



Full wwPDB EM Validation Report ⓘ

Sep 21, 2023 – 04:42 pm BST

PDB ID : 8P99
EMDB ID : EMD-17576
Title : SARS-CoV-2 S-protein:D614G mutant in 1-up conformation
Authors : Adhav, A.; Forcada-Nadal, A.; Marco-Marin, C.; Lopez-Redondo, M.L.;
Llacer, J.L.
Deposited on : 2023-06-05
Resolution : 3.40 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

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.dev50
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.35.1

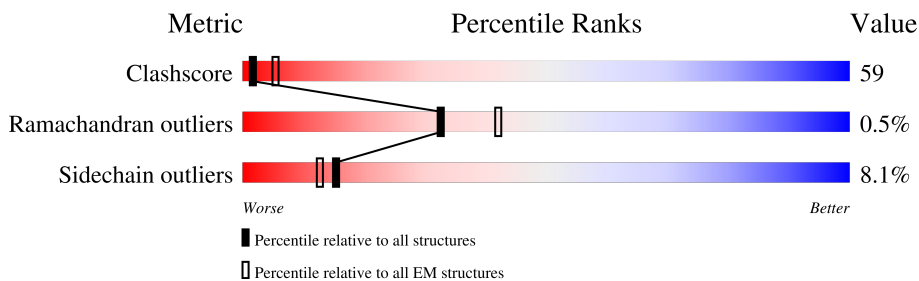
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 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	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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 ≥ 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	A	1270	
1	B	1270	
1	C	1270	
2	E	2	
2	F	2	
2	G	2	
2	I	2	
2	J	2	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	K	2	
2	L	2	
2	N	2	
2	O	2	
2	P	2	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	NAG	J	1	X	-	-	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 25713 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 Spike protein S1,Spike glycoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	1070	8354	5332	1392	1592	38	0	0
1	B	1073	8369	5342	1393	1596	38	0	0
1	C	1076	8374	5346	1395	1595	38	0	0

There are 234 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	MET	-	initiating methionine	UNP P0DTC2
A	-4	VAL	-	expression tag	UNP P0DTC2
A	-3	SER	-	expression tag	UNP P0DTC2
A	-2	ALA	-	expression tag	UNP P0DTC2
A	-1	ILE	-	expression tag	UNP P0DTC2
A	0	VAL	-	expression tag	UNP P0DTC2
A	1	LEU	-	expression tag	UNP P0DTC2
A	2	TYR	-	expression tag	UNP P0DTC2
A	3	VAL	-	expression tag	UNP P0DTC2
A	4	LEU	-	expression tag	UNP P0DTC2
A	5	LEU	-	expression tag	UNP P0DTC2
A	6	ALA	-	expression tag	UNP P0DTC2
A	7	ALA	-	expression tag	UNP P0DTC2
A	8	ALA	-	expression tag	UNP P0DTC2
A	9	ALA	-	expression tag	UNP P0DTC2
A	10	HIS	-	expression tag	UNP P0DTC2
A	11	SER	-	expression tag	UNP P0DTC2
A	12	ALA	-	expression tag	UNP P0DTC2
A	13	PHE	-	expression tag	UNP P0DTC2
A	14	ALA	-	expression tag	UNP P0DTC2
A	614	GLY	ASP	engineered mutation	UNP P0DTC2
A	685	ALA	ARG	engineered mutation	UNP P0DTC2
A	986	PRO	LYS	engineered mutation	UNP P0DTC2
A	987	PRO	VAL	engineered mutation	UNP P0DTC2

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	1214	LEU	-	expression tag	UNP P0DTC2
A	1215	VAL	-	expression tag	UNP P0DTC2
A	1216	PRO	-	expression tag	UNP P0DTC2
A	1217	ARG	-	expression tag	UNP P0DTC2
A	1218	GLY	-	expression tag	UNP P0DTC2
A	1219	SER	-	expression tag	UNP P0DTC2
A	1220	GLY	-	expression tag	UNP P0DTC2
A	1221	TYR	-	expression tag	UNP P0DTC2
A	1222	ILE	-	expression tag	UNP P0DTC2
A	1223	PRO	-	expression tag	UNP P0DTC2
A	1224	GLU	-	expression tag	UNP P0DTC2
A	1225	ALA	-	expression tag	UNP P0DTC2
A	1226	PRO	-	expression tag	UNP P0DTC2
A	1227	ARG	-	expression tag	UNP P0DTC2
A	1228	ASP	-	expression tag	UNP P0DTC2
A	1229	GLY	-	expression tag	UNP P0DTC2
A	1230	GLN	-	expression tag	UNP P0DTC2
A	1231	ALA	-	expression tag	UNP P0DTC2
A	1232	TYR	-	expression tag	UNP P0DTC2
A	1233	VAL	-	expression tag	UNP P0DTC2
A	1234	ARG	-	expression tag	UNP P0DTC2
A	1235	LYS	-	expression tag	UNP P0DTC2
A	1236	ASP	-	expression tag	UNP P0DTC2
A	1237	GLY	-	expression tag	UNP P0DTC2
A	1238	GLU	-	expression tag	UNP P0DTC2
A	1239	TRP	-	expression tag	UNP P0DTC2
A	1240	VAL	-	expression tag	UNP P0DTC2
A	1241	PHE	-	expression tag	UNP P0DTC2
A	1242	LEU	-	expression tag	UNP P0DTC2
A	1243	SER	-	expression tag	UNP P0DTC2
A	1244	THR	-	expression tag	UNP P0DTC2
A	1245	PHE	-	expression tag	UNP P0DTC2
A	1246	LEU	-	expression tag	UNP P0DTC2
A	1247	SER	-	expression tag	UNP P0DTC2
A	1248	PRO	-	expression tag	UNP P0DTC2
A	1249	HIS	-	expression tag	UNP P0DTC2
A	1250	HIS	-	expression tag	UNP P0DTC2
A	1251	HIS	-	expression tag	UNP P0DTC2
A	1252	HIS	-	expression tag	UNP P0DTC2
A	1253	HIS	-	expression tag	UNP P0DTC2
A	1254	HIS	-	expression tag	UNP P0DTC2
A	1255	HIS	-	expression tag	UNP P0DTC2

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	1256	HIS	-	expression tag	UNP P0DTC2
A	1257	HIS	-	expression tag	UNP P0DTC2
A	1258	GLU	-	expression tag	UNP P0DTC2
A	1259	GLN	-	expression tag	UNP P0DTC2
A	1260	LYS	-	expression tag	UNP P0DTC2
A	1261	LEU	-	expression tag	UNP P0DTC2
A	1262	ILE	-	expression tag	UNP P0DTC2
A	1263	SER	-	expression tag	UNP P0DTC2
A	1264	GLU	-	expression tag	UNP P0DTC2
A	1265	GLU	-	expression tag	UNP P0DTC2
A	1266	ASP	-	expression tag	UNP P0DTC2
A	1267	LEU	-	expression tag	UNP P0DTC2
B	-5	MET	-	initiating methionine	UNP P0DTC2
B	-4	VAL	-	expression tag	UNP P0DTC2
B	-3	SER	-	expression tag	UNP P0DTC2
B	-2	ALA	-	expression tag	UNP P0DTC2
B	-1	ILE	-	expression tag	UNP P0DTC2
B	0	VAL	-	expression tag	UNP P0DTC2
B	1	LEU	-	expression tag	UNP P0DTC2
B	2	TYR	-	expression tag	UNP P0DTC2
B	3	VAL	-	expression tag	UNP P0DTC2
B	4	LEU	-	expression tag	UNP P0DTC2
B	5	LEU	-	expression tag	UNP P0DTC2
B	6	ALA	-	expression tag	UNP P0DTC2
B	7	ALA	-	expression tag	UNP P0DTC2
B	8	ALA	-	expression tag	UNP P0DTC2
B	9	ALA	-	expression tag	UNP P0DTC2
B	10	HIS	-	expression tag	UNP P0DTC2
B	11	SER	-	expression tag	UNP P0DTC2
B	12	ALA	-	expression tag	UNP P0DTC2
B	13	PHE	-	expression tag	UNP P0DTC2
B	14	ALA	-	expression tag	UNP P0DTC2
B	614	GLY	ASP	engineered mutation	UNP P0DTC2
B	685	ALA	ARG	engineered mutation	UNP P0DTC2
B	986	PRO	LYS	engineered mutation	UNP P0DTC2
B	987	PRO	VAL	engineered mutation	UNP P0DTC2
B	1214	LEU	-	expression tag	UNP P0DTC2
B	1215	VAL	-	expression tag	UNP P0DTC2
B	1216	PRO	-	expression tag	UNP P0DTC2
B	1217	ARG	-	expression tag	UNP P0DTC2
B	1218	GLY	-	expression tag	UNP P0DTC2
B	1219	SER	-	expression tag	UNP P0DTC2

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	1220	GLY	-	expression tag	UNP P0DTC2
B	1221	TYR	-	expression tag	UNP P0DTC2
B	1222	ILE	-	expression tag	UNP P0DTC2
B	1223	PRO	-	expression tag	UNP P0DTC2
B	1224	GLU	-	expression tag	UNP P0DTC2
B	1225	ALA	-	expression tag	UNP P0DTC2
B	1226	PRO	-	expression tag	UNP P0DTC2
B	1227	ARG	-	expression tag	UNP P0DTC2
B	1228	ASP	-	expression tag	UNP P0DTC2
B	1229	GLY	-	expression tag	UNP P0DTC2
B	1230	GLN	-	expression tag	UNP P0DTC2
B	1231	ALA	-	expression tag	UNP P0DTC2
B	1232	TYR	-	expression tag	UNP P0DTC2
B	1233	VAL	-	expression tag	UNP P0DTC2
B	1234	ARG	-	expression tag	UNP P0DTC2
B	1235	LYS	-	expression tag	UNP P0DTC2
B	1236	ASP	-	expression tag	UNP P0DTC2
B	1237	GLY	-	expression tag	UNP P0DTC2
B	1238	GLU	-	expression tag	UNP P0DTC2
B	1239	TRP	-	expression tag	UNP P0DTC2
B	1240	VAL	-	expression tag	UNP P0DTC2
B	1241	PHE	-	expression tag	UNP P0DTC2
B	1242	LEU	-	expression tag	UNP P0DTC2
B	1243	SER	-	expression tag	UNP P0DTC2
B	1244	THR	-	expression tag	UNP P0DTC2
B	1245	PHE	-	expression tag	UNP P0DTC2
B	1246	LEU	-	expression tag	UNP P0DTC2
B	1247	SER	-	expression tag	UNP P0DTC2
B	1248	PRO	-	expression tag	UNP P0DTC2
B	1249	HIS	-	expression tag	UNP P0DTC2
B	1250	HIS	-	expression tag	UNP P0DTC2
B	1251	HIS	-	expression tag	UNP P0DTC2
B	1252	HIS	-	expression tag	UNP P0DTC2
B	1253	HIS	-	expression tag	UNP P0DTC2
B	1254	HIS	-	expression tag	UNP P0DTC2
B	1255	HIS	-	expression tag	UNP P0DTC2
B	1256	HIS	-	expression tag	UNP P0DTC2
B	1257	HIS	-	expression tag	UNP P0DTC2
B	1258	GLU	-	expression tag	UNP P0DTC2
B	1259	GLN	-	expression tag	UNP P0DTC2
B	1260	LYS	-	expression tag	UNP P0DTC2
B	1261	LEU	-	expression tag	UNP P0DTC2

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	1262	ILE	-	expression tag	UNP P0DTC2
B	1263	SER	-	expression tag	UNP P0DTC2
B	1264	GLU	-	expression tag	UNP P0DTC2
B	1265	GLU	-	expression tag	UNP P0DTC2
B	1266	ASP	-	expression tag	UNP P0DTC2
B	1267	LEU	-	expression tag	UNP P0DTC2
C	-5	MET	-	initiating methionine	UNP P0DTC2
C	-4	VAL	-	expression tag	UNP P0DTC2
C	-3	SER	-	expression tag	UNP P0DTC2
C	-2	ALA	-	expression tag	UNP P0DTC2
C	-1	ILE	-	expression tag	UNP P0DTC2
C	0	VAL	-	expression tag	UNP P0DTC2
C	1	LEU	-	expression tag	UNP P0DTC2
C	2	TYR	-	expression tag	UNP P0DTC2
C	3	VAL	-	expression tag	UNP P0DTC2
C	4	LEU	-	expression tag	UNP P0DTC2
C	5	LEU	-	expression tag	UNP P0DTC2
C	6	ALA	-	expression tag	UNP P0DTC2
C	7	ALA	-	expression tag	UNP P0DTC2
C	8	ALA	-	expression tag	UNP P0DTC2
C	9	ALA	-	expression tag	UNP P0DTC2
C	10	HIS	-	expression tag	UNP P0DTC2
C	11	SER	-	expression tag	UNP P0DTC2
C	12	ALA	-	expression tag	UNP P0DTC2
C	13	PHE	-	expression tag	UNP P0DTC2
C	14	ALA	-	expression tag	UNP P0DTC2
C	614	GLY	ASP	engineered mutation	UNP P0DTC2
C	685	ALA	ARG	engineered mutation	UNP P0DTC2
C	986	PRO	LYS	engineered mutation	UNP P0DTC2
C	987	PRO	VAL	engineered mutation	UNP P0DTC2
C	1214	LEU	-	expression tag	UNP P0DTC2
C	1215	VAL	-	expression tag	UNP P0DTC2
C	1216	PRO	-	expression tag	UNP P0DTC2
C	1217	ARG	-	expression tag	UNP P0DTC2
C	1218	GLY	-	expression tag	UNP P0DTC2
C	1219	SER	-	expression tag	UNP P0DTC2
C	1220	GLY	-	expression tag	UNP P0DTC2
C	1221	TYR	-	expression tag	UNP P0DTC2
C	1222	ILE	-	expression tag	UNP P0DTC2
C	1223	PRO	-	expression tag	UNP P0DTC2
C	1224	GLU	-	expression tag	UNP P0DTC2
C	1225	ALA	-	expression tag	UNP P0DTC2

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	1226	PRO	-	expression tag	UNP P0DTC2
C	1227	ARG	-	expression tag	UNP P0DTC2
C	1228	ASP	-	expression tag	UNP P0DTC2
C	1229	GLY	-	expression tag	UNP P0DTC2
C	1230	GLN	-	expression tag	UNP P0DTC2
C	1231	ALA	-	expression tag	UNP P0DTC2
C	1232	TYR	-	expression tag	UNP P0DTC2
C	1233	VAL	-	expression tag	UNP P0DTC2
C	1234	ARG	-	expression tag	UNP P0DTC2
C	1235	LYS	-	expression tag	UNP P0DTC2
C	1236	ASP	-	expression tag	UNP P0DTC2
C	1237	GLY	-	expression tag	UNP P0DTC2
C	1238	GLU	-	expression tag	UNP P0DTC2
C	1239	TRP	-	expression tag	UNP P0DTC2
C	1240	VAL	-	expression tag	UNP P0DTC2
C	1241	PHE	-	expression tag	UNP P0DTC2
C	1242	LEU	-	expression tag	UNP P0DTC2
C	1243	SER	-	expression tag	UNP P0DTC2
C	1244	THR	-	expression tag	UNP P0DTC2
C	1245	PHE	-	expression tag	UNP P0DTC2
C	1246	LEU	-	expression tag	UNP P0DTC2
C	1247	SER	-	expression tag	UNP P0DTC2
C	1248	PRO	-	expression tag	UNP P0DTC2
C	1249	HIS	-	expression tag	UNP P0DTC2
C	1250	HIS	-	expression tag	UNP P0DTC2
C	1251	HIS	-	expression tag	UNP P0DTC2
C	1252	HIS	-	expression tag	UNP P0DTC2
C	1253	HIS	-	expression tag	UNP P0DTC2
C	1254	HIS	-	expression tag	UNP P0DTC2
C	1255	HIS	-	expression tag	UNP P0DTC2
C	1256	HIS	-	expression tag	UNP P0DTC2
C	1257	HIS	-	expression tag	UNP P0DTC2
C	1258	GLU	-	expression tag	UNP P0DTC2
C	1259	GLN	-	expression tag	UNP P0DTC2
C	1260	LYS	-	expression tag	UNP P0DTC2
C	1261	LEU	-	expression tag	UNP P0DTC2
C	1262	ILE	-	expression tag	UNP P0DTC2
C	1263	SER	-	expression tag	UNP P0DTC2
C	1264	GLU	-	expression tag	UNP P0DTC2
C	1265	GLU	-	expression tag	UNP P0DTC2
C	1266	ASP	-	expression tag	UNP P0DTC2
C	1267	LEU	-	expression tag	UNP P0DTC2

- Molecule 2 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
2	E	2	28	16	2	10	0	0
2	F	2	28	16	2	10	0	0
2	G	2	28	16	2	10	0	0
2	I	2	28	16	2	10	0	0
2	J	2	28	16	2	10	0	0
2	K	2	28	16	2	10	0	0
2	L	2	28	16	2	10	0	0
2	N	2	28	16	2	10	0	0
2	O	2	28	16	2	10	0	0
2	P	2	28	16	2	10	0	0

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C₈H₁₅NO₆).

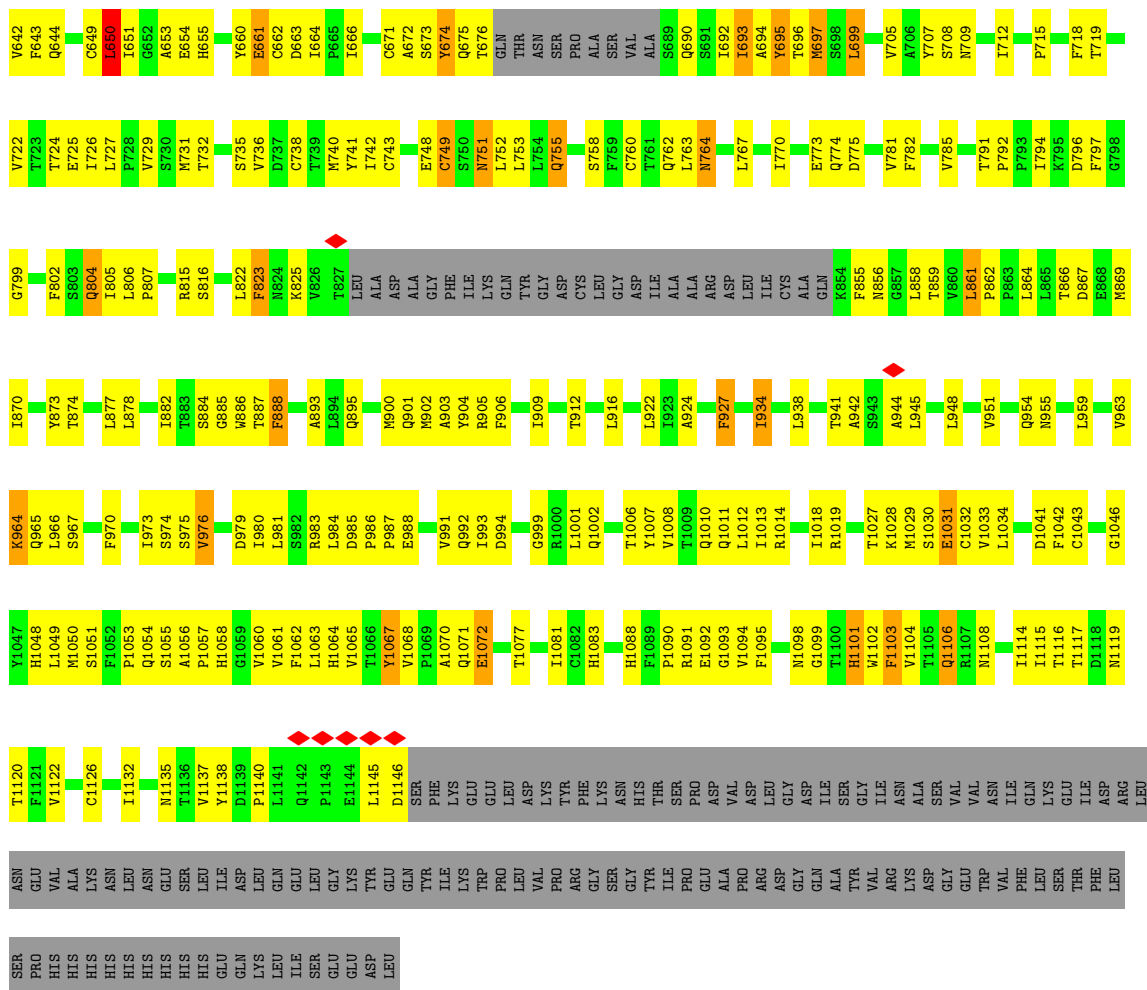


Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
3	A	1	Total	C	N	O	0
			14	8	1	5	
3	A	1	Total	C	N	O	0
			14	8	1	5	
3	A	1	Total	C	N	O	0
			14	8	1	5	
3	A	1	Total	C	N	O	0
			14	8	1	5	
3	A	1	Total	C	N	O	0
			14	8	1	5	
3	A	1	Total	C	N	O	0
			14	8	1	5	
3	A	1	Total	C	N	O	0
			14	8	1	5	
3	B	1	Total	C	N	O	0
			14	8	1	5	
3	B	1	Total	C	N	O	0
			14	8	1	5	
3	B	1	Total	C	N	O	0
			14	8	1	5	
3	B	1	Total	C	N	O	0
			14	8	1	5	
3	B	1	Total	C	N	O	0
			14	8	1	5	
3	B	1	Total	C	N	O	0
			14	8	1	5	

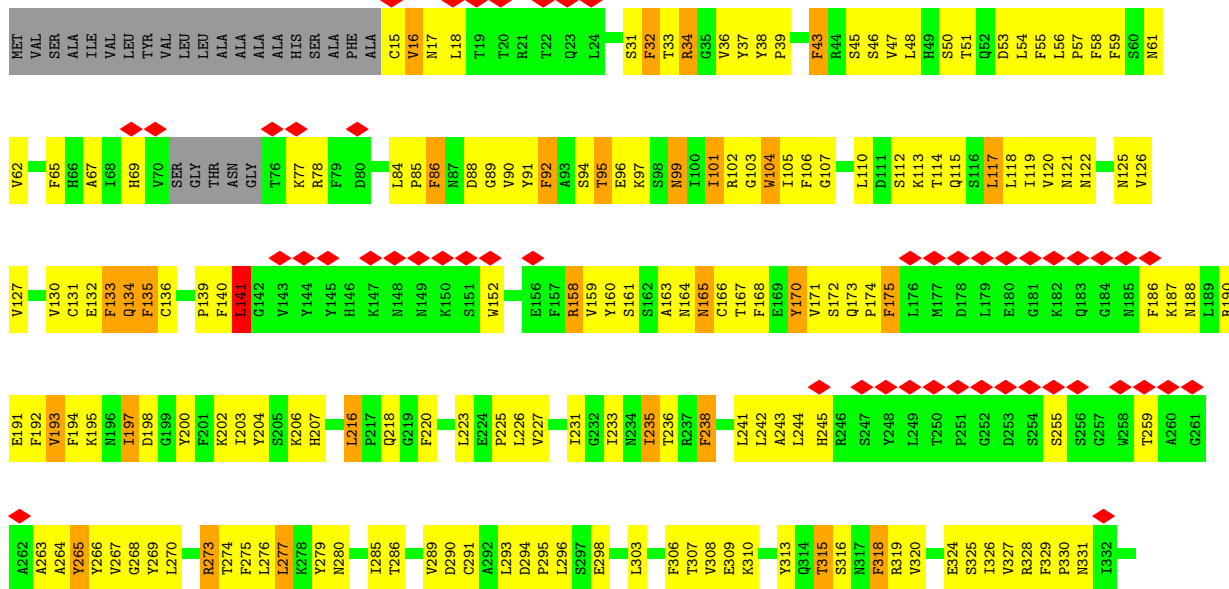
Continued on next page...

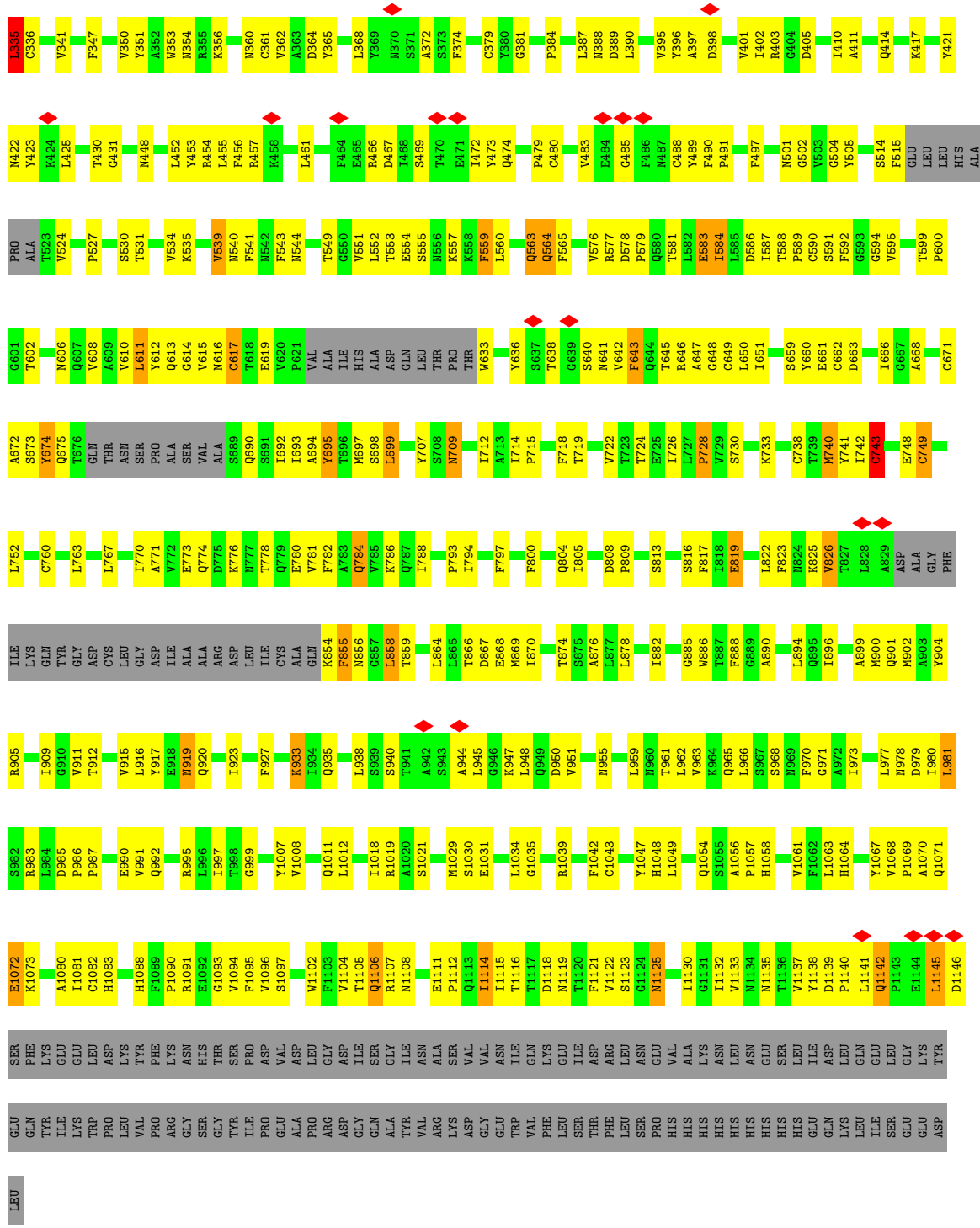
Continued from previous page...

Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
3	B	1	Total 14	8	1	5	0
3	B	1	Total 14	8	1	5	0
3	B	1	Total 14	8	1	5	0
3	C	1	Total 14	8	1	5	0
3	C	1	Total 14	8	1	5	0
3	C	1	Total 14	8	1	5	0
3	C	1	Total 14	8	1	5	0
3	C	1	Total 14	8	1	5	0
3	C	1	Total 14	8	1	5	0
3	C	1	Total 14	8	1	5	0

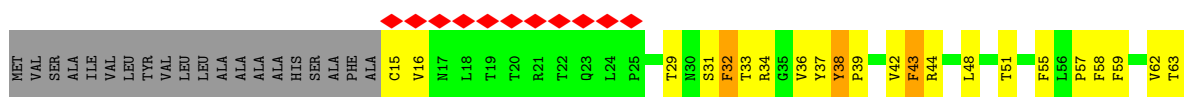
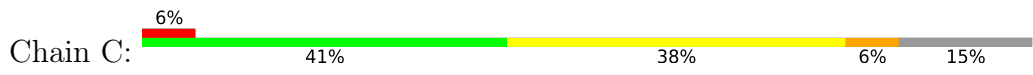


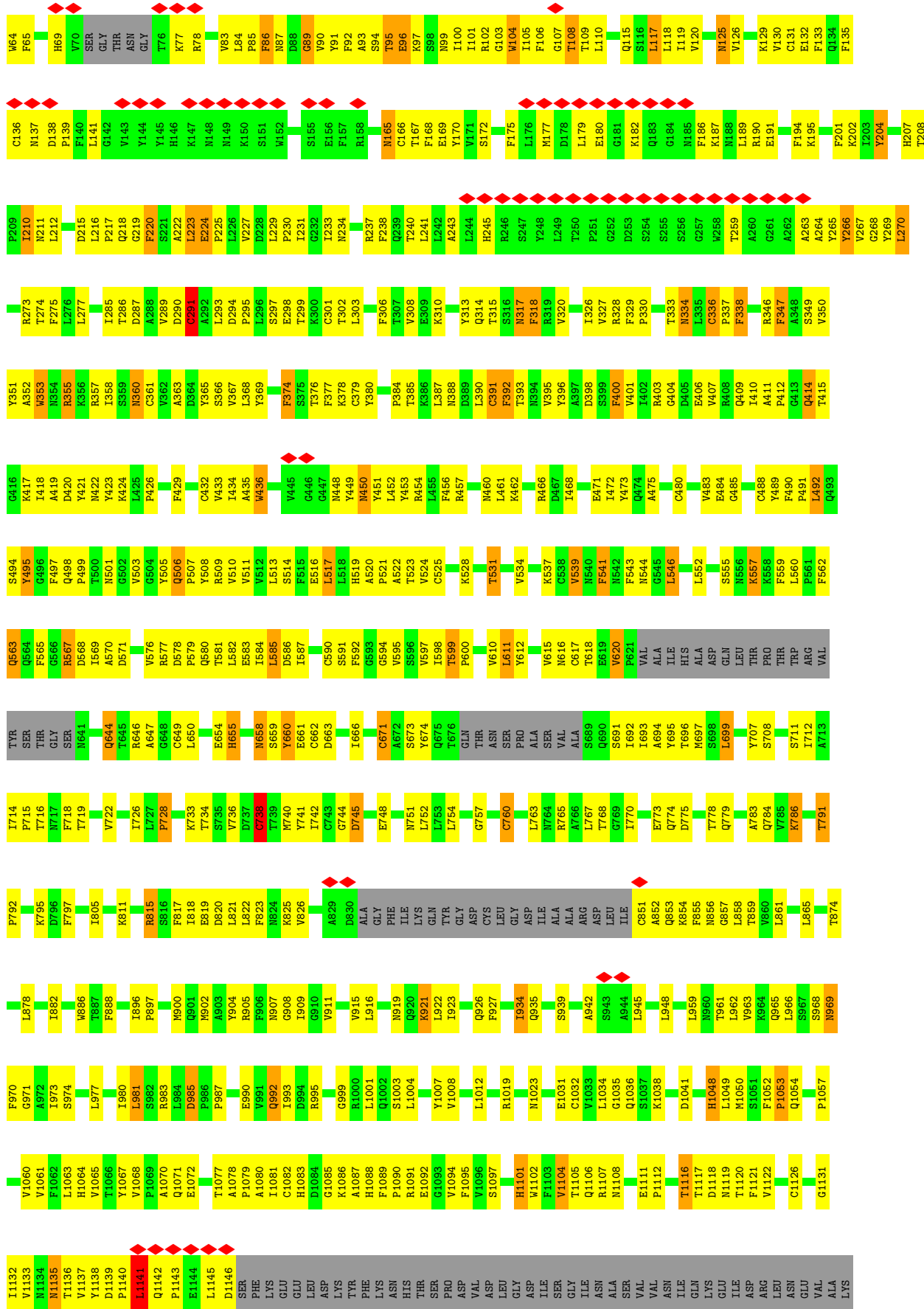
• Molecule 1: Spike protein S1,Spike glycoprotein





● Molecule 1: Spike protein S1, Spike glycoprotein






ASN LEU ASN ASN GLU SER SER LEU ILE ASP LEU GLN GLU LEU GLY LYS TYR GLN TYR ILE LYS TRP PRO VAL PRO ARG GLY SER GLY TYR ILE PRO GLU ALA PRO ARG ASP GLY ALA TYR VAL ARG LYS ASP GLY TRP VAL PHE LEU SER THR PHE LEU SER PRO HIS HIS

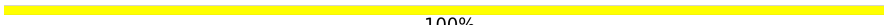
HIS HIS HIS HIS HIS HIS GLU GLN LYS LEU ILE SER GLU ASP LEU

- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain E:  50% 50%


MAG1
MAG2

- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain F:  100%

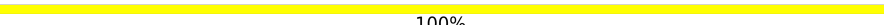
MAG1
MAG2

- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain G:  50% 50%


MAG1
MAG2

- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain I:  100%

MAG1
MAG2

- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain J:  50% 50%

MAG1
MAG2

- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain K:  50% 100%



- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain L:  50% 50%




- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain N:  100%



- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain O:  50% 50%



- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain P:  100%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	278833	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	1.916	Depositor
Minimum map value	-0.002	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.021	Depositor
Recommended contour level	0.01	Depositor
Map size (\AA)	420.66, 420.66, 420.66	wwPDB
Map dimensions	492, 492, 492	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.855, 0.855, 0.855	Depositor

5 Model quality i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: NAG

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	A	0.67	6/8550 (0.1%)	0.71	8/11641 (0.1%)
1	B	0.64	5/8565 (0.1%)	0.76	11/11661 (0.1%)
1	C	0.58	5/8570 (0.1%)	0.67	8/11670 (0.1%)
All	All	0.63	16/25685 (0.1%)	0.71	27/34972 (0.1%)

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	1

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1146	ASP	C-O	33.46	1.86	1.23
1	B	1146	ASP	C-O	-22.08	0.81	1.23
1	C	1146	ASP	C-O	19.99	1.61	1.23
1	A	749	CYS	CB-SG	-9.58	1.66	1.82
1	B	643	PHE	CE2-CZ	8.20	1.52	1.37
1	B	743	CYS	CB-SG	-7.73	1.69	1.82
1	A	37	TYR	CE1-CZ	-7.25	1.29	1.38
1	C	495	TYR	CE1-CZ	-6.93	1.29	1.38
1	C	347	PHE	CG-CD1	-6.74	1.28	1.38
1	C	815	ARG	CZ-NH1	-6.32	1.24	1.33
1	C	336	CYS	CB-SG	-5.92	1.72	1.81
1	B	749	CYS	CB-SG	-5.89	1.72	1.81
1	A	1122	VAL	CB-CG1	-5.74	1.40	1.52
1	A	1032	CYS	CB-SG	-5.48	1.72	1.81
1	A	1031	GLU	CD-OE1	-5.25	1.19	1.25

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	315	THR	CB-CG2	-5.03	1.35	1.52

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1146	ASP	CA-C-O	-15.93	86.64	120.10
1	A	336	CYS	C-N-CD	-11.26	95.82	120.60
1	B	1146	ASP	CA-C-O	10.67	142.51	120.10
1	A	1032	CYS	CA-CB-SG	-10.08	95.86	114.00
1	B	617	CYS	O-C-N	9.10	137.26	122.70
1	B	141	LEU	CB-CG-CD1	-8.80	96.05	111.00
1	B	141	LEU	CD1-CG-CD2	7.76	133.79	110.50
1	A	336	CYS	C-N-CA	7.63	154.03	122.00
1	C	1146	ASP	CA-C-O	-7.27	104.83	120.10
1	B	335	LEU	CA-CB-CG	6.97	131.33	115.30
1	B	617	CYS	CA-C-O	-6.96	105.49	120.10
1	A	650	LEU	CA-CB-CG	6.86	131.07	115.30
1	C	1032	CYS	CA-CB-SG	-6.69	101.96	114.00
1	B	16	VAL	CG1-CB-CG2	6.60	121.47	110.90
1	B	273	ARG	NE-CZ-NH1	-6.38	117.11	120.30
1	C	1141	LEU	CA-CB-CG	6.25	129.66	115.30
1	C	1141	LEU	CB-CG-CD2	6.20	121.54	111.00
1	B	158	ARG	NE-CZ-NH1	6.03	123.31	120.30
1	C	760	CYS	CA-CB-SG	5.91	124.64	114.00
1	A	462	LYS	C-N-CD	5.71	140.39	128.40
1	A	749	CYS	CB-CA-C	5.68	121.76	110.40
1	C	336	CYS	CA-CB-SG	5.49	123.88	114.00
1	A	341	VAL	CB-CA-C	-5.39	101.15	111.40
1	B	1145	LEU	CB-CG-CD1	-5.25	102.07	111.00
1	C	738	CYS	CA-CB-SG	-5.23	104.58	114.00
1	C	291	CYS	CA-CB-SG	5.17	123.31	114.00
1	B	819	GLU	OE1-CD-OE2	-5.14	117.13	123.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	940	SER	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	A	8354	0	8126	974	0
1	B	8369	0	8124	992	0
1	C	8374	0	8124	1111	0
2	E	28	0	25	1	0
2	F	28	0	25	0	0
2	G	28	0	25	1	0
2	I	28	0	25	0	0
2	J	28	0	25	2	0
2	K	28	0	25	0	0
2	L	28	0	25	1	0
2	N	28	0	25	0	0
2	O	28	0	25	1	0
2	P	28	0	25	0	0
3	A	112	0	104	1	0
3	B	126	0	117	4	0
3	C	98	0	91	3	0
All	All	25713	0	24936	3008	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 59.

All (3008) 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:B:1116:THR:CG2	1:B:1140:PRO:HG2	1.18	1.66
1:B:131:CYS:HB2	1:B:133:PHE:CZ	1.10	1.62
1:B:1116:THR:HG22	1:B:1140:PRO:CG	1.28	1.61
1:C:126:VAL:CG2	1:C:172:SER:HB3	1.23	1.58
1:A:125:ASN:HD21	1:A:171:VAL:CG1	1.07	1.57
1:B:105:ILE:CD1	1:B:241:LEU:HD11	1.12	1.56
1:A:64:TRP:CD1	1:A:266:TYR:CE1	1.94	1.55
1:B:65:PHE:HB2	1:B:265:TYR:CE1	1.37	1.54
1:A:37:TYR:CD1	1:A:55:PHE:HE1	1.22	1.53
1:C:347:PHE:CZ	1:C:509:ARG:HD3	1.40	1.51
1:B:1116:THR:CG2	1:B:1140:PRO:CG	1.79	1.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:37:TYR:CE1	1:A:55:PHE:CE1	2.00	1.47
1:C:65:PHE:CE2	1:C:84:LEU:HD11	1.43	1.47
1:C:65:PHE:CE2	1:C:84:LEU:CD1	1.95	1.46
1:C:718:PHE:HB2	1:C:1067:TYR:CE1	1.50	1.46
1:A:64:TRP:NE1	1:A:266:TYR:CE1	1.84	1.46
1:B:131:CYS:CB	1:B:133:PHE:CZ	1.95	1.46
1:C:126:VAL:HG13	1:C:175:PHE:CE1	1.48	1.45
1:C:126:VAL:CG2	1:C:172:SER:CB	1.96	1.44
1:B:817:PHE:CE1	1:B:935:GLN:NE2	1.73	1.44
1:C:391:CYS:SG	1:C:525:CYS:HA	1.58	1.44
1:A:64:TRP:NE1	1:A:266:TYR:HE1	1.13	1.43
1:B:57:PRO:CB	1:B:273:ARG:HH12	1.27	1.43
1:B:825:LYS:HZ3	1:B:944:ALA:N	1.18	1.42
1:B:105:ILE:HD13	1:B:241:LEU:CD1	1.47	1.42
1:B:65:PHE:CB	1:B:265:TYR:HE1	1.34	1.41
1:B:105:ILE:CD1	1:B:241:LEU:CD1	1.99	1.41
1:B:55:PHE:C	1:B:270:LEU:CD2	1.89	1.40
1:B:65:PHE:CB	1:B:265:TYR:CE1	2.02	1.40
1:B:131:CYS:HB2	1:B:133:PHE:CE2	1.57	1.39
1:B:110:LEU:HD22	1:B:135:PHE:CE2	1.58	1.39
1:C:815:ARG:NH1	1:C:823:PHE:CD2	1.89	1.38
1:C:826:VAL:HG11	1:C:1057:PRO:CG	1.49	1.37
1:B:741:TYR:CE1	1:B:966:LEU:HD11	1.59	1.36
1:A:37:TYR:CD1	1:A:55:PHE:CE1	2.10	1.36
1:A:125:ASN:ND2	1:A:171:VAL:HG13	1.36	1.36
1:A:64:TRP:CD1	1:A:266:TYR:HE1	1.30	1.35
1:C:187:LYS:HD2	1:C:211:ASN:ND2	1.37	1.35
1:C:29:THR:HG23	1:C:62:VAL:CG1	1.57	1.34
1:B:16:VAL:CG2	1:B:158:ARG:NH2	1.88	1.34
1:B:564:GLN:NE2	1:B:577:ARG:HD2	1.41	1.34
1:C:65:PHE:HE2	1:C:84:LEU:CD1	1.28	1.33
1:C:105:ILE:CD1	1:C:241:LEU:HD11	1.57	1.33
1:C:166:CYS:HB3	1:C:169:GLU:OE2	1.16	1.33
1:C:726:ILE:CD1	1:C:1061:VAL:HG22	1.57	1.32
1:B:885:GLY:HA2	1:B:901:GLN:NE2	1.39	1.32
1:B:718:PHE:HB2	1:B:1067:TYR:CE1	1.63	1.31
1:C:337:PRO:CG	1:C:358:ILE:HD11	1.61	1.31
1:A:342:PHE:CE1	1:A:511:VAL:HG11	1.65	1.30
1:A:126:VAL:HG22	1:A:172:SER:CB	1.60	1.29
1:B:826:VAL:CG1	1:B:945:LEU:HD13	1.60	1.29
1:B:130:VAL:HG11	1:B:167:THR:OG1	1.24	1.28

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:115:GLN:O	1:C:233:ILE:HD11	1.25	1.28
1:C:29:THR:O	1:C:62:VAL:HG12	1.14	1.28
1:C:89:GLY:O	1:C:270:LEU:HD13	1.31	1.27
1:C:905:ARG:NH1	1:C:1050:MET:HB3	1.43	1.27
1:B:1115:ILE:O	1:B:1138:TYR:CB	1.81	1.27
1:B:310:LYS:HB2	1:B:600:PRO:O	1.35	1.26
1:C:89:GLY:O	1:C:270:LEU:CD1	1.82	1.26
1:C:826:VAL:CG1	1:C:1057:PRO:HG3	1.63	1.26
1:A:342:PHE:HE1	1:A:511:VAL:CB	1.47	1.25
1:B:104:TRP:HZ3	1:B:119:ILE:CG2	1.48	1.25
1:C:472:ILE:HG22	1:C:490:PHE:CA	1.64	1.25
1:C:718:PHE:CB	1:C:1067:TYR:HE1	1.48	1.25
1:B:102:ARG:NH2	1:B:141:LEU:HD21	1.51	1.25
1:C:1083:HIS:CG	1:C:1137:VAL:HG22	1.70	1.25
1:B:387:LEU:O	1:B:390:LEU:HG	1.36	1.24
1:B:130:VAL:CG1	1:B:167:THR:OG1	1.85	1.24
1:B:718:PHE:CB	1:B:1067:TYR:HE1	1.50	1.24
1:B:294:ASP:OD1	1:B:295:PRO:HD2	1.32	1.23
1:C:453:TYR:HD1	1:C:495:TYR:CE1	1.54	1.23
1:A:1102:TRP:HB2	1:A:1135:ASN:ND2	1.51	1.23
1:C:390:LEU:HD11	1:C:392:PHE:CE2	1.74	1.23
1:A:1031:GLU:OE1	1:A:1042:PHE:CD2	1.92	1.22
1:C:472:ILE:CG2	1:C:490:PHE:HA	1.69	1.22
1:B:106:PHE:CB	1:B:235:ILE:HD13	1.68	1.22
1:A:126:VAL:CG2	1:A:172:SER:CB	2.17	1.22
1:C:615:VAL:CG2	1:C:649:CYS:HB3	1.69	1.21
1:A:64:TRP:CD1	1:A:266:TYR:CD1	2.28	1.21
1:C:453:TYR:CD1	1:C:495:TYR:HE1	1.58	1.21
1:B:555:SER:HB2	1:B:586:ASP:CG	1.62	1.21
1:C:404:GLY:O	1:C:407:VAL:HG12	1.38	1.20
1:A:125:ASN:ND2	1:A:171:VAL:CG1	1.91	1.20
1:A:106:PHE:HZ	1:A:194:PHE:CD2	1.60	1.20
1:A:33:THR:HA	1:A:58:PHE:CE2	1.77	1.20
1:B:1116:THR:CB	1:B:1140:PRO:HG2	1.69	1.20
1:C:115:GLN:O	1:C:233:ILE:CD1	1.89	1.20
1:B:57:PRO:HB3	1:B:273:ARG:NH1	1.56	1.19
1:B:885:GLY:CA	1:B:901:GLN:HE21	1.54	1.19
1:B:55:PHE:O	1:B:270:LEU:HD23	1.41	1.19
1:A:1031:GLU:OE1	1:A:1042:PHE:CE2	1.96	1.19
1:B:104:TRP:CZ3	1:B:119:ILE:HG21	1.78	1.19
1:C:752:LEU:HD21	1:C:990:GLU:OE2	1.42	1.19

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:324:GLU:O	1:B:539:VAL:CG2	1.91	1.19
1:C:497:PHE:CD1	1:C:507:PRO:HD3	1.77	1.19
1:C:726:ILE:HD12	1:C:1061:VAL:CG2	1.73	1.18
1:C:347:PHE:CE2	1:C:509:ARG:HD3	1.78	1.18
1:A:96:GLU:HA	1:A:186:PHE:CD1	1.78	1.18
1:B:555:SER:HB2	1:B:586:ASP:OD1	1.40	1.18
1:C:85:PRO:O	1:C:269:TYR:OH	1.57	1.18
1:B:85:PRO:HG2	1:B:269:TYR:OH	1.44	1.18
1:B:770:ILE:HD11	1:B:1012:LEU:HD12	1.26	1.18
1:A:318:PHE:CE2	1:A:615:VAL:HG11	1.78	1.17
1:C:337:PRO:CD	1:C:358:ILE:HD11	1.72	1.17
1:C:598:ILE:HD11	1:C:666:ILE:CD1	1.73	1.17
1:B:104:TRP:CZ3	1:B:119:ILE:CG2	2.27	1.17
1:C:420:ASP:O	1:C:460:ASN:OD1	1.62	1.17
1:B:1043:CYS:HB2	1:B:1048:HIS:CD2	1.79	1.17
1:B:1115:ILE:O	1:B:1138:TYR:HB3	1.36	1.16
1:C:452:LEU:HB2	1:C:492:LEU:HD12	1.25	1.16
1:C:905:ARG:NH1	1:C:1050:MET:CB	2.09	1.16
1:C:29:THR:CG2	1:C:62:VAL:CG1	2.23	1.16
1:C:166:CYS:CB	1:C:169:GLU:OE2	1.93	1.16
1:A:166:CYS:HB3	1:A:169:GLU:OE2	1.45	1.15
1:B:55:PHE:C	1:B:270:LEU:HD21	1.65	1.15
1:A:133:PHE:CE1	1:A:160:TYR:CE1	2.33	1.15
1:B:112:SER:CB	1:B:134:GLN:CG	2.25	1.15
1:C:37:TYR:OH	1:C:195:LYS:NZ	1.79	1.15
1:B:57:PRO:CB	1:B:273:ARG:NH1	2.08	1.15
1:B:105:ILE:HD12	1:B:241:LEU:HD11	1.25	1.15
1:B:58:PHE:CE1	1:B:275:PHE:CZ	2.35	1.15
1:A:552:LEU:HD22	1:A:587:ILE:HD13	1.17	1.14
1:B:564:GLN:HE22	1:B:577:ARG:CD	1.60	1.14
1:C:83:VAL:HG21	1:C:237:ARG:CZ	1.77	1.14
1:A:497:PHE:CE2	1:A:507:PRO:HB3	1.79	1.14
1:A:785:VAL:HG13	1:A:877:LEU:HD21	1.28	1.14
1:B:825:LYS:NZ	1:B:944:ALA:H	1.45	1.14
1:A:342:PHE:CE1	1:A:511:VAL:CG1	2.29	1.14
1:C:37:TYR:CB	1:C:223:LEU:HD21	1.77	1.14
1:C:126:VAL:CG1	1:C:175:PHE:CE1	2.31	1.14
1:A:115:GLN:NE2	1:A:132:GLU:HG3	1.60	1.13
1:B:16:VAL:HG22	1:B:158:ARG:NH2	1.57	1.13
1:B:57:PRO:CA	1:B:273:ARG:HH12	1.59	1.13
1:B:106:PHE:HB3	1:B:235:ILE:HD13	1.14	1.13

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:37:TYR:HB3	1:C:223:LEU:HD21	1.16	1.13
1:C:856:ASN:O	1:C:858:LEU:HD12	1.48	1.13
1:A:1050:MET:HG2	1:A:1065:VAL:HG21	1.28	1.13
1:A:620:VAL:CG2	1:A:621:PRO:HD2	1.78	1.12
1:A:741:TYR:CE1	1:A:966:LEU:HD21	1.82	1.12
1:B:131:CYS:HB2	1:B:133:PHE:CE1	1.84	1.12
1:A:220:PHE:CD2	1:A:287:ASP:HA	1.85	1.12
1:A:318:PHE:HE2	1:A:615:VAL:HG11	1.04	1.12
1:A:617:CYS:SG	1:A:644:GLN:HB2	1.88	1.12
1:A:319:ARG:HG2	1:A:592:PHE:HD1	1.11	1.12
1:B:105:ILE:HD11	1:B:241:LEU:HD21	1.30	1.11
1:C:767:LEU:CD2	1:C:1008:VAL:HG22	1.80	1.11
1:C:366:SER:HB3	1:C:388:ASN:OD1	1.47	1.11
1:B:112:SER:HB3	1:B:134:GLN:CG	1.79	1.11
1:C:346:ARG:NH2	1:C:450:ASN:HB2	1.64	1.11
1:C:462:LYS:HA	1:C:462:LYS:HE2	1.30	1.11
1:A:126:VAL:HG22	1:A:172:SER:HB3	1.11	1.11
1:A:389:ASP:OD1	1:A:528:LYS:NZ	1.83	1.11
1:B:16:VAL:CG2	1:B:158:ARG:HH22	1.56	1.11
1:B:388:ASN:OD1	1:B:527:PRO:HD2	1.48	1.11
1:C:187:LYS:CD	1:C:211:ASN:HD22	1.64	1.11
1:C:105:ILE:HD11	1:C:241:LEU:HD11	1.19	1.10
1:C:32:PHE:HB3	1:C:59:PHE:CE1	1.86	1.10
1:B:372:ALA:HB1	1:B:374:PHE:CE2	1.85	1.10
1:C:598:ILE:HD11	1:C:666:ILE:HD12	1.27	1.10
1:C:65:PHE:HE2	1:C:84:LEU:HD13	1.12	1.10
1:C:347:PHE:CZ	1:C:509:ARG:CD	2.35	1.10
1:C:471:GLU:O	1:C:491:PRO:HD3	1.49	1.10
1:C:497:PHE:HD1	1:C:507:PRO:HD3	1.03	1.10
1:B:67:ALA:HB3	1:B:263:ALA:HB3	1.31	1.10
1:A:130:VAL:HG11	1:A:231:ILE:HD11	1.13	1.09
1:A:342:PHE:CE1	1:A:511:VAL:CB	2.34	1.09
1:A:342:PHE:HE1	1:A:511:VAL:CG1	1.64	1.09
1:C:320:VAL:HG23	1:C:591:SER:HB2	1.30	1.09
1:A:166:CYS:CB	1:A:169:GLU:OE2	2.00	1.09
1:B:16:VAL:HG21	1:B:158:ARG:NH2	1.65	1.09
1:C:337:PRO:HG2	1:C:358:ILE:HD11	1.35	1.09
1:A:203:ILE:CG2	1:A:227:VAL:CG2	2.31	1.08
1:B:310:LYS:CB	1:B:600:PRO:O	2.01	1.08
1:C:187:LYS:CD	1:C:211:ASN:ND2	2.14	1.08
1:A:203:ILE:CG2	1:A:227:VAL:HG23	1.83	1.08

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:453:TYR:CE2	1:A:493:GLN:HG2	1.88	1.08
1:A:888:PHE:CZ	1:A:1034:LEU:CD2	2.35	1.08
1:A:984:LEU:CD2	1:A:988:GLU:HG2	1.82	1.08
1:B:617:CYS:N	1:B:649:CYS:SG	2.26	1.08
1:B:112:SER:CB	1:B:134:GLN:HG2	1.83	1.08
1:B:131:CYS:O	1:B:133:PHE:CD1	2.06	1.08
1:A:328:ARG:CZ	1:A:578:ASP:OD2	2.01	1.07
1:A:673:SER:O	1:A:693:ILE:HD13	1.51	1.07
1:B:106:PHE:HB3	1:B:235:ILE:CD1	1.84	1.07
1:B:826:VAL:HG21	1:B:1057:PRO:HG3	1.29	1.07
1:A:130:VAL:HG23	1:A:168:PHE:O	1.55	1.07
1:B:826:VAL:HG13	1:B:945:LEU:CD1	1.85	1.07
1:B:947:LYS:O	1:B:950:ASP:OD1	1.72	1.07
1:C:89:GLY:C	1:C:270:LEU:HD13	1.74	1.07
1:A:106:PHE:HB3	1:A:235:ILE:HG21	1.12	1.07
1:A:984:LEU:HD22	1:A:988:GLU:CG	1.84	1.07
1:B:825:LYS:NZ	1:B:944:ALA:N	1.97	1.07
1:C:105:ILE:CD1	1:C:241:LEU:CD1	2.32	1.07
1:C:826:VAL:HG11	1:C:1057:PRO:HG3	1.18	1.07
1:B:115:GLN:NE2	1:B:167:THR:CG2	2.17	1.07
1:B:555:SER:CB	1:B:586:ASP:OD1	2.02	1.07
1:C:615:VAL:HG23	1:C:649:CYS:CB	1.85	1.07
1:A:345:THR:HG23	1:A:346:ARG:N	1.69	1.06
1:A:729:VAL:HG21	1:A:1060:VAL:HG23	1.34	1.06
1:C:29:THR:CG2	1:C:62:VAL:HG11	1.84	1.06
1:C:791:THR:HG22	1:C:792:PRO:HD2	1.37	1.06
1:A:126:VAL:CG2	1:A:172:SER:HB2	1.81	1.06
1:B:1043:CYS:HB2	1:B:1048:HIS:HD2	0.94	1.06
1:C:33:THR:HA	1:C:58:PHE:CE1	1.90	1.06
1:A:106:PHE:CZ	1:A:194:PHE:CD2	2.43	1.06
1:B:298:GLU:CD	1:B:315:THR:CG2	2.24	1.06
1:B:826:VAL:HG13	1:B:945:LEU:HD13	1.14	1.06
1:C:115:GLN:C	1:C:233:ILE:HD11	1.76	1.06
1:C:436:TRP:HD1	1:C:509:ARG:O	1.36	1.06
1:C:856:ASN:OD1	1:C:966:LEU:HD12	1.55	1.06
1:C:400:PHE:HE2	1:C:423:TYR:CD2	1.74	1.06
1:C:752:LEU:HD11	1:C:990:GLU:OE1	1.55	1.06
1:A:36:VAL:HG21	1:A:220:PHE:CZ	1.90	1.05
1:A:673:SER:O	1:A:693:ILE:CD1	2.04	1.05
1:A:210:ILE:HD13	1:A:217:PRO:HB3	1.32	1.05
1:A:674:TYR:HE1	1:A:690:GLN:HB3	1.19	1.05

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:34:ARG:NH1	1:B:191:GLU:HG2	1.71	1.05
1:B:94:SER:OG	1:B:96:GLU:OE2	1.74	1.05
1:B:112:SER:CB	1:B:134:GLN:HG3	1.86	1.05
1:C:520:ALA:HB1	1:C:521:PRO:HD2	1.34	1.05
1:A:203:ILE:HG21	1:A:227:VAL:CG2	1.86	1.05
1:B:56:LEU:N	1:B:270:LEU:HD21	1.70	1.05
1:C:497:PHE:CD1	1:C:507:PRO:CD	2.40	1.05
1:A:106:PHE:HB3	1:A:235:ILE:CG2	1.86	1.04
1:A:319:ARG:HG2	1:A:592:PHE:CD1	1.90	1.04
1:B:324:GLU:O	1:B:539:VAL:HG23	1.54	1.04
1:B:1039:ARG:NE	1:C:1031:GLU:OE2	1.89	1.04
1:B:1116:THR:HG21	1:B:1140:PRO:HG2	1.08	1.04
1:C:337:PRO:HG2	1:C:358:ILE:CD1	1.87	1.04
1:A:106:PHE:CB	1:A:235:ILE:HG21	1.88	1.04
1:B:55:PHE:C	1:B:270:LEU:HD23	1.60	1.04
1:C:741:TYR:OH	1:C:962:LEU:O	1.75	1.04
1:A:620:VAL:HG23	1:A:621:PRO:HD2	1.09	1.04
1:C:337:PRO:HD2	1:C:358:ILE:HD11	1.38	1.04
1:A:620:VAL:HB	1:A:621:PRO:HD3	1.39	1.03
1:B:57:PRO:HB3	1:B:273:ARG:HH12	1.03	1.03
1:B:102:ARG:HG3	1:B:141:LEU:HD13	1.36	1.03
1:B:102:ARG:CG	1:B:141:LEU:HD13	1.89	1.03
1:B:613:GLN:O	1:B:647:ALA:O	1.75	1.03
1:B:1114:ILE:CG2	1:B:1138:TYR:HD2	1.69	1.03
1:A:805:ILE:O	1:A:816:SER:OG	1.72	1.03
1:C:1090:PRO:HA	1:C:1120:THR:HG22	1.37	1.03
1:B:324:GLU:O	1:B:539:VAL:HG22	1.59	1.03
1:C:581:THR:HG22	1:C:583:GLU:HG3	1.37	1.03
1:B:825:LYS:CE	1:B:944:ALA:H	1.72	1.02
1:B:1116:THR:HG22	1:B:1140:PRO:HG3	1.03	1.02
1:C:126:VAL:HG21	1:C:172:SER:CB	1.85	1.02
1:A:275:PHE:HE1	1:A:290:ASP:HB2	1.23	1.02
1:A:984:LEU:HD22	1:A:988:GLU:HG2	1.03	1.02
1:B:104:TRP:HZ3	1:B:119:ILE:HG22	1.20	1.02
1:C:391:CYS:SG	1:C:525:CYS:CA	2.47	1.02
1:A:81:ASN:HD22	1:A:242:LEU:HD23	1.23	1.02
1:C:598:ILE:CD1	1:C:666:ILE:HD11	1.90	1.02
1:A:96:GLU:HA	1:A:186:PHE:HD1	1.22	1.01
1:B:740:MET:HA	1:B:740:MET:HE3	1.39	1.01
1:B:1114:ILE:HG21	1:B:1138:TYR:HD2	1.24	1.01
1:C:400:PHE:HE2	1:C:423:TYR:CE2	1.79	1.01

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:64:TRP:HD1	1:A:266:TYR:CD1	1.70	1.01
1:B:298:GLU:CD	1:B:315:THR:HG21	1.80	1.01
1:C:767:LEU:HD21	1:C:1008:VAL:HG22	1.04	1.01
1:B:110:LEU:CD2	1:B:135:PHE:CE2	2.43	1.01
1:B:741:TYR:HE1	1:B:966:LEU:HD11	1.25	1.01
1:B:822:LEU:HD11	1:B:938:LEU:HD13	1.42	1.01
1:A:115:GLN:HE22	1:A:132:GLU:HG3	1.19	1.01
1:C:436:TRP:CD1	1:C:509:ARG:O	2.12	1.01
1:C:559:PHE:CZ	1:C:565:PHE:O	2.14	1.01
1:C:992:GLN:HE21	1:C:992:GLN:HA	1.25	1.01
1:C:471:GLU:O	1:C:491:PRO:CD	2.08	1.01
1:C:497:PHE:CD1	1:C:507:PRO:CG	2.44	1.00
1:A:125:ASN:HD21	1:A:171:VAL:HG12	1.26	1.00
1:B:65:PHE:HB3	1:B:265:TYR:HE1	1.24	1.00
1:C:126:VAL:CG1	1:C:175:PHE:CZ	2.44	1.00
1:B:784:GLN:HA	1:B:784:GLN:HE21	1.24	1.00
1:A:83:VAL:C	1:A:84:LEU:HD23	1.82	1.00
1:B:57:PRO:HB3	1:B:273:ARG:CZ	1.92	1.00
1:C:187:LYS:HD2	1:C:211:ASN:HD22	0.84	0.99
1:B:298:GLU:OE2	1:B:315:THR:HG22	1.63	0.99
1:C:1083:HIS:CB	1:C:1137:VAL:HG22	1.91	0.99
1:A:785:VAL:CG1	1:A:877:LEU:CD2	2.40	0.99
1:A:954:GLN:HB3	1:A:1014:ARG:NH1	1.75	0.99
1:A:126:VAL:CG2	1:A:172:SER:HB3	1.85	0.99
1:B:298:GLU:HG2	1:B:315:THR:HG23	1.43	0.99
1:A:1102:TRP:HB2	1:A:1135:ASN:HD21	1.06	0.99
1:A:617:CYS:HA	1:A:649:CYS:SG	2.03	0.99
1:C:353:TRP:CZ3	1:C:423:TYR:CD1	2.50	0.99
1:A:785:VAL:HG11	1:A:877:LEU:HD23	1.42	0.99
1:C:452:LEU:CB	1:C:492:LEU:HD12	1.92	0.99
1:C:453:TYR:CD1	1:C:495:TYR:CE1	2.41	0.99
1:C:29:THR:O	1:C:62:VAL:CG1	2.10	0.98
1:C:534:VAL:HG11	1:C:539:VAL:HG11	1.43	0.98
1:A:96:GLU:OE1	1:A:101:ILE:CD1	2.11	0.98
1:A:674:TYR:CE1	1:A:690:GLN:HB3	1.97	0.98
1:B:461:LEU:HD21	1:B:467:ASP:HB2	1.41	0.98
1:C:826:VAL:CG1	1:C:1057:PRO:CG	2.31	0.98
1:A:342:PHE:CE1	1:A:511:VAL:HG21	1.99	0.98
1:B:962:LEU:HD11	1:B:1007:TYR:HB2	1.45	0.98
1:C:773:GLU:OE2	1:C:1019:ARG:HD2	1.64	0.98
1:C:615:VAL:HG11	1:C:620:VAL:HG12	1.42	0.97

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:620:VAL:HB	1:A:621:PRO:CD	1.94	0.97
1:B:131:CYS:O	1:B:133:PHE:CE1	2.16	0.97
1:B:773:GLU:OE2	1:B:1019:ARG:NH1	1.97	0.97
1:C:970:PHE:CE2	1:C:999:GLY:CA	2.46	0.97
1:A:106:PHE:CZ	1:A:194:PHE:HD2	1.78	0.97
1:B:341:VAL:HG22	1:B:356:LYS:NZ	1.79	0.97
1:C:726:ILE:HD12	1:C:1061:VAL:HG22	0.97	0.97
1:C:65:PHE:CZ	1:C:84:LEU:HD11	1.98	0.97
1:C:595:VAL:CG1	1:C:610:VAL:CG1	2.41	0.97
1:A:712:ILE:HB	1:A:1077:THR:HG21	1.41	0.97
1:A:888:PHE:CZ	1:A:1034:LEU:HD22	1.99	0.97
1:C:615:VAL:HG23	1:C:649:CYS:HB3	1.40	0.97
1:A:1050:MET:HG2	1:A:1065:VAL:CG2	1.94	0.97
1:C:220:PHE:CE1	1:C:287:ASP:HA	2.00	0.97
1:C:826:VAL:HG11	1:C:1057:PRO:HG2	1.41	0.97
1:B:825:LYS:HZ3	1:B:944:ALA:CA	1.77	0.97
1:C:34:ARG:NH1	1:C:219:GLY:O	1.96	0.97
1:C:352:ALA:HB2	1:C:468:ILE:CG2	1.94	0.97
1:C:436:TRP:NE1	1:C:509:ARG:HB3	1.80	0.97
1:C:581:THR:HG22	1:C:583:GLU:CG	1.95	0.96
1:B:55:PHE:CA	1:B:270:LEU:CD2	2.43	0.96
1:C:1083:HIS:CG	1:C:1137:VAL:CG2	2.48	0.96
1:C:115:GLN:C	1:C:233:ILE:CD1	2.32	0.96
1:C:856:ASN:O	1:C:858:LEU:CD1	2.12	0.96
1:A:388:ASN:OD1	1:A:527:PRO:CD	2.14	0.96
1:B:102:ARG:CZ	1:B:141:LEU:CD2	2.41	0.96
1:A:994:ASP:OD2	1:C:995:ARG:NH2	1.98	0.96
1:C:567:ARG:HH11	1:C:567:ARG:HG3	1.27	0.96
1:A:342:PHE:HE1	1:A:511:VAL:CG2	1.78	0.96
1:B:67:ALA:HB3	1:B:263:ALA:CB	1.96	0.96
1:B:298:GLU:HG2	1:B:315:THR:CG2	1.96	0.96
1:A:130:VAL:HG11	1:A:231:ILE:CD1	1.95	0.95
1:B:1115:ILE:O	1:B:1138:TYR:HB2	1.60	0.95
1:C:65:PHE:CE2	1:C:84:LEU:HD13	1.86	0.95
1:A:719:THR:HG23	1:A:1070:ALA:HB2	1.47	0.95
1:B:164:ASN:OD1	1:B:165:ASN:ND2	1.98	0.95
1:C:970:PHE:CD2	1:C:999:GLY:HA3	2.01	0.95
1:B:1082:CYS:SG	1:B:1132:ILE:CD1	2.55	0.95
1:A:220:PHE:HE2	1:A:288:ALA:N	1.62	0.95
1:C:390:LEU:CD1	1:C:392:PHE:CE2	2.48	0.95
1:A:86:PHE:CD2	1:A:106:PHE:HE2	1.84	0.95

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:112:SER:HB3	1:B:134:GLN:HG2	1.44	0.95
1:C:726:ILE:CD1	1:C:1061:VAL:CG2	2.37	0.95
1:C:970:PHE:CE2	1:C:999:GLY:HA3	2.01	0.95
1:C:598:ILE:CD1	1:C:666:ILE:CD1	2.45	0.95
1:A:96:GLU:OE1	1:A:101:ILE:HD12	1.64	0.95
1:C:126:VAL:HG22	1:C:172:SER:CB	1.71	0.95
1:C:763:LEU:HD13	1:C:1004:LEU:HD22	1.48	0.95
1:C:811:LYS:HD3	1:C:820:ASP:OD2	1.65	0.95
1:B:106:PHE:HB2	1:B:117:LEU:HD22	1.47	0.95
1:A:1050:MET:CG	1:A:1065:VAL:HG21	1.95	0.95
1:A:303:LEU:HD23	1:A:308:VAL:HG12	1.46	0.95
1:A:125:ASN:ND2	1:A:172:SER:O	1.98	0.94
1:B:131:CYS:CA	1:B:133:PHE:CE1	2.49	0.94
1:B:277:LEU:H	1:B:277:LEU:HD12	1.28	0.94
1:C:337:PRO:CG	1:C:358:ILE:CD1	2.43	0.94
1:A:1102:TRP:CB	1:A:1135:ASN:ND2	2.30	0.94
1:C:380:TYR:CE2	1:C:412:PRO:CD	2.50	0.94
1:C:497:PHE:CE1	1:C:507:PRO:HB3	2.01	0.94
1:B:826:VAL:CG1	1:B:945:LEU:CD1	2.45	0.94
1:C:497:PHE:CG	1:C:507:PRO:HG3	2.02	0.94
1:C:822:LEU:HD21	1:C:945:LEU:HD21	1.47	0.94
1:A:86:PHE:CD2	1:A:106:PHE:CE2	2.56	0.94
1:A:133:PHE:CD1	1:A:160:TYR:CD1	2.55	0.94
1:C:805:ILE:HG22	1:C:878:LEU:HD13	1.48	0.94
1:B:1104:VAL:HG11	1:B:1119:ASN:ND2	1.82	0.94
1:C:352:ALA:CB	1:C:468:ILE:CG2	2.45	0.94
1:A:130:VAL:CG1	1:A:231:ILE:HD11	1.97	0.94
1:C:377:PHE:CE1	1:C:434:ILE:HD11	2.03	0.94
1:A:541:PHE:CE2	1:A:587:ILE:HD12	2.01	0.93
1:C:29:THR:HG23	1:C:62:VAL:HG11	0.94	0.93
1:B:298:GLU:CG	1:B:315:THR:CG2	2.46	0.93
1:C:1082:CYS:HB2	1:C:1132:ILE:HD11	1.47	0.93
1:C:347:PHE:CE2	1:C:509:ARG:CD	2.49	0.93
1:A:726:ILE:HD13	1:A:945:LEU:HD23	1.51	0.93
1:C:346:ARG:HH22	1:C:450:ASN:CB	1.81	0.93
1:A:617:CYS:SG	1:A:644:GLN:OE1	2.27	0.93
1:B:130:VAL:HG11	1:B:167:THR:HG1	1.00	0.93
1:C:89:GLY:O	1:C:270:LEU:HD12	1.67	0.93
1:A:424:LYS:O	1:A:463:PRO:HA	1.69	0.93
1:C:353:TRP:HZ3	1:C:423:TYR:CB	1.80	0.93
1:A:802:PHE:HE1	1:A:927:PHE:CZ	1.87	0.92

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:563:GLN:HE21	1:C:563:GLN:H	1.08	0.92
1:A:310:LYS:CG	1:A:664:ILE:HD11	1.99	0.92
1:A:336:CYS:HB3	1:A:337:PRO:HD2	1.50	0.92
1:B:107:GLY:N	1:B:235:ILE:CG2	2.32	0.92
1:C:644:GLN:HA	1:C:644:GLN:HE21	1.31	0.92
1:C:977:LEU:HD22	1:C:993:ILE:CD1	1.99	0.92
1:A:426:PRO:HG3	1:A:463:PRO:HB3	1.52	0.92
1:A:1030:SER:OG	1:C:1041:ASP:HB3	1.68	0.92
1:C:497:PHE:CD1	1:C:507:PRO:HG3	2.04	0.92
1:C:815:ARG:NH1	1:C:823:PHE:CE2	2.24	0.92
1:C:858:LEU:HD23	1:C:959:LEU:HD11	1.51	0.92
1:B:16:VAL:CG2	1:B:158:ARG:HH21	1.71	0.92
1:B:56:LEU:HD12	1:B:57:PRO:HD2	1.51	0.92
1:C:126:VAL:HG12	1:C:175:PHE:CZ	2.05	0.92
1:C:615:VAL:CG1	1:C:620:VAL:HG12	2.00	0.92
1:B:457:ARG:CZ	1:B:467:ASP:OD2	2.17	0.92
1:C:346:ARG:HH22	1:C:450:ASN:HB2	1.28	0.92
1:A:133:PHE:CE1	1:A:160:TYR:CD1	2.58	0.92
1:B:564:GLN:HE22	1:B:577:ARG:HD2	0.79	0.92
1:B:1043:CYS:CB	1:B:1048:HIS:HD2	1.83	0.92
1:B:947:LYS:HA	1:B:950:ASP:OD2	1.70	0.92
1:B:1116:THR:CB	1:B:1140:PRO:CD	2.48	0.92
1:C:130:VAL:HG11	1:C:167:THR:OG1	1.68	0.92
1:A:726:ILE:HD12	1:A:944:ALA:O	1.68	0.92
1:A:552:LEU:HD22	1:A:587:ILE:CD1	2.00	0.92
1:B:817:PHE:CD1	1:B:935:GLN:NE2	2.38	0.92
1:C:29:THR:HG22	1:C:62:VAL:HG13	1.50	0.92
1:A:37:TYR:HE1	1:A:55:PHE:CE1	1.63	0.91
1:A:106:PHE:C	1:A:235:ILE:HG22	1.90	0.91
1:B:387:LEU:HA	1:B:390:LEU:CD2	2.00	0.91
1:B:1043:CYS:CB	1:B:1048:HIS:CD2	2.53	0.91
1:B:718:PHE:HB2	1:B:1067:TYR:HE1	0.79	0.91
1:B:718:PHE:CB	1:B:1067:TYR:CE1	2.38	0.91
1:A:37:TYR:CE1	1:A:55:PHE:CD1	2.58	0.91
1:A:712:ILE:HB	1:A:1077:THR:CG2	2.00	0.91
1:C:378:LYS:HD3	1:C:380:TYR:OH	1.69	0.91
1:B:1116:THR:HG22	1:B:1140:PRO:CD	2.01	0.91
1:B:57:PRO:CA	1:B:273:ARG:NH1	2.33	0.91
1:B:125:ASN:HA	1:B:175:PHE:CE1	2.05	0.91
1:C:346:ARG:NH2	1:C:450:ASN:CB	2.33	0.91
1:B:1116:THR:CB	1:B:1140:PRO:CG	2.37	0.91

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:318:PHE:HE2	1:B:615:VAL:HG21	1.35	0.91
1:B:65:PHE:HB3	1:B:265:TYR:CE1	1.96	0.91
1:B:1088:HIS:CE1	1:B:1122:VAL:HG23	2.06	0.91
1:C:791:THR:CG2	1:C:792:PRO:HD2	2.01	0.91
1:C:826:VAL:HG13	1:C:1057:PRO:HG3	1.53	0.91
1:B:599:THR:HG22	1:B:608:VAL:HG12	1.53	0.90
1:C:662:CYS:SG	1:C:697:MET:SD	2.69	0.90
1:B:58:PHE:HE1	1:B:275:PHE:CZ	1.85	0.90
1:B:1082:CYS:SG	1:B:1132:ILE:HD13	2.11	0.90
1:A:37:TYR:HE1	1:A:55:PHE:CD1	1.88	0.90
1:B:388:ASN:OD1	1:B:527:PRO:CD	2.19	0.90
1:C:347:PHE:CE1	1:C:509:ARG:HD3	2.05	0.90
1:A:676:THR:OG1	1:A:690:GLN:NE2	2.05	0.90
1:B:480:CYS:O	1:B:483:VAL:HG12	1.71	0.90
1:C:1083:HIS:CB	1:C:1137:VAL:CG2	2.49	0.90
1:C:83:VAL:HG21	1:C:237:ARG:NH2	1.86	0.90
1:C:355:ARG:HG3	1:C:398:ASP:OD1	1.72	0.90
1:C:400:PHE:CE2	1:C:423:TYR:CD2	2.58	0.90
1:B:457:ARG:NE	1:B:467:ASP:OD2	2.04	0.90
1:C:130:VAL:O	1:C:131:CYS:SG	2.29	0.90
1:B:365:TYR:O	1:B:368:LEU:HD23	1.70	0.90
1:A:345:THR:HG23	1:A:346:ARG:H	1.35	0.90
1:A:785:VAL:HG13	1:A:877:LEU:CD2	2.00	0.90
1:C:352:ALA:CB	1:C:468:ILE:HG22	2.02	0.90
1:C:480:CYS:SG	1:C:485:GLY:N	2.45	0.90
1:C:497:PHE:CZ	1:C:507:PRO:HB3	2.06	0.90
1:A:452:LEU:HD13	1:A:493:GLN:O	1.72	0.90
1:B:191:GLU:OE1	1:B:206:LYS:O	1.90	0.90
1:A:107:GLY:N	1:A:235:ILE:HG22	1.87	0.90
1:B:102:ARG:CZ	1:B:141:LEU:HD21	1.99	0.90
1:B:141:LEU:O	1:B:243:ALA:HA	1.72	0.90
1:B:817:PHE:HE1	1:B:935:GLN:HE21	0.93	0.90
1:C:352:ALA:HB2	1:C:468:ILE:HG22	1.51	0.90
1:C:909:ILE:HD12	1:C:1067:TYR:HD2	1.34	0.90
1:A:388:ASN:OD1	1:A:526:GLY:HA3	1.72	0.89
1:C:329:PHE:HB3	1:C:330:PRO:HD2	1.53	0.89
1:C:615:VAL:CG2	1:C:649:CYS:CB	2.46	0.89
1:C:662:CYS:SG	1:C:697:MET:HB3	2.12	0.89
1:A:203:ILE:HG23	1:A:227:VAL:CG2	2.02	0.89
1:B:826:VAL:HG12	1:B:945:LEU:HD13	1.51	0.89
1:C:29:THR:CG2	1:C:62:VAL:HG13	1.98	0.89

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:559:PHE:CE2	1:C:565:PHE:O	2.26	0.89
1:C:329:PHE:O	1:C:580:GLN:NE2	2.04	0.89
1:C:767:LEU:HD21	1:C:1008:VAL:CG2	1.98	0.89
1:B:915:VAL:O	1:B:919:ASN:ND2	2.05	0.89
1:C:65:PHE:CZ	1:C:84:LEU:CD1	2.55	0.89
1:C:414:GLN:HE21	1:C:414:GLN:HA	1.34	0.89
1:A:41:LYS:O	1:C:563:GLN:HB3	1.72	0.89
1:A:126:VAL:HG23	1:A:172:SER:HB2	1.54	0.89
1:A:318:PHE:HE2	1:A:615:VAL:CG1	1.85	0.89
1:A:1101:HIS:HB3	1:A:1103:PHE:CE1	2.08	0.89
1:B:112:SER:HB2	1:B:134:GLN:HG3	1.55	0.89
1:A:785:VAL:CG1	1:A:877:LEU:HD23	2.01	0.89
1:C:126:VAL:CG2	1:C:172:SER:HB2	2.03	0.89
1:C:126:VAL:HG13	1:C:175:PHE:CZ	2.05	0.89
1:C:1082:CYS:HB2	1:C:1132:ILE:CD1	2.03	0.89
1:C:1140:PRO:O	1:C:1143:PRO:HD2	1.73	0.89
1:B:56:LEU:N	1:B:270:LEU:CD2	2.33	0.88
1:B:102:ARG:NH2	1:B:141:LEU:CD2	2.37	0.88
1:B:107:GLY:N	1:B:235:ILE:HG23	1.87	0.88
1:C:353:TRP:HZ3	1:C:423:TYR:CA	1.86	0.88
1:A:57:PRO:HB3	1:A:273:ARG:HE	1.34	0.88
1:A:277:LEU:HD22	1:A:285:ILE:HD13	1.55	0.88
1:B:131:CYS:C	1:B:133:PHE:CE1	2.47	0.88
1:C:126:VAL:HG13	1:C:175:PHE:HE1	0.85	0.88
1:C:905:ARG:HH11	1:C:1050:MET:HB3	1.26	0.88
1:B:105:ILE:HD11	1:B:241:LEU:CD2	2.03	0.88
1:B:715:PRO:HA	1:B:1071:GLN:O	1.74	0.88
1:B:817:PHE:CZ	1:B:935:GLN:NE2	2.40	0.88
1:C:1139:ASP:OD1	1:C:1140:PRO:HD2	1.71	0.88
1:A:620:VAL:CB	1:A:621:PRO:CD	2.50	0.88
1:C:32:PHE:HB3	1:C:59:PHE:CD1	2.07	0.88
1:C:338:PHE:HZ	1:C:365:TYR:CZ	1.90	0.88
1:A:742:ILE:HD11	1:A:1001:LEU:HD23	1.55	0.88
1:A:785:VAL:CG1	1:A:877:LEU:HD21	2.00	0.88
1:B:152:TRP:CH2	1:B:245:HIS:CE1	2.61	0.88
1:B:1116:THR:HA	1:B:1140:PRO:HD3	1.54	0.88
1:A:37:TYR:HD1	1:A:55:PHE:HE1	1.10	0.88
1:A:715:PRO:HA	1:A:1071:GLN:O	1.73	0.88
1:A:342:PHE:CE1	1:A:511:VAL:CG2	2.55	0.88
1:A:388:ASN:OD1	1:A:527:PRO:HD2	1.74	0.88
1:C:351:TYR:HD2	1:C:452:LEU:O	1.57	0.88

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:404:GLY:HA2	1:C:508:TYR:HD2	1.39	0.88
1:B:826:VAL:N	1:B:945:LEU:HD11	1.88	0.88
1:C:380:TYR:HE2	1:C:412:PRO:CD	1.85	0.87
1:A:905:ARG:HD3	1:A:1049:LEU:O	1.73	0.87
1:C:37:TYR:CB	1:C:223:LEU:CD2	2.52	0.87
1:C:105:ILE:HD13	1:C:241:LEU:HD11	1.54	0.87
1:B:106:PHE:HB2	1:B:235:ILE:HD13	1.56	0.87
1:B:48:LEU:HB3	1:B:276:LEU:HD21	1.55	0.87
1:B:454:ARG:NH1	1:B:469:SER:OG	2.07	0.87
1:C:699:LEU:H	1:C:699:LEU:HD22	1.37	0.87
1:C:595:VAL:CG1	1:C:610:VAL:HG11	2.04	0.87
1:A:106:PHE:HZ	1:A:194:PHE:HD2	0.90	0.87
1:C:353:TRP:CZ3	1:C:423:TYR:CB	2.57	0.87
1:B:719:THR:HG23	1:B:1070:ALA:HB2	1.57	0.87
1:C:320:VAL:HG23	1:C:591:SER:CB	2.05	0.87
1:A:1050:MET:CG	1:A:1065:VAL:CG2	2.53	0.87
1:B:106:PHE:HB3	1:B:235:ILE:HG21	1.57	0.87
1:B:472:ILE:CG2	1:B:489:TYR:O	2.22	0.87
1:A:33:THR:HA	1:A:58:PHE:CD2	2.10	0.86
1:A:310:LYS:HG3	1:A:664:ILE:HD11	1.55	0.86
1:A:598:ILE:HG23	1:A:664:ILE:HG21	1.57	0.86
1:B:454:ARG:HA	1:B:491:PRO:O	1.73	0.86
1:A:342:PHE:CE1	1:A:511:VAL:HB	2.08	0.86
1:A:741:TYR:CZ	1:A:966:LEU:HD21	2.10	0.86
1:B:16:VAL:HG22	1:B:158:ARG:HH21	1.26	0.86
1:B:58:PHE:CD1	1:B:275:PHE:HZ	1.92	0.86
1:B:318:PHE:CE2	1:B:615:VAL:HG21	2.11	0.86
1:C:718:PHE:CB	1:C:1067:TYR:CE1	2.33	0.86
1:B:126:VAL:HB	1:B:175:PHE:HZ	1.38	0.86
1:B:559:PHE:HE1	1:C:43:PHE:CD2	1.91	0.86
1:B:105:ILE:CD1	1:B:241:LEU:CG	2.54	0.86
1:B:294:ASP:CG	1:B:295:PRO:HD2	1.95	0.86
1:B:365:TYR:C	1:B:368:LEU:HD23	1.96	0.86
1:A:559:PHE:HB2	1:A:563:GLN:OE1	1.75	0.86
1:C:58:PHE:CE2	1:C:275:PHE:CE2	2.63	0.86
1:B:1142:GLN:HA	1:B:1142:GLN:HE21	1.41	0.85
1:C:58:PHE:HE2	1:C:275:PHE:CE2	1.94	0.85
1:C:353:TRP:CZ3	1:C:423:TYR:CG	2.64	0.85
1:A:235:ILE:H	1:A:235:ILE:HD12	1.39	0.85
1:B:741:TYR:CZ	1:B:966:LEU:HD11	2.11	0.85
1:B:823:PHE:CZ	1:B:867:ASP:OD2	2.28	0.85

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:37:TYR:HA	1:C:223:LEU:CD2	2.06	0.85
1:C:471:GLU:O	1:C:491:PRO:CG	2.23	0.85
1:C:852:ALA:HB1	1:C:859:THR:HG22	1.58	0.85
1:A:58:PHE:CE1	1:A:275:PHE:CZ	2.65	0.85
1:B:763:LEU:HD22	1:B:1008:VAL:HG21	1.57	0.85
1:B:822:LEU:CD1	1:B:938:LEU:HD13	2.07	0.85
1:C:366:SER:N	1:C:388:ASN:HD21	1.74	0.85
1:B:16:VAL:CB	1:B:158:ARG:HH22	1.90	0.85
1:B:331:ASN:HD22	2:J:1:NAG:H82	1.41	0.85
1:C:977:LEU:HD22	1:C:993:ILE:HD12	1.58	0.85
1:B:825:LYS:HZ3	1:B:944:ALA:H	0.96	0.85
1:A:365:TYR:O	1:A:369:TYR:CB	2.23	0.85
1:A:770:ILE:HD11	1:A:1012:LEU:HD23	1.59	0.85
1:B:564:GLN:HE21	1:B:564:GLN:HA	1.41	0.85
1:B:1114:ILE:HG21	1:B:1138:TYR:CD2	2.09	0.85
1:C:105:ILE:HD11	1:C:241:LEU:CD1	2.03	0.85
1:B:741:TYR:CE1	1:B:966:LEU:CD1	2.54	0.85
1:B:826:VAL:HG21	1:B:1057:PRO:CG	2.06	0.85
1:A:275:PHE:CE1	1:A:290:ASP:HB2	2.10	0.85
1:B:303:LEU:HD12	1:B:308:VAL:HG22	1.59	0.85
1:B:336:CYS:HG	1:B:361:CYS:HG	0.85	0.85
1:B:126:VAL:HB	1:B:175:PHE:CZ	2.11	0.84
1:C:969:ASN:O	1:C:969:ASN:ND2	2.10	0.84
1:C:58:PHE:CE2	1:C:275:PHE:HE2	1.95	0.84
1:C:303:LEU:HD11	1:C:313:TYR:CE2	2.12	0.84
1:C:472:ILE:HG22	1:C:490:PHE:HA	0.85	0.84
1:A:366:SER:O	1:A:370:ASN:N	2.10	0.84
1:A:388:ASN:CG	1:A:527:PRO:HD2	1.96	0.84
1:B:94:SER:HB2	1:B:264:ALA:O	1.77	0.84
1:B:485:GLY:O	1:B:488:CYS:HB2	1.77	0.84
1:C:303:LEU:HD12	1:C:308:VAL:HG13	1.60	0.84
1:C:380:TYR:HE2	1:C:412:PRO:HD2	1.38	0.84
1:C:770:ILE:HD11	1:C:1012:LEU:HD23	1.59	0.84
1:C:856:ASN:CG	1:C:966:LEU:HD12	1.98	0.84
1:C:905:ARG:HH12	1:C:1050:MET:HA	1.42	0.84
1:A:125:ASN:ND2	1:A:171:VAL:HG12	1.85	0.84
1:C:126:VAL:HG23	1:C:172:SER:CB	2.07	0.84
1:A:611:LEU:HB2	1:A:650:LEU:HD22	1.57	0.84
1:A:220:PHE:HE2	1:A:288:ALA:H	1.23	0.84
1:A:388:ASN:ND2	1:A:527:PRO:HD2	1.93	0.84
1:B:294:ASP:OD1	1:B:295:PRO:CD	2.22	0.84

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:104:TRP:HE3	1:B:119:ILE:HB	1.42	0.84
1:A:620:VAL:HG23	1:A:621:PRO:CD	2.03	0.83
1:A:773:GLU:OE2	1:A:1019:ARG:CZ	2.26	0.83
1:B:1082:CYS:SG	1:B:1132:ILE:HD11	2.17	0.83
1:C:380:TYR:CE2	1:C:412:PRO:HD2	2.11	0.83
1:C:655:HIS:HB2	1:C:694:ALA:O	1.78	0.83
1:A:391:CYS:HA	1:A:525:CYS:HB3	1.57	0.83
1:A:420:ASP:HB3	1:A:460:ASN:OD1	1.78	0.83
1:C:786:LYS:O	1:C:786:LYS:NZ	2.11	0.83
1:C:878:LEU:HD21	1:C:1052:PHE:HB3	1.59	0.83
1:B:472:ILE:HG23	1:B:489:TYR:O	1.78	0.83
1:C:100:ILE:HA	1:C:243:ALA:HB3	1.60	0.83
1:C:33:THR:HA	1:C:58:PHE:HE1	1.39	0.83
1:C:544:ASN:HD21	1:C:579:PRO:HG3	1.42	0.83
1:A:345:THR:CG2	1:A:346:ARG:N	2.39	0.83
1:C:1078:ALA:HB2	1:C:1133:VAL:HG11	1.61	0.83
1:A:96:GLU:CA	1:A:186:PHE:HD1	1.91	0.83
1:B:559:PHE:CE1	1:C:43:PHE:CD2	2.66	0.83
1:C:105:ILE:CG2	1:C:135:PHE:HE2	1.91	0.83
1:A:319:ARG:CG	1:A:592:PHE:CD1	2.61	0.83
1:A:324:GLU:O	1:A:539:VAL:HB	1.79	0.83
1:B:193:VAL:HG13	1:B:204:TYR:HB2	1.61	0.83
1:C:421:TYR:O	1:C:461:LEU:CD1	2.26	0.83
1:A:453:TYR:CE2	1:A:493:GLN:CG	2.62	0.83
1:B:770:ILE:CD1	1:B:1012:LEU:HD12	2.07	0.82
1:C:595:VAL:HG12	1:C:610:VAL:CG1	2.08	0.82
1:C:921:LYS:HA	1:C:921:LYS:CE	2.09	0.82
1:B:65:PHE:HB2	1:B:265:TYR:CZ	2.12	0.82
1:C:126:VAL:HG12	1:C:175:PHE:HZ	1.41	0.82
1:C:350:VAL:HG12	1:C:422:ASN:HB3	1.61	0.82
1:A:36:VAL:HG21	1:A:220:PHE:HZ	1.36	0.82
1:A:55:PHE:CD2	1:A:275:PHE:HD2	1.98	0.82
1:B:1116:THR:HB	1:B:1140:PRO:HD2	1.60	0.82
1:A:86:PHE:HD2	1:A:106:PHE:CE2	1.93	0.82
1:A:220:PHE:CE2	1:A:287:ASP:HA	2.14	0.82
1:B:107:GLY:CA	1:B:235:ILE:HG23	2.09	0.82
1:C:822:LEU:HD11	1:C:1061:VAL:HG21	1.60	0.82
1:A:64:TRP:HD1	1:A:266:TYR:HD1	1.23	0.82
1:A:729:VAL:CG2	1:A:1060:VAL:HG23	2.10	0.82
1:A:676:THR:CB	1:A:690:GLN:HE22	1.93	0.82
1:B:112:SER:OG	1:B:134:GLN:HG2	1.79	0.82

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:788:ILE:HG23	1:B:876:ALA:HB2	1.62	0.82
1:C:130:VAL:HB	1:C:168:PHE:O	1.80	0.82
1:A:970:PHE:CD2	1:A:999:GLY:HA3	2.14	0.82
1:B:858:LEU:HD12	1:B:959:LEU:HD12	1.61	0.82
1:B:112:SER:HB3	1:B:134:GLN:HG3	1.52	0.82
1:C:353:TRP:HZ3	1:C:423:TYR:HA	1.44	0.82
1:A:773:GLU:HG3	1:A:1019:ARG:HH21	1.44	0.82
1:B:97:LYS:N	1:B:186:PHE:CD1	2.47	0.82
1:A:125:ASN:HD21	1:A:171:VAL:HG13	0.65	0.81
1:B:813:SER:O	1:B:868:GLU:OE1	1.98	0.81
1:B:947:LYS:O	1:B:950:ASP:CG	2.17	0.81
1:A:101:ILE:HD12	1:A:101:ILE:H	1.45	0.81
1:A:1051:SER:OG	1:A:1064:HIS:HD2	1.61	0.81
1:B:106:PHE:HB2	1:B:117:LEU:CD2	2.10	0.81
1:B:712:ILE:CD1	1:B:1094:VAL:HG11	2.10	0.81
1:C:115:GLN:HA	1:C:115:GLN:HE21	1.45	0.81
1:B:298:GLU:CG	1:B:315:THR:HG21	2.10	0.81
1:B:308:VAL:H	1:B:602:THR:HB	1.45	0.81
1:C:355:ARG:NH2	1:C:396:TYR:CE2	2.47	0.81
1:C:1090:PRO:CA	1:C:1120:THR:HG22	2.10	0.81
1:C:366:SER:CB	1:C:388:ASN:OD1	2.29	0.81
1:A:564:GLN:HA	1:A:564:GLN:HE21	1.46	0.81
1:B:57:PRO:HA	1:B:273:ARG:NH1	1.95	0.81
1:A:58:PHE:HE1	1:A:275:PHE:CZ	1.98	0.81
1:C:126:VAL:HG23	1:C:172:SER:HB3	1.56	0.81
1:C:905:ARG:NH1	1:C:1050:MET:CA	2.43	0.81
1:A:370:ASN:HD22	1:A:371:SER:N	1.78	0.81
1:B:962:LEU:HD11	1:B:1007:TYR:CB	2.11	0.81
1:B:1116:THR:HB	1:B:1140:PRO:CD	2.09	0.81
1:A:986:PRO:N	1:A:987:PRO:HD2	1.96	0.81
1:A:1081:ILE:CG1	1:A:1095:PHE:CE2	2.64	0.81
1:C:29:THR:C	1:C:62:VAL:HG12	2.02	0.80
1:C:392:PHE:O	1:C:522:ALA:HB1	1.80	0.80
1:C:752:LEU:CD2	1:C:990:GLU:OE2	2.27	0.80
1:A:321:GLN:HA	1:A:321:GLN:HE21	1.44	0.80
1:A:516:GLU:N	1:A:516:GLU:OE1	2.13	0.80
1:B:1104:VAL:HG11	1:B:1119:ASN:HD21	1.44	0.80
1:B:1114:ILE:CG2	1:B:1138:TYR:CD2	2.61	0.80
1:C:328:ARG:NE	1:C:578:ASP:OD2	2.14	0.80
1:B:39:PRO:HG3	1:B:51:THR:HG21	1.60	0.80
1:A:141:LEU:N	1:A:242:LEU:O	2.12	0.80

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:85:PRO:CG	1:B:269:TYR:OH	2.28	0.80
1:C:615:VAL:HG23	1:C:649:CYS:HB2	1.61	0.80
1:C:726:ILE:HD13	1:C:1061:VAL:HG22	1.61	0.80
1:B:203:ILE:HB	1:B:227:VAL:HG23	1.62	0.80
1:A:1041:ASP:HB3	1:B:1030:SER:OG	1.81	0.80
1:C:105:ILE:HG21	1:C:135:PHE:CE2	2.17	0.80
1:A:86:PHE:CE2	1:A:106:PHE:HE2	1.99	0.80
1:A:453:TYR:CZ	1:A:493:GLN:HG3	2.16	0.80
1:B:115:GLN:CD	1:B:167:THR:HG21	2.02	0.80
1:B:555:SER:CB	1:B:586:ASP:CG	2.46	0.80
1:B:885:GLY:HA2	1:B:901:GLN:HE22	1.47	0.80
1:C:83:VAL:HG21	1:C:237:ARG:NE	1.97	0.80
1:A:365:TYR:O	1:A:369:TYR:N	2.14	0.80
1:B:303:LEU:HD11	1:B:308:VAL:HG13	1.63	0.80
1:C:497:PHE:CE1	1:C:507:PRO:CB	2.65	0.80
1:A:620:VAL:CG2	1:A:621:PRO:CD	2.58	0.80
1:B:365:TYR:HA	1:B:368:LEU:HD23	1.62	0.80
1:C:1117:THR:HG23	1:C:1139:ASP:OD1	1.82	0.80
1:A:57:PRO:CB	1:A:273:ARG:HE	1.94	0.79
1:C:352:ALA:CB	1:C:468:ILE:HG21	2.11	0.79
1:A:203:ILE:CG2	1:A:227:VAL:HG22	2.09	0.79
1:C:741:TYR:CE2	1:C:962:LEU:HD11	2.17	0.79
1:A:115:GLN:NE2	1:A:132:GLU:CG	2.44	0.79
1:A:435:ALA:CB	1:A:510:VAL:HG22	2.12	0.79
1:B:104:TRP:CZ3	1:B:119:ILE:HG22	2.08	0.79
1:B:341:VAL:HG22	1:B:356:LYS:HZ1	1.45	0.79
1:B:564:GLN:NE2	1:B:577:ARG:CD	2.31	0.79
1:C:390:LEU:HD11	1:C:392:PHE:HE2	1.47	0.79
1:A:31:SER:HB2	1:A:216:LEU:HD22	1.62	0.79
1:B:57:PRO:HB3	1:B:273:ARG:NH2	1.97	0.79
1:A:984:LEU:HD13	1:A:988:GLU:HG3	1.65	0.79
1:B:141:LEU:HB3	1:B:243:ALA:HB2	1.61	0.79
1:C:495:TYR:HD2	1:C:497:PHE:HE2	1.30	0.79
1:C:905:ARG:HH12	1:C:1050:MET:CA	1.95	0.79
1:A:166:CYS:HB2	1:A:169:GLU:OE2	1.80	0.79
1:A:755:GLN:O	1:C:968:SER:OG	2.00	0.79
1:B:130:VAL:HB	1:B:168:PHE:H	1.46	0.79
1:B:131:CYS:CB	1:B:133:PHE:CE2	2.43	0.79
1:C:126:VAL:CG1	1:C:175:PHE:HE1	1.81	0.79
1:A:86:PHE:CE2	1:A:106:PHE:CE2	2.70	0.79
1:A:470:THR:HB	1:A:492:LEU:HD11	1.65	0.79

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:741:TYR:CE1	1:A:966:LEU:CD2	2.65	0.79
1:C:429:PHE:HE1	1:C:514:SER:HB2	1.46	0.79
1:A:303:LEU:CD2	1:A:308:VAL:HG12	2.13	0.79
1:B:58:PHE:CD1	1:B:275:PHE:CZ	2.67	0.79
1:B:1081:ILE:HD12	1:B:1133:VAL:HG23	1.65	0.79
1:A:299:THR:OG1	1:A:597:VAL:HG21	1.82	0.79
1:A:319:ARG:CG	1:A:592:PHE:HD1	1.95	0.79
1:A:345:THR:CG2	1:A:346:ARG:H	1.93	0.79
1:A:310:LYS:HB2	1:A:600:PRO:O	1.82	0.79
1:A:675:GLN:HB2	1:A:693:ILE:CD1	2.13	0.79
1:C:352:ALA:CA	1:C:468:ILE:HG22	2.13	0.79
1:A:350:VAL:HG12	1:A:452:LEU:O	1.82	0.78
1:B:55:PHE:CA	1:B:270:LEU:HD21	2.10	0.78
1:B:1090:PRO:HB3	1:B:1095:PHE:CE1	2.18	0.78
1:C:400:PHE:CZ	1:C:410:ILE:HD12	2.18	0.78
1:B:599:THR:HG22	1:B:608:VAL:CG1	2.13	0.78
1:B:902:MET:HB3	1:B:916:LEU:CD2	2.13	0.78
1:C:326:ILE:HA	1:C:531:THR:HG21	1.62	0.78
1:C:805:ILE:CG2	1:C:878:LEU:CD1	2.61	0.78
1:C:32:PHE:CB	1:C:59:PHE:CE1	2.65	0.78
1:C:380:TYR:CE2	1:C:412:PRO:HD3	2.18	0.78
1:C:811:LYS:CD	1:C:820:ASP:OD2	2.31	0.78
1:A:676:THR:CB	1:A:690:GLN:NE2	2.47	0.78
1:B:274:THR:HB	1:B:291:CYS:SG	2.23	0.78
1:B:885:GLY:HA2	1:B:901:GLN:HE21	0.96	0.78
1:C:37:TYR:CA	1:C:223:LEU:CD2	2.62	0.78
1:A:115:GLN:NE2	1:A:115:GLN:HA	1.98	0.78
1:A:617:CYS:SG	1:A:644:GLN:CB	2.69	0.78
1:C:327:VAL:H	1:C:531:THR:CG2	1.96	0.78
1:A:67:ALA:HB3	1:A:263:ALA:HB3	1.66	0.78
1:A:168:PHE:CE2	1:A:230:PRO:HD2	2.19	0.78
1:B:34:ARG:HH12	1:B:191:GLU:HG2	1.46	0.78
1:B:387:LEU:HA	1:B:390:LEU:HD21	1.66	0.78
1:A:210:ILE:HD11	1:A:213:VAL:HB	1.66	0.78
1:A:762:GLN:OE1	1:C:961:THR:HG21	1.83	0.78
1:C:210:ILE:HD13	1:C:210:ILE:H	1.49	0.78
1:C:400:PHE:CE2	1:C:423:TYR:CE2	2.68	0.78
1:C:581:THR:HG22	1:C:583:GLU:CD	2.04	0.78
1:A:105:ILE:HG13	1:A:118:LEU:HD12	1.65	0.78
1:A:985:ASP:OD1	1:A:986:PRO:HD2	1.82	0.78
1:C:103:GLY:C	1:C:104:TRP:HE3	1.86	0.78

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:400:PHE:CE2	1:C:423:TYR:HD2	2.00	0.78
1:C:878:LEU:HG	1:C:1053:PRO:HD2	1.65	0.78
1:A:1081:ILE:HG13	1:A:1095:PHE:CE2	2.18	0.78
1:A:130:VAL:HG21	1:A:168:PHE:HB3	1.66	0.78
1:B:106:PHE:HZ	1:B:194:PHE:CD2	2.00	0.78
1:B:115:GLN:HE22	1:B:167:THR:CG2	1.96	0.78
1:C:274:THR:O	1:C:291:CYS:HB2	1.84	0.78
1:A:567:ARG:NH1	1:A:571:ASP:OD1	2.17	0.77
1:B:885:GLY:CA	1:B:901:GLN:NE2	2.23	0.77
1:B:110:LEU:HD22	1:B:135:PHE:CZ	2.19	0.77
1:A:31:SER:CB	1:A:216:LEU:HD22	2.13	0.77
1:A:342:PHE:CD1	1:A:511:VAL:HG21	2.18	0.77
1:A:128:ILE:HD13	1:A:229:LEU:HD21	1.66	0.77
1:A:326:ILE:HG21	1:A:534:VAL:HG22	1.66	0.77
1:A:552:LEU:CD2	1:A:587:ILE:HD13	2.06	0.77
1:A:985:ASP:OD1	1:A:986:PRO:CD	2.32	0.77
1:B:131:CYS:N	1:B:133:PHE:CE1	2.52	0.77
1:C:189:LEU:HG	1:C:191:GLU:OE2	1.84	0.77
1:A:370:ASN:HD22	1:A:371:SER:H	1.31	0.77
1:A:712:ILE:CD1	1:A:1094:VAL:HG21	2.15	0.77
1:B:16:VAL:CG1	1:B:158:ARG:HH22	1.97	0.77
1:B:97:LYS:N	1:B:186:PHE:HD1	1.82	0.77
1:B:743:CYS:O	1:B:977:LEU:HD13	1.85	0.77
1:A:1051:SER:OG	1:A:1064:HIS:CD2	2.38	0.77
1:B:1090:PRO:CB	1:B:1095:PHE:HE1	1.98	0.77
1:C:337:PRO:HD2	1:C:358:ILE:CD1	2.14	0.77
1:C:429:PHE:CE1	1:C:514:SER:HB2	2.19	0.77
1:A:102:ARG:NH2	1:A:179:LEU:HD22	1.99	0.77
1:A:888:PHE:CZ	1:A:1034:LEU:HD21	2.18	0.77
1:B:56:LEU:HD12	1:B:57:PRO:CD	2.15	0.77
1:B:65:PHE:CB	1:B:265:TYR:CZ	2.66	0.77
1:B:387:LEU:O	1:B:390:LEU:CG	2.27	0.77
1:A:471:GLU:O	1:A:491:PRO:HG3	1.84	0.77
1:C:220:PHE:HE1	1:C:286:THR:C	1.88	0.77
1:C:934:ILE:O	1:C:934:ILE:HD12	1.85	0.76
1:A:64:TRP:CE2	1:A:266:TYR:HE1	2.00	0.76
1:B:1083:HIS:HB2	1:B:1137:VAL:HG23	1.67	0.76
1:C:347:PHE:CB	1:C:401:VAL:HG23	2.15	0.76
1:B:131:CYS:CA	1:B:133:PHE:CZ	2.68	0.76
1:C:117:LEU:HD23	1:C:117:LEU:O	1.84	0.76
1:C:429:PHE:HE1	1:C:514:SER:CB	1.98	0.76

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:495:TYR:CD2	1:C:497:PHE:CE2	2.73	0.76
1:A:1031:GLU:OE1	1:A:1042:PHE:HD2	1.66	0.76
1:C:1083:HIS:HB2	1:C:1137:VAL:HG22	1.66	0.76
1:A:125:ASN:CG	1:A:171:VAL:HG13	2.05	0.76
1:A:805:ILE:O	1:A:816:SER:CB	2.34	0.76
1:B:105:ILE:HD12	1:B:241:LEU:CD1	1.91	0.76
1:C:34:ARG:CZ	1:C:219:GLY:O	2.33	0.76
1:C:117:LEU:HD21	1:C:119:ILE:HD13	1.67	0.76
1:C:805:ILE:HG22	1:C:878:LEU:CD1	2.14	0.76
1:B:104:TRP:CE3	1:B:119:ILE:HB	2.20	0.76
1:A:37:TYR:HD1	1:A:55:PHE:CE1	1.85	0.76
1:B:62:VAL:HG13	1:B:268:GLY:CA	2.16	0.76
1:B:825:LYS:HE2	1:B:944:ALA:H	1.50	0.76
1:B:365:TYR:CA	1:B:368:LEU:HD23	2.15	0.76
1:C:404:GLY:O	1:C:407:VAL:CG1	2.29	0.76
1:A:96:GLU:OE1	1:A:101:ILE:HD13	1.84	0.75
1:A:322:PRO:HG2	1:A:540:ASN:OD1	1.86	0.75
1:A:976:VAL:HG22	1:A:979:ASP:H	1.50	0.75
1:B:131:CYS:SG	1:B:133:PHE:CZ	2.78	0.75
1:C:220:PHE:CE1	1:C:286:THR:O	2.38	0.75
1:B:115:GLN:NE2	1:B:167:THR:HG21	1.99	0.75
1:B:726:ILE:HD12	1:B:1061:VAL:HG22	1.68	0.75
1:A:1102:TRP:CB	1:A:1135:ASN:HD21	1.93	0.75
1:B:125:ASN:HA	1:B:175:PHE:HE1	1.49	0.75
1:C:36:VAL:O	1:C:223:LEU:HD22	1.86	0.75
1:C:495:TYR:HD2	1:C:497:PHE:CE2	2.04	0.75
1:A:435:ALA:HB2	1:A:510:VAL:HG22	1.68	0.75
1:B:106:PHE:CB	1:B:235:ILE:CD1	2.50	0.75
1:C:1117:THR:CG2	1:C:1139:ASP:OD1	2.34	0.75
1:B:770:ILE:HD11	1:B:1012:LEU:CD1	2.12	0.75
1:C:421:TYR:O	1:C:461:LEU:HD11	1.84	0.75
1:A:403:ARG:HG3	1:A:495:TYR:OH	1.87	0.75
1:A:902:MET:HB3	1:A:916:LEU:HD11	1.67	0.75
1:C:39:PRO:HG3	1:C:51:THR:HG21	1.67	0.75
1:C:745:ASP:OD1	1:C:745:ASP:N	2.20	0.75
1:C:1048:HIS:ND1	1:C:1048:HIS:O	2.19	0.75
1:A:36:VAL:HG21	1:A:220:PHE:CE1	2.22	0.75
1:C:404:GLY:HA2	1:C:508:TYR:CD2	2.22	0.75
1:C:598:ILE:HD13	1:C:666:ILE:HD11	1.66	0.75
1:C:1078:ALA:HB1	1:C:1133:VAL:HG13	1.67	0.75
1:C:1090:PRO:HA	1:C:1120:THR:CG2	2.15	0.75

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:742:ILE:CD1	1:A:1001:LEU:CD2	2.65	0.74
1:A:791:THR:HG22	1:A:792:PRO:HD2	1.69	0.74
1:B:472:ILE:HG23	1:B:489:TYR:C	2.07	0.74
1:A:453:TYR:CZ	1:A:493:GLN:CG	2.70	0.74
1:B:97:LYS:H	1:B:186:PHE:HD1	1.35	0.74
1:B:105:ILE:CD1	1:B:241:LEU:HD21	2.13	0.74
1:B:1107:ARG:CZ	1:C:896:ILE:CD1	2.65	0.74
1:C:377:PHE:CD1	1:C:434:ILE:HD11	2.22	0.74
1:A:68:ILE:HA	1:A:261:GLY:O	1.85	0.74
1:B:726:ILE:HG22	1:B:948:LEU:HD21	1.69	0.74
1:B:743:CYS:O	1:B:977:LEU:CD1	2.35	0.74
1:C:126:VAL:HG22	1:C:172:SER:HB3	0.75	0.74
1:C:462:LYS:HA	1:C:462:LYS:CE	2.13	0.74
1:C:905:ARG:NH1	1:C:1049:LEU:O	2.19	0.74
1:C:1031:GLU:O	1:C:1035:GLY:O	2.04	0.74
1:B:117:LEU:HD23	1:B:117:LEU:O	1.87	0.74
1:A:328:ARG:NH1	1:A:578:ASP:OD2	2.20	0.74
1:B:559:PHE:HE1	1:C:43:PHE:CE2	2.04	0.74
1:C:108:THR:HG22	1:C:109:THR:HG23	1.70	0.74
1:C:210:ILE:HB	1:C:212:LEU:HD23	1.69	0.74
1:A:1081:ILE:HG13	1:A:1095:PHE:HE2	1.52	0.74
1:B:275:PHE:HE1	1:B:290:ASP:CB	2.00	0.74
1:C:115:GLN:HB3	1:C:233:ILE:CD1	2.16	0.74
1:C:436:TRP:CD1	1:C:509:ARG:HB3	2.23	0.74
1:A:866:THR:H	1:A:869:MET:HE3	1.52	0.74
1:B:351:TYR:HB3	1:B:422:ASN:ND2	2.02	0.74
1:A:83:VAL:O	1:A:84:LEU:HD23	1.88	0.74
1:A:322:PRO:HG3	1:A:549:THR:HG21	1.69	0.74
1:B:58:PHE:HE1	1:B:275:PHE:CE2	2.05	0.74
1:B:115:GLN:NE2	1:B:167:THR:HG23	2.02	0.74
1:B:152:TRP:HH2	1:B:245:HIS:CE1	2.06	0.74
1:C:805:ILE:CG2	1:C:878:LEU:HD11	2.18	0.74
1:C:905:ARG:HH12	1:C:1050:MET:CB	1.94	0.74
1:B:307:THR:HB	1:B:602:THR:HG21	1.69	0.74
1:B:1107:ARG:CZ	1:C:896:ILE:HD11	2.16	0.74
1:C:773:GLU:OE2	1:C:1019:ARG:CD	2.34	0.74
1:C:916:LEU:HD12	1:C:923:ILE:HD12	1.69	0.74
1:B:125:ASN:HB3	1:B:174:PRO:HA	1.70	0.73
1:B:1116:THR:HB	1:B:1140:PRO:CG	2.18	0.73
1:B:1116:THR:HB	1:B:1140:PRO:HG2	1.67	0.73
1:C:400:PHE:CZ	1:C:410:ILE:CD1	2.70	0.73

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:115:GLN:CB	1:C:233:ILE:HD12	2.18	0.73
1:A:774:GLN:NE2	1:A:774:GLN:HA	2.04	0.73
1:B:191:GLU:O	1:B:192:PHE:HD1	1.71	0.73
1:C:104:TRP:NE1	1:C:194:PHE:CZ	2.57	0.73
1:C:115:GLN:O	1:C:233:ILE:HD13	1.86	0.73
1:A:965:GLN:HA	1:A:965:GLN:HE21	1.54	0.73
1:C:355:ARG:NE	1:C:396:TYR:CE2	2.57	0.73
1:A:33:THR:CA	1:A:58:PHE:CE2	2.65	0.73
1:A:365:TYR:O	1:A:369:TYR:HB3	1.89	0.73
1:A:299:THR:OG1	1:A:597:VAL:CG2	2.36	0.73
1:A:388:ASN:HD21	1:A:527:PRO:CD	2.01	0.73
1:A:600:PRO:HD3	1:A:692:ILE:HD11	1.70	0.73
1:B:54:LEU:HD23	1:B:88:ASP:HB3	1.70	0.73
1:B:289:VAL:HG23	1:B:306:PHE:CZ	2.23	0.73
1:C:69:HIS:HA	1:C:78:ARG:O	1.88	0.73
1:C:277:LEU:HD13	1:C:285:ILE:HD13	1.70	0.73
1:A:742:ILE:CD1	1:A:1001:LEU:HD23	2.18	0.73
1:C:37:TYR:CA	1:C:223:LEU:HD21	2.18	0.73
1:C:208:THR:HG22	1:C:210:ILE:HD13	1.71	0.73
1:A:1002:GLN:HA	1:A:1002:GLN:HE21	1.54	0.73
1:B:103:GLY:O	1:B:241:LEU:N	2.19	0.73
1:B:139:PRO:HB3	1:B:159:VAL:HG22	1.69	0.73
1:C:360:ASN:H	1:C:523:THR:HB	1.53	0.73
1:A:96:GLU:HA	1:A:186:PHE:CE1	2.24	0.73
1:C:520:ALA:HB1	1:C:521:PRO:CD	2.16	0.73
1:C:786:LYS:HA	1:C:786:LYS:HE2	1.71	0.73
1:B:351:TYR:HB3	1:B:422:ASN:HD22	1.54	0.73
1:B:858:LEU:HD12	1:B:959:LEU:CD1	2.18	0.73
1:C:220:PHE:HE1	1:C:286:THR:O	1.70	0.73
1:C:1117:THR:CG2	1:C:1139:ASP:CG	2.57	0.73
1:B:559:PHE:CE1	1:C:43:PHE:CE2	2.77	0.72
1:C:353:TRP:CZ3	1:C:423:TYR:HB2	2.23	0.72
1:C:791:THR:HG22	1:C:792:PRO:CD	2.18	0.72
1:A:791:THR:CG2	1:A:792:PRO:HD2	2.18	0.72
1:C:105:ILE:HG23	1:C:135:PHE:HE2	1.54	0.72
1:C:517:LEU:H	1:C:517:LEU:HD12	1.52	0.72
1:A:128:ILE:CD1	1:A:229:LEU:HD21	2.20	0.72
1:C:102:ARG:HH12	1:C:179:LEU:CD2	2.01	0.72
1:C:353:TRP:CZ3	1:C:423:TYR:HA	2.24	0.72
1:C:874:THR:HG23	1:C:1053:PRO:O	1.88	0.72
1:B:457:ARG:NH2	1:B:467:ASP:OD2	2.23	0.72

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:671:CYS:SG	1:C:697:MET:HB3	2.29	0.72
1:A:211:ASN:ND2	1:A:211:ASN:O	2.22	0.72
1:A:220:PHE:HD2	1:A:287:ASP:HA	1.46	0.72
1:B:130:VAL:HG12	1:B:167:THR:OG1	1.87	0.72
1:C:752:LEU:HD11	1:C:990:GLU:CD	2.08	0.72
1:A:521:PRO:HG3	1:A:564:GLN:HB2	1.72	0.72
1:C:37:TYR:HA	1:C:223:LEU:HD23	1.70	0.72
1:A:954:GLN:CB	1:A:1014:ARG:NH1	2.53	0.72
1:B:560:LEU:HB2	1:B:563:GLN:OE1	1.90	0.72
1:B:805:ILE:HG22	1:B:878:LEU:CD1	2.19	0.72
1:B:34:ARG:HH11	1:B:191:GLU:HG2	1.50	0.72
1:B:102:ARG:HG3	1:B:141:LEU:CD1	2.19	0.72
1:B:106:PHE:HZ	1:B:194:PHE:HD2	1.36	0.72
1:B:316:SER:O	1:B:595:VAL:HG22	1.88	0.72
1:A:403:ARG:CG	1:A:495:TYR:CE1	2.73	0.72
1:B:501:ASN:HB3	1:B:505:TYR:HB3	1.70	0.72
1:B:592:PHE:O	1:C:852:ALA:HB2	1.89	0.72
1:B:825:LYS:NZ	1:B:944:ALA:CB	2.52	0.72
1:B:909:ILE:HD12	1:B:1067:TYR:HD2	1.52	0.72
1:C:83:VAL:CG2	1:C:237:ARG:NH2	2.52	0.72
1:C:336:CYS:HB2	1:C:363:ALA:HB2	1.72	0.72
1:A:388:ASN:OD1	1:A:527:PRO:HD3	1.89	0.72
1:B:90:VAL:HG21	1:B:238:PHE:CE2	2.25	0.72
1:C:1078:ALA:HB2	1:C:1133:VAL:CG1	2.20	0.72
1:A:36:VAL:CG2	1:A:220:PHE:CE1	2.73	0.71
1:C:337:PRO:HG2	1:C:358:ILE:HD13	1.72	0.71
1:C:366:SER:H	1:C:388:ASN:HD21	1.36	0.71
1:A:379:CYS:HB2	1:A:384:PRO:HD3	1.72	0.71
1:B:612:TYR:O	1:B:648:GLY:HA3	1.88	0.71
1:C:1117:THR:HG23	1:C:1139:ASP:CG	2.10	0.71
1:B:65:PHE:CE2	1:B:84:LEU:HD11	2.24	0.71
1:B:543:PHE:CE2	1:B:576:VAL:HG11	2.25	0.71
1:B:962:LEU:CD1	1:B:1007:TYR:HB2	2.20	0.71
1:B:1145:LEU:HD11	1:C:1141:LEU:HG	1.72	0.71
1:C:187:LYS:HA	1:C:211:ASN:HB3	1.70	0.71
1:C:611:LEU:O	1:C:611:LEU:HD23	1.90	0.71
1:A:210:ILE:HD13	1:A:217:PRO:CB	2.18	0.71
1:A:563:GLN:NE2	1:B:43:PHE:HB2	2.05	0.71
1:B:308:VAL:O	1:B:602:THR:HG22	1.90	0.71
1:B:740:MET:HE3	1:B:740:MET:CA	2.20	0.71
1:B:1090:PRO:CA	1:B:1095:PHE:HE1	2.04	0.71

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:347:PHE:HB3	1:C:401:VAL:HG23	1.71	0.71
1:A:390:LEU:HD23	1:A:390:LEU:H	1.54	0.71
1:B:365:TYR:HA	1:B:368:LEU:CD2	2.20	0.71
1:B:805:ILE:HG22	1:B:878:LEU:HD13	1.71	0.71
1:C:560:LEU:O	1:C:563:GLN:NE2	2.24	0.71
1:C:856:ASN:C	1:C:858:LEU:HD12	2.11	0.71
1:B:34:ARG:HH12	1:B:191:GLU:CG	2.04	0.71
1:B:303:LEU:CD1	1:B:308:VAL:HG13	2.19	0.71
1:C:290:ASP:O	1:C:297:SER:HB3	1.90	0.71
1:C:970:PHE:CD2	1:C:999:GLY:CA	2.72	0.71
1:C:1136:THR:HG21	1:C:1138:TYR:CE2	2.26	0.71
1:B:541:PHE:CZ	1:B:587:ILE:HD13	2.25	0.71
1:B:164:ASN:C	1:B:165:ASN:HD22	1.93	0.71
1:C:115:GLN:HB3	1:C:233:ILE:HD12	1.71	0.71
1:C:581:THR:CG2	1:C:583:GLU:CD	2.59	0.71
1:B:1104:VAL:CG1	1:B:1119:ASN:HD21	2.03	0.71
1:C:104:TRP:CD1	1:C:194:PHE:CZ	2.79	0.71
1:C:472:ILE:CB	1:C:489:TYR:O	2.39	0.71
1:A:203:ILE:HG23	1:A:227:VAL:HG22	1.68	0.70
1:A:1102:TRP:CG	1:A:1135:ASN:ND2	2.59	0.70
1:C:103:GLY:C	1:C:104:TRP:CE3	2.65	0.70
1:C:338:PHE:CZ	1:C:365:TYR:CZ	2.78	0.70
1:B:389:ASP:OD1	1:B:390:LEU:N	2.25	0.70
1:B:1106:GLN:HE21	1:B:1111:GLU:CD	1.95	0.70
1:C:216:LEU:HD12	1:C:216:LEU:O	1.91	0.70
1:C:786:LYS:HA	1:C:786:LYS:CE	2.21	0.70
1:B:126:VAL:N	1:B:175:PHE:CE1	2.59	0.70
1:A:773:GLU:OE2	1:A:1019:ARG:NH2	2.24	0.70
1:B:325:SER:OG	1:B:540:ASN:HB2	1.92	0.70
1:C:92:PHE:HE1	1:C:94:SER:HB3	1.55	0.70
1:C:563:GLN:HE21	1:C:563:GLN:N	1.86	0.70
1:C:921:LYS:HA	1:C:921:LYS:HE2	1.72	0.70
1:A:822:LEU:HD13	1:A:1061:VAL:HG21	1.74	0.70
1:B:105:ILE:CD1	1:B:241:LEU:CD2	2.67	0.70
1:C:615:VAL:HB	1:C:620:VAL:CG1	2.22	0.70
1:C:805:ILE:HD11	1:C:1063:LEU:CD1	2.21	0.70
1:A:36:VAL:HB	1:A:220:PHE:HE1	1.55	0.70
1:A:370:ASN:ND2	1:A:371:SER:N	2.39	0.70
1:B:191:GLU:C	1:B:192:PHE:CD1	2.65	0.70
1:B:193:VAL:CG1	1:B:223:LEU:HD12	2.21	0.70
1:B:1011:GLN:HE21	1:B:1011:GLN:HA	1.54	0.70

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:102:ARG:HD2	1:C:141:LEU:HD13	1.73	0.70
1:A:108:THR:HA	1:A:236:THR:H	1.56	0.70
1:A:878:LEU:O	1:A:878:LEU:HD23	1.92	0.70
1:C:615:VAL:HG21	1:C:649:CYS:HB3	1.72	0.70
1:C:826:VAL:HG11	1:C:1057:PRO:CD	2.22	0.70
1:A:426:PRO:CG	1:A:463:PRO:HB3	2.22	0.70
1:A:675:GLN:HE21	1:A:693:ILE:HG13	1.57	0.70
1:B:131:CYS:N	1:B:133:PHE:HE1	1.90	0.70
1:B:615:VAL:HG13	1:B:619:GLU:HB2	1.74	0.70
1:A:336:CYS:CB	1:A:337:PRO:HD2	1.95	0.69
1:A:357:ARG:HG2	1:A:357:ARG:HH11	1.56	0.69
1:A:822:LEU:HD21	1:A:938:LEU:HD13	1.74	0.69
1:B:826:VAL:CA	1:B:945:LEU:HD11	2.22	0.69
1:B:970:PHE:CD2	1:B:999:GLY:HA3	2.26	0.69
1:C:97:LYS:O	1:C:97:LYS:HD3	1.92	0.69
1:A:1048:HIS:ND1	1:A:1048:HIS:O	2.25	0.69
1:B:55:PHE:N	1:B:270:LEU:HD22	2.07	0.69
1:B:274:THR:CB	1:B:291:CYS:SG	2.79	0.69
1:C:973:ILE:HG13	1:C:980:ILE:HD12	1.73	0.69
1:A:426:PRO:HG3	1:A:463:PRO:CB	2.21	0.69
1:A:676:THR:HB	1:A:690:GLN:HE22	1.58	0.69
1:B:130:VAL:CG2	1:B:231:ILE:HD13	2.22	0.69
1:C:347:PHE:O	1:C:451:TYR:HE2	1.74	0.69
1:C:353:TRP:CE2	1:C:466:ARG:HB3	2.28	0.69
1:C:902:MET:HB3	1:C:916:LEU:CD2	2.23	0.69
1:B:36:VAL:HG21	1:B:220:PHE:HE2	1.57	0.69
1:B:105:ILE:HD13	1:B:241:LEU:CG	2.20	0.69
1:C:555:SER:HB2	1:C:586:ASP:HB2	1.75	0.69
1:A:105:ILE:O	1:A:238:PHE:HA	1.91	0.69
1:A:902:MET:CB	1:A:916:LEU:HD11	2.22	0.69
1:A:334:ASN:ND2	1:A:334:ASN:H	1.88	0.69
1:A:934:ILE:HD12	1:A:938:LEU:HG	1.74	0.69
1:A:1101:HIS:HB3	1:A:1103:PHE:HE1	1.55	0.69
1:B:34:ARG:NH1	1:B:191:GLU:CG	2.54	0.69
1:B:933:LYS:HA	1:B:933:LYS:CE	2.23	0.69
1:A:226:LEU:HG	1:A:227:VAL:HG13	1.74	0.69
1:A:497:PHE:CD2	1:A:507:PRO:HB3	2.27	0.69
1:A:855:PHE:CZ	1:C:568:ASP:OD2	2.46	0.69
1:A:888:PHE:HZ	1:A:1034:LEU:CD2	2.03	0.69
1:B:298:GLU:CD	1:B:315:THR:HG22	2.05	0.69
1:C:472:ILE:HB	1:C:489:TYR:O	1.93	0.69

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:970:PHE:CE2	1:C:999:GLY:HA2	2.28	0.69
1:A:357:ARG:HG3	1:A:396:TYR:CE1	2.26	0.69
1:C:33:THR:HA	1:C:58:PHE:CD1	2.28	0.69
1:C:101:ILE:HD11	1:C:263:ALA:HB1	1.73	0.69
1:C:563:GLN:H	1:C:563:GLN:NE2	1.89	0.69
1:C:611:LEU:HB2	1:C:650:LEU:HD13	1.75	0.69
1:B:114:THR:N	1:B:132:GLU:OE1	2.26	0.69
1:B:805:ILE:CG2	1:B:878:LEU:HD11	2.22	0.69
1:C:902:MET:CB	1:C:916:LEU:HD21	2.23	0.69
1:C:909:ILE:CD1	1:C:1067:TYR:HD2	2.06	0.69
1:A:864:LEU:HD12	1:A:864:LEU:O	1.93	0.68
1:B:110:LEU:CD2	1:B:135:PHE:HE2	1.95	0.68
1:C:450:ASN:OD1	1:C:450:ASN:N	2.25	0.68
1:A:275:PHE:HE1	1:A:290:ASP:CB	2.04	0.68
1:C:378:LYS:HG3	1:C:433:VAL:HG12	1.75	0.68
1:C:380:TYR:CD2	1:C:412:PRO:HD3	2.29	0.68
1:A:1043:CYS:HB3	1:A:1048:HIS:CD2	2.28	0.68
1:C:1078:ALA:CB	1:C:1133:VAL:CG1	2.72	0.68
1:A:564:GLN:HA	1:A:564:GLN:NE2	2.08	0.68
1:A:1002:GLN:HA	1:A:1002:GLN:NE2	2.08	0.68
1:C:107:GLY:HA3	1:C:110:LEU:HD23	1.76	0.68
1:A:37:TYR:HD2	1:A:204:TYR:CD2	2.11	0.68
1:A:1090:PRO:HB3	1:A:1095:PHE:CE1	2.29	0.68
1:B:1107:ARG:NH2	1:C:896:ILE:HD11	2.08	0.68
1:C:105:ILE:CG2	1:C:135:PHE:CE2	2.73	0.68
1:C:327:VAL:H	1:C:531:THR:HG22	1.58	0.68
1:C:358:ILE:HG22	1:C:395:VAL:HB	1.76	0.68
1:A:1090:PRO:HB3	1:A:1095:PHE:HE1	1.59	0.68
1:A:68:ILE:HD12	1:A:262:ALA:HB2	1.75	0.68
1:A:973:ILE:HG13	1:A:992:GLN:OE1	1.93	0.68
1:B:55:PHE:CA	1:B:270:LEU:HD22	2.21	0.68
1:B:360:ASN:ND2	1:C:168:PHE:HD1	1.92	0.68
1:B:1081:ILE:HD12	1:B:1133:VAL:CG2	2.24	0.68
1:C:595:VAL:HG12	1:C:610:VAL:HG13	1.76	0.68
1:C:992:GLN:HA	1:C:992:GLN:NE2	2.05	0.68
1:A:57:PRO:CG	1:A:273:ARG:HE	2.05	0.68
1:A:902:MET:HG3	1:A:916:LEU:HD11	1.74	0.68
1:B:106:PHE:CZ	1:B:194:PHE:CD2	2.82	0.68
1:B:784:GLN:HE21	1:B:784:GLN:CA	2.02	0.68
1:C:346:ARG:HH21	1:C:450:ASN:HB2	1.58	0.68
1:C:819:GLU:OE2	1:C:1054:GLN:OE1	2.12	0.68

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:105:ILE:HD13	1:B:241:LEU:HD11	0.68	0.68
1:A:68:ILE:HB	1:A:262:ALA:HA	1.76	0.67
1:A:388:ASN:ND2	1:A:527:PRO:CD	2.56	0.67
1:C:498:GLN:O	1:C:501:ASN:HB3	1.94	0.67
1:C:541:PHE:CZ	1:C:587:ILE:HD13	2.29	0.67
1:B:193:VAL:HG11	1:B:223:LEU:HD12	1.74	0.67
1:B:825:LYS:HZ3	1:B:944:ALA:CB	2.06	0.67
1:C:411:ALA:HB1	1:C:412:PRO:HD2	1.76	0.67
1:C:905:ARG:NH1	1:C:1050:MET:HA	2.09	0.67
1:C:992:GLN:HE21	1:C:992:GLN:CA	2.06	0.67
1:A:906:PHE:CE1	1:A:1049:LEU:HD11	2.29	0.67
1:B:164:ASN:C	1:B:165:ASN:ND2	2.48	0.67
1:C:490:PHE:CG	1:C:491:PRO:HD2	2.29	0.67
1:C:1078:ALA:CB	1:C:1133:VAL:HG13	2.24	0.67
1:A:220:PHE:CE2	1:A:288:ALA:N	2.54	0.67
1:B:296:LEU:HD12	1:B:296:LEU:O	1.95	0.67
1:B:616:ASN:C	1:B:649:CYS:SG	2.72	0.67
1:C:378:LYS:HG3	1:C:433:VAL:CG1	2.23	0.67
1:C:662:CYS:SG	1:C:697:MET:CB	2.82	0.67
1:C:971:GLY:HA3	1:C:995:ARG:NH1	2.09	0.67
1:A:99:ASN:HD22	1:A:99:ASN:N	1.92	0.67
1:A:231:ILE:HG12	1:A:233:ILE:HG23	1.75	0.67
1:B:730:SER:O	1:B:1058:HIS:HB3	1.93	0.67
1:B:856:ASN:ND2	1:B:966:LEU:CD2	2.58	0.67
1:C:115:GLN:HA	1:C:115:GLN:NE2	2.09	0.67
1:C:329:PHE:CB	1:C:330:PRO:HD2	2.24	0.67
1:C:858:LEU:HD23	1:C:959:LEU:CD1	2.23	0.67
1:A:986:PRO:CD	1:A:987:PRO:HD2	2.25	0.67
1:B:616:ASN:ND2	3:B:1302:NAG:O7	2.28	0.67
1:C:1081:ILE:HD13	1:C:1133:VAL:CG2	2.24	0.67
1:A:55:PHE:CD2	1:A:275:PHE:CD2	2.82	0.67
1:A:916:LEU:O	1:A:916:LEU:HD23	1.94	0.67
1:A:1088:HIS:CD2	1:A:1137:VAL:HG21	2.29	0.67
1:B:642:VAL:HA	1:B:650:LEU:O	1.95	0.67
1:C:852:ALA:HB1	1:C:859:THR:CG2	2.24	0.67
1:A:296:LEU:HD12	1:A:296:LEU:O	1.94	0.67
1:A:390:LEU:HD23	1:A:390:LEU:N	2.09	0.67
1:A:497:PHE:CZ	1:A:507:PRO:HB3	2.28	0.67
1:B:1081:ILE:CD1	1:B:1133:VAL:CG2	2.73	0.67
1:C:97:LYS:HB2	1:C:186:PHE:HA	1.76	0.67
1:C:578:ASP:HB3	1:C:581:THR:HB	1.76	0.67

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:767:LEU:CD2	1:C:1008:VAL:CG2	2.65	0.67
1:A:676:THR:HB	1:A:690:GLN:NE2	2.10	0.67
1:A:822:LEU:CD2	1:A:938:LEU:HD13	2.25	0.67
1:B:106:PHE:CZ	1:B:194:PHE:HD2	2.13	0.67
1:B:131:CYS:C	1:B:133:PHE:CD1	2.68	0.67
1:B:275:PHE:CE1	1:B:290:ASP:HA	2.30	0.67
1:B:387:LEU:HA	1:B:390:LEU:HD23	1.75	0.67
1:C:401:VAL:HG21	1:C:509:ARG:NH1	2.10	0.67
1:C:520:ALA:CB	1:C:521:PRO:HD2	2.20	0.67
1:C:644:GLN:HA	1:C:644:GLN:NE2	2.09	0.67
1:C:310:LYS:HB2	1:C:600:PRO:O	1.95	0.67
1:C:352:ALA:HB1	1:C:468:ILE:HG21	1.74	0.67
1:A:203:ILE:HG23	1:A:227:VAL:HG23	1.64	0.66
1:A:521:PRO:HG3	1:A:564:GLN:CB	2.24	0.66
1:A:1031:GLU:OE1	1:A:1042:PHE:HE2	1.71	0.66
1:B:69:HIS:CE1	1:B:77:LYS:H	2.13	0.66
1:C:1083:HIS:HB2	1:C:1137:VAL:CG2	2.22	0.66
1:A:130:VAL:CG2	1:A:168:PHE:O	2.40	0.66
1:A:273:ARG:HH21	1:A:273:ARG:HG2	1.60	0.66
1:B:387:LEU:C	1:B:387:LEU:HD23	2.16	0.66
1:C:492:LEU:N	1:C:492:LEU:HD23	2.10	0.66
1:C:654:GLU:OE2	1:C:693:ILE:HG22	1.96	0.66
1:A:126:VAL:HG23	1:A:172:SER:CB	2.13	0.66
1:A:309:GLU:OE1	1:A:309:GLU:N	2.27	0.66
1:B:38:TYR:CD1	1:B:223:LEU:O	2.48	0.66
1:B:856:ASN:HD21	1:B:966:LEU:CD2	2.08	0.66
1:C:754:LEU:HD23	1:C:754:LEU:O	1.96	0.66
1:A:581:THR:HG22	1:A:583:GLU:HG2	1.78	0.66
1:B:69:HIS:HA	1:B:78:ARG:O	1.95	0.66
1:B:1031:GLU:O	1:B:1035:GLY:O	2.12	0.66
1:C:349:SER:HB2	1:C:351:TYR:CE2	2.31	0.66
1:B:909:ILE:HD12	1:B:1067:TYR:CD2	2.29	0.66
1:A:331:ASN:HB3	1:A:580:GLN:HE22	1.60	0.66
1:A:1081:ILE:HG12	1:A:1095:PHE:CE2	2.29	0.66
1:B:473:TYR:N	1:B:489:TYR:O	2.28	0.66
1:C:559:PHE:HZ	1:C:565:PHE:O	1.72	0.66
1:A:96:GLU:CD	1:A:101:ILE:HD13	2.16	0.66
1:A:612:TYR:HE1	1:A:651:ILE:HD12	1.59	0.66
1:B:275:PHE:CD1	1:B:290:ASP:HA	2.31	0.66
1:B:555:SER:HB2	1:B:586:ASP:OD2	1.95	0.66
1:B:673:SER:O	1:B:693:ILE:HG12	1.94	0.66

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1139:ASP:N	1:B:1140:PRO:HD3	2.10	0.66
1:C:32:PHE:HB3	1:C:59:PHE:HE1	1.53	0.66
1:A:480:CYS:HG	1:A:488:CYS:CB	2.07	0.66
1:A:597:VAL:HG12	1:A:610:VAL:HG22	1.78	0.66
1:A:773:GLU:CD	1:A:1019:ARG:NH2	2.48	0.66
1:B:1116:THR:HG21	1:B:1140:PRO:CG	1.85	0.66
1:A:954:GLN:CD	1:A:1014:ARG:HH12	1.98	0.66
1:B:141:LEU:N	1:B:242:LEU:O	2.26	0.66
1:B:501:ASN:HB3	1:B:505:TYR:CB	2.25	0.66
1:B:973:ILE:HD11	1:B:980:ILE:HD13	1.78	0.66
1:C:414:GLN:HA	1:C:414:GLN:NE2	2.10	0.66
1:B:126:VAL:N	1:B:175:PHE:CZ	2.64	0.65
1:B:1081:ILE:O	1:B:1088:HIS:HB2	1.96	0.65
1:A:605:SER:HB3	1:A:674:TYR:HE2	1.61	0.65
1:B:293:LEU:O	1:B:293:LEU:HD12	1.96	0.65
1:B:902:MET:CB	1:B:916:LEU:HD21	2.27	0.65
1:B:1116:THR:CG2	1:B:1140:PRO:HG3	1.81	0.65
1:C:103:GLY:CA	1:C:104:TRP:HE3	2.08	0.65
1:A:620:VAL:CB	1:A:621:PRO:HD2	2.23	0.65
1:B:84:LEU:HB3	1:B:85:PRO:HD2	1.79	0.65
1:B:330:PRO:HA	1:B:579:PRO:HB2	1.78	0.65
1:B:1093:GLY:HA3	1:B:1105:THR:O	1.97	0.65
1:C:347:PHE:CE2	1:C:509:ARG:NE	2.50	0.65
1:C:595:VAL:HG13	1:C:610:VAL:CG1	2.26	0.65
1:A:34:ARG:NE	1:A:191:GLU:OE2	2.28	0.65
1:A:101:ILE:HD12	1:A:101:ILE:N	2.10	0.65
1:A:1102:TRP:CB	1:A:1135:ASN:HD22	2.09	0.65
1:B:59:PHE:HD2	1:B:293:LEU:HD21	1.59	0.65
1:B:220:PHE:CE1	1:B:285:ILE:O	2.50	0.65
1:B:1116:THR:CA	1:B:1140:PRO:CD	2.75	0.65
1:C:1137:VAL:HG23	1:C:1137:VAL:O	1.96	0.65
1:A:58:PHE:CD1	1:A:275:PHE:CZ	2.85	0.65
1:A:906:PHE:HE1	1:A:1049:LEU:HD11	1.60	0.65
1:B:173:GLN:NE2	1:B:226:LEU:HD11	2.11	0.65
1:B:776:LYS:NZ	1:B:780:GLU:OE2	2.24	0.65
1:C:102:ARG:NH2	1:C:177:MET:CE	2.59	0.65
1:C:273:ARG:HG2	1:C:273:ARG:HH11	1.61	0.65
1:C:644:GLN:HE21	1:C:644:GLN:CA	2.05	0.65
1:C:115:GLN:CA	1:C:233:ILE:HD11	2.27	0.65
1:C:130:VAL:CG1	1:C:167:THR:OG1	2.44	0.65
1:C:210:ILE:H	1:C:210:ILE:CD1	2.09	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:270:LEU:HD12	1:C:270:LEU:N	2.12	0.65
1:C:448:ASN:HD21	1:C:451:TYR:HE1	1.44	0.65
1:C:1091:ARG:HB3	1:C:1119:ASN:O	1.96	0.65
1:A:81:ASN:ND2	1:A:242:LEU:HD23	2.05	0.65
1:A:902:MET:CG	1:A:916:LEU:HD11	2.26	0.65
1:B:1031:GLU:OE2	1:B:1039:ARG:HD2	1.97	0.65
1:B:1116:THR:HA	1:B:1140:PRO:CD	2.25	0.65
1:B:141:LEU:O	1:B:243:ALA:CA	2.42	0.65
1:B:329:PHE:HB3	1:B:330:PRO:HD2	1.78	0.65
1:B:933:LYS:HA	1:B:933:LYS:HZ1	1.61	0.65
1:C:69:HIS:CE1	1:C:77:LYS:H	2.15	0.65
1:C:765:ARG:HA	1:C:768:THR:HG22	1.78	0.65
1:A:64:TRP:NE1	1:A:266:TYR:CZ	2.60	0.65
1:A:82:PRO:O	1:A:84:LEU:HD21	1.97	0.65
1:A:133:PHE:CZ	1:A:160:TYR:CE1	2.85	0.65
1:B:726:ILE:CD1	1:B:1061:VAL:HG13	2.27	0.65
1:C:115:GLN:CB	1:C:233:ILE:CD1	2.74	0.65
1:C:355:ARG:NE	1:C:396:TYR:CD2	2.62	0.65
1:C:380:TYR:CD2	1:C:412:PRO:CD	2.80	0.65
1:C:825:LYS:NZ	1:C:942:ALA:HB2	2.12	0.65
1:A:86:PHE:HA	1:A:90:VAL:HG11	1.79	0.64
1:A:560:LEU:HB2	1:A:562:PHE:CE1	2.32	0.64
1:C:495:TYR:CD2	1:C:497:PHE:HE2	2.09	0.64
1:B:298:GLU:OE2	1:B:315:THR:CG2	2.33	0.64
1:B:318:PHE:HE2	1:B:615:VAL:CG2	2.10	0.64
1:C:96:GLU:HG2	1:C:101:ILE:HD13	1.79	0.64
1:C:104:TRP:HE3	1:C:104:TRP:N	1.95	0.64
1:C:615:VAL:CB	1:C:620:VAL:CG1	2.76	0.64
1:C:658:ASN:OD1	1:C:658:ASN:N	2.26	0.64
1:A:480:CYS:SG	1:A:488:CYS:HA	2.37	0.64
1:B:57:PRO:HB3	1:B:273:ARG:HH22	1.60	0.64
1:B:559:PHE:CE1	1:C:43:PHE:HD2	2.12	0.64
1:C:97:LYS:HD3	1:C:97:LYS:C	2.18	0.64
1:C:1082:CYS:CB	1:C:1132:ILE:HD11	2.24	0.64
1:A:551:VAL:C	1:A:552:LEU:HD23	2.18	0.64
1:B:102:ARG:CD	1:B:141:LEU:HD13	2.26	0.64
1:B:1142:GLN:HE21	1:B:1142:GLN:CA	2.02	0.64
1:A:38:TYR:HD1	1:A:223:LEU:O	1.79	0.64
1:A:403:ARG:HD3	1:A:495:TYR:HE1	1.62	0.64
1:A:825:LYS:HD2	1:A:938:LEU:O	1.97	0.64
1:B:105:ILE:HG13	1:B:118:LEU:HD13	1.77	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:695:TYR:O	1:B:695:TYR:HD1	1.80	0.64
1:A:712:ILE:HD12	1:A:1094:VAL:HG21	1.79	0.64
1:B:57:PRO:CG	1:B:273:ARG:NH1	2.59	0.64
1:B:615:VAL:CG1	1:B:619:GLU:HB2	2.27	0.64
1:C:401:VAL:HG22	1:C:509:ARG:HG3	1.78	0.64
1:A:321:GLN:HA	1:A:321:GLN:NE2	2.10	0.64
1:C:390:LEU:C	1:C:390:LEU:HD12	2.18	0.64
1:C:471:GLU:O	1:C:491:PRO:CB	2.46	0.64
1:C:718:PHE:HB2	1:C:1067:TYR:HE1	0.58	0.64
1:C:805:ILE:CG2	1:C:878:LEU:HD13	2.22	0.64
1:A:388:ASN:CG	1:A:527:PRO:CD	2.64	0.64
1:B:94:SER:HA	1:B:265:TYR:HA	1.79	0.64
1:B:1073:LYS:HB3	1:B:1073:LYS:NZ	2.13	0.64
1:C:977:LEU:CD2	1:C:993:ILE:CD1	2.75	0.64
1:A:102:ARG:HH22	1:A:179:LEU:HD22	1.62	0.64
1:B:308:VAL:H	1:B:602:THR:CB	2.11	0.64
1:C:351:TYR:CD2	1:C:452:LEU:O	2.46	0.64
1:A:115:GLN:OE1	1:A:131:CYS:N	2.30	0.64
1:A:322:PRO:CG	1:A:540:ASN:OD1	2.45	0.64
1:A:1116:THR:HB	1:A:1140:PRO:HD3	1.80	0.64
1:B:110:LEU:HB3	1:B:135:PHE:CD2	2.33	0.64
1:A:729:VAL:HG21	1:A:1060:VAL:CG2	2.19	0.63
1:A:806:LEU:HD23	1:A:807:PRO:HD3	1.80	0.63
1:B:168:PHE:HE2	1:B:170:TYR:HB2	1.63	0.63
1:B:502:GLY:O	1:B:505:TYR:N	2.30	0.63
1:C:436:TRP:CZ2	1:C:509:ARG:HD2	2.33	0.63
1:C:909:ILE:HD12	1:C:1067:TYR:CD2	2.26	0.63
1:C:916:LEU:CD1	1:C:923:ILE:HD12	2.28	0.63
1:C:220:PHE:CE1	1:C:287:ASP:CA	2.79	0.63
1:C:317:ASN:OD1	1:C:317:ASN:N	2.31	0.63
1:A:650:LEU:HD21	1:A:666:ILE:HD13	1.80	0.63
1:B:933:LYS:HA	1:B:933:LYS:NZ	2.12	0.63
1:B:1088:HIS:CE1	1:B:1122:VAL:CG2	2.80	0.63
1:C:390:LEU:HD12	1:C:390:LEU:O	1.97	0.63
1:C:612:TYR:HB2	1:C:615:VAL:HG22	1.80	0.63
1:C:874:THR:CG2	1:C:1053:PRO:O	2.46	0.63
1:C:909:ILE:HD13	1:C:1049:LEU:HD21	1.81	0.63
1:B:804:GLN:OE1	1:B:804:GLN:N	2.32	0.63
1:C:102:ARG:NH1	1:C:179:LEU:CD2	2.61	0.63
1:C:471:GLU:C	1:C:491:PRO:HD3	2.17	0.63
1:A:472:ILE:CD1	1:A:482:GLY:HA2	2.29	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:62:VAL:HG12	1:B:267:VAL:O	1.97	0.63
1:B:372:ALA:CB	1:B:374:PHE:CE2	2.74	0.63
1:B:633:TRP:HA	1:B:636:TYR:HB2	1.81	0.63
1:B:823:PHE:CZ	1:B:867:ASP:CG	2.72	0.63
1:C:115:GLN:CG	1:C:233:ILE:HD12	2.28	0.63
1:A:421:TYR:CD1	1:A:457:ARG:HB3	2.34	0.63
1:A:413:GLY:O	1:C:987:PRO:HG3	1.98	0.63
1:A:617:CYS:HG	1:A:644:GLN:CD	2.00	0.63
1:B:805:ILE:CG2	1:B:878:LEU:CD1	2.76	0.63
1:B:933:LYS:HA	1:B:933:LYS:HE3	1.80	0.63
1:C:115:GLN:HG3	1:C:233:ILE:HD12	1.81	0.63
1:A:203:ILE:HG21	1:A:227:VAL:HG23	1.61	0.63
1:A:731:MET:HB2	1:A:955:ASN:ND2	2.14	0.63
1:B:65:PHE:CA	1:B:265:TYR:HE1	2.07	0.63
1:B:565:PHE:HB2	1:C:42:VAL:HG12	1.80	0.63
1:B:611:LEU:HD22	1:B:666:ILE:HG23	1.80	0.63
1:A:934:ILE:HD12	1:A:934:ILE:O	1.99	0.63
1:A:992:GLN:HA	1:A:992:GLN:NE2	2.14	0.63
1:B:97:LYS:C	1:B:97:LYS:HD3	2.19	0.63
1:B:131:CYS:CB	1:B:133:PHE:CE1	2.53	0.63
1:B:1088:HIS:ND1	1:B:1122:VAL:HG23	2.13	0.63
1:C:352:ALA:HA	1:C:468:ILE:HG22	1.80	0.63
1:A:106:PHE:C	1:A:235:ILE:CG2	2.67	0.62
1:B:106:PHE:CB	1:B:235:ILE:HG21	2.28	0.62
1:B:535:LYS:NZ	1:B:554:GLU:OE2	2.32	0.62
1:B:971:GLY:O	1:B:995:ARG:NE	2.32	0.62
1:B:1011:GLN:HA	1:B:1011:GLN:NE2	2.13	0.62
1:C:326:ILE:HG13	1:C:326:ILE:O	1.98	0.62
1:A:117:LEU:C	1:A:117:LEU:HD23	2.19	0.62
1:A:328:ARG:NH1	1:A:578:ASP:CG	2.53	0.62
1:A:1050:MET:HG3	1:A:1065:VAL:CG2	2.28	0.62
1:B:110:LEU:HB3	1:B:135:PHE:HD2	1.63	0.62
1:C:104:TRP:NE1	1:C:194:PHE:HZ	1.96	0.62
1:C:1085:GLY:C	1:C:1126:CYS:SG	2.78	0.62
1:A:612:TYR:CE1	1:A:651:ILE:HD12	2.34	0.62
1:B:763:LEU:HD22	1:B:1008:VAL:CG2	2.28	0.62
1:B:905:ARG:HD2	1:B:1049:LEU:O	1.98	0.62
1:C:100:ILE:HG23	1:C:243:ALA:O	2.00	0.62
1:C:805:ILE:HG23	1:C:878:LEU:HD11	1.81	0.62
1:A:57:PRO:HB3	1:A:273:ARG:NE	2.10	0.62
1:A:118:LEU:HD22	1:A:135:PHE:CE1	2.34	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:521:PRO:HG3	1:A:564:GLN:CG	2.29	0.62
1:B:543:PHE:CD2	1:B:576:VAL:HG11	2.35	0.62
1:B:902:MET:HB3	1:B:916:LEU:HD22	1.80	0.62
1:C:902:MET:HB2	1:C:916:LEU:HD21	1.81	0.62
1:A:675:GLN:H	1:A:693:ILE:CD1	2.13	0.62
1:A:770:ILE:HD11	1:A:1012:LEU:CD2	2.29	0.62
1:A:888:PHE:HZ	1:A:1034:LEU:HD21	1.61	0.62
1:B:474:GLN:OE1	1:B:479:PRO:HB3	1.98	0.62
1:B:1031:GLU:OE1	1:B:1042:PHE:CE2	2.53	0.62
1:C:115:GLN:OE1	1:C:130:VAL:HG12	2.00	0.62
1:C:329:PHE:CE2	1:C:528:LYS:HB2	2.35	0.62
1:A:741:TYR:CZ	1:A:966:LEU:CD2	2.83	0.62
1:B:1097:SER:HB3	1:B:1102:TRP:CD2	2.34	0.62
1:A:34:ARG:NH2	1:A:217:PRO:O	2.33	0.62
1:A:403:ARG:HG3	1:A:495:TYR:CZ	2.34	0.62
1:A:417:LYS:NZ	1:A:455:LEU:O	2.32	0.62
1:A:693:ILE:HD13	1:A:693:ILE:H	1.62	0.62
1:B:277:LEU:HD12	1:B:277:LEU:N	2.08	0.62
1:B:320:VAL:HG23	1:B:591:SER:O	2.00	0.62
1:B:329:PHE:HB3	1:B:330:PRO:CD	2.30	0.62
1:C:615:VAL:CB	1:C:620:VAL:HG12	2.29	0.62
1:C:1001:LEU:O	1:C:1001:LEU:HD13	2.00	0.62
1:A:102:ARG:HG3	1:A:141:LEU:HD13	1.81	0.62
1:A:965:GLN:HA	1:A:965:GLN:NE2	2.15	0.62
1:A:36:VAL:HB	1:A:220:PHE:CE1	2.34	0.62
1:A:117:LEU:HB2	1:A:233:ILE:CD1	2.29	0.62
1:A:1081:ILE:HD11	1:A:1095:PHE:CD2	2.35	0.62
1:C:65:PHE:HD2	1:C:265:TYR:CE2	2.18	0.62
1:C:110:LEU:HD12	1:C:237:ARG:HH12	1.64	0.62
1:C:115:GLN:NE2	1:C:132:GLU:HG2	2.15	0.62
1:C:303:LEU:HD11	1:C:313:TYR:CD2	2.35	0.62
1:A:86:PHE:HA	1:A:90:VAL:CG1	2.29	0.61
1:A:715:PRO:CA	1:A:1071:GLN:O	2.46	0.61
1:B:85:PRO:HG2	1:B:269:TYR:CZ	2.35	0.61
1:C:497:PHE:CD1	1:C:507:PRO:CB	2.83	0.61
1:C:537:LYS:HB2	1:C:537:LYS:NZ	2.15	0.61
1:C:1116:THR:CB	1:C:1118:ASP:OD1	2.48	0.61
1:A:108:THR:OG1	1:A:234:ASN:O	2.12	0.61
1:B:94:SER:HB3	1:B:265:TYR:CB	2.30	0.61
1:C:400:PHE:HZ	1:C:410:ILE:HD12	1.63	0.61
1:A:117:LEU:HD21	1:A:119:ILE:HG13	1.81	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:366:SER:O	1:A:370:ASN:HB3	2.00	0.61
1:A:954:GLN:CD	1:A:1014:ARG:NH1	2.54	0.61
1:B:50:SER:HA	1:B:275:PHE:O	2.00	0.61
1:B:324:GLU:C	1:B:539:VAL:HG23	2.20	0.61
1:B:911:VAL:HG21	1:B:1067:TYR:CE2	2.35	0.61
1:A:189:LEU:HB3	1:A:208:THR:O	2.01	0.61
1:B:115:GLN:HE22	1:B:167:THR:HG22	1.64	0.61
1:B:885:GLY:HA3	1:B:901:GLN:HE21	1.58	0.61
1:C:31:SER:O	1:C:59:PHE:HA	2.00	0.61
1:C:338:PHE:CZ	1:C:365:TYR:CE1	2.88	0.61
1:C:378:LYS:CD	1:C:380:TYR:OH	2.48	0.61
1:C:472:ILE:HG22	1:C:490:PHE:N	2.16	0.61
1:B:38:TYR:HD1	1:B:223:LEU:O	1.81	0.61
1:B:902:MET:HB3	1:B:916:LEU:HD21	1.80	0.61
1:A:26:PRO:HB2	1:A:28:TYR:HE1	1.64	0.61
1:C:692:ILE:N	1:C:692:ILE:HD12	2.16	0.61
1:C:752:LEU:CD1	1:C:990:GLU:OE1	2.43	0.61
1:A:45:SER:O	1:A:47:VAL:HG13	2.01	0.61
1:A:106:PHE:CZ	1:A:194:PHE:CE2	2.88	0.61
1:B:564:GLN:NE2	1:B:564:GLN:HA	2.14	0.61
1:C:409:GLN:NE2	1:C:409:GLN:H	1.99	0.61
1:C:498:GLN:CG	1:C:499:PRO:HD2	2.30	0.61
1:C:654:GLU:OE2	1:C:693:ILE:CG2	2.49	0.61
1:A:96:GLU:CA	1:A:186:PHE:CD1	2.66	0.61
1:B:388:ASN:OD1	1:B:527:PRO:HG2	2.01	0.61
1:C:329:PHE:HE2	1:C:528:LYS:HB2	1.66	0.61
1:A:342:PHE:CZ	1:A:511:VAL:HB	2.34	0.61
1:A:742:ILE:HD13	1:A:1001:LEU:HG	1.82	0.61
1:A:973:ILE:HD12	1:A:984:LEU:HD11	1.83	0.61
1:C:210:ILE:HD13	1:C:210:ILE:N	2.14	0.61
1:C:380:TYR:CD2	1:C:412:PRO:HG3	2.36	0.61
1:C:1116:THR:OG1	1:C:1118:ASP:OD1	2.19	0.61
1:B:67:ALA:CB	1:B:263:ALA:HB3	2.18	0.61
1:B:69:HIS:CD2	1:B:77:LYS:HA	2.35	0.61
1:B:131:CYS:H	1:B:133:PHE:HE1	1.47	0.61
1:C:115:GLN:HE22	1:C:132:GLU:HG2	1.66	0.61
1:C:327:VAL:N	1:C:531:THR:CG2	2.63	0.61
1:C:921:LYS:HA	1:C:921:LYS:HE3	1.82	0.61
1:A:319:ARG:HD3	1:A:592:PHE:CE1	2.36	0.60
1:A:748:GLU:OE1	1:A:748:GLU:HA	2.01	0.60
1:A:802:PHE:CE1	1:A:927:PHE:CZ	2.79	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:825:LYS:CE	1:A:942:ALA:HA	2.30	0.60
1:B:104:TRP:CE3	1:B:119:ILE:CG2	2.84	0.60
1:B:422:ASN:HD21	1:B:454:ARG:H	1.49	0.60
1:B:748:GLU:CD	1:B:981:LEU:HD21	2.20	0.60
1:A:884:SER:HB2	1:A:893:ALA:HB1	1.84	0.60
1:B:672:ALA:HA	1:B:693:ILE:O	2.01	0.60
1:C:37:TYR:HB3	1:C:223:LEU:CD2	2.10	0.60
1:A:617:CYS:CA	1:A:649:CYS:SG	2.85	0.60
1:A:782:PHE:CZ	1:A:1060:VAL:HG22	2.35	0.60
1:B:90:VAL:HG21	1:B:238:PHE:CD2	2.36	0.60
1:B:115:GLN:CD	1:B:167:THR:CG2	2.65	0.60
1:B:388:ASN:OD1	1:B:527:PRO:CG	2.49	0.60
1:B:1114:ILE:HD12	1:B:1114:ILE:N	2.17	0.60
1:C:353:TRP:CE3	1:C:423:TYR:HB2	2.36	0.60
1:A:314:GLN:HG3	1:A:314:GLN:O	2.01	0.60
1:A:342:PHE:CZ	1:A:511:VAL:HG11	2.31	0.60
1:A:389:ASP:OD1	1:A:528:LYS:CE	2.49	0.60
1:A:1114:ILE:CG2	1:A:1138:TYR:HD2	2.14	0.60
1:B:641:ASN:O	1:B:651:ILE:HA	2.01	0.60
1:A:342:PHE:CZ	1:A:511:VAL:CG1	2.83	0.60
1:B:1011:GLN:HE21	1:B:1011:GLN:CA	2.11	0.60
1:C:861:LEU:HD22	1:C:861:LEU:N	2.16	0.60
1:A:885:GLY:HA2	1:A:901:GLN:OE1	2.02	0.60
1:B:34:ARG:HH12	1:B:191:GLU:CD	2.05	0.60
1:B:277:LEU:H	1:B:277:LEU:CD1	2.07	0.60
1:C:856:ASN:C	1:C:858:LEU:CD1	2.68	0.60
1:A:986:PRO:HD2	1:A:987:PRO:HD2	1.83	0.60
1:B:48:LEU:HB3	1:B:276:LEU:CD2	2.30	0.60
1:B:133:PHE:HB3	1:B:160:TYR:HB2	1.84	0.60
1:B:193:VAL:HG12	1:B:223:LEU:CD1	2.31	0.60
1:B:728:PRO:HD2	1:B:1021:SER:OG	2.01	0.60
1:B:1107:ARG:NH2	1:C:904:TYR:CD1	2.70	0.60
1:C:744:GLY:C	1:C:745:ASP:OD1	2.40	0.60
1:A:309:GLU:O	1:A:313:TYR:OH	2.14	0.60
1:B:15:CYS:SG	1:B:16:VAL:N	2.74	0.60
1:B:191:GLU:OE1	1:B:191:GLU:N	2.35	0.60
1:B:965:GLN:NE2	1:B:965:GLN:HA	2.16	0.60
1:C:110:LEU:CD1	1:C:237:ARG:HH12	2.14	0.60
1:C:118:LEU:HD11	1:C:120:VAL:HG22	1.84	0.60
1:C:299:THR:CG2	1:C:597:VAL:HB	2.32	0.60
1:A:86:PHE:CD2	1:A:106:PHE:CD2	2.89	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:877:LEU:HD13	1:A:1029:MET:HE1	1.84	0.60
1:A:1145:LEU:HD23	1:A:1145:LEU:O	2.02	0.60
1:B:97:LYS:HD3	1:B:97:LYS:O	2.01	0.60
1:B:303:LEU:HD12	1:B:308:VAL:CG2	2.30	0.60
1:B:707:TYR:HB3	1:C:792:PRO:HG3	1.82	0.60
1:C:69:HIS:NE2	1:C:77:LYS:HD3	2.17	0.60
1:C:368:LEU:HD12	1:C:368:LEU:N	2.16	0.60
1:C:1116:THR:HB	1:C:1118:ASP:OD1	2.02	0.60
1:A:84:LEU:HD23	1:A:84:LEU:N	2.13	0.60
1:A:743:CYS:O	1:A:749:CYS:CB	2.50	0.60
1:A:1114:ILE:HG21	1:A:1138:TYR:HD2	1.67	0.60
1:B:206:LYS:HB2	1:B:223:LEU:HA	1.83	0.60
1:B:1090:PRO:CB	1:B:1095:PHE:CE1	2.79	0.60
1:B:104:TRP:CE3	1:B:119:ILE:CB	2.85	0.59
1:A:366:SER:HA	1:A:369:TYR:HB3	1.84	0.59
1:B:95:THR:OG1	1:B:186:PHE:CB	2.51	0.59
1:B:786:LYS:HD2	1:B:786:LYS:N	2.17	0.59
1:B:866:THR:HG23	1:B:869:MET:H	1.67	0.59
1:B:1081:ILE:CD1	1:B:1133:VAL:HG23	2.32	0.59
1:C:208:THR:CG2	1:C:210:ILE:CD1	2.80	0.59
1:A:611:LEU:HD22	1:A:666:ILE:HG23	1.84	0.59
1:B:280:ASN:HB3	1:B:286:THR:CG2	2.33	0.59
1:C:395:VAL:HG21	1:C:524:VAL:HG21	1.84	0.59
1:C:448:ASN:O	1:C:449:TYR:CD1	2.55	0.59
1:A:328:ARG:NH2	1:A:578:ASP:OD2	2.34	0.59
1:A:536:ASN:HD22	1:A:536:ASN:N	2.01	0.59
1:A:731:MET:HB2	1:A:955:ASN:HD21	1.68	0.59
1:C:115:GLN:OE1	1:C:131:CYS:N	2.35	0.59
1:C:129:LYS:HE3	1:C:133:PHE:CE2	2.38	0.59
1:C:186:PHE:O	1:C:211:ASN:CB	2.50	0.59
1:C:204:TYR:HA	1:C:225:PRO:HA	1.83	0.59
1:C:403:ARG:HA	1:C:507:PRO:HA	1.82	0.59
1:C:595:VAL:HG11	1:C:610:VAL:HG11	1.81	0.59
1:C:615:VAL:HG21	1:C:620:VAL:HG11	1.84	0.59
1:A:322:PRO:CB	1:A:540:ASN:OD1	2.50	0.59
1:B:115:GLN:OE1	1:B:167:THR:HG21	2.01	0.59
1:B:1104:VAL:CG1	1:B:1119:ASN:ND2	2.59	0.59
1:C:118:LEU:C	1:C:119:ILE:HD12	2.23	0.59
1:C:472:ILE:CA	1:C:489:TYR:O	2.51	0.59
1:C:611:LEU:HD23	1:C:611:LEU:C	2.22	0.59
1:A:435:ALA:HB1	1:A:510:VAL:HG22	1.83	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:552:LEU:HD23	1:A:552:LEU:N	2.18	0.59
1:A:736:VAL:HG22	1:A:858:LEU:CD2	2.32	0.59
1:B:170:TYR:CZ	1:B:172:SER:HB3	2.38	0.59
1:B:324:GLU:C	1:B:539:VAL:CG2	2.69	0.59
1:B:773:GLU:OE2	1:B:1019:ARG:CZ	2.51	0.59
1:B:971:GLY:O	1:B:995:ARG:NH2	2.34	0.59
1:C:541:PHE:CZ	1:C:587:ILE:CD1	2.86	0.59
1:A:472:ILE:HD13	1:A:482:GLY:HA2	1.85	0.59
1:A:825:LYS:HE2	1:A:941:THR:O	2.03	0.59
1:A:1054:GLN:OE1	1:A:1054:GLN:HA	2.02	0.59
1:B:69:HIS:NE2	1:B:77:LYS:HD3	2.17	0.59
1:B:372:ALA:HB1	1:B:374:PHE:CD2	2.36	0.59
1:B:1114:ILE:HD12	1:B:1114:ILE:H	1.67	0.59
1:C:517:LEU:HD12	1:C:517:LEU:N	2.18	0.59
1:C:578:ASP:OD1	1:C:579:PRO:HD2	2.02	0.59
1:C:815:ARG:NH1	1:C:823:PHE:CG	2.62	0.59
1:B:90:VAL:HG11	1:B:238:PHE:CE2	2.38	0.59
1:B:140:PHE:HB2	1:B:242:LEU:O	2.03	0.59
1:B:461:LEU:HD21	1:B:467:ASP:CB	2.24	0.59
1:C:909:ILE:O	1:C:1108:ASN:ND2	2.35	0.59
1:C:1054:GLN:OE1	1:C:1054:GLN:HA	2.03	0.59
1:A:472:ILE:HD12	1:A:472:ILE:N	2.18	0.59
1:B:594:GLY:O	1:B:613:GLN:OE1	2.20	0.59
1:B:722:VAL:HA	1:B:1064:HIS:O	2.03	0.59
1:B:1072:GLU:OE1	1:B:1072:GLU:N	2.36	0.59
1:C:858:LEU:HD12	1:C:858:LEU:N	2.17	0.59
1:A:319:ARG:CG	1:A:592:PHE:CE1	2.86	0.58
1:A:758:SER:HG	1:C:965:GLN:CD	2.05	0.58
1:A:855:PHE:CZ	1:C:570:ALA:HB3	2.38	0.58
1:A:1027:THR:HG22	1:A:1042:PHE:CZ	2.38	0.58
1:B:216:LEU:HD23	1:B:266:TYR:CD2	2.37	0.58
1:B:583:GLU:OE1	1:B:583:GLU:HA	2.02	0.58
1:C:567:ARG:HH11	1:C:567:ARG:CG	2.10	0.58
1:C:595:VAL:HG13	1:C:610:VAL:HG12	1.85	0.58
1:C:611:LEU:CD1	1:C:666:ILE:HG23	2.32	0.58
1:C:822:LEU:HD21	1:C:945:LEU:CD2	2.28	0.58
1:A:214:ARG:O	1:A:266:TYR:OH	2.20	0.58
1:A:770:ILE:O	1:A:774:GLN:HG2	2.03	0.58
1:C:117:LEU:HD21	1:C:119:ILE:CD1	2.33	0.58
1:C:187:LYS:NZ	1:C:211:ASN:HD21	2.00	0.58
1:C:1083:HIS:CB	1:C:1137:VAL:HG21	2.30	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:118:LEU:HB2	1:A:135:PHE:HZ	1.68	0.58
1:B:715:PRO:HG2	1:B:1108:ASN:O	2.03	0.58
1:C:48:LEU:N	1:C:48:LEU:HD12	2.18	0.58
1:C:360:ASN:N	1:C:523:THR:HB	2.18	0.58
1:C:786:LYS:NZ	1:C:786:LYS:HA	2.19	0.58
1:A:365:TYR:O	1:A:369:TYR:HB2	2.03	0.58
1:A:471:GLU:OE1	1:A:471:GLU:HA	2.03	0.58
1:B:126:VAL:HG12	1:B:173:GLN:HB3	1.86	0.58
1:C:353:TRP:CZ3	1:C:423:TYR:HD1	2.20	0.58
1:A:275:PHE:CE1	1:A:290:ASP:CB	2.83	0.58
1:B:126:VAL:CG1	1:B:173:GLN:HB3	2.33	0.58
1:C:734:THR:HG21	1:C:1007:TYR:OH	2.04	0.58
1:A:699:LEU:N	1:A:699:LEU:HD23	2.19	0.58
1:A:755:GLN:HA	1:A:755:GLN:HE21	1.68	0.58
1:C:360:ASN:H	1:C:523:THR:CB	2.16	0.58
1:C:902:MET:HB3	1:C:916:LEU:HD22	1.85	0.58
1:C:973:ILE:HD12	1:C:983:ARG:HD3	1.84	0.58
1:A:220:PHE:CD2	1:A:287:ASP:OD1	2.57	0.58
1:B:341:VAL:HG22	1:B:356:LYS:HZ2	1.63	0.58
1:C:349:SER:OG	1:C:451:TYR:HA	2.04	0.58
1:C:716:THR:N	1:C:1071:GLN:O	2.30	0.58
1:C:822:LEU:CD2	1:C:945:LEU:HD21	2.27	0.58
1:A:564:GLN:HE21	1:A:564:GLN:CA	2.14	0.58
1:B:825:LYS:NZ	1:B:944:ALA:HB2	2.18	0.58
1:C:368:LEU:HD12	1:C:368:LEU:H	1.67	0.58
1:C:390:LEU:CD1	1:C:392:PHE:CD2	2.87	0.58
1:A:643:PHE:CE2	1:A:655:HIS:CG	2.92	0.58
1:A:675:GLN:NE2	1:A:693:ILE:HG13	2.19	0.58
1:B:164:ASN:O	1:B:165:ASN:ND2	2.32	0.58
1:B:245:HIS:HB3	1:B:259:THR:O	2.04	0.58
1:C:317:ASN:HA	1:C:594:GLY:HA2	1.85	0.58
1:C:353:TRP:CH2	1:C:423:TYR:CD1	2.91	0.58
1:C:378:LYS:CG	1:C:433:VAL:CG1	2.82	0.58
1:A:115:GLN:HE21	1:A:132:GLU:HG3	1.62	0.58
1:A:210:ILE:CD1	1:A:217:PRO:HB3	2.23	0.58
1:A:785:VAL:HG11	1:A:877:LEU:CD2	2.13	0.58
1:A:884:SER:CB	1:A:893:ALA:HB1	2.34	0.58
1:A:329:PHE:CD1	1:A:391:CYS:SG	2.97	0.57
1:B:336:CYS:N	1:B:362:VAL:O	2.34	0.57
1:C:355:ARG:CZ	1:C:396:TYR:CE2	2.87	0.57
1:C:546:LEU:HD23	1:C:546:LEU:C	2.24	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1004:LEU:O	1:C:1004:LEU:HD23	2.04	0.57
1:A:48:LEU:HD23	1:A:276:LEU:HD21	1.87	0.57
1:A:328:ARG:O	1:A:579:PRO:HG3	2.04	0.57
1:A:413:GLY:C	1:C:987:PRO:HG3	2.23	0.57
1:A:474:GLN:OE1	1:A:479:PRO:HB3	2.04	0.57
1:A:643:PHE:CD2	1:A:655:HIS:CB	2.86	0.57
1:B:310:LYS:CA	1:B:600:PRO:O	2.52	0.57
1:B:541:PHE:CZ	1:B:587:ILE:CD1	2.87	0.57
1:C:347:PHE:CB	1:C:401:VAL:CG2	2.83	0.57
1:C:977:LEU:CD2	1:C:993:ILE:HD12	2.33	0.57
1:A:472:ILE:HG23	1:A:489:TYR:O	2.05	0.57
1:A:934:ILE:CD1	1:A:938:LEU:HG	2.33	0.57
1:B:158:ARG:HG2	1:B:158:ARG:O	2.04	0.57
1:C:567:ARG:HD3	1:C:571:ASP:CG	2.24	0.57
1:C:779:GLN:O	1:C:783:ALA:HB3	2.04	0.57
1:C:1117:THR:HG21	1:C:1139:ASP:CG	2.23	0.57
1:A:105:ILE:HG13	1:A:118:LEU:CD1	2.32	0.57
1:A:906:PHE:HE1	1:A:1049:LEU:CD1	2.17	0.57
1:B:126:VAL:CB	1:B:175:PHE:HZ	2.14	0.57
1:C:661:GLU:H	1:C:661:GLU:CD	2.06	0.57
1:B:741:TYR:CZ	1:B:966:LEU:CD1	2.87	0.57
1:C:97:LYS:HB2	1:C:186:PHE:HD1	1.70	0.57
1:C:329:PHE:HB3	1:C:330:PRO:CD	2.32	0.57
1:C:908:GLY:O	1:C:1038:LYS:NZ	2.37	0.57
1:A:598:ILE:HD12	1:A:598:ILE:N	2.19	0.57
1:A:1072:GLU:N	1:A:1072:GLU:OE2	2.38	0.57
1:B:719:THR:OG1	1:B:1068:VAL:CG2	2.52	0.57
1:B:947:LYS:CA	1:B:950:ASP:OD2	2.49	0.57
1:C:103:GLY:CA	1:C:104:TRP:CE3	2.86	0.57
1:C:355:ARG:HE	1:C:396:TYR:HD2	1.49	0.57
1:C:355:ARG:CG	1:C:398:ASP:OD1	2.49	0.57
1:C:454:ARG:HD3	1:C:457:ARG:HB2	1.86	0.57
1:A:123:ALA:O	1:A:175:PHE:O	2.21	0.57
1:A:472:ILE:HA	1:A:491:PRO:HD3	1.85	0.57
1:A:521:PRO:HG3	1:A:564:GLN:HG3	1.86	0.57
1:B:55:PHE:HA	1:B:270:LEU:HD21	1.87	0.57
1:B:886:TRP:CH2	1:B:904:TYR:HD2	2.23	0.57
1:B:1122:VAL:O	1:B:1122:VAL:HG22	2.05	0.57
1:C:117:LEU:HD23	1:C:117:LEU:C	2.25	0.57
1:C:303:LEU:CD1	1:C:313:TYR:CE2	2.86	0.57
1:C:328:ARG:NH2	1:C:578:ASP:OD2	2.37	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:774:GLN:OE1	1:C:774:GLN:HA	2.03	0.57
1:C:985:ASP:OD1	1:C:985:ASP:N	2.32	0.57
1:A:58:PHE:CD1	1:A:275:PHE:HZ	2.23	0.57
1:A:986:PRO:N	1:A:987:PRO:CD	2.66	0.57
1:C:350:VAL:CG1	1:C:422:ASN:HB3	2.33	0.57
1:C:902:MET:CB	1:C:916:LEU:CD2	2.82	0.57
1:A:36:VAL:CB	1:A:220:PHE:HE1	2.18	0.57
1:A:709:ASN:OD1	1:A:709:ASN:N	2.36	0.57
1:A:1090:PRO:CB	1:A:1095:PHE:HE1	2.16	0.57
1:B:220:PHE:HE1	1:B:285:ILE:O	1.87	0.57
1:B:726:ILE:HG22	1:B:948:LEU:CD2	2.34	0.57
1:B:825:LYS:HZ2	1:B:944:ALA:HB2	1.69	0.57
1:C:99:ASN:N	1:C:99:ASN:HD22	2.03	0.57
1:C:378:LYS:HB2	1:C:380:TYR:HE1	1.70	0.57
1:C:909:ILE:CD1	1:C:1067:TYR:CD2	2.87	0.57
1:B:125:ASN:CA	1:B:175:PHE:HE1	2.15	0.57
1:B:715:PRO:CG	1:B:1069:PRO:HB3	2.34	0.57
1:A:402:ILE:HD11	1:A:418:ILE:HG21	1.86	0.56
1:B:95:THR:HG1	1:B:186:PHE:CB	2.18	0.56
1:C:349:SER:CB	1:C:351:TYR:CE2	2.88	0.56
1:A:403:ARG:HG3	1:A:495:TYR:CE1	2.39	0.56
1:A:1007:TYR:CE1	1:A:1011:GLN:OE1	2.57	0.56
1:B:105:ILE:HD11	1:B:241:LEU:CG	2.31	0.56
1:B:368:LEU:HD22	1:B:368:LEU:N	2.20	0.56
1:B:555:SER:CB	1:B:586:ASP:OD2	2.52	0.56
1:B:564:GLN:HE21	1:B:564:GLN:CA	2.12	0.56
1:B:1094:VAL:HG23	1:C:900:MET:CE	2.34	0.56
1:C:302:THR:OG1	1:C:315:THR:HG22	2.05	0.56
1:C:434:ILE:HG22	1:C:511:VAL:HG12	1.86	0.56
1:C:541:PHE:CE2	1:C:587:ILE:HD11	2.40	0.56
1:C:825:LYS:HZ1	1:C:942:ALA:HB2	1.70	0.56
1:C:856:ASN:CG	1:C:966:LEU:CD1	2.72	0.56
1:A:37:TYR:CD1	1:A:55:PHE:CD1	2.86	0.56
1:A:118:LEU:HD22	1:A:135:PHE:CZ	2.41	0.56
1:A:130:VAL:HG21	1:A:231:ILE:CD1	2.36	0.56
1:A:421:TYR:HB3	1:A:454:ARG:HD2	1.87	0.56
1:A:462:LYS:O	1:A:463:PRO:C	2.40	0.56
1:A:552:LEU:CD2	1:A:587:ILE:CD1	2.74	0.56
1:B:117:LEU:HG	1:B:119:ILE:CD1	2.36	0.56
1:B:422:ASN:HD21	1:B:453:TYR:HA	1.69	0.56
1:B:455:LEU:N	1:B:491:PRO:O	2.37	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:724:THR:HG22	1:B:1063:LEU:CD2	2.35	0.56
1:B:1031:GLU:OE2	1:B:1039:ARG:CD	2.53	0.56
1:C:187:LYS:HD2	1:C:211:ASN:HD21	1.55	0.56
1:C:189:LEU:HB3	1:C:208:THR:HB	1.87	0.56
1:C:338:PHE:HZ	1:C:365:TYR:CE1	2.23	0.56
1:C:377:PHE:HE2	1:C:384:PRO:HB3	1.70	0.56
1:C:567:ARG:HG3	1:C:567:ARG:NH1	2.07	0.56
1:C:1083:HIS:HB3	1:C:1137:VAL:HG21	1.86	0.56
1:A:269:TYR:N	1:A:269:TYR:CD1	2.74	0.56
1:A:964:LYS:HB2	1:A:964:LYS:NZ	2.21	0.56
1:B:94:SER:OG	1:B:101:ILE:HD12	2.04	0.56
1:B:310:LYS:CG	1:B:600:PRO:O	2.52	0.56
1:B:356:LYS:HB3	1:B:397:ALA:HB3	1.88	0.56
1:C:503:VAL:HA	1:C:506:GLN:HB3	1.88	0.56
1:C:204:TYR:CD2	1:C:225:PRO:HB3	2.40	0.56
1:C:223:LEU:CD2	1:C:223:LEU:H	2.18	0.56
1:C:560:LEU:HB3	1:C:562:PHE:CE1	2.40	0.56
1:C:617:CYS:HG	1:C:649:CYS:CB	2.17	0.56
1:A:57:PRO:HG3	1:A:273:ARG:NE	2.20	0.56
1:A:68:ILE:CB	1:A:262:ALA:HA	2.35	0.56
1:A:487:ASN:HA	1:A:489:TYR:HE1	1.71	0.56
1:B:57:PRO:CG	1:B:273:ARG:HH12	2.06	0.56
1:C:83:VAL:CB	1:C:237:ARG:HH21	2.18	0.56
1:C:126:VAL:HG21	1:C:172:SER:HB2	1.79	0.56
1:C:660:TYR:N	1:C:660:TYR:CD1	2.74	0.56
1:A:310:LYS:HG2	1:A:664:ILE:HD11	1.83	0.56
1:B:106:PHE:C	1:B:235:ILE:CG2	2.74	0.56
1:B:784:GLN:HA	1:B:784:GLN:NE2	2.08	0.56
1:A:34:ARG:NH2	1:A:217:PRO:HG2	2.20	0.56
1:A:983:ARG:O	1:A:983:ARG:HG3	2.06	0.56
1:B:119:ILE:N	1:B:119:ILE:HD12	2.21	0.56
1:B:131:CYS:SG	1:B:133:PHE:HZ	2.27	0.56
1:B:645:THR:OG1	1:B:648:GLY:N	2.31	0.56
1:B:909:ILE:O	1:B:1108:ASN:ND2	2.39	0.56
1:A:742:ILE:HD13	1:A:1001:LEU:CD2	2.36	0.56
1:A:973:ILE:HG21	1:A:983:ARG:NH2	2.21	0.56
1:A:1090:PRO:CB	1:A:1093:GLY:O	2.54	0.56
1:A:1145:LEU:HD23	1:A:1145:LEU:C	2.25	0.56
1:B:65:PHE:HB3	1:B:265:TYR:CZ	2.40	0.56
1:B:106:PHE:C	1:B:235:ILE:HG21	2.27	0.56
1:B:411:ALA:HB3	1:B:414:GLN:CG	2.36	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:186:PHE:O	1:C:211:ASN:HB3	2.05	0.56
1:A:1027:THR:HG22	1:A:1042:PHE:HZ	1.71	0.56
1:B:310:LYS:HE2	1:B:663:ASP:OD1	2.05	0.56
1:C:595:VAL:CG1	1:C:610:VAL:HG12	2.36	0.56
1:C:699:LEU:HD22	1:C:699:LEU:N	2.15	0.56
1:C:741:TYR:CE1	1:C:966:LEU:HG	2.41	0.56
1:C:1118:ASP:OD1	1:C:1118:ASP:N	2.39	0.56
1:A:105:ILE:CG1	1:A:118:LEU:CD1	2.84	0.55
1:A:133:PHE:HE1	1:A:160:TYR:CE1	2.15	0.55
1:A:357:ARG:HG3	1:A:396:TYR:CD1	2.41	0.55
1:A:856:ASN:ND2	1:A:966:LEU:CD1	2.69	0.55
1:A:862:PRO:HG3	1:C:647:ALA:HA	1.87	0.55
1:A:954:GLN:HB3	1:A:1014:ARG:CZ	2.33	0.55
1:A:1083:HIS:HB2	1:A:1137:VAL:HG23	1.88	0.55
1:B:130:VAL:HB	1:B:168:PHE:N	2.20	0.55
1:B:187:LYS:C	1:B:188:ASN:OD1	2.44	0.55
1:B:642:VAL:HG12	1:B:651:ILE:HG22	1.88	0.55
1:C:368:LEU:H	1:C:368:LEU:CD1	2.19	0.55
1:C:498:GLN:HG3	1:C:499:PRO:HD2	1.88	0.55
1:A:741:TYR:CE1	1:A:966:LEU:HD11	2.41	0.55
1:A:758:SER:OG	1:C:965:GLN:NE2	2.38	0.55
1:B:36:VAL:HG21	1:B:220:PHE:CE2	2.40	0.55
1:C:103:GLY:HA2	1:C:104:TRP:HE3	1.70	0.55
1:C:327:VAL:H	1:C:531:THR:HG21	1.70	0.55
1:C:1088:HIS:CE1	1:C:1137:VAL:HG21	2.40	0.55
1:A:273:ARG:HG2	1:A:273:ARG:NH2	2.22	0.55
1:A:903:ALA:N	1:A:916:LEU:HD13	2.21	0.55
1:B:130:VAL:HG21	1:B:231:ILE:HD13	1.87	0.55
1:B:826:VAL:CA	1:B:945:LEU:CD1	2.84	0.55
1:C:83:VAL:CB	1:C:237:ARG:NH2	2.70	0.55
1:C:361:CYS:O	1:C:524:VAL:HA	2.06	0.55
1:C:480:CYS:SG	1:C:485:GLY:CA	2.94	0.55
1:A:216:LEU:HD12	1:A:216:LEU:N	2.21	0.55
1:B:106:PHE:CB	1:B:117:LEU:HD22	2.27	0.55
1:B:275:PHE:HE1	1:B:290:ASP:HB2	1.70	0.55
1:A:654:GLU:HG3	1:A:693:ILE:HG22	1.87	0.55
1:C:360:ASN:HA	1:C:523:THR:HB	1.89	0.55
1:A:546:LEU:HD23	1:A:547:THR:N	2.21	0.55
1:A:985:ASP:OD1	1:A:986:PRO:HD3	2.07	0.55
1:B:388:ASN:ND2	1:B:527:PRO:HG2	2.21	0.55
1:B:584:ILE:N	1:B:584:ILE:HD12	2.22	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:661:GLU:OE1	1:C:661:GLU:N	2.24	0.55
1:A:329:PHE:CE1	1:A:391:CYS:SG	3.00	0.55
1:A:954:GLN:CG	1:A:1014:ARG:HH12	2.20	0.55
1:A:1043:CYS:CB	1:A:1048:HIS:CD2	2.89	0.55
1:B:474:GLN:OE1	1:B:479:PRO:CB	2.54	0.55
1:C:102:ARG:HH12	1:C:179:LEU:HD21	1.71	0.55
1:C:490:PHE:CD1	1:C:491:PRO:HD2	2.42	0.55
1:A:48:LEU:N	1:A:48:LEU:HD12	2.22	0.55
1:A:234:ASN:HD22	3:C:1301:NAG:C1	2.19	0.55
1:A:973:ILE:CD1	1:A:984:LEU:HD11	2.37	0.55
1:B:85:PRO:O	1:B:269:TYR:OH	2.19	0.55
1:B:117:LEU:HB2	1:B:233:ILE:CD1	2.37	0.55
1:B:1056:ALA:HB1	1:B:1057:PRO:HD2	1.89	0.55
1:A:334:ASN:H	1:A:334:ASN:HD22	1.55	0.55
1:A:752:LEU:HD12	1:A:993:ILE:HG21	1.89	0.55
1:B:62:VAL:CG1	1:B:267:VAL:O	2.55	0.55
1:B:103:GLY:O	1:B:241:LEU:HB2	2.07	0.55
1:B:555:SER:HB3	1:B:586:ASP:OD1	2.00	0.55
1:C:552:LEU:CD2	1:C:587:ILE:HG12	2.37	0.55
1:A:719:THR:OG1	1:A:1068:VAL:HG13	2.07	0.55
1:A:1102:TRP:CD1	1:A:1135:ASN:ND2	2.75	0.55
1:B:95:THR:OG1	1:B:186:PHE:HB3	2.05	0.55
1:C:69:HIS:CD2	1:C:77:LYS:HA	2.42	0.55
1:C:719:THR:HG23	1:C:1070:ALA:HB2	1.89	0.55
1:C:741:TYR:CE2	1:C:962:LEU:CD1	2.89	0.55
1:A:277:LEU:HD23	1:A:288:ALA:HB2	1.89	0.54
1:A:403:ARG:HD3	1:A:495:TYR:CE1	2.42	0.54
1:A:408:ARG:O	1:A:414:GLN:NE2	2.38	0.54
1:A:773:GLU:CG	1:A:1019:ARG:HH21	2.16	0.54
1:B:16:VAL:HG21	1:B:158:ARG:HH22	1.38	0.54
1:B:103:GLY:O	1:B:241:LEU:HD13	2.08	0.54
1:B:187:LYS:O	1:B:188:ASN:OD1	2.25	0.54
1:B:749:CYS:SG	1:B:997:ILE:HD11	2.47	0.54
1:B:916:LEU:CD1	1:B:923:ILE:HD12	2.37	0.54
1:C:822:LEU:HD23	1:C:945:LEU:HD11	1.88	0.54
1:A:130:VAL:CG1	1:A:231:ILE:CD1	2.72	0.54
1:A:874:THR:HG21	1:A:1055:SER:HB3	1.88	0.54
1:B:805:ILE:HG23	1:B:878:LEU:HD11	1.88	0.54
1:B:911:VAL:HG21	1:B:1067:TYR:HE2	1.72	0.54
1:C:204:TYR:N	1:C:204:TYR:CD1	2.75	0.54
1:C:366:SER:H	1:C:388:ASN:ND2	2.04	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:410:ILE:O	1:C:410:ILE:HG22	2.06	0.54
1:A:707:TYR:CD1	1:A:708:SER:N	2.75	0.54
1:A:870:ILE:O	1:A:874:THR:HG23	2.07	0.54
1:C:105:ILE:HD12	1:C:241:LEU:CD1	2.32	0.54
1:C:224:GLU:H	1:C:224:GLU:CD	2.11	0.54
1:C:347:PHE:O	1:C:451:TYR:CE2	2.59	0.54
1:A:68:ILE:HD12	1:A:262:ALA:CB	2.38	0.54
1:A:165:ASN:HD21	2:G:1:NAG:C1	2.20	0.54
1:A:480:CYS:HG	1:A:488:CYS:CA	2.20	0.54
1:A:878:LEU:HD23	1:A:878:LEU:C	2.27	0.54
1:B:104:TRP:CE3	1:B:104:TRP:N	2.75	0.54
1:B:125:ASN:HA	1:B:175:PHE:CD1	2.41	0.54
1:B:660:TYR:CD1	1:B:695:TYR:CD2	2.96	0.54
1:B:741:TYR:HE1	1:B:966:LEU:CD1	2.05	0.54
1:C:277:LEU:HD13	1:C:285:ILE:CD1	2.35	0.54
1:C:391:CYS:SG	1:C:525:CYS:CB	2.95	0.54
1:A:65:PHE:HB2	1:A:265:TYR:CE1	2.43	0.54
1:A:235:ILE:H	1:A:235:ILE:CD1	2.14	0.54
1:A:535:LYS:C	1:A:536:ASN:HD22	2.10	0.54
1:A:822:LEU:HD21	1:A:938:LEU:CD1	2.36	0.54
1:A:970:PHE:CE2	1:A:999:GLY:HA3	2.42	0.54
1:B:551:VAL:HG22	1:B:588:THR:O	2.07	0.54
1:B:1142:GLN:CA	1:B:1142:GLN:NE2	2.69	0.54
1:C:104:TRP:CE3	1:C:104:TRP:N	2.74	0.54
1:C:208:THR:CG2	1:C:210:ILE:HD13	2.37	0.54
1:C:223:LEU:HD23	1:C:223:LEU:O	2.08	0.54
1:C:303:LEU:HD21	1:C:313:TYR:CD2	2.43	0.54
1:C:738:CYS:SG	1:C:760:CYS:O	2.65	0.54
1:A:468:ILE:HG22	1:A:468:ILE:O	2.08	0.54
1:A:697:MET:O	1:A:697:MET:HG2	2.07	0.54
1:A:797:PHE:CE1	1:A:882:ILE:HG22	2.43	0.54
1:A:974:SER:H	1:A:980:ILE:HD11	1.73	0.54
1:A:1072:GLU:HG2	1:B:894:LEU:HD22	1.90	0.54
1:B:106:PHE:CD1	1:B:117:LEU:CD2	2.90	0.54
1:C:1083:HIS:ND1	1:C:1137:VAL:CG2	2.71	0.54
1:A:36:VAL:CG2	1:A:220:PHE:HE1	2.20	0.54
1:C:126:VAL:HG23	1:C:172:SER:HB2	1.82	0.54
1:C:826:VAL:O	1:C:826:VAL:HG22	2.08	0.54
1:C:970:PHE:N	1:C:970:PHE:HD1	2.06	0.54
1:A:36:VAL:CB	1:A:220:PHE:CE1	2.91	0.54
1:A:736:VAL:HG22	1:A:858:LEU:HD22	1.89	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1103:PHE:N	1:A:1103:PHE:CD1	2.76	0.54
1:B:280:ASN:HB3	1:B:286:THR:HG23	1.88	0.54
1:B:328:ARG:NH2	1:B:530:SER:OG	2.40	0.54
1:B:902:MET:CB	1:B:916:LEU:CD2	2.82	0.54
1:B:1080:ALA:O	1:B:1132:ILE:HG13	2.08	0.54
1:C:85:PRO:O	1:C:269:TYR:CZ	2.59	0.54
1:A:366:SER:O	1:A:370:ASN:CB	2.56	0.54
1:B:118:LEU:HG	1:B:120:VAL:HG23	1.89	0.54
1:C:552:LEU:HD23	1:C:587:ILE:HG12	1.89	0.54
1:C:915:VAL:HG23	1:C:1111:GLU:OE2	2.08	0.54
1:A:203:ILE:HG23	1:A:227:VAL:O	2.07	0.54
1:A:600:PRO:CD	1:A:692:ILE:HD11	2.36	0.54
1:B:126:VAL:CB	1:B:175:PHE:CZ	2.88	0.54
1:B:131:CYS:HB3	1:B:163:ALA:HB1	1.88	0.54
1:B:241:LEU:N	1:B:241:LEU:HD12	2.21	0.54
1:B:325:SER:OG	1:B:540:ASN:CB	2.54	0.54
1:B:472:ILE:HG22	1:B:489:TYR:O	2.03	0.54
1:B:719:THR:OG1	1:B:1068:VAL:HG22	2.07	0.54
1:B:822:LEU:HD23	1:B:1061:VAL:HG21	1.89	0.54
1:B:1047:TYR:HD2	1:B:1067:TYR:O	1.91	0.54
1:C:269:TYR:CD1	1:C:269:TYR:N	2.76	0.54
1:C:376:THR:HG23	1:C:378:LYS:HE3	1.90	0.54
1:A:326:ILE:HG13	1:A:326:ILE:O	2.08	0.53
1:A:726:ILE:CD1	1:A:945:LEU:HD23	2.33	0.53
1:A:1081:ILE:O	1:A:1088:HIS:HB2	2.08	0.53
1:B:326:ILE:HD13	1:B:534:VAL:HG12	1.90	0.53
1:B:368:LEU:O	1:B:372:ALA:CB	2.56	0.53
1:B:551:VAL:CG2	1:B:588:THR:HB	2.38	0.53
1:C:34:ARG:NH2	1:C:219:GLY:O	2.40	0.53
1:C:326:ILE:CA	1:C:531:THR:HG21	2.36	0.53
1:C:480:CYS:N	1:C:488:CYS:SG	2.81	0.53
1:C:754:LEU:HD23	1:C:754:LEU:C	2.28	0.53
1:A:643:PHE:CD2	1:A:655:HIS:HB2	2.43	0.53
1:B:130:VAL:O	1:B:131:CYS:SG	2.64	0.53
1:C:888:PHE:CZ	1:C:1034:LEU:CD2	2.92	0.53
1:C:1095:PHE:HZ	1:C:1120:THR:HG21	1.74	0.53
1:A:781:VAL:HG11	1:A:1060:VAL:HG21	1.90	0.53
1:A:888:PHE:CE1	1:A:1034:LEU:HD22	2.43	0.53
1:A:1090:PRO:HB2	1:A:1093:GLY:O	2.08	0.53
1:B:422:ASN:ND2	1:B:454:ARG:H	2.05	0.53
1:C:374:PHE:N	1:C:374:PHE:CD1	2.75	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:453:TYR:CD1	1:C:495:TYR:CD1	2.94	0.53
1:A:965:GLN:HE21	1:A:965:GLN:CA	2.12	0.53
1:A:1114:ILE:N	1:A:1114:ILE:HD12	2.23	0.53
1:B:793:PRO:HG2	1:B:794:ILE:HD12	1.89	0.53
1:C:102:ARG:NH2	1:C:177:MET:HE1	2.22	0.53
1:C:985:ASP:HB2	1:C:987:PRO:HD2	1.91	0.53
1:B:104:TRP:HB2	1:B:106:PHE:HE1	1.74	0.53
1:C:57:PRO:HB3	1:C:273:ARG:HE	1.74	0.53
1:C:289:VAL:HG23	1:C:306:PHE:CZ	2.43	0.53
1:C:471:GLU:O	1:C:491:PRO:HB3	2.09	0.53
1:C:797:PHE:HE2	1:C:882:ILE:HB	1.74	0.53
1:A:82:PRO:O	1:A:84:LEU:CD2	2.56	0.53
1:A:104:TRP:N	1:A:104:TRP:CE3	2.76	0.53
1:A:954:GLN:OE1	1:A:1014:ARG:NH1	2.41	0.53
1:A:1050:MET:O	1:A:1065:VAL:HG22	2.09	0.53
1:B:17:ASN:O	1:B:255:SER:HA	2.07	0.53
1:B:32:PHE:N	1:B:32:PHE:CD1	2.76	0.53
1:C:269:TYR:N	1:C:269:TYR:HD1	2.06	0.53
1:A:55:PHE:HB3	1:A:275:PHE:HE2	1.74	0.53
1:A:276:LEU:HD22	1:A:306:PHE:HE1	1.74	0.53
1:A:302:THR:HG21	1:A:315:THR:HA	1.90	0.53
1:B:303:LEU:CD1	1:B:308:VAL:HG22	2.36	0.53
1:B:961:THR:O	1:B:965:GLN:HG2	2.08	0.53
1:C:218:GLN:OE1	1:C:218:GLN:N	2.25	0.53
1:C:417:LYS:O	1:C:421:TYR:HB2	2.09	0.53
1:C:770:ILE:CD1	1:C:1012:LEU:HD23	2.34	0.53
1:C:905:ARG:CZ	1:C:1050:MET:HB3	2.31	0.53
3:C:1306:NAG:O7	3:C:1306:NAG:H3	2.08	0.53
1:A:41:LYS:O	1:C:563:GLN:CB	2.52	0.53
1:A:403:ARG:CD	1:A:495:TYR:HE1	2.21	0.53
1:A:675:GLN:HB2	1:A:693:ILE:HD11	1.90	0.53
1:A:712:ILE:HG13	1:B:896:ILE:HD12	1.90	0.53
1:A:815:ARG:NH1	1:A:823:PHE:CD1	2.77	0.53
1:A:1043:CYS:HB3	1:A:1048:HIS:HD2	1.69	0.53
1:B:97:LYS:HB2	1:B:186:PHE:HA	1.91	0.53
1:B:307:THR:CB	1:B:602:THR:HG21	2.38	0.53
1:B:797:PHE:CZ	1:B:882:ILE:HG21	2.44	0.53
1:C:32:PHE:N	1:C:32:PHE:CD1	2.76	0.53
1:C:37:TYR:CE1	1:C:55:PHE:CD1	2.97	0.53
1:C:37:TYR:CE1	1:C:55:PHE:CE1	2.97	0.53
1:C:105:ILE:HG21	1:C:135:PHE:CD2	2.44	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:125:ASN:N	1:C:125:ASN:HD22	2.04	0.53
1:C:392:PHE:CD1	1:C:392:PHE:N	2.76	0.53
1:C:466:ARG:O	1:C:466:ARG:HG3	2.08	0.53
1:C:617:CYS:SG	1:C:649:CYS:HB2	2.48	0.53
1:C:970:PHE:N	1:C:970:PHE:CD1	2.77	0.53
1:A:115:GLN:OE1	1:A:131:CYS:CA	2.57	0.53
1:A:310:LYS:CB	1:A:600:PRO:O	2.55	0.53
1:A:546:LEU:HD23	1:A:546:LEU:C	2.29	0.53
1:A:1050:MET:H	1:A:1065:VAL:HG23	1.74	0.53
1:B:712:ILE:HD12	1:B:1094:VAL:HG21	1.90	0.53
1:B:886:TRP:CH2	1:B:904:TYR:CD2	2.96	0.53
1:C:103:GLY:HA2	1:C:104:TRP:CE3	2.44	0.53
1:C:742:ILE:HD13	1:C:1001:LEU:HD23	1.90	0.53
1:A:457:ARG:HG3	1:A:459:SER:O	2.09	0.53
1:A:660:TYR:CE1	1:A:675:GLN:OE1	2.62	0.53
1:A:743:CYS:O	1:A:749:CYS:HB3	2.08	0.53
1:A:976:VAL:HG13	1:A:979:ASP:HB3	1.91	0.53
1:B:69:HIS:NE2	1:B:77:LYS:HA	2.24	0.53
1:B:131:CYS:O	1:B:133:PHE:HD1	1.83	0.53
1:B:191:GLU:C	1:B:192:PHE:HD1	2.10	0.53
1:B:822:LEU:HD11	1:B:938:LEU:CD1	2.26	0.53
1:B:1142:GLN:HA	1:B:1142:GLN:NE2	2.18	0.53
1:C:187:LYS:CD	1:C:211:ASN:HD21	2.13	0.53
1:C:858:LEU:HD21	1:C:963:VAL:CG2	2.38	0.53
1:A:121:ASN:ND2	1:A:190:ARG:HH22	2.07	0.52
1:A:298:GLU:OE2	1:A:316:SER:HB3	2.09	0.52
1:A:383:SER:OG	1:B:985:ASP:HB3	2.09	0.52
1:B:113:LYS:C	1:B:132:GLU:OE1	2.47	0.52
1:B:171:VAL:O	1:B:171:VAL:HG22	2.09	0.52
1:B:191:GLU:O	1:B:192:PHE:CD1	2.56	0.52
1:B:551:VAL:HG22	1:B:588:THR:HB	1.91	0.52
1:C:337:PRO:HD2	1:C:358:ILE:CG1	2.39	0.52
1:C:615:VAL:HB	1:C:620:VAL:HG13	1.90	0.52
1:C:1081:ILE:HD13	1:C:1133:VAL:HG23	1.90	0.52
1:A:379:CYS:CB	1:A:384:PRO:HD3	2.38	0.52
1:A:1033:VAL:CG2	1:A:1062:PHE:HE1	2.21	0.52
1:B:275:PHE:HE1	1:B:290:ASP:CA	2.22	0.52
1:B:797:PHE:CE2	1:B:882:ILE:HG21	2.45	0.52
1:C:180:GLU:HB3	1:C:182:LYS:HE2	1.92	0.52
1:C:1086:LYS:HB3	1:C:1122:VAL:CG2	2.39	0.52
1:A:1081:ILE:CG1	1:A:1095:PHE:CD2	2.92	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:709:ASN:N	1:B:709:ASN:OD1	2.41	0.52
1:C:105:ILE:HD13	1:C:241:LEU:CD1	2.25	0.52
1:C:409:GLN:HB2	1:C:418:ILE:HD11	1.91	0.52
1:C:471:GLU:CG	1:C:472:ILE:N	2.72	0.52
1:C:483:VAL:HG12	1:C:485:GLY:N	2.24	0.52
1:C:611:LEU:HD13	1:C:666:ILE:HG23	1.90	0.52
1:C:655:HIS:CB	1:C:694:ALA:O	2.55	0.52
1:B:97:LYS:HB2	1:B:186:PHE:HD1	1.75	0.52
1:B:140:PHE:CA	1:B:242:LEU:O	2.58	0.52
1:C:347:PHE:CD2	1:C:509:ARG:HD3	2.39	0.52
1:B:175:PHE:CD1	1:B:175:PHE:N	2.76	0.52
1:B:353:TRP:O	1:B:466:ARG:NH2	2.42	0.52
1:B:645:THR:HG1	1:B:648:GLY:H	1.55	0.52
1:B:1107:ARG:CZ	1:C:904:TYR:CD1	2.92	0.52
1:C:102:ARG:HH12	1:C:179:LEU:HD23	1.73	0.52
1:C:352:ALA:CA	1:C:468:ILE:CG2	2.84	0.52
1:C:393:THR:O	1:C:516:GLU:O	2.28	0.52
1:C:452:LEU:HB2	1:C:492:LEU:CD1	2.19	0.52
1:A:131:CYS:HB3	1:A:163:ALA:HB1	1.92	0.52
1:A:204:TYR:CE2	1:A:225:PRO:HG3	2.45	0.52
1:A:1081:ILE:HG21	1:A:1135:ASN:HB3	1.91	0.52
1:B:826:VAL:HA	1:B:945:LEU:CD1	2.40	0.52
1:C:333:THR:O	1:C:333:THR:HG22	2.09	0.52
1:C:1145:LEU:C	1:C:1145:LEU:HD13	2.30	0.52
1:A:115:GLN:HG3	1:A:130:VAL:HG12	1.92	0.52
1:A:353:TRP:H	1:A:466:ARG:HD2	1.75	0.52
1:B:18:LEU:HD11	1:B:244:LEU:HD11	1.92	0.52
1:B:57:PRO:CB	1:B:273:ARG:HH22	2.23	0.52
1:B:241:LEU:CD1	1:B:241:LEU:N	2.73	0.52
1:C:102:ARG:NH1	1:C:179:LEU:HD23	2.24	0.52
1:C:436:TRP:NE1	1:C:509:ARG:CB	2.65	0.52
1:A:65:PHE:CB	1:A:265:TYR:CZ	2.93	0.52
1:B:823:PHE:CE2	1:B:867:ASP:OD2	2.63	0.52
1:C:742:ILE:HD11	1:C:1001:LEU:HD22	1.92	0.52
1:A:407:VAL:HG21	1:A:508:TYR:HD2	1.75	0.52
1:A:774:GLN:HA	1:A:774:GLN:HE21	1.74	0.52
1:B:62:VAL:HG13	1:B:268:GLY:HA2	1.90	0.52
1:B:699:LEU:HD22	1:B:699:LEU:H	1.74	0.52
1:C:400:PHE:HZ	1:C:410:ILE:CD1	2.18	0.52
1:C:436:TRP:O	1:C:509:ARG:N	2.37	0.52
1:C:611:LEU:HD12	1:C:666:ILE:CG2	2.40	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1090:PRO:HB3	1:C:1095:PHE:CE1	2.45	0.52
1:A:106:PHE:CB	1:A:235:ILE:CG2	2.67	0.52
1:A:560:LEU:HD12	1:A:562:PHE:HE1	1.75	0.52
1:B:37:TYR:CE2	1:B:55:PHE:CE1	2.97	0.52
1:B:94:SER:HB3	1:B:265:TYR:HB3	1.92	0.52
1:B:106:PHE:CA	1:B:235:ILE:HG21	2.40	0.52
1:B:308:VAL:N	1:B:602:THR:HG21	2.25	0.52
1:C:422:ASN:CA	1:C:461:LEU:HD12	2.39	0.52
1:C:516:GLU:HB3	1:C:519:HIS:NE2	2.25	0.52
1:C:699:LEU:H	1:C:699:LEU:CD2	2.14	0.52
1:B:104:TRP:N	1:B:104:TRP:CD2	2.77	0.51
1:B:125:ASN:CA	1:B:175:PHE:CE1	2.85	0.51
1:A:29:THR:O	1:A:62:VAL:HG12	2.10	0.51
1:A:611:LEU:HG	1:A:611:LEU:O	2.09	0.51
1:A:1116:THR:HA	1:A:1138:TYR:H	1.75	0.51
1:B:32:PHE:HB3	1:B:59:PHE:CE1	2.45	0.51
1:B:331:ASN:HD22	2:J:1:NAG:C8	2.18	0.51
1:C:101:ILE:HD12	1:C:101:ILE:N	2.26	0.51
1:C:818:ILE:HD11	1:C:935:GLN:HB2	1.92	0.51
1:C:858:LEU:HD21	1:C:963:VAL:HG23	1.92	0.51
1:A:36:VAL:CG2	1:A:220:PHE:CZ	2.76	0.51
1:A:47:VAL:HG12	1:C:569:ILE:HG12	1.91	0.51
1:A:1083:HIS:CB	1:A:1137:VAL:HG23	2.39	0.51
1:B:55:PHE:O	1:B:270:LEU:CD2	2.19	0.51
1:B:472:ILE:CD1	1:B:490:PHE:HB2	2.40	0.51
1:B:715:PRO:HG3	1:B:1069:PRO:CB	2.40	0.51
1:B:980:ILE:HD12	1:B:980:ILE:O	2.10	0.51
1:C:303:LEU:CD1	1:C:308:VAL:HG13	2.36	0.51
1:C:559:PHE:CD2	1:C:563:GLN:O	2.63	0.51
1:A:265:TYR:N	1:A:265:TYR:CD1	2.78	0.51
1:A:1050:MET:HG3	1:A:1065:VAL:HG22	1.93	0.51
1:B:37:TYR:CE2	1:B:55:PHE:CD1	2.99	0.51
1:C:452:LEU:HB3	1:C:492:LEU:HD12	1.86	0.51
1:A:231:ILE:HG23	1:A:233:ILE:H	1.76	0.51
1:A:822:LEU:HD22	1:A:945:LEU:HD11	1.93	0.51
1:A:916:LEU:HD23	1:A:916:LEU:C	2.30	0.51
1:B:274:THR:HG22	1:B:291:CYS:SG	2.50	0.51
1:B:715:PRO:HG3	1:B:1069:PRO:HB3	1.92	0.51
1:B:1114:ILE:HG22	1:B:1138:TYR:HD2	1.67	0.51
1:C:119:ILE:HD12	1:C:119:ILE:N	2.26	0.51
1:A:215:ASP:OD1	1:A:215:ASP:N	2.38	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:308:VAL:N	1:B:602:THR:HB	2.20	0.51
1:B:1116:THR:CA	1:B:1140:PRO:HD3	2.29	0.51
1:C:91:TYR:HE1	1:C:93:ALA:HB2	1.76	0.51
1:C:100:ILE:O	1:C:243:ALA:N	2.44	0.51
1:C:902:MET:HB3	1:C:916:LEU:HD21	1.85	0.51
1:A:660:TYR:CD1	1:A:675:GLN:OE1	2.64	0.51
1:A:738:CYS:SG	1:A:760:CYS:O	2.68	0.51
1:A:885:GLY:CA	1:A:901:GLN:OE1	2.59	0.51
1:B:57:PRO:HG3	1:B:273:ARG:NH1	2.25	0.51
1:B:308:VAL:N	1:B:602:THR:CG2	2.74	0.51
1:B:388:ASN:HD21	1:B:527:PRO:HG2	1.75	0.51
1:B:559:PHE:HE1	1:C:43:PHE:HD2	1.43	0.51
1:B:671:CYS:O	1:B:694:ALA:HA	2.11	0.51
1:C:38:TYR:N	1:C:38:TYR:CD1	2.77	0.51
1:C:346:ARG:HH22	1:C:450:ASN:CG	2.13	0.51
1:C:1068:VAL:O	1:C:1068:VAL:HG23	2.11	0.51
1:C:1082:CYS:HB2	1:C:1132:ILE:HD13	1.89	0.51
1:A:38:TYR:CD1	1:A:223:LEU:O	2.63	0.51
1:A:108:THR:O	1:A:236:THR:HB	2.11	0.51
1:B:102:ARG:CB	1:B:141:LEU:HD13	2.41	0.51
1:B:117:LEU:HG	1:B:119:ILE:HD11	1.93	0.51
1:B:1116:THR:CB	1:B:1140:PRO:HD2	2.26	0.51
1:B:1125:ASN:OD1	1:B:1125:ASN:N	2.44	0.51
1:C:471:GLU:O	1:C:491:PRO:HG3	2.07	0.51
1:C:971:GLY:CA	1:C:995:ARG:NH1	2.74	0.51
1:A:33:THR:CA	1:A:58:PHE:CD2	2.88	0.51
1:A:81:ASN:CB	1:A:242:LEU:HD21	2.41	0.51
1:A:220:PHE:CE2	1:A:287:ASP:CA	2.93	0.51
1:A:600:PRO:CB	1:A:674:TYR:HD2	2.24	0.51
1:A:663:ASP:N	1:A:695:TYR:OH	2.44	0.51
1:A:725:GLU:OE1	1:A:1028:LYS:HE2	2.10	0.51
1:C:37:TYR:CD1	1:C:55:PHE:CE1	2.99	0.51
1:C:328:ARG:CZ	1:C:578:ASP:OD2	2.59	0.51
1:C:353:TRP:CZ3	1:C:423:TYR:CA	2.78	0.51
1:C:353:TRP:CE3	1:C:423:TYR:CG	2.98	0.51
1:C:360:ASN:HD22	1:C:523:THR:HG21	1.76	0.51
1:C:546:LEU:HD23	1:C:546:LEU:O	2.11	0.51
1:C:1072:GLU:OE1	1:C:1072:GLU:N	2.44	0.51
1:A:135:PHE:CD1	1:A:160:TYR:HB3	2.46	0.51
1:A:322:PRO:HG3	1:A:549:THR:CG2	2.39	0.51
1:A:480:CYS:HG	1:A:488:CYS:HA	1.75	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:719:THR:O	1:A:1068:VAL:HG12	2.11	0.51
1:A:726:ILE:HG21	1:A:948:LEU:HG	1.92	0.51
1:B:916:LEU:HD12	1:B:923:ILE:HD12	1.92	0.51
1:B:983:ARG:NH1	1:B:983:ARG:HB3	2.24	0.51
1:C:336:CYS:SG	1:C:361:CYS:O	2.53	0.51
1:C:615:VAL:HG22	1:C:649:CYS:HB3	1.82	0.51
1:A:65:PHE:CB	1:A:265:TYR:CE1	2.94	0.50
1:A:751:ASN:HD22	1:A:751:ASN:N	2.09	0.50
1:A:902:MET:HB3	1:A:916:LEU:CD1	2.41	0.50
1:C:91:TYR:HB3	1:C:268:GLY:O	2.11	0.50
1:C:537:LYS:HB2	1:C:537:LYS:HZ3	1.76	0.50
1:C:971:GLY:HA3	1:C:995:ARG:HH11	1.75	0.50
1:B:193:VAL:CG1	1:B:223:LEU:CD1	2.88	0.50
1:B:351:TYR:CE1	1:B:452:LEU:HB2	2.45	0.50
1:B:1097:SER:HB3	1:B:1102:TRP:CE2	2.46	0.50
1:B:1138:TYR:CD1	1:B:1140:PRO:HG3	2.46	0.50
1:C:934:ILE:HD12	1:C:934:ILE:C	2.31	0.50
1:C:971:GLY:O	1:C:995:ARG:HD3	2.11	0.50
1:A:521:PRO:CG	1:A:564:GLN:HG3	2.42	0.50
1:A:675:GLN:H	1:A:693:ILE:HD12	1.77	0.50
1:A:741:TYR:CE1	1:A:966:LEU:CG	2.94	0.50
1:B:46:SER:HA	1:B:279:TYR:O	2.12	0.50
1:B:396:TYR:N	1:B:514:SER:O	2.43	0.50
1:B:659:SER:HB3	1:B:698:SER:HB3	1.92	0.50
1:B:986:PRO:N	1:B:987:PRO:HD2	2.26	0.50
1:C:168:PHE:CE2	1:C:170:TYR:HB2	2.46	0.50
1:C:715:PRO:HA	1:C:1071:GLN:O	2.11	0.50
1:C:784:GLN:OE1	1:C:784:GLN:HA	2.12	0.50
1:A:822:LEU:HD22	1:A:945:LEU:HD21	1.93	0.50
1:B:173:GLN:HG3	1:B:173:GLN:O	2.12	0.50
1:B:856:ASN:HD21	1:B:966:LEU:HD23	1.77	0.50
1:B:1081:ILE:HG21	1:B:1135:ASN:HB2	1.94	0.50
1:C:103:GLY:O	1:C:241:LEU:N	2.33	0.50
1:C:400:PHE:CE2	1:C:410:ILE:HD12	2.47	0.50
1:A:133:PHE:CZ	1:A:160:TYR:CZ	3.00	0.50
1:A:727:LEU:HD11	1:A:1028:LYS:HD2	1.93	0.50
1:B:107:GLY:N	1:B:235:ILE:HG21	2.23	0.50
1:B:360:ASN:H	1:B:524:VAL:HG22	1.75	0.50
1:C:436:TRP:CD1	1:C:436:TRP:N	2.79	0.50
1:B:134:GLN:HE21	1:B:161:SER:HB2	1.77	0.50
1:B:968:SER:OG	1:C:757:GLY:HA3	2.11	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:224:GLU:OE1	1:C:224:GLU:N	2.37	0.50
1:C:805:ILE:CD1	1:C:1063:LEU:CD1	2.90	0.50
1:A:559:PHE:HE1	1:A:577:ARG:NE	2.10	0.50
1:B:718:PHE:HB3	1:B:1067:TYR:CE1	2.38	0.50
1:C:92:PHE:HE2	1:C:240:THR:HG1	1.59	0.50
1:C:406:GLU:OE1	1:C:406:GLU:HA	2.12	0.50
1:A:64:TRP:CE2	1:A:266:TYR:CE1	2.86	0.50
1:A:285:ILE:O	1:A:285:ILE:HG22	2.11	0.50
1:A:328:ARG:HH22	1:A:533:LEU:HB2	1.77	0.50
1:A:662:CYS:HA	1:A:695:TYR:OH	2.12	0.50
1:B:194:PHE:N	1:B:194:PHE:CD1	2.78	0.50
1:B:327:VAL:N	1:B:531:THR:OG1	2.43	0.50
1:C:220:PHE:CD1	1:C:286:THR:O	2.64	0.50
1:C:422:ASN:HA	1:C:461:LEU:HD12	1.94	0.50
1:A:547:THR:OG1	1:B:978:ASN:HB3	2.12	0.50
1:A:973:ILE:CG2	1:A:983:ARG:NH2	2.75	0.50
1:B:54:LEU:N	1:B:54:LEU:HD12	2.27	0.50
1:B:699:LEU:HD22	1:B:699:LEU:N	2.27	0.50
1:C:329:PHE:CB	1:C:330:PRO:CD	2.89	0.50
1:C:400:PHE:CE2	1:C:423:TYR:HE2	2.24	0.50
1:A:62:VAL:HG21	1:A:266:TYR:HB3	1.93	0.49
1:A:85:PRO:O	1:A:269:TYR:HE2	1.95	0.49
1:A:230:PRO:HG3	1:C:357:ARG:NH2	2.27	0.49
1:A:992:GLN:NE2	1:A:992:GLN:CA	2.74	0.49
1:C:391:CYS:SG	1:C:525:CYS:SG	3.08	0.49
1:C:400:PHE:O	1:C:400:PHE:HD1	1.95	0.49
1:C:421:TYR:O	1:C:461:LEU:HD12	2.12	0.49
1:C:654:GLU:OE2	1:C:691:SER:OG	2.28	0.49
1:A:31:SER:HB2	1:A:216:LEU:CD2	2.37	0.49
1:A:391:CYS:SG	1:A:544:ASN:HA	2.52	0.49
1:A:430:THR:HG21	1:A:517:LEU:HD21	1.94	0.49
1:B:192:PHE:CD1	1:B:192:PHE:N	2.78	0.49
1:B:295:PRO:HD3	1:B:633:TRP:N	2.27	0.49
1:B:616:ASN:HD22	3:B:1302:NAG:C7	2.24	0.49
1:C:65:PHE:HD2	1:C:265:TYR:HE2	1.60	0.49
1:C:187:LYS:HA	1:C:211:ASN:HD22	1.76	0.49
1:A:26:PRO:HB2	1:A:28:TYR:CE1	2.46	0.49
1:A:86:PHE:CD1	1:A:86:PHE:C	2.86	0.49
1:A:357:ARG:HG3	1:A:396:TYR:HE1	1.71	0.49
1:A:945:LEU:HD22	1:A:948:LEU:HD12	1.93	0.49
1:A:1013:ILE:HD13	1:B:1012:LEU:HB3	1.95	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:125:ASN:C	1:B:175:PHE:HE1	2.16	0.49
1:B:902:MET:HB2	1:B:916:LEU:HD21	1.92	0.49
1:C:330:PRO:HG3	1:C:525:CYS:SG	2.51	0.49
1:C:577:ARG:HB2	1:C:584:ILE:HD13	1.93	0.49
1:A:567:ARG:HD3	1:A:571:ASP:OD1	2.11	0.49
1:A:650:LEU:HD12	1:A:653:ALA:HB3	1.94	0.49
1:C:484:GLU:HG2	1:C:484:GLU:O	2.12	0.49
1:C:555:SER:CB	1:C:586:ASP:HB2	2.41	0.49
1:A:216:LEU:HD12	1:A:216:LEU:H	1.78	0.49
1:B:559:PHE:CD1	1:C:43:PHE:CD2	3.00	0.49
1:B:595:VAL:HG12	1:B:612:TYR:CD1	2.48	0.49
1:C:222:ALA:HB2	1:C:285:ILE:HB	1.94	0.49
1:A:695:TYR:CD1	1:A:695:TYR:N	2.81	0.49
1:A:804:GLN:O	1:A:816:SER:HB3	2.13	0.49
1:B:127:VAL:HG22	1:B:171:VAL:HG23	1.94	0.49
1:B:610:VAL:HG23	1:B:651:ILE:HG12	1.94	0.49
1:B:715:PRO:CA	1:B:1071:GLN:O	2.53	0.49
1:C:353:TRP:CH2	1:C:423:TYR:HD1	2.30	0.49
1:C:615:VAL:HG11	1:C:620:VAL:CG1	2.29	0.49
1:C:654:GLU:HG2	1:C:654:GLU:O	2.11	0.49
1:C:728:PRO:HB3	1:C:948:LEU:HD23	1.94	0.49
1:C:778:THR:HG22	1:C:865:LEU:HD12	1.94	0.49
1:C:1105:THR:HB	1:C:1111:GLU:O	2.12	0.49
1:A:83:VAL:CG1	1:A:237:ARG:NE	2.76	0.49
1:A:141:LEU:O	1:A:243:ALA:HA	2.12	0.49
1:A:797:PHE:CE1	1:A:882:ILE:CG2	2.95	0.49
1:B:59:PHE:HD2	1:B:293:LEU:CD2	2.25	0.49
1:B:610:VAL:CG2	1:B:651:ILE:HD11	2.43	0.49
1:B:983:ARG:HB3	1:B:983:ARG:HH11	1.77	0.49
1:C:1052:PHE:HE2	1:C:1065:VAL:CG2	2.25	0.49
1:A:1081:ILE:CG1	1:A:1095:PHE:HE2	2.15	0.49
1:B:938:LEU:HD22	1:B:944:ALA:HB1	1.94	0.49
1:C:38:TYR:H	1:C:38:TYR:HD1	1.61	0.49
1:C:117:LEU:HD11	1:C:119:ILE:HD11	1.94	0.49
1:C:216:LEU:HA	1:C:217:PRO:HD3	1.65	0.49
1:A:80:ASP:CG	1:A:82:PRO:HD3	2.33	0.49
1:A:92:PHE:C	1:A:92:PHE:CD1	2.86	0.49
1:A:413:GLY:O	1:C:987:PRO:CG	2.60	0.49
1:B:277:LEU:HD23	1:B:285:ILE:HD13	1.94	0.49
1:B:388:ASN:CG	1:B:527:PRO:HG2	2.34	0.49
1:B:816:SER:OG	1:B:819:GLU:HG3	2.13	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1090:PRO:N	1:B:1095:PHE:HE1	2.11	0.49
1:B:1093:GLY:CA	1:B:1105:THR:O	2.61	0.49
1:C:168:PHE:HE2	1:C:170:TYR:HB2	1.78	0.49
1:C:347:PHE:HB2	1:C:401:VAL:CG2	2.43	0.49
1:A:490:PHE:CE2	1:A:492:LEU:HB2	2.48	0.49
1:A:675:GLN:HB2	1:A:693:ILE:HD12	1.91	0.49
1:B:170:TYR:CE1	1:B:172:SER:HB3	2.47	0.49
1:C:83:VAL:HB	1:C:237:ARG:NH2	2.28	0.49
1:C:208:THR:CG2	1:C:210:ILE:HD11	2.42	0.49
1:C:318:PHE:CZ	1:C:615:VAL:CG1	2.96	0.49
1:C:449:TYR:HB3	1:C:494:SER:OG	2.13	0.49
1:C:662:CYS:SG	1:C:697:MET:HE3	2.53	0.49
1:C:741:TYR:HD1	1:C:856:ASN:HB3	1.76	0.49
1:C:826:VAL:HG13	1:C:826:VAL:O	2.13	0.49
1:A:806:LEU:CD2	1:A:807:PRO:HD3	2.43	0.48
1:B:131:CYS:CB	1:B:133:PHE:HZ	2.03	0.48
1:B:403:ARG:HG3	1:B:497:PHE:HE1	1.78	0.48
1:B:472:ILE:CG2	1:B:489:TYR:C	2.76	0.48
1:B:552:LEU:HD23	1:B:587:ILE:HG12	1.95	0.48
1:C:89:GLY:C	1:C:270:LEU:CD1	2.52	0.48
1:C:273:ARG:HG2	1:C:273:ARG:NH1	2.28	0.48
1:A:275:PHE:CD1	1:A:290:ASP:HA	2.48	0.48
1:A:331:ASN:CB	1:A:580:GLN:HE22	2.26	0.48
1:B:308:VAL:O	1:B:602:THR:N	2.43	0.48
1:C:352:ALA:HA	1:C:468:ILE:CG2	2.44	0.48
1:C:559:PHE:HD2	1:C:563:GLN:O	1.96	0.48
1:C:795:LYS:HB3	1:C:797:PHE:CE1	2.48	0.48
1:A:250:THR:HG22	1:A:259:THR:HG23	1.93	0.48
1:A:671:CYS:O	1:A:694:ALA:HA	2.14	0.48
1:A:712:ILE:HD11	1:B:896:ILE:HD11	1.94	0.48
1:A:967:SER:O	1:A:975:SER:HB2	2.13	0.48
1:B:86:PHE:C	1:B:86:PHE:CD1	2.87	0.48
1:B:236:THR:O	1:B:236:THR:HG22	2.12	0.48
1:B:329:PHE:CE1	1:B:544:ASN:HA	2.48	0.48
1:C:379:CYS:HA	1:C:432:CYS:HA	1.95	0.48
1:C:663:ASP:HB2	1:C:673:SER:HB3	1.94	0.48
1:C:971:GLY:CA	1:C:995:ARG:HH11	2.25	0.48
1:A:562:PHE:CD2	1:B:225:PRO:HG2	2.49	0.48
1:B:309:GLU:HA	1:B:309:GLU:OE2	2.13	0.48
1:B:589:PRO:HD3	1:C:855:PHE:CE2	2.48	0.48
1:B:610:VAL:HG23	1:B:651:ILE:CG1	2.44	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:965:GLN:NE2	1:B:965:GLN:CA	2.75	0.48
1:C:567:ARG:HD3	1:C:571:ASP:OD1	2.13	0.48
1:A:480:CYS:SG	1:A:488:CYS:CB	3.01	0.48
1:A:617:CYS:SG	1:A:644:GLN:CD	2.90	0.48
1:A:755:GLN:HE21	1:A:755:GLN:CA	2.25	0.48
1:B:197:ILE:HD11	1:B:202:LYS:HD2	1.94	0.48
1:B:65:PHE:HB2	1:B:265:TYR:CD1	2.25	0.48
1:B:125:ASN:N	1:B:125:ASN:OD1	2.45	0.48
1:B:661:GLU:OE1	1:B:661:GLU:HA	2.14	0.48
1:A:189:LEU:HB2	1:A:210:ILE:HG22	1.95	0.48
1:A:390:LEU:HG	1:A:392:PHE:CZ	2.48	0.48
1:A:1029:MET:SD	1:A:1033:VAL:HG21	2.53	0.48
1:B:329:PHE:CD1	1:B:544:ASN:HA	2.47	0.48
1:B:868:GLU:OE1	1:B:868:GLU:HA	2.13	0.48
1:C:99:ASN:N	1:C:99:ASN:ND2	2.62	0.48
1:C:223:LEU:CD2	1:C:223:LEU:N	2.77	0.48
1:C:377:PHE:CD1	1:C:434:ILE:CD1	2.96	0.48
1:C:1089:PHE:O	1:C:1120:THR:HG22	2.13	0.48
1:A:54:LEU:HD12	1:A:54:LEU:N	2.28	0.48
1:A:413:GLY:C	1:C:987:PRO:CG	2.82	0.48
1:A:605:SER:HB3	1:A:674:TYR:CE2	2.46	0.48
1:B:326:ILE:O	1:B:326:ILE:HG13	2.13	0.48
1:C:433:VAL:HG13	1:C:433:VAL:O	2.12	0.48
1:C:497:PHE:CD1	1:C:507:PRO:HB3	2.44	0.48
1:C:611:LEU:CD1	1:C:666:ILE:CG2	2.92	0.48
1:A:58:PHE:CE1	1:A:275:PHE:CE1	3.02	0.48
1:A:85:PRO:O	1:A:269:TYR:CE2	2.67	0.48
1:A:560:LEU:CD1	1:A:562:PHE:HE1	2.26	0.48
1:A:954:GLN:CG	1:A:1014:ARG:NH1	2.76	0.48
1:B:117:LEU:CB	1:B:233:ILE:HD12	2.44	0.48
1:B:472:ILE:HD13	1:B:490:PHE:HD1	1.79	0.48
1:B:819:GLU:OE2	1:B:1054:GLN:OE1	2.32	0.48
1:B:1090:PRO:HB3	1:B:1095:PHE:CD1	2.48	0.48
1:C:83:VAL:HB	1:C:237:ARG:HH21	1.79	0.48
1:C:395:VAL:CG2	1:C:524:VAL:HG21	2.44	0.48
1:C:471:GLU:HG2	1:C:472:ILE:N	2.28	0.48
1:C:617:CYS:SG	1:C:649:CYS:CB	3.01	0.48
1:C:797:PHE:CE2	1:C:882:ILE:HD12	2.49	0.48
1:C:1142:GLN:N	1:C:1143:PRO:CD	2.76	0.48
1:A:86:PHE:HE2	1:A:106:PHE:CE2	2.25	0.48
1:A:421:TYR:CE1	1:A:457:ARG:HB3	2.48	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:794:ILE:HD12	1:B:794:ILE:N	2.29	0.48
1:B:1081:ILE:CG2	1:B:1135:ASN:O	2.62	0.48
1:C:32:PHE:CB	1:C:59:PHE:HE1	2.20	0.48
1:C:69:HIS:NE2	1:C:77:LYS:HA	2.28	0.48
1:C:404:GLY:CA	1:C:508:TYR:CD2	2.95	0.48
1:A:413:GLY:CA	1:C:987:PRO:HG3	2.44	0.47
1:A:474:GLN:OE1	1:A:479:PRO:CB	2.62	0.47
1:A:643:PHE:CE2	1:A:655:HIS:CB	2.97	0.47
1:A:970:PHE:CE2	1:A:999:GLY:CA	2.97	0.47
1:B:55:PHE:HA	1:B:270:LEU:CD2	2.41	0.47
1:B:99:ASN:HD22	1:B:99:ASN:N	2.12	0.47
1:B:970:PHE:CE2	1:B:999:GLY:HA3	2.49	0.47
1:C:95:THR:HG23	1:C:95:THR:O	2.14	0.47
1:C:299:THR:HG21	1:C:597:VAL:HB	1.95	0.47
1:C:492:LEU:HD23	1:C:492:LEU:H	1.78	0.47
1:C:1095:PHE:HB3	1:C:1102:TRP:CZ3	2.49	0.47
1:A:33:THR:HG22	1:A:58:PHE:CD2	2.50	0.47
1:A:65:PHE:HE2	1:A:84:LEU:HD13	1.79	0.47
1:A:86:PHE:HB2	1:A:238:PHE:HD1	1.79	0.47
1:A:91:TYR:C	1:A:91:TYR:CD1	2.86	0.47
1:A:331:ASN:HB3	1:A:580:GLN:NE2	2.27	0.47
1:A:471:GLU:O	1:A:491:PRO:CG	2.57	0.47
1:A:855:PHE:HZ	1:C:568:ASP:OD2	1.94	0.47
1:B:34:ARG:HD3	1:B:91:TYR:OH	2.14	0.47
1:B:55:PHE:CD2	1:B:275:PHE:CD2	3.03	0.47
1:B:216:LEU:HD23	1:B:266:TYR:HD2	1.78	0.47
1:B:220:PHE:CD1	1:B:220:PHE:C	2.88	0.47
1:B:541:PHE:HZ	1:B:587:ILE:HD13	1.75	0.47
1:C:659:SER:HB3	1:C:696:THR:O	2.14	0.47
1:C:922:LEU:HD11	1:C:926:GLN:HE21	1.78	0.47
1:C:1086:LYS:HB3	1:C:1122:VAL:HG21	1.95	0.47
1:A:296:LEU:HB2	1:A:608:VAL:HG11	1.96	0.47
1:A:299:THR:HG22	1:A:308:VAL:HG11	1.96	0.47
1:A:403:ARG:HG2	1:A:495:TYR:CE1	2.48	0.47
1:A:480:CYS:CB	1:A:488:CYS:HG	2.27	0.47
1:B:62:VAL:CG1	1:B:267:VAL:C	2.82	0.47
1:B:106:PHE:CD1	1:B:117:LEU:HD21	2.49	0.47
1:B:190:ARG:HB3	1:B:192:PHE:CZ	2.49	0.47
1:B:405:ASP:N	1:B:504:GLY:O	2.46	0.47
1:B:675:GLN:HB3	1:B:693:ILE:CD1	2.44	0.47
1:B:900:MET:HG2	1:B:917:TYR:OH	2.14	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1094:VAL:HG23	1:C:900:MET:HE1	1.95	0.47
1:C:129:LYS:HE3	1:C:133:PHE:CZ	2.49	0.47
1:C:366:SER:HB3	1:C:388:ASN:CG	2.27	0.47
1:C:376:THR:HB	1:C:435:ALA:HB3	1.96	0.47
1:C:483:VAL:O	1:C:484:GLU:HB3	2.14	0.47
1:A:101:ILE:CD1	1:A:101:ILE:H	2.20	0.47
1:B:33:THR:HA	1:B:58:PHE:CD2	2.49	0.47
1:B:92:PHE:CD1	1:B:92:PHE:C	2.87	0.47
1:B:139:PRO:CB	1:B:159:VAL:HG22	2.41	0.47
1:B:170:TYR:CD1	1:B:170:TYR:C	2.87	0.47
1:B:919:ASN:C	1:B:919:ASN:HD22	2.17	0.47
1:C:215:ASP:OD1	1:C:215:ASP:N	2.38	0.47
1:C:353:TRP:NE1	1:C:466:ARG:HB3	2.29	0.47
1:C:400:PHE:CZ	1:C:410:ILE:HG13	2.48	0.47
1:C:858:LEU:CD2	1:C:963:VAL:CG2	2.92	0.47
1:A:107:GLY:CA	1:A:235:ILE:HG22	2.44	0.47
1:A:740:MET:CE	1:C:592:PHE:CE1	2.97	0.47
1:B:133:PHE:CD1	1:B:133:PHE:N	2.76	0.47
1:B:553:THR:O	1:B:586:ASP:N	2.48	0.47
1:B:600:PRO:HD3	1:B:692:ILE:HD11	1.96	0.47
1:B:659:SER:CB	1:B:698:SER:HB3	2.45	0.47
1:C:400:PHE:CD1	1:C:400:PHE:C	2.88	0.47
1:C:733:LYS:HD3	1:C:775:ASP:OD1	2.15	0.47
1:C:927:PHE:CD1	1:C:927:PHE:C	2.88	0.47
1:A:220:PHE:HD2	1:A:287:ASP:OD1	1.96	0.47
1:A:560:LEU:HB2	1:A:562:PHE:HE1	1.77	0.47
1:A:661:GLU:O	1:A:695:TYR:CE2	2.67	0.47
1:A:741:TYR:HE1	1:A:966:LEU:HD11	1.79	0.47
1:B:117:LEU:HB3	1:B:233:ILE:HD12	1.96	0.47
1:B:275:PHE:CE1	1:B:290:ASP:CA	2.96	0.47
1:C:380:TYR:CD2	1:C:412:PRO:CG	2.97	0.47
1:C:897:PRO:HB2	1:C:900:MET:HG3	1.97	0.47
1:A:107:GLY:O	1:A:236:THR:N	2.48	0.47
1:A:121:ASN:HD21	1:A:190:ARG:HH22	1.63	0.47
1:A:336:CYS:SG	1:A:361:CYS:C	2.93	0.47
1:A:403:ARG:CG	1:A:495:TYR:CZ	2.98	0.47
1:A:664:ILE:HB	1:A:672:ALA:O	2.14	0.47
1:A:724:THR:HG22	1:A:1063:LEU:CD2	2.45	0.47
1:A:963:VAL:HG11	1:C:570:ALA:HB1	1.95	0.47
1:A:1067:TYR:C	1:A:1067:TYR:CD1	2.88	0.47
1:A:1108:ASN:HD22	1:A:1108:ASN:N	2.13	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:58:PHE:HD1	1:B:275:PHE:HZ	1.54	0.47
1:B:99:ASN:N	1:B:99:ASN:ND2	2.61	0.47
1:B:105:ILE:CG1	1:B:118:LEU:HD13	2.42	0.47
1:B:134:GLN:NE2	1:B:161:SER:HB2	2.29	0.47
1:B:411:ALA:HB3	1:B:414:GLN:HG2	1.97	0.47
1:B:718:PHE:O	1:B:718:PHE:CD1	2.68	0.47
1:B:1130:ILE:N	1:B:1130:ILE:HD12	2.30	0.47
1:C:33:THR:CA	1:C:58:PHE:HE1	2.18	0.47
1:C:65:PHE:CZ	1:C:84:LEU:HD13	2.33	0.47
1:C:91:TYR:CE1	1:C:93:ALA:HB2	2.50	0.47
1:C:165:ASN:N	1:C:165:ASN:OD1	2.46	0.47
1:C:218:GLN:H	1:C:218:GLN:CD	2.14	0.47
1:C:409:GLN:H	1:C:409:GLN:HE21	1.63	0.47
1:C:591:SER:O	1:C:592:PHE:CD1	2.67	0.47
1:C:741:TYR:OH	1:C:962:LEU:HD12	2.15	0.47
1:C:786:LYS:CE	1:C:786:LYS:CA	2.89	0.47
1:A:401:VAL:HG11	1:A:451:TYR:CE2	2.50	0.47
1:C:115:GLN:CA	1:C:233:ILE:CD1	2.92	0.47
1:C:291:CYS:O	1:C:298:GLU:HG3	2.15	0.47
1:C:360:ASN:CA	1:C:523:THR:HB	2.44	0.47
1:C:1079:PRO:HD2	1:C:1131:GLY:O	2.14	0.47
1:C:1095:PHE:HB3	1:C:1102:TRP:HZ3	1.79	0.47
1:A:63:THR:O	1:A:63:THR:OG1	2.33	0.47
1:A:472:ILE:HA	1:A:491:PRO:CD	2.45	0.47
1:A:927:PHE:CD1	1:A:927:PHE:C	2.88	0.47
1:A:1019:ARG:HG2	1:A:1019:ARG:HH11	1.79	0.47
1:B:97:LYS:CB	1:B:186:PHE:HD1	2.28	0.47
1:C:64:TRP:HE1	1:C:264:ALA:HB1	1.79	0.47
1:C:125:ASN:N	1:C:125:ASN:ND2	2.63	0.47
2:O:2:NAG:O7	2:O:2:NAG:H3	2.14	0.47
1:A:722:VAL:HA	1:A:1064:HIS:O	2.15	0.47
1:A:884:SER:OG	1:A:887:THR:OG1	2.32	0.47
1:B:1114:ILE:H	1:B:1114:ILE:CD1	2.27	0.47
1:C:911:VAL:HG21	1:C:1067:TYR:CE2	2.50	0.47
1:A:104:TRP:N	1:A:104:TRP:CD2	2.82	0.46
1:A:903:ALA:CA	1:A:916:LEU:HD13	2.45	0.46
1:B:614:GLY:O	1:C:851:CYS:N	2.48	0.46
1:B:616:ASN:ND2	3:B:1302:NAG:C7	2.78	0.46
1:C:1081:ILE:HD13	1:C:1133:VAL:HG22	1.95	0.46
2:L:2:NAG:O7	2:L:2:NAG:H3	2.14	0.46
1:A:86:PHE:CE2	1:A:90:VAL:HG22	2.50	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:600:PRO:HB3	1:A:674:TYR:HD2	1.80	0.46
1:A:742:ILE:HD13	1:A:1001:LEU:CG	2.44	0.46
1:B:102:ARG:CD	1:B:141:LEU:CD1	2.93	0.46
1:B:140:PHE:HA	1:B:242:LEU:O	2.15	0.46
1:B:870:ILE:O	1:B:874:THR:HG23	2.14	0.46
1:C:426:PRO:HD2	1:C:429:PHE:HB2	1.96	0.46
1:C:436:TRP:CE2	1:C:509:ARG:HB3	2.48	0.46
1:A:455:LEU:HG	1:A:456:PHE:CD2	2.51	0.46
1:B:395:VAL:HG22	1:B:515:PHE:HB3	1.96	0.46
1:C:115:GLN:OE1	1:C:130:VAL:CG1	2.64	0.46
1:C:398:ASP:O	1:C:511:VAL:HG23	2.14	0.46
1:A:289:VAL:HG23	1:A:306:PHE:CZ	2.50	0.46
1:A:675:GLN:CB	1:A:693:ILE:HD11	2.44	0.46
1:A:693:ILE:CD1	1:A:693:ILE:H	2.27	0.46
1:B:347:PHE:HB2	1:B:401:VAL:HG23	1.97	0.46
1:C:87:ASN:N	1:C:87:ASN:HD22	2.13	0.46
1:C:102:ARG:HH22	1:C:177:MET:CE	2.29	0.46
1:C:821:LEU:HD21	1:C:939:SER:HB3	1.98	0.46
1:C:861:LEU:N	1:C:861:LEU:CD2	2.78	0.46
1:C:1001:LEU:HD13	1:C:1001:LEU:C	2.36	0.46
1:A:125:ASN:HB2	1:A:172:SER:O	2.16	0.46
1:A:203:ILE:HG21	1:A:227:VAL:HG22	1.78	0.46
1:A:718:PHE:HA	1:A:1070:ALA:H	1.80	0.46
1:A:856:ASN:HD21	1:A:966:LEU:CD1	2.28	0.46
1:A:885:GLY:HA2	1:A:901:GLN:CD	2.35	0.46
1:B:615:VAL:HG12	1:B:616:ASN:O	2.16	0.46
1:C:320:VAL:HB	1:C:590:CYS:SG	2.56	0.46
1:C:403:ARG:O	1:C:406:GLU:HB2	2.15	0.46
1:C:718:PHE:CD1	1:C:718:PHE:C	2.89	0.46
1:A:86:PHE:C	1:A:86:PHE:HD1	2.19	0.46
1:A:102:ARG:NH2	1:A:179:LEU:CD2	2.73	0.46
1:A:641:ASN:OD1	1:A:641:ASN:N	2.49	0.46
1:A:886:TRP:CD1	1:A:886:TRP:C	2.88	0.46
1:B:57:PRO:CB	1:B:273:ARG:CZ	2.73	0.46
1:B:774:GLN:OE1	1:B:774:GLN:HA	2.16	0.46
1:C:409:GLN:NE2	1:C:409:GLN:N	2.63	0.46
1:C:888:PHE:CE2	1:C:1034:LEU:CD2	2.98	0.46
1:A:822:LEU:CD1	1:A:1061:VAL:HG21	2.44	0.46
1:B:356:LYS:N	1:B:397:ALA:O	2.46	0.46
1:B:490:PHE:CD1	1:B:491:PRO:HD2	2.51	0.46
1:C:541:PHE:HZ	1:C:587:ILE:HD13	1.78	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:62:VAL:HG23	1:A:267:VAL:C	2.36	0.46
1:A:1081:ILE:CG2	1:A:1135:ASN:HB3	2.45	0.46
1:A:216:LEU:H	1:A:216:LEU:CD1	2.29	0.46
1:A:229:LEU:HD12	1:A:229:LEU:N	2.31	0.46
1:A:912:THR:OG1	1:A:1106:GLN:NE2	2.49	0.46
1:A:963:VAL:CG1	1:C:570:ALA:HB1	2.44	0.46
1:B:31:SER:HA	1:B:216:LEU:CD1	2.46	0.46
1:C:102:ARG:NH2	1:C:177:MET:SD	2.86	0.46
1:C:119:ILE:CD1	1:C:119:ILE:N	2.79	0.46
1:C:202:LYS:HB3	1:C:204:TYR:CE1	2.50	0.46
1:C:368:LEU:N	1:C:368:LEU:CD1	2.78	0.46
1:A:62:VAL:CG2	1:A:266:TYR:HB3	2.46	0.46
1:A:411:ALA:HB3	1:A:414:GLN:HE21	1.81	0.46
1:C:741:TYR:CD1	1:C:856:ASN:HB3	2.51	0.46
1:C:1080:ALA:O	1:C:1132:ILE:HG13	2.16	0.46
1:A:557:LYS:O	1:A:584:ILE:HD13	2.15	0.45
1:A:773:GLU:CG	1:A:1019:ARG:NH2	2.78	0.45
1:A:1091:ARG:HB2	1:A:1119:ASN:O	2.17	0.45
1:B:48:LEU:HD12	1:B:48:LEU:N	2.30	0.45
1:B:584:ILE:N	1:B:584:ILE:CD1	2.78	0.45
1:B:610:VAL:CG2	1:B:651:ILE:CG1	2.95	0.45
1:B:1141:LEU:HD23	1:B:1141:LEU:C	2.36	0.45
1:C:126:VAL:HG21	1:C:172:SER:OG	2.15	0.45
1:C:338:PHE:HZ	1:C:365:TYR:HH	1.63	0.45
1:C:421:TYR:C	1:C:461:LEU:HD12	2.36	0.45
1:C:856:ASN:HB2	1:C:858:LEU:HD11	1.98	0.45
1:C:1036:GLN:HA	1:C:1048:HIS:HE1	1.81	0.45
1:A:310:LYS:HG2	1:A:664:ILE:CD1	2.45	0.45
1:A:429:PHE:CD1	1:A:429:PHE:C	2.89	0.45
1:B:57:PRO:CB	1:B:273:ARG:NH2	2.75	0.45
1:B:94:SER:CB	1:B:96:GLU:OE2	2.62	0.45
1:B:273:ARG:HH11	1:B:273:ARG:HG3	1.81	0.45
1:B:350:VAL:HB	1:B:402:ILE:HG22	1.97	0.45
1:B:714:ILE:HG23	1:B:1107:ARG:O	2.17	0.45
1:B:724:THR:HG22	1:B:1063:LEU:HD22	1.99	0.45
1:B:742:ILE:HG22	1:B:997:ILE:HD12	1.98	0.45
1:B:886:TRP:HA	1:B:1034:LEU:O	2.17	0.45
1:B:1121:PHE:HD1	1:B:1123:SER:H	1.64	0.45
1:C:360:ASN:N	1:C:360:ASN:ND2	2.63	0.45
1:A:54:LEU:N	1:A:54:LEU:CD1	2.80	0.45
1:A:448:ASN:HB2	1:A:497:PHE:HB2	1.97	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:823:PHE:HZ	1:A:867:ASP:OD2	1.99	0.45
1:A:988:GLU:OE1	1:A:988:GLU:HA	2.17	0.45
1:B:1049:LEU:N	1:B:1049:LEU:HD12	2.31	0.45
1:C:96:GLU:HG3	1:C:101:ILE:H	1.82	0.45
1:C:103:GLY:HA3	1:C:241:LEU:HD22	1.98	0.45
1:C:334:ASN:N	1:C:334:ASN:OD1	2.49	0.45
1:C:414:GLN:HE21	1:C:414:GLN:CA	2.07	0.45
1:A:65:PHE:CE2	1:A:84:LEU:HD13	2.51	0.45
1:A:115:GLN:HE22	1:A:132:GLU:CG	2.09	0.45
1:A:384:PRO:HA	1:A:387:LEU:HD12	1.97	0.45
1:A:643:PHE:CD2	1:A:655:HIS:HB3	2.51	0.45
1:B:140:PHE:CB	1:B:242:LEU:O	2.65	0.45
1:B:559:PHE:CE1	1:C:43:PHE:HE2	2.34	0.45
1:B:977:LEU:HA	1:B:980:ILE:HG22	1.98	0.45
1:C:695:TYR:CD1	1:C:695:TYR:C	2.89	0.45
1:C:748:GLU:OE1	1:C:981:LEU:HG	2.16	0.45
1:A:81:ASN:HB2	1:A:242:LEU:HD21	1.97	0.45
1:A:130:VAL:HG21	1:A:231:ILE:HD12	1.99	0.45
1:A:1050:MET:N	1:A:1065:VAL:HG23	2.32	0.45
1:B:86:PHE:O	1:B:86:PHE:HD1	1.99	0.45
1:B:364:ASP:O	1:B:368:LEU:HD21	2.16	0.45
1:B:396:TYR:HB2	1:B:514:SER:HB3	1.97	0.45
1:B:454:ARG:CA	1:B:491:PRO:O	2.55	0.45
1:C:42:VAL:HG23	1:C:44:ARG:NH1	2.32	0.45
1:C:318:PHE:HZ	1:C:615:VAL:HG12	1.82	0.45
1:A:135:PHE:HD1	1:A:160:TYR:HB3	1.82	0.45
1:A:472:ILE:HD12	1:A:472:ILE:H	1.81	0.45
1:A:732:THR:HG23	1:A:1058:HIS:CE1	2.52	0.45
1:C:210:ILE:O	1:C:210:ILE:HG12	2.17	0.45
1:C:293:LEU:HD12	1:C:293:LEU:O	2.17	0.45
1:C:353:TRP:HD1	1:C:353:TRP:O	2.00	0.45
1:C:534:VAL:HG13	1:C:534:VAL:O	2.16	0.45
1:C:666:ILE:O	1:C:666:ILE:HG22	2.16	0.45
1:C:742:ILE:CD1	1:C:1001:LEU:CD2	2.94	0.45
1:A:81:ASN:N	1:A:82:PRO:CD	2.79	0.45
1:A:115:GLN:HA	1:A:115:GLN:HE21	1.78	0.45
1:A:130:VAL:HG21	1:A:231:ILE:HD11	1.98	0.45
1:A:388:ASN:HD21	1:A:527:PRO:CG	2.29	0.45
1:A:489:TYR:N	1:A:489:TYR:CD1	2.84	0.45
1:A:991:VAL:HG22	1:A:992:GLN:HE21	1.82	0.45
1:B:54:LEU:HD13	1:B:195:LYS:NZ	2.32	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:106:PHE:CB	1:B:117:LEU:CD2	2.90	0.45
1:B:117:LEU:CG	1:B:119:ILE:HD11	2.46	0.45
1:B:131:CYS:SG	1:B:166:CYS:HB3	2.56	0.45
1:C:117:LEU:CD2	1:C:119:ILE:HD13	2.43	0.45
1:C:543:PHE:CD2	1:C:576:VAL:HG21	2.52	0.45
1:A:115:GLN:HA	1:A:132:GLU:HG2	1.99	0.45
1:A:398:ASP:OD2	1:A:423:TYR:OH	2.28	0.45
1:A:562:PHE:CD2	1:B:225:PRO:CG	3.00	0.45
1:A:600:PRO:CB	1:A:674:TYR:CD2	2.99	0.45
1:A:736:VAL:HG22	1:A:858:LEU:HD23	1.98	0.45
1:A:902:MET:C	1:A:916:LEU:CD1	2.85	0.45
1:B:325:SER:HA	1:B:540:ASN:O	2.16	0.45
1:C:136:CYS:SG	1:C:137:ASN:N	2.90	0.45
1:C:346:ARG:HH22	1:C:450:ASN:ND2	2.15	0.45
1:C:497:PHE:CE1	1:C:507:PRO:CD	2.96	0.45
1:C:557:LYS:H	1:C:557:LYS:HG2	1.50	0.45
1:C:559:PHE:HE2	1:C:565:PHE:O	1.95	0.45
1:C:708:SER:HB2	1:C:711:SER:OG	2.17	0.45
1:C:795:LYS:HB3	1:C:797:PHE:HE1	1.81	0.45
1:C:1083:HIS:HB2	1:C:1137:VAL:CG1	2.46	0.45
1:A:855:PHE:HZ	1:C:570:ALA:HB3	1.82	0.45
1:B:197:ILE:H	1:B:197:ILE:HD12	1.82	0.45
1:C:105:ILE:HD12	1:C:241:LEU:HD13	1.98	0.45
1:C:318:PHE:HZ	1:C:615:VAL:CG1	2.30	0.45
1:C:400:PHE:HD1	1:C:400:PHE:C	2.19	0.45
1:C:577:ARG:HA	1:C:583:GLU:O	2.16	0.45
1:C:822:LEU:CD2	1:C:945:LEU:HD11	2.47	0.45
1:A:16:VAL:HG13	1:A:158:ARG:NH2	2.32	0.45
1:A:31:SER:CB	1:A:216:LEU:CD2	2.92	0.45
1:A:34:ARG:CZ	1:A:217:PRO:HG2	2.47	0.45
1:A:712:ILE:CG1	1:B:896:ILE:HD12	2.46	0.45
1:B:899:ALA:HB2	1:B:920:GLN:HE22	1.82	0.45
1:C:95:THR:OG1	1:C:186:PHE:CD2	2.65	0.45
1:C:303:LEU:HD11	1:C:313:TYR:CZ	2.52	0.45
1:C:415:THR:HG23	1:C:415:THR:O	2.16	0.45
1:C:435:ALA:CB	1:C:510:VAL:HG22	2.47	0.45
1:C:712:ILE:HB	1:C:1077:THR:HG21	1.98	0.45
1:C:736:VAL:HG23	1:C:857:GLY:O	2.17	0.45
1:A:33:THR:HG22	1:A:58:PHE:HD2	1.83	0.44
1:A:791:THR:HG22	1:A:792:PRO:CD	2.43	0.44
1:B:38:TYR:CE1	1:B:223:LEU:O	2.70	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:950:ASP:OD1	1:B:951:VAL:N	2.50	0.44
1:C:62:VAL:HG22	1:C:266:TYR:HB3	1.99	0.44
1:C:358:ILE:HG13	1:C:361:CYS:SG	2.57	0.44
1:C:369:TYR:CD1	1:C:369:TYR:C	2.90	0.44
1:C:726:ILE:CD1	1:C:1061:VAL:HG13	2.48	0.44
1:A:65:PHE:CE2	1:A:84:LEU:CD1	3.01	0.44
1:B:274:THR:CG2	1:B:291:CYS:SG	3.05	0.44
1:C:187:LYS:CA	1:C:211:ASN:HB3	2.43	0.44
1:C:380:TYR:N	1:C:380:TYR:CD1	2.80	0.44
1:C:805:ILE:CD1	1:C:1063:LEU:HD12	2.47	0.44
1:C:1136:THR:CG2	1:C:1138:TYR:CE2	2.99	0.44
1:A:273:ARG:HD3	1:A:290:ASP:OD2	2.17	0.44
1:A:742:ILE:HG21	1:A:753:LEU:HD13	2.00	0.44
1:A:781:VAL:O	1:A:1029:MET:HG3	2.17	0.44
1:A:877:LEU:HD13	1:A:1029:MET:CE	2.47	0.44
1:B:864:LEU:HD12	1:B:864:LEU:O	2.16	0.44
1:B:1043:CYS:SG	1:B:1048:HIS:CD2	3.10	0.44
1:C:104:TRP:HB3	1:C:106:PHE:HE1	1.81	0.44
1:C:585:LEU:N	1:C:585:LEU:HD23	2.31	0.44
1:C:654:GLU:OE1	1:C:654:GLU:N	2.47	0.44
1:C:738:CYS:SG	1:C:760:CYS:C	2.96	0.44
1:C:974:SER:HB3	1:C:980:ILE:HD11	1.99	0.44
1:A:33:THR:CB	1:A:58:PHE:HE2	2.31	0.44
1:A:329:PHE:CE2	1:A:528:LYS:HG3	2.52	0.44
1:A:409:GLN:NE2	1:A:418:ILE:HG22	2.33	0.44
1:A:541:PHE:O	1:A:541:PHE:CD1	2.71	0.44
1:A:581:THR:HG22	1:A:581:THR:O	2.17	0.44
1:A:1002:GLN:HE21	1:A:1002:GLN:CA	2.20	0.44
1:B:97:LYS:HB2	1:B:186:PHE:CD1	2.52	0.44
1:B:119:ILE:CD1	1:B:119:ILE:N	2.80	0.44
1:B:592:PHE:CZ	1:C:857:GLY:HA2	2.52	0.44
1:B:741:TYR:OH	1:B:966:LEU:CD1	2.66	0.44
1:B:916:LEU:HD12	1:B:916:LEU:O	2.17	0.44
1:C:62:VAL:HG13	1:C:62:VAL:O	2.17	0.44
1:C:294:ASP:HB2	1:C:295:PRO:CD	2.48	0.44
1:C:360:ASN:HD22	1:C:523:THR:CG2	2.31	0.44
1:C:714:ILE:HG23	1:C:1107:ARG:O	2.17	0.44
1:C:1081:ILE:HG12	1:C:1095:PHE:CE2	2.51	0.44
1:A:105:ILE:HG12	1:A:118:LEU:CD1	2.48	0.44
1:A:365:TYR:CD2	1:A:387:LEU:HB3	2.52	0.44
1:A:426:PRO:HA	1:A:463:PRO:HG3	1.98	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:643:PHE:CD1	1:A:643:PHE:C	2.90	0.44
1:A:856:ASN:ND2	1:A:966:LEU:HD12	2.33	0.44
1:C:392:PHE:C	1:C:522:ALA:HB1	2.37	0.44
1:C:662:CYS:SG	1:C:697:MET:CE	3.05	0.44
1:C:786:LYS:HA	1:C:786:LYS:HZ1	1.81	0.44
1:C:970:PHE:CE2	1:C:999:GLY:C	2.90	0.44
1:C:1116:THR:HA	1:C:1138:TYR:O	2.17	0.44
1:A:336:CYS:HA	1:A:337:PRO:HD3	1.15	0.44
1:A:457:ARG:CG	1:A:459:SER:O	2.65	0.44
1:A:794:ILE:HG22	1:A:796:ASP:OD1	2.17	0.44
1:B:206:LYS:HB3	1:B:223:LEU:HD22	1.99	0.44
1:B:712:ILE:HD11	1:B:1094:VAL:HG11	1.95	0.44
1:C:390:LEU:HD13	1:C:392:PHE:CD2	2.51	0.44
1:C:786:LYS:NZ	1:C:786:LYS:CA	2.80	0.44
1:C:1083:HIS:HB2	1:C:1137:VAL:HG13	1.99	0.44
1:A:37:TYR:HD2	1:A:204:TYR:CE2	2.36	0.44
1:A:612:TYR:HB3	1:A:615:VAL:CG2	2.48	0.44
1:A:1081:ILE:HD11	1:A:1095:PHE:HD2	1.82	0.44
1:B:335:LEU:HA	1:B:362:VAL:O	2.18	0.44
1:B:641:ASN:HD22	1:B:641:ASN:HA	1.63	0.44
1:C:492:LEU:N	1:C:492:LEU:CD2	2.80	0.44
1:C:692:ILE:N	1:C:692:ILE:CD1	2.79	0.44
1:A:321:GLN:NE2	1:A:321:GLN:CA	2.75	0.44
1:A:900:MET:HB3	1:C:1107:ARG:NH1	2.33	0.44
1:A:1090:PRO:HD3	1:A:1095:PHE:CE1	2.53	0.44
1:B:329:PHE:CB	1:B:330:PRO:CD	2.93	0.44
1:B:965:GLN:CA	1:B:965:GLN:HE21	2.30	0.44
1:C:559:PHE:HB3	1:C:577:ARG:HH21	1.82	0.44
1:C:886:TRP:CD1	1:C:886:TRP:C	2.90	0.44
1:A:572:THR:HG21	1:B:855:PHE:CZ	2.52	0.44
1:A:770:ILE:CD1	1:A:1012:LEU:HD23	2.40	0.44
1:A:1126:CYS:HB2	1:A:1132:ILE:HD13	2.00	0.44
1:B:310:LYS:HA	1:B:600:PRO:O	2.18	0.44
1:B:552:LEU:CD2	1:B:587:ILE:HG12	2.48	0.44
1:B:599:THR:CG2	1:B:608:VAL:HG12	2.35	0.44
1:C:125:ASN:HD22	1:C:125:ASN:H	1.66	0.44
1:C:351:TYR:CD2	1:C:492:LEU:HD13	2.53	0.44
1:C:365:TYR:HE1	1:C:513:LEU:CD2	2.31	0.44
1:C:456:PHE:HB3	1:C:473:TYR:CG	2.53	0.44
1:A:133:PHE:CE1	1:A:163:ALA:HB2	2.52	0.43
1:A:201:PHE:CD1	1:A:201:PHE:C	2.91	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:324:GLU:O	1:A:539:VAL:CB	2.61	0.43
1:A:501:ASN:N	1:A:501:ASN:ND2	2.66	0.43
1:A:563:GLN:NE2	1:B:43:PHE:CB	2.79	0.43
1:A:600:PRO:CG	1:A:692:ILE:HD11	2.48	0.43
1:A:718:PHE:CD1	1:A:718:PHE:C	2.92	0.43
1:B:89:GLY:CA	1:B:194:PHE:O	2.66	0.43
1:B:557:LYS:H	1:B:557:LYS:HG3	1.57	0.43
1:B:854:LYS:N	1:B:859:THR:HG22	2.32	0.43
1:C:360:ASN:ND2	1:C:523:THR:HG21	2.33	0.43
1:C:726:ILE:HD13	1:C:1061:VAL:HG13	2.00	0.43
1:A:68:ILE:CG1	1:A:262:ALA:HA	2.47	0.43
1:A:96:GLU:HB3	1:A:101:ILE:CD1	2.47	0.43
1:A:332:ILE:HD12	1:A:332:ILE:N	2.33	0.43
1:A:546:LEU:HD13	1:A:565:PHE:CZ	2.52	0.43
1:A:902:MET:CE	1:A:1050:MET:HE1	2.48	0.43
1:B:92:PHE:HZ	1:B:101:ILE:CD1	2.31	0.43
1:B:104:TRP:HE3	1:B:104:TRP:H	1.63	0.43
1:B:448:ASN:HB3	1:B:497:PHE:HB2	1.99	0.43
1:B:613:GLN:HG2	1:C:861:LEU:HD11	1.99	0.43
1:C:616:ASN:O	1:C:617:CYS:HB2	2.17	0.43
1:C:1060:VAL:HG13	1:C:1060:VAL:O	2.18	0.43
1:A:125:ASN:CB	1:A:172:SER:O	2.66	0.43
1:B:33:THR:HA	1:B:58:PHE:CE2	2.54	0.43
1:B:697:MET:CE	1:C:865:LEU:HD23	2.48	0.43
1:B:726:ILE:HD13	1:B:1061:VAL:HG13	2.00	0.43
1:B:1081:ILE:HG21	1:B:1135:ASN:O	2.19	0.43
1:C:220:PHE:CD1	1:C:220:PHE:O	2.71	0.43
1:C:387:LEU:HD11	1:C:432:CYS:SG	2.59	0.43
1:C:480:CYS:HB2	1:C:488:CYS:HB3	1.86	0.43
1:C:560:LEU:N	1:C:563:GLN:HE22	2.16	0.43
1:C:712:ILE:CD1	1:C:714:ILE:HD11	2.48	0.43
1:C:718:PHE:CE1	1:C:923:ILE:HG12	2.52	0.43
1:C:741:TYR:CE1	1:C:966:LEU:CG	3.01	0.43
1:A:108:THR:HA	1:A:236:THR:OG1	2.18	0.43
1:A:815:ARG:NH1	1:A:823:PHE:CE1	2.87	0.43
1:A:991:VAL:HG22	1:A:992:GLN:NE2	2.34	0.43
1:A:1006:THR:O	1:A:1010:GLN:HG2	2.18	0.43
1:B:303:LEU:HD21	1:B:313:TYR:CE2	2.54	0.43
1:B:646:ARG:HB2	1:B:668:ALA:HB1	2.00	0.43
1:C:722:VAL:HA	1:C:1064:HIS:O	2.17	0.43
1:C:770:ILE:HG23	1:C:774:GLN:HE21	1.82	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1029:MET:CA	1:A:1029:MET:HE3	2.48	0.43
1:B:16:VAL:CG1	1:B:158:ARG:NH2	2.74	0.43
1:B:350:VAL:HG13	1:B:422:ASN:ND2	2.34	0.43
1:B:979:ASP:O	1:B:983:ARG:HG3	2.18	0.43
1:C:102:ARG:CD	1:C:141:LEU:HD13	2.43	0.43
1:C:222:ALA:CB	1:C:285:ILE:HB	2.49	0.43
1:C:971:GLY:HA3	1:C:995:ARG:HD3	2.00	0.43
1:C:1095:PHE:CE1	1:C:1104:VAL:HB	2.54	0.43
1:A:775:ASP:OD2	1:A:864:LEU:HD23	2.19	0.43
1:A:797:PHE:CZ	1:A:882:ILE:HG21	2.54	0.43
1:A:981:LEU:HD12	1:A:981:LEU:HA	1.91	0.43
1:B:62:VAL:HG13	1:B:268:GLY:HA3	1.96	0.43
1:B:472:ILE:HD12	1:B:490:PHE:HB2	1.99	0.43
1:C:498:GLN:O	1:C:501:ASN:CB	2.65	0.43
1:C:718:PHE:CG	1:C:1067:TYR:CE1	3.04	0.43
1:C:908:GLY:CA	1:C:1038:LYS:NZ	2.82	0.43
1:C:1121:PHE:O	1:C:1121:PHE:CD1	2.72	0.43
1:C:1140:PRO:C	1:C:1143:PRO:HD2	2.38	0.43
1:A:96:GLU:C	1:A:186:PHE:HD1	2.22	0.43
1:A:570:ALA:HB1	1:B:963:VAL:CG1	2.48	0.43
1:A:741:TYR:CD1	1:A:966:LEU:HD21	2.46	0.43
1:A:992:GLN:HE21	1:A:992:GLN:N	2.17	0.43
1:B:773:GLU:HG2	1:B:1019:ARG:NH2	2.34	0.43
1:B:1114:ILE:HG22	1:B:1138:TYR:HB2	1.99	0.43
1:A:81:ASN:CB	1:A:242:LEU:CD2	2.97	0.43
1:A:612:TYR:CB	1:A:615:VAL:CG2	2.96	0.43
1:B:106:PHE:HB2	1:B:235:ILE:CD1	2.37	0.43
1:C:1081:ILE:CD1	1:C:1133:VAL:CG2	2.94	0.43
1:A:37:TYR:CD2	1:A:204:TYR:CE2	3.07	0.43
1:A:65:PHE:HB2	1:A:265:TYR:CZ	2.54	0.43
1:A:106:PHE:CE1	1:A:194:PHE:CE2	3.07	0.43
1:A:422:ASN:HD21	1:A:454:ARG:H	1.65	0.43
1:A:675:GLN:HG3	1:A:693:ILE:HD11	2.00	0.43
1:B:54:LEU:HD12	1:B:54:LEU:H	1.82	0.43
1:B:319:ARG:HG3	1:B:319:ARG:O	2.19	0.43
1:C:65:PHE:CD2	1:C:265:TYR:CE2	3.03	0.43
1:C:86:PHE:CD1	1:C:86:PHE:O	2.72	0.43
1:C:194:PHE:CD1	1:C:194:PHE:N	2.86	0.43
1:C:223:LEU:HD22	1:C:223:LEU:H	1.83	0.43
1:C:707:TYR:CD1	1:C:707:TYR:C	2.92	0.43
1:C:726:ILE:HD12	1:C:1061:VAL:HG21	1.87	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:965:GLN:HG2	1:C:1003:SER:OG	2.19	0.43
1:A:86:PHE:CD2	1:A:90:VAL:HG22	2.54	0.43
1:A:128:ILE:HD12	1:A:229:LEU:HD21	2.00	0.43
1:A:275:PHE:HD1	1:A:290:ASP:HA	1.84	0.43
1:A:612:TYR:CB	1:A:615:VAL:HG22	2.48	0.43
1:A:782:PHE:CE1	1:A:874:THR:HG22	2.53	0.43
1:A:903:ALA:HA	1:A:916:LEU:HD13	2.01	0.43
1:A:927:PHE:C	1:A:927:PHE:HD1	2.23	0.43
1:A:1104:VAL:HG13	1:A:1104:VAL:O	2.19	0.43
1:B:469:SER:O	1:B:491:PRO:HG3	2.19	0.43
1:B:671:CYS:O	1:B:695:TYR:CD1	2.72	0.43
1:C:32:PHE:HE2	1:C:218:GLN:HB3	1.83	0.43
1:C:86:PHE:HD2	1:C:90:VAL:HB	1.84	0.43
1:C:347:PHE:CD2	1:C:509:ARG:CD	2.96	0.43
1:C:582:LEU:O	1:C:582:LEU:HD23	2.18	0.43
1:A:55:PHE:HB3	1:A:275:PHE:CE2	2.53	0.42
1:A:65:PHE:HB3	1:A:265:TYR:CE1	2.54	0.42
1:A:126:VAL:HG22	1:A:172:SER:OG	2.10	0.42
1:A:742:ILE:CD1	1:A:1001:LEU:HD21	2.47	0.42
1:A:822:LEU:CD2	1:A:945:LEU:HD11	2.49	0.42
1:A:974:SER:N	1:A:980:ILE:HD11	2.34	0.42
1:B:18:LEU:HA	1:B:255:SER:O	2.18	0.42
1:B:53:ASP:OD1	1:B:195:LYS:NZ	2.52	0.42
1:B:89:GLY:HA2	1:B:194:PHE:O	2.19	0.42
1:B:307:THR:C	1:B:602:THR:HG21	2.39	0.42
1:B:1107:ARG:NH1	1:C:896:ILE:CD1	2.82	0.42
1:B:1145:LEU:CD1	1:C:1141:LEU:HG	2.46	0.42
1:C:1082:CYS:CB	1:C:1132:ILE:CD1	2.85	0.42
1:A:490:PHE:HE2	1:A:492:LEU:HB2	1.84	0.42
1:B:216:LEU:HD23	1:B:266:TYR:CE2	2.54	0.42
1:B:341:VAL:HG22	1:B:356:LYS:CE	2.48	0.42
1:B:368:LEU:CD2	1:B:368:LEU:N	2.81	0.42
1:B:501:ASN:HB3	1:B:505:TYR:HB2	2.01	0.42
1:B:938:LEU:CD2	1:B:944:ALA:HB1	2.49	0.42
1:B:1118:ASP:OD1	1:B:1119:ASN:N	2.53	0.42
1:C:186:PHE:O	1:C:211:ASN:HB2	2.19	0.42
1:C:390:LEU:CD1	1:C:390:LEU:C	2.87	0.42
1:C:400:PHE:CZ	1:C:410:ILE:CG1	3.02	0.42
1:C:473:TYR:HE1	1:C:475:ALA:HB2	1.84	0.42
1:A:612:TYR:HB3	1:A:615:VAL:HG22	2.00	0.42
1:A:799:GLY:O	1:A:924:ALA:HB1	2.19	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:861:LEU:CD1	1:A:861:LEU:N	2.82	0.42
1:B:193:VAL:HG12	1:B:223:LEU:HD13	2.00	0.42
1:B:888:PHE:CE1	1:B:1034:LEU:CD2	3.03	0.42
1:C:977:LEU:HD23	1:C:977:LEU:HA	1.85	0.42
1:C:1083:HIS:CD2	1:C:1137:VAL:HG22	2.42	0.42
1:A:310:LYS:CG	1:A:600:PRO:O	2.67	0.42
1:A:1046:GLY:HA2	1:B:890:ALA:HB1	2.01	0.42
3:A:1305:NAG:C8	3:A:1305:NAG:C1	2.98	0.42
1:B:318:PHE:CD2	1:B:318:PHE:O	2.72	0.42
1:B:354:ASN:O	1:B:398:ASP:HA	2.19	0.42
1:C:238:PHE:HZ	1:C:267:VAL:HG21	1.84	0.42
1:C:825:LYS:HB2	1:C:945:LEU:HD12	2.01	0.42
1:A:43:PHE:CD1	1:A:43:PHE:O	2.72	0.42
1:A:426:PRO:CD	1:A:463:PRO:HB3	2.49	0.42
1:A:675:GLN:HB2	1:A:693:ILE:HG13	2.02	0.42
1:A:1051:SER:CB	1:A:1064:HIS:HD2	2.33	0.42
1:A:1115:ILE:CG2	1:A:1120:THR:HG21	2.49	0.42
1:B:45:SER:O	1:B:47:VAL:HG13	2.20	0.42
1:B:275:PHE:HD1	1:B:290:ASP:HA	1.80	0.42
1:B:595:VAL:HG12	1:B:612:TYR:CE1	2.54	0.42
1:B:825:LYS:CD	1:B:944:ALA:HB3	2.49	0.42
1:B:1106:GLN:NE2	1:B:1111:GLU:CD	2.70	0.42
1:B:1114:ILE:N	1:B:1114:ILE:CD1	2.82	0.42
1:C:245:HIS:HB3	1:C:259:THR:O	2.19	0.42
1:C:353:TRP:O	1:C:353:TRP:CD1	2.72	0.42
1:C:615:VAL:HG21	1:C:620:VAL:CG1	2.49	0.42
1:C:718:PHE:HE2	1:C:919:ASN:HD22	1.66	0.42
1:C:742:ILE:CD1	1:C:1001:LEU:HD23	2.49	0.42
1:C:817:PHE:CD1	1:C:817:PHE:C	2.93	0.42
1:C:1081:ILE:CG1	1:C:1095:PHE:CE2	3.02	0.42
1:C:1145:LEU:HD13	1:C:1145:LEU:O	2.18	0.42
1:A:437:ASN:OD1	1:A:438:SER:N	2.52	0.42
1:B:125:ASN:C	1:B:175:PHE:CE1	2.92	0.42
1:B:195:LYS:HE3	1:B:195:LYS:HB2	1.91	0.42
1:B:379:CYS:SG	1:B:384:PRO:HB3	2.59	0.42
1:B:1039:ARG:H	1:B:1039:ARG:HG3	1.65	0.42
1:C:201:PHE:HB3	1:C:229:LEU:HB2	2.01	0.42
1:C:973:ILE:HB	1:C:983:ARG:NH2	2.35	0.42
1:B:16:VAL:HG11	1:B:158:ARG:HH22	1.83	0.42
1:B:112:SER:OG	1:B:134:GLN:CG	2.55	0.42
1:B:238:PHE:CD1	1:B:238:PHE:C	2.92	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:308:VAL:O	1:B:602:THR:CG2	2.63	0.42
1:B:560:LEU:HB2	1:B:563:GLN:CD	2.40	0.42
1:C:83:VAL:HG11	1:C:237:ARG:HH21	1.85	0.42
1:C:856:ASN:O	1:C:858:LEU:HD11	2.10	0.42
1:C:1052:PHE:CE2	1:C:1065:VAL:CG2	3.03	0.42
1:A:312:ILE:O	1:A:312:ILE:HG23	2.20	0.42
1:A:675:GLN:HB2	1:A:693:ILE:CG1	2.50	0.42
1:A:707:TYR:CD1	1:A:707:TYR:C	2.93	0.42
1:A:763:LEU:HD22	1:A:1008:VAL:HG21	2.01	0.42
1:A:984:LEU:CD2	1:A:988:GLU:CG	2.67	0.42
1:A:1101:HIS:HB3	1:A:1103:PHE:CZ	2.54	0.42
1:B:197:ILE:HD12	1:B:197:ILE:O	2.19	0.42
1:B:353:TRP:CZ3	1:B:423:TYR:HD1	2.37	0.42
1:B:675:GLN:NE2	1:B:675:GLN:HA	2.34	0.42
1:C:138:ASP:N	1:C:139:PRO:HD3	2.35	0.42
1:C:400:PHE:O	1:C:400:PHE:CD1	2.73	0.42
1:C:1086:LYS:HE2	1:C:1122:VAL:HG21	2.01	0.42
1:C:1101:HIS:NE2	3:C:1303:NAG:H5	2.35	0.42
1:A:296:LEU:HB2	1:A:608:VAL:CG1	2.50	0.42
1:A:353:TRP:CD1	1:A:353:TRP:N	2.88	0.42
1:A:357:ARG:HH11	1:A:357:ARG:CG	2.29	0.42
1:A:735:SER:OG	1:A:861:LEU:HD11	2.20	0.42
1:A:764:ASN:O	1:A:764:ASN:ND2	2.53	0.42
1:A:927:PHE:HD1	1:A:927:PHE:O	2.02	0.42
1:A:951:VAL:HG21	1:A:1018:ILE:HD11	2.01	0.42
1:B:55:PHE:CD2	1:B:275:PHE:HD2	2.37	0.42
1:B:307:THR:HB	1:B:602:THR:CG2	2.45	0.42
1:B:472:ILE:HD13	1:B:490:PHE:CD1	2.54	0.42
1:B:726:ILE:HG21	1:B:948:LEU:HG	2.01	0.42
1:B:738:CYS:SG	1:B:760:CYS:O	2.78	0.42
1:B:752:LEU:HD11	1:B:990:GLU:CG	2.49	0.42
1:C:208:THR:HG22	1:C:210:ILE:CD1	2.39	0.42
1:C:376:THR:CG2	1:C:378:LYS:HE3	2.50	0.42
1:C:436:TRP:HD1	1:C:436:TRP:N	2.18	0.42
1:C:1087:ALA:O	1:C:1122:VAL:HA	2.19	0.42
1:A:888:PHE:CD1	1:A:888:PHE:C	2.92	0.42
1:A:985:ASP:CG	1:A:986:PRO:HD2	2.38	0.42
1:B:131:CYS:N	1:B:133:PHE:CZ	2.86	0.42
1:B:808:ASP:HA	1:B:809:PRO:HD3	1.92	0.42
1:B:971:GLY:O	1:B:995:ARG:CZ	2.68	0.42
1:B:1090:PRO:CA	1:B:1095:PHE:CE1	2.93	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1091:ARG:HB2	1:B:1119:ASN:O	2.20	0.42
1:C:15:CYS:SG	1:C:16:VAL:N	2.93	0.42
1:C:462:LYS:CE	1:C:462:LYS:CA	2.92	0.42
1:C:611:LEU:HB2	1:C:650:LEU:CD1	2.45	0.42
1:A:472:ILE:CD1	1:A:472:ILE:N	2.82	0.41
1:A:735:SER:HB2	1:A:859:THR:HG23	2.02	0.41
1:A:866:THR:HG22	1:C:646:ARG:NH2	2.35	0.41
1:B:16:VAL:CG1	1:B:158:ARG:HH12	2.33	0.41
1:B:16:VAL:O	1:B:17:ASN:OD1	2.37	0.41
1:B:55:PHE:N	1:B:270:LEU:CD2	2.75	0.41
1:B:387:LEU:O	1:B:387:LEU:HD23	2.20	0.41
1:B:712:ILE:HD12	1:B:1094:VAL:HG11	2.00	0.41
1:B:718:PHE:CZ	1:B:919:ASN:OD1	2.73	0.41
1:B:856:ASN:ND2	1:B:966:LEU:HD21	2.34	0.41
1:C:38:TYR:N	1:C:38:TYR:HD1	2.17	0.41
1:C:118:LEU:HD11	1:C:120:VAL:CG2	2.50	0.41
1:C:126:VAL:HG23	1:C:126:VAL:O	2.19	0.41
1:C:318:PHE:O	1:C:318:PHE:CD1	2.73	0.41
1:C:973:ILE:HD12	1:C:983:ARG:CD	2.48	0.41
1:C:1089:PHE:N	1:C:1089:PHE:CD1	2.88	0.41
1:A:327:VAL:O	1:A:327:VAL:HG23	2.20	0.41
1:A:328:ARG:NH1	1:A:578:ASP:OD1	2.53	0.41
1:A:365:TYR:O	1:A:369:TYR:CA	2.66	0.41
1:A:973:ILE:CG1	1:A:992:GLN:OE1	2.67	0.41
1:B:86:PHE:CD1	1:B:86:PHE:O	2.72	0.41
1:B:91:TYR:CD1	1:B:91:TYR:C	2.93	0.41
1:B:94:SER:CB	1:B:265:TYR:HB3	2.50	0.41
1:B:381:GLY:HA3	1:B:430:THR:HG23	2.01	0.41
1:B:778:THR:HG23	1:B:782:PHE:HD2	1.86	0.41
1:C:229:LEU:CD1	1:C:230:PRO:HD2	2.50	0.41
1:C:241:LEU:CD1	1:C:241:LEU:N	2.83	0.41
1:C:421:TYR:C	1:C:461:LEU:CD1	2.87	0.41
1:C:434:ILE:HG22	1:C:511:VAL:CG1	2.50	0.41
1:C:695:TYR:CD1	1:C:695:TYR:O	2.72	0.41
1:A:230:PRO:CG	1:C:357:ARG:NH2	2.83	0.41
1:A:605:SER:CB	1:A:674:TYR:HE2	2.29	0.41
1:A:922:LEU:HD21	2:E:1:NAG:H5	2.02	0.41
1:A:1081:ILE:CD1	1:A:1095:PHE:CD2	3.03	0.41
1:B:164:ASN:OD1	3:B:1305:NAG:N2	2.53	0.41
1:B:549:THR:HG22	1:B:590:CYS:SG	2.60	0.41
1:B:1096:VAL:HG22	1:B:1105:THR:HG22	2.03	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1102:TRP:NE1	1:B:1135:ASN:OD1	2.40	0.41
1:C:318:PHE:O	1:C:318:PHE:CG	2.73	0.41
1:C:980:ILE:N	1:C:980:ILE:HD13	2.36	0.41
1:A:216:LEU:N	1:A:216:LEU:CD1	2.84	0.41
1:A:347:PHE:CE2	1:A:399:SER:HB2	2.55	0.41
1:A:1081:ILE:HG13	1:A:1095:PHE:CD2	2.55	0.41
1:B:85:PRO:CD	1:B:269:TYR:OH	2.68	0.41
1:B:410:ILE:HG23	1:B:425:LEU:HD11	2.03	0.41
1:B:733:LYS:HB3	1:B:771:ALA:CB	2.51	0.41
1:B:819:GLU:HG2	1:B:1054:GLN:HB3	2.02	0.41
1:B:962:LEU:O	1:B:965:GLN:HB2	2.21	0.41
1:B:966:LEU:CD1	1:B:966:LEU:N	2.83	0.41
1:C:472:ILE:HA	1:C:489:TYR:O	2.19	0.41
1:C:878:LEU:CD2	1:C:1052:PHE:HD1	2.33	0.41
1:A:403:ARG:CD	1:A:495:TYR:CE1	3.00	0.41
1:A:642:VAL:HG13	1:A:651:ILE:HG12	2.03	0.41
1:B:141:LEU:O	1:B:243:ALA:CB	2.68	0.41
1:B:1107:ARG:NH1	1:C:904:TYR:CG	2.88	0.41
1:C:400:PHE:HZ	1:C:410:ILE:CG1	2.33	0.41
1:C:856:ASN:HB2	1:C:858:LEU:CD1	2.50	0.41
1:C:1094:VAL:HG13	1:C:1094:VAL:O	2.19	0.41
1:A:17:ASN:O	1:A:255:SER:HA	2.21	0.41
1:A:600:PRO:HB3	1:A:674:TYR:CD2	2.55	0.41
1:A:1048:HIS:ND1	1:A:1048:HIS:C	2.74	0.41
1:B:139:PRO:HB3	1:B:159:VAL:HG13	2.01	0.41
1:B:160:TYR:O	1:B:160:TYR:CG	2.73	0.41
1:B:231:ILE:HG22	1:B:233:ILE:HG23	2.02	0.41
1:B:541:PHE:CD1	1:B:541:PHE:C	2.93	0.41
1:B:640:SER:O	1:B:641:ASN:ND2	2.54	0.41
1:B:767:LEU:HD23	1:B:767:LEU:HA	1.77	0.41
1:C:353:TRP:CD1	1:C:353:TRP:C	2.94	0.41
1:C:365:TYR:HE1	1:C:513:LEU:HD23	1.85	0.41
1:C:434:ILE:HB	1:C:511:VAL:HG13	2.02	0.41
1:C:505:TYR:O	1:C:505:TYR:CD2	2.73	0.41
1:C:718:PHE:CD1	1:C:718:PHE:O	2.73	0.41
1:C:1139:ASP:OD1	1:C:1140:PRO:CD	2.57	0.41
1:A:33:THR:HA	1:A:58:PHE:HE2	1.66	0.41
1:A:91:TYR:HB3	1:A:268:GLY:O	2.20	0.41
1:A:108:THR:HG23	1:A:236:THR:OG1	2.20	0.41
1:A:319:ARG:CD	1:A:592:PHE:CE1	3.01	0.41
1:A:970:PHE:CD2	1:A:999:GLY:CA	2.97	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:983:ARG:NH1	1:C:517:LEU:HD11	2.36	0.41
1:B:223:LEU:N	1:B:223:LEU:HD23	2.36	0.41
1:B:368:LEU:O	1:B:372:ALA:HB3	2.21	0.41
1:B:800:PHE:HD2	1:B:927:PHE:HD2	1.69	0.41
1:B:1049:LEU:HD11	1:B:1067:TYR:HB3	2.02	0.41
1:C:36:VAL:O	1:C:223:LEU:CD2	2.61	0.41
1:C:472:ILE:CG2	1:C:490:PHE:CA	2.56	0.41
1:C:858:LEU:CD1	1:C:858:LEU:N	2.83	0.41
1:A:536:ASN:N	1:A:536:ASN:ND2	2.67	0.41
1:B:733:LYS:HD2	1:B:771:ALA:O	2.21	0.41
1:C:220:PHE:HE1	1:C:287:ASP:N	2.19	0.41
1:A:37:TYR:HE2	1:A:204:TYR:CZ	2.39	0.41
1:A:53:ASP:OD1	1:A:54:LEU:N	2.54	0.41
1:A:54:LEU:CD1	1:A:54:LEU:H	2.33	0.41
1:A:86:PHE:CD2	1:A:90:VAL:CG2	3.03	0.41
1:A:168:PHE:CZ	1:A:230:PRO:HD2	2.55	0.41
1:A:204:TYR:CD1	1:A:204:TYR:N	2.89	0.41
1:A:350:VAL:HG13	1:A:422:ASN:ND2	2.35	0.41
1:A:386:LYS:O	1:A:390:LEU:CD2	2.69	0.41
1:A:438:SER:HB2	1:A:442:ASP:HB2	2.02	0.41
1:A:483:VAL:HG13	1:A:485:GLY:H	1.86	0.41
1:A:825:LYS:HE2	1:A:942:ALA:HA	2.01	0.41
1:B:114:THR:O	1:B:132:GLU:OE1	2.30	0.41
1:B:165:ASN:ND2	1:B:165:ASN:N	2.64	0.41
1:B:431:GLY:HA2	1:B:515:PHE:HZ	1.85	0.41
1:B:472:ILE:CA	1:B:489:TYR:O	2.69	0.41
1:B:578:ASP:OD1	1:B:578:ASP:N	2.54	0.41
1:B:781:VAL:HG12	1:B:1029:MET:CE	2.51	0.41
1:B:822:LEU:CD2	1:B:1061:VAL:HG21	2.50	0.41
1:B:858:LEU:N	1:B:858:LEU:CD2	2.84	0.41
1:C:190:ARG:HD3	1:C:207:HIS:CE1	2.56	0.41
1:C:367:VAL:HG23	1:C:368:LEU:HD12	2.03	0.41
1:C:498:GLN:HG2	1:C:499:PRO:HD2	2.03	0.41
1:C:599:THR:HA	1:C:600:PRO:HD3	1.93	0.41
1:C:712:ILE:HD12	1:C:1094:VAL:HG21	2.03	0.41
1:A:752:LEU:CD1	1:A:993:ILE:HG21	2.50	0.41
1:A:1056:ALA:HB1	1:A:1057:PRO:HD2	2.02	0.41
1:B:62:VAL:HG12	1:B:267:VAL:C	2.41	0.41
1:B:555:SER:OG	1:B:586:ASP:OD2	2.34	0.41
1:C:86:PHE:CD1	1:C:86:PHE:C	2.94	0.41
1:A:298:GLU:OE2	1:A:316:SER:CB	2.69	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:349:SER:O	1:A:352:ALA:O	2.39	0.40
1:A:693:ILE:HD13	1:A:693:ILE:N	2.33	0.40
1:A:764:ASN:ND2	1:A:764:ASN:C	2.75	0.40
1:A:1115:ILE:O	1:A:1138:TYR:N	2.48	0.40
1:B:417:LYS:O	1:B:421:TYR:HB2	2.21	0.40
1:B:1116:THR:CG2	1:B:1140:PRO:CD	2.60	0.40
1:C:1091:ARG:NH1	1:C:1118:ASP:O	2.55	0.40
1:A:453:TYR:OH	1:A:493:GLN:HG3	2.20	0.40
1:A:806:LEU:CD2	1:A:807:PRO:CD	2.99	0.40
1:B:130:VAL:N	1:B:168:PHE:O	2.46	0.40
1:B:139:PRO:HB3	1:B:159:VAL:CG2	2.43	0.40
1:B:296:LEU:HD22	1:B:606:ASN:O	2.21	0.40
1:B:726:ILE:CG2	1:B:948:LEU:HG	2.52	0.40
1:B:825:LYS:HZ2	1:B:944:ALA:CB	2.24	0.40
1:A:715:PRO:HA	1:A:1072:GLU:HA	2.03	0.40
1:A:767:LEU:HD23	1:A:767:LEU:HA	1.86	0.40
1:B:168:PHE:CE2	1:B:170:TYR:HB2	2.50	0.40
1:B:592:PHE:CD1	1:B:592:PHE:C	2.94	0.40
1:B:973:ILE:HD12	1:B:983:ARG:NH2	2.37	0.40
1:B:1107:ARG:CZ	1:C:904:TYR:CG	3.04	0.40
1:C:92:PHE:HE2	1:C:240:THR:OG1	2.04	0.40
1:C:699:LEU:N	1:C:699:LEU:HD13	2.36	0.40
1:C:718:PHE:CZ	1:C:923:ILE:HD11	2.57	0.40
1:C:1089:PHE:C	1:C:1120:THR:HG22	2.41	0.40
1:C:1097:SER:HB3	1:C:1102:TRP:CD2	2.56	0.40
1:A:130:VAL:O	1:A:166:CYS:HA	2.21	0.40
1:A:332:ILE:N	1:A:332:ILE:CD1	2.84	0.40
1:A:403:ARG:HB2	1:A:406:GLU:OE1	2.22	0.40
1:A:560:LEU:HD12	1:A:562:PHE:CE1	2.53	0.40
1:A:611:LEU:HB2	1:A:650:LEU:CD2	2.41	0.40
1:B:16:VAL:HG11	1:B:158:ARG:HH12	1.86	0.40
1:B:308:VAL:N	1:B:602:THR:CB	2.80	0.40
1:B:973:ILE:HD12	1:B:983:ARG:HH22	1.87	0.40
1:B:1018:ILE:HD13	1:B:1018:ILE:HA	1.95	0.40
1:C:419:ALA:O	1:C:424:LYS:HB2	2.20	0.40
1:A:117:LEU:C	1:A:117:LEU:CD2	2.89	0.40
1:A:560:LEU:CB	1:A:562:PHE:HE1	2.33	0.40
1:A:671:CYS:HB2	1:A:695:TYR:CZ	2.56	0.40
1:A:895:GLN:O	1:A:895:GLN:HG2	2.20	0.40
1:B:141:LEU:HB3	1:B:243:ALA:CB	2.41	0.40
1:B:456:PHE:CD1	1:B:490:PHE:O	2.75	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:674:TYR:CE1	1:B:690:GLN:HB3	2.57	0.40
1:B:947:LYS:O	1:B:950:ASP:OD2	2.37	0.40
1:C:97:LYS:C	1:C:97:LYS:CD	2.89	0.40
1:C:302:THR:OG1	1:C:315:THR:CG2	2.69	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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	A	1060/1270 (84%)	1016 (96%)	37 (4%)	7 (1%)	22	55
1	B	1061/1270 (84%)	1018 (96%)	40 (4%)	3 (0%)	41	72
1	C	1066/1270 (84%)	1019 (96%)	40 (4%)	7 (1%)	22	55
All	All	3187/3810 (84%)	3053 (96%)	117 (4%)	17 (0%)	32	61

All (17) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	620	VAL
1	A	1117	THR
1	C	854	LYS
1	A	502	GLY
1	C	89	GLY
1	B	136	CYS
1	C	853	GLN
1	A	230	PRO
1	A	293	LEU
1	A	1053	PRO
1	B	728	PRO
1	C	728	PRO
1	C	1112	PRO

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	1135	ASN
1	C	1053	PRO
1	B	1112	PRO
1	A	1099	GLY

5.3.2 Protein sidechains [i](#)

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	A	932/1102 (85%)	857 (92%)	75 (8%)	12	38
1	B	932/1102 (85%)	866 (93%)	66 (7%)	14	44
1	C	929/1102 (84%)	845 (91%)	84 (9%)	9	32
All	All	2793/3306 (84%)	2568 (92%)	225 (8%)	15	38

All (225) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	32	PHE
1	A	37	TYR
1	A	43	PHE
1	A	64	TRP
1	A	84	LEU
1	A	86	PHE
1	A	91	TYR
1	A	92	PHE
1	A	99	ASN
1	A	104	TRP
1	A	130	VAL
1	A	136	CYS
1	A	200	TYR
1	A	201	PHE
1	A	203	ILE
1	A	211	ASN
1	A	215	ASP
1	A	220	PHE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	229	LEU
1	A	235	ILE
1	A	242	LEU
1	A	265	TYR
1	A	271	GLN
1	A	275	PHE
1	A	293	LEU
1	A	306	PHE
1	A	318	PHE
1	A	334	ASN
1	A	338	PHE
1	A	353	TRP
1	A	367	VAL
1	A	370	ASN
1	A	390	LEU
1	A	452	LEU
1	A	465	GLU
1	A	515	PHE
1	A	518	LEU
1	A	536	ASN
1	A	559	PHE
1	A	580	GLN
1	A	595	VAL
1	A	599	THR
1	A	611	LEU
1	A	619	GLU
1	A	650	LEU
1	A	661	GLU
1	A	674	TYR
1	A	693	ILE
1	A	695	TYR
1	A	696	THR
1	A	697	MET
1	A	699	LEU
1	A	705	VAL
1	A	751	ASN
1	A	755	GLN
1	A	764	ASN
1	A	804	GLN
1	A	823	PHE
1	A	861	LEU
1	A	873	TYR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	888	PHE
1	A	904	TYR
1	A	909	ILE
1	A	927	PHE
1	A	934	ILE
1	A	959	LEU
1	A	964	LYS
1	A	976	VAL
1	A	1067	TYR
1	A	1072	GLU
1	A	1092	GLU
1	A	1098	ASN
1	A	1101	HIS
1	A	1103	PHE
1	A	1106	GLN
1	B	32	PHE
1	B	34	ARG
1	B	43	PHE
1	B	61	ASN
1	B	86	PHE
1	B	92	PHE
1	B	95	THR
1	B	99	ASN
1	B	101	ILE
1	B	104	TRP
1	B	117	LEU
1	B	121	ASN
1	B	122	ASN
1	B	133	PHE
1	B	134	GLN
1	B	135	PHE
1	B	141	LEU
1	B	165	ASN
1	B	170	TYR
1	B	175	PHE
1	B	193	VAL
1	B	197	ILE
1	B	198	ASP
1	B	200	TYR
1	B	207	HIS
1	B	216	LEU
1	B	218	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	235	ILE
1	B	238	PHE
1	B	265	TYR
1	B	277	LEU
1	B	318	PHE
1	B	335	LEU
1	B	539	VAL
1	B	559	PHE
1	B	563	GLN
1	B	564	GLN
1	B	581	THR
1	B	583	GLU
1	B	584	ILE
1	B	611	LEU
1	B	638	THR
1	B	643	PHE
1	B	662	CYS
1	B	674	TYR
1	B	695	TYR
1	B	699	LEU
1	B	709	ASN
1	B	740	MET
1	B	743	CYS
1	B	784	GLN
1	B	826	VAL
1	B	855	PHE
1	B	858	LEU
1	B	912	THR
1	B	919	ASN
1	B	933	LYS
1	B	955	ASN
1	B	981	LEU
1	B	991	VAL
1	B	992	GLN
1	B	1072	GLU
1	B	1106	GLN
1	B	1114	ILE
1	B	1125	ASN
1	B	1142	GLN
1	C	32	PHE
1	C	38	TYR
1	C	43	PHE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	63	THR
1	C	86	PHE
1	C	95	THR
1	C	96	GLU
1	C	104	TRP
1	C	108	THR
1	C	117	LEU
1	C	125	ASN
1	C	165	ASN
1	C	204	TYR
1	C	210	ILE
1	C	220	PHE
1	C	223	LEU
1	C	224	GLU
1	C	227	VAL
1	C	231	ILE
1	C	234	ASN
1	C	266	TYR
1	C	270	LEU
1	C	291	CYS
1	C	301	CYS
1	C	314	GLN
1	C	317	ASN
1	C	318	PHE
1	C	334	ASN
1	C	338	PHE
1	C	353	TRP
1	C	355	ARG
1	C	360	ASN
1	C	374	PHE
1	C	385	THR
1	C	391	CYS
1	C	392	PHE
1	C	400	PHE
1	C	414	GLN
1	C	436	TRP
1	C	450	ASN
1	C	492	LEU
1	C	506	GLN
1	C	517	LEU
1	C	531	THR
1	C	539	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	541	PHE
1	C	546	LEU
1	C	557	LYS
1	C	563	GLN
1	C	567	ARG
1	C	585	LEU
1	C	599	THR
1	C	611	LEU
1	C	618	THR
1	C	620	VAL
1	C	644	GLN
1	C	655	HIS
1	C	658	ASN
1	C	660	TYR
1	C	671	CYS
1	C	674	TYR
1	C	699	LEU
1	C	738	CYS
1	C	740	MET
1	C	745	ASP
1	C	751	ASN
1	C	786	LYS
1	C	791	THR
1	C	907	ASN
1	C	921	LYS
1	C	934	ILE
1	C	969	ASN
1	C	981	LEU
1	C	985	ASP
1	C	992	GLN
1	C	1023	ASN
1	C	1048	HIS
1	C	1092	GLU
1	C	1101	HIS
1	C	1104	VAL
1	C	1106	GLN
1	C	1116	THR
1	C	1135	ASN
1	C	1141	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (86) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	81	ASN
1	A	99	ASN
1	A	125	ASN
1	A	164	ASN
1	A	165	ASN
1	A	211	ASN
1	A	234	ASN
1	A	317	ASN
1	A	321	GLN
1	A	334	ASN
1	A	370	ASN
1	A	409	GLN
1	A	501	ASN
1	A	536	ASN
1	A	564	GLN
1	A	580	GLN
1	A	613	GLN
1	A	641	ASN
1	A	675	GLN
1	A	690	GLN
1	A	751	ASN
1	A	755	GLN
1	A	764	ASN
1	A	774	GLN
1	A	804	GLN
1	A	949	GLN
1	A	965	GLN
1	A	1002	GLN
1	A	1058	HIS
1	A	1064	HIS
1	A	1108	ASN
1	A	1135	ASN
1	B	99	ASN
1	B	115	GLN
1	B	121	ASN
1	B	122	ASN
1	B	134	GLN
1	B	211	ASN
1	B	218	GLN
1	B	245	HIS
1	B	422	ASN
1	B	501	ASN
1	B	564	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	606	ASN
1	B	641	ASN
1	B	675	GLN
1	B	690	GLN
1	B	784	GLN
1	B	856	ASN
1	B	901	GLN
1	B	913	GLN
1	B	919	ASN
1	B	920	GLN
1	B	955	ASN
1	B	965	GLN
1	B	1011	GLN
1	B	1036	GLN
1	B	1106	GLN
1	B	1119	ASN
1	B	1142	GLN
1	C	87	ASN
1	C	99	ASN
1	C	125	ASN
1	C	164	ASN
1	C	207	HIS
1	C	211	ASN
1	C	360	ASN
1	C	388	ASN
1	C	394	ASN
1	C	409	GLN
1	C	414	GLN
1	C	532	ASN
1	C	544	ASN
1	C	563	GLN
1	C	644	GLN
1	C	751	ASN
1	C	762	GLN
1	C	779	GLN
1	C	824	ASN
1	C	969	ASN
1	C	992	GLN
1	C	1002	GLN
1	C	1005	GLN
1	C	1071	GLN
1	C	1125	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	1135	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](#)

20 monosaccharides are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	E	1	1,2	14,14,15	0.79	0	17,19,21	2.94	6 (35%)
2	NAG	E	2	2	14,14,15	0.66	0	17,19,21	1.08	2 (11%)
2	NAG	F	1	1,2	14,14,15	0.83	0	17,19,21	2.94	5 (29%)
2	NAG	F	2	2	14,14,15	0.64	0	17,19,21	1.11	2 (11%)
2	NAG	G	1	2	14,14,15	0.82	0	17,19,21	3.01	7 (41%)
2	NAG	G	2	2	14,14,15	0.62	0	17,19,21	1.07	2 (11%)
2	NAG	I	1	1,2	14,14,15	0.84	0	17,19,21	2.60	5 (29%)
2	NAG	I	2	2	14,14,15	0.63	0	17,19,21	1.08	2 (11%)
2	NAG	J	1	1,2	14,14,15	0.79	0	17,19,21	2.89	6 (35%)
2	NAG	J	2	2	14,14,15	0.62	0	17,19,21	1.11	2 (11%)
2	NAG	K	1	1,2	14,14,15	0.47	0	17,19,21	0.50	0
2	NAG	K	2	2	14,14,15	0.29	0	17,19,21	0.52	0
2	NAG	L	1	1,2	14,14,15	0.48	0	17,19,21	1.78	2 (11%)
2	NAG	L	2	2	14,14,15	0.49	0	17,19,21	2.06	5 (29%)
2	NAG	N	1	1,2	14,14,15	0.89	0	17,19,21	2.99	7 (41%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	N	2	2	14,14,15	0.66	0	17,19,21	1.10	2 (11%)
2	NAG	O	1	1,2	14,14,15	0.58	0	17,19,21	1.88	3 (17%)
2	NAG	O	2	2	14,14,15	0.53	0	17,19,21	2.05	5 (29%)
2	NAG	P	1	1,2	14,14,15	0.90	0	17,19,21	2.95	6 (35%)
2	NAG	P	2	2	14,14,15	0.65	0	17,19,21	1.11	2 (11%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	E	1	1,2	-	3/6/23/26	0/1/1/1
2	NAG	E	2	2	-	2/6/23/26	0/1/1/1
2	NAG	F	1	1,2	-	3/6/23/26	0/1/1/1
2	NAG	F	2	2	-	2/6/23/26	0/1/1/1
2	NAG	G	1	2	-	3/6/23/26	0/1/1/1
2	NAG	G	2	2	-	2/6/23/26	0/1/1/1
2	NAG	I	1	1,2	-	3/6/23/26	0/1/1/1
2	NAG	I	2	2	-	2/6/23/26	0/1/1/1
2	NAG	J	1	1,2	1/1/5/7	3/6/23/26	0/1/1/1
2	NAG	J	2	2	-	2/6/23/26	0/1/1/1
2	NAG	K	1	1,2	-	1/6/23/26	0/1/1/1
2	NAG	K	2	2	-	0/6/23/26	0/1/1/1
2	NAG	L	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	L	2	2	-	2/6/23/26	0/1/1/1
2	NAG	N	1	1,2	-	3/6/23/26	0/1/1/1
2	NAG	N	2	2	-	2/6/23/26	0/1/1/1
2	NAG	O	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	O	2	2	-	2/6/23/26	0/1/1/1
2	NAG	P	1	1,2	-	3/6/23/26	0/1/1/1
2	NAG	P	2	2	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (71) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	1	NAG	C8-C7-N2	7.53	128.84	116.10
2	G	1	NAG	C8-C7-N2	7.25	128.38	116.10
2	E	1	NAG	C8-C7-N2	7.24	128.35	116.10
2	N	1	NAG	C8-C7-N2	7.18	128.26	116.10
2	J	1	NAG	C8-C7-N2	6.92	127.82	116.10
2	P	1	NAG	C8-C7-N2	6.83	127.66	116.10
2	G	1	NAG	C2-N2-C7	6.53	132.21	122.90
2	J	1	NAG	C2-N2-C7	6.49	132.15	122.90
2	N	1	NAG	C2-N2-C7	6.45	132.09	122.90
2	E	1	NAG	C2-N2-C7	6.38	131.98	122.90
2	F	1	NAG	C2-N2-C7	6.25	131.80	122.90
2	P	1	NAG	C2-N2-C7	6.00	131.45	122.90
2	I	1	NAG	C8-C7-N2	5.93	126.14	116.10
2	L	2	NAG	C2-N2-C7	5.69	131.00	122.90
2	O	2	NAG	C2-N2-C7	5.63	130.92	122.90
2	O	1	NAG	C1-O5-C5	5.45	119.58	112.19
2	F	1	NAG	O7-C7-N2	-5.15	112.49	121.95
2	I	1	NAG	C2-N2-C7	4.99	130.01	122.90
2	E	1	NAG	O7-C7-N2	-4.72	113.27	121.95
2	G	1	NAG	O7-C7-N2	-4.71	113.30	121.95
2	P	1	NAG	O7-C7-N2	-4.69	113.32	121.95
2	L	1	NAG	C1-O5-C5	4.61	118.43	112.19
2	N	1	NAG	O7-C7-N2	-4.60	113.50	121.95
2	J	1	NAG	O7-C7-N2	-4.55	113.59	121.95
2	L	1	NAG	O5-C1-C2	-4.45	104.25	111.29
2	P	1	NAG	C1-O5-C5	-4.37	106.27	112.19
2	I	1	NAG	C4-C3-C2	-4.26	104.78	111.02
2	I	1	NAG	O7-C7-N2	-4.10	114.41	121.95
2	N	1	NAG	C1-O5-C5	-3.97	106.81	112.19
2	O	1	NAG	O5-C1-C2	-3.77	105.34	111.29
2	I	1	NAG	C1-O5-C5	-3.74	107.13	112.19
2	L	2	NAG	C8-C7-N2	-3.44	110.28	116.10
2	O	2	NAG	C8-C7-N2	-3.42	110.31	116.10
2	L	2	NAG	C1-O5-C5	3.41	116.81	112.19
2	O	2	NAG	C1-O5-C5	3.39	116.79	112.19
2	P	1	NAG	C4-C3-C2	-3.24	106.28	111.02
2	F	1	NAG	C1-O5-C5	-3.13	107.95	112.19
2	N	1	NAG	C4-C3-C2	-3.11	106.47	111.02
2	J	1	NAG	C4-C3-C2	-2.99	106.63	111.02
2	E	1	NAG	C4-C3-C2	-2.92	106.74	111.02
2	G	1	NAG	C1-C2-N2	-2.89	105.55	110.49
2	G	1	NAG	C4-C3-C2	-2.74	107.00	111.02
2	J	1	NAG	C1-O5-C5	-2.71	108.52	112.19

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	1	NAG	C1-C2-N2	-2.69	105.89	110.49
2	G	1	NAG	C1-O5-C5	-2.65	108.61	112.19
2	O	1	NAG	C2-N2-C7	2.62	126.64	122.90
2	J	1	NAG	C1-C2-N2	-2.52	106.18	110.49
2	P	2	NAG	C2-N2-C7	-2.49	119.36	122.90
2	E	1	NAG	C1-O5-C5	-2.48	108.83	112.19
2	I	2	NAG	C1-C2-N2	-2.42	106.36	110.49
2	F	2	NAG	C2-N2-C7	-2.41	119.47	122.90
2	N	2	NAG	C2-N2-C7	-2.40	119.48	122.90
2	J	2	NAG	C2-N2-C7	-2.40	119.49	122.90
2	G	2	NAG	C1-C2-N2	-2.37	106.44	110.49
2	E	2	NAG	C1-C2-N2	-2.36	106.45	110.49
2	O	2	NAG	C1-C2-N2	-2.33	106.52	110.49
2	J	2	NAG	C1-C2-N2	-2.32	106.53	110.49
2	P	2	NAG	C1-C2-N2	-2.32	106.53	110.49
2	N	2	NAG	C1-C2-N2	-2.31	106.55	110.49
2	F	2	NAG	C1-C2-N2	-2.30	106.55	110.49
2	G	2	NAG	C2-N2-C7	-2.30	119.63	122.90
2	I	2	NAG	C2-N2-C7	-2.30	119.63	122.90
2	E	2	NAG	C2-N2-C7	-2.29	119.64	122.90
2	L	2	NAG	C1-C2-N2	-2.29	106.58	110.49
2	P	1	NAG	C1-C2-N2	-2.27	106.62	110.49
2	F	1	NAG	C4-C3-C2	-2.21	107.78	111.02
2	O	2	NAG	O7-C7-N2	2.19	125.98	121.95
2	L	2	NAG	O7-C7-N2	2.13	125.87	121.95
2	N	1	NAG	O7-C7-C8	-2.06	118.23	122.06
2	G	1	NAG	O7-C7-C8	-2.02	118.30	122.06
2	N	1	NAG	C1-C2-N2	-2.01	107.06	110.49

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	J	1	NAG	C1

All (44) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	L	2	NAG	C3-C2-N2-C7
2	O	2	NAG	C3-C2-N2-C7
2	E	1	NAG	C8-C7-N2-C2
2	E	1	NAG	O7-C7-N2-C2
2	F	1	NAG	C8-C7-N2-C2

Continued on next page...

Continued from previous page...

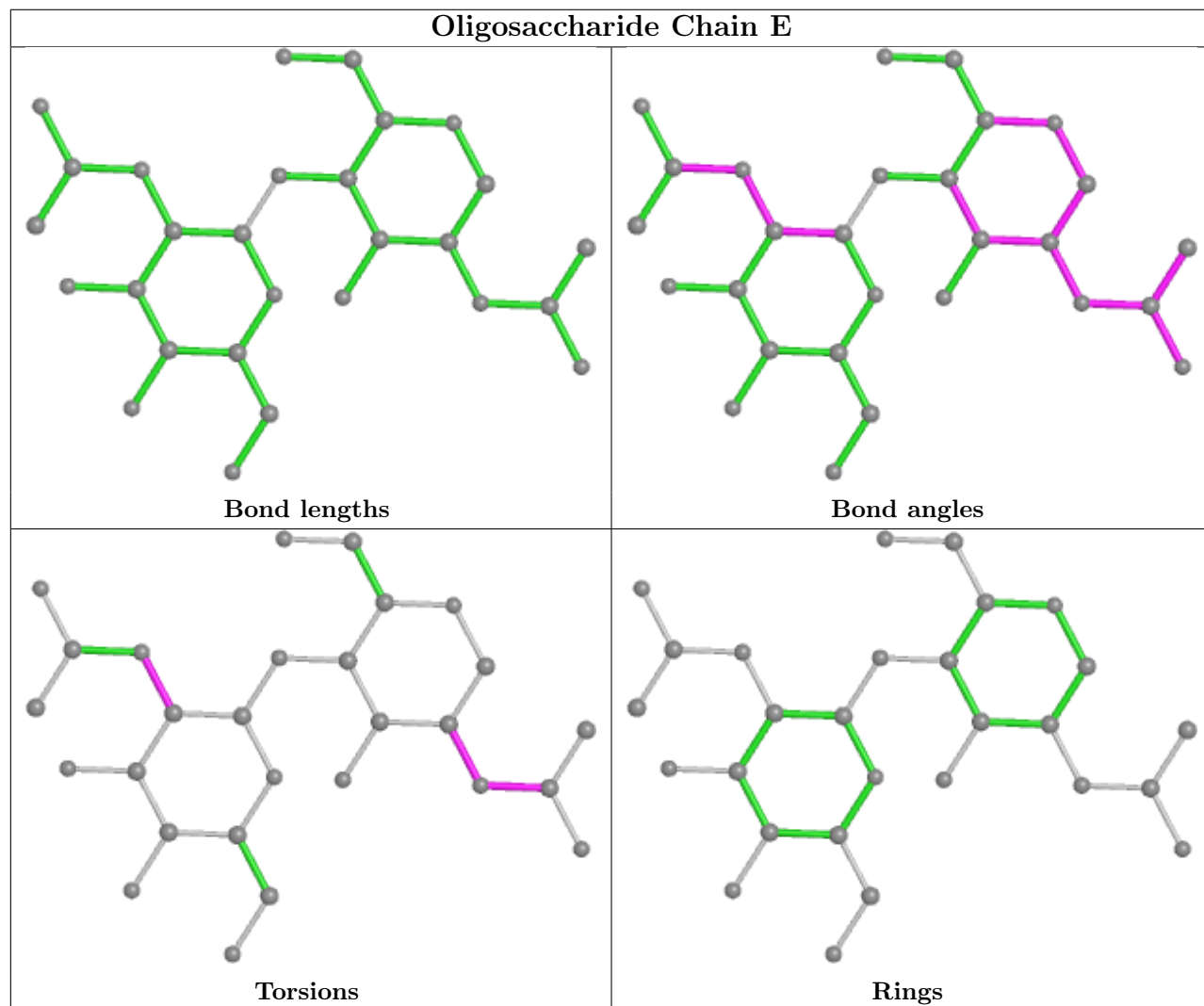
Mol	Chain	Res	Type	Atoms
2	F	1	NAG	O7-C7-N2-C2
2	G	1	NAG	C8-C7-N2-C2
2	G	1	NAG	O7-C7-N2-C2
2	I	1	NAG	C8-C7-N2-C2
2	I	1	NAG	O7-C7-N2-C2
2	J	1	NAG	C8-C7-N2-C2
2	J	1	NAG	O7-C7-N2-C2
2	L	1	NAG	C8-C7-N2-C2
2	L	1	NAG	O7-C7-N2-C2
2	N	1	NAG	C8-C7-N2-C2
2	N	1	NAG	O7-C7-N2-C2
2	O	1	NAG	C8-C7-N2-C2
2	O	1	NAG	O7-C7-N2-C2
2	P	1	NAG	C8-C7-N2-C2
2	P	1	NAG	O7-C7-N2-C2
2	L	2	NAG	O5-C5-C6-O6
2	O	2	NAG	O5-C5-C6-O6
2	G	1	NAG	C3-C2-N2-C7
2	E	2	NAG	C1-C2-N2-C7
2	F	2	NAG	C1-C2-N2-C7
2	G	2	NAG	C1-C2-N2-C7
2	I	2	NAG	C1-C2-N2-C7
2	J	2	NAG	C1-C2-N2-C7
2	N	2	NAG	C1-C2-N2-C7
2	P	2	NAG	C1-C2-N2-C7
2	E	1	NAG	C3-C2-N2-C7
2	F	1	NAG	C3-C2-N2-C7
2	I	1	NAG	C3-C2-N2-C7
2	J	1	NAG	C3-C2-N2-C7
2	K	1	NAG	C3-C2-N2-C7
2	N	1	NAG	C3-C2-N2-C7
2	P	1	NAG	C3-C2-N2-C7
2	E	2	NAG	C3-C2-N2-C7
2	F	2	NAG	C3-C2-N2-C7
2	G	2	NAG	C3-C2-N2-C7
2	I	2	NAG	C3-C2-N2-C7
2	J	2	NAG	C3-C2-N2-C7
2	N	2	NAG	C3-C2-N2-C7
2	P	2	NAG	C3-C2-N2-C7

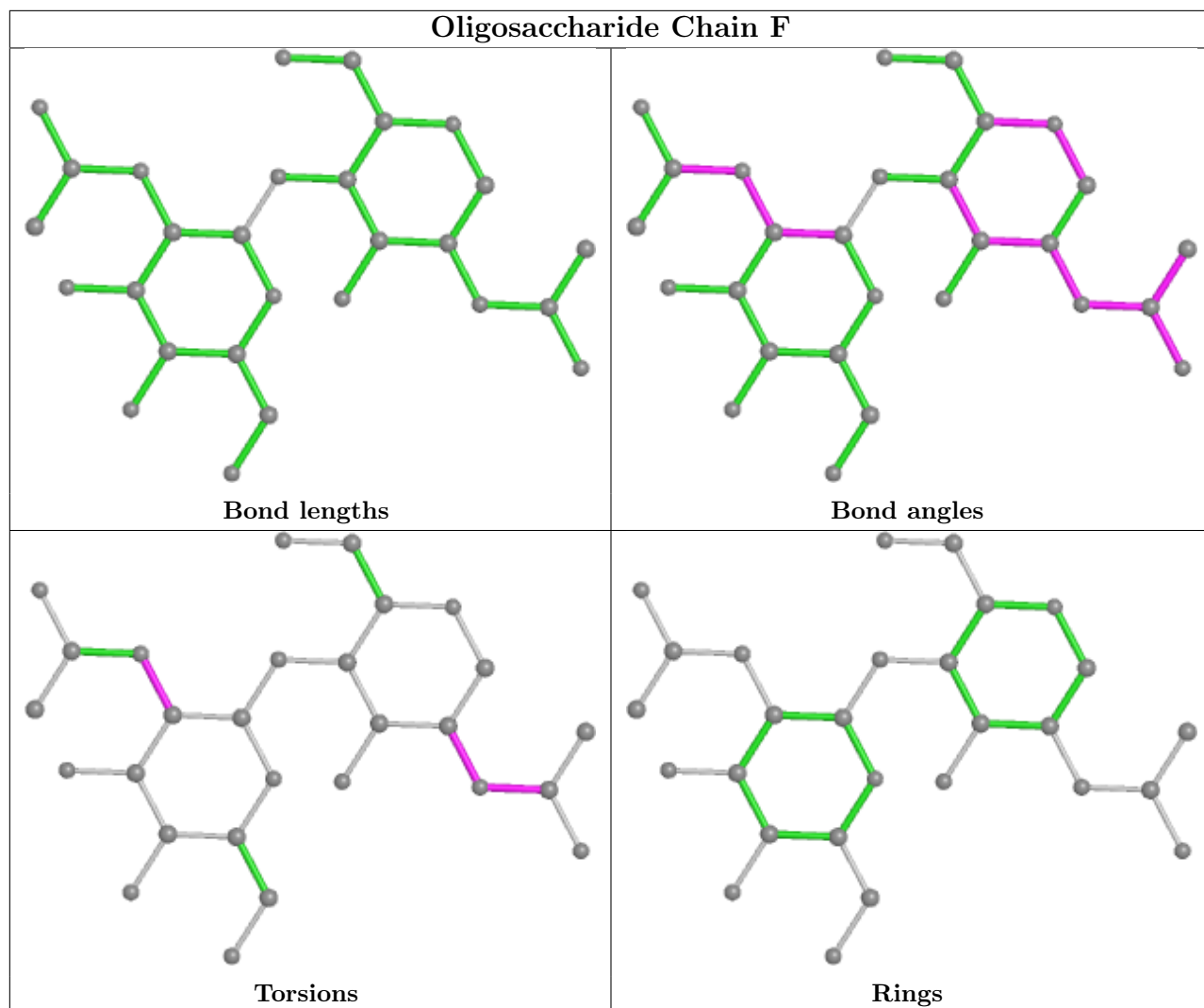
There are no ring outliers.

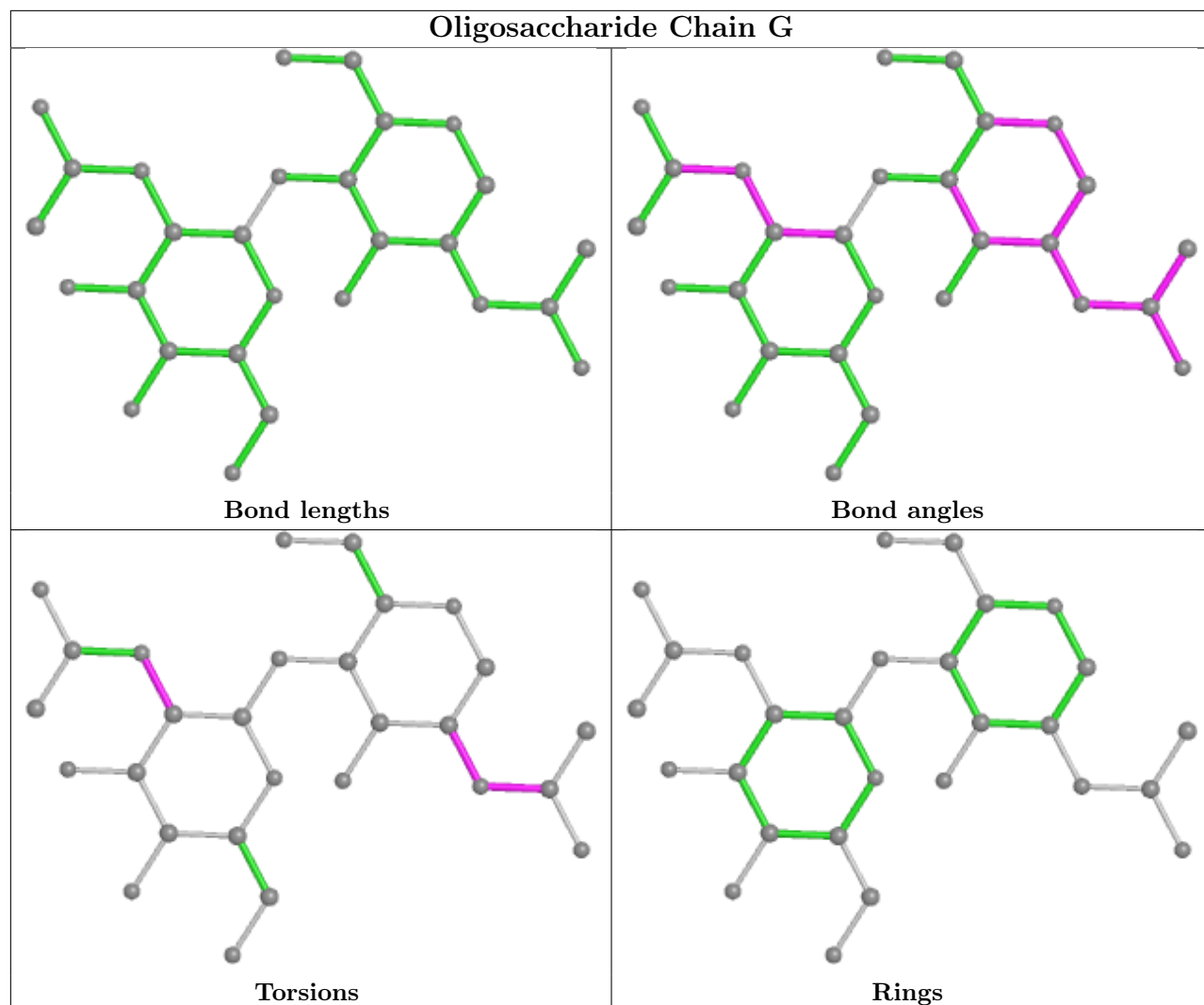
5 monomers are involved in 6 short contacts:

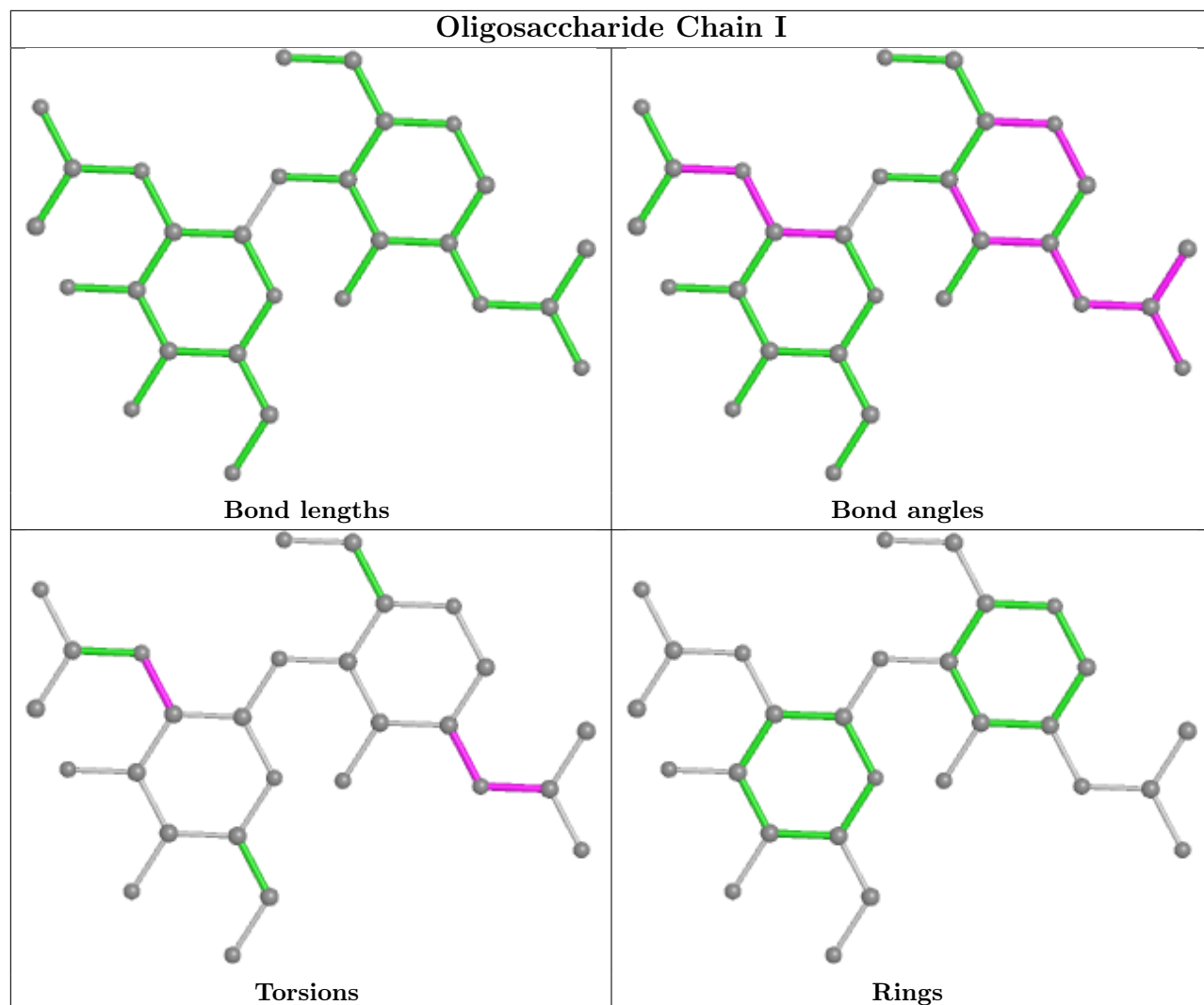
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	1	NAG	1	0
2	O	2	NAG	1	0
2	G	1	NAG	1	0
2	L	2	NAG	1	0
2	J	1	NAG	2	0

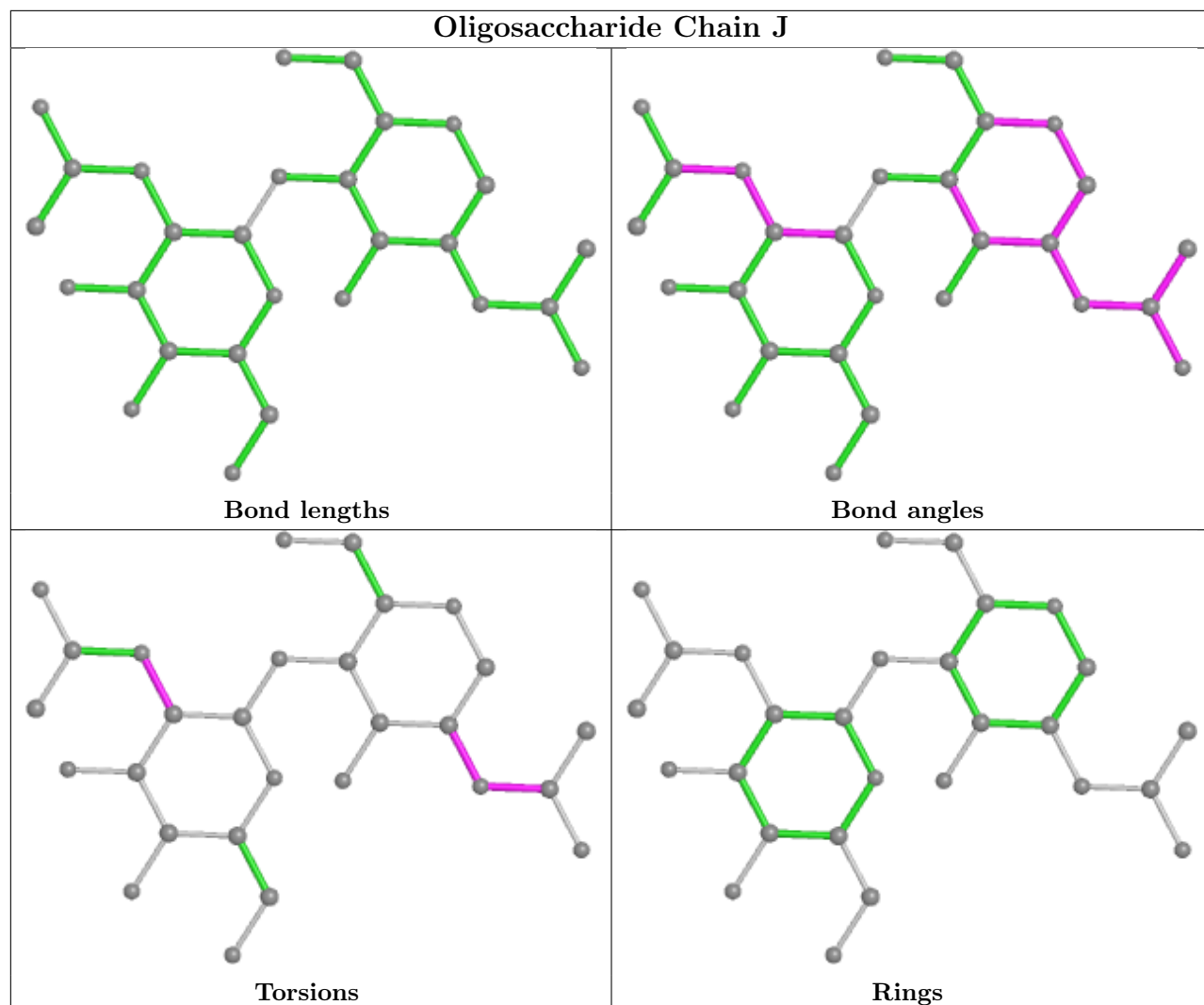
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

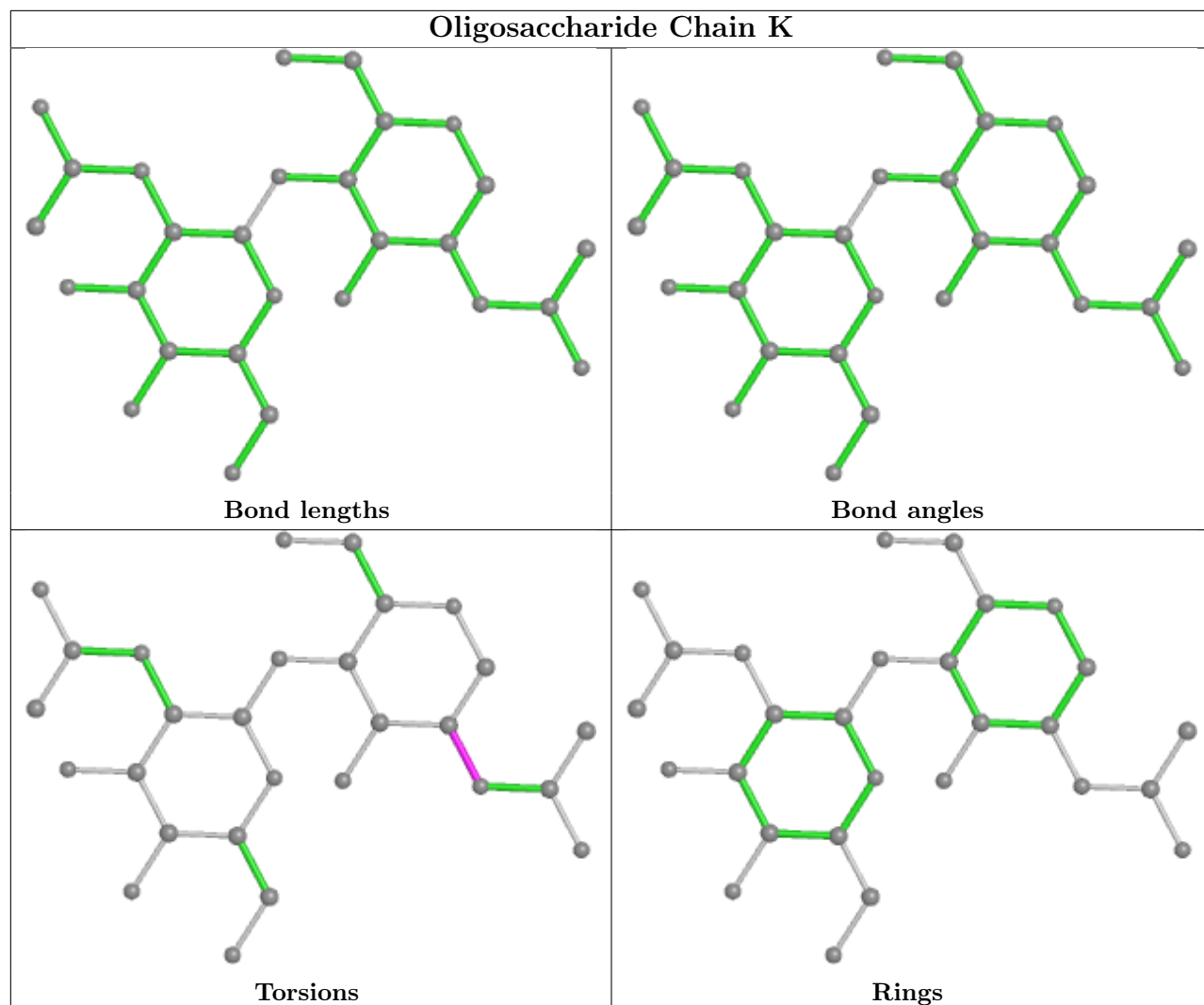


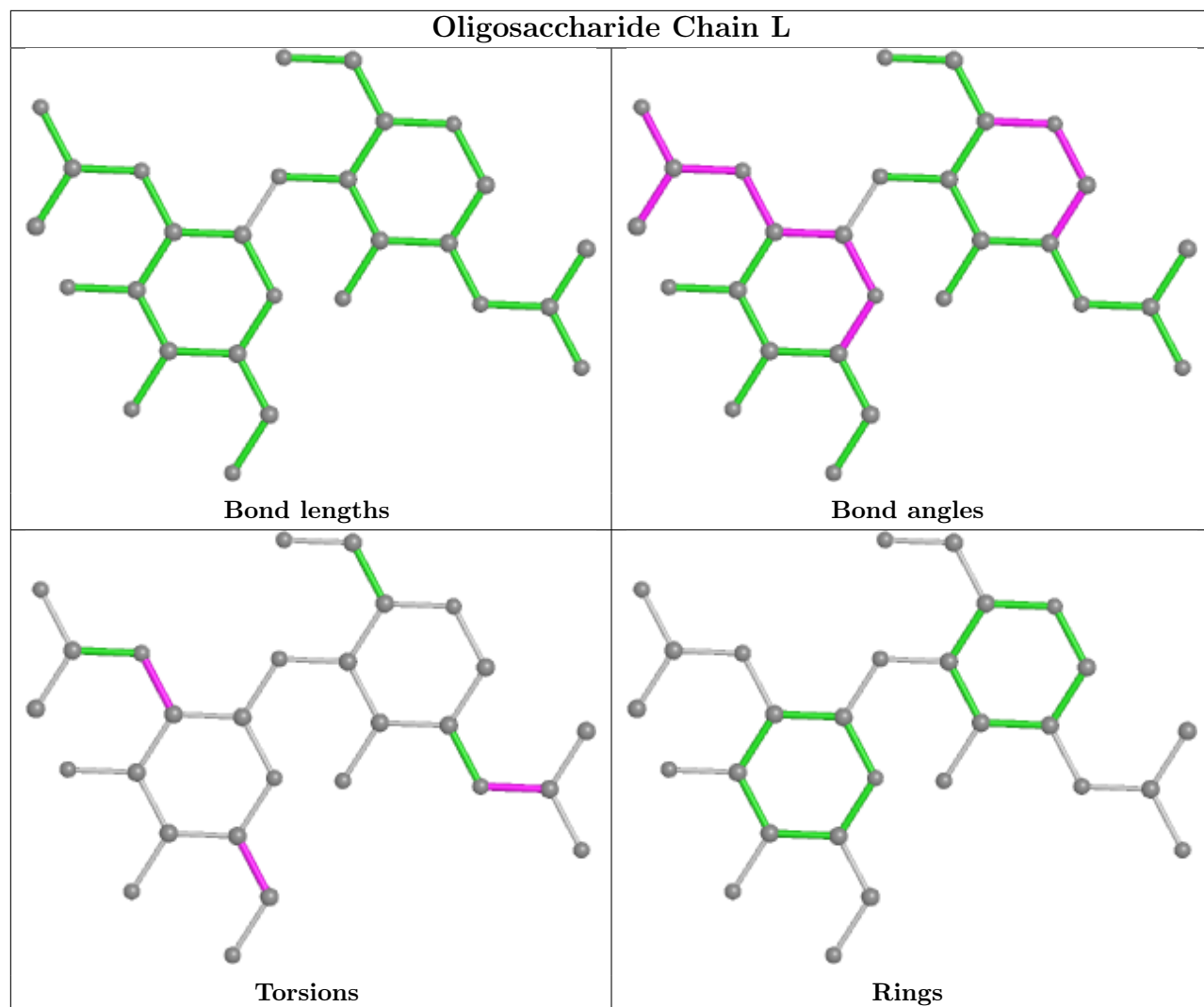


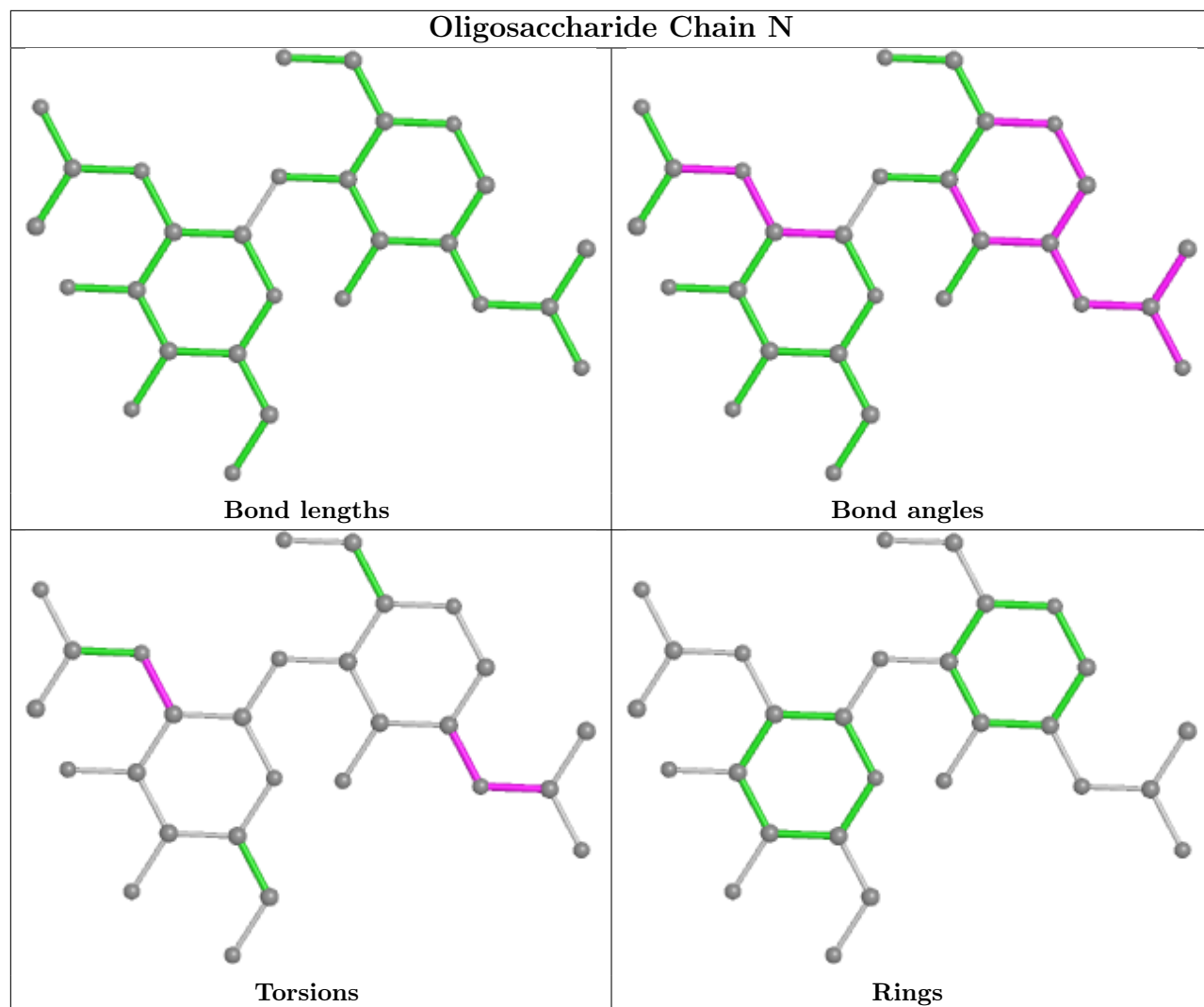


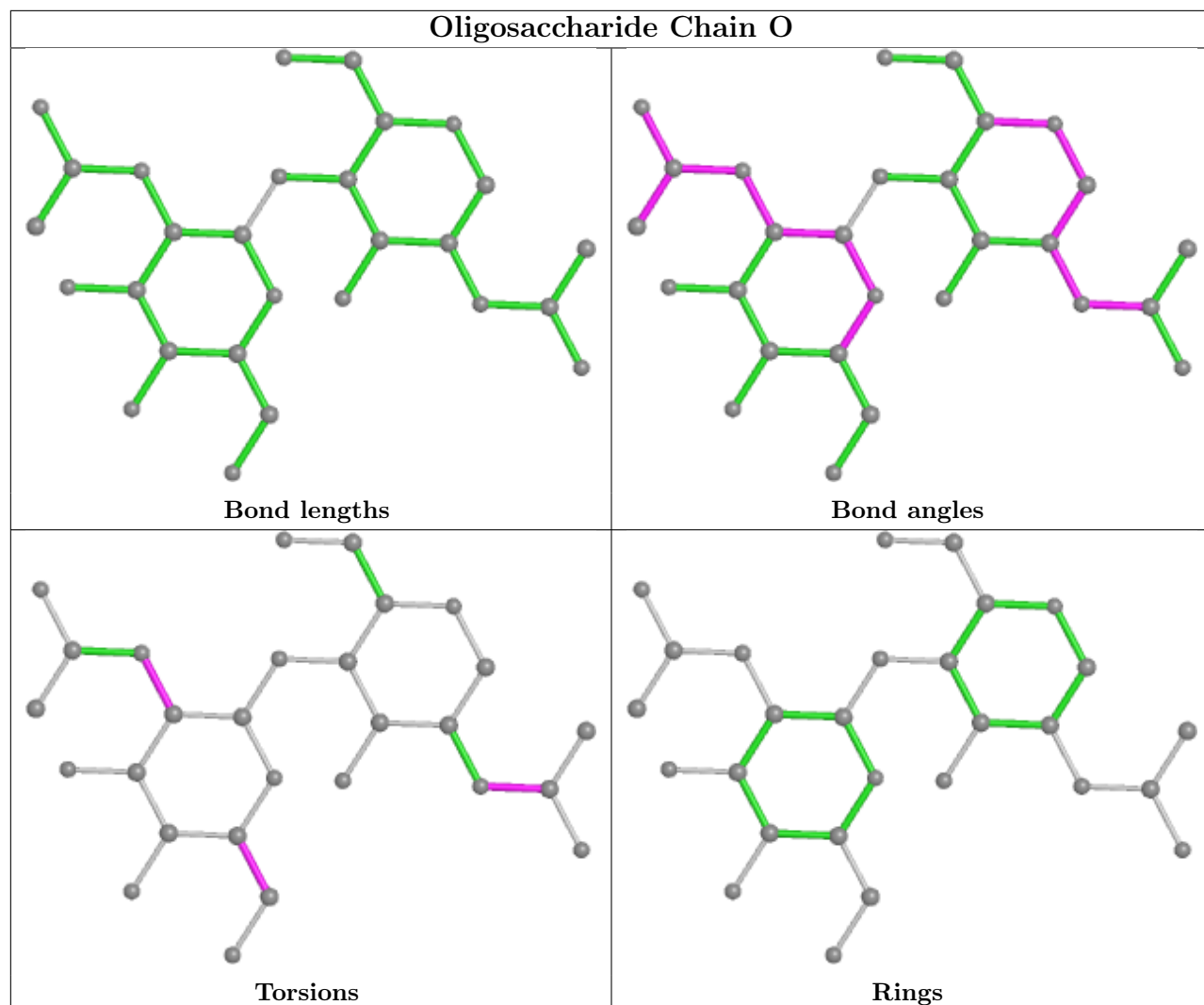


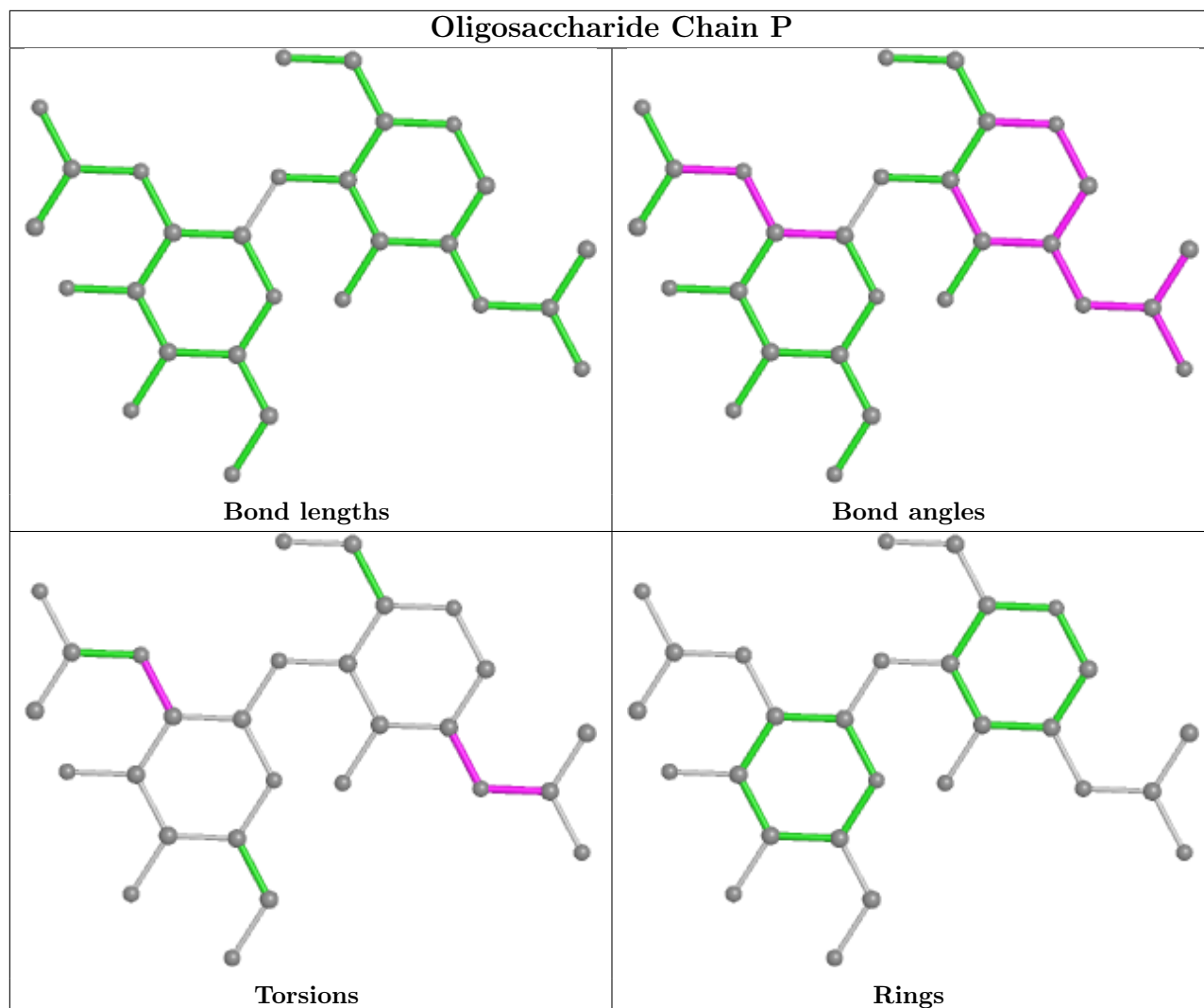












5.6 Ligand geometry [i](#)

24 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	NAG	B	1302	1	14,14,15	0.74	0	17,19,21	1.06	2 (11%)
3	NAG	B	1304	1	14,14,15	0.43	0	17,19,21	0.96	0
3	NAG	B	1305	1	14,14,15	0.48	0	17,19,21	1.23	2 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	A	1304	1	14,14,15	0.37	0	17,19,21	0.63	0
3	NAG	C	1303	1	14,14,15	0.66	0	17,19,21	1.99	5 (29%)
3	NAG	C	1302	-	14,14,15	0.46	0	17,19,21	1.38	3 (17%)
3	NAG	B	1309	1	14,14,15	0.45	0	17,19,21	2.28	4 (23%)
3	NAG	A	1301	1	14,14,15	0.31	0	17,19,21	0.67	0
3	NAG	C	1307	1	14,14,15	0.54	0	17,19,21	1.45	3 (17%)
3	NAG	C	1305	1	14,14,15	0.48	0	17,19,21	1.63	4 (23%)
3	NAG	A	1302	1	14,14,15	0.34	0	17,19,21	0.63	0
3	NAG	B	1301	1	14,14,15	0.33	0	17,19,21	1.46	3 (17%)
3	NAG	A	1303	1	14,14,15	0.24	0	17,19,21	1.38	3 (17%)
3	NAG	B	1303	1	14,14,15	0.45	0	17,19,21	0.61	0
3	NAG	A	1308	1	14,14,15	0.40	0	17,19,21	1.08	1 (5%)
3	NAG	A	1307	1	14,14,15	0.45	0	17,19,21	0.59	0
3	NAG	A	1306	1	14,14,15	0.28	0	17,19,21	1.33	3 (17%)
3	NAG	C	1306	1	14,14,15	0.56	0	17,19,21	0.78	0
3	NAG	C	1304	1	14,14,15	0.68	0	17,19,21	2.81	6 (35%)
3	NAG	B	1308	1	14,14,15	0.50	0	17,19,21	1.75	4 (23%)
3	NAG	C	1301	-	14,14,15	0.44	0	17,19,21	0.66	0
3	NAG	A	1305	1	14,14,15	0.40	0	17,19,21	2.66	6 (35%)
3	NAG	B	1307	1	14,14,15	0.55	0	17,19,21	1.26	2 (11%)
3	NAG	B	1306	1	14,14,15	0.27	0	17,19,21	1.41	4 (23%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	B	1302	1	-	1/6/23/26	0/1/1/1
3	NAG	B	1304	1	-	2/6/23/26	0/1/1/1
3	NAG	B	1305	1	-	2/6/23/26	0/1/1/1
3	NAG	A	1304	1	-	1/6/23/26	0/1/1/1
3	NAG	C	1303	1	-	4/6/23/26	0/1/1/1
3	NAG	C	1302	-	-	4/6/23/26	0/1/1/1
3	NAG	B	1309	1	-	2/6/23/26	0/1/1/1
3	NAG	A	1301	1	-	1/6/23/26	0/1/1/1
3	NAG	C	1307	1	-	4/6/23/26	0/1/1/1
3	NAG	C	1305	1	-	4/6/23/26	0/1/1/1

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	A	1302	1	-	1/6/23/26	0/1/1/1
3	NAG	B	1301	1	-	1/6/23/26	0/1/1/1
3	NAG	A	1303	1	-	1/6/23/26	0/1/1/1
3	NAG	B	1303	1	-	0/6/23/26	0/1/1/1
3	NAG	A	1308	1	-	1/6/23/26	0/1/1/1
3	NAG	A	1307	1	-	1/6/23/26	0/1/1/1
3	NAG	A	1306	1	-	1/6/23/26	0/1/1/1
3	NAG	C	1306	1	-	3/6/23/26	0/1/1/1
3	NAG	C	1304	1	-	0/6/23/26	0/1/1/1
3	NAG	B	1308	1	-	4/6/23/26	0/1/1/1
3	NAG	C	1301	-	-	1/6/23/26	0/1/1/1
3	NAG	A	1305	1	-	5/6/23/26	0/1/1/1
3	NAG	B	1307	1	-	1/6/23/26	0/1/1/1
3	NAG	B	1306	1	-	1/6/23/26	0/1/1/1

There are no bond length outliers.

All (55) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	1304	NAG	C1-O5-C5	9.52	125.10	112.19
3	A	1305	NAG	C2-N2-C7	6.63	132.35	122.90
3	A	1305	NAG	C8-C7-N2	6.40	126.94	116.10
3	B	1309	NAG	C1-O5-C5	6.36	120.81	112.19
3	C	1303	NAG	C1-O5-C5	5.52	119.67	112.19
3	B	1309	NAG	C1-C2-N2	-4.25	103.22	110.49
3	B	1301	NAG	C1-O5-C5	4.11	117.76	112.19
3	C	1307	NAG	C8-C7-N2	4.08	123.01	116.10
3	B	1308	NAG	C8-C7-N2	3.83	122.58	116.10
3	B	1308	NAG	C1-C2-N2	-3.62	104.30	110.49
3	A	1303	NAG	O5-C1-C2	-3.54	105.70	111.29
3	B	1308	NAG	C2-N2-C7	3.49	127.87	122.90
3	C	1305	NAG	C1-O5-C5	3.47	116.89	112.19
3	C	1302	NAG	C8-C7-N2	3.47	121.97	116.10
3	B	1307	NAG	C2-N2-C7	3.44	127.80	122.90
3	C	1305	NAG	C8-C7-N2	3.40	121.86	116.10
3	B	1306	NAG	O5-C1-C2	-3.39	105.93	111.29
3	C	1303	NAG	C8-C7-N2	3.36	121.79	116.10
3	A	1305	NAG	O7-C7-N2	-3.15	116.16	121.95
3	A	1308	NAG	O5-C1-C2	-3.10	106.39	111.29
3	C	1305	NAG	C2-N2-C7	3.07	127.28	122.90
3	C	1304	NAG	O5-C1-C2	3.05	116.11	111.29

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1309	NAG	O7-C7-N2	3.04	127.54	121.95
3	B	1305	NAG	O5-C5-C6	3.01	111.92	107.20
3	A	1306	NAG	C1-O5-C5	2.95	116.18	112.19
3	A	1306	NAG	O5-C1-C2	-2.89	106.72	111.29
3	B	1305	NAG	O5-C1-C2	-2.80	106.86	111.29
3	A	1305	NAG	O7-C7-C8	-2.78	116.90	122.06
3	C	1307	NAG	C2-N2-C7	2.75	126.82	122.90
3	C	1304	NAG	C2-N2-C7	2.69	126.73	122.90
3	C	1302	NAG	C2-N2-C7	2.61	126.62	122.90
3	B	1308	NAG	O7-C7-N2	-2.57	117.22	121.95
3	B	1306	NAG	C1-O5-C5	2.50	115.58	112.19
3	A	1305	NAG	C1-O5-C5	2.49	115.57	112.19
3	C	1303	NAG	C3-C4-C5	2.48	114.67	110.24
3	B	1301	NAG	C2-N2-C7	2.46	126.41	122.90
3	B	1309	NAG	C3-C4-C5	2.44	114.58	110.24
3	B	1301	NAG	O5-C1-C2	-2.41	107.48	111.29
3	A	1305	NAG	O5-C5-C6	2.40	110.96	107.20
3	B	1307	NAG	O7-C7-N2	2.37	126.31	121.95
3	B	1306	NAG	C2-N2-C7	2.35	126.25	122.90
3	C	1303	NAG	O7-C7-N2	-2.31	117.71	121.95
3	A	1303	NAG	C4-C3-C2	-2.29	107.67	111.02
3	B	1302	NAG	C1-C2-N2	-2.26	106.62	110.49
3	C	1304	NAG	O5-C5-C6	2.26	110.74	107.20
3	B	1302	NAG	C2-N2-C7	-2.23	119.73	122.90
3	C	1304	NAG	C3-C4-C5	2.22	114.20	110.24
3	B	1306	NAG	C4-C3-C2	-2.21	107.78	111.02
3	A	1303	NAG	C2-N2-C7	2.20	126.04	122.90
3	C	1307	NAG	O7-C7-N2	-2.19	117.93	121.95
3	C	1304	NAG	O5-C5-C4	2.12	115.99	110.83
3	C	1305	NAG	O7-C7-N2	-2.07	118.14	121.95
3	A	1306	NAG	C2-N2-C7	2.07	125.84	122.90
3	C	1303	NAG	C2-N2-C7	2.05	125.82	122.90
3	C	1302	NAG	O7-C7-N2	-2.01	118.25	121.95

There are no chirality outliers.

All (46) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1303	NAG	C3-C2-N2-C7
3	A	1305	NAG	C1-C2-N2-C7
3	A	1306	NAG	C3-C2-N2-C7
3	B	1301	NAG	C3-C2-N2-C7

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
3	B	1306	NAG	C3-C2-N2-C7
3	B	1308	NAG	C4-C5-C6-O6
3	B	1305	NAG	O5-C5-C6-O6
3	C	1306	NAG	O5-C5-C6-O6
3	C	1302	NAG	O5-C5-C6-O6
3	B	1309	NAG	O5-C5-C6-O6
3	C	1307	NAG	O5-C5-C6-O6
3	A	1305	NAG	C8-C7-N2-C2
3	A	1305	NAG	O7-C7-N2-C2
3	B	1308	NAG	C8-C7-N2-C2
3	B	1308	NAG	O7-C7-N2-C2
3	C	1302	NAG	C8-C7-N2-C2
3	C	1302	NAG	O7-C7-N2-C2
3	C	1303	NAG	C8-C7-N2-C2
3	C	1303	NAG	O7-C7-N2-C2
3	C	1305	NAG	C8-C7-N2-C2
3	C	1305	NAG	O7-C7-N2-C2
3	C	1307	NAG	C8-C7-N2-C2
3	C	1307	NAG	O7-C7-N2-C2
3	B	1308	NAG	O5-C5-C6-O6
3	C	1303	NAG	O5-C5-C6-O6
3	C	1305	NAG	O5-C5-C6-O6
3	B	1304	NAG	O5-C5-C6-O6
3	A	1305	NAG	O5-C5-C6-O6
3	A	1301	NAG	O5-C5-C6-O6
3	A	1302	NAG	O5-C5-C6-O6
3	C	1306	NAG	C4-C5-C6-O6
3	C	1301	NAG	O5-C5-C6-O6
3	A	1307	NAG	O5-C5-C6-O6
3	A	1304	NAG	O5-C5-C6-O6
3	A	1308	NAG	O5-C5-C6-O6
3	B	1305	NAG	C4-C5-C6-O6
3	C	1302	NAG	C4-C5-C6-O6
3	B	1309	NAG	C4-C5-C6-O6
3	B	1302	NAG	C3-C2-N2-C7
3	C	1306	NAG	C3-C2-N2-C7
3	C	1307	NAG	C4-C5-C6-O6
3	C	1303	NAG	C4-C5-C6-O6
3	C	1305	NAG	C4-C5-C6-O6
3	A	1305	NAG	C4-C5-C6-O6
3	B	1307	NAG	C4-C5-C6-O6
3	B	1304	NAG	C4-C5-C6-O6

There are no ring outliers.

6 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	1302	NAG	3	0
3	B	1305	NAG	1	0
3	C	1303	NAG	1	0
3	C	1306	NAG	1	0
3	C	1301	NAG	1	0
3	A	1305	NAG	1	0

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.

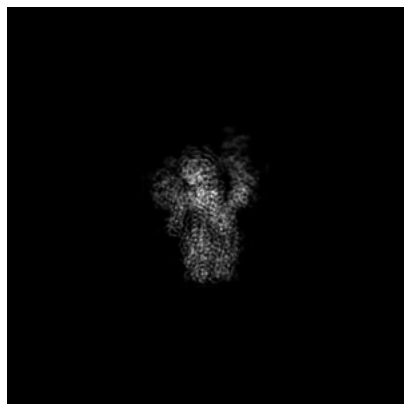
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-17576. These allow visual inspection of the internal detail of the map and identification of artifacts.

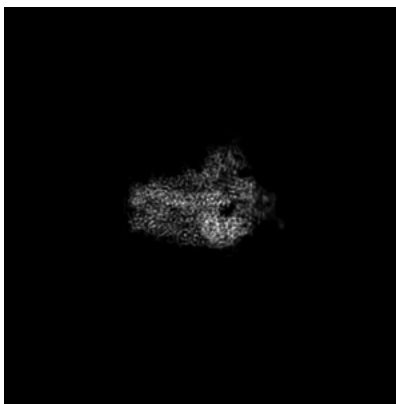
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

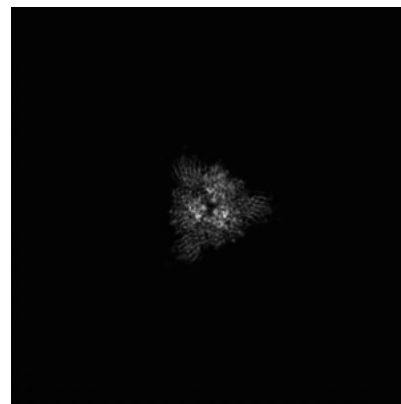
6.1.1 Primary map



X

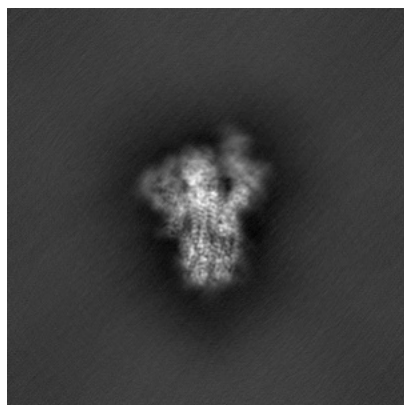


Y

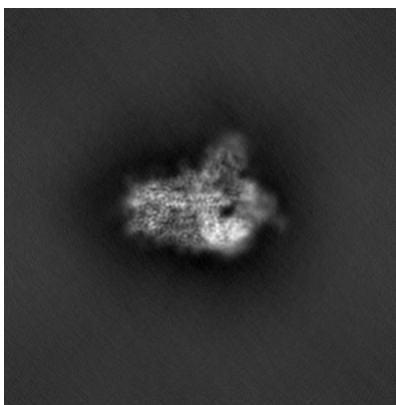


Z

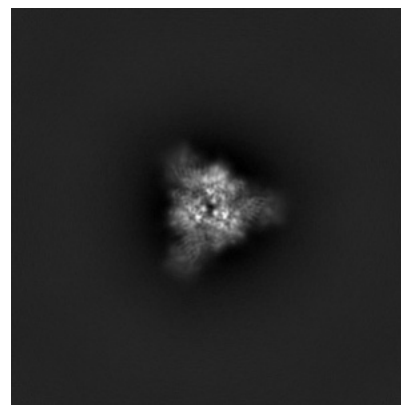
6.1.2 Raw map



X



Y



Z

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

6.2 Central slices [i](#)

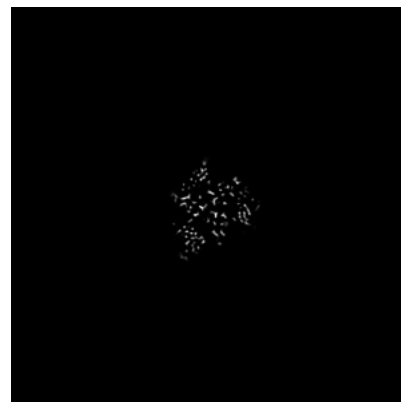
6.2.1 Primary map



X Index: 246

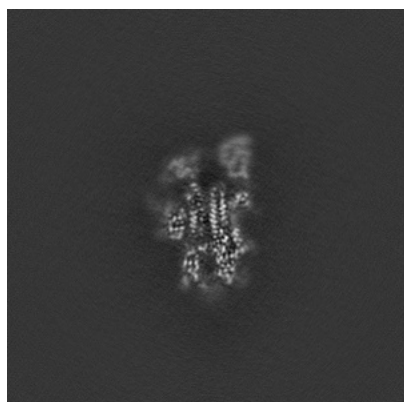


Y Index: 246

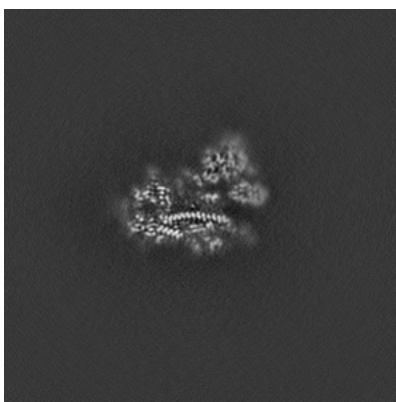


Z Index: 246

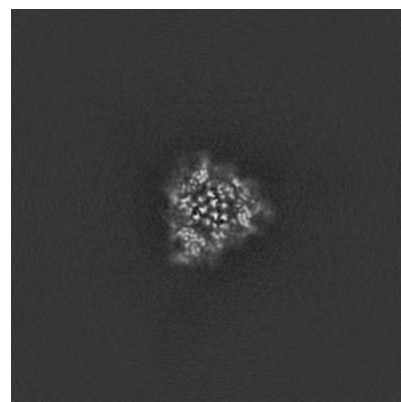
6.2.2 Raw map



X Index: 246



Y Index: 246



Z Index: 246

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: 251

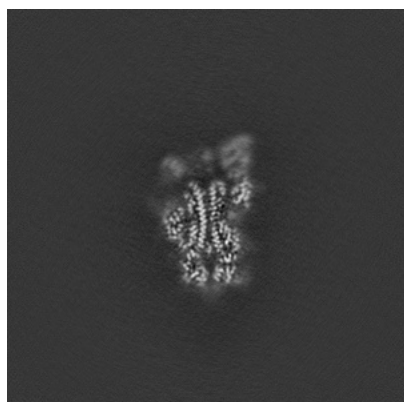


Y Index: 239

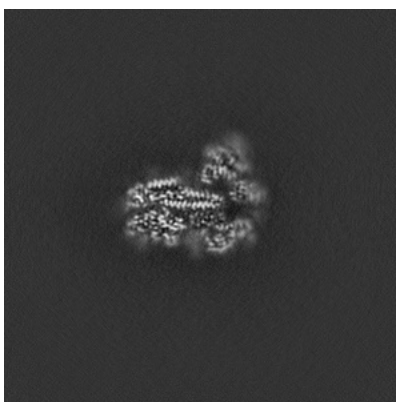


Z Index: 262

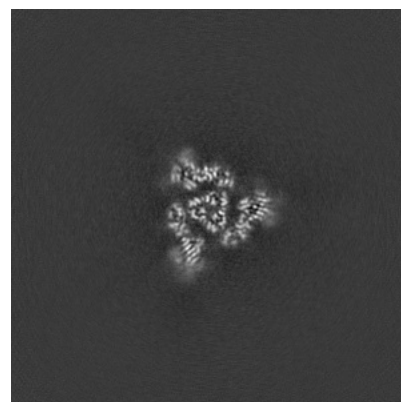
6.3.2 Raw map



X Index: 251



Y Index: 239

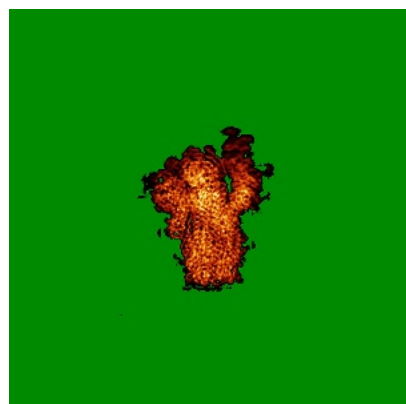


Z Index: 262

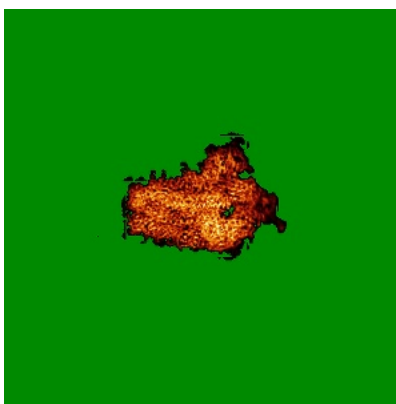
The images above show the largest variance slices of the map in three orthogonal directions.

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

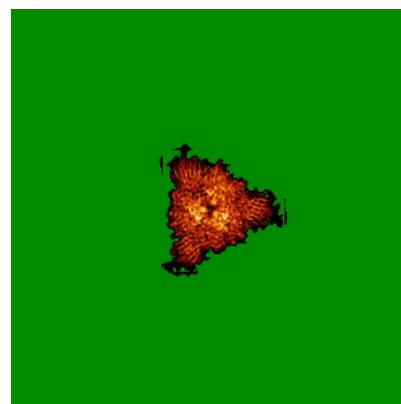
6.4.1 Primary map



X

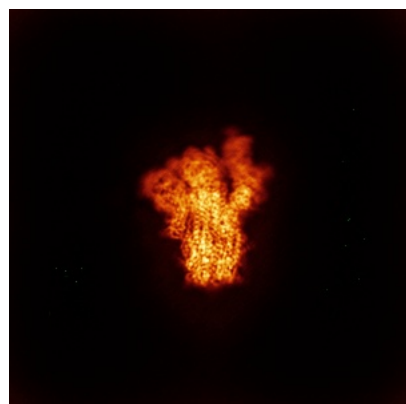


Y

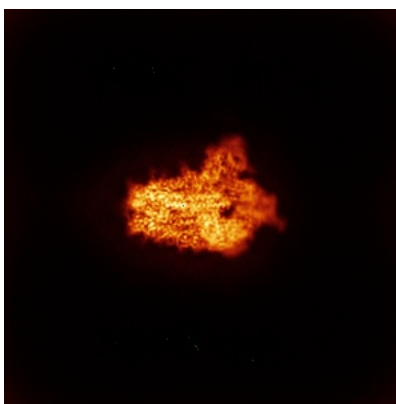


Z

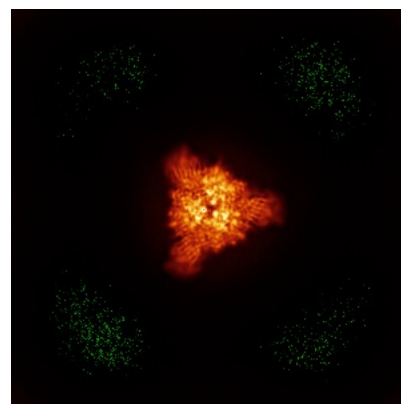
6.4.2 Raw map



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.

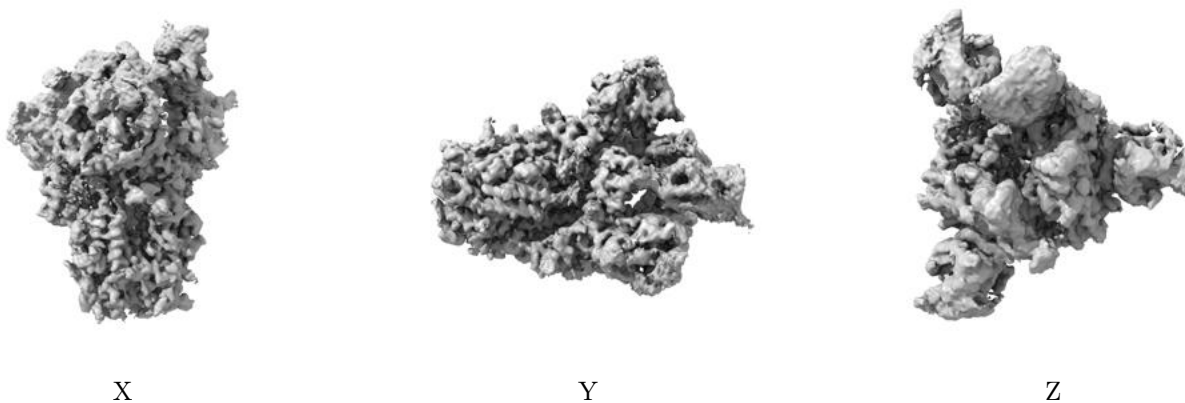
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.01. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

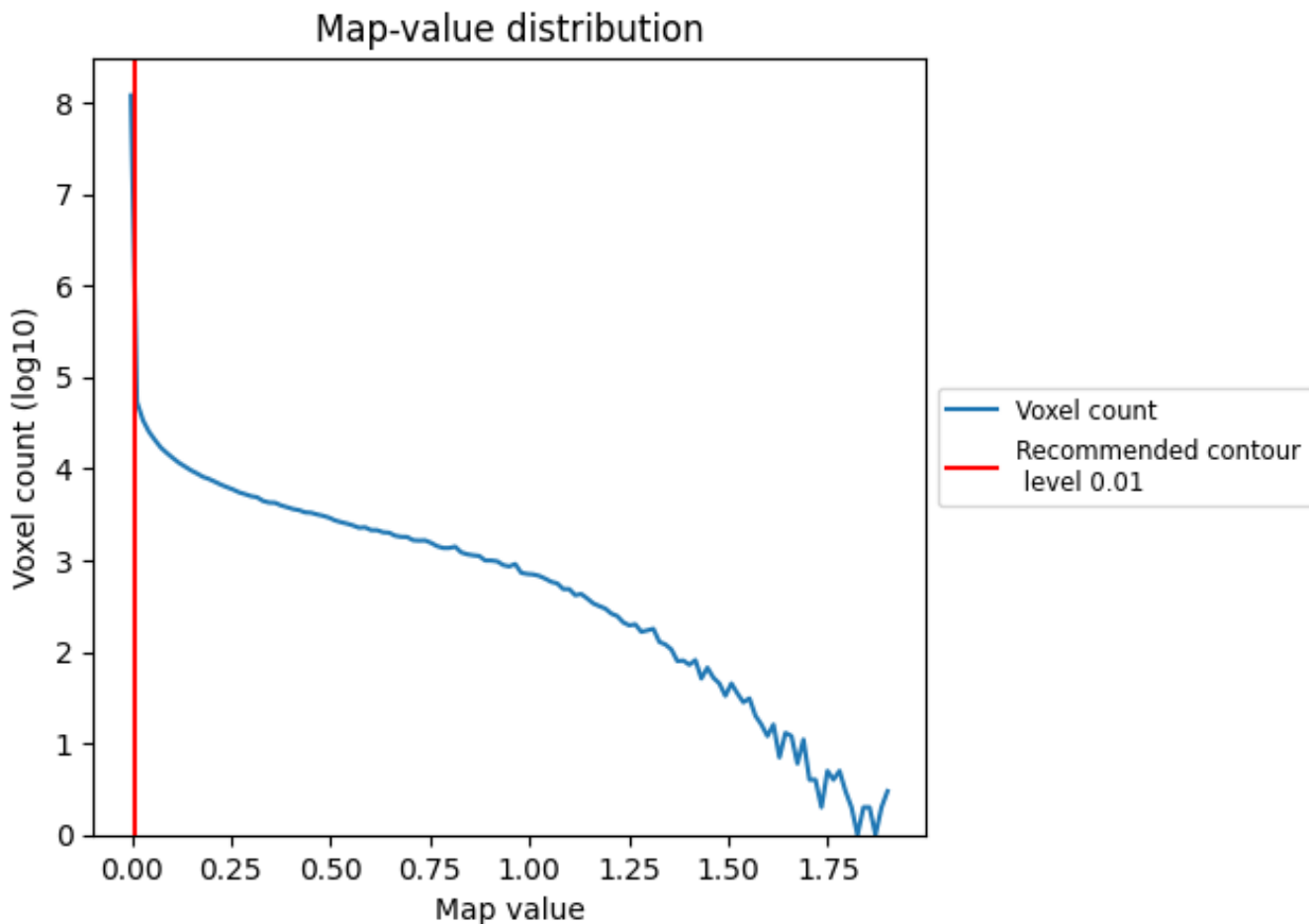
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

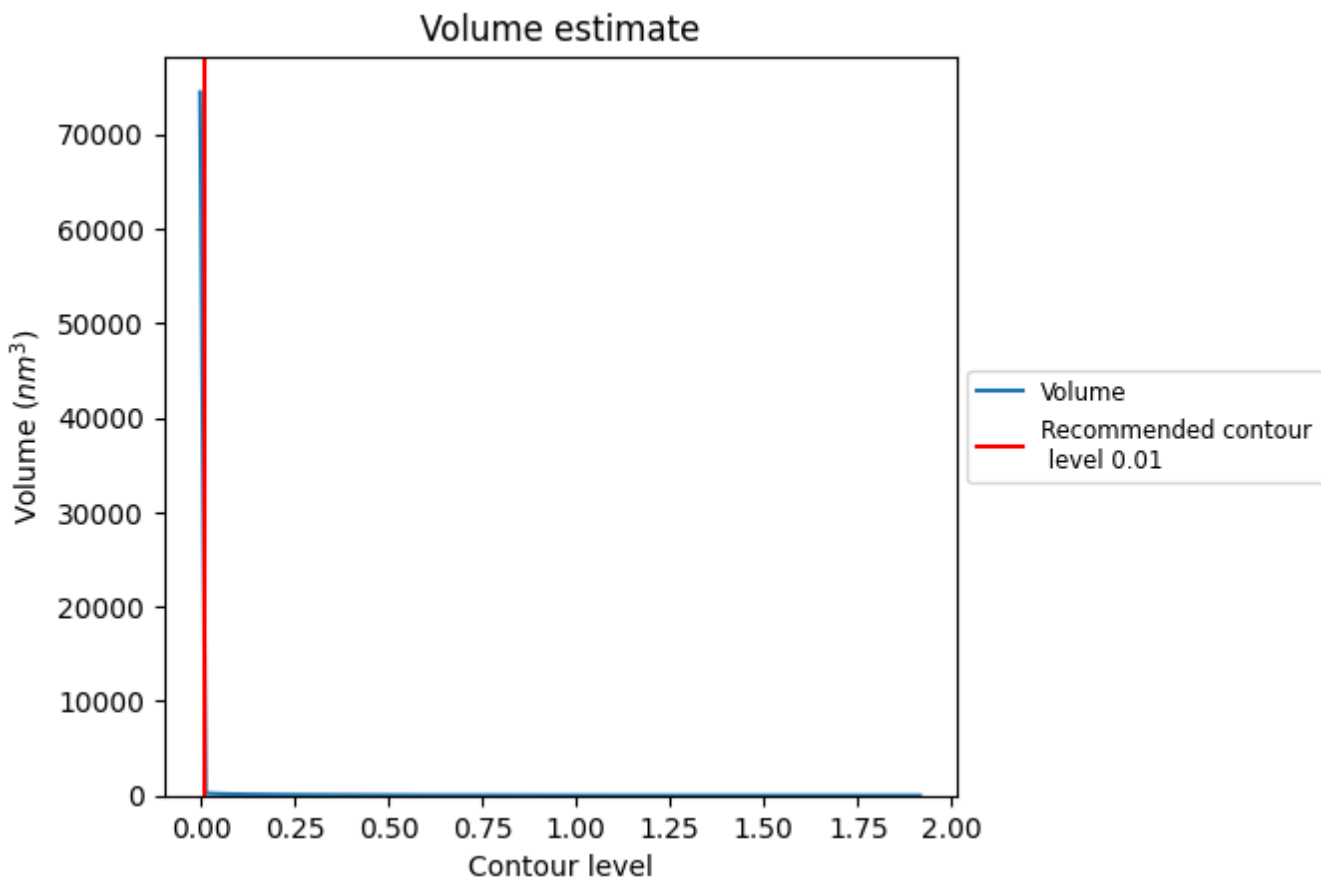
This section contains the results of statistical analysis of the map.

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.

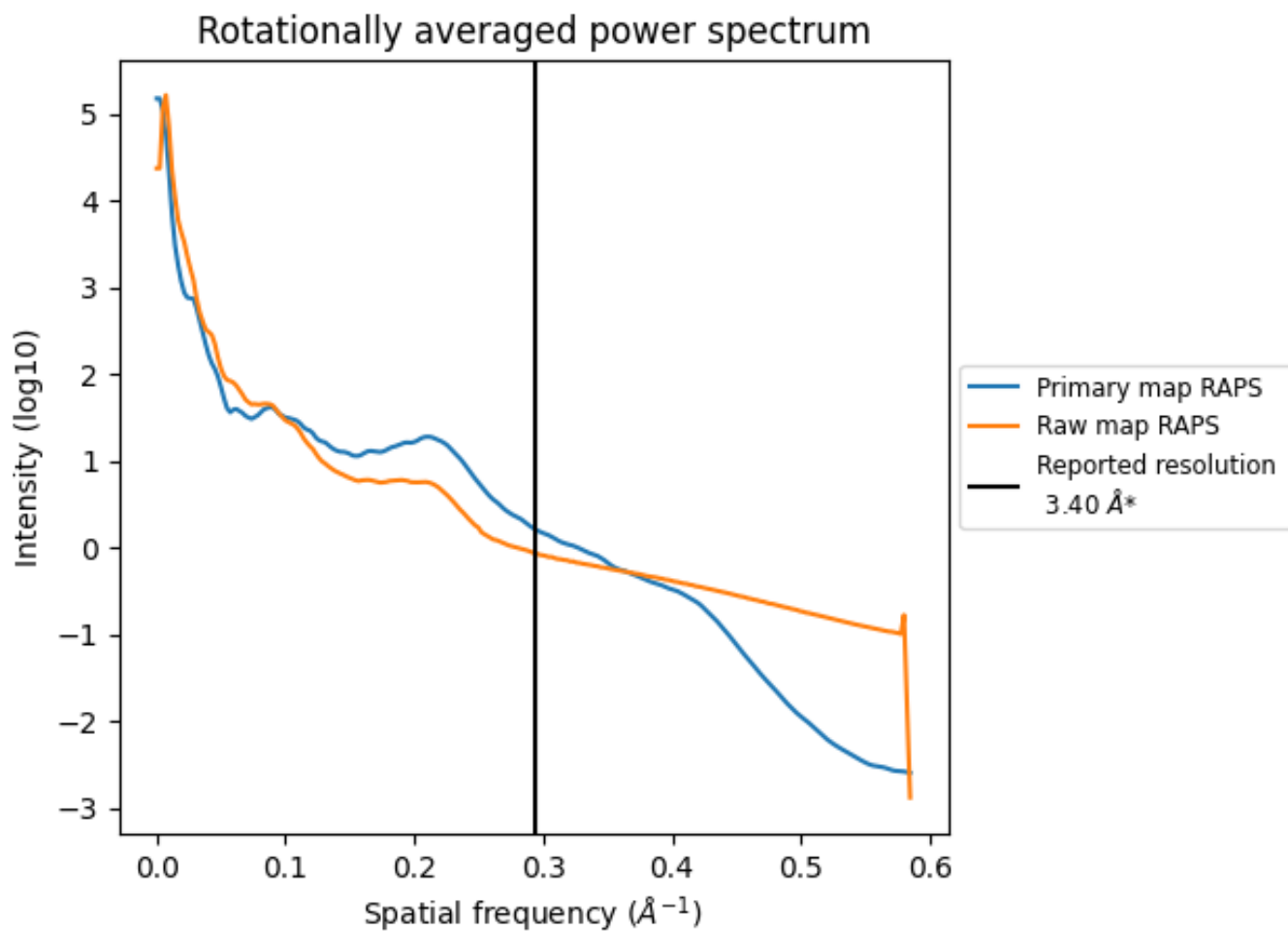
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 16639 nm^3 ; this corresponds to an approximate mass of 15030 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 i

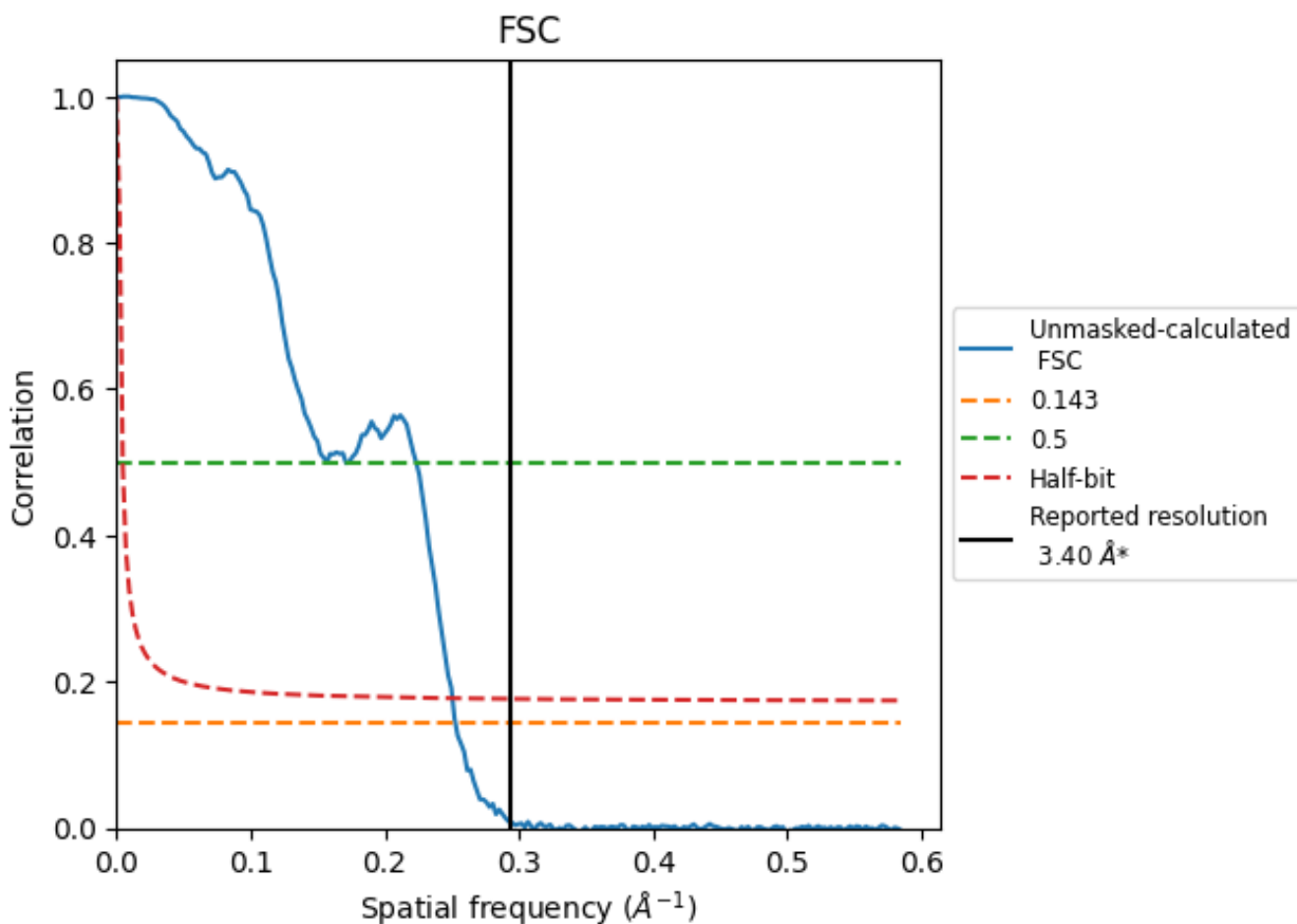


*Reported resolution corresponds to spatial frequency of 0.294 \AA^{-1}

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.294 \AA^{-1}

8.2 Resolution estimates [i](#)

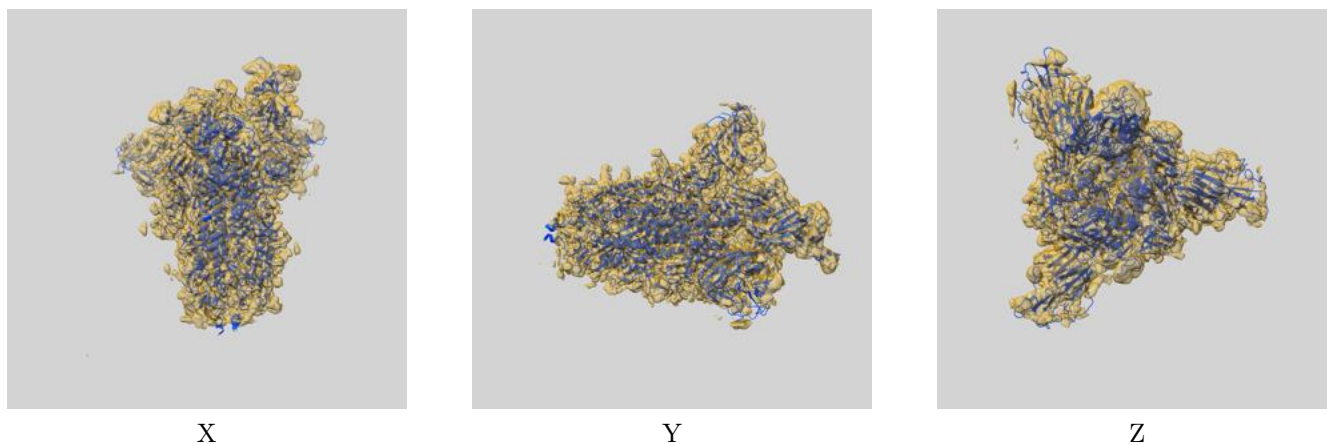
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.96	6.38	3.99

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.96 differs from the reported value 3.4 by more than 10 %

9 Map-model fit [i](#)

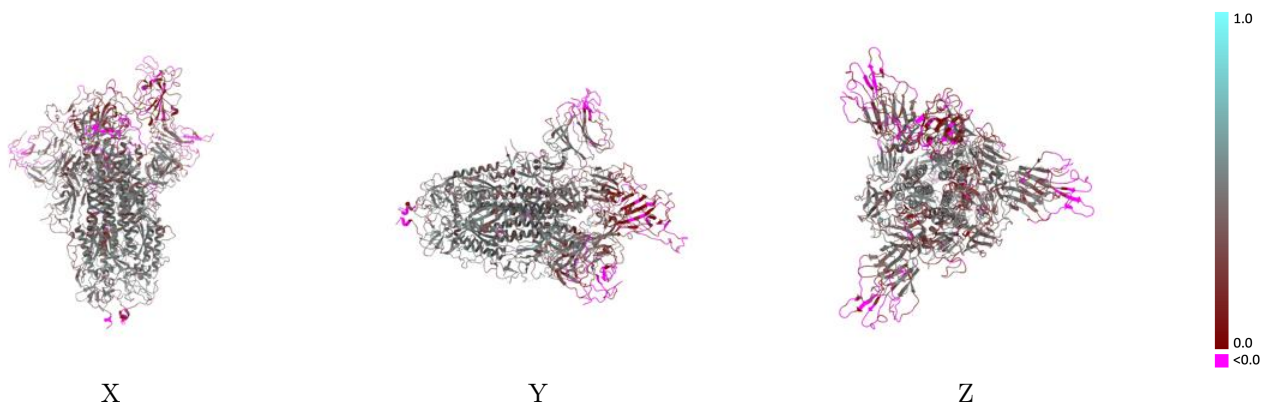
This section contains information regarding the fit between EMDB map EMD-17576 and PDB model 8P99. Per-residue inclusion information can be found in section 3 on page 13.

9.1 Map-model overlay [i](#)



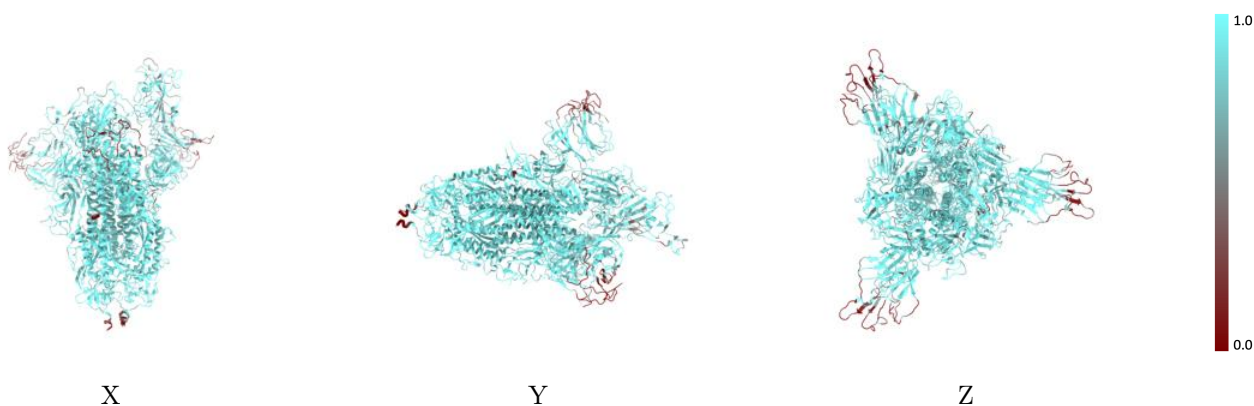
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



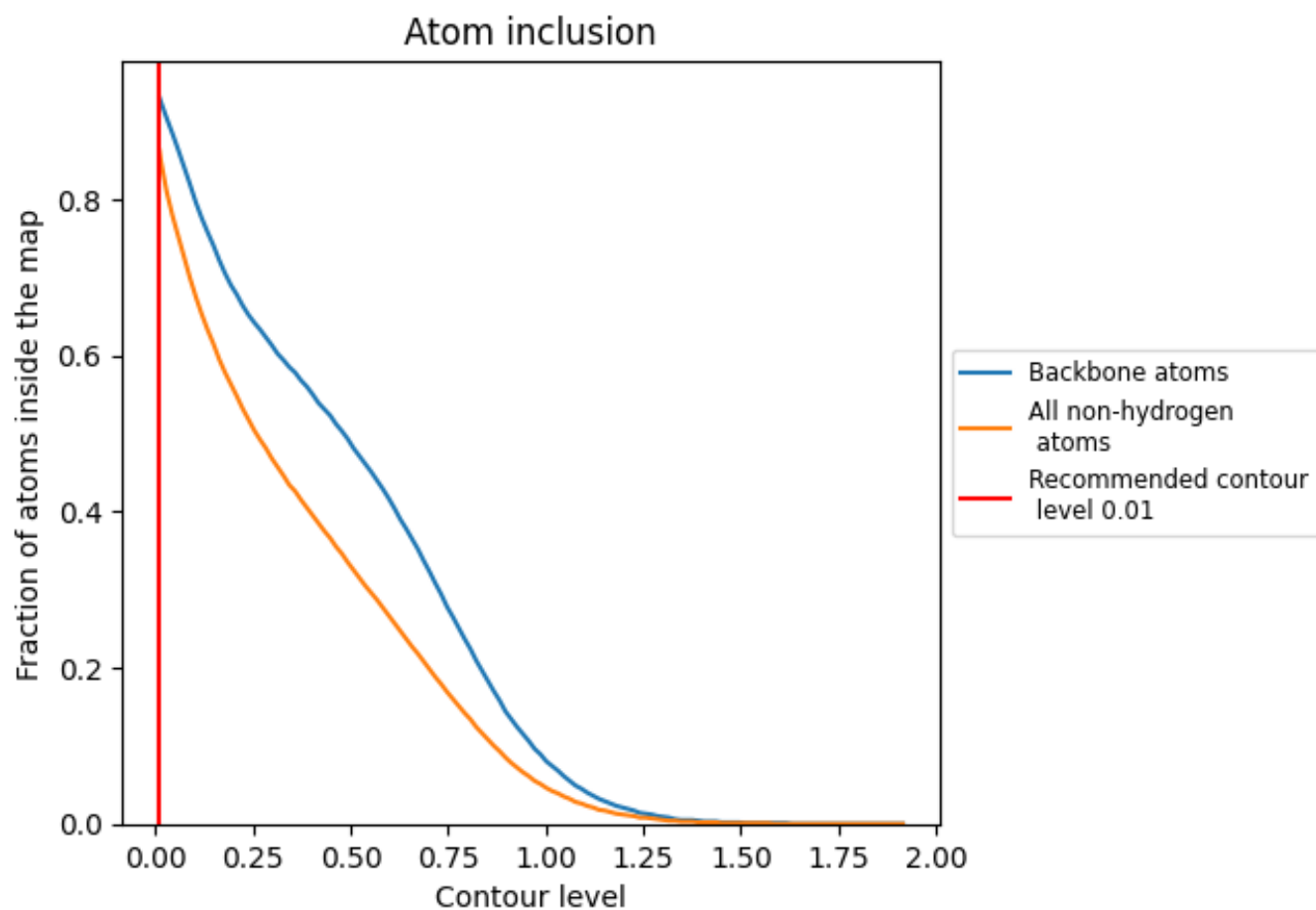
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.01).





























9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 86% 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 (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8620	 0.3430
A	 0.8670	 0.3520
B	 0.8570	 0.3210
C	 0.8640	 0.3590
E	 0.8210	 0.2620
F	 0.8210	 0.2090
G	 0.8210	 0.2070
I	 0.8930	 0.3210
J	 0.8570	 0.2170
K	 0.5360	 0.0450
L	 0.7500	 0.1370
N	 0.9290	 0.3650
O	 0.7140	 0.1090
P	 0.6430	 0.1570

