



## Full wwPDB EM Validation Report ⓘ

Apr 5, 2025 – 09:14 am BST

PDB ID : 5NOJ / pdb\_00005noj  
EMDB ID : EMD-3666  
Title : Ca<sup>2+</sup>-induced Movement of Tropomyosin on Native Cardiac Thin Filaments  
- "OPEN" state  
Authors : Risi, C.; Eisner, J.; Belknap, B.; Heeley, D.H.; White, H.D.; Schroeder, G.F.;  
Galkin, V.E.  
Deposited on : 2017-04-12  
Resolution : 11.00 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

---

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

EMDB validation analysis : 0.0.1.dev117  
Mogul : 1.8.4, CSD as541be (2020)  
MolProbity : 4.02b-467  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.42

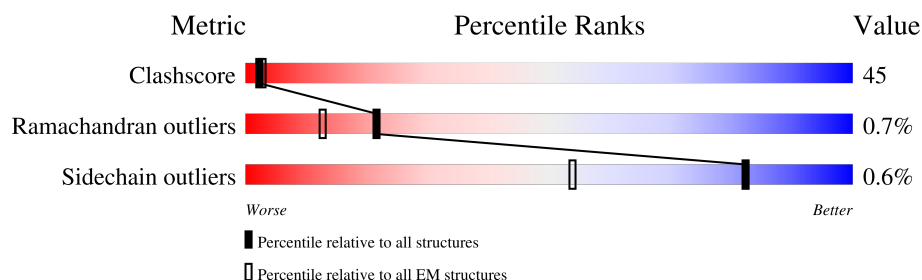
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 11.00 Å.

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



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

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

Mol	Chain	Length	Quality of chain
1	A	367	<div> <div>15%</div> <div>52%</div> <div>46%</div> <div>.</div> </div>
1	B	367	<div> <div>14%</div> <div>52%</div> <div>46%</div> <div>.</div> </div>
1	C	367	<div> <div>13%</div> <div>51%</div> <div>47%</div> <div>.</div> </div>
1	D	367	<div> <div>13%</div> <div>51%</div> <div>47%</div> <div>.</div> </div>
1	E	367	<div> <div>13%</div> <div>51%</div> <div>47%</div> <div>.</div> </div>
2	F	136	<div> <div>9%</div> <div>93%</div> <div>7%</div> </div>
2	H	136	<div> <div>12%</div> <div>93%</div> <div>7%</div> </div>

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 16077 atoms, of which 270 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 Actin, alpha skeletal muscle.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	367	Total	C	N	O	S	0	0
			2861	1813	481	548	19		
1	B	367	Total	C	N	O	S	0	0
			2861	1813	481	548	19		
1	C	367	Total	C	N	O	S	0	0
			2861	1813	481	548	19		
1	D	367	Total	C	N	O	S	0	0
			2861	1813	481	548	19		
1	E	367	Total	C	N	O	S	0	0
			2861	1813	481	548	19		

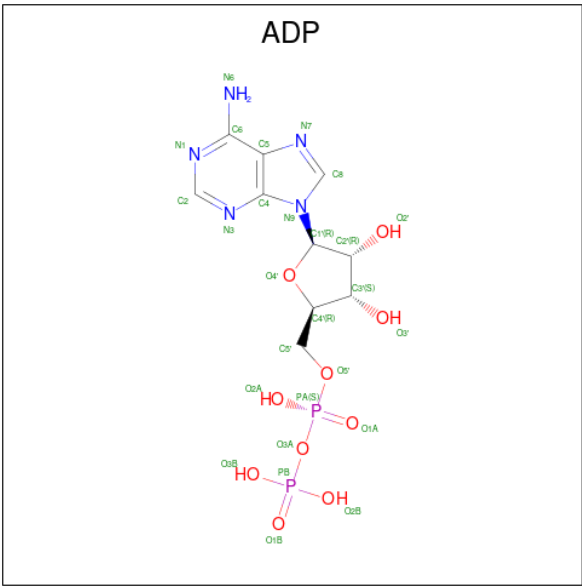
There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	299	LEU	MET	conflict	UNP P68137
A	358	SER	THR	conflict	UNP P68137
B	299	LEU	MET	conflict	UNP P68137
B	358	SER	THR	conflict	UNP P68137
C	299	LEU	MET	conflict	UNP P68137
C	358	SER	THR	conflict	UNP P68137
D	299	LEU	MET	conflict	UNP P68137
D	358	SER	THR	conflict	UNP P68137
E	299	LEU	MET	conflict	UNP P68137
E	358	SER	THR	conflict	UNP P68137

- Molecule 2 is a protein called cardiac alpha tropomyosin.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	F	136	Total	C	H	N	O	0	0
			816	408	135	136	137		
2	H	136	Total	C	H	N	O	0	0
			816	408	135	136	137		

- Molecule 3 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C<sub>10</sub>H<sub>15</sub>N<sub>5</sub>O<sub>10</sub>P<sub>2</sub>).

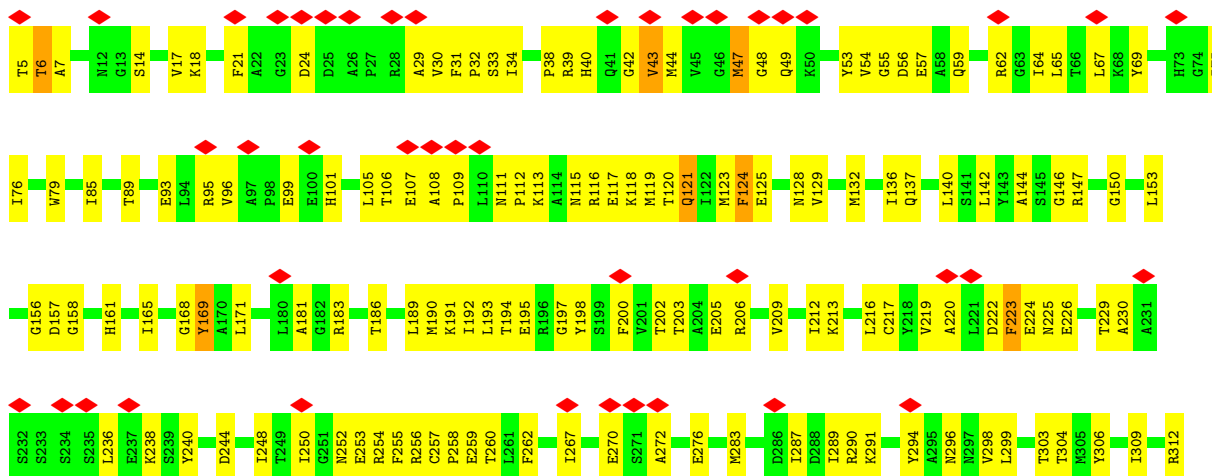


Mol	Chain	Residues	Atoms					AltConf
3	A	1	Total	C	N	O	P	0
			27	10	5	10	2	
3	B	1	Total	C	N	O	P	0
			27	10	5	10	2	
3	C	1	Total	C	N	O	P	0
			27	10	5	10	2	
3	D	1	Total	C	N	O	P	0
			27	10	5	10	2	
3	E	1	Total	C	N	O	P	0
			27	10	5	10	2	

- Molecule 4 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

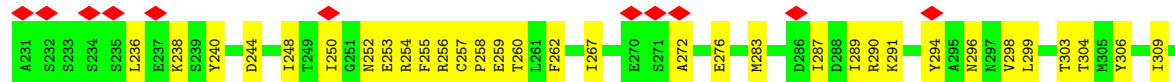
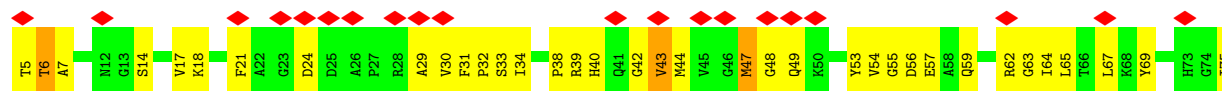
Mol	Chain	Residues	Atoms		AltConf
4	A	1	Total	Mg	0
			1	1	
4	B	1	Total	Mg	0
			1	1	
4	C	1	Total	Mg	0
			1	1	
4	D	1	Total	Mg	0
			1	1	
4	E	1	Total	Mg	0
			1	1	



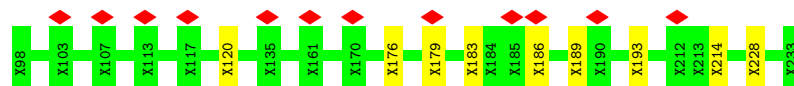
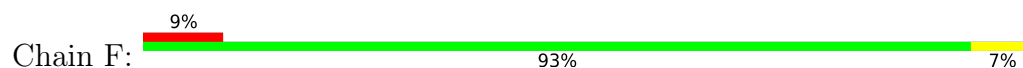




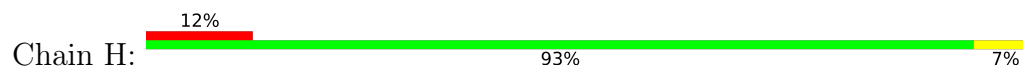
• Molecule 1: Actin, alpha skeletal muscle



• Molecule 2: cardiac alpha tropomyosin



• Molecule 2: cardiac alpha tropomyosin



## 4 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=-166.7°, rise=27.4 Å, axial sym=C1	Depositor
Number of segments used	3809	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	30.0	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	107.592	Depositor
Minimum map value	-36.052	Depositor
Average map value	-0.050	Depositor
Map value standard deviation	17.890	Depositor
Recommended contour level	45	Depositor
Map size (Å)	157.5, 157.5, 315.0	wwPDB
Map dimensions	150, 150, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.05, 1.05, 1.05	Depositor



## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, HIC, ADP

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	0.37	2/2910 (0.1%)	0.52	0/3944
1	B	0.37	2/2910 (0.1%)	0.52	0/3944
1	C	0.37	2/2910 (0.1%)	0.52	0/3944
1	D	0.37	2/2910 (0.1%)	0.52	0/3944
1	E	0.37	2/2910 (0.1%)	0.52	0/3944
All	All	0.37	10/14550 (0.1%)	0.52	0/19720

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	A	0	2
1	B	0	2
1	C	0	2
1	D	0	1
1	E	0	1
All	All	0	8

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	124	PHE	CE2-CZ	6.66	1.50	1.37
1	C	124	PHE	CE2-CZ	6.64	1.50	1.37
1	B	124	PHE	CE2-CZ	6.63	1.50	1.37
1	D	124	PHE	CE2-CZ	6.61	1.50	1.37
1	E	124	PHE	CE2-CZ	6.59	1.49	1.37
1	B	223	PHE	CE1-CZ	5.15	1.47	1.37
1	A	223	PHE	CE1-CZ	5.15	1.47	1.37
1	D	223	PHE	CE1-CZ	5.14	1.47	1.37

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	223	PHE	CE1-CZ	5.14	1.47	1.37
1	C	223	PHE	CE1-CZ	5.13	1.47	1.37

There are no bond angle outliers.

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	168	GLY	Peptide
1	A	5	THR	Peptide
1	B	168	GLY	Peptide
1	B	5	THR	Peptide
1	C	168	GLY	Peptide
1	C	5	THR	Peptide
1	D	5	THR	Peptide
1	E	5	THR	Peptide

## 5.2 Too-close contacts [i](#)

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	2861	0	2832	272	0
1	B	2861	0	2832	278	0
1	C	2861	0	2832	293	0
1	D	2861	0	2832	276	0
1	E	2861	0	2832	270	0
2	F	681	135	138	19	0
2	H	681	135	138	19	0
3	A	27	0	12	0	0
3	B	27	0	12	0	0
3	C	27	0	12	0	0
3	D	27	0	12	0	0
3	E	27	0	12	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	E	1	0	0	0	0
All	All	15807	270	14496	1355	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 45.

All (1355) 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:124:PHE:HB3	1:B:359:LYS:NZ	1.58	1.19
1:D:124:PHE:HB3	1:D:359:LYS:NZ	1.58	1.19
1:E:124:PHE:HB3	1:E:359:LYS:NZ	1.58	1.18
1:A:124:PHE:HB3	1:A:359:LYS:NZ	1.58	1.18
1:D:365:ALA:HB1	1:D:369:ILE:HG12	1.18	1.18
1:B:365:ALA:HB1	1:B:369:ILE:HG12	1.18	1.17
1:C:124:PHE:HB3	1:C:359:LYS:NZ	1.58	1.17
1:C:365:ALA:HB1	1:C:369:ILE:HG12	1.18	1.13
1:D:109:PRO:HB3	1:D:136:ILE:HD11	1.28	1.13
1:A:365:ALA:HB1	1:A:369:ILE:HG12	1.18	1.12
1:E:365:ALA:HB1	1:E:369:ILE:HG12	1.18	1.13
1:B:109:PRO:HB3	1:B:136:ILE:HD11	1.28	1.11
1:D:331:ALA:HB1	1:D:335:ARG:HH21	0.94	1.11
1:E:109:PRO:HB3	1:E:136:ILE:HD11	1.28	1.09
1:A:109:PRO:HB3	1:A:136:ILE:HD11	1.28	1.09
1:A:331:ALA:HB1	1:A:335:ARG:HH21	0.95	1.09
1:E:331:ALA:HB1	1:E:335:ARG:HH21	0.95	1.08
2:F:183:UNK:HA	2:H:183:UNK:HA	1.31	1.08
1:D:230:ALA:HA	1:D:236:LEU:HD12	1.35	1.08
1:C:331:ALA:HB1	1:C:335:ARG:HH21	0.95	1.08
1:B:230:ALA:HA	1:B:236:LEU:HD12	1.35	1.07
1:B:331:ALA:HB1	1:B:335:ARG:HH21	0.95	1.07
1:D:223:PHE:CZ	1:D:259:GLU:HB2	1.90	1.07
1:B:223:PHE:CZ	1:B:259:GLU:HB2	1.90	1.06
1:E:223:PHE:CZ	1:E:259:GLU:HB2	1.90	1.06
1:C:109:PRO:HB3	1:C:136:ILE:HD11	1.28	1.06
1:C:223:PHE:CZ	1:C:259:GLU:HB2	1.90	1.05
1:C:230:ALA:HA	1:C:236:LEU:HD12	1.35	1.05
1:A:165:ILE:HD11	1:C:44:MET:SD	1.97	1.05
1:A:230:ALA:HA	1:A:236:LEU:HD12	1.35	1.05
1:C:116:ARG:HB2	1:C:371:HIS:CE1	1.92	1.05
1:C:165:ILE:HD11	1:E:44:MET:SD	1.97	1.04

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:223:PHE:CZ	1:A:259:GLU:HB2	1.90	1.04
1:B:116:ARG:HB2	1:B:371:HIS:CE1	1.92	1.04
1:B:331:ALA:HB1	1:B:335:ARG:NH2	1.73	1.04
1:D:116:ARG:HB2	1:D:371:HIS:CE1	1.92	1.04
1:B:165:ILE:HD11	1:D:44:MET:SD	1.97	1.04
1:D:331:ALA:HB1	1:D:335:ARG:NH2	1.73	1.04
1:E:116:ARG:HB2	1:E:371:HIS:CE1	1.92	1.03
1:A:116:ARG:HB2	1:A:371:HIS:CE1	1.92	1.03
1:E:229:THR:HG23	1:E:236:LEU:CD1	1.89	1.03
1:B:168:GLY:HA3	1:D:47:MET:HB3	1.41	1.02
1:C:229:THR:HG23	1:C:236:LEU:CD1	1.89	1.02
1:B:229:THR:HG23	1:B:236:LEU:CD1	1.89	1.02
1:E:331:ALA:HB1	1:E:335:ARG:NH2	1.73	1.02
1:C:331:ALA:HB1	1:C:335:ARG:NH2	1.73	1.02
1:E:230:ALA:HA	1:E:236:LEU:HD12	1.35	1.02
1:A:331:ALA:HB1	1:A:335:ARG:NH2	1.73	1.01
1:D:229:THR:HG23	1:D:236:LEU:CD1	1.89	1.01
1:A:229:THR:HG23	1:A:236:LEU:CD1	1.89	1.01
1:A:168:GLY:HA3	1:C:47:MET:HB3	1.41	1.00
1:A:229:THR:CG2	1:A:236:LEU:HD11	1.91	1.00
1:D:216:LEU:HD12	1:D:250:ILE:HD11	1.44	1.00
1:B:216:LEU:HD12	1:B:250:ILE:HD11	1.43	1.00
1:C:229:THR:CG2	1:C:236:LEU:HD11	1.91	1.00
1:C:168:GLY:HA3	1:E:47:MET:HB3	1.41	1.00
1:D:229:THR:CG2	1:D:236:LEU:HD11	1.91	1.00
1:E:229:THR:CG2	1:E:236:LEU:HD11	1.91	0.99
1:E:216:LEU:HD12	1:E:250:ILE:HD11	1.43	0.99
1:C:124:PHE:CZ	1:C:132:MET:HG2	1.98	0.99
1:C:216:LEU:HD12	1:C:250:ILE:HD11	1.43	0.99
1:A:216:LEU:HD12	1:A:250:ILE:HD11	1.44	0.99
1:B:229:THR:CG2	1:B:236:LEU:HD11	1.91	0.99
1:E:124:PHE:CZ	1:E:132:MET:HG2	1.98	0.99
1:A:124:PHE:CZ	1:A:132:MET:HG2	1.98	0.99
1:B:124:PHE:CZ	1:B:132:MET:HG2	1.98	0.98
1:D:124:PHE:CZ	1:D:132:MET:HG2	1.98	0.98
1:A:224:GLU:N	1:A:224:GLU:OE1	1.97	0.97
1:C:224:GLU:N	1:C:224:GLU:OE1	1.97	0.97
1:C:124:PHE:HB3	1:C:359:LYS:CD	1.94	0.97
1:A:124:PHE:HB3	1:A:359:LYS:CD	1.94	0.97
1:E:224:GLU:OE1	1:E:224:GLU:N	1.97	0.97
1:E:124:PHE:HB3	1:E:359:LYS:CD	1.94	0.97

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:124:PHE:HB3	1:D:359:LYS:CD	1.94	0.97
1:D:365:ALA:CB	1:D:369:ILE:HG12	1.95	0.97
1:A:365:ALA:CB	1:A:369:ILE:HG12	1.95	0.96
1:B:124:PHE:HB3	1:B:359:LYS:CD	1.94	0.96
1:B:224:GLU:N	1:B:224:GLU:OE1	1.97	0.96
1:C:365:ALA:CB	1:C:369:ILE:HG12	1.95	0.96
1:D:224:GLU:N	1:D:224:GLU:OE1	1.97	0.96
1:E:124:PHE:CB	1:E:359:LYS:HD3	1.97	0.95
1:B:365:ALA:CB	1:B:369:ILE:HG12	1.95	0.95
1:C:124:PHE:CB	1:C:359:LYS:HD3	1.97	0.95
1:E:365:ALA:CB	1:E:369:ILE:HG12	1.95	0.95
1:D:124:PHE:CB	1:D:359:LYS:HD3	1.97	0.95
1:B:124:PHE:CB	1:B:359:LYS:HD3	1.97	0.95
1:A:124:PHE:CB	1:A:359:LYS:HD3	1.97	0.94
1:D:230:ALA:CA	1:D:236:LEU:HD12	1.97	0.94
1:B:230:ALA:CA	1:B:236:LEU:HD12	1.97	0.94
1:C:230:ALA:CA	1:C:236:LEU:HD12	1.97	0.94
1:A:230:ALA:CA	1:A:236:LEU:HD12	1.97	0.93
1:E:230:ALA:CA	1:E:236:LEU:HD12	1.97	0.93
1:B:32:PRO:HG2	1:B:59:GLN:HE21	1.34	0.93
1:E:6:THR:HG23	1:E:7:ALA:H	1.34	0.92
1:E:306:TYR:HB2	1:E:309:ILE:HD11	1.51	0.92
1:D:220:ALA:HB2	1:D:226:GLU:HG3	1.50	0.92
1:A:124:PHE:HB3	1:A:359:LYS:HZ2	1.30	0.92
1:C:6:THR:HG23	1:C:7:ALA:H	1.34	0.92
1:A:6:THR:HG23	1:A:7:ALA:H	1.34	0.92
1:B:223:PHE:CE2	1:B:255:PHE:HD1	1.88	0.92
2:F:183:UNK:CA	2:H:183:UNK:HA	2.00	0.92
1:E:223:PHE:CE2	1:E:255:PHE:HD1	1.88	0.92
1:C:223:PHE:CE2	1:C:255:PHE:HD1	1.88	0.91
1:A:32:PRO:HG2	1:A:59:GLN:HE21	1.33	0.91
1:C:32:PRO:HG2	1:C:59:GLN:HE21	1.34	0.91
1:D:223:PHE:CE2	1:D:255:PHE:HD1	1.88	0.91
1:B:220:ALA:HB2	1:B:226:GLU:HG3	1.50	0.91
1:D:32:PRO:HG2	1:D:59:GLN:HE21	1.33	0.91
1:D:306:TYR:HB2	1:D:309:ILE:HD11	1.50	0.91
1:E:32:PRO:HG2	1:E:59:GLN:HE21	1.33	0.91
1:C:306:TYR:HB2	1:C:309:ILE:HD11	1.51	0.91
1:D:6:THR:HG23	1:D:7:ALA:H	1.34	0.91
1:E:220:ALA:HB2	1:E:226:GLU:HG3	1.50	0.91
1:A:306:TYR:HB2	1:A:309:ILE:HD11	1.51	0.90

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:124:PHE:HB3	1:B:359:LYS:CE	2.01	0.90
1:B:306:TYR:HB2	1:B:309:ILE:HD11	1.50	0.90
1:D:124:PHE:HB3	1:D:359:LYS:CE	2.01	0.90
1:A:223:PHE:CE2	1:A:255:PHE:HD1	1.88	0.90
1:C:220:ALA:HB2	1:C:226:GLU:HG3	1.50	0.90
1:B:6:THR:HG23	1:B:7:ALA:H	1.34	0.90
1:D:220:ALA:CB	1:D:226:GLU:HG3	2.03	0.89
1:A:220:ALA:HB2	1:A:226:GLU:HG3	1.50	0.89
1:E:124:PHE:HB3	1:E:359:LYS:CE	2.01	0.89
1:B:220:ALA:CB	1:B:226:GLU:HG3	2.03	0.89
1:C:220:ALA:CB	1:C:226:GLU:HG3	2.03	0.89
1:A:124:PHE:HB3	1:A:359:LYS:CE	2.01	0.89
1:A:220:ALA:CB	1:A:226:GLU:HG3	2.03	0.88
1:C:124:PHE:HB3	1:C:359:LYS:CE	2.01	0.88
1:D:111:ASN:OD1	1:D:112:PRO:HD2	1.75	0.88
1:E:220:ALA:CB	1:E:226:GLU:HG3	2.03	0.87
1:A:365:ALA:HB1	1:A:369:ILE:CG1	2.04	0.87
1:E:124:PHE:HB3	1:E:359:LYS:HZ2	1.30	0.87
1:C:365:ALA:HB1	1:C:369:ILE:CG1	2.04	0.87
1:B:111:ASN:OD1	1:B:112:PRO:HD2	1.75	0.87
1:E:365:ALA:HB1	1:E:369:ILE:CG1	2.04	0.86
1:E:229:THR:HG23	1:E:236:LEU:HD11	0.94	0.86
1:B:109:PRO:HB3	1:B:136:ILE:CD1	2.06	0.86
1:D:109:PRO:HB3	1:D:136:ILE:CD1	2.06	0.86
1:B:365:ALA:HB1	1:B:369:ILE:CG1	2.04	0.85
1:C:229:THR:HG23	1:C:236:LEU:HD11	0.94	0.85
1:C:111:ASN:OD1	1:C:112:PRO:HD2	1.74	0.85
1:E:111:ASN:OD1	1:E:112:PRO:HD2	1.75	0.85
1:A:229:THR:HG23	1:A:236:LEU:HD11	0.94	0.85
1:A:111:ASN:OD1	1:A:112:PRO:HD2	1.75	0.85
1:B:124:PHE:HB3	1:B:359:LYS:HZ2	1.39	0.85
1:B:331:ALA:CB	1:B:335:ARG:HH21	1.86	0.84
1:E:331:ALA:CB	1:E:335:ARG:HH21	1.86	0.84
1:C:109:PRO:HB3	1:C:136:ILE:CD1	2.06	0.84
1:E:109:PRO:HB3	1:E:136:ILE:CD1	2.06	0.84
1:E:39:ARG:HG2	1:E:64:ILE:O	1.78	0.84
1:A:109:PRO:HB3	1:A:136:ILE:CD1	2.06	0.84
1:D:365:ALA:HB1	1:D:369:ILE:CG1	2.04	0.84
1:D:229:THR:HG23	1:D:236:LEU:HD11	0.94	0.84
1:A:39:ARG:HG2	1:A:64:ILE:O	1.78	0.83
1:C:331:ALA:CB	1:C:335:ARG:HH21	1.86	0.83

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:331:ALA:CB	1:D:335:ARG:HH21	1.86	0.83
1:A:124:PHE:CB	1:A:359:LYS:CD	2.56	0.83
1:B:124:PHE:CB	1:B:359:LYS:CD	2.56	0.83
1:E:124:PHE:CG	1:E:359:LYS:HD3	2.13	0.83
1:D:124:PHE:CB	1:D:359:LYS:CD	2.56	0.82
1:A:331:ALA:CB	1:A:335:ARG:HH21	1.86	0.82
1:B:124:PHE:CG	1:B:359:LYS:HD3	2.14	0.82
1:C:124:PHE:CB	1:C:359:LYS:CD	2.56	0.82
1:D:39:ARG:HG2	1:D:64:ILE:O	1.78	0.82
1:A:124:PHE:CG	1:A:359:LYS:HD3	2.14	0.82
1:C:124:PHE:CG	1:C:359:LYS:HD3	2.13	0.82
1:C:39:ARG:HG2	1:C:64:ILE:O	1.78	0.82
1:D:124:PHE:CD1	1:D:359:LYS:HD3	2.14	0.82
1:D:124:PHE:CG	1:D:359:LYS:HD3	2.13	0.82
1:E:124:PHE:CB	1:E:359:LYS:CD	2.56	0.82
1:B:39:ARG:HG2	1:B:64:ILE:O	1.78	0.82
1:C:150:GLY:O	1:C:165:ILE:HG22	1.79	0.82
1:B:124:PHE:CD1	1:B:359:LYS:HD3	2.14	0.82
1:B:150:GLY:O	1:B:165:ILE:HG22	1.79	0.82
1:B:229:THR:HG23	1:B:236:LEU:HD11	0.94	0.81
1:C:124:PHE:CD1	1:C:359:LYS:HD3	2.14	0.81
1:E:124:PHE:CD1	1:E:359:LYS:HD3	2.14	0.81
1:A:124:PHE:CD1	1:A:359:LYS:HD3	2.14	0.81
1:A:150:GLY:O	1:A:165:ILE:HG22	1.79	0.81
1:C:117:GLU:HB3	1:C:367:PRO:HB3	1.62	0.81
1:D:117:GLU:HB3	1:D:367:PRO:HB3	1.62	0.81
1:E:117:GLU:HB3	1:E:367:PRO:HB3	1.62	0.80
1:C:47:MET:O	1:C:49:GLN:HA	1.81	0.80
1:D:47:MET:O	1:D:49:GLN:HA	1.81	0.80
1:B:47:MET:O	1:B:49:GLN:HA	1.81	0.80
1:E:47:MET:O	1:E:49:GLN:HA	1.81	0.80
1:A:47:MET:O	1:A:49:GLN:HA	1.81	0.80
1:B:117:GLU:HB3	1:B:367:PRO:HB3	1.62	0.80
1:D:150:GLY:O	1:D:165:ILE:HG22	1.82	0.79
1:E:222:ASP:HB2	1:E:225:ASN:HD22	1.46	0.79
1:C:168:GLY:HA3	1:E:47:MET:CB	2.13	0.79
1:A:117:GLU:HB3	1:A:367:PRO:HB3	1.62	0.79
1:A:168:GLY:HA3	1:C:47:MET:CB	2.13	0.79
1:B:168:GLY:HA3	1:D:47:MET:CB	2.13	0.79
1:D:222:ASP:HB2	1:D:225:ASN:HD22	1.46	0.79
1:B:222:ASP:HB2	1:B:225:ASN:HD22	1.46	0.79

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:124:PHE:HB3	1:D:359:LYS:HZ3	1.46	0.78
1:C:222:ASP:HB2	1:C:225:ASN:HD22	1.46	0.78
1:B:299:LEU:HB3	1:B:304:THR:HG21	1.66	0.78
1:C:299:LEU:HB3	1:C:304:THR:HG21	1.65	0.78
1:A:222:ASP:HB2	1:A:225:ASN:HD22	1.46	0.77
1:A:299:LEU:HB3	1:A:304:THR:HG21	1.65	0.77
1:E:150:GLY:O	1:E:165:ILE:HG22	1.82	0.77
1:E:299:LEU:HB3	1:E:304:THR:HG21	1.65	0.77
1:D:124:PHE:CB	1:D:359:LYS:NZ	2.46	0.77
1:B:168:GLY:CA	1:D:47:MET:HB3	2.15	0.77
1:C:168:GLY:CA	1:E:47:MET:HB3	2.15	0.77
1:D:124:PHE:HB3	1:D:359:LYS:HZ2	1.48	0.76
1:D:299:LEU:HB3	1:D:304:THR:HG21	1.66	0.76
1:A:168:GLY:CA	1:C:47:MET:HB3	2.15	0.76
1:A:168:GLY:O	1:C:44:MET:SD	2.44	0.76
1:C:168:GLY:O	1:E:44:MET:SD	2.44	0.75
1:D:32:PRO:HG2	1:D:59:GLN:NE2	2.02	0.75
1:B:168:GLY:O	1:D:44:MET:SD	2.44	0.75
1:D:39:ARG:HG3	1:D:40:HIS:CD2	2.21	0.75
1:C:39:ARG:HG3	1:C:40:HIS:CD2	2.21	0.75
1:E:39:ARG:HG3	1:E:40:HIS:CD2	2.21	0.75
1:A:39:ARG:HG3	1:A:40:HIS:CD2	2.21	0.75
1:B:32:PRO:HG2	1:B:59:GLN:NE2	2.02	0.75
1:D:360:GLN:O	1:D:364:GLU:OE1	2.05	0.75
1:B:39:ARG:HG3	1:B:40:HIS:CD2	2.21	0.75
1:B:360:GLN:O	1:B:364:GLU:OE1	2.05	0.75
1:A:32:PRO:HG2	1:A:59:GLN:NE2	2.02	0.74
1:C:124:PHE:HB3	1:C:359:LYS:HZ3	1.47	0.74
1:C:32:PRO:HG2	1:C:59:GLN:NE2	2.02	0.74
1:E:32:PRO:HG2	1:E:59:GLN:NE2	2.02	0.74
1:C:345:ILE:O	1:C:349:LEU:HD13	1.88	0.74
1:A:345:ILE:O	1:A:349:LEU:HD13	1.88	0.74
1:D:345:ILE:O	1:D:349:LEU:HD13	1.88	0.74
1:E:345:ILE:O	1:E:349:LEU:HD13	1.88	0.74
1:A:124:PHE:O	1:A:359:LYS:HE2	1.88	0.74
1:E:360:GLN:O	1:E:364:GLU:OE1	2.05	0.74
1:B:345:ILE:O	1:B:349:LEU:HD13	1.88	0.74
1:D:124:PHE:O	1:D:359:LYS:HE2	1.87	0.74
1:C:360:GLN:O	1:C:364:GLU:OE1	2.05	0.74
1:C:124:PHE:O	1:C:359:LYS:HE2	1.88	0.73
1:A:360:GLN:O	1:A:364:GLU:OE1	2.05	0.73

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:124:PHE:O	1:B:359:LYS:HE2	1.87	0.73
1:E:124:PHE:O	1:E:359:LYS:HE2	1.88	0.73
1:A:317:ILE:HG22	1:A:327:ILE:HD13	1.71	0.73
1:C:124:PHE:HB3	1:C:359:LYS:HZ2	1.46	0.73
1:E:223:PHE:CE2	1:E:259:GLU:HB2	2.24	0.73
1:B:223:PHE:CE2	1:B:259:GLU:HB2	2.24	0.72
1:C:168:GLY:O	1:C:169:TYR:O	2.08	0.72
1:D:223:PHE:CE2	1:D:259:GLU:HB2	2.24	0.72
1:C:317:ILE:HG22	1:C:327:ILE:HD13	1.71	0.72
1:A:223:PHE:CE2	1:A:259:GLU:HB2	2.24	0.71
1:A:124:PHE:CG	1:A:359:LYS:CD	2.74	0.71
1:A:168:GLY:O	1:A:169:TYR:O	2.08	0.71
1:B:168:GLY:O	1:B:169:TYR:O	2.08	0.71
1:C:124:PHE:CG	1:C:359:LYS:CD	2.74	0.71
1:C:223:PHE:CE2	1:C:259:GLU:HB2	2.24	0.71
1:E:124:PHE:CG	1:E:359:LYS:CD	2.74	0.71
1:A:124:PHE:CB	1:A:359:LYS:NZ	2.46	0.71
1:A:34:ILE:HG12	1:A:59:GLN:NE2	2.05	0.71
1:B:124:PHE:CB	1:B:359:LYS:NZ	2.46	0.71
1:D:34:ILE:HG12	1:D:59:GLN:NE2	2.05	0.71
1:B:34:ILE:HG12	1:B:59:GLN:NE2	2.06	0.70
1:B:124:PHE:CG	1:B:359:LYS:CD	2.74	0.70
1:B:317:ILE:HG22	1:B:327:ILE:HD13	1.71	0.70
1:D:124:PHE:CG	1:D:359:LYS:CD	2.74	0.70
1:D:317:ILE:HG22	1:D:327:ILE:HD13	1.71	0.70
1:E:34:ILE:HG12	1:E:59:GLN:NE2	2.05	0.70
1:B:223:PHE:HE2	1:B:256:ARG:HA	1.56	0.70
1:E:317:ILE:HG22	1:E:327:ILE:HD13	1.71	0.70
1:C:34:ILE:HG12	1:C:59:GLN:NE2	2.05	0.70
1:A:223:PHE:HE2	1:A:256:ARG:HA	1.56	0.70
1:D:223:PHE:HE2	1:D:256:ARG:HA	1.56	0.70
1:E:223:PHE:HE2	1:E:256:ARG:HA	1.56	0.69
1:E:116:ARG:HD2	1:E:371:HIS:ND1	2.07	0.69
1:B:6:THR:HG23	1:B:7:ALA:N	2.07	0.69
1:B:59:GLN:O	1:B:62:ARG:HG3	1.93	0.69
1:D:116:ARG:HD2	1:D:371:HIS:ND1	2.07	0.69
1:E:124:PHE:CB	1:E:359:LYS:NZ	2.46	0.69
1:A:257:CYS:HB3	1:A:258:PRO:HD3	1.75	0.69
1:C:75:ILE:HA	1:C:115:ASN:HD21	1.58	0.69
1:A:75:ILE:HA	1:A:115:ASN:HD21	1.58	0.69
1:C:124:PHE:CB	1:C:359:LYS:NZ	2.46	0.69

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:59:GLN:O	1:D:62:ARG:HG3	1.93	0.69
1:E:257:CYS:HB3	1:E:258:PRO:HD3	1.75	0.69
1:C:116:ARG:HD2	1:C:371:HIS:ND1	2.07	0.69
1:C:257:CYS:HB3	1:C:258:PRO:HD3	1.75	0.69
1:D:140:LEU:O	1:D:342:GLY:HA3	1.93	0.69
1:C:223:PHE:HE2	1:C:256:ARG:HA	1.57	0.69
1:A:116:ARG:HD2	1:A:371:HIS:ND1	2.07	0.68
1:A:223:PHE:CE2	1:A:256:ARG:HA	2.28	0.68
1:E:140:LEU:O	1:E:342:GLY:HA3	1.93	0.68
1:D:6:THR:HG23	1:D:7:ALA:N	2.07	0.68
1:A:166:TYR:HB3	1:C:64:ILE:HD11	1.75	0.68
1:B:116:ARG:HD2	1:B:371:HIS:ND1	2.07	0.68
1:C:223:PHE:CE2	1:C:256:ARG:HA	2.29	0.68
1:E:75:ILE:HA	1:E:115:ASN:HD21	1.58	0.68
1:B:166:TYR:HB3	1:D:64:ILE:HD11	1.75	0.68
1:C:140:LEU:O	1:C:342:GLY:HA3	1.93	0.68
1:D:223:PHE:CE2	1:D:256:ARG:HA	2.28	0.68
1:D:230:ALA:CA	1:D:236:LEU:CD1	2.72	0.68
1:B:223:PHE:CE2	1:B:256:ARG:HA	2.28	0.68
1:B:306:TYR:HB2	1:B:309:ILE:CD1	2.24	0.68
1:A:42:GLY:HA3	1:A:47:MET:SD	2.34	0.68
1:B:75:ILE:HA	1:B:115:ASN:HD21	1.58	0.68
1:B:230:ALA:CA	1:B:236:LEU:CD1	2.72	0.68
1:D:333:PRO:O	1:D:334:GLU:HB2	1.94	0.68
1:E:59:GLN:O	1:E:62:ARG:HG3	1.93	0.68
1:E:116:ARG:HB2	1:E:371:HIS:NE2	2.09	0.68
1:B:190:MET:CE	1:B:206:ARG:HG2	2.24	0.68
1:C:116:ARG:HB2	1:C:371:HIS:NE2	2.09	0.68
1:D:116:ARG:HB2	1:D:371:HIS:NE2	2.09	0.68
1:D:306:TYR:HB2	1:D:309:ILE:CD1	2.24	0.68
1:E:6:THR:HG23	1:E:7:ALA:N	2.07	0.68
1:E:190:MET:CE	1:E:206:ARG:HG2	2.24	0.68
1:A:190:MET:CE	1:A:206:ARG:HG2	2.24	0.68
1:D:257:CYS:HB3	1:D:258:PRO:HD3	1.75	0.68
1:E:54:VAL:CG2	1:E:85:ILE:HG22	2.24	0.68
1:A:54:VAL:CG2	1:A:85:ILE:HG22	2.24	0.68
1:A:333:PRO:O	1:A:334:GLU:HB2	1.94	0.68
1:B:42:GLY:HA3	1:B:47:MET:SD	2.34	0.68
1:C:54:VAL:CG2	1:C:85:ILE:HG22	2.24	0.68
1:C:190:MET:CE	1:C:206:ARG:HG2	2.24	0.68
1:A:6:THR:HG23	1:A:7:ALA:N	2.07	0.68

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:59:GLN:O	1:A:62:ARG:HG3	1.93	0.68
1:D:190:MET:CE	1:D:206:ARG:HG2	2.24	0.68
1:D:222:ASP:HB2	1:D:225:ASN:ND2	2.10	0.67
1:E:223:PHE:CE2	1:E:256:ARG:HA	2.28	0.67
1:A:222:ASP:HB2	1:A:225:ASN:ND2	2.09	0.67
1:B:140:LEU:O	1:B:342:GLY:HA3	1.93	0.67
1:B:257:CYS:HB3	1:B:258:PRO:HD3	1.75	0.67
1:C:59:GLN:O	1:C:62:ARG:HG3	1.93	0.67
1:D:75:ILE:HA	1:D:115:ASN:HD21	1.58	0.67
1:E:190:MET:HE3	1:E:206:ARG:HG2	1.76	0.67
1:B:222:ASP:HB2	1:B:225:ASN:ND2	2.09	0.67
1:C:230:ALA:CA	1:C:236:LEU:CD1	2.72	0.67
1:E:230:ALA:CA	1:E:236:LEU:CD1	2.72	0.67
1:C:6:THR:HG23	1:C:7:ALA:N	2.07	0.67
1:A:140:LEU:O	1:A:342:GLY:HA3	1.93	0.67
1:B:116:ARG:HB2	1:B:371:HIS:NE2	2.09	0.67
1:C:166:TYR:HB3	1:E:64:ILE:HD11	1.75	0.67
2:F:176:UNK:HA	2:H:176:UNK:HA	1.75	0.67
1:A:230:ALA:CA	1:A:236:LEU:CD1	2.72	0.67
1:C:222:ASP:HB2	1:C:225:ASN:ND2	2.09	0.66
1:A:116:ARG:HB2	1:A:371:HIS:NE2	2.09	0.66
1:C:333:PRO:O	1:C:334:GLU:HB2	1.94	0.66
1:B:54:VAL:CG2	1:B:85:ILE:HG22	2.24	0.66
1:B:333:PRO:O	1:B:334:GLU:HB2	1.94	0.66
1:D:54:VAL:CG2	1:D:85:ILE:HG22	2.24	0.66
2:F:186:UNK:CB	2:H:186:UNK:C	2.73	0.66
2:F:186:UNK:CB	2:H:187:UNK:N	2.58	0.66
1:E:222:ASP:HB2	1:E:225:ASN:ND2	2.09	0.66
1:E:333:PRO:O	1:E:334:GLU:HB2	1.94	0.66
1:E:55:GLY:O	1:E:59:GLN:HG2	1.95	0.66
1:B:55:GLY:O	1:B:59:GLN:HG2	1.95	0.66
1:D:168:GLY:O	1:D:169:TYR:O	2.14	0.66
1:C:55:GLY:O	1:C:59:GLN:HG2	1.95	0.66
1:C:54:VAL:HG23	1:C:85:ILE:HG22	1.79	0.65
1:C:216:LEU:HD11	1:C:240:TYR:HB2	1.79	0.65
1:C:220:ALA:HB1	1:C:226:GLU:CG	2.26	0.65
1:A:216:LEU:HD11	1:A:240:TYR:HB2	1.79	0.65
1:D:342:GLY:O	1:D:345:ILE:HG22	1.96	0.65
1:E:220:ALA:HB1	1:E:226:GLU:CG	2.26	0.65
1:B:220:ALA:HB1	1:B:226:GLU:CG	2.26	0.65
1:D:55:GLY:O	1:D:59:GLN:HG2	1.95	0.65

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:124:PHE:HB3	1:B:359:LYS:HZ3	1.54	0.65
1:D:190:MET:HE1	1:D:206:ARG:HA	1.78	0.65
1:E:216:LEU:HD11	1:E:240:TYR:HB2	1.79	0.65
1:C:342:GLY:O	1:C:345:ILE:HG22	1.96	0.65
1:A:55:GLY:O	1:A:59:GLN:HG2	1.95	0.65
1:D:222:ASP:HB3	1:D:224:GLU:CD	2.17	0.65
1:A:230:ALA:HB2	1:A:236:LEU:HD13	1.79	0.65
1:E:191:LYS:O	1:E:194:THR:HG22	1.97	0.65
1:A:54:VAL:HG23	1:A:85:ILE:HG22	1.79	0.65
1:B:216:LEU:HD11	1:B:240:TYR:HB2	1.79	0.65
1:A:222:ASP:HB3	1:A:224:GLU:CD	2.17	0.65
1:C:222:ASP:HB3	1:C:224:GLU:CD	2.17	0.65
1:D:220:ALA:HB1	1:D:226:GLU:CG	2.27	0.65
1:E:190:MET:HE1	1:E:206:ARG:HA	1.78	0.65
1:B:222:ASP:HB3	1:B:224:GLU:CD	2.17	0.64
1:C:191:LYS:O	1:C:194:THR:HG22	1.97	0.64
1:E:222:ASP:HB3	1:E:224:GLU:CD	2.17	0.64
1:A:192:ILE:O	1:A:195:GLU:HG2	1.98	0.64
1:B:342:GLY:O	1:B:345:ILE:HG22	1.96	0.64
1:D:216:LEU:HD11	1:D:240:TYR:HB2	1.79	0.64
1:E:168:GLY:O	1:E:169:TYR:O	2.14	0.64
1:E:192:ILE:O	1:E:195:GLU:HG2	1.98	0.64
1:A:306:TYR:HB2	1:A:309:ILE:CD1	2.24	0.64
1:B:54:VAL:HG23	1:B:85:ILE:HG22	1.78	0.64
1:E:54:VAL:HG23	1:E:85:ILE:HG22	1.78	0.64
1:E:220:ALA:HB1	1:E:226:GLU:OE2	1.97	0.64
1:A:220:ALA:HB1	1:A:226:GLU:CG	2.27	0.64
1:A:342:GLY:O	1:A:345:ILE:HG22	1.96	0.64
1:C:230:ALA:HB2	1:C:236:LEU:HD13	1.79	0.64
1:D:220:ALA:HB1	1:D:226:GLU:OE2	1.97	0.64
1:C:220:ALA:HB1	1:C:226:GLU:OE2	1.97	0.64
1:D:54:VAL:HG23	1:D:85:ILE:HG22	1.78	0.64
1:C:190:MET:HE1	1:C:206:ARG:HA	1.80	0.64
1:E:306:TYR:HB2	1:E:309:ILE:CD1	2.24	0.64
1:E:342:GLY:O	1:E:345:ILE:HG22	1.96	0.64
1:B:220:ALA:CB	1:B:226:GLU:CG	2.75	0.64
1:C:192:ILE:O	1:C:195:GLU:HG2	1.98	0.64
1:C:306:TYR:HB2	1:C:309:ILE:CD1	2.24	0.64
1:D:220:ALA:CB	1:D:226:GLU:CG	2.75	0.64
1:E:124:PHE:CD1	1:E:359:LYS:CD	2.81	0.64
1:A:34:ILE:HD12	1:A:67:LEU:HD22	1.80	0.64

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:124:PHE:CE1	1:C:359:LYS:HA	2.33	0.64
1:E:124:PHE:CE1	1:E:359:LYS:HA	2.33	0.64
1:A:124:PHE:CD1	1:A:359:LYS:CD	2.81	0.64
1:A:191:LYS:O	1:A:194:THR:HG22	1.97	0.64
1:D:124:PHE:CE1	1:D:359:LYS:HA	2.33	0.64
1:D:216:LEU:CD1	1:D:250:ILE:HD11	2.26	0.64
2:F:183:UNK:CB	2:H:183:UNK:HA	2.28	0.64
1:A:190:MET:HE1	1:A:206:ARG:HA	1.79	0.64
1:B:191:LYS:O	1:B:194:THR:HG22	1.97	0.64
1:B:192:ILE:O	1:B:195:GLU:HG2	1.98	0.64
1:B:220:ALA:HB1	1:B:226:GLU:OE2	1.97	0.64
1:A:124:PHE:CE1	1:A:359:LYS:HA	2.33	0.63
1:A:165:ILE:CD1	1:C:44:MET:SD	2.83	0.63
1:B:124:PHE:CD1	1:B:359:LYS:CD	2.81	0.63
1:D:192:ILE:O	1:D:195:GLU:HG2	1.98	0.63
1:D:32:PRO:CG	1:D:59:GLN:HE21	2.10	0.63
1:D:191:LYS:O	1:D:194:THR:HG22	1.97	0.63
1:E:17:VAL:HG23	1:E:33:SER:OG	1.98	0.63
1:A:220:ALA:HB1	1:A:226:GLU:OE2	1.97	0.63
1:B:34:ILE:HD12	1:B:67:LEU:HD22	1.80	0.63
1:B:17:VAL:HG23	1:B:33:SER:OG	1.98	0.63
1:E:53:TYR:CD2	1:E:65:LEU:HD11	2.34	0.63
1:C:17:VAL:HG23	1:C:33:SER:OG	1.99	0.63
1:D:53:TYR:CD2	1:D:65:LEU:HD11	2.34	0.63
1:E:34:ILE:HD12	1:E:67:LEU:HD22	1.80	0.63
1:E:230:ALA:HB2	1:E:236:LEU:HD13	1.79	0.63
1:B:124:PHE:CE1	1:B:359:LYS:HA	2.33	0.63
1:B:230:ALA:HB2	1:B:236:LEU:HD13	1.79	0.63
1:C:53:TYR:CD2	1:C:65:LEU:HD11	2.34	0.63
1:D:17:VAL:HG23	1:D:33:SER:OG	1.98	0.63
1:A:220:ALA:CB	1:A:226:GLU:CG	2.75	0.63
1:B:190:MET:HE1	1:B:206:ARG:HA	1.80	0.63
1:C:124:PHE:CD1	1:C:359:LYS:CD	2.81	0.63
1:D:124:PHE:CD1	1:D:359:LYS:CD	2.80	0.63
1:E:129:VAL:O	1:E:359:LYS:HB2	1.99	0.63
1:A:53:TYR:CD2	1:A:65:LEU:HD11	2.34	0.63
1:C:34:ILE:HD12	1:C:67:LEU:HD22	1.80	0.63
1:C:125:GLU:HG3	1:C:359:LYS:NZ	2.14	0.63
1:D:34:ILE:HD12	1:D:67:LEU:HD22	1.80	0.63
1:B:216:LEU:CD1	1:B:250:ILE:HD11	2.26	0.62
1:C:129:VAL:O	1:C:359:LYS:HB2	1.99	0.62

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:129:VAL:O	1:D:359:LYS:HB2	1.99	0.62
1:A:125:GLU:HG3	1:A:359:LYS:NZ	2.14	0.62
1:B:129:VAL:O	1:B:359:LYS:HB2	1.99	0.62
1:C:220:ALA:CB	1:C:226:GLU:CG	2.75	0.62
1:D:213:LYS:HD2	1:D:306:TYR:OH	1.99	0.62
1:B:53:TYR:CD2	1:B:65:LEU:HD11	2.34	0.62
1:B:113:LYS:O	1:B:117:GLU:HG2	1.99	0.62
1:C:32:PRO:CG	1:C:59:GLN:HE21	2.10	0.62
1:D:113:LYS:O	1:D:117:GLU:HG2	1.99	0.62
1:D:230:ALA:HB2	1:D:236:LEU:HD13	1.79	0.62
1:A:17:VAL:HG23	1:A:33:SER:OG	1.99	0.62
1:E:125:GLU:HG3	1:E:359:LYS:NZ	2.14	0.62
1:A:116:ARG:HD2	1:A:371:HIS:CE1	2.35	0.62
1:A:223:PHE:CD2	1:A:255:PHE:HD1	2.17	0.62
1:E:116:ARG:HD2	1:E:371:HIS:CE1	2.35	0.62
1:E:213:LYS:HD2	1:E:306:TYR:OH	1.99	0.62
1:B:156:GLY:O	1:B:181:ALA:HB1	2.00	0.62
1:C:223:PHE:CD2	1:C:255:PHE:HD1	2.18	0.62
1:A:124:PHE:HB3	1:A:359:LYS:HZ3	1.63	0.62
1:A:129:VAL:O	1:A:359:LYS:HB2	1.99	0.62
1:D:116:ARG:HD2	1:D:371:HIS:CE1	2.34	0.62
1:D:156:GLY:O	1:D:181:ALA:HB1	2.00	0.62
1:C:116:ARG:HD2	1:C:371:HIS:CE1	2.34	0.61
1:C:216:LEU:CD1	1:C:250:ILE:HD11	2.26	0.61
1:D:223:PHE:CD2	1:D:255:PHE:HD1	2.17	0.61
1:A:113:LYS:O	1:A:117:GLU:HG2	1.99	0.61
1:B:165:ILE:CD1	1:D:44:MET:SD	2.83	0.61
1:B:213:LYS:HD2	1:B:306:TYR:OH	1.99	0.61
1:B:223:PHE:CD2	1:B:255:PHE:HD1	2.18	0.61
1:E:113:LYS:O	1:E:117:GLU:HG2	1.99	0.61
1:B:116:ARG:HD2	1:B:371:HIS:CE1	2.35	0.61
1:C:213:LYS:HD2	1:C:306:TYR:OH	1.99	0.61
1:D:124:PHE:CB	1:D:359:LYS:HZ3	2.10	0.61
1:A:213:LYS:HD2	1:A:306:TYR:OH	2.00	0.61
1:D:125:GLU:HG3	1:D:359:LYS:NZ	2.14	0.61
1:B:125:GLU:HG3	1:B:359:LYS:NZ	2.14	0.61
1:E:216:LEU:CD1	1:E:250:ILE:HD11	2.26	0.61
1:E:223:PHE:CD2	1:E:255:PHE:HD1	2.18	0.61
1:A:358:SER:HB3	1:A:361:GLU:HB3	1.83	0.61
1:C:358:SER:HB3	1:C:361:GLU:HB3	1.83	0.61
1:E:32:PRO:CG	1:E:59:GLN:HE21	2.10	0.61

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:109:PRO:HD2	1:B:161:HIS:CD2	2.36	0.61
1:C:113:LYS:O	1:C:117:GLU:HG2	1.99	0.61
1:D:109:PRO:HD2	1:D:161:HIS:CD2	2.36	0.61
1:B:198:TYR:CE2	1:B:248:ILE:HG23	2.36	0.61
1:C:34:ILE:CD1	1:C:59:GLN:NE2	2.64	0.61
1:A:34:ILE:CD1	1:A:59:GLN:NE2	2.64	0.61
1:D:198:TYR:CE2	1:D:248:ILE:HG23	2.36	0.61
1:E:358:SER:HB3	1:E:361:GLU:HB3	1.83	0.61
1:B:124:PHE:CE2	1:B:362:TYR:CG	2.89	0.60
1:C:165:ILE:CD1	1:E:44:MET:SD	2.83	0.60
1:D:34:ILE:CD1	1:D:59:GLN:NE2	2.64	0.60
1:A:216:LEU:CD1	1:A:250:ILE:HD11	2.26	0.60
1:D:190:MET:HE3	1:D:206:ARG:HG2	1.82	0.60
1:E:156:GLY:O	1:E:181:ALA:HB1	2.00	0.60
1:A:198:TYR:CE2	1:A:248:ILE:HG23	2.36	0.60
1:B:223:PHE:CE2	1:B:255:PHE:CD1	2.80	0.60
1:C:198:TYR:CE2	1:C:248:ILE:HG23	2.36	0.60
1:E:125:GLU:HG3	1:E:359:LYS:HZ3	1.66	0.60
1:A:32:PRO:CG	1:A:59:GLN:NE2	2.64	0.60
1:A:223:PHE:CE2	1:A:255:PHE:CD1	2.80	0.60
1:E:198:TYR:CE2	1:E:248:ILE:HG23	2.36	0.60
1:C:156:GLY:O	1:C:181:ALA:HB1	2.00	0.60
1:D:124:PHE:CE2	1:D:362:TYR:CG	2.89	0.60
1:E:34:ILE:CD1	1:E:59:GLN:NE2	2.64	0.60
1:A:124:PHE:CE2	1:A:362:TYR:CG	2.89	0.60
1:A:156:GLY:O	1:A:181:ALA:HB1	2.00	0.60
1:C:109:PRO:HD2	1:C:161:HIS:CD2	2.36	0.60
1:A:109:PRO:HD2	1:A:161:HIS:CD2	2.36	0.60
1:B:14:SER:O	1:B:157:ASP:HB3	2.02	0.60
1:B:34:ILE:CD1	1:B:59:GLN:NE2	2.64	0.60
1:A:32:PRO:CG	1:A:59:GLN:HE21	2.10	0.60
1:E:109:PRO:HD2	1:E:161:HIS:CD2	2.36	0.60
1:E:124:PHE:CE2	1:E:362:TYR:CG	2.89	0.60
1:A:14:SER:O	1:A:157:ASP:HB3	2.02	0.59
1:C:14:SER:O	1:C:157:ASP:HB3	2.02	0.59
1:C:169:TYR:CE1	1:E:47:MET:HE1	2.37	0.59
1:D:32:PRO:CG	1:D:59:GLN:NE2	2.64	0.59
1:A:125:GLU:HG3	1:A:359:LYS:HZ3	1.66	0.59
1:B:169:TYR:CE1	1:D:47:MET:HE1	2.37	0.59
1:C:124:PHE:CE2	1:C:362:TYR:CG	2.89	0.59
1:E:14:SER:O	1:E:157:ASP:HB3	2.02	0.59

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:124:PHE:HB3	1:E:359:LYS:HZ3	1.63	0.59
1:A:144:ALA:CB	1:A:338:SER:O	2.51	0.59
1:C:124:PHE:CB	1:C:359:LYS:HZ3	2.11	0.59
1:C:144:ALA:CB	1:C:338:SER:O	2.51	0.59
1:D:144:ALA:CB	1:D:338:SER:O	2.51	0.59
1:E:223:PHE:CE2	1:E:255:PHE:CD1	2.80	0.59
1:E:223:PHE:HA	1:E:226:GLU:HG2	1.84	0.59
1:B:32:PRO:CG	1:B:59:GLN:NE2	2.65	0.59
1:B:358:SER:HB3	1:B:361:GLU:HB3	1.83	0.59
1:E:32:PRO:CG	1:E:59:GLN:NE2	2.64	0.59
1:B:144:ALA:CB	1:B:338:SER:O	2.51	0.59
1:B:304:THR:O	1:B:304:THR:HG22	2.03	0.59
1:C:223:PHE:HA	1:C:226:GLU:HG2	1.84	0.59
1:D:223:PHE:HA	1:D:226:GLU:HG2	1.84	0.59
1:E:144:ALA:CB	1:E:338:SER:O	2.51	0.59
1:C:223:PHE:CE2	1:C:255:PHE:CD1	2.80	0.59
1:E:304:THR:O	1:E:304:THR:HG22	2.03	0.59
1:A:124:PHE:CA	1:A:359:LYS:HD3	2.33	0.59
1:A:304:THR:HG22	1:A:304:THR:O	2.03	0.59
1:C:304:THR:HG22	1:C:304:THR:O	2.03	0.59
1:D:14:SER:O	1:D:157:ASP:HB3	2.02	0.59
1:E:117:GLU:CB	1:E:367:PRO:HB3	2.33	0.59
1:A:223:PHE:CD2	1:A:255:PHE:CD1	2.91	0.59
1:B:117:GLU:CB	1:B:367:PRO:HB3	2.33	0.59
1:C:32:PRO:CG	1:C:59:GLN:NE2	2.65	0.59
1:C:117:GLU:CB	1:C:367:PRO:HB3	2.33	0.59
1:A:222:ASP:O	1:A:226:GLU:HG2	2.03	0.59
1:A:223:PHE:HA	1:A:226:GLU:HG2	1.84	0.59
1:B:34:ILE:HD11	1:B:59:GLN:CD	2.24	0.59
1:B:222:ASP:O	1:B:226:GLU:HG2	2.03	0.59
1:D:222:ASP:O	1:D:226:GLU:HG2	2.03	0.59
1:E:34:ILE:HD11	1:E:59:GLN:CD	2.24	0.58
1:A:117:GLU:CB	1:A:367:PRO:HB3	2.33	0.58
1:B:223:PHE:HA	1:B:226:GLU:HG2	1.84	0.58
1:C:34:ILE:HD11	1:C:59:GLN:CD	2.24	0.58
1:C:124:PHE:CA	1:C:359:LYS:HD3	2.33	0.58
1:D:34:ILE:HD11	1:D:59:GLN:CD	2.24	0.58
1:C:222:ASP:O	1:C:226:GLU:HG2	2.03	0.58
1:D:117:GLU:CB	1:D:367:PRO:HB3	2.33	0.58
1:D:223:PHE:CD2	1:D:255:PHE:CD1	2.91	0.58
1:D:358:SER:HB3	1:D:361:GLU:HB3	1.83	0.58

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:223:PHE:CD2	1:C:255:PHE:CD1	2.91	0.58
1:E:124:PHE:CA	1:E:359:LYS:HD3	2.33	0.58
1:B:223:PHE:CD2	1:B:255:PHE:CD1	2.91	0.58
1:D:144:ALA:HB2	1:D:338:SER:O	2.03	0.58
1:E:189:LEU:HA	1:E:192:ILE:HG22	1.86	0.58
1:E:223:PHE:CD2	1:E:255:PHE:CD1	2.91	0.58
2:F:186:UNK:CB	2:H:186:UNK:CB	2.82	0.58
1:A:34:ILE:HD11	1:A:59:GLN:CD	2.24	0.58
1:C:144:ALA:HB2	1:C:338:SER:O	2.03	0.58
1:C:189:LEU:HA	1:C:192:ILE:HG22	1.86	0.58
1:D:304:THR:HG22	1:D:304:THR:O	2.03	0.58
1:E:108:ALA:HB1	1:E:161:HIS:NE2	2.18	0.58
1:A:144:ALA:HB2	1:A:338:SER:O	2.03	0.58
1:A:223:PHE:CZ	1:A:255:PHE:O	2.57	0.58
1:D:108:ALA:HB1	1:D:161:HIS:NE2	2.18	0.58
1:B:124:PHE:CA	1:B:359:LYS:HD3	2.33	0.58
1:B:144:ALA:HB2	1:B:338:SER:O	2.03	0.58
1:B:223:PHE:CZ	1:B:255:PHE:O	2.57	0.58
1:D:306:TYR:CB	1:D:309:ILE:HD11	2.30	0.58
1:E:144:ALA:HB2	1:E:338:SER:O	2.03	0.58
1:E:222:ASP:O	1:E:226:GLU:HG2	2.03	0.57
1:A:189:LEU:HA	1:A:192:ILE:HG22	1.86	0.57
1:C:223:PHE:HZ	1:C:255:PHE:O	1.87	0.57
1:A:108:ALA:HB1	1:A:161:HIS:NE2	2.18	0.57
1:A:223:PHE:HZ	1:A:255:PHE:O	1.87	0.57
1:B:32:PRO:CG	1:B:59:GLN:HE21	2.10	0.57
1:B:108:ALA:HB1	1:B:161:HIS:NE2	2.18	0.57
1:D:124:PHE:CA	1:D:359:LYS:HD3	2.33	0.57
1:E:223:PHE:HZ	1:E:255:PHE:O	1.87	0.57
1:C:43:VAL:HG12	1:C:43:VAL:O	2.05	0.57
1:C:108:ALA:HB1	1:C:161:HIS:NE2	2.18	0.57
1:C:223:PHE:CZ	1:C:255:PHE:O	2.57	0.57
1:D:223:PHE:CZ	1:D:255:PHE:O	2.57	0.57
1:B:223:PHE:HZ	1:B:255:PHE:O	1.87	0.57
1:B:306:TYR:CB	1:B:309:ILE:HD11	2.30	0.57
1:C:190:MET:HE1	1:C:206:ARG:HG2	1.87	0.57
1:D:223:PHE:HZ	1:D:255:PHE:O	1.87	0.57
1:E:223:PHE:CZ	1:E:255:PHE:O	2.57	0.57
1:B:230:ALA:N	1:B:236:LEU:CD1	2.68	0.57
1:C:303:THR:HG22	1:C:303:THR:O	2.05	0.57
1:D:142:LEU:HD22	1:D:165:ILE:HG21	1.87	0.57

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:124:PHE:CB	1:E:359:LYS:HZ2	2.11	0.57
1:D:230:ALA:N	1:D:236:LEU:CD1	2.68	0.57
1:B:190:MET:HE1	1:B:206:ARG:HG2	1.87	0.57
1:E:306:TYR:CB	1:E:309:ILE:HD11	2.30	0.57
1:A:303:THR:O	1:A:303:THR:HG22	2.05	0.57
1:D:124:PHE:CD2	1:D:362:TYR:CD2	2.93	0.57
1:B:124:PHE:CD2	1:B:362:TYR:CD2	2.93	0.56
1:B:255:PHE:O	1:B:258:PRO:HD2	2.05	0.56
1:A:24:ASP:O	1:A:340:TRP:HZ3	1.88	0.56
1:A:230:ALA:N	1:A:236:LEU:CD1	2.68	0.56
1:C:107:GLU:OE2	1:C:116:ARG:NE	2.38	0.56
1:C:255:PHE:O	1:C:258:PRO:HD2	2.05	0.56
1:D:44:MET:HB2	1:D:47:MET:HG2	1.88	0.56
1:E:220:ALA:CB	1:E:226:GLU:CG	2.75	0.56
1:A:43:VAL:HG12	1:A:43:VAL:O	2.05	0.56
1:A:124:PHE:CB	1:A:359:LYS:HZ2	2.11	0.56
1:A:124:PHE:CD2	1:A:362:TYR:CD2	2.93	0.56
1:B:313:MET:O	1:B:317:ILE:HD12	2.06	0.56
1:E:107:GLU:OE2	1:E:116:ARG:NE	2.38	0.56
1:E:313:MET:O	1:E:317:ILE:HD12	2.06	0.56
1:C:24:ASP:O	1:C:340:TRP:HZ3	1.88	0.56
1:C:230:ALA:N	1:C:236:LEU:CD1	2.68	0.56
1:D:107:GLU:OE2	1:D:116:ARG:NE	2.38	0.56
1:D:255:PHE:O	1:D:258:PRO:HD2	2.05	0.56
1:E:24:ASP:O	1:E:340:TRP:HZ3	1.88	0.56
1:A:223:PHE:CE1	1:A:259:GLU:HB2	2.39	0.56
1:E:124:PHE:CD2	1:E:362:TYR:CD2	2.93	0.56
1:A:190:MET:HE1	1:A:206:ARG:HG2	1.88	0.56
1:A:255:PHE:O	1:A:258:PRO:HD2	2.05	0.56
1:B:107:GLU:OE2	1:B:116:ARG:NE	2.38	0.56
1:B:190:MET:HE3	1:B:206:ARG:HG2	1.88	0.56
1:C:42:GLY:HA3	1:C:47:MET:SD	2.46	0.56
1:D:189:LEU:HA	1:D:192:ILE:HG22	1.86	0.56
1:D:313:MET:O	1:D:317:ILE:HD12	2.06	0.56
1:B:252:ASN:HA	1:B:255:PHE:CE2	2.41	0.56
1:C:124:PHE:CD2	1:C:362:TYR:CD2	2.93	0.56
1:D:43:VAL:HG12	1:D:43:VAL:O	2.05	0.56
1:E:43:VAL:HG12	1:E:43:VAL:O	2.04	0.56
1:E:230:ALA:N	1:E:236:LEU:CD1	2.68	0.56
1:E:252:ASN:HA	1:E:255:PHE:CE2	2.41	0.56
1:E:255:PHE:O	1:E:258:PRO:HD2	2.05	0.56

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:142:LEU:HD22	1:B:165:ILE:HG21	1.88	0.56
1:B:189:LEU:HA	1:B:192:ILE:HG22	1.86	0.56
1:A:53:TYR:HD2	1:A:65:LEU:HD21	1.71	0.56
1:A:313:MET:O	1:A:317:ILE:HD12	2.06	0.56
1:B:24:ASP:O	1:B:340:TRP:HZ3	1.88	0.56
1:C:306:TYR:CB	1:C:309:ILE:HD11	2.30	0.56
1:D:48:GLY:HA3	1:D:49:GLN:C	2.27	0.56
1:D:252:ASN:HA	1:D:255:PHE:CE2	2.41	0.56
1:E:48:GLY:HA3	1:E:49:GLN:C	2.26	0.56
1:A:252:ASN:HA	1:A:255:PHE:CE2	2.41	0.56
1:B:43:VAL:HG12	1:B:43:VAL:O	2.05	0.56
1:C:291:LYS:HA	1:C:325:MET:HE1	1.87	0.56
1:D:42:GLY:HA3	1:D:47:MET:SD	2.46	0.56
1:E:53:TYR:HD2	1:E:65:LEU:HD21	1.71	0.56
1:E:140:LEU:HG	1:E:343:GLY:CA	2.36	0.56
1:C:223:PHE:CE1	1:C:259:GLU:HB2	2.39	0.55
1:C:252:ASN:HA	1:C:255:PHE:CE2	2.41	0.55
1:D:189:LEU:O	1:D:193:LEU:HB2	2.06	0.55
1:E:142:LEU:HD22	1:E:165:ILE:HG21	1.87	0.55
1:E:303:THR:HG22	1:E:303:THR:O	2.05	0.55
1:A:107:GLU:OE2	1:A:116:ARG:NE	2.38	0.55
1:A:169:TYR:CE1	1:C:47:MET:HE1	2.41	0.55
1:B:303:THR:HG22	1:B:303:THR:O	2.05	0.55
1:D:223:PHE:CE2	1:D:255:PHE:CD1	2.80	0.55
1:A:189:LEU:O	1:A:193:LEU:HB2	2.06	0.55
1:C:313:MET:O	1:C:317:ILE:HD12	2.06	0.55
1:D:6:THR:CG2	1:D:7:ALA:H	2.15	0.55
1:A:140:LEU:HG	1:A:343:GLY:CA	2.36	0.55
1:A:190:MET:HE3	1:A:206:ARG:HG2	1.87	0.55
1:C:44:MET:HB2	1:C:47:MET:HG2	1.88	0.55
1:C:140:LEU:HG	1:C:343:GLY:CA	2.36	0.55
1:A:142:LEU:HD22	1:A:165:ILE:HG21	1.88	0.55
1:B:53:TYR:HD2	1:B:65:LEU:HD21	1.71	0.55
1:B:140:LEU:HG	1:B:343:GLY:HA2	1.89	0.55
1:B:216:LEU:HD22	1:B:238:LYS:HD2	1.88	0.55
1:D:140:LEU:HG	1:D:343:GLY:HA2	1.89	0.55
1:E:189:LEU:O	1:E:193:LEU:HB2	2.06	0.55
1:B:48:GLY:HA3	1:B:49:GLN:C	2.27	0.55
1:C:216:LEU:HD22	1:C:238:LYS:HD2	1.88	0.55
1:D:303:THR:HG22	1:D:303:THR:O	2.05	0.55
1:D:318:THR:HA	1:D:327:ILE:HD12	1.88	0.55

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:189:LEU:O	1:B:193:LEU:HB2	2.06	0.55
1:B:330:ILE:HG23	1:B:330:ILE:O	2.07	0.55
1:C:190:MET:HE3	1:C:206:ARG:HG2	1.88	0.55
1:D:53:TYR:HD2	1:D:65:LEU:HD21	1.71	0.55
1:D:223:PHE:CE1	1:D:259:GLU:HB2	2.39	0.55
1:E:42:GLY:HA3	1:E:47:MET:SD	2.46	0.55
1:E:44:MET:HB2	1:E:47:MET:HG2	1.88	0.55
1:E:216:LEU:HD22	1:E:238:LYS:HD2	1.88	0.55
1:C:318:THR:HA	1:C:327:ILE:HD12	1.88	0.55
1:C:330:ILE:HG23	1:C:330:ILE:O	2.07	0.55
1:D:24:ASP:O	1:D:340:TRP:HZ3	1.88	0.55
1:D:140:LEU:HG	1:D:343:GLY:CA	2.36	0.55
1:B:140:LEU:HG	1:B:343:GLY:CA	2.36	0.55
1:C:48:GLY:HA3	1:C:49:GLN:C	2.26	0.55
1:C:142:LEU:HD22	1:C:165:ILE:HG21	1.88	0.55
1:C:189:LEU:O	1:C:193:LEU:HB2	2.06	0.55
2:F:183:UNK:HA	2:H:183:UNK:CA	2.20	0.55
1:A:318:THR:HA	1:A:327:ILE:HD12	1.88	0.55
1:E:318:THR:HA	1:E:327:ILE:HD12	1.88	0.55
1:A:140:LEU:HG	1:A:343:GLY:HA2	1.89	0.54
1:A:216:LEU:HD22	1:A:238:LYS:HD2	1.88	0.54
1:B:6:THR:CG2	1:B:7:ALA:H	2.15	0.54
1:B:318:THR:HA	1:B:327:ILE:HD12	1.88	0.54
1:E:18:LYS:HG2	1:E:30:VAL:HG12	1.90	0.54
1:E:223:PHE:CE1	1:E:259:GLU:HB2	2.39	0.54
1:E:291:LYS:HA	1:E:325:MET:HE1	1.89	0.54
1:A:48:GLY:HA3	1:A:49:GLN:C	2.27	0.54
1:A:330:ILE:HG23	1:A:330:ILE:O	2.07	0.54
1:C:190:MET:HE2	1:C:209:VAL:HG21	1.89	0.54
1:B:223:PHE:CE1	1:B:259:GLU:HB2	2.39	0.54
1:D:34:ILE:HG12	1:D:59:GLN:HE22	1.71	0.54
1:D:216:LEU:HD22	1:D:238:LYS:HD2	1.89	0.54
1:A:34:ILE:HG12	1:A:59:GLN:HE22	1.71	0.54
1:C:324:THR:O	1:C:324:THR:HG22	2.08	0.54
1:D:330:ILE:HG23	1:D:330:ILE:O	2.07	0.54
1:E:140:LEU:HG	1:E:343:GLY:HA2	1.89	0.54
1:B:190:MET:HE2	1:B:209:VAL:HG21	1.89	0.54
1:C:222:ASP:HB3	1:C:224:GLU:OE2	2.08	0.54
1:A:306:TYR:CB	1:A:309:ILE:HD11	2.30	0.54
1:C:53:TYR:HD2	1:C:65:LEU:HD21	1.71	0.54
1:C:18:LYS:HG2	1:C:30:VAL:HG12	1.90	0.54

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:272:ALA:HB1	1:C:276:GLU:HB2	1.90	0.54
1:D:222:ASP:HB3	1:D:224:GLU:OE2	2.08	0.54
1:E:222:ASP:HB3	1:E:224:GLU:OE2	2.08	0.54
1:A:18:LYS:HG2	1:A:30:VAL:HG12	1.90	0.54
1:A:324:THR:O	1:A:324:THR:HG22	2.08	0.54
1:E:330:ILE:O	1:E:330:ILE:HG23	2.07	0.54
1:A:112:PRO:HG3	1:B:197:GLY:HA2	1.90	0.54
1:A:272:ALA:HB1	1:A:276:GLU:HB2	1.90	0.54
1:B:124:PHE:CB	1:B:359:LYS:HZ3	2.18	0.54
1:B:222:ASP:HB3	1:B:224:GLU:OE2	2.08	0.54
1:C:112:PRO:HG3	1:D:197:GLY:HA2	1.90	0.53
1:C:140:LEU:HG	1:C:343:GLY:HA2	1.89	0.53
1:E:272:ALA:HB1	1:E:276:GLU:HB2	1.90	0.53
1:A:190:MET:HE2	1:A:209:VAL:HG21	1.90	0.53
1:B:272:ALA:HB1	1:B:276:GLU:HB2	1.90	0.53
1:E:324:THR:HG22	1:E:324:THR:O	2.08	0.53
1:D:324:THR:HG22	1:D:324:THR:O	2.08	0.53
1:A:299:LEU:HD12	1:A:331:ALA:HB2	1.90	0.53
1:D:112:PRO:HG3	1:E:197:GLY:HA2	1.90	0.53
1:E:6:THR:CG2	1:E:7:ALA:H	2.15	0.53
1:B:18:LYS:HG2	1:B:30:VAL:HG12	1.89	0.53
1:B:34:ILE:HG12	1:B:59:GLN:HE22	1.71	0.53
1:C:299:LEU:HD12	1:C:331:ALA:HB2	1.90	0.53
1:A:169:TYR:CE1	1:C:47:MET:CE	2.92	0.53
1:A:222:ASP:HB3	1:A:224:GLU:OE2	2.08	0.53
1:B:202:THR:HG22	1:B:203:THR:N	2.24	0.53
1:B:299:LEU:HD12	1:B:331:ALA:HB2	1.90	0.53
1:D:202:THR:HG22	1:D:203:THR:N	2.24	0.53
1:B:6:THR:O	1:B:7:ALA:HB2	2.09	0.53
1:B:321:ALA:HB3	1:B:327:ILE:HD11	1.91	0.53
1:A:53:TYR:HD2	1:A:65:LEU:HD11	1.75	0.53
1:D:272:ALA:HB1	1:D:276:GLU:HB2	1.90	0.53
1:B:112:PRO:HG3	1:C:197:GLY:HA2	1.90	0.52
1:D:6:THR:O	1:D:7:ALA:HB2	2.09	0.52
1:D:18:LYS:HG2	1:D:30:VAL:HG12	1.90	0.52
1:D:53:TYR:HD2	1:D:65:LEU:HD11	1.75	0.52
1:D:369:ILE:HD12	1:D:370:VAL:N	2.25	0.52
1:E:299:LEU:HD12	1:E:331:ALA:HB2	1.90	0.52
1:A:202:THR:HG22	1:A:203:THR:N	2.24	0.52
1:A:321:ALA:HB3	1:A:327:ILE:HD11	1.91	0.52
1:C:34:ILE:HG12	1:C:59:GLN:HE22	1.71	0.52

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:53:TYR:HD2	1:C:65:LEU:HD11	1.75	0.52
1:D:299:LEU:HD12	1:D:331:ALA:HB2	1.90	0.52
1:B:53:TYR:HD2	1:B:65:LEU:HD11	1.75	0.52
1:B:369:ILE:HD12	1:B:370:VAL:N	2.24	0.52
1:D:291:LYS:HA	1:D:325:MET:HE1	1.90	0.52
1:E:202:THR:HG22	1:E:203:THR:N	2.24	0.52
1:C:6:THR:CG2	1:C:7:ALA:H	2.15	0.52
1:C:169:TYR:CE1	1:E:47:MET:CE	2.92	0.52
1:B:125:GLU:HG3	1:B:359:LYS:HZ3	1.75	0.52
1:B:324:THR:HG22	1:B:324:THR:O	2.08	0.52
1:C:6:THR:O	1:C:7:ALA:HB2	2.09	0.52
1:E:6:THR:O	1:E:7:ALA:HB2	2.09	0.52
1:E:34:ILE:HG12	1:E:59:GLN:HE22	1.71	0.52
1:E:53:TYR:HD2	1:E:65:LEU:HD11	1.74	0.52
1:A:262:PHE:CE2	1:A:312:ARG:HD3	2.45	0.52
1:A:369:ILE:HD12	1:A:370:VAL:N	2.24	0.52
1:D:53:TYR:CD2	1:D:65:LEU:HD21	2.45	0.52
1:E:53:TYR:CD2	1:E:65:LEU:HD21	2.45	0.52
1:C:262:PHE:CE2	1:C:312:ARG:HD3	2.45	0.52
1:C:321:ALA:HB3	1:C:327:ILE:HD11	1.91	0.52
1:D:321:ALA:HB3	1:D:327:ILE:HD11	1.90	0.52
1:A:6:THR:O	1:A:7:ALA:HB2	2.09	0.52
1:B:53:TYR:CD2	1:B:65:LEU:HD21	2.45	0.52
1:D:124:PHE:CD2	1:D:362:TYR:CG	2.98	0.52
1:D:219:VAL:HG22	1:D:258:PRO:HB2	1.92	0.52
1:A:220:ALA:HB3	1:A:223:PHE:CD1	2.45	0.52
1:B:34:ILE:CG1	1:B:59:GLN:NE2	2.73	0.52
1:C:53:TYR:CD2	1:C:65:LEU:HD21	2.45	0.52
1:D:262:PHE:CE2	1:D:312:ARG:HD3	2.45	0.52
1:B:169:TYR:CE1	1:D:47:MET:CE	2.92	0.52
1:B:219:VAL:HG22	1:B:258:PRO:HB2	1.92	0.52
1:C:202:THR:HG22	1:C:203:THR:N	2.24	0.52
1:D:287:ILE:HA	1:D:290:ARG:HD3	1.92	0.52
1:E:262:PHE:CE2	1:E:312:ARG:HD3	2.45	0.52
1:B:124:PHE:CD1	1:B:359:LYS:HB2	2.45	0.51
1:B:124:PHE:CD2	1:B:362:TYR:CG	2.98	0.51
1:C:153:LEU:HB3	1:C:299:LEU:HD23	1.93	0.51
1:D:220:ALA:HB3	1:D:223:PHE:CD1	2.45	0.51
1:E:124:PHE:CD2	1:E:362:TYR:CG	2.98	0.51
1:E:321:ALA:HB3	1:E:327:ILE:HD11	1.91	0.51
2:F:183:UNK:CA	2:H:183:UNK:CA	2.83	0.51

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:124:PHE:CD1	1:D:359:LYS:HB2	2.45	0.51
1:A:124:PHE:CD2	1:A:362:TYR:CG	2.98	0.51
1:A:153:LEU:HB3	1:A:299:LEU:HD23	1.92	0.51
1:B:270:GLU:OE2	1:C:39:ARG:CZ	2.58	0.51
1:C:220:ALA:HB3	1:C:223:PHE:CD1	2.45	0.51
1:C:369:ILE:HD12	1:C:370:VAL:N	2.24	0.51
1:E:287:ILE:HA	1:E:290:ARG:HD3	1.92	0.51
1:A:53:TYR:CD2	1:A:65:LEU:HD21	2.45	0.51
1:A:124:PHE:CD1	1:A:359:LYS:HB2	2.45	0.51
1:A:270:GLU:OE2	1:B:39:ARG:CZ	2.58	0.51
1:B:262:PHE:CE2	1:B:312:ARG:HD3	2.45	0.51
1:B:287:ILE:HA	1:B:290:ARG:HD3	1.93	0.51
1:B:294:TYR:HB2	1:B:325:MET:HE1	1.93	0.51
1:C:124:PHE:CD2	1:C:362:TYR:CG	2.98	0.51
1:C:223:PHE:HE2	1:C:256:ARG:CA	2.23	0.51
1:D:190:MET:HE1	1:D:206:ARG:HG2	1.93	0.51
1:D:270:GLU:OE2	1:E:39:ARG:CZ	2.58	0.51
1:E:219:VAL:HG22	1:E:258:PRO:HB2	1.92	0.51
1:E:153:LEU:HB3	1:E:299:LEU:HD23	1.93	0.51
1:E:223:PHE:HE2	1:E:256:ARG:CA	2.23	0.51
1:E:230:ALA:HB2	1:E:236:LEU:CD1	2.41	0.51
2:F:228:UNK:CB	2:H:228:UNK:CB	2.88	0.51
1:E:369:ILE:HD12	1:E:370:VAL:N	2.24	0.51
2:F:189:UNK:CB	2:H:190:UNK:CB	2.89	0.51
1:B:220:ALA:HB3	1:B:223:PHE:CD1	2.45	0.51
1:D:125:GLU:HG3	1:D:359:LYS:HZ1	1.75	0.51
1:B:230:ALA:HB2	1:B:236:LEU:CD1	2.41	0.51
1:C:116:ARG:CB	1:C:371:HIS:CE1	2.82	0.51
1:D:153:LEU:HB3	1:D:299:LEU:HD23	1.93	0.51
1:A:6:THR:CG2	1:A:7:ALA:H	2.15	0.51
1:D:223:PHE:HE2	1:D:256:ARG:CA	2.23	0.51
1:B:153:LEU:HB3	1:B:299:LEU:HD23	1.92	0.51
1:C:124:PHE:CD1	1:C:359:LYS:HB2	2.45	0.51
1:C:125:GLU:HG3	1:C:359:LYS:HZ1	1.76	0.51
1:C:270:GLU:OE2	1:D:39:ARG:CZ	2.58	0.51
1:D:230:ALA:HB2	1:D:236:LEU:CD1	2.41	0.51
1:B:120:THR:HG22	1:B:132:MET:CE	2.42	0.50
1:C:230:ALA:HB2	1:C:236:LEU:CD1	2.41	0.50
1:C:230:ALA:N	1:C:236:LEU:HD12	2.26	0.50
1:C:287:ILE:HA	1:C:290:ARG:HD3	1.93	0.50
1:D:120:THR:HG22	1:D:132:MET:CE	2.41	0.50

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:220:ALA:HB3	1:E:223:PHE:CD1	2.45	0.50
1:E:230:ALA:N	1:E:236:LEU:HD12	2.26	0.50
2:F:214:UNK:CB	2:H:214:UNK:CB	2.89	0.50
1:A:124:PHE:CG	1:A:359:LYS:HD2	2.47	0.50
1:A:219:VAL:HG22	1:A:258:PRO:HB2	1.92	0.50
1:A:230:ALA:N	1:A:236:LEU:HD12	2.26	0.50
1:C:219:VAL:HG22	1:C:258:PRO:HB2	1.92	0.50
1:A:223:PHE:HE2	1:A:256:ARG:CA	2.23	0.50
1:C:34:ILE:CG1	1:C:59:GLN:NE2	2.73	0.50
1:A:34:ILE:CG1	1:A:59:GLN:NE2	2.73	0.50
1:B:53:TYR:CE1	1:B:57:GLU:OE2	2.65	0.50
1:E:124:PHE:CD1	1:E:359:LYS:HB2	2.45	0.50
1:B:124:PHE:CG	1:B:359:LYS:HD2	2.47	0.50
1:C:53:TYR:CE1	1:C:57:GLU:OE2	2.65	0.50
1:E:53:TYR:CE1	1:E:57:GLU:OE2	2.65	0.50
1:E:120:THR:HG22	1:E:132:MET:CE	2.42	0.50
1:A:120:THR:HG22	1:A:132:MET:CE	2.41	0.50
1:C:124:PHE:CG	1:C:359:LYS:HD2	2.47	0.50
1:D:165:ILE:CD1	1:D:169:TYR:O	2.60	0.50
1:D:198:TYR:CG	1:D:248:ILE:HD12	2.47	0.50
1:E:165:ILE:CD1	1:E:169:TYR:O	2.60	0.50
1:B:44:MET:HB2	1:B:47:MET:HG2	1.93	0.50
1:B:115:ASN:O	1:B:119:MET:HB2	2.12	0.50
1:A:53:TYR:CE1	1:A:57:GLU:OE2	2.65	0.50
1:C:120:THR:HG22	1:C:132:MET:CE	2.41	0.50
1:D:358:SER:OG	1:D:360:GLN:HG2	2.12	0.50
1:E:34:ILE:CG1	1:E:59:GLN:NE2	2.73	0.50
1:E:267:ILE:HG22	1:E:267:ILE:O	2.12	0.50
1:B:198:TYR:CG	1:B:248:ILE:HD12	2.47	0.49
1:D:217:CYS:HA	1:D:254:ARG:HG2	1.93	0.49
1:E:358:SER:OG	1:E:360:GLN:HG2	2.11	0.49
1:A:115:ASN:O	1:A:119:MET:HB2	2.12	0.49
1:A:267:ILE:HG22	1:A:267:ILE:O	2.12	0.49
1:A:365:ALA:O	1:A:369:ILE:HG23	2.12	0.49
1:B:31:PHE:HZ	1:B:89:THR:OG1	1.95	0.49
1:B:217:CYS:HA	1:B:254:ARG:HG2	1.93	0.49
1:D:34:ILE:CG1	1:D:59:GLN:NE2	2.73	0.49
1:A:287:ILE:HA	1:A:290:ARG:HD3	1.93	0.49
1:C:31:PHE:HZ	1:C:89:THR:OG1	1.95	0.49
1:D:124:PHE:CG	1:D:359:LYS:HD2	2.47	0.49
1:D:365:ALA:O	1:D:369:ILE:HG23	2.12	0.49

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:230:ALA:HB2	1:A:236:LEU:CD1	2.41	0.49
1:B:223:PHE:HE2	1:B:256:ARG:CA	2.23	0.49
1:B:365:ALA:O	1:B:369:ILE:HG23	2.12	0.49
1:C:267:ILE:HG22	1:C:267:ILE:O	2.12	0.49
1:C:365:ALA:O	1:C:369:ILE:HG23	2.12	0.49
1:D:115:ASN:O	1:D:119:MET:HB2	2.12	0.49
1:D:165:ILE:HG23	1:D:165:ILE:O	2.12	0.49
1:E:165:ILE:O	1:E:165:ILE:HG23	2.12	0.49
1:A:44:MET:HB2	1:A:47:MET:HG2	1.93	0.49
1:C:115:ASN:O	1:C:119:MET:HB2	2.12	0.49
1:C:217:CYS:HA	1:C:254:ARG:HG2	1.93	0.49
1:D:53:TYR:CE1	1:D:57:GLU:OE2	2.65	0.49
1:E:365:ALA:O	1:E:369:ILE:HG23	2.12	0.49
1:A:116:ARG:CB	1:A:371:HIS:CE1	2.82	0.49
1:B:358:SER:OG	1:B:360:GLN:HG2	2.12	0.49
1:C:358:SER:OG	1:C:360:GLN:HG2	2.12	0.49
1:E:124:PHE:CG	1:E:359:LYS:HD2	2.47	0.49
1:E:217:CYS:HA	1:E:254:ARG:HG2	1.93	0.49
1:A:358:SER:OG	1:A:360:GLN:HG2	2.12	0.49
1:E:31:PHE:HZ	1:E:89:THR:OG1	1.95	0.49
1:B:166:TYR:HD2	1:D:64:ILE:CG1	2.26	0.49
1:E:198:TYR:CG	1:E:248:ILE:HD12	2.47	0.49
1:A:124:PHE:C	1:A:359:LYS:HE2	2.33	0.49
1:B:223:PHE:CE1	1:B:259:GLU:OE1	2.66	0.49
1:C:165:ILE:HG23	1:C:165:ILE:O	2.13	0.49
1:A:217:CYS:HA	1:A:254:ARG:HG2	1.94	0.49
1:B:124:PHE:C	1:B:359:LYS:HE2	2.33	0.49
1:E:115:ASN:O	1:E:119:MET:HB2	2.12	0.49
1:E:124:PHE:C	1:E:359:LYS:HE2	2.33	0.49
1:A:31:PHE:HZ	1:A:89:THR:OG1	1.95	0.48
1:A:294:TYR:HB2	1:A:325:MET:HE1	1.95	0.48
1:C:124:PHE:C	1:C:359:LYS:HE2	2.33	0.48
1:D:267:ILE:O	1:D:267:ILE:HG22	2.12	0.48
1:A:190:MET:CE	1:A:209:VAL:HG21	2.43	0.48
1:C:198:TYR:CG	1:C:248:ILE:HD12	2.47	0.48
1:D:223:PHE:CE1	1:D:259:GLU:OE1	2.66	0.48
1:E:99:GLU:HG3	1:E:128:ASN:HB3	1.95	0.48
1:A:99:GLU:HG3	1:A:128:ASN:HB3	1.96	0.48
1:A:223:PHE:CE1	1:A:259:GLU:OE1	2.66	0.48
1:C:34:ILE:HG22	1:C:69:TYR:CD1	2.49	0.48
1:C:99:GLU:HG3	1:C:128:ASN:HB3	1.95	0.48

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:120:THR:HB	1:C:362:TYR:CE1	2.49	0.48
1:E:34:ILE:HG22	1:E:69:TYR:CD1	2.49	0.48
1:A:198:TYR:CG	1:A:248:ILE:HD12	2.47	0.48
1:B:34:ILE:HG22	1:B:69:TYR:CD1	2.49	0.48
1:B:190:MET:CE	1:B:209:VAL:HG21	2.43	0.48
1:B:190:MET:SD	1:B:200:PHE:HB2	2.53	0.48
1:C:190:MET:SD	1:C:200:PHE:HB2	2.53	0.48
1:C:223:PHE:CE1	1:C:259:GLU:OE1	2.66	0.48
1:A:190:MET:SD	1:A:200:PHE:HB2	2.53	0.48
1:A:206:ARG:O	1:A:209:VAL:HG22	2.14	0.48
1:B:120:THR:HB	1:B:362:TYR:CE1	2.49	0.48
1:D:31:PHE:HZ	1:D:89:THR:OG1	1.95	0.48
1:D:120:THR:HB	1:D:362:TYR:CE1	2.49	0.48
1:D:124:PHE:HZ	1:D:132:MET:HG2	1.72	0.48
1:D:190:MET:SD	1:D:200:PHE:HB2	2.53	0.48
1:E:190:MET:CE	1:E:209:VAL:HG21	2.43	0.48
1:A:34:ILE:HG22	1:A:69:TYR:CD1	2.49	0.48
1:B:337:TYR:O	1:B:341:ILE:HG13	2.14	0.48
1:E:190:MET:SD	1:E:200:PHE:HB2	2.53	0.48
1:A:165:ILE:HG23	1:A:165:ILE:O	2.13	0.48
1:B:116:ARG:CB	1:B:371:HIS:CE1	2.82	0.48
1:B:147:ARG:HH22	1:B:296:ASN:HB3	1.79	0.48
1:B:120:THR:HG22	1:B:132:MET:SD	2.54	0.48
1:C:190:MET:CE	1:C:209:VAL:HG21	2.43	0.48
1:D:34:ILE:HG22	1:D:69:TYR:CD1	2.49	0.48
1:D:206:ARG:O	1:D:209:VAL:HG22	2.14	0.48
1:D:337:TYR:O	1:D:341:ILE:HG13	2.14	0.48
1:A:253:GLU:HA	1:A:256:ARG:HG2	1.96	0.48
1:D:124:PHE:C	1:D:359:LYS:HE2	2.33	0.48
1:D:147:ARG:HH22	1:D:296:ASN:HB3	1.79	0.48
1:D:190:MET:CE	1:D:209:VAL:HG21	2.43	0.48
1:E:116:ARG:CB	1:E:371:HIS:CE1	2.82	0.48
1:E:206:ARG:O	1:E:209:VAL:HG22	2.14	0.48
1:E:358:SER:O	1:E:362:TYR:N	2.47	0.48
1:B:165:ILE:HG23	1:B:165:ILE:O	2.13	0.48
1:B:206:ARG:O	1:B:209:VAL:HG22	2.14	0.48
1:B:267:ILE:O	1:B:267:ILE:HG22	2.12	0.48
1:C:166:TYR:HD2	1:E:64:ILE:CG1	2.26	0.48
1:C:206:ARG:O	1:C:209:VAL:HG22	2.14	0.48
1:D:120:THR:HG22	1:D:132:MET:SD	2.54	0.48
1:D:358:SER:O	1:D:362:TYR:N	2.47	0.48

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:120:THR:HG22	1:E:132:MET:SD	2.54	0.48
1:E:223:PHE:CE1	1:E:259:GLU:OE1	2.66	0.48
1:A:337:TYR:O	1:A:341:ILE:HG13	2.14	0.47
1:C:120:THR:HG22	1:C:132:MET:SD	2.54	0.47
1:D:116:ARG:CB	1:D:371:HIS:CE1	2.82	0.47
1:E:260:THR:HG21	1:E:267:ILE:CD1	2.45	0.47
1:A:166:TYR:HD2	1:C:64:ILE:CG1	2.26	0.47
1:B:34:ILE:CD1	1:B:59:GLN:CD	2.83	0.47
1:B:169:TYR:CE1	1:D:38:PRO:HB3	2.50	0.47
1:E:253:GLU:HA	1:E:256:ARG:HG2	1.96	0.47
1:A:120:THR:HB	1:A:362:TYR:CE1	2.49	0.47
1:D:34:ILE:CD1	1:D:59:GLN:CD	2.83	0.47
1:A:358:SER:O	1:A:362:TYR:N	2.47	0.47
1:B:99:GLU:HG3	1:B:128:ASN:HB3	1.96	0.47
1:C:260:THR:HG21	1:C:267:ILE:CD1	2.45	0.47
1:C:358:SER:HB3	1:C:361:GLU:CB	2.44	0.47
1:D:99:GLU:HG3	1:D:128:ASN:HB3	1.96	0.47
1:E:34:ILE:CD1	1:E:59:GLN:CD	2.83	0.47
1:E:120:THR:HB	1:E:362:TYR:CE1	2.49	0.47
1:A:120:THR:HG22	1:A:132:MET:SD	2.54	0.47
1:C:147:ARG:HH22	1:C:296:ASN:HB3	1.78	0.47
1:E:337:TYR:O	1:E:341:ILE:HG13	2.14	0.47
1:E:358:SER:HB3	1:E:361:GLU:CB	2.44	0.47
1:A:260:THR:HG21	1:A:267:ILE:CD1	2.45	0.47
1:C:34:ILE:CD1	1:C:59:GLN:CD	2.83	0.47
1:C:253:GLU:HA	1:C:256:ARG:HG2	1.96	0.47
1:C:337:TYR:O	1:C:341:ILE:HG13	2.14	0.47
1:D:253:GLU:HA	1:D:256:ARG:HG2	1.96	0.47
1:E:147:ARG:HH22	1:E:296:ASN:HB3	1.78	0.47
2:F:183:UNK:CB	2:H:183:UNK:CA	2.93	0.47
1:A:358:SER:HB3	1:A:361:GLU:CB	2.44	0.47
1:B:14:SER:OG	1:B:158:GLY:N	2.48	0.47
1:B:67:LEU:HB2	1:B:203:THR:HG22	1.97	0.47
1:D:190:MET:HE2	1:D:209:VAL:HG21	1.96	0.47
1:A:34:ILE:CD1	1:A:59:GLN:CD	2.83	0.47
1:A:147:ARG:HH22	1:A:296:ASN:HB3	1.79	0.47
1:B:165:ILE:HG13	1:B:168:GLY:O	2.15	0.47
1:B:253:GLU:HA	1:B:256:ARG:HG2	1.96	0.47
1:B:260:THR:HG21	1:B:267:ILE:CD1	2.45	0.47
1:C:116:ARG:HH11	1:C:371:HIS:CE1	2.33	0.47
1:C:358:SER:O	1:C:362:TYR:N	2.47	0.47

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:67:LEU:HB2	1:E:203:THR:CG2	2.45	0.47
1:E:116:ARG:HH11	1:E:371:HIS:CE1	2.33	0.47
1:B:358:SER:HB3	1:B:361:GLU:CB	2.44	0.47
1:C:169:TYR:CE1	1:E:38:PRO:HB3	2.49	0.47
1:D:67:LEU:HB2	1:D:203:THR:HG22	1.97	0.47
1:D:260:THR:HG21	1:D:267:ILE:CD1	2.45	0.47
1:A:14:SER:OG	1:A:158:GLY:N	2.48	0.46
1:A:116:ARG:HH11	1:A:371:HIS:CE1	2.33	0.46
1:A:165:ILE:HG13	1:A:168:GLY:O	2.15	0.46
1:C:165:ILE:HG13	1:C:168:GLY:O	2.15	0.46
1:C:216:LEU:O	1:C:254:ARG:HD3	2.16	0.46
1:D:358:SER:HB3	1:D:361:GLU:CB	2.44	0.46
1:E:147:ARG:HH12	1:E:296:ASN:HB3	1.81	0.46
1:C:67:LEU:HB2	1:C:203:THR:CG2	2.46	0.46
1:E:105:LEU:HD11	1:E:123:MET:HG3	1.97	0.46
1:E:216:LEU:O	1:E:254:ARG:HD3	2.16	0.46
1:A:169:TYR:CE1	1:C:38:PRO:HB3	2.49	0.46
1:A:216:LEU:O	1:A:254:ARG:HD3	2.16	0.46
1:C:147:ARG:HH12	1:C:296:ASN:HB3	1.81	0.46
1:A:142:LEU:CD2	1:A:165:ILE:HG21	2.45	0.46
1:A:147:ARG:HH12	1:A:296:ASN:HB3	1.81	0.46
1:D:147:ARG:HH12	1:D:296:ASN:HB3	1.81	0.46
1:A:67:LEU:HB2	1:A:203:THR:HG22	1.97	0.46
1:D:14:SER:OG	1:D:158:GLY:N	2.48	0.46
1:E:14:SER:OG	1:E:158:GLY:N	2.48	0.46
1:E:257:CYS:CB	1:E:258:PRO:HD3	2.45	0.46
2:F:193:UNK:CB	2:H:193:UNK:CB	2.94	0.46
1:A:67:LEU:HB2	1:A:203:THR:CG2	2.45	0.46
1:B:56:ASP:OD1	1:B:57:GLU:N	2.49	0.46
1:C:105:LEU:HD11	1:C:123:MET:HG3	1.97	0.46
1:D:56:ASP:OD1	1:D:57:GLU:N	2.49	0.46
1:A:56:ASP:OD1	1:A:57:GLU:N	2.49	0.46
1:B:67:LEU:HB2	1:B:203:THR:CG2	2.45	0.46
1:D:216:LEU:O	1:D:254:ARG:HD3	2.16	0.46
1:A:105:LEU:HD11	1:A:123:MET:HG3	1.97	0.46
1:B:147:ARG:HH12	1:B:296:ASN:HB3	1.81	0.46
1:B:342:GLY:O	1:B:345:ILE:CG2	2.64	0.46
1:C:67:LEU:HB2	1:C:203:THR:HG22	1.97	0.46
1:C:142:LEU:CD2	1:C:165:ILE:HG21	2.45	0.46
1:D:116:ARG:HH11	1:D:371:HIS:CE1	2.33	0.46
1:A:59:GLN:OE1	1:A:59:GLN:HA	2.16	0.46

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:216:LEU:O	1:B:254:ARG:HD3	2.16	0.46
1:E:96:VAL:CG2	1:E:101:HIS:CD2	2.99	0.46
1:C:257:CYS:CB	1:C:258:PRO:HD3	2.45	0.45
1:E:56:ASP:OD1	1:E:57:GLU:N	2.49	0.45
1:A:96:VAL:CG2	1:A:101:HIS:CD2	2.99	0.45
1:B:105:LEU:HD11	1:B:123:MET:HG3	1.97	0.45
1:B:116:ARG:HH11	1:B:371:HIS:CE1	2.33	0.45
1:E:142:LEU:CD2	1:E:165:ILE:HG21	2.46	0.45
1:B:59:GLN:HA	1:B:59:GLN:OE1	2.16	0.45
1:C:306:TYR:O	1:C:309:ILE:HG13	2.17	0.45
1:A:257:CYS:CB	1:A:258:PRO:HD3	2.45	0.45
1:B:358:SER:O	1:B:362:TYR:N	2.47	0.45
1:C:14:SER:OG	1:C:158:GLY:N	2.48	0.45
1:B:76:ILE:HG21	1:B:79:TRP:CE3	2.52	0.45
1:D:142:LEU:CD2	1:D:165:ILE:HG21	2.46	0.45
1:E:6:THR:CG2	1:E:7:ALA:N	2.78	0.45
1:E:67:LEU:HB2	1:E:203:THR:HG22	1.97	0.45
1:B:113:LYS:HG3	1:C:195:GLU:HB2	1.99	0.45
1:D:59:GLN:HA	1:D:59:GLN:OE1	2.16	0.45
1:D:76:ILE:HG21	1:D:79:TRP:CE3	2.51	0.45
1:D:113:LYS:HG3	1:E:195:GLU:HB2	1.99	0.45
1:E:59:GLN:OE1	1:E:59:GLN:HA	2.16	0.45
1:A:367:PRO:O	1:A:371:HIS:HD2	2.00	0.45
1:B:142:LEU:CD2	1:B:165:ILE:HG21	2.45	0.45
1:C:96:VAL:CG2	1:C:101:HIS:CD2	2.99	0.45
1:B:306:TYR:O	1:B:309:ILE:HG13	2.17	0.45
1:C:56:ASP:OD1	1:C:57:GLU:N	2.49	0.45
1:C:59:GLN:OE1	1:C:59:GLN:HA	2.16	0.45
1:C:123:MET:O	1:C:129:VAL:HG23	2.17	0.45
1:D:67:LEU:HB2	1:D:203:THR:CG2	2.45	0.45
1:D:306:TYR:O	1:D:309:ILE:HG13	2.17	0.45
1:E:190:MET:HE1	1:E:206:ARG:HG2	1.99	0.45
1:E:306:TYR:O	1:E:309:ILE:HG13	2.17	0.45
1:A:291:LYS:HA	1:A:325:MET:HE1	1.98	0.45
1:C:125:GLU:HG3	1:C:359:LYS:HZ3	1.81	0.45
1:D:96:VAL:CG2	1:D:101:HIS:CD2	2.99	0.45
1:D:105:LEU:HD11	1:D:123:MET:HG3	1.97	0.45
1:D:125:GLU:HG3	1:D:359:LYS:HZ3	1.82	0.45
1:E:76:ILE:HG21	1:E:79:TRP:CE3	2.52	0.45
1:E:367:PRO:O	1:E:371:HIS:HD2	2.00	0.45
1:A:123:MET:O	1:A:129:VAL:HG23	2.17	0.45

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:76:ILE:HG21	1:C:79:TRP:CE3	2.52	0.45
1:A:226:GLU:HA	1:A:229:THR:HG22	1.99	0.44
1:A:306:TYR:O	1:A:309:ILE:HG13	2.17	0.44
1:B:123:MET:O	1:B:129:VAL:HG23	2.17	0.44
1:B:226:GLU:HA	1:B:229:THR:HG22	1.99	0.44
1:B:230:ALA:N	1:B:236:LEU:HD12	2.26	0.44
1:B:367:PRO:O	1:B:371:HIS:HD2	2.00	0.44
1:D:342:GLY:O	1:D:345:ILE:CG2	2.64	0.44
1:E:226:GLU:HA	1:E:229:THR:HG22	1.99	0.44
1:A:24:ASP:O	1:A:340:TRP:CZ3	2.71	0.44
1:A:76:ILE:HG21	1:A:79:TRP:CE3	2.52	0.44
1:A:219:VAL:HG21	1:A:309:ILE:HG12	2.00	0.44
1:B:147:ARG:HH22	1:B:296:ASN:CB	2.30	0.44
1:C:219:VAL:HG21	1:C:309:ILE:HG12	1.99	0.44
1:A:113:LYS:HG3	1:B:195:GLU:HB2	1.99	0.44
1:B:219:VAL:HG21	1:B:309:ILE:HG12	2.00	0.44
1:B:276:GLU:HG3	1:B:320:LEU:HD11	1.99	0.44
1:D:123:MET:O	1:D:129:VAL:HG23	2.17	0.44
2:F:179:UNK:CB	2:H:180:UNK:N	2.81	0.44
1:E:123:MET:O	1:E:129:VAL:HG23	2.17	0.44
1:E:219:VAL:HG21	1:E:309:ILE:HG12	2.00	0.44
1:B:96:VAL:CG2	1:B:101:HIS:CD2	2.99	0.44
1:D:219:VAL:HG21	1:D:309:ILE:HG12	2.00	0.44
1:D:369:ILE:HD12	1:D:369:ILE:C	2.38	0.44
1:B:369:ILE:HD12	1:B:369:ILE:C	2.38	0.44
1:D:147:ARG:HH22	1:D:296:ASN:CB	2.30	0.44
1:E:24:ASP:O	1:E:340:TRP:CZ3	2.71	0.44
1:C:147:ARG:HH22	1:C:296:ASN:CG	2.22	0.44
1:D:276:GLU:HG3	1:D:320:LEU:HD11	2.00	0.44
1:B:106:THR:CG2	1:B:137:GLN:HG2	2.48	0.43
1:C:113:LYS:HG3	1:D:195:GLU:HB2	1.99	0.43
1:C:124:PHE:CE2	1:C:362:TYR:CD1	3.06	0.43
2:F:176:UNK:HA	2:H:176:UNK:CA	2.44	0.43
1:A:124:PHE:CE2	1:A:362:TYR:CD1	3.06	0.43
1:D:226:GLU:HA	1:D:229:THR:HG22	1.99	0.43
1:E:124:PHE:CE2	1:E:362:TYR:CD1	3.06	0.43
1:E:147:ARG:HH22	1:E:296:ASN:CB	2.30	0.43
1:E:147:ARG:HH22	1:E:296:ASN:CG	2.22	0.43
1:E:331:ALA:CB	1:E:335:ARG:NH2	2.62	0.43
1:A:147:ARG:HH22	1:A:296:ASN:CB	2.30	0.43
1:B:34:ILE:HD11	1:B:59:GLN:NE2	2.33	0.43

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:124:PHE:HZ	1:B:132:MET:HG2	1.72	0.43
1:C:96:VAL:HG21	1:C:101:HIS:CD2	2.54	0.43
1:C:147:ARG:HH22	1:C:296:ASN:CB	2.30	0.43
1:C:342:GLY:O	1:C:345:ILE:CG2	2.64	0.43
1:D:106:THR:CG2	1:D:137:GLN:HG2	2.48	0.43
1:A:106:THR:CG2	1:A:137:GLN:HG2	2.48	0.43
1:A:342:GLY:O	1:A:345:ILE:CG2	2.64	0.43
1:C:34:ILE:HD11	1:C:59:GLN:NE2	2.33	0.43
1:C:226:GLU:HA	1:C:229:THR:HG22	1.99	0.43
1:D:34:ILE:HD11	1:D:59:GLN:NE2	2.33	0.43
1:D:298:VAL:HG12	1:D:299:LEU:N	2.34	0.43
1:D:367:PRO:O	1:D:371:HIS:HD2	2.00	0.43
1:E:276:GLU:HG3	1:E:320:LEU:HD11	2.00	0.43
1:B:166:TYR:CD2	1:D:64:ILE:HG12	2.53	0.43
1:A:166:TYR:CD2	1:C:64:ILE:HG12	2.54	0.43
1:A:276:GLU:HG3	1:A:320:LEU:HD11	2.00	0.43
1:B:298:VAL:HG12	1:B:299:LEU:N	2.34	0.43
1:C:283:MET:HE1	1:C:294:TYR:OH	2.17	0.43
1:C:367:PRO:O	1:C:371:HIS:HD2	2.00	0.43
1:D:124:PHE:CE2	1:D:362:TYR:CD1	3.06	0.43
1:E:369:ILE:HD12	1:E:369:ILE:C	2.38	0.43
1:A:212:ILE:HG12	1:A:240:TYR:CD2	2.54	0.43
1:A:222:ASP:CB	1:A:225:ASN:ND2	2.81	0.43
1:A:298:VAL:HG12	1:A:299:LEU:N	2.34	0.43
1:B:146:GLY:C	1:B:147:ARG:HG3	2.39	0.43
1:C:106:THR:CG2	1:C:137:GLN:HG2	2.48	0.43
1:A:147:ARG:HH22	1:A:296:ASN:CG	2.22	0.43
1:B:287:ILE:HG23	1:D:244:ASP:HB2	2.01	0.43
1:C:24:ASP:O	1:C:340:TRP:CZ3	2.70	0.43
1:C:212:ILE:HG12	1:C:240:TYR:CD2	2.54	0.43
1:C:276:GLU:HG3	1:C:320:LEU:HD11	2.00	0.43
1:D:146:GLY:C	1:D:147:ARG:HG3	2.39	0.43
1:E:34:ILE:HD11	1:E:59:GLN:NE2	2.33	0.43
1:E:106:THR:CG2	1:E:137:GLN:HG2	2.48	0.43
1:E:118:LYS:NZ	1:E:121:GLN:HE22	2.17	0.43
1:E:342:GLY:O	1:E:345:ILE:CG2	2.64	0.43
1:A:369:ILE:HD12	1:A:369:ILE:C	2.38	0.43
1:B:331:ALA:CB	1:B:335:ARG:NH2	2.62	0.43
1:C:298:VAL:HG12	1:C:299:LEU:N	2.34	0.43
1:A:169:TYR:CZ	1:C:47:MET:HE3	2.54	0.43
1:B:118:LYS:NZ	1:B:121:GLN:HE22	2.17	0.43

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:124:PHE:CE2	1:B:362:TYR:CD1	3.06	0.43
1:B:283:MET:HE1	1:B:294:TYR:OH	2.19	0.43
1:C:166:TYR:CD2	1:E:64:ILE:HG12	2.53	0.43
1:C:331:ALA:CB	1:C:335:ARG:NH2	2.62	0.43
1:C:369:ILE:HD12	1:C:369:ILE:C	2.38	0.43
1:D:21:PHE:O	1:D:340:TRP:CZ2	2.72	0.43
1:D:118:LYS:NZ	1:D:121:GLN:HE22	2.17	0.43
1:D:147:ARG:HH22	1:D:296:ASN:CG	2.22	0.43
1:E:212:ILE:HG12	1:E:240:TYR:CD2	2.54	0.43
1:A:116:ARG:NH1	1:A:371:HIS:ND1	2.66	0.42
1:A:124:PHE:HZ	1:A:132:MET:HG2	1.72	0.42
1:A:206:ARG:O	1:A:209:VAL:CG2	2.67	0.42
1:B:21:PHE:O	1:B:340:TRP:CZ2	2.72	0.42
1:B:106:THR:HG22	1:B:107:GLU:N	2.34	0.42
1:B:147:ARG:HH22	1:B:296:ASN:CG	2.22	0.42
1:C:120:THR:OG1	1:C:362:TYR:CE1	2.72	0.42
1:D:95:ARG:HH11	1:D:95:ARG:HD3	1.70	0.42
1:D:116:ARG:NH1	1:D:371:HIS:ND1	2.66	0.42
1:E:206:ARG:O	1:E:209:VAL:CG2	2.67	0.42
1:D:183:ARG:O	1:D:186:THR:HG22	2.20	0.42
1:E:96:VAL:HG21	1:E:101:HIS:CD2	2.54	0.42
1:A:96:VAL:HG21	1:A:101:HIS:CD2	2.54	0.42
1:B:124:PHE:CE1	1:B:359:LYS:CA	3.02	0.42
1:B:206:ARG:O	1:B:209:VAL:CG2	2.67	0.42
1:C:192:ILE:HD12	1:C:192:ILE:HA	1.94	0.42
1:D:24:ASP:O	1:D:340:TRP:CZ3	2.71	0.42
1:D:124:PHE:CE1	1:D:359:LYS:CA	3.02	0.42
2:F:176:UNK:CA	2:H:176:UNK:HA	2.45	0.42
1:A:364:GLU:OE1	1:A:364:GLU:N	2.49	0.42
1:B:96:VAL:HG21	1:B:101:HIS:CD2	2.54	0.42
1:D:96:VAL:HG21	1:D:101:HIS:CD2	2.53	0.42
1:D:206:ARG:O	1:D:209:VAL:CG2	2.67	0.42
1:D:230:ALA:N	1:D:236:LEU:HD12	2.26	0.42
1:E:124:PHE:CD1	1:E:359:LYS:CB	3.03	0.42
1:E:298:VAL:HG12	1:E:299:LEU:N	2.34	0.42
1:A:53:TYR:CD1	1:A:57:GLU:CD	2.93	0.42
1:B:39:ARG:CG	1:B:40:HIS:CD2	2.99	0.42
1:C:124:PHE:CD1	1:C:359:LYS:CB	3.03	0.42
1:C:206:ARG:O	1:C:209:VAL:CG2	2.67	0.42
1:C:6:THR:CG2	1:C:7:ALA:N	2.78	0.42
1:C:53:TYR:CD1	1:C:57:GLU:CD	2.93	0.42

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:118:LYS:NZ	1:C:121:GLN:HE22	2.17	0.42
1:D:183:ARG:HA	1:D:186:THR:HG22	2.02	0.42
1:D:212:ILE:HG12	1:D:240:TYR:CD2	2.54	0.42
1:D:331:ALA:CB	1:D:335:ARG:NH2	2.62	0.42
1:D:333:PRO:O	1:D:334:GLU:CB	2.66	0.42
1:A:106:THR:HG22	1:A:107:GLU:N	2.34	0.42
1:B:53:TYR:CD1	1:B:57:GLU:CD	2.93	0.42
1:B:116:ARG:NH1	1:B:371:HIS:ND1	2.66	0.42
1:D:53:TYR:CD1	1:D:57:GLU:CD	2.93	0.42
1:E:39:ARG:CG	1:E:40:HIS:CD2	2.99	0.42
1:A:124:PHE:CD1	1:A:359:LYS:CB	3.03	0.42
1:A:183:ARG:O	1:A:186:THR:HG22	2.20	0.42
1:B:183:ARG:O	1:B:186:THR:HG22	2.20	0.42
1:C:106:THR:HG22	1:C:107:GLU:N	2.34	0.42
1:E:53:TYR:CD1	1:E:57:GLU:CD	2.93	0.42
1:A:220:ALA:HB1	1:A:226:GLU:CD	2.41	0.42
1:B:183:ARG:HA	1:B:186:THR:HG22	2.01	0.42
1:C:116:ARG:NH1	1:C:371:HIS:ND1	2.66	0.42
1:D:124:PHE:CD1	1:D:359:LYS:CB	3.03	0.42
1:D:222:ASP:CB	1:D:225:ASN:ND2	2.81	0.42
1:E:283:MET:HE1	1:E:294:TYR:OH	2.20	0.42
1:A:34:ILE:HD11	1:A:59:GLN:NE2	2.33	0.42
1:A:146:GLY:C	1:A:147:ARG:HG3	2.39	0.42
1:A:171:LEU:HD11	1:A:289:ILE:HD11	2.02	0.42
1:A:183:ARG:HA	1:A:186:THR:HG22	2.01	0.42
1:B:24:ASP:O	1:B:340:TRP:CZ3	2.71	0.42
1:B:212:ILE:HG12	1:B:240:TYR:CD2	2.54	0.42
1:B:226:GLU:O	1:B:229:THR:HG22	2.20	0.42
1:C:183:ARG:O	1:C:186:THR:HG22	2.20	0.42
1:C:220:ALA:HB1	1:C:226:GLU:CD	2.41	0.42
1:D:96:VAL:O	1:D:96:VAL:HG13	2.20	0.42
1:D:345:ILE:HG12	1:D:349:LEU:HD13	2.02	0.42
1:E:106:THR:HG22	1:E:107:GLU:N	2.34	0.42
1:E:198:TYR:CD2	1:E:248:ILE:HG23	2.55	0.42
1:A:287:ILE:HG23	1:C:244:ASP:HB2	2.01	0.41
1:B:345:ILE:HG12	1:B:349:LEU:HD13	2.02	0.41
1:C:120:THR:CB	1:C:362:TYR:CE1	3.03	0.41
1:D:294:TYR:HB2	1:D:325:MET:HE1	2.01	0.41
1:A:165:ILE:O	1:A:165:ILE:CG2	2.68	0.41
1:A:226:GLU:O	1:A:229:THR:HG22	2.20	0.41
1:B:96:VAL:O	1:B:96:VAL:HG13	2.20	0.41

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:230:ALA:CB	1:B:236:LEU:CD1	2.99	0.41
1:B:324:THR:O	1:B:324:THR:CG2	2.68	0.41
1:C:21:PHE:O	1:C:340:TRP:CZ2	2.73	0.41
1:D:120:THR:CB	1:D:362:TYR:CE1	3.03	0.41
1:D:171:LEU:HD11	1:D:289:ILE:HD11	2.02	0.41
1:D:230:ALA:CB	1:D:236:LEU:CD1	2.99	0.41
1:E:96:VAL:O	1:E:96:VAL:HG13	2.20	0.41
2:F:176:UNK:CB	2:H:176:UNK:CB	2.98	0.41
1:A:345:ILE:HG12	1:A:349:LEU:HD13	2.02	0.41
1:B:120:THR:CB	1:B:362:TYR:CE1	3.04	0.41
1:B:171:LEU:HD11	1:B:289:ILE:HD11	2.02	0.41
1:B:198:TYR:CD2	1:B:248:ILE:HG23	2.55	0.41
1:E:220:ALA:HB1	1:E:226:GLU:CD	2.41	0.41
1:E:267:ILE:O	1:E:267:ILE:CG2	2.68	0.41
1:E:294:TYR:HB2	1:E:325:MET:HE1	2.02	0.41
1:A:29:ALA:HB2	1:A:93:GLU:HB3	2.03	0.41
1:A:118:LYS:NZ	1:A:121:GLN:HE22	2.17	0.41
1:B:124:PHE:CD1	1:B:359:LYS:CB	3.03	0.41
1:C:171:LEU:HD11	1:C:289:ILE:HD11	2.02	0.41
1:C:324:THR:O	1:C:324:THR:CG2	2.68	0.41
1:D:283:MET:HE1	1:D:294:TYR:OH	2.19	0.41
1:B:125:GLU:HG3	1:B:359:LYS:HZ1	1.82	0.41
1:B:267:ILE:O	1:B:267:ILE:CG2	2.68	0.41
1:D:106:THR:HG22	1:D:107:GLU:N	2.34	0.41
1:D:226:GLU:O	1:D:229:THR:HG22	2.20	0.41
1:E:29:ALA:HB2	1:E:93:GLU:HB3	2.03	0.41
1:E:223:PHE:N	1:E:224:GLU:OE1	2.54	0.41
1:A:205:GLU:N	1:A:205:GLU:OE1	2.54	0.41
1:A:223:PHE:N	1:A:224:GLU:OE1	2.54	0.41
1:A:267:ILE:O	1:A:267:ILE:CG2	2.68	0.41
1:C:146:GLY:C	1:C:147:ARG:HG3	2.39	0.41
1:C:183:ARG:HA	1:C:186:THR:HG22	2.01	0.41
1:C:205:GLU:OE1	1:C:205:GLU:N	2.54	0.41
1:C:226:GLU:O	1:C:229:THR:HG22	2.20	0.41
1:E:202:THR:CG2	1:E:203:THR:N	2.84	0.41
2:F:120:UNK:HA	2:H:120:UNK:HA	2.03	0.41
1:A:21:PHE:O	1:A:340:TRP:CZ2	2.73	0.41
1:A:96:VAL:HG13	1:A:96:VAL:O	2.20	0.41
1:B:120:THR:OG1	1:B:362:TYR:CE1	2.72	0.41
1:B:205:GLU:N	1:B:205:GLU:OE1	2.54	0.41
1:C:96:VAL:HG13	1:C:96:VAL:O	2.20	0.41

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:267:ILE:O	1:C:267:ILE:CG2	2.68	0.41
1:C:287:ILE:HG23	1:E:244:ASP:HB2	2.01	0.41
1:D:29:ALA:HB2	1:D:93:GLU:HB3	2.03	0.41
1:E:21:PHE:O	1:E:340:TRP:CZ2	2.72	0.41
1:E:205:GLU:OE1	1:E:205:GLU:N	2.54	0.41
1:B:220:ALA:HB1	1:B:226:GLU:CD	2.41	0.41
1:C:345:ILE:HG12	1:C:349:LEU:HD13	2.02	0.41
1:D:205:GLU:N	1:D:205:GLU:OE1	2.54	0.41
1:D:324:THR:O	1:D:324:THR:CG2	2.68	0.41
1:E:146:GLY:C	1:E:147:ARG:HG3	2.39	0.41
1:E:183:ARG:O	1:E:186:THR:HG22	2.20	0.41
1:E:223:PHE:CE2	1:E:255:PHE:C	2.94	0.41
1:E:345:ILE:HG12	1:E:349:LEU:HD13	2.01	0.41
1:A:120:THR:CB	1:A:362:TYR:CE1	3.04	0.41
1:A:202:THR:CG2	1:A:203:THR:N	2.84	0.41
1:A:223:PHE:CE2	1:A:255:PHE:C	2.94	0.41
1:B:223:PHE:N	1:B:224:GLU:OE1	2.54	0.41
1:C:39:ARG:CG	1:C:40:HIS:CD2	2.99	0.41
1:C:165:ILE:O	1:C:165:ILE:CG2	2.68	0.41
1:C:223:PHE:CE2	1:C:255:PHE:C	2.94	0.41
1:D:198:TYR:CD2	1:D:248:ILE:HG23	2.55	0.41
1:E:116:ARG:NH1	1:E:371:HIS:ND1	2.66	0.41
1:E:171:LEU:HD11	1:E:289:ILE:HD11	2.02	0.41
1:E:226:GLU:O	1:E:229:THR:HG22	2.20	0.41
1:B:202:THR:CG2	1:B:203:THR:N	2.84	0.41
1:D:267:ILE:O	1:D:267:ILE:CG2	2.68	0.41
1:E:120:THR:CB	1:E:362:TYR:CE1	3.04	0.41
1:E:183:ARG:HA	1:E:186:THR:HG22	2.01	0.41
1:A:202:THR:HB	1:A:205:GLU:OE1	2.21	0.40
1:D:53:TYR:HE1	1:D:57:GLU:OE2	2.04	0.40
1:C:202:THR:CG2	1:C:203:THR:N	2.84	0.40
1:C:223:PHE:N	1:C:224:GLU:OE1	2.54	0.40
1:D:220:ALA:HB1	1:D:226:GLU:CD	2.41	0.40
1:D:223:PHE:CE2	1:D:255:PHE:C	2.94	0.40
1:A:324:THR:O	1:A:324:THR:CG2	2.68	0.40
1:B:165:ILE:O	1:B:165:ILE:CG2	2.68	0.40
1:B:224:GLU:HG2	1:B:225:ASN:N	2.37	0.40
1:C:80:ASP:OD1	1:C:80:ASP:N	2.53	0.40
1:C:202:THR:HB	1:C:205:GLU:OE1	2.21	0.40
1:D:202:THR:CG2	1:D:203:THR:N	2.84	0.40
1:E:222:ASP:CB	1:E:225:ASN:ND2	2.81	0.40

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:124:PHE:CB	1:B:359:LYS:HZ2	2.21	0.40
1:B:291:LYS:HA	1:B:325:MET:HE1	2.02	0.40
1:C:29:ALA:HB2	1:C:93:GLU:HB3	2.03	0.40
1:C:198:TYR:CD2	1:C:248:ILE:HG23	2.55	0.40
1:A:198:TYR:CD2	1:A:248:ILE:HG23	2.55	0.40
1:A:230:ALA:CB	1:A:236:LEU:CD1	2.99	0.40
1:B:53:TYR:HE1	1:B:57:GLU:OE2	2.04	0.40
1:B:222:ASP:CB	1:B:225:ASN:ND2	2.81	0.40
1:C:230:ALA:CB	1:C:236:LEU:CD1	2.99	0.40
1:C:289:ILE:HG23	1:E:63:GLY:HA3	2.04	0.40
1:E:324:THR:O	1:E:324:THR:CG2	2.68	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	364/367 (99%)	349 (96%)	13 (4%)	2 (0%)	25 64
1	B	364/367 (99%)	349 (96%)	13 (4%)	2 (0%)	25 64
1	C	364/367 (99%)	349 (96%)	12 (3%)	3 (1%)	16 55
1	D	364/367 (99%)	349 (96%)	12 (3%)	3 (1%)	16 55
1	E	364/367 (99%)	349 (96%)	12 (3%)	3 (1%)	16 55
All	All	1820/1835 (99%)	1745 (96%)	62 (3%)	13 (1%)	21 57

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	169	TYR
1	B	169	TYR
1	C	169	TYR

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	D	169	TYR
1	E	169	TYR
1	A	6	THR
1	B	6	THR
1	C	6	THR
1	D	6	THR
1	E	6	THR
1	C	43	VAL
1	D	43	VAL
1	E	43	VAL

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	309/309 (100%)	307 (99%)	2 (1%)	84	88
1	B	309/309 (100%)	307 (99%)	2 (1%)	84	88
1	C	309/309 (100%)	307 (99%)	2 (1%)	84	88
1	D	309/309 (100%)	307 (99%)	2 (1%)	84	88
1	E	309/309 (100%)	307 (99%)	2 (1%)	84	88
All	All	1545/1545 (100%)	1535 (99%)	10 (1%)	82	88

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	47	MET
1	A	121	GLN
1	B	47	MET
1	B	121	GLN
1	C	47	MET
1	C	121	GLN
1	D	47	MET
1	D	121	GLN
1	E	47	MET

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	E	121	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (43) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	59	GLN
1	A	88	HIS
1	A	92	ASN
1	A	101	HIS
1	A	115	ASN
1	A	121	GLN
1	A	225	ASN
1	A	314	GLN
1	B	59	GLN
1	B	88	HIS
1	B	92	ASN
1	B	101	HIS
1	B	115	ASN
1	B	121	GLN
1	B	225	ASN
1	B	314	GLN
1	C	40	HIS
1	C	59	GLN
1	C	88	HIS
1	C	92	ASN
1	C	101	HIS
1	C	115	ASN
1	C	121	GLN
1	C	225	ASN
1	C	314	GLN
1	D	40	HIS
1	D	59	GLN
1	D	88	HIS
1	D	92	ASN
1	D	101	HIS
1	D	115	ASN
1	D	121	GLN
1	D	225	ASN
1	D	314	GLN
1	E	40	HIS
1	E	59	GLN
1	E	88	HIS

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	E	92	ASN
1	E	101	HIS
1	E	115	ASN
1	E	121	GLN
1	E	225	ASN
1	E	314	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

5 non-standard protein/DNA/RNA residues 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	$\# Z  > 2$
1	HIC	D	73	1	8,11,12	0.63	0	6,14,16	1.06	0
1	HIC	B	73	1	8,11,12	0.63	0	6,14,16	1.06	0
1	HIC	A	73	1	8,11,12	0.65	0	6,14,16	1.06	0
1	HIC	C	73	1	8,11,12	0.66	0	6,14,16	1.07	0
1	HIC	E	73	1	8,11,12	0.66	0	6,14,16	1.06	0

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
1	HIC	D	73	1	-	2/5/6/8	0/1/1/1
1	HIC	B	73	1	-	2/5/6/8	0/1/1/1
1	HIC	A	73	1	-	2/5/6/8	0/1/1/1
1	HIC	C	73	1	-	2/5/6/8	0/1/1/1

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	HIC	E	73	1	-	2/5/6/8	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	73	HIC	N-CA-CB-CG
1	A	73	HIC	CA-CB-CG-ND1
1	B	73	HIC	N-CA-CB-CG
1	C	73	HIC	N-CA-CB-CG
1	C	73	HIC	CA-CB-CG-ND1
1	D	73	HIC	N-CA-CB-CG
1	D	73	HIC	CA-CB-CG-ND1
1	E	73	HIC	N-CA-CB-CG
1	B	73	HIC	CA-CB-CG-ND1
1	E	73	HIC	CA-CB-CG-ND1

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 5 are monoatomic - leaving 5 for Mogul analysis.

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	ADP	C	401	4	24,29,29	0.95	1 (4%)	29,45,45	1.45	4 (13%)
3	ADP	B	401	4	24,29,29	0.95	1 (4%)	29,45,45	1.45	4 (13%)
3	ADP	E	401	4	24,29,29	0.95	1 (4%)	29,45,45	1.45	4 (13%)
3	ADP	A	401	4	24,29,29	0.95	1 (4%)	29,45,45	1.45	4 (13%)
3	ADP	D	401	4	24,29,29	0.95	1 (4%)	29,45,45	1.44	4 (13%)

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	ADP	C	401	4	-	2/12/32/32	0/3/3/3
3	ADP	B	401	4	-	2/12/32/32	0/3/3/3
3	ADP	E	401	4	-	2/12/32/32	0/3/3/3
3	ADP	A	401	4	-	2/12/32/32	0/3/3/3
3	ADP	D	401	4	-	2/12/32/32	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	401	ADP	C5-C4	2.51	1.47	1.40
3	E	401	ADP	C5-C4	2.51	1.47	1.40
3	A	401	ADP	C5-C4	2.50	1.47	1.40
3	C	401	ADP	C5-C4	2.49	1.47	1.40
3	B	401	ADP	C5-C4	2.49	1.47	1.40

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	401	ADP	PA-O3A-PB	-3.33	121.41	132.83
3	A	401	ADP	PA-O3A-PB	-3.32	121.42	132.83
3	E	401	ADP	PA-O3A-PB	-3.32	121.43	132.83
3	C	401	ADP	PA-O3A-PB	-3.32	121.44	132.83
3	D	401	ADP	PA-O3A-PB	-3.32	121.45	132.83
3	A	401	ADP	N3-C2-N1	-3.20	123.68	128.68
3	D	401	ADP	C3'-C2'-C1'	3.20	105.79	100.98
3	C	401	ADP	N3-C2-N1	-3.19	123.69	128.68
3	C	401	ADP	C3'-C2'-C1'	3.19	105.78	100.98
3	A	401	ADP	C3'-C2'-C1'	3.19	105.78	100.98

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	401	ADP	C3'-C2'-C1'	3.19	105.78	100.98
3	E	401	ADP	N3-C2-N1	-3.18	123.70	128.68
3	E	401	ADP	C3'-C2'-C1'	3.18	105.77	100.98
3	B	401	ADP	N3-C2-N1	-3.18	123.71	128.68
3	D	401	ADP	N3-C2-N1	-3.13	123.78	128.68
3	E	401	ADP	C4-C5-N7	-2.52	106.77	109.40
3	C	401	ADP	C4-C5-N7	-2.50	106.79	109.40
3	B	401	ADP	C4-C5-N7	-2.48	106.82	109.40
3	A	401	ADP	C4-C5-N7	-2.48	106.82	109.40
3	D	401	ADP	C4-C5-N7	-2.48	106.82	109.40

There are no chirality outliers.

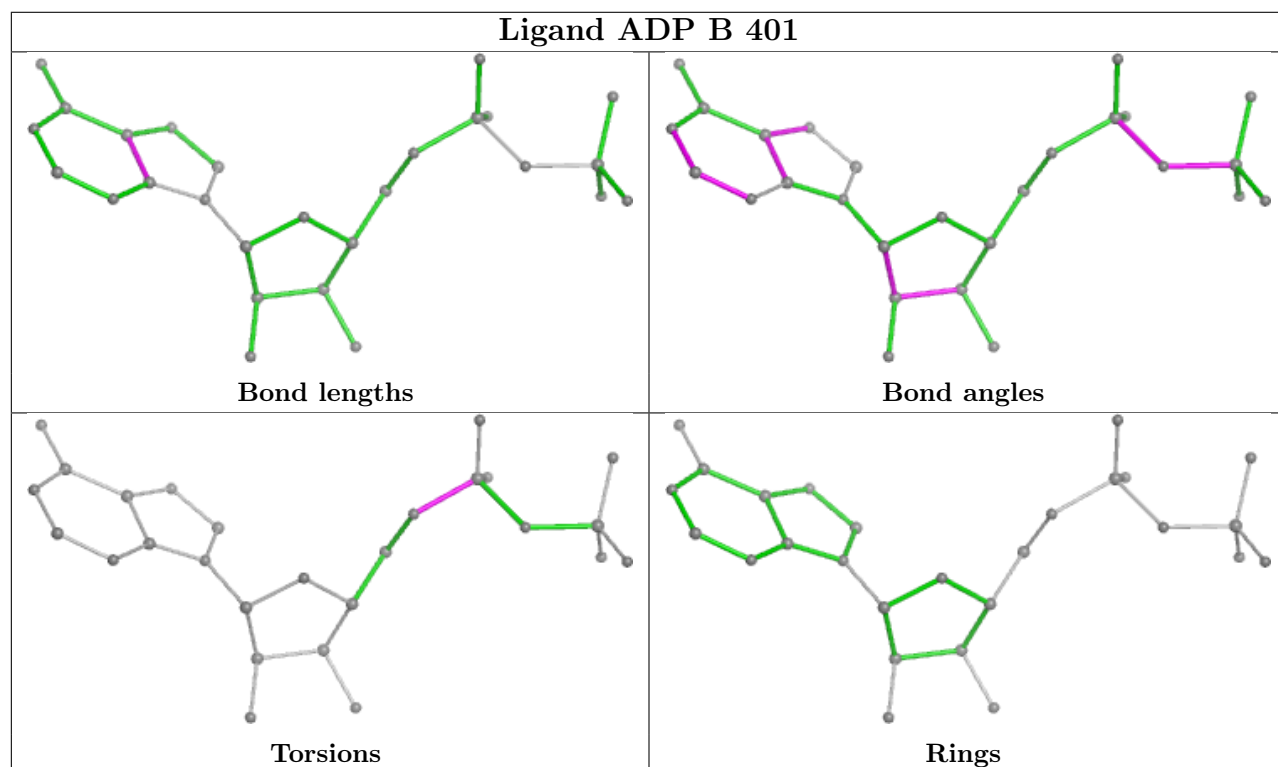
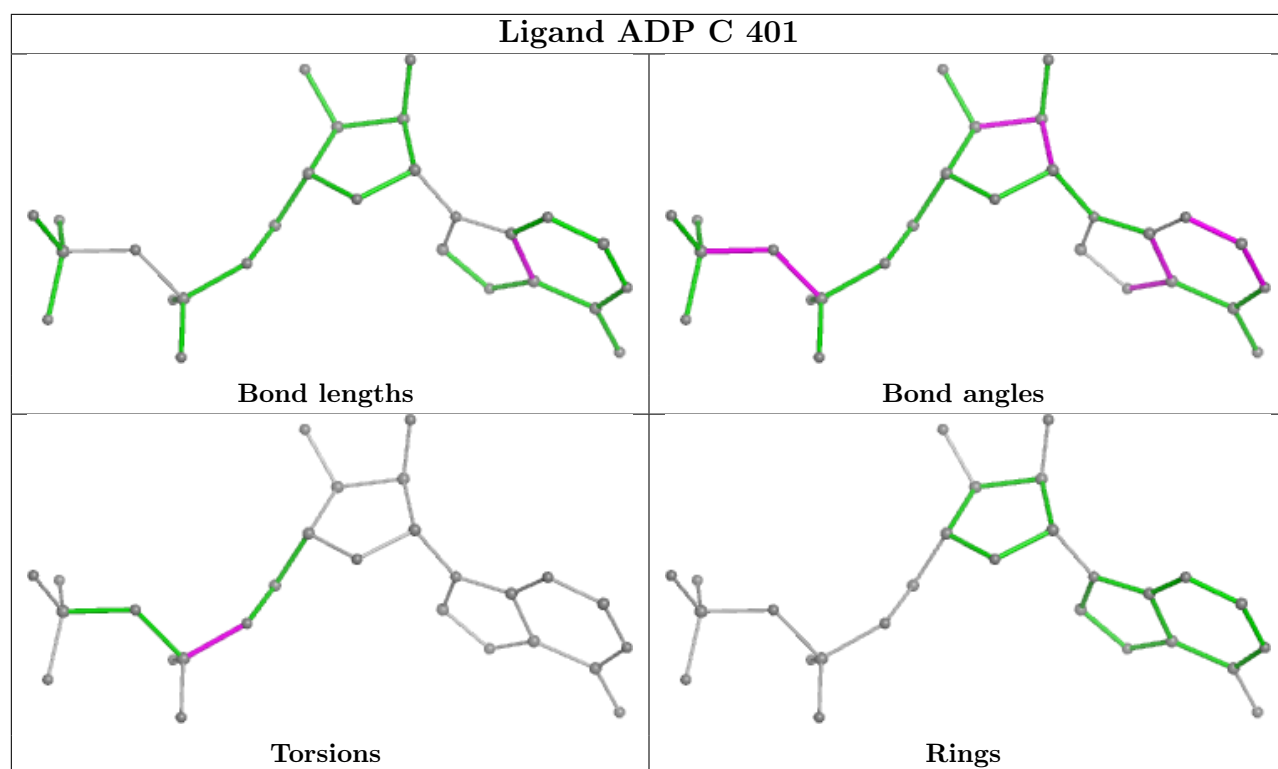
All (10) torsion outliers are listed below:

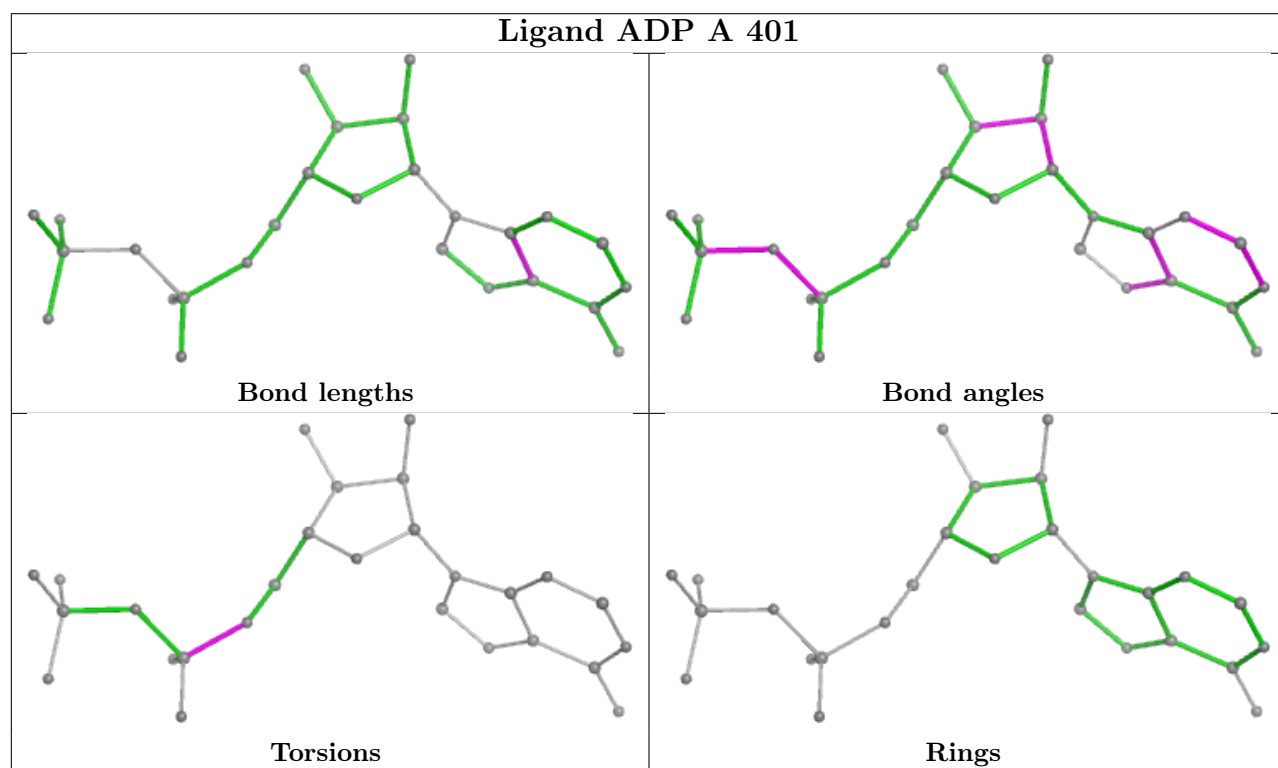
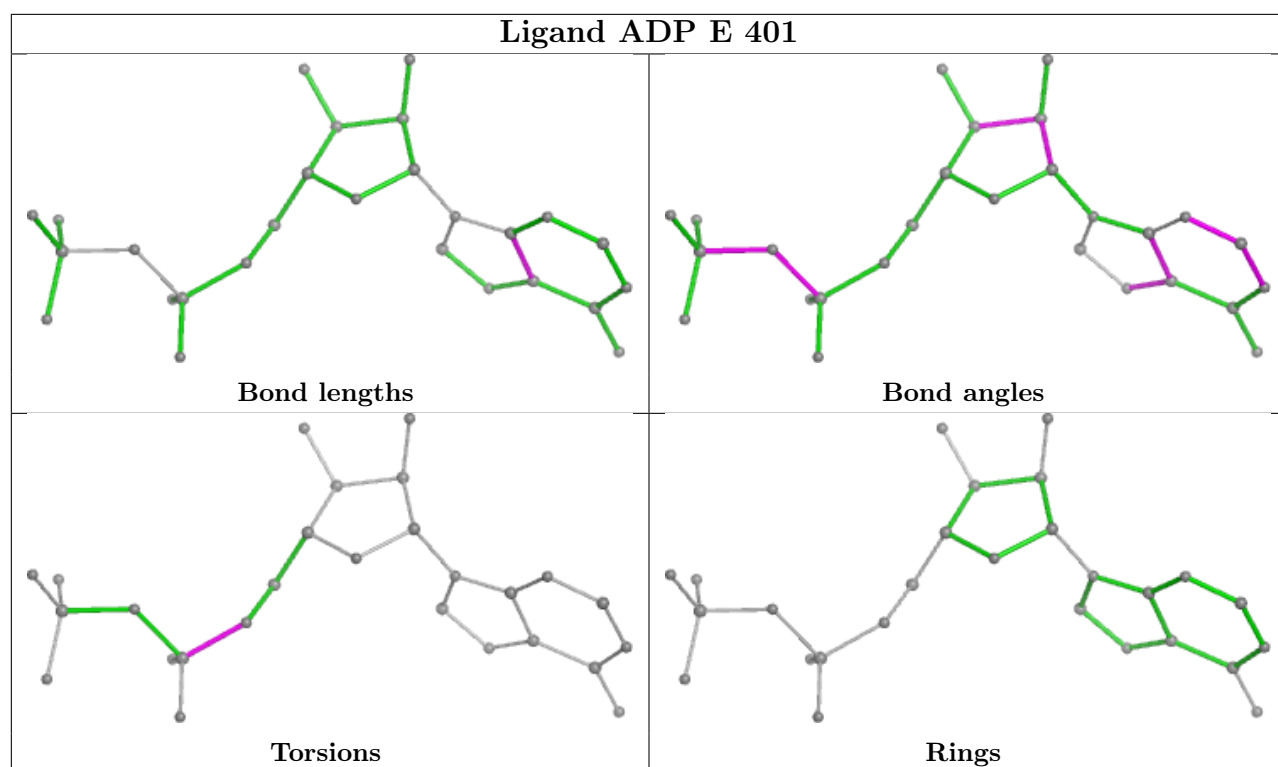
Mol	Chain	Res	Type	Atoms
3	A	401	ADP	C5'-O5'-PA-O1A
3	B	401	ADP	C5'-O5'-PA-O1A
3	C	401	ADP	C5'-O5'-PA-O1A
3	D	401	ADP	C5'-O5'-PA-O1A
3	E	401	ADP	C5'-O5'-PA-O1A
3	A	401	ADP	C5'-O5'-PA-O3A
3	B	401	ADP	C5'-O5'-PA-O3A
3	C	401	ADP	C5'-O5'-PA-O3A
3	D	401	ADP	C5'-O5'-PA-O3A
3	E	401	ADP	C5'-O5'-PA-O3A

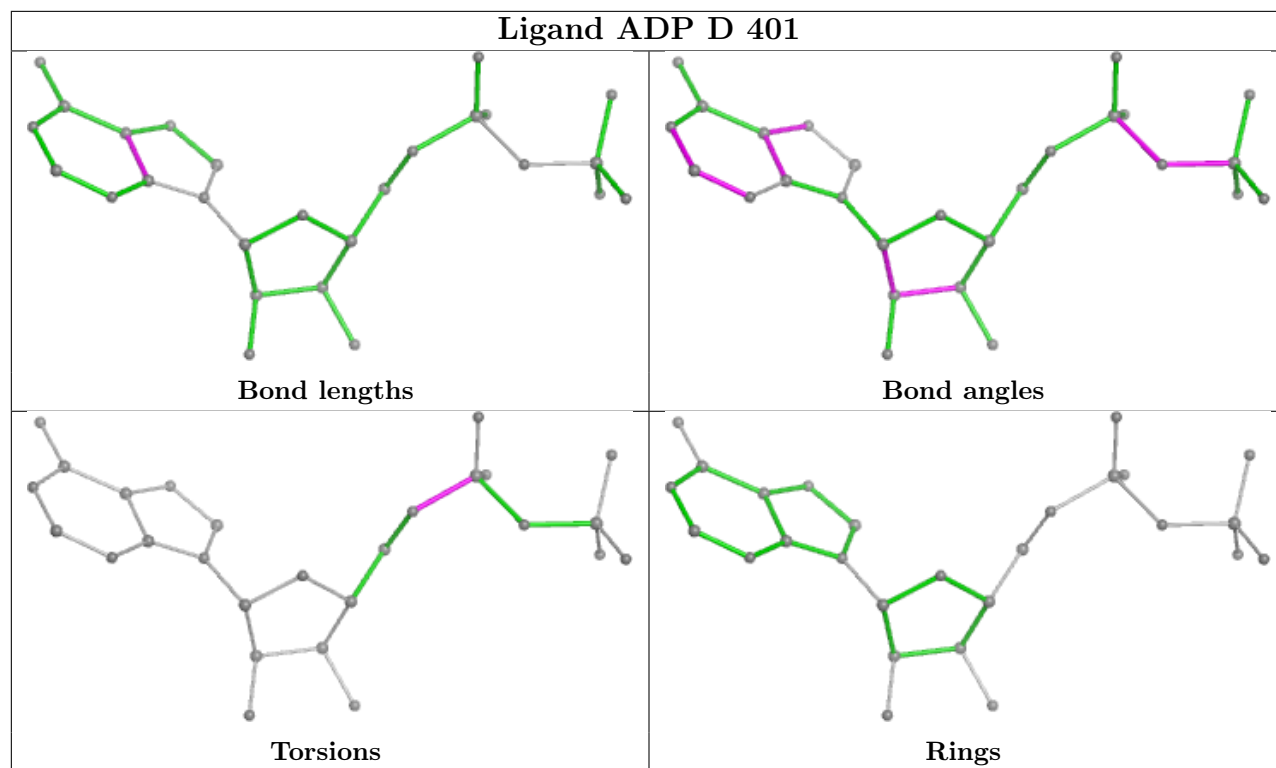
There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.







## 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-3666. These allow visual inspection of the internal detail of the map and identification of artifacts.

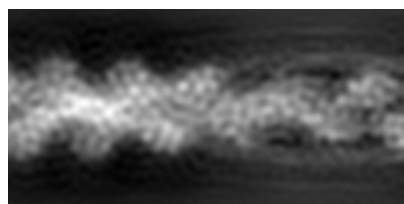
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

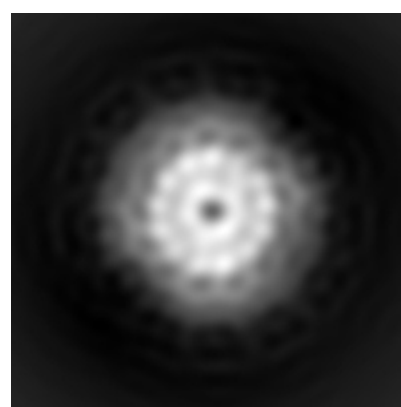
#### 6.1.1 Primary map



X



Y

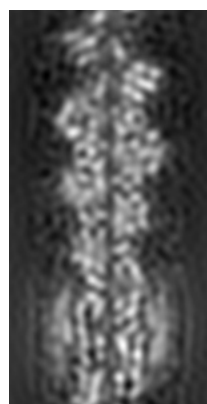


Z

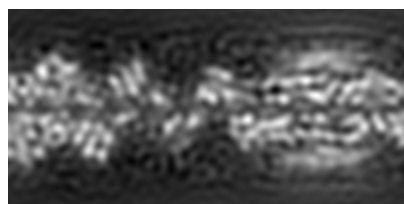
The images above show the map projected in three orthogonal directions.

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

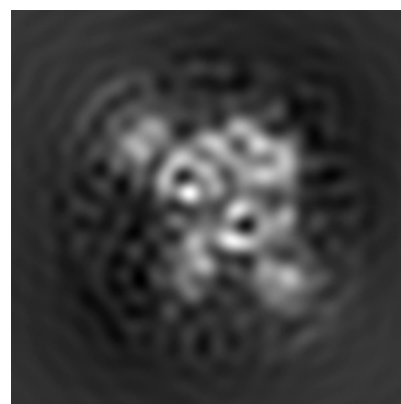
#### 6.2.1 Primary map



X Index: 75



Y Index: 75



Z Index: 150

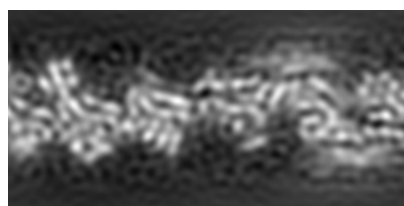
The images above show central slices of the map in three orthogonal directions.

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

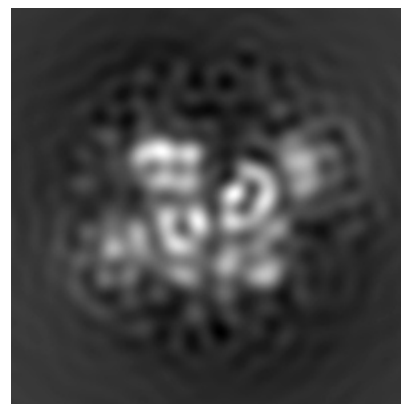
### 6.3.1 Primary map



X Index: 67



Y Index: 68

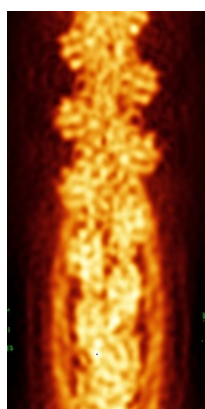


Z Index: 285

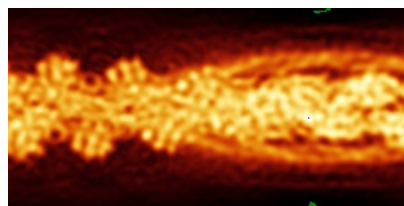
The images above show the largest variance slices of the map in three orthogonal directions.

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

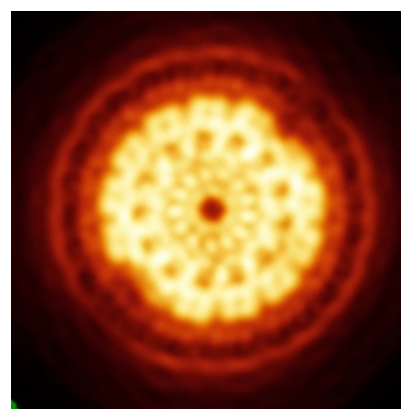
### 6.4.1 Primary map



X



Y



Z

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

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

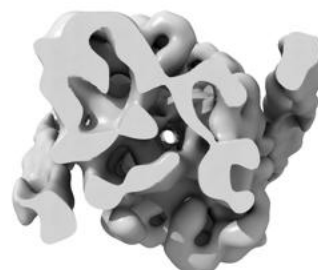
### 6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 45.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

## 6.6 Mask visualisation [i](#)

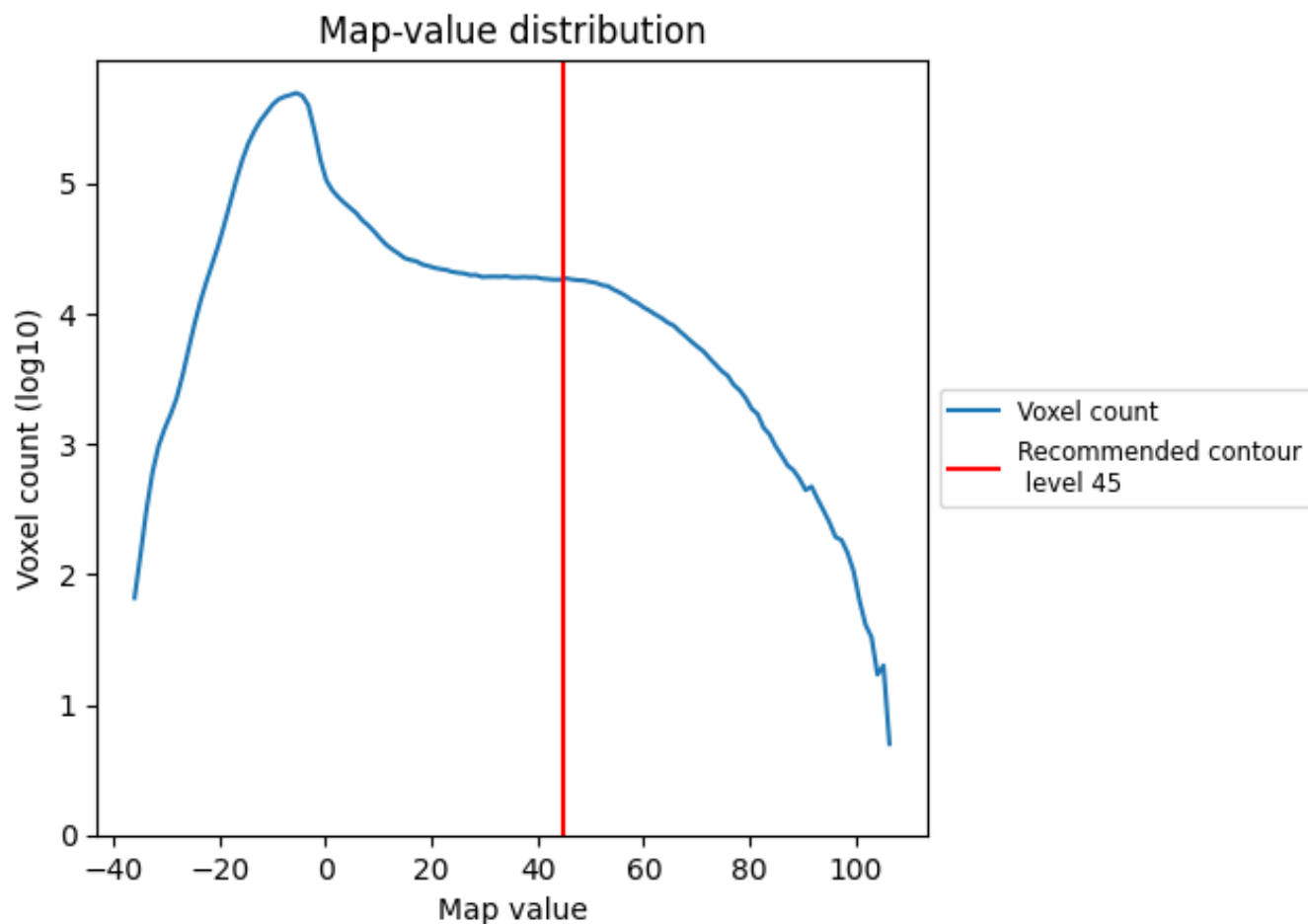
This section was not generated. No masks/segmentation were deposited.



## 7 Map analysis [i](#)

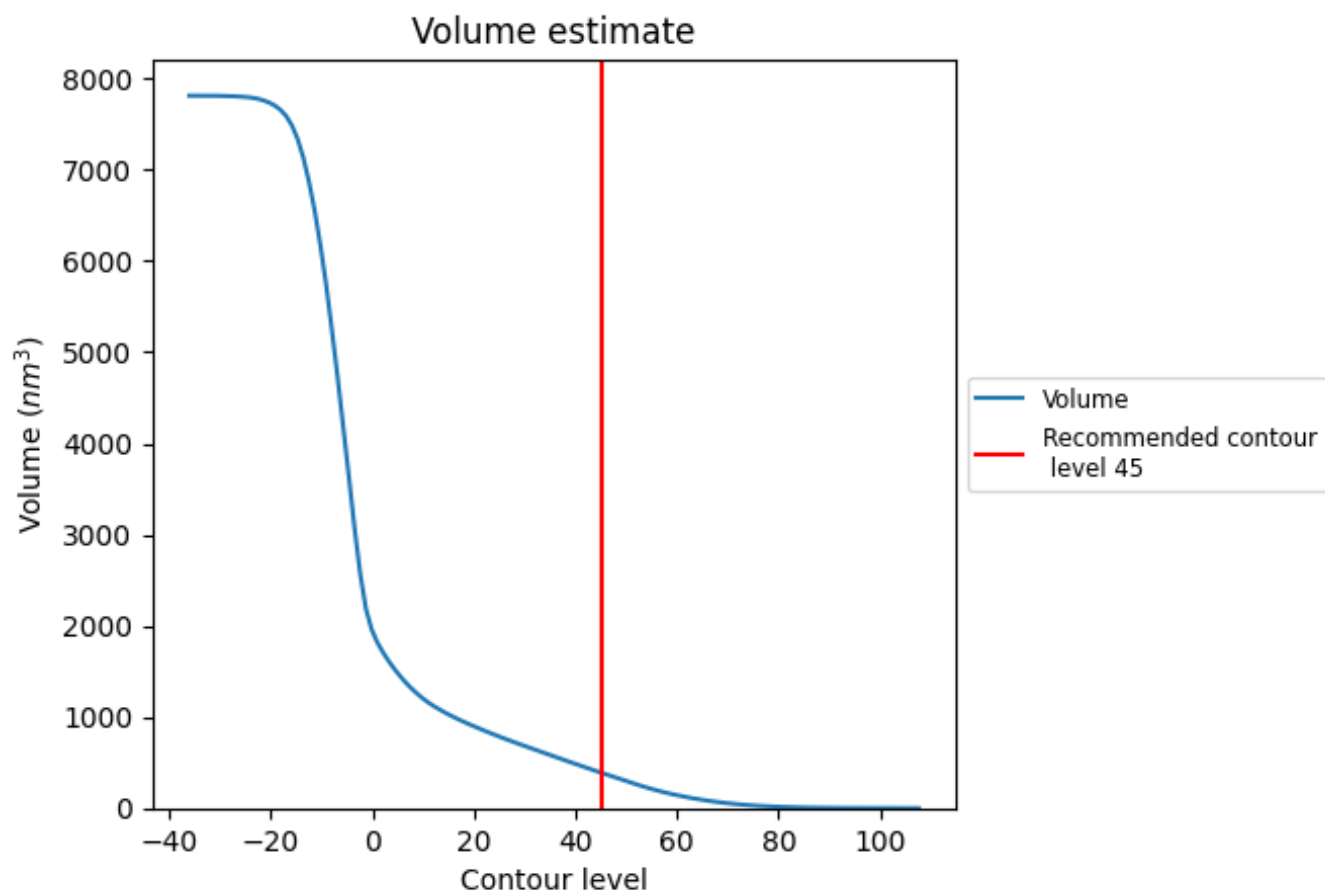
This section contains the results of statistical analysis of the map.

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



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

## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 390 nm<sup>3</sup>; this corresponds to an approximate mass of 352 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](#)

This section was not generated. The rotationally averaged power spectrum is only generated for cubic maps.

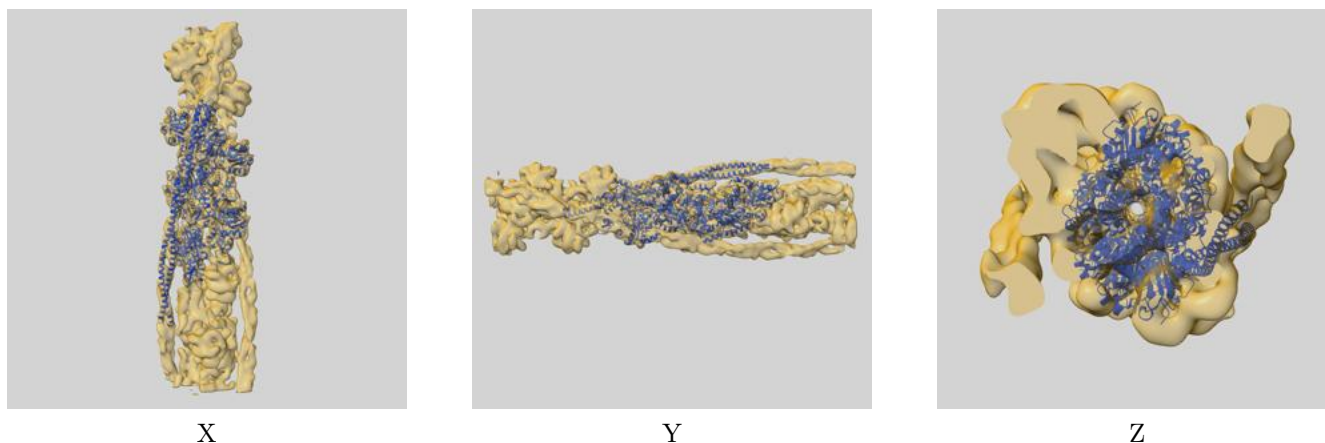
## 8 Fourier-Shell correlation ⓘ

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

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

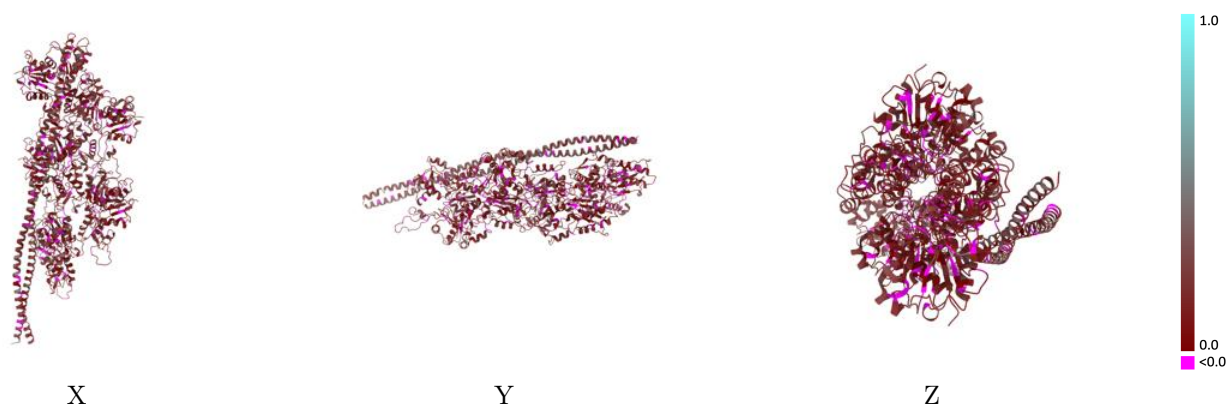
This section contains information regarding the fit between EMDB map EMD-3666 and PDB model 5NOJ. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

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



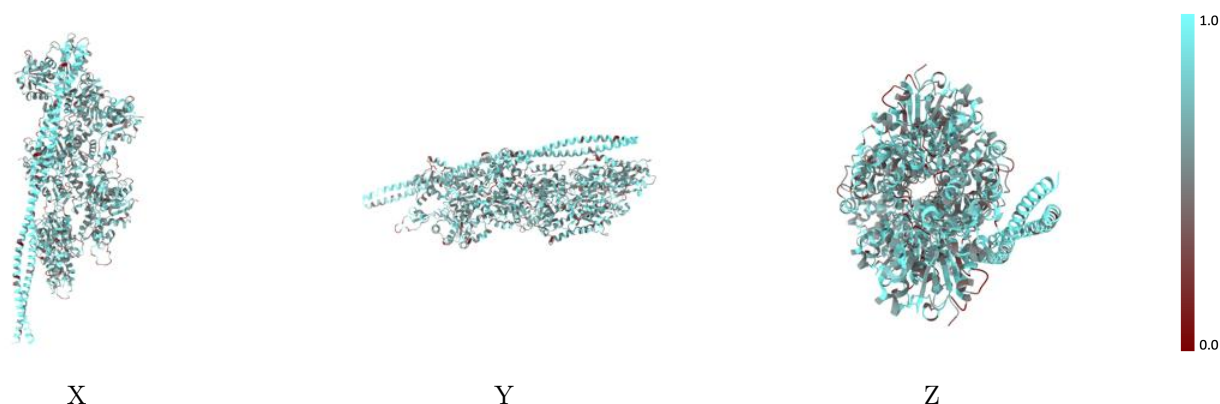
The images above show the 3D surface view of the map at the recommended contour level 45.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



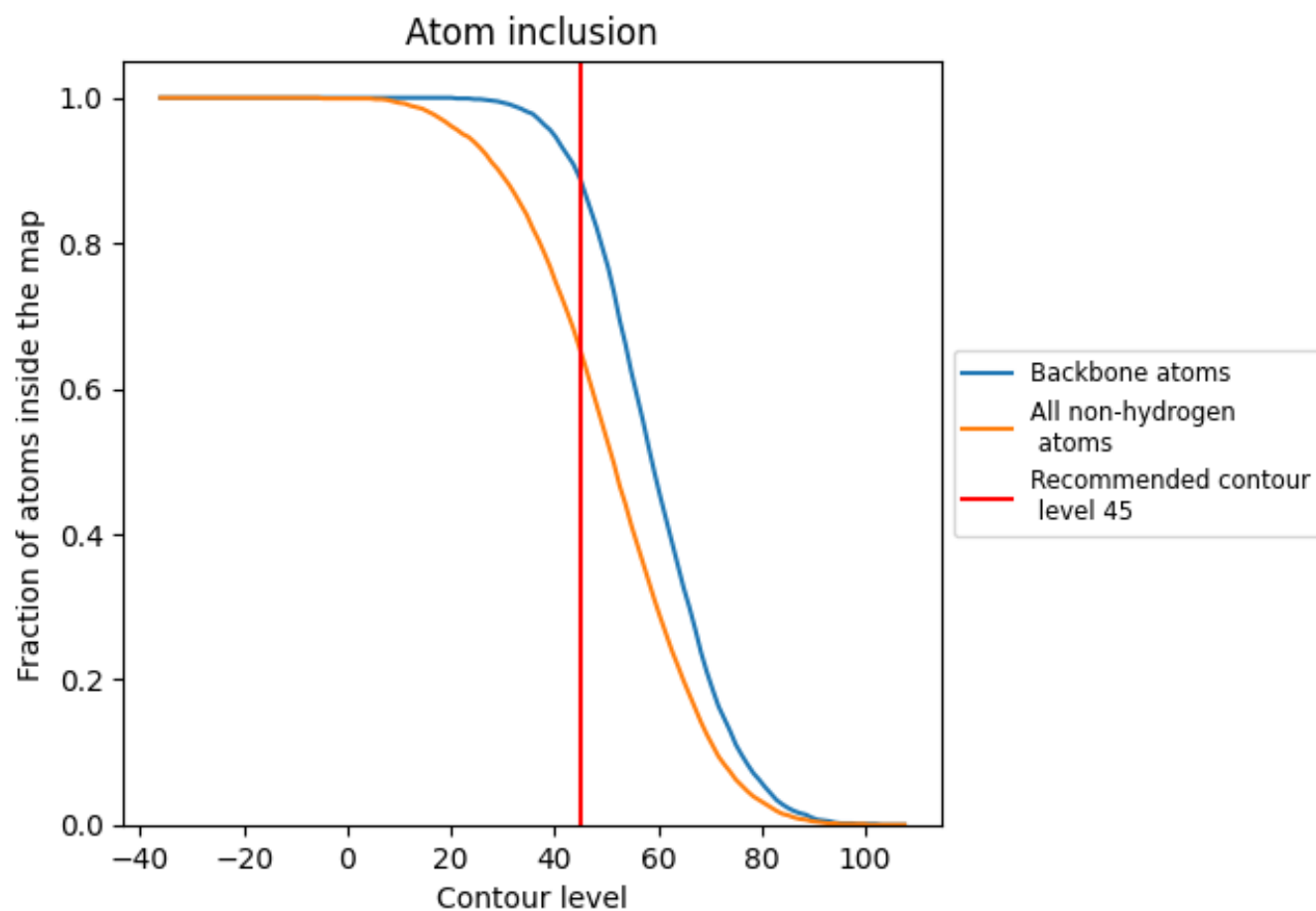
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (45).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 65% 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 (45) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.6530	<div></div> 0.1430
A	<div></div> 0.6350	<div></div> 0.1350
B	<div></div> 0.6330	<div></div> 0.1350
C	<div></div> 0.6340	<div></div> 0.1360
D	<div></div> 0.6410	<div></div> 0.1360
E	<div></div> 0.6420	<div></div> 0.1360
F	<div></div> 0.8590	<div></div> 0.2290
H	<div></div> 0.8410	<div></div> 0.2250

1.0

0.0

<0.0