	-6.48	1.16	1.24
1	C	77	THR	CA-C	6.47	1.60	1.52
1	C	437	ALA	C-O	-6.47	1.15	1.24
1	C	1169	HIS	CA-C	-6.47	1.44	1.52
1	C	116	SER	CA-C	-6.46	1.46	1.53
1	C	532	ILE	CA-CB	-6.44	1.46	1.54
1	C	336	TYR	CA-C	-6.44	1.44	1.52
1	C	1075	ARG	C-O	-6.44	1.16	1.24
1	C	737	PRO	C-O	-6.43	1.16	1.24
1	C	725	ALA	CA-C	-6.42	1.44	1.52
1	C	558	TYR	N-CA	-6.41	1.38	1.46
1	C	361	ASN	CA-C	-6.41	1.44	1.52
1	C	384	MET	C-O	-6.41	1.16	1.23
1	C	311	ASN	C-O	-6.41	1.16	1.24
1	C	1275	ASP	C-O	-6.39	1.15	1.23
1	C	957	PHE	C-O	-6.38	1.15	1.23
1	C	421	ARG	C-O	-6.37	1.16	1.24
1	C	410	ARG	CA-C	-6.37	1.44	1.52
1	C	417	ALA	CA-C	-6.36	1.44	1.52
1	C	1200	LYS	CA-C	-6.36	1.44	1.52
1	C	552	ILE	CA-C	-6.35	1.44	1.52
1	C	684	LEU	C-O	-6.35	1.16	1.24
1	C	1014	MET	C-O	-6.34	1.16	1.24
1	C	84	THR	CA-C	-6.34	1.44	1.52
1	C	767	LEU	C-O	-6.33	1.15	1.24
1	C	360	ILE	CA-C	-6.33	1.44	1.52
1	C	762	ILE	C-O	-6.33	1.15	1.24
1	C	673	GLN	C-O	-6.32	1.16	1.24
1	C	1147	MET	C-O	-6.32	1.16	1.24
1	C	1290	LYS	C-O	-6.31	1.16	1.24
1	C	457	GLN	CA-C	6.29	1.61	1.52
1	C	998	GLY	CA-C	-6.29	1.43	1.51
1	C	1225	GLU	CA-CB	6.29	1.62	1.53
1	C	393	ASN	CA-C	-6.28	1.44	1.52
1	C	618	LEU	C-O	-6.27	1.16	1.24
1	C	1254	PRO	C-O	-6.27	1.15	1.23
1	C	508	ILE	N-CA	-6.26	1.38	1.46
1	C	1246	VAL	CA-C	-6.25	1.45	1.52

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	626	ARG	C-O	-6.25	1.16	1.24
1	C	756	THR	C-O	-6.25	1.16	1.24
1	C	768	CYS	C-N	-6.25	1.25	1.33
1	C	1009	THR	CA-C	-6.25	1.45	1.52
1	C	801	SER	C-O	-6.24	1.16	1.24
1	C	811	SER	C-O	-6.24	1.17	1.24
1	C	774	LEU	CA-C	-6.23	1.44	1.52
1	C	864	HIS	CA-C	-6.23	1.44	1.52
1	C	705	VAL	C-O	-6.22	1.17	1.24
1	C	325	TYR	CA-C	-6.22	1.45	1.52
1	C	693	ASN	C-O	6.22	1.31	1.24
1	C	1099	VAL	CA-C	-6.21	1.45	1.52
1	C	458	SER	C-O	6.21	1.31	1.24
1	C	1157	ALA	CA-C	-6.21	1.45	1.52
1	C	696	VAL	CA-C	-6.20	1.45	1.52
1	C	620	ILE	C-O	-6.20	1.16	1.24
1	C	763	VAL	CA-C	-6.19	1.45	1.52
1	C	930	ALA	CA-C	-6.18	1.45	1.52
1	C	416	ALA	CA-C	-6.17	1.44	1.52
1	C	475	ILE	CA-CB	-6.17	1.46	1.54
1	C	1205	GLN	C-O	-6.17	1.16	1.24
1	C	539	PHE	C-O	-6.16	1.17	1.24
1	C	546	VAL	CA-CB	-6.16	1.47	1.54
1	C	353	PHE	C-O	-6.15	1.16	1.24
1	C	1289	PRO	C-O	-6.15	1.16	1.23
1	C	706	TYR	CA-CB	-6.14	1.43	1.53
1	C	542	ARG	CA-C	-6.14	1.43	1.52
1	C	423	GLU	CA-C	-6.14	1.45	1.52
1	C	916	LEU	CA-C	-6.14	1.45	1.52
1	C	1201	LEU	C-O	-6.14	1.16	1.24
1	C	438	ASN	CA-C	-6.13	1.46	1.53
1	C	807	ALA	C-O	-6.13	1.17	1.24
1	C	727	PHE	C-O	-6.12	1.17	1.24
1	C	309	TRP	C-O	-6.08	1.17	1.24
1	C	886	SER	CA-C	-6.08	1.44	1.52
1	C	373	ASP	C-O	-6.07	1.16	1.24
1	C	522	PRO	CA-CB	-6.07	1.45	1.53
1	C	653	ARG	CA-C	-6.07	1.45	1.52
1	C	108	LYS	CA-C	-6.07	1.45	1.52
1	C	388	GLN	C-O	-6.07	1.16	1.24
1	C	417	ALA	C-O	-6.05	1.17	1.24
1	C	976	THR	C-O	-6.05	1.16	1.24

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	156	GLN	C-O	-6.05	1.16	1.24
1	C	680	THR	C-O	-6.05	1.17	1.24
1	C	1017	ALA	CA-C	-6.04	1.45	1.52
1	C	383	SER	C-O	-6.04	1.16	1.24
1	C	353	PHE	CA-CB	-6.03	1.43	1.53
1	C	710	SER	C-O	-6.03	1.16	1.24
1	C	1005	LEU	CA-C	-6.03	1.45	1.52
1	C	579	LEU	N-CA	-6.02	1.39	1.46
1	C	683	TRP	CA-CB	-6.02	1.44	1.53
1	C	756	THR	CA-C	-6.02	1.45	1.52
1	C	413	MET	C-O	-6.01	1.17	1.24
1	C	426	ILE	CA-CB	-6.01	1.46	1.54
1	C	706	TYR	C-O	-6.01	1.17	1.24
1	C	746	GLU	C-O	-6.00	1.16	1.23
1	C	1253	ARG	C-O	-6.00	1.16	1.24
1	C	963	ALA	C-O	-6.00	1.17	1.24
1	B	479	HIS	CG-ND1	-6.00	1.31	1.38
1	C	506	SER	CA-CB	-6.00	1.42	1.53
1	C	1198	LYS	C-O	-5.99	1.16	1.24
1	C	744	ILE	CA-C	-5.99	1.45	1.52
1	C	999	LYS	C-O	-5.99	1.15	1.23
1	C	688	GLU	C-O	-5.98	1.17	1.24
1	C	577	GLN	CA-C	-5.97	1.44	1.52
1	C	558	TYR	CA-C	-5.97	1.45	1.52
1	C	703	SER	N-CA	-5.96	1.39	1.46
1	C	613	LEU	CA-C	-5.96	1.45	1.52
1	C	864	HIS	C-O	-5.95	1.17	1.24
1	C	100	ASP	N-CA	-5.94	1.38	1.46
1	C	682	GLN	C-O	-5.94	1.17	1.24
1	C	759	ASP	CA-C	-5.94	1.45	1.52
1	C	462	LEU	C-O	-5.92	1.17	1.24
1	C	556	ALA	CA-C	-5.92	1.44	1.52
1	C	975	SER	N-CA	-5.92	1.42	1.46
1	C	883	ILE	C-O	-5.91	1.17	1.24
1	C	679	CYS	C-O	-5.91	1.17	1.24
1	C	1015	GLN	C-O	-5.91	1.16	1.24
1	C	1264	GLU	CA-C	-5.90	1.44	1.52
1	C	467	LYS	CA-CB	-5.89	1.46	1.54
1	C	1068	ALA	N-CA	-5.89	1.39	1.46
1	C	401	LEU	CA-C	-5.89	1.45	1.52
1	C	1326	ARG	N-CA	-5.88	1.39	1.46
1	C	763	VAL	C-O	-5.87	1.17	1.24

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	111	PRO	C-O	-5.87	1.16	1.23
1	C	794	PRO	CA-C	-5.87	1.44	1.52
1	C	1038	GLU	C-O	-5.87	1.17	1.24
1	C	484	ARG	C-N	-5.86	1.26	1.34
1	C	279	SER	C-N	5.86	1.41	1.33
1	C	517	PHE	CA-C	-5.85	1.45	1.52
1	C	1174	THR	C-O	-5.85	1.17	1.24
1	C	814	THR	N-CA	-5.85	1.39	1.46
1	C	101	ASP	C-N	-5.85	1.27	1.33
1	C	577	GLN	C-O	-5.85	1.16	1.24
1	C	580	TYR	CA-C	-5.84	1.45	1.52
1	C	1231	TYR	CA-C	-5.84	1.45	1.52
1	C	938	ASN	CA-C	5.84	1.60	1.52
1	C	457	GLN	C-O	5.83	1.30	1.24
1	C	1177	VAL	C-O	-5.83	1.18	1.23
1	C	715	ASN	CA-C	-5.83	1.45	1.52
1	C	297	ASN	CG-ND2	-5.82	1.21	1.33
1	C	503	GLU	C-O	-5.81	1.16	1.24
1	C	517	PHE	C-O	-5.81	1.17	1.24
1	C	351	ASP	C-O	-5.80	1.16	1.23
1	C	1267	THR	N-CA	-5.80	1.39	1.46
1	C	401	LEU	N-CA	-5.79	1.39	1.46
1	C	354	ALA	N-CA	-5.79	1.39	1.46
1	C	1176	GLU	CA-CB	-5.79	1.44	1.53
1	C	1045	TYR	C-O	-5.78	1.16	1.24
1	C	507	SER	N-CA	-5.78	1.38	1.46
1	C	540	PHE	C-O	-5.78	1.17	1.24
1	C	805	SER	C-O	-5.77	1.17	1.24
1	C	515	ILE	CA-CB	-5.77	1.47	1.54
1	C	1163	ASN	CA-C	-5.77	1.45	1.53
1	C	440	ILE	CA-CB	-5.77	1.46	1.55
1	C	1073	GLY	C-O	-5.77	1.16	1.23
1	C	546	VAL	CA-C	-5.76	1.45	1.52
1	C	386	SER	CA-CB	-5.76	1.46	1.53
1	C	1181	SER	CA-C	-5.75	1.45	1.52
1	C	565	GLU	C-O	-5.75	1.16	1.24
1	C	701	HIS	N-CA	-5.75	1.39	1.46
1	C	666	ARG	CA-C	-5.75	1.45	1.52
1	C	132	PRO	CA-C	-5.74	1.44	1.52
1	C	589	PHE	C-O	-5.74	1.16	1.24
1	C	709	MET	CA-C	-5.74	1.44	1.52
1	C	918	VAL	C-O	-5.74	1.17	1.24

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	359	ASN	N-CA	-5.73	1.39	1.46
1	C	329	LEU	C-O	-5.73	1.16	1.23
1	C	463	VAL	CA-C	-5.72	1.45	1.52
1	C	764	TRP	C-O	-5.72	1.19	1.24
1	C	134	THR	C-O	-5.72	1.17	1.24
1	C	552	ILE	CA-CB	-5.72	1.47	1.54
1	C	508	ILE	C-O	-5.71	1.16	1.24
1	C	804	LEU	CA-C	-5.71	1.45	1.52
1	C	1214	GLU	C-O	-5.70	1.18	1.23
1	C	1122	PRO	CA-C	-5.69	1.46	1.52
1	C	797	SER	N-CA	-5.69	1.39	1.46
1	C	381	ALA	CA-CB	-5.69	1.44	1.53
1	C	98	ASN	CA-CB	-5.68	1.44	1.53
1	C	514	PHE	C-O	-5.68	1.17	1.24
1	C	802	GLN	CA-C	-5.68	1.45	1.52
1	C	1328	ILE	N-CA	-5.68	1.39	1.46
1	C	481	ALA	C-O	-5.68	1.17	1.24
1	C	541	SER	CA-CB	-5.68	1.44	1.53
1	C	425	ILE	C-O	-5.67	1.17	1.24
1	C	689	THR	CA-CB	-5.67	1.44	1.53
1	C	875	THR	CA-C	5.67	1.60	1.52
1	C	653	ARG	CA-CB	-5.67	1.44	1.53
1	C	723	ASN	C-O	-5.67	1.17	1.24
1	C	1150	LEU	CA-C	-5.67	1.45	1.52
1	C	398	ARG	C-O	-5.66	1.19	1.24
1	C	366	MET	C-O	-5.65	1.15	1.23
1	C	1110	LEU	C-O	-5.65	1.17	1.23
1	C	1001	THR	C-O	-5.64	1.17	1.24
1	C	1223	SER	CA-CB	-5.64	1.44	1.53
1	C	1251	VAL	N-CA	-5.64	1.39	1.46
1	C	1312	GLY	C-N	-5.64	1.26	1.33
1	C	1001	THR	CA-C	-5.64	1.45	1.52
1	C	398	ARG	CA-CB	-5.64	1.46	1.53
1	C	434	VAL	CA-CB	-5.64	1.47	1.54
1	C	459	ALA	C-O	-5.64	1.17	1.24
1	C	742	LYS	CA-C	-5.64	1.45	1.52
1	C	592	VAL	CA-C	-5.63	1.46	1.52
1	C	625	PRO	N-CA	-5.63	1.41	1.47
1	C	1308	ASN	CA-CB	-5.63	1.44	1.53
1	C	553	GLN	C-O	-5.62	1.17	1.24
1	C	915	VAL	CA-C	-5.62	1.46	1.52
1	C	415	ALA	C-O	-5.62	1.17	1.24

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	469	ARG	N-CA	-5.62	1.39	1.46
1	C	435	ALA	CA-C	-5.60	1.45	1.52
1	C	661	ASN	C-N	-5.60	1.27	1.33
1	C	495	LEU	C-O	-5.59	1.17	1.23
1	C	1126	MET	C-O	-5.59	1.17	1.24
1	C	498	ILE	CA-C	-5.59	1.45	1.52
1	C	619	ALA	CA-CB	-5.59	1.44	1.53
1	C	418	ASN	CA-C	-5.57	1.45	1.52
1	C	646	ASN	C-O	-5.57	1.17	1.24
1	C	814	THR	C-O	-5.57	1.17	1.24
1	C	484	ARG	CA-C	-5.57	1.45	1.52
1	C	387	THR	C-O	-5.56	1.16	1.23
1	C	408	ILE	CA-CB	-5.56	1.47	1.54
1	C	699	THR	CA-C	-5.55	1.44	1.52
1	C	1109	SER	C-O	-5.55	1.17	1.24
1	C	311	ASN	CA-C	-5.55	1.45	1.52
1	C	363	ARG	C-O	-5.54	1.17	1.24
1	C	1154	ASN	CA-CB	-5.54	1.44	1.53
1	C	643	THR	CA-C	-5.54	1.45	1.52
1	C	606	LEU	C-O	-5.54	1.16	1.24
1	C	1177	VAL	CA-C	-5.54	1.46	1.53
1	C	158	SER	C-O	-5.53	1.17	1.24
1	C	736	SER	C-O	-5.53	1.18	1.24
1	C	1325	VAL	C-O	-5.53	1.17	1.24
1	C	760	THR	CA-C	-5.52	1.45	1.52
1	C	1067	ILE	C-O	-5.52	1.17	1.24
1	C	1111	ALA	CA-C	-5.52	1.45	1.52
1	C	1116	ARG	C-O	-5.51	1.17	1.23
1	C	680	THR	CA-CB	-5.51	1.44	1.53
1	C	799	THR	C-O	-5.51	1.17	1.24
1	C	569	SER	CA-C	-5.51	1.46	1.52
1	C	1092	VAL	CA-C	-5.50	1.46	1.52
1	C	1243	ARG	CA-C	-5.50	1.45	1.52
1	C	467	LYS	CA-C	-5.50	1.44	1.52
1	C	1199	GLY	CA-C	-5.49	1.44	1.51
1	C	112	THR	C-O	-5.48	1.17	1.24
1	C	465	ALA	C-O	-5.48	1.17	1.24
1	C	1192	SER	C-O	-5.48	1.17	1.24
1	C	408	ILE	N-CA	-5.48	1.39	1.46
1	C	1252	ASP	C-O	-5.47	1.17	1.23
1	C	644	VAL	N-CA	-5.47	1.39	1.46
1	C	1229	LEU	CA-C	-5.47	1.46	1.52

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	527	ARG	CA-C	-5.47	1.45	1.52
1	C	635	ILE	C-O	-5.47	1.17	1.24
1	C	496	LYS	CA-C	-5.47	1.46	1.52
1	C	1058	GLY	C-O	-5.46	1.17	1.23
1	C	1273	ASN	C-O	-5.46	1.18	1.24
1	C	116	SER	N-CA	-5.46	1.40	1.46
1	C	810	LEU	CA-C	-5.46	1.45	1.52
1	C	475	ILE	C-O	-5.46	1.17	1.24
1	C	499	ALA	N-CA	-5.46	1.39	1.46
1	C	1168	ILE	C-O	-5.46	1.17	1.24
1	C	733	VAL	C-O	-5.45	1.18	1.24
1	C	765	PRO	CA-CB	-5.45	1.45	1.53
1	C	1244	ALA	CA-C	-5.44	1.47	1.53
1	C	326	GLY	C-O	-5.44	1.17	1.23
1	C	430	ASN	CB-CG	-5.43	1.38	1.52
1	C	1004	PHE	C-O	-5.43	1.16	1.24
1	C	519	LEU	C-O	-5.43	1.17	1.24
1	C	1037	ILE	CA-C	-5.43	1.47	1.53
1	C	1223	SER	CA-C	-5.42	1.45	1.52
1	C	374	ASP	CA-C	-5.42	1.45	1.52
1	C	823	ILE	C-O	-5.42	1.17	1.24
1	C	1138	HIS	N-CA	-5.42	1.39	1.46
1	C	1119	TYR	CA-C	-5.41	1.46	1.52
1	C	520	PHE	CA-C	-5.41	1.45	1.52
1	C	524	GLU	CA-C	-5.40	1.45	1.52
1	C	676	THR	CA-C	-5.40	1.45	1.52
1	C	86	VAL	C-O	-5.40	1.18	1.24
1	B	469	ARG	C-O	-5.39	1.17	1.24
1	C	1247	ASN	CA-C	-5.39	1.45	1.52
1	C	96	ILE	C-O	-5.39	1.18	1.24
1	C	875	THR	N-CA	5.38	1.53	1.46
1	C	637	TYR	CA-C	-5.38	1.46	1.52
1	C	362	LEU	CA-C	-5.37	1.45	1.52
1	C	1103	HIS	CA-C	-5.37	1.45	1.52
1	C	802	GLN	C-O	-5.37	1.18	1.24
1	C	1068	ALA	CA-C	-5.37	1.47	1.53
1	C	538	LEU	C-O	-5.36	1.18	1.24
1	C	160	PRO	C-O	-5.36	1.17	1.23
1	C	640	GLN	CA-C	-5.36	1.46	1.52
1	C	1010	ARG	CA-CB	-5.36	1.45	1.53
1	C	1104	ARG	N-CA	-5.35	1.40	1.46
1	C	711	ASN	C-O	-5.35	1.16	1.23

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	1097	VAL	C-O	-5.34	1.17	1.24
1	C	150	LEU	C-O	-5.34	1.17	1.23
1	C	478	ILE	CA-C	-5.34	1.45	1.52
1	C	1310	ARG	CA-C	5.34	1.59	1.52
1	C	808	GLN	C-O	-5.34	1.17	1.24
1	C	796	PRO	N-CA	-5.33	1.40	1.47
1	C	381	ALA	C-O	-5.33	1.18	1.24
1	C	971	MET	C-O	-5.33	1.17	1.24
1	C	922	TYR	C-O	-5.33	1.16	1.23
1	C	794	PRO	CA-CB	-5.33	1.46	1.53
1	C	1245	ILE	C-O	-5.33	1.17	1.24
1	C	651	ARG	C-O	-5.33	1.17	1.24
1	C	1093	PRO	C-O	-5.33	1.17	1.24
1	C	811	SER	N-CA	-5.32	1.40	1.46
1	C	977	SER	CA-CB	-5.31	1.44	1.53
1	C	318	LEU	CA-C	-5.31	1.45	1.52
1	C	551	PHE	CA-C	-5.31	1.45	1.52
1	C	90	ALA	C-O	-5.30	1.17	1.23
1	C	961	SER	C-O	-5.30	1.18	1.23
1	C	1023	ARG	C-O	-5.30	1.17	1.24
1	C	1292	GLU	CA-C	-5.30	1.45	1.52
1	C	1090	PRO	C-O	-5.29	1.17	1.23
1	C	646	ASN	CA-C	-5.29	1.45	1.52
1	C	1055	LEU	CA-CB	-5.28	1.44	1.53
1	C	751	THR	C-O	-5.28	1.16	1.23
1	C	768	CYS	C-O	-5.28	1.17	1.24
1	C	862	ARG	CA-C	-5.28	1.46	1.52
1	C	347	ALA	CA-C	-5.27	1.46	1.52
1	C	353	PHE	CA-C	-5.25	1.46	1.52
1	C	363	ARG	N-CA	-5.24	1.40	1.46
1	C	1157	ALA	N-CA	-5.23	1.40	1.46
1	C	99	VAL	C-O	-5.23	1.17	1.24
1	C	748	GLN	CA-C	-5.23	1.46	1.52
1	C	675	ALA	CA-C	-5.23	1.46	1.52
1	C	607	PHE	C-O	-5.23	1.17	1.24
1	C	706	TYR	CA-C	-5.23	1.46	1.52
1	C	472	GLU	C-O	-5.23	1.17	1.23
1	C	1266	ASP	C-O	-5.23	1.17	1.23
1	C	1203	HIS	C-O	-5.22	1.18	1.24
1	C	358	LEU	CA-C	-5.22	1.46	1.52
1	C	120	VAL	CA-CB	-5.22	1.47	1.54
1	C	442	PRO	C-O	-5.22	1.17	1.24

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	510	VAL	C-O	-5.22	1.18	1.24
1	C	701	HIS	CA-CB	-5.22	1.45	1.53
1	C	1157	ALA	CA-CB	-5.21	1.45	1.53
1	C	1214	GLU	CA-C	-5.21	1.44	1.52
1	C	377	LYS	N-CA	-5.20	1.40	1.46
1	C	1115	ASN	CA-C	-5.20	1.45	1.52
1	C	1297	SER	CA-C	-5.20	1.46	1.52
1	C	1250	GLU	C-O	-5.20	1.18	1.24
1	C	947	GLU	C-O	-5.20	1.18	1.24
1	C	307	VAL	CA-CB	-5.19	1.47	1.53
1	C	1063	THR	C-O	-5.19	1.17	1.24
1	C	569	SER	C-O	-5.19	1.17	1.24
1	C	1043	SER	N-CA	5.18	1.52	1.46
1	C	750	GLU	CA-C	-5.18	1.46	1.52
1	C	477	SER	C-O	-5.18	1.17	1.24
1	C	528	ILE	CA-CB	-5.18	1.47	1.54
1	C	557	THR	C-O	-5.18	1.17	1.23
1	C	771	THR	CA-C	-5.18	1.46	1.52
1	C	859	ILE	N-CA	-5.17	1.40	1.46
1	C	1280	PRO	N-CD	5.17	1.55	1.47
1	C	430	ASN	C-O	-5.16	1.17	1.24
1	C	1215	PRO	CA-CB	-5.16	1.46	1.53
1	B	971	MET	C-N	-5.16	1.21	1.33
1	C	682	GLN	CA-CB	-5.16	1.45	1.53
1	C	1246	VAL	C-O	-5.16	1.18	1.24
1	C	306	GLN	CA-CB	-5.16	1.45	1.53
1	C	1072	ASP	CA-C	-5.15	1.46	1.52
1	C	304	PHE	C-O	-5.15	1.17	1.24
1	C	296	VAL	CA-C	-5.15	1.46	1.52
1	C	431	THR	C-O	-5.15	1.18	1.24
1	C	770	CYS	CA-C	-5.13	1.46	1.52
1	C	118	THR	C-O	-5.13	1.17	1.24
1	C	1012	LEU	N-CA	-5.12	1.39	1.46
1	C	333	ARG	C-O	-5.12	1.18	1.24
1	C	423	GLU	C-O	-5.12	1.18	1.24
1	C	694	ILE	C-O	-5.12	1.17	1.24
1	C	172	ASP	C-N	5.12	1.40	1.33
1	C	583	GLU	C-O	-5.12	1.17	1.24
1	C	861	GLU	CA-C	-5.12	1.46	1.52
1	C	1169	HIS	C-N	-5.11	1.27	1.33
1	C	1274	GLY	C-O	-5.11	1.17	1.23
1	C	607	PHE	CA-C	-5.11	1.46	1.52

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	560	ILE	C-O	-5.11	1.18	1.24
1	C	858	HIS	CA-CB	-5.11	1.45	1.53
1	C	1238	VAL	CA-CB	-5.11	1.47	1.54
1	C	707	ALA	N-CA	-5.10	1.40	1.46
1	C	123	GLU	C-O	-5.10	1.17	1.23
1	C	600	ILE	CA-CB	-5.09	1.47	1.54
1	C	737	PRO	CA-C	-5.09	1.43	1.52
1	C	1143	GLU	N-CA	-5.09	1.39	1.46
1	C	362	LEU	C-O	-5.08	1.18	1.24
1	C	1327	ALA	N-CA	-5.08	1.39	1.46
1	C	544	TYR	CB-CG	-5.08	1.40	1.51
1	C	377	LYS	C-O	-5.08	1.18	1.24
1	C	1015	GLN	CA-C	-5.07	1.46	1.52
1	C	1232	PRO	CA-CB	-5.07	1.47	1.53
1	C	1285	GLN	CA-C	5.07	1.59	1.52
1	C	1036	ASP	C-O	-5.07	1.17	1.23
1	C	1084	PRO	N-CD	5.07	1.54	1.47
1	C	682	GLN	CA-C	-5.06	1.46	1.52
1	C	697	ALA	CA-C	-5.06	1.45	1.52
1	C	691	PHE	N-CA	-5.06	1.40	1.46
1	C	577	GLN	C-N	-5.05	1.27	1.33
1	C	579	LEU	C-O	-5.05	1.17	1.24
1	C	1238	VAL	C-O	-5.05	1.17	1.24
1	C	1010	ARG	CA-C	-5.04	1.46	1.52
1	C	1119	TYR	C-O	-5.04	1.18	1.23
1	C	752	VAL	N-CA	-5.04	1.40	1.46
1	C	587	ALA	C-O	-5.04	1.18	1.24
1	C	1315	MET	C-O	-5.04	1.17	1.23
1	C	273	PRO	N-CD	5.03	1.54	1.47
1	C	997	TYR	C-N	-5.03	1.26	1.33
1	C	126	ALA	N-CA	-5.03	1.40	1.46
1	C	707	ALA	CA-CB	-5.03	1.45	1.53
1	C	560	ILE	CA-C	-5.03	1.46	1.52
1	C	675	ALA	CA-CB	-5.03	1.45	1.53
1	C	595	ALA	CA-C	-5.02	1.46	1.52
1	C	828	ASP	C-O	-5.02	1.15	1.24
1	C	1089	VAL	C-O	-5.02	1.18	1.24
1	C	1262	SER	CA-C	-5.02	1.46	1.52
1	C	813	LEU	C-O	5.02	1.29	1.24
1	C	819	PHE	CA-CB	-5.02	1.45	1.53
1	C	1210	LEU	C-O	-5.01	1.17	1.24
1	C	961	SER	CA-C	-5.01	1.47	1.53

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	382	HIS	CA-CB	-5.01	1.44	1.53
1	C	1037	ILE	C-O	-5.01	1.16	1.23
1	C	361	ASN	CA-CB	-5.00	1.45	1.53
1	C	1028	VAL	C-O	-5.00	1.18	1.24

All (572) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	285	VAL	O-C-N	27.50	151.47	122.04
1	C	172	ASP	CA-C-N	-20.92	92.00	123.17
1	C	172	ASP	C-N-CA	-20.92	92.00	123.17
1	C	1307	ALA	N-CA-C	-20.83	88.36	113.15
1	C	398	ARG	N-CA-C	20.81	140.24	112.35
1	C	285	VAL	CA-C-N	-20.37	93.47	122.19
1	C	285	VAL	C-N-CA	-20.37	93.47	122.19
1	C	173	GLN	O-C-N	-20.26	94.62	121.97
1	C	171	GLU	O-C-N	-19.89	98.10	123.16
1	C	449	PHE	O-C-N	-19.54	98.85	121.32
1	C	638	THR	N-CA-C	16.84	129.71	111.36
1	C	279	SER	O-C-N	-16.53	101.03	123.01
1	C	226	PRO	O-C-N	15.53	143.61	122.64
1	C	226	PRO	CA-C-N	-15.40	101.47	122.72
1	C	226	PRO	C-N-CA	-15.40	101.47	122.72
1	C	772	TYR	C-N-CD	-15.09	63.15	125.00
1	C	172	ASP	O-C-N	13.30	136.73	122.23
1	C	158	SER	N-CA-C	13.24	125.44	111.14
1	C	484	ARG	N-CA-C	-12.93	97.19	113.23
1	C	655	ILE	CB-CA-C	-12.90	94.72	112.14
1	C	360	ILE	CB-CA-C	-12.58	95.15	112.14
1	C	954	GLN	N-CA-C	12.55	129.12	110.17
1	C	721	SER	N-CA-C	-12.39	87.01	108.56
1	C	278	LEU	O-C-N	12.13	137.30	123.48
1	C	1300	ASN	N-CA-C	12.02	132.83	107.70
1	C	661	ASN	CA-C-N	-11.96	107.08	122.16
1	C	661	ASN	C-N-CA	-11.96	107.08	122.16
1	C	1230	ILE	N-CA-C	11.94	125.84	108.53
1	C	700	ASP	N-CA-C	11.94	128.59	113.55
1	C	152	ASP	N-CA-C	11.90	124.83	110.91
1	C	773	PRO	N-CA-C	-11.84	88.07	112.47
1	C	244	SER	O-C-N	11.77	134.80	122.09
1	C	756	THR	N-CA-C	11.72	124.05	111.28
1	C	1286	VAL	N-CA-C	11.67	133.61	109.34

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	1285	GLN	N-CA-C	11.65	135.62	110.80
1	C	439	VAL	N-CA-C	11.65	124.40	113.10
1	C	336	TYR	N-CA-C	11.55	135.41	110.80
1	C	244	SER	CA-C-N	-11.54	99.50	121.54
1	C	244	SER	C-N-CA	-11.54	99.50	121.54
1	C	313	ASP	N-CA-C	11.47	123.87	111.36
1	C	635	ILE	CA-C-N	11.46	131.77	119.05
1	C	635	ILE	C-N-CA	11.46	131.77	119.05
1	C	448	TYR	O-C-N	-11.40	107.42	122.59
1	C	1121	HIS	C-N-CD	-11.35	78.48	125.00
1	C	457	GLN	N-CA-C	11.16	124.83	111.33
1	C	85	ASP	N-CA-C	11.14	127.05	108.90
1	C	119	ASP	N-CA-C	-11.08	93.68	110.30
1	C	947	GLU	N-CA-C	11.06	123.34	111.28
1	C	870	ASP	C-N-CD	-11.00	79.91	125.00
1	C	151	SER	N-CA-C	10.98	124.34	111.71
1	C	185	ALA	O-C-N	-10.94	110.38	122.08
1	C	816	PRO	CA-N-CD	-10.74	96.96	112.00
1	C	1098	ALA	N-CA-C	10.56	127.02	111.81
1	C	1179	THR	N-CA-C	10.46	122.92	109.64
1	C	173	GLN	CA-C-N	10.46	147.83	122.95
1	C	173	GLN	C-N-CA	10.46	147.83	122.95
1	C	1299	SER	N-CA-C	10.39	124.07	109.31
1	C	361	ASN	O-C-N	-10.32	109.58	122.27
1	C	495	LEU	N-CA-C	10.30	123.64	110.24
1	C	124	GLN	N-CA-C	10.27	129.41	113.19
1	C	350	ILE	CB-CA-C	-10.20	95.12	110.82
1	C	635	ILE	N-CA-C	10.12	130.74	108.88
1	C	883	ILE	N-CA-C	-10.11	101.03	110.53
1	C	1178	MET	CB-CG-SD	-10.03	82.61	112.70
1	C	1042	TRP	N-CA-C	10.02	132.15	110.80
1	C	874	ILE	N-CA-C	10.02	122.19	107.37
1	C	279	SER	CA-C-N	9.99	140.61	121.54
1	C	279	SER	C-N-CA	9.99	140.61	121.54
1	C	827	GLY	N-CA-C	-9.94	89.63	113.18
1	C	497	LYS	N-CA-C	9.93	124.63	110.23
1	C	458	SER	CA-C-O	9.91	131.05	120.55
1	C	352	HIS	N-CA-C	9.82	124.79	113.01
1	C	163	TYR	N-CA-C	9.81	122.05	111.36
1	C	75	ILE	O-C-N	9.80	133.69	122.81
1	C	456	ASN	O-C-N	-9.73	111.39	123.27
1	C	444	SER	N-CA-C	9.53	121.67	111.28

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	521	PHE	C-N-CD	-9.51	86.03	125.00
1	C	136	VAL	CA-C-N	9.47	136.14	120.62
1	C	136	VAL	C-N-CA	9.47	136.14	120.62
1	C	348	LEU	N-CA-C	9.41	124.44	110.52
1	C	866	THR	N-CA-C	-9.40	89.85	107.71
1	C	120	VAL	N-CA-C	9.40	128.89	109.34
1	C	546	VAL	CB-CA-C	-9.37	99.97	111.97
1	C	278	LEU	CA-C-N	-9.35	107.19	121.02
1	C	278	LEU	C-N-CA	-9.35	107.19	121.02
1	C	114	VAL	CB-CA-C	-9.34	99.01	111.15
1	C	1198	LYS	N-CA-C	9.31	124.95	113.50
1	C	1230	ILE	CB-CA-C	-9.31	96.66	110.81
1	C	1147	MET	N-CA-C	9.29	130.58	110.80
1	C	1043	SER	N-CA-C	9.20	130.39	110.80
1	C	144	ASN	N-CA-CB	9.12	125.91	110.49
1	C	475	ILE	N-CA-C	9.12	128.32	109.34
1	C	855	TYR	CA-C-O	-9.12	110.89	120.55
1	C	418	ASN	N-CA-C	9.11	124.52	113.41
1	C	768	CYS	N-CA-C	9.10	128.26	113.89
1	C	75	ILE	CA-C-N	9.05	134.41	121.02
1	C	75	ILE	C-N-CA	9.05	134.41	121.02
1	C	137	ILE	N-CA-C	8.98	123.56	111.17
1	B	1317	VAL	N-CA-C	-8.97	96.50	108.35
1	C	1321	ASN	N-CA-C	8.94	124.35	109.87
1	C	1320	VAL	N-CA-C	8.91	120.97	108.93
1	C	731	GLN	N-CA-C	8.82	129.59	110.80
1	C	758	ILE	CB-CA-C	-8.81	98.09	110.96
1	C	1043	SER	CA-C-N	8.77	137.30	120.99
1	C	1043	SER	C-N-CA	8.77	137.30	120.99
1	C	408	ILE	CB-CA-C	-8.73	100.17	112.22
1	C	654	THR	CB-CA-C	-8.67	97.27	110.88
1	C	879	THR	C-N-CD	-8.66	89.50	125.00
1	C	632	GLN	N-CA-C	-8.65	96.25	109.14
1	C	645	THR	N-CA-C	8.65	124.77	114.04
1	C	713	MET	N-CA-C	8.57	120.70	111.36
1	C	418	ASN	CB-CA-C	-8.56	94.25	109.24
1	C	1092	VAL	CB-CA-C	-8.55	102.50	110.88
1	C	1279	SER	C-N-CD	8.49	139.27	120.60
1	C	308	ASN	N-CA-C	8.46	120.50	111.28
1	C	1199	GLY	N-CA-C	-8.45	93.16	113.18
1	C	1214	GLU	N-CA-CB	8.44	119.35	109.72
1	B	441	ARG	CA-C-N	8.43	130.38	119.84

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	441	ARG	C-N-CA	8.43	130.38	119.84
1	C	671	ASP	O-C-N	-8.35	112.66	122.93
1	C	938	ASN	CB-CA-C	8.35	125.75	109.72
1	C	121	PHE	CA-C-N	8.33	137.45	121.54
1	C	121	PHE	C-N-CA	8.33	137.45	121.54
1	C	891	HIS	N-CA-C	8.29	128.47	110.80
1	C	501	SER	N-CA-C	8.28	122.95	113.02
1	C	716	PHE	N-CA-C	8.21	123.47	112.30
1	C	314	ILE	CB-CA-C	-8.19	100.91	112.22
1	C	744	ILE	N-CA-C	8.18	118.22	110.53
1	C	496	LYS	N-CA-C	-8.18	95.99	108.67
1	C	696	VAL	CB-CA-C	-8.16	101.12	112.14
1	C	616	ASP	N-CA-C	8.12	122.69	108.56
1	C	1259	ALA	CA-C-N	8.12	129.99	119.84
1	C	1259	ALA	C-N-CA	8.12	129.99	119.84
1	C	755	LEU	CA-C-N	8.10	131.14	120.28
1	C	755	LEU	C-N-CA	8.10	131.14	120.28
1	C	347	ALA	N-CA-C	8.10	122.25	107.99
1	C	1229	LEU	CA-C-O	-8.09	112.57	120.90
1	C	797	SER	N-CA-C	8.06	120.98	111.71
1	C	688	GLU	CB-CA-C	7.99	124.05	110.79
1	C	100	ASP	N-CA-CB	-7.98	98.36	110.73
1	C	899	SER	N-CA-C	7.97	122.08	110.28
1	C	511	VAL	CB-CA-C	-7.90	101.48	112.14
1	C	1225	GLU	N-CA-CB	7.88	121.18	110.38
1	C	342	THR	CA-C-N	7.88	132.53	121.66
1	C	342	THR	C-N-CA	7.88	132.53	121.66
1	B	1317	VAL	CA-C-N	7.85	135.83	121.70
1	B	1317	VAL	C-N-CA	7.85	135.83	121.70
1	C	1298	PHE	CA-C-N	7.84	135.78	122.15
1	C	1298	PHE	C-N-CA	7.84	135.78	122.15
1	C	1149	LYS	N-CA-C	-7.83	102.36	108.78
1	C	1023	ARG	CA-C-N	7.82	129.62	119.84
1	C	1023	ARG	C-N-CA	7.82	129.62	119.84
1	C	1113	LYS	N-CA-C	7.79	124.85	113.40
1	C	971	MET	N-CA-C	7.77	119.44	109.72
1	C	525	PHE	CB-CA-C	-7.76	97.90	110.79
1	C	446	LYS	CA-C-N	7.76	134.08	122.67
1	C	446	LYS	C-N-CA	7.76	134.08	122.67
1	C	1108	SER	N-CA-C	7.76	121.86	109.83
1	C	390	HIS	N-CA-C	7.75	121.19	109.41
1	C	346	HIS	N-CA-CB	-7.68	97.77	110.68

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	921	ASP	CA-C-N	-7.68	111.41	123.24
1	C	921	ASP	C-N-CA	-7.68	111.41	123.24
1	C	849	MET	CB-CG-SD	-7.67	89.69	112.70
1	C	106	GLN	N-CA-C	7.64	120.16	109.15
1	C	575	TRP	N-CA-C	7.63	119.24	111.07
1	C	719	ASN	CB-CA-C	-7.62	96.30	110.01
1	C	774	LEU	N-CA-C	7.61	120.54	111.33
1	C	397	LEU	CA-C-N	7.59	129.19	119.78
1	C	397	LEU	C-N-CA	7.59	129.19	119.78
1	C	83	GLN	CA-C-N	-7.59	110.67	122.59
1	C	83	GLN	C-N-CA	-7.59	110.67	122.59
1	C	670	ASP	CB-CA-C	-7.58	97.79	109.99
1	C	864	HIS	N-CA-C	7.55	119.51	111.28
1	C	83	GLN	N-CA-C	-7.55	100.57	110.53
1	C	1325	VAL	N-CA-C	7.55	125.04	109.34
1	C	461	ARG	N-CA-CB	7.49	121.13	110.12
1	C	1003	ARG	N-CA-C	7.48	119.22	111.14
1	C	859	ILE	CB-CA-C	7.46	122.23	112.24
1	C	1181	SER	CA-C-N	7.45	135.76	121.54
1	C	1181	SER	C-N-CA	7.45	135.76	121.54
1	C	95	THR	N-CA-C	7.43	121.00	108.90
1	C	841	ASP	CA-C-N	7.42	135.71	121.54
1	C	841	ASP	C-N-CA	7.42	135.71	121.54
1	C	1122	PRO	N-CA-C	7.40	119.73	110.70
1	C	864	HIS	CB-CA-C	-7.38	98.53	110.79
1	C	545	PRO	CB-CA-C	-7.32	101.43	113.06
1	C	875	THR	CA-C-N	7.30	134.84	121.70
1	C	875	THR	C-N-CA	7.30	134.84	121.70
1	C	343	ILE	CB-CA-C	-7.30	101.67	111.15
1	C	715	ASN	N-CA-C	-7.30	95.15	107.99
1	C	952	PHE	N-CA-C	7.29	118.87	111.07
1	C	700	ASP	O-C-N	7.28	133.05	122.13
1	C	1167	ASP	N-CA-CB	-7.26	98.22	110.49
1	C	1044	ARG	N-CA-C	7.26	121.58	112.87
1	C	1221	PRO	N-CA-C	7.26	127.42	112.47
1	C	1298	PHE	N-CA-C	7.25	120.77	107.73
1	C	925	VAL	CA-C-N	7.22	130.68	120.42
1	C	925	VAL	C-N-CA	7.22	130.68	120.42
1	C	611	GLY	N-CA-C	7.20	121.76	112.54
1	C	460	ALA	CA-C-O	-7.19	113.27	120.82
1	C	638	THR	CB-CA-C	-7.18	98.65	110.85
1	C	1187	HIS	N-CA-C	7.15	120.64	107.99

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	610	GLN	N-CA-C	7.14	120.11	111.40
1	C	926	VAL	N-CA-C	7.13	117.92	110.72
1	C	468	ALA	N-CA-C	-7.12	103.60	111.36
1	C	1087	ASP	N-CA-C	7.12	120.98	111.30
1	C	1191	GLU	N-CA-C	-7.12	95.64	110.80
1	C	1270	LEU	O-C-N	-7.09	114.94	123.16
1	C	976	THR	CA-C-N	-7.09	110.08	120.28
1	C	976	THR	C-N-CA	-7.09	110.08	120.28
1	C	640	GLN	N-CA-C	7.08	119.97	110.35
1	C	874	ILE	CA-C-N	7.04	134.99	121.54
1	C	874	ILE	C-N-CA	7.04	134.99	121.54
1	C	1191	GLU	O-C-N	7.04	131.95	122.59
1	C	460	ALA	CA-C-N	-6.99	110.91	120.28
1	C	460	ALA	C-N-CA	-6.99	110.91	120.28
1	C	706	TYR	CB-CA-C	-6.98	99.20	110.79
1	C	722	GLY	N-CA-C	-6.98	104.40	112.50
1	C	1188	VAL	CB-CA-C	-6.95	99.89	111.29
1	C	547	GLU	CB-CA-C	-6.94	99.26	110.79
1	C	111	PRO	CA-C-O	-6.93	113.53	121.56
1	C	928	ARG	CB-CA-C	-6.92	99.96	110.90
1	C	534	ASN	CB-CA-C	-6.90	100.04	110.88
1	C	1026	GLY	CA-C-O	6.86	128.36	119.44
1	C	119	ASP	CA-C-N	6.85	134.31	121.97
1	C	119	ASP	C-N-CA	6.85	134.31	121.97
1	C	520	PHE	N-CA-C	6.84	118.82	111.36
1	C	630	ASN	CA-C-N	6.83	127.07	119.90
1	C	630	ASN	C-N-CA	6.83	127.07	119.90
1	B	478	ILE	CB-CA-C	-6.83	103.14	111.88
1	C	948	ILE	N-CA-C	6.82	123.52	109.34
1	C	77	THR	N-CA-C	-6.75	98.92	109.72
1	C	1212	ARG	C-N-CD	-6.72	97.44	125.00
1	C	699	THR	CA-C-N	-6.72	110.83	122.79
1	C	699	THR	C-N-CA	-6.72	110.83	122.79
1	C	708	THR	N-CA-CB	6.72	119.72	109.91
1	B	466	VAL	CB-CA-C	-6.71	103.08	112.14
1	C	1025	ASP	CB-CA-C	-6.71	97.08	110.42
1	C	96	ILE	CB-CA-C	-6.70	101.34	111.33
1	C	577	GLN	N-CA-CB	6.69	121.80	110.49
1	C	718	ASN	N-CA-C	-6.69	96.31	108.02
1	C	1032	ASP	N-CA-C	-6.69	100.27	110.30
1	C	946	LEU	N-CA-C	6.68	119.41	108.52
1	C	136	VAL	N-CA-C	6.68	117.25	107.37

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	752	VAL	N-CA-C	6.68	116.78	110.30
1	C	617	ASP	N-CA-C	6.66	119.37	111.71
1	C	620	ILE	CB-CA-C	6.66	121.41	112.22
1	C	840	ASP	N-CA-C	6.65	121.00	113.02
1	C	585	PHE	CB-CA-C	6.64	119.17	109.48
1	C	812	LYS	N-CA-C	6.63	118.51	111.28
1	C	1037	ILE	CA-C-N	6.62	129.05	120.44
1	C	1037	ILE	C-N-CA	6.62	129.05	120.44
1	C	298	PRO	CA-C-N	6.60	134.15	121.54
1	C	298	PRO	C-N-CA	6.60	134.15	121.54
1	C	972	PRO	CB-CA-C	-6.59	102.96	111.46
1	C	102	VAL	N-CA-C	-6.58	98.05	107.98
1	C	1330	ILE	N-CA-C	-6.57	104.35	110.53
1	C	1267	THR	N-CA-C	-6.56	96.94	108.23
1	C	1154	ASN	N-CA-C	6.56	118.09	111.07
1	C	646	ASN	N-CA-C	6.56	124.77	110.80
1	C	490	PHE	N-CA-C	6.54	121.54	112.45
1	C	1271	SER	CB-CA-C	-6.53	97.44	110.42
1	C	1236	ILE	N-CA-C	6.52	122.91	109.34
1	C	488	PRO	CA-C-O	-6.52	113.91	121.34
1	C	148	GLN	N-CA-CB	-6.52	100.33	110.11
1	C	143	VAL	CA-C-N	6.51	133.98	121.54
1	C	143	VAL	C-N-CA	6.51	133.98	121.54
1	C	630	ASN	N-CA-C	-6.50	95.44	109.81
1	C	730	ASP	N-CA-C	6.48	124.59	110.80
1	C	1286	VAL	CB-CA-C	-6.47	100.67	111.29
1	C	769	GLN	N-CA-C	-6.46	100.82	110.06
1	C	1037	ILE	CB-CA-C	-6.44	104.50	111.59
1	C	970	LEU	N-CA-C	6.44	119.29	111.82
1	C	484	ARG	CA-C-N	-6.43	111.02	120.28
1	C	484	ARG	C-N-CA	-6.43	111.02	120.28
1	C	828	ASP	N-CA-C	6.43	120.70	112.86
1	C	1300	ASN	CB-CA-C	-6.42	101.28	111.17
1	C	494	GLU	N-CA-C	6.42	119.47	109.52
1	C	747	ARG	N-CA-C	6.42	119.59	109.96
1	C	1259	ALA	C-N-CD	-6.42	98.69	125.00
1	C	540	PHE	CA-C-O	-6.42	113.75	120.55
1	C	1037	ILE	N-CA-C	6.41	117.04	110.05
1	C	653	ARG	CB-CA-C	-6.41	100.82	110.88
1	C	673	GLN	N-CA-C	-6.40	104.16	112.23
1	C	1304	MET	CB-CG-SD	-6.40	93.49	112.70
1	C	975	SER	N-CA-C	-6.40	103.53	108.78

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	469	ARG	N-CA-CB	-6.39	102.73	110.53
1	C	141	LEU	N-CA-C	6.39	120.53	107.69
1	C	607	PHE	CB-CA-C	-6.39	100.56	110.78
1	C	449	PHE	C-N-CD	-6.36	98.92	125.00
1	C	1004	PHE	N-CA-C	6.36	120.74	112.92
1	C	957	PHE	O-C-N	-6.34	115.56	122.79
1	C	1075	ARG	CA-C-O	-6.34	113.52	120.43
1	C	775	VAL	CA-CB-CG2	6.34	121.18	110.40
1	C	698	HIS	CB-CA-C	-6.33	100.09	110.85
1	C	997	TYR	N-CA-C	-6.33	97.94	108.32
1	C	305	THR	CB-CA-C	-6.32	99.22	109.72
1	C	311	ASN	CA-C-O	-6.32	114.18	120.82
1	C	1281	VAL	CG1-CB-CG2	6.28	124.61	110.80
1	C	317	MET	N-CA-C	6.27	118.92	111.71
1	C	315	THR	CA-C-O	-6.26	113.91	120.55
1	C	956	ASP	CB-CA-C	6.26	121.17	110.79
1	C	673	GLN	CA-C-N	6.25	128.66	120.28
1	C	673	GLN	C-N-CA	6.25	128.66	120.28
1	C	1069	ARG	N-CA-C	6.24	119.84	112.72
1	C	596	GLY	N-CA-C	6.24	120.22	112.73
1	C	459	ALA	CA-C-O	-6.23	113.06	120.10
1	C	83	GLN	O-C-N	-6.23	115.69	122.79
1	C	390	HIS	CA-C-N	-6.22	112.10	121.87
1	C	390	HIS	C-N-CA	-6.22	112.10	121.87
1	C	488	PRO	CB-CA-C	-6.22	103.43	111.46
1	C	1179	THR	C-N-CD	-6.22	99.49	125.00
1	C	449	PHE	CA-C-N	6.21	127.61	119.84
1	C	449	PHE	C-N-CA	6.21	127.61	119.84
1	C	756	THR	CB-CA-C	-6.21	100.48	110.79
1	C	1160	ILE	N-CA-C	-6.21	106.71	111.62
1	C	856	LEU	CB-CA-C	-6.21	101.40	110.96
1	C	627	ALA	N-CA-C	6.21	119.02	111.82
1	C	1229	LEU	N-CA-C	6.21	117.92	111.03
1	C	811	SER	CA-C-O	-6.20	114.31	120.82
1	C	456	ASN	N-CA-CB	-6.20	99.78	111.00
1	C	473	ALA	N-CA-C	-6.20	100.48	109.59
1	C	1145	ALA	N-CA-C	6.19	123.99	110.80
1	C	671	ASP	N-CA-CB	6.18	119.06	109.85
1	C	1225	GLU	CA-CB-CG	6.18	126.45	114.10
1	C	320	GLN	N-CA-C	6.16	120.41	113.02
1	C	118	THR	CA-C-O	-6.14	113.73	120.36
1	C	534	ASN	N-CA-C	6.14	117.64	111.07

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	119	ASP	CA-CB-CG	6.13	118.73	112.60
1	C	726	THR	N-CA-C	6.13	121.22	108.53
1	C	847	ILE	N-CA-C	-6.13	98.70	107.77
1	C	647	GLU	CB-CA-C	-6.12	100.63	110.79
1	C	864	HIS	CA-C-N	6.11	130.91	121.19
1	C	864	HIS	C-N-CA	6.11	130.91	121.19
1	C	1244	ALA	N-CA-C	6.11	118.65	111.02
1	C	852	TYR	CA-C-O	-6.09	114.38	120.90
1	C	1275	ASP	CA-C-N	6.09	130.39	121.31
1	C	1275	ASP	C-N-CA	6.09	130.39	121.31
1	C	707	ALA	CA-C-O	-6.09	114.10	120.55
1	C	761	SER	CA-C-O	6.08	126.79	119.43
1	C	589	PHE	N-CA-C	6.08	120.69	113.16
1	C	506	SER	CA-CB-OG	-6.07	98.97	111.10
1	C	1038	GLU	CB-CA-C	-6.06	101.36	110.88
1	C	696	VAL	N-CA-CB	6.05	118.77	110.54
1	C	853	ASP	N-CA-C	6.05	117.87	111.28
1	C	926	VAL	CB-CA-C	-6.05	103.88	112.22
1	C	507	SER	CA-C-N	-6.04	110.39	120.30
1	C	507	SER	C-N-CA	-6.04	110.39	120.30
1	C	1308	ASN	N-CA-C	6.04	123.67	110.80
1	C	1305	MET	CB-CG-SD	-6.04	94.59	112.70
1	C	123	GLU	N-CA-C	6.02	118.96	110.23
1	C	1215	PRO	CB-CA-C	-6.01	103.08	110.95
1	C	105	MET	CA-C-O	-6.00	114.59	121.19
1	C	115	GLN	N-CA-C	-5.99	100.65	109.81
1	C	121	PHE	N-CA-CB	-5.99	100.37	110.49
1	C	440	ILE	N-CA-C	-5.95	99.22	108.44
1	C	1070	ARG	N-CA-C	-5.92	95.78	107.69
1	C	1212	ARG	CA-C-N	5.92	127.24	119.84
1	C	1212	ARG	C-N-CA	5.92	127.24	119.84
1	C	361	ASN	N-CA-C	-5.92	104.96	111.82
1	C	930	ALA	N-CA-C	-5.92	98.08	108.20
1	C	687	LEU	CB-CA-C	5.91	120.59	110.79
1	C	904	GLY	N-CA-C	5.90	119.81	112.73
1	C	157	ILE	CA-C-N	5.89	128.46	120.44
1	C	157	ILE	C-N-CA	5.89	128.46	120.44
1	C	793	TYR	C-N-CD	-5.89	100.84	125.00
1	C	674	LYS	CD-CE-NZ	-5.89	93.06	111.90
1	C	745	ILE	CB-CA-C	-5.88	103.34	110.99
1	C	560	ILE	CB-CA-C	-5.87	103.09	111.31
1	C	939	ASN	N-CA-C	5.87	117.75	111.36

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	585	PHE	O-C-N	5.86	125.36	121.14
1	C	498	ILE	CB-CA-C	-5.85	103.12	111.31
1	C	897	TYR	N-CA-C	5.84	118.99	110.17
1	C	378	ALA	CA-C-O	-5.84	114.36	120.55
1	C	1122	PRO	C-N-CD	-5.84	101.07	125.00
1	C	625	PRO	N-CA-CB	-5.83	99.65	102.92
1	C	307	VAL	N-CA-CB	-5.83	104.12	111.41
1	C	310	LEU	CA-C-O	-5.83	114.37	120.55
1	C	1214	GLU	CA-C-N	5.82	125.79	120.03
1	C	1214	GLU	C-N-CA	5.82	125.79	120.03
1	C	546	VAL	N-CA-C	5.82	116.00	110.42
1	C	160	PRO	CA-C-O	-5.80	114.66	122.08
1	C	844	ASP	N-CA-CB	5.79	120.28	110.49
1	C	595	ALA	N-CA-C	-5.78	98.48	110.80
1	C	767	LEU	CA-CB-CG	5.78	136.53	116.30
1	C	752	VAL	CB-CA-C	-5.76	104.61	111.81
1	C	875	THR	N-CA-CB	5.75	120.21	110.49
1	C	108	LYS	CA-C-N	5.74	131.10	121.92
1	C	108	LYS	C-N-CA	5.74	131.10	121.92
1	C	692	ASP	N-CA-C	5.74	117.21	111.07
1	C	1296	ILE	CB-CA-C	5.74	118.03	110.91
1	C	1166	VAL	CB-CA-C	-5.74	101.88	111.29
1	C	445	GLU	N-CA-C	5.71	118.52	110.23
1	C	1149	LYS	CB-CA-C	-5.70	108.87	117.07
1	C	796	PRO	N-CA-C	-5.69	105.62	113.53
1	C	342	THR	O-C-N	5.69	129.72	123.01
1	C	878	SER	CA-C-N	5.68	135.66	121.80
1	C	878	SER	C-N-CA	5.68	135.66	121.80
1	C	298	PRO	N-CA-C	-5.68	100.78	112.47
1	C	413	MET	CB-CG-SD	-5.68	95.67	112.70
1	C	767	LEU	CB-CA-C	-5.67	98.83	109.72
1	C	956	ASP	N-CA-C	-5.67	105.10	111.28
1	C	138	PHE	CB-CA-C	-5.67	99.92	109.72
1	C	144	ASN	CB-CA-C	5.67	121.70	110.42
1	C	557	THR	N-CA-CB	-5.66	102.20	111.66
1	C	1325	VAL	CB-CA-C	-5.66	102.00	111.29
1	C	104	ILE	N-CA-C	5.64	121.07	109.34
1	C	1031	TYR	O-C-N	5.64	130.56	121.53
1	C	947	GLU	CB-CA-C	-5.63	101.44	110.79
1	C	1275	ASP	CB-CA-C	-5.63	98.73	109.66
1	C	638	THR	CA-C-N	5.63	132.29	121.54
1	C	638	THR	C-N-CA	5.63	132.29	121.54

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	1035	ILE	CG1-CB-CG2	-5.63	93.82	110.70
1	C	639	ASN	N-CA-CB	5.61	119.97	110.49
1	C	791	ILE	CB-CA-C	-5.61	102.73	111.26
1	C	638	THR	CA-C-O	-5.60	114.49	120.42
1	C	1323	ASP	N-CA-C	5.60	122.72	110.80
1	C	528	ILE	CB-CA-C	-5.59	104.22	111.88
1	C	1143	GLU	N-CA-C	-5.59	97.67	107.73
1	C	436	SER	CA-C-O	-5.58	114.51	120.42
1	C	1106	PHE	N-CA-C	-5.57	98.93	110.80
1	C	157	ILE	CB-CA-C	-5.57	102.86	110.77
1	C	129	ALA	CA-C-N	5.56	132.16	121.54
1	C	129	ALA	C-N-CA	5.56	132.16	121.54
1	C	1275	ASP	N-CA-C	5.56	118.63	109.85
1	C	1291	LEU	N-CA-C	-5.55	101.63	109.96
1	C	1281	VAL	N-CA-C	5.55	120.89	109.34
1	C	1202	PHE	CB-CA-C	5.55	119.00	109.51
1	C	1024	PRO	N-CA-C	5.55	123.90	112.47
1	C	130	LEU	N-CA-CB	5.54	119.86	110.49
1	C	826	GLY	N-CA-C	-5.54	100.08	110.77
1	C	315	THR	N-CA-CB	5.53	118.25	110.12
1	C	721	SER	CA-C-O	-5.53	116.01	122.37
1	C	1109	SER	N-CA-C	5.53	122.58	110.80
1	C	815	LEU	CA-C-O	-5.53	113.31	118.73
1	C	601	ILE	O-C-N	-5.53	116.29	121.87
1	C	1232	PRO	CA-C-N	-5.53	114.94	123.17
1	C	1232	PRO	C-N-CA	-5.53	114.94	123.17
1	C	156	GLN	CB-CA-C	-5.52	99.43	110.42
1	C	949	ALA	N-CA-C	5.51	119.04	111.54
1	C	795	ASP	CA-C-O	5.51	125.90	120.17
1	C	890	THR	N-CA-C	5.51	119.10	112.93
1	C	810	LEU	CA-C-N	-5.50	113.29	120.44
1	C	810	LEU	C-N-CA	-5.50	113.29	120.44
1	C	1014	MET	N-CA-C	-5.49	96.66	107.69
1	C	430	ASN	N-CA-C	5.48	119.97	113.28
1	C	1292	GLU	N-CA-CB	5.48	119.75	110.49
1	C	585	PHE	N-CA-C	-5.47	102.04	110.58
1	C	1240	ARG	N-CA-C	5.47	122.45	110.80
1	C	1304	MET	CB-CA-C	-5.47	102.58	113.80
1	C	86	VAL	CB-CA-C	-5.45	103.00	110.96
1	C	848	ARG	CA-CB-CG	-5.44	103.21	114.10
1	C	1201	LEU	CA-CB-CG	5.43	135.31	116.30
1	C	543	TRP	N-CA-CB	-5.43	101.31	110.49

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	1139	MET	CB-CA-C	-5.43	100.71	109.72
1	C	156	GLN	N-CA-C	5.42	122.36	110.80
1	C	958	ILE	N-CA-CB	5.42	120.18	111.23
1	C	498	ILE	CB-CG1-CD1	-5.42	102.42	113.80
1	C	841	ASP	N-CA-C	5.42	117.24	108.08
1	C	557	THR	CA-C-O	-5.41	115.48	121.33
1	C	772	TYR	CA-C-N	5.41	126.60	119.84
1	C	772	TYR	C-N-CA	5.41	126.60	119.84
1	C	503	GLU	N-CA-C	5.41	119.72	113.18
1	C	624	PHE	CB-CA-C	5.39	117.20	109.11
1	C	1117	VAL	CB-CA-C	-5.39	103.30	111.33
1	C	699	THR	N-CA-CB	5.38	118.67	110.44
1	C	484	ARG	CA-C-O	5.38	125.56	119.27
1	C	1182	GLU	N-CA-CB	5.37	119.57	110.49
1	C	1037	ILE	O-C-N	5.37	129.23	122.52
1	C	306	GLN	CA-CB-CG	-5.37	103.36	114.10
1	C	698	HIS	N-CA-C	5.36	117.21	111.36
1	B	150	LEU	CA-C-N	5.35	131.76	121.54
1	B	150	LEU	C-N-CA	5.35	131.76	121.54
1	C	457	GLN	O-C-N	-5.35	116.45	122.12
1	C	1094	GLU	N-CA-C	5.35	122.19	110.80
1	C	860	ARG	N-CA-CB	5.34	118.07	110.16
1	C	1044	ARG	CA-C-O	5.34	125.83	119.10
1	C	583	GLU	CA-C-N	5.33	129.12	121.50
1	C	583	GLU	C-N-CA	5.33	129.12	121.50
1	C	759	ASP	N-CA-C	-5.33	101.97	109.96
1	C	859	ILE	N-CA-CB	5.32	119.45	110.56
1	C	1148	SER	CB-CA-C	-5.32	108.87	115.89
1	C	1222	ALA	O-C-N	5.32	129.67	122.59
1	C	1167	ASP	N-CA-C	5.31	122.12	110.80
1	C	851	THR	CB-CA-C	5.31	118.53	109.72
1	C	123	GLU	CA-C-O	-5.30	115.36	121.19
1	C	320	GLN	CB-CA-C	5.30	119.80	110.37
1	C	855	TYR	N-CA-CB	5.29	117.90	110.12
1	C	1249	ASN	N-CA-C	-5.29	99.53	110.80
1	C	998	GLY	CA-C-N	-5.28	111.36	120.97
1	C	998	GLY	C-N-CA	-5.28	111.36	120.97
1	C	774	LEU	CA-C-O	-5.26	114.95	120.63
1	C	1044	ARG	CA-C-N	5.26	131.59	121.54
1	C	1044	ARG	C-N-CA	5.26	131.59	121.54
1	C	997	TYR	O-C-N	-5.25	117.44	123.42
1	C	708	THR	CA-C-O	-5.24	115.50	121.00

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	881	ASP	O-C-N	5.24	129.05	122.19
1	B	1317	VAL	CA-C-O	-5.24	115.30	120.90
1	C	86	VAL	N-CA-CB	-5.24	104.86	111.46
1	C	447	ARG	CA-C-N	-5.23	111.54	121.54
1	C	447	ARG	C-N-CA	-5.23	111.54	121.54
1	C	546	VAL	O-C-N	5.23	127.03	121.91
1	C	447	ARG	O-C-N	5.22	131.23	121.63
1	C	632	GLN	CA-C-O	5.22	127.35	121.51
1	C	505	PRO	CA-C-O	5.21	126.64	119.18
1	C	96	ILE	CG1-CB-CG2	-5.21	95.06	110.70
1	C	1234	GLN	CA-C-N	-5.21	113.33	119.84
1	C	1234	GLN	C-N-CA	-5.21	113.33	119.84
1	C	1212	ARG	O-C-N	5.21	127.31	121.32
1	C	1245	ILE	N-CA-C	5.21	120.18	109.34
1	C	720	PHE	CA-C-N	-5.21	114.35	122.16
1	C	720	PHE	C-N-CA	-5.21	114.35	122.16
1	C	735	THR	CB-CA-C	-5.21	100.01	109.38
1	C	1274	GLY	N-CA-C	5.21	125.52	113.18
1	C	1153	ASP	N-CA-C	-5.20	105.69	111.36
1	C	444	SER	CA-C-N	5.20	128.09	120.71
1	C	444	SER	C-N-CA	5.20	128.09	120.71
1	C	429	ILE	N-CA-CB	5.19	118.37	110.58
1	C	143	VAL	CB-CA-C	-5.19	102.77	111.29
1	C	1146	GLY	CA-C-N	5.19	131.46	121.54
1	C	1146	GLY	C-N-CA	5.19	131.46	121.54
1	C	151	SER	CA-C-O	-5.19	114.24	120.10
1	C	737	PRO	CB-CA-C	-5.18	104.13	112.21
1	C	602	ALA	N-CA-C	5.18	116.61	111.07
1	C	272	THR	CA-C-N	-5.17	113.37	119.84
1	C	272	THR	C-N-CA	-5.17	113.37	119.84
1	C	565	GLU	CB-CA-C	5.17	120.72	110.42
1	C	1248	HIS	N-CA-CB	-5.15	102.61	110.85
1	C	121	PHE	CA-C-O	-5.14	113.15	120.51
1	C	736	SER	CA-C-N	5.14	124.94	119.28
1	C	736	SER	C-N-CA	5.14	124.94	119.28
1	C	586	PRO	CA-C-O	5.14	129.96	120.60
1	C	1083	ASP	CA-C-N	-5.13	113.42	119.84
1	C	1083	ASP	C-N-CA	-5.13	113.42	119.84
1	C	1134	ARG	CA-C-N	-5.13	113.42	119.84
1	C	1134	ARG	C-N-CA	-5.13	113.42	119.84
1	C	502	PHE	N-CA-C	5.13	118.52	111.54
1	C	709	MET	CB-CG-SD	-5.13	97.32	112.70

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	1155	ILE	CB-CA-C	-5.12	104.22	112.16
1	C	639	ASN	CA-C-N	5.12	128.49	120.75
1	C	639	ASN	C-N-CA	5.12	128.49	120.75
1	C	875	THR	CB-CA-C	5.11	120.59	110.42
1	C	1032	ASP	CB-CA-C	5.11	117.17	110.06
1	C	916	LEU	CB-CA-C	-5.11	101.24	109.72
1	C	1135	PRO	CA-N-CD	-5.11	104.85	112.00
1	B	461	ARG	N-CA-C	-5.11	105.79	111.36
1	C	691	PHE	CA-C-O	-5.09	115.15	120.55
1	C	1071	PHE	CB-CA-C	-5.09	100.80	109.51
1	B	464	SER	N-CA-C	-5.08	105.74	111.28
1	C	85	ASP	CA-C-N	5.08	129.73	123.12
1	C	85	ASP	C-N-CA	5.08	129.73	123.12
1	C	1128	TYR	CA-C-N	-5.08	113.50	119.84
1	C	1128	TYR	C-N-CA	-5.08	113.50	119.84
1	C	1276	LEU	N-CA-C	5.08	117.46	110.35
1	C	938	ASN	N-CA-CB	-5.07	102.50	110.46
1	C	710	SER	CA-C-N	-5.07	116.24	123.03
1	C	710	SER	C-N-CA	-5.07	116.24	123.03
1	C	796	PRO	CB-CA-C	-5.05	104.29	112.62
1	B	467	LYS	N-CA-C	-5.04	105.79	111.28
1	B	504	ASP	CA-C-N	5.04	132.22	120.89
1	B	504	ASP	C-N-CA	5.04	132.22	120.89
1	C	162	GLY	N-CA-C	5.04	118.32	111.72
1	C	493	HIS	N-CA-C	5.04	117.46	109.50
1	C	813	LEU	CA-C-O	5.03	126.10	120.82
1	B	1236	ILE	N-CA-C	5.03	119.79	109.34
1	C	137	ILE	CB-CA-C	-5.01	104.74	112.05
1	C	383	SER	CA-C-N	5.01	127.96	120.90
1	C	383	SER	C-N-CA	5.01	127.96	120.90
1	C	857	SER	CA-C-N	-5.01	113.63	120.44
1	C	857	SER	C-N-CA	-5.01	113.63	120.44
1	C	98	ASN	CB-CA-C	-5.01	101.92	111.48
1	C	1043	SER	O-C-N	5.01	129.25	122.59

There are no chirality outliers.

All (39) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	1193	ILE	Peptide
1	B	1235	PRO	Peptide
1	B	1236	ILE	Peptide

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Res	Type	Group
1	B	261	ASP	Peptide
1	B	506	SER	Peptide
1	B	717	THR	Peptide
1	B	825	SER	Peptide
1	B	875	THR	Peptide
1	B	895	VAL	Peptide
1	C	1031	TYR	Mainchain
1	C	1068	ALA	Mainchain
1	C	1093	PRO	Mainchain
1	C	121	PHE	Mainchain
1	C	171	GLU	Mainchain
1	C	172	ASP	Mainchain
1	C	173	GLN	Mainchain
1	C	185	ALA	Mainchain
1	C	244	SER	Mainchain
1	C	279	SER	Mainchain
1	C	317	MET	Mainchain
1	C	334	LEU	Mainchain
1	C	351	ASP	Mainchain
1	C	361	ASN	Mainchain
1	C	398	ARG	Peptide
1	C	436	SER	Mainchain
1	C	448	TYR	Mainchain
1	C	449	PHE	Mainchain
1	C	456	ASN	Mainchain
1	C	503	GLU	Mainchain
1	C	519	LEU	Mainchain
1	C	533	GLN	Mainchain
1	C	635	ILE	Mainchain,Peptide
1	C	661	ASN	Mainchain
1	C	662	VAL	Mainchain
1	C	697	ALA	Mainchain
1	C	768	CYS	Mainchain
1	C	897	TYR	Mainchain
1	C	997	TYR	Mainchain

## 5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	9058	0	8964	546	0
1	C	9827	0	9719	2017	0
All	All	18885	0	18683	2518	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 67.

All (2518) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:835:TYR:CE1	1:C:942:HIS:HB3	1.27	1.68
1:C:1278:TYR:CD2	1:C:1288:ILE:HG13	1.23	1.64
1:C:910:LEU:HD23	1:C:915:VAL:CG2	1.27	1.63
1:C:233:VAL:CG2	1:C:234:PRO:HD2	1.28	1.62
1:C:1093:PRO:HG2	1:C:1096:TYR:CE1	1.30	1.61
1:C:233:VAL:HG11	1:C:981:HIS:CE1	1.31	1.60
1:C:829:SER:CB	1:C:965:ARG:HD2	1.15	1.59
1:C:838:GLU:CB	1:C:934:LEU:HB2	1.12	1.55
1:C:1278:TYR:HD2	1:C:1288:ILE:CG1	1.15	1.55
1:C:910:LEU:CD2	1:C:915:VAL:HG23	1.23	1.55
1:C:835:TYR:CE2	1:C:925:VAL:CG2	1.88	1.53
1:C:1080:THR:C	1:C:1227:MET:HG2	1.28	1.53
1:C:835:TYR:CE2	1:C:925:VAL:HG21	1.00	1.52
1:C:838:GLU:CG	1:C:934:LEU:C	1.81	1.50
1:C:838:GLU:HB2	1:C:934:LEU:CB	1.42	1.49
1:C:835:TYR:CD2	1:C:925:VAL:HG21	1.49	1.47
1:C:301:LEU:HD13	1:C:305:THR:CG2	1.41	1.46
1:C:230:ASP:CB	1:C:985:ARG:NE	1.76	1.46
1:B:469:ARG:NH1	1:B:498:ILE:CD1	1.78	1.45
1:C:1080:THR:HA	1:C:1227:MET:CG	0.98	1.45
1:C:829:SER:CB	1:C:965:ARG:CD	1.92	1.45
1:C:843:LEU:HD11	1:C:943:GLU:CG	1.01	1.45
1:C:841:ASP:H	1:C:940:ARG:NH1	1.07	1.44
1:C:180:LEU:HD22	1:C:306:GLN:NE2	1.29	1.44
1:C:449:PHE:HB2	1:C:683:TRP:NE1	1.24	1.44
1:C:1080:THR:CA	1:C:1227:MET:HG2	1.22	1.43
1:C:837:THR:O	1:C:934:LEU:CD1	1.67	1.43
1:C:1080:THR:CA	1:C:1227:MET:CG	1.78	1.43
1:C:233:VAL:HG11	1:C:981:HIS:NE2	1.18	1.43
1:C:843:LEU:CD1	1:C:943:GLU:HG3	0.95	1.42
1:B:442:PRO:HB2	1:B:475:ILE:CD1	1.45	1.42
1:C:838:GLU:HG3	1:C:934:LEU:CA	1.50	1.42

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:233:VAL:HG22	1:C:234:PRO:CD	1.49	1.41
1:B:389:PHE:CE1	1:B:1319:ARG:HG3	1.54	1.39
1:C:248:VAL:CG1	1:C:970:LEU:HB3	1.53	1.39
1:C:81:ALA:HB2	1:C:170:TYR:CE2	1.59	1.37
1:C:838:GLU:CB	1:C:934:LEU:CB	1.96	1.36
1:C:1093:PRO:CG	1:C:1096:TYR:CE1	2.08	1.36
1:C:449:PHE:CB	1:C:683:TRP:NE1	1.87	1.35
1:C:1214:GLU:CB	1:C:1215:PRO:CD	1.96	1.34
1:C:835:TYR:CD1	1:C:942:HIS:HB3	1.60	1.34
1:C:233:VAL:CG1	1:C:981:HIS:CE1	2.08	1.33
1:C:449:PHE:CB	1:C:683:TRP:HE1	1.39	1.33
1:C:1219:ASP:OD1	1:C:1220:PRO:HD2	1.16	1.33
1:C:835:TYR:CE1	1:C:942:HIS:CB	2.12	1.32
1:C:338:ARG:CG	1:C:342:THR:HG22	1.57	1.32
1:B:135:LYS:CE	1:C:468:ALA:O	1.77	1.32
1:C:383:SER:OG	1:C:796:PRO:CG	1.78	1.32
1:C:233:VAL:CG1	1:C:981:HIS:NE2	1.91	1.31
1:C:838:GLU:HG3	1:C:934:LEU:C	0.90	1.31
1:C:230:ASP:HB3	1:C:985:ARG:CD	1.59	1.31
1:C:864:HIS:CE1	1:C:1030:ARG:NH2	2.01	1.29
1:C:1109:SER:OG	1:C:1118:THR:HG21	1.19	1.29
1:C:835:TYR:CZ	1:C:925:VAL:HG21	1.69	1.28
1:C:151:SER:HB3	1:C:400:GLU:OE1	1.24	1.28
1:C:230:ASP:CG	1:C:985:ARG:HD3	1.57	1.27
1:C:836:GLN:CB	1:C:940:ARG:HG2	1.62	1.27
1:C:230:ASP:CB	1:C:985:ARG:HE	1.36	1.27
1:C:836:GLN:HB2	1:C:940:ARG:CG	1.62	1.27
1:C:230:ASP:CG	1:C:985:ARG:CD	2.07	1.26
1:C:1089:VAL:HG23	1:C:1232:PRO:O	1.30	1.26
1:C:1214:GLU:HB3	1:C:1215:PRO:CD	1.59	1.26
1:C:230:ASP:C	1:C:985:ARG:HG2	1.58	1.26
1:C:445:GLU:OE2	1:C:447:ARG:HG2	1.27	1.26
1:C:829:SER:HB2	1:C:965:ARG:CD	1.52	1.26
1:C:230:ASP:OD1	1:C:985:ARG:HD3	1.30	1.26
1:B:442:PRO:CB	1:B:475:ILE:HD11	1.66	1.26
1:C:835:TYR:CZ	1:C:925:VAL:CG2	2.20	1.25
1:C:910:LEU:CD2	1:C:915:VAL:CG2	1.96	1.25
1:C:838:GLU:CG	1:C:935:GLN:N	1.98	1.25
1:C:186:ASP:OD1	1:C:279:SER:N	1.69	1.25
1:C:446:LYS:HD3	1:C:448:TYR:OH	1.34	1.25
1:C:659:LEU:O	1:C:662:VAL:HG23	1.27	1.25

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:153:ASP:OD2	1:C:401:LEU:HB2	1.10	1.24
1:C:450:PRO:HA	1:C:454:GLU:CG	1.67	1.24
1:C:180:LEU:CD2	1:C:306:GLN:NE2	2.01	1.23
1:C:830:VAL:CG2	1:C:947:GLU:CB	2.15	1.23
1:B:274:MET:HE1	1:C:978:GLN:OE1	1.11	1.23
1:C:1191:GLU:O	1:C:1195:THR:OG1	1.55	1.23
1:C:225:ILE:HG21	1:C:247:TYR:CD1	1.73	1.22
1:B:135:LYS:HE2	1:C:468:ALA:O	1.30	1.22
1:C:372:ALA:HB1	1:C:1315:MET:CE	1.68	1.22
1:C:449:PHE:HB2	1:C:683:TRP:CD1	1.74	1.22
1:C:230:ASP:CG	1:C:985:ARG:NE	1.95	1.22
1:C:660:ALA:O	1:C:662:VAL:N	1.72	1.22
1:C:1119:TYR:O	1:C:1127:ALA:O	1.54	1.22
1:C:830:VAL:CG2	1:C:947:GLU:HB2	1.68	1.22
1:C:230:ASP:CB	1:C:985:ARG:CD	2.14	1.21
1:C:230:ASP:HB3	1:C:985:ARG:CG	1.68	1.21
1:C:892:VAL:CG1	1:C:894:VAL:CG1	2.19	1.21
1:C:81:ALA:CB	1:C:170:TYR:CE2	2.24	1.20
1:C:446:LYS:CD	1:C:448:TYR:OH	1.88	1.20
1:C:613:LEU:CD2	1:C:632:GLN:HB3	1.71	1.20
1:C:1079:LEU:CD1	1:C:1231:TYR:OH	1.90	1.20
1:C:1214:GLU:CB	1:C:1215:PRO:HD2	1.60	1.19
1:C:845:GLU:OE2	1:C:911:ARG:NE	1.72	1.19
1:C:449:PHE:CA	1:C:683:TRP:HE1	1.54	1.19
1:C:81:ALA:CB	1:C:170:TYR:HE2	1.55	1.19
1:C:225:ILE:CG2	1:C:247:TYR:HD1	1.56	1.18
1:C:654:THR:O	1:C:658:THR:HG22	1.41	1.18
1:C:1263:TYR:CE1	1:C:1278:TYR:CE1	2.32	1.18
1:C:838:GLU:HG3	1:C:935:GLN:N	1.58	1.18
1:C:213:PHE:CB	1:C:219:ILE:HG21	1.74	1.17
1:C:251:LEU:HD23	1:C:1062:ILE:HG13	1.21	1.17
1:C:1292:GLU:O	1:C:1293:VAL:HG23	1.40	1.17
1:B:388:GLN:HB2	1:B:1320:VAL:HG11	1.18	1.17
1:B:472:GLU:HB3	1:B:761:SER:OG	1.43	1.17
1:C:230:ASP:CG	1:C:985:ARG:HE	1.49	1.17
1:C:334:LEU:HD21	1:C:366:MET:HE1	1.21	1.17
1:C:841:ASP:N	1:C:940:ARG:NH1	1.93	1.17
1:C:835:TYR:O	1:C:846:GLY:HA2	1.42	1.16
1:C:184:GLU:O	1:C:187:ASP:HB3	1.41	1.16
1:C:232:LEU:CD2	1:C:249:SER:HB3	1.74	1.16
1:C:232:LEU:HD21	1:C:249:SER:CB	1.75	1.16

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:383:SER:OG	1:C:796:PRO:HG3	1.01	1.16
1:C:240:GLY:O	1:C:242:GLU:N	1.79	1.15
1:C:660:ALA:C	1:C:662:VAL:H	1.39	1.15
1:C:407:HIS:CD2	1:C:1047:LEU:HA	1.80	1.15
1:C:829:SER:OG	1:C:965:ARG:CD	1.74	1.15
1:C:230:ASP:HB3	1:C:985:ARG:NE	1.38	1.15
1:C:406:ASP:OD1	1:C:1039:ALA:HB2	1.41	1.15
1:C:1306:THR:OG1	1:C:1308:ASN:HA	1.47	1.15
1:C:875:THR:OG1	1:C:899:SER:O	1.61	1.15
1:C:338:ARG:HG3	1:C:342:THR:CG2	1.77	1.15
1:C:1072:ASP:O	1:C:1234:GLN:NE2	1.78	1.15
1:C:837:THR:HG22	1:C:934:LEU:CD1	1.77	1.14
1:B:274:MET:CE	1:C:978:GLN:OE1	1.95	1.14
1:C:638:THR:HG21	1:C:1331:ARG:NH2	1.60	1.14
1:C:838:GLU:OE1	1:C:935:GLN:HB2	1.43	1.14
1:B:469:ARG:NH1	1:B:498:ILE:HD12	0.82	1.14
1:C:1219:ASP:OD1	1:C:1220:PRO:CD	1.94	1.14
1:C:1278:TYR:CD2	1:C:1288:ILE:CG1	1.99	1.14
1:C:233:VAL:CG1	1:C:981:HIS:CD2	2.29	1.13
1:C:362:LEU:HD12	1:C:1302:VAL:CG1	1.79	1.13
1:C:843:LEU:HD11	1:C:943:GLU:HG2	1.29	1.13
1:C:901:VAL:HG22	1:C:930:ALA:HB2	1.30	1.13
1:C:838:GLU:OE1	1:C:935:GLN:N	1.80	1.13
1:C:1000:LEU:CD2	1:C:1010:ARG:HH21	1.62	1.13
1:C:248:VAL:HG13	1:C:970:LEU:HB3	1.15	1.13
1:C:671:ASP:O	1:C:672:MET:HB3	1.49	1.13
1:C:451:GLU:OE1	1:C:685:ARG:HG3	1.46	1.13
1:C:383:SER:HG	1:C:796:PRO:CG	1.55	1.12
1:C:613:LEU:HD21	1:C:632:GLN:CB	1.79	1.12
1:C:668:VAL:CG2	1:C:673:GLN:HB3	1.78	1.12
1:C:1278:TYR:CE2	1:C:1288:ILE:HG13	1.82	1.12
1:C:713:MET:HE1	1:C:804:LEU:HD23	1.28	1.12
1:C:1079:LEU:HD11	1:C:1231:TYR:OH	0.97	1.12
1:B:472:GLU:O	1:B:761:SER:HB2	1.47	1.11
1:C:144:ASN:HB3	1:C:1318:GLU:OE1	1.47	1.11
1:C:252:LEU:HD13	1:C:971:MET:CE	1.80	1.11
1:C:323:THR:HB	1:C:1266:ASP:HB2	1.27	1.11
1:C:822:MET:HG3	1:C:1044:ARG:HD3	1.25	1.11
1:B:135:LYS:CD	1:C:468:ALA:O	1.97	1.11
1:C:843:LEU:CG	1:C:943:GLU:HG3	1.79	1.11
1:C:157:ILE:HD11	1:C:263:ARG:CG	1.80	1.11

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:338:ARG:HG2	1:C:342:THR:N	1.64	1.11
1:C:362:LEU:CD1	1:C:1302:VAL:CG1	2.29	1.11
1:C:701:HIS:HE1	1:C:791:ILE:HG23	1.12	1.10
1:C:1093:PRO:HB2	1:C:1096:TYR:CD1	1.86	1.10
1:B:469:ARG:CZ	1:B:498:ILE:HD12	1.81	1.10
1:C:879:THR:H	1:C:880:PRO:CD	1.63	1.10
1:C:1219:ASP:HB2	1:C:1220:PRO:HD3	1.33	1.10
1:C:252:LEU:HD11	1:C:823:ILE:HG21	1.29	1.09
1:C:410:ARG:NH1	1:C:1048:ASP:OD2	1.85	1.09
1:C:830:VAL:HG21	1:C:947:GLU:CB	1.77	1.09
1:C:1084:PRO:O	1:C:1208:ASP:O	1.68	1.09
1:C:478:ILE:CD1	1:C:762:ILE:HD11	1.82	1.09
1:C:841:ASP:H	1:C:940:ARG:CZ	1.65	1.09
1:C:892:VAL:CG1	1:C:894:VAL:HG13	1.80	1.09
1:B:472:GLU:CB	1:B:761:SER:OG	2.00	1.09
1:C:1171:ILE:HD11	1:C:1202:PHE:CZ	1.86	1.09
1:C:338:ARG:HG3	1:C:342:THR:HG22	1.14	1.08
1:C:338:ARG:CD	1:C:342:THR:HG22	1.83	1.08
1:C:1047:LEU:HB2	1:C:1051:ARG:HB2	1.34	1.08
1:B:135:LYS:HE3	1:C:470:ALA:H	1.06	1.08
1:C:838:GLU:CD	1:C:935:GLN:N	2.11	1.08
1:C:864:HIS:CE1	1:C:1030:ARG:HH21	1.66	1.08
1:C:342:THR:O	1:C:1305:MET:SD	2.12	1.08
1:C:528:ILE:HG21	1:C:758:ILE:HD11	1.26	1.08
1:C:1263:TYR:CZ	1:C:1278:TYR:OH	2.06	1.08
1:C:301:LEU:CD1	1:C:305:THR:CG2	2.32	1.07
1:C:362:LEU:CD1	1:C:1302:VAL:HG12	1.80	1.07
1:C:633:THR:HG21	1:C:710:SER:OG	1.53	1.07
1:C:656:VAL:HG11	1:C:688:GLU:HB3	1.27	1.07
1:C:225:ILE:HG21	1:C:247:TYR:HD1	0.97	1.07
1:C:611:GLY:O	1:C:634:TYR:CZ	2.06	1.07
1:C:148:GLN:NE2	1:C:375:ARG:HH12	1.51	1.06
1:C:713:MET:HE1	1:C:804:LEU:CD2	1.84	1.06
1:C:864:HIS:HE1	1:C:1030:ARG:NH2	1.44	1.06
1:C:1289:PRO:O	1:C:1293:VAL:HG21	1.53	1.06
1:C:310:LEU:HD21	1:C:1242:MET:HE1	1.36	1.06
1:C:450:PRO:HA	1:C:454:GLU:HG2	1.34	1.06
1:C:929:PHE:CG	1:C:936:MET:HE1	1.89	1.06
1:C:1289:PRO:O	1:C:1293:VAL:CG2	2.02	1.06
1:C:892:VAL:HG12	1:C:894:VAL:HG13	1.32	1.06
1:C:606:LEU:HD13	1:C:655:ILE:HG23	1.25	1.05

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:472:GLU:HB3	1:B:761:SER:CB	1.84	1.05
1:C:654:THR:HG22	1:C:658:THR:HG21	1.38	1.05
1:C:1263:TYR:CE1	1:C:1278:TYR:CZ	2.43	1.05
1:C:892:VAL:HG12	1:C:894:VAL:CG1	1.84	1.05
1:C:1000:LEU:CD2	1:C:1010:ARG:NH2	2.20	1.05
1:C:1179:THR:OG1	1:C:1180:PRO:HD2	1.54	1.05
1:B:461:ARG:HB2	1:B:461:ARG:HH11	1.20	1.05
1:B:388:GLN:HB2	1:B:1320:VAL:CG1	1.87	1.04
1:C:153:ASP:OD2	1:C:401:LEU:CB	2.03	1.04
1:C:251:LEU:CD2	1:C:1062:ILE:HG13	1.86	1.04
1:C:838:GLU:CG	1:C:934:LEU:HB2	1.86	1.04
1:C:839:ALA:C	1:C:940:ARG:NH1	2.14	1.04
1:B:459:ALA:O	1:B:463:VAL:HG13	1.56	1.04
1:C:1179:THR:OG1	1:C:1180:PRO:CD	2.05	1.04
1:C:1306:THR:CB	1:C:1308:ASN:H	1.63	1.04
1:C:151:SER:CB	1:C:400:GLU:OE1	2.04	1.04
1:C:736:SER:HB2	1:C:1016:ASN:O	1.57	1.04
1:C:835:TYR:CD1	1:C:942:HIS:CB	2.38	1.04
1:C:887:VAL:HG11	1:C:893:ALA:HB2	1.37	1.03
1:C:1089:VAL:HG21	1:C:1233:LEU:HA	1.38	1.03
1:C:701:HIS:CE1	1:C:791:ILE:HG23	1.94	1.03
1:C:830:VAL:CG2	1:C:947:GLU:HB3	1.83	1.03
1:C:837:THR:HG22	1:C:934:LEU:HD11	1.39	1.03
1:C:839:ALA:O	1:C:940:ARG:NH2	1.91	1.03
1:B:388:GLN:O	1:B:1320:VAL:HG12	1.56	1.03
1:C:252:LEU:CD1	1:C:971:MET:HE1	1.89	1.03
1:C:233:VAL:CG2	1:C:234:PRO:CD	2.22	1.02
1:C:879:THR:H	1:C:880:PRO:HD3	1.22	1.02
1:C:231:LEU:O	1:C:982:ALA:HA	1.59	1.02
1:C:1280:PRO:HB3	1:C:1287:GLY:HA2	1.41	1.02
1:C:157:ILE:HD11	1:C:263:ARG:HG2	1.39	1.02
1:C:668:VAL:HG21	1:C:673:GLN:HB3	1.05	1.02
1:C:874:ILE:HG21	1:C:902:ILE:HD11	1.42	1.02
1:C:1214:GLU:HB2	1:C:1215:PRO:HD2	1.02	1.02
1:C:248:VAL:HG11	1:C:970:LEU:HB3	1.41	1.02
1:C:1093:PRO:CB	1:C:1096:TYR:CE1	2.41	1.02
1:C:157:ILE:CG1	1:C:263:ARG:HG2	1.90	1.01
1:B:135:LYS:HD3	1:C:468:ALA:O	1.59	1.01
1:C:232:LEU:HD21	1:C:249:SER:HB3	1.03	1.01
1:C:450:PRO:HA	1:C:454:GLU:HG3	1.39	1.01
1:C:611:GLY:N	1:C:636:PRO:O	1.93	1.01

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:830:VAL:HG22	1:C:947:GLU:HB3	1.40	1.01
1:C:838:GLU:CG	1:C:934:LEU:CA	2.27	1.01
1:B:793:TYR:HD2	1:B:1321:ASN:ND2	1.57	1.00
1:C:929:PHE:CB	1:C:936:MET:HE1	1.91	1.00
1:B:135:LYS:HE3	1:C:470:ALA:N	1.76	1.00
1:B:469:ARG:HH12	1:B:498:ILE:HD12	1.21	1.00
1:B:469:ARG:HH11	1:B:498:ILE:CD1	1.52	1.00
1:C:822:MET:HE2	1:C:1046:PHE:HE2	1.25	1.00
1:C:301:LEU:CD1	1:C:305:THR:HG23	1.92	1.00
1:C:924:ASP:OD1	1:C:927:SER:HB2	1.61	0.99
1:C:384:MET:HA	1:C:708:THR:HG21	1.45	0.99
1:C:1171:ILE:HD11	1:C:1202:PHE:CE1	1.96	0.99
1:C:235:ILE:HD11	1:C:978:GLN:NE2	1.76	0.99
1:C:638:THR:HG21	1:C:1331:ARG:HH21	1.24	0.99
1:C:341:LYS:HG3	1:C:1306:THR:HB	1.43	0.99
1:C:362:LEU:HD12	1:C:1302:VAL:HG12	1.00	0.99
1:C:820:ILE:HG21	1:C:983:ILE:CG1	1.93	0.99
1:C:1093:PRO:CG	1:C:1096:TYR:HE1	1.65	0.99
1:C:252:LEU:HD13	1:C:971:MET:HE1	0.99	0.99
1:B:389:PHE:HE1	1:B:1319:ARG:CG	1.76	0.99
1:C:301:LEU:HD13	1:C:305:THR:HG23	1.01	0.99
1:C:879:THR:N	1:C:880:PRO:HD3	1.77	0.99
1:C:157:ILE:CD1	1:C:263:ARG:HG2	1.92	0.99
1:C:248:VAL:HG11	1:C:970:LEU:C	1.88	0.99
1:C:896:LEU:HD22	1:C:918:VAL:HG21	1.44	0.99
1:C:1219:ASP:CB	1:C:1220:PRO:HD3	1.89	0.99
1:C:1089:VAL:CG2	1:C:1232:PRO:O	2.11	0.98
1:C:835:TYR:HE2	1:C:925:VAL:HG11	1.28	0.98
1:C:243:GLN:O	1:C:246:GLU:HB2	1.61	0.98
1:C:440:ILE:HD13	1:C:478:ILE:HG21	1.43	0.98
1:C:301:LEU:HD13	1:C:305:THR:HG21	1.45	0.98
1:C:654:THR:HG22	1:C:658:THR:CG2	1.93	0.98
1:C:254:VAL:CG1	1:C:1062:ILE:HD11	1.93	0.98
1:C:835:TYR:CZ	1:C:925:VAL:HG22	1.95	0.98
1:C:1173:TYR:CD1	1:C:1204:LEU:HD12	1.98	0.98
1:C:242:GLU:HB3	1:C:1200:LYS:HD2	1.46	0.98
1:C:1109:SER:OG	1:C:1118:THR:CG2	2.12	0.98
1:C:261:ASP:O	1:C:1054:ARG:NH2	1.96	0.98
1:C:840:ASP:N	1:C:940:ARG:HH12	1.60	0.98
1:C:1093:PRO:HG2	1:C:1096:TYR:CZ	1.98	0.98
1:C:213:PHE:HB2	1:C:219:ILE:HG21	1.41	0.98

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:815:LEU:HB3	1:C:816:PRO:HD2	1.45	0.98
1:C:1000:LEU:HD22	1:C:1010:ARG:NH2	1.78	0.97
1:C:1214:GLU:HB3	1:C:1215:PRO:HD3	0.98	0.97
1:C:180:LEU:HD22	1:C:306:GLN:HE21	1.23	0.97
1:C:509:VAL:HG23	1:C:683:TRP:CZ3	1.99	0.97
1:C:879:THR:N	1:C:880:PRO:CD	2.23	0.97
1:C:148:GLN:HE21	1:C:375:ARG:NH1	1.62	0.97
1:C:554:ARG:HD2	1:C:594:LEU:HD21	1.47	0.97
1:C:451:GLU:OE1	1:C:685:ARG:CG	2.12	0.97
1:C:1137:VAL:O	1:C:1139:MET:N	1.97	0.97
1:C:452:ASN:O	1:C:453:LEU:HB2	1.64	0.97
1:C:668:VAL:HG21	1:C:673:GLN:CB	1.94	0.97
1:C:845:GLU:CD	1:C:911:ARG:HE	1.73	0.97
1:C:870:ASP:O	1:C:871:PRO:C	2.06	0.97
1:C:638:THR:CG2	1:C:1331:ARG:NH2	2.27	0.96
1:C:1155:ILE:CG2	1:C:1166:VAL:HG11	1.94	0.96
1:C:522:PRO:HG2	1:C:636:PRO:HB3	1.47	0.96
1:C:1278:TYR:HD2	1:C:1288:ILE:HG12	1.28	0.96
1:C:372:ALA:HB1	1:C:1315:MET:HE1	1.42	0.96
1:C:841:ASP:N	1:C:940:ARG:CZ	2.28	0.96
1:C:450:PRO:CA	1:C:454:GLU:HG2	1.96	0.96
1:C:963:ALA:HB3	1:C:1059:LEU:HG	1.48	0.96
1:C:862:ARG:HB3	1:C:952:PHE:CZ	2.01	0.95
1:C:929:PHE:CD2	1:C:936:MET:HE1	1.99	0.95
1:C:1031:TYR:HE2	1:C:1041:ARG:NH1	1.63	0.95
1:C:338:ARG:HG3	1:C:342:THR:CB	1.96	0.95
1:C:371:THR:O	1:C:374:ASP:N	1.98	0.95
1:C:837:THR:O	1:C:934:LEU:HD13	0.78	0.95
1:C:184:GLU:O	1:C:187:ASP:CB	2.15	0.95
1:C:372:ALA:CB	1:C:1315:MET:CE	2.43	0.95
1:C:449:PHE:O	1:C:683:TRP:HD1	1.46	0.95
1:C:659:LEU:O	1:C:662:VAL:CG2	2.15	0.95
1:C:1079:LEU:H	1:C:1079:LEU:HD12	1.27	0.95
1:C:85:ASP:OD2	1:C:161:LYS:HG3	1.65	0.95
1:C:1120:THR:O	1:C:1122:PRO:HD3	1.67	0.95
1:C:372:ALA:CB	1:C:1315:MET:HE1	1.96	0.95
1:C:910:LEU:HD21	1:C:915:VAL:HG23	1.46	0.95
1:C:321:ALA:HB3	1:C:1283:ASN:ND2	1.81	0.95
1:C:815:LEU:HD13	1:C:1051:ARG:NH2	1.81	0.95
1:C:741:TYR:CE2	1:C:1022:ILE:HD11	2.01	0.94
1:C:1080:THR:C	1:C:1227:MET:CG	2.25	0.94

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1093:PRO:HB2	1:C:1096:TYR:CE1	2.02	0.94
1:C:874:ILE:HD11	1:C:883:ILE:CD1	1.97	0.94
1:C:909:TYR:CE1	1:C:913:ASN:OD1	2.20	0.94
1:C:1121:HIS:CD2	1:C:1135:PRO:CG	2.50	0.94
1:C:1310:ARG:CZ	1:C:1310:ARG:HA	1.96	0.94
1:C:829:SER:HB3	1:C:965:ARG:HD2	1.49	0.94
1:C:1243:ARG:HB3	1:C:1258:VAL:HG22	1.47	0.94
1:C:148:GLN:NE2	1:C:375:ARG:NH1	2.15	0.94
1:C:838:GLU:OE1	1:C:935:GLN:CB	2.15	0.94
1:C:999:LYS:HB2	1:C:1008:LEU:O	1.67	0.94
1:C:1206:PHE:CD2	1:C:1236:ILE:CD1	2.50	0.94
1:C:1292:GLU:O	1:C:1293:VAL:CG2	2.14	0.94
1:B:472:GLU:CB	1:B:761:SER:CB	2.45	0.94
1:C:837:THR:C	1:C:934:LEU:HD13	1.91	0.93
1:C:1081:ASP:N	1:C:1227:MET:HG2	1.82	0.93
1:C:338:ARG:CG	1:C:342:THR:CG2	2.42	0.93
1:C:176:LYS:HG3	1:C:177:LYS:H	1.32	0.93
1:C:849:MET:HG3	1:C:919:MET:HE2	1.49	0.93
1:C:887:VAL:CG1	1:C:893:ALA:HB2	1.97	0.93
1:C:317:MET:SD	1:C:1262:SER:HB2	2.08	0.93
1:C:1134:ARG:HB3	1:C:1135:PRO:HD3	1.51	0.93
1:B:262:ASN:O	1:B:361:ASN:ND2	2.02	0.93
1:C:449:PHE:HA	1:C:683:TRP:HE1	1.32	0.93
1:C:838:GLU:CG	1:C:934:LEU:CB	2.42	0.93
1:B:389:PHE:CE1	1:B:1319:ARG:CG	2.50	0.93
1:C:233:VAL:HG13	1:C:981:HIS:CD2	2.05	0.92
1:C:259:MET:HG3	1:C:1055:LEU:HB2	1.49	0.92
1:C:226:PRO:O	1:C:250:GLY:HA3	1.70	0.92
1:C:311:ASN:O	1:C:315:THR:HG23	1.69	0.92
1:C:892:VAL:HG11	1:C:894:VAL:CG1	1.96	0.92
1:C:445:GLU:OE2	1:C:447:ARG:CG	2.17	0.92
1:B:235:ILE:HG13	1:B:978:GLN:HE21	1.33	0.92
1:C:230:ASP:CB	1:C:985:ARG:CG	2.45	0.92
1:C:822:MET:CG	1:C:1044:ARG:HD3	1.99	0.92
1:C:956:ASP:O	1:C:959:GLN:OE1	1.85	0.92
1:C:701:HIS:CE1	1:C:791:ILE:CG2	2.53	0.92
1:C:839:ALA:O	1:C:940:ARG:CZ	2.18	0.92
1:C:843:LEU:HD12	1:C:943:GLU:HG3	1.46	0.92
1:C:213:PHE:HB3	1:C:219:ILE:HG21	1.47	0.92
1:C:478:ILE:HD12	1:C:762:ILE:HD11	1.50	0.92
1:C:1121:HIS:HD2	1:C:1135:PRO:HG3	1.35	0.92

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:405:HIS:CD2	1:C:625:PRO:HA	2.03	0.92
1:B:1249:ASN:OD1	1:C:1115:ASN:OD1	1.88	0.92
1:C:230:ASP:HB2	1:C:985:ARG:HE	1.35	0.92
1:C:841:ASP:H	1:C:940:ARG:HH12	0.97	0.92
1:C:372:ALA:HB1	1:C:1315:MET:HE2	1.53	0.91
1:C:225:ILE:CG2	1:C:247:TYR:CD1	2.41	0.91
1:C:838:GLU:CD	1:C:935:GLN:H	1.76	0.91
1:C:924:ASP:CG	1:C:927:SER:HB2	1.95	0.91
1:C:935:GLN:HB3	1:C:939:ASN:HB3	1.51	0.91
1:C:528:ILE:HD13	1:C:758:ILE:HD11	1.53	0.91
1:C:701:HIS:HE1	1:C:791:ILE:CG2	1.83	0.91
1:C:1155:ILE:HG21	1:C:1166:VAL:HG11	1.51	0.91
1:C:1306:THR:C	1:C:1308:ASN:H	1.56	0.91
1:C:495:LEU:HD11	1:C:531:ASP:HB3	1.50	0.90
1:C:838:GLU:O	1:C:940:ARG:NH1	2.04	0.90
1:C:1089:VAL:CG2	1:C:1233:LEU:HA	1.98	0.90
1:C:248:VAL:CG1	1:C:970:LEU:CB	2.47	0.90
1:C:452:ASN:O	1:C:453:LEU:CD2	2.18	0.90
1:C:660:ALA:O	1:C:663:VAL:N	2.05	0.90
1:C:1279:SER:N	1:C:1280:PRO:HA	1.87	0.90
1:C:334:LEU:CD2	1:C:366:MET:HE1	2.01	0.90
1:C:1084:PRO:HD2	1:C:1085:ASP:OD1	1.72	0.90
1:C:870:ASP:O	1:C:871:PRO:O	1.89	0.90
1:C:446:LYS:HD2	1:C:448:TYR:OH	1.71	0.90
1:C:838:GLU:HB3	1:C:934:LEU:CB	2.02	0.90
1:C:1306:THR:OG1	1:C:1308:ASN:CA	2.19	0.90
1:C:87:GLU:HB2	1:C:159:ASP:O	1.72	0.90
1:C:338:ARG:HG2	1:C:341:LYS:C	1.97	0.89
1:C:509:VAL:CG2	1:C:683:TRP:CH2	2.55	0.89
1:C:1306:THR:C	1:C:1308:ASN:N	2.21	0.89
1:C:835:TYR:HE1	1:C:942:HIS:HB3	1.17	0.89
1:C:157:ILE:HD11	1:C:263:ARG:CB	2.01	0.89
1:C:1085:ASP:HB2	1:C:1086:PRO:CD	2.02	0.89
1:C:312:ARG:HG3	1:C:312:ARG:HH21	1.38	0.89
1:C:610:GLN:HA	1:C:610:GLN:HE21	1.36	0.89
1:C:892:VAL:CG1	1:C:894:VAL:HG12	2.00	0.89
1:C:1306:THR:OG1	1:C:1308:ASN:N	2.06	0.89
1:C:671:ASP:O	1:C:672:MET:CB	2.14	0.88
1:C:252:LEU:CD1	1:C:971:MET:CE	2.50	0.88
1:C:338:ARG:HA	1:C:342:THR:HA	1.52	0.88
1:C:204:VAL:O	1:C:1240:ARG:O	1.90	0.88

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:81:ALA:HB2	1:C:170:TYR:HE2	0.75	0.88
1:B:898:GLN:HE21	1:B:917:VAL:HB	1.38	0.88
1:C:323:THR:HA	1:C:1279:SER:OG	1.72	0.88
1:C:389:PHE:CE1	1:C:1319:ARG:HB3	2.08	0.88
1:C:829:SER:OG	1:C:965:ARG:HD3	1.73	0.88
1:C:843:LEU:CD1	1:C:943:GLU:CG	1.86	0.88
1:C:1134:ARG:HB3	1:C:1135:PRO:CD	2.03	0.88
1:B:276:ASN:HD21	1:C:244:SER:HB3	1.39	0.88
1:C:839:ALA:C	1:C:940:ARG:CZ	2.46	0.88
1:C:849:MET:HA	1:C:917:VAL:O	1.74	0.88
1:C:323:THR:HB	1:C:1266:ASP:CB	2.04	0.88
1:C:1322:PRO:HB3	1:C:1328:ILE:HD13	1.54	0.88
1:C:924:ASP:OD1	1:C:927:SER:N	2.06	0.88
1:C:129:ALA:HB3	1:C:133:MET:HG2	1.57	0.87
1:C:77:THR:O	1:C:172:ASP:HB2	1.74	0.87
1:C:334:LEU:HD21	1:C:366:MET:CE	2.04	0.87
1:C:1093:PRO:HB2	1:C:1096:TYR:HD1	1.36	0.87
1:C:735:THR:HG21	1:C:1028:VAL:HG21	1.57	0.87
1:C:610:GLN:OE1	1:C:651:ARG:HG2	1.74	0.87
1:C:910:LEU:CD2	1:C:915:VAL:HG21	2.04	0.87
1:C:96:ILE:CD1	1:C:103:GLY:HA2	2.04	0.87
1:C:266:ILE:HD13	1:C:1304:MET:HB2	1.56	0.87
1:C:449:PHE:CA	1:C:683:TRP:NE1	2.22	0.87
1:C:1271:SER:HA	1:C:1277:LEU:HD13	1.56	0.87
1:C:213:PHE:CB	1:C:219:ILE:CG2	2.53	0.87
1:C:213:PHE:HB3	1:C:219:ILE:CG2	2.05	0.87
1:C:830:VAL:HG22	1:C:947:GLU:CB	2.00	0.87
1:C:838:GLU:HG3	1:C:934:LEU:O	1.75	0.87
1:C:448:TYR:C	1:C:450:PRO:HD2	1.98	0.86
1:C:503:GLU:OE2	1:C:542:ARG:HD2	1.75	0.86
1:C:660:ALA:C	1:C:662:VAL:N	2.17	0.86
1:C:874:ILE:HD11	1:C:883:ILE:HD11	1.57	0.86
1:C:886:SER:O	1:C:890:THR:HG22	1.74	0.86
1:C:248:VAL:HG13	1:C:970:LEU:CB	2.03	0.86
1:C:449:PHE:HA	1:C:683:TRP:NE1	1.89	0.86
1:C:841:ASP:N	1:C:940:ARG:HH12	1.63	0.86
1:C:849:MET:CG	1:C:919:MET:HE2	2.05	0.86
1:C:1093:PRO:CB	1:C:1096:TYR:HE1	1.85	0.86
1:C:122:ASN:O	1:C:122:ASN:ND2	2.07	0.86
1:C:265:VAL:HG21	1:C:1301:VAL:HG23	1.57	0.86
1:C:666:ARG:HG2	1:C:666:ARG:HH11	1.40	0.86

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1093:PRO:CB	1:C:1096:TYR:CD1	2.59	0.86
1:C:1109:SER:HG	1:C:1118:THR:HG21	1.40	0.86
1:C:1211:LEU:HD11	1:C:1246:VAL:HG23	1.55	0.86
1:C:493:HIS:HB2	1:C:756:THR:O	1.74	0.86
1:C:901:VAL:CG2	1:C:930:ALA:HB2	2.06	0.86
1:C:1121:HIS:CD2	1:C:1135:PRO:HG3	2.08	0.86
1:B:442:PRO:CB	1:B:475:ILE:CD1	2.39	0.86
1:B:461:ARG:HE	1:B:504:ASP:CB	1.89	0.85
1:C:206:ILE:O	1:C:1239:ALA:HB1	1.76	0.85
1:C:230:ASP:C	1:C:985:ARG:CG	2.47	0.85
1:C:323:THR:CB	1:C:1266:ASP:HB2	2.06	0.85
1:C:530:GLY:HA3	1:C:575:TRP:CD1	2.11	0.85
1:C:375:ARG:HG2	1:C:375:ARG:HH11	1.38	0.85
1:C:213:PHE:HB3	1:C:219:ILE:CB	2.05	0.85
1:C:199:TYR:OH	1:C:1247:ASN:ND2	2.09	0.85
1:C:462:LEU:O	1:C:462:LEU:HD22	1.76	0.85
1:C:1219:ASP:CB	1:C:1220:PRO:CD	2.54	0.85
1:B:525:PHE:O	1:B:529:LYS:HB3	1.76	0.85
1:C:163:TYR:CE2	1:C:258:VAL:HG23	2.11	0.85
1:C:148:GLN:HE21	1:C:375:ARG:HH12	1.11	0.85
1:C:1072:ASP:H	1:C:1234:GLN:HE22	1.25	0.85
1:C:820:ILE:HG21	1:C:983:ILE:HG12	1.58	0.84
1:C:371:THR:O	1:C:373:ASP:N	2.09	0.84
1:C:552:ILE:HD12	1:C:572:ASN:HB2	1.58	0.84
1:C:929:PHE:CB	1:C:936:MET:CE	2.55	0.84
1:B:919:MET:SD	1:B:928:ARG:NH1	2.51	0.84
1:C:405:HIS:NE2	1:C:625:PRO:HA	1.90	0.84
1:C:96:ILE:HD12	1:C:103:GLY:HA2	1.57	0.84
1:C:301:LEU:CD1	1:C:305:THR:HG21	2.05	0.84
1:C:454:GLU:O	1:C:455:GLN:HB3	1.76	0.84
1:C:663:VAL:O	1:C:677:ARG:HD2	1.76	0.84
1:B:269:GLU:HB3	1:B:292:ASN:HD22	1.40	0.84
1:B:461:ARG:HH11	1:B:461:ARG:CB	1.89	0.84
1:C:833:ARG:NH1	1:C:942:HIS:NE2	2.26	0.84
1:B:472:GLU:HA	1:B:473:ALA:HB2	1.57	0.84
1:B:1276:LEU:HB3	1:B:1290:LYS:HD3	1.59	0.84
1:C:154:PHE:CE1	1:C:361:ASN:ND2	2.46	0.84
1:C:700:ASP:OD2	1:C:1326:ARG:HG3	1.77	0.84
1:C:733:VAL:HG21	1:C:1022:ILE:HD12	1.60	0.84
1:C:874:ILE:HG13	1:C:895:VAL:CG1	2.08	0.84
1:C:1263:TYR:HE1	1:C:1278:TYR:CE1	1.95	0.84

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:459:ALA:O	1:B:463:VAL:CG1	2.26	0.83
1:C:414:LEU:HD23	1:C:814:THR:OG1	1.77	0.83
1:C:1285:GLN:HE21	1:C:1285:GLN:H	1.24	0.83
1:C:495:LEU:H	1:C:495:LEU:HD12	1.43	0.83
1:C:929:PHE:HB2	1:C:936:MET:HE1	1.59	0.83
1:C:1079:LEU:HD11	1:C:1231:TYR:HH	1.38	0.83
1:C:258:VAL:HG11	1:C:1058:GLY:HA2	1.60	0.83
1:C:656:VAL:HG11	1:C:688:GLU:CB	2.08	0.83
1:C:887:VAL:HG11	1:C:893:ALA:CB	2.07	0.83
1:B:440:ILE:HG12	1:B:772:TYR:CE2	2.13	0.83
1:C:321:ALA:HB3	1:C:1283:ASN:HD21	1.40	0.83
1:C:1021:ARG:HB2	1:C:1021:ARG:HH11	1.43	0.83
1:C:1322:PRO:HB3	1:C:1328:ILE:CD1	2.06	0.83
1:C:550:ILE:HD12	1:C:550:ILE:O	1.78	0.83
1:C:341:LYS:HG3	1:C:1306:THR:CB	2.09	0.83
1:C:615:THR:H	1:C:1333:ALA:C	1.87	0.83
1:C:865:ILE:HG21	1:C:957:PHE:HE2	1.41	0.83
1:C:874:ILE:CG2	1:C:902:ILE:HD11	2.08	0.83
1:C:1072:ASP:N	1:C:1234:GLN:HE22	1.75	0.83
1:C:107:GLN:OE1	1:C:107:GLN:N	2.11	0.83
1:C:352:HIS:HD2	1:C:1297:SER:H	1.26	0.83
1:C:446:LYS:HD3	1:C:448:TYR:HH	1.43	0.83
1:C:1000:LEU:HD22	1:C:1010:ARG:HH21	1.38	0.83
1:C:230:ASP:CA	1:C:985:ARG:HG2	2.07	0.83
1:C:838:GLU:HG3	1:C:934:LEU:CB	2.06	0.83
1:C:865:ILE:CG2	1:C:957:PHE:HE2	1.91	0.83
1:C:1263:TYR:CE1	1:C:1278:TYR:OH	2.27	0.83
1:B:1249:ASN:O	1:C:1109:SER:HA	1.78	0.83
1:C:265:VAL:HG13	1:C:358:LEU:HD13	1.60	0.83
1:C:1210:LEU:O	1:C:1210:LEU:HG	1.78	0.83
1:C:452:ASN:O	1:C:453:LEU:HD23	1.79	0.82
1:C:896:LEU:HA	1:C:918:VAL:CG2	2.09	0.82
1:C:1263:TYR:CD1	1:C:1278:TYR:HE1	1.97	0.82
1:C:509:VAL:CG2	1:C:683:TRP:CZ3	2.61	0.82
1:C:449:PHE:C	1:C:686:HIS:HD2	1.87	0.82
1:C:1219:ASP:CG	1:C:1220:PRO:CD	2.52	0.82
1:C:815:LEU:HB3	1:C:816:PRO:CD	2.08	0.82
1:C:449:PHE:CZ	1:C:463:VAL:HG22	2.14	0.82
1:B:461:ARG:HE	1:B:504:ASP:HB2	1.45	0.82
1:C:494:GLU:N	1:C:494:GLU:OE2	2.13	0.82
1:C:1049:GLU:O	1:C:1053:ARG:HG3	1.80	0.82

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1210:LEU:CD2	1:C:1244:ALA:CB	2.58	0.82
1:B:272:THR:HG22	1:B:289:THR:HG22	1.61	0.82
1:C:180:LEU:CD2	1:C:306:GLN:HE22	1.91	0.82
1:C:333:ARG:HE	1:C:1272:ARG:HA	1.44	0.82
1:C:830:VAL:HG23	1:C:947:GLU:HB2	1.60	0.82
1:C:879:THR:H	1:C:880:PRO:HD2	1.44	0.82
1:C:965:ARG:HH11	1:C:968:ARG:NH1	1.78	0.81
1:C:1179:THR:OG1	1:C:1180:PRO:HD3	1.81	0.81
1:B:135:LYS:HE2	1:C:469:ARG:HA	1.61	0.81
1:C:611:GLY:O	1:C:634:TYR:OH	1.98	0.81
1:C:230:ASP:O	1:C:985:ARG:HG2	1.79	0.81
1:C:446:LYS:HB2	1:C:448:TYR:CE1	2.15	0.81
1:C:843:LEU:HD21	1:C:943:GLU:CD	2.04	0.81
1:C:929:PHE:CG	1:C:936:MET:CE	2.63	0.81
1:C:654:THR:O	1:C:658:THR:CG2	2.26	0.81
1:C:157:ILE:HD11	1:C:263:ARG:HB3	1.59	0.81
1:C:164:LEU:HD11	1:C:353:PHE:HE2	1.42	0.81
1:C:946:LEU:HD21	1:C:965:ARG:HG2	1.63	0.81
1:C:838:GLU:O	1:C:940:ARG:NE	2.11	0.81
1:C:1289:PRO:O	1:C:1293:VAL:HG23	1.80	0.81
1:B:826:GLY:O	1:B:968:ARG:NH2	2.13	0.81
1:C:233:VAL:HG23	1:C:234:PRO:HD2	1.55	0.81
1:C:493:HIS:CB	1:C:756:THR:O	2.28	0.81
1:C:963:ALA:CB	1:C:1059:LEU:HG	2.09	0.81
1:C:230:ASP:O	1:C:985:ARG:CG	2.29	0.81
1:C:656:VAL:CG1	1:C:688:GLU:HG2	2.11	0.81
1:C:687:LEU:HD23	1:C:687:LEU:C	2.04	0.81
1:C:838:GLU:C	1:C:940:ARG:NE	2.38	0.81
1:C:1120:THR:O	1:C:1122:PRO:CD	2.28	0.81
1:C:1210:LEU:HD23	1:C:1244:ALA:CB	2.10	0.81
1:C:87:GLU:CB	1:C:159:ASP:O	2.29	0.81
1:C:495:LEU:HD12	1:C:495:LEU:N	1.93	0.81
1:C:741:TYR:HE2	1:C:1022:ILE:HD11	1.42	0.81
1:C:494:GLU:HB3	1:C:577:GLN:NE2	1.96	0.80
1:C:1273:ASN:O	1:C:1273:ASN:ND2	2.14	0.80
1:C:213:PHE:O	1:C:219:ILE:HB	1.80	0.80
1:C:81:ALA:HB3	1:C:170:TYR:CE2	2.16	0.80
1:C:1306:THR:HG1	1:C:1308:ASN:HA	1.46	0.80
1:C:556:ALA:C	1:C:587:ALA:HB2	2.07	0.80
1:C:629:ARG:HB2	1:C:1037:ILE:HG23	1.61	0.80
1:C:452:ASN:O	1:C:453:LEU:CB	2.29	0.80

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1079:LEU:O	1:C:1227:MET:CB	2.29	0.80
1:C:1081:ASP:H	1:C:1227:MET:HB3	1.46	0.80
1:B:793:TYR:CD2	1:B:1321:ASN:ND2	2.48	0.80
1:C:434:VAL:HG23	1:C:709:MET:HE1	1.63	0.80
1:C:144:ASN:CB	1:C:1318:GLU:OE1	2.28	0.80
1:C:835:TYR:CE2	1:C:925:VAL:HG11	2.17	0.80
1:C:685:ARG:HB3	1:C:685:ARG:HH11	1.45	0.80
1:B:394:GLN:HB2	1:C:1005:LEU:HD21	1.63	0.80
1:C:310:LEU:HD21	1:C:1242:MET:CE	2.11	0.80
1:C:528:ILE:HD13	1:C:758:ILE:CD1	2.11	0.80
1:C:837:THR:HG22	1:C:934:LEU:HD12	1.64	0.79
1:C:1134:ARG:HH22	1:C:1154:ASN:HD21	1.30	0.79
1:C:233:VAL:CG1	1:C:981:HIS:CG	2.65	0.79
1:C:1121:HIS:HD2	1:C:1135:PRO:CG	1.91	0.79
1:C:1281:VAL:O	1:C:1283:ASN:N	2.15	0.79
1:C:332:THR:O	1:C:335:ASP:HB2	1.83	0.79
1:C:847:ILE:HG12	1:C:911:ARG:HB2	1.63	0.79
1:C:1214:GLU:HB2	1:C:1215:PRO:CD	1.80	0.79
1:C:659:LEU:O	1:C:659:LEU:HD22	1.83	0.79
1:C:233:VAL:HG12	1:C:981:HIS:CE1	2.17	0.79
1:C:406:ASP:OD1	1:C:1039:ALA:CB	2.29	0.79
1:C:384:MET:HA	1:C:708:THR:CG2	2.13	0.79
1:C:449:PHE:CD1	1:C:450:PRO:HD3	2.18	0.79
1:C:1076:ILE:HB	1:C:1230:ILE:HG22	1.65	0.79
1:C:252:LEU:CD1	1:C:823:ILE:HG21	2.12	0.78
1:C:261:ASP:O	1:C:1054:ARG:CZ	2.30	0.78
1:C:924:ASP:OD1	1:C:927:SER:CB	2.30	0.78
1:C:1263:TYR:CD1	1:C:1278:TYR:CE1	2.71	0.78
1:C:372:ALA:CA	1:C:1315:MET:HE1	2.14	0.78
1:C:441:ARG:HG2	1:C:441:ARG:HH21	1.48	0.78
1:B:342:THR:HB	1:B:1309:ILE:HD11	1.65	0.78
1:C:685:ARG:HH11	1:C:685:ARG:CB	1.95	0.78
1:C:985:ARG:O	1:C:985:ARG:NH2	2.15	0.78
1:C:1060:ARG:NH1	1:C:1292:GLU:H	1.82	0.78
1:C:1091:ASP:OD1	1:C:1091:ASP:N	2.15	0.78
1:C:821:ASN:HA	1:C:824:LEU:HD22	1.66	0.78
1:C:297:ASN:ND2	1:C:298:PRO:HD2	1.99	0.77
1:C:614:ARG:HD3	1:C:635:ILE:HD12	1.64	0.77
1:C:896:LEU:HD22	1:C:918:VAL:CG2	2.14	0.77
1:C:948:ILE:HG13	1:C:962:ASP:HB3	1.65	0.77
1:C:1313:ASP:OD1	1:C:1313:ASP:N	2.12	0.77

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:536:LEU:HD13	1:B:604:MET:HE1	1.66	0.77
1:C:449:PHE:CB	1:C:683:TRP:CD1	2.51	0.77
1:C:901:VAL:HA	1:C:928:ARG:O	1.85	0.77
1:C:986:ILE:O	1:C:989:ILE:HG22	1.83	0.77
1:C:77:THR:O	1:C:172:ASP:CB	2.32	0.77
1:C:333:ARG:HG2	1:C:333:ARG:HH21	1.49	0.77
1:C:910:LEU:HD23	1:C:915:VAL:HG22	1.61	0.77
1:C:184:GLU:O	1:C:187:ASP:N	2.16	0.77
1:C:338:ARG:CG	1:C:342:THR:N	2.47	0.77
1:C:449:PHE:O	1:C:683:TRP:CD1	2.34	0.77
1:C:830:VAL:HG21	1:C:947:GLU:HB2	1.43	0.77
1:C:835:TYR:CD2	1:C:925:VAL:CG2	2.40	0.77
1:C:946:LEU:N	1:C:946:LEU:HD12	2.00	0.77
1:B:352:HIS:HA	1:B:1300:ASN:HD21	1.50	0.77
1:C:265:VAL:HG21	1:C:1301:VAL:CG2	2.14	0.77
1:C:371:THR:C	1:C:373:ASP:N	2.42	0.77
1:C:407:HIS:NE2	1:C:1047:LEU:HD12	2.00	0.77
1:C:484:ARG:CZ	1:C:758:ILE:HG22	2.15	0.77
1:C:896:LEU:CD2	1:C:918:VAL:HG21	2.14	0.77
1:C:1074:VAL:HB	1:C:1173:TYR:HE2	1.50	0.77
1:C:485:GLU:OE1	1:C:486:VAL:HG13	1.85	0.76
1:C:822:MET:HE2	1:C:1046:PHE:CE2	2.14	0.76
1:C:840:ASP:N	1:C:940:ARG:NH1	2.26	0.76
1:B:1064:ASN:HD21	1:B:1296:ILE:HD11	1.50	0.76
1:C:516:LEU:HB3	1:C:763:VAL:HG11	1.66	0.76
1:C:492:VAL:HG22	1:C:747:ARG:HA	1.66	0.76
1:C:81:ALA:CB	1:C:170:TYR:CZ	2.69	0.76
1:C:339:LEU:HD21	1:C:366:MET:HA	1.68	0.76
1:C:129:ALA:CB	1:C:133:MET:HG2	2.16	0.76
1:C:232:LEU:CG	1:C:249:SER:HB3	2.14	0.76
1:C:364:ALA:CB	1:C:1050:LEU:HD21	2.15	0.76
1:C:1104:ARG:HG2	1:C:1104:ARG:HH11	1.49	0.76
1:C:838:GLU:O	1:C:940:ARG:CZ	2.34	0.76
1:B:388:GLN:H	1:B:1320:VAL:CG1	1.98	0.76
1:C:835:TYR:CE2	1:C:925:VAL:CB	2.69	0.76
1:C:128:GLU:OE1	1:C:133:MET:HE2	1.86	0.76
1:C:230:ASP:CB	1:C:985:ARG:HG2	2.13	0.76
1:C:613:LEU:HD21	1:C:632:GLN:HB3	0.86	0.76
1:C:874:ILE:HD11	1:C:883:ILE:HD12	1.67	0.76
1:C:897:TYR:CD1	1:C:898:GLN:N	2.54	0.76
1:C:480:LEU:O	1:C:480:LEU:HD23	1.85	0.76

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1044:ARG:HG3	1:C:1044:ARG:HH11	1.51	0.76
1:B:397:LEU:CD2	1:C:1008:LEU:HD11	2.16	0.75
1:C:321:ALA:CB	1:C:1283:ASN:ND2	2.49	0.75
1:C:734:ILE:HG23	1:C:1017:ALA:HB1	1.68	0.75
1:B:903:ASN:O	1:B:907:SER:CB	2.34	0.75
1:C:225:ILE:HD11	1:C:1069:ARG:C	2.11	0.75
1:C:1250:GLU:C	1:C:1251:VAL:HG23	2.10	0.75
1:B:793:TYR:HD2	1:B:1321:ASN:HD21	1.31	0.75
1:C:341:LYS:CG	1:C:1306:THR:HB	2.17	0.75
1:C:910:LEU:HD21	1:C:915:VAL:CG2	2.10	0.75
1:B:343:ILE:HD11	1:B:366:MET:HE3	1.67	0.75
1:C:449:PHE:CG	1:C:466:VAL:HG11	2.22	0.75
1:C:659:LEU:HD22	1:C:662:VAL:HG21	1.67	0.75
1:C:1285:GLN:HE21	1:C:1285:GLN:N	1.85	0.75
1:C:77:THR:O	1:C:172:ASP:CG	2.29	0.75
1:C:179:LYS:HE3	1:C:181:ARG:HB3	1.67	0.75
1:C:1031:TYR:HE2	1:C:1041:ARG:HH11	1.31	0.75
1:C:254:VAL:HG13	1:C:1062:ILE:CD1	2.17	0.75
1:C:1093:PRO:HG2	1:C:1096:TYR:CD1	2.17	0.75
1:C:1173:TYR:CE1	1:C:1204:LEU:HD12	2.22	0.75
1:C:910:LEU:HG	1:C:915:VAL:HG21	1.69	0.75
1:C:964:VAL:HG13	1:C:1059:LEU:HD21	1.69	0.75
1:B:873:TYR:HB3	1:B:897:TYR:HB2	1.68	0.75
1:C:333:ARG:HG2	1:C:333:ARG:NH2	2.01	0.75
1:B:1185:THR:O	1:B:1205:GLN:NE2	2.20	0.75
1:C:654:THR:CG2	1:C:658:THR:HG21	2.16	0.75
1:C:865:ILE:CG2	1:C:957:PHE:CE2	2.70	0.75
1:C:1085:ASP:HA	1:C:1208:ASP:O	1.87	0.75
1:C:1144:ARG:HD3	1:C:1168:ILE:HG21	1.68	0.75
1:C:1292:GLU:C	1:C:1293:VAL:HG23	2.11	0.75
1:C:233:VAL:HG12	1:C:981:HIS:CG	2.22	0.74
1:C:525:PHE:CE1	1:C:532:ILE:HD12	2.22	0.74
1:C:495:LEU:HD11	1:C:531:ASP:CB	2.17	0.74
1:C:266:ILE:HD13	1:C:1304:MET:CB	2.16	0.74
1:C:451:GLU:HB2	1:C:686:HIS:HB3	1.68	0.74
1:C:611:GLY:CA	1:C:636:PRO:O	2.35	0.74
1:C:1280:PRO:HG3	1:C:1286:VAL:O	1.87	0.74
1:C:87:GLU:OE1	1:C:157:ILE:HG21	1.88	0.74
1:C:449:PHE:CE2	1:C:463:VAL:HG22	2.22	0.74
1:B:436:SER:O	1:B:437:ALA:HB3	1.86	0.74
1:C:404:ASP:O	1:C:408:ILE:HG12	1.87	0.74

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:449:PHE:CA	1:C:683:TRP:CD1	2.71	0.74
1:C:838:GLU:OE1	1:C:935:GLN:CA	2.35	0.74
1:C:910:LEU:CG	1:C:915:VAL:CG2	2.65	0.74
1:C:934:LEU:O	1:C:936:MET:N	2.19	0.74
1:C:449:PHE:C	1:C:686:HIS:CD2	2.65	0.74
1:B:196:LEU:HD23	1:B:296:VAL:HG11	1.70	0.74
1:B:442:PRO:HB2	1:B:475:ILE:HD11	0.76	0.74
1:C:213:PHE:HB3	1:C:219:ILE:HG13	1.68	0.74
1:C:429:ILE:C	1:C:429:ILE:HD12	2.13	0.74
1:C:1296:ILE:O	1:C:1296:ILE:HD13	1.87	0.74
1:B:439:VAL:O	1:B:440:ILE:HG13	1.87	0.74
1:C:87:GLU:HG3	1:C:87:GLU:O	1.87	0.74
1:B:139:ASN:O	1:C:757:ILE:HB	1.88	0.74
1:B:338:ARG:HH12	1:C:1005:LEU:HD22	1.52	0.74
1:B:699:THR:O	1:B:703:SER:OG	2.04	0.74
1:C:422:LEU:CD1	1:C:490:PHE:CE2	2.71	0.73
1:C:449:PHE:HB2	1:C:683:TRP:CE2	2.19	0.73
1:C:509:VAL:HG22	1:C:683:TRP:CH2	2.23	0.73
1:C:1280:PRO:CB	1:C:1287:GLY:HA2	2.18	0.73
1:C:259:MET:CG	1:C:1055:LEU:HB2	2.18	0.73
1:C:265:VAL:HG23	1:C:1303:SER:HA	1.70	0.73
1:C:901:VAL:HG22	1:C:930:ALA:CB	2.15	0.73
1:C:1281:VAL:C	1:C:1283:ASN:H	1.94	0.73
1:C:1112:ASN:O	1:C:1112:ASN:ND2	2.15	0.73
1:B:442:PRO:HB2	1:B:475:ILE:HD13	1.64	0.73
1:B:505:PRO:HG2	1:B:672:MET:HE1	1.71	0.73
1:C:108:LYS:HB2	1:C:108:LYS:NZ	2.03	0.73
1:C:371:THR:C	1:C:373:ASP:H	1.94	0.73
1:C:1079:LEU:HD11	1:C:1231:TYR:CZ	2.16	0.73
1:C:1104:ARG:HD2	1:C:1104:ARG:O	1.88	0.73
1:C:1250:GLU:C	1:C:1251:VAL:CG2	2.61	0.73
1:C:338:ARG:O	1:C:340:VAL:N	2.20	0.73
1:C:795:ASP:OD1	1:C:795:ASP:N	2.17	0.73
1:C:837:THR:C	1:C:934:LEU:CD1	2.58	0.73
1:C:1278:TYR:CD2	1:C:1288:ILE:CD1	2.71	0.73
1:C:168:VAL:HG23	1:C:204:VAL:HG13	1.70	0.73
1:C:516:LEU:CB	1:C:763:VAL:HG11	2.17	0.73
1:C:338:ARG:O	1:C:341:LYS:O	2.06	0.73
1:B:903:ASN:O	1:B:907:SER:HB2	1.89	0.73
1:C:146:GLU:N	1:C:146:GLU:OE1	2.21	0.73
1:C:254:VAL:HG13	1:C:1062:ILE:HD11	1.70	0.73

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1081:ASP:N	1:C:1227:MET:HB3	2.03	0.73
1:B:462:LEU:HD23	1:B:462:LEU:C	2.14	0.72
1:C:247:TYR:CD2	1:C:1070:ARG:HD3	2.24	0.72
1:C:448:TYR:C	1:C:450:PRO:CD	2.61	0.72
1:C:571:ARG:HB3	1:C:571:ARG:HH11	1.53	0.72
1:C:838:GLU:HG2	1:C:935:GLN:C	2.14	0.72
1:C:1259:ALA:HB1	1:C:1260:PRO:CD	2.19	0.72
1:C:81:ALA:HB3	1:C:170:TYR:CZ	2.24	0.72
1:C:327:LEU:HD13	1:C:327:LEU:O	1.88	0.72
1:C:985:ARG:NH1	1:C:989:ILE:HD12	2.05	0.72
1:C:1231:TYR:HB3	1:C:1232:PRO:HD2	1.72	0.72
1:C:339:LEU:HD13	1:C:397:LEU:CD2	2.19	0.72
1:C:829:SER:HB2	1:C:965:ARG:HD2	0.72	0.72
1:C:1210:LEU:HD23	1:C:1244:ALA:HB2	1.70	0.72
1:C:1306:THR:CA	1:C:1308:ASN:H	2.01	0.72
1:C:120:VAL:O	1:C:121:PHE:O	2.07	0.72
1:C:233:VAL:CG1	1:C:981:HIS:ND1	2.52	0.72
1:C:985:ARG:NH2	1:C:988:GLN:HG3	2.03	0.72
1:C:244:SER:C	1:C:246:GLU:N	2.47	0.72
1:C:849:MET:CE	1:C:929:PHE:HE2	2.02	0.72
1:C:240:GLY:C	1:C:242:GLU:N	2.47	0.72
1:C:1168:ILE:HD13	1:C:1168:ILE:N	2.05	0.72
1:C:265:VAL:HG11	1:C:1301:VAL:HG21	1.70	0.72
1:C:362:LEU:HD13	1:C:1302:VAL:CG1	2.19	0.72
1:C:954:GLN:O	1:C:958:ILE:HD11	1.90	0.72
1:B:372:ALA:O	1:B:375:ARG:HG2	1.89	0.72
1:C:666:ARG:HH11	1:C:666:ARG:CG	2.03	0.72
1:C:733:VAL:CG2	1:C:1022:ILE:HD12	2.19	0.72
1:C:835:TYR:CE1	1:C:942:HIS:CG	2.77	0.72
1:B:394:GLN:CB	1:C:1005:LEU:HD21	2.19	0.72
1:C:864:HIS:CE1	1:C:1030:ARG:CZ	2.73	0.72
1:C:874:ILE:HG13	1:C:895:VAL:HG11	1.71	0.72
1:B:1131:PRO:O	1:B:1162:SER:OG	2.07	0.71
1:C:462:LEU:HD13	1:C:462:LEU:C	2.15	0.71
1:C:835:TYR:HE2	1:C:925:VAL:CG1	2.01	0.71
1:C:1176:GLU:OE1	1:C:1203:HIS:CE1	2.43	0.71
1:B:533:GLN:HG3	1:B:588:LEU:HD12	1.72	0.71
1:C:213:PHE:HB2	1:C:219:ILE:CG2	2.16	0.71
1:C:829:SER:CB	1:C:965:ARG:HD3	2.12	0.71
1:B:388:GLN:C	1:B:1320:VAL:HG12	2.14	0.71
1:C:109:LYS:HD2	1:C:110:PRO:HD3	1.72	0.71

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:302:ARG:HD2	1:C:318:LEU:HD23	1.70	0.71
1:C:450:PRO:CA	1:C:454:GLU:CG	2.55	0.71
1:C:554:ARG:HG2	1:C:554:ARG:O	1.91	0.71
1:C:935:GLN:CB	1:C:939:ASN:HB3	2.20	0.71
1:C:108:LYS:HB2	1:C:108:LYS:HZ2	1.56	0.71
1:C:235:ILE:HD11	1:C:978:GLN:HE21	1.55	0.71
1:C:1276:LEU:N	1:C:1276:LEU:HD23	2.05	0.71
1:C:339:LEU:HD13	1:C:397:LEU:HD23	1.72	0.71
1:C:1211:LEU:HD11	1:C:1246:VAL:CG2	2.20	0.71
1:B:272:THR:HG23	1:C:235:ILE:HG21	1.72	0.71
1:C:502:PHE:CD1	1:C:507:SER:HB3	2.24	0.71
1:C:1044:ARG:HH11	1:C:1044:ARG:CG	2.03	0.71
1:C:375:ARG:HH11	1:C:375:ARG:CG	2.04	0.71
1:C:613:LEU:O	1:C:613:LEU:HD13	1.90	0.71
1:C:659:LEU:C	1:C:659:LEU:HD13	2.15	0.71
1:C:832:MET:HG3	1:C:832:MET:O	1.88	0.71
1:C:841:ASP:N	1:C:940:ARG:NH2	2.37	0.71
1:B:472:GLU:HB2	1:B:761:SER:OG	1.87	0.71
1:C:96:ILE:HD13	1:C:96:ILE:N	2.05	0.71
1:C:606:LEU:HD11	1:C:659:LEU:HB2	1.72	0.71
1:C:511:VAL:HG21	1:C:539:PHE:CE2	2.26	0.71
1:C:1023:ARG:NH2	1:C:1023:ARG:HB3	2.05	0.71
1:B:316:ASN:O	1:B:320:GLN:NE2	2.24	0.71
1:B:903:ASN:O	1:B:907:SER:OG	2.09	0.71
1:C:502:PHE:HD1	1:C:507:SER:HB3	1.55	0.71
1:C:366:MET:HG2	1:C:366:MET:O	1.88	0.70
1:C:265:VAL:CG1	1:C:358:LEU:HD13	2.21	0.70
1:C:862:ARG:HH21	1:C:1042:TRP:HZ2	1.38	0.70
1:C:1000:LEU:HD23	1:C:1010:ARG:NE	2.04	0.70
1:C:1076:ILE:O	1:C:1076:ILE:HG12	1.90	0.70
1:B:313:ASP:O	1:B:317:MET:CB	2.39	0.70
1:C:210:ARG:HA	1:C:221:LEU:HD11	1.72	0.70
1:C:213:PHE:HB3	1:C:219:ILE:CG1	2.21	0.70
1:C:258:VAL:HG11	1:C:1058:GLY:CA	2.21	0.70
1:C:611:GLY:HA3	1:C:636:PRO:O	1.91	0.70
1:C:713:MET:HE1	1:C:804:LEU:HD21	1.73	0.70
1:C:850:THR:OG1	1:C:916:LEU:HD22	1.91	0.70
1:C:897:TYR:CZ	1:C:898:GLN:O	2.43	0.70
1:C:301:LEU:HD12	1:C:301:LEU:O	1.91	0.70
1:C:835:TYR:CE2	1:C:925:VAL:CG1	2.74	0.70
1:C:383:SER:OG	1:C:796:PRO:HG2	1.88	0.70

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:656:VAL:CG1	1:C:688:GLU:HB3	2.15	0.70
1:B:898:GLN:HG2	1:B:919:MET:HE2	1.73	0.70
1:C:910:LEU:CG	1:C:915:VAL:HG21	2.22	0.70
1:C:1259:ALA:HB1	1:C:1260:PRO:HD3	1.73	0.70
1:C:1263:TYR:CZ	1:C:1278:TYR:CZ	2.74	0.70
1:B:875:THR:H	1:B:878:SER:HB3	1.55	0.70
1:B:1282:ALA:HB1	1:B:1283:ASN:HA	1.73	0.70
1:C:141:LEU:O	1:C:141:LEU:HG	1.91	0.70
1:C:179:LYS:HD2	1:C:179:LYS:C	2.16	0.70
1:C:204:VAL:HG23	1:C:1242:MET:O	1.92	0.70
1:C:230:ASP:HB2	1:C:985:ARG:NE	1.95	0.70
1:C:896:LEU:HD13	1:C:918:VAL:CG2	2.22	0.70
1:C:1261:SER:O	1:C:1263:TYR:N	2.25	0.70
1:C:154:PHE:HE1	1:C:361:ASN:ND2	1.89	0.70
1:C:659:LEU:HD22	1:C:662:VAL:CG2	2.22	0.70
1:C:1031:TYR:CE2	1:C:1041:ARG:NH1	2.55	0.70
1:C:558:TYR:CZ	1:C:585:PHE:HB2	2.27	0.69
1:C:835:TYR:O	1:C:846:GLY:CA	2.32	0.69
1:C:1122:PRO:HB2	1:C:1123:PRO:HD3	1.74	0.69
1:B:472:GLU:CA	1:B:473:ALA:HB2	2.22	0.69
1:C:206:ILE:HD11	1:C:1066:ARG:HD3	1.74	0.69
1:B:606:LEU:HD11	1:B:658:THR:HG21	1.72	0.69
1:C:233:VAL:HG12	1:C:981:HIS:ND1	2.06	0.69
1:C:407:HIS:CD2	1:C:1047:LEU:CA	2.69	0.69
1:C:1270:LEU:O	1:C:1271:SER:O	2.10	0.69
1:B:139:ASN:O	1:C:757:ILE:O	2.10	0.69
1:B:564:GLY:HA2	1:B:565:GLU:HB3	1.73	0.69
1:B:1189:ASP:O	1:B:1192:SER:N	2.21	0.69
1:C:176:LYS:CG	1:C:177:LYS:H	2.05	0.69
1:C:375:ARG:HD3	1:C:398:ARG:NH2	2.07	0.69
1:C:485:GLU:OE1	1:C:706:TYR:CE1	2.46	0.69
1:C:897:TYR:CG	1:C:898:GLN:N	2.57	0.69
1:C:999:LYS:HE2	1:C:1009:THR:HG22	1.74	0.69
1:C:1047:LEU:HD22	1:C:1051:ARG:HD3	1.71	0.69
1:C:1296:ILE:HD11	1:C:1298:PHE:HE1	1.58	0.69
1:C:180:LEU:CD2	1:C:306:GLN:HE21	1.87	0.69
1:C:615:THR:HG23	1:C:1333:ALA:C	2.18	0.69
1:C:843:LEU:HD11	1:C:943:GLU:CD	2.09	0.69
1:C:1046:PHE:HD2	1:C:1052:LEU:HD21	1.56	0.69
1:B:388:GLN:CB	1:B:1320:VAL:CG1	2.67	0.69
1:C:1000:LEU:HD21	1:C:1010:ARG:HH21	1.56	0.69

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1176:GLU:HG2	1:C:1203:HIS:CE1	2.26	0.69
1:B:475:ILE:HD13	1:B:475:ILE:O	1.93	0.69
1:B:640:GLN:HE21	1:B:647:GLU:HB3	1.58	0.69
1:B:1112:ASN:OD1	1:B:1113:LYS:N	2.26	0.69
1:C:830:VAL:O	1:C:854:GLN:HG2	1.92	0.69
1:C:836:GLN:HB2	1:C:940:ARG:HG2	0.77	0.69
1:C:1322:PRO:CB	1:C:1328:ILE:CD1	2.70	0.69
1:B:469:ARG:HH11	1:B:498:ILE:HD12	0.87	0.69
1:B:926:VAL:HG21	1:B:938:ASN:H	1.56	0.69
1:C:1219:ASP:CG	1:C:1220:PRO:HD2	2.08	0.69
1:C:1243:ARG:HG2	1:C:1243:ARG:HH11	1.57	0.69
1:C:77:THR:O	1:C:172:ASP:OD2	2.10	0.69
1:C:251:LEU:HD23	1:C:1062:ILE:CG1	2.12	0.69
1:C:314:ILE:HG22	1:C:318:LEU:CD2	2.22	0.69
1:C:338:ARG:CG	1:C:342:THR:CA	2.70	0.69
1:C:865:ILE:HG21	1:C:957:PHE:CE2	2.26	0.69
1:B:209:ASN:ND2	1:B:211:ASP:OD1	2.25	0.69
1:B:961:SER:HB2	1:B:964:VAL:HG12	1.75	0.69
1:C:333:ARG:O	1:C:335:ASP:N	2.25	0.69
1:C:365:LEU:O	1:C:365:LEU:HD22	1.93	0.69
1:C:540:PHE:CE2	1:C:604:MET:HE3	2.28	0.69
1:B:699:THR:O	1:B:703:SER:CB	2.41	0.68
1:B:1249:ASN:HB3	1:C:1110:LEU:CB	2.22	0.68
1:C:509:VAL:HG23	1:C:683:TRP:HZ3	1.57	0.68
1:C:232:LEU:HD21	1:C:249:SER:CA	2.23	0.68
1:C:583:GLU:HG3	1:C:583:GLU:O	1.94	0.68
1:C:1085:ASP:OD1	1:C:1085:ASP:N	2.26	0.68
1:C:1173:TYR:CD1	1:C:1204:LEU:CD1	2.74	0.68
1:C:146:GLU:HB2	1:C:1317:VAL:CG1	2.23	0.68
1:C:1093:PRO:CG	1:C:1096:TYR:CD1	2.73	0.68
1:B:1331:ARG:HG2	1:B:1332:ASN:H	1.58	0.68
1:C:180:LEU:HG	1:C:180:LEU:O	1.93	0.68
1:C:185:ALA:C	1:C:187:ASP:N	2.50	0.68
1:C:297:ASN:C	1:C:297:ASN:HD22	2.01	0.68
1:C:320:GLN:O	1:C:321:ALA:HB3	1.93	0.68
1:C:542:ARG:HG3	1:C:542:ARG:O	1.91	0.68
1:C:619:ALA:HB2	1:C:711:ASN:HB2	1.75	0.68
1:C:629:ARG:HG3	1:C:629:ARG:O	1.91	0.68
1:B:472:GLU:HB3	1:B:761:SER:HB2	1.74	0.68
1:C:240:GLY:O	1:C:241:ALA:C	2.37	0.68
1:C:733:VAL:CB	1:C:1022:ILE:HD12	2.23	0.68

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1206:PHE:CD2	1:C:1236:ILE:HD11	2.28	0.68
1:C:168:VAL:HG23	1:C:204:VAL:CG1	2.23	0.68
1:C:168:VAL:HB	1:C:204:VAL:HG12	1.76	0.68
1:C:838:GLU:CB	1:C:934:LEU:HB3	2.16	0.68
1:C:939:ASN:HD22	1:C:939:ASN:C	2.00	0.68
1:B:135:LYS:HE2	1:C:468:ALA:C	2.14	0.68
1:C:278:LEU:HD22	1:C:282:VAL:HB	1.76	0.68
1:C:849:MET:CG	1:C:919:MET:CE	2.72	0.68
1:C:1079:LEU:HD12	1:C:1079:LEU:N	2.02	0.68
1:C:1132:THR:O	1:C:1133:GLY:C	2.37	0.68
1:C:259:MET:HG3	1:C:1055:LEU:CB	2.23	0.68
1:C:389:PHE:CE1	1:C:1319:ARG:CB	2.76	0.68
1:C:509:VAL:HG22	1:C:683:TRP:HH2	1.59	0.68
1:C:674:LYS:HB2	1:C:674:LYS:NZ	2.08	0.68
1:C:180:LEU:HD22	1:C:306:GLN:CD	2.15	0.67
1:C:231:LEU:O	1:C:982:ALA:CA	2.40	0.67
1:C:516:LEU:HB3	1:C:763:VAL:CG1	2.24	0.67
1:C:896:LEU:HD13	1:C:918:VAL:HG21	1.75	0.67
1:C:440:ILE:CD1	1:C:478:ILE:HG21	2.22	0.67
1:C:958:ILE:O	1:C:958:ILE:HG12	1.92	0.67
1:C:1000:LEU:HD23	1:C:1010:ARG:CZ	2.25	0.67
1:B:234:PRO:HB3	1:B:972:PRO:HB3	1.75	0.67
1:B:440:ILE:HG21	1:B:770:CYS:SG	2.34	0.67
1:B:821:ASN:ND2	1:B:1015:GLN:OE1	2.26	0.67
1:C:385:ILE:O	1:C:1328:ILE:HG21	1.95	0.67
1:C:450:PRO:O	1:C:451:GLU:HB3	1.93	0.67
1:C:285:VAL:HG13	1:C:325:TYR:O	1.94	0.67
1:C:791:ILE:HG13	1:C:1325:VAL:CG2	2.25	0.67
1:C:909:TYR:HE1	1:C:913:ASN:OD1	1.77	0.67
1:C:1272:ARG:O	1:C:1272:ARG:HD3	1.93	0.67
1:B:898:GLN:NE2	1:B:917:VAL:HB	2.09	0.67
1:B:409:ILE:HD11	1:B:627:ALA:HA	1.76	0.67
1:C:365:LEU:O	1:C:365:LEU:HD13	1.93	0.67
1:C:550:ILE:HD12	1:C:550:ILE:C	2.20	0.67
1:C:820:ILE:CG2	1:C:983:ILE:HG12	2.24	0.67
1:C:1079:LEU:O	1:C:1227:MET:HB2	1.93	0.67
1:C:1149:LYS:O	1:C:1151:VAL:N	2.27	0.67
1:B:397:LEU:O	1:B:398:ARG:NH1	2.24	0.67
1:B:439:VAL:HG23	1:B:440:ILE:H	1.58	0.67
1:C:702:LEU:HD12	1:C:702:LEU:O	1.93	0.67
1:C:838:GLU:HB3	1:C:934:LEU:HB3	1.76	0.67

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:928:ARG:HH11	1:C:928:ARG:HG3	1.60	0.67
1:B:301:LEU:O	1:B:305:THR:OG1	2.13	0.67
1:C:1296:ILE:HD13	1:C:1296:ILE:C	2.20	0.67
1:C:896:LEU:HA	1:C:918:VAL:HG22	1.76	0.67
1:C:945:VAL:C	1:C:946:LEU:HD12	2.20	0.67
1:B:388:GLN:H	1:B:1320:VAL:HG13	1.58	0.67
1:B:1119:TYR:HB3	1:B:1134:ARG:HE	1.58	0.67
1:C:607:PHE:O	1:C:608:THR:CG2	2.43	0.66
1:C:540:PHE:HE2	1:C:604:MET:HE3	1.60	0.66
1:C:791:ILE:HG13	1:C:1325:VAL:HG21	1.76	0.66
1:C:1105:LEU:H	1:C:1105:LEU:HD12	1.61	0.66
1:C:1206:PHE:HD2	1:C:1236:ILE:CD1	2.04	0.66
1:C:297:ASN:HD22	1:C:298:PRO:HD2	1.58	0.66
1:C:309:TRP:CZ2	1:C:1257:ALA:HB1	2.31	0.66
1:C:327:LEU:C	1:C:327:LEU:HD22	2.21	0.66
1:C:394:GLN:HG3	1:C:394:GLN:O	1.96	0.66
1:C:1021:ARG:HH11	1:C:1021:ARG:CB	2.08	0.66
1:C:422:LEU:HD11	1:C:490:PHE:CE2	2.31	0.66
1:C:434:VAL:CG2	1:C:709:MET:HE1	2.26	0.66
1:C:685:ARG:HB3	1:C:685:ARG:NH1	2.10	0.66
1:B:522:PRO:HG2	1:B:636:PRO:HB3	1.78	0.66
1:C:1293:VAL:O	1:C:1294:ASP:HB2	1.95	0.66
1:C:610:GLN:HA	1:C:610:GLN:NE2	2.08	0.66
1:C:838:GLU:HG2	1:C:934:LEU:C	2.13	0.66
1:B:147:VAL:HB	1:B:379:LEU:HD22	1.78	0.66
1:B:461:ARG:HB2	1:B:461:ARG:NH1	2.03	0.66
1:B:1066:ARG:HG3	1:B:1239:ALA:HA	1.78	0.66
1:C:144:ASN:HD22	1:C:1318:GLU:CD	2.03	0.66
1:C:255:LEU:HD23	1:C:1058:GLY:C	2.20	0.66
1:C:85:ASP:OD2	1:C:161:LYS:CG	2.41	0.66
1:C:1030:ARG:C	1:C:1032:ASP:H	2.02	0.66
1:C:1077:MET:HG3	1:C:1077:MET:O	1.96	0.66
1:C:389:PHE:HZ	1:C:796:PRO:HG2	1.62	0.65
1:C:467:LYS:HZ2	1:C:467:LYS:HB3	1.62	0.65
1:C:449:PHE:CG	1:C:450:PRO:N	2.65	0.65
1:B:529:LYS:HB2	1:B:589:PHE:CE2	2.31	0.65
1:B:856:LEU:HD12	1:B:860:ARG:HE	1.60	0.65
1:C:833:ARG:NH1	1:C:942:HIS:CE1	2.63	0.65
1:B:1188:VAL:HG11	1:B:1204:LEU:HD23	1.77	0.65
1:C:1277:LEU:HD23	1:C:1287:GLY:HA3	1.78	0.65
1:C:225:ILE:HD12	1:C:247:TYR:CE1	2.32	0.65

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:607:PHE:C	1:C:608:THR:HG23	2.20	0.65
1:C:766:ILE:HD12	1:C:766:ILE:O	1.97	0.65
1:C:887:VAL:CG1	1:C:893:ALA:CB	2.72	0.65
1:C:1227:MET:O	1:C:1228:ARG:HB3	1.97	0.65
1:C:663:VAL:HG11	1:C:680:THR:HG23	1.77	0.65
1:C:926:VAL:HG11	1:C:937:ASN:HD22	1.62	0.65
1:B:397:LEU:HD21	1:C:1008:LEU:HD11	1.78	0.65
1:B:1176:GLU:HG2	1:B:1203:HIS:HE1	1.62	0.65
1:C:144:ASN:ND2	1:C:1318:GLU:OE1	2.28	0.65
1:C:157:ILE:HG12	1:C:263:ARG:HG2	1.75	0.65
1:C:317:MET:SD	1:C:1262:SER:CB	2.83	0.65
1:C:612:PHE:HD1	1:C:612:PHE:H	1.45	0.65
1:C:843:LEU:CD1	1:C:943:GLU:CB	2.73	0.65
1:C:865:ILE:HG22	1:C:957:PHE:CE2	2.30	0.65
1:C:893:ALA:HB1	1:C:915:VAL:HG12	1.77	0.65
1:B:388:GLN:CA	1:B:1320:VAL:HG12	2.27	0.65
1:C:146:GLU:O	1:C:1316:ALA:HA	1.97	0.65
1:C:924:ASP:CG	1:C:927:SER:CB	2.69	0.65
1:C:1060:ARG:HH12	1:C:1292:GLU:H	1.42	0.65
1:B:709:MET:O	1:B:715:ASN:ND2	2.30	0.65
1:C:446:LYS:HD3	1:C:448:TYR:CZ	2.31	0.65
1:C:849:MET:N	1:C:849:MET:SD	2.70	0.65
1:C:180:LEU:HD23	1:C:180:LEU:H	1.62	0.65
1:C:1268:GLY:HA3	1:C:1277:LEU:O	1.97	0.65
1:C:240:GLY:C	1:C:242:GLU:H	2.06	0.64
1:C:243:GLN:HB2	1:C:246:GLU:HG3	1.77	0.64
1:C:382:HIS:CD2	1:C:800:LEU:HD23	2.31	0.64
1:C:1074:VAL:CA	1:C:1233:LEU:HD22	2.25	0.64
1:C:213:PHE:CZ	1:C:254:VAL:HG23	2.32	0.64
1:C:741:TYR:OH	1:C:1022:ILE:HD13	1.96	0.64
1:C:1135:PRO:HG2	1:C:1137:VAL:HG13	1.78	0.64
1:B:436:SER:O	1:B:437:ALA:CB	2.45	0.64
1:C:117:ARG:HG3	1:C:121:PHE:CZ	2.32	0.64
1:B:1060:ARG:NH1	1:B:1291:LEU:O	2.29	0.64
1:C:840:ASP:CA	1:C:940:ARG:HH12	2.11	0.64
1:C:873:TYR:HD2	1:C:898:GLN:HG3	1.62	0.64
1:C:1127:ALA:O	1:C:1128:TYR:HB2	1.97	0.64
1:C:1143:GLU:C	1:C:1145:ALA:H	2.04	0.64
1:C:148:GLN:NE2	1:C:148:GLN:HA	2.12	0.64
1:C:734:ILE:O	1:C:734:ILE:HG22	1.98	0.64
1:C:741:TYR:CE2	1:C:1022:ILE:CD1	2.80	0.64

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1279:SER:HB2	1:C:1280:PRO:O	1.97	0.64
1:C:1280:PRO:HG3	1:C:1286:VAL:C	2.22	0.64
1:C:254:VAL:CG1	1:C:1062:ILE:CD1	2.70	0.64
1:C:547:GLU:HG2	1:C:600:ILE:HG13	1.79	0.64
1:C:750:GLU:HG3	1:C:750:GLU:O	1.96	0.64
1:B:313:ASP:O	1:B:317:MET:HB3	1.97	0.64
1:B:1022:ILE:HG22	1:B:1028:VAL:HA	1.79	0.64
1:C:208:LEU:HB2	1:C:221:LEU:HD22	1.77	0.64
1:C:528:ILE:HG21	1:C:758:ILE:CD1	2.18	0.64
1:C:430:ASN:C	1:C:430:ASN:HD22	2.05	0.64
1:C:334:LEU:HD11	1:C:366:MET:HE1	1.80	0.64
1:C:338:ARG:HG3	1:C:342:THR:CA	2.28	0.64
1:C:362:LEU:HD13	1:C:1302:VAL:HG11	1.79	0.64
1:C:838:GLU:C	1:C:940:ARG:HE	2.01	0.64
1:C:1020:ARG:NH1	1:C:1041:ARG:O	2.30	0.64
1:C:1210:LEU:CD2	1:C:1244:ALA:HB2	2.28	0.64
1:C:297:ASN:HD22	1:C:298:PRO:CD	2.11	0.64
1:C:753:ASP:N	1:C:753:ASP:OD1	2.30	0.64
1:C:1245:ILE:O	1:C:1245:ILE:HG13	1.98	0.64
1:B:390:HIS:HB2	1:B:1318:GLU:HG2	1.80	0.63
1:C:312:ARG:HH21	1:C:312:ARG:CG	2.09	0.63
1:C:441:ARG:HG2	1:C:441:ARG:NH2	2.12	0.63
1:C:909:TYR:CZ	1:C:913:ASN:OD1	2.50	0.63
1:B:135:LYS:CE	1:C:469:ARG:HA	2.28	0.63
1:B:440:ILE:CG2	1:B:770:CYS:SG	2.87	0.63
1:B:1185:THR:H	1:B:1205:GLN:NE2	1.95	0.63
1:C:1206:PHE:CE2	1:C:1236:ILE:CD1	2.82	0.63
1:B:204:VAL:HG11	1:B:1242:MET:HE3	1.79	0.63
1:B:1249:ASN:HB3	1:C:1110:LEU:HB2	1.81	0.63
1:C:480:LEU:HD23	1:C:480:LEU:C	2.23	0.63
1:C:452:ASN:C	1:C:453:LEU:HD22	2.23	0.63
1:C:764:TRP:HB2	1:C:765:PRO:HD3	1.79	0.63
1:C:870:ASP:OD1	1:C:870:ASP:N	2.24	0.63
1:C:1080:THR:N	1:C:1227:MET:SD	2.55	0.63
1:C:258:VAL:CG1	1:C:1058:GLY:CA	2.76	0.63
1:C:1074:VAL:O	1:C:1074:VAL:HG13	1.99	0.63
1:C:422:LEU:HD11	1:C:490:PHE:HE2	1.63	0.63
1:C:616:ASP:OD1	1:C:631:PRO:HB2	1.97	0.63
1:C:836:GLN:O	1:C:838:GLU:N	2.28	0.63
1:C:1137:VAL:CG2	1:C:1164:TRP:CE2	2.81	0.63
1:B:658:THR:HA	1:B:661:ASN:HD22	1.64	0.63

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:185:ALA:C	1:C:187:ASP:H	2.07	0.63
1:C:389:PHE:HD1	1:C:1317:VAL:CG2	2.11	0.63
1:C:655:ILE:O	1:C:659:LEU:HB3	1.98	0.63
1:C:663:VAL:O	1:C:677:ARG:CD	2.45	0.63
1:C:815:LEU:HD13	1:C:1051:ARG:HH21	1.62	0.63
1:C:1049:GLU:O	1:C:1053:ARG:CG	2.46	0.63
1:B:489:MET:SD	1:B:492:VAL:HA	2.39	0.63
1:B:529:LYS:HB2	1:B:589:PHE:HE2	1.64	0.63
1:B:897:TYR:CZ	1:B:899:SER:HB3	2.34	0.63
1:C:849:MET:HE2	1:C:929:PHE:HE2	1.64	0.63
1:C:1046:PHE:CD2	1:C:1052:LEU:HD21	2.34	0.63
1:C:75:ILE:HG23	1:C:75:ILE:O	1.98	0.63
1:C:154:PHE:CE2	1:C:365:LEU:HB2	2.34	0.63
1:C:230:ASP:O	1:C:985:ARG:HG3	1.98	0.63
1:C:1173:TYR:HB2	1:C:1202:PHE:O	1.99	0.63
1:B:848:ARG:NH1	1:B:914:GLU:O	2.32	0.62
1:B:1048:ASP:OD1	1:B:1049:GLU:N	2.32	0.62
1:C:1054:ARG:CG	1:C:1054:ARG:HH11	2.12	0.62
1:C:225:ILE:HG23	1:C:226:PRO:HD2	1.81	0.62
1:C:233:VAL:O	1:C:234:PRO:O	2.18	0.62
1:C:259:MET:O	1:C:1054:ARG:NH1	2.31	0.62
1:C:389:PHE:HE1	1:C:1319:ARG:HB3	1.64	0.62
1:B:1047:LEU:HA	1:B:1051:ARG:HH21	1.64	0.62
1:C:156:GLN:NE2	1:C:1309:ILE:HG12	2.13	0.62
1:C:164:LEU:HD11	1:C:353:PHE:CE2	2.31	0.62
1:C:571:ARG:HB3	1:C:571:ARG:NH1	2.14	0.62
1:B:1214:GLU:HG2	1:B:1215:PRO:HD2	1.80	0.62
1:C:81:ALA:CB	1:C:170:TYR:OH	2.47	0.62
1:C:478:ILE:CD1	1:C:762:ILE:CD1	2.68	0.62
1:C:834:THR:HG22	1:C:848:ARG:HG2	1.81	0.62
1:C:964:VAL:CG1	1:C:1059:LEU:HD21	2.28	0.62
1:C:1173:TYR:CD2	1:C:1204:LEU:HD11	2.35	0.62
1:B:629:ARG:NH2	1:B:1033:ASP:O	2.31	0.62
1:C:333:ARG:HH21	1:C:333:ARG:CG	2.12	0.62
1:C:389:PHE:CD1	1:C:1317:VAL:HG21	2.35	0.62
1:C:428:GLN:OE1	1:C:428:GLN:HA	1.99	0.62
1:C:1135:PRO:HD2	1:C:1164:TRP:HE1	1.64	0.62
1:C:338:ARG:HG2	1:C:342:THR:CA	2.29	0.62
1:C:611:GLY:O	1:C:634:TYR:CE2	2.50	0.62
1:C:827:GLY:HA3	1:C:964:VAL:HG21	1.80	0.62
1:C:830:VAL:HG21	1:C:947:GLU:HB3	1.62	0.62

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:985:ARG:NH2	1:C:989:ILE:HB	2.15	0.62
1:B:867:ASN:OD1	1:B:1030:ARG:HD3	2.00	0.62
1:C:656:VAL:HG12	1:C:688:GLU:HG2	1.81	0.62
1:C:1000:LEU:HD23	1:C:1010:ARG:NH2	2.13	0.62
1:C:1129:PRO:O	1:C:1130:SER:HB3	2.00	0.62
1:B:439:VAL:C	1:B:440:ILE:HG13	2.24	0.62
1:C:606:LEU:CD1	1:C:655:ILE:HG23	2.16	0.62
1:C:824:LEU:O	1:C:824:LEU:HD23	1.98	0.62
1:C:180:LEU:HD23	1:C:306:GLN:HE22	1.64	0.62
1:C:820:ILE:HD13	1:C:820:ILE:O	2.00	0.62
1:C:1060:ARG:HA	1:C:1060:ARG:NE	2.14	0.62
1:B:588:LEU:HD13	1:B:604:MET:HE3	1.81	0.62
1:B:985:ARG:HH21	1:B:988:GLN:HE21	1.46	0.62
1:C:845:GLU:CD	1:C:911:ARG:HH21	2.08	0.62
1:B:667:ALA:HA	1:B:672:MET:HE3	1.81	0.61
1:B:702:LEU:HA	1:B:705:VAL:HG22	1.82	0.61
1:B:772:TYR:HB2	1:B:775:VAL:HG12	1.81	0.61
1:C:143:VAL:HG23	1:C:143:VAL:O	2.00	0.61
1:C:206:ILE:O	1:C:1239:ALA:CB	2.46	0.61
1:C:733:VAL:HG12	1:C:1020:ARG:O	2.00	0.61
1:C:155:LYS:HD2	1:C:155:LYS:O	2.00	0.61
1:C:462:LEU:HD22	1:C:462:LEU:C	2.23	0.61
1:C:718:ASN:OD1	1:C:718:ASN:N	2.29	0.61
1:C:1134:ARG:NH2	1:C:1154:ASN:HD21	1.95	0.61
1:C:1278:TYR:CD2	1:C:1288:ILE:HG12	2.12	0.61
1:B:135:LYS:HE2	1:C:469:ARG:CA	2.30	0.61
1:C:120:VAL:O	1:C:120:VAL:HG22	2.00	0.61
1:C:255:LEU:CD2	1:C:1058:GLY:C	2.73	0.61
1:C:720:PHE:O	1:C:727:PHE:CE1	2.53	0.61
1:C:849:MET:HG2	1:C:919:MET:CE	2.30	0.61
1:C:1165:VAL:O	1:C:1165:VAL:HG12	2.01	0.61
1:C:1206:PHE:CD2	1:C:1236:ILE:HD12	2.34	0.61
1:C:163:TYR:HE2	1:C:258:VAL:HG23	1.65	0.61
1:C:579:LEU:HB2	1:C:582:SER:OG	2.00	0.61
1:C:1111:ALA:HB2	1:C:1129:PRO:HB2	1.83	0.61
1:B:793:TYR:HD2	1:B:1321:ASN:CG	2.08	0.61
1:C:508:ILE:O	1:C:508:ILE:HG13	2.00	0.61
1:C:820:ILE:CG2	1:C:983:ILE:HD11	2.30	0.61
1:B:472:GLU:N	1:B:473:ALA:HA	2.16	0.61
1:C:146:GLU:HB2	1:C:1317:VAL:HG12	1.82	0.61
1:C:232:LEU:CD2	1:C:249:SER:CB	2.52	0.61

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:674:LYS:HG3	1:C:677:ARG:HH21	1.66	0.61
1:C:1173:TYR:CG	1:C:1204:LEU:HD11	2.36	0.61
1:B:1254:PRO:O	1:B:1256:GLY:N	2.32	0.61
1:C:99:VAL:HG22	1:C:99:VAL:O	2.01	0.61
1:C:837:THR:O	1:C:838:GLU:HB2	1.99	0.61
1:C:1036:ASP:OD1	1:C:1036:ASP:N	2.34	0.61
1:C:258:VAL:CG1	1:C:1058:GLY:HA3	2.30	0.61
1:C:849:MET:CE	1:C:929:PHE:CE2	2.84	0.61
1:C:1014:MET:HG3	1:C:1017:ALA:HB2	1.81	0.61
1:C:1277:LEU:O	1:C:1278:TYR:O	2.19	0.61
1:C:348:LEU:CD1	1:C:1301:VAL:HG22	2.30	0.61
1:C:897:TYR:O	1:C:898:GLN:HG2	2.00	0.61
1:B:271:THR:HG23	1:C:237:VAL:CG2	2.31	0.61
1:B:629:ARG:NH2	1:B:1036:ASP:O	2.34	0.61
1:C:101:ASP:OD1	1:C:101:ASP:N	2.31	0.61
1:C:309:TRP:CH2	1:C:1257:ALA:HB1	2.36	0.61
1:C:372:ALA:HA	1:C:1315:MET:HE1	1.83	0.61
1:C:659:LEU:CD2	1:C:662:VAL:HG21	2.31	0.61
1:C:838:GLU:HB2	1:C:934:LEU:CG	2.26	0.61
1:C:965:ARG:NH1	1:C:968:ARG:NH1	2.48	0.61
1:C:1242:MET:SD	1:C:1260:PRO:HG3	2.41	0.61
1:C:114:VAL:HG23	1:C:114:VAL:O	2.00	0.60
1:C:873:TYR:HD2	1:C:898:GLN:CG	2.12	0.60
1:C:1271:SER:HB2	1:C:1275:ASP:O	2.01	0.60
1:B:385:ILE:HG13	1:B:1330:ILE:HG22	1.83	0.60
1:C:466:VAL:HG13	1:C:466:VAL:O	1.99	0.60
1:B:1021:ARG:O	1:B:1029:LEU:HB2	2.01	0.60
1:C:204:VAL:HG21	1:C:1242:MET:HG3	1.81	0.60
1:C:656:VAL:HG13	1:C:656:VAL:O	2.01	0.60
1:C:668:VAL:CG2	1:C:673:GLN:CB	2.66	0.60
1:B:530:GLY:O	1:B:533:GLN:HB3	2.02	0.60
1:B:590:SER:HA	1:B:725:ALA:HB2	1.81	0.60
1:C:843:LEU:HD21	1:C:943:GLU:OE2	2.01	0.60
1:C:1081:ASP:N	1:C:1227:MET:CG	2.57	0.60
1:B:1077:MET:HE2	1:B:1079:LEU:HD21	1.83	0.60
1:C:91:ASP:OD1	1:C:91:ASP:N	2.28	0.60
1:C:123:GLU:O	1:C:123:GLU:HG2	2.00	0.60
1:B:145:THR:HB	1:B:1317:VAL:HG13	1.83	0.60
1:B:453:LEU:HD12	1:B:682:GLN:HE21	1.66	0.60
1:B:1179:THR:OG1	1:B:1181:SER:O	2.18	0.60
1:C:449:PHE:CD1	1:C:450:PRO:CD	2.83	0.60

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:874:ILE:HG13	1:C:895:VAL:HG13	1.81	0.60
1:B:427:VAL:HG11	1:B:755:LEU:HD21	1.84	0.60
1:B:849:MET:SD	1:B:919:MET:HE3	2.42	0.60
1:C:184:GLU:O	1:C:187:ASP:CA	2.48	0.60
1:C:1173:TYR:CG	1:C:1204:LEU:CD1	2.85	0.60
1:C:1271:SER:HB3	1:C:1274:GLY:H	1.66	0.60
1:C:1176:GLU:HG3	1:C:1176:GLU:O	2.00	0.60
1:C:837:THR:CG2	1:C:934:LEU:HD11	2.24	0.60
1:C:874:ILE:CD1	1:C:883:ILE:HD11	2.30	0.60
1:B:475:ILE:O	1:B:475:ILE:HG23	2.01	0.60
1:C:446:LYS:CB	1:C:448:TYR:CE1	2.84	0.60
1:C:870:ASP:C	1:C:871:PRO:O	2.44	0.60
1:B:1234:GLN:HB3	1:B:1235:PRO:HD2	1.82	0.59
1:C:122:ASN:HD22	1:C:122:ASN:C	2.04	0.59
1:C:492:VAL:HG23	1:C:492:VAL:O	2.01	0.59
1:C:733:VAL:HG21	1:C:1022:ILE:CD1	2.30	0.59
1:C:862:ARG:HG2	1:C:952:PHE:CE2	2.37	0.59
1:C:1219:ASP:CG	1:C:1220:PRO:HD3	2.25	0.59
1:B:833:ARG:HD3	1:B:922:TYR:CZ	2.36	0.59
1:B:862:ARG:NH1	1:B:948:ILE:HG21	2.17	0.59
1:C:258:VAL:HG13	1:C:1058:GLY:HA3	1.84	0.59
1:C:980:ARG:O	1:C:984:GLU:HB2	2.02	0.59
1:B:1238:VAL:HG23	1:B:1239:ALA:H	1.67	0.59
1:B:1249:ASN:HB3	1:C:1110:LEU:HB3	1.84	0.59
1:C:1171:ILE:O	1:C:1171:ILE:HG12	2.02	0.59
1:C:146:GLU:HG2	1:C:1317:VAL:HG13	1.84	0.59
1:C:189:ILE:HG12	1:C:286:LEU:CD1	2.32	0.59
1:C:614:ARG:HD3	1:C:635:ILE:CD1	2.32	0.59
1:C:1044:ARG:HG3	1:C:1044:ARG:O	2.02	0.59
1:B:397:LEU:HD21	1:C:1008:LEU:CD1	2.32	0.59
1:C:120:VAL:O	1:C:120:VAL:HG13	2.01	0.59
1:C:176:LYS:HG3	1:C:177:LYS:N	2.11	0.59
1:C:948:ILE:HG23	1:C:948:ILE:O	2.03	0.59
1:B:637:TYR:HB2	1:B:703:SER:HB3	1.84	0.59
1:C:113:VAL:O	1:C:113:VAL:HG13	2.03	0.59
1:C:154:PHE:HE2	1:C:365:LEU:HB2	1.68	0.59
1:C:208:LEU:CB	1:C:221:LEU:HD22	2.32	0.59
1:C:343:ILE:CD1	1:C:366:MET:HE3	2.33	0.59
1:C:609:PRO:HB2	1:C:634:TYR:CE2	2.37	0.59
1:C:674:LYS:HB2	1:C:674:LYS:HZ2	1.67	0.59
1:C:989:ILE:HG23	1:C:990:THR:HG23	1.83	0.59

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1094:GLU:HA	1:C:1094:GLU:OE2	2.01	0.59
1:C:1298:PHE:N	1:C:1298:PHE:CD1	2.70	0.59
1:C:1325:VAL:O	1:C:1325:VAL:HG12	2.01	0.59
1:C:493:HIS:HB3	1:C:756:THR:O	2.02	0.59
1:C:494:GLU:O	1:C:494:GLU:HG2	2.02	0.59
1:C:606:LEU:HD13	1:C:655:ILE:CG2	2.17	0.59
1:C:1298:PHE:N	1:C:1298:PHE:HD1	2.00	0.59
1:B:167:SER:OG	1:B:205:ASN:OD1	2.21	0.59
1:B:313:ASP:O	1:B:317:MET:HB2	2.02	0.59
1:C:128:GLU:OE1	1:C:133:MET:CE	2.51	0.59
1:C:422:LEU:CD1	1:C:490:PHE:HE2	2.12	0.59
1:C:1280:PRO:HB3	1:C:1287:GLY:CA	2.27	0.59
1:B:1071:PHE:CZ	1:B:1236:ILE:HD13	2.38	0.59
1:C:928:ARG:H	1:C:928:ARG:CD	2.15	0.59
1:B:231:LEU:HB2	1:B:249:SER:HB2	1.85	0.59
1:C:213:PHE:CE1	1:C:254:VAL:HG23	2.37	0.59
1:C:230:ASP:OD2	1:C:985:ARG:NE	2.27	0.59
1:C:244:SER:O	1:C:247:TYR:HB3	2.03	0.59
1:C:1079:LEU:O	1:C:1227:MET:HB3	2.03	0.59
1:C:1104:ARG:HG2	1:C:1104:ARG:NH1	2.18	0.59
1:B:188:ARG:HH22	1:C:237:VAL:CG1	2.16	0.58
1:B:388:GLN:N	1:B:1320:VAL:CG1	2.64	0.58
1:C:108:LYS:HG3	1:C:108:LYS:O	2.02	0.58
1:C:1060:ARG:HA	1:C:1060:ARG:HE	1.68	0.58
1:B:272:THR:CG2	1:C:235:ILE:HG21	2.33	0.58
1:B:472:GLU:HB2	1:B:761:SER:CB	2.33	0.58
1:B:1285:GLN:O	1:B:1286:VAL:HG23	2.03	0.58
1:C:197:PHE:CD1	1:C:1242:MET:HE2	2.38	0.58
1:C:248:VAL:HG11	1:C:970:LEU:CB	2.21	0.58
1:C:389:PHE:CD1	1:C:1319:ARG:HB3	2.37	0.58
1:C:451:GLU:HB2	1:C:686:HIS:CB	2.33	0.58
1:C:840:ASP:C	1:C:940:ARG:HH22	2.11	0.58
1:C:1174:THR:HG23	1:C:1174:THR:O	2.03	0.58
1:C:463:VAL:O	1:C:467:LYS:HG3	2.03	0.58
1:C:654:THR:HG22	1:C:658:THR:HG22	1.82	0.58
1:C:756:THR:O	1:C:756:THR:HG22	2.01	0.58
1:C:408:ILE:HG22	1:C:408:ILE:O	2.04	0.58
1:C:1070:ARG:O	1:C:1070:ARG:HG2	2.02	0.58
1:C:81:ALA:HB3	1:C:170:TYR:OH	2.02	0.58
1:C:427:VAL:O	1:C:431:THR:HG22	2.03	0.58
1:C:560:ILE:HG23	1:C:560:ILE:O	2.02	0.58

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:820:ILE:HG21	1:C:983:ILE:CD1	2.33	0.58
1:C:850:THR:OG1	1:C:916:LEU:CD2	2.52	0.58
1:C:901:VAL:HG13	1:C:901:VAL:O	2.04	0.58
1:C:963:ALA:HB3	1:C:1059:LEU:CG	2.30	0.58
1:C:1135:PRO:O	1:C:1136:HIS:HB2	2.04	0.58
1:C:1276:LEU:HD23	1:C:1276:LEU:H	1.68	0.58
1:C:256:PHE:HD1	1:C:819:PHE:CE2	2.21	0.58
1:C:822:MET:CE	1:C:1046:PHE:HE2	2.08	0.58
1:B:699:THR:O	1:B:703:SER:HB3	2.04	0.58
1:B:922:TYR:O	1:B:925:VAL:HG13	2.04	0.58
1:C:668:VAL:HG23	1:C:673:GLN:HE21	1.68	0.58
1:C:849:MET:CA	1:C:917:VAL:O	2.50	0.58
1:C:892:VAL:HG11	1:C:894:VAL:HG13	1.63	0.58
1:C:935:GLN:HB3	1:C:939:ASN:CB	2.31	0.58
1:C:957:PHE:CD1	1:C:957:PHE:N	2.72	0.58
1:C:1121:HIS:CD2	1:C:1135:PRO:HG2	2.37	0.58
1:C:615:THR:N	1:C:1333:ALA:C	2.59	0.58
1:C:1055:LEU:O	1:C:1055:LEU:HG	2.01	0.58
1:B:893:ALA:HB1	1:B:915:VAL:HA	1.86	0.58
1:C:360:ILE:HG22	1:C:360:ILE:O	2.03	0.58
1:C:607:PHE:C	1:C:608:THR:CG2	2.77	0.58
1:C:1198:LYS:O	1:C:1198:LYS:HD3	2.03	0.58
1:B:1250:GLU:O	1:B:1251:VAL:HG13	2.04	0.58
1:C:389:PHE:CD1	1:C:1317:VAL:CG2	2.86	0.58
1:C:452:ASN:O	1:C:453:LEU:HD22	2.03	0.58
1:C:644:VAL:HG13	1:C:644:VAL:O	2.03	0.58
1:C:644:VAL:O	1:C:644:VAL:HG22	2.02	0.58
1:C:918:VAL:HG23	1:C:918:VAL:O	2.02	0.58
1:B:824:LEU:HD22	1:B:979:ILE:HD12	1.86	0.57
1:C:1014:MET:CG	1:C:1017:ALA:HB2	2.34	0.57
1:B:372:ALA:HB3	1:B:1315:MET:HE3	1.86	0.57
1:B:461:ARG:HH11	1:B:461:ARG:CG	2.15	0.57
1:B:1076:ILE:HG12	1:B:1230:ILE:HG22	1.85	0.57
1:C:259:MET:HA	1:C:1054:ARG:HB3	1.86	0.57
1:C:439:VAL:HG22	1:C:439:VAL:O	2.03	0.57
1:C:1085:ASP:HB2	1:C:1086:PRO:HD2	1.83	0.57
1:B:1064:ASN:ND2	1:B:1296:ILE:HD11	2.18	0.57
1:C:314:ILE:HG22	1:C:318:LEU:HD22	1.87	0.57
1:C:422:LEU:C	1:C:422:LEU:HD13	2.29	0.57
1:C:656:VAL:CG1	1:C:688:GLU:CG	2.82	0.57
1:C:668:VAL:CG2	1:C:673:GLN:HE21	2.17	0.57

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:747:ARG:HG2	1:C:747:ARG:HH11	1.68	0.57
1:C:965:ARG:HH11	1:C:968:ARG:HH12	1.50	0.57
1:C:1121:HIS:CD2	1:C:1135:PRO:CB	2.87	0.57
1:C:154:PHE:HE1	1:C:361:ASN:HD21	1.50	0.57
1:C:405:HIS:CD2	1:C:625:PRO:CA	2.83	0.57
1:C:610:GLN:HE21	1:C:610:GLN:CA	2.12	0.57
1:C:709:MET:O	1:C:715:ASN:ND2	2.37	0.57
1:C:1140:THR:HA	1:C:1167:ASP:HB3	1.86	0.57
1:B:261:ASP:OD2	1:B:263:ARG:NH2	2.37	0.57
1:B:577:GLN:O	1:B:580:TYR:N	2.37	0.57
1:C:838:GLU:C	1:C:940:ARG:CZ	2.77	0.57
1:C:1023:ARG:HB3	1:C:1023:ARG:HH21	1.68	0.57
1:C:1310:ARG:HA	1:C:1310:ARG:NE	2.19	0.57
1:B:141:LEU:HD11	1:B:1318:GLU:HG2	1.87	0.57
1:B:874:ILE:HG23	1:B:895:VAL:HG21	1.86	0.57
1:C:309:TRP:CD1	1:C:309:TRP:C	2.83	0.57
1:C:403:PHE:CZ	1:C:408:ILE:HG13	2.39	0.57
1:C:736:SER:HB2	1:C:1016:ASN:C	2.28	0.57
1:C:342:THR:O	1:C:1305:MET:CE	2.52	0.57
1:C:654:THR:CG2	1:C:658:THR:CG2	2.77	0.57
1:C:635:ILE:HD11	1:C:707:ALA:HA	1.85	0.57
1:C:1261:SER:C	1:C:1263:TYR:H	2.12	0.57
1:C:451:GLU:OE1	1:C:685:ARG:HG2	2.03	0.57
1:C:585:PHE:CE1	1:C:728:LYS:HE2	2.40	0.57
1:C:762:ILE:HD12	1:C:762:ILE:O	2.04	0.57
1:B:469:ARG:NH1	1:B:498:ILE:CG1	2.61	0.57
1:C:389:PHE:HD1	1:C:1317:VAL:HG22	1.70	0.57
1:C:434:VAL:HG23	1:C:709:MET:CE	2.33	0.57
1:B:472:GLU:C	1:B:761:SER:HB2	2.27	0.56
1:C:339:LEU:CD1	1:C:397:LEU:HD23	2.34	0.56
1:C:478:ILE:HD13	1:C:762:ILE:HD11	1.80	0.56
1:C:521:PHE:N	1:C:521:PHE:CD1	2.71	0.56
1:C:668:VAL:CG1	1:C:674:LYS:HD3	2.35	0.56
1:C:820:ILE:HG21	1:C:983:ILE:HG13	1.83	0.56
1:C:915:VAL:HG23	1:C:915:VAL:O	2.04	0.56
1:C:1231:TYR:N	1:C:1231:TYR:CD1	2.72	0.56
1:B:184:GLU:O	1:B:188:ARG:HG2	2.04	0.56
1:B:831:VAL:H	1:B:854:GLN:HE21	1.52	0.56
1:B:957:PHE:HB2	1:B:1042:TRP:CZ3	2.40	0.56
1:B:383:SER:HB3	1:B:387:THR:HG21	1.86	0.56
1:B:461:ARG:NE	1:B:504:ASP:HB2	2.18	0.56

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:472:GLU:O	1:B:761:SER:CB	2.38	0.56
1:C:109:LYS:HB3	1:C:109:LYS:NZ	2.21	0.56
1:C:362:LEU:HD23	1:C:362:LEU:O	2.04	0.56
1:C:446:LYS:HB3	1:C:448:TYR:CZ	2.40	0.56
1:C:471:SER:HB3	1:C:765:PRO:HG2	1.87	0.56
1:C:503:GLU:OE2	1:C:542:ARG:CD	2.50	0.56
1:C:747:ARG:HH11	1:C:747:ARG:CG	2.18	0.56
1:C:890:THR:O	1:C:890:THR:OG1	2.21	0.56
1:C:928:ARG:H	1:C:928:ARG:HD3	1.70	0.56
1:C:1054:ARG:NH1	1:C:1054:ARG:HG2	2.19	0.56
1:C:613:LEU:HD22	1:C:613:LEU:C	2.29	0.56
1:C:661:ASN:O	1:C:665:GLU:HB3	2.05	0.56
1:C:1000:LEU:CD2	1:C:1010:ARG:CZ	2.81	0.56
1:B:637:TYR:HB3	1:B:699:THR:HA	1.88	0.56
1:C:874:ILE:CG2	1:C:902:ILE:CD1	2.82	0.56
1:C:1135:PRO:HG2	1:C:1137:VAL:CG1	2.34	0.56
1:B:1121:HIS:HD2	1:B:1124:THR:HG22	1.69	0.56
1:C:225:ILE:HD11	1:C:1069:ARG:CB	2.36	0.56
1:C:929:PHE:HB2	1:C:936:MET:CE	2.29	0.56
1:C:498:ILE:CD1	1:C:514:PHE:HZ	2.19	0.56
1:C:579:LEU:C	1:C:579:LEU:HD12	2.31	0.56
1:C:582:SER:O	1:C:728:LYS:HD2	2.05	0.56
1:C:1317:VAL:HG13	1:C:1317:VAL:O	2.05	0.56
1:B:338:ARG:NH1	1:C:1005:LEU:HD22	2.21	0.56
1:B:558:TYR:CZ	1:B:590:SER:HB3	2.41	0.56
1:C:96:ILE:HD11	1:C:103:GLY:HA2	1.84	0.56
1:C:449:PHE:HZ	1:C:463:VAL:HG22	1.70	0.56
1:C:556:ALA:O	1:C:587:ALA:HB2	2.04	0.56
1:C:1290:LYS:HZ1	1:C:1299:SER:HB3	1.71	0.56
1:B:489:MET:SD	1:B:527:ARG:HD2	2.46	0.56
1:C:538:LEU:HD21	1:C:542:ARG:HH21	1.70	0.56
1:C:772:TYR:N	1:C:772:TYR:CD1	2.74	0.56
1:B:310:LEU:O	1:B:314:ILE:HG12	2.05	0.56
1:C:554:ARG:CD	1:C:594:LEU:HD21	2.30	0.56
1:C:1111:ALA:HB2	1:C:1129:PRO:CB	2.36	0.56
1:B:287:ARG:HH11	1:B:330:THR:HB	1.71	0.55
1:B:303:ASP:HA	1:B:311:ASN:HD21	1.71	0.55
1:B:1306:THR:HG22	1:B:1307:ALA:H	1.69	0.55
1:C:694:ILE:C	1:C:694:ILE:HD12	2.31	0.55
1:C:758:ILE:HG13	1:C:758:ILE:O	2.06	0.55
1:C:987:ALA:O	1:C:992:VAL:HG13	2.06	0.55

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1081:ASP:N	1:C:1227:MET:CB	2.68	0.55
1:C:1332:ASN:O	1:C:1333:ALA:OXT	2.24	0.55
1:B:264:LEU:HD11	1:B:365:LEU:HD11	1.88	0.55
1:B:414:LEU:HA	1:B:734:ILE:HD11	1.88	0.55
1:B:1290:LYS:HE2	1:B:1300:ASN:HB3	1.87	0.55
1:B:198:LYS:O	1:B:200:GLY:HA2	2.06	0.55
1:C:213:PHE:CZ	1:C:254:VAL:CG2	2.88	0.55
1:C:259:MET:O	1:C:1054:ARG:HG2	2.07	0.55
1:C:348:LEU:HD12	1:C:1301:VAL:HG22	1.88	0.55
1:C:654:THR:C	1:C:658:THR:HG22	2.25	0.55
1:C:672:MET:SD	1:C:672:MET:C	2.89	0.55
1:C:838:GLU:HB2	1:C:934:LEU:CD1	2.36	0.55
1:C:874:ILE:HG22	1:C:874:ILE:O	2.06	0.55
1:C:1175:ALA:HA	1:C:1204:LEU:O	2.07	0.55
1:C:1176:GLU:HG2	1:C:1203:HIS:HE1	1.72	0.55
1:B:924:ASP:OD1	1:B:927:SER:HB2	2.07	0.55
1:C:304:PHE:N	1:C:304:PHE:CD1	2.71	0.55
1:C:387:THR:HG23	1:C:387:THR:O	2.06	0.55
1:C:465:ALA:CB	1:C:506:SER:HB3	2.36	0.55
1:C:838:GLU:HG2	1:C:935:GLN:N	2.14	0.55
1:C:878:SER:HB3	1:C:903:ASN:CG	2.31	0.55
1:C:986:ILE:C	1:C:989:ILE:HG22	2.32	0.55
1:C:1074:VAL:HB	1:C:1173:TYR:CE2	2.37	0.55
1:C:117:ARG:CG	1:C:121:PHE:CZ	2.89	0.55
1:C:461:ARG:HG3	1:C:461:ARG:O	2.06	0.55
1:C:607:PHE:O	1:C:608:THR:HG22	2.06	0.55
1:B:309:TRP:CH2	1:B:1257:ALA:HB1	2.42	0.55
1:B:576:ASP:OD1	1:B:577:GLN:N	2.39	0.55
1:C:225:ILE:HD11	1:C:1069:ARG:CA	2.37	0.55
1:C:230:ASP:HB3	1:C:985:ARG:HG3	1.77	0.55
1:C:446:LYS:CD	1:C:448:TYR:CZ	2.89	0.55
1:C:735:THR:HG21	1:C:1028:VAL:CG2	2.34	0.55
1:C:926:VAL:CG1	1:C:937:ASN:HD22	2.19	0.55
1:C:1000:LEU:HD23	1:C:1010:ARG:HE	1.71	0.55
1:B:276:ASN:OD1	1:C:1199:GLY:HA3	2.07	0.55
1:B:315:THR:O	1:B:319:GLN:HB2	2.06	0.55
1:C:254:VAL:HG13	1:C:1062:ILE:HD13	1.89	0.55
1:C:469:ARG:NH2	1:C:498:ILE:HG23	2.21	0.55
1:B:157:ILE:HD11	1:B:265:VAL:HG22	1.88	0.55
1:B:307:VAL:HG13	1:B:310:LEU:HB3	1.88	0.55
1:C:588:LEU:HG	1:C:604:MET:SD	2.47	0.55

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:738:GLU:HB3	1:C:1015:GLN:HG3	1.87	0.55
1:C:838:GLU:HA	1:C:940:ARG:HD3	1.89	0.55
1:C:1054:ARG:HH11	1:C:1054:ARG:HG2	1.71	0.55
1:C:1116:ARG:NH1	1:C:1130:SER:HB2	2.22	0.55
1:C:1290:LYS:NZ	1:C:1299:SER:HB3	2.22	0.55
1:B:332:THR:HG23	1:B:344:VAL:HG12	1.89	0.55
1:C:144:ASN:HB3	1:C:1318:GLU:CD	2.27	0.55
1:C:334:LEU:HD11	1:C:366:MET:CE	2.37	0.55
1:C:547:GLU:HG3	1:C:597:ALA:HA	1.90	0.55
1:C:551:PHE:CD1	1:C:551:PHE:C	2.85	0.55
1:C:714:LEU:HD11	1:C:806:VAL:HG12	1.89	0.55
1:C:1044:ARG:CG	1:C:1044:ARG:NH1	2.70	0.55
1:B:1124:THR:HG23	1:B:1126:MET:H	1.72	0.54
1:C:146:GLU:CB	1:C:1317:VAL:CG1	2.85	0.54
1:B:235:ILE:HG13	1:B:978:GLN:NE2	2.14	0.54
1:B:832:MET:SD	1:B:848:ARG:HD2	2.47	0.54
1:C:157:ILE:HG13	1:C:263:ARG:HG2	1.86	0.54
1:C:163:TYR:N	1:C:163:TYR:CD1	2.71	0.54
1:C:498:ILE:H	1:C:498:ILE:HD12	1.72	0.54
1:C:547:GLU:CD	1:C:599:THR:HG23	2.32	0.54
1:C:1097:VAL:O	1:C:1097:VAL:HG13	2.06	0.54
1:B:875:THR:OG1	1:B:876:GLY:HA2	2.07	0.54
1:C:225:ILE:HG23	1:C:247:TYR:CD1	2.40	0.54
1:C:837:THR:CG2	1:C:934:LEU:CD1	2.68	0.54
1:C:892:VAL:HG12	1:C:894:VAL:H	1.72	0.54
1:C:1171:ILE:CD1	1:C:1202:PHE:CZ	2.78	0.54
1:B:926:VAL:CG2	1:B:938:ASN:H	2.20	0.54
1:C:1281:VAL:C	1:C:1283:ASN:N	2.58	0.54
1:B:515:ILE:HG21	1:B:655:ILE:HG21	1.90	0.54
1:C:495:LEU:N	1:C:495:LEU:CD1	2.70	0.54
1:C:972:PRO:O	1:C:972:PRO:HG2	2.08	0.54
1:C:1310:ARG:HH21	1:C:1312:GLY:H	1.55	0.54
1:B:291:HIS:CD2	1:B:348:LEU:HD21	2.43	0.54
1:B:1276:LEU:HD22	1:B:1300:ASN:HB2	1.89	0.54
1:C:820:ILE:CG2	1:C:983:ILE:CG1	2.77	0.54
1:C:1310:ARG:NE	1:C:1310:ARG:CA	2.70	0.54
1:C:511:VAL:HG21	1:C:539:PHE:CZ	2.43	0.54
1:C:887:VAL:HG22	1:C:893:ALA:HA	1.90	0.54
1:C:1134:ARG:HH22	1:C:1154:ASN:ND2	2.04	0.54
1:C:1179:THR:HG23	1:C:1179:THR:O	2.07	0.54
1:C:1193:ILE:HG23	1:C:1193:ILE:O	2.06	0.54

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:291:HIS:CE1	1:B:1304:MET:HE1	2.43	0.54
1:B:1314:ASP:N	1:B:1314:ASP:OD1	2.40	0.54
1:C:168:VAL:CG2	1:C:204:VAL:CG1	2.85	0.54
1:C:220:ASP:OD1	1:C:222:THR:HG23	2.08	0.54
1:C:265:VAL:O	1:C:1303:SER:HA	2.08	0.54
1:C:364:ALA:CB	1:C:1050:LEU:CD2	2.85	0.54
1:C:446:LYS:CB	1:C:448:TYR:CZ	2.91	0.54
1:B:225:ILE:HG23	1:B:1069:ARG:HB2	1.90	0.54
1:C:81:ALA:HB3	1:C:168:VAL:CG1	2.38	0.54
1:C:427:VAL:O	1:C:427:VAL:HG12	2.07	0.54
1:C:458:SER:HB3	1:C:675:ALA:HB1	1.90	0.54
1:C:500:GLU:HA	1:C:500:GLU:OE1	2.08	0.54
1:C:515:ILE:HG21	1:C:655:ILE:HG21	1.89	0.54
1:C:559:THR:HG22	1:C:583:GLU:HG3	1.90	0.54
1:C:612:PHE:N	1:C:612:PHE:CD1	2.73	0.54
1:C:736:SER:CB	1:C:1016:ASN:O	2.46	0.54
1:C:1242:MET:HE3	1:C:1245:ILE:HG21	1.90	0.54
1:B:206:ILE:HB	1:B:1066:ARG:HD3	1.90	0.53
1:B:434:VAL:O	1:B:439:VAL:HG22	2.09	0.53
1:C:258:VAL:CG1	1:C:1058:GLY:HA2	2.34	0.53
1:C:449:PHE:N	1:C:450:PRO:HD3	2.22	0.53
1:C:666:ARG:HG2	1:C:666:ARG:NH1	2.18	0.53
1:C:843:LEU:CD2	1:C:943:GLU:HG3	2.38	0.53
1:C:297:ASN:ND2	1:C:298:PRO:CD	2.67	0.53
1:C:385:ILE:O	1:C:1328:ILE:CG2	2.56	0.53
1:C:929:PHE:CD2	1:C:936:MET:CE	2.84	0.53
1:C:985:ARG:HH22	1:C:989:ILE:HB	1.71	0.53
1:B:139:ASN:O	1:C:757:ILE:CB	2.56	0.53
1:B:1282:ALA:HB1	1:B:1283:ASN:CA	2.39	0.53
1:C:146:GLU:HB2	1:C:1317:VAL:HG13	1.90	0.53
1:C:505:PRO:O	1:C:508:ILE:HG22	2.08	0.53
1:C:741:TYR:CZ	1:C:1022:ILE:CD1	2.91	0.53
1:C:1173:TYR:CE1	1:C:1204:LEU:CD1	2.91	0.53
1:C:1202:PHE:CD1	1:C:1202:PHE:C	2.84	0.53
1:C:1297:SER:C	1:C:1298:PHE:HD1	2.16	0.53
1:B:1250:GLU:OE1	1:B:1250:GLU:N	2.41	0.53
1:C:259:MET:SD	1:C:1055:LEU:HB2	2.48	0.53
1:C:445:GLU:CD	1:C:447:ARG:HG2	2.22	0.53
1:C:543:TRP:HD1	1:C:544:TYR:HD1	1.54	0.53
1:C:635:ILE:HG23	1:C:635:ILE:O	2.08	0.53
1:C:849:MET:CG	1:C:919:MET:HG3	2.39	0.53

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:352:HIS:CD2	1:C:1297:SER:H	2.17	0.53
1:C:571:ARG:NH1	1:C:571:ARG:CB	2.71	0.53
1:C:1046:PHE:HB2	1:C:1052:LEU:HD21	1.90	0.53
1:C:1118:THR:HB	1:C:1129:PRO:HA	1.91	0.53
1:C:1322:PRO:CB	1:C:1328:ILE:HD11	2.38	0.53
1:B:1242:MET:SD	1:B:1260:PRO:HG3	2.49	0.53
1:C:157:ILE:CD1	1:C:263:ARG:HB3	2.36	0.53
1:C:206:ILE:HD11	1:C:1066:ARG:CD	2.39	0.53
1:C:652:PHE:HE1	1:C:688:GLU:HB3	1.74	0.53
1:C:836:GLN:C	1:C:838:GLU:H	2.14	0.53
1:C:1319:ARG:HG3	1:C:1319:ARG:O	2.08	0.53
1:B:1158:SER:O	1:B:1162:SER:HB2	2.09	0.53
1:C:154:PHE:HD1	1:C:262:ASN:HB2	1.73	0.53
1:C:651:ARG:HD2	1:C:651:ARG:O	2.08	0.53
1:C:865:ILE:HD13	1:C:865:ILE:N	2.23	0.53
1:C:1307:ALA:O	1:C:1309:ILE:N	2.39	0.53
1:C:1318:GLU:O	1:C:1318:GLU:HG2	2.08	0.53
1:C:144:ASN:HA	1:C:1318:GLU:HB3	1.91	0.53
1:C:1159:VAL:O	1:C:1159:VAL:HG22	2.09	0.53
1:B:373:ASP:O	1:B:376:ILE:HB	2.09	0.53
1:C:840:ASP:CA	1:C:940:ARG:HH22	2.22	0.53
1:C:1014:MET:HG3	1:C:1017:ALA:CB	2.38	0.53
1:C:1022:ILE:HG12	1:C:1027:THR:O	2.08	0.53
1:C:1231:TYR:HB3	1:C:1232:PRO:CD	2.39	0.53
1:B:388:GLN:N	1:B:1320:VAL:HG12	2.24	0.53
1:B:1148:SER:HB2	1:B:1151:VAL:H	1.74	0.53
1:C:256:PHE:HD1	1:C:819:PHE:CD2	2.26	0.53
1:C:910:LEU:HD23	1:C:915:VAL:HG23	0.57	0.53
1:C:1258:VAL:HG23	1:C:1258:VAL:O	2.07	0.53
1:C:1283:ASN:N	1:C:1283:ASN:OD1	2.41	0.53
1:B:309:TRP:HB3	1:B:1252:ASP:O	2.10	0.52
1:C:434:VAL:O	1:C:434:VAL:HG12	2.09	0.52
1:C:466:VAL:O	1:C:466:VAL:HG22	2.07	0.52
1:C:1002:LEU:HD13	1:C:1005:LEU:HD13	1.91	0.52
1:B:197:PHE:HD2	1:B:301:LEU:HD22	1.74	0.52
1:B:874:ILE:H	1:B:897:TYR:HB3	1.75	0.52
1:B:1071:PHE:HZ	1:B:1236:ILE:HD13	1.74	0.52
1:C:189:ILE:HG12	1:C:286:LEU:HD12	1.91	0.52
1:C:498:ILE:HD11	1:C:514:PHE:HZ	1.75	0.52
1:C:1084:PRO:C	1:C:1208:ASP:O	2.50	0.52
1:C:1322:PRO:HB2	1:C:1328:ILE:HD11	1.91	0.52

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:144:ASN:H	1:B:1318:GLU:H	1.58	0.52
1:C:168:VAL:CB	1:C:204:VAL:HG12	2.38	0.52
1:C:233:VAL:HG22	1:C:234:PRO:HD2	0.57	0.52
1:C:403:PHE:CE1	1:C:408:ILE:HG13	2.44	0.52
1:C:536:LEU:HD11	1:C:607:PHE:CZ	2.44	0.52
1:B:472:GLU:HB3	1:B:761:SER:HG	1.66	0.52
1:B:626:ARG:NH2	1:B:712:PHE:O	2.43	0.52
1:C:186:ASP:CG	1:C:279:SER:N	2.62	0.52
1:C:285:VAL:HG13	1:C:326:GLY:HA2	1.91	0.52
1:C:607:PHE:O	1:C:608:THR:HG23	2.09	0.52
1:C:1046:PHE:CD2	1:C:1052:LEU:CD2	2.93	0.52
1:B:352:HIS:HD2	1:B:1297:SER:H	1.57	0.52
1:C:822:MET:C	1:C:822:MET:SD	2.92	0.52
1:C:855:TYR:CD1	1:C:859:ILE:HB	2.44	0.52
1:C:879:THR:N	1:C:880:PRO:HD2	2.09	0.52
1:B:388:GLN:CA	1:B:1320:VAL:CG1	2.87	0.52
1:B:472:GLU:N	1:B:473:ALA:CA	2.73	0.52
1:B:817:ASP:OD1	1:B:983:ILE:HG21	2.09	0.52
1:C:350:ILE:O	1:C:350:ILE:HG13	2.09	0.52
1:C:397:LEU:H	1:C:397:LEU:HD12	1.72	0.52
1:C:603:ILE:HD13	1:C:659:LEU:HD23	1.91	0.52
1:C:838:GLU:HB2	1:C:934:LEU:HB2	0.53	0.52
1:C:1097:VAL:HG12	1:C:1136:HIS:O	2.10	0.52
1:C:1099:VAL:O	1:C:1139:MET:HA	2.10	0.52
1:C:1105:LEU:HD12	1:C:1105:LEU:N	2.20	0.52
1:B:451:GLU:HG2	1:B:452:ASN:N	2.25	0.52
1:B:588:LEU:HD22	1:B:604:MET:HE3	1.91	0.52
1:C:157:ILE:HD11	1:C:263:ARG:NE	2.24	0.52
1:C:157:ILE:CD1	1:C:263:ARG:CG	2.61	0.52
1:C:341:LYS:CB	1:C:1306:THR:HB	2.39	0.52
1:C:449:PHE:N	1:C:450:PRO:CD	2.72	0.52
1:C:713:MET:CE	1:C:804:LEU:CD2	2.74	0.52
1:C:750:GLU:HA	1:C:756:THR:HG21	1.90	0.52
1:C:937:ASN:OD1	1:C:937:ASN:N	2.41	0.52
1:C:1193:ILE:HG13	1:C:1202:PHE:CZ	2.43	0.52
1:B:878:SER:O	1:B:879:THR:HG23	2.09	0.52
1:C:193:THR:HG21	1:C:300:LEU:HB3	1.91	0.52
1:C:1105:LEU:HD12	1:C:1105:LEU:C	2.35	0.52
1:B:559:THR:HG23	1:B:583:GLU:HG3	1.90	0.52
1:C:118:THR:O	1:C:119:ASP:C	2.52	0.52
1:C:285:VAL:CG1	1:C:326:GLY:HA2	2.39	0.52

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:830:VAL:HG21	1:C:947:GLU:CG	2.38	0.52
1:C:929:PHE:HB3	1:C:936:MET:CE	2.38	0.52
1:C:967:LEU:HD22	1:C:1062:ILE:HG21	1.92	0.52
1:C:1021:ARG:CB	1:C:1021:ARG:NH1	2.72	0.52
1:B:897:TYR:CE2	1:B:899:SER:HB3	2.44	0.52
1:C:146:GLU:CB	1:C:1317:VAL:HG12	2.40	0.52
1:C:442:PRO:HG2	1:C:442:PRO:O	2.09	0.52
1:C:543:TRP:CD1	1:C:543:TRP:C	2.86	0.52
1:C:656:VAL:HG11	1:C:688:GLU:CG	2.39	0.52
1:C:686:HIS:ND1	1:C:686:HIS:C	2.68	0.52
1:C:835:TYR:CE1	1:C:942:HIS:CD2	2.98	0.52
1:C:924:ASP:OD1	1:C:927:SER:CA	2.57	0.52
1:C:1230:ILE:O	1:C:1230:ILE:HG13	2.09	0.52
1:C:1247:ASN:HD22	1:C:1247:ASN:N	2.07	0.52
1:B:188:ARG:HH22	1:C:237:VAL:HG13	1.75	0.51
1:B:440:ILE:CG2	1:B:770:CYS:HB2	2.41	0.51
1:B:924:ASP:HB3	1:B:928:ARG:CZ	2.40	0.51
1:C:338:ARG:O	1:C:341:LYS:N	2.42	0.51
1:C:467:LYS:HZ2	1:C:467:LYS:CB	2.22	0.51
1:C:1081:ASP:O	1:C:1227:MET:HB3	2.10	0.51
1:C:1279:SER:H	1:C:1280:PRO:HA	1.70	0.51
1:C:339:LEU:O	1:C:397:LEU:HD21	2.10	0.51
1:C:511:VAL:CG2	1:C:539:PHE:CE2	2.93	0.51
1:C:612:PHE:CE2	1:C:614:ARG:HB3	2.45	0.51
1:C:928:ARG:CD	1:C:928:ARG:N	2.73	0.51
1:B:1103:HIS:CE1	1:B:1145:ALA:HB3	2.45	0.51
1:C:210:ARG:HA	1:C:221:LEU:CD1	2.39	0.51
1:C:254:VAL:HG11	1:C:1062:ILE:HD11	1.87	0.51
1:C:310:LEU:CD2	1:C:1242:MET:HE1	2.25	0.51
1:C:452:ASN:C	1:C:453:LEU:CD2	2.81	0.51
1:C:484:ARG:O	1:C:485:GLU:C	2.47	0.51
1:B:1306:THR:HG22	1:B:1307:ALA:N	2.25	0.51
1:C:1112:ASN:HD22	1:C:1112:ASN:C	2.01	0.51
1:B:517:PHE:CE2	1:B:528:ILE:HD11	2.46	0.51
1:C:434:VAL:CG2	1:C:709:MET:CE	2.88	0.51
1:C:669:GLN:OE1	1:C:669:GLN:N	2.43	0.51
1:C:815:LEU:CB	1:C:816:PRO:CD	2.81	0.51
1:C:1054:ARG:HH11	1:C:1054:ARG:CB	2.23	0.51
1:C:1259:ALA:HB1	1:C:1260:PRO:HD2	1.91	0.51
1:B:150:LEU:HD21	1:B:378:ALA:HB3	1.93	0.51
1:B:489:MET:SD	1:B:493:HIS:ND1	2.81	0.51

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:735:THR:HG21	1:B:1028:VAL:HG11	1.92	0.51
1:B:1128:TYR:HB3	1:B:1134:ARG:HG2	1.93	0.51
1:C:264:LEU:O	1:C:266:ILE:HG12	2.11	0.51
1:C:336:TYR:O	1:C:337:VAL:O	2.29	0.51
1:C:502:PHE:HA	1:C:507:SER:CB	2.41	0.51
1:C:1310:ARG:HG3	1:C:1310:ARG:O	2.11	0.51
1:B:461:ARG:NH1	1:B:461:ARG:CG	2.73	0.51
1:B:531:ASP:OD1	1:B:531:ASP:N	2.37	0.51
1:B:974:LEU:HA	1:B:978:GLN:OE1	2.10	0.51
1:B:1066:ARG:HD2	1:B:1296:ILE:HD13	1.92	0.51
1:C:409:ILE:HG23	1:C:1040:PHE:CZ	2.44	0.51
1:C:849:MET:HG2	1:C:919:MET:HG3	1.92	0.51
1:C:1222:ALA:O	1:C:1223:SER:HB2	2.10	0.51
1:B:1121:HIS:CD2	1:B:1123:PRO:HD2	2.45	0.51
1:B:1134:ARG:NH1	1:B:1158:SER:OG	2.44	0.51
1:C:285:VAL:O	1:C:327:LEU:N	2.39	0.51
1:C:285:VAL:O	1:C:326:GLY:HA2	2.11	0.51
1:C:320:GLN:O	1:C:321:ALA:CB	2.58	0.51
1:C:450:PRO:C	1:C:454:GLU:HG2	2.35	0.51
1:C:516:LEU:HB2	1:C:763:VAL:HG11	1.90	0.51
1:C:668:VAL:CG1	1:C:674:LYS:CD	2.88	0.51
1:B:388:GLN:CB	1:B:1320:VAL:HG11	2.12	0.51
1:C:190:VAL:HG11	1:C:304:PHE:CZ	2.46	0.51
1:C:231:LEU:HD13	1:C:982:ALA:HB1	1.93	0.51
1:C:485:GLU:OE1	1:C:486:VAL:CG1	2.56	0.51
1:C:849:MET:HG2	1:C:919:MET:HE3	1.93	0.51
1:B:879:THR:O	1:B:883:ILE:HD12	2.09	0.51
1:C:1101:TYR:OH	1:C:1147:MET:HG2	2.10	0.51
1:B:231:LEU:HD23	1:B:985:ARG:HB3	1.93	0.50
1:B:305:THR:HG22	1:B:307:VAL:HG12	1.92	0.50
1:B:526:ASN:HB2	1:B:721:SER:HB3	1.92	0.50
1:C:233:VAL:HG11	1:C:981:HIS:HE2	1.53	0.50
1:C:252:LEU:CD1	1:C:971:MET:HE3	2.38	0.50
1:C:337:VAL:HG12	1:C:338:ARG:H	1.76	0.50
1:C:741:TYR:CZ	1:C:1022:ILE:HD11	2.45	0.50
1:C:873:TYR:HA	1:C:896:LEU:O	2.11	0.50
1:C:887:VAL:O	1:C:887:VAL:HG12	2.10	0.50
1:C:954:GLN:CA	1:C:958:ILE:HD13	2.41	0.50
1:C:1077:MET:HB2	1:C:1165:VAL:HG22	1.91	0.50
1:C:1206:PHE:CE2	1:C:1236:ILE:HD13	2.46	0.50
1:B:524:GLU:O	1:B:528:ILE:HG13	2.12	0.50

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:339:LEU:CD1	1:C:397:LEU:CD2	2.87	0.50
1:C:559:THR:CG2	1:C:583:GLU:HG3	2.41	0.50
1:C:568:PHE:N	1:C:568:PHE:CD1	2.77	0.50
1:C:716:PHE:CD1	1:C:716:PHE:C	2.88	0.50
1:C:820:ILE:HG22	1:C:983:ILE:HD11	1.92	0.50
1:C:1259:ALA:CB	1:C:1260:PRO:HD3	2.29	0.50
1:B:490:PHE:HA	1:B:745:ILE:HG12	1.92	0.50
1:B:735:THR:O	1:B:1017:ALA:HA	2.11	0.50
1:C:334:LEU:CG	1:C:366:MET:HE1	2.40	0.50
1:C:1078:TYR:HD2	1:C:1229:LEU:CD1	2.25	0.50
1:C:638:THR:HG22	1:C:638:THR:O	2.11	0.50
1:C:713:MET:CE	1:C:804:LEU:HD21	2.41	0.50
1:C:836:GLN:HB2	1:C:940:ARG:CB	2.38	0.50
1:C:947:GLU:O	1:C:947:GLU:HG3	2.11	0.50
1:C:1105:LEU:C	1:C:1105:LEU:CD1	2.85	0.50
1:C:1119:TYR:HE2	1:C:1135:PRO:HG3	1.76	0.50
1:C:614:ARG:HG3	1:C:614:ARG:O	2.10	0.50
1:C:617:ASP:HA	1:C:620:ILE:HG22	1.93	0.50
1:C:652:PHE:HZ	1:C:687:LEU:HD21	1.76	0.50
1:C:835:TYR:CE1	1:C:925:VAL:CG2	2.89	0.50
1:C:1248:HIS:HB3	1:C:1252:ASP:O	2.11	0.50
1:C:157:ILE:HD11	1:C:263:ARG:CD	2.41	0.50
1:C:204:VAL:CG2	1:C:1242:MET:O	2.58	0.50
1:C:255:LEU:HD23	1:C:1058:GLY:O	2.10	0.50
1:C:338:ARG:HG3	1:C:342:THR:HB	1.88	0.50
1:C:405:HIS:CD2	1:C:624:PHE:O	2.64	0.50
1:C:409:ILE:HD13	1:C:409:ILE:O	2.12	0.50
1:C:881:ASP:O	1:C:884:ALA:HB3	2.12	0.50
1:C:987:ALA:O	1:C:992:VAL:CG1	2.60	0.50
1:C:1206:PHE:CD2	1:C:1236:ILE:HD13	2.45	0.50
1:C:1233:LEU:C	1:C:1234:GLN:HG3	2.37	0.50
1:B:683:TRP:CH2	1:B:687:LEU:HD11	2.46	0.50
1:C:235:ILE:HG22	1:C:236:GLY:N	2.27	0.50
1:C:304:PHE:N	1:C:304:PHE:HD1	2.10	0.50
1:C:1071:PHE:HB3	1:C:1234:GLN:OE1	2.12	0.50
1:C:1122:PRO:CB	1:C:1123:PRO:HD3	2.41	0.50
1:C:1137:VAL:C	1:C:1139:MET:N	2.66	0.50
1:C:232:LEU:HD11	1:C:245:ALA:O	2.11	0.50
1:C:251:LEU:HD21	1:C:1062:ILE:HG13	1.87	0.50
1:C:338:ARG:HD3	1:C:342:THR:HG22	1.83	0.50
1:C:109:LYS:HD2	1:C:110:PRO:CD	2.39	0.50

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:449:PHE:HA	1:C:683:TRP:CD1	2.45	0.50
1:C:485:GLU:OE1	1:C:706:TYR:CD1	2.65	0.50
1:C:1031:TYR:CE2	1:C:1041:ARG:HG3	2.47	0.50
1:B:461:ARG:NE	1:B:504:ASP:CB	2.69	0.49
1:B:1021:ARG:HH22	1:B:1032:ASP:HB2	1.77	0.49
1:C:270:THR:HG22	1:C:291:HIS:HA	1.94	0.49
1:C:462:LEU:HD23	1:C:506:SER:OG	2.11	0.49
1:C:887:VAL:CG2	1:C:893:ALA:HA	2.42	0.49
1:C:1085:ASP:CB	1:C:1086:PRO:CD	2.79	0.49
1:B:793:TYR:CD2	1:B:1321:ASN:CG	2.87	0.49
1:C:248:VAL:HG11	1:C:970:LEU:O	2.12	0.49
1:C:1088:PHE:CG	1:C:1088:PHE:O	2.65	0.49
1:C:1290:LYS:NZ	1:C:1297:SER:OG	2.44	0.49
1:B:269:GLU:HB3	1:B:292:ASN:ND2	2.20	0.49
1:C:334:LEU:CD1	1:C:366:MET:HE1	2.42	0.49
1:C:446:LYS:HE2	1:C:472:GLU:OE2	2.12	0.49
1:C:686:HIS:ND1	1:C:686:HIS:O	2.45	0.49
1:C:1297:SER:C	1:C:1298:PHE:CD1	2.91	0.49
1:B:526:ASN:HD21	1:B:727:PHE:HD2	1.60	0.49
1:B:1245:ILE:O	1:B:1246:VAL:HG13	2.12	0.49
1:C:157:ILE:CD1	1:C:263:ARG:NE	2.75	0.49
1:C:314:ILE:N	1:C:314:ILE:HD13	2.28	0.49
1:C:347:ALA:CB	1:C:1300:ASN:HB3	2.43	0.49
1:C:820:ILE:CG2	1:C:983:ILE:CD1	2.90	0.49
1:C:832:MET:HE3	1:C:945:VAL:HG23	1.95	0.49
1:C:840:ASP:C	1:C:940:ARG:HH12	2.18	0.49
1:C:997:TYR:C	1:C:999:LYS:N	2.67	0.49
1:C:1250:GLU:O	1:C:1251:VAL:CG2	2.60	0.49
1:B:206:ILE:O	1:B:1239:ALA:HB1	2.12	0.49
1:C:171:GLU:OE2	1:C:1179:THR:OG1	2.21	0.49
1:C:268:GLY:O	1:C:269:GLU:HB2	2.11	0.49
1:C:409:ILE:HD12	1:C:1040:PHE:CZ	2.47	0.49
1:C:467:LYS:CB	1:C:467:LYS:NZ	2.72	0.49
1:C:606:LEU:HD22	1:C:655:ILE:HD13	1.94	0.49
1:C:853:ASP:OD1	1:C:854:GLN:N	2.46	0.49
1:C:199:TYR:CZ	1:C:1246:VAL:HG12	2.47	0.49
1:C:362:LEU:C	1:C:362:LEU:CD2	2.85	0.49
1:C:720:PHE:C	1:C:722:GLY:N	2.68	0.49
1:B:427:VAL:HG11	1:B:755:LEU:CD2	2.42	0.49
1:B:845:GLU:N	1:B:846:GLY:HA2	2.26	0.49
1:B:1269:THR:HG22	1:B:1270:LEU:H	1.78	0.49

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:449:PHE:C	1:C:683:TRP:CD1	2.89	0.49
1:C:555:GLY:HA2	1:C:570:GLY:HA2	1.95	0.49
1:C:639:ASN:HB3	1:C:1330:ILE:CD1	2.43	0.49
1:C:862:ARG:HB3	1:C:952:PHE:HZ	1.70	0.49
1:B:243:GLN:O	1:B:246:GLU:HB2	2.13	0.49
1:B:437:ALA:O	1:B:701:HIS:CE1	2.66	0.49
1:C:441:ARG:NH2	1:C:441:ARG:CG	2.73	0.49
1:C:494:GLU:HB2	1:C:531:ASP:OD2	2.13	0.49
1:C:912:GLU:O	1:C:912:GLU:HG2	2.12	0.49
1:C:1101:TYR:CD1	1:C:1101:TYR:C	2.91	0.49
1:C:1270:LEU:O	1:C:1271:SER:C	2.52	0.49
1:B:271:THR:HG23	1:C:237:VAL:HG23	1.94	0.49
1:C:339:LEU:HD13	1:C:397:LEU:HD21	1.91	0.49
1:B:631:PRO:HA	1:B:718:ASN:HD21	1.78	0.49
1:B:649:ALA:HB1	1:B:692:ASP:OD1	2.12	0.49
1:B:996:ASP:HB2	1:B:999:LYS:HG3	1.94	0.49
1:B:1210:LEU:HD11	1:B:1256:GLY:HA3	1.95	0.49
1:C:225:ILE:HD12	1:C:247:TYR:HE1	1.76	0.49
1:C:312:ARG:CG	1:C:312:ARG:NH2	2.71	0.49
1:C:558:TYR:CZ	1:C:585:PHE:CB	2.96	0.49
1:B:558:TYR:CE1	1:B:590:SER:HB3	2.48	0.48
1:B:893:ALA:HB1	1:B:915:VAL:HG12	1.94	0.48
1:C:541:SER:C	1:C:543:TRP:H	2.17	0.48
1:C:1101:TYR:CD1	1:C:1101:TYR:O	2.66	0.48
1:B:150:LEU:HD12	1:B:150:LEU:O	2.12	0.48
1:B:1082:ASP:CG	1:B:1212:ARG:HH12	2.21	0.48
1:C:565:GLU:HG2	1:C:566:PHE:N	2.29	0.48
1:B:276:ASN:OD1	1:C:1199:GLY:CA	2.62	0.48
1:B:970:LEU:HD21	1:B:1070:ARG:HH21	1.79	0.48
1:C:348:LEU:HD11	1:C:1301:VAL:HG22	1.95	0.48
1:C:833:ARG:HH11	1:C:942:HIS:CE1	2.27	0.48
1:C:892:VAL:HG11	1:C:894:VAL:HG11	1.90	0.48
1:C:987:ALA:O	1:C:992:VAL:O	2.31	0.48
1:C:1143:GLU:C	1:C:1145:ALA:N	2.69	0.48
1:C:1186:GLN:H	1:C:1205:GLN:HE22	1.60	0.48
1:B:439:VAL:HG23	1:B:440:ILE:N	2.27	0.48
1:C:96:ILE:HD12	1:C:96:ILE:HG23	1.62	0.48
1:C:365:LEU:HD13	1:C:365:LEU:C	2.38	0.48
1:C:820:ILE:HG21	1:C:983:ILE:HD11	1.94	0.48
1:C:1210:LEU:HD23	1:C:1244:ALA:HB1	1.92	0.48
1:B:361:ASN:OD1	1:B:1054:ARG:NH2	2.36	0.48

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:379:LEU:O	1:C:380:GLN:C	2.51	0.48
1:C:492:VAL:CG1	1:C:580:TYR:HD2	2.26	0.48
1:C:605:ARG:HG3	1:C:605:ARG:O	2.13	0.48
1:C:741:TYR:OH	1:C:1022:ILE:CD1	2.61	0.48
1:C:828:ASP:OD1	1:C:828:ASP:N	2.45	0.48
1:C:985:ARG:NH2	1:C:988:GLN:CG	2.76	0.48
1:C:1276:LEU:HB3	1:C:1290:LYS:HG3	1.95	0.48
1:B:505:PRO:HG3	1:B:670:ASP:OD2	2.14	0.48
1:B:560:ILE:HG23	1:B:564:GLY:HA3	1.96	0.48
1:B:862:ARG:NH1	1:B:948:ILE:HD13	2.29	0.48
1:B:1103:HIS:NE2	1:B:1146:GLY:O	2.46	0.48
1:B:1117:VAL:HB	1:B:1154:ASN:HD22	1.78	0.48
1:C:144:ASN:CG	1:C:1318:GLU:OE1	2.56	0.48
1:C:302:ARG:CD	1:C:318:LEU:HD23	2.43	0.48
1:C:840:ASP:HA	1:C:940:ARG:HH22	1.77	0.48
1:C:1137:VAL:HG22	1:C:1164:TRP:NE1	2.28	0.48
1:C:1259:ALA:CB	1:C:1260:PRO:CD	2.76	0.48
1:B:157:ILE:O	1:B:158:SER:OG	2.26	0.48
1:B:614:ARG:NH1	1:B:707:ALA:HB1	2.29	0.48
1:B:1088:PHE:CE2	1:B:1090:PRO:HG3	2.48	0.48
1:C:592:VAL:HG13	1:C:593:PRO:HD2	1.95	0.48
1:C:843:LEU:HD12	1:C:943:GLU:CG	2.15	0.48
1:C:849:MET:HG3	1:C:919:MET:CE	2.30	0.48
1:C:878:SER:HB2	1:C:880:PRO:HD3	1.95	0.48
1:C:1066:ARG:HG2	1:C:1238:VAL:O	2.14	0.48
1:C:339:LEU:HD12	1:C:399:PRO:HB3	1.94	0.48
1:C:539:PHE:O	1:C:543:TRP:HB3	2.12	0.48
1:C:1247:ASN:ND2	1:C:1247:ASN:N	2.58	0.48
1:B:434:VAL:O	1:B:439:VAL:CG2	2.62	0.48
1:B:549:GLY:O	1:B:553:GLN:HG2	2.14	0.48
1:B:634:TYR:HB2	1:B:720:PHE:HD1	1.79	0.48
1:C:824:LEU:HA	1:C:968:ARG:HD2	1.96	0.48
1:C:892:VAL:HG12	1:C:894:VAL:HG12	1.69	0.48
1:C:1137:VAL:HG21	1:C:1164:TRP:CE2	2.48	0.48
1:B:157:ILE:HG21	1:B:263:ARG:HD2	1.95	0.48
1:B:426:ILE:HG12	1:B:714:LEU:HD21	1.95	0.48
1:C:189:ILE:HG12	1:C:286:LEU:HD11	1.96	0.48
1:C:290:TYR:HA	1:C:328:GLY:HA2	1.96	0.48
1:C:530:GLY:HA3	1:C:575:TRP:NE1	2.29	0.48
1:C:629:ARG:HB2	1:C:1037:ILE:CG2	2.38	0.48
1:C:1104:ARG:NH1	1:C:1104:ARG:CG	2.71	0.48

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1243:ARG:HG2	1:C:1243:ARG:NH1	2.24	0.48
1:C:1310:ARG:NE	1:C:1310:ARG:C	2.72	0.48
1:B:868:VAL:HB	1:B:890:THR:HA	1.96	0.47
1:C:408:ILE:N	1:C:408:ILE:HD13	2.29	0.47
1:C:494:GLU:N	1:C:494:GLU:CD	2.72	0.47
1:C:560:ILE:HG22	1:C:585:PHE:HE2	1.79	0.47
1:C:671:ASP:HA	1:C:674:LYS:HZ1	1.78	0.47
1:C:730:ASP:OD1	1:C:731:GLN:N	2.46	0.47
1:C:1116:ARG:NH1	1:C:1130:SER:CB	2.77	0.47
1:B:199:TYR:CE1	1:B:1246:VAL:HA	2.48	0.47
1:C:82:ARG:HH22	1:C:209:ASN:HD22	1.62	0.47
1:C:121:PHE:HB3	1:C:122:ASN:H	1.34	0.47
1:C:450:PRO:O	1:C:451:GLU:CB	2.60	0.47
1:C:451:GLU:CB	1:C:686:HIS:CB	2.92	0.47
1:B:148:GLN:HB2	1:B:149:PRO:HD2	1.96	0.47
1:C:247:TYR:CG	1:C:1070:ARG:HD3	2.48	0.47
1:C:259:MET:O	1:C:1054:ARG:HB3	2.14	0.47
1:C:312:ARG:HG3	1:C:312:ARG:NH2	2.18	0.47
1:C:382:HIS:NE2	1:C:800:LEU:HD23	2.28	0.47
1:C:835:TYR:CD1	1:C:942:HIS:HB2	2.44	0.47
1:C:1250:GLU:O	1:C:1251:VAL:HG22	2.14	0.47
1:B:426:ILE:HG12	1:B:714:LEU:CD2	2.44	0.47
1:B:558:TYR:CZ	1:B:585:PHE:HB2	2.48	0.47
1:B:880:PRO:HG3	1:B:905:SER:C	2.39	0.47
1:C:514:PHE:HE2	1:C:535:VAL:HG13	1.80	0.47
1:C:838:GLU:O	1:C:839:ALA:HB3	2.14	0.47
1:C:1046:PHE:HD2	1:C:1052:LEU:CD2	2.22	0.47
1:C:1155:ILE:CG2	1:C:1166:VAL:CG1	2.81	0.47
1:B:139:ASN:O	1:C:757:ILE:CG2	2.63	0.47
1:B:537:LEU:O	1:B:541:SER:OG	2.18	0.47
1:B:863:LEU:HD21	1:B:871:PRO:HD3	1.95	0.47
1:B:1131:PRO:HA	1:B:1134:ARG:NH1	2.29	0.47
1:C:227:LEU:HD23	1:C:246:GLU:O	2.14	0.47
1:C:338:ARG:NE	1:C:342:THR:HG22	2.26	0.47
1:C:370:VAL:CG1	1:C:398:ARG:HB2	2.44	0.47
1:C:1021:ARG:HB2	1:C:1021:ARG:NH1	2.22	0.47
1:C:1105:LEU:O	1:C:1105:LEU:HD13	2.15	0.47
1:B:156:GLN:HG2	1:B:266:ILE:HD11	1.96	0.47
1:B:204:VAL:CG1	1:B:1242:MET:HB2	2.45	0.47
1:B:752:VAL:O	1:B:753:ASP:HB2	2.15	0.47
1:B:971:MET:HA	1:B:972:PRO:HD3	1.60	0.47

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1023:ARG:NE	1:B:1027:THR:OG1	2.48	0.47
1:C:498:ILE:HD11	1:C:514:PHE:CZ	2.50	0.47
1:C:516:LEU:HA	1:C:516:LEU:HD23	1.72	0.47
1:C:552:ILE:CD1	1:C:572:ASN:HB2	2.39	0.47
1:C:826:GLY:H	1:C:968:ARG:CD	2.27	0.47
1:C:896:LEU:CD1	1:C:918:VAL:HG21	2.42	0.47
1:C:928:ARG:HG3	1:C:928:ARG:NH1	2.29	0.47
1:B:154:PHE:CG	1:B:264:LEU:HG	2.50	0.47
1:B:383:SER:O	1:B:708:THR:HG23	2.15	0.47
1:B:500:GLU:CD	1:B:502:PHE:H	2.22	0.47
1:B:528:ILE:HG13	1:B:528:ILE:H	1.56	0.47
1:B:697:ALA:HA	1:B:774:LEU:HD12	1.97	0.47
1:B:1200:LYS:HD3	1:B:1202:PHE:HE1	1.79	0.47
1:C:203:VAL:HG12	1:C:1243:ARG:HD2	1.97	0.47
1:C:579:LEU:HD12	1:C:579:LEU:O	2.15	0.47
1:C:843:LEU:HD12	1:C:943:GLU:CB	2.44	0.47
1:C:954:GLN:C	1:C:958:ILE:CD1	2.88	0.47
1:C:1262:SER:O	1:C:1262:SER:OG	2.30	0.47
1:C:1273:ASN:ND2	1:C:1273:ASN:C	2.72	0.47
1:B:298:PRO:O	1:B:301:LEU:HB3	2.15	0.47
1:B:694:ILE:HG22	1:B:698:HIS:ND1	2.30	0.47
1:B:733:VAL:HG21	1:B:741:TYR:CD1	2.50	0.47
1:B:960:THR:HG23	1:B:965:ARG:NH1	2.30	0.47
1:B:1066:ARG:HH21	1:B:1296:ILE:HD12	1.79	0.47
1:C:200:GLY:HA2	1:C:1246:VAL:HG22	1.95	0.47
1:C:323:THR:CG2	1:C:1266:ASP:HB2	2.44	0.47
1:C:835:TYR:HE1	1:C:942:HIS:CD2	2.33	0.47
1:C:1084:PRO:O	1:C:1209:GLY:C	2.58	0.47
1:C:1206:PHE:HD2	1:C:1236:ILE:HD11	1.73	0.47
1:B:231:LEU:HB2	1:B:249:SER:CB	2.45	0.47
1:B:323:THR:HA	1:B:1266:ASP:OD1	2.15	0.47
1:B:329:LEU:HD21	1:B:332:THR:OG1	2.14	0.47
1:B:482:ILE:HG23	1:B:706:TYR:CE1	2.50	0.47
1:B:530:GLY:HA3	1:B:575:TRP:CD1	2.49	0.47
1:C:525:PHE:O	1:C:525:PHE:CG	2.68	0.47
1:C:1034:GLN:N	1:C:1034:GLN:CD	2.72	0.47
1:C:1228:ARG:HG3	1:C:1228:ARG:O	2.15	0.47
1:B:154:PHE:HA	1:B:262:ASN:OD1	2.15	0.47
1:B:232:LEU:HD22	1:B:974:LEU:HD21	1.96	0.47
1:B:265:VAL:HG21	1:B:358:LEU:HD13	1.97	0.47
1:B:957:PHE:CD2	1:B:958:ILE:HG13	2.50	0.47

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:107:GLN:N	1:C:107:GLN:CD	2.73	0.47
1:C:652:PHE:HB3	1:C:691:PHE:CD2	2.50	0.47
1:C:1021:ARG:O	1:C:1029:LEU:HB2	2.15	0.47
1:C:1031:TYR:O	1:C:1031:TYR:CG	2.68	0.47
1:C:1062:ILE:HG23	1:C:1062:ILE:O	2.15	0.47
1:C:1205:GLN:O	1:C:1205:GLN:HG3	2.15	0.47
1:C:1254:PRO:HG2	1:C:1257:ALA:HB2	1.97	0.47
1:C:237:VAL:HG12	1:C:238:THR:H	1.80	0.46
1:C:560:ILE:CG2	1:C:585:PHE:HE2	2.28	0.46
1:C:733:VAL:HB	1:C:1022:ILE:HD12	1.94	0.46
1:C:804:LEU:HD23	1:C:804:LEU:HA	1.66	0.46
1:C:873:TYR:CD2	1:C:898:GLN:HG3	2.48	0.46
1:C:946:LEU:N	1:C:946:LEU:CD1	2.73	0.46
1:B:274:MET:HB2	1:B:277:THR:HG23	1.97	0.46
1:B:424:GLY:HA2	1:B:427:VAL:HG12	1.98	0.46
1:B:701:HIS:CD2	1:B:791:ILE:HD11	2.50	0.46
1:C:451:GLU:OE1	1:C:686:HIS:N	2.49	0.46
1:C:741:TYR:O	1:C:741:TYR:CD1	2.68	0.46
1:C:839:ALA:C	1:C:940:ARG:NH2	2.66	0.46
1:C:1149:LYS:O	1:C:1150:LEU:C	2.59	0.46
1:C:1176:GLU:OE1	1:C:1203:HIS:HE1	1.96	0.46
1:B:617:ASP:OD1	1:B:618:LEU:N	2.48	0.46
1:B:880:PRO:HB3	1:B:909:TYR:HB2	1.96	0.46
1:B:1210:LEU:HD13	1:B:1243:ARG:NH1	2.30	0.46
1:B:1271:SER:HB3	1:B:1275:ASP:OD2	2.15	0.46
1:C:163:TYR:CE2	1:C:258:VAL:CG2	2.93	0.46
1:C:370:VAL:HG13	1:C:398:ARG:H	1.79	0.46
1:C:492:VAL:HG22	1:C:747:ARG:CA	2.41	0.46
1:C:342:THR:O	1:C:1305:MET:HE1	2.15	0.46
1:C:430:ASN:C	1:C:430:ASN:ND2	2.73	0.46
1:C:962:ASP:O	1:C:965:ARG:HB3	2.15	0.46
1:B:1064:ASN:OD1	1:B:1065:PRO:HD2	2.16	0.46
1:B:1269:THR:HG22	1:B:1270:LEU:N	2.30	0.46
1:B:1278:TYR:CE2	1:B:1290:LYS:HA	2.50	0.46
1:C:371:THR:O	1:C:372:ALA:C	2.56	0.46
1:C:480:LEU:C	1:C:480:LEU:CD2	2.88	0.46
1:C:947:GLU:HA	1:C:947:GLU:OE2	2.16	0.46
1:B:482:ILE:O	1:B:485:GLU:HB2	2.16	0.46
1:B:926:VAL:HG21	1:B:937:ASN:N	2.30	0.46
1:B:1174:THR:HG23	1:B:1201:LEU:HD21	1.97	0.46
1:C:700:ASP:CG	1:C:1326:ARG:HG3	2.38	0.46

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:820:ILE:HD12	1:C:820:ILE:HG23	1.58	0.46
1:C:901:VAL:CG2	1:C:930:ALA:CB	2.85	0.46
1:B:219:ILE:HA	1:B:228:VAL:HG22	1.98	0.46
1:C:77:THR:C	1:C:172:ASP:OD2	2.58	0.46
1:C:652:PHE:HE1	1:C:688:GLU:CB	2.29	0.46
1:C:663:VAL:HG11	1:C:680:THR:CG2	2.46	0.46
1:B:231:LEU:HD12	1:B:249:SER:HB2	1.97	0.46
1:B:285:VAL:HG21	1:B:325:TYR:CE2	2.50	0.46
1:C:338:ARG:CG	1:C:342:THR:HA	2.44	0.46
1:C:520:PHE:C	1:C:521:PHE:CD1	2.94	0.46
1:C:747:ARG:CG	1:C:747:ARG:NH1	2.72	0.46
1:B:352:HIS:O	1:B:356:SER:OG	2.30	0.46
1:B:919:MET:SD	1:B:925:VAL:HG12	2.56	0.46
1:B:1216:SER:O	1:B:1219:ASP:HB2	2.16	0.46
1:C:178:ASP:O	1:C:306:GLN:OE1	2.34	0.46
1:C:329:LEU:HA	1:C:329:LEU:HD23	1.67	0.46
1:C:514:PHE:CD2	1:C:532:ILE:HG23	2.51	0.46
1:C:716:PHE:CD1	1:C:716:PHE:O	2.69	0.46
1:C:872:ILE:HD12	1:C:873:TYR:H	1.81	0.46
1:C:887:VAL:HG13	1:C:893:ALA:HA	1.98	0.46
1:B:822:MET:HG3	1:B:1045:TYR:CD1	2.51	0.46
1:B:845:GLU:HG2	1:B:911:ARG:HD2	1.98	0.46
1:C:81:ALA:HB3	1:C:168:VAL:HG13	1.98	0.46
1:C:322:GLY:O	1:C:1279:SER:CB	2.64	0.46
1:C:455:GLN:HG2	1:C:455:GLN:O	2.15	0.46
1:C:525:PHE:CE1	1:C:532:ILE:CD1	2.96	0.46
1:C:543:TRP:CD1	1:C:543:TRP:O	2.69	0.46
1:C:558:TYR:CE1	1:C:585:PHE:HB2	2.51	0.46
1:C:579:LEU:CB	1:C:582:SER:OG	2.63	0.46
1:C:585:PHE:HA	1:C:586:PRO:HD3	1.56	0.46
1:C:822:MET:CE	1:C:1046:PHE:CE2	2.89	0.46
1:C:825:SER:O	1:C:825:SER:OG	2.34	0.46
1:C:897:TYR:CD1	1:C:897:TYR:C	2.94	0.46
1:C:1078:TYR:O	1:C:1078:TYR:CD1	2.68	0.46
1:C:1132:THR:O	1:C:1133:GLY:O	2.33	0.46
1:C:1275:ASP:OD1	1:C:1275:ASP:N	2.34	0.46
1:B:342:THR:HB	1:B:1309:ILE:CD1	2.42	0.45
1:B:793:TYR:CD2	1:B:1322:PRO:HD2	2.51	0.45
1:B:890:THR:C	1:B:892:VAL:H	2.24	0.45
1:B:1204:LEU:HD21	1:B:1230:ILE:HD11	1.98	0.45
1:C:262:ASN:HA	1:C:361:ASN:OD1	2.16	0.45

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:696:VAL:O	1:C:696:VAL:HG12	2.15	0.45
1:C:720:PHE:O	1:C:720:PHE:CD1	2.70	0.45
1:C:1047:LEU:HB2	1:C:1051:ARG:HD3	1.98	0.45
1:B:165:THR:HG22	1:B:166:TYR:N	2.30	0.45
1:B:230:ASP:OD1	1:B:230:ASP:N	2.49	0.45
1:B:231:LEU:CD2	1:B:986:ILE:HG13	2.46	0.45
1:B:554:ARG:CZ	1:B:594:LEU:HD12	2.46	0.45
1:B:1122:PRO:HB2	1:B:1123:PRO:HD3	1.98	0.45
1:C:439:VAL:O	1:C:439:VAL:HG13	2.16	0.45
1:C:603:ILE:HD13	1:C:659:LEU:CD2	2.46	0.45
1:C:874:ILE:HG21	1:C:902:ILE:CD1	2.29	0.45
1:C:928:ARG:HH11	1:C:928:ARG:CG	2.23	0.45
1:B:329:LEU:HD12	1:B:346:HIS:CE1	2.51	0.45
1:B:504:ASP:O	1:B:506:SER:HA	2.16	0.45
1:C:96:ILE:HD13	1:C:96:ILE:H	1.76	0.45
1:C:108:LYS:NZ	1:C:108:LYS:CB	2.72	0.45
1:C:497:LYS:H	1:C:497:LYS:HG2	1.49	0.45
1:C:1127:ALA:O	1:C:1128:TYR:CB	2.64	0.45
1:C:1206:PHE:CE2	1:C:1236:ILE:HD12	2.51	0.45
1:B:479:HIS:O	1:B:482:ILE:N	2.50	0.45
1:B:1238:VAL:HG23	1:B:1239:ALA:N	2.31	0.45
1:C:160:PRO:HG3	1:C:265:VAL:HG12	1.98	0.45
1:C:213:PHE:HB3	1:C:219:ILE:HB	1.92	0.45
1:C:236:GLY:C	1:C:237:VAL:CG2	2.88	0.45
1:C:525:PHE:HE1	1:C:532:ILE:CD1	2.30	0.45
1:C:629:ARG:CB	1:C:1037:ILE:HG23	2.41	0.45
1:C:643:THR:HG22	1:C:644:VAL:HG12	1.97	0.45
1:C:674:LYS:NZ	1:C:674:LYS:CB	2.73	0.45
1:C:1062:ILE:HD12	1:C:1062:ILE:HA	1.53	0.45
1:C:1078:TYR:HB2	1:C:1229:LEU:CD1	2.47	0.45
1:B:307:VAL:HG11	1:B:1245:ILE:HG23	1.98	0.45
1:B:370:VAL:HG23	1:B:374:ASP:OD2	2.17	0.45
1:B:1278:TYR:HD2	1:B:1288:ILE:HG23	1.82	0.45
1:C:285:VAL:O	1:C:326:GLY:CA	2.65	0.45
1:C:341:LYS:HB2	1:C:1306:THR:HB	1.98	0.45
1:C:375:ARG:NH1	1:C:375:ARG:CG	2.69	0.45
1:C:376:ILE:HA	1:C:376:ILE:HD12	1.62	0.45
1:C:407:HIS:HD2	1:C:1047:LEU:HA	1.63	0.45
1:C:407:HIS:CE1	1:C:1047:LEU:HD12	2.52	0.45
1:C:441:ARG:O	1:C:770:CYS:HA	2.16	0.45
1:C:742:LYS:HA	1:C:743:PRO:HD3	1.84	0.45

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:986:ILE:HA	1:C:989:ILE:HG22	1.97	0.45
1:C:1079:LEU:CD1	1:C:1231:TYR:HH	2.06	0.45
1:B:166:TYR:OH	1:B:1264:GLU:OE2	2.31	0.45
1:B:340:VAL:HG21	1:C:1008:LEU:HB3	1.98	0.45
1:B:696:VAL:HG21	1:B:1326:ARG:HH12	1.81	0.45
1:B:716:PHE:O	1:B:717:THR:HB	2.16	0.45
1:C:377:LYS:HE2	1:C:621:ALA:O	2.16	0.45
1:C:746:GLU:N	1:C:746:GLU:OE2	2.49	0.45
1:C:838:GLU:CG	1:C:934:LEU:HA	2.36	0.45
1:C:838:GLU:CG	1:C:935:GLN:CA	2.89	0.45
1:C:997:TYR:C	1:C:999:LYS:H	2.25	0.45
1:C:1168:ILE:N	1:C:1168:ILE:CD1	2.73	0.45
1:C:1285:GLN:CA	1:C:1285:GLN:NE2	2.80	0.45
1:B:147:VAL:HG13	1:B:375:ARG:HD2	1.99	0.45
1:B:270:THR:HG23	1:B:289:THR:HB	1.99	0.45
1:B:461:ARG:HE	1:B:504:ASP:HB3	1.75	0.45
1:C:484:ARG:NE	1:C:758:ILE:HG22	2.31	0.45
1:C:517:PHE:CE1	1:C:521:PHE:CD2	3.04	0.45
1:C:674:LYS:HB2	1:C:674:LYS:HZ3	1.80	0.45
1:C:829:SER:O	1:C:965:ARG:NH2	2.49	0.45
1:C:240:GLY:O	1:C:242:GLU:CA	2.59	0.45
1:C:270:THR:HB	1:C:289:THR:CG2	2.47	0.45
1:C:849:MET:CG	1:C:919:MET:CG	2.94	0.45
1:C:853:ASP:HA	1:C:856:LEU:HB2	1.98	0.45
1:C:1060:ARG:NH1	1:C:1292:GLU:N	2.59	0.45
1:B:231:LEU:HD21	1:B:986:ILE:HG13	1.99	0.45
1:B:301:LEU:HG	1:B:305:THR:OG1	2.17	0.45
1:B:875:THR:OG1	1:B:901:VAL:O	2.34	0.45
1:B:1096:TYR:CE1	1:B:1136:HIS:HB3	2.51	0.45
1:B:1181:SER:O	1:B:1182:GLU:HB3	2.17	0.45
1:C:180:LEU:HD11	1:C:304:PHE:O	2.16	0.45
1:C:208:LEU:HB3	1:C:221:LEU:CD2	2.47	0.45
1:C:407:HIS:NE2	1:C:1047:LEU:HA	2.22	0.45
1:C:1212:ARG:HA	1:C:1213:PRO:HD3	1.73	0.45
1:B:1176:GLU:HG2	1:B:1203:HIS:CE1	2.46	0.45
1:C:737:PRO:HD2	1:C:1016:ASN:O	2.17	0.45
1:C:1202:PHE:C	1:C:1202:PHE:HD1	2.24	0.45
1:B:338:ARG:O	1:B:339:LEU:HB2	2.17	0.44
1:B:594:LEU:HD23	1:B:595:ALA:N	2.32	0.44
1:B:863:LEU:HD21	1:B:871:PRO:CD	2.47	0.44
1:C:109:LYS:HB3	1:C:110:PRO:CD	2.48	0.44

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:225:ILE:O	1:C:227:LEU:N	2.50	0.44
1:C:362:LEU:HD23	1:C:362:LEU:C	2.39	0.44
1:C:504:ASP:OD2	1:C:506:SER:HB2	2.16	0.44
1:C:839:ALA:CA	1:C:940:ARG:NH1	2.80	0.44
1:C:905:SER:O	1:C:908:THR:HG22	2.16	0.44
1:C:1034:GLN:OE1	1:C:1034:GLN:HA	2.17	0.44
1:C:1111:ALA:HB2	1:C:1129:PRO:CG	2.47	0.44
1:B:462:LEU:HD23	1:B:462:LEU:O	2.17	0.44
1:B:484:ARG:O	1:B:527:ARG:NH1	2.51	0.44
1:C:214:ASP:C	1:C:216:ALA:N	2.73	0.44
1:C:492:VAL:CG2	1:C:747:ARG:HA	2.42	0.44
1:C:564:GLY:O	1:C:565:GLU:HB3	2.17	0.44
1:C:1046:PHE:C	1:C:1048:ASP:N	2.73	0.44
1:C:1191:GLU:C	1:C:1195:THR:OG1	2.48	0.44
1:B:588:LEU:HD13	1:B:604:MET:CE	2.47	0.44
1:B:1332:ASN:HA	1:B:1333:ALA:HA	1.58	0.44
1:C:211:ASP:O	1:C:212:PHE:C	2.60	0.44
1:C:1263:TYR:CE2	1:C:1278:TYR:OH	2.55	0.44
1:C:1294:ASP:O	1:C:1295:HIS:CG	2.71	0.44
1:B:135:LYS:CE	1:C:469:ARG:CA	2.93	0.44
1:B:575:TRP:CG	1:B:576:ASP:N	2.85	0.44
1:C:252:LEU:HD11	1:C:823:ILE:CG2	2.22	0.44
1:C:279:SER:C	1:C:281:VAL:H	2.25	0.44
1:C:543:TRP:HD1	1:C:544:TYR:CD1	2.34	0.44
1:C:883:ILE:HG23	1:C:895:VAL:HG21	2.00	0.44
1:B:1242:MET:HA	1:B:1258:VAL:O	2.17	0.44
1:C:81:ALA:O	1:C:168:VAL:HG12	2.17	0.44
1:C:176:LYS:HA	1:C:176:LYS:HD3	1.81	0.44
1:C:204:VAL:CG2	1:C:1242:MET:HB2	2.48	0.44
1:C:214:ASP:C	1:C:216:ALA:H	2.26	0.44
1:C:449:PHE:CE2	1:C:454:GLU:HG3	2.53	0.44
1:C:451:GLU:OE2	1:C:682:GLN:HB3	2.18	0.44
1:C:836:GLN:O	1:C:940:ARG:HB3	2.17	0.44
1:C:954:GLN:HG2	1:C:957:PHE:CD1	2.53	0.44
1:C:1099:VAL:O	1:C:1099:VAL:CG2	2.66	0.44
1:C:1144:ARG:HE	1:C:1144:ARG:HB3	1.49	0.44
1:B:261:ASP:HA	1:B:262:ASN:HB3	1.99	0.44
1:B:540:PHE:CD1	1:B:600:ILE:HG12	2.53	0.44
1:C:259:MET:HG3	1:C:1055:LEU:CA	2.46	0.44
1:C:375:ARG:HA	1:C:375:ARG:HD2	1.74	0.44
1:C:985:ARG:HH22	1:C:989:ILE:CA	2.31	0.44

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1247:ASN:HD22	1:C:1247:ASN:C	2.21	0.44
1:C:1282:ALA:C	1:C:1284:GLY:N	2.73	0.44
1:B:157:ILE:HD13	1:B:263:ARG:HD2	1.98	0.44
1:B:349:ASN:HA	1:B:1299:SER:HA	1.99	0.44
1:C:146:GLU:CB	1:C:1317:VAL:HG13	2.47	0.44
1:C:153:ASP:OD1	1:C:153:ASP:N	2.48	0.44
1:C:256:PHE:CD1	1:C:819:PHE:CD2	3.06	0.44
1:B:733:VAL:HG22	1:B:734:ILE:N	2.33	0.44
1:B:886:SER:O	1:B:890:THR:HG22	2.17	0.44
1:C:161:LYS:HB2	1:C:161:LYS:HE2	1.79	0.44
1:C:168:VAL:CG2	1:C:204:VAL:HG12	2.47	0.44
1:C:176:LYS:HB2	1:C:199:TYR:CD2	2.53	0.44
1:C:738:GLU:O	1:C:738:GLU:CG	2.66	0.44
1:C:865:ILE:HG22	1:C:865:ILE:O	2.17	0.44
1:C:1073:GLY:HA3	1:C:1233:LEU:HD21	1.78	0.44
1:B:312:ARG:HA	1:B:315:THR:HG22	1.99	0.44
1:B:387:THR:HG22	1:B:1322:PRO:HD3	2.00	0.44
1:B:389:PHE:CD1	1:B:1319:ARG:HG3	2.34	0.44
1:B:895:VAL:HG22	1:B:896:LEU:H	1.83	0.44
1:B:1076:ILE:HB	1:B:1166:VAL:HG13	2.00	0.44
1:C:233:VAL:HG23	1:C:234:PRO:CD	2.28	0.44
1:C:302:ARG:HH11	1:C:302:ARG:CG	2.31	0.44
1:C:426:ILE:HG21	1:C:426:ILE:HD13	1.74	0.44
1:C:714:LEU:HA	1:C:714:LEU:HD23	1.58	0.44
1:C:935:GLN:C	1:C:937:ASN:H	2.25	0.44
1:C:970:LEU:HA	1:C:970:LEU:HD23	1.64	0.44
1:C:979:ILE:HD13	1:C:979:ILE:HG21	1.77	0.44
1:C:1014:MET:O	1:C:1014:MET:HG2	2.17	0.44
1:C:1138:HIS:CG	1:C:1138:HIS:O	2.68	0.44
1:B:272:THR:HG21	1:C:235:ILE:HD13	1.63	0.43
1:B:833:ARG:O	1:B:849:MET:N	2.49	0.43
1:C:556:ALA:O	1:C:587:ALA:CB	2.64	0.43
1:C:1122:PRO:N	1:C:1123:PRO:CD	2.81	0.43
1:B:285:VAL:HG23	1:B:326:GLY:HA2	1.99	0.43
1:C:314:ILE:HG23	1:C:314:ILE:HD12	1.61	0.43
1:C:541:SER:C	1:C:543:TRP:N	2.75	0.43
1:C:1023:ARG:NH1	1:C:1029:LEU:HD21	2.33	0.43
1:C:1050:LEU:HA	1:C:1050:LEU:HD13	1.72	0.43
1:C:1094:GLU:OE2	1:C:1094:GLU:CA	2.66	0.43
1:C:1137:VAL:HG22	1:C:1164:TRP:CE2	2.52	0.43
1:C:1310:ARG:HA	1:C:1310:ARG:NH1	2.31	0.43

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1180:PRO:HB3	1:B:1212:ARG:HB3	1.99	0.43
1:C:153:ASP:OD2	1:C:401:LEU:HD22	2.17	0.43
1:C:522:PRO:O	1:C:523:THR:C	2.58	0.43
1:C:614:ARG:O	1:C:614:ARG:CG	2.66	0.43
1:C:652:PHE:CB	1:C:691:PHE:CE2	3.01	0.43
1:C:1078:TYR:HB2	1:C:1229:LEU:HD11	2.00	0.43
1:C:1176:GLU:OE1	1:C:1203:HIS:NE2	2.51	0.43
1:C:1250:GLU:O	1:C:1250:GLU:HG3	2.18	0.43
1:C:1263:TYR:O	1:C:1297:SER:HB2	2.18	0.43
1:B:251:LEU:HA	1:B:254:VAL:HG22	2.01	0.43
1:B:267:VAL:HA	1:B:1304:MET:HE2	2.00	0.43
1:B:823:ILE:HG23	1:B:964:VAL:HG23	2.00	0.43
1:B:849:MET:SD	1:B:917:VAL:HG23	2.59	0.43
1:B:908:THR:HG23	1:B:911:ARG:NH1	2.33	0.43
1:C:733:VAL:HG23	1:C:743:PRO:HA	2.01	0.43
1:C:880:PRO:HB3	1:C:906:ALA:HA	1.66	0.43
1:B:381:ALA:HB3	1:B:624:PHE:HE2	1.82	0.43
1:B:388:GLN:OE1	1:B:1320:VAL:CG1	2.66	0.43
1:B:515:ILE:HD12	1:B:659:LEU:HD11	2.01	0.43
1:B:540:PHE:CE2	1:B:604:MET:HE2	2.53	0.43
1:B:733:VAL:HG22	1:B:734:ILE:H	1.84	0.43
1:B:895:VAL:HG12	1:B:917:VAL:HG12	2.00	0.43
1:B:1121:HIS:CD2	1:B:1124:THR:HG22	2.51	0.43
1:C:237:VAL:HG12	1:C:238:THR:N	2.34	0.43
1:C:310:LEU:HA	1:C:310:LEU:HD12	1.51	0.43
1:C:635:ILE:O	1:C:635:ILE:CG2	2.67	0.43
1:C:928:ARG:N	1:C:928:ARG:HD2	2.34	0.43
1:C:954:GLN:C	1:C:958:ILE:HD11	2.42	0.43
1:C:954:GLN:HG2	1:C:957:PHE:HD1	1.83	0.43
1:C:1075:ARG:O	1:C:1075:ARG:CG	2.64	0.43
1:C:1120:THR:O	1:C:1122:PRO:HD2	2.12	0.43
1:B:922:TYR:HD1	1:B:925:VAL:HG11	1.82	0.43
1:C:144:ASN:HB3	1:C:1318:GLU:H	1.83	0.43
1:C:674:LYS:CB	1:C:674:LYS:HZ3	2.32	0.43
1:C:716:PHE:O	1:C:716:PHE:HD1	2.00	0.43
1:C:760:THR:O	1:C:760:THR:OG1	2.29	0.43
1:C:923:TYR:N	1:C:923:TYR:CD1	2.86	0.43
1:C:1023:ARG:HG2	1:C:1024:PRO:HD2	2.00	0.43
1:C:1029:LEU:HA	1:C:1029:LEU:HD23	1.71	0.43
1:C:1202:PHE:O	1:C:1202:PHE:HD1	2.01	0.43
1:B:213:PHE:HB3	1:B:219:ILE:HD12	1.99	0.43

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:895:VAL:O	1:B:918:VAL:HG12	2.18	0.43
1:B:1175:ALA:HA	1:B:1204:LEU:O	2.18	0.43
1:B:1209:GLY:O	1:B:1212:ARG:HG2	2.18	0.43
1:B:1254:PRO:C	1:B:1256:GLY:H	2.20	0.43
1:C:156:GLN:HE22	1:C:1309:ILE:HG12	1.79	0.43
1:C:548:TYR:CZ	1:C:552:ILE:HG13	2.53	0.43
1:C:1038:GLU:C	1:C:1040:PHE:H	2.26	0.43
1:C:1156:ILE:O	1:C:1156:ILE:HG22	2.17	0.43
1:C:1159:VAL:HG23	1:C:1164:TRP:O	2.18	0.43
1:C:1186:GLN:H	1:C:1205:GLN:NE2	2.16	0.43
1:B:188:ARG:HH22	1:C:237:VAL:HG11	1.84	0.43
1:B:442:PRO:HB3	1:B:770:CYS:HB3	1.99	0.43
1:C:343:ILE:HD13	1:C:343:ILE:HG21	1.73	0.43
1:C:614:ARG:CD	1:C:635:ILE:HD12	2.42	0.43
1:C:639:ASN:HB3	1:C:1330:ILE:HD13	2.01	0.43
1:C:672:MET:O	1:C:672:MET:HG2	2.18	0.43
1:C:830:VAL:HA	1:C:854:GLN:HG2	2.00	0.43
1:C:1099:VAL:HG11	1:C:1119:TYR:OH	2.19	0.43
1:B:417:ALA:HB3	1:B:734:ILE:HD12	2.00	0.43
1:B:540:PHE:HE2	1:B:604:MET:HE2	1.84	0.43
1:B:619:ALA:HA	1:B:624:PHE:HD2	1.84	0.43
1:C:233:VAL:HG13	1:C:981:HIS:NE2	2.04	0.43
1:C:451:GLU:OE2	1:C:682:GLN:CB	2.64	0.43
1:C:550:ILE:HD11	1:C:594:LEU:CD1	2.48	0.43
1:C:1050:LEU:HD12	1:C:1054:ARG:CZ	2.48	0.43
1:C:1060:ARG:HH12	1:C:1292:GLU:N	2.14	0.43
1:C:1074:VAL:HG12	1:C:1171:ILE:CG2	2.48	0.43
1:B:450:PRO:HG3	1:B:686:HIS:HB2	2.00	0.43
1:B:1236:ILE:HD12	1:B:1238:VAL:N	2.34	0.43
1:C:429:ILE:HD12	1:C:429:ILE:O	2.16	0.43
1:C:601:ILE:HD12	1:C:601:ILE:HG23	1.70	0.43
1:C:887:VAL:HG13	1:C:893:ALA:CA	2.49	0.43
1:C:896:LEU:HD22	1:C:896:LEU:HA	1.76	0.43
1:C:1072:ASP:HB3	1:C:1172:GLU:HG2	2.01	0.43
1:C:1193:ILE:HG13	1:C:1202:PHE:CE2	2.54	0.43
1:C:1193:ILE:HG21	1:C:1193:ILE:HD13	1.65	0.43
1:B:505:PRO:HA	1:B:506:SER:HA	1.59	0.42
1:B:873:TYR:HD1	1:B:896:LEU:HB2	1.83	0.42
1:C:136:VAL:O	1:C:136:VAL:HG13	2.19	0.42
1:C:151:SER:N	1:C:400:GLU:OE1	2.50	0.42
1:C:265:VAL:O	1:C:1303:SER:CA	2.67	0.42

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:357:VAL:HG22	1:C:1054:ARG:HD2	2.01	0.42
1:C:469:ARG:HD3	1:C:513:GLU:OE1	2.18	0.42
1:C:738:GLU:O	1:C:738:GLU:HG3	2.17	0.42
1:C:810:LEU:HD23	1:C:810:LEU:HA	1.42	0.42
1:C:833:ARG:HH11	1:C:942:HIS:CD2	2.37	0.42
1:C:1074:VAL:O	1:C:1074:VAL:CG1	2.67	0.42
1:C:1085:ASP:HB3	1:C:1243:ARG:NH2	2.34	0.42
1:C:1270:LEU:HA	1:C:1270:LEU:HD23	1.57	0.42
1:C:1276:LEU:CB	1:C:1290:LYS:HG3	2.49	0.42
1:B:153:ASP:OD2	1:B:401:LEU:HD21	2.19	0.42
1:B:701:HIS:NE2	1:B:791:ILE:HD11	2.34	0.42
1:B:952:PHE:HB2	1:B:958:ILE:HD12	2.02	0.42
1:B:1128:TYR:CE2	1:B:1135:PRO:HD3	2.53	0.42
1:C:155:LYS:O	1:C:155:LYS:CG	2.67	0.42
1:C:448:TYR:HB2	1:C:449:PHE:H	1.10	0.42
1:C:936:MET:O	1:C:936:MET:SD	2.77	0.42
1:C:1013:LYS:HE3	1:C:1015:GLN:NE2	2.34	0.42
1:C:1014:MET:HB3	1:C:1014:MET:HE3	1.66	0.42
1:C:1022:ILE:O	1:C:1022:ILE:HG22	2.17	0.42
1:C:1059:LEU:HD12	1:C:1059:LEU:HA	1.80	0.42
1:C:1134:ARG:CB	1:C:1135:PRO:CD	2.85	0.42
1:B:228:VAL:HG11	1:B:253:MET:HG3	2.01	0.42
1:B:1066:ARG:HH21	1:B:1296:ILE:CD1	2.32	0.42
1:B:1236:ILE:CD1	1:B:1238:VAL:HG22	2.49	0.42
1:C:143:VAL:C	1:C:1318:GLU:HB3	2.44	0.42
1:C:197:PHE:HE1	1:C:1242:MET:HG3	1.83	0.42
1:C:225:ILE:CG2	1:C:226:PRO:HD2	2.48	0.42
1:C:454:GLU:OE2	1:C:454:GLU:HA	2.19	0.42
1:C:720:PHE:O	1:C:720:PHE:CG	2.69	0.42
1:C:791:ILE:HG21	1:C:1325:VAL:HG21	2.01	0.42
1:C:845:GLU:HB3	1:C:846:GLY:H	1.54	0.42
1:C:976:THR:O	1:C:977:SER:C	2.53	0.42
1:C:1014:MET:CG	1:C:1014:MET:O	2.67	0.42
1:C:1137:VAL:CG2	1:C:1164:TRP:CD2	3.03	0.42
1:C:1177:VAL:O	1:C:1177:VAL:CG2	2.66	0.42
1:C:1178:MET:HE2	1:C:1205:GLN:HB2	1.65	0.42
1:C:1178:MET:HG3	1:C:1178:MET:O	2.20	0.42
1:B:372:ALA:HB3	1:B:1315:MET:CE	2.49	0.42
1:B:720:PHE:HD2	1:B:727:PHE:CD1	2.36	0.42
1:B:1051:ARG:O	1:B:1055:LEU:HB2	2.20	0.42
1:C:267:VAL:HG21	1:C:344:VAL:CG2	2.49	0.42

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:409:ILE:HG23	1:C:409:ILE:HD12	1.58	0.42
1:C:494:GLU:HB3	1:C:577:GLN:HE22	1.79	0.42
1:C:504:ASP:OD1	1:C:504:ASP:N	2.52	0.42
1:C:892:VAL:HG13	1:C:894:VAL:HG12	1.94	0.42
1:C:941:TYR:HD1	1:C:941:TYR:HA	1.72	0.42
1:C:1193:ILE:HG13	1:C:1202:PHE:HZ	1.84	0.42
1:C:1321:ASN:HB3	1:C:1322:PRO:HD2	2.01	0.42
1:B:188:ARG:NH2	1:C:237:VAL:HG11	2.35	0.42
1:B:287:ARG:HB2	1:B:328:GLY:HA3	2.00	0.42
1:B:434:VAL:HB	1:B:439:VAL:HG11	2.01	0.42
1:B:734:ILE:HG12	1:B:1019:ILE:HD13	2.01	0.42
1:C:144:ASN:CA	1:C:1318:GLU:HB3	2.49	0.42
1:C:389:PHE:CZ	1:C:796:PRO:HG2	2.50	0.42
1:C:560:ILE:HG22	1:C:585:PHE:CE2	2.54	0.42
1:C:830:VAL:HA	1:C:854:GLN:CG	2.50	0.42
1:C:985:ARG:HH21	1:C:988:GLN:HG3	1.79	0.42
1:C:1205:GLN:O	1:C:1205:GLN:CG	2.67	0.42
1:C:1330:ILE:H	1:C:1330:ILE:HD12	1.85	0.42
1:B:135:LYS:CE	1:C:470:ALA:N	2.65	0.42
1:B:139:ASN:O	1:C:757:ILE:HG22	2.20	0.42
1:B:190:VAL:HG12	1:B:300:LEU:HB3	2.01	0.42
1:B:193:THR:HA	1:B:296:VAL:HG13	2.01	0.42
1:C:314:ILE:O	1:C:318:LEU:HD22	2.18	0.42
1:C:342:THR:OG1	1:C:1305:MET:HE1	2.20	0.42
1:C:519:LEU:HA	1:C:519:LEU:HD23	1.51	0.42
1:C:520:PHE:CZ	1:C:691:PHE:HE1	2.38	0.42
1:C:652:PHE:CD1	1:C:652:PHE:C	2.96	0.42
1:C:851:THR:O	1:C:852:TYR:C	2.62	0.42
1:C:1079:LEU:O	1:C:1079:LEU:HD13	2.19	0.42
1:C:1089:VAL:O	1:C:1089:VAL:CG1	2.68	0.42
1:B:390:HIS:HB2	1:B:1318:GLU:CG	2.47	0.42
1:B:440:ILE:CG2	1:B:770:CYS:CB	2.98	0.42
1:C:455:GLN:O	1:C:455:GLN:CG	2.68	0.42
1:C:543:TRP:HD1	1:C:543:TRP:C	2.27	0.42
1:C:1078:TYR:O	1:C:1078:TYR:HD1	2.02	0.42
1:C:1155:ILE:O	1:C:1155:ILE:HG22	2.16	0.42
1:C:1159:VAL:O	1:C:1159:VAL:CG2	2.67	0.42
1:C:208:LEU:CB	1:C:221:LEU:CD2	2.98	0.42
1:C:220:ASP:CG	1:C:222:THR:HG23	2.44	0.42
1:C:333:ARG:NE	1:C:1272:ARG:HA	2.24	0.42
1:C:613:LEU:HD22	1:C:614:ARG:N	2.35	0.42

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:836:GLN:C	1:C:838:GLU:N	2.74	0.42
1:C:965:ARG:NH1	1:C:968:ARG:CZ	2.82	0.42
1:C:986:ILE:HA	1:C:989:ILE:CG2	2.49	0.42
1:C:1278:TYR:CE2	1:C:1288:ILE:CD1	3.01	0.42
1:B:614:ARG:O	1:B:633:THR:HG22	2.19	0.42
1:B:712:PHE:HB2	1:B:715:ASN:ND2	2.34	0.42
1:B:1060:ARG:HA	1:B:1063:THR:HG22	2.02	0.42
1:C:124:GLN:OE1	1:C:124:GLN:CA	2.68	0.42
1:C:405:HIS:CD2	1:C:624:PHE:C	2.98	0.42
1:C:923:TYR:N	1:C:923:TYR:HD1	2.17	0.42
1:B:274:MET:O	1:B:277:THR:N	2.49	0.42
1:B:852:TYR:CE2	1:B:856:LEU:HD22	2.54	0.42
1:B:1105:LEU:HD11	1:B:1122:PRO:HD3	2.01	0.42
1:B:1248:HIS:HB2	1:B:1251:VAL:HG22	2.01	0.42
1:B:1260:PRO:HB2	1:B:1265:MET:HE3	2.01	0.42
1:C:391:GLY:O	1:C:392:PRO:C	2.61	0.42
1:C:489:MET:HE2	1:C:489:MET:HB3	1.94	0.42
1:C:810:LEU:O	1:C:811:SER:C	2.58	0.42
1:C:1247:ASN:ND2	1:C:1247:ASN:O	2.51	0.42
1:B:455:GLN:H	1:B:455:GLN:CD	2.24	0.41
1:B:632:GLN:H	1:B:718:ASN:ND2	2.18	0.41
1:B:649:ALA:HA	1:B:691:PHE:HE1	1.85	0.41
1:B:1289:PRO:HG2	1:B:1292:GLU:HG2	2.00	0.41
1:C:385:ILE:H	1:C:708:THR:HG22	1.85	0.41
1:C:503:GLU:OE2	1:C:542:ARG:CG	2.68	0.41
1:C:838:GLU:CD	1:C:934:LEU:HA	2.44	0.41
1:C:913:ASN:HD22	1:C:913:ASN:HA	1.72	0.41
1:C:1212:ARG:O	1:C:1212:ARG:HG3	2.20	0.41
1:B:472:GLU:CB	1:B:761:SER:HB3	2.42	0.41
1:B:1276:LEU:HD13	1:B:1300:ASN:ND2	2.35	0.41
1:C:179:LYS:HD2	1:C:180:LEU:N	2.35	0.41
1:C:244:SER:C	1:C:246:GLU:H	2.27	0.41
1:C:612:PHE:O	1:C:612:PHE:CG	2.70	0.41
1:C:656:VAL:CG1	1:C:688:GLU:CB	2.85	0.41
1:C:743:PRO:HD2	1:C:743:PRO:O	2.19	0.41
1:C:838:GLU:CD	1:C:934:LEU:CA	2.90	0.41
1:C:870:ASP:CB	1:C:871:PRO:HD2	2.47	0.41
1:C:971:MET:HE2	1:C:971:MET:HB3	1.50	0.41
1:C:1137:VAL:HG22	1:C:1164:TRP:CD1	2.55	0.41
1:C:1278:TYR:CD2	1:C:1288:ILE:HD11	2.53	0.41
1:C:1288:ILE:HG12	1:C:1288:ILE:H	1.55	0.41

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:303:ASP:O	1:C:1103:HIS:HE1	2.03	0.41
1:B:451:GLU:HG2	1:B:452:ASN:H	1.85	0.41
1:B:479:HIS:ND1	1:B:479:HIS:N	2.67	0.41
1:B:683:TRP:O	1:B:686:HIS:HB3	2.19	0.41
1:B:862:ARG:HH12	1:B:948:ILE:HG21	1.84	0.41
1:B:892:VAL:HG21	1:B:952:PHE:CE1	2.56	0.41
1:B:985:ARG:NH2	1:B:988:GLN:HE21	2.14	0.41
1:B:1119:TYR:HB3	1:B:1134:ARG:NE	2.31	0.41
1:B:1300:ASN:OD1	1:B:1300:ASN:N	2.52	0.41
1:C:202:ALA:O	1:C:1244:ALA:N	2.38	0.41
1:C:245:ALA:C	1:C:247:TYR:H	2.28	0.41
1:C:252:LEU:HD12	1:C:971:MET:HE3	2.01	0.41
1:C:289:THR:O	1:C:329:LEU:N	2.54	0.41
1:C:418:ASN:OD1	1:C:418:ASN:N	2.53	0.41
1:C:659:LEU:HD22	1:C:659:LEU:C	2.41	0.41
1:C:676:THR:O	1:C:676:THR:HG22	2.20	0.41
1:B:305:THR:CG2	1:B:307:VAL:HG12	2.51	0.41
1:B:694:ILE:HD12	1:B:772:TYR:CE1	2.55	0.41
1:C:133:MET:SD	1:C:133:MET:O	2.78	0.41
1:C:136:VAL:O	1:C:136:VAL:CG1	2.68	0.41
1:C:362:LEU:O	1:C:362:LEU:CD2	2.68	0.41
1:C:383:SER:HG	1:C:796:PRO:HG3	0.58	0.41
1:C:385:ILE:HG12	1:C:708:THR:HG22	2.00	0.41
1:C:612:PHE:HE2	1:C:614:ARG:HB3	1.85	0.41
1:C:734:ILE:HD13	1:C:734:ILE:HG21	1.74	0.41
1:C:883:ILE:HD12	1:C:883:ILE:HG23	1.76	0.41
1:C:407:HIS:HD2	1:C:1047:LEU:CA	2.28	0.41
1:C:427:VAL:O	1:C:427:VAL:CG1	2.69	0.41
1:C:449:PHE:HB3	1:C:683:TRP:HE1	1.61	0.41
1:C:536:LEU:HD23	1:C:536:LEU:HA	1.56	0.41
1:C:934:LEU:H	1:C:934:LEU:HG	1.66	0.41
1:C:971:MET:HB2	1:C:972:PRO:HD2	2.03	0.41
1:C:1072:ASP:N	1:C:1072:ASP:OD1	2.52	0.41
1:C:1078:TYR:HB3	1:C:1159:VAL:O	2.20	0.41
1:C:1147:MET:HB3	1:C:1147:MET:HE3	1.50	0.41
1:C:1251:VAL:O	1:C:1251:VAL:HG12	2.21	0.41
1:B:390:HIS:O	1:B:1317:VAL:HG23	2.20	0.41
1:B:437:ALA:O	1:B:701:HIS:HE1	2.04	0.41
1:B:1271:SER:OG	1:B:1272:ARG:N	2.53	0.41
1:C:485:GLU:HB3	1:C:706:TYR:HE1	1.86	0.41
1:C:651:ARG:HD2	1:C:655:ILE:HG12	2.02	0.41

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:729:PRO:O	1:C:731:GLN:N	2.53	0.41
1:C:845:GLU:CD	1:C:911:ARG:NH2	2.77	0.41
1:C:928:ARG:NH1	1:C:928:ARG:CG	2.77	0.41
1:C:1019:ILE:O	1:C:1019:ILE:HG13	2.19	0.41
1:C:1191:GLU:O	1:C:1191:GLU:HG3	2.16	0.41
1:C:1215:PRO:CD	1:C:1215:PRO:O	2.68	0.41
1:B:560:ILE:HG12	1:B:566:PHE:CD1	2.56	0.41
1:B:733:VAL:HG21	1:B:741:TYR:HD1	1.86	0.41
1:B:873:TYR:CB	1:B:897:TYR:HB2	2.43	0.41
1:B:1236:ILE:HD13	1:B:1238:VAL:HG22	2.02	0.41
1:C:265:VAL:HG23	1:C:1302:VAL:O	2.21	0.41
1:C:287:ARG:CB	1:C:329:LEU:O	2.68	0.41
1:C:370:VAL:HG13	1:C:370:VAL:O	2.21	0.41
1:C:548:TYR:CE2	1:C:552:ILE:HG13	2.55	0.41
1:C:1037:ILE:HD11	1:C:1040:PHE:CD2	2.56	0.41
1:B:765:PRO:O	1:B:769:GLN:HB2	2.20	0.41
1:C:77:THR:OG1	1:C:172:ASP:OD2	2.37	0.41
1:C:367:GLU:OE1	1:C:367:GLU:HA	2.21	0.41
1:C:571:ARG:HH11	1:C:571:ARG:CB	2.26	0.41
1:C:585:PHE:CE1	1:C:728:LYS:HG2	2.56	0.41
1:C:742:LYS:HE2	1:C:742:LYS:HB3	1.32	0.41
1:C:840:ASP:C	1:C:940:ARG:NH2	2.76	0.41
1:C:974:LEU:HA	1:C:974:LEU:HD23	1.83	0.41
1:C:1079:LEU:C	1:C:1227:MET:SD	3.04	0.41
1:C:1099:VAL:HG21	1:C:1119:TYR:OH	2.20	0.41
1:B:141:LEU:HD21	1:B:391:GLY:HA2	2.02	0.41
1:B:223:LYS:HD2	1:B:1203:HIS:ND1	2.35	0.41
1:B:262:ASN:H	1:B:1054:ARG:CZ	2.34	0.41
1:B:295:GLY:H	1:B:349:ASN:CG	2.28	0.41
1:B:418:ASN:O	1:B:420:PRO:HD3	2.21	0.41
1:B:584:HIS:C	1:B:585:PHE:HD1	2.29	0.41
1:B:694:ILE:HG23	1:B:772:TYR:CE1	2.56	0.41
1:B:752:VAL:O	1:B:752:VAL:HG12	2.20	0.41
1:B:791:ILE:HD12	1:B:791:ILE:HA	1.82	0.41
1:B:826:GLY:HA2	1:B:827:GLY:HA3	1.50	0.41
1:C:110:PRO:CB	1:C:111:PRO:CD	2.98	0.41
1:C:236:GLY:O	1:C:237:VAL:HG22	2.21	0.41
1:C:429:ILE:HD13	1:C:799:THR:HG22	2.01	0.41
1:C:501:SER:O	1:C:501:SER:OG	2.23	0.41
1:C:601:ILE:N	1:C:601:ILE:HD13	2.36	0.41
1:C:651:ARG:CD	1:C:651:ARG:C	2.91	0.41

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:731:GLN:O	1:C:731:GLN:CG	2.69	0.41
1:C:835:TYR:HE1	1:C:942:HIS:CG	2.29	0.41
1:C:990:THR:OG1	1:C:992:VAL:HG12	2.20	0.41
1:C:1085:ASP:HB2	1:C:1086:PRO:HD3	1.98	0.41
1:C:1186:GLN:HE21	1:C:1186:GLN:C	2.29	0.41
1:C:1280:PRO:HB2	1:C:1281:VAL:H	1.62	0.41
1:B:157:ILE:HG12	1:B:264:LEU:O	2.21	0.41
1:B:157:ILE:HD12	1:B:160:PRO:HA	2.02	0.41
1:B:648:PHE:CE2	1:B:691:PHE:HZ	2.39	0.41
1:B:1096:TYR:CD1	1:B:1136:HIS:HB3	2.55	0.41
1:C:364:ALA:HB1	1:C:1050:LEU:HD21	2.01	0.41
1:C:471:SER:O	1:C:765:PRO:HG3	2.20	0.41
1:C:837:THR:HA	1:C:936:MET:CG	2.51	0.41
1:C:865:ILE:HD11	1:C:1020:ARG:NH2	2.36	0.41
1:B:261:ASP:OD1	1:B:263:ARG:HB2	2.21	0.40
1:B:394:GLN:O	1:B:394:GLN:HG2	2.21	0.40
1:B:958:ILE:HG22	1:B:959:GLN:N	2.35	0.40
1:C:101:ASP:O	1:C:103:GLY:N	2.54	0.40
1:C:110:PRO:HB2	1:C:111:PRO:HD2	2.03	0.40
1:C:225:ILE:O	1:C:227:LEU:HG	2.21	0.40
1:C:399:PRO:O	1:C:399:PRO:CG	2.69	0.40
1:C:579:LEU:O	1:C:579:LEU:CD1	2.69	0.40
1:C:743:PRO:O	1:C:743:PRO:CD	2.69	0.40
1:C:762:ILE:CD1	1:C:762:ILE:O	2.69	0.40
1:C:979:ILE:O	1:C:983:ILE:HG13	2.21	0.40
1:C:1022:ILE:O	1:C:1022:ILE:CG2	2.68	0.40
1:C:1046:PHE:C	1:C:1048:ASP:H	2.30	0.40
1:C:408:ILE:HG22	1:C:412:LEU:HD12	2.02	0.40
1:C:730:ASP:O	1:C:731:GLN:HG2	2.22	0.40
1:C:897:TYR:OH	1:C:928:ARG:HG3	2.21	0.40
1:C:909:TYR:OH	1:C:913:ASN:OD1	2.32	0.40
1:C:978:GLN:HE21	1:C:978:GLN:HB2	1.75	0.40
1:C:1253:ARG:HA	1:C:1254:PRO:HD3	1.87	0.40
1:B:295:GLY:N	1:B:349:ASN:OD1	2.54	0.40
1:B:558:TYR:CE1	1:B:585:PHE:HB2	2.57	0.40
1:B:736:SER:HA	1:B:1016:ASN:O	2.21	0.40
1:B:830:VAL:HA	1:B:854:GLN:HE21	1.85	0.40
1:B:924:ASP:HB3	1:B:928:ARG:NH2	2.36	0.40
1:C:146:GLU:CG	1:C:1317:VAL:HG13	2.49	0.40
1:C:164:LEU:HD13	1:C:1296:ILE:HG13	2.03	0.40
1:C:166:TYR:HE1	1:C:1298:PHE:CZ	2.38	0.40

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:451:GLU:CB	1:C:686:HIS:HB2	2.51	0.40
1:C:750:GLU:HB3	1:C:757:ILE:HG13	2.03	0.40
1:C:822:MET:HE3	1:C:822:MET:HB3	1.75	0.40
1:C:1000:LEU:O	1:C:1000:LEU:CG	2.69	0.40
1:C:1185:THR:OG1	1:C:1186:GLN:N	2.55	0.40
1:C:1278:TYR:HB3	1:C:1279:SER:H	1.68	0.40
1:B:678:SER:O	1:B:682:GLN:HG2	2.21	0.40
1:B:1086:PRO:HB3	1:B:1177:VAL:HG22	2.02	0.40
1:B:1277:LEU:HA	1:B:1289:PRO:HA	2.02	0.40
1:C:554:ARG:CZ	1:C:594:LEU:CD2	2.99	0.40
1:C:985:ARG:HH22	1:C:989:ILE:CB	2.33	0.40
1:C:1033:ASP:HB3	1:C:1034:GLN:NE2	2.37	0.40
1:C:1245:ILE:HG21	1:C:1245:ILE:HD13	1.62	0.40
1:C:1254:PRO:O	1:C:1254:PRO:CD	2.69	0.40
1:C:1292:GLU:O	1:C:1292:GLU:CG	2.69	0.40
1:B:171:GLU:CD	1:B:1180:PRO:HG2	2.47	0.40
1:B:462:LEU:O	1:B:466:VAL:HG23	2.22	0.40
1:B:606:LEU:HD21	1:B:658:THR:HG23	2.02	0.40
1:B:874:ILE:HG23	1:B:895:VAL:CG2	2.50	0.40
1:B:898:GLN:O	1:B:928:ARG:HD3	2.21	0.40
1:C:322:GLY:O	1:C:1279:SER:HB2	2.20	0.40
1:C:343:ILE:HD11	1:C:366:MET:HE3	2.03	0.40
1:C:391:GLY:HA3	1:C:392:PRO:HD3	1.90	0.40
1:C:841:ASP:CA	1:C:940:ARG:CZ	2.98	0.40
1:C:1034:GLN:OE1	1:C:1034:GLN:CA	2.69	0.40
1:C:1105:LEU:CD1	1:C:1105:LEU:O	2.69	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.



Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	1132/1333 (85%)	999 (88%)	121 (11%)	12 (1%)	12	40
1	C	1243/1333 (93%)	937 (75%)	209 (17%)	97 (8%)	1	5
All	All	2375/2666 (89%)	1936 (82%)	330 (14%)	109 (5%)	3	13

All (109) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	120	VAL
1	C	121	PHE
1	C	122	ASN
1	C	129	ALA
1	C	144	ASN
1	C	186	ASP
1	C	234	PRO
1	C	241	ALA
1	C	280	THR
1	C	299	ALA
1	C	337	VAL
1	C	338	ARG
1	C	372	ALA
1	C	450	PRO
1	C	455	GLN
1	C	475	ILE
1	C	661	ASN
1	C	730	ASP
1	C	772	TYR
1	C	773	PRO
1	C	871	PRO
1	C	875	THR
1	C	879	THR
1	C	880	PRO
1	C	891	HIS
1	C	935	GLN
1	C	1024	PRO
1	C	1130	SER
1	C	1134	ARG
1	C	1138	HIS
1	C	1147	MET
1	C	1150	LEU
1	C	1182	GLU
1	C	1213	PRO
1	C	1221	PRO

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Res	Type
1	C	1262	SER
1	C	1271	SER
1	C	1278	TYR
1	C	1282	ALA
1	C	1293	VAL
1	C	1308	ASN
1	B	437	ALA
1	B	473	ALA
1	B	1251	VAL
1	B	1255	ARG
1	B	1286	VAL
1	C	130	LEU
1	C	184	GLU
1	C	339	LEU
1	C	403	PHE
1	C	453	LEU
1	C	565	GLU
1	C	639	ASN
1	C	837	THR
1	C	842	ASP
1	C	948	ILE
1	C	1049	GLU
1	C	1067	ILE
1	C	1190	ALA
1	C	1228	ARG
1	C	1251	VAL
1	C	1280	PRO
1	C	1295	HIS
1	C	1325	VAL
1	C	1329	ASN
1	C	1332	ASN
1	B	151	SER
1	B	753	ASP
1	C	231	LEU
1	C	235	ILE
1	C	442	PRO
1	C	448	TYR
1	C	522	PRO
1	C	1045	TYR
1	C	1129	PRO
1	C	1222	ALA
1	C	1294	ASP

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	C	265	VAL
1	C	646	ASN
1	C	731	GLN
1	C	1093	PRO
1	C	1136	HIS
1	C	1144	ARG
1	C	1191	GLU
1	C	1223	SER
1	C	1235	PRO
1	B	384	MET
1	B	1094	GLU
1	C	336	TYR
1	C	577	GLN
1	C	898	GLN
1	C	942	HIS
1	C	958	ILE
1	C	1260	PRO
1	B	879	THR
1	C	245	ALA
1	C	644	VAL
1	C	794	PRO
1	C	1109	SER
1	C	1234	GLN
1	C	1137	VAL
1	B	1236	ILE
1	C	273	PRO
1	C	635	ILE
1	B	1246	VAL
1	C	1128	TYR
1	C	1236	ILE
1	C	1274	GLY
1	C	1286	VAL

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	1000/1155 (87%)	987 (99%)	13 (1%)	65	79
1	C	1087/1155 (94%)	707 (65%)	380 (35%)	0	1
All	All	2087/2310 (90%)	1694 (81%)	393 (19%)	3	6

All (393) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	225	ILE
1	B	438	ASN
1	B	461	ARG
1	B	463	VAL
1	B	464	SER
1	B	467	LYS
1	B	471	SER
1	B	472	GLU
1	B	474	ASP
1	B	475	ILE
1	B	528	ILE
1	B	790	GLU
1	B	1171	ILE
1	C	74	LYS
1	C	79	SER
1	C	83	GLN
1	C	85	ASP
1	C	87	GLU
1	C	88	LYS
1	C	89	PRO
1	C	92	VAL
1	C	93	THR
1	C	96	ILE
1	C	97	GLU
1	C	101	ASP
1	C	102	VAL
1	C	104	ILE
1	C	105	MET
1	C	106	GLN
1	C	108	LYS
1	C	109	LYS
1	C	112	THR
1	C	113	VAL
1	C	119	ASP
1	C	120	VAL

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	C	122	ASN
1	C	123	GLU
1	C	124	GLN
1	C	132	PRO
1	C	133	MET
1	C	134	THR
1	C	135	LYS
1	C	136	VAL
1	C	137	ILE
1	C	141	LEU
1	C	143	VAL
1	C	145	THR
1	C	146	GLU
1	C	150	LEU
1	C	155	LYS
1	C	156	GLN
1	C	157	ILE
1	C	159	ASP
1	C	161	LYS
1	C	190	VAL
1	C	196	LEU
1	C	204	VAL
1	C	205	ASN
1	C	214	ASP
1	C	221	LEU
1	C	229	GLN
1	C	230	ASP
1	C	231	LEU
1	C	232	LEU
1	C	248	VAL
1	C	251	LEU
1	C	255	LEU
1	C	265	VAL
1	C	282	VAL
1	C	287	ARG
1	C	296	VAL
1	C	297	ASN
1	C	300	LEU
1	C	302	ARG
1	C	304	PHE
1	C	306	GLN
1	C	309	TRP

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	C	312	ARG
1	C	315	THR
1	C	316	ASN
1	C	318	LEU
1	C	319	GLN
1	C	320	GLN
1	C	327	LEU
1	C	330	THR
1	C	333	ARG
1	C	337	VAL
1	C	338	ARG
1	C	339	LEU
1	C	342	THR
1	C	348	LEU
1	C	350	ILE
1	C	351	ASP
1	C	356	SER
1	C	357	VAL
1	C	361	ASN
1	C	362	LEU
1	C	363	ARG
1	C	366	MET
1	C	375	ARG
1	C	376	ILE
1	C	377	LYS
1	C	384	MET
1	C	386	SER
1	C	397	LEU
1	C	409	ILE
1	C	422	LEU
1	C	425	ILE
1	C	429	ILE
1	C	430	ASN
1	C	439	VAL
1	C	440	ILE
1	C	441	ARG
1	C	445	GLU
1	C	446	LYS
1	C	448	TYR
1	C	452	ASN
1	C	453	LEU
1	C	454	GLU

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	C	455	GLN
1	C	462	LEU
1	C	466	VAL
1	C	472	GLU
1	C	480	LEU
1	C	482	ILE
1	C	495	LEU
1	C	497	LYS
1	C	498	ILE
1	C	505	PRO
1	C	509	VAL
1	C	513	GLU
1	C	522	PRO
1	C	523	THR
1	C	524	GLU
1	C	526	ASN
1	C	529	LYS
1	C	538	LEU
1	C	550	ILE
1	C	552	ILE
1	C	553	GLN
1	C	554	ARG
1	C	560	ILE
1	C	565	GLU
1	C	571	ARG
1	C	572	ASN
1	C	574	LYS
1	C	576	ASP
1	C	578	SER
1	C	581	LEU
1	C	583	GLU
1	C	591	ASP
1	C	592	VAL
1	C	594	LEU
1	C	599	THR
1	C	603	ILE
1	C	605	ARG
1	C	607	PHE
1	C	613	LEU
1	C	615	THR
1	C	617	ASP
1	C	623	ASN

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	C	628	SER
1	C	629	ARG
1	C	633	THR
1	C	635	ILE
1	C	637	TYR
1	C	639	ASN
1	C	641	ARG
1	C	643	THR
1	C	646	ASN
1	C	655	ILE
1	C	656	VAL
1	C	658	THR
1	C	659	LEU
1	C	666	ARG
1	C	669	GLN
1	C	673	GLN
1	C	674	LYS
1	C	685	ARG
1	C	686	HIS
1	C	687	LEU
1	C	694	ILE
1	C	702	LEU
1	C	708	THR
1	C	717	THR
1	C	720	PHE
1	C	729	PRO
1	C	734	ILE
1	C	736	SER
1	C	742	LYS
1	C	744	ILE
1	C	746	GLU
1	C	747	ARG
1	C	748	GLN
1	C	755	LEU
1	C	757	ILE
1	C	758	ILE
1	C	765	PRO
1	C	766	ILE
1	C	767	LEU
1	C	770	CYS
1	C	792	VAL
1	C	795	ASP

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Res	Type
1	C	797	SER
1	C	799	THR
1	C	800	LEU
1	C	802	GLN
1	C	804	LEU
1	C	806	VAL
1	C	812	LYS
1	C	813	LEU
1	C	814	THR
1	C	816	PRO
1	C	817	ASP
1	C	820	ILE
1	C	823	ILE
1	C	824	LEU
1	C	828	ASP
1	C	829	SER
1	C	831	VAL
1	C	837	THR
1	C	840	ASP
1	C	843	LEU
1	C	848	ARG
1	C	850	THR
1	C	851	THR
1	C	856	LEU
1	C	859	ILE
1	C	860	ARG
1	C	864	HIS
1	C	865	ILE
1	C	866	THR
1	C	867	ASN
1	C	870	ASP
1	C	872	ILE
1	C	874	ILE
1	C	888	GLN
1	C	892	VAL
1	C	894	VAL
1	C	895	VAL
1	C	896	LEU
1	C	897	TYR
1	C	898	GLN
1	C	902	ILE
1	C	907	SER

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	C	910	LEU
1	C	913	ASN
1	C	916	LEU
1	C	917	VAL
1	C	922	TYR
1	C	928	ARG
1	C	931	ASN
1	C	934	LEU
1	C	940	ARG
1	C	941	TYR
1	C	945	VAL
1	C	948	ILE
1	C	951	ILE
1	C	954	GLN
1	C	957	PHE
1	C	958	ILE
1	C	962	ASP
1	C	966	GLN
1	C	967	LEU
1	C	973	THR
1	C	976	THR
1	C	978	GLN
1	C	980	ARG
1	C	984	GLU
1	C	988	GLN
1	C	989	ILE
1	C	991	ASP
1	C	1002	LEU
1	C	1003	ARG
1	C	1008	LEU
1	C	1014	MET
1	C	1018	GLN
1	C	1021	ARG
1	C	1022	ILE
1	C	1023	ARG
1	C	1024	PRO
1	C	1034	GLN
1	C	1036	ASP
1	C	1038	GLU
1	C	1043	SER
1	C	1044	ARG
1	C	1049	GLU

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	C	1050	LEU
1	C	1051	ARG
1	C	1053	ARG
1	C	1054	ARG
1	C	1059	LEU
1	C	1061	LEU
1	C	1062	ILE
1	C	1063	THR
1	C	1070	ARG
1	C	1072	ASP
1	C	1075	ARG
1	C	1076	ILE
1	C	1077	MET
1	C	1079	LEU
1	C	1080	THR
1	C	1082	ASP
1	C	1083	ASP
1	C	1088	PHE
1	C	1089	VAL
1	C	1092	VAL
1	C	1099	VAL
1	C	1100	GLN
1	C	1104	ARG
1	C	1105	LEU
1	C	1110	LEU
1	C	1112	ASN
1	C	1113	LYS
1	C	1114	ARG
1	C	1116	ARG
1	C	1118	THR
1	C	1122	PRO
1	C	1123	PRO
1	C	1124	THR
1	C	1126	MET
1	C	1132	THR
1	C	1140	THR
1	C	1141	ILE
1	C	1147	MET
1	C	1149	LYS
1	C	1156	ILE
1	C	1158	SER
1	C	1161	LYS

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	C	1168	ILE
1	C	1169	HIS
1	C	1170	ASP
1	C	1171	ILE
1	C	1172	GLU
1	C	1177	VAL
1	C	1182	GLU
1	C	1185	THR
1	C	1186	GLN
1	C	1187	HIS
1	C	1191	GLU
1	C	1192	SER
1	C	1195	THR
1	C	1200	LYS
1	C	1201	LEU
1	C	1202	PHE
1	C	1204	LEU
1	C	1207	MET
1	C	1210	LEU
1	C	1211	LEU
1	C	1212	ARG
1	C	1213	PRO
1	C	1214	GLU
1	C	1219	ASP
1	C	1221	PRO
1	C	1227	MET
1	C	1229	LEU
1	C	1234	GLN
1	C	1236	ILE
1	C	1237	SER
1	C	1240	ARG
1	C	1242	MET
1	C	1243	ARG
1	C	1246	VAL
1	C	1247	ASN
1	C	1250	GLU
1	C	1263	TYR
1	C	1264	GLU
1	C	1272	ARG
1	C	1273	ASN
1	C	1276	LEU
1	C	1277	LEU

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	C	1283	ASN
1	C	1285	GLN
1	C	1286	VAL
1	C	1288	ILE
1	C	1290	LYS
1	C	1292	GLU
1	C	1295	HIS
1	C	1296	ILE
1	C	1298	PHE
1	C	1301	VAL
1	C	1302	VAL
1	C	1309	ILE
1	C	1310	ARG
1	C	1313	ASP
1	C	1319	ARG
1	C	1320	VAL
1	C	1323	ASP
1	C	1325	VAL
1	C	1326	ARG
1	C	1328	ILE
1	C	1331	ARG
1	C	1332	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (79) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	139	ASN
1	B	148	GLN
1	B	291	HIS
1	B	292	ASN
1	B	311	ASN
1	B	346	HIS
1	B	352	HIS
1	B	369	ASN
1	B	438	ASN
1	B	623	ASN
1	B	661	ASN
1	B	682	GLN
1	B	686	HIS
1	B	693	ASN
1	B	698	HIS
1	B	701	HIS

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	B	711	ASN
1	B	718	ASN
1	B	769	GLN
1	B	802	GLN
1	B	854	GLN
1	B	882	GLN
1	B	891	HIS
1	B	942	HIS
1	B	988	GLN
1	B	1016	ASN
1	B	1064	ASN
1	B	1169	HIS
1	B	1205	GLN
1	B	1295	HIS
1	B	1300	ASN
1	C	106	GLN
1	C	115	GLN
1	C	144	ASN
1	C	148	GLN
1	C	173	GLN
1	C	195	ASN
1	C	205	ASN
1	C	209	ASN
1	C	229	GLN
1	C	283	ASN
1	C	297	ASN
1	C	306	GLN
1	C	311	ASN
1	C	346	HIS
1	C	352	HIS
1	C	369	ASN
1	C	394	GLN
1	C	430	ASN
1	C	452	ASN
1	C	455	GLN
1	C	493	HIS
1	C	526	ASN
1	C	577	GLN
1	C	610	GLN
1	C	646	ASN
1	C	673	GLN
1	C	693	ASN

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	C	701	HIS
1	C	748	GLN
1	C	802	GLN
1	C	836	GLN
1	C	854	GLN
1	C	864	HIS
1	C	882	GLN
1	C	903	ASN
1	C	937	ASN
1	C	954	GLN
1	C	959	GLN
1	C	978	GLN
1	C	1103	HIS
1	C	1121	HIS
1	C	1154	ASN
1	C	1186	GLN
1	C	1203	HIS
1	C	1205	GLN
1	C	1247	ASN
1	C	1285	GLN
1	C	1308	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

### 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

### 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

There are no ligands in this entry.



## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

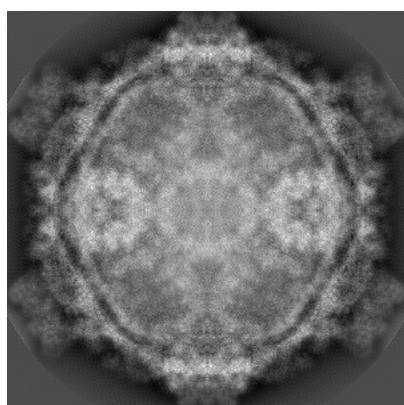
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9565. These allow visual inspection of the internal detail of the map and identification of artifacts.

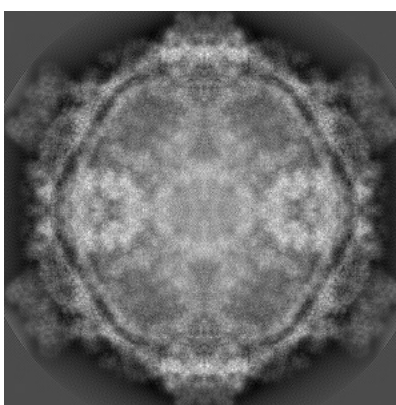
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

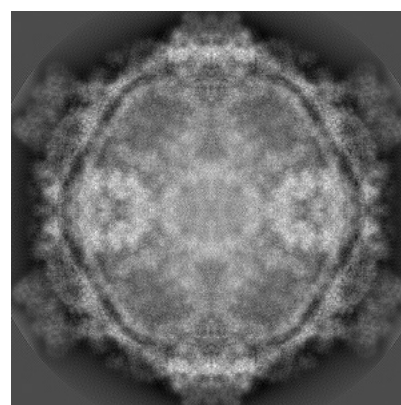
#### 6.1.1 Primary map



X



Y

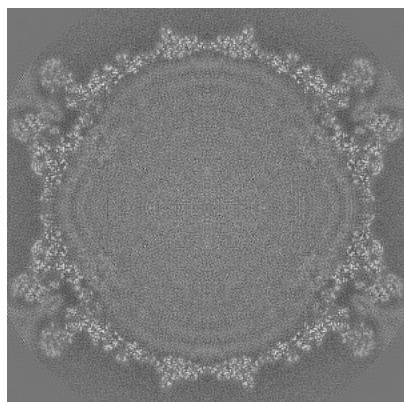


Z

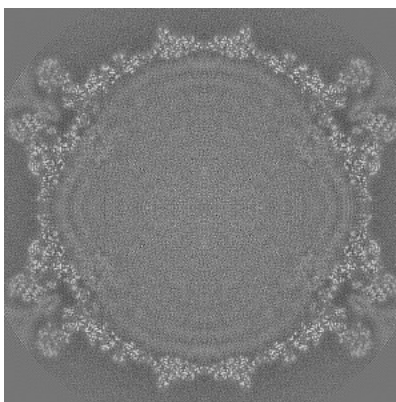
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

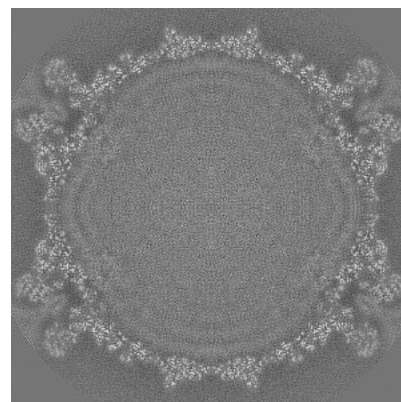
#### 6.2.1 Primary map



X Index: 350



Y Index: 350

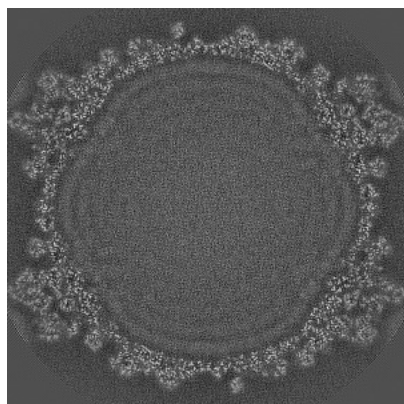


Z Index: 350

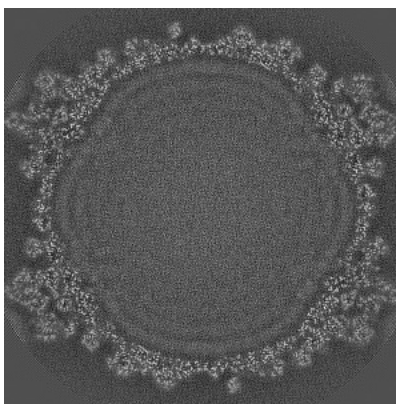
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

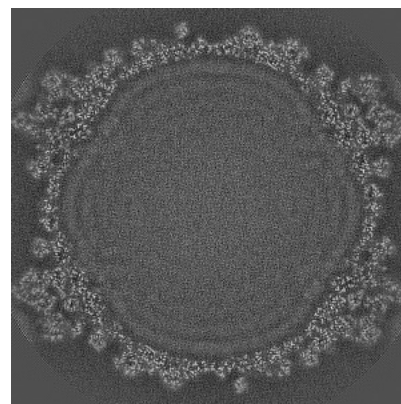
### 6.3.1 Primary map



X Index: 320



Y Index: 320

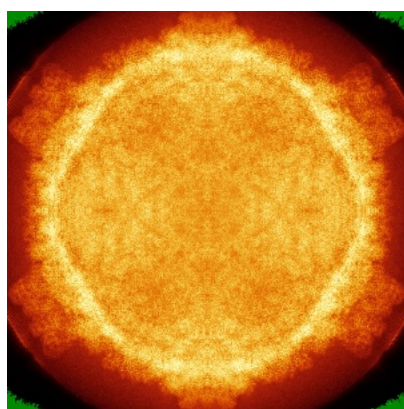


Z Index: 320

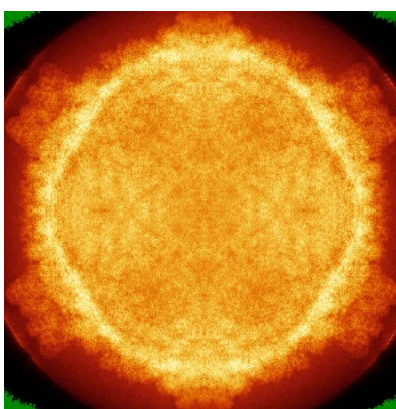
The images above show the largest variance slices of the map in three orthogonal directions.

## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

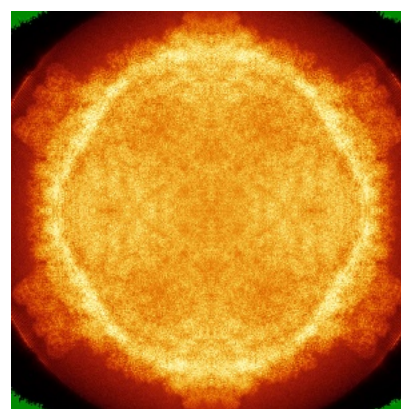
### 6.4.1 Primary map



X



Y

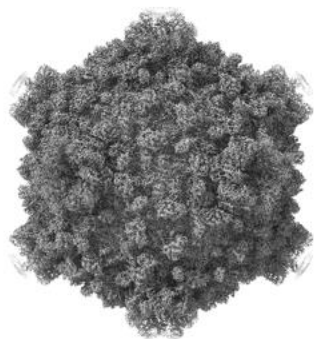


Z

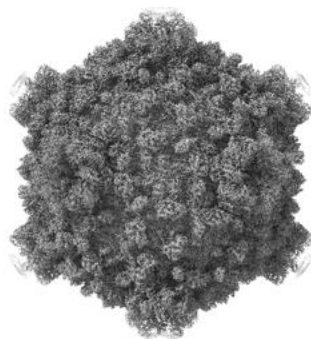
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

## 6.5 Orthogonal surface views [i](#)

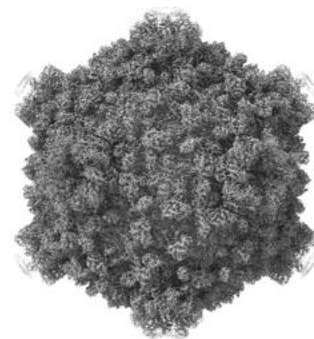
### 6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 17.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

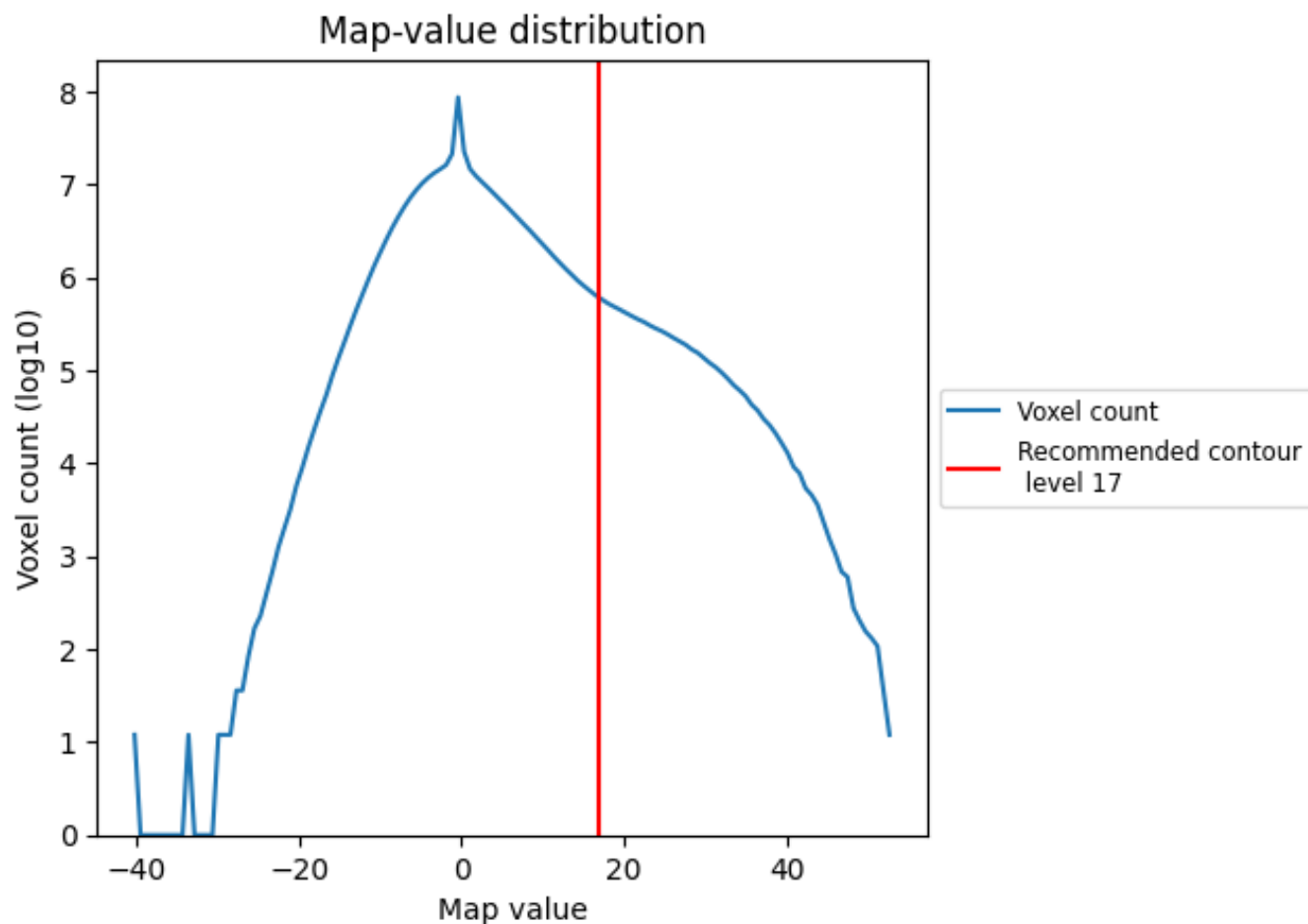
## 6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

## 7 Map analysis [i](#)

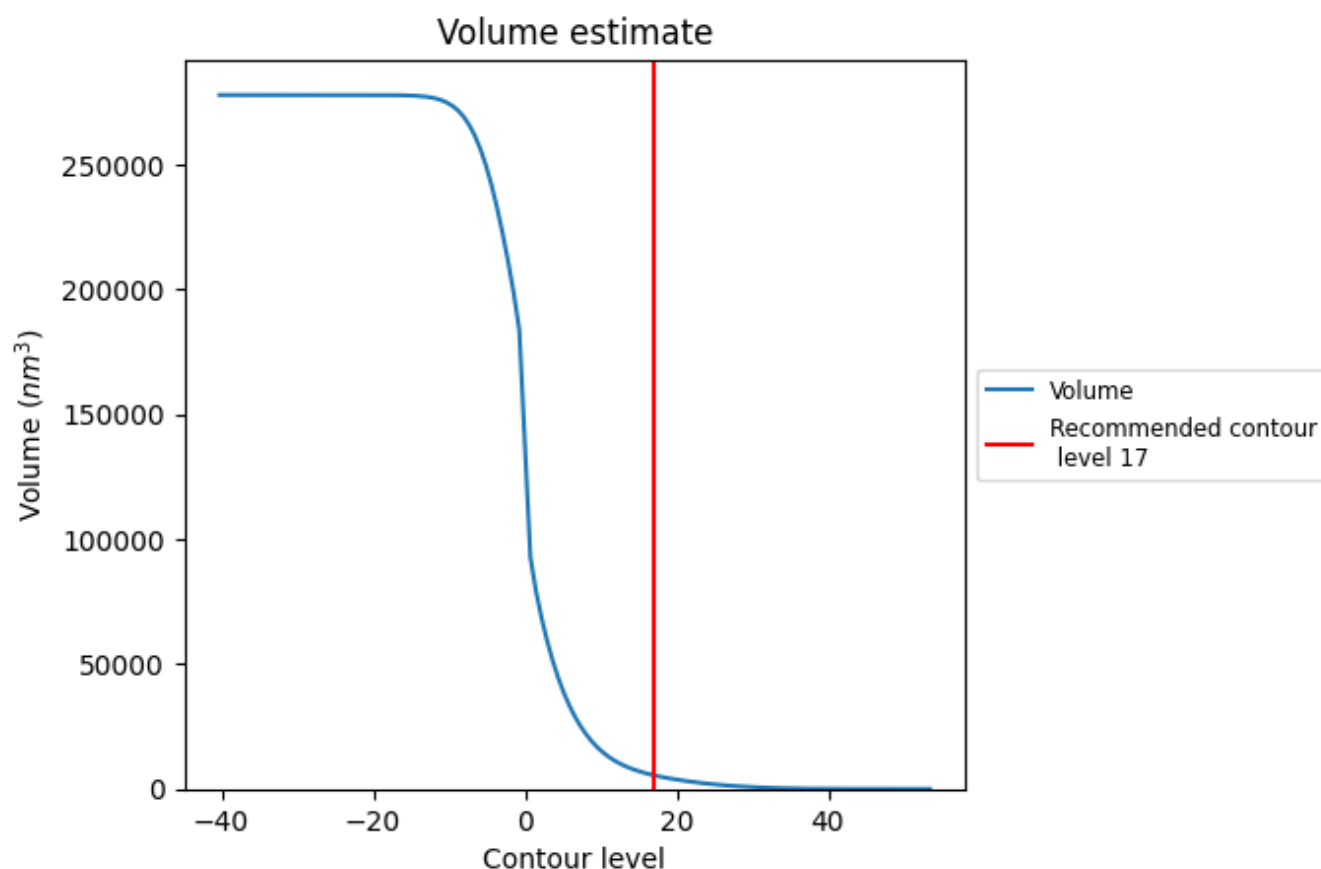
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

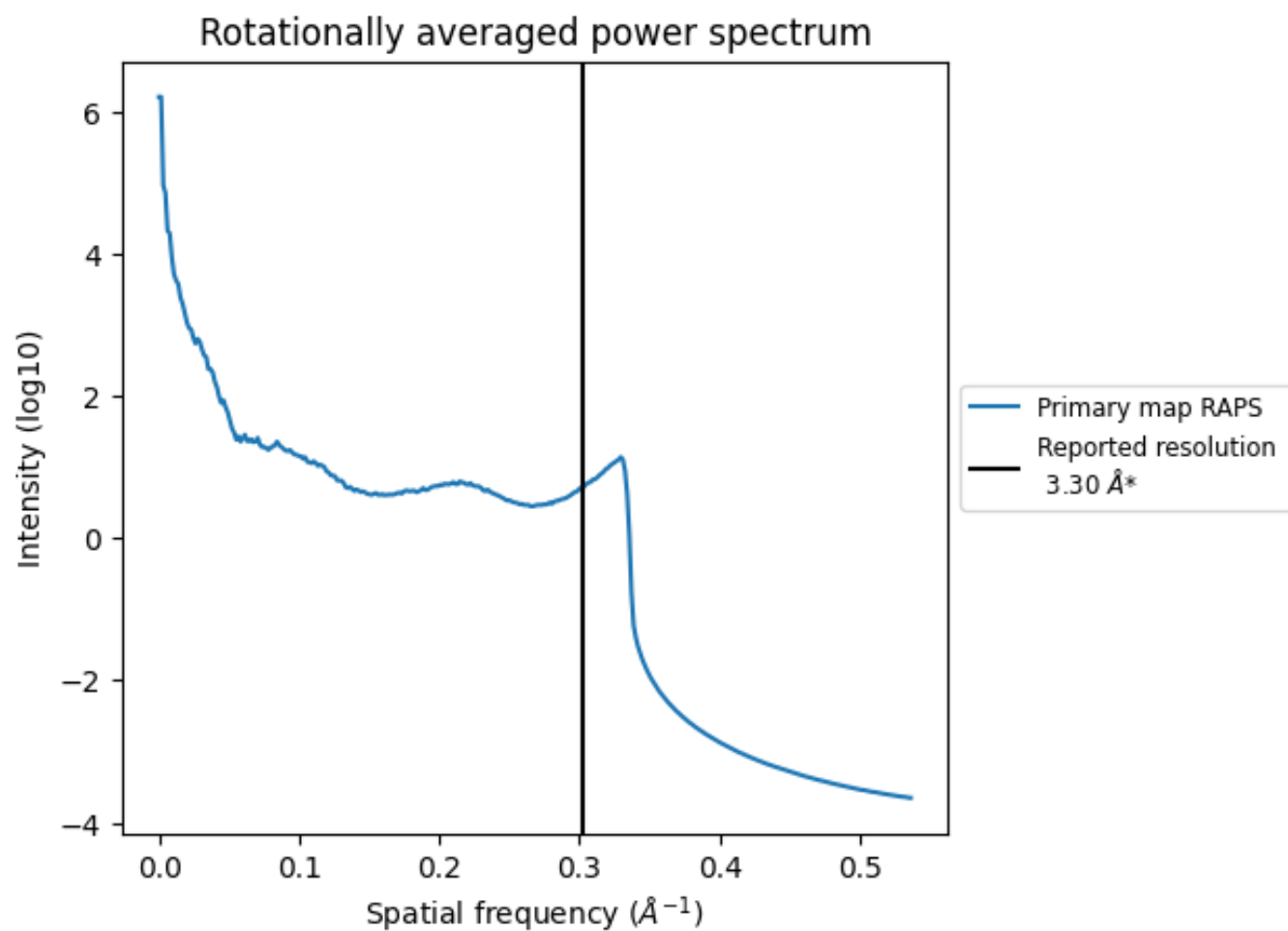
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 5491 nm<sup>3</sup>; this corresponds to an approximate mass of 4961 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

### 7.3 Rotationally averaged power spectrum ⓘ



\*Reported resolution corresponds to spatial frequency of 0.303 Å<sup>-1</sup>

## 8 Fourier-Shell correlation ⓘ

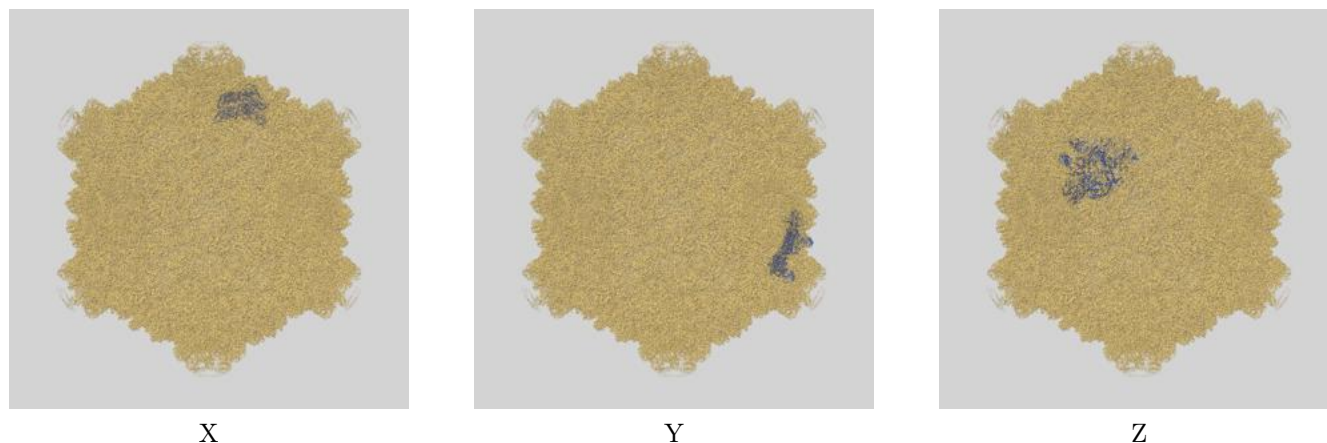
This section was not generated. No FSC curve or half-maps provided.



## 9 Map-model fit [i](#)

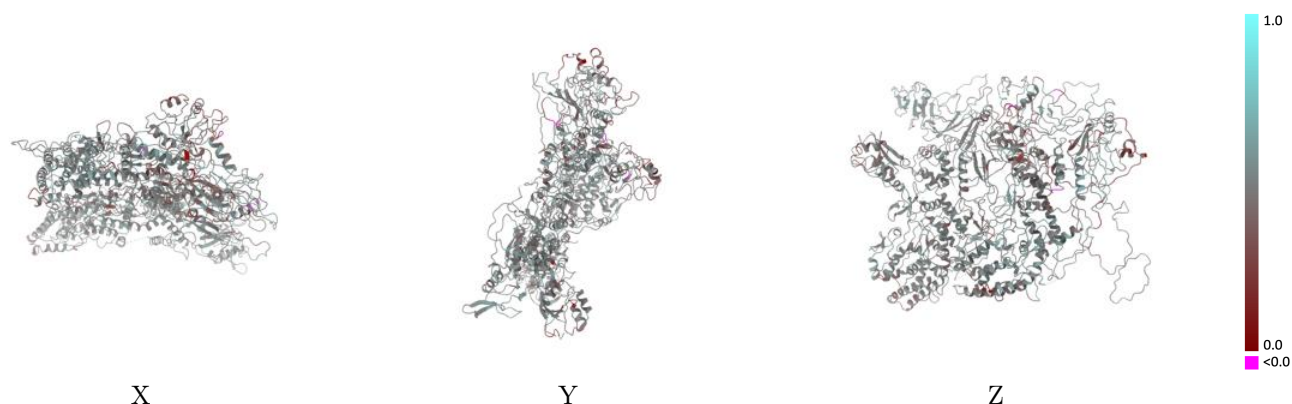
This section contains information regarding the fit between EMDB map EMD-9565 and PDB model 5H0S. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

### 9.1 Map-model overlay [i](#)



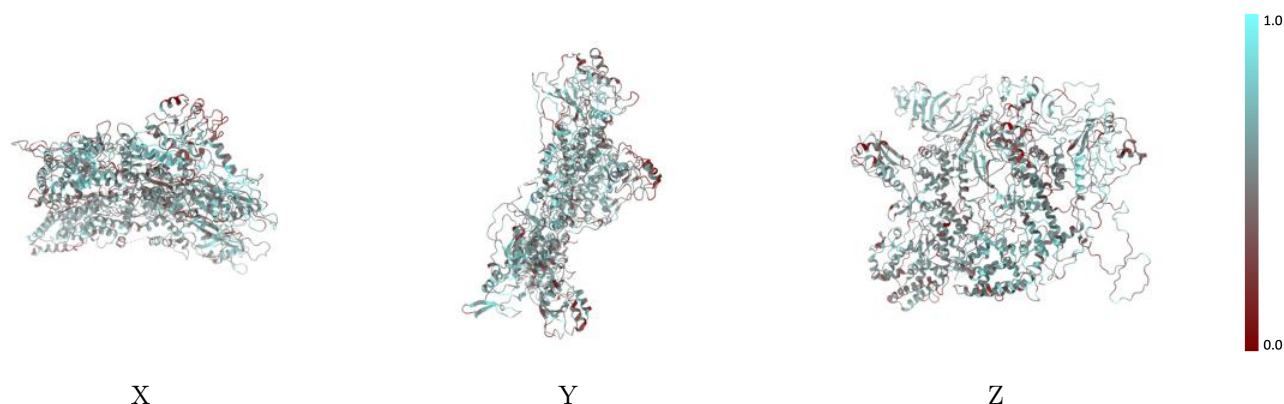
The images above show the 3D surface view of the map at the recommended contour level 17.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

## 9.2 Q-score mapped to coordinate model [i](#)



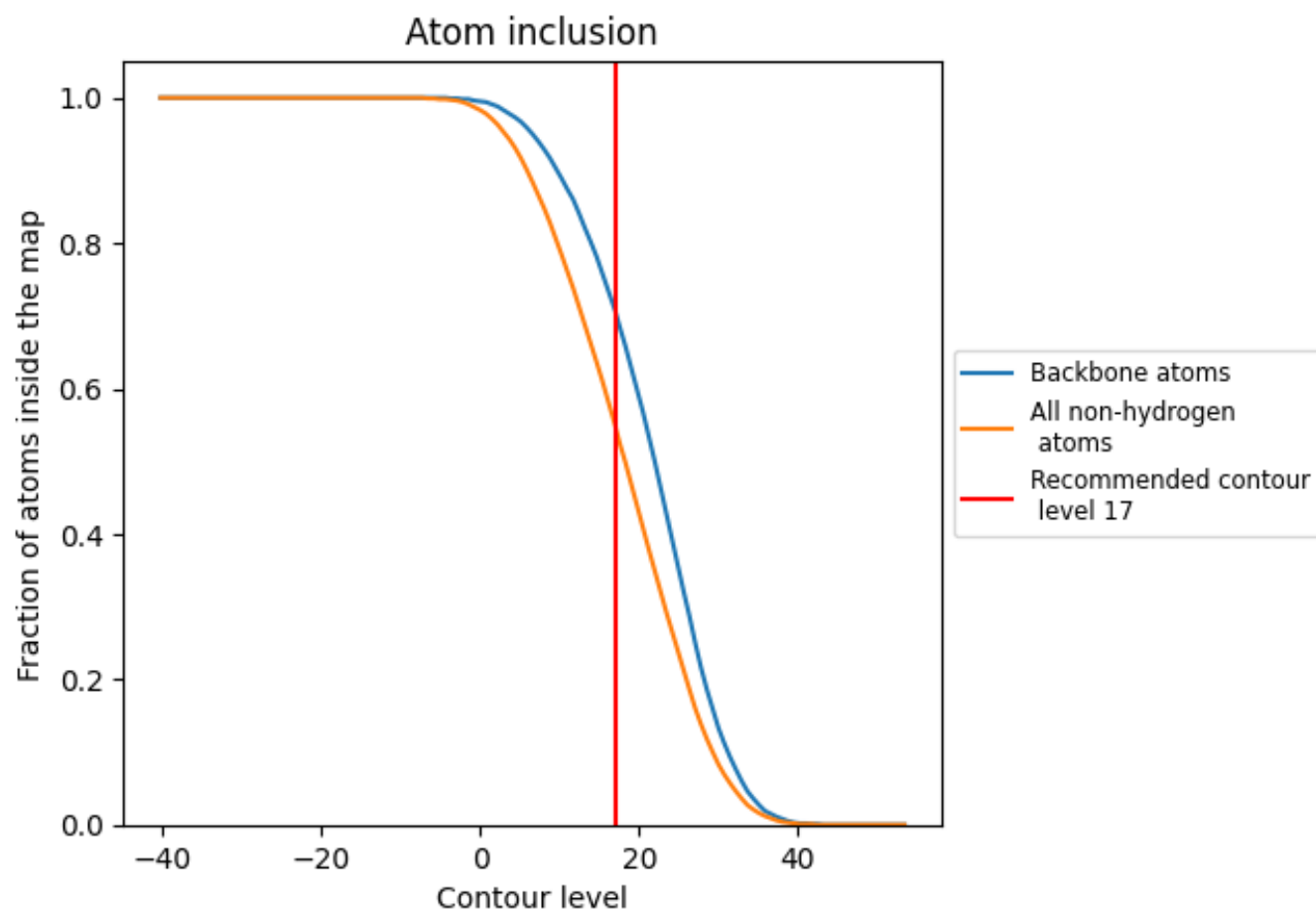
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

## 9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (17).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 71% of all backbone atoms, 55% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (17) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.5490	<div></div> 0.4770
B	<div></div> 0.5460	<div></div> 0.4780
C	<div></div> 0.5520	<div></div> 0.4760

