



# Full wwPDB X-ray Structure Validation Report ⓘ

May 21, 2020 – 07:53 am BST

PDB ID : 2CB6  
Title : Crystal structure of the catalytic domain of the mosquitocidal toxin from *Bacillus sphaericus*, mutant E195Q  
Authors : Reinert, D.J.; Carpusca, I.; Aktories, K.; Schulz, G.E.  
Deposited on : 2005-12-29  
Resolution : 3.00 Å(reported)

This is a Full wwPDB X-ray Structure 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/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

---

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

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

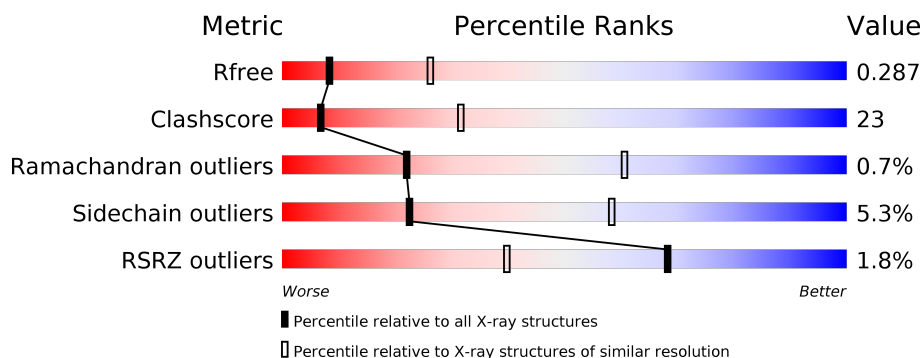
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.00 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.






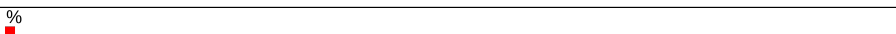
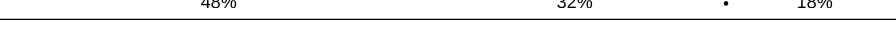




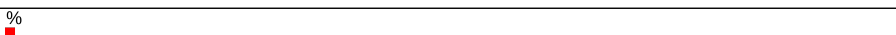
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower 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 electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	291	<div> <div>%</div> <div> <div></div> <div>51%</div> <div>28%</div> <div>•</div> <div>18%</div> </div> </div>
1	B	291	<div> <div>3%</div> <div> <div></div> <div>46%</div> <div>33%</div> <div>•</div> <div>18%</div> </div> </div>
1	C	291	<div> <div>%</div> <div> <div></div> <div>51%</div> <div>29%</div> <div>•</div> <div>16%</div> </div> </div>
1	D	291	<div> <div>%</div> <div> <div></div> <div>50%</div> <div>31%</div> <div>•</div> <div>16%</div> </div> </div>
1	E	291	<div> <div>%</div> <div> <div></div> <div>49%</div> <div>30%</div> <div>•</div> <div>18%</div> </div> </div>
1	F	291	<div> <div>3%</div> <div> <div></div> <div>46%</div> <div>32%</div> <div>•</div> <div>18%</div> </div> </div>

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Length	Quality of chain
1	G	291	
1	H	291	
1	I	291	
1	J	291	
1	K	291	
1	L	291	
1	M	291	
1	N	291	
1	O	291	
1	P	291	

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 31202 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 MOSQUITOCIDAL TOXIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	238	Total	C	N	O	S	0	0	0
			1939	1223	346	367	3			
1	B	238	Total	C	N	O	S	0	0	0
			1939	1223	346	367	3			
1	C	244	Total	C	N	O	S	0	0	0
			1986	1252	353	378	3			
1	D	244	Total	C	N	O	S	0	0	0
			1986	1252	353	378	3			
1	E	238	Total	C	N	O	S	0	0	0
			1939	1223	346	367	3			
1	F	238	Total	C	N	O	S	0	0	0
			1939	1223	346	367	3			
1	G	236	Total	C	N	O	S	0	0	0
			1918	1210	338	367	3			
1	H	245	Total	C	N	O	S	0	0	0
			1992	1255	354	380	3			
1	I	238	Total	C	N	O	S	0	0	0
			1939	1223	346	367	3			
1	J	238	Total	C	N	O	S	0	0	0
			1939	1223	346	367	3			
1	K	244	Total	C	N	O	S	0	0	0
			1986	1252	353	378	3			
1	L	236	Total	C	N	O	S	0	0	0
			1918	1210	338	367	3			
1	M	238	Total	C	N	O	S	0	0	0
			1939	1223	346	367	3			
1	N	238	Total	C	N	O	S	0	0	0
			1939	1223	346	367	3			
1	O	236	Total	C	N	O	S	0	0	0
			1918	1210	338	367	3			
1	P	244	Total	C	N	O	S	0	0	0
			1986	1252	353	378	3			

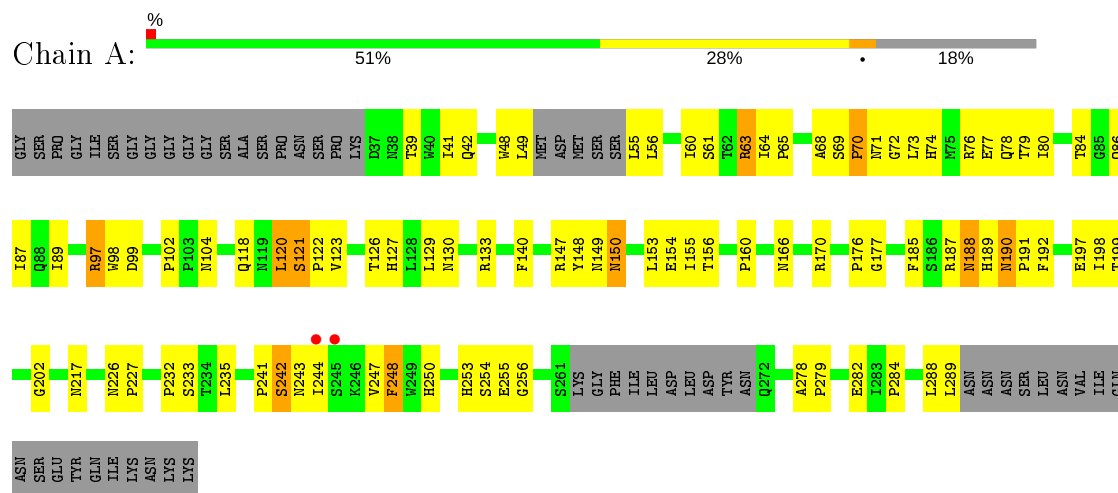
There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	195	GLN	GLU	engineered mutation	UNP Q03988
B	195	GLN	GLU	engineered mutation	UNP Q03988
C	195	GLN	GLU	engineered mutation	UNP Q03988
D	195	GLN	GLU	engineered mutation	UNP Q03988
E	195	GLN	GLU	engineered mutation	UNP Q03988
F	195	GLN	GLU	engineered mutation	UNP Q03988
G	195	GLN	GLU	engineered mutation	UNP Q03988
H	195	GLN	GLU	engineered mutation	UNP Q03988
I	195	GLN	GLU	engineered mutation	UNP Q03988
J	195	GLN	GLU	engineered mutation	UNP Q03988
K	195	GLN	GLU	engineered mutation	UNP Q03988
L	195	GLN	GLU	engineered mutation	UNP Q03988
M	195	GLN	GLU	engineered mutation	UNP Q03988
N	195	GLN	GLU	engineered mutation	UNP Q03988
O	195	GLN	GLU	engineered mutation	UNP Q03988
P	195	GLN	GLU	engineered mutation	UNP Q03988

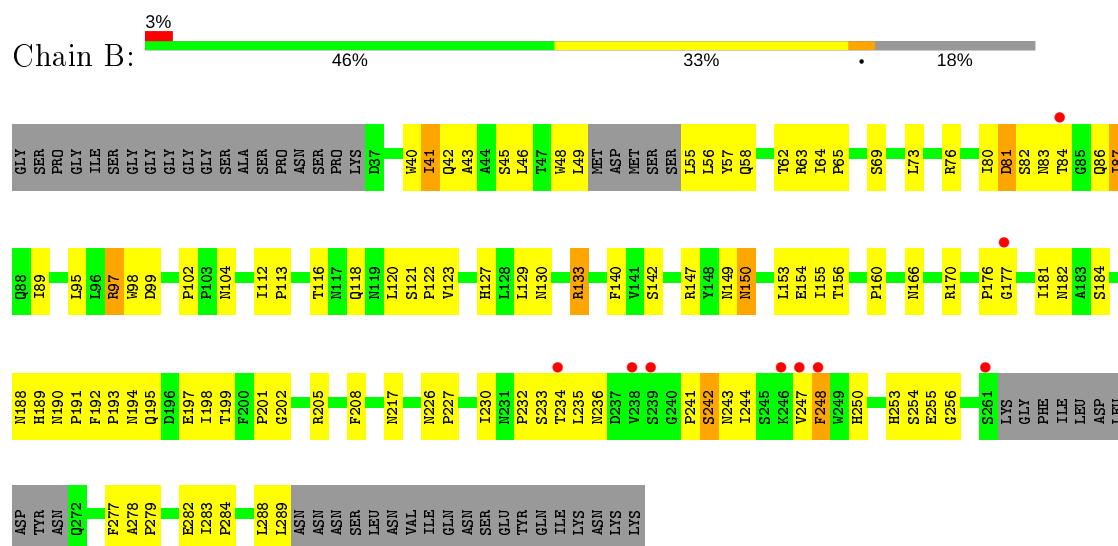
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

#### • Molecule 1: MOSQUITOCIDAL TOXIN

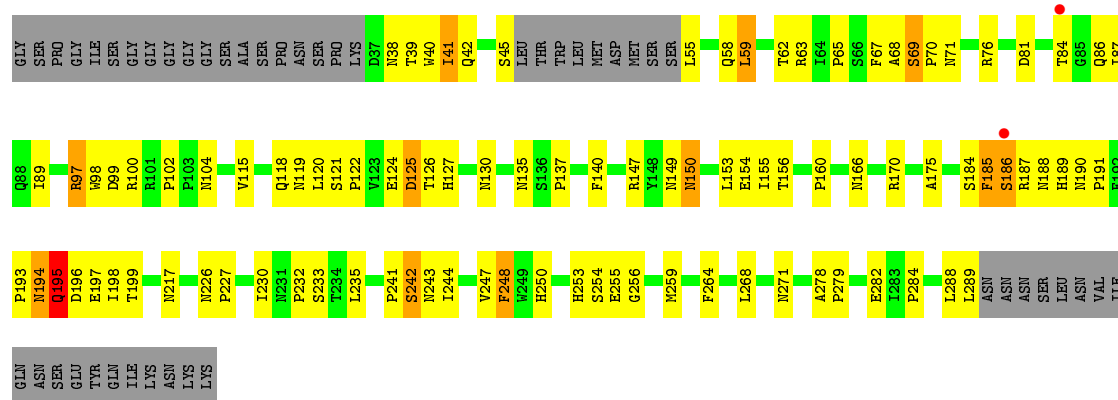


#### • Molecule 1: MOSQUITOCIDAL TOXIN

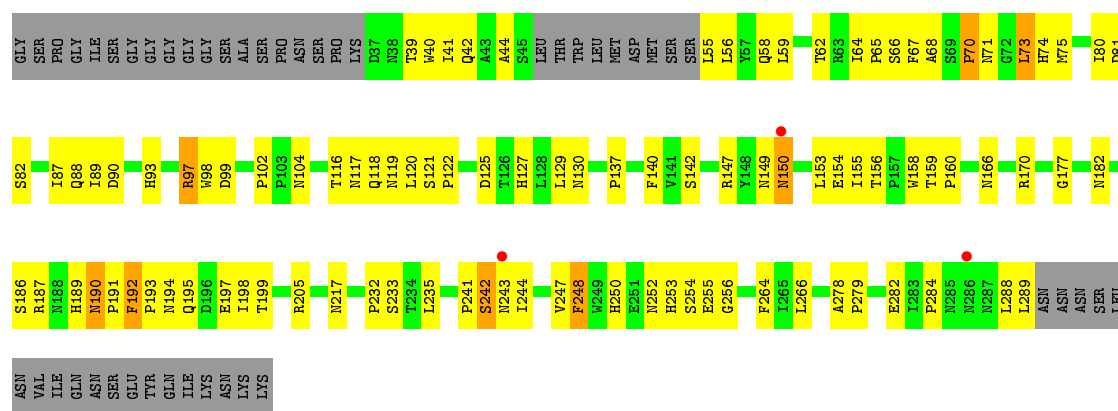


#### • Molecule 1: MOSQUITOCIDAL TOXIN

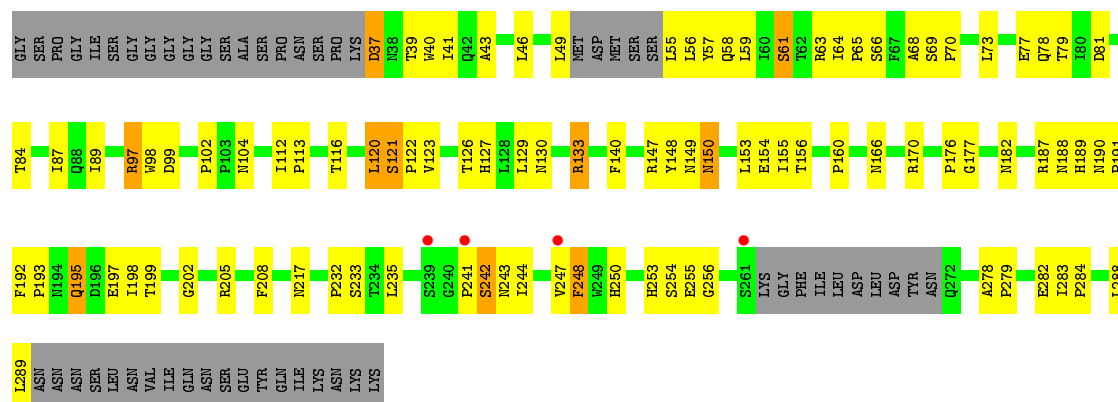




• Molecule 1: MOSQUITOCIDAL TOXIN

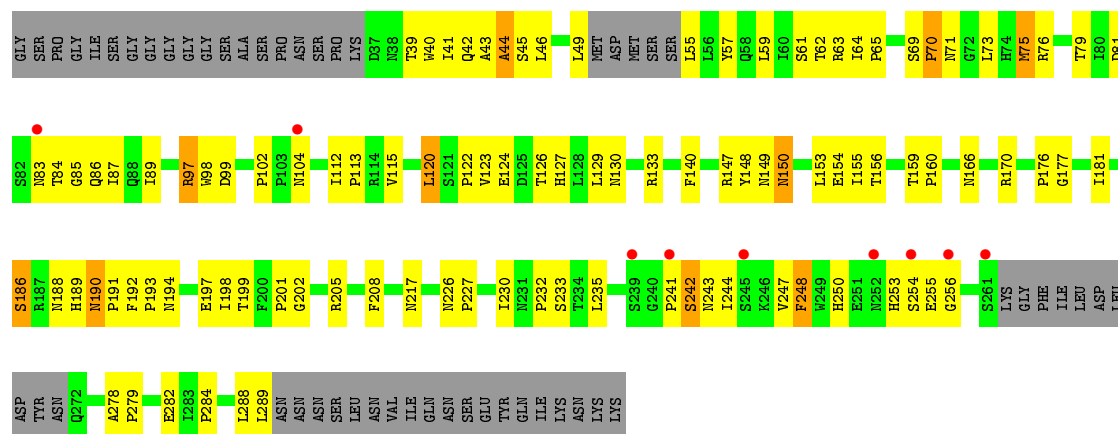


• Molecule 1: MOSQUITOCIDAL TOXIN



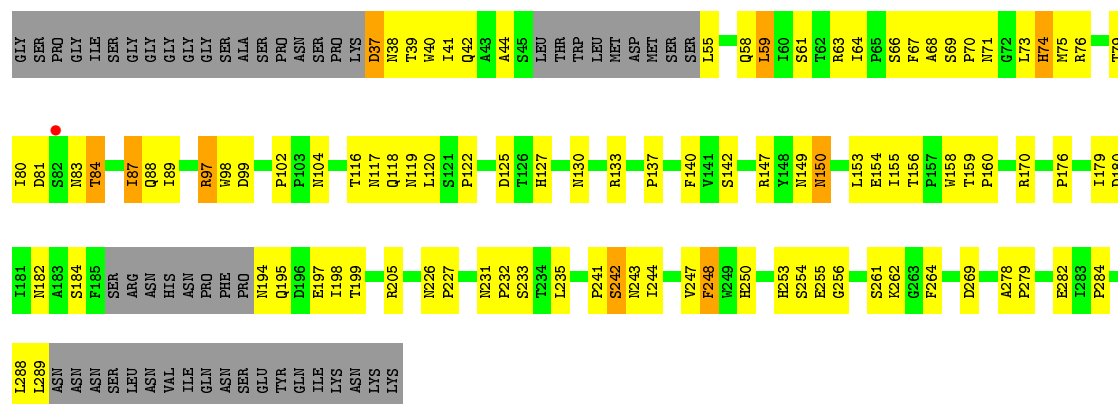
• Molecule 1: MOSQUITOCIDAL TOXIN





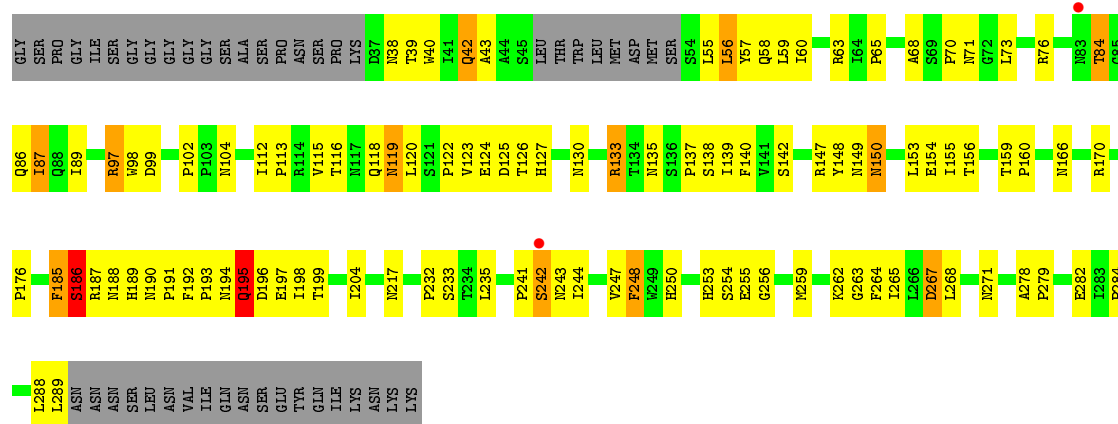
### • Molecule 1: MOSQUITOCIDAL TOXIN

Chain G: 47% 31% 19%



### • Molecule 1: MOSQUITOCIDAL TOXIN

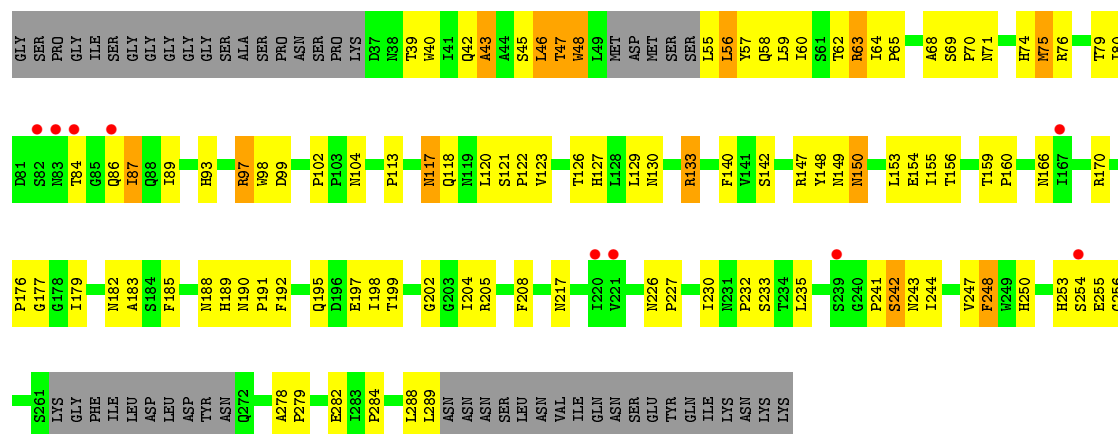
Chain H: 48% 32% 16%



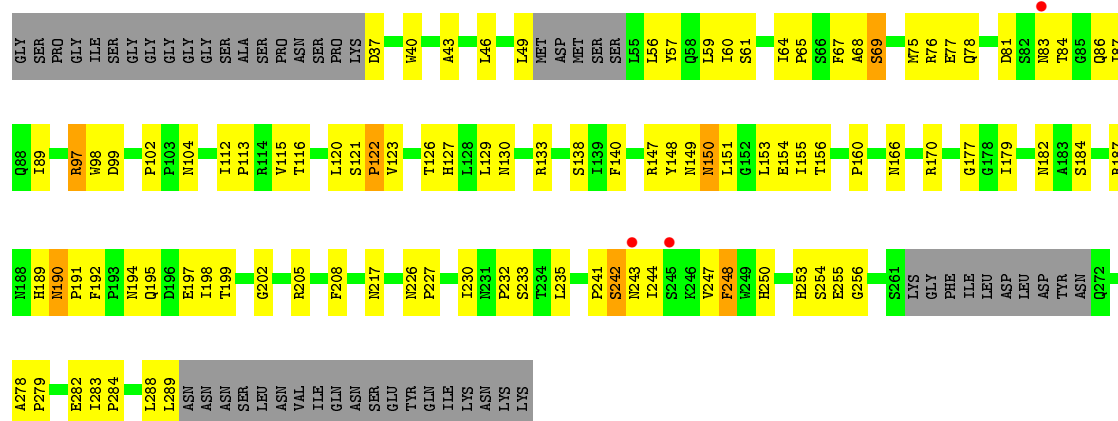
### • Molecule 1: MOSQUITOCIDAL TOXIN

Chain I: 45% 32% 5% 18%

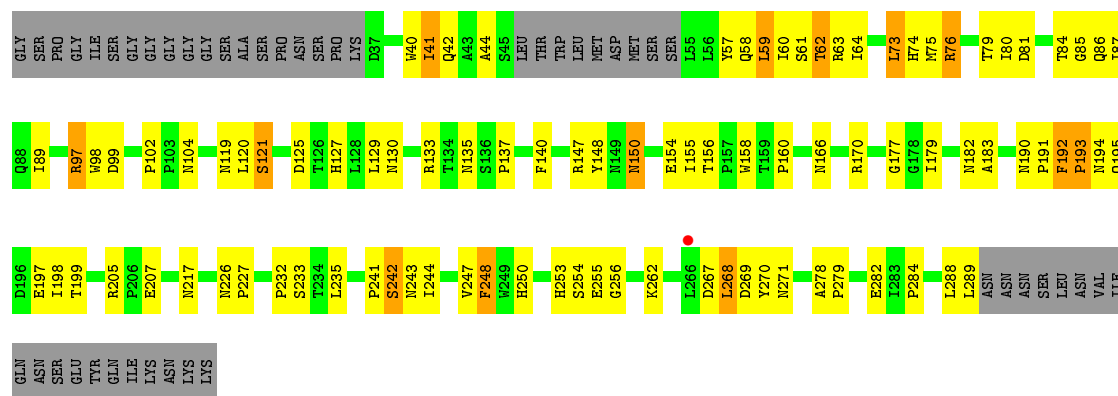




• Molecule 1: MOSQUITOCIDAL TOXIN

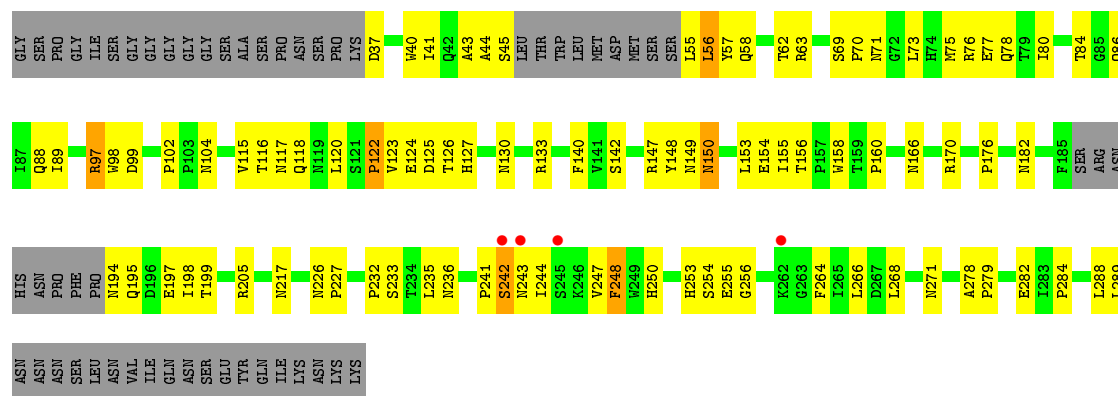


• Molecule 1: MOSQUITOCIDAL TOXIN

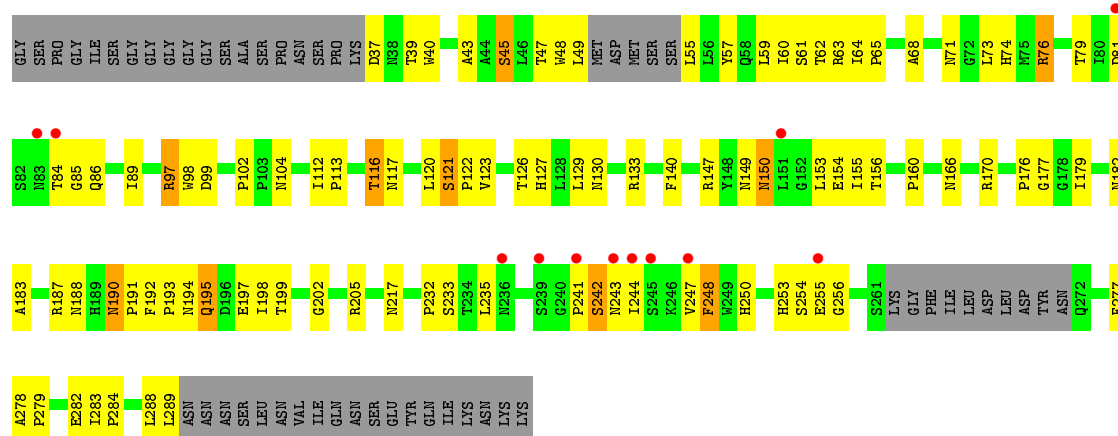


• Molecule 1: MOSQUITOCIDAL TOXIN

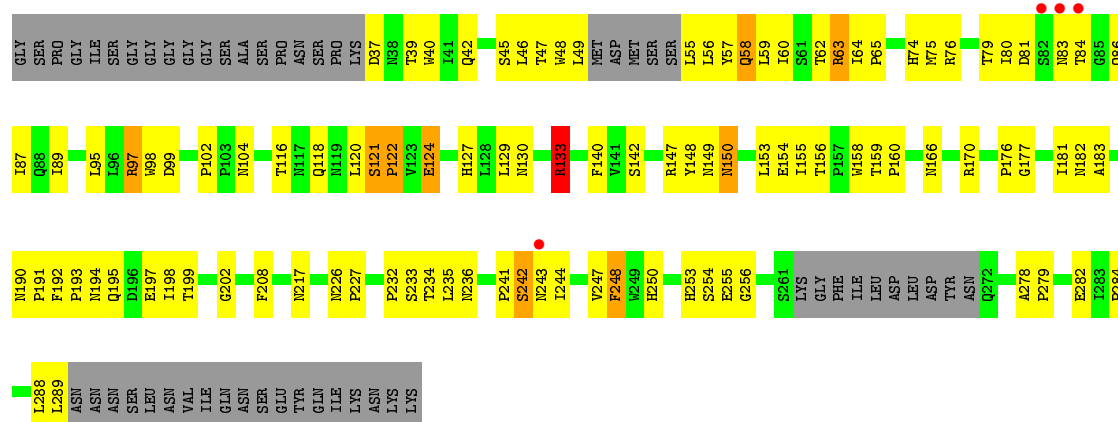




- Molecule 1: MOSQUITOCIDAL TOXIN

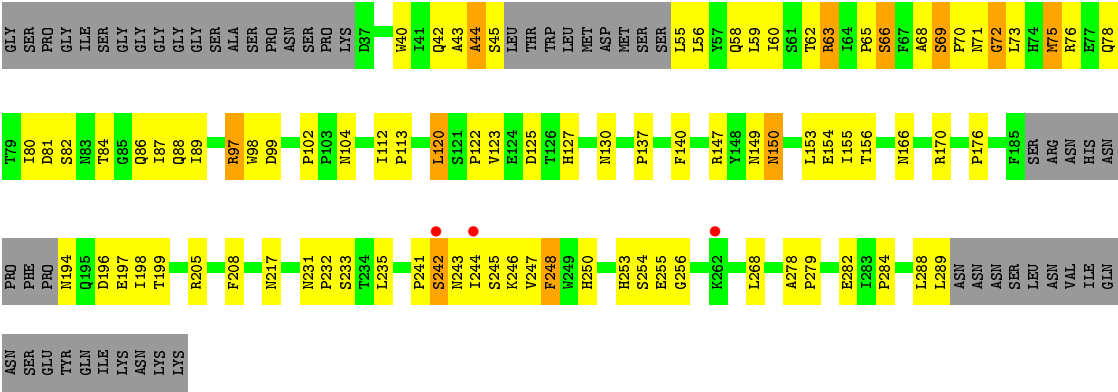


- Molecule 1: MOSQUITOCIDAL TOXIN

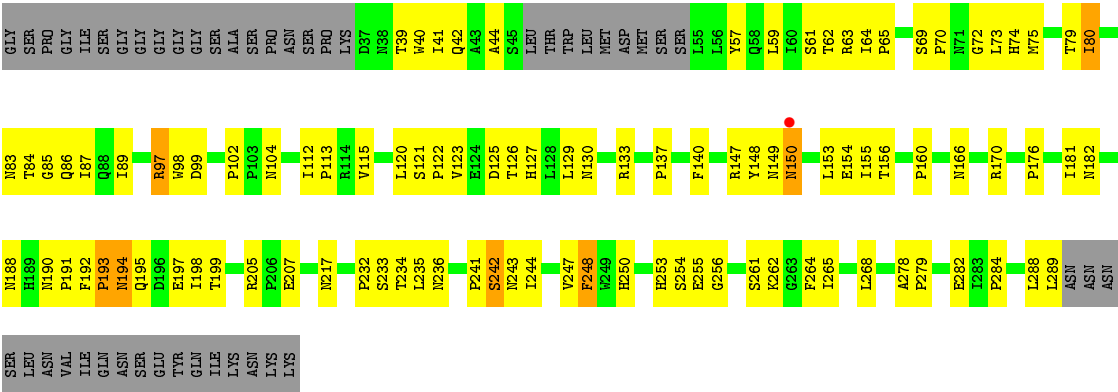


- Molecule 1: MOSQUITOCIDAL TOXIN





● Molecule 1: MOSQUITOCIDAL TOXIN



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	106.30Å 175.80Å 335.50Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 3.00 49.07 – 3.00	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-3.00) 99.6 (49.07-3.00)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.22 (at 3.01Å)	Xtriage
Refinement program	TNT 5.6.1	Depositor
R, $R_{free}$	0.227 , 0.246 0.267 , 0.287	Depositor DCC
$R_{free}$ test set	6301 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	49.0	Xtriage
Anisotropy	0.207	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 52.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.41$ , $\langle L^2 \rangle = 0.23$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.85	EDS
Total number of atoms	31202	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 24.83 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 3.5553e-03.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality

### 5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.48	0/1995	0.77	2/2726 (0.1%)
1	B	0.46	0/1995	0.73	1/2726 (0.0%)
1	C	0.49	0/2043	0.80	5/2790 (0.2%)
1	D	0.49	0/2043	0.80	3/2790 (0.1%)
1	E	0.47	0/1995	0.75	1/2726 (0.0%)
1	F	0.45	0/1995	0.72	0/2726
1	G	0.45	0/1970	0.73	0/2688
1	H	0.48	0/2049	0.82	7/2798 (0.3%)
1	I	0.46	0/1995	0.75	2/2726 (0.1%)
1	J	0.46	0/1995	0.76	2/2726 (0.1%)
1	K	0.46	0/2043	0.73	1/2790 (0.0%)
1	L	0.48	0/1970	0.77	1/2688 (0.0%)
1	M	0.44	0/1995	0.75	2/2726 (0.1%)
1	N	0.48	0/1995	0.76	1/2726 (0.0%)
1	O	0.49	0/1970	0.85	6/2688 (0.2%)
1	P	0.48	0/2043	0.74	1/2790 (0.0%)
All	All	0.47	0/32091	0.76	35/43830 (0.1%)

There are no bond length outliers.

All (35) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	O	69	SER	C-N-CD	-15.90	85.62	120.60
1	H	195	GLN	CB-CA-C	-8.77	92.87	110.40
1	D	190	ASN	C-N-CD	-8.13	102.72	120.60
1	H	186	SER	N-CA-CB	7.42	121.63	110.50
1	B	121	SER	C-N-CD	-7.13	104.91	120.60
1	J	121	SER	C-N-CD	-6.95	105.31	120.60
1	P	194	ASN	N-CA-C	-6.72	92.86	111.00
1	M	121	SER	C-N-CD	-6.71	105.84	120.60
1	C	195	GLN	CB-CA-C	-6.69	97.02	110.40
1	C	69	SER	C-N-CD	-6.59	106.10	120.60
1	C	185	PHE	O-C-N	-6.52	112.27	122.70

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	73	LEU	CB-CG-CD2	-6.32	100.25	111.00
1	C	185	PHE	C-N-CA	-6.27	106.02	121.70
1	E	121	SER	C-N-CD	-5.99	107.41	120.60
1	O	72	GLY	N-CA-C	5.97	128.03	113.10
1	H	187	ARG	N-CA-C	-5.89	95.09	111.00
1	I	46	LEU	CA-CB-CG	5.83	128.72	115.30
1	H	185	PHE	O-C-N	-5.82	113.39	122.70
1	A	121	SER	N-CA-C	-5.80	95.34	111.00
1	O	71	ASN	CA-C-N	-5.78	104.64	116.20
1	H	185	PHE	C-N-CA	-5.76	107.30	121.70
1	M	85	GLY	N-CA-C	-5.75	98.73	113.10
1	C	194	ASN	N-CA-C	-5.63	95.81	111.00
1	N	133	ARG	NE-CZ-NH2	5.60	123.10	120.30
1	A	187	ARG	N-CA-C	5.56	126.00	111.00
1	O	69	SER	N-CA-C	-5.53	96.06	111.00
1	J	187	ARG	N-CA-C	5.47	125.76	111.00
1	O	71	ASN	C-N-CA	5.43	133.70	122.30
1	O	73	LEU	N-CA-C	-5.41	96.40	111.00
1	D	55	LEU	CA-CB-CG	5.15	127.14	115.30
1	K	121	SER	N-CA-C	-5.12	97.19	111.00
1	I	87	ILE	N-CA-C	5.08	124.72	111.00
1	H	186	SER	CB-CA-C	5.08	119.75	110.10
1	H	56	LEU	CA-CB-CG	-5.07	103.63	115.30
1	L	271	ASN	N-CA-C	-5.04	97.38	111.00

There are no chirality outliers.

There are no planarity outliers.

## 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	1939	0	1829	100	0
1	B	1939	0	1829	108	0
1	C	1986	0	1872	95	0
1	D	1986	0	1872	88	1
1	E	1939	0	1829	116	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	1939	0	1829	106	0
1	G	1918	0	1811	93	0
1	H	1992	0	1877	101	1
1	I	1939	0	1829	107	0
1	J	1939	0	1829	86	0
1	K	1986	0	1872	101	0
1	L	1918	0	1811	85	0
1	M	1939	0	1829	85	0
1	N	1939	0	1829	94	0
1	O	1918	0	1811	83	0
1	P	1986	0	1872	88	0
All	All	31202	0	29430	1406	1

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 23.

All (1406) 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:J:87:ILE:HD12	1:J:230:ILE:HG21	1.22	1.15
1:I:64:ILE:HG23	1:I:129:LEU:HD11	1.25	1.11
1:A:84:THR:HB	1:A:86:GLN:HG2	1.11	1.10
1:A:64:ILE:HG23	1:A:129:LEU:HD11	1.17	1.08
1:D:254:SER:HB3	1:O:244:ILE:O	1.53	1.07
1:G:116:THR:HG22	1:G:118:GLN:H	1.18	1.07
1:E:133:ARG:HD3	1:E:190:ASN:HD21	1.20	1.06
1:K:133:ARG:HG3	1:K:191:PRO:HB3	1.37	1.06
1:D:254:SER:CB	1:O:244:ILE:O	2.03	1.06
1:I:63:ARG:HD2	1:L:123:VAL:HG21	1.28	1.06
1:A:63:ARG:HG2	1:A:63:ARG:HH11	1.17	1.05
1:E:46:LEU:HD12	1:E:202:GLY:HA2	1.37	1.04
1:E:133:ARG:HH11	1:E:190:ASN:ND2	1.54	1.03
1:D:116:THR:HG22	1:D:118:GLN:H	1.23	1.03
1:C:185:PHE:HB2	1:C:189:HIS:HD2	1.24	1.01
1:C:87:ILE:HD12	1:C:230:ILE:HG21	1.44	0.99
1:K:190:ASN:HA	1:K:192:PHE:HD2	1.27	0.99
1:C:40:TRP:CE2	1:C:41:ILE:HD13	2.00	0.97
1:E:129:LEU:HD23	1:E:191:PRO:HD3	1.48	0.96
1:M:84:THR:HG21	1:M:86:GLN:HB2	1.47	0.96
1:M:123:VAL:HG22	1:P:123:VAL:HG22	1.48	0.96
1:P:190:ASN:HB2	1:P:191:PRO:HA	1.45	0.96

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:80:ILE:HG22	1:G:87:ILE:HD13	1.46	0.95
1:I:43:ALA:HB2	1:I:176:PRO:HD2	1.45	0.95
1:F:64:ILE:HG23	1:F:129:LEU:HD11	1.46	0.95
1:F:87:ILE:HD12	1:F:230:ILE:HG12	1.48	0.94
1:I:46:LEU:HD12	1:I:202:GLY:HA2	1.48	0.93
1:G:254:SER:OG	1:L:243:ASN:N	2.01	0.93
1:P:133:ARG:HG3	1:P:191:PRO:HB3	1.50	0.93
1:G:254:SER:CB	1:L:243:ASN:H	1.83	0.92
1:H:120:LEU:HG	1:H:122:PRO:HD3	1.52	0.91
1:C:87:ILE:CD1	1:C:230:ILE:HG21	2.01	0.91
1:B:129:LEU:HD23	1:B:191:PRO:CG	2.00	0.91
1:I:87:ILE:HD12	1:I:230:ILE:HG21	1.53	0.91
1:J:190:ASN:HB2	1:J:191:PRO:HA	1.54	0.90
1:E:283:ILE:CG2	1:H:268:LEU:HD21	2.02	0.90
1:K:190:ASN:HB2	1:K:191:PRO:HA	1.54	0.89
1:J:129:LEU:HD23	1:J:191:PRO:HD3	1.54	0.89
1:G:254:SER:CB	1:L:243:ASN:N	2.36	0.89
1:O:69:SER:HB2	1:O:72:GLY:HA2	1.52	0.89
1:L:127:HIS:ND1	1:L:130:ASN:HB2	1.88	0.88
1:J:127:HIS:ND1	1:J:130:ASN:HB2	1.89	0.88
1:K:127:HIS:ND1	1:K:130:ASN:HB2	1.89	0.88
1:O:127:HIS:ND1	1:O:130:ASN:HB2	1.88	0.88
1:I:64:ILE:HG23	1:I:129:LEU:CD1	2.03	0.88
1:N:127:HIS:ND1	1:N:130:ASN:HB2	1.88	0.88
1:I:127:HIS:ND1	1:I:130:ASN:HB2	1.89	0.88
1:A:127:HIS:ND1	1:A:130:ASN:HB2	1.89	0.88
1:P:127:HIS:ND1	1:P:130:ASN:HB2	1.88	0.88
1:B:127:HIS:ND1	1:B:130:ASN:HB2	1.89	0.88
1:A:133:ARG:HD3	1:A:190:ASN:HD22	1.38	0.88
1:E:127:HIS:ND1	1:E:130:ASN:HB2	1.89	0.88
1:M:127:HIS:ND1	1:M:130:ASN:HB2	1.89	0.87
1:H:127:HIS:ND1	1:H:130:ASN:HB2	1.88	0.87
1:C:127:HIS:ND1	1:C:130:ASN:HB2	1.88	0.87
1:E:64:ILE:HG23	1:E:129:LEU:HD11	1.55	0.87
1:F:127:HIS:ND1	1:F:130:ASN:HB2	1.89	0.87
1:N:133:ARG:HE	1:N:190:ASN:HD21	1.23	0.87
1:G:127:HIS:ND1	1:G:130:ASN:HB2	1.88	0.87
1:K:133:ARG:CG	1:K:191:PRO:HB3	2.03	0.87
1:K:190:ASN:HA	1:K:192:PHE:CD2	2.08	0.86
1:A:190:ASN:HA	1:A:192:PHE:H	1.38	0.86
1:D:127:HIS:ND1	1:D:130:ASN:HB2	1.88	0.86

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:63:ARG:HD2	1:L:123:VAL:CG2	2.06	0.86
1:A:129:LEU:HD23	1:A:191:PRO:HD3	1.58	0.86
1:A:84:THR:CB	1:A:86:GLN:HG2	2.02	0.86
1:I:133:ARG:HH11	1:I:190:ASN:ND2	1.73	0.85
1:O:241:PRO:HB2	1:O:244:ILE:HD12	1.59	0.85
1:L:241:PRO:HB2	1:L:244:ILE:HD12	1.59	0.85
1:M:241:PRO:HB2	1:M:244:ILE:HD12	1.59	0.85
1:M:283:ILE:HB	1:O:268:LEU:HD22	1.57	0.85
1:D:241:PRO:HB2	1:D:244:ILE:HD12	1.59	0.84
1:G:254:SER:HB3	1:L:244:ILE:H	1.42	0.84
1:E:241:PRO:HB2	1:E:244:ILE:HD12	1.59	0.84
1:P:64:ILE:HD13	1:P:73:LEU:HD13	1.59	0.84
1:H:241:PRO:HB2	1:H:244:ILE:HD12	1.59	0.84
1:B:133:ARG:HG2	1:B:191:PRO:HB3	1.57	0.84
1:F:241:PRO:HB2	1:F:244:ILE:HD12	1.59	0.84
1:A:241:PRO:HB2	1:A:244:ILE:HD12	1.59	0.84
1:A:64:ILE:HG23	1:A:129:LEU:CD1	2.06	0.83
1:C:135:ASN:HD22	1:C:271:ASN:HD21	1.26	0.83
1:N:87:ILE:HD11	1:N:208:PHE:CE1	2.13	0.83
1:G:241:PRO:HB2	1:G:244:ILE:HD12	1.59	0.83
1:C:241:PRO:HB2	1:C:244:ILE:CD1	2.09	0.83
1:I:241:PRO:HB2	1:I:244:ILE:CD1	2.09	0.83
1:J:241:PRO:HB2	1:J:244:ILE:HD12	1.59	0.83
1:N:241:PRO:HB2	1:N:244:ILE:HD12	1.59	0.83
1:I:79:THR:HG21	1:I:177:GLY:H	1.43	0.83
1:E:241:PRO:HB2	1:E:244:ILE:CD1	2.09	0.83
1:G:241:PRO:HB2	1:G:244:ILE:CD1	2.09	0.83
1:F:241:PRO:HB2	1:F:244:ILE:CD1	2.09	0.83
1:A:241:PRO:HB2	1:A:244:ILE:CD1	2.09	0.83
1:F:87:ILE:HD12	1:F:230:ILE:HG21	1.61	0.83
1:L:78:GLN:O	1:L:88:GLN:HG3	1.78	0.82
1:N:241:PRO:HB2	1:N:244:ILE:CD1	2.09	0.82
1:P:241:PRO:HB2	1:P:244:ILE:CD1	2.09	0.82
1:C:185:PHE:HB2	1:C:189:HIS:CD2	2.13	0.82
1:O:241:PRO:HB2	1:O:244:ILE:CD1	2.09	0.82
1:N:48:TRP:CH2	1:N:120:LEU:HD23	2.13	0.82
1:B:241:PRO:HB2	1:B:244:ILE:CD1	2.09	0.82
1:K:194:ASN:HB3	1:K:197:GLU:HB2	1.61	0.82
1:K:241:PRO:HB2	1:K:244:ILE:CD1	2.09	0.82
1:P:241:PRO:HB2	1:P:244:ILE:HD12	1.59	0.82
1:C:40:TRP:CD2	1:C:41:ILE:HG23	2.15	0.82

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:241:PRO:HB2	1:H:244:ILE:CD1	2.09	0.82
1:K:241:PRO:HB2	1:K:244:ILE:HD12	1.59	0.82
1:B:241:PRO:HB2	1:B:244:ILE:HD12	1.59	0.82
1:D:241:PRO:HB2	1:D:244:ILE:CD1	2.09	0.81
1:C:241:PRO:HB2	1:C:244:ILE:HD12	1.59	0.81
1:I:241:PRO:HB2	1:I:244:ILE:HD12	1.59	0.81
1:G:254:SER:HB3	1:L:244:ILE:N	1.95	0.81
1:M:133:ARG:HH11	1:M:190:ASN:HB2	1.46	0.81
1:M:241:PRO:HB2	1:M:244:ILE:CD1	2.09	0.81
1:C:154:GLU:HG2	1:C:289:LEU:HD22	1.63	0.81
1:J:241:PRO:HB2	1:J:244:ILE:CD1	2.09	0.81
1:I:154:GLU:HG2	1:I:289:LEU:HD22	1.63	0.81
1:L:154:GLU:HG2	1:L:289:LEU:HD22	1.63	0.81
1:L:241:PRO:HB2	1:L:244:ILE:CD1	2.09	0.80
1:B:129:LEU:HD23	1:B:191:PRO:HG3	1.60	0.80
1:H:63:ARG:HH11	1:H:63:ARG:HG3	1.46	0.80
1:P:133:ARG:CG	1:P:191:PRO:HB3	2.10	0.80
1:D:186:SER:HB2	1:D:189:HIS:HB2	1.62	0.80
1:O:154:GLU:HG2	1:O:289:LEU:HD22	1.63	0.80
1:K:154:GLU:HG2	1:K:289:LEU:HD22	1.63	0.80
1:E:129:LEU:CD2	1:E:191:PRO:HD3	2.12	0.80
1:D:154:GLU:HG2	1:D:289:LEU:HD22	1.63	0.80
1:E:133:ARG:HH11	1:E:190:ASN:HD21	1.30	0.80
1:G:154:GLU:HG2	1:G:289:LEU:HD22	1.63	0.80
1:P:57:TYR:HE1	1:P:73:LEU:HD23	1.45	0.80
1:A:154:GLU:HG2	1:A:289:LEU:HD22	1.63	0.79
1:F:87:ILE:CD1	1:F:230:ILE:HG21	2.12	0.79
1:E:129:LEU:HD23	1:E:191:PRO:CD	2.13	0.79
1:N:154:GLU:HG2	1:N:289:LEU:HD22	1.63	0.79
1:J:154:GLU:HG2	1:J:289:LEU:HD22	1.63	0.79
1:D:255:GLU:OE2	1:O:242:SER:HB3	1.83	0.79
1:P:154:GLU:HG2	1:P:289:LEU:HD22	1.63	0.79
1:H:154:GLU:HG2	1:H:289:LEU:HD22	1.63	0.79
1:G:254:SER:HG	1:L:243:ASN:H	1.28	0.79
1:B:154:GLU:HG2	1:B:289:LEU:HD22	1.63	0.78
1:F:79:THR:HG21	1:F:177:GLY:H	1.48	0.78
1:M:84:THR:CG2	1:M:86:GLN:HB2	2.12	0.78
1:E:154:GLU:HG2	1:E:289:LEU:HD22	1.63	0.78
1:M:154:GLU:HG2	1:M:289:LEU:HD22	1.63	0.78
1:D:254:SER:HB3	1:O:244:ILE:C	2.03	0.78
1:F:154:GLU:HG2	1:F:289:LEU:HD22	1.63	0.78

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:133:ARG:HE	1:B:190:ASN:HD22	1.29	0.78
1:B:43:ALA:HB2	1:B:176:PRO:HD2	1.66	0.78
1:H:185:PHE:HB2	1:H:189:HIS:HD2	1.47	0.78
1:I:46:LEU:HD11	1:I:113:PRO:HG2	1.66	0.78
1:E:87:ILE:CD1	1:E:176:PRO:HD3	2.14	0.78
1:J:84:THR:HB	1:J:86:GLN:HG3	1.66	0.77
1:E:133:ARG:HD3	1:E:190:ASN:ND2	1.98	0.77
1:D:40:TRP:CD2	1:D:41:ILE:HG23	2.19	0.77
1:J:46:LEU:HD12	1:J:202:GLY:HA2	1.66	0.77
1:C:84:THR:OG1	1:C:86:GLN:HB2	1.85	0.77
1:H:115:VAL:HG11	1:H:125:ASP:HB3	1.66	0.77
1:J:87:ILE:CD1	1:J:230:ILE:HG21	2.12	0.77
1:A:49:LEU:HD21	1:A:56:LEU:HD21	1.65	0.76
1:F:87:ILE:CD1	1:F:230:ILE:HG12	2.15	0.76
1:G:39:THR:HA	1:G:42:GLN:HG3	1.67	0.76
1:B:122:PRO:HD3	1:D:62:THR:HG21	1.65	0.76
1:M:283:ILE:HB	1:O:268:LEU:CD2	2.14	0.76
1:D:252:ASN:O	1:O:245:SER:HA	1.85	0.76
1:N:182:ASN:HB2	1:N:195:GLN:O	1.85	0.76
1:G:87:ILE:HD11	1:G:176:PRO:HB3	1.67	0.76
1:A:63:ARG:HG2	1:A:63:ARG:NH1	1.97	0.76
1:I:129:LEU:HD23	1:I:191:PRO:HD3	1.67	0.76
1:G:254:SER:HB3	1:L:243:ASN:N	1.99	0.76
1:J:87:ILE:HD11	1:J:208:PHE:CE1	2.20	0.76
1:E:150:ASN:ND2	1:P:207:GLU:OE1	2.18	0.76
1:P:129:LEU:HD23	1:P:191:PRO:HD3	1.65	0.76
1:N:59:LEU:HA	1:O:122:PRO:HG2	1.67	0.76
1:C:40:TRP:NE1	1:C:41:ILE:HD13	2.01	0.75
1:D:254:SER:O	1:O:246:LYS:HE3	1.86	0.75
1:A:129:LEU:HD23	1:A:191:PRO:CD	2.17	0.75
1:D:58:GLN:O	1:D:62:THR:HG23	1.87	0.75
1:E:288:LEU:HD13	1:P:86:GLN:NE2	2.02	0.75
1:L:84:THR:OG1	1:L:86:GLN:HG2	1.85	0.74
1:F:76:ARG:HD2	1:F:198:ILE:HG21	1.69	0.74
1:L:56:LEU:HD12	1:L:56:LEU:O	1.85	0.74
1:N:133:ARG:HE	1:N:190:ASN:ND2	1.84	0.74
1:C:58:GLN:O	1:C:62:THR:HB	1.87	0.74
1:A:122:PRO:HG2	1:C:59:LEU:HA	1.70	0.74
1:E:133:ARG:NH1	1:E:190:ASN:ND2	2.33	0.74
1:G:254:SER:CB	1:L:244:ILE:H	2.01	0.74
1:O:80:ILE:HG22	1:O:81:ASP:O	1.87	0.74

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:129:LEU:HD23	1:B:191:PRO:CD	2.17	0.74
1:C:185:PHE:CB	1:C:189:HIS:HD2	2.00	0.74
1:N:59:LEU:HD13	1:O:122:PRO:HB2	1.68	0.73
1:M:64:ILE:HG12	1:M:129:LEU:HD12	1.70	0.73
1:I:40:TRP:CH2	1:I:57:TYR:HB2	2.24	0.73
1:N:76:ARG:NH1	1:N:95:LEU:HD11	2.04	0.73
1:B:129:LEU:HD23	1:B:191:PRO:HD3	1.70	0.73
1:M:187:ARG:NH1	1:M:195:GLN:HG3	2.03	0.73
1:J:129:LEU:CD2	1:J:191:PRO:HD3	2.18	0.73
1:E:87:ILE:O	1:E:89:ILE:HG13	1.89	0.73
1:F:79:THR:HB	1:F:176:PRO:HA	1.69	0.73
1:K:262:LYS:HG2	1:K:270:TYR:HE1	1.53	0.72
1:K:58:GLN:O	1:K:62:THR:HG23	1.89	0.72
1:K:133:ARG:CB	1:K:191:PRO:HB3	2.20	0.72
1:L:120:LEU:HG	1:L:122:PRO:HD3	1.71	0.72
1:P:79:THR:OG1	1:P:176:PRO:HA	1.89	0.72
1:N:84:THR:HB	1:N:86:GLN:HG2	1.72	0.72
1:E:65:PRO:HB3	1:F:62:THR:O	1.90	0.71
1:K:80:ILE:HG22	1:K:87:ILE:HD13	1.72	0.71
1:E:156:THR:HG21	1:E:284:PRO:HG2	1.73	0.71
1:O:76:ARG:HD3	1:O:198:ILE:HG13	1.71	0.71
1:G:156:THR:HG21	1:G:284:PRO:HG2	1.72	0.71
1:H:156:THR:HG21	1:H:284:PRO:HG2	1.73	0.71
1:J:156:THR:HG21	1:J:284:PRO:HG2	1.73	0.71
1:O:156:THR:HG21	1:O:284:PRO:HG2	1.72	0.71
1:H:115:VAL:HG12	1:H:115:VAL:O	1.89	0.71
1:P:65:PRO:HD3	1:P:129:LEU:CD1	2.21	0.71
1:A:129:LEU:CD2	1:A:191:PRO:HD3	2.20	0.71
1:A:156:THR:HG21	1:A:284:PRO:HG2	1.73	0.71
1:F:129:LEU:HD23	1:F:191:PRO:HD3	1.73	0.71
1:L:156:THR:HG21	1:L:284:PRO:HG2	1.72	0.71
1:D:156:THR:HG21	1:D:284:PRO:HG2	1.73	0.71
1:H:186:SER:N	1:H:188:ASN:OD1	2.24	0.71
1:I:156:THR:HG21	1:I:284:PRO:HG2	1.73	0.70
1:A:190:ASN:HA	1:A:192:PHE:N	2.06	0.70
1:K:268:LEU:HD23	1:K:268:LEU:N	2.05	0.70
1:B:156:THR:HG21	1:B:284:PRO:HG2	1.73	0.70
1:E:87:ILE:HD11	1:E:176:PRO:HD3	1.73	0.70
1:J:76:ARG:HD3	1:J:177:GLY:O	1.91	0.70
1:N:156:THR:HG21	1:N:284:PRO:HG2	1.73	0.70
1:K:156:THR:HG21	1:K:284:PRO:HG2	1.73	0.70

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:156:THR:HG21	1:C:284:PRO:HG2	1.73	0.70
1:I:64:ILE:CG2	1:I:129:LEU:HD11	2.14	0.70
1:K:135:ASN:ND2	1:K:271:ASN:HD21	1.90	0.70
1:G:182:ASN:HB2	1:G:195:GLN:O	1.92	0.70
1:B:40:TRP:HA	1:B:177:GLY:HA3	1.74	0.70
1:D:40:TRP:CE3	1:D:41:ILE:HG23	2.27	0.70
1:F:156:THR:HG21	1:F:284:PRO:HG2	1.73	0.70
1:P:133:ARG:CB	1:P:191:PRO:HB3	2.22	0.70
1:A:129:LEU:HD23	1:A:191:PRO:HG3	1.74	0.70
1:G:182:ASN:HA	1:G:195:GLN:OE1	1.92	0.70
1:J:194:ASN:HB3	1:J:197:GLU:HB2	1.72	0.69
1:M:156:THR:HG21	1:M:284:PRO:HG2	1.73	0.69
1:N:87:ILE:HD11	1:N:208:PHE:HE1	1.55	0.69
1:H:264:PHE:HB3	1:P:248:PHE:CD2	2.27	0.69
1:F:76:ARG:HD2	1:F:198:ILE:CG2	2.21	0.69
1:N:120:LEU:HD12	1:N:120:LEU:O	1.92	0.69
1:G:194:ASN:HD21	1:G:197:GLU:HB2	1.58	0.69
1:J:190:ASN:CB	1:J:191:PRO:HA	2.18	0.69
1:B:42:GLN:HE21	1:B:176:PRO:HG3	1.57	0.69
1:P:156:THR:HG21	1:P:284:PRO:HG2	1.73	0.69
1:N:76:ARG:HD2	1:N:198:ILE:HG23	1.74	0.69
1:A:76:ARG:NH1	1:A:177:GLY:O	2.26	0.69
1:K:44:ALA:O	1:K:205:ARG:NH1	2.26	0.69
1:A:87:ILE:CD1	1:A:176:PRO:HD3	2.23	0.68
1:I:63:ARG:NH2	1:I:123:VAL:O	2.26	0.68
1:M:64:ILE:HG23	1:M:129:LEU:HD11	1.74	0.68
1:G:254:SER:HB3	1:L:243:ASN:CA	2.24	0.68
1:L:45:SER:HA	1:L:205:ARG:HG2	1.75	0.68
1:P:57:TYR:CE1	1:P:73:LEU:HD23	2.29	0.68
1:J:84:THR:CB	1:J:86:GLN:HG3	2.24	0.68
1:J:43:ALA:O	1:J:205:ARG:HG3	1.94	0.67
1:J:87:ILE:HD12	1:J:230:ILE:CG2	2.14	0.67
1:L:116:THR:HG22	1:L:117:ASN:H	1.58	0.67
1:I:129:LEU:CD2	1:I:191:PRO:HD3	2.24	0.67
1:H:185:PHE:HB2	1:H:189:HIS:CD2	2.30	0.67
1:L:116:THR:CG2	1:L:117:ASN:H	2.07	0.67
1:F:79:THR:HG21	1:F:177:GLY:N	2.09	0.67
1:B:129:LEU:CD2	1:B:191:PRO:HD3	2.25	0.67
1:E:49:LEU:HD21	1:E:56:LEU:HD22	1.76	0.67
1:A:70:PRO:HG2	1:A:71:ASN:H	1.58	0.67
1:F:64:ILE:CG2	1:F:69:SER:HB3	2.24	0.67

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:264:PHE:O	1:L:266:LEU:HG	1.95	0.67
1:E:283:ILE:HG22	1:H:268:LEU:HD21	1.76	0.66
1:P:194:ASN:HB3	1:P:197:GLU:HB2	1.77	0.66
1:G:116:THR:HG22	1:G:118:GLN:N	2.01	0.66
1:N:48:TRP:HH2	1:N:120:LEU:HD23	1.57	0.66
1:O:59:LEU:O	1:O:63:ARG:NH1	2.28	0.66
1:D:254:SER:HB2	1:O:244:ILE:O	1.93	0.66
1:I:188:ASN:OD1	1:K:119:ASN:ND2	2.28	0.66
1:N:76:ARG:HD2	1:N:198:ILE:CG2	2.25	0.66
1:I:48:TRP:HB2	1:I:118:GLN:HG3	1.79	0.65
1:B:150:ASN:ND2	1:K:207:GLU:OE1	2.30	0.65
1:H:59:LEU:O	1:H:63:ARG:NH1	2.29	0.65
1:I:133:ARG:NH2	1:K:137:PRO:O	2.29	0.65
1:L:44:ALA:O	1:L:205:ARG:NH1	2.30	0.65
1:K:182:ASN:HB2	1:K:195:GLN:O	1.96	0.65
1:L:116:THR:HG22	1:L:117:ASN:N	2.12	0.65
1:N:87:ILE:HD11	1:N:208:PHE:CD1	2.32	0.65
1:H:120:LEU:HD12	1:H:125:ASP:HB2	1.77	0.65
1:A:129:LEU:HD23	1:A:191:PRO:CG	2.27	0.65
1:O:63:ARG:CG	1:O:63:ARG:HH11	2.09	0.65
1:O:69:SER:CB	1:O:72:GLY:HA2	2.25	0.65
1:A:49:LEU:HD21	1:A:56:LEU:CD2	2.27	0.65
1:I:87:ILE:HD11	1:I:208:PHE:HE1	1.62	0.65
1:F:192:PHE:CG	1:G:137:PRO:HG2	2.32	0.64
1:N:46:LEU:HD21	1:N:116:THR:HA	1.77	0.64
1:A:48:TRP:CG	1:A:118:GLN:HG2	2.32	0.64
1:M:190:ASN:CB	1:M:191:PRO:HA	2.26	0.64
1:M:190:ASN:HB2	1:M:191:PRO:HA	1.77	0.64
1:M:182:ASN:HB2	1:M:195:GLN:O	1.96	0.64
1:F:63:ARG:O	1:F:65:PRO:HD3	1.96	0.64
1:H:65:PRO:O	1:H:68:ALA:HB3	1.97	0.64
1:B:194:ASN:O	1:B:197:GLU:N	2.28	0.64
1:K:129:LEU:HD23	1:K:191:PRO:HD3	1.80	0.64
1:E:46:LEU:HD11	1:E:113:PRO:HG2	1.79	0.64
1:J:123:VAL:CB	1:K:63:ARG:HH21	2.10	0.64
1:E:187:ARG:O	1:E:189:HIS:ND1	2.30	0.64
1:H:84:THR:OG1	1:H:86:GLN:HB2	1.98	0.64
1:I:87:ILE:HD11	1:I:208:PHE:CE1	2.33	0.64
1:B:84:THR:CB	1:B:86:GLN:HG3	2.28	0.64
1:E:68:ALA:HB1	1:E:129:LEU:HD21	1.78	0.64
1:M:76:ARG:HB3	1:M:79:THR:CG2	2.28	0.64

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:81:ASP:HB3	1:C:84:THR:OG1	1.98	0.64
1:E:55:LEU:HD23	1:G:55:LEU:HD23	1.80	0.64
1:M:133:ARG:NH1	1:M:190:ASN:HB2	2.13	0.64
1:F:87:ILE:HD12	1:F:230:ILE:CG1	2.25	0.63
1:I:123:VAL:HG21	1:L:63:ARG:HH11	1.62	0.63
1:I:43:ALA:HB2	1:I:176:PRO:CD	2.24	0.63
1:N:133:ARG:NH2	1:P:125:ASP:OD1	2.30	0.63
1:J:123:VAL:HB	1:K:63:ARG:HH21	1.64	0.63
1:G:194:ASN:ND2	1:G:197:GLU:HB2	2.13	0.63
1:I:48:TRP:CB	1:I:118:GLN:HG3	2.28	0.63
1:N:64:ILE:HG23	1:N:129:LEU:HD11	1.79	0.63
1:N:40:TRP:CZ2	1:N:57:TYR:HB2	2.33	0.63
1:J:123:VAL:CG1	1:K:63:ARG:HH21	2.11	0.63
1:E:283:ILE:HB	1:H:268:LEU:CD2	2.27	0.63
1:K:74:HIS:HD2	1:K:183:ALA:O	1.81	0.63
1:N:84:THR:CB	1:N:86:GLN:HG2	2.28	0.63
1:B:76:ARG:NH1	1:B:95:LEU:HD11	2.12	0.63
1:F:76:ARG:HD3	1:F:177:GLY:O	1.99	0.63
1:B:64:ILE:HG23	1:B:129:LEU:HD11	1.79	0.63
1:B:64:ILE:HG21	1:B:69:SER:HB3	1.81	0.62
1:F:49:LEU:HD22	1:F:202:GLY:HA3	1.79	0.62
1:M:194:ASN:O	1:M:197:GLU:N	2.28	0.62
1:A:120:LEU:O	1:A:122:PRO:HD3	1.99	0.62
1:A:55:LEU:HD12	1:A:55:LEU:O	1.98	0.62
1:N:59:LEU:CA	1:O:122:PRO:HG2	2.28	0.62
1:A:68:ALA:HB1	1:A:129:LEU:HD21	1.82	0.62
1:C:120:LEU:HD21	1:C:122:PRO:HG3	1.80	0.62
1:D:155:ILE:HG22	1:D:288:LEU:HD23	1.82	0.62
1:E:155:ILE:HG22	1:E:288:LEU:HD23	1.82	0.62
1:H:155:ILE:HG22	1:H:288:LEU:HD23	1.82	0.62
1:H:38:ASN:OD1	1:H:42:GLN:NE2	2.32	0.62
1:B:42:GLN:NE2	1:B:176:PRO:HG3	2.15	0.62
1:N:155:ILE:HG22	1:N:288:LEU:HD23	1.82	0.62
1:K:135:ASN:HD22	1:K:271:ASN:HD21	1.45	0.62
1:A:155:ILE:HG22	1:A:288:LEU:HD23	1.82	0.62
1:E:133:ARG:CD	1:E:190:ASN:HD21	2.05	0.62
1:J:182:ASN:HB2	1:J:195:GLN:O	1.99	0.62
1:M:155:ILE:HG22	1:M:288:LEU:HD23	1.82	0.62
1:G:155:ILE:HG22	1:G:288:LEU:HD23	1.82	0.62
1:G:264:PHE:HE2	1:L:236:ASN:HA	1.64	0.62
1:O:63:ARG:HH11	1:O:63:ARG:HG3	1.64	0.62

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:63:ARG:CG	1:A:63:ARG:HH11	2.03	0.61
1:B:155:ILE:HG22	1:B:288:LEU:HD23	1.82	0.61
1:C:135:ASN:ND2	1:C:271:ASN:HD21	1.96	0.61
1:I:133:ARG:NH1	1:I:190:ASN:ND2	2.47	0.61
1:K:262:LYS:HG2	1:K:270:TYR:CE1	2.35	0.61
1:I:40:TRP:CZ2	1:I:57:TYR:HB2	2.35	0.61
1:B:133:ARG:HE	1:B:190:ASN:ND2	1.98	0.61
1:F:129:LEU:CD2	1:F:191:PRO:HD3	2.30	0.61
1:B:76:ARG:HD3	1:B:177:GLY:O	2.00	0.61
1:F:155:ILE:HG22	1:F:288:LEU:HD23	1.82	0.61
1:J:155:ILE:HG22	1:J:288:LEU:HD23	1.82	0.61
1:D:39:THR:HA	1:D:42:GLN:HG3	1.83	0.61
1:E:43:ALA:O	1:E:205:ARG:HG3	2.00	0.61
1:M:64:ILE:HG12	1:M:129:LEU:CD1	2.31	0.61
1:O:56:LEU:O	1:O:60:ILE:HD12	2.00	0.61
1:E:39:THR:HG23	1:E:40:TRP:N	2.16	0.61
1:H:87:ILE:HD13	1:H:87:ILE:N	2.16	0.61
1:I:155:ILE:HG22	1:I:288:LEU:HD23	1.82	0.61
1:L:76:ARG:HD3	1:L:198:ILE:HG13	1.81	0.61
1:L:155:ILE:HG22	1:L:288:LEU:HD23	1.82	0.61
1:P:155:ILE:HG22	1:P:288:LEU:HD23	1.82	0.61
1:F:87:ILE:HD12	1:F:230:ILE:CG2	2.31	0.61
1:L:57:TYR:CE1	1:L:75:MET:HE3	2.36	0.61
1:C:155:ILE:HG22	1:C:288:LEU:HD23	1.82	0.61
1:K:155:ILE:HG22	1:K:288:LEU:HD23	1.82	0.61
1:C:62:THR:HG23	1:C:63:ARG:HG3	1.81	0.60
1:A:133:ARG:NH1	1:A:190:ASN:HB2	2.17	0.60
1:C:39:THR:HA	1:C:42:GLN:HG2	1.83	0.60
1:E:40:TRP:CE3	1:E:41:ILE:HG23	2.36	0.60
1:O:155:ILE:HG22	1:O:288:LEU:HD23	1.82	0.60
1:G:116:THR:N	1:G:119:ASN:OD1	2.33	0.60
1:O:78:GLN:O	1:O:88:GLN:HG3	2.00	0.60
1:B:65:PRO:HD2	1:B:129:LEU:CD1	2.31	0.60
1:F:64:ILE:HG21	1:F:69:SER:HB3	1.82	0.60
1:J:64:ILE:HG21	1:J:69:SER:HB3	1.82	0.60
1:B:65:PRO:HD2	1:B:129:LEU:HD13	1.82	0.60
1:G:261:SER:O	1:G:264:PHE:HB2	2.02	0.60
1:M:55:LEU:HD12	1:M:55:LEU:O	2.02	0.60
1:E:283:ILE:CB	1:H:268:LEU:HD21	2.31	0.60
1:I:190:ASN:ND2	1:I:191:PRO:HA	2.17	0.60
1:N:133:ARG:NE	1:N:190:ASN:ND2	2.48	0.60

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:87:ILE:HG13	1:B:230:ILE:HG21	1.84	0.59
1:P:84:THR:OG1	1:P:85:GLY:N	2.35	0.59
1:J:87:ILE:HD11	1:J:208:PHE:HE1	1.65	0.59
1:J:64:ILE:HG23	1:J:129:LEU:HD11	1.85	0.59
1:P:65:PRO:HD3	1:P:129:LEU:HD11	1.83	0.59
1:I:129:LEU:HD23	1:I:191:PRO:CD	2.33	0.59
1:N:121:SER:HA	1:O:62:THR:HG21	1.84	0.59
1:E:61:SER:HA	1:E:64:ILE:CD1	2.33	0.59
1:O:63:ARG:NH1	1:O:63:ARG:HG3	2.17	0.59
1:A:133:ARG:HD3	1:A:190:ASN:ND2	2.15	0.59
1:J:123:VAL:HG11	1:K:63:ARG:HH21	1.68	0.59
1:A:133:ARG:HH11	1:A:190:ASN:HB2	1.68	0.58
1:H:135:ASN:HD22	1:H:271:ASN:HD21	1.50	0.58
1:H:63:ARG:NH1	1:H:63:ARG:HG3	2.13	0.58
1:N:55:LEU:HD23	1:O:55:LEU:HD23	1.85	0.58
1:E:283:ILE:HB	1:H:268:LEU:HD21	1.83	0.58
1:J:129:LEU:HD23	1:J:191:PRO:CD	2.30	0.58
1:E:40:TRP:CD2	1:E:41:ILE:HG23	2.38	0.58
1:D:252:ASN:O	1:O:245:SER:CA	2.51	0.58
1:F:70:PRO:HG2	1:F:71:ASN:H	1.68	0.58
1:E:77:GLU:O	1:E:78:GLN:HB2	2.02	0.58
1:F:42:GLN:O	1:F:205:ARG:NH1	2.37	0.58
1:I:65:PRO:HA	1:J:65:PRO:HA	1.84	0.58
1:B:63:ARG:NH1	1:B:123:VAL:O	2.35	0.58
1:F:70:PRO:CG	1:F:71:ASN:H	2.15	0.58
1:O:58:GLN:O	1:O:62:THR:HG23	2.03	0.58
1:B:55:LEU:HD12	1:B:55:LEU:O	2.03	0.58
1:B:64:ILE:CD1	1:B:73:LEU:HD11	2.34	0.58
1:F:123:VAL:HG21	1:H:63:ARG:HD3	1.85	0.58
1:I:75:MET:HE2	1:I:75:MET:HA	1.85	0.58
1:M:43:ALA:HB2	1:M:176:PRO:HD2	1.86	0.58
1:B:43:ALA:O	1:B:205:ARG:HG3	2.04	0.58
1:G:254:SER:OG	1:G:255:GLU:HG3	2.04	0.58
1:H:190:ASN:CG	1:H:191:PRO:HD2	2.23	0.58
1:A:254:SER:OG	1:A:255:GLU:HG3	2.04	0.57
1:B:288:LEU:HD13	1:K:86:GLN:NE2	2.19	0.57
1:B:42:GLN:O	1:B:205:ARG:NH1	2.35	0.57
1:H:194:ASN:OD1	1:H:196:ASP:HB2	2.04	0.57
1:G:80:ILE:HG22	1:G:87:ILE:CD1	2.28	0.57
1:H:254:SER:OG	1:H:255:GLU:HG3	2.04	0.57
1:H:264:PHE:HB3	1:P:248:PHE:HD2	1.70	0.57

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:254:SER:OG	1:I:255:GLU:HG3	2.04	0.57
1:B:87:ILE:CD1	1:B:208:PHE:HE1	2.16	0.57
1:C:62:THR:CG2	1:C:63:ARG:HG3	2.34	0.57
1:D:254:SER:OG	1:D:255:GLU:HG3	2.04	0.57
1:M:68:ALA:HB1	1:M:129:LEU:HD21	1.86	0.57
1:B:122:PRO:HD2	1:B:123:VAL:H	1.70	0.57
1:B:254:SER:OG	1:B:255:GLU:HG3	2.04	0.57
1:O:194:ASN:HD21	1:O:196:ASP:HB2	1.68	0.57
1:E:254:SER:OG	1:E:255:GLU:HG3	2.04	0.57
1:I:84:THR:HB	1:I:86:GLN:HG2	1.87	0.57
1:K:254:SER:OG	1:K:255:GLU:HG3	2.04	0.57
1:P:254:SER:OG	1:P:255:GLU:HG3	2.05	0.57
1:B:49:LEU:CD1	1:B:202:GLY:HA3	2.35	0.57
1:J:56:LEU:O	1:J:60:ILE:HG13	2.05	0.57
1:A:79:THR:HG21	1:A:177:GLY:H	1.70	0.57
1:J:254:SER:OG	1:J:255:GLU:HG3	2.04	0.57
1:M:254:SER:OG	1:M:255:GLU:HG3	2.04	0.57
1:N:42:GLN:HG2	1:N:176:PRO:HG3	1.87	0.57
1:C:120:LEU:CD2	1:C:122:PRO:HG3	2.35	0.56
1:F:63:ARG:HE	1:F:127:HIS:CD2	2.22	0.56
1:L:116:THR:CG2	1:L:117:ASN:N	2.68	0.56
1:B:84:THR:HB	1:B:86:GLN:HG3	1.87	0.56
1:A:61:SER:HB2	1:A:73:LEU:HD12	1.87	0.56
1:C:40:TRP:CE2	1:C:41:ILE:HG23	2.39	0.56
1:F:254:SER:OG	1:F:255:GLU:HG3	2.04	0.56
1:N:254:SER:OG	1:N:255:GLU:HG3	2.04	0.56
1:B:192:PHE:CE2	1:C:137:PRO:HB2	2.40	0.56
1:C:254:SER:OG	1:C:255:GLU:HG3	2.05	0.56
1:C:65:PRO:HG2	1:C:68:ALA:HB2	1.86	0.56
1:K:61:SER:HA	1:K:64:ILE:HD12	1.86	0.56
1:F:81:ASP:OD1	1:F:83:ASN:HB2	2.05	0.56
1:O:254:SER:OG	1:O:255:GLU:HG3	2.04	0.56
1:G:116:THR:HG22	1:G:117:ASN:N	2.21	0.56
1:K:42:GLN:O	1:K:42:GLN:HG2	2.04	0.56
1:L:254:SER:OG	1:L:255:GLU:HG3	2.04	0.56
1:M:65:PRO:HA	1:N:64:ILE:O	2.06	0.56
1:H:118:GLN:HG3	1:H:118:GLN:O	2.04	0.56
1:B:133:ARG:HG3	1:B:190:ASN:HD21	1.71	0.56
1:B:63:ARG:O	1:B:65:PRO:HD3	2.06	0.56
1:K:129:LEU:HD23	1:K:191:PRO:CD	2.36	0.56
1:C:76:ARG:HD3	1:C:198:ILE:HG13	1.88	0.56

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:116:THR:CG2	1:D:117:ASN:N	2.69	0.56
1:F:129:LEU:HD23	1:F:191:PRO:HG3	1.88	0.56
1:C:264:PHE:HB3	1:K:248:PHE:CD2	2.41	0.56
1:B:49:LEU:O	1:B:49:LEU:HD23	2.06	0.56
1:I:123:VAL:HG21	1:L:63:ARG:NH1	2.20	0.56
1:F:87:ILE:HD11	1:F:208:PHE:CE1	2.42	0.55
1:A:65:PRO:HB3	1:B:62:THR:O	2.07	0.55
1:B:84:THR:OG1	1:B:86:GLN:HG3	2.05	0.55
1:C:264:PHE:HB3	1:K:248:PHE:HD2	1.70	0.55
1:P:190:ASN:HA	1:P:192:PHE:H	1.72	0.55
1:B:188:ASN:HD21	1:C:119:ASN:ND2	2.03	0.55
1:I:59:LEU:HA	1:L:122:PRO:HG2	1.88	0.55
1:O:87:ILE:HD11	1:O:208:PHE:HE1	1.70	0.55
1:E:43:ALA:HB2	1:E:176:PRO:HD2	1.88	0.55
1:F:45:SER:OG	1:F:112:ILE:HG12	2.06	0.55
1:F:43:ALA:O	1:F:205:ARG:HG3	2.07	0.55
1:F:55:LEU:HG	1:H:55:LEU:HD23	1.87	0.55
1:A:87:ILE:HD12	1:A:176:PRO:HD3	1.88	0.55
1:H:197:GLU:O	1:H:198:ILE:HD13	2.07	0.55
1:L:57:TYR:HE1	1:L:75:MET:HE3	1.72	0.55
1:N:197:GLU:O	1:N:198:ILE:HD13	2.07	0.55
1:D:197:GLU:O	1:D:198:ILE:HD13	2.07	0.55
1:I:133:ARG:NH1	1:I:190:ASN:HD22	2.05	0.55
1:I:197:GLU:O	1:I:198:ILE:HD13	2.07	0.55
1:J:197:GLU:O	1:J:198:ILE:HD13	2.07	0.55
1:K:158:TRP:CG	1:K:194:ASN:ND2	2.75	0.55
1:L:197:GLU:O	1:L:198:ILE:HD13	2.07	0.55
1:D:116:THR:HG22	1:D:118:GLN:N	2.06	0.55
1:E:87:ILE:HD11	1:E:208:PHE:HE1	1.72	0.55
1:D:67:PHE:CD1	1:D:68:ALA:N	2.75	0.55
1:F:197:GLU:O	1:F:198:ILE:HD13	2.07	0.55
1:F:64:ILE:HG21	1:F:69:SER:CB	2.37	0.55
1:K:192:PHE:N	1:K:193:PRO:HD3	2.21	0.55
1:N:158:TRP:CD1	1:N:194:ASN:ND2	2.75	0.55
1:E:197:GLU:O	1:E:198:ILE:HD13	2.07	0.55
1:P:197:GLU:O	1:P:198:ILE:HD13	2.07	0.55
1:B:80:ILE:HG13	1:B:80:ILE:O	2.06	0.54
1:F:81:ASP:HB3	1:F:84:THR:HB	1.90	0.54
1:K:197:GLU:O	1:K:198:ILE:HD13	2.07	0.54
1:A:64:ILE:HG12	1:A:129:LEU:HD12	1.89	0.54
1:C:278:ALA:HB3	1:C:279:PRO:HD3	1.90	0.54

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:197:GLU:O	1:M:198:ILE:HD13	2.07	0.54
1:N:120:LEU:O	1:N:122:PRO:HD3	2.06	0.54
1:P:40:TRP:CE3	1:P:75:MET:HE1	2.42	0.54
1:P:61:SER:HA	1:P:64:ILE:HD12	1.89	0.54
1:B:197:GLU:O	1:B:198:ILE:HD13	2.07	0.54
1:P:64:ILE:CD1	1:P:73:LEU:HD13	2.34	0.54
1:A:48:TRP:CD2	1:A:118:GLN:HG2	2.43	0.54
1:I:247:VAL:HG12	1:I:248:PHE:N	2.23	0.54
1:K:247:VAL:HG12	1:K:248:PHE:N	2.23	0.54
1:O:278:ALA:HB3	1:O:279:PRO:HD3	1.90	0.54
1:C:186:SER:C	1:C:188:ASN:H	2.10	0.54
1:I:182:ASN:HB2	1:I:195:GLN:O	2.07	0.54
1:I:278:ALA:HB3	1:I:279:PRO:HD3	1.90	0.54
1:O:197:GLU:O	1:O:198:ILE:HD13	2.07	0.54
1:A:247:VAL:HG12	1:A:248:PHE:N	2.23	0.54
1:B:192:PHE:CG	1:C:137:PRO:HG2	2.42	0.54
1:C:247:VAL:HG12	1:C:248:PHE:N	2.23	0.54
1:D:278:ALA:HB3	1:D:279:PRO:HD3	1.90	0.54
1:G:197:GLU:O	1:G:198:ILE:HD13	2.07	0.54
1:J:68:ALA:HB1	1:J:129:LEU:HD21	1.88	0.54
1:J:283:ILE:O	1:L:268:LEU:HD13	2.07	0.54
1:J:40:TRP:CE3	1:J:75:MET:HE2	2.43	0.54
1:K:81:ASP:HB3	1:K:84:THR:OG1	2.07	0.54
1:L:278:ALA:HB3	1:L:279:PRO:HD3	1.90	0.54
1:P:65:PRO:CD	1:P:129:LEU:HD11	2.38	0.54
1:A:79:THR:HG21	1:A:177:GLY:N	2.22	0.54
1:E:116:THR:HG23	1:E:116:THR:O	2.08	0.54
1:G:247:VAL:HG12	1:G:248:PHE:N	2.23	0.54
1:K:278:ALA:HB3	1:K:279:PRO:HD3	1.90	0.54
1:L:247:VAL:HG12	1:L:248:PHE:N	2.23	0.54
1:M:247:VAL:HG12	1:M:248:PHE:N	2.23	0.54
1:E:188:ASN:O	1:H:119:ASN:HB2	2.08	0.54
1:F:192:PHE:CD1	1:G:137:PRO:HG2	2.43	0.54
1:G:278:ALA:HB3	1:G:279:PRO:HD3	1.90	0.54
1:A:49:LEU:HD13	1:A:202:GLY:HA3	1.89	0.54
1:B:247:VAL:HG12	1:B:248:PHE:N	2.23	0.54
1:C:118:GLN:HG3	1:C:118:GLN:O	2.08	0.54
1:C:197:GLU:O	1:C:198:ILE:HD13	2.07	0.54
1:E:40:TRP:HA	1:E:177:GLY:HA3	1.90	0.54
1:N:74:HIS:HD2	1:N:183:ALA:O	1.91	0.54
1:A:197:GLU:O	1:A:198:ILE:HD13	2.07	0.53

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:278:ALA:HB3	1:A:279:PRO:HD3	1.90	0.53
1:E:56:LEU:O	1:E:59:LEU:HB3	2.09	0.53
1:F:278:ALA:HB3	1:F:279:PRO:HD3	1.90	0.53
1:I:122:PRO:O	1:I:126:THR:HG23	2.07	0.53
1:K:40:TRP:CZ2	1:K:57:TYR:HB2	2.42	0.53
1:E:79:THR:HG21	1:E:177:GLY:H	1.72	0.53
1:E:97:ARG:NH1	1:E:99:ASP:OD2	2.41	0.53
1:H:115:VAL:HB	1:H:138:SER:C	2.28	0.53
1:C:194:ASN:C	1:C:196:ASP:H	2.10	0.53
1:E:190:ASN:CG	1:E:191:PRO:HA	2.28	0.53
1:H:97:ARG:NH1	1:H:99:ASP:OD2	2.41	0.53
1:J:112:ILE:HG22	1:J:116:THR:HG22	1.90	0.53
1:B:278:ALA:HB3	1:B:279:PRO:HD3	1.90	0.53
1:H:115:VAL:HB	1:H:138:SER:O	2.08	0.53
1:H:278:ALA:HB3	1:H:279:PRO:HD3	1.90	0.53
1:C:87:ILE:HD11	1:C:230:ILE:HG21	1.87	0.53
1:D:97:ARG:NH1	1:D:99:ASP:OD2	2.42	0.53
1:F:79:THR:CG2	1:F:177:GLY:H	2.20	0.53
1:M:60:ILE:HG12	1:M:126:THR:HB	1.90	0.53
1:N:247:VAL:HG12	1:N:248:PHE:N	2.23	0.53
1:P:278:ALA:HB3	1:P:279:PRO:HD3	1.90	0.53
1:E:278:ALA:HB3	1:E:279:PRO:HD3	1.90	0.53
1:F:129:LEU:HD23	1:F:191:PRO:CD	2.38	0.53
1:F:97:ARG:NH1	1:F:99:ASP:OD2	2.42	0.53
1:H:247:VAL:HG12	1:H:248:PHE:N	2.23	0.53
1:K:120:LEU:HD12	1:K:125:ASP:HB2	1.91	0.53
1:K:73:LEU:HD21	1:K:179:ILE:HG23	1.91	0.53
1:L:97:ARG:NH1	1:L:99:ASP:OD2	2.41	0.53
1:O:97:ARG:NH1	1:O:99:ASP:OD2	2.42	0.53
1:P:87:ILE:N	1:P:87:ILE:HD13	2.22	0.53
1:E:49:LEU:HD23	1:E:49:LEU:C	2.29	0.53
1:F:87:ILE:HD13	1:F:230:ILE:HG21	1.90	0.53
1:J:247:VAL:HG12	1:J:248:PHE:N	2.23	0.53
1:J:278:ALA:HB3	1:J:279:PRO:HD3	1.90	0.53
1:N:97:ARG:NH1	1:N:99:ASP:OD2	2.42	0.53
1:O:44:ALA:O	1:O:205:ARG:NH1	2.37	0.53
1:O:63:ARG:HB2	1:O:63:ARG:HH11	1.73	0.53
1:C:97:ARG:NH1	1:C:99:ASP:OD2	2.41	0.53
1:P:97:ARG:NH1	1:P:99:ASP:OD2	2.42	0.53
1:I:64:ILE:O	1:J:65:PRO:HA	2.09	0.53
1:I:97:ARG:NH1	1:I:99:ASP:OD2	2.41	0.53

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:97:ARG:NH1	1:K:99:ASP:OD2	2.42	0.53
1:O:247:VAL:HG12	1:O:248:PHE:N	2.23	0.53
1:P:247:VAL:HG12	1:P:248:PHE:N	2.23	0.53
1:B:97:ARG:NH1	1:B:99:ASP:OD2	2.42	0.53
1:F:46:LEU:HD11	1:F:115:VAL:O	2.09	0.53
1:G:116:THR:CG2	1:G:117:ASN:N	2.72	0.53
1:G:97:ARG:NH1	1:G:99:ASP:OD2	2.42	0.53
1:I:63:ARG:CD	1:L:123:VAL:HG21	2.19	0.53
1:M:278:ALA:HB3	1:M:279:PRO:HD3	1.90	0.53
1:D:254:SER:HB3	1:O:244:ILE:H	1.74	0.53
1:A:80:ILE:HD11	1:A:176:PRO:HB3	1.91	0.52
1:D:247:VAL:HG12	1:D:248:PHE:N	2.23	0.52
1:J:97:ARG:NH1	1:J:99:ASP:OD2	2.42	0.52
1:N:80:ILE:HD13	1:N:87:ILE:HA	1.91	0.52
1:C:76:ARG:NH2	1:C:175:ALA:O	2.42	0.52
1:E:247:VAL:HG12	1:E:248:PHE:N	2.23	0.52
1:K:76:ARG:NH2	1:K:79:THR:HG22	2.24	0.52
1:M:59:LEU:HD13	1:P:122:PRO:HB2	1.91	0.52
1:A:97:ARG:NH1	1:A:99:ASP:OD2	2.41	0.52
1:E:63:ARG:NH1	1:E:123:VAL:O	2.28	0.52
1:I:55:LEU:HD23	1:L:55:LEU:HD23	1.90	0.52
1:M:97:ARG:NH1	1:M:99:ASP:OD2	2.41	0.52
1:O:78:GLN:OE1	1:O:78:GLN:HA	2.09	0.52
1:C:70:PRO:HG2	1:C:71:ASN:H	1.74	0.52
1:L:40:TRP:CE3	1:L:41:ILE:HG23	2.43	0.52
1:M:45:SER:HA	1:M:205:ARG:HG2	1.90	0.52
1:P:115:VAL:HG11	1:P:120:LEU:HD12	1.90	0.52
1:I:79:THR:OG1	1:I:176:PRO:HA	2.09	0.52
1:K:192:PHE:N	1:K:192:PHE:CD2	2.77	0.52
1:N:278:ALA:HB3	1:N:279:PRO:HD3	1.90	0.52
1:C:40:TRP:CZ2	1:C:41:ILE:HD13	2.44	0.52
1:E:120:LEU:O	1:E:122:PRO:HD3	2.10	0.52
1:F:247:VAL:HG12	1:F:248:PHE:N	2.23	0.52
1:A:189:HIS:CD2	1:D:119:ASN:HB2	2.45	0.52
1:D:70:PRO:CG	1:D:71:ASN:H	2.22	0.52
1:G:40:TRP:HB3	1:G:75:MET:HG3	1.91	0.52
1:I:46:LEU:CD1	1:I:202:GLY:HA2	2.31	0.52
1:D:44:ALA:O	1:D:205:ARG:NH1	2.41	0.52
1:F:64:ILE:HG22	1:F:69:SER:HB3	1.91	0.52
1:L:56:LEU:HD12	1:L:56:LEU:C	2.28	0.52
1:L:57:TYR:CE1	1:L:75:MET:CE	2.93	0.52

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:79:THR:HG21	1:M:177:GLY:H	1.75	0.52
1:B:58:GLN:NE2	1:D:120:LEU:O	2.43	0.51
1:L:40:TRP:CD2	1:L:41:ILE:HG23	2.45	0.51
1:M:48:TRP:HH2	1:M:120:LEU:HD23	1.75	0.51
1:H:265:ILE:HG22	1:H:267:ASP:HB2	1.92	0.51
1:N:42:GLN:HG2	1:N:176:PRO:CG	2.40	0.51
1:A:79:THR:HB	1:A:176:PRO:HA	1.91	0.51
1:F:46:LEU:HG	1:F:113:PRO:HD2	1.93	0.51
1:F:122:PRO:HG2	1:H:59:LEU:HA	1.93	0.51
1:E:65:PRO:HA	1:F:65:PRO:HA	1.92	0.51
1:G:87:ILE:HD11	1:G:176:PRO:CB	2.38	0.51
1:I:48:TRP:CG	1:I:118:GLN:HG3	2.46	0.51
1:I:76:ARG:HD2	1:I:198:ILE:HG13	1.93	0.51
1:N:56:LEU:HD11	1:N:60:ILE:HD11	1.93	0.51
1:O:66:SER:O	1:O:69:SER:O	2.28	0.51
1:A:122:PRO:HG2	1:C:59:LEU:CA	2.39	0.51
1:B:45:SER:HA	1:B:205:ARG:HG2	1.92	0.51
1:H:133:ARG:HG3	1:H:133:ARG:O	2.09	0.51
1:I:150:ASN:OD1	1:I:150:ASN:N	2.44	0.51
1:J:122:PRO:HB2	1:K:59:LEU:HD13	1.93	0.51
1:J:40:TRP:HB2	1:J:75:MET:HE2	1.93	0.51
1:K:133:ARG:HG3	1:K:191:PRO:CB	2.25	0.51
1:N:181:ILE:HG21	1:N:193:PRO:HB2	1.92	0.51
1:P:181:ILE:HG21	1:P:193:PRO:HB2	1.92	0.51
1:A:150:ASN:N	1:A:150:ASN:OD1	2.44	0.51
1:H:194:ASN:C	1:H:196:ASP:H	2.12	0.51
1:K:150:ASN:OD1	1:K:150:ASN:N	2.44	0.51
1:J:69:SER:HB2	1:J:184:SER:O	2.11	0.51
1:I:46:LEU:HD12	1:I:202:GLY:CA	2.33	0.51
1:J:67:PHE:CZ	1:J:189:HIS:CD2	2.99	0.51
1:N:150:ASN:OD1	1:N:150:ASN:N	2.44	0.51
1:B:181:ILE:HG21	1:B:193:PRO:HB2	1.93	0.50
1:B:87:ILE:HD12	1:B:208:PHE:HE1	1.76	0.50
1:F:250:HIS:O	1:F:253:HIS:HB2	2.12	0.50
1:E:250:HIS:O	1:E:253:HIS:HB2	2.12	0.50
1:H:264:PHE:CB	1:P:248:PHE:CD2	2.93	0.50
1:M:129:LEU:HD23	1:M:191:PRO:HD3	1.94	0.50
1:D:254:SER:HA	1:O:246:LYS:HB2	1.93	0.50
1:A:48:TRP:CG	1:A:118:GLN:CG	2.94	0.50
1:C:120:LEU:HD12	1:C:125:ASP:HB2	1.93	0.50
1:E:288:LEU:HD13	1:P:86:GLN:HE21	1.77	0.50

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:40:TRP:HA	1:J:177:GLY:HA3	1.94	0.50
1:K:250:HIS:O	1:K:253:HIS:HB2	2.12	0.50
1:K:73:LEU:HD21	1:K:179:ILE:CG2	2.41	0.50
1:N:250:HIS:O	1:N:253:HIS:HB2	2.12	0.50
1:F:87:ILE:O	1:F:89:ILE:HG13	2.12	0.50
1:I:250:HIS:O	1:I:253:HIS:HB2	2.12	0.50
1:G:264:PHE:CE2	1:L:236:ASN:HA	2.45	0.50
1:M:250:HIS:O	1:M:253:HIS:HB2	2.12	0.50
1:O:45:SER:HA	1:O:205:ARG:HG2	1.94	0.50
1:P:63:ARG:NH2	1:P:126:THR:OG1	2.44	0.50
1:C:150:ASN:N	1:C:150:ASN:OD1	2.44	0.50
1:G:250:HIS:O	1:G:253:HIS:HB2	2.12	0.50
1:H:262:LYS:C	1:H:264:PHE:H	2.14	0.50
1:L:182:ASN:HB2	1:L:195:GLN:O	2.11	0.50
1:N:49:LEU:HD13	1:N:202:GLY:HA3	1.93	0.50
1:C:39:THR:HA	1:C:42:GLN:CG	2.41	0.49
1:E:129:LEU:HD23	1:E:191:PRO:CG	2.42	0.49
1:E:192:PHE:CD1	1:H:137:PRO:HG2	2.47	0.49
1:E:49:LEU:HD21	1:E:56:LEU:CD2	2.40	0.49
1:F:181:ILE:HG21	1:F:193:PRO:HB2	1.93	0.49
1:H:185:PHE:CB	1:H:189:HIS:HD2	2.18	0.49
1:B:49:LEU:C	1:B:49:LEU:HD23	2.33	0.49
1:D:40:TRP:HA	1:D:177:GLY:HA3	1.94	0.49
1:J:250:HIS:O	1:J:253:HIS:HB2	2.12	0.49
1:L:250:HIS:O	1:L:253:HIS:HB2	2.12	0.49
1:M:79:THR:HB	1:M:176:PRO:HA	1.94	0.49
1:F:61:SER:HB3	1:F:73:LEU:HD23	1.95	0.49
1:P:250:HIS:O	1:P:253:HIS:HB2	2.12	0.49
1:D:250:HIS:O	1:D:253:HIS:HB2	2.12	0.49
1:I:63:ARG:NH1	1:I:63:ARG:HG2	2.28	0.49
1:J:75:MET:HE3	1:J:179:ILE:HG13	1.95	0.49
1:K:158:TRP:CD1	1:K:194:ASN:ND2	2.80	0.49
1:I:123:VAL:CG2	1:L:63:ARG:NH1	2.75	0.49
1:O:250:HIS:O	1:O:253:HIS:HB2	2.12	0.49
1:P:39:THR:HA	1:P:42:GLN:HB2	1.93	0.49
1:M:74:HIS:HD2	1:M:183:ALA:O	1.95	0.49
1:B:232:PRO:HA	1:B:235:LEU:HG	1.95	0.49
1:E:192:PHE:N	1:E:193:PRO:HD3	2.28	0.49
1:F:87:ILE:HD11	1:F:208:PHE:HE1	1.78	0.49
1:M:57:TYR:CD2	1:M:57:TYR:C	2.86	0.49
1:I:76:ARG:HH21	1:I:93:HIS:HB3	1.76	0.49

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:64:ILE:HG12	1:J:129:LEU:CD1	2.43	0.49
1:K:232:PRO:HA	1:K:235:LEU:HG	1.95	0.49
1:P:40:TRP:CE3	1:P:75:MET:CE	2.96	0.49
1:A:250:HIS:O	1:A:253:HIS:HB2	2.12	0.49
1:B:250:HIS:O	1:B:253:HIS:HB2	2.12	0.49
1:F:232:PRO:HA	1:F:235:LEU:HG	1.95	0.49
1:H:250:HIS:O	1:H:253:HIS:HB2	2.12	0.49
1:H:104:ASN:HB2	1:H:256:GLY:O	2.13	0.49
1:H:265:ILE:HG22	1:H:267:ASP:CB	2.42	0.49
1:L:150:ASN:OD1	1:L:150:ASN:N	2.44	0.49
1:L:232:PRO:HA	1:L:235:LEU:HG	1.95	0.49
1:A:70:PRO:HG2	1:A:71:ASN:ND2	2.28	0.49
1:A:77:GLU:O	1:A:78:GLN:HB2	2.13	0.49
1:B:104:ASN:HB2	1:B:256:GLY:O	2.13	0.49
1:C:250:HIS:O	1:C:253:HIS:HB2	2.12	0.49
1:G:254:SER:OG	1:L:242:SER:HA	2.12	0.49
1:I:59:LEU:HD21	1:I:126:THR:HG21	1.93	0.49
1:J:115:VAL:HG23	1:J:138:SER:O	2.13	0.49
1:J:69:SER:OG	1:J:69:SER:O	2.27	0.49
1:K:104:ASN:HB2	1:K:256:GLY:O	2.13	0.49
1:O:232:PRO:HA	1:O:235:LEU:HG	1.95	0.49
1:N:55:LEU:CD2	1:O:55:LEU:HD23	2.43	0.49
1:A:192:PHE:CG	1:D:137:PRO:HG2	2.48	0.48
1:B:48:TRP:HB2	1:B:118:GLN:HG3	1.95	0.48
1:E:79:THR:HG21	1:E:177:GLY:N	2.28	0.48
1:I:232:PRO:HA	1:I:235:LEU:HG	1.95	0.48
1:J:112:ILE:HG22	1:J:116:THR:CG2	2.42	0.48
1:O:84:THR:OG1	1:O:86:GLN:HG2	2.13	0.48
1:P:232:PRO:HA	1:P:235:LEU:HG	1.95	0.48
1:P:59:LEU:HD12	1:P:63:ARG:HH12	1.77	0.48
1:E:104:ASN:HB2	1:E:256:GLY:O	2.13	0.48
1:E:79:THR:OG1	1:E:176:PRO:HA	2.13	0.48
1:G:76:ARG:HD3	1:G:198:ILE:HG13	1.94	0.48
1:K:81:ASP:HB3	1:K:84:THR:HG1	1.78	0.48
1:M:63:ARG:NH1	1:M:123:VAL:O	2.34	0.48
1:P:190:ASN:HB2	1:P:191:PRO:CA	2.32	0.48
1:E:232:PRO:HA	1:E:235:LEU:HG	1.95	0.48
1:J:60:ILE:HG12	1:J:126:THR:HB	1.95	0.48
1:F:63:ARG:HH11	1:H:123:VAL:HG21	1.79	0.48
1:O:63:ARG:CB	1:O:63:ARG:HH11	2.25	0.48
1:C:104:ASN:HB2	1:C:256:GLY:O	2.13	0.48

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:40:TRP:CE3	1:D:41:ILE:CG2	2.96	0.48
1:G:158:TRP:CD1	1:G:194:ASN:HB3	2.48	0.48
1:J:123:VAL:HG11	1:K:63:ARG:NH2	2.29	0.48
1:K:81:ASP:OD1	1:K:84:THR:HG23	2.14	0.48
1:M:104:ASN:HB2	1:M:256:GLY:O	2.13	0.48
1:M:49:LEU:HD22	1:M:202:GLY:HA3	1.95	0.48
1:P:182:ASN:HB2	1:P:195:GLN:O	2.11	0.48
1:P:242:SER:O	1:P:243:ASN:HB2	2.14	0.48
1:B:69:SER:OG	1:B:69:SER:O	2.26	0.48
1:D:129:LEU:HD23	1:D:191:PRO:CD	2.44	0.48
1:F:242:SER:O	1:F:243:ASN:HB2	2.14	0.48
1:H:242:SER:O	1:H:243:ASN:HB2	2.14	0.48
1:H:40:TRP:CH2	1:H:57:TYR:HA	2.48	0.48
1:I:45:SER:CB	1:I:205:ARG:HG2	2.43	0.48
1:B:46:LEU:HA	1:B:46:LEU:HD23	1.53	0.48
1:D:40:TRP:CZ3	1:D:41:ILE:CG2	2.97	0.48
1:G:242:SER:O	1:G:243:ASN:HB2	2.14	0.48
1:H:259:MET:CG	1:H:264:PHE:CE2	2.96	0.48
1:I:242:SER:O	1:I:243:ASN:HB2	2.14	0.48
1:M:242:SER:O	1:M:243:ASN:HB2	2.14	0.48
1:P:104:ASN:HB2	1:P:256:GLY:O	2.13	0.48
1:B:242:SER:O	1:B:243:ASN:HB2	2.14	0.48
1:C:65:PRO:HB3	1:C:67:PHE:CE2	2.48	0.48
1:G:39:THR:CA	1:G:42:GLN:HG3	2.42	0.48
1:N:104:ASN:HB2	1:N:256:GLY:O	2.13	0.48
1:H:265:ILE:C	1:H:267:ASP:H	2.16	0.48
1:K:192:PHE:N	1:K:192:PHE:HD2	2.12	0.48
1:D:232:PRO:HA	1:D:235:LEU:HG	1.95	0.48
1:F:104:ASN:HB2	1:F:256:GLY:O	2.13	0.48
1:G:232:PRO:HA	1:G:235:LEU:HG	1.95	0.48
1:H:232:PRO:HA	1:H:235:LEU:HG	1.95	0.48
1:I:104:ASN:HB2	1:I:256:GLY:O	2.13	0.48
1:J:242:SER:O	1:J:243:ASN:HB2	2.14	0.48
1:J:104:ASN:HB2	1:J:256:GLY:O	2.13	0.48
1:L:104:ASN:HB2	1:L:256:GLY:O	2.13	0.48
1:M:133:ARG:NH1	1:M:190:ASN:CB	2.75	0.48
1:N:80:ILE:CG2	1:N:81:ASP:N	2.76	0.48
1:O:104:ASN:HB2	1:O:256:GLY:O	2.13	0.48
1:P:64:ILE:HA	1:P:129:LEU:HD11	1.96	0.48
1:C:264:PHE:CB	1:K:248:PHE:CD2	2.97	0.47
1:J:232:PRO:HA	1:J:235:LEU:HG	1.95	0.47

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:48:TRP:HB2	1:A:118:GLN:HE21	1.79	0.47
1:C:242:SER:O	1:C:243:ASN:HB2	2.14	0.47
1:F:120:LEU:O	1:F:120:LEU:HD13	2.13	0.47
1:K:40:TRP:CE3	1:K:75:MET:CE	2.97	0.47
1:P:150:ASN:N	1:P:150:ASN:OD1	2.44	0.47
1:P:40:TRP:CE3	1:P:41:ILE:HG23	2.50	0.47
1:B:87:ILE:HD12	1:B:208:PHE:CE1	2.49	0.47
1:N:80:ILE:HG22	1:N:81:ASP:N	2.28	0.47
1:P:65:PRO:HD3	1:P:129:LEU:HD13	1.95	0.47
1:C:232:PRO:HA	1:C:235:LEU:HG	1.95	0.47
1:D:39:THR:HA	1:D:42:GLN:CG	2.44	0.47
1:G:120:LEU:CD1	1:G:125:ASP:HB2	2.44	0.47
1:G:104:ASN:HB2	1:G:256:GLY:O	2.13	0.47
1:I:63:ARG:HH11	1:I:63:ARG:HG2	1.78	0.47
1:N:242:SER:O	1:N:243:ASN:HB2	2.14	0.47
1:A:242:SER:O	1:A:243:ASN:HB2	2.14	0.47
1:A:60:ILE:HG22	1:A:73:LEU:HD11	1.95	0.47
1:B:41:ILE:HG22	1:B:201:PRO:O	2.15	0.47
1:C:70:PRO:CG	1:C:71:ASN:H	2.26	0.47
1:D:242:SER:O	1:D:243:ASN:HB2	2.14	0.47
1:E:133:ARG:NH1	1:E:190:ASN:HD22	2.10	0.47
1:I:43:ALA:H	1:I:176:PRO:HG2	1.79	0.47
1:I:189:HIS:CD2	1:K:119:ASN:HB2	2.50	0.47
1:K:89:ILE:O	1:K:89:ILE:HG22	2.15	0.47
1:O:65:PRO:HG2	1:O:68:ALA:HB3	1.96	0.47
1:O:89:ILE:HG22	1:O:89:ILE:O	2.15	0.47
1:A:188:ASN:O	1:D:119:ASN:ND2	2.43	0.47
1:A:190:ASN:ND2	1:A:191:PRO:HA	2.30	0.47
1:A:104:ASN:HB2	1:A:256:GLY:O	2.13	0.47
1:D:104:ASN:HB2	1:D:256:GLY:O	2.13	0.47
1:F:41:ILE:HG22	1:F:201:PRO:HB2	1.97	0.47
1:F:89:ILE:HG22	1:F:89:ILE:O	2.15	0.47
1:G:70:PRO:HD2	1:G:71:ASN:H	1.80	0.47
1:I:89:ILE:HG22	1:I:89:ILE:O	2.15	0.47
1:J:40:TRP:CE3	1:J:75:MET:CE	2.97	0.47
1:K:60:ILE:HG22	1:K:61:SER:N	2.29	0.47
1:B:288:LEU:CD1	1:K:86:GLN:NE2	2.78	0.47
1:M:232:PRO:HA	1:M:235:LEU:HG	1.95	0.47
1:N:124:GLU:HG2	1:N:124:GLU:H	1.57	0.47
1:C:120:LEU:HG	1:C:121:SER:N	2.29	0.47
1:E:89:ILE:HG22	1:E:89:ILE:O	2.15	0.47

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:188:ASN:C	1:I:189:HIS:HD2	2.18	0.47
1:L:242:SER:O	1:L:243:ASN:HB2	2.14	0.47
1:L:89:ILE:HG22	1:L:89:ILE:O	2.15	0.47
1:N:48:TRP:CZ3	1:N:120:LEU:HD23	2.49	0.47
1:P:115:VAL:CG1	1:P:120:LEU:HD12	2.44	0.47
1:A:232:PRO:HA	1:A:235:LEU:HG	1.95	0.47
1:D:142:SER:OG	1:D:197:GLU:OE2	2.27	0.47
1:H:89:ILE:HG22	1:H:89:ILE:O	2.15	0.47
1:N:40:TRP:HA	1:N:177:GLY:HA3	1.97	0.47
1:N:232:PRO:HA	1:N:235:LEU:HG	1.95	0.47
1:N:89:ILE:O	1:N:89:ILE:HG22	2.15	0.47
1:C:190:ASN:OD1	1:C:191:PRO:HD2	2.15	0.47
1:D:89:ILE:O	1:D:89:ILE:HG22	2.15	0.47
1:F:73:LEU:HG	1:F:75:MET:HE2	1.95	0.47
1:J:133:ARG:NH1	1:J:192:PHE:HE2	2.12	0.47
1:J:89:ILE:HG22	1:J:89:ILE:O	2.15	0.47
1:O:242:SER:O	1:O:243:ASN:HB2	2.14	0.47
1:E:242:SER:O	1:E:243:ASN:HB2	2.14	0.47
1:E:64:ILE:H	1:E:64:ILE:HD12	1.79	0.47
1:F:129:LEU:HD23	1:F:191:PRO:CG	2.44	0.47
1:H:150:ASN:N	1:H:150:ASN:OD1	2.44	0.47
1:L:43:ALA:O	1:L:205:ARG:HG3	2.15	0.47
1:M:40:TRP:CZ2	1:M:57:TYR:HB2	2.49	0.47
1:O:150:ASN:N	1:O:150:ASN:OD1	2.44	0.47
1:P:133:ARG:HB2	1:P:191:PRO:HB3	1.97	0.47
1:C:98:TRP:CH2	1:C:170:ARG:HD2	2.50	0.46
1:D:70:PRO:HG2	1:D:71:ASN:H	1.80	0.46
1:G:147:ARG:HD3	1:G:156:THR:O	2.16	0.46
1:H:98:TRP:CH2	1:H:170:ARG:HD2	2.51	0.46
1:I:142:SER:OG	1:I:197:GLU:OE2	2.27	0.46
1:I:68:ALA:O	1:I:185:PHE:HA	2.15	0.46
1:K:147:ARG:HD3	1:K:156:THR:O	2.16	0.46
1:O:81:ASP:OD1	1:O:82:SER:N	2.47	0.46
1:P:64:ILE:HA	1:P:129:LEU:CD1	2.46	0.46
1:A:122:PRO:HB2	1:C:59:LEU:HD13	1.97	0.46
1:C:89:ILE:HG22	1:C:89:ILE:O	2.15	0.46
1:D:40:TRP:HB2	1:D:75:MET:SD	2.55	0.46
1:E:147:ARG:HD3	1:E:156:THR:O	2.16	0.46
1:E:133:ARG:CD	1:E:190:ASN:ND2	2.73	0.46
1:H:59:LEU:HD21	1:H:122:PRO:HB3	1.96	0.46
1:I:188:ASN:O	1:I:189:HIS:HD2	1.99	0.46

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:98:TRP:CH2	1:K:170:ARG:HD2	2.50	0.46
1:K:190:ASN:CB	1:K:191:PRO:HA	2.29	0.46
1:J:59:LEU:HD13	1:K:59:LEU:HD21	1.97	0.46
1:L:147:ARG:HD3	1:L:156:THR:O	2.16	0.46
1:L:45:SER:HA	1:L:205:ARG:CG	2.44	0.46
1:O:120:LEU:HD12	1:O:125:ASP:HB2	1.97	0.46
1:O:98:TRP:CH2	1:O:170:ARG:HD2	2.51	0.46
1:O:81:ASP:HB3	1:O:84:THR:OG1	2.15	0.46
1:A:55:LEU:HG	1:C:55:LEU:HD23	1.97	0.46
1:D:98:TRP:CH2	1:D:170:ARG:HD2	2.51	0.46
1:E:153:LEU:HD13	1:P:86:GLN:HG2	1.97	0.46
1:F:98:TRP:CH2	1:F:170:ARG:HD2	2.51	0.46
1:H:147:ARG:HD3	1:H:156:THR:O	2.16	0.46
1:J:98:TRP:CH2	1:J:170:ARG:HD2	2.50	0.46
1:N:87:ILE:CD1	1:N:208:PHE:CD1	2.99	0.46
1:N:98:TRP:CH2	1:N:170:ARG:HD2	2.51	0.46
1:B:192:PHE:CZ	1:C:137:PRO:HB2	2.51	0.46
1:D:150:ASN:OD1	1:D:150:ASN:N	2.44	0.46
1:E:123:VAL:HG21	1:G:63:ARG:HD2	1.98	0.46
1:F:150:ASN:N	1:F:150:ASN:OD1	2.44	0.46
1:G:98:TRP:CH2	1:G:170:ARG:HD2	2.51	0.46
1:I:147:ARG:HD3	1:I:156:THR:O	2.16	0.46
1:M:98:TRP:CH2	1:M:170:ARG:HD2	2.51	0.46
1:N:46:LEU:HD22	1:N:48:TRP:CE2	2.51	0.46
1:A:147:ARG:HD3	1:A:156:THR:O	2.16	0.46
1:B:98:TRP:CH2	1:B:170:ARG:HD2	2.51	0.46
1:D:147:ARG:HD3	1:D:156:THR:O	2.16	0.46
1:I:121:SER:HA	1:I:122:PRO:HD3	1.68	0.46
1:I:98:TRP:CH2	1:I:170:ARG:HD2	2.51	0.46
1:B:153:LEU:HD21	1:K:84:THR:O	2.16	0.46
1:L:158:TRP:CD1	1:L:194:ASN:ND2	2.84	0.46
1:M:68:ALA:CB	1:M:129:LEU:HD21	2.46	0.46
1:N:147:ARG:HD3	1:N:156:THR:O	2.16	0.46
1:N:46:LEU:HD22	1:N:48:TRP:NE1	2.30	0.46
1:N:40:TRP:HB3	1:N:75:MET:HG3	1.98	0.46
1:C:147:ARG:HD3	1:C:156:THR:O	2.16	0.46
1:E:49:LEU:HD23	1:E:49:LEU:O	2.15	0.46
1:F:147:ARG:HD3	1:F:156:THR:O	2.16	0.46
1:H:259:MET:HG2	1:H:264:PHE:CZ	2.50	0.46
1:H:135:ASN:ND2	1:H:271:ASN:HD21	2.13	0.46
1:I:58:GLN:O	1:I:62:THR:HG22	2.16	0.46

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:133:ARG:HB2	1:K:191:PRO:CG	2.46	0.46
1:K:242:SER:O	1:K:243:ASN:HB2	2.14	0.46
1:N:37:ASP:OD1	1:N:39:THR:OG1	2.32	0.46
1:D:254:SER:HB3	1:O:244:ILE:N	2.29	0.46
1:A:98:TRP:CH2	1:A:170:ARG:HD2	2.51	0.46
1:B:133:ARG:O	1:B:277:PHE:HZ	1.98	0.46
1:B:192:PHE:HZ	1:C:115:VAL:HG22	1.80	0.46
1:C:65:PRO:CB	1:C:67:PHE:CE2	2.99	0.46
1:G:73:LEU:HD22	1:G:179:ILE:CG2	2.46	0.46
1:G:37:ASP:HB2	1:G:38:ASN:H	1.56	0.46
1:G:40:TRP:CB	1:G:75:MET:HG3	2.45	0.46
1:J:147:ARG:HD3	1:J:156:THR:O	2.16	0.46
1:M:55:LEU:HD12	1:M:55:LEU:C	2.35	0.46
1:A:122:PRO:O	1:A:126:THR:HG23	2.16	0.46
1:A:89:ILE:HG22	1:A:89:ILE:O	2.15	0.46
1:B:89:ILE:HG22	1:B:89:ILE:O	2.15	0.46
1:C:186:SER:O	1:C:188:ASN:N	2.45	0.46
1:E:81:ASP:HB3	1:E:84:THR:OG1	2.15	0.46
1:H:189:HIS:CE1	1:H:193:PRO:HB3	2.51	0.46
1:H:247:VAL:CG1	1:H:248:PHE:N	2.79	0.46
1:I:48:TRP:CD1	1:I:118:GLN:HB2	2.50	0.46
1:I:247:VAL:CG1	1:I:248:PHE:N	2.79	0.46
1:N:64:ILE:HA	1:N:65:PRO:HD3	1.80	0.46
1:O:147:ARG:HD3	1:O:156:THR:O	2.16	0.46
1:P:247:VAL:CG1	1:P:248:PHE:N	2.79	0.46
1:A:133:ARG:HH11	1:A:190:ASN:HD22	1.64	0.46
1:C:187:ARG:HB3	1:C:193:PRO:HG3	1.97	0.46
1:E:150:ASN:OD1	1:E:150:ASN:N	2.44	0.46
1:O:40:TRP:HB2	1:O:75:MET:SD	2.56	0.46
1:P:147:ARG:HD3	1:P:156:THR:O	2.16	0.46
1:P:89:ILE:O	1:P:89:ILE:HG22	2.15	0.46
1:B:147:ARG:HD3	1:B:156:THR:O	2.16	0.46
1:D:192:PHE:N	1:D:193:PRO:HD3	2.31	0.46
1:G:74:HIS:O	1:G:180:ASP:HB3	2.16	0.46
1:K:84:THR:OG1	1:K:85:GLY:N	2.48	0.46
1:M:283:ILE:O	1:O:268:LEU:HD13	2.16	0.46
1:A:123:VAL:HG21	1:C:63:ARG:HD2	1.97	0.45
1:D:80:ILE:HG12	1:D:87:ILE:HD13	1.97	0.45
1:M:133:ARG:HH11	1:M:190:ASN:CB	2.21	0.45
1:M:147:ARG:HD3	1:M:156:THR:O	2.16	0.45
1:M:89:ILE:HG22	1:M:89:ILE:O	2.15	0.45

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:247:VAL:CG1	1:N:248:PHE:N	2.79	0.45
1:A:226:ASN:HA	1:A:227:PRO:HD2	1.82	0.45
1:B:142:SER:OG	1:B:197:GLU:OE2	2.27	0.45
1:C:247:VAL:CG1	1:C:248:PHE:N	2.79	0.45
1:E:57:TYR:CD2	1:E:58:GLN:N	2.84	0.45
1:F:87:ILE:CD1	1:F:208:PHE:CE1	3.00	0.45
1:F:65:PRO:HD2	1:F:129:LEU:HD13	1.96	0.45
1:F:61:SER:HB3	1:F:73:LEU:CD2	2.47	0.45
1:K:64:ILE:HA	1:K:129:LEU:HD11	1.98	0.45
1:K:190:ASN:CA	1:K:192:PHE:CD2	2.93	0.45
1:N:48:TRP:CZ3	1:N:120:LEU:CD2	2.99	0.45
1:E:40:TRP:CZ2	1:E:57:TYR:HB2	2.51	0.45
1:F:70:PRO:CG	1:F:71:ASN:N	2.78	0.45
1:G:247:VAL:CG1	1:G:248:PHE:N	2.79	0.45
1:N:192:PHE:CG	1:P:137:PRO:HG2	2.51	0.45
1:P:61:SER:C	1:P:63:ARG:H	2.20	0.45
1:I:56:LEU:CD2	1:I:60:ILE:HD11	2.46	0.45
1:I:75:MET:HE2	1:I:75:MET:CA	2.46	0.45
1:K:247:VAL:CG1	1:K:248:PHE:N	2.79	0.45
1:L:247:VAL:CG1	1:L:248:PHE:N	2.79	0.45
1:L:73:LEU:CD2	1:L:75:MET:HE1	2.46	0.45
1:M:121:SER:HA	1:M:122:PRO:HD3	1.63	0.45
1:O:247:VAL:CG1	1:O:248:PHE:N	2.79	0.45
1:D:182:ASN:HB2	1:D:195:GLN:O	2.15	0.45
1:E:98:TRP:CH2	1:E:170:ARG:HD2	2.51	0.45
1:G:89:ILE:HG22	1:G:89:ILE:O	2.15	0.45
1:I:129:LEU:HD23	1:I:191:PRO:CG	2.47	0.45
1:L:98:TRP:CH2	1:L:170:ARG:HD2	2.51	0.45
1:B:247:VAL:CG1	1:B:248:PHE:N	2.79	0.45
1:B:57:TYR:C	1:B:57:TYR:CD2	2.88	0.45
1:B:64:ILE:HD13	1:B:73:LEU:HD11	1.98	0.45
1:D:264:PHE:O	1:D:266:LEU:HD13	2.17	0.45
1:F:247:VAL:CG1	1:F:248:PHE:N	2.79	0.45
1:K:268:LEU:CD2	1:K:268:LEU:N	2.76	0.45
1:M:113:PRO:O	1:M:116:THR:HG22	2.17	0.45
1:M:192:PHE:CG	1:O:137:PRO:HG2	2.51	0.45
1:P:98:TRP:CH2	1:P:170:ARG:HD2	2.50	0.45
1:G:67:PHE:CD1	1:G:68:ALA:N	2.85	0.45
1:H:56:LEU:HD12	1:H:56:LEU:HA	1.60	0.45
1:J:247:VAL:CG1	1:J:248:PHE:N	2.79	0.45
1:K:40:TRP:CE3	1:K:75:MET:HE3	2.52	0.45

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:150:ASN:OD1	1:M:150:ASN:N	2.44	0.45
1:C:65:PRO:O	1:C:68:ALA:HB3	2.17	0.45
1:D:116:THR:HG22	1:D:117:ASN:N	2.32	0.45
1:G:41:ILE:O	1:G:41:ILE:HG12	2.17	0.45
1:G:55:LEU:O	1:G:58:GLN:N	2.50	0.45
1:H:115:VAL:HG12	1:H:139:ILE:HG22	1.97	0.45
1:H:42:GLN:HB3	1:H:176:PRO:CG	2.47	0.45
1:I:117:ASN:OD1	1:I:117:ASN:N	2.43	0.45
1:I:226:ASN:HA	1:I:227:PRO:HD2	1.82	0.45
1:A:48:TRP:HB2	1:A:118:GLN:NE2	2.32	0.45
1:A:156:THR:HG21	1:A:284:PRO:CG	2.46	0.45
1:A:247:VAL:CG1	1:A:248:PHE:N	2.79	0.45
1:D:282:GLU:O	1:D:284:PRO:HD3	2.17	0.45
1:F:282:GLU:O	1:F:284:PRO:HD3	2.17	0.45
1:K:73:LEU:CD2	1:K:179:ILE:HG23	2.47	0.45
1:N:49:LEU:HD13	1:N:202:GLY:CA	2.47	0.45
1:P:72:GLY:O	1:P:74:HIS:HD2	1.99	0.45
1:A:87:ILE:HD11	1:A:176:PRO:HD3	1.98	0.45
1:B:156:THR:HG21	1:B:284:PRO:CG	2.46	0.45
1:D:247:VAL:CG1	1:D:248:PHE:N	2.79	0.45
1:E:46:LEU:HD12	1:E:202:GLY:CA	2.28	0.45
1:K:156:THR:HG21	1:K:284:PRO:CG	2.46	0.45
1:E:182:ASN:HB2	1:E:195:GLN:O	2.17	0.44
1:E:247:VAL:CG1	1:E:248:PHE:N	2.79	0.44
1:E:282:GLU:O	1:E:284:PRO:HD3	2.17	0.44
1:F:133:ARG:HH11	1:F:190:ASN:HD22	1.64	0.44
1:M:63:ARG:C	1:M:64:ILE:HG13	2.37	0.44
1:A:69:SER:HB2	1:A:185:PHE:CE1	2.52	0.44
1:A:282:GLU:O	1:A:284:PRO:HD3	2.17	0.44
1:A:72:GLY:O	1:A:74:HIS:HD2	2.01	0.44
1:G:150:ASN:OD1	1:G:150:ASN:N	2.44	0.44
1:G:156:THR:HG21	1:G:284:PRO:CG	2.46	0.44
1:H:282:GLU:O	1:H:284:PRO:HD3	2.17	0.44
1:I:64:ILE:HA	1:I:65:PRO:HD3	1.92	0.44
1:L:226:ASN:HA	1:L:227:PRO:HD2	1.82	0.44
1:E:41:ILE:HD12	1:E:49:LEU:HD22	1.97	0.44
1:K:226:ASN:HA	1:K:227:PRO:HD2	1.82	0.44
1:L:282:GLU:O	1:L:284:PRO:HD3	2.17	0.44
1:M:37:ASP:OD2	1:M:39:THR:OG1	2.35	0.44
1:N:120:LEU:C	1:N:120:LEU:HD12	2.37	0.44
1:P:282:GLU:O	1:P:284:PRO:HD3	2.17	0.44

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:142:SER:OG	1:H:197:GLU:OE2	2.27	0.44
1:M:84:THR:HB	1:M:86:GLN:H	1.82	0.44
1:O:282:GLU:O	1:O:284:PRO:HD3	2.17	0.44
1:M:122:PRO:HG2	1:P:59:LEU:HA	1.99	0.44
1:B:182:ASN:HB2	1:B:195:GLN:O	2.18	0.44
1:C:195:GLN:HB2	1:C:195:GLN:HE21	1.48	0.44
1:C:259:MET:HG2	1:C:264:PHE:CZ	2.52	0.44
1:H:70:PRO:CD	1:H:71:ASN:H	2.31	0.44
1:J:81:ASP:HB3	1:J:84:THR:OG1	2.18	0.44
1:M:247:VAL:CG1	1:M:248:PHE:N	2.79	0.44
1:N:282:GLU:O	1:N:284:PRO:HD3	2.17	0.44
1:P:261:SER:O	1:P:264:PHE:HB2	2.18	0.44
1:B:122:PRO:HG2	1:D:59:LEU:HA	1.99	0.44
1:E:87:ILE:HD11	1:E:208:PHE:CE1	2.53	0.44
1:G:262:LYS:C	1:G:264:PHE:H	2.20	0.44
1:G:282:GLU:O	1:G:284:PRO:HD3	2.17	0.44
1:G:87:ILE:HG22	1:G:87:ILE:O	2.17	0.44
1:H:59:LEU:HD23	1:H:126:THR:HG21	2.00	0.44
1:K:129:LEU:CD2	1:K:191:PRO:HD3	2.45	0.44
1:K:190:ASN:HA	1:K:192:PHE:N	2.32	0.44
1:L:140:PHE:HB3	1:L:199:THR:CG2	2.48	0.44
1:N:58:GLN:NE2	1:O:120:LEU:O	2.50	0.44
1:B:81:ASP:OD1	1:B:83:ASN:HB2	2.17	0.44
1:E:140:PHE:HB3	1:E:199:THR:CG2	2.48	0.44
1:F:140:PHE:HB3	1:F:199:THR:CG2	2.48	0.44
1:H:140:PHE:HB3	1:H:199:THR:CG2	2.48	0.44
1:K:282:GLU:O	1:K:284:PRO:HD3	2.17	0.44
1:M:61:SER:OG	1:M:62:THR:N	2.50	0.44
1:B:140:PHE:HB3	1:B:199:THR:CG2	2.48	0.44
1:B:282:GLU:O	1:B:284:PRO:HD3	2.17	0.44
1:C:69:SER:HB2	1:C:184:SER:O	2.17	0.44
1:C:190:ASN:CG	1:C:191:PRO:HD2	2.37	0.44
1:O:81:ASP:OD2	1:O:84:THR:HG23	2.18	0.44
1:B:283:ILE:CG2	1:C:268:LEU:HD21	2.48	0.44
1:E:64:ILE:HG21	1:E:69:SER:HB2	1.99	0.44
1:F:186:SER:OG	1:F:189:HIS:HB2	2.18	0.44
1:I:140:PHE:HB3	1:I:199:THR:CG2	2.48	0.44
1:K:102:PRO:HB2	1:K:256:GLY:O	2.18	0.44
1:M:140:PHE:HB3	1:M:199:THR:CG2	2.48	0.44
1:M:282:GLU:O	1:M:284:PRO:HD3	2.17	0.44
1:M:76:ARG:NH1	1:M:177:GLY:O	2.51	0.44

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:84:THR:HB	1:N:86:GLN:H	1.83	0.44
1:A:140:PHE:HB3	1:A:199:THR:CG2	2.48	0.43
1:B:112:ILE:HA	1:B:113:PRO:HD3	1.91	0.43
1:B:46:LEU:HD13	1:B:48:TRP:CZ2	2.53	0.43
1:B:64:ILE:HD12	1:B:73:LEU:CD1	2.48	0.43
1:D:102:PRO:HB2	1:D:256:GLY:O	2.18	0.43
1:F:120:LEU:O	1:F:122:PRO:HD3	2.18	0.43
1:F:64:ILE:HA	1:F:65:PRO:HD2	1.94	0.43
1:I:102:PRO:HB2	1:I:256:GLY:O	2.18	0.43
1:I:56:LEU:O	1:I:56:LEU:HD23	2.18	0.43
1:J:102:PRO:HB2	1:J:256:GLY:O	2.18	0.43
1:J:37:ASP:OD1	1:J:37:ASP:N	2.51	0.43
1:P:188:ASN:O	1:P:192:PHE:HE1	2.00	0.43
1:H:192:PHE:N	1:H:193:PRO:CD	2.81	0.43
1:J:140:PHE:HB3	1:J:199:THR:CG2	2.48	0.43
1:L:102:PRO:HB2	1:L:256:GLY:O	2.18	0.43
1:N:45:SER:N	1:N:202:GLY:O	2.51	0.43
1:N:76:ARG:HH12	1:N:95:LEU:HD11	1.81	0.43
1:O:154:GLU:CG	1:O:289:LEU:HD22	2.43	0.43
1:B:122:PRO:HG2	1:D:59:LEU:HD23	2.00	0.43
1:C:282:GLU:O	1:C:284:PRO:HD3	2.17	0.43
1:E:122:PRO:O	1:E:126:THR:HG23	2.18	0.43
1:E:102:PRO:HB2	1:E:256:GLY:O	2.18	0.43
1:G:102:PRO:HB2	1:G:256:GLY:O	2.18	0.43
1:H:56:LEU:HG	1:H:60:ILE:HD12	1.99	0.43
1:J:133:ARG:HG3	1:J:133:ARG:O	2.16	0.43
1:K:120:LEU:HG	1:K:121:SER:N	2.33	0.43
1:N:102:PRO:HB2	1:N:256:GLY:O	2.18	0.43
1:N:156:THR:HG21	1:N:284:PRO:CG	2.46	0.43
1:A:69:SER:HA	1:A:70:PRO:HD2	1.83	0.43
1:C:84:THR:HB	1:C:86:GLN:HG3	2.00	0.43
1:E:68:ALA:CB	1:E:129:LEU:HD21	2.46	0.43
1:F:76:ARG:NH1	1:F:177:GLY:O	2.48	0.43
1:G:194:ASN:HD21	1:G:197:GLU:CB	2.30	0.43
1:H:76:ARG:HD3	1:H:198:ILE:HG13	2.00	0.43
1:I:133:ARG:HD2	1:I:190:ASN:HD21	1.84	0.43
1:M:129:LEU:HD23	1:M:191:PRO:HG3	2.00	0.43
1:M:102:PRO:HB2	1:M:256:GLY:O	2.18	0.43
1:O:102:PRO:HB2	1:O:256:GLY:O	2.18	0.43
1:A:154:GLU:CG	1:A:289:LEU:HD22	2.43	0.43
1:D:120:LEU:HG	1:D:121:SER:N	2.27	0.43

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:65:PRO:HB2	1:D:67:PHE:CD2	2.53	0.43
1:H:156:THR:HG21	1:H:284:PRO:CG	2.46	0.43
1:I:63:ARG:CG	1:I:63:ARG:HH11	2.31	0.43
1:J:282:GLU:O	1:J:284:PRO:HD3	2.17	0.43
1:M:112:ILE:HA	1:M:113:PRO:HD3	1.91	0.43
1:O:140:PHE:HB3	1:O:199:THR:CG2	2.48	0.43
1:A:102:PRO:HB2	1:A:256:GLY:O	2.18	0.43
1:D:140:PHE:HB3	1:D:199:THR:CG2	2.48	0.43
1:E:283:ILE:O	1:H:268:LEU:HD23	2.19	0.43
1:G:44:ALA:O	1:G:205:ARG:NH1	2.50	0.43
1:H:124:GLU:N	1:H:124:GLU:OE1	2.52	0.43
1:I:43:ALA:CB	1:I:176:PRO:HD2	2.33	0.43
1:I:282:GLU:O	1:I:284:PRO:HD3	2.17	0.43
1:K:76:ARG:NH2	1:K:79:THR:CG2	2.82	0.43
1:C:186:SER:C	1:C:188:ASN:N	2.72	0.43
1:I:45:SER:HB3	1:I:204:ILE:C	2.39	0.43
1:K:140:PHE:HB3	1:K:199:THR:CG2	2.48	0.43
1:K:40:TRP:HA	1:K:177:GLY:HA3	1.99	0.43
1:M:283:ILE:HB	1:O:268:LEU:HD21	1.97	0.43
1:P:190:ASN:HA	1:P:192:PHE:N	2.33	0.43
1:P:140:PHE:HB3	1:P:199:THR:CG2	2.48	0.43
1:P:40:TRP:HB3	1:P:75:MET:HG3	2.01	0.43
1:B:69:SER:HA	1:B:184:SER:O	2.18	0.43
1:B:64:ILE:CG2	1:B:69:SER:HB3	2.48	0.43
1:C:102:PRO:HB2	1:C:256:GLY:O	2.18	0.43
1:D:154:GLU:CG	1:D:289:LEU:HD22	2.43	0.43
1:E:46:LEU:CD1	1:E:113:PRO:HG2	2.48	0.43
1:E:39:THR:CG2	1:E:40:TRP:N	2.81	0.43
1:K:267:ASP:HB2	1:K:268:LEU:HD23	2.00	0.43
1:M:79:THR:HG21	1:M:177:GLY:N	2.33	0.43
1:O:156:THR:HG21	1:O:284:PRO:CG	2.46	0.43
1:N:284:PRO:O	1:P:262:LYS:HD3	2.18	0.43
1:B:102:PRO:HB2	1:B:256:GLY:O	2.18	0.43
1:C:140:PHE:HB3	1:C:199:THR:CG2	2.48	0.43
1:E:190:ASN:ND2	1:E:191:PRO:HA	2.34	0.43
1:F:120:LEU:HD12	1:F:120:LEU:H	1.84	0.43
1:F:189:HIS:HD2	1:G:119:ASN:HB2	1.84	0.43
1:E:59:LEU:HA	1:G:122:PRO:HG2	2.01	0.43
1:F:192:PHE:CZ	1:G:137:PRO:HB2	2.54	0.43
1:G:80:ILE:CG2	1:G:87:ILE:HD13	2.33	0.43
1:D:88:GLN:NE2	1:D:90:ASP:OD2	2.51	0.43

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:64:ILE:HA	1:F:129:LEU:CD1	2.48	0.43
1:G:140:PHE:HB3	1:G:199:THR:CG2	2.48	0.43
1:J:87:ILE:CD1	1:J:208:PHE:CD1	3.01	0.43
1:E:288:LEU:CD1	1:P:86:GLN:NE2	2.76	0.43
1:D:120:LEU:HD12	1:D:125:ASP:HB2	2.01	0.42
1:D:80:ILE:HG22	1:D:81:ASP:N	2.34	0.42
1:L:76:ARG:HD3	1:L:198:ILE:CG1	2.46	0.42
1:N:140:PHE:HB3	1:N:199:THR:CG2	2.48	0.42
1:N:226:ASN:HA	1:N:227:PRO:HD2	1.82	0.42
1:P:102:PRO:HB2	1:P:256:GLY:O	2.18	0.42
1:A:133:ARG:O	1:A:133:ARG:HG3	2.19	0.42
1:A:192:PHE:CD1	1:D:137:PRO:HG2	2.54	0.42
1:B:49:LEU:HD21	1:B:56:LEU:HD22	2.01	0.42
1:J:226:ASN:HA	1:J:227:PRO:HD2	1.82	0.42
1:A:39:THR:O	1:A:42:GLN:HB3	2.19	0.42
1:A:65:PRO:HA	1:B:65:PRO:HA	2.01	0.42
1:B:192:PHE:CD1	1:C:137:PRO:HG2	2.55	0.42
1:D:159:THR:HA	1:D:160:PRO:HD3	1.93	0.42
1:D:65:PRO:HB2	1:D:67:PHE:CE2	2.55	0.42
1:E:79:THR:CB	1:E:176:PRO:HA	2.49	0.42
1:F:59:LEU:HD23	1:F:126:THR:HG21	2.01	0.42
1:G:55:LEU:O	1:G:59:LEU:N	2.41	0.42
1:H:102:PRO:HB2	1:H:256:GLY:O	2.18	0.42
1:J:87:ILE:CD1	1:J:208:PHE:CE1	2.97	0.42
1:J:64:ILE:HA	1:J:65:PRO:HD3	1.67	0.42
1:K:80:ILE:HG22	1:K:87:ILE:CD1	2.47	0.42
1:N:190:ASN:CG	1:N:191:PRO:HA	2.40	0.42
1:N:37:ASP:OD1	1:N:39:THR:N	2.40	0.42
1:N:81:ASP:OD1	1:N:83:ASN:HB2	2.19	0.42
1:B:288:LEU:HD13	1:K:86:GLN:HE21	1.85	0.42
1:D:56:LEU:C	1:D:56:LEU:HD23	2.38	0.42
1:E:156:THR:HG21	1:E:284:PRO:CG	2.46	0.42
1:G:194:ASN:ND2	1:G:197:GLU:N	2.67	0.42
1:E:283:ILE:HG21	1:H:268:LEU:HD21	1.94	0.42
1:J:77:GLU:HB3	1:J:78:GLN:NE2	2.34	0.42
1:N:48:TRP:HB3	1:N:118:GLN:OE1	2.19	0.42
1:D:158:TRP:CD1	1:D:194:ASN:HB3	2.55	0.42
1:D:40:TRP:CD1	1:D:40:TRP:N	2.81	0.42
1:I:47:THR:HG23	1:I:48:TRP:H	1.84	0.42
1:L:115:VAL:HG12	1:L:116:THR:O	2.19	0.42
1:N:57:TYR:CD2	1:N:57:TYR:C	2.92	0.42

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:186:SER:HB2	1:D:189:HIS:CB	2.43	0.42
1:H:123:VAL:HG23	1:H:123:VAL:H	1.62	0.42
1:H:84:THR:C	1:H:86:GLN:H	2.23	0.42
1:P:188:ASN:O	1:P:192:PHE:CE1	2.72	0.42
1:F:226:ASN:HA	1:F:227:PRO:HD2	1.82	0.42
1:F:84:THR:HG21	1:F:86:GLN:HB2	2.02	0.42
1:H:112:ILE:HA	1:H:113:PRO:HD3	1.91	0.42
1:I:56:LEU:HD21	1:I:60:ILE:HD11	2.02	0.42
1:M:156:THR:HG21	1:M:284:PRO:CG	2.46	0.42
1:E:61:SER:HA	1:E:64:ILE:HD12	2.00	0.42
1:F:159:THR:HA	1:F:160:PRO:HD3	1.93	0.42
1:L:73:LEU:HD23	1:L:75:MET:CE	2.50	0.42
1:O:42:GLN:HB3	1:O:42:GLN:HE21	1.69	0.42
1:O:65:PRO:HG2	1:O:68:ALA:CB	2.50	0.42
1:A:68:ALA:CB	1:A:129:LEU:HD21	2.47	0.42
1:C:67:PHE:C	1:C:67:PHE:CD1	2.93	0.42
1:F:102:PRO:HB2	1:F:256:GLY:O	2.18	0.42
1:F:55:LEU:CD2	1:H:55:LEU:HD23	2.49	0.42
1:I:70:PRO:HD2	1:I:71:ASN:H	1.84	0.42
1:L:78:GLN:OE1	1:L:78:GLN:HA	2.19	0.42
1:N:142:SER:OG	1:N:197:GLU:OE2	2.27	0.42
1:B:226:ASN:HA	1:B:227:PRO:HD2	1.82	0.42
1:B:64:ILE:CD1	1:B:73:LEU:CD1	2.97	0.42
1:D:149:ASN:HD21	1:D:153:LEU:HD12	1.85	0.42
1:M:73:LEU:HD23	1:M:73:LEU:HA	1.83	0.42
1:H:60:ILE:HG22	1:H:73:LEU:HD11	2.01	0.41
1:I:74:HIS:HD2	1:I:183:ALA:O	2.03	0.41
1:J:166:ASN:H	1:J:217:ASN:ND2	2.18	0.41
1:J:87:ILE:HD11	1:J:208:PHE:CD1	2.54	0.41
1:L:116:THR:HG22	1:L:118:GLN:H	1.85	0.41
1:L:156:THR:HG21	1:L:284:PRO:CG	2.46	0.41
1:M:133:ARG:O	1:M:277:PHE:HZ	2.03	0.41
1:M:192:PHE:N	1:M:193:PRO:HD3	2.35	0.41
1:O:166:ASN:H	1:O:217:ASN:ND2	2.18	0.41
1:B:98:TRP:CD1	1:B:160:PRO:HD3	2.56	0.41
1:B:87:ILE:HD11	1:B:208:PHE:HE1	1.84	0.41
1:F:166:ASN:H	1:F:217:ASN:ND2	2.18	0.41
1:F:81:ASP:HB3	1:F:85:GLY:H	1.85	0.41
1:H:166:ASN:H	1:H:217:ASN:ND2	2.18	0.41
1:I:159:THR:HA	1:I:160:PRO:HD3	1.93	0.41
1:I:166:ASN:H	1:I:217:ASN:ND2	2.18	0.41

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:98:TRP:CD1	1:J:160:PRO:HD3	2.56	0.41
1:L:80:ILE:HD11	1:L:176:PRO:HB3	2.02	0.41
1:L:142:SER:OG	1:L:197:GLU:OE2	2.27	0.41
1:M:129:LEU:HD23	1:M:191:PRO:CG	2.51	0.41
1:M:149:ASN:HD21	1:M:153:LEU:HD12	1.85	0.41
1:A:98:TRP:CD1	1:A:160:PRO:HD3	2.56	0.41
1:C:156:THR:HG21	1:C:284:PRO:CG	2.46	0.41
1:D:156:THR:HG21	1:D:284:PRO:CG	2.46	0.41
1:G:69:SER:OG	1:G:184:SER:O	2.28	0.41
1:H:55:LEU:O	1:H:58:GLN:HB2	2.20	0.41
1:L:124:GLU:C	1:L:126:THR:H	2.24	0.41
1:A:48:TRP:O	1:A:48:TRP:HE3	2.03	0.41
1:D:98:TRP:CD1	1:D:160:PRO:HD3	2.56	0.41
1:D:194:ASN:OD1	1:D:194:ASN:N	2.53	0.41
1:E:59:LEU:CA	1:G:122:PRO:HG2	2.50	0.41
1:G:98:TRP:CD1	1:G:160:PRO:HD3	2.56	0.41
1:H:149:ASN:HD21	1:H:153:LEU:HD12	1.85	0.41
1:N:98:TRP:CD1	1:N:160:PRO:HD3	2.56	0.41
1:O:112:ILE:HA	1:O:113:PRO:HD3	1.91	0.41
1:O:76:ARG:HD3	1:O:198:ILE:CG1	2.45	0.41
1:P:166:ASN:H	1:P:217:ASN:ND2	2.18	0.41
1:B:166:ASN:H	1:B:217:ASN:ND2	2.18	0.41
1:E:37:ASP:OD1	1:E:37:ASP:N	2.54	0.41
1:E:64:ILE:HG21	1:E:69:SER:CB	2.51	0.41
1:F:190:ASN:HA	1:F:191:PRO:HA	1.83	0.41
1:H:241:PRO:HB2	1:H:244:ILE:HD11	2.00	0.41
1:I:149:ASN:HD21	1:I:153:LEU:HD12	1.86	0.41
1:L:58:GLN:O	1:L:62:THR:OG1	2.28	0.41
1:M:73:LEU:HD22	1:M:179:ILE:HG23	2.01	0.41
1:P:98:TRP:CD1	1:P:160:PRO:HD3	2.56	0.41
1:P:69:SER:HA	1:P:70:PRO:HD2	1.77	0.41
1:A:60:ILE:HG22	1:A:61:SER:N	2.36	0.41
1:B:149:ASN:HD21	1:B:153:LEU:HD12	1.85	0.41
1:C:154:GLU:CG	1:C:289:LEU:HD22	2.43	0.41
1:D:80:ILE:CG2	1:D:81:ASP:N	2.83	0.41
1:E:187:ARG:HG2	1:E:195:GLN:NE2	2.35	0.41
1:E:241:PRO:HB2	1:E:244:ILE:HD11	2.00	0.41
1:H:98:TRP:CD1	1:H:160:PRO:HD3	2.56	0.41
1:I:98:TRP:CD1	1:I:160:PRO:HD3	2.56	0.41
1:L:98:TRP:CD1	1:L:160:PRO:HD3	2.56	0.41
1:L:166:ASN:H	1:L:217:ASN:ND2	2.18	0.41

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:129:LEU:CD2	1:M:191:PRO:HD3	2.51	0.41
1:B:48:TRP:CD2	1:B:118:GLN:HA	2.55	0.41
1:C:98:TRP:CD1	1:C:160:PRO:HD3	2.56	0.41
1:D:56:LEU:HD23	1:D:56:LEU:O	2.21	0.41
1:F:76:ARG:HD2	1:F:198:ILE:HG23	2.02	0.41
1:G:254:SER:HB3	1:L:243:ASN:C	2.39	0.41
1:I:74:HIS:C	1:I:75:MET:HE3	2.41	0.41
1:I:75:MET:HE2	1:I:179:ILE:HA	2.01	0.41
1:K:98:TRP:CD1	1:K:160:PRO:HD3	2.56	0.41
1:L:69:SER:HA	1:L:70:PRO:HD2	1.49	0.41
1:N:159:THR:HA	1:N:160:PRO:HD3	1.93	0.41
1:B:64:ILE:HD12	1:B:73:LEU:HD13	2.01	0.41
1:A:123:VAL:HG11	1:C:63:ARG:NH1	2.36	0.41
1:D:166:ASN:H	1:D:217:ASN:ND2	2.18	0.41
1:E:40:TRP:N	1:E:40:TRP:CD1	2.89	0.41
1:F:156:THR:HG21	1:F:284:PRO:CG	2.46	0.41
1:F:98:TRP:CD1	1:F:160:PRO:HD3	2.56	0.41
1:E:59:LEU:N	1:G:122:PRO:HG2	2.36	0.41
1:G:120:LEU:HD11	1:G:125:ASP:HB2	2.01	0.41
1:G:61:SER:HA	1:G:64:ILE:HD12	2.02	0.41
1:H:159:THR:HA	1:H:160:PRO:HD3	1.93	0.41
1:H:59:LEU:HA	1:H:59:LEU:HD12	1.90	0.41
1:J:151:LEU:HD23	1:J:151:LEU:HA	1.90	0.41
1:P:112:ILE:HA	1:P:113:PRO:HD3	1.91	0.41
1:A:149:ASN:HD21	1:A:153:LEU:HD12	1.85	0.41
1:E:192:PHE:CG	1:H:137:PRO:HG2	2.56	0.41
1:F:148:TYR:CE1	1:F:154:GLU:HB2	2.56	0.41
1:F:149:ASN:HD21	1:F:153:LEU:HD12	1.85	0.41
1:H:262:LYS:O	1:H:264:PHE:N	2.53	0.41
1:I:43:ALA:N	1:I:176:PRO:HG2	2.35	0.41
1:K:148:TYR:CE1	1:K:154:GLU:HB2	2.56	0.41
1:K:166:ASN:H	1:K:217:ASN:ND2	2.18	0.41
1:L:149:ASN:HD21	1:L:153:LEU:HD12	1.85	0.41
1:L:148:TYR:CE1	1:L:154:GLU:HB2	2.56	0.41
1:A:42:GLN:HG3	1:A:42:GLN:O	2.21	0.41
1:C:100:ARG:HH11	1:C:100:ARG:HD3	1.75	0.41
1:C:124:GLU:C	1:C:126:THR:H	2.24	0.41
1:E:133:ARG:HB2	1:E:191:PRO:HB2	2.03	0.41
1:E:98:TRP:CD1	1:E:160:PRO:HD3	2.56	0.41
1:F:154:GLU:CG	1:F:289:LEU:HD22	2.43	0.41
1:F:40:TRP:CZ2	1:F:57:TYR:HB2	2.56	0.41

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:148:TYR:CE1	1:H:154:GLU:HB2	2.56	0.41
1:I:148:TYR:CE1	1:I:154:GLU:HB2	2.56	0.41
1:I:79:THR:HG23	1:I:80:ILE:N	2.36	0.41
1:O:43:ALA:HB2	1:O:176:PRO:O	2.21	0.41
1:A:166:ASN:H	1:A:217:ASN:ND2	2.18	0.41
1:C:41:ILE:HG23	1:C:41:ILE:HD13	1.89	0.41
1:D:129:LEU:HD23	1:D:191:PRO:HD3	2.02	0.41
1:D:88:GLN:HG2	1:D:93:HIS:ND1	2.36	0.41
1:E:149:ASN:HD21	1:E:153:LEU:HD12	1.85	0.41
1:G:142:SER:OG	1:G:197:GLU:OE2	2.27	0.41
1:I:42:GLN:HE21	1:I:176:PRO:HG3	1.84	0.41
1:J:112:ILE:HA	1:J:113:PRO:HD3	1.91	0.41
1:J:149:ASN:HD21	1:J:153:LEU:HD12	1.85	0.41
1:J:148:TYR:CE1	1:J:154:GLU:HB2	2.56	0.41
1:J:156:THR:HG21	1:J:284:PRO:CG	2.46	0.41
1:M:129:LEU:HD23	1:M:191:PRO:CD	2.50	0.41
1:M:98:TRP:CD1	1:M:160:PRO:HD3	2.56	0.41
1:N:148:TYR:CE1	1:N:154:GLU:HB2	2.56	0.41
1:P:149:ASN:HD21	1:P:153:LEU:HD12	1.85	0.41
1:P:156:THR:HG21	1:P:284:PRO:CG	2.46	0.41
1:P:44:ALA:O	1:P:205:ARG:NH1	2.42	0.41
1:B:122:PRO:CD	1:B:123:VAL:H	2.34	0.40
1:D:64:ILE:HD12	1:D:73:LEU:HG	2.03	0.40
1:F:76:ARG:CD	1:F:198:ILE:HG21	2.45	0.40
1:G:231:ASN:HA	1:G:232:PRO:HD3	1.85	0.40
1:G:73:LEU:HD23	1:G:184:SER:HB3	2.01	0.40
1:N:127:HIS:CE1	1:N:130:ASN:HB2	2.55	0.40
1:N:166:ASN:H	1:N:217:ASN:ND2	2.18	0.40
1:O:63:ARG:HH21	1:O:123:VAL:HA	1.85	0.40
1:P:148:TYR:CE1	1:P:154:GLU:HB2	2.56	0.40
1:C:226:ASN:HA	1:C:227:PRO:HD2	1.82	0.40
1:E:148:TYR:CE1	1:E:154:GLU:HB2	2.56	0.40
1:E:166:ASN:H	1:E:217:ASN:ND2	2.18	0.40
1:F:120:LEU:C	1:F:120:LEU:HD13	2.42	0.40
1:G:81:ASP:OD2	1:G:84:THR:OG1	2.40	0.40
1:J:68:ALA:CB	1:J:129:LEU:HD21	2.51	0.40
1:M:166:ASN:H	1:M:217:ASN:ND2	2.18	0.40
1:N:234:THR:C	1:N:236:ASN:N	2.75	0.40
1:P:262:LYS:NZ	1:P:268:LEU:HB3	2.37	0.40
1:P:79:THR:HG23	1:P:80:ILE:HG23	2.02	0.40
1:B:190:ASN:ND2	1:B:191:PRO:HA	2.36	0.40

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:40:TRP:CD2	1:C:41:ILE:CG2	2.98	0.40
1:H:259:MET:HG2	1:H:264:PHE:CE2	2.56	0.40
1:K:40:TRP:CE3	1:K:75:MET:HE1	2.57	0.40
1:K:40:TRP:CD2	1:K:41:ILE:HG23	2.56	0.40
1:L:77:GLU:O	1:L:78:GLN:HB2	2.20	0.40
1:O:149:ASN:HD21	1:O:153:LEU:HD12	1.85	0.40
1:A:120:LEU:O	1:A:120:LEU:HD12	2.21	0.40
1:A:148:TYR:CE1	1:A:154:GLU:HB2	2.56	0.40
1:B:234:THR:C	1:B:236:ASN:N	2.75	0.40
1:C:149:ASN:HD21	1:C:153:LEU:HD12	1.85	0.40
1:C:166:ASN:H	1:C:217:ASN:ND2	2.18	0.40
1:C:185:PHE:CB	1:C:189:HIS:CD2	2.89	0.40
1:G:226:ASN:HA	1:G:227:PRO:HD2	1.82	0.40
1:H:43:ALA:O	1:H:204:ILE:HA	2.22	0.40
1:J:150:ASN:N	1:J:150:ASN:OD1	2.44	0.40
1:O:231:ASN:HA	1:O:232:PRO:HD3	1.85	0.40
1:A:133:ARG:HB2	1:A:191:PRO:HB3	2.02	0.40
1:A:48:TRP:O	1:A:48:TRP:CE3	2.74	0.40
1:E:112:ILE:HA	1:E:113:PRO:HD3	1.91	0.40
1:E:127:HIS:CE1	1:E:130:ASN:HB2	2.55	0.40
1:F:44:ALA:HA	1:F:202:GLY:O	2.22	0.40
1:G:149:ASN:HD21	1:G:153:LEU:HD12	1.85	0.40
1:G:159:THR:HA	1:G:160:PRO:HD3	1.93	0.40
1:G:79:THR:O	1:G:88:GLN:HB3	2.21	0.40
1:H:154:GLU:CG	1:H:289:LEU:HD22	2.43	0.40
1:J:40:TRP:CZ2	1:J:57:TYR:HB2	2.57	0.40
1:I:192:PHE:CG	1:K:137:PRO:HG2	2.56	0.40
1:M:235:LEU:HA	1:M:235:LEU:HD23	1.91	0.40
1:N:149:ASN:HD21	1:N:153:LEU:HD12	1.85	0.40
1:N:63:ARG:HE	1:N:63:ARG:HB2	1.37	0.40
1:P:234:THR:C	1:P:236:ASN:N	2.75	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:150:ASN:O	1:H:148:TYR:N[2_664]	1.96	0.24

## 5.3 Torsion angles

### 5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	232/291 (80%)	202 (87%)	29 (12%)	1 (0%)	34	72
1	B	232/291 (80%)	205 (88%)	27 (12%)	0	100	100
1	C	240/291 (82%)	211 (88%)	28 (12%)	1 (0%)	34	72
1	D	240/291 (82%)	216 (90%)	21 (9%)	3 (1%)	12	45
1	E	232/291 (80%)	200 (86%)	30 (13%)	2 (1%)	17	55
1	F	232/291 (80%)	205 (88%)	25 (11%)	2 (1%)	17	55
1	G	230/291 (79%)	208 (90%)	22 (10%)	0	100	100
1	H	241/291 (83%)	211 (88%)	27 (11%)	3 (1%)	13	48
1	I	232/291 (80%)	208 (90%)	21 (9%)	3 (1%)	12	45
1	J	232/291 (80%)	208 (90%)	23 (10%)	1 (0%)	34	72
1	K	240/291 (82%)	211 (88%)	28 (12%)	1 (0%)	34	72
1	L	230/291 (79%)	202 (88%)	26 (11%)	2 (1%)	17	55
1	M	232/291 (80%)	206 (89%)	25 (11%)	1 (0%)	34	72
1	N	232/291 (80%)	206 (89%)	23 (10%)	3 (1%)	12	45
1	O	230/291 (79%)	201 (87%)	27 (12%)	2 (1%)	17	55
1	P	240/291 (82%)	212 (88%)	25 (10%)	3 (1%)	12	45
All	All	3747/4656 (80%)	3312 (88%)	407 (11%)	28 (1%)	22	60

All (28) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	70	PRO
1	O	70	PRO
1	A	70	PRO
1	N	62	THR
1	P	83	ASN
1	C	125	ASP

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	H	39	THR
1	K	62	THR
1	L	125	ASP
1	D	122	PRO
1	E	70	PRO
1	E	121	SER
1	I	43	ALA
1	I	47	THR
1	M	195	GLN
1	N	122	PRO
1	O	44	ALA
1	P	62	THR
1	D	82	SER
1	H	195	GLN
1	P	193	PRO
1	D	70	PRO
1	F	44	ALA
1	H	263	GLY
1	I	48	TRP
1	J	122	PRO
1	N	121	SER
1	L	122	PRO

### 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 X-ray entries followed by that with respect to entries of similar resolution.

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	218/262 (83%)	207 (95%)	11 (5%)	24	60
1	B	218/262 (83%)	205 (94%)	13 (6%)	19	53
1	C	223/262 (85%)	212 (95%)	11 (5%)	25	61
1	D	223/262 (85%)	213 (96%)	10 (4%)	27	64
1	E	218/262 (83%)	206 (94%)	12 (6%)	21	57
1	F	218/262 (83%)	205 (94%)	13 (6%)	19	53
1	G	215/262 (82%)	201 (94%)	14 (6%)	17	50

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	H	224/262 (86%)	210 (94%)	14 (6%)	18	51
1	I	218/262 (83%)	205 (94%)	13 (6%)	19	53
1	J	218/262 (83%)	207 (95%)	11 (5%)	24	60
1	K	223/262 (85%)	210 (94%)	13 (6%)	20	55
1	L	215/262 (82%)	206 (96%)	9 (4%)	30	66
1	M	218/262 (83%)	204 (94%)	14 (6%)	17	51
1	N	218/262 (83%)	207 (95%)	11 (5%)	24	60
1	O	215/262 (82%)	206 (96%)	9 (4%)	30	66
1	P	223/262 (85%)	215 (96%)	8 (4%)	35	70
All	All	3505/4192 (84%)	3319 (95%)	186 (5%)	22	58

All (186) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	41	ILE
1	A	63	ARG
1	A	97	ARG
1	A	120	LEU
1	A	121	SER
1	A	150	ASN
1	A	188	ASN
1	A	190	ASN
1	A	233	SER
1	A	242	SER
1	A	248	PHE
1	B	41	ILE
1	B	81	ASP
1	B	82	SER
1	B	87	ILE
1	B	97	ARG
1	B	116	THR
1	B	120	LEU
1	B	133	ARG
1	B	150	ASN
1	B	189	HIS
1	B	233	SER
1	B	242	SER
1	B	248	PHE
1	C	38	ASN

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	C	41	ILE
1	C	45	SER
1	C	59	LEU
1	C	97	ARG
1	C	150	ASN
1	C	186	SER
1	C	195	GLN
1	C	233	SER
1	C	242	SER
1	C	248	PHE
1	D	66	SER
1	D	74	HIS
1	D	97	ARG
1	D	150	ASN
1	D	187	ARG
1	D	190	ASN
1	D	192	PHE
1	D	233	SER
1	D	242	SER
1	D	248	PHE
1	E	37	ASP
1	E	61	SER
1	E	66	SER
1	E	73	LEU
1	E	97	ARG
1	E	120	LEU
1	E	133	ARG
1	E	150	ASN
1	E	195	GLN
1	E	233	SER
1	E	242	SER
1	E	248	PHE
1	F	39	THR
1	F	75	MET
1	F	97	ARG
1	F	120	LEU
1	F	124	GLU
1	F	150	ASN
1	F	186	SER
1	F	188	ASN
1	F	190	ASN
1	F	194	ASN

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	F	233	SER
1	F	242	SER
1	F	248	PHE
1	G	37	ASP
1	G	59	LEU
1	G	66	SER
1	G	74	HIS
1	G	83	ASN
1	G	84	THR
1	G	87	ILE
1	G	97	ARG
1	G	133	ARG
1	G	150	ASN
1	G	233	SER
1	G	242	SER
1	G	248	PHE
1	G	269	ASP
1	H	42	GLN
1	H	84	THR
1	H	87	ILE
1	H	97	ARG
1	H	116	THR
1	H	119	ASN
1	H	133	ARG
1	H	150	ASN
1	H	186	SER
1	H	195	GLN
1	H	233	SER
1	H	242	SER
1	H	248	PHE
1	H	267	ASP
1	I	39	THR
1	I	56	LEU
1	I	63	ARG
1	I	69	SER
1	I	75	MET
1	I	97	ARG
1	I	117	ASN
1	I	120	LEU
1	I	133	ARG
1	I	150	ASN
1	I	233	SER

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	I	242	SER
1	I	248	PHE
1	J	49	LEU
1	J	61	SER
1	J	69	SER
1	J	83	ASN
1	J	97	ARG
1	J	120	LEU
1	J	150	ASN
1	J	190	ASN
1	J	233	SER
1	J	242	SER
1	J	248	PHE
1	K	41	ILE
1	K	59	LEU
1	K	73	LEU
1	K	76	ARG
1	K	97	ARG
1	K	150	ASN
1	K	192	PHE
1	K	193	PRO
1	K	233	SER
1	K	242	SER
1	K	248	PHE
1	K	268	LEU
1	K	269	ASP
1	L	37	ASP
1	L	56	LEU
1	L	71	ASN
1	L	97	ARG
1	L	133	ARG
1	L	150	ASN
1	L	233	SER
1	L	242	SER
1	L	248	PHE
1	M	45	SER
1	M	47	THR
1	M	71	ASN
1	M	76	ARG
1	M	81	ASP
1	M	97	ARG
1	M	116	THR

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	M	117	ASN
1	M	150	ASN
1	M	188	ASN
1	M	190	ASN
1	M	233	SER
1	M	242	SER
1	M	248	PHE
1	N	47	THR
1	N	58	GLN
1	N	63	ARG
1	N	79	THR
1	N	97	ARG
1	N	124	GLU
1	N	133	ARG
1	N	150	ASN
1	N	233	SER
1	N	242	SER
1	N	248	PHE
1	O	63	ARG
1	O	66	SER
1	O	75	MET
1	O	97	ARG
1	O	120	LEU
1	O	150	ASN
1	O	233	SER
1	O	242	SER
1	O	248	PHE
1	P	80	ILE
1	P	97	ARG
1	P	121	SER
1	P	150	ASN
1	P	233	SER
1	P	242	SER
1	P	248	PHE
1	P	265	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (75) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	71	ASN
1	A	74	HIS
1	A	118	GLN

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Res	Type
1	A	119	ASN
1	A	189	HIS
1	A	190	ASN
1	A	217	ASN
1	B	42	GLN
1	B	58	GLN
1	B	188	ASN
1	B	190	ASN
1	B	217	ASN
1	C	83	ASN
1	C	119	ASN
1	C	135	ASN
1	C	189	HIS
1	C	195	GLN
1	C	217	ASN
1	D	189	HIS
1	D	217	ASN
1	E	86	GLN
1	E	190	ASN
1	E	217	ASN
1	F	86	GLN
1	F	182	ASN
1	F	189	HIS
1	F	190	ASN
1	F	217	ASN
1	G	135	ASN
1	G	182	ASN
1	G	194	ASN
1	G	217	ASN
1	H	135	ASN
1	H	189	HIS
1	H	195	GLN
1	H	217	ASN
1	I	42	GLN
1	I	58	GLN
1	I	74	HIS
1	I	189	HIS
1	I	190	ASN
1	I	217	ASN
1	J	74	HIS
1	J	78	GLN
1	J	83	ASN

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	J	182	ASN
1	J	189	HIS
1	J	195	GLN
1	J	217	ASN
1	K	74	HIS
1	K	86	GLN
1	K	135	ASN
1	K	217	ASN
1	L	42	GLN
1	L	194	ASN
1	L	217	ASN
1	M	74	HIS
1	M	188	ASN
1	M	190	ASN
1	M	217	ASN
1	N	42	GLN
1	N	58	GLN
1	N	74	HIS
1	N	182	ASN
1	N	189	HIS
1	N	190	ASN
1	N	194	ASN
1	N	195	GLN
1	N	217	ASN
1	O	42	GLN
1	O	217	ASN
1	P	74	HIS
1	P	135	ASN
1	P	182	ASN
1	P	217	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	238/291 (81%)	-0.08	2 (0%) 86 65	15, 35, 66, 84	0
1	B	238/291 (81%)	0.16	9 (3%) 40 16	17, 41, 71, 84	0
1	C	244/291 (83%)	-0.19	2 (0%) 86 65	13, 32, 58, 78	0
1	D	244/291 (83%)	-0.09	3 (1%) 79 54	14, 36, 65, 92	0
1	E	238/291 (81%)	0.06	4 (1%) 70 41	15, 40, 71, 83	0
1	F	238/291 (81%)	0.14	9 (3%) 40 16	14, 36, 67, 86	0
1	G	236/291 (81%)	-0.09	1 (0%) 92 79	18, 37, 66, 77	0
1	H	245/291 (84%)	-0.01	2 (0%) 86 65	13, 30, 57, 71	0
1	I	238/291 (81%)	0.08	9 (3%) 40 16	23, 42, 72, 85	0
1	J	238/291 (81%)	-0.13	3 (1%) 77 51	16, 39, 68, 81	0
1	K	244/291 (83%)	-0.22	1 (0%) 92 79	10, 35, 68, 85	0
1	L	236/291 (81%)	-0.04	4 (1%) 70 41	18, 34, 64, 76	0
1	M	238/291 (81%)	0.19	12 (5%) 28 10	17, 40, 71, 87	0
1	N	238/291 (81%)	-0.19	4 (1%) 70 41	14, 40, 69, 83	0
1	O	236/291 (81%)	-0.17	3 (1%) 77 51	9, 34, 64, 79	0
1	P	244/291 (83%)	-0.13	1 (0%) 92 79	12, 35, 67, 87	0
All	All	3833/4656 (82%)	-0.04	69 (1%) 68 40	9, 37, 67, 92	0

All (69) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	261	SER	4.4
1	M	83	ASN	4.1
1	D	150	ASN	3.9
1	I	83	ASN	3.9
1	L	243	ASN	3.7

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	L	262	LYS	3.6
1	A	245	SER	3.5
1	J	83	ASN	3.5
1	N	243	ASN	3.4
1	M	151	LEU	3.4
1	M	244	ILE	3.3
1	M	243	ASN	3.3
1	J	245	SER	3.3
1	L	242	SER	3.1
1	B	247	VAL	3.0
1	M	236	ASN	3.0
1	F	256	GLY	2.9
1	M	247	VAL	2.9
1	N	82	SER	2.9
1	E	241	PRO	2.9
1	D	243	ASN	2.9
1	I	254	SER	2.8
1	P	150	ASN	2.8
1	N	84	THR	2.8
1	B	246	LYS	2.8
1	M	239	SER	2.8
1	F	254	SER	2.7
1	L	245	SER	2.6
1	H	83	ASN	2.6
1	O	244	ILE	2.6
1	M	241	PRO	2.6
1	M	245	SER	2.5
1	G	82	SER	2.5
1	H	242	SER	2.5
1	F	252	ASN	2.4
1	I	86	GLN	2.4
1	E	261	SER	2.4
1	F	245	SER	2.4
1	B	239	SER	2.4
1	K	266	LEU	2.4
1	I	84	THR	2.4
1	J	243	ASN	2.4
1	E	239	SER	2.3
1	I	82	SER	2.3
1	A	244	ILE	2.3
1	B	248	PHE	2.3
1	I	239	SER	2.3

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	E	247	VAL	2.3
1	O	262	LYS	2.3
1	F	261	SER	2.2
1	C	186	SER	2.2
1	F	83	ASN	2.2
1	F	241	PRO	2.2
1	B	238	VAL	2.2
1	I	221	VAL	2.1
1	M	84	THR	2.1
1	F	104	ASN	2.1
1	B	84	THR	2.1
1	C	84	THR	2.1
1	M	255	GLU	2.1
1	M	81	ASP	2.1
1	D	286	ASN	2.1
1	B	234	THR	2.1
1	F	239	SER	2.0
1	I	167	ILE	2.0
1	B	177	GLY	2.0
1	N	83	ASN	2.0
1	O	242	SER	2.0
1	I	220	ILE	2.0

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

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

## 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

There are no ligands in this entry.

## 6.5 Other polymers ⓘ

There are no such residues in this entry.