



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 19, 2016 – 10:39 PM GMT

PDB ID : 4WIZ
Title : Crystal structure of Grouper nervous necrosis virus-like particle at 3.6Å
Authors : Chen, N.C.; Chen, C.J.; Yoshimura, M.; Guan, H.H.; Chen, T.Y.
Deposited on : 2014-09-28
Resolution : 3.60 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
A user guide is available at
<http://wwpdb.org/validation/2016/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
Mogul : unknown
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026982
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20026982

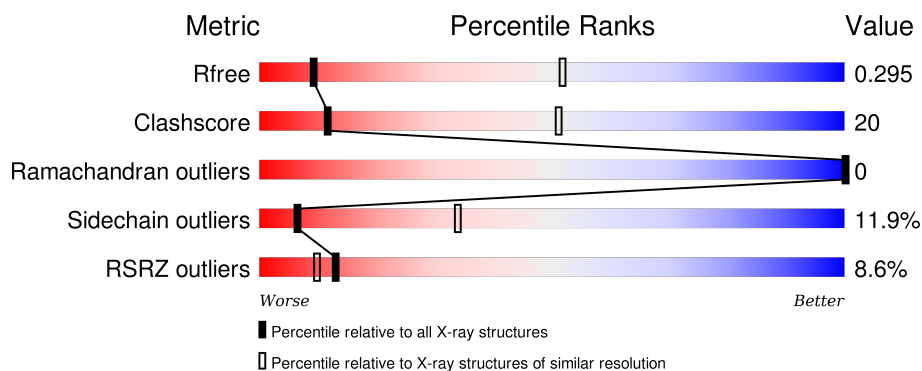
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.60 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}	91344	1408 (3.80-3.40)
Clashscore	102246	1010 (3.74-3.46)
Ramachandran outliers	100387	1007 (3.76-3.44)
Sidechain outliers	100360	1007 (3.76-3.44)
RSRZ outliers	91569	1003 (3.78-3.42)

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 ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	AA	338	<div> <div>18%</div> <div>49% 33% 15%</div> </div>
1	AB	338	<div> <div>8%</div> <div>48% 33% 15%</div> </div>
1	AC	338	<div> <div>5%</div> <div>47% 33% 15%</div> </div>
1	AD	338	<div> <div>2%</div> <div>48% 31% 5% 15%</div> </div>
1	AE	338	<div> <div>2%</div> <div>51% 29% 15%</div> </div>

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	AF	338	
1	AG	338	
1	AH	338	
1	AI	338	
1	AJ	338	
1	AK	338	
1	AL	338	
1	AM	338	
1	AN	338	
1	AO	338	
1	AP	338	
1	AQ	338	
1	AR	338	
1	AS	338	
1	AT	338	
1	AU	338	
1	AV	338	
1	AW	338	
1	AX	338	
1	AY	338	
1	AZ	338	
1	Aa	338	
1	Ab	338	
1	Ac	338	
1	Ad	338	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	BA	338	
1	BB	338	
1	BC	338	
1	BD	338	
1	BE	338	
1	BF	338	
1	BG	338	
1	BH	338	
1	BI	338	
1	BJ	338	
1	BK	338	
1	BL	338	
1	BM	338	
1	BN	338	
1	BO	338	
1	BP	338	
1	BQ	338	
1	BR	338	
1	BS	338	
1	BT	338	
1	BU	338	
1	BV	338	
1	BW	338	
1	BX	338	
1	BY	338	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	BZ	338	
1	Ba	338	
1	Bb	338	
1	Bc	338	
1	Bd	338	
1	CA	338	
1	CB	338	
1	CC	338	
1	CD	338	
1	CE	338	
1	CF	338	
1	CG	338	
1	CH	338	
1	CI	338	
1	CJ	338	
1	CK	338	
1	CL	338	
1	CM	338	
1	CN	338	
1	CO	338	
1	CP	338	
1	CQ	338	
1	CR	338	
1	CS	338	
1	CT	338	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	CU	338	
1	CV	338	
1	CW	338	
1	CX	338	
1	CY	338	
1	CZ	338	
1	Ca	338	
1	Cb	338	
1	Cc	338	
1	Cd	338	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 203250 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 Coat protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	BA	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			
1	AA	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	CA	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	BB	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			
1	AB	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	CB	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	BC	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			
1	AC	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	CC	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	BD	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			
1	AD	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	CD	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	BE	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			
1	AE	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	CE	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	BF	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AF	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	CF	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	BG	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			
1	AG	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	CG	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	BH	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			
1	AH	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	CH	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	BI	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			
1	AI	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	CI	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	BJ	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			
1	AJ	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	CJ	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	BK	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			
1	AK	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	CK	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	BL	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			
1	AL	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	CL	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	BM	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AM	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	CM	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	BN	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			
1	AN	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	CN	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	BO	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			
1	AO	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	CO	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	BP	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			
1	AP	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	CP	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	BQ	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			
1	AQ	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	CQ	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	BR	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			
1	AR	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	CR	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	BS	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			
1	AS	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	CS	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	BT	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AT	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	CT	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	BU	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			
1	AU	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	CU	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	BV	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			
1	AV	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	CV	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	BW	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			
1	AW	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	CW	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	BX	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			
1	AX	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	CX	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	BY	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			
1	AY	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	CY	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	BZ	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			
1	AZ	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	CZ	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	Ba	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Aa	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	Ca	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	Bb	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			
1	Ab	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	Cb	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	Bc	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			
1	Ac	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	Cc	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			
1	Bd	286	Total	C	N	O	S	0	0	0
			2214	1401	381	425	7			
1	Ad	287	Total	C	N	O	S	0	0	0
			2218	1403	382	426	7			
1	Cd	304	Total	C	N	O	S	0	0	0
			2340	1477	406	450	7			

There are 90 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BA	214	ASN	THR	engineered mutation	UNP Q8JNX5
AA	214	ASN	THR	engineered mutation	UNP Q8JNX5
CA	214	ASN	THR	engineered mutation	UNP Q8JNX5
BB	214	ASN	THR	engineered mutation	UNP Q8JNX5
AB	214	ASN	THR	engineered mutation	UNP Q8JNX5
CB	214	ASN	THR	engineered mutation	UNP Q8JNX5
BC	214	ASN	THR	engineered mutation	UNP Q8JNX5
AC	214	ASN	THR	engineered mutation	UNP Q8JNX5
CC	214	ASN	THR	engineered mutation	UNP Q8JNX5
BD	214	ASN	THR	engineered mutation	UNP Q8JNX5
AD	214	ASN	THR	engineered mutation	UNP Q8JNX5
CD	214	ASN	THR	engineered mutation	UNP Q8JNX5
BE	214	ASN	THR	engineered mutation	UNP Q8JNX5
AE	214	ASN	THR	engineered mutation	UNP Q8JNX5
CE	214	ASN	THR	engineered mutation	UNP Q8JNX5
BF	214	ASN	THR	engineered mutation	UNP Q8JNX5
AF	214	ASN	THR	engineered mutation	UNP Q8JNX5

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
CF	214	ASN	THR	engineered mutation	UNP Q8JNX5
BG	214	ASN	THR	engineered mutation	UNP Q8JNX5
AG	214	ASN	THR	engineered mutation	UNP Q8JNX5
CG	214	ASN	THR	engineered mutation	UNP Q8JNX5
BH	214	ASN	THR	engineered mutation	UNP Q8JNX5
AH	214	ASN	THR	engineered mutation	UNP Q8JNX5
CH	214	ASN	THR	engineered mutation	UNP Q8JNX5
BI	214	ASN	THR	engineered mutation	UNP Q8JNX5
AI	214	ASN	THR	engineered mutation	UNP Q8JNX5
CI	214	ASN	THR	engineered mutation	UNP Q8JNX5
BJ	214	ASN	THR	engineered mutation	UNP Q8JNX5
AJ	214	ASN	THR	engineered mutation	UNP Q8JNX5
CJ	214	ASN	THR	engineered mutation	UNP Q8JNX5
BK	214	ASN	THR	engineered mutation	UNP Q8JNX5
AK	214	ASN	THR	engineered mutation	UNP Q8JNX5
CK	214	ASN	THR	engineered mutation	UNP Q8JNX5
BL	214	ASN	THR	engineered mutation	UNP Q8JNX5
AL	214	ASN	THR	engineered mutation	UNP Q8JNX5
CL	214	ASN	THR	engineered mutation	UNP Q8JNX5
BM	214	ASN	THR	engineered mutation	UNP Q8JNX5
AM	214	ASN	THR	engineered mutation	UNP Q8JNX5
CM	214	ASN	THR	engineered mutation	UNP Q8JNX5
BN	214	ASN	THR	engineered mutation	UNP Q8JNX5
AN	214	ASN	THR	engineered mutation	UNP Q8JNX5
CN	214	ASN	THR	engineered mutation	UNP Q8JNX5
BO	214	ASN	THR	engineered mutation	UNP Q8JNX5
AO	214	ASN	THR	engineered mutation	UNP Q8JNX5
CO	214	ASN	THR	engineered mutation	UNP Q8JNX5
BP	214	ASN	THR	engineered mutation	UNP Q8JNX5
AP	214	ASN	THR	engineered mutation	UNP Q8JNX5
CP	214	ASN	THR	engineered mutation	UNP Q8JNX5
BQ	214	ASN	THR	engineered mutation	UNP Q8JNX5
AQ	214	ASN	THR	engineered mutation	UNP Q8JNX5
CQ	214	ASN	THR	engineered mutation	UNP Q8JNX5
BR	214	ASN	THR	engineered mutation	UNP Q8JNX5
AR	214	ASN	THR	engineered mutation	UNP Q8JNX5
CR	214	ASN	THR	engineered mutation	UNP Q8JNX5
BS	214	ASN	THR	engineered mutation	UNP Q8JNX5
AS	214	ASN	THR	engineered mutation	UNP Q8JNX5
CS	214	ASN	THR	engineered mutation	UNP Q8JNX5
BT	214	ASN	THR	engineered mutation	UNP Q8JNX5
AT	214	ASN	THR	engineered mutation	UNP Q8JNX5

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
CT	214	ASN	THR	engineered mutation	UNP Q8JNX5
BU	214	ASN	THR	engineered mutation	UNP Q8JNX5
AU	214	ASN	THR	engineered mutation	UNP Q8JNX5
CU	214	ASN	THR	engineered mutation	UNP Q8JNX5
BV	214	ASN	THR	engineered mutation	UNP Q8JNX5
AV	214	ASN	THR	engineered mutation	UNP Q8JNX5
CV	214	ASN	THR	engineered mutation	UNP Q8JNX5
BW	214	ASN	THR	engineered mutation	UNP Q8JNX5
AW	214	ASN	THR	engineered mutation	UNP Q8JNX5
CW	214	ASN	THR	engineered mutation	UNP Q8JNX5
BX	214	ASN	THR	engineered mutation	UNP Q8JNX5
AX	214	ASN	THR	engineered mutation	UNP Q8JNX5
CX	214	ASN	THR	engineered mutation	UNP Q8JNX5
BY	214	ASN	THR	engineered mutation	UNP Q8JNX5
AY	214	ASN	THR	engineered mutation	UNP Q8JNX5
CY	214	ASN	THR	engineered mutation	UNP Q8JNX5
BZ	214	ASN	THR	engineered mutation	UNP Q8JNX5
AZ	214	ASN	THR	engineered mutation	UNP Q8JNX5
CZ	214	ASN	THR	engineered mutation	UNP Q8JNX5
Ba	214	ASN	THR	engineered mutation	UNP Q8JNX5
Aa	214	ASN	THR	engineered mutation	UNP Q8JNX5
Ca	214	ASN	THR	engineered mutation	UNP Q8JNX5
Bb	214	ASN	THR	engineered mutation	UNP Q8JNX5
Ab	214	ASN	THR	engineered mutation	UNP Q8JNX5
Cb	214	ASN	THR	engineered mutation	UNP Q8JNX5
Bc	214	ASN	THR	engineered mutation	UNP Q8JNX5
Ac	214	ASN	THR	engineered mutation	UNP Q8JNX5
Cc	214	ASN	THR	engineered mutation	UNP Q8JNX5
Bd	214	ASN	THR	engineered mutation	UNP Q8JNX5
Ad	214	ASN	THR	engineered mutation	UNP Q8JNX5
Cd	214	ASN	THR	engineered mutation	UNP Q8JNX5

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	AP	1	Total Ca 1 1	0	0
2	BA	2	Total Ca 2 2	0	0
2	AK	1	Total Ca 1 1	0	0
2	AB	1	Total Ca 1 1	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	BL	2	Total 2	Ca 2	0	0
2	Ac	1	Total 1	Ca 1	0	0
2	BE	2	Total 2	Ca 2	0	0
2	AW	1	Total 1	Ca 1	0	0
2	Bd	2	Total 2	Ca 2	0	0
2	AN	1	Total 1	Ca 1	0	0
2	BP	2	Total 2	Ca 2	0	0
2	AX	1	Total 1	Ca 1	0	0
2	BI	2	Total 2	Ca 2	0	0
2	AS	1	Total 1	Ca 1	0	0
2	BB	2	Total 2	Ca 2	0	0
2	AJ	1	Total 1	Ca 1	0	0
2	BT	2	Total 2	Ca 2	0	0
2	Ba	2	Total 2	Ca 2	0	0
2	AE	1	Total 1	Ca 1	0	0
2	BM	2	Total 2	Ca 2	0	0
2	Ab	1	Total 1	Ca 1	0	0
2	BF	2	Total 2	Ca 2	0	0
2	AV	1	Total 1	Ca 1	0	0
2	BX	2	Total 2	Ca 2	0	0
2	AA	1	Total 1	Ca 1	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	BQ	2	Total 2	Ca 2	0	0
2	BJ	2	Total 2	Ca 2	0	0
2	AR	1	Total 1	Ca 1	0	0
2	BC	2	Total 2	Ca 2	0	0
2	AM	1	Total 1	Ca 1	0	0
2	BU	2	Total 2	Ca 2	0	0
2	Bb	2	Total 2	Ca 2	0	0
2	AD	1	Total 1	Ca 1	0	0
2	BN	2	Total 2	Ca 2	0	0
2	BG	2	Total 2	Ca 2	0	0
2	AI	1	Total 1	Ca 1	0	0
2	BY	2	Total 2	Ca 2	0	0
2	BR	2	Total 2	Ca 2	0	0
2	AZ	1	Total 1	Ca 1	0	0
2	Aa	1	Total 1	Ca 1	0	0
2	BK	2	Total 2	Ca 2	0	0
2	AU	1	Total 1	Ca 1	0	0
2	AL	1	Total 1	Ca 1	0	0
2	BV	2	Total 2	Ca 2	0	0
2	Bc	2	Total 2	Ca 2	0	0
2	AG	1	Total 1	Ca 1	0	0

Continued on next page...

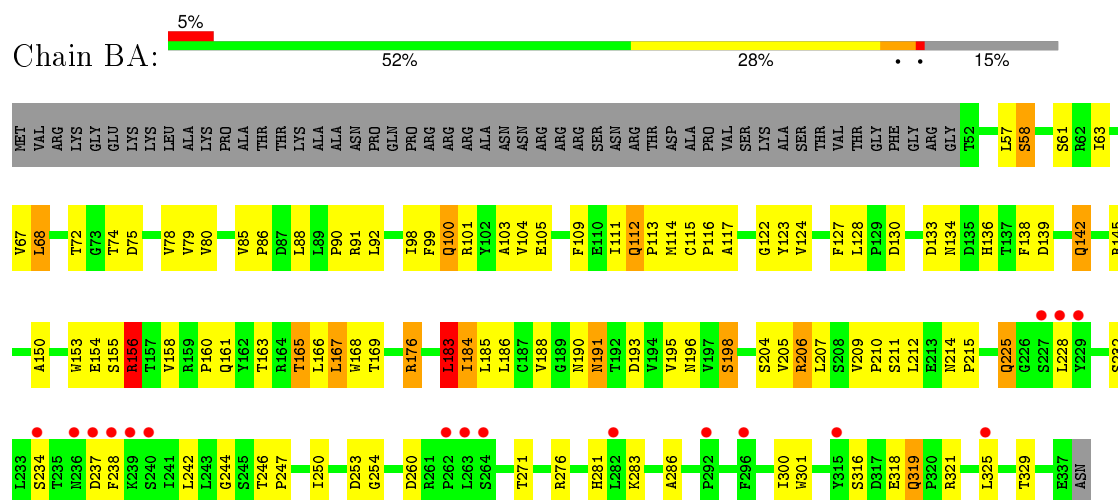
Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	BO	2	Total 2	Ca 2	0	0
2	AQ	1	Total 1	Ca 1	0	0
2	Ad	1	Total 1	Ca 1	0	0
2	AH	1	Total 1	Ca 1	0	0
2	BZ	2	Total 2	Ca 2	0	0
2	AC	1	Total 1	Ca 1	0	0
2	BS	2	Total 2	Ca 2	0	0
2	BD	2	Total 2	Ca 2	0	0
2	AT	1	Total 1	Ca 1	0	0
2	AO	1	Total 1	Ca 1	0	0
2	BW	2	Total 2	Ca 2	0	0
2	AY	1	Total 1	Ca 1	0	0
2	AF	1	Total 1	Ca 1	0	0
2	BH	2	Total 2	Ca 2	0	0

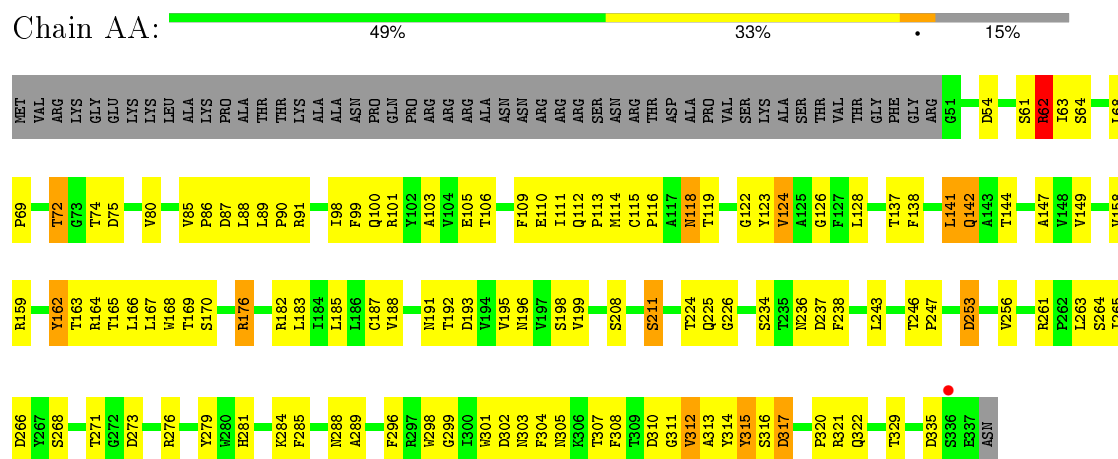
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

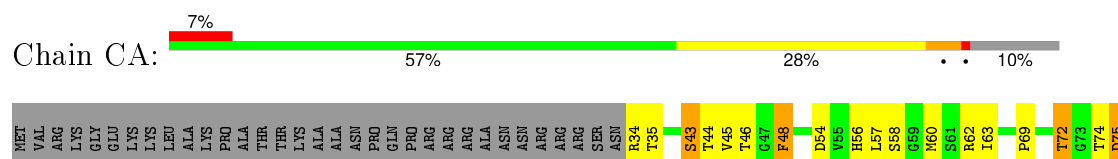
• Molecule 1: Coat protein

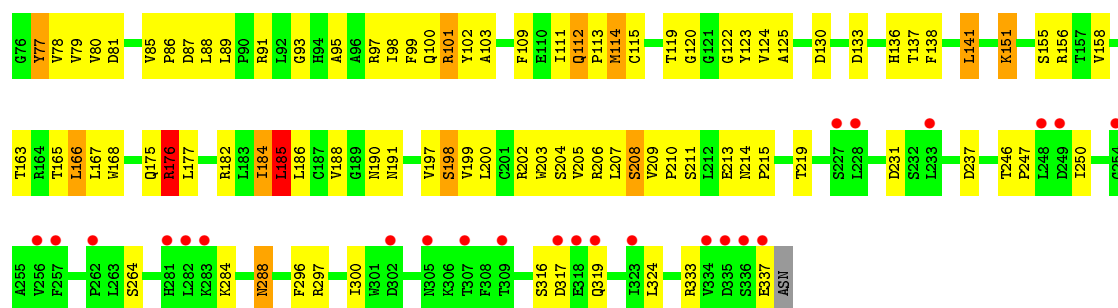


• Molecule 1: Coat protein

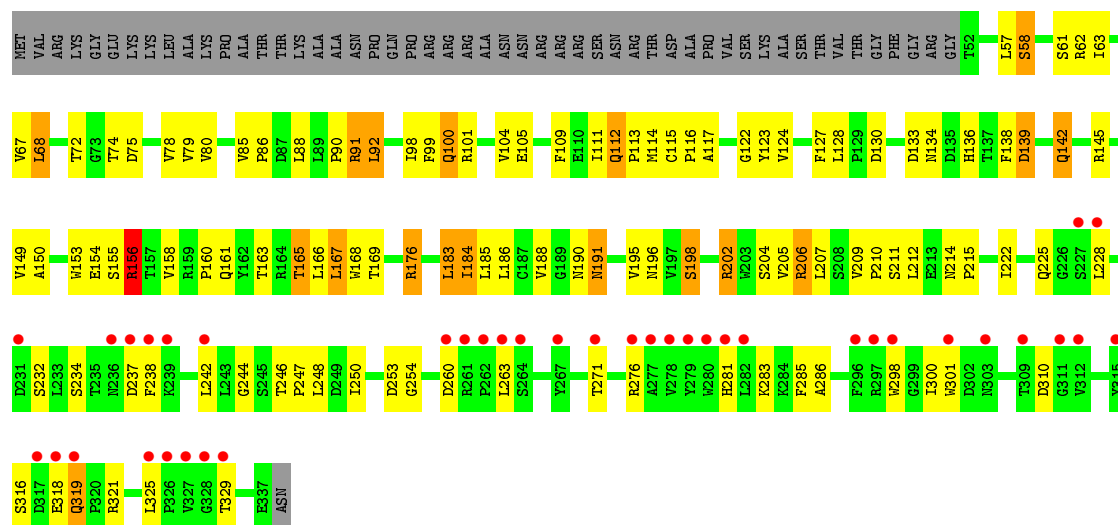


• Molecule 1: Coat protein

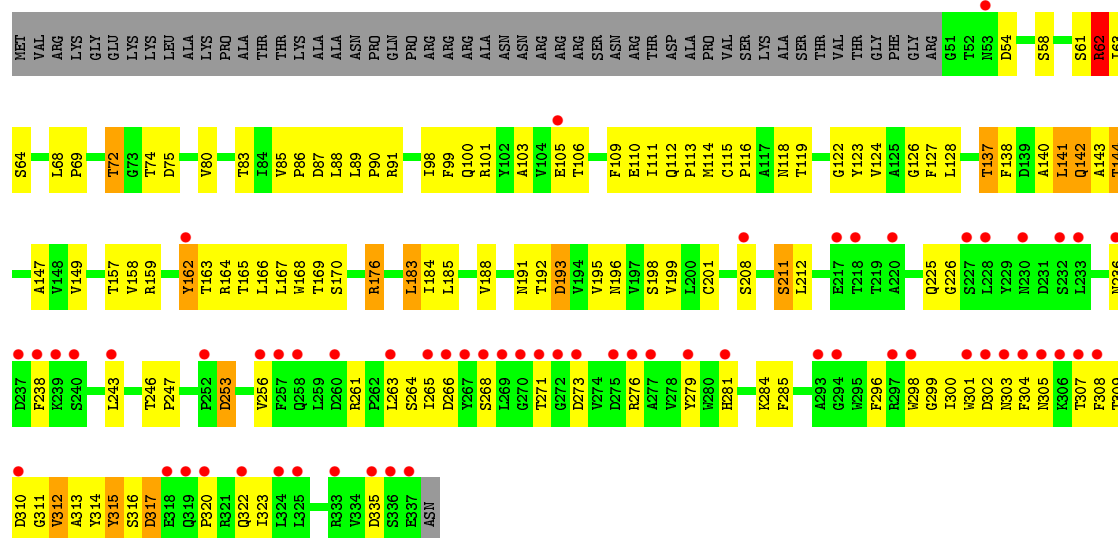




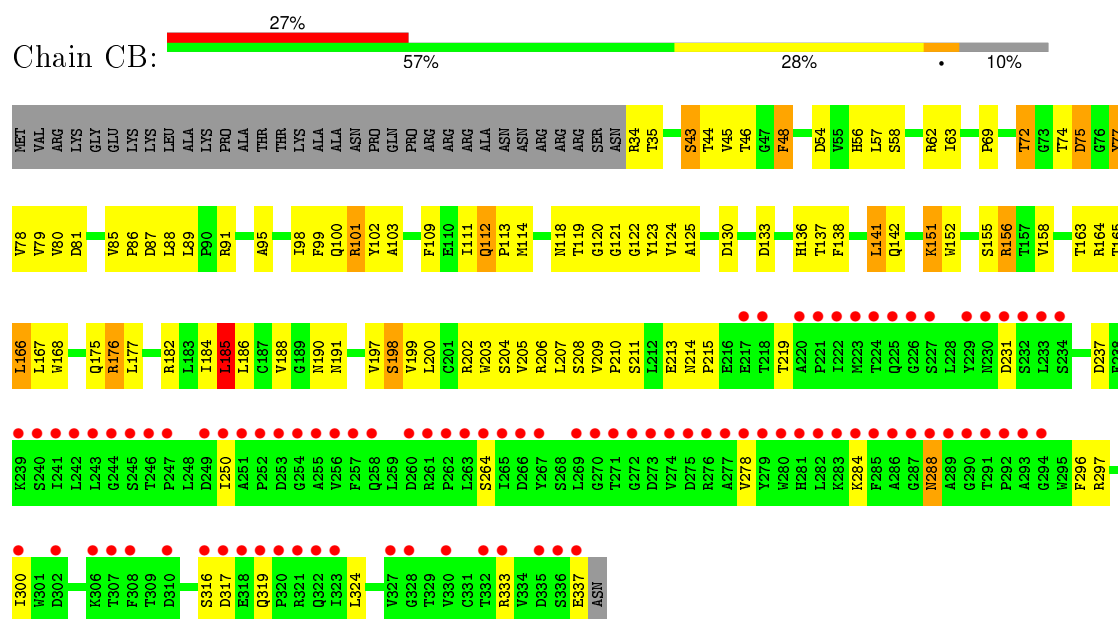
• Molecule 1: Coat protein



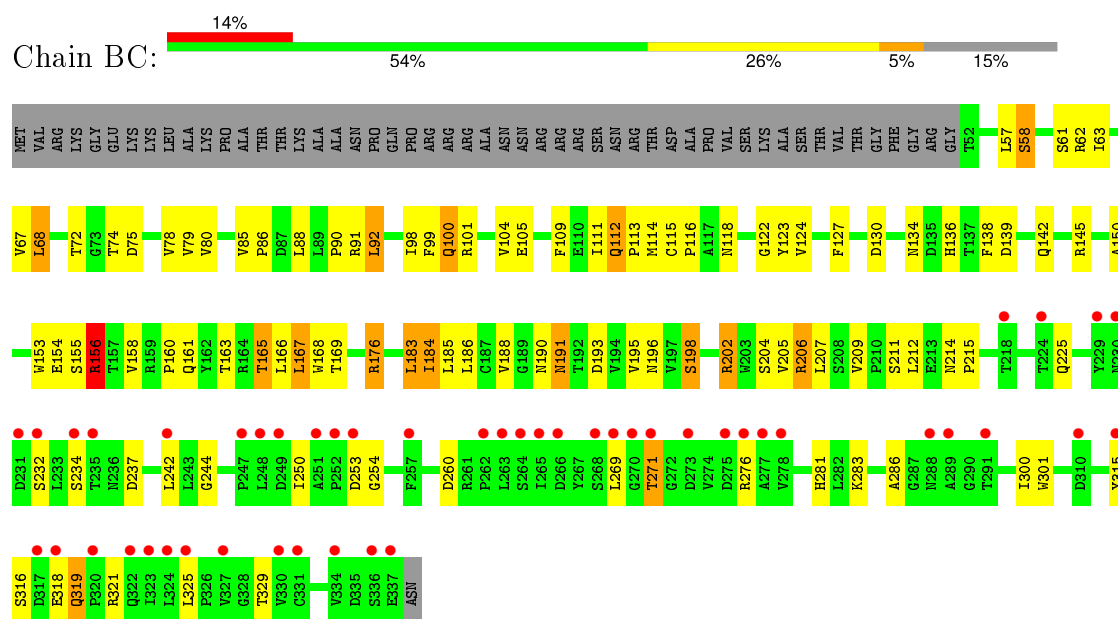
• Molecule 1: Coat protein



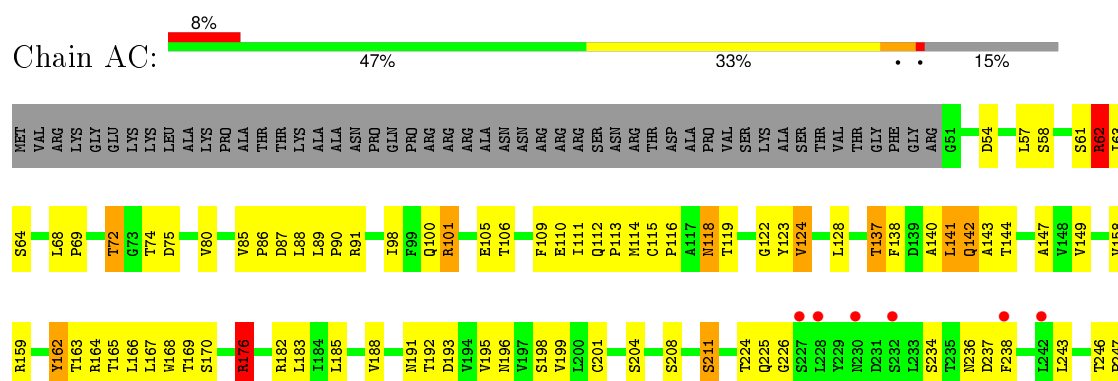
• Molecule 1: Coat protein

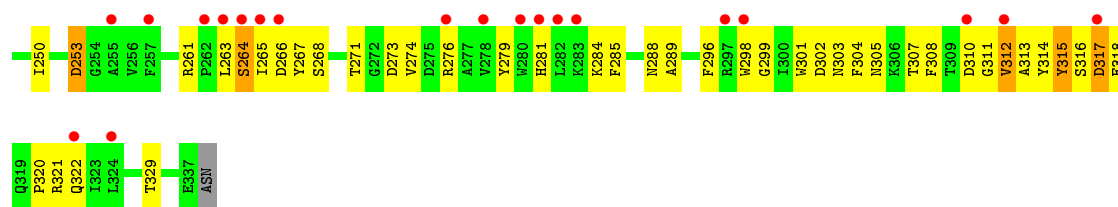


• Molecule 1: Coat protein

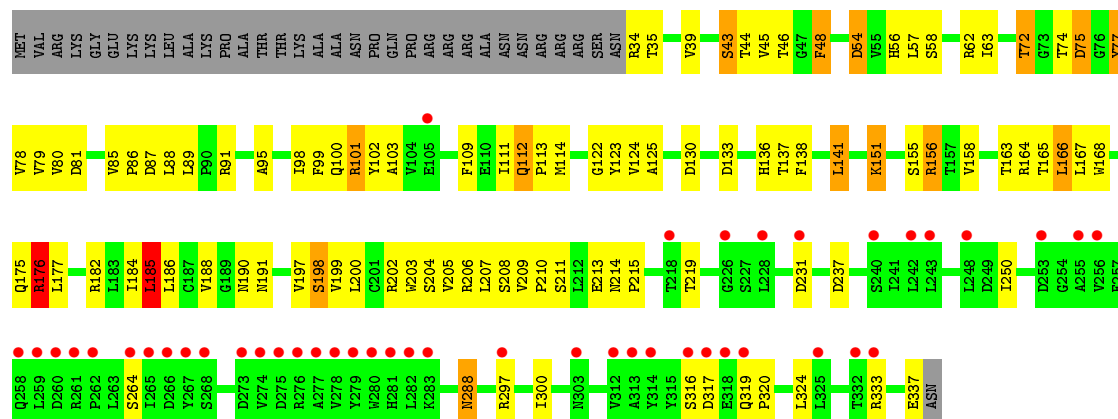


• Molecule 1: Coat protein

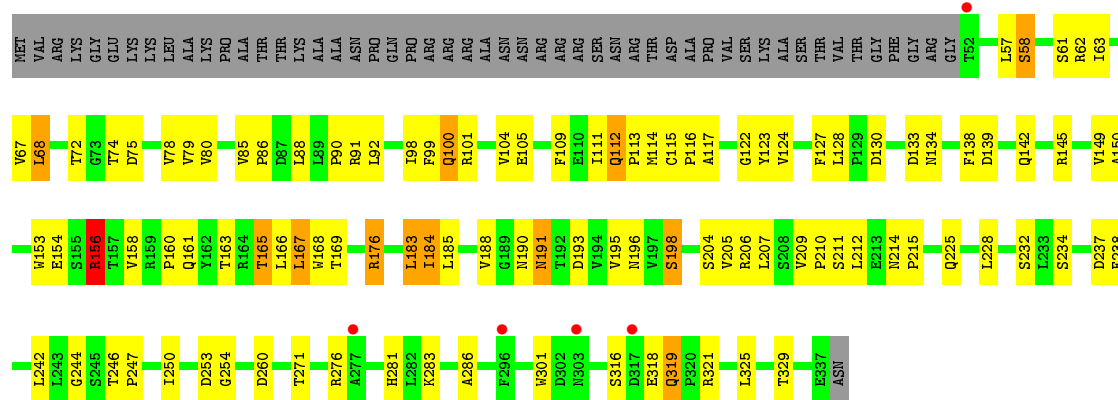




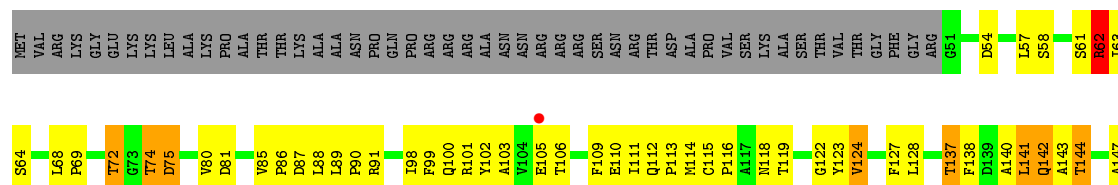
● Molecule 1: Coat protein

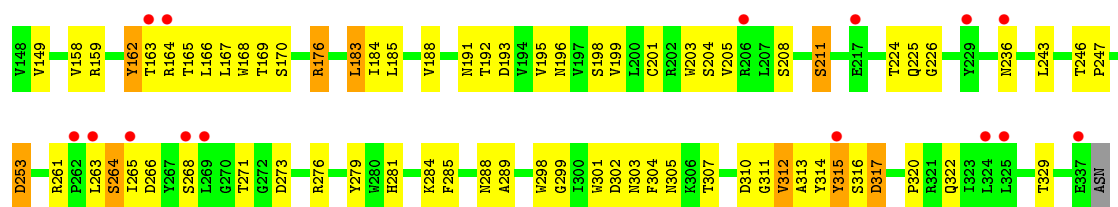


● Molecule 1: Coat protein

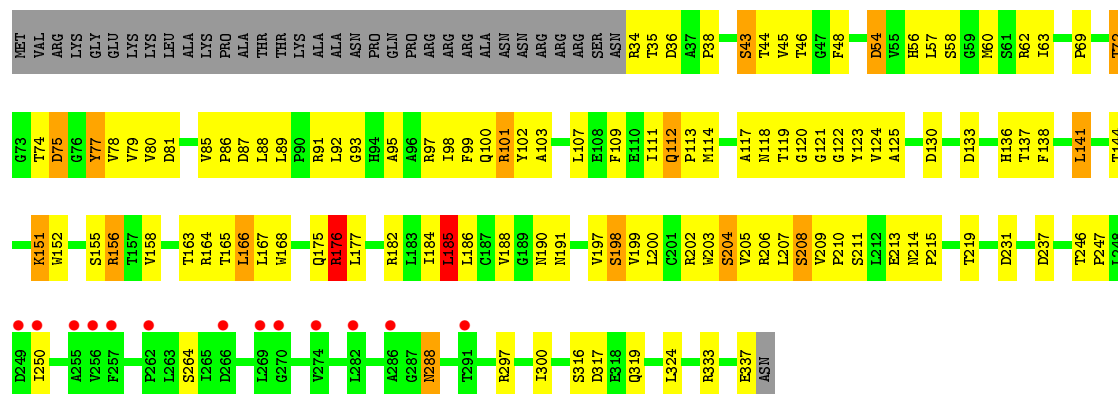


● Molecule 1: Coat protein

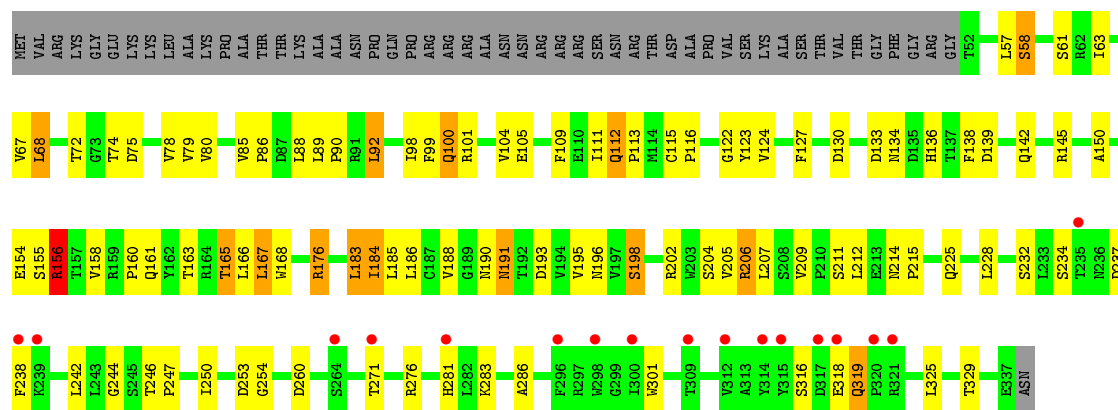




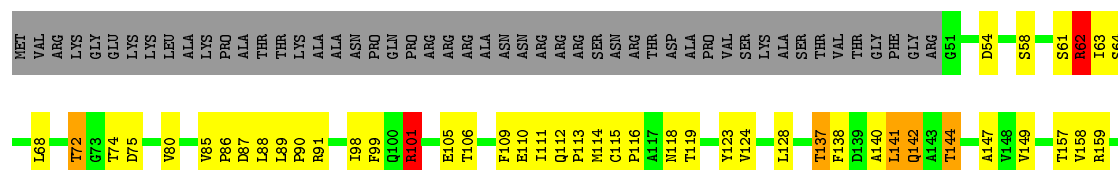
• Molecule 1: Coat protein

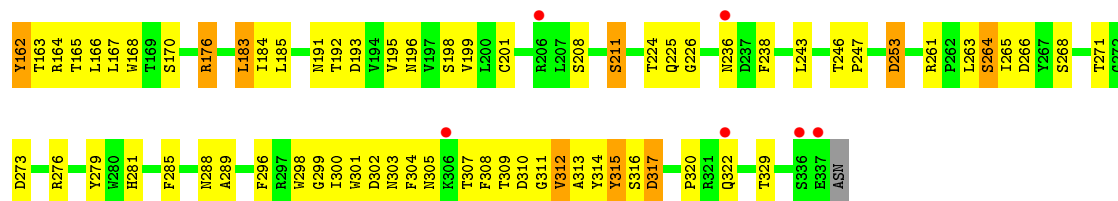


• Molecule 1: Coat protein

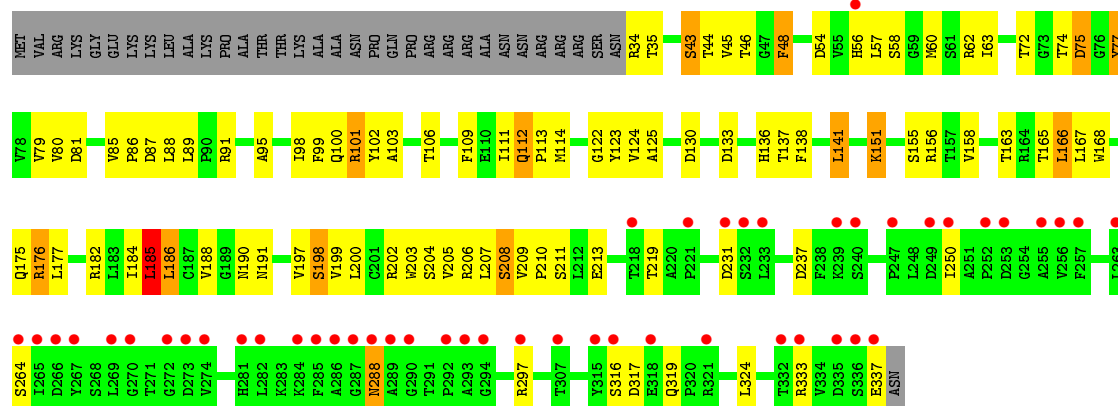


• Molecule 1: Coat protein

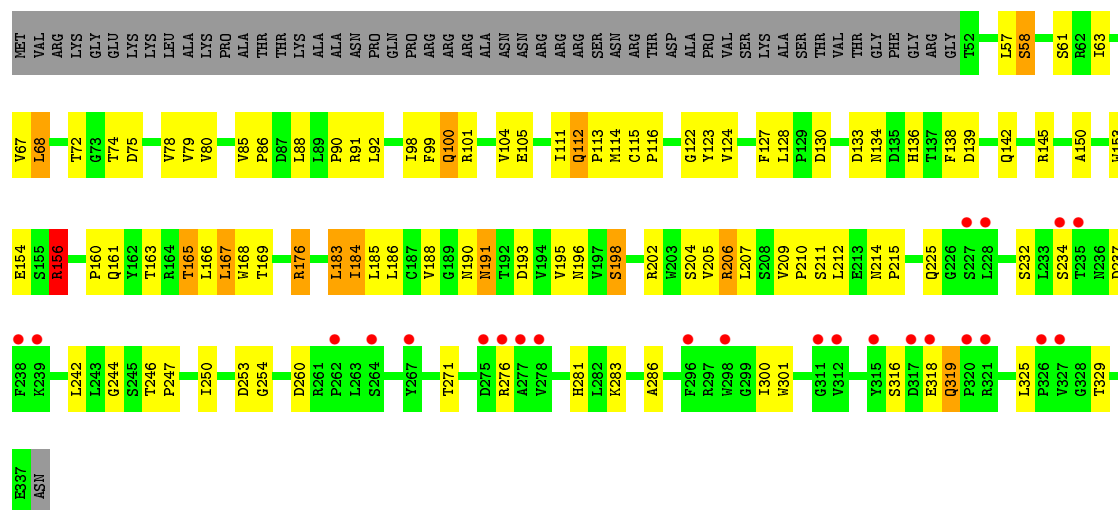




• Molecule 1: Coat protein



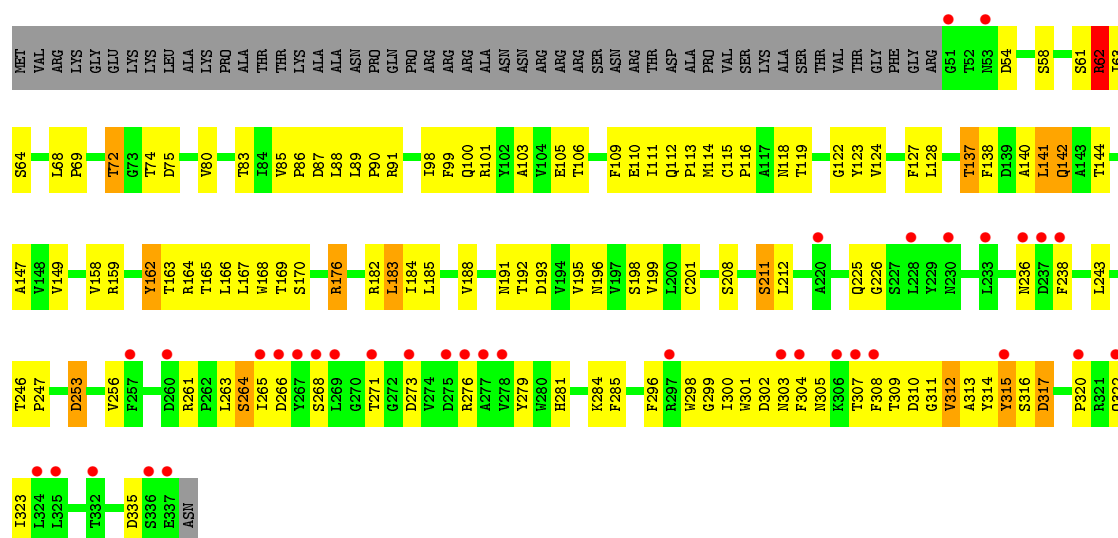
• Molecule 1: Coat protein



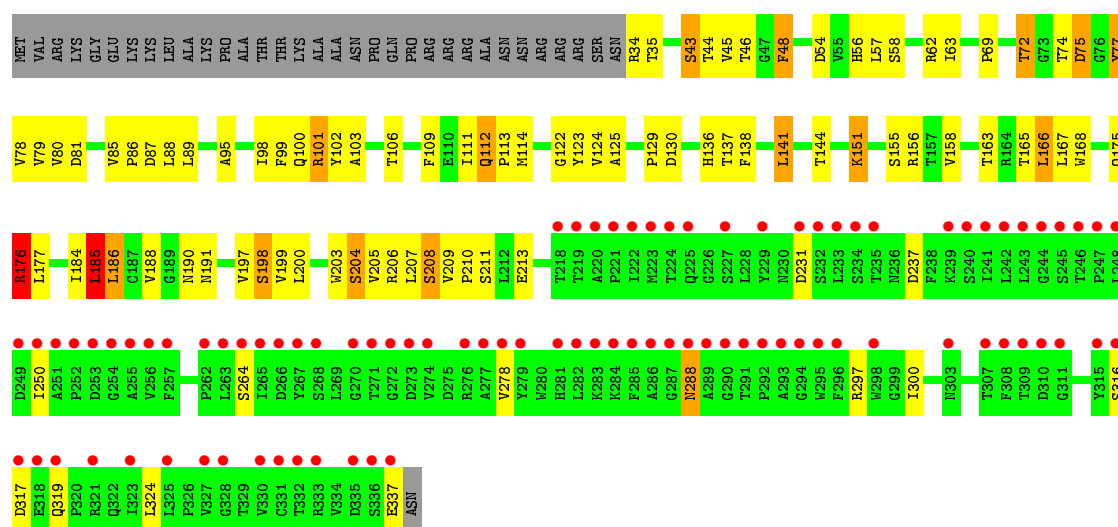
• Molecule 1: Coat protein



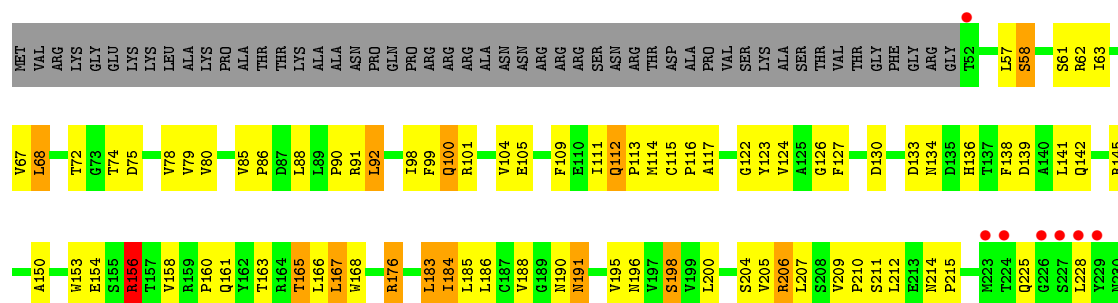




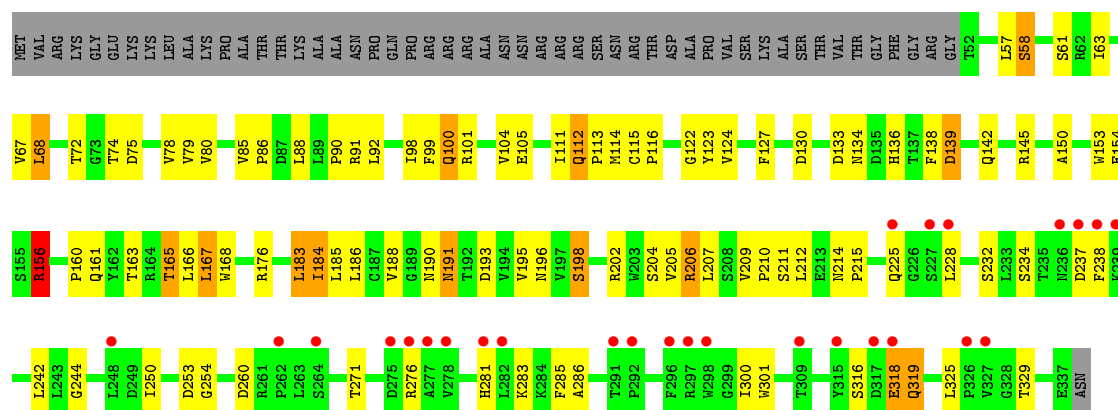
• Molecule 1: Coat protein



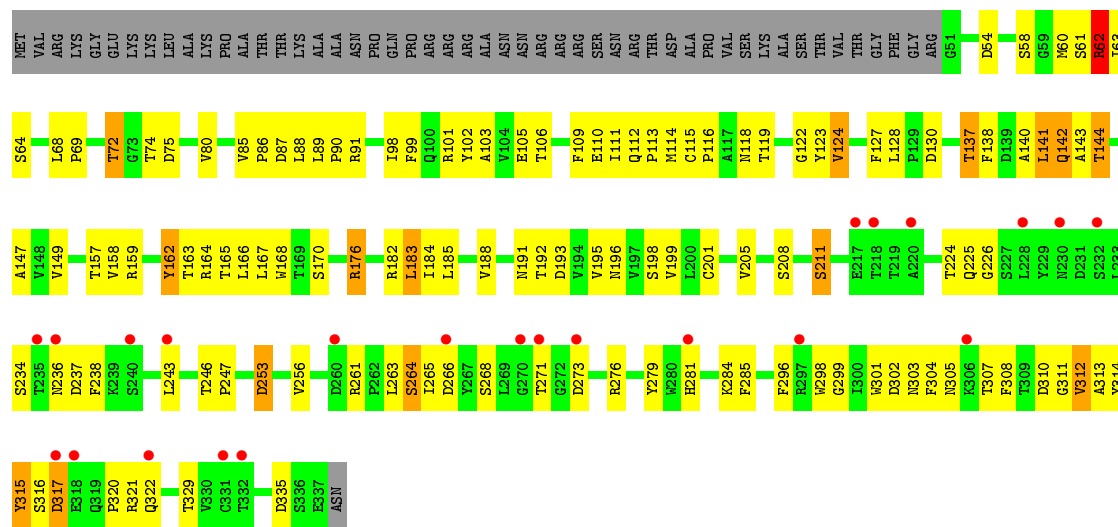
• Molecule 1: Coat protein



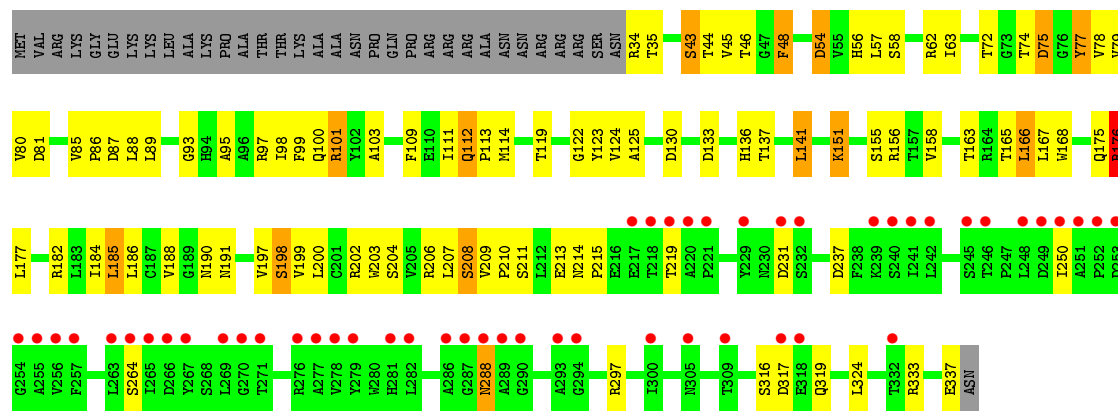




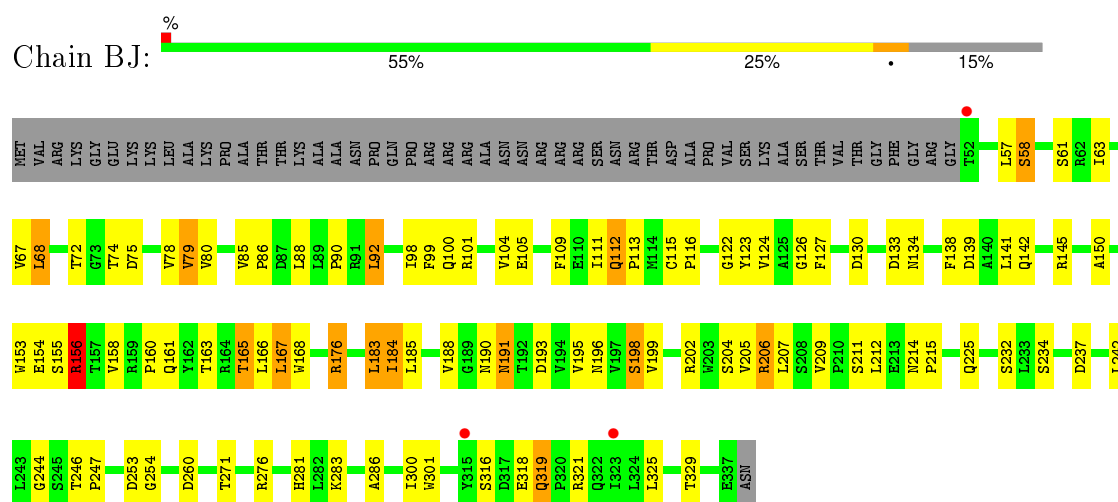
• Molecule 1: Coat protein



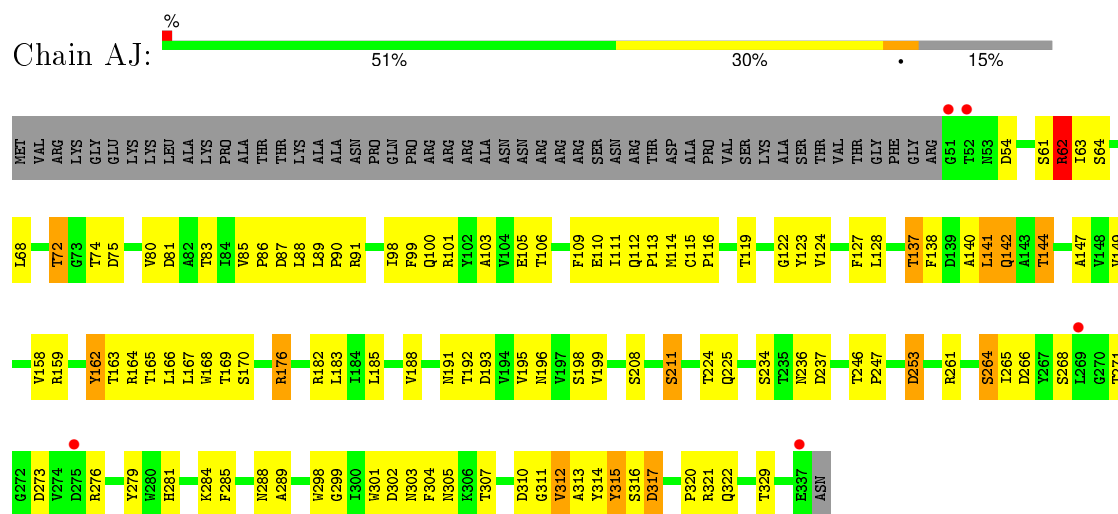
• Molecule 1: Coat protein



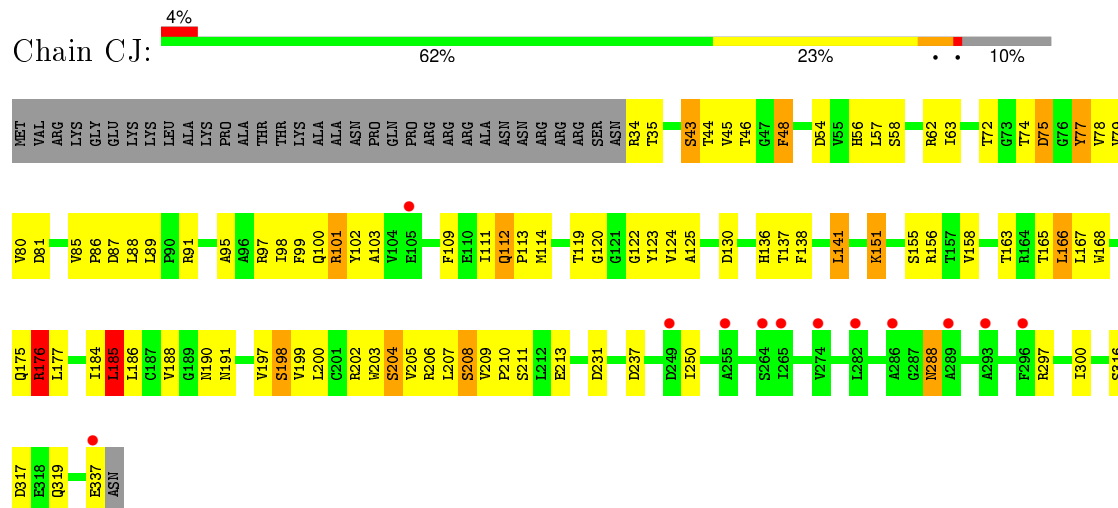
• Molecule 1: Coat protein



- Molecule 1: Coat protein

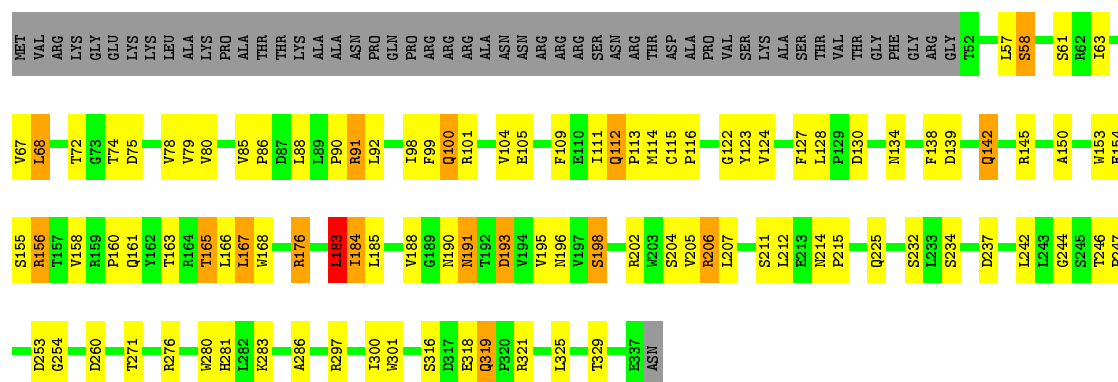


- Molecule 1: Coat protein

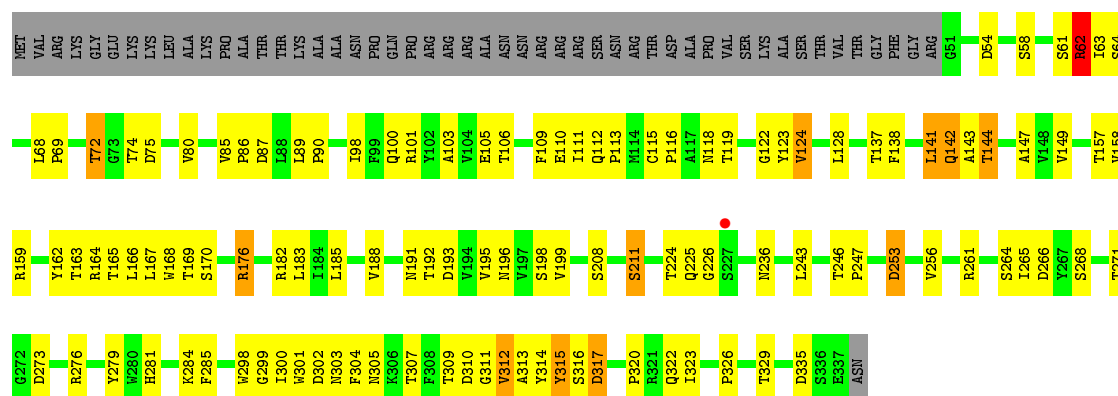


- Molecule 1: Coat protein

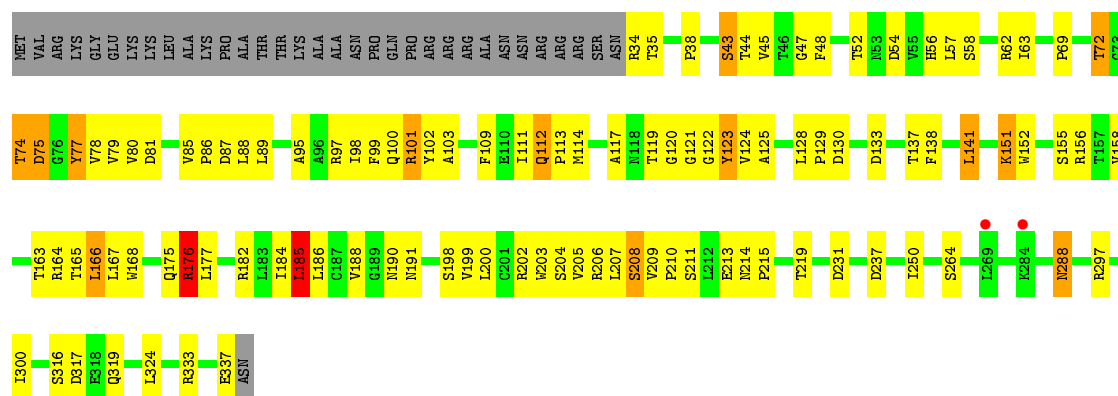




- Molecule 1: Coat protein

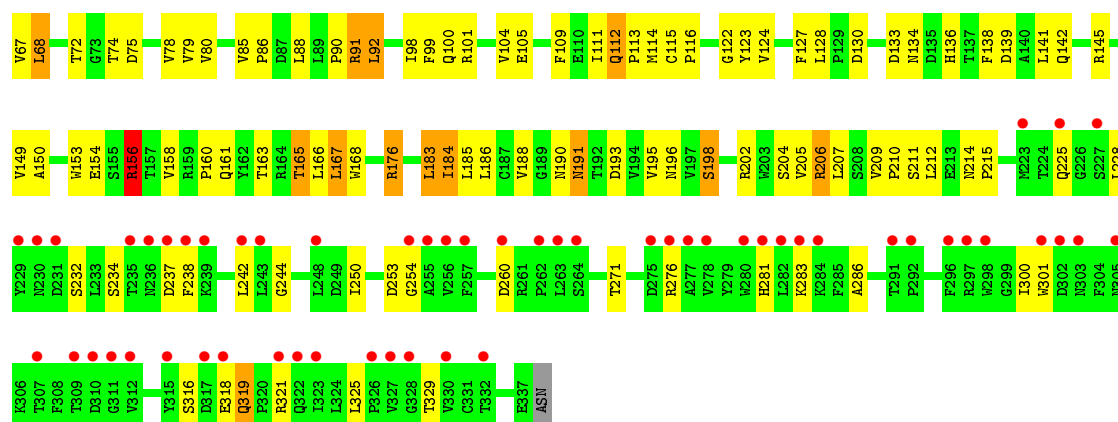


- Molecule 1: Coat protein

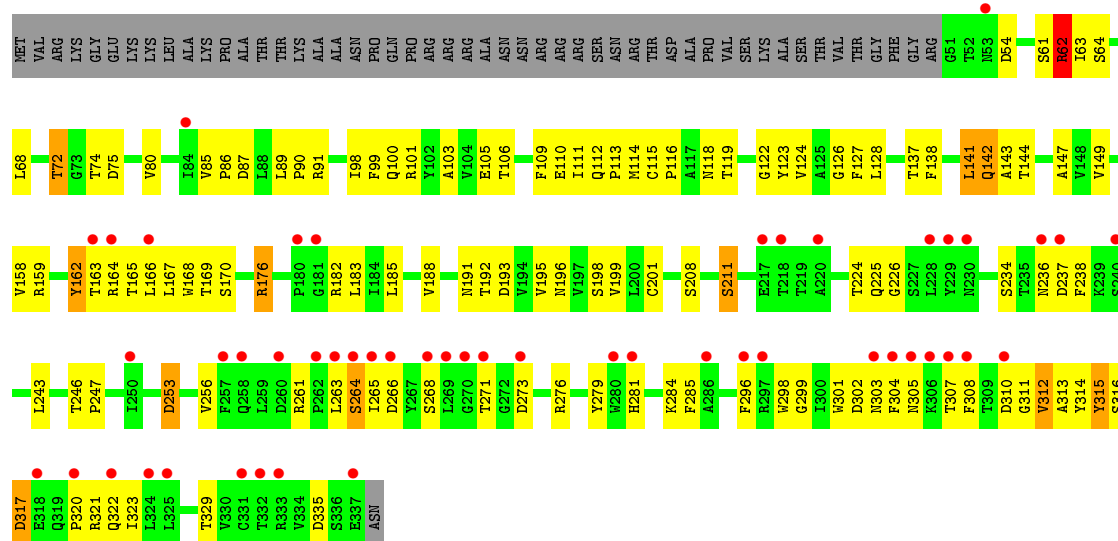


- Molecule 1: Coat protein

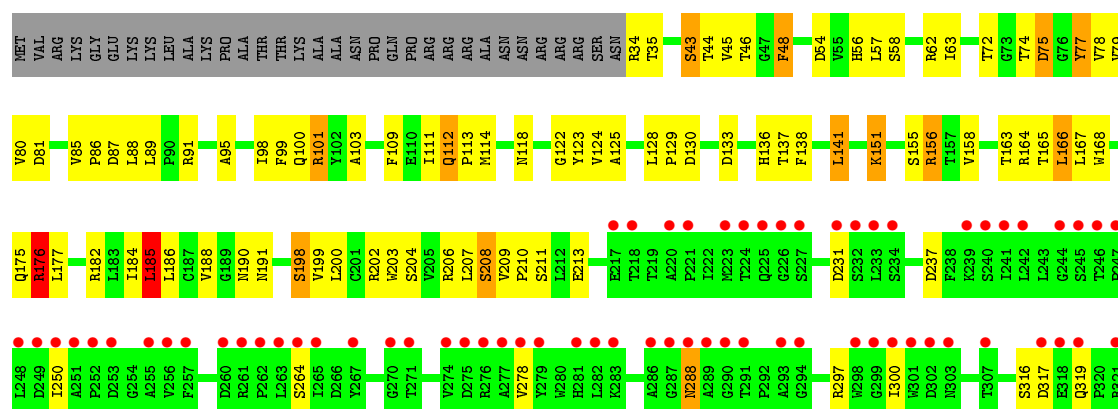


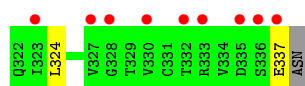


• Molecule 1: Coat protein

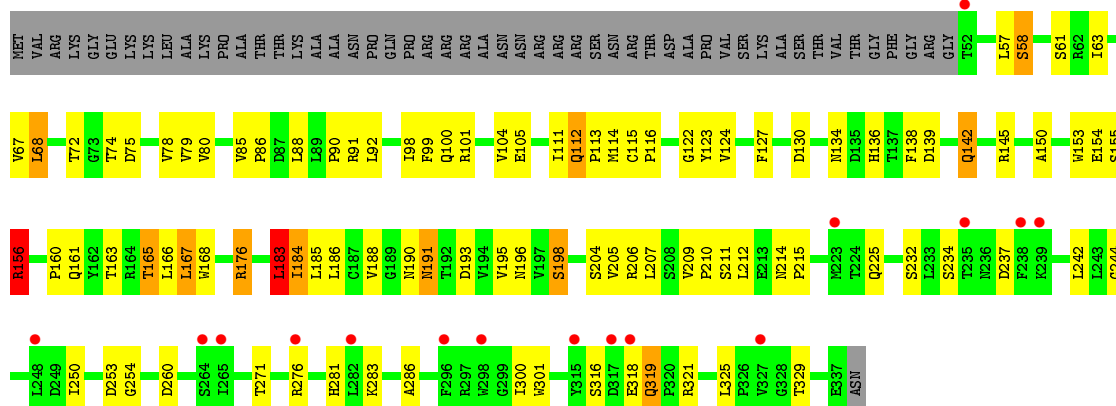


• Molecule 1: Coat protein

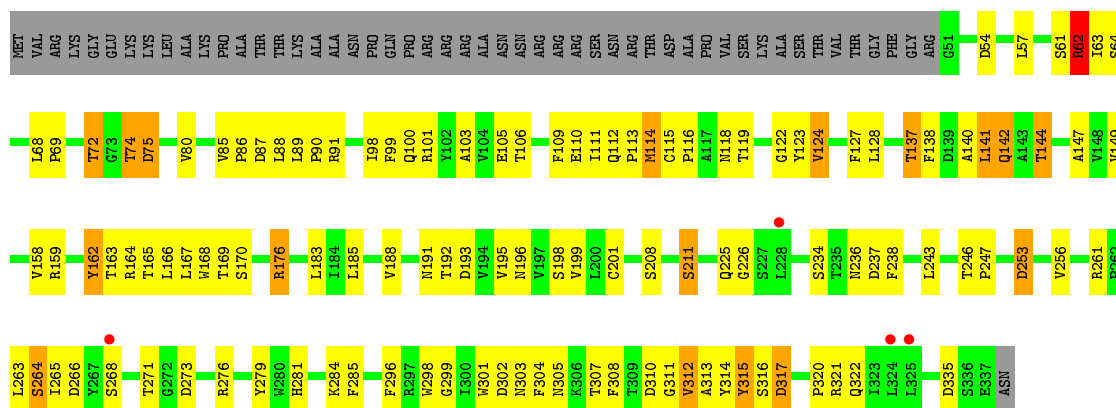




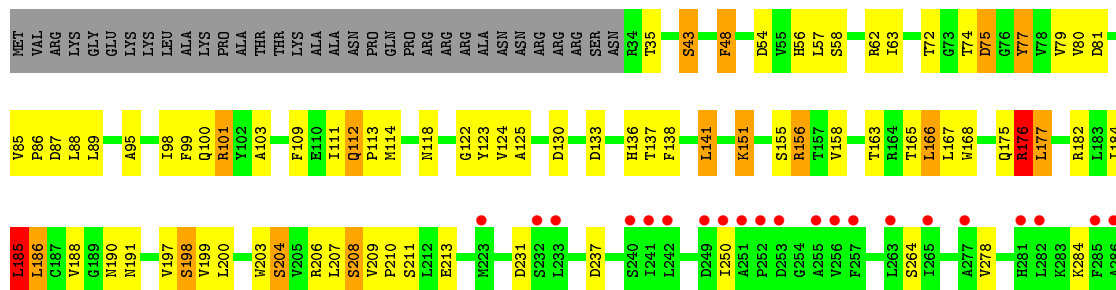
• Molecule 1: Coat protein

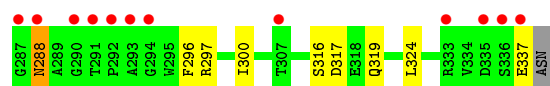


• Molecule 1: Coat protein

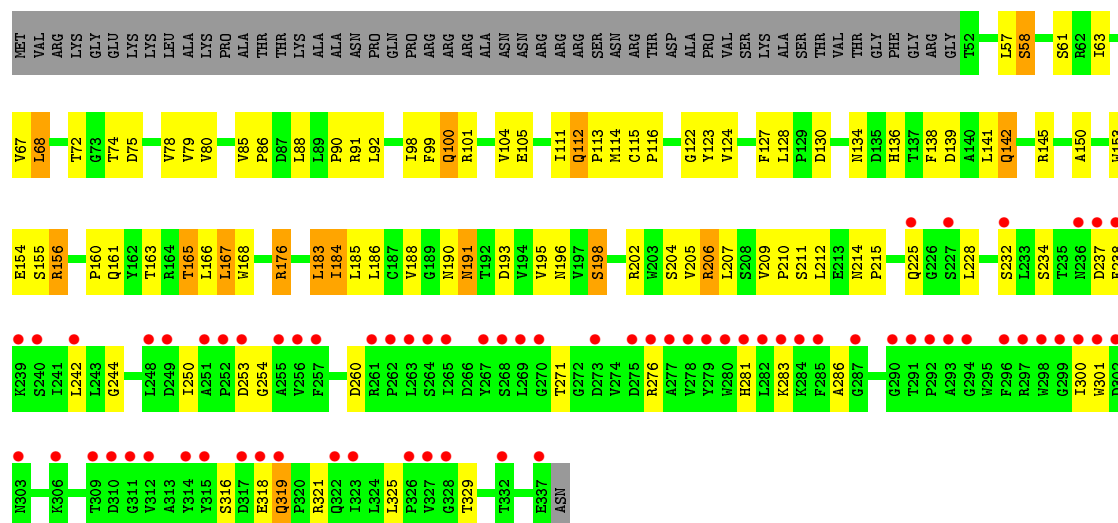


• Molecule 1: Coat protein

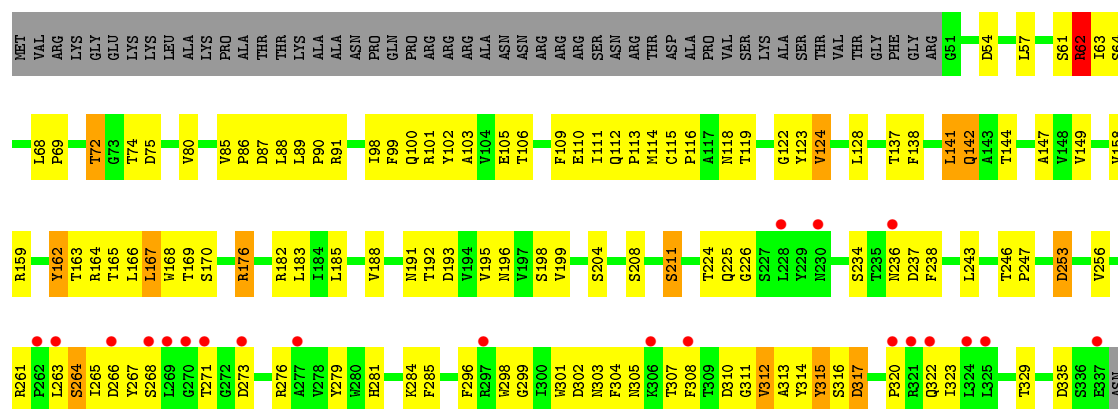




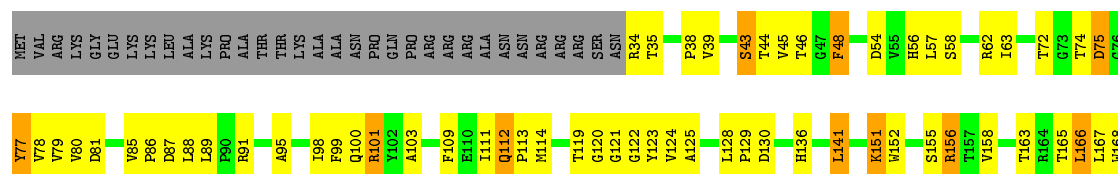
• Molecule 1: Coat protein

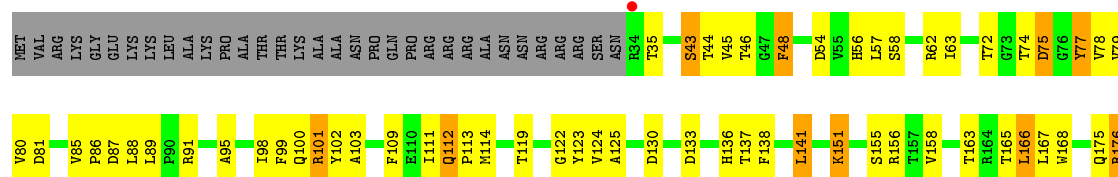


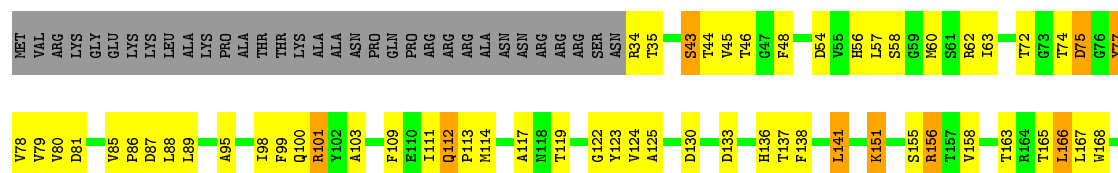
• Molecule 1: Coat protein

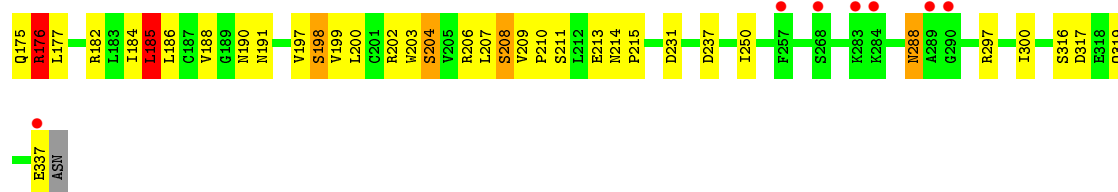


• Molecule 1: Coat protein

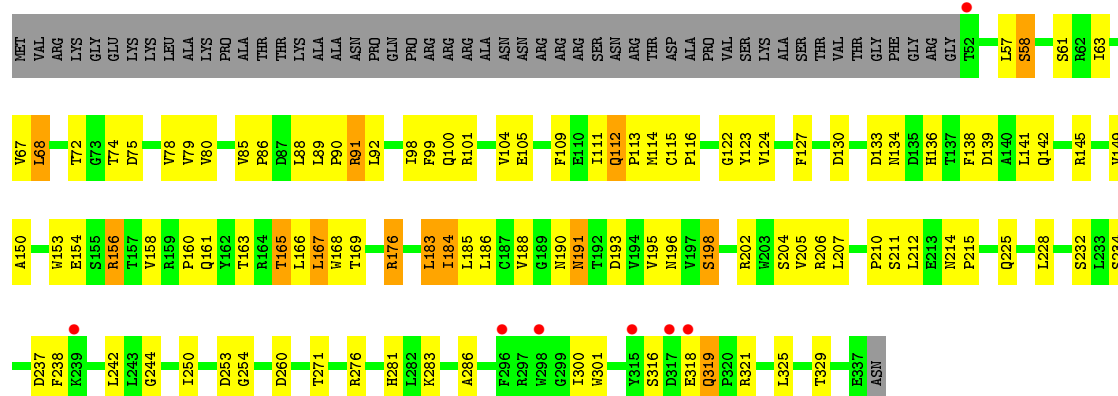




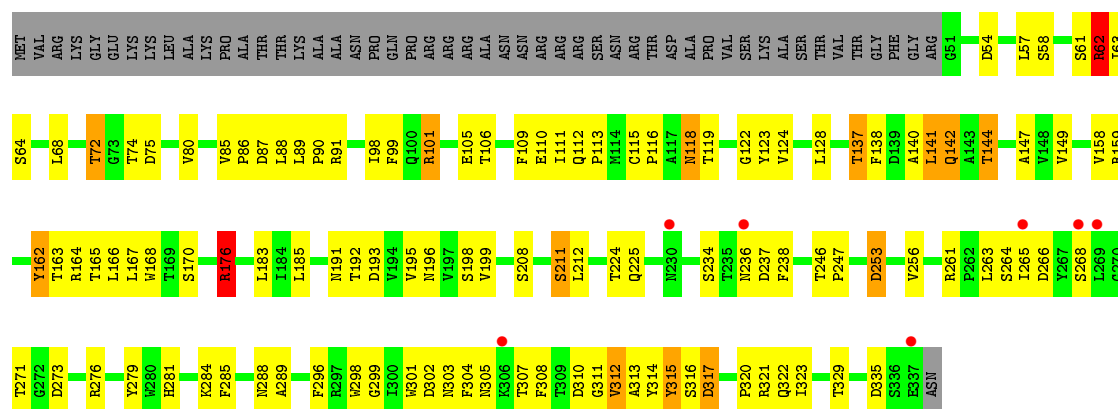




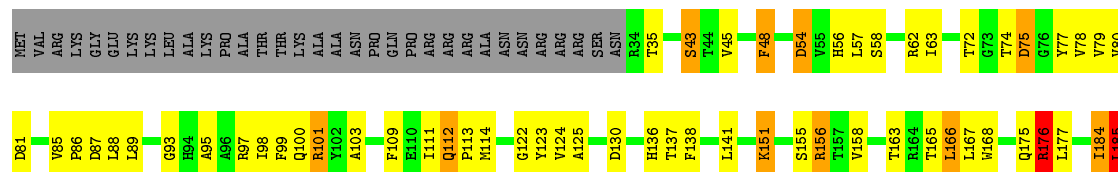
- Molecule 1: Coat protein

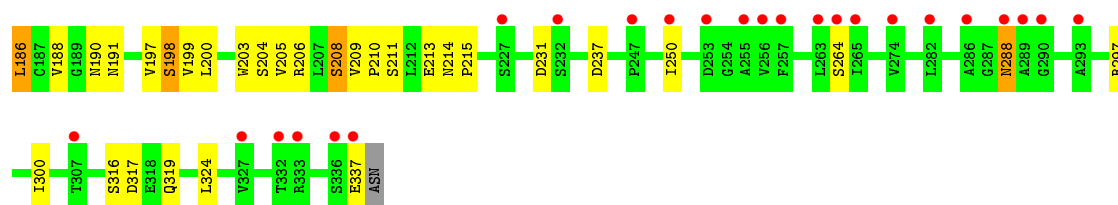


- Molecule 1: Coat protein

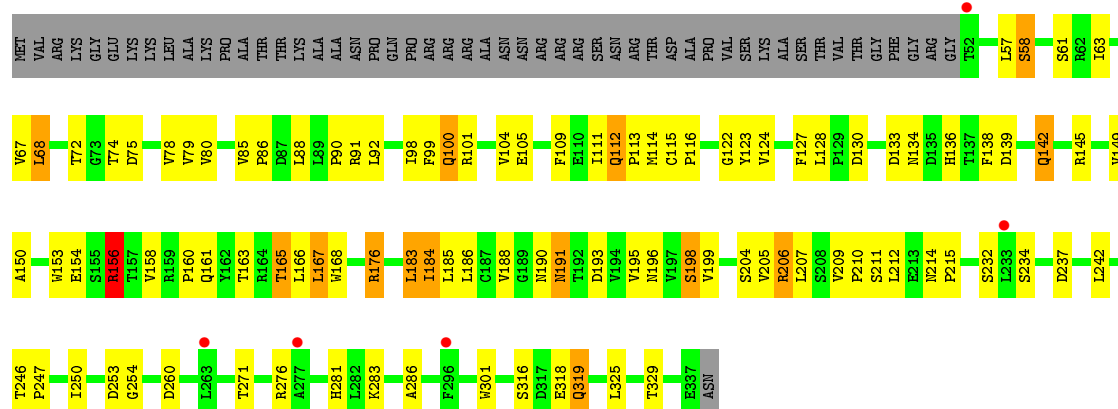


- Molecule 1: Coat protein

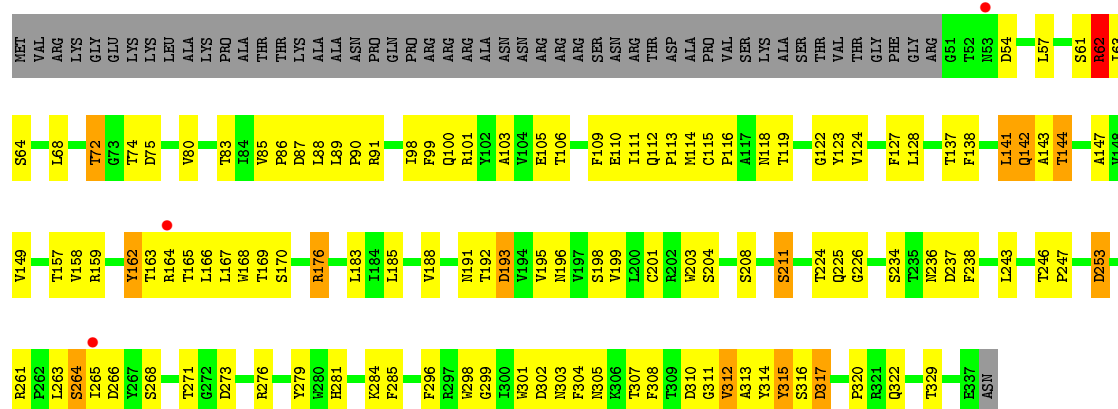




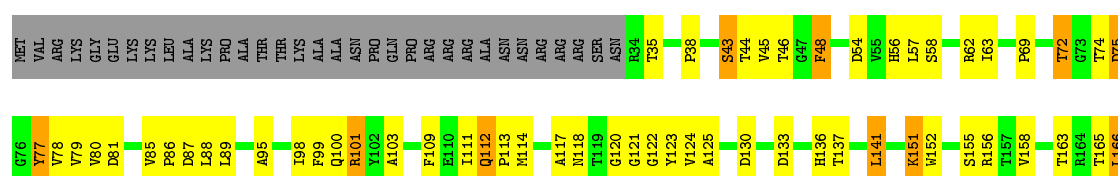
• Molecule 1: Coat protein

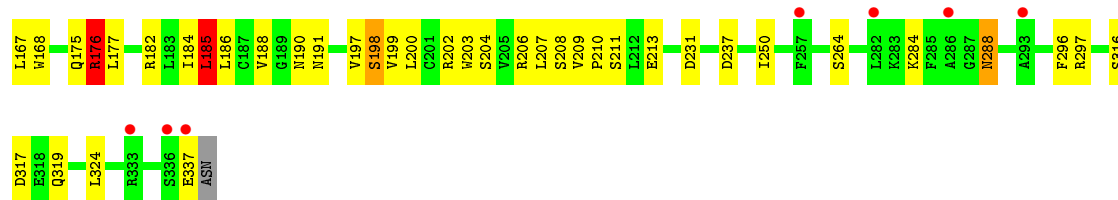


• Molecule 1: Coat protein

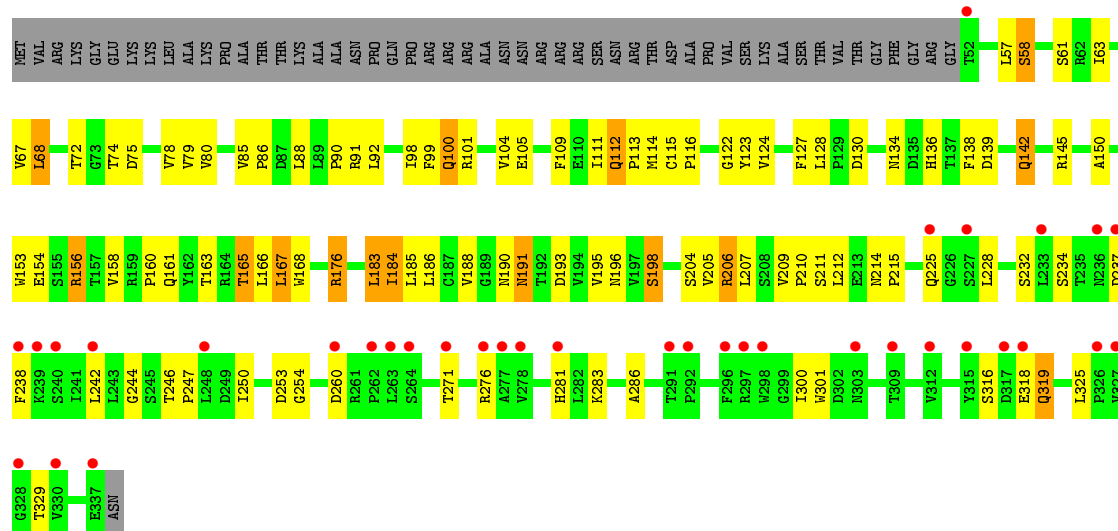


• Molecule 1: Coat protein

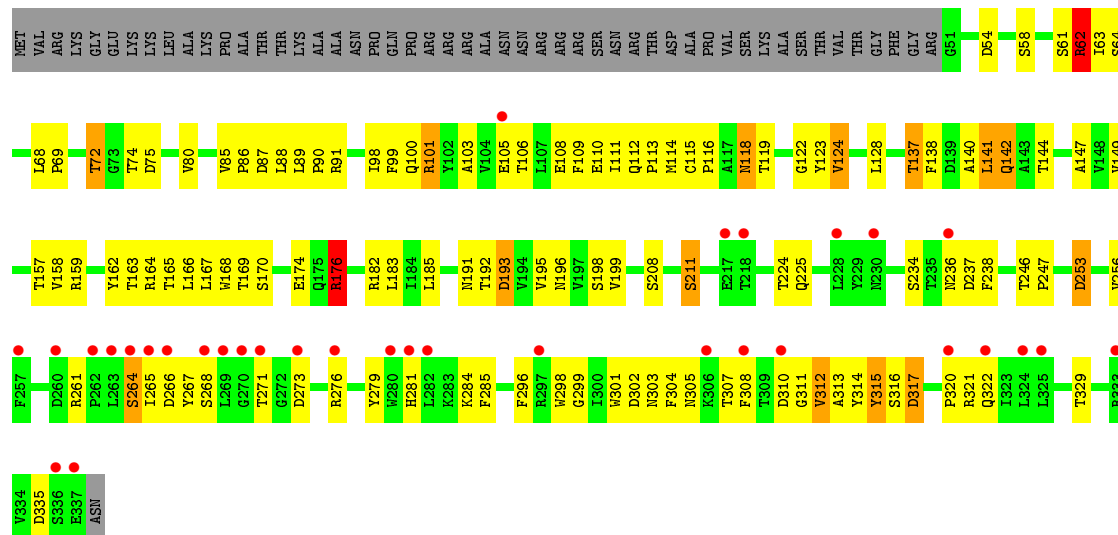




• Molecule 1: Coat protein

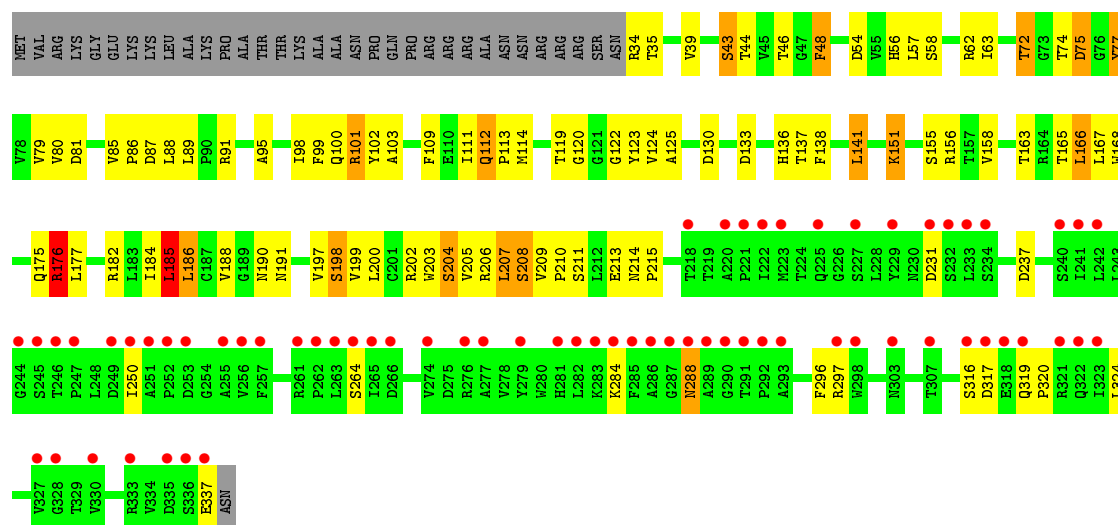


• Molecule 1: Coat protein

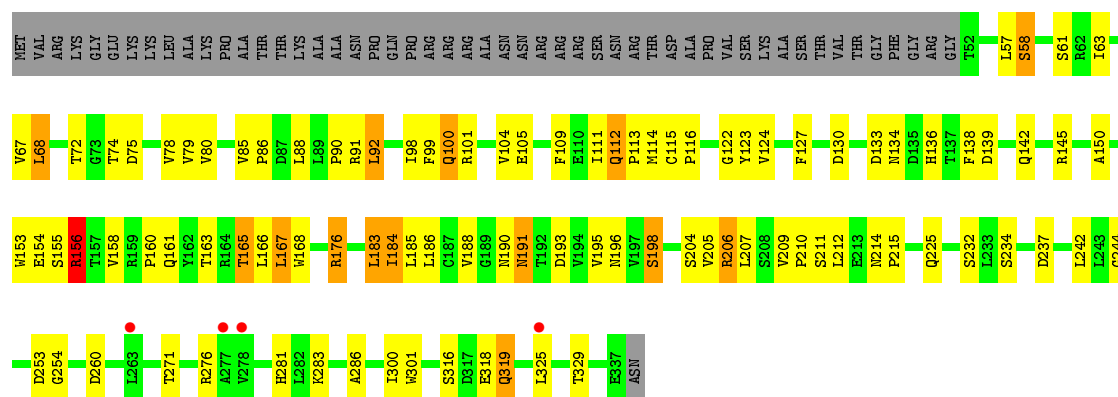


• Molecule 1: Coat protein

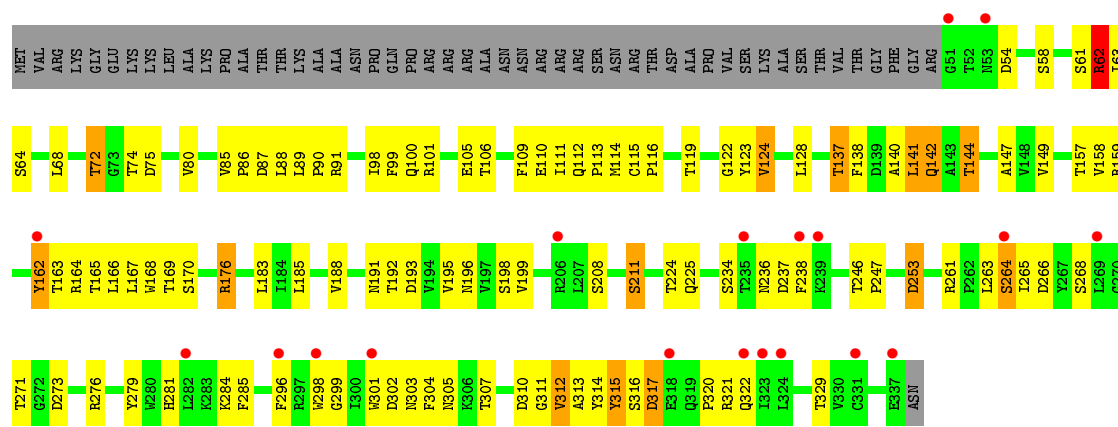




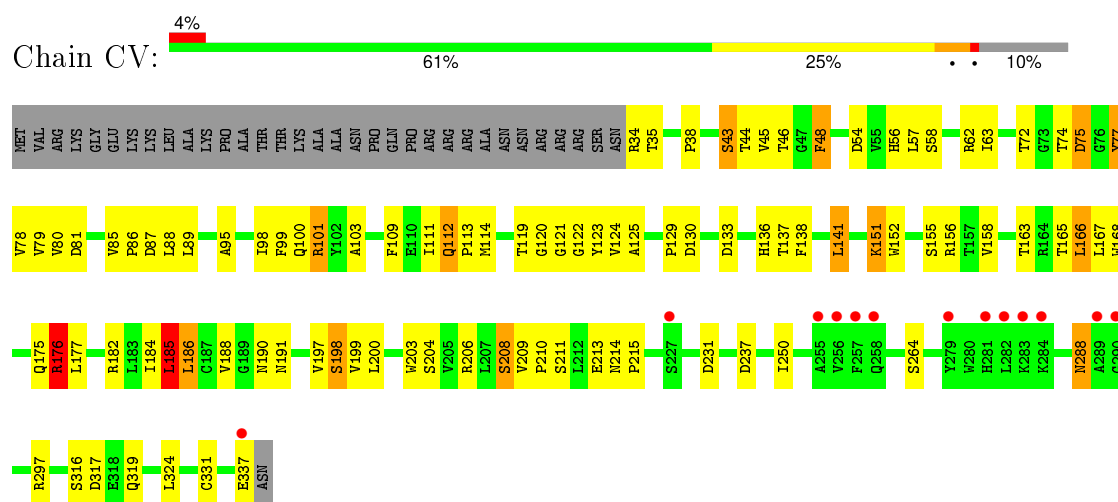
- Molecule 1: Coat protein



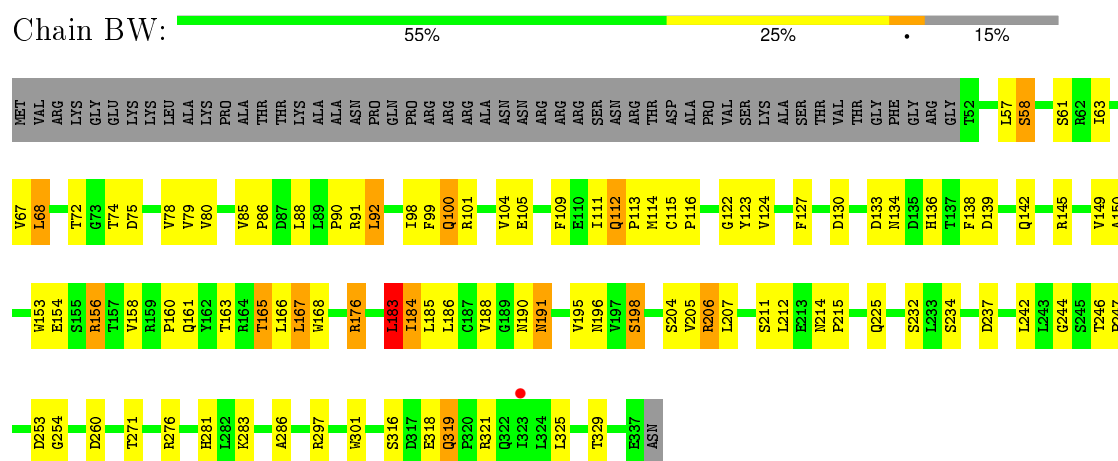
- Molecule 1: Coat protein



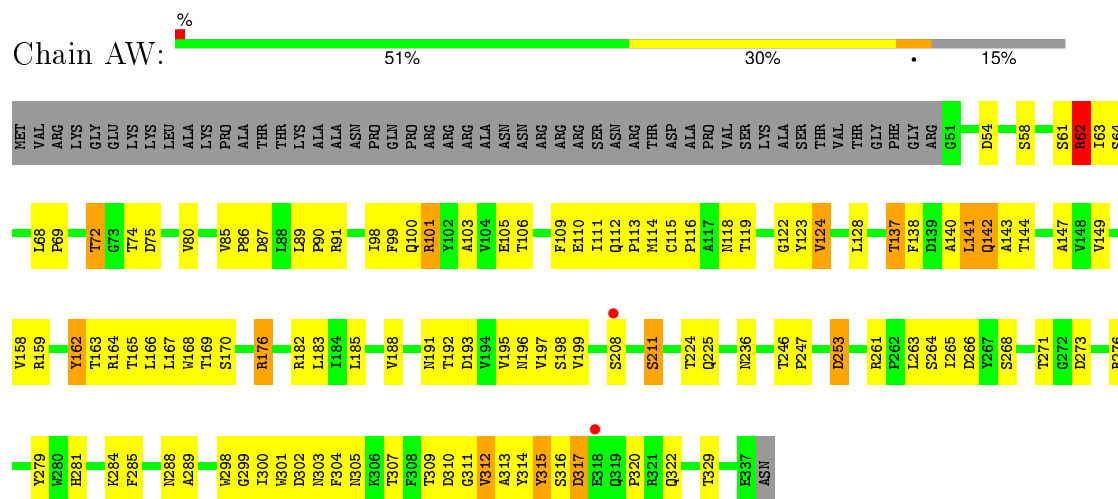
- Molecule 1: Coat protein



- Molecule 1: Coat protein



- Molecule 1: Coat protein

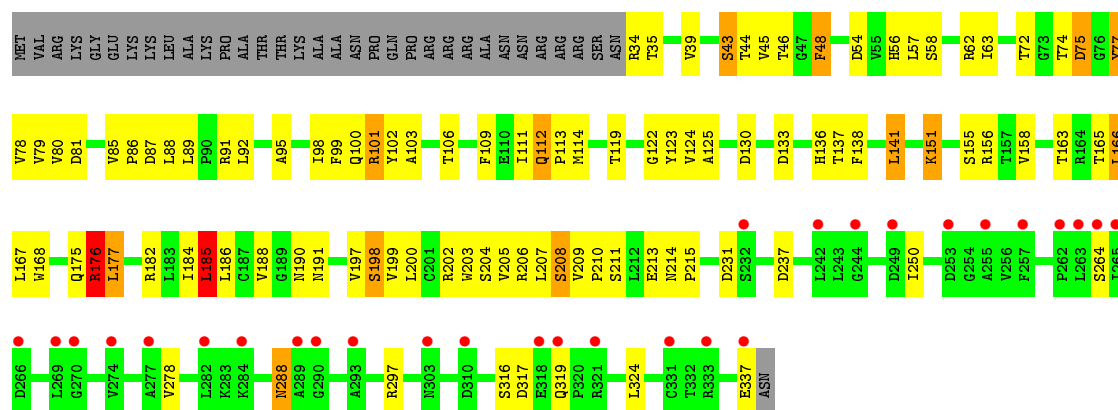


- Molecule 1: Coat protein

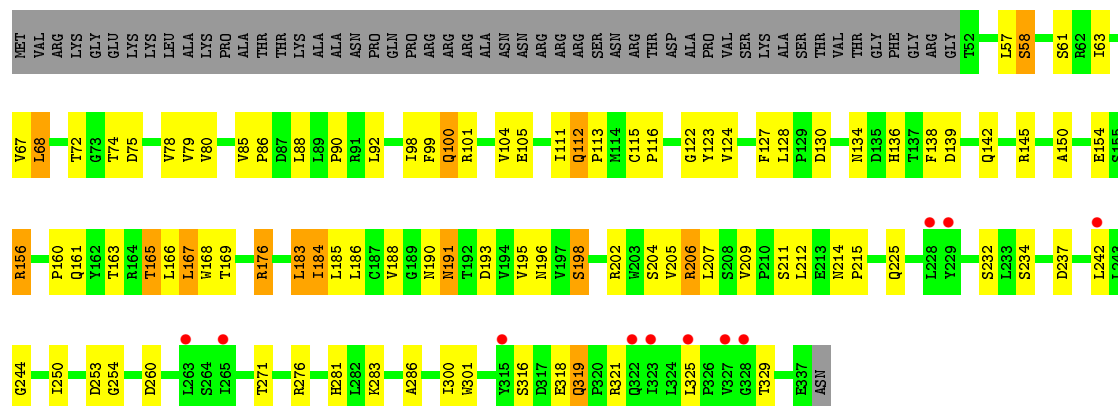




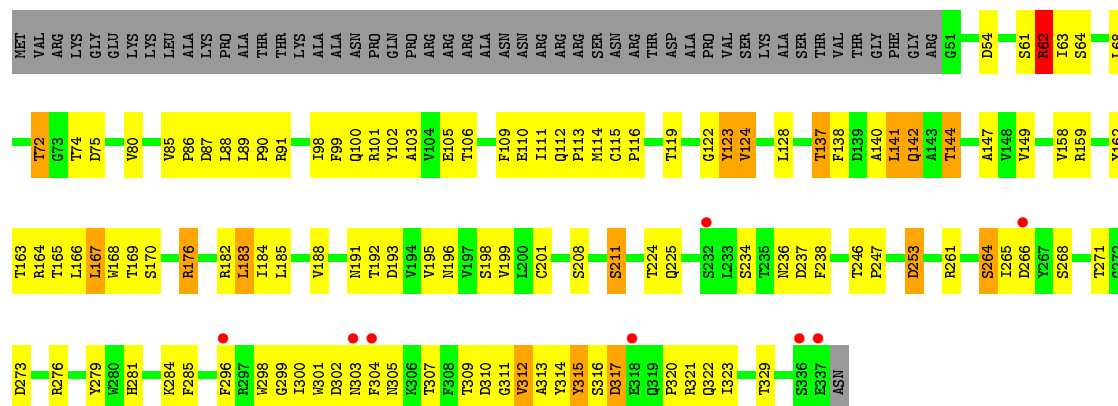




• Molecule 1: Coat protein

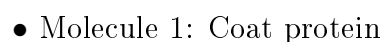


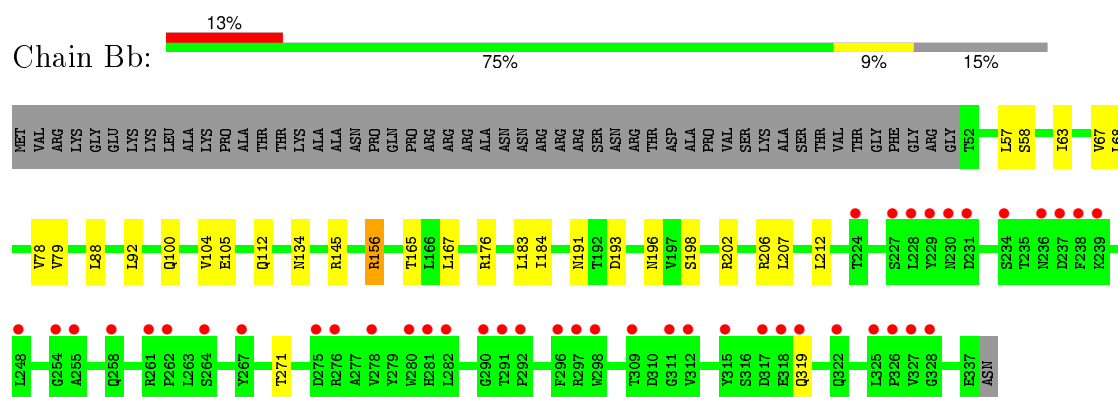
• Molecule 1: Coat protein



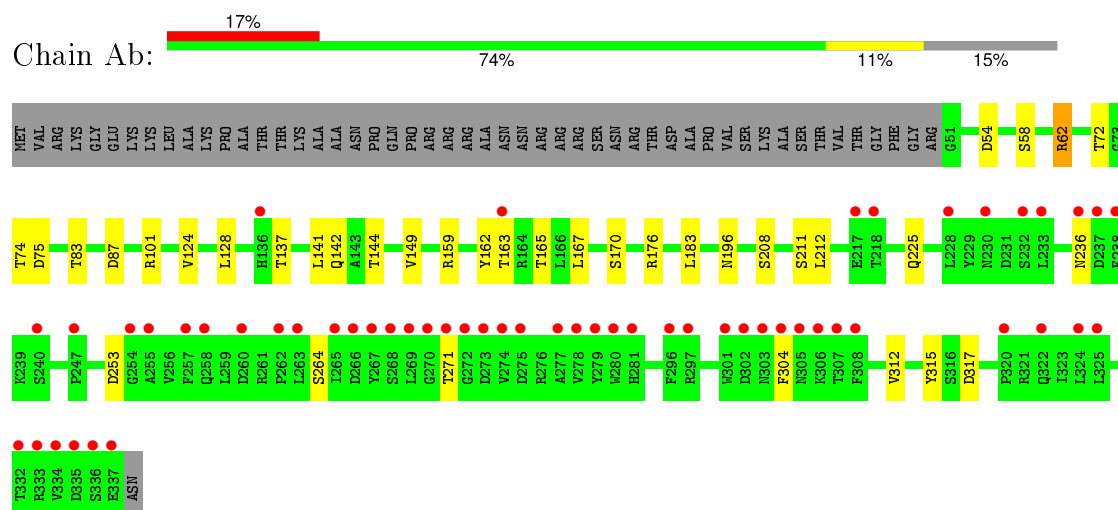
• Molecule 1: Coat protein



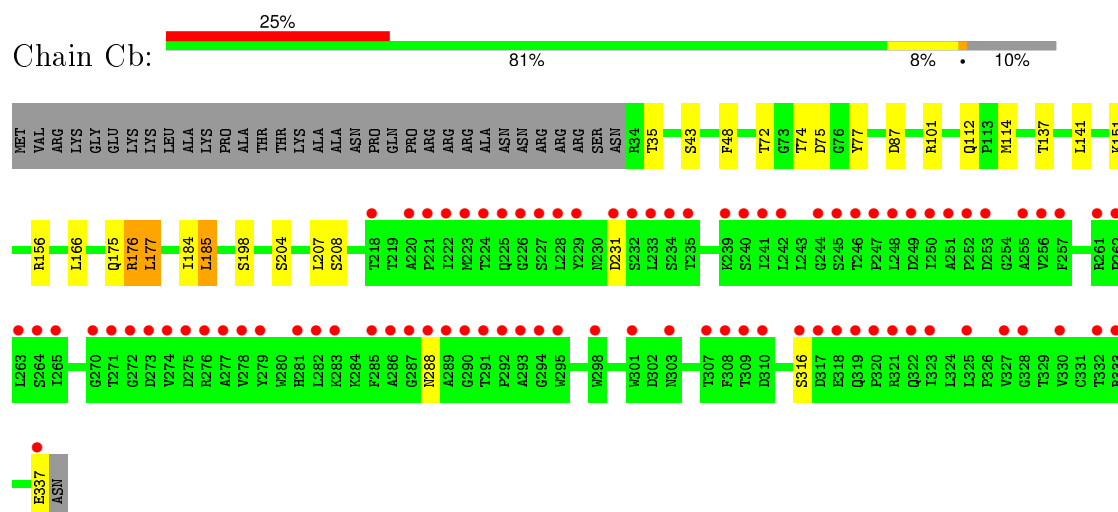




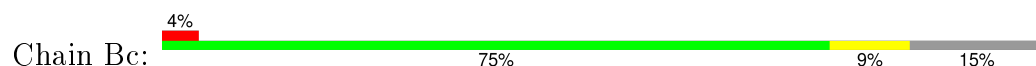
• Molecule 1: Coat protein

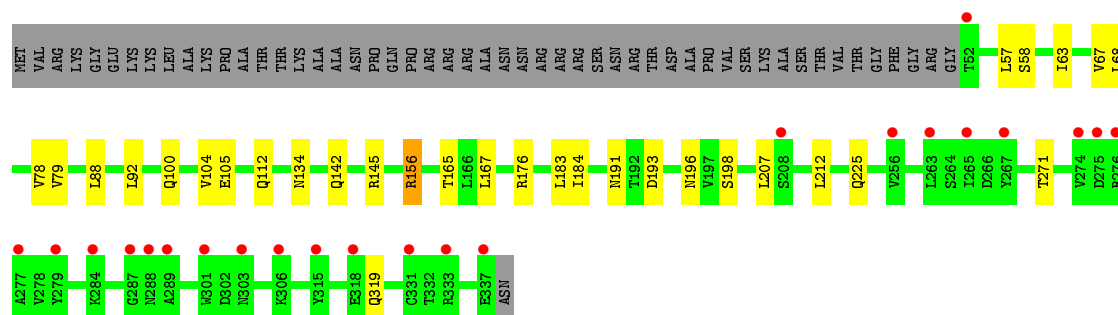


• Molecule 1: Coat protein

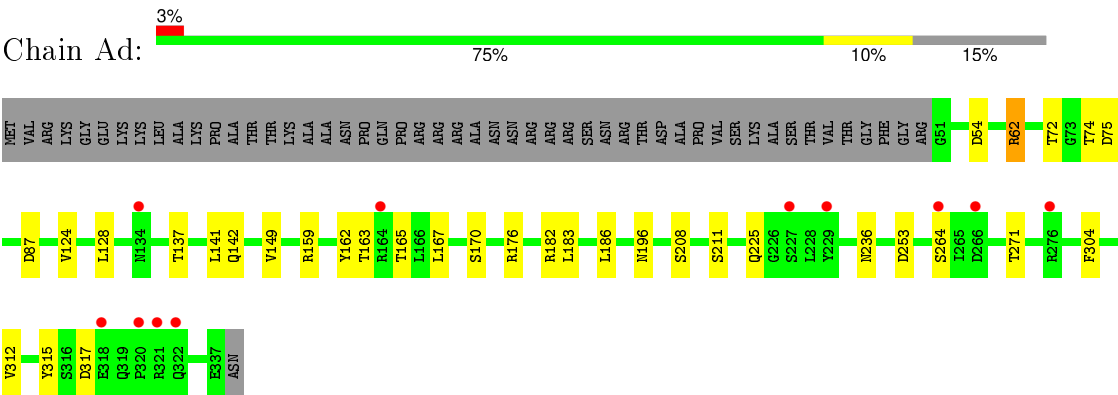


• Molecule 1: Coat protein

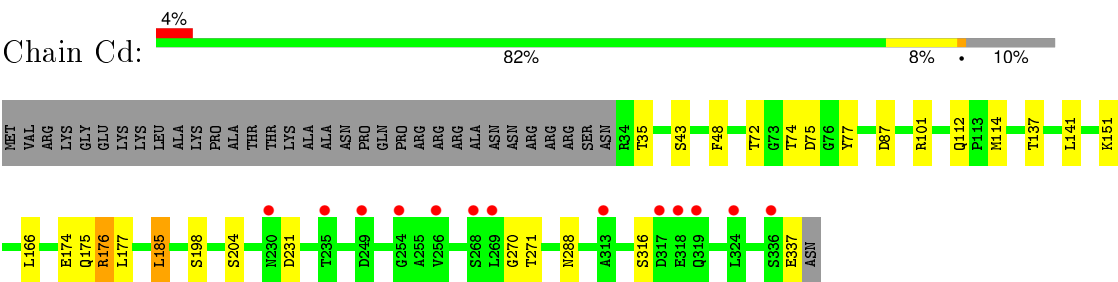




● Molecule 1: Coat protein



● Molecule 1: Coat protein



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	477.36 Å 422.74 Å 337.89 Å 90.00° 134.03° 90.00°	Depositor
Resolution (Å)	263.91 – 3.60 263.91 – 3.60	Depositor EDS
% Data completeness (in resolution range)	99.2 (263.91-3.60) 99.3 (263.91-3.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.85 (at 3.58 Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.255 , 0.297 0.255 , 0.295	Depositor DCC
R_{free} test set	27556 reflections (5.28%)	DCC
Wilson B-factor (Å ²)	75.1	Xtriage
Anisotropy	0.054	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 72.0	EDS
Estimated twinning fraction	0.000 for h+2*k,-h-l 0.000 for h,-k,-h-l 0.000 for -h-2*k,-k,l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	4 of 549703 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.85	EDS
Total number of atoms	203250	wwPDB-VP
Average B, all atoms (Å ²)	103.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.66% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	AA	0.71	0/2274	0.89	4/3112 (0.1%)
1	AB	0.80	0/2274	0.92	3/3112 (0.1%)
1	AC	0.79	0/2274	0.90	4/3112 (0.1%)
1	AD	0.73	0/2274	0.90	2/3112 (0.1%)
1	AE	0.75	0/2274	0.92	3/3112 (0.1%)
1	AF	0.77	1/2274 (0.0%)	0.92	3/3112 (0.1%)
1	AG	0.72	0/2274	0.89	3/3112 (0.1%)
1	AH	0.77	0/2274	0.90	2/3112 (0.1%)
1	AI	0.73	0/2274	0.89	3/3112 (0.1%)
1	AJ	0.78	0/2274	0.92	3/3112 (0.1%)
1	AK	0.92	0/2274	0.99	3/3112 (0.1%)
1	AL	0.85	0/2274	0.95	3/3112 (0.1%)
1	AM	0.72	0/2274	0.88	2/3112 (0.1%)
1	AN	0.72	0/2274	0.89	2/3112 (0.1%)
1	AO	0.76	0/2274	0.91	2/3112 (0.1%)
1	AP	0.77	0/2274	0.91	2/3112 (0.1%)
1	AQ	0.74	0/2274	0.91	4/3112 (0.1%)
1	AR	0.78	0/2274	0.91	3/3112 (0.1%)
1	AS	0.80	0/2274	0.91	2/3112 (0.1%)
1	AT	0.71	0/2274	0.89	3/3112 (0.1%)
1	AU	0.81	2/2274 (0.1%)	0.92	5/3112 (0.2%)
1	AV	0.72	0/2274	0.89	2/3112 (0.1%)
1	AW	0.80	0/2274	0.93	4/3112 (0.1%)
1	AX	0.77	0/2274	0.91	4/3112 (0.1%)
1	AY	0.78	0/2274	0.91	3/3112 (0.1%)
1	AZ	0.75	1/2274 (0.0%)	0.89	4/3112 (0.1%)
1	Aa	0.71	0/2274	0.88	2/3112 (0.1%)
1	Ab	0.78	0/2274	0.92	3/3112 (0.1%)
1	Ac	0.76	0/2274	0.92	5/3112 (0.2%)
1	Ad	0.82	0/2274	0.94	3/3112 (0.1%)
1	BA	0.76	0/2270	0.94	5/3107 (0.2%)
1	BB	0.87	0/2270	0.99	7/3107 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	BC	0.77	0/2270	0.92	5/3107 (0.2%)
1	BD	0.78	0/2270	0.92	3/3107 (0.1%)
1	BE	0.79	0/2270	0.95	6/3107 (0.2%)
1	BF	0.80	0/2270	0.95	6/3107 (0.2%)
1	BG	0.80	0/2270	0.94	4/3107 (0.1%)
1	BH	0.81	0/2270	0.95	5/3107 (0.2%)
1	BI	0.79	1/2270 (0.0%)	0.93	4/3107 (0.1%)
1	BJ	0.86	0/2270	0.97	7/3107 (0.2%)
1	BK	0.92	1/2270 (0.0%)	0.98	5/3107 (0.2%)
1	BL	0.93	0/2270	0.98	8/3107 (0.3%)
1	BM	0.83	0/2270	0.95	5/3107 (0.2%)
1	BN	0.80	0/2270	0.95	5/3107 (0.2%)
1	BO	0.82	0/2270	0.96	6/3107 (0.2%)
1	BP	0.80	0/2270	0.94	5/3107 (0.2%)
1	BQ	0.80	0/2270	0.93	4/3107 (0.1%)
1	BR	0.83	0/2270	0.93	4/3107 (0.1%)
1	BS	0.85	0/2270	0.97	4/3107 (0.1%)
1	BT	0.77	0/2270	0.94	5/3107 (0.2%)
1	BU	0.84	0/2270	0.96	4/3107 (0.1%)
1	BV	0.78	0/2270	0.92	5/3107 (0.2%)
1	BW	0.87	0/2270	0.95	4/3107 (0.1%)
1	BX	0.79	1/2270 (0.0%)	0.93	4/3107 (0.1%)
1	BY	0.79	0/2270	0.92	4/3107 (0.1%)
1	BZ	0.77	0/2270	0.93	4/3107 (0.1%)
1	Ba	0.79	0/2270	0.93	4/3107 (0.1%)
1	Bb	0.85	0/2270	0.98	6/3107 (0.2%)
1	Bc	0.80	0/2270	0.93	4/3107 (0.1%)
1	Bd	0.82	0/2270	0.94	3/3107 (0.1%)
1	CA	0.72	0/2398	0.87	5/3280 (0.2%)
1	CB	0.78	0/2398	0.86	2/3280 (0.1%)
1	CC	0.84	0/2398	0.90	4/3280 (0.1%)
1	CD	0.75	0/2398	0.87	5/3280 (0.2%)
1	CE	0.79	0/2398	0.88	2/3280 (0.1%)
1	CF	0.80	1/2398 (0.0%)	0.88	3/3280 (0.1%)
1	CG	0.73	0/2398	0.86	4/3280 (0.1%)
1	CH	0.75	0/2398	0.87	3/3280 (0.1%)
1	CI	0.73	0/2398	0.86	3/3280 (0.1%)
1	CJ	0.80	0/2398	0.88	5/3280 (0.2%)
1	CK	0.94	0/2398	0.98	4/3280 (0.1%)
1	CL	0.87	1/2398 (0.0%)	0.92	4/3280 (0.1%)
1	CM	0.76	0/2398	0.88	3/3280 (0.1%)
1	CN	0.74	0/2398	0.86	4/3280 (0.1%)
1	CO	0.78	0/2398	0.89	4/3280 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	CP	0.75	0/2398	0.86	2/3280 (0.1%)
1	CQ	0.77	0/2398	0.87	4/3280 (0.1%)
1	CR	0.76	0/2398	0.87	4/3280 (0.1%)
1	CS	0.82	0/2398	0.91	4/3280 (0.1%)
1	CT	0.74	0/2398	0.88	4/3280 (0.1%)
1	CU	0.81	0/2398	0.90	4/3280 (0.1%)
1	CV	0.73	0/2398	0.86	3/3280 (0.1%)
1	CW	0.81	0/2398	0.91	4/3280 (0.1%)
1	CX	0.77	0/2398	0.87	3/3280 (0.1%)
1	CY	0.78	0/2398	0.88	4/3280 (0.1%)
1	CZ	0.74	1/2398 (0.0%)	0.87	3/3280 (0.1%)
1	Ca	0.74	0/2398	0.86	2/3280 (0.1%)
1	Cb	0.79	0/2398	0.88	5/3280 (0.2%)
1	Cc	0.78	0/2398	0.88	5/3280 (0.2%)
1	Cd	0.86	1/2398 (0.0%)	0.94	4/3280 (0.1%)
All	All	0.79	11/208260 (0.0%)	0.91	346/284970 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	CU	0	1
1	Cb	0	1
All	All	0	2

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	BI	318	GLU	CD-OE2	7.13	1.33	1.25
1	Cd	174	GLU	CD-OE1	6.83	1.33	1.25
1	CF	174	GLU	CD-OE1	6.23	1.32	1.25
1	AF	174	GLU	CD-OE2	5.70	1.31	1.25
1	AU	108	GLU	CD-OE1	5.60	1.31	1.25
1	BK	203	TRP	CE3-CZ3	5.27	1.47	1.38
1	AU	174	GLU	CD-OE2	5.21	1.31	1.25
1	BX	115	CYS	CB-SG	-5.12	1.73	1.81
1	AZ	123	TYR	CE1-CZ	-5.12	1.31	1.38
1	CL	123	TYR	CE2-CZ	-5.04	1.31	1.38
1	CZ	174	GLU	CD-OE1	5.03	1.31	1.25

All (346) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CO	176	ARG	NE-CZ-NH2	8.79	124.70	120.30
1	AE	62	ARG	NE-CZ-NH1	8.55	124.58	120.30
1	CT	176	ARG	NE-CZ-NH2	8.44	124.52	120.30
1	CU	176	ARG	NE-CZ-NH2	8.25	124.42	120.30
1	CW	176	ARG	NE-CZ-NH2	8.08	124.34	120.30
1	BO	176	ARG	NE-CZ-NH1	-7.94	116.33	120.30
1	AV	62	ARG	NE-CZ-NH1	7.74	124.17	120.30
1	BJ	156	ARG	NE-CZ-NH2	-7.70	116.45	120.30
1	Ab	101	ARG	NE-CZ-NH1	7.68	124.14	120.30
1	Ad	62	ARG	NE-CZ-NH1	7.62	124.11	120.30
1	Cd	176	ARG	NE-CZ-NH2	7.51	124.05	120.30
1	BO	176	ARG	NE-CZ-NH2	7.46	124.03	120.30
1	Ba	176	ARG	NE-CZ-NH2	7.39	123.99	120.30
1	BJ	176	ARG	NE-CZ-NH2	7.39	123.99	120.30
1	BB	176	ARG	NE-CZ-NH1	-7.35	116.63	120.30
1	AA	62	ARG	NE-CZ-NH1	7.30	123.95	120.30
1	BN	176	ARG	NE-CZ-NH1	-7.28	116.66	120.30
1	BT	156	ARG	NE-CZ-NH2	-7.26	116.67	120.30
1	BQ	156	ARG	NE-CZ-NH2	-7.18	116.71	120.30
1	AB	62	ARG	NE-CZ-NH1	7.14	123.87	120.30
1	CK	176	ARG	NE-CZ-NH2	7.12	123.86	120.30
1	BN	176	ARG	NE-CZ-NH2	7.05	123.83	120.30
1	BL	91	ARG	NE-CZ-NH1	-7.02	116.79	120.30
1	CK	176	ARG	NE-CZ-NH1	-6.97	116.81	120.30
1	CA	176	ARG	NE-CZ-NH2	6.94	123.77	120.30
1	CP	166	LEU	CA-CB-CG	6.91	131.19	115.30
1	BD	156	ARG	NE-CZ-NH2	-6.86	116.87	120.30
1	BJ	206	ARG	NE-CZ-NH1	6.86	123.73	120.30
1	CZ	176	ARG	NE-CZ-NH2	6.84	123.72	120.30
1	BK	91	ARG	NE-CZ-NH1	-6.80	116.90	120.30
1	BZ	176	ARG	NE-CZ-NH2	6.79	123.69	120.30
1	CI	176	ARG	NE-CZ-NH2	6.68	123.64	120.30
1	Ba	156	ARG	NE-CZ-NH2	-6.68	116.96	120.30
1	BO	206	ARG	NE-CZ-NH1	6.67	123.64	120.30
1	CM	176	ARG	NE-CZ-NH2	6.66	123.63	120.30
1	CQ	176	ARG	NE-CZ-NH2	6.63	123.61	120.30
1	Ac	62	ARG	NE-CZ-NH1	6.62	123.61	120.30
1	AH	62	ARG	NE-CZ-NH1	6.59	123.60	120.30
1	AG	62	ARG	NE-CZ-NH1	6.54	123.57	120.30
1	AK	182	ARG	NE-CZ-NH2	-6.50	117.05	120.30
1	AW	101	ARG	NE-CZ-NH1	6.50	123.55	120.30
1	AF	62	ARG	NE-CZ-NH1	6.47	123.53	120.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CT	176	ARG	NE-CZ-NH1	-6.47	117.07	120.30
1	AM	182	ARG	NE-CZ-NH2	-6.46	117.07	120.30
1	AX	62	ARG	NE-CZ-NH1	6.46	123.53	120.30
1	CI	176	ARG	NE-CZ-NH1	-6.45	117.08	120.30
1	Bd	156	ARG	NE-CZ-NH2	-6.42	117.09	120.30
1	BT	176	ARG	NE-CZ-NH1	-6.41	117.09	120.30
1	CO	166	LEU	CA-CB-CG	6.40	130.02	115.30
1	AP	176	ARG	NE-CZ-NH2	6.38	123.49	120.30
1	CX	166	LEU	CA-CB-CG	6.37	129.95	115.30
1	BF	156	ARG	NE-CZ-NH2	-6.35	117.12	120.30
1	BK	156	ARG	NE-CZ-NH2	-6.35	117.12	120.30
1	CD	176	ARG	NE-CZ-NH1	-6.34	117.13	120.30
1	CD	166	LEU	CA-CB-CG	6.33	129.86	115.30
1	BT	176	ARG	NE-CZ-NH2	6.33	123.46	120.30
1	CQ	166	LEU	CA-CB-CG	6.33	129.85	115.30
1	BM	156	ARG	NE-CZ-NH2	-6.32	117.14	120.30
1	CZ	166	LEU	CA-CB-CG	6.30	129.79	115.30
1	CQ	176	ARG	NE-CZ-NH1	-6.29	117.16	120.30
1	CW	176	ARG	NE-CZ-NH1	-6.27	117.17	120.30
1	Cd	176	ARG	NE-CZ-NH1	-6.27	117.17	120.30
1	BH	156	ARG	NE-CZ-NH2	-6.25	117.18	120.30
1	BJ	176	ARG	NE-CZ-NH1	-6.23	117.18	120.30
1	Cc	166	LEU	CA-CB-CG	6.23	129.62	115.30
1	Bb	206	ARG	NE-CZ-NH2	-6.22	117.19	120.30
1	CK	166	LEU	CA-CB-CG	6.22	129.60	115.30
1	BN	156	ARG	NE-CZ-NH2	-6.21	117.20	120.30
1	CB	166	LEU	CA-CB-CG	6.20	129.56	115.30
1	CG	176	ARG	NE-CZ-NH1	-6.18	117.21	120.30
1	BS	91	ARG	NE-CZ-NH1	-6.18	117.21	120.30
1	BA	156	ARG	NE-CZ-NH2	-6.17	117.22	120.30
1	BY	91	ARG	NE-CZ-NH1	-6.14	117.23	120.30
1	CF	166	LEU	CA-CB-CG	6.14	129.42	115.30
1	CW	166	LEU	CA-CB-CG	6.13	129.40	115.30
1	BK	112	GLN	N-CA-C	6.13	127.54	111.00
1	CX	185	LEU	CA-CB-CG	6.13	129.39	115.30
1	CS	166	LEU	CA-CB-CG	6.10	129.33	115.30
1	Bb	176	ARG	NE-CZ-NH1	-6.10	117.25	120.30
1	BV	176	ARG	NE-CZ-NH2	6.10	123.35	120.30
1	CY	166	LEU	CA-CB-CG	6.09	129.31	115.30
1	BA	112	GLN	N-CA-C	6.08	127.43	111.00
1	Cd	166	LEU	CA-CB-CG	6.08	129.27	115.30
1	CC	166	LEU	CA-CB-CG	6.07	129.26	115.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	BC	112	GLN	N-CA-C	6.07	127.39	111.00
1	CC	176	ARG	NE-CZ-NH2	6.05	123.33	120.30
1	CJ	176	ARG	NE-CZ-NH2	6.05	123.33	120.30
1	BE	176	ARG	NE-CZ-NH2	6.04	123.32	120.30
1	Cc	176	ARG	NE-CZ-NH2	6.03	123.32	120.30
1	BP	112	GLN	N-CA-C	6.03	127.28	111.00
1	AU	182	ARG	NE-CZ-NH2	-6.03	117.29	120.30
1	CR	166	LEU	CA-CB-CG	6.02	129.15	115.30
1	BE	156	ARG	NE-CZ-NH2	-6.01	117.30	120.30
1	BH	112	GLN	N-CA-C	6.00	127.20	111.00
1	BZ	176	ARG	NE-CZ-NH1	-5.99	117.31	120.30
1	BW	176	ARG	NE-CZ-NH1	-5.98	117.31	120.30
1	BU	206	ARG	NE-CZ-NH1	5.97	123.29	120.30
1	BF	112	GLN	N-CA-C	5.96	127.08	111.00
1	BC	176	ARG	NE-CZ-NH1	-5.95	117.32	120.30
1	AQ	62	ARG	NE-CZ-NH1	5.95	123.28	120.30
1	CJ	176	ARG	NE-CZ-NH1	-5.94	117.33	120.30
1	BV	112	GLN	N-CA-C	5.94	127.03	111.00
1	CS	176	ARG	NE-CZ-NH2	5.93	123.27	120.30
1	CV	185	LEU	CA-CB-CG	5.93	128.93	115.30
1	Ab	62	ARG	NE-CZ-NH1	5.92	123.26	120.30
1	AL	182	ARG	NE-CZ-NH2	-5.92	117.34	120.30
1	Bd	112	GLN	N-CA-C	5.92	126.99	111.00
1	BO	112	GLN	N-CA-C	5.92	126.97	111.00
1	CA	176	ARG	NE-CZ-NH1	-5.91	117.35	120.30
1	BZ	112	GLN	N-CA-C	5.90	126.92	111.00
1	BC	156	ARG	NE-CZ-NH2	-5.89	117.35	120.30
1	BW	112	GLN	N-CA-C	5.88	126.88	111.00
1	Ca	166	LEU	CA-CB-CG	5.88	128.83	115.30
1	BK	176	ARG	NE-CZ-NH2	5.88	123.24	120.30
1	CL	166	LEU	CA-CB-CG	5.87	128.80	115.30
1	BX	206	ARG	NE-CZ-NH2	-5.87	117.37	120.30
1	BU	112	GLN	N-CA-C	5.87	126.84	111.00
1	BX	112	GLN	N-CA-C	5.87	126.83	111.00
1	CT	166	LEU	CA-CB-CG	5.86	128.78	115.30
1	BF	176	ARG	NE-CZ-NH1	-5.86	117.37	120.30
1	BI	112	GLN	N-CA-C	5.86	126.81	111.00
1	CN	176	ARG	NE-CZ-NH2	5.85	123.23	120.30
1	BN	112	GLN	N-CA-C	5.85	126.78	111.00
1	AG	62	ARG	CG-CD-NE	5.84	124.07	111.80
1	CH	166	LEU	CA-CB-CG	5.83	128.71	115.30
1	BB	112	GLN	N-CA-C	5.83	126.73	111.00

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AL	62	ARG	NE-CZ-NH1	5.83	123.21	120.30
1	CL	97	ARG	NE-CZ-NH1	5.82	123.21	120.30
1	AF	176	ARG	NE-CZ-NH2	5.82	123.21	120.30
1	AU	176	ARG	NE-CZ-NH1	-5.82	117.39	120.30
1	BD	112	GLN	N-CA-C	5.82	126.71	111.00
1	AZ	62	ARG	NE-CZ-NH1	5.81	123.21	120.30
1	CI	166	LEU	CA-CB-CG	5.81	128.66	115.30
1	Bc	176	ARG	NE-CZ-NH2	5.81	123.20	120.30
1	CU	166	LEU	CA-CB-CG	5.80	128.64	115.30
1	BR	112	GLN	N-CA-C	5.80	126.65	111.00
1	BT	206	ARG	NE-CZ-NH1	5.79	123.20	120.30
1	CR	176	ARG	NE-CZ-NH2	5.79	123.19	120.30
1	CJ	166	LEU	CA-CB-CG	5.78	128.60	115.30
1	AW	62	ARG	NE-CZ-NH1	5.78	123.19	120.30
1	AU	62	ARG	CG-CD-NE	5.78	123.93	111.80
1	Cc	185	LEU	CA-CB-CG	5.77	128.56	115.30
1	CE	166	LEU	CA-CB-CG	5.76	128.56	115.30
1	BG	176	ARG	NE-CZ-NH1	-5.76	117.42	120.30
1	CM	166	LEU	CA-CB-CG	5.76	128.54	115.30
1	BM	176	ARG	NE-CZ-NH1	-5.76	117.42	120.30
1	BX	156	ARG	NE-CZ-NH2	-5.76	117.42	120.30
1	Cb	166	LEU	CA-CB-CG	5.75	128.53	115.30
1	CG	176	ARG	NE-CZ-NH2	5.75	123.17	120.30
1	BH	176	ARG	NE-CZ-NH2	5.75	123.17	120.30
1	CV	166	LEU	CA-CB-CG	5.73	128.47	115.30
1	BL	112	GLN	N-CA-C	5.72	126.45	111.00
1	BG	112	GLN	N-CA-C	5.72	126.44	111.00
1	BH	206	ARG	NE-CZ-NH2	-5.72	117.44	120.30
1	Ab	62	ARG	CG-CD-NE	5.71	123.79	111.80
1	AS	62	ARG	CG-CD-NE	5.71	123.79	111.80
1	CF	185	LEU	CA-CB-CG	5.70	128.40	115.30
1	BQ	112	GLN	N-CA-C	5.70	126.38	111.00
1	Cb	185	LEU	CA-CB-CG	5.70	128.40	115.30
1	BE	112	GLN	N-CA-C	5.69	126.37	111.00
1	AR	62	ARG	NE-CZ-NH1	5.69	123.15	120.30
1	CC	176	ARG	NE-CZ-NH1	-5.68	117.46	120.30
1	Ca	185	LEU	CA-CB-CG	5.67	128.35	115.30
1	BS	112	GLN	N-CA-C	5.67	126.31	111.00
1	BY	112	GLN	N-CA-C	5.67	126.31	111.00
1	BJ	112	GLN	N-CA-C	5.66	126.28	111.00
1	Bb	156	ARG	NE-CZ-NH2	-5.66	117.47	120.30
1	BM	112	GLN	N-CA-C	5.65	126.26	111.00

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AI	62	ARG	CG-CD-NE	5.64	123.65	111.80
1	CA	185	LEU	CA-CB-CG	5.64	128.27	115.30
1	BB	176	ARG	NE-CZ-NH2	5.63	123.11	120.30
1	Ba	112	GLN	N-CA-C	5.63	126.19	111.00
1	AQ	193	ASP	CB-CG-OD2	5.62	123.36	118.30
1	CE	185	LEU	CA-CB-CG	5.62	128.22	115.30
1	Bb	206	ARG	NE-CZ-NH1	5.59	123.10	120.30
1	CY	176	ARG	NE-CZ-NH2	5.58	123.09	120.30
1	BB	156	ARG	NE-CZ-NH2	-5.58	117.51	120.30
1	CH	176	ARG	NE-CZ-NH2	5.58	123.09	120.30
1	BL	206	ARG	NE-CZ-NH2	-5.57	117.51	120.30
1	CN	185	LEU	CA-CB-CG	5.57	128.12	115.30
1	BL	176	ARG	NE-CZ-NH1	-5.57	117.52	120.30
1	Ac	62	ARG	CG-CD-NE	5.57	123.50	111.80
1	AG	182	ARG	NE-CZ-NH2	-5.56	117.52	120.30
1	CS	184	ILE	CG1-CB-CG2	-5.56	99.16	111.40
1	CP	185	LEU	CA-CB-CG	5.56	128.08	115.30
1	AR	193	ASP	CB-CG-OD2	5.56	123.30	118.30
1	BI	156	ARG	NE-CZ-NH2	-5.55	117.53	120.30
1	Aa	62	ARG	NE-CZ-NH2	-5.55	117.53	120.30
1	CA	166	LEU	CA-CB-CG	5.55	128.06	115.30
1	AY	62	ARG	CG-CD-NE	5.54	123.42	111.80
1	Ba	91	ARG	NE-CZ-NH1	-5.53	117.54	120.30
1	BF	176	ARG	NE-CZ-NH2	5.53	123.06	120.30
1	BE	176	ARG	NE-CZ-NH1	-5.52	117.54	120.30
1	CK	185	LEU	CA-CB-CG	5.52	128.00	115.30
1	CU	176	ARG	NE-CZ-NH1	-5.52	117.54	120.30
1	CS	185	LEU	CA-CB-CG	5.51	127.98	115.30
1	BI	206	ARG	NE-CZ-NH1	5.51	123.06	120.30
1	CB	185	LEU	CA-CB-CG	5.51	127.96	115.30
1	Bc	112	GLN	N-CA-C	5.50	125.85	111.00
1	BO	206	ARG	NE-CZ-NH2	-5.50	117.55	120.30
1	BG	206	ARG	NE-CZ-NH1	5.49	123.05	120.30
1	BJ	202	ARG	NE-CZ-NH1	5.49	123.05	120.30
1	BP	176	ARG	NE-CZ-NH2	5.49	123.05	120.30
1	BA	176	ARG	NE-CZ-NH1	-5.49	117.56	120.30
1	Cc	176	ARG	NE-CZ-NH1	-5.49	117.56	120.30
1	BV	156	ARG	NE-CZ-NH2	-5.47	117.56	120.30
1	AD	62	ARG	CG-CD-NE	5.46	123.26	111.80
1	CJ	185	LEU	CA-CB-CG	5.45	127.84	115.30
1	BU	176	ARG	NE-CZ-NH2	5.45	123.03	120.30
1	BJ	206	ARG	NE-CZ-NH2	-5.45	117.58	120.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	BU	206	ARG	NE-CZ-NH2	-5.44	117.58	120.30
1	AM	62	ARG	CG-CD-NE	5.44	123.23	111.80
1	AI	182	ARG	NE-CZ-NH2	-5.44	117.58	120.30
1	BT	112	GLN	N-CA-C	5.44	125.68	111.00
1	CJ	97	ARG	NE-CZ-NH1	5.43	123.02	120.30
1	Bc	176	ARG	NE-CZ-NH1	-5.43	117.58	120.30
1	AC	62	ARG	CG-CD-NE	5.43	123.21	111.80
1	AJ	62	ARG	CG-CD-NE	5.43	123.20	111.80
1	CD	176	ARG	NE-CZ-NH2	5.42	123.01	120.30
1	AN	114	MET	CG-SD-CE	5.42	108.86	100.20
1	AX	62	ARG	CG-CD-NE	5.42	123.17	111.80
1	BR	156	ARG	NE-CZ-NH2	-5.42	117.59	120.30
1	BF	206	ARG	NE-CZ-NH2	-5.41	117.59	120.30
1	BL	202	ARG	NE-CZ-NH1	5.41	123.01	120.30
1	Bb	112	GLN	N-CA-C	5.41	125.60	111.00
1	BA	206	ARG	NE-CZ-NH1	5.41	123.00	120.30
1	BE	202	ARG	NE-CZ-NH1	5.41	123.00	120.30
1	Bc	156	ARG	NE-CZ-NH2	-5.39	117.61	120.30
1	BO	202	ARG	NE-CZ-NH1	5.39	123.00	120.30
1	AT	62	ARG	CG-CD-NE	5.38	123.09	111.80
1	BH	176	ARG	NE-CZ-NH1	-5.37	117.61	120.30
1	Ad	62	ARG	CG-CD-NE	5.37	123.08	111.80
1	AU	193	ASP	CB-CG-OD2	5.36	123.12	118.30
1	BZ	206	ARG	NE-CZ-NH1	5.35	122.98	120.30
1	AA	62	ARG	CG-CD-NE	5.35	123.04	111.80
1	AB	193	ASP	CB-CG-OD2	5.35	123.12	118.30
1	BS	176	ARG	NE-CZ-NH2	5.35	122.97	120.30
1	AO	182	ARG	NE-CZ-NH2	-5.35	117.63	120.30
1	AK	62	ARG	CG-CD-NE	5.34	123.03	111.80
1	CF	184	ILE	CG1-CB-CG2	-5.34	99.65	111.40
1	BF	206	ARG	NE-CZ-NH1	5.33	122.97	120.30
1	BY	206	ARG	NE-CZ-NH2	-5.33	117.63	120.30
1	BB	91	ARG	NE-CZ-NH1	-5.32	117.64	120.30
1	AJ	182	ARG	NE-CZ-NH2	-5.32	117.64	120.30
1	CG	166	LEU	CA-CB-CG	5.32	127.54	115.30
1	AB	62	ARG	CG-CD-NE	5.32	122.96	111.80
1	CM	185	LEU	CA-CB-CG	5.31	127.52	115.30
1	AP	62	ARG	CG-CD-NE	5.31	122.96	111.80
1	CH	185	LEU	CA-CB-CG	5.30	127.49	115.30
1	AV	62	ARG	CG-CD-NE	5.30	122.93	111.80
1	CN	166	LEU	CA-CB-CG	5.30	127.48	115.30
1	CX	176	ARG	NE-CZ-NH1	-5.29	117.66	120.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CO	176	ARG	NE-CZ-NH1	-5.28	117.66	120.30
1	CY	185	LEU	CA-CB-CG	5.28	127.44	115.30
1	BW	206	ARG	NE-CZ-NH2	-5.28	117.66	120.30
1	AX	193	ASP	CB-CG-OD2	5.27	123.05	118.30
1	CN	177	LEU	CA-CB-CG	5.27	127.43	115.30
1	Ac	159	ARG	NE-CZ-NH1	5.27	122.94	120.30
1	BP	156	ARG	NE-CZ-NH2	-5.26	117.67	120.30
1	AX	182	ARG	NE-CZ-NH2	-5.26	117.67	120.30
1	AT	62	ARG	NE-CZ-NH1	5.26	122.93	120.30
1	AY	182	ARG	NE-CZ-NH2	-5.26	117.67	120.30
1	Cb	177	LEU	CA-CB-CG	5.26	127.39	115.30
1	BA	183	LEU	CA-CB-CG	5.26	127.39	115.30
1	AA	182	ARG	NE-CZ-NH2	-5.25	117.67	120.30
1	BC	202	ARG	NE-CZ-NH1	5.25	122.92	120.30
1	AR	62	ARG	CG-CD-NE	5.25	122.83	111.80
1	AA	187	CYS	CA-CB-SG	5.25	123.44	114.00
1	BB	202	ARG	NE-CZ-NH1	5.25	122.92	120.30
1	AN	62	ARG	CG-CD-NE	5.23	122.79	111.80
1	Cd	185	LEU	CA-CB-CG	5.23	127.34	115.30
1	CV	176	ARG	NE-CZ-NH2	5.23	122.92	120.30
1	BI	206	ARG	NE-CZ-NH2	-5.22	117.69	120.30
1	BL	183	LEU	CA-CB-CG	5.22	127.30	115.30
1	AF	62	ARG	CG-CD-NE	5.21	122.75	111.80
1	CZ	176	ARG	NE-CZ-NH1	-5.21	117.69	120.30
1	CL	176	ARG	NE-CZ-NH2	5.21	122.90	120.30
1	CD	107	LEU	CB-CA-C	-5.20	100.32	110.20
1	AE	101	ARG	NE-CZ-NH1	5.20	122.90	120.30
1	AW	182	ARG	NE-CZ-NH2	-5.19	117.70	120.30
1	CD	185	LEU	CA-CB-CG	5.19	127.24	115.30
1	BL	176	ARG	NE-CZ-NH2	5.19	122.89	120.30
1	AW	62	ARG	CG-CD-NE	5.19	122.70	111.80
1	Ac	101	ARG	NE-CZ-NH1	5.19	122.89	120.30
1	CQ	185	LEU	CA-CB-CG	5.19	127.23	115.30
1	BY	206	ARG	NE-CZ-NH1	5.19	122.89	120.30
1	CT	185	LEU	CA-CB-CG	5.18	127.22	115.30
1	Cb	176	ARG	NE-CZ-NH1	-5.18	117.71	120.30
1	AQ	62	ARG	CG-CD-NE	5.18	122.67	111.80
1	BW	183	LEU	CA-CB-CG	5.17	127.20	115.30
1	BR	202	ARG	NE-CZ-NH1	5.17	122.89	120.30
1	AC	176	ARG	NE-CZ-NH1	-5.17	117.72	120.30
1	AD	62	ARG	NE-CZ-NH1	5.16	122.88	120.30
1	BN	183	LEU	CA-CB-CG	5.16	127.17	115.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Bb	176	ARG	NE-CZ-NH2	5.16	122.88	120.30
1	AK	62	ARG	NE-CZ-NH1	5.16	122.88	120.30
1	BQ	183	LEU	CA-CB-CG	5.16	127.17	115.30
1	Ad	182	ARG	NE-CZ-NH2	-5.16	117.72	120.30
1	Bd	176	ARG	NE-CZ-NH1	-5.16	117.72	120.30
1	BG	156	ARG	NE-CZ-NH2	-5.15	117.72	120.30
1	AC	62	ARG	CD-NE-CZ	5.15	130.81	123.60
1	BR	176	ARG	NE-CZ-NH2	5.15	122.87	120.30
1	Cb	184	ILE	CG1-CB-CG2	-5.14	100.08	111.40
1	CU	185	LEU	CA-CB-CG	5.14	127.13	115.30
1	AU	62	ARG	CD-NE-CZ	5.14	130.79	123.60
1	BK	176	ARG	NE-CZ-NH1	-5.13	117.73	120.30
1	BV	206	ARG	NE-CZ-NH1	5.13	122.86	120.30
1	BX	183	LEU	CA-CB-CG	5.13	127.09	115.30
1	AZ	182	ARG	NE-CZ-NH2	-5.13	117.74	120.30
1	AI	62	ARG	NE-CZ-NH1	5.12	122.86	120.30
1	AY	176	ARG	NE-CZ-NH1	-5.12	117.74	120.30
1	BD	176	ARG	NE-CZ-NH1	-5.11	117.75	120.30
1	BB	206	ARG	NE-CZ-NH2	-5.11	117.75	120.30
1	BP	91	ARG	NE-CZ-NH1	-5.11	117.75	120.30
1	AC	182	ARG	NE-CZ-NH2	-5.11	117.75	120.30
1	CC	185	LEU	CA-CB-CG	5.10	127.04	115.30
1	CY	177	LEU	CA-CB-CG	5.10	127.03	115.30
1	AZ	62	ARG	CG-CD-NE	5.10	122.52	111.80
1	BC	206	ARG	NE-CZ-NH2	-5.10	117.75	120.30
1	CL	185	LEU	CA-CB-CG	5.09	127.01	115.30
1	AS	176	ARG	NE-CZ-NH2	5.09	122.84	120.30
1	AH	62	ARG	CG-CD-NE	5.08	122.47	111.80
1	Cc	75	ASP	CB-CG-OD1	-5.08	113.73	118.30
1	CG	185	LEU	CA-CB-CG	5.08	126.98	115.30
1	BL	193	ASP	CB-CG-OD2	-5.06	113.74	118.30
1	BV	206	ARG	NE-CZ-NH2	-5.06	117.77	120.30
1	AT	193	ASP	CB-CG-OD2	5.06	122.85	118.30
1	BE	206	ARG	NE-CZ-NH2	-5.06	117.77	120.30
1	AJ	62	ARG	NE-CZ-NH1	5.05	122.83	120.30
1	CO	185	LEU	CA-CB-CG	5.05	126.91	115.30
1	CR	176	ARG	NE-CZ-NH1	-5.05	117.78	120.30
1	BM	206	ARG	NE-CZ-NH2	-5.04	117.78	120.30
1	BS	202	ARG	NE-CZ-NH1	5.04	122.82	120.30
1	CW	107	LEU	CB-CA-C	-5.04	100.62	110.20
1	CA	184	ILE	CG1-CB-CG2	-5.04	100.32	111.40
1	AQ	182	ARG	NE-CZ-NH2	-5.04	117.78	120.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Aa	62	ARG	CG-CD-NE	5.04	122.38	111.80
1	AZ	62	ARG	CD-NE-CZ	5.03	130.65	123.60
1	AO	62	ARG	CD-NE-CZ	5.02	130.63	123.60
1	BQ	156	ARG	NE-CZ-NH1	5.01	122.80	120.30
1	BM	91	ARG	NE-CZ-NH1	-5.01	117.80	120.30
1	CR	185	LEU	CA-CB-CG	5.01	126.81	115.30
1	BP	176	ARG	NE-CZ-NH1	-5.00	117.80	120.30
1	Ac	193	ASP	CB-CG-OD2	5.00	122.80	118.30
1	AL	62	ARG	CG-CD-NE	5.00	122.31	111.80
1	AE	62	ARG	CD-NE-CZ	5.00	130.60	123.60

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	CU	207	LEU	Peptide
1	Cb	207	LEU	Peptide

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	AA	2218	0	2155	158	0
1	AB	2218	0	2155	156	0
1	AC	2218	0	2155	146	19
1	AD	2218	0	2155	161	0
1	AE	2218	0	2155	128	0
1	AF	2218	0	2155	132	0
1	AG	2218	0	2155	144	0
1	AH	2218	0	2155	136	0
1	AI	2218	0	2155	142	0
1	AJ	2218	0	2155	136	1
1	AK	2218	0	2155	127	0
1	AL	2218	0	2155	117	0
1	AM	2218	0	2155	139	0
1	AN	2218	0	2155	138	0
1	AO	2218	0	2155	137	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AP	2218	0	2155	130	1
1	AQ	2218	0	2155	127	0
1	AR	2218	0	2155	122	0
1	AS	2218	0	2155	136	0
1	AT	2218	0	2155	136	0
1	AU	2218	0	2155	135	0
1	AV	2218	0	2155	133	0
1	AW	2218	0	2155	136	0
1	AX	2218	0	2155	125	0
1	AY	2218	0	2155	131	0
1	AZ	2218	0	2155	135	0
1	Aa	2218	0	2155	0	0
1	Ab	2218	0	2155	0	0
1	Ac	2218	0	2155	0	0
1	Ad	2218	0	2155	0	0
1	BA	2214	0	2153	114	0
1	BB	2214	0	2153	125	0
1	BC	2214	0	2153	116	13
1	BD	2214	0	2153	118	0
1	BE	2214	0	2153	83	0
1	BF	2214	0	2153	92	0
1	BG	2214	0	2153	92	0
1	BH	2214	0	2153	106	0
1	BI	2214	0	2153	93	8
1	BJ	2214	0	2153	84	1
1	BK	2214	0	2153	94	0
1	BL	2214	0	2153	88	7
1	BM	2214	0	2153	101	0
1	BN	2214	0	2153	84	0
1	BO	2214	0	2153	97	0
1	BP	2214	0	2153	92	0
1	BQ	2214	0	2153	94	0
1	BR	2214	0	2153	85	1
1	BS	2214	0	2153	95	0
1	BT	2214	0	2153	92	0
1	BU	2214	0	2153	88	0
1	BV	2214	0	2153	93	0
1	BW	2214	0	2153	89	6
1	BX	2214	0	2153	79	1
1	BY	2214	0	2153	97	0
1	BZ	2214	0	2153	79	0
1	Ba	2214	0	2153	0	11

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	Bb	2214	0	2153	0	0
1	Bc	2214	0	2153	0	1
1	Bd	2214	0	2153	0	0
1	CA	2340	0	2280	135	1
1	CB	2340	0	2280	154	0
1	CC	2340	0	2280	136	0
1	CD	2340	0	2280	162	0
1	CE	2340	0	2280	110	0
1	CF	2340	0	2280	121	0
1	CG	2340	0	2280	110	0
1	CH	2340	0	2280	119	0
1	CI	2340	0	2280	116	0
1	CJ	2340	0	2280	114	0
1	CK	2340	0	2280	123	6
1	CL	2340	0	2280	125	1
1	CM	2340	0	2280	120	0
1	CN	2340	0	2280	99	0
1	CO	2340	0	2280	120	0
1	CP	2340	0	2280	111	2
1	CQ	2340	0	2280	118	11
1	CR	2340	0	2280	116	1
1	CS	2340	0	2280	102	0
1	CT	2340	0	2280	116	2
1	CU	2340	0	2280	112	0
1	CV	2340	0	2280	112	0
1	CW	2340	0	2280	120	0
1	CX	2340	0	2280	109	0
1	CY	2340	0	2280	117	0
1	CZ	2340	0	2280	113	32
1	Ca	2340	0	2280	0	0
1	Cb	2340	0	2280	0	0
1	Cc	2340	0	2280	0	0
1	Cd	2340	0	2280	0	7
2	AA	1	0	0	0	0
2	AB	1	0	0	0	0
2	AC	1	0	0	0	0
2	AD	1	0	0	0	0
2	AE	1	0	0	0	0
2	AF	1	0	0	0	0
2	AG	1	0	0	0	0
2	AH	1	0	0	0	0
2	AI	1	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	AJ	1	0	0	0	0
2	AK	1	0	0	0	0
2	AL	1	0	0	0	0
2	AM	1	0	0	0	0
2	AN	1	0	0	0	0
2	AO	1	0	0	0	0
2	AP	1	0	0	0	0
2	AQ	1	0	0	0	0
2	AR	1	0	0	0	0
2	AS	1	0	0	0	0
2	AT	1	0	0	0	0
2	AU	1	0	0	0	0
2	AV	1	0	0	0	0
2	AW	1	0	0	0	0
2	AX	1	0	0	0	0
2	AY	1	0	0	0	0
2	AZ	1	0	0	0	0
2	Aa	1	0	0	0	0
2	Ab	1	0	0	0	0
2	Ac	1	0	0	0	0
2	Ad	1	0	0	0	0
2	BA	2	0	0	0	0
2	BB	2	0	0	0	0
2	BC	2	0	0	0	0
2	BD	2	0	0	0	0
2	BE	2	0	0	0	0
2	BF	2	0	0	0	0
2	BG	2	0	0	0	0
2	BH	2	0	0	0	0
2	BI	2	0	0	0	0
2	BJ	2	0	0	0	0
2	BK	2	0	0	0	0
2	BL	2	0	0	0	0
2	BM	2	0	0	0	0
2	BN	2	0	0	0	0
2	BO	2	0	0	0	0
2	BP	2	0	0	0	0
2	BQ	2	0	0	0	0
2	BR	2	0	0	0	0
2	BS	2	0	0	0	0
2	BT	2	0	0	0	0
2	BU	2	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	BV	2	0	0	0	0
2	BW	2	0	0	0	0
2	BX	2	0	0	0	0
2	BY	2	0	0	0	0
2	BZ	2	0	0	0	0
2	Ba	2	0	0	0	0
2	Bb	2	0	0	0	0
2	Bc	2	0	0	0	0
2	Bd	2	0	0	0	0
All	All	203250	0	197640	8152	71

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 20.

All (8152) 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:AD:298:TRP:NE1	1:AD:312:VAL:HG12	1.23	1.53
1:AA:298:TRP:NE1	1:AA:312:VAL:HG12	1.24	1.53
1:AK:298:TRP:NE1	1:AK:312:VAL:HG12	1.21	1.50
1:AI:298:TRP:NE1	1:AI:312:VAL:HG12	1.24	1.50
1:AB:298:TRP:NE1	1:AB:312:VAL:HG12	1.23	1.49
1:AC:298:TRP:NE1	1:AC:312:VAL:HG12	1.24	1.48
1:AU:298:TRP:NE1	1:AU:312:VAL:HG12	1.23	1.48
1:AO:298:TRP:NE1	1:AO:312:VAL:HG12	1.22	1.47
1:AJ:298:TRP:NE1	1:AJ:312:VAL:HG12	1.22	1.46
1:AL:298:TRP:NE1	1:AL:312:VAL:HG12	1.21	1.46
1:AS:298:TRP:NE1	1:AS:312:VAL:HG12	1.22	1.46
1:AF:298:TRP:NE1	1:AF:312:VAL:HG12	1.22	1.45
1:AN:298:TRP:NE1	1:AN:312:VAL:HG12	1.23	1.45
1:AV:298:TRP:NE1	1:AV:312:VAL:HG12	1.24	1.44
1:AM:298:TRP:NE1	1:AM:312:VAL:HG12	1.22	1.44
1:AH:298:TRP:NE1	1:AH:312:VAL:HG12	1.23	1.43
1:AY:298:TRP:NE1	1:AY:312:VAL:HG12	1.23	1.43
1:AW:298:TRP:NE1	1:AW:312:VAL:HG12	1.21	1.43
1:AD:298:TRP:CE2	1:AD:312:VAL:HG12	1.55	1.43
1:AZ:298:TRP:NE1	1:AZ:312:VAL:HG12	1.24	1.43
1:AX:298:TRP:NE1	1:AX:312:VAL:HG12	1.23	1.42
1:AQ:298:TRP:NE1	1:AQ:312:VAL:HG12	1.23	1.41
1:AZ:298:TRP:CE2	1:AZ:312:VAL:HG12	1.54	1.41
1:AG:298:TRP:NE1	1:AG:312:VAL:HG12	1.22	1.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AP:298:TRP:NE1	1:AP:312:VAL:HG12	1.22	1.41
1:AA:298:TRP:CE2	1:AA:312:VAL:HG12	1.55	1.41
1:AC:298:TRP:CE2	1:AC:312:VAL:HG12	1.54	1.41
1:AR:298:TRP:NE1	1:AR:312:VAL:HG12	1.24	1.41
1:AI:298:TRP:CE2	1:AI:312:VAL:HG12	1.56	1.40
1:AL:298:TRP:CE2	1:AL:312:VAL:HG12	1.53	1.40
1:AN:298:TRP:CE2	1:AN:312:VAL:HG12	1.56	1.40
1:AT:298:TRP:CE2	1:AT:312:VAL:HG12	1.54	1.40
1:AE:298:TRP:NE1	1:AE:312:VAL:HG12	1.24	1.40
1:AP:298:TRP:CE2	1:AP:312:VAL:HG12	1.54	1.40
1:AQ:298:TRP:CE2	1:AQ:312:VAL:HG12	1.56	1.40
1:AV:298:TRP:CE2	1:AV:312:VAL:HG12	1.54	1.39
1:AW:298:TRP:CE2	1:AW:312:VAL:HG12	1.54	1.39
1:AT:298:TRP:NE1	1:AT:312:VAL:HG12	1.23	1.39
1:AE:298:TRP:CE2	1:AE:312:VAL:HG12	1.56	1.39
1:AO:298:TRP:CE2	1:AO:312:VAL:HG12	1.56	1.39
1:AR:298:TRP:CE2	1:AR:312:VAL:HG12	1.56	1.39
1:AK:298:TRP:CE2	1:AK:312:VAL:HG12	1.54	1.39
1:AJ:298:TRP:CE2	1:AJ:312:VAL:HG12	1.56	1.39
1:AM:298:TRP:CE2	1:AM:312:VAL:HG12	1.57	1.39
1:AX:298:TRP:CE2	1:AX:312:VAL:HG12	1.56	1.39
1:AY:298:TRP:CE2	1:AY:312:VAL:HG12	1.55	1.38
1:AF:298:TRP:CE2	1:AF:312:VAL:HG12	1.56	1.38
1:AH:298:TRP:CE2	1:AH:312:VAL:HG12	1.56	1.38
1:AB:298:TRP:CE2	1:AB:312:VAL:HG12	1.57	1.38
1:AU:298:TRP:CE2	1:AU:312:VAL:HG12	1.56	1.38
1:AG:298:TRP:CE2	1:AG:312:VAL:HG12	1.56	1.37
1:AD:298:TRP:CD1	1:AD:312:VAL:HG12	1.62	1.37
1:AR:298:TRP:CD1	1:AR:312:VAL:HG12	1.60	1.36
1:AS:298:TRP:CE2	1:AS:312:VAL:HG12	1.57	1.36
1:AK:298:TRP:CD1	1:AK:312:VAL:HG12	1.61	1.35
1:AB:298:TRP:CD1	1:AB:312:VAL:HG12	1.62	1.35
1:AL:298:TRP:CD1	1:AL:312:VAL:HG12	1.60	1.35
1:AA:298:TRP:CD1	1:AA:312:VAL:HG12	1.63	1.35
1:AG:298:TRP:CD1	1:AG:312:VAL:HG12	1.62	1.35
1:AW:298:TRP:CD1	1:AW:312:VAL:HG12	1.60	1.34
1:AT:298:TRP:CD1	1:AT:312:VAL:HG12	1.61	1.34
1:AJ:298:TRP:CD1	1:AJ:312:VAL:HG12	1.62	1.34
1:AC:298:TRP:CD1	1:AC:312:VAL:HG12	1.61	1.33
1:AO:298:TRP:CD1	1:AO:312:VAL:HG12	1.62	1.33
1:AH:298:TRP:CD1	1:AH:312:VAL:HG12	1.62	1.33

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AV:298:TRP:CD1	1:AV:312:VAL:HG12	1.62	1.33
1:AZ:298:TRP:CD1	1:AZ:312:VAL:HG12	1.62	1.33
1:AX:298:TRP:CD1	1:AX:312:VAL:HG12	1.62	1.33
1:AP:298:TRP:CD1	1:AP:312:VAL:HG12	1.61	1.33
1:AE:298:TRP:CD1	1:AE:312:VAL:HG12	1.63	1.32
1:AN:298:TRP:CD1	1:AN:312:VAL:HG12	1.62	1.32
1:AQ:298:TRP:CD1	1:AQ:312:VAL:HG12	1.62	1.32
1:AU:298:TRP:CD1	1:AU:312:VAL:HG12	1.64	1.31
1:AM:298:TRP:CD1	1:AM:312:VAL:HG12	1.62	1.31
1:AI:298:TRP:CD1	1:AI:312:VAL:HG12	1.63	1.31
1:AF:298:TRP:CD1	1:AF:312:VAL:HG12	1.62	1.31
1:AY:298:TRP:CD1	1:AY:312:VAL:HG12	1.63	1.30
1:AS:298:TRP:CD1	1:AS:312:VAL:HG12	1.64	1.29
1:AH:253:ASP:OD1	1:AH:284:LYS:O	1.52	1.27
1:AM:253:ASP:OD1	1:AM:284:LYS:O	1.53	1.27
1:AT:253:ASP:OD1	1:AT:284:LYS:O	1.53	1.27
1:AN:253:ASP:OD1	1:AN:284:LYS:O	1.53	1.27
1:AO:253:ASP:OD1	1:AO:284:LYS:O	1.53	1.26
1:AB:253:ASP:OD1	1:AB:284:LYS:O	1.52	1.26
1:AP:253:ASP:OD1	1:AP:284:LYS:O	1.53	1.26
1:AV:253:ASP:OD1	1:AV:284:LYS:O	1.53	1.25
1:AI:253:ASP:OD1	1:AI:284:LYS:O	1.53	1.25
1:AU:253:ASP:OD1	1:AU:284:LYS:O	1.52	1.25
1:AW:253:ASP:OD1	1:AW:284:LYS:O	1.54	1.25
1:AZ:253:ASP:OD1	1:AZ:284:LYS:O	1.54	1.24
1:AJ:253:ASP:OD1	1:AJ:284:LYS:O	1.54	1.24
1:AA:253:ASP:OD1	1:AA:284:LYS:O	1.53	1.24
1:AD:253:ASP:OD1	1:AD:284:LYS:O	1.54	1.24
1:AC:253:ASP:OD1	1:AC:284:LYS:O	1.53	1.24
1:AQ:253:ASP:OD1	1:AQ:284:LYS:O	1.52	1.23
1:AG:253:ASP:OD1	1:AG:284:LYS:O	1.53	1.23
1:AS:253:ASP:OD1	1:AS:284:LYS:O	1.53	1.23
1:AR:253:ASP:OD1	1:AR:284:LYS:O	1.54	1.22
1:AL:253:ASP:OD1	1:AL:284:LYS:O	1.53	1.22
1:AF:253:ASP:OD1	1:AF:284:LYS:O	1.53	1.22
1:AK:253:ASP:OD1	1:AK:284:LYS:O	1.54	1.22
1:AX:253:ASP:OD1	1:AX:284:LYS:O	1.53	1.21
1:AY:253:ASP:OD1	1:AY:284:LYS:O	1.53	1.21
1:AM:298:TRP:CD1	1:AM:312:VAL:CG1	2.26	1.19
1:AT:298:TRP:CD1	1:AT:312:VAL:CG1	2.26	1.19
1:AC:298:TRP:CD1	1:AC:312:VAL:CG1	2.27	1.18

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AN:298:TRP:CD1	1:AN:312:VAL:CG1	2.27	1.18
1:AP:298:TRP:CD1	1:AP:312:VAL:CG1	2.26	1.18
1:AL:298:TRP:CD1	1:AL:312:VAL:CG1	2.26	1.18
1:AW:298:TRP:CD1	1:AW:312:VAL:CG1	2.26	1.18
1:AH:298:TRP:CD1	1:AH:312:VAL:CG1	2.27	1.17
1:AQ:298:TRP:CD1	1:AQ:312:VAL:CG1	2.28	1.17
1:AA:298:TRP:CD1	1:AA:312:VAL:CG1	2.28	1.17
1:AI:298:TRP:CD1	1:AI:312:VAL:CG1	2.28	1.17
1:AR:298:TRP:CD1	1:AR:312:VAL:CG1	2.26	1.17
1:AD:298:TRP:CD1	1:AD:312:VAL:CG1	2.27	1.17
1:AB:298:TRP:CD1	1:AB:312:VAL:CG1	2.26	1.17
1:AF:298:TRP:CD1	1:AF:312:VAL:CG1	2.28	1.17
1:CD:141:LEU:HD21	1:CD:184:ILE:HD11	1.31	1.17
1:AK:302:ASP:C	1:AK:305:ASN:OD1	1.83	1.17
1:AC:302:ASP:C	1:AC:305:ASN:OD1	1.84	1.17
1:AO:298:TRP:CD1	1:AO:312:VAL:CG1	2.27	1.16
1:AT:302:ASP:C	1:AT:305:ASN:OD1	1.84	1.16
1:AP:302:ASP:C	1:AP:305:ASN:OD1	1.84	1.16
1:AE:298:TRP:CD1	1:AE:312:VAL:CG1	2.29	1.16
1:AA:302:ASP:C	1:AA:305:ASN:OD1	1.83	1.16
1:AX:302:ASP:C	1:AX:305:ASN:OD1	1.84	1.16
1:AJ:302:ASP:C	1:AJ:305:ASN:OD1	1.84	1.16
1:AB:302:ASP:C	1:AB:305:ASN:OD1	1.84	1.16
1:AG:302:ASP:C	1:AG:305:ASN:OD1	1.84	1.16
1:AG:298:TRP:CD1	1:AG:312:VAL:CG1	2.27	1.16
1:AK:298:TRP:CD1	1:AK:312:VAL:CG1	2.28	1.16
1:AU:298:TRP:CD1	1:AU:312:VAL:CG1	2.29	1.16
1:AV:298:TRP:CD1	1:AV:312:VAL:CG1	2.28	1.16
1:AZ:298:TRP:CD1	1:AZ:312:VAL:CG1	2.28	1.16
1:AX:298:TRP:CD1	1:AX:312:VAL:CG1	2.28	1.16
1:AI:302:ASP:C	1:AI:305:ASN:OD1	1.84	1.16
1:AU:302:ASP:C	1:AU:305:ASN:OD1	1.84	1.16
1:AD:302:ASP:C	1:AD:305:ASN:OD1	1.84	1.15
1:AJ:298:TRP:CD1	1:AJ:312:VAL:CG1	2.28	1.15
1:AQ:302:ASP:C	1:AQ:305:ASN:OD1	1.84	1.15
1:AO:302:ASP:C	1:AO:305:ASN:OD1	1.85	1.15
1:AS:298:TRP:CD1	1:AS:312:VAL:CG1	2.29	1.15
1:AE:302:ASP:C	1:AE:305:ASN:OD1	1.84	1.15
1:AH:302:ASP:C	1:AH:305:ASN:OD1	1.84	1.15
1:AM:302:ASP:C	1:AM:305:ASN:OD1	1.84	1.15
1:AR:302:ASP:C	1:AR:305:ASN:OD1	1.83	1.15

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AZ:302:ASP:C	1:AZ:305:ASN:OD1	1.84	1.15
1:CR:141:LEU:HD21	1:CR:184:ILE:HD11	1.30	1.14
1:AS:302:ASP:C	1:AS:305:ASN:OD1	1.84	1.14
1:AV:302:ASP:C	1:AV:305:ASN:OD1	1.84	1.14
1:AY:302:ASP:C	1:AY:305:ASN:OD1	1.84	1.14
1:AN:302:ASP:C	1:AN:305:ASN:OD1	1.84	1.14
1:AL:302:ASP:C	1:AL:305:ASN:OD1	1.84	1.14
1:AF:302:ASP:C	1:AF:305:ASN:OD1	1.84	1.14
1:AY:298:TRP:CD1	1:AY:312:VAL:CG1	2.30	1.14
1:CX:141:LEU:HD21	1:CX:184:ILE:HD11	1.27	1.14
1:AP:298:TRP:NE1	1:AP:312:VAL:CG1	2.12	1.13
1:AW:302:ASP:C	1:AW:305:ASN:OD1	1.85	1.13
1:CT:141:LEU:HD21	1:CT:184:ILE:HD11	1.29	1.13
1:CI:141:LEU:HD21	1:CI:184:ILE:HD11	1.30	1.13
1:CW:141:LEU:HD21	1:CW:184:ILE:HD11	1.31	1.13
1:AG:298:TRP:NE1	1:AG:312:VAL:CG1	2.12	1.12
1:CM:141:LEU:HD21	1:CM:184:ILE:HD11	1.30	1.12
1:AF:298:TRP:NE1	1:AF:312:VAL:CG1	2.13	1.12
1:CZ:141:LEU:HD21	1:CZ:184:ILE:HD11	1.26	1.12
1:AM:298:TRP:NE1	1:AM:312:VAL:CG1	2.13	1.12
1:AW:298:TRP:NE1	1:AW:312:VAL:CG1	2.12	1.12
1:AU:298:TRP:NE1	1:AU:312:VAL:CG1	2.13	1.11
1:AY:298:TRP:NE1	1:AY:312:VAL:CG1	2.13	1.11
1:CP:141:LEU:HD21	1:CP:184:ILE:HD11	1.31	1.11
1:AK:298:TRP:NE1	1:AK:312:VAL:CG1	2.13	1.11
1:CB:141:LEU:HD21	1:CB:184:ILE:HD11	1.29	1.11
1:AC:298:TRP:NE1	1:AC:312:VAL:CG1	2.13	1.11
1:AH:298:TRP:NE1	1:AH:312:VAL:CG1	2.13	1.11
1:AS:298:TRP:NE1	1:AS:312:VAL:CG1	2.13	1.11
1:AE:298:TRP:NE1	1:AE:312:VAL:CG1	2.14	1.11
1:AB:298:TRP:NE1	1:AB:312:VAL:CG1	2.13	1.10
1:AO:298:TRP:NE1	1:AO:312:VAL:CG1	2.13	1.10
1:CO:141:LEU:HD21	1:CO:184:ILE:HD11	1.31	1.10
1:AJ:298:TRP:NE1	1:AJ:312:VAL:CG1	2.13	1.10
1:AX:298:TRP:NE1	1:AX:312:VAL:CG1	2.14	1.10
1:CN:141:LEU:HD21	1:CN:184:ILE:HD11	1.32	1.10
1:AI:141:LEU:O	1:AI:144:THR:HG22	1.50	1.10
1:AQ:298:TRP:NE1	1:AQ:312:VAL:CG1	2.13	1.10
1:AD:141:LEU:O	1:AD:144:THR:HG22	1.58	1.10
1:AA:298:TRP:NE1	1:AA:312:VAL:CG1	2.14	1.10
1:AL:298:TRP:NE1	1:AL:312:VAL:CG1	2.12	1.10

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AN:298:TRP:NE1	1:AN:312:VAL:CG1	2.13	1.10
1:AD:298:TRP:NE1	1:AD:312:VAL:CG1	2.13	1.10
1:AV:298:TRP:NE1	1:AV:312:VAL:CG1	2.14	1.09
1:CL:141:LEU:HD21	1:CL:184:ILE:HD11	1.31	1.09
1:AI:298:TRP:NE1	1:AI:312:VAL:CG1	2.14	1.09
1:AA:141:LEU:O	1:AA:144:THR:HG22	1.52	1.09
1:AT:298:TRP:NE1	1:AT:312:VAL:CG1	2.13	1.09
1:CK:141:LEU:HD21	1:CK:184:ILE:HD11	1.31	1.09
1:CH:141:LEU:HD21	1:CH:184:ILE:HD11	1.31	1.09
1:CA:141:LEU:HD21	1:CA:184:ILE:HD11	1.35	1.09
1:CD:122:GLY:HA3	1:BH:114:MET:SD	141.29	1.08
1:AZ:298:TRP:NE1	1:AZ:312:VAL:CG1	2.13	1.08
1:CY:141:LEU:HD21	1:CY:184:ILE:HD11	1.36	1.08
1:CS:141:LEU:HD21	1:CS:184:ILE:HD11	1.34	1.08
1:AR:298:TRP:NE1	1:AR:312:VAL:CG1	2.14	1.07
1:CV:141:LEU:HD21	1:CV:184:ILE:HD11	1.34	1.07
1:AX:141:LEU:O	1:AX:144:THR:HG22	1.53	1.07
1:CC:141:LEU:HD21	1:CC:184:ILE:HD11	1.33	1.07
1:CJ:141:LEU:HD21	1:CJ:184:ILE:HD11	1.37	1.07
1:BN:61:SER:HB3	1:BN:90:PRO:HD2	1.37	1.06
1:CG:141:LEU:HD21	1:CG:184:ILE:HD11	1.32	1.06
1:AL:298:TRP:CE2	1:AL:312:VAL:CG1	2.39	1.06
1:AC:141:LEU:O	1:AC:144:THR:HG22	1.55	1.06
1:CE:141:LEU:HD21	1:CE:184:ILE:HD11	1.36	1.06
1:BO:61:SER:HB3	1:BO:90:PRO:HD2	1.36	1.06
1:BC:61:SER:HB3	1:BC:90:PRO:HD2	1.42	1.06
1:CQ:141:LEU:HD21	1:CQ:184:ILE:HD11	1.30	1.06
1:AQ:141:LEU:O	1:AQ:144:THR:HG22	1.55	1.05
1:AT:141:LEU:O	1:AT:144:THR:HG22	1.55	1.05
1:AU:141:LEU:O	1:AU:144:THR:HG22	1.55	1.05
1:AN:141:LEU:O	1:AN:144:THR:HG22	1.56	1.05
1:AK:298:TRP:CE2	1:AK:312:VAL:CG1	2.39	1.05
1:AK:141:LEU:O	1:AK:144:THR:HG22	1.57	1.05
1:AD:298:TRP:CE2	1:AD:312:VAL:CG1	2.41	1.05
1:BG:61:SER:HB3	1:BG:90:PRO:HD2	1.39	1.05
1:AV:298:TRP:CE2	1:AV:312:VAL:CG1	2.40	1.04
1:AT:298:TRP:CE2	1:AT:312:VAL:CG1	2.40	1.04
1:BE:61:SER:HB3	1:BE:90:PRO:HD2	1.38	1.04
1:CF:141:LEU:HD21	1:CF:184:ILE:HD11	1.35	1.04
1:BI:61:SER:HB3	1:BI:90:PRO:HD2	1.37	1.04
1:BA:61:SER:HB3	1:BA:90:PRO:HD2	1.40	1.04

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AM:141:LEU:O	1:AM:144:THR:HG22	1.55	1.04
1:BY:254:GLY:HA2	1:BY:283:LYS:HE3	1.39	1.04
1:AY:298:TRP:CE2	1:AY:312:VAL:CG1	2.41	1.04
1:AZ:298:TRP:CE2	1:AZ:312:VAL:CG1	2.40	1.04
1:AY:141:LEU:O	1:AY:144:THR:HG22	1.56	1.04
1:AH:141:LEU:O	1:AH:144:THR:HG22	1.58	1.04
1:AV:141:LEU:O	1:AV:144:THR:HG22	1.56	1.04
1:BH:61:SER:HB3	1:BH:90:PRO:HD2	1.39	1.04
1:BV:61:SER:HB3	1:BV:90:PRO:HD2	1.38	1.04
1:AO:141:LEU:O	1:AO:144:THR:HG22	1.58	1.04
1:BD:254:GLY:HA2	1:BD:283:LYS:HE3	1.39	1.04
1:BS:61:SER:HB3	1:BS:90:PRO:HD2	1.36	1.03
1:AW:141:LEU:O	1:AW:144:THR:HG22	1.58	1.03
1:BI:254:GLY:HA2	1:BI:283:LYS:HE3	1.37	1.03
1:AC:298:TRP:CE2	1:AC:312:VAL:CG1	2.41	1.03
1:AW:298:TRP:CE2	1:AW:312:VAL:CG1	2.40	1.03
1:BA:254:GLY:HA2	1:BA:283:LYS:HE3	1.38	1.03
1:BZ:61:SER:HB3	1:BZ:90:PRO:HD2	1.39	1.03
1:BG:254:GLY:HA2	1:BG:283:LYS:HE3	1.40	1.03
1:AE:141:LEU:O	1:AE:144:THR:HG22	1.56	1.03
1:AB:141:LEU:O	1:AB:144:THR:HG22	1.59	1.03
1:AJ:141:LEU:O	1:AJ:144:THR:HG22	1.58	1.03
1:BE:254:GLY:HA2	1:BE:283:LYS:HE3	1.41	1.03
1:AN:298:TRP:CE2	1:AN:312:VAL:CG1	2.42	1.03
1:AP:298:TRP:CE2	1:AP:312:VAL:CG1	2.40	1.03
1:AA:298:TRP:CE2	1:AA:312:VAL:CG1	2.42	1.03
1:AF:141:LEU:O	1:AF:144:THR:HG22	1.59	1.03
1:BB:61:SER:HB3	1:BB:90:PRO:HD2	1.41	1.03
1:AR:298:TRP:CE2	1:AR:312:VAL:CG1	2.42	1.02
1:BB:254:GLY:HA2	1:BB:283:LYS:HE3	1.41	1.02
1:AG:141:LEU:O	1:AG:144:THR:HG22	1.57	1.02
1:BX:61:SER:HB3	1:BX:90:PRO:HD2	1.40	1.02
1:BK:254:GLY:HA2	1:BK:283:LYS:HE3	1.41	1.02
1:AI:298:TRP:CE2	1:AI:312:VAL:CG1	2.43	1.02
1:AU:298:TRP:CE2	1:AU:312:VAL:CG1	2.43	1.02
1:BL:254:GLY:HA2	1:BL:283:LYS:HE3	1.39	1.02
1:BM:61:SER:HB3	1:BM:90:PRO:HD2	1.41	1.02
1:BC:254:GLY:HA2	1:BC:283:LYS:HE3	1.42	1.02
1:AO:298:TRP:CE2	1:AO:312:VAL:CG1	2.42	1.02
1:AH:298:TRP:CE2	1:AH:312:VAL:CG1	2.43	1.02
1:AL:279:TYR:CZ	1:AL:311:GLY:O	2.13	1.02

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CC:101:ARG:HB2	1:CC:208:SER:OG	1.59	1.02
1:BL:61:SER:HB3	1:BL:90:PRO:HD2	1.40	1.02
1:AJ:298:TRP:CE2	1:AJ:312:VAL:CG1	2.43	1.01
1:AQ:298:TRP:CE2	1:AQ:312:VAL:CG1	2.42	1.01
1:AE:298:TRP:CE2	1:AE:312:VAL:CG1	2.42	1.01
1:BT:254:GLY:HA2	1:BT:283:LYS:HE3	1.41	1.01
1:CU:141:LEU:HD21	1:CU:184:ILE:HD11	1.35	1.01
1:AX:298:TRP:CE2	1:AX:312:VAL:CG1	2.42	1.01
1:BJ:61:SER:HB3	1:BJ:90:PRO:HD2	1.40	1.01
1:AF:279:TYR:CZ	1:AF:311:GLY:O	2.14	1.01
1:AF:298:TRP:CE2	1:AF:312:VAL:CG1	2.42	1.01
1:AG:298:TRP:CE2	1:AG:312:VAL:CG1	2.42	1.01
1:CM:75:ASP:OD1	1:CM:188:VAL:O	1.79	1.01
1:BM:254:GLY:HA2	1:BM:283:LYS:HE3	1.41	1.01
1:BN:254:GLY:HA2	1:BN:283:LYS:HE3	1.42	1.01
1:BU:61:SER:HB3	1:BU:90:PRO:HD2	1.39	1.01
1:AH:279:TYR:CZ	1:AH:311:GLY:O	2.14	1.01
1:AC:279:TYR:CZ	1:AC:311:GLY:O	2.14	1.01
1:BK:98:ILE:O	1:BK:211:SER:O	1.79	1.01
1:BS:254:GLY:HA2	1:BS:283:LYS:HE3	1.39	1.01
1:AR:141:LEU:O	1:AR:144:THR:HG22	1.60	1.01
1:BX:254:GLY:HA2	1:BX:283:LYS:HE3	1.41	1.01
1:AM:279:TYR:CZ	1:AM:311:GLY:O	2.14	1.01
1:AB:298:TRP:CE2	1:AB:312:VAL:CG1	2.44	1.00
1:AM:298:TRP:CE2	1:AM:312:VAL:CG1	2.43	1.00
1:AE:279:TYR:CZ	1:AE:311:GLY:O	2.14	1.00
1:BR:254:GLY:HA2	1:BR:283:LYS:HE3	1.41	1.00
1:AP:279:TYR:CZ	1:AP:311:GLY:O	2.15	1.00
1:AJ:279:TYR:CZ	1:AJ:311:GLY:O	2.14	1.00
1:AS:141:LEU:O	1:AS:144:THR:HG22	1.60	1.00
1:BK:61:SER:HB3	1:BK:90:PRO:HD2	1.42	1.00
1:AA:279:TYR:CZ	1:AA:311:GLY:O	2.14	1.00
1:BY:61:SER:HB3	1:BY:90:PRO:HD2	1.41	1.00
1:AP:141:LEU:O	1:AP:144:THR:HG22	1.62	1.00
1:BP:61:SER:HB3	1:BP:90:PRO:HD2	1.40	1.00
1:AI:279:TYR:CZ	1:AI:311:GLY:O	2.14	1.00
1:AD:279:TYR:CZ	1:AD:311:GLY:O	2.14	1.00
1:BH:254:GLY:HA2	1:BH:283:LYS:HE3	1.40	1.00
1:AB:279:TYR:CZ	1:AB:311:GLY:O	2.15	1.00
1:BO:254:GLY:HA2	1:BO:283:LYS:HE3	1.40	1.00
1:AA:299:GLY:HA3	1:AA:310:ASP:O	1.63	0.99

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BQ:61:SER:HB3	1:BQ:90:PRO:HD2	1.40	0.99
1:BD:98:ILE:O	1:BD:211:SER:O	1.81	0.99
1:CZ:101:ARG:HB2	1:CZ:208:SER:OG	1.63	0.99
1:AR:279:TYR:CZ	1:AR:311:GLY:O	2.15	0.99
1:BV:254:GLY:HA2	1:BV:283:LYS:HE3	1.41	0.99
1:BP:254:GLY:HA2	1:BP:283:LYS:HE3	1.41	0.99
1:BZ:254:GLY:HA2	1:BZ:283:LYS:HE3	1.41	0.99
1:AB:299:GLY:HA3	1:AB:310:ASP:O	1.63	0.99
1:AT:279:TYR:CZ	1:AT:311:GLY:O	2.14	0.99
1:AQ:279:TYR:CZ	1:AQ:311:GLY:O	2.15	0.99
1:AK:279:TYR:CZ	1:AK:311:GLY:O	2.16	0.99
1:AZ:141:LEU:O	1:AZ:144:THR:HG22	1.60	0.99
1:BM:98:ILE:O	1:BM:211:SER:O	1.80	0.99
1:AS:298:TRP:CE2	1:AS:312:VAL:CG1	2.43	0.99
1:AZ:299:GLY:HA3	1:AZ:310:ASP:O	1.62	0.99
1:CI:75:ASP:OD1	1:CI:188:VAL:O	1.81	0.99
1:BP:98:ILE:O	1:BP:211:SER:O	1.81	0.99
1:AN:279:TYR:CZ	1:AN:311:GLY:O	2.15	0.99
1:BF:61:SER:HB3	1:BF:90:PRO:HD2	1.44	0.99
1:AL:298:TRP:CD2	1:AL:312:VAL:HG12	1.98	0.99
1:CL:75:ASP:OD1	1:CL:188:VAL:O	1.79	0.99
1:BT:61:SER:HB3	1:BT:90:PRO:HD2	1.41	0.99
1:BQ:254:GLY:HA2	1:BQ:283:LYS:HE3	1.41	0.99
1:BV:98:ILE:O	1:BV:211:SER:O	1.81	0.99
1:BD:61:SER:HB3	1:BD:90:PRO:HD2	1.41	0.99
1:AW:279:TYR:CZ	1:AW:311:GLY:O	2.14	0.99
1:BW:254:GLY:HA2	1:BW:283:LYS:HE3	1.43	0.99
1:AW:298:TRP:CD2	1:AW:312:VAL:HG12	1.98	0.99
1:AZ:279:TYR:CZ	1:AZ:311:GLY:O	2.16	0.99
1:BU:254:GLY:HA2	1:BU:283:LYS:HE3	1.41	0.99
1:AO:279:TYR:CZ	1:AO:311:GLY:O	2.15	0.99
1:AV:279:TYR:CZ	1:AV:311:GLY:O	2.16	0.99
1:BF:98:ILE:O	1:BF:211:SER:O	1.81	0.98
1:AG:279:TYR:CZ	1:AG:311:GLY:O	2.15	0.98
1:BW:61:SER:HB3	1:BW:90:PRO:HD2	1.41	0.98
1:AS:279:TYR:CZ	1:AS:311:GLY:O	2.16	0.98
1:BI:98:ILE:O	1:BI:211:SER:O	1.81	0.98
1:AN:299:GLY:HA3	1:AN:310:ASP:O	1.63	0.98
1:AL:141:LEU:O	1:AL:144:THR:HG22	1.61	0.98
1:AU:299:GLY:HA3	1:AU:310:ASP:O	1.63	0.98
1:AG:299:GLY:HA3	1:AG:310:ASP:O	1.63	0.98

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AK:298:TRP:CD2	1:AK:312:VAL:HG12	1.99	0.98
1:AC:299:GLY:HA3	1:AC:310:ASP:O	1.63	0.98
1:AV:299:GLY:HA3	1:AV:310:ASP:O	1.63	0.98
1:AM:299:GLY:HA3	1:AM:310:ASP:O	1.62	0.98
1:CW:75:ASP:OD1	1:CW:188:VAL:O	1.81	0.98
1:BP:98:ILE:O	1:BP:211:SER:N	1.95	0.98
1:AU:279:TYR:CZ	1:AU:311:GLY:O	2.15	0.98
1:AT:299:GLY:HA3	1:AT:310:ASP:O	1.64	0.98
1:BR:61:SER:HB3	1:BR:90:PRO:HD2	1.42	0.98
1:BB:98:ILE:O	1:BB:211:SER:O	1.81	0.98
1:CL:101:ARG:HB2	1:CL:208:SER:OG	1.64	0.98
1:BX:98:ILE:O	1:BX:211:SER:O	1.80	0.98
1:AD:298:TRP:CD2	1:AD:312:VAL:HG12	2.00	0.98
1:AI:299:GLY:HA3	1:AI:310:ASP:O	1.62	0.98
1:AH:299:GLY:HA3	1:AH:310:ASP:O	1.62	0.98
1:CH:101:ARG:HB2	1:CH:208:SER:OG	1.64	0.98
1:AP:299:GLY:HA3	1:AP:310:ASP:O	1.64	0.98
1:AE:299:GLY:HA3	1:AE:310:ASP:O	1.63	0.98
1:BJ:254:GLY:HA2	1:BJ:283:LYS:HE3	1.42	0.98
1:CU:101:ARG:HB2	1:CU:208:SER:OG	1.64	0.98
1:BS:98:ILE:O	1:BS:211:SER:O	1.82	0.98
1:AX:299:GLY:HA3	1:AX:310:ASP:O	1.64	0.97
1:AR:298:TRP:CD2	1:AR:312:VAL:HG12	1.98	0.97
1:CR:101:ARG:HB2	1:CR:208:SER:OG	1.64	0.97
1:AY:279:TYR:CZ	1:AY:311:GLY:O	2.16	0.97
1:AV:298:TRP:CD2	1:AV:312:VAL:HG12	1.99	0.97
1:CB:101:ARG:HB2	1:CB:208:SER:OG	1.63	0.97
1:BC:98:ILE:O	1:BC:211:SER:O	1.82	0.97
1:BO:98:ILE:O	1:BO:211:SER:O	1.82	0.97
1:BL:98:ILE:O	1:BL:211:SER:O	1.82	0.97
1:CX:101:ARG:HB2	1:CX:208:SER:OG	1.65	0.97
1:AX:279:TYR:CZ	1:AX:311:GLY:O	2.17	0.97
1:AF:299:GLY:HA3	1:AF:310:ASP:O	1.64	0.97
1:BJ:98:ILE:O	1:BJ:211:SER:O	1.81	0.97
1:CO:75:ASP:OD1	1:CO:188:VAL:O	1.83	0.97
1:AT:298:TRP:CD2	1:AT:312:VAL:HG12	2.00	0.97
1:AM:253:ASP:OD1	1:AM:284:LYS:C	2.03	0.97
1:CB:75:ASP:OD1	1:CB:188:VAL:O	1.82	0.97
1:CA:122:GLY:HA3	1:BV:114:MET:SD	2.04	0.97
1:AL:299:GLY:HA3	1:AL:310:ASP:O	1.65	0.97
1:BU:98:ILE:O	1:BU:211:SER:O	1.81	0.97

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AJ:299:GLY:HA3	1:AJ:310:ASP:O	1.65	0.97
1:CI:101:ARG:HB2	1:CI:208:SER:OG	1.64	0.97
1:CD:101:ARG:HB2	1:CD:208:SER:OG	1.65	0.97
1:CY:75:ASP:OD1	1:CY:188:VAL:O	1.83	0.97
1:CC:75:ASP:OD1	1:CC:188:VAL:O	1.82	0.97
1:CQ:75:ASP:OD1	1:CQ:188:VAL:O	1.83	0.97
1:BN:98:ILE:O	1:BN:211:SER:N	1.98	0.97
1:AR:299:GLY:HA3	1:AR:310:ASP:O	1.64	0.96
1:AN:253:ASP:OD1	1:AN:284:LYS:C	2.03	0.96
1:AC:253:ASP:OD1	1:AC:284:LYS:C	2.04	0.96
1:BE:98:ILE:O	1:BE:211:SER:O	1.83	0.96
1:CP:101:ARG:HB2	1:CP:208:SER:OG	1.65	0.96
1:BA:98:ILE:O	1:BA:211:SER:O	1.82	0.96
1:CF:75:ASP:OD1	1:CF:188:VAL:O	1.83	0.96
1:BN:98:ILE:O	1:BN:211:SER:O	1.82	0.96
1:CE:101:ARG:HB2	1:CE:208:SER:OG	1.64	0.96
1:AZ:298:TRP:CD2	1:AZ:312:VAL:HG12	1.98	0.96
1:AJ:302:ASP:O	1:AJ:305:ASN:OD1	1.83	0.96
1:AC:298:TRP:CD2	1:AC:312:VAL:HG12	2.00	0.96
1:AQ:299:GLY:HA3	1:AQ:310:ASP:O	1.65	0.96
1:AQ:298:TRP:CD2	1:AQ:312:VAL:HG12	2.00	0.96
1:CI:80:VAL:HG12	1:CI:185:LEU:HB3	1.47	0.96
1:CA:75:ASP:OD1	1:CA:188:VAL:O	1.84	0.96
1:CJ:101:ARG:HB2	1:CJ:208:SER:OG	1.64	0.96
1:AR:253:ASP:OD1	1:AR:284:LYS:C	2.04	0.96
1:CW:101:ARG:HB2	1:CW:208:SER:OG	1.66	0.96
1:AA:298:TRP:CD2	1:AA:312:VAL:HG12	2.00	0.96
1:AV:253:ASP:OD1	1:AV:284:LYS:C	2.04	0.96
1:AD:253:ASP:OD1	1:AD:284:LYS:C	2.04	0.96
1:AK:253:ASP:OD1	1:AK:284:LYS:C	2.04	0.96
1:BD:98:ILE:O	1:BD:211:SER:N	1.98	0.96
1:BA:98:ILE:O	1:BA:211:SER:N	1.99	0.96
1:CT:101:ARG:HB2	1:CT:208:SER:OG	1.65	0.96
1:AD:299:GLY:HA3	1:AD:310:ASP:O	1.65	0.96
1:AB:253:ASP:OD1	1:AB:284:LYS:C	2.03	0.96
1:AA:253:ASP:OD1	1:AA:284:LYS:C	2.04	0.96
1:AV:302:ASP:O	1:AV:305:ASN:OD1	1.84	0.96
1:CQ:101:ARG:HB2	1:CQ:208:SER:OG	1.64	0.96
1:BT:98:ILE:O	1:BT:211:SER:O	1.82	0.96
1:AH:253:ASP:OD1	1:AH:284:LYS:C	2.03	0.96
1:AF:253:ASP:OD1	1:AF:284:LYS:C	2.04	0.96

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BZ:98:ILE:O	1:BZ:211:SER:N	1.98	0.96
1:BW:98:ILE:O	1:BW:211:SER:O	1.81	0.96
1:AO:299:GLY:HA3	1:AO:310:ASP:O	1.64	0.96
1:AI:253:ASP:OD1	1:AI:284:LYS:C	2.03	0.96
1:AO:302:ASP:O	1:AO:305:ASN:OD1	1.84	0.96
1:BH:98:ILE:O	1:BH:211:SER:N	1.97	0.96
1:CQ:80:VAL:HG12	1:CQ:185:LEU:HB3	1.47	0.96
1:BF:254:GLY:HA2	1:BF:283:LYS:HE3	1.44	0.96
1:AM:314:TYR:CE1	1:AM:315:TYR:C	2.40	0.96
1:AZ:253:ASP:OD1	1:AZ:284:LYS:C	2.04	0.96
1:AX:253:ASP:OD1	1:AX:284:LYS:C	2.04	0.96
1:AT:302:ASP:O	1:AT:305:ASN:OD1	1.84	0.96
1:AP:302:ASP:O	1:AP:305:ASN:OD1	1.84	0.96
1:CZ:75:ASP:OD1	1:CZ:188:VAL:O	1.83	0.96
1:BV:98:ILE:O	1:BV:211:SER:N	1.99	0.96
1:BZ:98:ILE:O	1:BZ:211:SER:O	1.84	0.96
1:AO:314:TYR:CE1	1:AO:315:TYR:C	2.39	0.96
1:CG:75:ASP:OD1	1:CG:188:VAL:O	1.84	0.95
1:AX:314:TYR:CE1	1:AX:315:TYR:C	2.39	0.95
1:CR:98:ILE:O	1:CR:211:SER:O	1.84	0.95
1:AV:61:SER:HB3	1:AV:90:PRO:HD2	1.48	0.95
1:CV:101:ARG:HB2	1:CV:208:SER:OG	1.64	0.95
1:AC:302:ASP:O	1:AC:305:ASN:OD1	1.84	0.95
1:AB:302:ASP:O	1:AB:305:ASN:OD1	1.84	0.95
1:CD:75:ASP:OD1	1:CD:188:VAL:O	1.85	0.95
1:BR:98:ILE:O	1:BR:211:SER:O	1.84	0.95
1:AS:299:GLY:HA3	1:AS:310:ASP:O	1.65	0.95
1:AW:299:GLY:HA3	1:AW:310:ASP:O	1.66	0.95
1:AA:302:ASP:O	1:AA:305:ASN:OD1	1.84	0.95
1:BH:98:ILE:O	1:BH:211:SER:O	1.82	0.95
1:BO:98:ILE:O	1:BO:211:SER:N	1.99	0.95
1:BY:98:ILE:O	1:BY:211:SER:N	1.99	0.95
1:BE:98:ILE:O	1:BE:211:SER:N	1.98	0.95
1:AX:298:TRP:CD2	1:AX:312:VAL:HG12	2.01	0.95
1:AU:253:ASP:OD1	1:AU:284:LYS:C	2.04	0.95
1:AX:302:ASP:O	1:AX:305:ASN:OD1	1.83	0.95
1:BQ:98:ILE:O	1:BQ:211:SER:O	1.83	0.95
1:CK:56:HIS:CE1	1:CK:206:ARG:HD2	2.01	0.95
1:CC:98:ILE:O	1:CC:211:SER:O	1.91	0.95
1:CO:101:ARG:HB2	1:CO:208:SER:OG	1.66	0.95
1:AL:253:ASP:OD1	1:AL:284:LYS:C	2.04	0.95

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AT:253:ASP:OD1	1:AT:284:LYS:C	2.04	0.95
1:BC:98:ILE:O	1:BC:211:SER:N	1.99	0.95
1:AU:314:TYR:CE1	1:AU:315:TYR:C	2.40	0.95
1:CH:80:VAL:HG12	1:CH:185:LEU:HB3	1.48	0.95
1:AG:253:ASP:OD1	1:AG:284:LYS:C	2.04	0.95
1:AD:302:ASP:O	1:AD:305:ASN:OD1	1.84	0.95
1:AN:302:ASP:O	1:AN:305:ASN:OD1	1.84	0.95
1:AP:298:TRP:CD2	1:AP:312:VAL:HG12	2.01	0.95
1:AP:253:ASP:OD1	1:AP:284:LYS:C	2.04	0.95
1:AE:302:ASP:O	1:AE:305:ASN:OD1	1.84	0.95
1:AL:298:TRP:CG	1:AL:312:VAL:HG12	2.02	0.95
1:AY:298:TRP:CD2	1:AY:312:VAL:HG12	2.01	0.95
1:AO:253:ASP:OD1	1:AO:284:LYS:C	2.04	0.95
1:AF:302:ASP:O	1:AF:305:ASN:OD1	1.84	0.95
1:BK:98:ILE:O	1:BK:211:SER:N	1.99	0.95
1:BI:98:ILE:O	1:BI:211:SER:N	1.98	0.95
1:AQ:314:TYR:CE1	1:AQ:315:TYR:C	2.41	0.95
1:CL:56:HIS:CE1	1:CL:206:ARG:HD2	2.01	0.95
1:CI:98:ILE:O	1:CI:211:SER:O	1.85	0.95
1:BG:98:ILE:O	1:BG:211:SER:O	1.83	0.94
1:AI:298:TRP:CD2	1:AI:312:VAL:HG12	2.02	0.94
1:AH:298:TRP:CD2	1:AH:312:VAL:HG12	2.02	0.94
1:AW:253:ASP:OD1	1:AW:284:LYS:C	2.04	0.94
1:AI:302:ASP:O	1:AI:305:ASN:OD1	1.84	0.94
1:AG:61:SER:HB3	1:AG:90:PRO:HD2	1.47	0.94
1:AA:314:TYR:CE1	1:AA:315:TYR:C	2.40	0.94
1:AS:302:ASP:O	1:AS:305:ASN:OD1	1.84	0.94
1:BQ:98:ILE:O	1:BQ:211:SER:N	1.99	0.94
1:CD:98:ILE:O	1:CD:211:SER:O	1.85	0.94
1:AD:298:TRP:CG	1:AD:312:VAL:HG12	2.04	0.94
1:AN:298:TRP:CD2	1:AN:312:VAL:HG12	2.02	0.94
1:BT:98:ILE:O	1:BT:211:SER:N	2.01	0.94
1:CW:80:VAL:HG12	1:CW:185:LEU:HB3	1.46	0.94
1:CK:80:VAL:HG12	1:CK:185:LEU:HB3	1.49	0.94
1:BG:98:ILE:O	1:BG:211:SER:N	2.01	0.94
1:CS:101:ARG:HB2	1:CS:208:SER:OG	1.67	0.94
1:CX:56:HIS:CE1	1:CX:206:ARG:HD2	2.01	0.94
1:CM:101:ARG:HB2	1:CM:208:SER:OG	1.67	0.94
1:AO:298:TRP:CD2	1:AO:312:VAL:HG12	2.02	0.94
1:AJ:253:ASP:OD1	1:AJ:284:LYS:C	2.05	0.94
1:BY:98:ILE:O	1:BY:211:SER:O	1.85	0.94

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CH:75:ASP:OD1	1:CH:188:VAL:O	1.84	0.94
1:CX:75:ASP:OD1	1:CX:188:VAL:O	1.86	0.94
1:AB:314:TYR:CE1	1:AB:315:TYR:C	2.40	0.94
1:CF:101:ARG:HB2	1:CF:208:SER:OG	1.65	0.94
1:AG:314:TYR:CE1	1:AG:315:TYR:C	2.41	0.94
1:CO:98:ILE:O	1:CO:211:SER:O	1.86	0.94
1:AV:314:TYR:CE1	1:AV:315:TYR:C	2.41	0.94
1:CB:98:ILE:O	1:CB:211:SER:O	1.86	0.94
1:AR:298:TRP:CG	1:AR:312:VAL:HG12	2.01	0.94
1:AQ:253:ASP:OD1	1:AQ:284:LYS:C	2.04	0.94
1:AY:302:ASP:O	1:AY:305:ASN:OD1	1.85	0.94
1:CE:75:ASP:OD1	1:CE:188:VAL:O	1.84	0.94
1:BB:98:ILE:O	1:BB:211:SER:N	1.99	0.94
1:BR:98:ILE:O	1:BR:211:SER:N	1.99	0.94
1:CI:56:HIS:CE1	1:CI:206:ARG:HD2	2.03	0.94
1:CR:75:ASP:OD1	1:CR:188:VAL:O	1.84	0.94
1:CT:317:ASP:HB3	1:CT:319:GLN:HG3	1.50	0.94
1:CG:101:ARG:HB2	1:CG:208:SER:OG	1.65	0.94
1:CU:56:HIS:CE1	1:CU:206:ARG:HD2	2.03	0.94
1:CB:317:ASP:HB3	1:CB:319:GLN:HG3	1.50	0.94
1:AW:298:TRP:CG	1:AW:312:VAL:HG12	2.02	0.94
1:CP:75:ASP:OD1	1:CP:188:VAL:O	1.85	0.94
1:CU:98:ILE:O	1:CU:211:SER:O	1.86	0.94
1:AK:302:ASP:O	1:AK:305:ASN:OD1	1.86	0.94
1:AH:314:TYR:CE1	1:AH:315:TYR:C	2.41	0.94
1:AS:253:ASP:OD1	1:AS:284:LYS:C	2.04	0.93
1:BU:98:ILE:O	1:BU:211:SER:N	2.01	0.93
1:CS:75:ASP:OD1	1:CS:188:VAL:O	1.86	0.93
1:CY:101:ARG:HB2	1:CY:208:SER:OG	1.67	0.93
1:CV:75:ASP:OD1	1:CV:188:VAL:O	1.86	0.93
1:AY:299:GLY:HA3	1:AY:310:ASP:O	1.68	0.93
1:AY:253:ASP:OD1	1:AY:284:LYS:C	2.06	0.93
1:AL:302:ASP:O	1:AL:305:ASN:OD1	1.85	0.93
1:AC:314:TYR:CE1	1:AC:315:TYR:C	2.42	0.93
1:AI:314:TYR:CE1	1:AI:315:TYR:C	2.41	0.93
1:AS:314:TYR:CE1	1:AS:315:TYR:C	2.41	0.93
1:CH:317:ASP:HB3	1:CH:319:GLN:HG3	1.50	0.93
1:CC:56:HIS:CE1	1:CC:206:ARG:HD2	2.03	0.93
1:AN:314:TYR:CE1	1:AN:315:TYR:C	2.41	0.93
1:AF:314:TYR:CE1	1:AF:315:TYR:C	2.41	0.93
1:CU:317:ASP:HB3	1:CU:319:GLN:HG3	1.51	0.93

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AE:298:TRP:CD2	1:AE:312:VAL:HG12	2.02	0.93
1:CP:80:VAL:HG12	1:CP:185:LEU:HB3	1.50	0.93
1:AJ:298:TRP:CD2	1:AJ:312:VAL:HG12	2.02	0.93
1:AG:302:ASP:O	1:AG:305:ASN:OD1	1.85	0.93
1:AH:302:ASP:O	1:AH:305:ASN:OD1	1.84	0.93
1:CG:80:VAL:HG12	1:CG:185:LEU:HB3	1.49	0.93
1:BM:98:ILE:O	1:BM:211:SER:N	2.00	0.93
1:CM:317:ASP:HB3	1:CM:319:GLN:HG3	1.50	0.93
1:CK:101:ARG:HB2	1:CK:208:SER:OG	1.67	0.93
1:AJ:314:TYR:CE1	1:AJ:315:TYR:C	2.42	0.93
1:CR:56:HIS:CE1	1:CR:206:ARG:HD2	2.04	0.93
1:CB:56:HIS:CE1	1:CB:206:ARG:HD2	2.04	0.93
1:CL:317:ASP:HB3	1:CL:319:GLN:HG3	1.50	0.93
1:BD:114:MET:SD	1:CW:122:GLY:HA3	2.09	0.93
1:CE:56:HIS:CE1	1:CE:206:ARG:HD2	2.03	0.93
1:AA:298:TRP:CG	1:AA:312:VAL:HG12	2.05	0.93
1:AB:298:TRP:CD2	1:AB:312:VAL:HG12	2.03	0.93
1:AF:298:TRP:CD2	1:AF:312:VAL:HG12	2.02	0.93
1:CL:80:VAL:HG12	1:CL:185:LEU:HB3	1.49	0.93
1:BW:98:ILE:O	1:BW:211:SER:N	2.02	0.93
1:CQ:98:ILE:O	1:CQ:211:SER:O	1.85	0.93
1:AE:314:TYR:CE1	1:AE:315:TYR:C	2.41	0.93
1:CD:56:HIS:CE1	1:CD:206:ARG:HD2	2.04	0.93
1:AS:298:TRP:CD2	1:AS:312:VAL:HG12	2.04	0.93
1:AU:302:ASP:O	1:AU:305:ASN:OD1	1.84	0.93
1:BF:98:ILE:O	1:BF:211:SER:N	2.02	0.93
1:AX:314:TYR:CE1	1:AX:315:TYR:O	2.22	0.93
1:CA:101:ARG:HB2	1:CA:208:SER:OG	1.67	0.93
1:AD:314:TYR:CE1	1:AD:315:TYR:C	2.42	0.93
1:AK:298:TRP:CG	1:AK:312:VAL:HG12	2.02	0.93
1:BL:98:ILE:O	1:BL:211:SER:N	2.02	0.93
1:CS:56:HIS:CE1	1:CS:206:ARG:HD2	2.02	0.93
1:CA:317:ASP:HB3	1:CA:319:GLN:HG3	1.50	0.93
1:AU:298:TRP:CD2	1:AU:312:VAL:HG12	2.04	0.93
1:CU:75:ASP:OD1	1:CU:188:VAL:O	1.85	0.93
1:CK:75:ASP:OD1	1:CK:188:VAL:O	1.85	0.93
1:AP:314:TYR:CE1	1:AP:315:TYR:C	2.43	0.93
1:AL:314:TYR:CE1	1:AL:315:TYR:C	2.42	0.93
1:CA:56:HIS:CE1	1:CA:206:ARG:HD2	2.04	0.93
1:AQ:302:ASP:O	1:AQ:305:ASN:OD1	1.84	0.93
1:AR:302:ASP:O	1:AR:305:ASN:OD1	1.84	0.93

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BJ:98:ILE:O	1:BJ:211:SER:N	2.00	0.93
1:AZ:314:TYR:CE1	1:AZ:315:TYR:C	2.42	0.93
1:AG:298:TRP:CD2	1:AG:312:VAL:HG12	2.03	0.92
1:CN:75:ASP:OD1	1:CN:188:VAL:O	1.86	0.92
1:AM:298:TRP:CD2	1:AM:312:VAL:HG12	2.03	0.92
1:AZ:302:ASP:O	1:AZ:305:ASN:OD1	1.85	0.92
1:AT:314:TYR:CE1	1:AT:315:TYR:C	2.42	0.92
1:CT:56:HIS:CE1	1:CT:206:ARG:HD2	2.04	0.92
1:CK:317:ASP:HB3	1:CK:319:GLN:HG3	1.52	0.92
1:CD:80:VAL:HG12	1:CD:185:LEU:HB3	1.53	0.92
1:AY:314:TYR:CE1	1:AY:315:TYR:C	2.43	0.92
1:CY:56:HIS:CE1	1:CY:206:ARG:HD2	2.05	0.92
1:CR:317:ASP:HB3	1:CR:319:GLN:HG3	1.52	0.92
1:AW:314:TYR:CE1	1:AW:315:TYR:C	2.42	0.92
1:CC:317:ASP:HB3	1:CC:319:GLN:HG3	1.50	0.92
1:AK:299:GLY:HA3	1:AK:310:ASP:O	1.70	0.92
1:AC:298:TRP:CG	1:AC:312:VAL:HG12	2.04	0.92
1:AQ:298:TRP:CG	1:AQ:312:VAL:HG12	2.04	0.92
1:AM:302:ASP:O	1:AM:305:ASN:OD1	1.84	0.92
1:CB:80:VAL:HG12	1:CB:185:LEU:HB3	1.49	0.92
1:CW:317:ASP:HB3	1:CW:319:GLN:HG3	1.52	0.92
1:BB:114:MET:SD	1:CK:122:GLY:HA3	2.09	0.92
1:CV:56:HIS:CE1	1:CV:206:ARG:HD2	2.05	0.92
1:AZ:298:TRP:CG	1:AZ:312:VAL:HG12	2.04	0.92
1:BX:98:ILE:O	1:BX:211:SER:N	2.01	0.92
1:CO:80:VAL:HG12	1:CO:185:LEU:HB3	1.50	0.92
1:CD:317:ASP:HB3	1:CD:319:GLN:HG3	1.51	0.92
1:BA:101:ARG:CZ	1:BA:166:LEU:HD12	2.00	0.92
1:CZ:80:VAL:HG12	1:CZ:185:LEU:HB3	1.51	0.92
1:CW:56:HIS:CE1	1:CW:206:ARG:HD2	2.05	0.92
1:CT:80:VAL:HG12	1:CT:185:LEU:HB3	1.50	0.92
1:CG:56:HIS:CE1	1:CG:206:ARG:HD2	2.03	0.92
1:CF:317:ASP:HB3	1:CF:319:GLN:HG3	1.51	0.92
1:CX:317:ASP:HB3	1:CX:319:GLN:HG3	1.50	0.92
1:CG:317:ASP:HB3	1:CG:319:GLN:HG3	1.51	0.92
1:CS:317:ASP:HB3	1:CS:319:GLN:HG3	1.51	0.92
1:AT:298:TRP:CG	1:AT:312:VAL:HG12	2.04	0.92
1:AO:314:TYR:CE1	1:AO:315:TYR:O	2.23	0.92
1:CJ:56:HIS:CE1	1:CJ:206:ARG:HD2	2.05	0.92
1:AK:314:TYR:CE1	1:AK:315:TYR:C	2.43	0.92
1:AV:314:TYR:CE1	1:AV:315:TYR:O	2.23	0.92

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AR:314:TYR:CE1	1:AR:315:TYR:C	2.43	0.92
1:AO:298:TRP:CG	1:AO:312:VAL:HG12	2.05	0.91
1:CO:317:ASP:HB3	1:CO:319:GLN:HG3	1.52	0.91
1:CA:98:ILE:O	1:CA:211:SER:O	1.88	0.91
1:CT:98:ILE:O	1:CT:211:SER:O	1.88	0.91
1:CJ:75:ASP:OD1	1:CJ:188:VAL:O	1.88	0.91
1:CM:98:ILE:O	1:CM:211:SER:O	1.88	0.91
1:AM:298:TRP:CG	1:AM:312:VAL:HG12	2.06	0.91
1:AH:61:SER:HB3	1:AH:90:PRO:HD2	1.52	0.91
1:CN:101:ARG:HB2	1:CN:208:SER:OG	1.69	0.91
1:AU:61:SER:HB3	1:AU:90:PRO:HD2	1.52	0.91
1:AO:61:SER:HB3	1:AO:90:PRO:HD2	1.51	0.91
1:AW:302:ASP:O	1:AW:305:ASN:OD1	1.86	0.91
1:CN:56:HIS:CE1	1:CN:206:ARG:HD2	2.05	0.91
1:AY:302:ASP:HB3	1:AY:305:ASN:ND2	1.86	0.91
1:AU:314:TYR:CE1	1:AU:315:TYR:O	2.24	0.91
1:CR:80:VAL:HG12	1:CR:185:LEU:HB3	1.49	0.91
1:CJ:98:ILE:O	1:CJ:211:SER:O	1.89	0.91
1:CF:56:HIS:CE1	1:CF:206:ARG:HD2	2.04	0.91
1:AJ:302:ASP:HB3	1:AJ:305:ASN:ND2	1.86	0.91
1:CJ:80:VAL:HG12	1:CJ:185:LEU:HB3	1.53	0.91
1:AQ:61:SER:HB3	1:AQ:90:PRO:HD2	1.52	0.91
1:AA:61:SER:HB3	1:AA:90:PRO:HD2	1.52	0.91
1:CH:98:ILE:O	1:CH:211:SER:O	1.89	0.91
1:CZ:98:ILE:O	1:CZ:211:SER:O	1.88	0.91
1:AF:302:ASP:HB3	1:AF:305:ASN:ND2	1.86	0.91
1:CE:98:ILE:O	1:CE:211:SER:O	1.89	0.91
1:AV:298:TRP:CG	1:AV:312:VAL:HG12	2.04	0.91
1:CL:98:ILE:O	1:CL:211:SER:O	1.88	0.91
1:AJ:298:TRP:CG	1:AJ:312:VAL:HG12	2.06	0.91
1:AO:302:ASP:HB3	1:AO:305:ASN:ND2	1.86	0.91
1:CM:80:VAL:HG12	1:CM:185:LEU:HB3	1.53	0.91
1:CE:317:ASP:HB3	1:CE:319:GLN:HG3	1.51	0.91
1:CN:317:ASP:HB3	1:CN:319:GLN:HG3	1.51	0.91
1:CP:56:HIS:CE1	1:CP:206:ARG:HD2	2.05	0.91
1:CS:98:ILE:O	1:CS:211:SER:O	1.89	0.91
1:AY:298:TRP:CG	1:AY:312:VAL:HG12	2.06	0.91
1:AM:302:ASP:HB3	1:AM:305:ASN:ND2	1.86	0.91
1:CH:56:HIS:CE1	1:CH:206:ARG:HD2	2.06	0.91
1:CZ:56:HIS:CE1	1:CZ:206:ARG:HD2	2.05	0.91
1:AX:298:TRP:CG	1:AX:312:VAL:HG12	2.05	0.90

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AI:314:TYR:CE1	1:AI:315:TYR:O	2.24	0.90
1:AE:298:TRP:CG	1:AE:312:VAL:HG12	2.06	0.90
1:AH:302:ASP:HB3	1:AH:305:ASN:ND2	1.86	0.90
1:CN:98:ILE:O	1:CN:211:SER:O	1.87	0.90
1:CV:317:ASP:HB3	1:CV:319:GLN:HG3	1.50	0.90
1:CP:98:ILE:O	1:CP:211:SER:O	1.89	0.90
1:CQ:56:HIS:CE1	1:CQ:206:ARG:HD2	2.06	0.90
1:AB:314:TYR:CE1	1:AB:315:TYR:O	2.23	0.90
1:CX:98:ILE:O	1:CX:211:SER:O	1.88	0.90
1:CG:98:ILE:O	1:CG:211:SER:O	1.89	0.90
1:AN:302:ASP:HB3	1:AN:305:ASN:ND2	1.87	0.90
1:AS:314:TYR:CE1	1:AS:315:TYR:O	2.24	0.90
1:AN:314:TYR:CE1	1:AN:315:TYR:O	2.25	0.90
1:CQ:317:ASP:HB3	1:CQ:319:GLN:HG3	1.51	0.90
1:AC:61:SER:HB3	1:AC:90:PRO:HD2	1.56	0.90
1:AB:298:TRP:CG	1:AB:312:VAL:HG12	2.06	0.90
1:AF:298:TRP:CG	1:AF:312:VAL:HG12	2.07	0.90
1:AA:302:ASP:HB3	1:AA:305:ASN:ND2	1.87	0.90
1:CF:98:ILE:O	1:CF:211:SER:O	1.88	0.90
1:AZ:314:TYR:CE1	1:AZ:315:TYR:O	2.25	0.90
1:AH:298:TRP:CG	1:AH:312:VAL:HG12	2.06	0.90
1:CD:141:LEU:HD21	1:CD:184:ILE:CD1	2.05	0.90
1:AI:302:ASP:HB3	1:AI:305:ASN:ND2	1.87	0.90
1:CY:80:VAL:HG12	1:CY:185:LEU:HB3	1.52	0.90
1:CY:317:ASP:HB3	1:CY:319:GLN:HG3	1.51	0.90
1:AP:298:TRP:CG	1:AP:312:VAL:HG12	2.05	0.90
1:AE:302:ASP:HB3	1:AE:305:ASN:ND2	1.86	0.90
1:AG:314:TYR:CE1	1:AG:315:TYR:O	2.25	0.90
1:AH:314:TYR:CE1	1:AH:315:TYR:O	2.25	0.90
1:CM:56:HIS:CE1	1:CM:206:ARG:HD2	2.06	0.90
1:AI:298:TRP:CG	1:AI:312:VAL:HG12	2.06	0.90
1:AG:298:TRP:CG	1:AG:312:VAL:HG12	2.07	0.90
1:AS:302:ASP:HB3	1:AS:305:ASN:ND2	1.86	0.90
1:CO:56:HIS:CE1	1:CO:206:ARG:HD2	2.06	0.90
1:AT:61:SER:HB3	1:AT:90:PRO:HD2	1.52	0.90
1:AB:302:ASP:HB3	1:AB:305:ASN:ND2	1.87	0.90
1:CU:80:VAL:HG12	1:CU:185:LEU:HB3	1.51	0.90
1:AM:314:TYR:CE1	1:AM:315:TYR:O	2.24	0.90
1:AC:314:TYR:CE1	1:AC:315:TYR:O	2.25	0.90
1:AE:61:SER:HB3	1:AE:90:PRO:HD2	1.53	0.90
1:AQ:302:ASP:HB3	1:AQ:305:ASN:ND2	1.87	0.90

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:314:TYR:CE1	1:AA:315:TYR:O	2.25	0.90
1:CJ:317:ASP:HB3	1:CJ:319:GLN:HG3	1.52	0.90
1:AT:302:ASP:HB3	1:AT:305:ASN:ND2	1.87	0.89
1:AL:279:TYR:OH	1:AL:311:GLY:O	1.89	0.89
1:AE:314:TYR:CE1	1:AE:315:TYR:O	2.26	0.89
1:AC:302:ASP:HB3	1:AC:305:ASN:ND2	1.88	0.89
1:AP:302:ASP:HB3	1:AP:305:ASN:ND2	1.87	0.89
1:BS:98:ILE:O	1:BS:211:SER:N	2.05	0.89
1:AD:314:TYR:CE1	1:AD:315:TYR:O	2.25	0.89
1:CP:317:ASP:HB3	1:CP:319:GLN:HG3	1.50	0.89
1:AY:61:SER:HB3	1:AY:90:PRO:HD2	1.53	0.89
1:CC:80:VAL:HG12	1:CC:185:LEU:HB3	1.53	0.89
1:CT:75:ASP:OD1	1:CT:188:VAL:O	1.89	0.89
1:CY:98:ILE:O	1:CY:211:SER:O	1.87	0.89
1:AD:302:ASP:HB3	1:AD:305:ASN:ND2	1.87	0.89
1:AP:314:TYR:CE1	1:AP:315:TYR:O	2.26	0.89
1:AR:314:TYR:CE1	1:AR:315:TYR:O	2.25	0.89
1:AS:298:TRP:CG	1:AS:312:VAL:HG12	2.08	0.89
1:AN:298:TRP:CG	1:AN:312:VAL:HG12	2.06	0.89
1:AG:302:ASP:HB3	1:AG:305:ASN:ND2	1.87	0.89
1:CA:80:VAL:HG12	1:CA:185:LEU:HB3	1.51	0.89
1:CI:317:ASP:HB3	1:CI:319:GLN:HG3	1.52	0.89
1:CS:80:VAL:HG12	1:CS:185:LEU:HB3	1.55	0.89
1:AL:314:TYR:CE1	1:AL:315:TYR:O	2.25	0.89
1:BC:101:ARG:CZ	1:BC:166:LEU:HD12	2.03	0.89
1:AZ:302:ASP:HB3	1:AZ:305:ASN:ND2	1.88	0.89
1:AW:302:ASP:HB3	1:AW:305:ASN:ND2	1.86	0.89
1:AK:279:TYR:OH	1:AK:311:GLY:O	1.91	0.89
1:AD:61:SER:HB3	1:AD:90:PRO:HD2	1.54	0.89
1:AQ:314:TYR:CE1	1:AQ:315:TYR:O	2.24	0.89
1:AK:314:TYR:CE1	1:AK:315:TYR:O	2.25	0.89
1:BK:101:ARG:CZ	1:BK:166:LEU:HD12	2.03	0.89
1:AV:302:ASP:HB3	1:AV:305:ASN:ND2	1.88	0.89
1:AT:314:TYR:CE1	1:AT:315:TYR:O	2.25	0.89
1:CE:80:VAL:HG12	1:CE:185:LEU:HB3	1.54	0.89
1:BI:101:ARG:CZ	1:BI:166:LEU:HD12	2.02	0.89
1:AU:298:TRP:CG	1:AU:312:VAL:HG12	2.08	0.88
1:AB:61:SER:HB3	1:AB:90:PRO:HD2	1.58	0.88
1:AD:298:TRP:CG	1:AD:312:VAL:CG1	2.58	0.88
1:AK:302:ASP:HB3	1:AK:305:ASN:ND2	1.88	0.88
1:AF:314:TYR:CE1	1:AF:315:TYR:O	2.26	0.88

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BH:101:ARG:CZ	1:BH:166:LEU:HD12	2.03	0.88
1:CN:80:VAL:HG12	1:CN:185:LEU:HB3	1.53	0.88
1:AU:302:ASP:HB3	1:AU:305:ASN:ND2	1.86	0.88
1:AR:61:SER:HB3	1:AR:90:PRO:HD2	1.53	0.88
1:CX:80:VAL:HG12	1:CX:185:LEU:HB3	1.55	0.88
1:AX:61:SER:HB3	1:AX:90:PRO:HD2	1.55	0.88
1:BD:153:TRP:O	1:CW:151:LYS:NZ	2.07	0.88
1:BN:101:ARG:CZ	1:BN:166:LEU:HD12	2.03	0.88
1:BT:101:ARG:CZ	1:BT:166:LEU:HD12	2.03	0.88
1:AK:298:TRP:CG	1:AK:312:VAL:CG1	2.57	0.88
1:CV:79:VAL:HG12	1:CV:185:LEU:O	1.74	0.88
1:CZ:317:ASP:HB3	1:CZ:319:GLN:HG3	1.52	0.88
1:AW:298:TRP:CG	1:AW:312:VAL:CG1	2.57	0.88
1:CK:98:ILE:O	1:CK:211:SER:O	1.90	0.88
1:CW:98:ILE:O	1:CW:211:SER:O	1.90	0.88
1:AX:302:ASP:HB3	1:AX:305:ASN:ND2	1.87	0.88
1:AR:302:ASP:HB3	1:AR:305:ASN:ND2	1.88	0.88
1:AJ:314:TYR:CE1	1:AJ:315:TYR:O	2.27	0.88
1:BU:101:ARG:CZ	1:BU:166:LEU:HD12	2.03	0.88
1:BA:114:MET:SD	1:CT:122:GLY:HA3	122.96	0.88
1:CV:80:VAL:HG12	1:CV:185:LEU:HB3	1.55	0.88
1:BG:114:MET:SD	1:CP:122:GLY:HA3	2.13	0.87
1:AK:61:SER:HB3	1:AK:90:PRO:HD2	1.54	0.87
1:CF:80:VAL:HG12	1:CF:185:LEU:HB3	1.53	0.87
1:AE:279:TYR:OH	1:AE:311:GLY:O	1.91	0.87
1:AA:279:TYR:OH	1:AA:311:GLY:O	1.92	0.87
1:AW:279:TYR:OH	1:AW:311:GLY:O	1.92	0.87
1:CS:79:VAL:HG12	1:CS:185:LEU:O	1.73	0.87
1:AN:61:SER:HB3	1:AN:90:PRO:HD2	1.54	0.87
1:AR:298:TRP:CG	1:AR:312:VAL:CG1	2.57	0.87
1:BD:101:ARG:CZ	1:BD:166:LEU:HD12	2.06	0.87
1:AJ:61:SER:HB3	1:AJ:90:PRO:HD2	1.56	0.87
1:AA:298:TRP:CG	1:AA:312:VAL:CG1	2.59	0.87
1:BJ:101:ARG:CZ	1:BJ:166:LEU:HD12	2.04	0.87
1:BT:114:MET:SD	1:CV:122:GLY:HA3	2.15	0.87
1:CD:151:LYS:NZ	1:BH:153:TRP:O	144.20	0.87
1:AF:279:TYR:OH	1:AF:311:GLY:O	1.92	0.86
1:AY:314:TYR:CE1	1:AY:315:TYR:O	2.27	0.86
1:AW:314:TYR:CE1	1:AW:315:TYR:O	2.27	0.86
1:BY:101:ARG:CZ	1:BY:166:LEU:HD12	2.04	0.86
1:CG:79:VAL:HG12	1:CG:185:LEU:O	1.75	0.86

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AL:298:TRP:CG	1:AL:312:VAL:CG1	2.56	0.86
1:AT:298:TRP:CG	1:AT:312:VAL:CG1	2.59	0.86
1:AR:279:TYR:OH	1:AR:311:GLY:O	1.93	0.86
1:AT:279:TYR:OH	1:AT:311:GLY:O	1.94	0.86
1:BX:101:ARG:CZ	1:BX:166:LEU:HD12	2.05	0.86
1:BP:101:ARG:CZ	1:BP:166:LEU:HD12	2.05	0.86
1:CD:79:VAL:HG12	1:CD:185:LEU:O	1.74	0.86
1:CH:79:VAL:HG12	1:CH:185:LEU:O	1.75	0.86
1:AI:61:SER:HB3	1:AI:90:PRO:HD2	1.57	0.86
1:BV:101:ARG:CZ	1:BV:166:LEU:HD12	2.05	0.86
1:AM:61:SER:HB3	1:AM:90:PRO:HD2	1.56	0.86
1:AL:98:ILE:O	1:AL:211:SER:O	1.93	0.86
1:AL:302:ASP:HB3	1:AL:305:ASN:ND2	1.89	0.86
1:CX:141:LEU:HD21	1:CX:184:ILE:CD1	2.04	0.86
1:AZ:98:ILE:O	1:AZ:211:SER:O	1.94	0.86
1:BF:101:ARG:CZ	1:BF:166:LEU:HD12	2.06	0.86
1:AB:305:ASN:ND2	1:AB:307:THR:O	2.09	0.86
1:CR:79:VAL:HG12	1:CR:185:LEU:O	1.76	0.86
1:BL:101:ARG:CZ	1:BL:166:LEU:HD12	2.05	0.86
1:AC:305:ASN:ND2	1:AC:307:THR:O	2.10	0.86
1:AI:98:ILE:O	1:AI:211:SER:O	1.92	0.86
1:AW:61:SER:HB3	1:AW:90:PRO:HD2	1.56	0.86
1:AJ:305:ASN:ND2	1:AJ:307:THR:O	2.08	0.86
1:CY:79:VAL:HG12	1:CY:185:LEU:O	1.74	0.86
1:AA:305:ASN:ND2	1:AA:307:THR:O	2.11	0.85
1:AQ:279:TYR:OH	1:AQ:311:GLY:O	1.93	0.85
1:BQ:101:ARG:CZ	1:BQ:166:LEU:HD12	2.06	0.85
1:BG:101:ARG:CZ	1:BG:166:LEU:HD12	2.07	0.85
1:CW:141:LEU:HD21	1:CW:184:ILE:CD1	2.06	0.85
1:CG:141:LEU:HD21	1:CG:184:ILE:CD1	2.06	0.85
1:AD:279:TYR:OH	1:AD:311:GLY:O	1.93	0.85
1:CV:98:ILE:O	1:CV:211:SER:O	1.93	0.85
1:AP:298:TRP:CG	1:AP:312:VAL:CG1	2.59	0.85
1:AJ:279:TYR:OH	1:AJ:311:GLY:O	1.93	0.85
1:BW:101:ARG:CZ	1:BW:166:LEU:HD12	2.05	0.85
1:BB:101:ARG:CZ	1:BB:166:LEU:HD12	2.06	0.85
1:AQ:298:TRP:CG	1:AQ:312:VAL:CG1	2.59	0.85
1:AM:305:ASN:ND2	1:AM:307:THR:O	2.09	0.85
1:BO:101:ARG:CZ	1:BO:166:LEU:HD12	2.05	0.85
1:AI:305:ASN:ND2	1:AI:307:THR:O	2.09	0.85
1:AS:305:ASN:ND2	1:AS:307:THR:O	2.09	0.85

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CZ:79:VAL:HG12	1:CZ:185:LEU:O	1.76	0.85
1:AO:98:ILE:O	1:AO:211:SER:O	1.95	0.85
1:CD:117:ALA:HB2	1:CW:38:PRO:O	144.47	0.85
1:BA:114:MET:SD	1:CI:122:GLY:HA3	2.16	0.85
1:BR:101:ARG:CZ	1:BR:166:LEU:HD12	2.07	0.85
1:CO:100:GLN:CG	1:CO:211:SER:OG	2.24	0.85
1:CJ:79:VAL:HG12	1:CJ:185:LEU:O	1.77	0.85
1:BS:101:ARG:CZ	1:BS:166:LEU:HD12	2.06	0.85
1:AE:98:ILE:O	1:AE:211:SER:O	1.95	0.85
1:AB:298:TRP:CG	1:AB:312:VAL:CG1	2.60	0.85
1:AN:298:TRP:CG	1:AN:312:VAL:CG1	2.60	0.85
1:AV:298:TRP:CG	1:AV:312:VAL:CG1	2.59	0.85
1:AE:298:TRP:CG	1:AE:312:VAL:CG1	2.60	0.85
1:AW:98:ILE:O	1:AW:211:SER:O	1.93	0.85
1:AS:61:SER:HB3	1:AS:90:PRO:HD2	1.56	0.85
1:AZ:61:SER:HB3	1:AZ:90:PRO:HD2	1.58	0.85
1:AO:305:ASN:ND2	1:AO:307:THR:O	2.09	0.85
1:CT:141:LEU:HD21	1:CT:184:ILE:CD1	2.05	0.85
1:CL:141:LEU:HD21	1:CL:184:ILE:CD1	2.07	0.85
1:CT:79:VAL:HG12	1:CT:185:LEU:O	1.76	0.85
1:AL:61:SER:HB3	1:AL:90:PRO:HD2	1.59	0.85
1:AK:98:ILE:O	1:AK:211:SER:O	1.93	0.85
1:AO:298:TRP:CG	1:AO:312:VAL:CG1	2.60	0.84
1:AH:298:TRP:CG	1:AH:312:VAL:CG1	2.60	0.84
1:CB:79:VAL:HG12	1:CB:185:LEU:O	1.76	0.84
1:AA:105:GLU:O	1:AA:162:TYR:OH	1.95	0.84
1:AM:298:TRP:CG	1:AM:312:VAL:CG1	2.60	0.84
1:AO:279:TYR:OH	1:AO:311:GLY:O	1.95	0.84
1:AY:279:TYR:OH	1:AY:311:GLY:O	1.94	0.84
1:AX:279:TYR:OH	1:AX:311:GLY:O	1.95	0.84
1:AI:298:TRP:CG	1:AI:312:VAL:CG1	2.60	0.84
1:AJ:298:TRP:CG	1:AJ:312:VAL:CG1	2.60	0.84
1:AG:298:TRP:CG	1:AG:312:VAL:CG1	2.61	0.84
1:AG:305:ASN:ND2	1:AG:307:THR:O	2.10	0.84
1:AH:305:ASN:ND2	1:AH:307:THR:O	2.09	0.84
1:AP:61:SER:HB3	1:AP:90:PRO:HD2	1.58	0.84
1:AD:98:ILE:O	1:AD:211:SER:O	1.94	0.84
1:AV:98:ILE:O	1:AV:211:SER:O	1.94	0.84
1:AC:298:TRP:CG	1:AC:312:VAL:CG1	2.59	0.84
1:AX:305:ASN:ND2	1:AX:307:THR:O	2.10	0.84
1:CR:141:LEU:HD21	1:CR:184:ILE:CD1	2.06	0.84

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CZ:141:LEU:HD21	1:CZ:184:ILE:CD1	2.04	0.84
1:CH:141:LEU:HD21	1:CH:184:ILE:CD1	2.08	0.84
1:AC:279:TYR:OH	1:AC:311:GLY:O	1.96	0.84
1:AI:105:GLU:O	1:AI:162:TYR:OH	1.94	0.84
1:AM:279:TYR:OH	1:AM:311:GLY:O	1.94	0.84
1:CA:79:VAL:HG12	1:CA:185:LEU:O	1.77	0.84
1:CN:100:GLN:CG	1:CN:211:SER:OG	2.26	0.84
1:BZ:101:ARG:CZ	1:BZ:166:LEU:HD12	2.07	0.84
1:AU:305:ASN:ND2	1:AU:307:THR:O	2.09	0.84
1:CB:141:LEU:HD21	1:CB:184:ILE:CD1	2.06	0.84
1:AS:279:TYR:OH	1:AS:311:GLY:O	1.95	0.84
1:AF:61:SER:HB3	1:AF:90:PRO:HD2	1.58	0.84
1:AJ:302:ASP:O	1:AJ:305:ASN:ND2	2.10	0.84
1:AP:98:ILE:O	1:AP:211:SER:O	1.96	0.84
1:AZ:298:TRP:CG	1:AZ:312:VAL:CG1	2.59	0.84
1:BB:153:TRP:O	1:CK:151:LYS:NZ	2.11	0.84
1:BE:101:ARG:CZ	1:BE:166:LEU:HD12	2.07	0.84
1:AH:105:GLU:O	1:AH:162:TYR:OH	1.96	0.84
1:AA:302:ASP:O	1:AA:305:ASN:ND2	2.11	0.84
1:AZ:302:ASP:O	1:AZ:305:ASN:ND2	2.11	0.84
1:AF:305:ASN:ND2	1:AF:307:THR:O	2.10	0.84
1:AP:279:TYR:OH	1:AP:311:GLY:O	1.95	0.84
1:AP:305:ASN:ND2	1:AP:307:THR:O	2.11	0.83
1:AH:279:TYR:OH	1:AH:311:GLY:O	1.95	0.83
1:AA:98:ILE:O	1:AA:211:SER:O	1.96	0.83
1:AV:302:ASP:O	1:AV:305:ASN:ND2	2.11	0.83
1:CM:79:VAL:HG12	1:CM:185:LEU:O	1.78	0.83
1:AJ:98:ILE:O	1:AJ:211:SER:O	1.95	0.83
1:AX:298:TRP:CG	1:AX:312:VAL:CG1	2.59	0.83
1:AX:302:ASP:O	1:AX:305:ASN:ND2	2.11	0.83
1:AI:302:ASP:O	1:AI:305:ASN:ND2	2.11	0.83
1:AF:302:ASP:O	1:AF:305:ASN:ND2	2.11	0.83
1:CM:141:LEU:HD21	1:CM:184:ILE:CD1	2.06	0.83
1:AN:279:TYR:OH	1:AN:311:GLY:O	1.95	0.83
1:AB:98:ILE:O	1:AB:211:SER:O	1.95	0.83
1:AC:302:ASP:O	1:AC:305:ASN:ND2	2.11	0.83
1:AU:302:ASP:O	1:AU:305:ASN:ND2	2.11	0.83
1:AE:302:ASP:O	1:AE:305:ASN:ND2	2.11	0.83
1:CE:79:VAL:HG12	1:CE:185:LEU:O	1.79	0.83
1:AI:279:TYR:OH	1:AI:311:GLY:O	1.96	0.83
1:AS:298:TRP:CG	1:AS:312:VAL:CG1	2.61	0.83

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AM:302:ASP:O	1:AM:305:ASN:ND2	2.11	0.83
1:AN:305:ASN:ND2	1:AN:307:THR:O	2.10	0.83
1:AG:279:TYR:OH	1:AG:311:GLY:O	1.95	0.83
1:AV:305:ASN:ND2	1:AV:307:THR:O	2.11	0.83
1:CP:141:LEU:HD21	1:CP:184:ILE:CD1	2.07	0.83
1:CC:79:VAL:HG12	1:CC:185:LEU:O	1.78	0.83
1:CU:79:VAL:HG12	1:CU:185:LEU:O	1.79	0.83
1:AU:279:TYR:OH	1:AU:311:GLY:O	1.95	0.83
1:CB:100:GLN:CG	1:CB:211:SER:OG	2.27	0.83
1:CF:79:VAL:HG12	1:CF:185:LEU:O	1.79	0.83
1:AS:98:ILE:O	1:AS:211:SER:O	1.95	0.83
1:AU:98:ILE:O	1:AU:211:SER:O	1.97	0.83
1:AE:305:ASN:ND2	1:AE:307:THR:O	2.09	0.83
1:AH:302:ASP:O	1:AH:305:ASN:ND2	2.11	0.83
1:AS:302:ASP:O	1:AS:305:ASN:ND2	2.11	0.83
1:CO:79:VAL:HG12	1:CO:185:LEU:O	1.79	0.83
1:AT:105:GLU:O	1:AT:162:TYR:OH	1.97	0.83
1:AT:302:ASP:OD2	1:AT:305:ASN:HB3	1.79	0.83
1:AB:302:ASP:O	1:AB:305:ASN:ND2	2.11	0.83
1:AD:305:ASN:ND2	1:AD:307:THR:O	2.11	0.83
1:AQ:302:ASP:O	1:AQ:305:ASN:ND2	2.12	0.83
1:AY:305:ASN:ND2	1:AY:307:THR:O	2.11	0.83
1:AN:302:ASP:O	1:AN:305:ASN:ND2	2.11	0.83
1:CF:141:LEU:HD21	1:CF:184:ILE:CD1	2.09	0.83
1:AB:279:TYR:OH	1:AB:311:GLY:O	1.95	0.83
1:AG:302:ASP:O	1:AG:305:ASN:ND2	2.11	0.83
1:AZ:305:ASN:ND2	1:AZ:307:THR:O	2.12	0.83
1:CO:141:LEU:HD21	1:CO:184:ILE:CD1	2.08	0.83
1:AC:98:ILE:O	1:AC:211:SER:O	1.97	0.83
1:AJ:91:ARG:HE	1:BR:98:ILE:HG22	1.44	0.82
1:CT:317:ASP:HB3	1:CT:319:GLN:CG	2.10	0.82
1:AR:98:ILE:O	1:AR:211:SER:O	1.96	0.82
1:AT:302:ASP:O	1:AT:305:ASN:ND2	2.11	0.82
1:AQ:305:ASN:ND2	1:AQ:307:THR:O	2.12	0.82
1:CQ:141:LEU:HD21	1:CQ:184:ILE:CD1	2.07	0.82
1:AV:279:TYR:OH	1:AV:311:GLY:O	1.94	0.82
1:CK:79:VAL:HG12	1:CK:185:LEU:O	1.79	0.82
1:AT:98:ILE:O	1:AT:211:SER:O	1.97	0.82
1:AN:98:ILE:O	1:AN:211:SER:O	1.97	0.82
1:AU:298:TRP:CG	1:AU:312:VAL:CG1	2.62	0.82
1:AP:302:ASP:O	1:AP:305:ASN:ND2	2.12	0.82

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AH:98:ILE:O	1:AH:211:SER:O	1.95	0.82
1:AD:302:ASP:O	1:AD:305:ASN:ND2	2.11	0.82
1:AW:305:ASN:ND2	1:AW:307:THR:O	2.12	0.82
1:CK:141:LEU:HD21	1:CK:184:ILE:CD1	2.09	0.82
1:CD:100:GLN:CG	1:CD:211:SER:OG	2.30	0.82
1:CX:79:VAL:HG12	1:CX:185:LEU:O	1.78	0.82
1:AF:298:TRP:CG	1:AF:312:VAL:CG1	2.61	0.82
1:AO:302:ASP:O	1:AO:305:ASN:ND2	2.11	0.82
1:AL:302:ASP:O	1:AL:305:ASN:ND2	2.12	0.82
1:AL:305:ASN:ND2	1:AL:307:THR:O	2.13	0.82
1:CI:141:LEU:HD21	1:CI:184:ILE:CD1	2.07	0.82
1:AM:105:GLU:O	1:AM:162:TYR:OH	1.96	0.82
1:AY:98:ILE:O	1:AY:211:SER:O	1.97	0.82
1:AW:105:GLU:O	1:AW:162:TYR:OH	1.97	0.82
1:AR:302:ASP:O	1:AR:305:ASN:ND2	2.12	0.82
1:AR:305:ASN:ND2	1:AR:307:THR:O	2.12	0.82
1:CN:141:LEU:HD21	1:CN:184:ILE:CD1	2.07	0.82
1:AQ:98:ILE:O	1:AQ:211:SER:O	1.98	0.82
1:AI:302:ASP:OD2	1:AI:305:ASN:HB3	1.80	0.82
1:CI:79:VAL:HG12	1:CI:185:LEU:O	1.79	0.82
1:CE:100:GLN:CG	1:CE:211:SER:OG	2.28	0.82
1:CV:317:ASP:HB3	1:CV:319:GLN:CG	2.10	0.82
1:AY:298:TRP:CG	1:AY:312:VAL:CG1	2.62	0.82
1:AR:302:ASP:OD2	1:AR:305:ASN:HB3	1.80	0.82
1:AY:302:ASP:O	1:AY:305:ASN:ND2	2.11	0.82
1:CA:317:ASP:HB3	1:CA:319:GLN:CG	2.10	0.82
1:CK:100:GLN:CG	1:CK:211:SER:OG	2.27	0.82
1:BM:101:ARG:CZ	1:BM:166:LEU:HD12	2.08	0.82
1:BM:122:GLY:C	1:BM:188:VAL:HG22	2.00	0.82
1:AW:302:ASP:O	1:AW:305:ASN:ND2	2.12	0.82
1:CA:141:LEU:HD21	1:CA:184:ILE:CD1	2.10	0.82
1:CC:141:LEU:HD21	1:CC:184:ILE:CD1	2.12	0.82
1:CD:101:ARG:NH1	1:CD:166:LEU:HD12	2.01	0.82
1:CN:79:VAL:HG12	1:CN:185:LEU:O	1.80	0.82
1:AG:98:ILE:O	1:AG:211:SER:O	1.98	0.82
1:AO:253:ASP:OD1	1:AO:285:PHE:HA	1.80	0.82
1:CL:79:VAL:HG12	1:CL:185:LEU:O	1.80	0.82
1:CU:141:LEU:HD21	1:CU:184:ILE:CD1	2.10	0.82
1:CC:317:ASP:HB3	1:CC:319:GLN:CG	2.10	0.82
1:AP:105:GLU:O	1:AP:162:TYR:OH	1.98	0.82
1:CY:141:LEU:HD21	1:CY:184:ILE:CD1	2.10	0.81

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CM:317:ASP:HB3	1:CM:319:GLN:CG	2.10	0.81
1:AT:305:ASN:ND2	1:AT:307:THR:O	2.13	0.81
1:AP:302:ASP:OD2	1:AP:305:ASN:HB3	1.79	0.81
1:AZ:279:TYR:OH	1:AZ:311:GLY:O	1.97	0.81
1:AM:98:ILE:O	1:AM:211:SER:O	1.98	0.81
1:AL:298:TRP:CD2	1:AL:312:VAL:CG1	2.63	0.81
1:AB:253:ASP:OD1	1:AB:285:PHE:HA	1.81	0.81
1:CB:317:ASP:HB3	1:CB:319:GLN:CG	2.10	0.81
1:CH:317:ASP:HB3	1:CH:319:GLN:CG	2.10	0.81
1:AO:105:GLU:O	1:AO:162:TYR:OH	1.97	0.81
1:AX:105:GLU:O	1:AX:162:TYR:OH	1.97	0.81
1:AW:253:ASP:OD1	1:AW:285:PHE:HA	1.81	0.81
1:AK:302:ASP:O	1:AK:305:ASN:ND2	2.13	0.81
1:CG:317:ASP:HB3	1:CG:319:GLN:CG	2.10	0.81
1:CW:100:GLN:CG	1:CW:211:SER:OG	2.28	0.81
1:AR:105:GLU:O	1:AR:162:TYR:OH	1.98	0.81
1:AN:253:ASP:OD1	1:AN:285:PHE:HA	1.81	0.81
1:AA:253:ASP:OD1	1:AA:285:PHE:HA	1.80	0.81
1:BG:122:GLY:C	1:BG:188:VAL:HG22	2.01	0.81
1:AN:105:GLU:O	1:AN:162:TYR:OH	1.99	0.81
1:AC:105:GLU:O	1:AC:162:TYR:OH	1.98	0.81
1:AD:298:TRP:CD2	1:AD:312:VAL:CG1	2.66	0.81
1:CP:101:ARG:NH1	1:CP:166:LEU:HD12	1.95	0.81
1:CU:317:ASP:HB3	1:CU:319:GLN:CG	2.10	0.81
1:CP:79:VAL:HG12	1:CP:185:LEU:O	1.79	0.81
1:AE:253:ASP:OD1	1:AE:285:PHE:HA	1.80	0.81
1:AG:105:GLU:O	1:AG:162:TYR:OH	1.98	0.81
1:AC:253:ASP:OD1	1:AC:285:PHE:HA	1.81	0.81
1:AS:253:ASP:OD1	1:AS:285:PHE:HA	1.81	0.81
1:AD:91:ARG:HE	1:BH:98:ILE:HG22	132.58	0.81
1:CC:100:GLN:CG	1:CC:211:SER:OG	2.32	0.81
1:CT:100:GLN:CG	1:CT:211:SER:OG	2.29	0.81
1:AU:253:ASP:OD1	1:AU:285:PHE:HA	1.80	0.81
1:AM:302:ASP:OD2	1:AM:305:ASN:HB3	1.81	0.81
1:CJ:141:LEU:HD21	1:CJ:184:ILE:CD1	2.10	0.81
1:CK:317:ASP:HB3	1:CK:319:GLN:CG	2.11	0.81
1:CN:317:ASP:HB3	1:CN:319:GLN:CG	2.10	0.81
1:CD:117:ALA:CB	1:CW:38:PRO:O	144.83	0.81
1:AQ:253:ASP:OD1	1:AQ:285:PHE:HA	1.81	0.81
1:AK:253:ASP:OD1	1:AK:285:PHE:HA	1.81	0.81
1:AX:253:ASP:OD1	1:AX:285:PHE:HA	1.81	0.81

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AU:302:ASP:OD2	1:AU:305:ASN:HB3	1.81	0.81
1:CE:317:ASP:HB3	1:CE:319:GLN:CG	2.10	0.81
1:AM:298:TRP:CD1	1:AM:312:VAL:HG13	2.16	0.80
1:AH:253:ASP:OD1	1:AH:285:PHE:HA	1.81	0.80
1:AD:253:ASP:OD1	1:AD:285:PHE:HA	1.81	0.80
1:CE:141:LEU:HD21	1:CE:184:ILE:CD1	2.09	0.80
1:AS:105:GLU:O	1:AS:162:TYR:OH	1.99	0.80
1:AQ:302:ASP:OD2	1:AQ:305:ASN:HB3	1.81	0.80
1:BD:98:ILE:HG22	1:AW:91:ARG:HE	1.47	0.80
1:CQ:100:GLN:CG	1:CQ:211:SER:OG	2.29	0.80
1:CO:317:ASP:HB3	1:CO:319:GLN:CG	2.11	0.80
1:CP:317:ASP:HB3	1:CP:319:GLN:CG	2.10	0.80
1:AW:298:TRP:CD2	1:AW:312:VAL:CG1	2.64	0.80
1:AV:253:ASP:OD1	1:AV:285:PHE:HA	1.81	0.80
1:AA:302:ASP:OD2	1:AA:305:ASN:HB3	1.81	0.80
1:CL:101:ARG:NH1	1:CL:166:LEU:HD12	1.96	0.80
1:CX:317:ASP:HB3	1:CX:319:GLN:CG	2.10	0.80
1:AV:105:GLU:O	1:AV:162:TYR:OH	1.99	0.80
1:AX:302:ASP:OD2	1:AX:305:ASN:HB3	1.81	0.80
1:AN:302:ASP:OD2	1:AN:305:ASN:HB3	1.82	0.80
1:CR:317:ASP:HB3	1:CR:319:GLN:CG	2.11	0.80
1:CW:317:ASP:HB3	1:CW:319:GLN:CG	2.12	0.80
1:CQ:317:ASP:HB3	1:CQ:319:GLN:CG	2.11	0.80
1:BD:122:GLY:C	1:BD:188:VAL:HG22	2.02	0.80
1:BV:122:GLY:C	1:BV:188:VAL:HG22	2.02	0.80
1:AM:253:ASP:OD1	1:AM:285:PHE:HA	1.81	0.80
1:AJ:302:ASP:O	1:AJ:305:ASN:CG	2.20	0.80
1:AZ:302:ASP:OD2	1:AZ:305:ASN:HB3	1.82	0.80
1:CX:100:GLN:CG	1:CX:211:SER:OG	2.30	0.80
1:CY:317:ASP:HB3	1:CY:319:GLN:CG	2.10	0.80
1:BO:122:GLY:C	1:BO:188:VAL:HG22	2.02	0.80
1:AC:298:TRP:CD1	1:AC:312:VAL:HG13	2.16	0.80
1:AW:298:TRP:CD1	1:AW:312:VAL:HG13	2.16	0.80
1:CV:141:LEU:HD21	1:CV:184:ILE:CD1	2.09	0.80
1:CJ:100:GLN:CG	1:CJ:211:SER:OG	2.30	0.80
1:AD:105:GLU:O	1:AD:162:TYR:OH	2.03	0.80
1:AH:298:TRP:CD1	1:AH:312:VAL:HG13	2.16	0.80
1:CD:141:LEU:CD2	1:CD:184:ILE:HD11	2.13	0.80
1:AD:302:ASP:OD2	1:AD:305:ASN:HB3	1.82	0.80
1:AE:302:ASP:OD2	1:AE:305:ASN:HB3	1.82	0.80
1:CS:317:ASP:HB3	1:CS:319:GLN:CG	2.10	0.80

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BD:154:GLU:OE1	1:CD:43:SER:OG	1.99	0.80
1:AG:298:TRP:CD1	1:AG:312:VAL:HG13	2.17	0.80
1:CM:100:GLN:CG	1:CM:211:SER:OG	2.29	0.80
1:AL:298:TRP:CD1	1:AL:312:VAL:HG13	2.17	0.80
1:AA:298:TRP:CD1	1:AA:312:VAL:HG13	2.17	0.80
1:AN:298:TRP:CD1	1:AN:312:VAL:HG13	2.17	0.80
1:AY:253:ASP:OD1	1:AY:285:PHE:HA	1.82	0.80
1:CF:100:GLN:CG	1:CF:211:SER:OG	2.30	0.80
1:AY:105:GLU:O	1:AY:162:TYR:OH	1.99	0.80
1:AX:98:ILE:O	1:AX:211:SER:O	2.00	0.80
1:AV:302:ASP:OD2	1:AV:305:ASN:HB3	1.82	0.79
1:CN:122:GLY:HA3	1:BP:114:MET:SD	2.23	0.79
1:CD:317:ASP:HB3	1:CD:319:GLN:CG	2.12	0.79
1:CZ:100:GLN:CG	1:CZ:211:SER:OG	2.30	0.79
1:BA:122:GLY:C	1:BA:188:VAL:HG22	2.03	0.79
1:BT:122:GLY:C	1:BT:188:VAL:HG22	2.02	0.79
1:AL:253:ASP:OD1	1:AL:285:PHE:HA	1.82	0.79
1:AJ:302:ASP:OD2	1:AJ:305:ASN:HB3	1.83	0.79
1:CR:100:GLN:CG	1:CR:211:SER:OG	2.30	0.79
1:CA:100:GLN:CG	1:CA:211:SER:OG	2.32	0.79
1:CP:100:GLN:CG	1:CP:211:SER:OG	2.30	0.79
1:BX:122:GLY:C	1:BX:188:VAL:HG22	2.02	0.79
1:AU:105:GLU:O	1:AU:162:TYR:OH	1.99	0.79
1:AK:302:ASP:OD2	1:AK:305:ASN:HB3	1.81	0.79
1:AU:302:ASP:O	1:AU:305:ASN:CG	2.21	0.79
1:CO:100:GLN:HG3	1:CO:211:SER:OG	1.83	0.79
1:CL:317:ASP:HB3	1:CL:319:GLN:CG	2.11	0.79
1:CH:100:GLN:CG	1:CH:211:SER:OG	2.30	0.79
1:AD:302:ASP:O	1:AD:305:ASN:CG	2.21	0.79
1:CR:101:ARG:NH1	1:CR:166:LEU:HD12	1.98	0.79
1:CI:100:GLN:CG	1:CI:211:SER:OG	2.30	0.79
1:CF:317:ASP:HB3	1:CF:319:GLN:CG	2.10	0.79
1:AB:105:GLU:O	1:AB:162:TYR:OH	2.00	0.79
1:AZ:105:GLU:O	1:AZ:162:TYR:OH	2.00	0.79
1:AS:298:TRP:CD1	1:AS:312:VAL:HG13	2.18	0.79
1:AP:298:TRP:CD1	1:AP:312:VAL:HG13	2.16	0.79
1:AC:302:ASP:O	1:AC:305:ASN:CG	2.21	0.79
1:AB:302:ASP:OD2	1:AB:305:ASN:HB3	1.83	0.79
1:CW:79:VAL:HG12	1:CW:185:LEU:O	1.82	0.79
1:AD:298:TRP:CD1	1:AD:312:VAL:HG13	2.18	0.79
1:AO:298:TRP:CD1	1:AO:312:VAL:HG13	2.18	0.79

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AZ:253:ASP:OD1	1:AZ:285:PHE:HA	1.82	0.79
1:CI:101:ARG:NH1	1:CI:166:LEU:HD12	1.98	0.79
1:AU:314:TYR:HE1	1:AU:316:SER:CA	1.96	0.79
1:CZ:317:ASP:HB3	1:CZ:319:GLN:CG	2.12	0.79
1:BA:154:GLU:OE1	1:CA:43:SER:OG	1.99	0.79
1:AF:302:ASP:OD2	1:AF:305:ASN:HB3	1.81	0.79
1:AB:314:TYR:HE1	1:AB:316:SER:CA	1.96	0.79
1:BG:154:GLU:OE1	1:CG:43:SER:OG	2.01	0.79
1:CK:101:ARG:NH1	1:CK:166:LEU:HD12	1.98	0.79
1:CG:100:GLN:CG	1:CG:211:SER:OG	2.31	0.79
1:AF:298:TRP:CD1	1:AF:312:VAL:HG13	2.18	0.79
1:AI:253:ASP:OD1	1:AI:285:PHE:HA	1.81	0.79
1:AM:302:ASP:O	1:AM:305:ASN:CG	2.22	0.79
1:AV:302:ASP:O	1:AV:305:ASN:CG	2.20	0.79
1:AJ:98:ILE:HG23	1:BR:91:ARG:NH1	1.98	0.79
1:BY:122:GLY:C	1:BY:188:VAL:HG22	2.02	0.79
1:BU:154:GLU:OE1	1:CU:43:SER:OG	2.01	0.79
1:AT:253:ASP:OD1	1:AT:285:PHE:HA	1.81	0.79
1:AJ:253:ASP:OD1	1:AJ:285:PHE:HA	1.83	0.79
1:AG:253:ASP:OD1	1:AG:285:PHE:HA	1.82	0.79
1:AK:305:ASN:ND2	1:AK:307:THR:O	2.16	0.79
1:AA:302:ASP:O	1:AA:305:ASN:CG	2.21	0.79
1:AH:302:ASP:OD2	1:AH:305:ASN:HB3	1.81	0.79
1:CC:101:ARG:NH1	1:CC:166:LEU:HD12	1.99	0.79
1:CI:317:ASP:HB3	1:CI:319:GLN:CG	2.12	0.79
1:BQ:122:GLY:C	1:BQ:188:VAL:HG22	2.03	0.79
1:AX:298:TRP:CD1	1:AX:312:VAL:HG13	2.18	0.78
1:AR:253:ASP:OD1	1:AR:285:PHE:HA	1.82	0.78
1:AX:302:ASP:O	1:AX:305:ASN:CG	2.21	0.78
1:AB:302:ASP:O	1:AB:305:ASN:CG	2.21	0.78
1:AL:302:ASP:OD2	1:AL:305:ASN:HB3	1.81	0.78
1:AX:314:TYR:HE1	1:AX:316:SER:CA	1.96	0.78
1:CJ:317:ASP:HB3	1:CJ:319:GLN:CG	2.12	0.78
1:AJ:298:TRP:CD1	1:AJ:312:VAL:HG13	2.18	0.78
1:AT:302:ASP:O	1:AT:305:ASN:CG	2.21	0.78
1:AO:302:ASP:O	1:AO:305:ASN:CG	2.22	0.78
1:CV:101:ARG:NH1	1:CV:166:LEU:HD12	1.99	0.78
1:CT:100:GLN:HG2	1:CT:213:GLU:OE2	1.83	0.78
1:BZ:122:GLY:C	1:BZ:188:VAL:HG22	2.03	0.78
1:AZ:298:TRP:CD2	1:AZ:312:VAL:CG1	2.65	0.78
1:AS:302:ASP:OD2	1:AS:305:ASN:HB3	1.83	0.78

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CN:100:GLN:HG2	1:CN:211:SER:OG	1.84	0.78
1:BL:122:GLY:C	1:BL:188:VAL:HG22	2.04	0.78
1:AL:105:GLU:O	1:AL:162:TYR:OH	1.99	0.78
1:AQ:105:GLU:O	1:AQ:162:TYR:OH	1.98	0.78
1:AF:253:ASP:OD1	1:AF:285:PHE:HA	1.81	0.78
1:AP:302:ASP:O	1:AP:305:ASN:CG	2.21	0.78
1:AF:302:ASP:O	1:AF:305:ASN:CG	2.21	0.78
1:AJ:91:ARG:NE	1:BR:98:ILE:HG22	1.99	0.78
1:BY:154:GLU:OE1	1:CY:43:SER:OG	2.00	0.78
1:AJ:105:GLU:O	1:AJ:162:TYR:OH	2.01	0.78
1:BN:122:GLY:C	1:BN:188:VAL:HG22	2.04	0.78
1:AE:105:GLU:O	1:AE:162:TYR:OH	2.00	0.78
1:AG:302:ASP:OD2	1:AG:305:ASN:HB3	1.83	0.78
1:AN:302:ASP:O	1:AN:305:ASN:CG	2.21	0.78
1:CD:200:LEU:HD13	1:CW:45:VAL:HG23	111.46	0.78
1:AF:105:GLU:O	1:AF:162:TYR:OH	2.01	0.78
1:AV:298:TRP:CD1	1:AV:312:VAL:HG13	2.19	0.78
1:CS:101:ARG:NH1	1:CS:166:LEU:HD12	1.98	0.78
1:AY:302:ASP:OD2	1:AY:305:ASN:HB3	1.82	0.78
1:CS:141:LEU:HD21	1:CS:184:ILE:CD1	2.11	0.78
1:BF:122:GLY:C	1:BF:188:VAL:HG22	2.04	0.78
1:BH:154:GLU:OE1	1:CH:43:SER:OG	2.02	0.78
1:AK:298:TRP:CD1	1:AK:312:VAL:HG13	2.19	0.78
1:AQ:302:ASP:O	1:AQ:305:ASN:CG	2.22	0.78
1:AZ:302:ASP:O	1:AZ:305:ASN:CG	2.22	0.78
1:CW:80:VAL:CG1	1:CW:185:LEU:HB3	2.14	0.78
1:AT:298:TRP:CD1	1:AT:312:VAL:HG13	2.17	0.78
1:AE:302:ASP:O	1:AE:305:ASN:CG	2.22	0.78
1:CJ:101:ARG:NH1	1:CJ:166:LEU:HD12	1.99	0.78
1:BJ:122:GLY:C	1:BJ:188:VAL:HG22	2.03	0.78
1:BS:122:GLY:C	1:BS:188:VAL:HG22	2.04	0.78
1:BP:122:GLY:C	1:BP:188:VAL:HG22	2.03	0.78
1:AZ:298:TRP:CD1	1:AZ:312:VAL:HG13	2.18	0.77
1:AP:253:ASP:OD1	1:AP:285:PHE:HA	1.84	0.77
1:AI:302:ASP:O	1:AI:305:ASN:CG	2.21	0.77
1:AS:302:ASP:O	1:AS:305:ASN:CG	2.21	0.77
1:CK:100:GLN:HG2	1:CK:211:SER:OG	1.85	0.77
1:BC:122:GLY:C	1:BC:188:VAL:HG22	2.04	0.77
1:AB:298:TRP:CD1	1:AB:312:VAL:HG13	2.16	0.77
1:AC:302:ASP:OD2	1:AC:305:ASN:HB3	1.84	0.77
1:BD:98:ILE:HG22	1:AW:91:ARG:NE	1.99	0.77

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CQ:79:VAL:HG12	1:CQ:185:LEU:O	1.84	0.77
1:AO:314:TYR:HE1	1:AO:316:SER:CA	1.97	0.77
1:BK:122:GLY:C	1:BK:188:VAL:HG22	2.03	0.77
1:BA:153:TRP:O	1:CT:151:LYS:NZ	128.67	0.77
1:AA:298:TRP:CD2	1:AA:312:VAL:CG1	2.67	0.77
1:AD:91:ARG:NE	1:BH:98:ILE:HG22	131.79	0.77
1:CB:101:ARG:NH1	1:CB:166:LEU:HD12	1.99	0.77
1:AI:314:TYR:HE1	1:AI:316:SER:CA	1.97	0.77
1:AF:98:ILE:O	1:AF:211:SER:O	2.02	0.77
1:AG:302:ASP:O	1:AG:305:ASN:CG	2.22	0.77
1:CZ:101:ARG:NH1	1:CZ:166:LEU:HD12	2.00	0.77
1:AH:302:ASP:O	1:AH:305:ASN:CG	2.21	0.77
1:AR:302:ASP:O	1:AR:305:ASN:CG	2.22	0.77
1:AL:302:ASP:O	1:AL:305:ASN:CG	2.22	0.77
1:CI:141:LEU:CD2	1:CI:184:ILE:HD11	2.14	0.77
1:CX:101:ARG:NH1	1:CX:166:LEU:HD12	2.00	0.77
1:CN:101:ARG:NH1	1:CN:166:LEU:HD12	1.98	0.77
1:BW:122:GLY:C	1:BW:188:VAL:HG22	2.04	0.77
1:AD:111:ILE:HG22	1:AD:113:PRO:HD3	1.73	0.77
1:CU:100:GLN:CG	1:CU:211:SER:OG	2.33	0.77
1:AC:314:TYR:HE1	1:AC:316:SER:CA	1.99	0.77
1:AE:314:TYR:HE1	1:AE:316:SER:CA	1.97	0.77
1:BH:122:GLY:C	1:BH:188:VAL:HG22	2.05	0.77
1:AG:72:THR:O	1:AG:191:ASN:ND2	2.18	0.77
1:AE:298:TRP:CD2	1:AE:312:VAL:CG1	2.68	0.77
1:AW:302:ASP:OD2	1:AW:305:ASN:HB3	1.83	0.77
1:CH:101:ARG:NH1	1:CH:166:LEU:HD12	2.00	0.77
1:CV:100:GLN:CG	1:CV:211:SER:OG	2.32	0.77
1:BE:122:GLY:C	1:BE:188:VAL:HG22	2.05	0.77
1:AI:298:TRP:CD1	1:AI:312:VAL:HG13	2.18	0.77
1:AX:298:TRP:CD2	1:AX:312:VAL:CG1	2.67	0.77
1:CG:141:LEU:CD2	1:CG:184:ILE:HD11	2.15	0.77
1:BL:91:ARG:NH1	1:AU:98:ILE:HG23	1.99	0.77
1:BS:154:GLU:OE1	1:CS:43:SER:OG	2.02	0.77
1:BB:122:GLY:C	1:BB:188:VAL:HG22	2.05	0.77
1:AO:302:ASP:OD2	1:AO:305:ASN:HB3	1.83	0.77
1:CU:101:ARG:NH1	1:CU:166:LEU:HD12	2.00	0.77
1:AM:314:TYR:HE1	1:AM:316:SER:CA	1.96	0.77
1:AG:314:TYR:HE1	1:AG:316:SER:CA	1.98	0.77
1:AN:314:TYR:HE1	1:AN:316:SER:CA	1.98	0.77
1:BI:122:GLY:C	1:BI:188:VAL:HG22	2.04	0.77

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AU:298:TRP:CD1	1:AU:312:VAL:HG13	2.19	0.77
1:AK:302:ASP:O	1:AK:305:ASN:CG	2.23	0.77
1:AY:302:ASP:O	1:AY:305:ASN:CG	2.22	0.77
1:AW:302:ASP:O	1:AW:305:ASN:CG	2.23	0.77
1:BU:114:MET:SD	1:CX:122:GLY:HA3	2.25	0.77
1:AS:314:TYR:HE1	1:AS:316:SER:CA	1.98	0.77
1:AK:298:TRP:CD2	1:AK:312:VAL:CG1	2.63	0.76
1:AE:298:TRP:CD1	1:AE:312:VAL:HG13	2.19	0.76
1:CQ:101:ARG:NH1	1:CQ:166:LEU:HD12	2.00	0.76
1:CO:101:ARG:NH1	1:CO:166:LEU:HD12	1.98	0.76
1:AA:314:TYR:HE1	1:AA:316:SER:CA	1.98	0.76
1:AI:72:THR:O	1:AI:191:ASN:ND2	2.18	0.76
1:AT:298:TRP:CD2	1:AT:312:VAL:CG1	2.66	0.76
1:AC:298:TRP:CD2	1:AC:312:VAL:CG1	2.67	0.76
1:AR:298:TRP:CD2	1:AR:312:VAL:CG1	2.65	0.76
1:CT:141:LEU:CD2	1:CT:184:ILE:HD11	2.12	0.76
1:CF:101:ARG:NH1	1:CF:166:LEU:HD12	1.99	0.76
1:AH:314:TYR:HE1	1:AH:316:SER:CA	1.97	0.76
1:CE:100:GLN:HG2	1:CE:211:SER:OG	1.85	0.76
1:BR:154:GLU:OE1	1:CR:43:SER:OG	2.03	0.76
1:AQ:298:TRP:CD1	1:AQ:312:VAL:HG13	2.18	0.76
1:BC:114:MET:SD	1:CY:122:GLY:HA3	2.26	0.76
1:CW:101:ARG:NH1	1:CW:166:LEU:HD12	2.01	0.76
1:CI:100:GLN:HG2	1:CI:213:GLU:OE2	1.85	0.76
1:CL:100:GLN:CG	1:CL:211:SER:OG	2.31	0.76
1:CT:100:GLN:HG3	1:CT:211:SER:OG	1.86	0.76
1:CL:99:PHE:HA	1:CL:209:VAL:O	1.86	0.76
1:BR:122:GLY:C	1:BR:188:VAL:HG22	2.05	0.76
1:AP:111:ILE:HG22	1:AP:113:PRO:HD3	1.66	0.76
1:AS:72:THR:O	1:AS:191:ASN:ND2	2.18	0.76
1:AY:298:TRP:CD2	1:AY:312:VAL:CG1	2.67	0.76
1:BQ:154:GLU:OE1	1:CQ:43:SER:OG	2.03	0.76
1:CW:80:VAL:CG1	1:CW:185:LEU:CB	2.64	0.76
1:CP:141:LEU:CD2	1:CP:184:ILE:HD11	2.14	0.76
1:CH:141:LEU:CD2	1:CH:184:ILE:HD11	2.15	0.76
1:BB:98:ILE:HG22	1:AK:91:ARG:HE	1.51	0.76
1:CD:99:PHE:HA	1:CD:209:VAL:O	1.87	0.76
1:BW:130:ASP:HB2	1:CW:100:GLN:HE22	1.49	0.76
1:BV:154:GLU:OE1	1:CV:43:SER:OG	2.03	0.76
1:AV:298:TRP:CD2	1:AV:312:VAL:CG1	2.65	0.76
1:CS:100:GLN:CG	1:CS:211:SER:OG	2.32	0.76

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CG:100:GLN:HG2	1:CG:213:GLU:OE2	1.84	0.76
1:BC:101:ARG:HB3	1:BC:166:LEU:HD11	1.72	0.76
1:AN:111:ILE:HG22	1:AN:113:PRO:HD3	1.67	0.76
1:CW:141:LEU:CD2	1:CW:184:ILE:HD11	2.14	0.75
1:CB:141:LEU:CD2	1:CB:184:ILE:HD11	2.13	0.75
1:CQ:80:VAL:CG1	1:CQ:185:LEU:HB3	2.15	0.75
1:AQ:314:TYR:HE1	1:AQ:316:SER:CA	1.98	0.75
1:AJ:314:TYR:HE1	1:AJ:316:SER:CA	1.99	0.75
1:BI:154:GLU:OE1	1:CI:43:SER:OG	2.03	0.75
1:AQ:298:TRP:CD2	1:AQ:312:VAL:CG1	2.67	0.75
1:CI:80:VAL:CG1	1:CI:185:LEU:HB3	2.15	0.75
1:BD:130:ASP:HB2	1:CD:100:GLN:HE22	1.54	0.75
1:CB:100:GLN:HG2	1:CB:211:SER:OG	1.85	0.75
1:CR:80:VAL:CG1	1:CR:185:LEU:HB3	2.16	0.75
1:BL:130:ASP:HB2	1:CL:100:GLN:HE22	1.51	0.75
1:CN:100:GLN:HG2	1:CN:213:GLU:OE2	1.86	0.75
1:BF:154:GLU:OE1	1:CF:43:SER:OG	2.03	0.75
1:BB:154:GLU:OE1	1:CB:43:SER:OG	2.03	0.75
1:CT:101:ARG:NH1	1:CT:166:LEU:HD12	2.01	0.75
1:CZ:100:GLN:HG2	1:CZ:213:GLU:OE2	1.87	0.75
1:AU:111:ILE:HG22	1:AU:113:PRO:HD3	1.67	0.75
1:AR:298:TRP:CD1	1:AR:312:VAL:HG13	2.17	0.75
1:CK:141:LEU:CD2	1:CK:184:ILE:HD11	2.13	0.75
1:CE:101:ARG:NH1	1:CE:166:LEU:HD12	2.01	0.75
1:CQ:99:PHE:HA	1:CQ:209:VAL:O	1.86	0.75
1:AP:314:TYR:HE1	1:AP:316:SER:CA	1.98	0.75
1:AY:314:TYR:HE1	1:AY:316:SER:CA	1.99	0.75
1:BP:101:ARG:HB3	1:BP:166:LEU:HD11	1.69	0.75
1:CD:122:GLY:HA3	1:BF:114:MET:SD	2.26	0.75
1:CR:99:PHE:HA	1:CR:209:VAL:O	1.86	0.75
1:AF:314:TYR:HE1	1:AF:316:SER:CA	1.98	0.75
1:BC:154:GLU:OE1	1:CC:43:SER:OG	2.04	0.75
1:CX:141:LEU:CD2	1:CX:184:ILE:HD11	2.13	0.75
1:CD:100:GLN:HG2	1:CD:211:SER:OG	1.90	0.75
1:CO:100:GLN:HG2	1:CO:211:SER:OG	1.85	0.75
1:CA:101:ARG:NH1	1:CA:166:LEU:HD12	2.00	0.75
1:BJ:154:GLU:OE1	1:CJ:43:SER:OG	2.03	0.75
1:AK:105:GLU:O	1:AK:162:TYR:OH	2.03	0.75
1:AF:298:TRP:CD2	1:AF:312:VAL:CG1	2.69	0.75
1:CR:141:LEU:CD2	1:CR:184:ILE:HD11	2.13	0.75
1:CC:99:PHE:HA	1:CC:209:VAL:O	1.85	0.75

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CD:100:GLN:HG2	1:CD:213:GLU:OE2	1.86	0.75
1:CA:100:GLN:HG2	1:CA:213:GLU:OE2	1.87	0.75
1:CW:100:GLN:HG2	1:CW:211:SER:OG	1.86	0.75
1:BM:154:GLU:OE1	1:CM:43:SER:OG	2.05	0.75
1:AF:72:THR:O	1:AF:191:ASN:ND2	2.20	0.75
1:CM:100:GLN:HG2	1:CM:211:SER:OG	1.87	0.74
1:CD:112:GLN:NE2	1:CW:43:SER:HA	123.09	0.74
1:AK:111:ILE:HG22	1:AK:113:PRO:HD3	1.69	0.74
1:CY:101:ARG:NH1	1:CY:166:LEU:HD12	2.01	0.74
1:CT:99:PHE:HA	1:CT:209:VAL:O	1.87	0.74
1:CN:100:GLN:HG3	1:CN:211:SER:OG	1.87	0.74
1:AL:111:ILE:HG22	1:AL:113:PRO:HD3	1.69	0.74
1:AW:111:ILE:HG22	1:AW:113:PRO:HD3	1.69	0.74
1:CB:80:VAL:CG1	1:CB:185:LEU:HB3	2.18	0.74
1:CU:122:GLY:O	1:CU:188:VAL:N	2.20	0.74
1:CT:80:VAL:CG1	1:CT:185:LEU:HB3	2.17	0.74
1:CH:100:GLN:HG2	1:CH:211:SER:OG	1.88	0.74
1:BL:154:GLU:OE1	1:CL:43:SER:OG	2.04	0.74
1:BC:75:ASP:OD2	1:CX:62:ARG:NH1	228.35	0.74
1:CC:63:ILE:HD12	1:CC:88:LEU:HG	1.76	0.74
1:CL:80:VAL:CG1	1:CL:185:LEU:HB3	2.18	0.74
1:AV:314:TYR:HE1	1:AV:316:SER:CA	2.00	0.74
1:AL:314:TYR:HE1	1:AL:316:SER:CA	2.00	0.74
1:AR:314:TYR:HE1	1:AR:316:SER:CA	2.00	0.74
1:CY:100:GLN:CG	1:CY:211:SER:OG	2.35	0.74
1:AM:298:TRP:CD2	1:AM:312:VAL:CG1	2.69	0.74
1:CI:80:VAL:CG1	1:CI:185:LEU:CB	2.65	0.74
1:AT:314:TYR:HE1	1:AT:316:SER:CA	2.00	0.74
1:CZ:80:VAL:CG1	1:CZ:185:LEU:CB	2.66	0.74
1:CH:80:VAL:CG1	1:CH:185:LEU:HB3	2.17	0.74
1:AD:98:ILE:HG23	1:BH:91:ARG:NH1	120.83	0.74
1:AE:72:THR:O	1:AE:191:ASN:ND2	2.19	0.74
1:AW:72:THR:O	1:AW:191:ASN:ND2	2.21	0.74
1:AO:111:ILE:HG22	1:AO:113:PRO:HD3	1.70	0.74
1:CF:100:GLN:HG2	1:CF:213:GLU:OE2	1.88	0.74
1:AH:72:THR:O	1:AH:191:ASN:ND2	2.21	0.74
1:AS:298:TRP:CD2	1:AS:312:VAL:CG1	2.69	0.74
1:AD:314:TYR:HE1	1:AD:316:SER:CA	2.00	0.74
1:AK:72:THR:O	1:AK:191:ASN:ND2	2.20	0.74
1:AP:72:THR:O	1:AP:191:ASN:ND2	2.20	0.74
1:AP:298:TRP:CD2	1:AP:312:VAL:CG1	2.67	0.74

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CM:100:GLN:HG2	1:CM:213:GLU:OE2	1.88	0.74
1:BT:153:TRP:O	1:CV:151:LYS:NZ	2.21	0.74
1:AG:298:TRP:CD2	1:AG:312:VAL:CG1	2.69	0.74
1:CC:100:GLN:HG3	1:CC:211:SER:OG	1.92	0.74
1:CZ:100:GLN:HG3	1:CZ:211:SER:OG	1.88	0.74
1:BU:130:ASP:HB2	1:CU:100:GLN:HE22	1.53	0.73
1:CQ:100:GLN:HG2	1:CQ:213:GLU:OE2	1.88	0.73
1:AZ:72:THR:O	1:AZ:191:ASN:ND2	2.21	0.73
1:AB:298:TRP:CD2	1:AB:312:VAL:CG1	2.69	0.73
1:AU:298:TRP:CD2	1:AU:312:VAL:CG1	2.70	0.73
1:CZ:141:LEU:CD2	1:CZ:184:ILE:HD11	2.12	0.73
1:CH:122:GLY:O	1:CH:188:VAL:N	2.21	0.73
1:CI:100:GLN:HG3	1:CI:211:SER:OG	1.87	0.73
1:CO:100:GLN:HG2	1:CO:213:GLU:OE2	1.87	0.73
1:CF:99:PHE:HA	1:CF:209:VAL:O	1.88	0.73
1:CH:99:PHE:HA	1:CH:209:VAL:O	1.87	0.73
1:BQ:101:ARG:HB3	1:BQ:166:LEU:HD11	1.69	0.73
1:CV:99:PHE:HA	1:CV:209:VAL:O	1.87	0.73
1:AB:72:THR:O	1:AB:191:ASN:ND2	2.20	0.73
1:AF:265:ILE:CG2	1:AF:313:ALA:O	2.36	0.73
1:BK:154:GLU:OE1	1:CK:43:SER:OG	2.06	0.73
1:CK:45:VAL:HG23	1:CL:200:LEU:HD13	1.69	0.73
1:AH:298:TRP:CD2	1:AH:312:VAL:CG1	2.69	0.73
1:AH:299:GLY:CA	1:AH:310:ASP:O	2.36	0.73
1:CB:122:GLY:O	1:CB:188:VAL:N	2.21	0.73
1:CC:100:GLN:HG2	1:CC:211:SER:OG	1.89	0.73
1:CB:100:GLN:HG3	1:CB:211:SER:OG	1.88	0.73
1:AZ:314:TYR:HE1	1:AZ:316:SER:CA	2.00	0.73
1:AT:72:THR:O	1:AT:191:ASN:ND2	2.21	0.73
1:AY:298:TRP:CD1	1:AY:312:VAL:HG13	2.20	0.73
1:CK:80:VAL:CG1	1:CK:185:LEU:CB	2.67	0.73
1:AW:314:TYR:HE1	1:AW:316:SER:CA	2.01	0.73
1:CA:99:PHE:HA	1:CA:209:VAL:O	1.88	0.73
1:AD:72:THR:O	1:AD:191:ASN:ND2	2.21	0.73
1:CQ:100:GLN:HG2	1:CQ:211:SER:OG	1.88	0.73
1:CJ:122:GLY:O	1:CJ:188:VAL:N	2.21	0.73
1:CG:99:PHE:HA	1:CG:209:VAL:O	1.87	0.73
1:AX:111:ILE:HG22	1:AX:113:PRO:HD3	1.71	0.73
1:CQ:141:LEU:CD2	1:CQ:184:ILE:HD11	2.15	0.73
1:CI:80:VAL:HG12	1:CI:185:LEU:CB	2.19	0.73
1:CR:100:GLN:HG3	1:CR:211:SER:OG	1.88	0.73

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CP:99:PHE:HA	1:CP:209:VAL:O	1.88	0.73
1:CP:100:GLN:HG2	1:CP:211:SER:OG	1.87	0.73
1:BV:130:ASP:HB2	1:CV:100:GLN:HE22	1.54	0.73
1:BX:154:GLU:OE1	1:CX:43:SER:OG	2.07	0.73
1:CA:63:ILE:HD12	1:CA:88:LEU:HG	1.75	0.73
1:AY:111:ILE:HG22	1:AY:113:PRO:HD3	1.69	0.73
1:CG:80:VAL:CG1	1:CG:185:LEU:HB3	2.17	0.73
1:CL:141:LEU:CD2	1:CL:184:ILE:HD11	2.14	0.73
1:CK:80:VAL:HG12	1:CK:185:LEU:CB	2.19	0.73
1:CU:100:GLN:HG2	1:CU:213:GLU:OE2	1.89	0.73
1:BJ:130:ASP:HB2	1:CJ:100:GLN:HE22	1.53	0.73
1:AO:72:THR:O	1:AO:191:ASN:ND2	2.22	0.73
1:AJ:298:TRP:CD2	1:AJ:312:VAL:CG1	2.68	0.73
1:AN:298:TRP:CD2	1:AN:312:VAL:CG1	2.68	0.73
1:CM:141:LEU:CD2	1:CM:184:ILE:HD11	2.14	0.73
1:CN:141:LEU:CD2	1:CN:184:ILE:HD11	2.16	0.73
1:CH:100:GLN:HG2	1:CH:213:GLU:OE2	1.88	0.73
1:CX:100:GLN:HG3	1:CX:211:SER:OG	1.89	0.73
1:AB:299:GLY:CA	1:AB:310:ASP:O	2.37	0.73
1:CD:100:GLN:HG3	1:CD:211:SER:OG	1.88	0.73
1:CB:99:PHE:HA	1:CB:209:VAL:O	1.89	0.73
1:CF:100:GLN:HG2	1:CF:211:SER:OG	1.88	0.73
1:AJ:72:THR:O	1:AJ:191:ASN:ND2	2.22	0.73
1:AU:265:ILE:CG2	1:AU:313:ALA:O	2.37	0.73
1:AO:265:ILE:CG2	1:AO:313:ALA:O	2.37	0.73
1:AM:299:GLY:CA	1:AM:310:ASP:O	2.36	0.73
1:CD:80:VAL:CG1	1:CD:185:LEU:CB	2.68	0.73
1:CA:80:VAL:CG1	1:CA:185:LEU:HB3	2.18	0.73
1:BR:130:ASP:HB2	1:CR:100:GLN:HE22	1.53	0.73
1:CB:100:GLN:HG2	1:CB:213:GLU:OE2	1.88	0.73
1:BT:130:ASP:HB2	1:CT:100:GLN:HE22	1.54	0.73
1:BZ:130:ASP:HB2	1:CZ:100:GLN:HE22	1.53	0.73
1:CE:99:PHE:HA	1:CE:209:VAL:O	1.89	0.73
1:CY:99:PHE:HA	1:CY:209:VAL:O	1.87	0.73
1:CW:100:GLN:HG3	1:CW:211:SER:OG	1.88	0.73
1:CW:100:GLN:HG2	1:CW:213:GLU:OE2	1.89	0.73
1:BU:122:GLY:C	1:BU:188:VAL:HG22	2.08	0.73
1:AA:265:ILE:CG2	1:AA:313:ALA:O	2.36	0.73
1:BN:154:GLU:OE1	1:CN:43:SER:OG	2.07	0.73
1:CF:63:ILE:HD12	1:CF:88:LEU:HG	1.71	0.73
1:CP:122:GLY:O	1:CP:188:VAL:N	2.22	0.72

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CO:80:VAL:CG1	1:CO:185:LEU:HB3	2.19	0.72
1:BE:130:ASP:HB2	1:CE:100:GLN:HE22	1.54	0.72
1:AV:111:ILE:HG22	1:AV:113:PRO:HD3	1.71	0.72
1:BP:154:GLU:OE1	1:CP:43:SER:OG	2.07	0.72
1:AG:111:ILE:HG22	1:AG:113:PRO:HD3	1.71	0.72
1:AC:299:GLY:CA	1:AC:310:ASP:O	2.37	0.72
1:BB:98:ILE:HG22	1:AK:91:ARG:NE	2.04	0.72
1:CQ:100:GLN:HG3	1:CQ:211:SER:OG	1.88	0.72
1:BM:130:ASP:HB2	1:CM:100:GLN:HE22	1.53	0.72
1:CP:100:GLN:HG2	1:CP:213:GLU:OE2	1.89	0.72
1:AB:119:THR:HG23	1:AB:193:ASP:HB2	1.72	0.72
1:AC:119:THR:HG23	1:AC:193:ASP:HB2	1.76	0.72
1:AE:265:ILE:CG2	1:AE:313:ALA:O	2.37	0.72
1:CE:122:GLY:O	1:CE:188:VAL:N	2.22	0.72
1:CO:122:GLY:O	1:CO:188:VAL:N	2.22	0.72
1:CG:100:GLN:HG3	1:CG:211:SER:OG	1.90	0.72
1:CV:100:GLN:HG2	1:CV:213:GLU:OE2	1.89	0.72
1:BO:154:GLU:OE1	1:CO:43:SER:OG	2.06	0.72
1:AC:265:ILE:CG2	1:AC:313:ALA:O	2.37	0.72
1:AC:111:ILE:HG22	1:AC:113:PRO:HD3	1.71	0.72
1:AV:299:GLY:CA	1:AV:310:ASP:O	2.37	0.72
1:AT:302:ASP:C	1:AT:305:ASN:CG	2.48	0.72
1:CP:80:VAL:CG1	1:CP:185:LEU:HB3	2.19	0.72
1:BC:98:ILE:HG22	1:AY:91:ARG:HE	1.54	0.72
1:AQ:111:ILE:HG22	1:AQ:113:PRO:HD3	1.71	0.72
1:CK:200:LEU:HD13	1:CL:45:VAL:HG23	1.71	0.72
1:AL:302:ASP:C	1:AL:305:ASN:CG	2.48	0.72
1:AA:91:ARG:HE	1:BI:98:ILE:HG22	58.33	0.72
1:CC:100:GLN:HG2	1:CC:213:GLU:OE2	1.89	0.72
1:BI:130:ASP:HB2	1:CI:100:GLN:HE22	1.55	0.72
1:CZ:99:PHE:HA	1:CZ:209:VAL:O	1.89	0.72
1:CX:99:PHE:HA	1:CX:209:VAL:O	1.88	0.72
1:BG:130:ASP:HB2	1:CG:100:GLN:HE22	1.54	0.72
1:CN:80:VAL:CG1	1:CN:185:LEU:HB3	2.19	0.72
1:BA:91:ARG:NH1	1:AI:98:ILE:HG23	2.04	0.72
1:CR:80:VAL:CG1	1:CR:185:LEU:CB	2.67	0.72
1:CL:100:GLN:HG2	1:CL:213:GLU:OE2	1.89	0.72
1:BK:130:ASP:HB2	1:CK:100:GLN:HE22	1.53	0.72
1:CK:100:GLN:HG3	1:CK:211:SER:OG	1.89	0.72
1:BW:154:GLU:OE1	1:CW:43:SER:OG	2.08	0.72
1:AM:72:THR:O	1:AM:191:ASN:ND2	2.21	0.72

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AI:298:TRP:CD2	1:AI:312:VAL:CG1	2.68	0.72
1:CL:80:VAL:CG1	1:CL:185:LEU:CB	2.68	0.72
1:BB:130:ASP:HB2	1:CB:100:GLN:HE22	1.53	0.72
1:CS:100:GLN:HG2	1:CS:213:GLU:OE2	1.89	0.72
1:CX:63:ILE:HD12	1:CX:88:LEU:HG	1.71	0.72
1:AN:72:THR:O	1:AN:191:ASN:ND2	2.23	0.72
1:AG:68:LEU:HB2	1:AG:195:VAL:HG22	1.71	0.72
1:AA:302:ASP:C	1:AA:305:ASN:CG	2.48	0.72
1:AR:302:ASP:C	1:AR:305:ASN:CG	2.48	0.72
1:AZ:302:ASP:C	1:AZ:305:ASN:CG	2.49	0.72
1:BC:130:ASP:HB2	1:CC:100:GLN:HE22	1.58	0.72
1:CM:101:ARG:NH1	1:CM:166:LEU:HD12	2.05	0.72
1:BA:130:ASP:HB2	1:CA:100:GLN:HE22	1.55	0.72
1:AB:265:ILE:CG2	1:AB:313:ALA:O	2.38	0.72
1:AR:72:THR:O	1:AR:191:ASN:ND2	2.22	0.72
1:BG:153:TRP:O	1:CP:151:LYS:NZ	2.22	0.72
1:AD:302:ASP:C	1:AD:305:ASN:CG	2.49	0.72
1:CG:80:VAL:CG1	1:CG:185:LEU:CB	2.68	0.72
1:CR:100:GLN:HG2	1:CR:211:SER:OG	1.90	0.72
1:CH:122:GLY:HA3	1:BN:114:MET:SD	2.30	0.72
1:AK:314:TYR:HE1	1:AK:316:SER:CA	2.03	0.72
1:CY:100:GLN:HG2	1:CY:213:GLU:OE2	1.90	0.72
1:BK:101:ARG:HB3	1:BK:166:LEU:HD11	1.70	0.72
1:AZ:111:ILE:HG22	1:AZ:113:PRO:HD3	1.72	0.72
1:CQ:80:VAL:CG1	1:CQ:185:LEU:CB	2.68	0.72
1:CK:80:VAL:CG1	1:CK:185:LEU:HB3	2.20	0.72
1:CR:100:GLN:HG2	1:CR:213:GLU:OE2	1.89	0.72
1:CJ:100:GLN:HG2	1:CJ:211:SER:OG	1.88	0.72
1:AC:98:ILE:HG23	1:BS:91:ARG:NH1	2.03	0.72
1:AA:68:LEU:HB2	1:AA:195:VAL:HG22	1.81	0.72
1:AA:119:THR:HG23	1:AA:193:ASP:HB2	1.71	0.72
1:AU:299:GLY:CA	1:AU:310:ASP:O	2.37	0.71
1:AK:302:ASP:C	1:AK:305:ASN:CG	2.48	0.71
1:AH:302:ASP:C	1:AH:305:ASN:CG	2.49	0.71
1:AN:302:ASP:C	1:AN:305:ASN:CG	2.49	0.71
1:CZ:80:VAL:CG1	1:CZ:185:LEU:HB3	2.19	0.71
1:BH:130:ASP:HB2	1:CH:100:GLN:HE22	1.54	0.71
1:CN:99:PHE:HA	1:CN:209:VAL:O	1.90	0.71
1:CD:34:ARG:HD3	1:CD:43:SER:O	22.32	0.71
1:CA:63:ILE:HD11	1:CA:89:LEU:HD23	1.76	0.71
1:AU:72:THR:O	1:AU:191:ASN:ND2	2.23	0.71

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CK:63:ILE:HD12	1:CK:88:LEU:HG	1.71	0.71
1:AP:302:ASP:C	1:AP:305:ASN:CG	2.48	0.71
1:AQ:302:ASP:C	1:AQ:305:ASN:CG	2.49	0.71
1:AA:91:ARG:NE	1:BI:98:ILE:HG22	57.55	0.71
1:BQ:130:ASP:HB2	1:CQ:100:GLN:HE22	1.55	0.71
1:AW:314:TYR:CD1	1:AW:315:TYR:N	2.58	0.71
1:CJ:100:GLN:HG3	1:CJ:211:SER:OG	1.90	0.71
1:CS:100:GLN:HG2	1:CS:211:SER:OG	1.90	0.71
1:CG:100:GLN:HG2	1:CG:211:SER:OG	1.90	0.71
1:AI:302:ASP:C	1:AI:305:ASN:CG	2.49	0.71
1:AU:302:ASP:C	1:AU:305:ASN:CG	2.49	0.71
1:AF:302:ASP:C	1:AF:305:ASN:CG	2.49	0.71
1:CT:80:VAL:CG1	1:CT:185:LEU:CB	2.68	0.71
1:CO:80:VAL:CG1	1:CO:185:LEU:CB	2.68	0.71
1:CI:99:PHE:HA	1:CI:209:VAL:O	1.90	0.71
1:BO:130:ASP:HB2	1:CO:100:GLN:HE22	1.55	0.71
1:CM:100:GLN:HG3	1:CM:211:SER:OG	1.90	0.71
1:CL:100:GLN:HG2	1:CL:211:SER:OG	1.90	0.71
1:CX:100:GLN:HG2	1:CX:211:SER:OG	1.89	0.71
1:CW:99:PHE:HA	1:CW:209:VAL:O	1.89	0.71
1:AK:253:ASP:OD1	1:AK:285:PHE:CA	2.37	0.71
1:AJ:302:ASP:C	1:AJ:305:ASN:CG	2.49	0.71
1:AG:302:ASP:C	1:AG:305:ASN:CG	2.49	0.71
1:AY:302:ASP:C	1:AY:305:ASN:CG	2.49	0.71
1:BA:98:ILE:HG22	1:AT:91:ARG:HE	58.14	0.71
1:BX:130:ASP:HB2	1:CX:100:GLN:HE22	1.54	0.71
1:AV:265:ILE:CG2	1:AV:313:ALA:O	2.38	0.71
1:BE:72:THR:O	1:BE:191:ASN:ND2	2.24	0.71
1:AO:298:TRP:CD2	1:AO:312:VAL:CG1	2.68	0.71
1:AD:253:ASP:OD1	1:AD:285:PHE:CA	2.39	0.71
1:AM:302:ASP:C	1:AM:305:ASN:CG	2.49	0.71
1:AS:302:ASP:C	1:AS:305:ASN:CG	2.49	0.71
1:CY:122:GLY:O	1:CY:188:VAL:N	2.23	0.71
1:CA:122:GLY:O	1:CA:188:VAL:N	2.25	0.71
1:CE:100:GLN:HG3	1:CE:211:SER:OG	1.89	0.71
1:AY:72:THR:O	1:AY:191:ASN:ND2	2.23	0.71
1:AF:299:GLY:CA	1:AF:310:ASP:O	2.38	0.71
1:AV:302:ASP:C	1:AV:305:ASN:CG	2.49	0.71
1:CZ:100:GLN:HG2	1:CZ:211:SER:OG	1.91	0.71
1:CX:100:GLN:HG2	1:CX:213:GLU:OE2	1.89	0.71
1:AR:299:GLY:CA	1:AR:310:ASP:O	2.38	0.71

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AC:302:ASP:C	1:AC:305:ASN:CG	2.48	0.71
1:AB:302:ASP:C	1:AB:305:ASN:CG	2.49	0.71
1:BA:98:ILE:HG22	1:AI:91:ARG:HE	1.54	0.71
1:CH:80:VAL:CG1	1:CH:185:LEU:CB	2.69	0.71
1:CG:101:ARG:NH1	1:CG:166:LEU:HD12	2.04	0.71
1:CS:122:GLY:O	1:CS:188:VAL:N	2.24	0.71
1:CA:100:GLN:HG3	1:CA:211:SER:OG	1.91	0.71
1:BH:101:ARG:HB3	1:BH:166:LEU:HD11	1.71	0.71
1:BK:72:THR:O	1:BK:191:ASN:ND2	2.24	0.71
1:BF:72:THR:O	1:BF:191:ASN:ND2	2.23	0.71
1:AA:72:THR:O	1:AA:191:ASN:ND2	2.24	0.71
1:AY:302:ASP:HB3	1:AY:305:ASN:CG	2.11	0.71
1:AB:91:ARG:HE	1:BY:98:ILE:HG22	1.56	0.71
1:CR:122:GLY:O	1:CR:188:VAL:N	2.23	0.71
1:CM:99:PHE:HA	1:CM:209:VAL:O	1.89	0.71
1:CK:99:PHE:HA	1:CK:209:VAL:O	1.90	0.71
1:BD:101:ARG:HB3	1:BD:166:LEU:HD11	1.75	0.71
1:AC:72:THR:O	1:AC:191:ASN:ND2	2.25	0.71
1:AL:72:THR:O	1:AL:191:ASN:ND2	2.24	0.71
1:AY:119:THR:HG23	1:AY:193:ASP:HB2	1.73	0.71
1:AN:265:ILE:CG2	1:AN:313:ALA:O	2.39	0.71
1:AR:111:ILE:HG22	1:AR:113:PRO:HD3	1.72	0.71
1:AS:119:THR:HG23	1:AS:193:ASP:HB2	1.73	0.71
1:AA:299:GLY:CA	1:AA:310:ASP:O	2.38	0.71
1:AN:299:GLY:CA	1:AN:310:ASP:O	2.38	0.71
1:AQ:299:GLY:CA	1:AQ:310:ASP:O	2.39	0.71
1:AW:302:ASP:C	1:AW:305:ASN:CG	2.49	0.71
1:CW:80:VAL:HG12	1:CW:185:LEU:CB	2.18	0.71
1:CB:80:VAL:CG1	1:CB:185:LEU:CB	2.69	0.71
1:CA:141:LEU:CD2	1:CA:184:ILE:HD11	2.19	0.71
1:CC:80:VAL:CG1	1:CC:185:LEU:HB3	2.22	0.71
1:BQ:98:ILE:HG22	1:AZ:91:ARG:HE	1.55	0.71
1:BF:130:ASP:HB2	1:CF:100:GLN:HE22	1.56	0.71
1:BA:101:ARG:HB3	1:BA:166:LEU:HD11	1.73	0.71
1:CR:63:ILE:HD12	1:CR:88:LEU:HG	1.73	0.71
1:AR:253:ASP:OD1	1:AR:285:PHE:CA	2.39	0.71
1:CD:80:VAL:HG12	1:CD:185:LEU:CB	2.21	0.71
1:CA:80:VAL:CG1	1:CA:185:LEU:CB	2.69	0.71
1:CY:100:GLN:HG2	1:CY:211:SER:OG	1.91	0.71
1:AV:72:THR:O	1:AV:191:ASN:ND2	2.23	0.71
1:AX:72:THR:O	1:AX:191:ASN:ND2	2.23	0.71

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AM:111:ILE:HG22	1:AM:113:PRO:HD3	1.72	0.71
1:AD:116:PRO:HB3	1:AH:118:ASN:O	154.57	0.71
1:CD:80:VAL:CG1	1:CD:185:LEU:HB3	2.23	0.70
1:AQ:314:TYR:CD1	1:AQ:315:TYR:N	2.59	0.70
1:CU:99:PHE:HA	1:CU:209:VAL:O	1.90	0.70
1:CL:100:GLN:HG3	1:CL:211:SER:OG	1.91	0.70
1:AH:265:ILE:CG2	1:AH:313:ALA:O	2.39	0.70
1:AZ:265:ILE:CG2	1:AZ:313:ALA:O	2.39	0.70
1:AJ:119:THR:HG23	1:AJ:193:ASP:HB2	1.73	0.70
1:BT:154:GLU:OE1	1:CT:43:SER:OG	2.08	0.70
1:BL:139:ASP:HA	1:BL:142:GLN:HG2	1.72	0.70
1:AZ:299:GLY:CA	1:AZ:310:ASP:O	2.36	0.70
1:CC:141:LEU:CD2	1:CC:184:ILE:HD11	2.19	0.70
1:BK:98:ILE:HG22	1:AS:91:ARG:HE	1.54	0.70
1:BU:98:ILE:HG22	1:AX:91:ARG:HE	1.56	0.70
1:CQ:122:GLY:O	1:CQ:188:VAL:N	2.24	0.70
1:AA:314:TYR:CD1	1:AA:315:TYR:N	2.59	0.70
1:AK:314:TYR:CD1	1:AK:315:TYR:N	2.59	0.70
1:CA:100:GLN:HG2	1:CA:211:SER:OG	1.91	0.70
1:BT:101:ARG:HB3	1:BT:166:LEU:HD11	1.73	0.70
1:CK:117:ALA:CB	1:CL:38:PRO:O	2.39	0.70
1:AZ:253:ASP:OD1	1:AZ:285:PHE:CA	2.39	0.70
1:AL:253:ASP:OD1	1:AL:285:PHE:CA	2.39	0.70
1:CM:122:GLY:O	1:CM:188:VAL:N	2.24	0.70
1:CV:141:LEU:CD2	1:CV:184:ILE:HD11	2.17	0.70
1:AA:91:ARG:HE	1:BV:98:ILE:HG22	1.56	0.70
1:AM:314:TYR:CD1	1:AM:315:TYR:N	2.60	0.70
1:CH:80:VAL:HG12	1:CH:185:LEU:CB	2.22	0.70
1:CO:99:PHE:HA	1:CO:209:VAL:O	1.90	0.70
1:CF:100:GLN:HG3	1:CF:211:SER:OG	1.90	0.70
1:AJ:314:TYR:CD1	1:AJ:315:TYR:N	2.59	0.70
1:BY:101:ARG:HB3	1:BY:166:LEU:HD11	1.73	0.70
1:AF:68:LEU:HB2	1:AF:195:VAL:HG22	1.74	0.70
1:AJ:68:LEU:HB2	1:AJ:195:VAL:HG22	1.73	0.70
1:AJ:299:GLY:CA	1:AJ:310:ASP:O	2.39	0.70
1:AX:314:TYR:CD1	1:AX:315:TYR:N	2.60	0.70
1:CR:80:VAL:HG12	1:CR:185:LEU:CB	2.21	0.70
1:AD:314:TYR:CD1	1:AD:315:TYR:N	2.60	0.70
1:CE:100:GLN:HG2	1:CE:213:GLU:OE2	1.91	0.70
1:CF:80:VAL:CG1	1:CF:185:LEU:HB3	2.21	0.70
1:BD:72:THR:O	1:BD:191:ASN:ND2	2.27	0.70

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AQ:72:THR:O	1:AQ:191:ASN:ND2	2.24	0.70
1:AJ:253:ASP:OD1	1:AJ:285:PHE:CA	2.39	0.70
1:CG:122:GLY:O	1:CG:188:VAL:N	2.24	0.70
1:CM:80:VAL:CG1	1:CM:185:LEU:HB3	2.21	0.70
1:CC:122:GLY:O	1:CC:188:VAL:N	2.24	0.70
1:CV:122:GLY:O	1:CV:188:VAL:N	2.24	0.70
1:CK:100:GLN:HG2	1:CK:213:GLU:OE2	1.90	0.70
1:BL:101:ARG:HB3	1:BL:166:LEU:HD11	1.73	0.70
1:BG:101:ARG:HB3	1:BG:166:LEU:HD11	1.73	0.70
1:CD:63:ILE:HD11	1:CD:89:LEU:HD23	1.73	0.70
1:AI:299:GLY:CA	1:AI:310:ASP:O	2.37	0.70
1:AW:299:GLY:CA	1:AW:310:ASP:O	2.39	0.70
1:AO:253:ASP:OD1	1:AO:285:PHE:CA	2.39	0.70
1:CY:141:LEU:CD2	1:CY:184:ILE:HD11	2.18	0.70
1:CX:80:VAL:CG1	1:CX:185:LEU:HB3	2.21	0.70
1:AS:314:TYR:CD1	1:AS:315:TYR:N	2.60	0.70
1:AT:314:TYR:CD1	1:AT:315:TYR:N	2.60	0.70
1:BA:101:ARG:CZ	1:BA:166:LEU:CD1	2.69	0.70
1:BI:101:ARG:HB3	1:BI:166:LEU:HD11	1.73	0.70
1:BE:101:ARG:HB3	1:BE:166:LEU:HD11	1.73	0.70
1:CO:63:ILE:HD12	1:CO:88:LEU:HG	1.74	0.70
1:CM:63:ILE:HD11	1:CM:89:LEU:HD23	1.74	0.70
1:AI:111:ILE:HG22	1:AI:113:PRO:HD3	1.74	0.70
1:BQ:72:THR:O	1:BQ:191:ASN:ND2	2.25	0.70
1:AO:302:ASP:C	1:AO:305:ASN:CG	2.49	0.70
1:CY:80:VAL:CG1	1:CY:185:LEU:HB3	2.20	0.70
1:CZ:80:VAL:HG12	1:CZ:185:LEU:CB	2.21	0.70
1:CG:63:ILE:HD12	1:CG:88:LEU:HG	1.71	0.70
1:BZ:154:GLU:OE1	1:CZ:43:SER:OG	2.09	0.70
1:AW:119:THR:HG23	1:AW:193:ASP:HB2	1.74	0.70
1:AM:253:ASP:OD1	1:AM:285:PHE:CA	2.39	0.70
1:AB:253:ASP:OD1	1:AB:285:PHE:CA	2.39	0.70
1:AX:253:ASP:OD1	1:AX:285:PHE:CA	2.40	0.70
1:AB:302:ASP:HB3	1:AB:305:ASN:CG	2.12	0.70
1:CC:122:GLY:HA3	1:BS:114:MET:SD	2.31	0.70
1:AM:314:TYR:CE1	1:AM:316:SER:N	2.60	0.70
1:AF:314:TYR:CD1	1:AF:315:TYR:N	2.60	0.70
1:AL:314:TYR:CD1	1:AL:315:TYR:N	2.60	0.70
1:CP:100:GLN:HG3	1:CP:211:SER:OG	1.91	0.70
1:AF:119:THR:HG23	1:AF:193:ASP:HB2	1.73	0.70
1:BE:75:ASP:OD2	1:CH:62:ARG:NH1	2.20	0.70

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AX:299:GLY:CA	1:AX:310:ASP:O	2.38	0.70
1:AV:253:ASP:OD1	1:AV:285:PHE:CA	2.39	0.70
1:AW:302:ASP:HB3	1:AW:305:ASN:CG	2.12	0.70
1:AJ:91:ARG:NE	1:BR:98:ILE:CG2	2.55	0.70
1:BQ:98:ILE:HG22	1:AZ:91:ARG:NE	2.06	0.70
1:CU:100:GLN:HG2	1:CU:211:SER:OG	1.92	0.70
1:BN:130:ASP:HB2	1:CN:100:GLN:HE22	1.53	0.70
1:CV:100:GLN:HG2	1:CV:211:SER:OG	1.89	0.70
1:BM:139:ASP:HA	1:BM:142:GLN:HG2	1.73	0.70
1:CQ:63:ILE:HD11	1:CQ:89:LEU:HD23	1.74	0.70
1:AT:253:ASP:OD1	1:AT:285:PHE:CA	2.40	0.70
1:AJ:302:ASP:HB3	1:AJ:305:ASN:CG	2.12	0.70
1:CD:122:GLY:O	1:CD:188:VAL:N	2.25	0.70
1:AE:314:TYR:CD1	1:AE:315:TYR:N	2.60	0.70
1:AR:314:TYR:CD1	1:AR:315:TYR:N	2.60	0.70
1:CT:100:GLN:HG2	1:CT:211:SER:OG	1.90	0.70
1:BP:130:ASP:HB2	1:CP:100:GLN:HE22	1.56	0.70
1:AZ:68:LEU:HB2	1:AZ:195:VAL:HG22	1.74	0.70
1:AL:299:GLY:CA	1:AL:310:ASP:O	2.40	0.69
1:AP:299:GLY:CA	1:AP:310:ASP:O	2.38	0.69
1:AX:302:ASP:C	1:AX:305:ASN:CG	2.49	0.69
1:AM:302:ASP:HB3	1:AM:305:ASN:CG	2.12	0.69
1:CU:80:VAL:CG1	1:CU:185:LEU:HB3	2.20	0.69
1:AV:314:TYR:CD1	1:AV:315:TYR:N	2.60	0.69
1:BI:139:ASP:HA	1:BI:142:GLN:HG2	1.74	0.69
1:AX:265:ILE:CG2	1:AX:313:ALA:O	2.39	0.69
1:AA:111:ILE:HG22	1:AA:113:PRO:HD3	1.72	0.69
1:AO:299:GLY:CA	1:AO:310:ASP:O	2.38	0.69
1:AH:253:ASP:OD1	1:AH:285:PHE:CA	2.40	0.69
1:AA:253:ASP:OD1	1:AA:285:PHE:CA	2.39	0.69
1:AC:253:ASP:OD1	1:AC:285:PHE:CA	2.39	0.69
1:AC:302:ASP:HB3	1:AC:305:ASN:CG	2.13	0.69
1:AA:302:ASP:HB3	1:AA:305:ASN:CG	2.13	0.69
1:AG:302:ASP:HB3	1:AG:305:ASN:CG	2.12	0.69
1:CT:122:GLY:O	1:CT:188:VAL:N	2.23	0.69
1:CU:100:GLN:HG3	1:CU:211:SER:OG	1.92	0.69
1:CJ:80:VAL:CG1	1:CJ:185:LEU:HB3	2.21	0.69
1:AF:111:ILE:HG22	1:AF:113:PRO:HD3	1.74	0.69
1:AD:302:ASP:HB3	1:AD:305:ASN:CG	2.13	0.69
1:AO:302:ASP:HB3	1:AO:305:ASN:CG	2.12	0.69
1:AA:141:LEU:O	1:AA:144:THR:CG2	2.37	0.69

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BA:98:ILE:HG22	1:AT:91:ARG:NE	57.75	0.69
1:AO:314:TYR:CD1	1:AO:315:TYR:N	2.60	0.69
1:AU:314:TYR:CD1	1:AU:315:TYR:N	2.60	0.69
1:BZ:101:ARG:HB3	1:BZ:166:LEU:HD11	1.74	0.69
1:BA:72:THR:O	1:BA:191:ASN:ND2	2.27	0.69
1:CE:62:ARG:NH1	1:BH:75:ASP:OD2	2.24	0.69
1:AD:265:ILE:CG2	1:AD:313:ALA:O	2.40	0.69
1:CW:63:ILE:HD12	1:CW:88:LEU:HG	1.72	0.69
1:AN:253:ASP:OD1	1:AN:285:PHE:CA	2.39	0.69
1:AU:253:ASP:OD1	1:AU:285:PHE:CA	2.39	0.69
1:AW:253:ASP:OD1	1:AW:285:PHE:CA	2.39	0.69
1:AT:302:ASP:HB3	1:AT:305:ASN:CG	2.12	0.69
1:AE:302:ASP:C	1:AE:305:ASN:CG	2.49	0.69
1:AF:302:ASP:HB3	1:AF:305:ASN:CG	2.11	0.69
1:CZ:122:GLY:O	1:CZ:188:VAL:N	2.25	0.69
1:CE:141:LEU:CD2	1:CE:184:ILE:HD11	2.18	0.69
1:AC:314:TYR:CD1	1:AC:315:TYR:N	2.60	0.69
1:BS:130:ASP:HB2	1:CS:100:GLN:HE22	1.56	0.69
1:AD:119:THR:HG23	1:AD:193:ASP:HB2	1.74	0.69
1:BO:139:ASP:HA	1:BO:142:GLN:HG2	1.74	0.69
1:CY:63:ILE:HD12	1:CY:88:LEU:HG	1.75	0.69
1:AQ:265:ILE:CG2	1:AQ:313:ALA:O	2.39	0.69
1:BJ:72:THR:O	1:BJ:191:ASN:ND2	2.25	0.69
1:BQ:153:TRP:O	1:CZ:151:LYS:NZ	2.25	0.69
1:AG:299:GLY:CA	1:AG:310:ASP:O	2.38	0.69
1:AT:299:GLY:CA	1:AT:310:ASP:O	2.39	0.69
1:AI:253:ASP:OD1	1:AI:285:PHE:CA	2.40	0.69
1:AZ:302:ASP:HB3	1:AZ:305:ASN:CG	2.13	0.69
1:CG:122:GLY:O	1:CG:188:VAL:HB	1.93	0.69
1:CO:80:VAL:HG12	1:CO:185:LEU:CB	2.22	0.69
1:BX:101:ARG:HB3	1:BX:166:LEU:HD11	1.74	0.69
1:BV:318:GLU:OE2	1:BV:318:GLU:N	2.26	0.69
1:AE:299:GLY:CA	1:AE:310:ASP:O	2.37	0.69
1:AX:302:ASP:HB3	1:AX:305:ASN:CG	2.12	0.69
1:AN:302:ASP:HB3	1:AN:305:ASN:CG	2.13	0.69
1:CA:122:GLY:O	1:CA:188:VAL:HB	1.93	0.69
1:AU:314:TYR:CE1	1:AU:316:SER:N	2.61	0.69
1:AN:314:TYR:CD1	1:AN:315:TYR:N	2.60	0.69
1:AZ:314:TYR:CD1	1:AZ:315:TYR:N	2.61	0.69
1:CJ:100:GLN:HG2	1:CJ:213:GLU:OE2	1.91	0.69
1:CS:99:PHE:HA	1:CS:209:VAL:O	1.93	0.69

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BN:101:ARG:HB3	1:BN:166:LEU:HD11	1.74	0.69
1:BR:101:ARG:HB3	1:BR:166:LEU:HD11	1.75	0.69
1:CK:117:ALA:HB2	1:CL:38:PRO:O	1.93	0.69
1:BB:75:ASP:OD2	1:CF:62:ARG:NH1	2.24	0.69
1:BQ:139:ASP:HA	1:BQ:142:GLN:HG2	1.75	0.69
1:AS:253:ASP:OD1	1:AS:285:PHE:CA	2.40	0.69
1:CM:80:VAL:CG1	1:CM:185:LEU:CB	2.70	0.69
1:CY:80:VAL:CG1	1:CY:185:LEU:CB	2.70	0.69
1:BS:101:ARG:HB3	1:BS:166:LEU:HD11	1.73	0.69
1:AJ:111:ILE:HG22	1:AJ:113:PRO:HD3	1.73	0.69
1:CT:63:ILE:HD12	1:CT:88:LEU:HG	1.74	0.69
1:CB:63:ILE:HD11	1:CB:89:LEU:HD23	1.75	0.69
1:CE:63:ILE:HD12	1:CE:88:LEU:HG	1.74	0.69
1:AF:253:ASP:OD1	1:AF:285:PHE:CA	2.40	0.69
1:AK:253:ASP:CG	1:AK:285:PHE:HA	2.13	0.69
1:AK:302:ASP:HB3	1:AK:305:ASN:CG	2.13	0.69
1:AP:302:ASP:HB3	1:AP:305:ASN:CG	2.13	0.69
1:AU:302:ASP:HB3	1:AU:305:ASN:CG	2.12	0.69
1:CP:80:VAL:CG1	1:CP:185:LEU:CB	2.71	0.69
1:CL:141:LEU:N	1:CL:141:LEU:HD23	2.08	0.69
1:CE:80:VAL:CG1	1:CE:185:LEU:HB3	2.23	0.69
1:CE:122:GLY:HA3	1:BM:114:MET:SD	2.33	0.69
1:BK:98:ILE:HG22	1:AS:91:ARG:NE	2.08	0.69
1:CI:100:GLN:HG2	1:CI:211:SER:OG	1.91	0.69
1:AB:314:TYR:CD1	1:AB:315:TYR:N	2.60	0.69
1:BT:101:ARG:CZ	1:BT:166:LEU:CD1	2.71	0.69
1:CF:80:VAL:CG1	1:CF:185:LEU:CB	2.71	0.69
1:CQ:63:ILE:HD12	1:CQ:88:LEU:HG	1.74	0.69
1:CP:63:ILE:HD12	1:CP:88:LEU:HG	1.72	0.69
1:AG:119:THR:HG23	1:AG:193:ASP:HB2	1.73	0.69
1:CA:151:LYS:NZ	1:BV:153:TRP:O	2.24	0.69
1:AS:299:GLY:CA	1:AS:310:ASP:O	2.39	0.69
1:AR:302:ASP:HB3	1:AR:305:ASN:CG	2.14	0.69
1:CQ:80:VAL:HG12	1:CQ:185:LEU:CB	2.21	0.69
1:AX:314:TYR:CE1	1:AX:316:SER:N	2.61	0.69
1:CN:80:VAL:CG1	1:CN:185:LEU:CB	2.71	0.69
1:BD:91:ARG:NH1	1:AG:98:ILE:HG23	66.31	0.69
1:BM:101:ARG:HB3	1:BM:166:LEU:HD11	1.73	0.69
1:AZ:68:LEU:HB2	1:AZ:195:VAL:CG2	2.23	0.69
1:AZ:119:THR:HG23	1:AZ:193:ASP:HB2	1.74	0.69
1:AP:265:ILE:CG2	1:AP:313:ALA:O	2.41	0.69

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AL:265:ILE:CG2	1:AL:313:ALA:O	2.41	0.69
1:BS:318:GLU:N	1:BS:318:GLU:OE2	2.26	0.69
1:BZ:72:THR:O	1:BZ:191:ASN:ND2	2.26	0.69
1:CW:122:GLY:O	1:CW:188:VAL:N	2.26	0.69
1:CU:80:VAL:CG1	1:CU:185:LEU:CB	2.70	0.69
1:CS:80:VAL:CG1	1:CS:185:LEU:HB3	2.23	0.69
1:CQ:99:PHE:CA	1:CQ:209:VAL:O	2.41	0.69
1:BJ:101:ARG:HB3	1:BJ:166:LEU:HD11	1.74	0.69
1:AB:68:LEU:HB2	1:AB:195:VAL:HG22	1.76	0.69
1:AK:68:LEU:HB2	1:AK:195:VAL:CG2	2.22	0.69
1:AI:265:ILE:CG2	1:AI:313:ALA:O	2.40	0.69
1:BO:72:THR:O	1:BO:191:ASN:ND2	2.26	0.69
1:CI:122:GLY:O	1:CI:188:VAL:HB	1.93	0.68
1:BN:101:ARG:CZ	1:BN:166:LEU:CD1	2.71	0.68
1:BC:91:ARG:NH1	1:AY:98:ILE:HG23	2.08	0.68
1:BU:91:ARG:NH1	1:AX:98:ILE:HG23	2.08	0.68
1:AG:265:ILE:CG2	1:AG:313:ALA:O	2.41	0.68
1:AT:68:LEU:HB2	1:AT:195:VAL:HG22	1.75	0.68
1:CI:63:ILE:HD12	1:CI:88:LEU:HG	1.75	0.68
1:AN:68:LEU:HB2	1:AN:195:VAL:HG22	1.75	0.68
1:CU:63:ILE:HD12	1:CU:88:LEU:HG	1.75	0.68
1:AX:119:THR:HG23	1:AX:193:ASP:HB2	1.75	0.68
1:AS:265:ILE:CG2	1:AS:313:ALA:O	2.41	0.68
1:AQ:253:ASP:OD1	1:AQ:285:PHE:CA	2.40	0.68
1:AC:91:ARG:HE	1:BS:98:ILE:HG22	1.58	0.68
1:CX:122:GLY:O	1:CX:188:VAL:N	2.25	0.68
1:AG:314:TYR:CD1	1:AG:315:TYR:N	2.61	0.68
1:AI:314:TYR:CD1	1:AI:315:TYR:N	2.61	0.68
1:BC:101:ARG:CZ	1:BC:166:LEU:CD1	2.71	0.68
1:AE:253:ASP:OD1	1:AE:285:PHE:CA	2.39	0.68
1:CM:62:ARG:NH1	1:BO:75:ASP:OD2	2.25	0.68
1:BE:154:GLU:OE1	1:CE:43:SER:OG	2.11	0.68
1:CV:63:ILE:HD11	1:CV:89:LEU:HD23	1.75	0.68
1:AS:302:ASP:HB3	1:AS:305:ASN:CG	2.12	0.68
1:BL:98:ILE:HG22	1:AU:91:ARG:HE	1.57	0.68
1:AH:314:TYR:CD1	1:AH:315:TYR:N	2.62	0.68
1:AJ:68:LEU:HB2	1:AJ:195:VAL:CG2	2.23	0.68
1:AH:119:THR:HG23	1:AH:193:ASP:HB2	1.74	0.68
1:AB:111:ILE:HG22	1:AB:113:PRO:HD3	1.74	0.68
1:CS:63:ILE:HD12	1:CS:88:LEU:HG	1.74	0.68
1:BA:318:GLU:OE2	1:BA:318:GLU:N	2.28	0.68

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AG:253:ASP:OD1	1:AG:285:PHE:CA	2.40	0.68
1:AQ:302:ASP:HB3	1:AQ:305:ASN:CG	2.12	0.68
1:CA:80:VAL:HG12	1:CA:185:LEU:CB	2.24	0.68
1:CD:99:PHE:CA	1:CD:209:VAL:O	2.43	0.68
1:AP:314:TYR:CD1	1:AP:315:TYR:N	2.61	0.68
1:BW:101:ARG:HB3	1:BW:166:LEU:HD11	1.75	0.68
1:CC:63:ILE:HD11	1:CC:89:LEU:HD23	1.79	0.68
1:CF:63:ILE:HD11	1:CF:89:LEU:HD23	1.75	0.68
1:AJ:265:ILE:CG2	1:AJ:313:ALA:O	2.42	0.68
1:BF:318:GLU:N	1:BF:318:GLU:OE2	2.27	0.68
1:AN:119:THR:HG23	1:AN:193:ASP:HB2	1.74	0.68
1:AD:299:GLY:CA	1:AD:310:ASP:O	2.40	0.68
1:AP:253:ASP:OD1	1:AP:285:PHE:CA	2.41	0.68
1:CG:80:VAL:HG12	1:CG:185:LEU:CB	2.22	0.68
1:CP:80:VAL:HG12	1:CP:185:LEU:CB	2.24	0.68
1:CO:141:LEU:CD2	1:CO:184:ILE:HD11	2.15	0.68
1:AC:314:TYR:CE1	1:AC:316:SER:N	2.64	0.68
1:CL:99:PHE:CA	1:CL:209:VAL:O	2.40	0.68
1:BB:101:ARG:HB3	1:BB:166:LEU:HD11	1.74	0.68
1:CG:63:ILE:HD11	1:CG:89:LEU:HD23	1.74	0.68
1:BJ:318:GLU:OE2	1:BJ:318:GLU:N	2.27	0.68
1:BW:72:THR:O	1:BW:191:ASN:ND2	2.27	0.68
1:AE:302:ASP:HB3	1:AE:305:ASN:CG	2.11	0.68
1:AH:302:ASP:HB3	1:AH:305:ASN:CG	2.13	0.68
1:CB:80:VAL:HG12	1:CB:185:LEU:CB	2.23	0.68
1:AO:314:TYR:CE1	1:AO:316:SER:N	2.61	0.68
1:AB:314:TYR:CE1	1:AB:316:SER:N	2.62	0.68
1:CH:100:GLN:HG3	1:CH:211:SER:OG	1.92	0.68
1:AK:68:LEU:HB2	1:AK:195:VAL:HG22	1.75	0.68
1:AH:111:ILE:HG22	1:AH:113:PRO:HD3	1.74	0.68
1:BX:318:GLU:OE2	1:BX:318:GLU:N	2.26	0.68
1:BG:318:GLU:N	1:BG:318:GLU:OE2	2.27	0.68
1:AV:302:ASP:HB3	1:AV:305:ASN:CG	2.12	0.68
1:CZ:122:GLY:O	1:CZ:188:VAL:HB	1.94	0.68
1:CJ:141:LEU:CD2	1:CJ:184:ILE:HD11	2.18	0.68
1:CS:100:GLN:HG3	1:CS:211:SER:OG	1.93	0.68
1:CY:99:PHE:CA	1:CY:209:VAL:O	2.42	0.68
1:CU:63:ILE:HD11	1:CU:89:LEU:HD23	1.74	0.68
1:CC:141:LEU:HD23	1:CC:141:LEU:N	2.08	0.68
1:CE:80:VAL:CG1	1:CE:185:LEU:CB	2.72	0.68
1:BA:98:ILE:HG22	1:AI:91:ARG:NE	2.09	0.68

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AN:314:TYR:CE1	1:AN:316:SER:N	2.62	0.68
1:CV:63:ILE:HD12	1:CV:88:LEU:HG	1.76	0.68
1:BR:72:THR:O	1:BR:191:ASN:ND2	2.27	0.68
1:BB:72:THR:O	1:BB:191:ASN:ND2	2.27	0.68
1:BT:318:GLU:N	1:BT:318:GLU:OE2	2.27	0.68
1:BY:318:GLU:N	1:BY:318:GLU:OE2	2.26	0.68
1:CK:38:PRO:O	1:CL:117:ALA:HB2	1.94	0.68
1:CK:141:LEU:N	1:CK:141:LEU:HD23	2.09	0.68
1:CA:141:LEU:N	1:CA:141:LEU:HD23	2.08	0.68
1:CQ:122:GLY:O	1:CQ:188:VAL:HB	1.94	0.68
1:CA:151:LYS:NZ	1:BI:153:TRP:O	127.41	0.68
1:AA:62:ARG:HG2	1:AA:62:ARG:HH11	1.69	0.68
1:AT:265:ILE:CG2	1:AT:313:ALA:O	2.42	0.68
1:BD:318:GLU:OE2	1:BD:318:GLU:N	2.27	0.68
1:CN:63:ILE:HD12	1:CN:88:LEU:HG	1.75	0.68
1:AW:253:ASP:CG	1:AW:285:PHE:HA	2.14	0.68
1:AY:253:ASP:OD1	1:AY:285:PHE:CA	2.41	0.68
1:AI:302:ASP:HB3	1:AI:305:ASN:CG	2.13	0.68
1:CF:122:GLY:O	1:CF:188:VAL:N	2.27	0.68
1:AI:314:TYR:CE1	1:AI:316:SER:N	2.61	0.68
1:CT:99:PHE:CA	1:CT:209:VAL:O	2.42	0.68
1:CJ:80:VAL:CG1	1:CJ:185:LEU:CB	2.72	0.68
1:CX:99:PHE:CA	1:CX:209:VAL:O	2.42	0.68
1:AT:111:ILE:HG22	1:AT:113:PRO:HD3	1.73	0.68
1:AO:68:LEU:HB2	1:AO:195:VAL:HG22	1.75	0.68
1:CM:80:VAL:HG12	1:CM:185:LEU:CB	2.24	0.67
1:CB:122:GLY:HA3	1:BY:114:MET:SD	2.34	0.67
1:CR:99:PHE:CA	1:CR:209:VAL:O	2.43	0.67
1:CS:80:VAL:CG1	1:CS:185:LEU:CB	2.71	0.67
1:AB:68:LEU:HB2	1:AB:195:VAL:CG2	2.26	0.67
1:AR:68:LEU:HB2	1:AR:195:VAL:HG22	1.76	0.67
1:CP:199:VAL:O	1:CP:199:VAL:HG13	1.94	0.67
1:BZ:318:GLU:N	1:BZ:318:GLU:OE2	2.26	0.67
1:CC:151:LYS:NZ	1:BS:153:TRP:O	2.27	0.67
1:AU:253:ASP:CG	1:AU:285:PHE:HA	2.14	0.67
1:AI:141:LEU:O	1:AI:144:THR:CG2	2.38	0.67
1:BV:101:ARG:HB3	1:BV:166:LEU:HD11	1.75	0.67
1:CB:63:ILE:HD12	1:CB:88:LEU:HG	1.76	0.67
1:AD:68:LEU:HB2	1:AD:195:VAL:HG22	1.76	0.67
1:CC:199:VAL:O	1:CC:199:VAL:HG13	1.95	0.67
1:AM:265:ILE:CG2	1:AM:313:ALA:O	2.41	0.67

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BN:72:THR:O	1:BN:191:ASN:ND2	2.27	0.67
1:CF:141:LEU:CD2	1:CF:184:ILE:HD11	2.19	0.67
1:CI:122:GLY:O	1:CI:188:VAL:N	2.26	0.67
1:AA:314:TYR:CE1	1:AA:316:SER:N	2.62	0.67
1:AH:314:TYR:CE1	1:AH:316:SER:N	2.61	0.67
1:CV:80:VAL:CG1	1:CV:185:LEU:HB3	2.24	0.67
1:CN:122:GLY:O	1:CN:188:VAL:N	2.27	0.67
1:AJ:119:THR:O	1:AJ:192:THR:HB	1.95	0.67
1:AR:265:ILE:CG2	1:AR:313:ALA:O	2.43	0.67
1:CR:200:LEU:HD13	1:CT:45:VAL:HG23	1.75	0.67
1:BB:318:GLU:OE2	1:BB:318:GLU:N	2.28	0.67
1:BE:318:GLU:OE2	1:BE:318:GLU:N	2.27	0.67
1:AM:119:THR:HG23	1:AM:193:ASP:HB2	1.75	0.67
1:CD:151:LYS:NZ	1:BF:153:TRP:O	2.28	0.67
1:BL:101:ARG:CZ	1:BL:166:LEU:CD1	2.73	0.67
1:AB:98:ILE:HG23	1:BO:91:ARG:NH1	122.36	0.67
1:AE:253:ASP:CG	1:AE:285:PHE:HA	2.14	0.67
1:BC:318:GLU:OE2	1:BC:318:GLU:N	2.27	0.67
1:BQ:318:GLU:N	1:BQ:318:GLU:OE2	2.27	0.67
1:AQ:314:TYR:CE1	1:AQ:316:SER:N	2.63	0.67
1:CV:80:VAL:CG1	1:CV:185:LEU:CB	2.73	0.67
1:AY:314:TYR:CD1	1:AY:315:TYR:N	2.62	0.67
1:BW:101:ARG:CZ	1:BW:166:LEU:CD1	2.72	0.67
1:BP:72:THR:O	1:BP:191:ASN:ND2	2.28	0.67
1:CJ:63:ILE:HD11	1:CJ:89:LEU:HD23	1.77	0.67
1:AE:119:THR:HG23	1:AE:193:ASP:HB2	1.76	0.67
1:AY:299:GLY:CA	1:AY:310:ASP:O	2.41	0.67
1:CY:80:VAL:HG12	1:CY:185:LEU:CB	2.25	0.67
1:BL:98:ILE:HG22	1:AU:91:ARG:NE	2.08	0.67
1:CJ:99:PHE:HA	1:CJ:209:VAL:O	1.95	0.67
1:AA:98:ILE:HG23	1:BV:91:ARG:NH1	2.08	0.67
1:CF:34:ARG:HD3	1:CY:43:SER:O	1.95	0.67
1:AY:265:ILE:CG2	1:AY:313:ALA:O	2.43	0.67
1:AM:62:ARG:HH11	1:AM:62:ARG:HG2	1.60	0.67
1:CG:199:VAL:HG13	1:CG:199:VAL:O	1.94	0.67
1:CX:80:VAL:CG1	1:CX:185:LEU:CB	2.73	0.67
1:AE:314:TYR:CE1	1:AE:316:SER:N	2.62	0.67
1:CA:99:PHE:CA	1:CA:209:VAL:O	2.44	0.67
1:BU:101:ARG:HB3	1:BU:166:LEU:HD11	1.74	0.67
1:BQ:101:ARG:NH1	1:BQ:166:LEU:HD12	2.10	0.67
1:AG:68:LEU:HB2	1:AG:195:VAL:CG2	2.25	0.67

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AS:111:ILE:HG22	1:AS:113:PRO:HD3	1.75	0.67
1:BP:139:ASP:HA	1:BP:142:GLN:HG2	1.77	0.67
1:BN:318:GLU:N	1:BN:318:GLU:OE2	2.28	0.67
1:BM:72:THR:O	1:BM:191:ASN:ND2	2.28	0.67
1:AC:122:GLY:HA3	1:AM:114:MET:SD	241.38	0.67
1:AO:253:ASP:CG	1:AO:285:PHE:HA	2.15	0.67
1:CC:80:VAL:CG1	1:CC:185:LEU:CB	2.72	0.67
1:CU:80:VAL:HG12	1:CU:185:LEU:CB	2.23	0.67
1:AC:91:ARG:NE	1:BS:98:ILE:HG22	2.10	0.67
1:AB:91:ARG:NE	1:BY:98:ILE:HG22	2.10	0.67
1:BY:130:ASP:HB2	1:CY:100:GLN:HE22	1.58	0.67
1:BO:101:ARG:HB3	1:BO:166:LEU:HD11	1.77	0.67
1:AT:119:THR:HG23	1:AT:193:ASP:HB2	1.74	0.67
1:BZ:139:ASP:HA	1:BZ:142:GLN:HG2	1.76	0.67
1:BK:318:GLU:OE2	1:BK:318:GLU:N	2.27	0.67
1:BO:318:GLU:N	1:BO:318:GLU:OE2	2.27	0.67
1:BG:72:THR:O	1:BG:191:ASN:ND2	2.28	0.67
1:AW:302:ASP:CB	1:AW:305:ASN:CG	2.64	0.67
1:AE:141:LEU:O	1:AE:144:THR:CG2	2.41	0.67
1:AD:91:ARG:NE	1:BF:98:ILE:HG22	2.10	0.67
1:AY:314:TYR:CE1	1:AY:316:SER:N	2.63	0.67
1:BA:101:ARG:NH1	1:BA:166:LEU:HD12	2.09	0.67
1:BY:101:ARG:CZ	1:BY:166:LEU:CD1	2.73	0.67
1:BB:91:ARG:NH1	1:AF:98:ILE:HG23	67.16	0.67
1:CM:34:ARG:HD3	1:CW:43:SER:O	1.95	0.67
1:AO:119:THR:HG23	1:AO:193:ASP:HB2	1.76	0.67
1:AJ:314:TYR:CE1	1:AJ:316:SER:N	2.63	0.67
1:CD:63:ILE:HD12	1:CD:88:LEU:HG	1.77	0.67
1:BS:72:THR:O	1:BS:191:ASN:ND2	2.28	0.67
1:AL:119:THR:HG23	1:AL:193:ASP:HB2	1.77	0.67
1:BH:318:GLU:OE2	1:BH:318:GLU:N	2.28	0.67
1:CK:199:VAL:O	1:CK:199:VAL:HG13	1.94	0.67
1:BC:153:TRP:O	1:CM:151:LYS:NZ	212.26	0.67
1:AE:302:ASP:CB	1:AE:305:ASN:CG	2.64	0.66
1:CN:122:GLY:O	1:CN:188:VAL:HB	1.96	0.66
1:BK:101:ARG:CZ	1:BK:166:LEU:CD1	2.73	0.66
1:BI:101:ARG:CZ	1:BI:166:LEU:CD1	2.72	0.66
1:CN:63:ILE:HD11	1:CN:89:LEU:HD23	1.76	0.66
1:BD:139:ASP:HA	1:BD:142:GLN:HG2	1.75	0.66
1:AX:253:ASP:CG	1:AX:285:PHE:HA	2.16	0.66
1:AS:314:TYR:CE1	1:AS:316:SER:N	2.63	0.66

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CH:99:PHE:CA	1:CH:209:VAL:O	2.43	0.66
1:CZ:99:PHE:CA	1:CZ:209:VAL:O	2.44	0.66
1:BJ:101:ARG:CZ	1:BJ:166:LEU:CD1	2.71	0.66
1:CV:100:GLN:HG3	1:CV:211:SER:OG	1.93	0.66
1:CX:63:ILE:HD11	1:CX:89:LEU:HD23	1.76	0.66
1:CK:38:PRO:O	1:CL:117:ALA:CB	2.43	0.66
1:AD:68:LEU:HB2	1:AD:195:VAL:CG2	2.30	0.66
1:BT:72:THR:O	1:BT:191:ASN:ND2	2.28	0.66
1:AV:119:THR:HG23	1:AV:193:ASP:HB2	1.76	0.66
1:AX:314:TYR:HE1	1:AX:316:SER:HA	1.61	0.66
1:BA:101:ARG:NH1	1:BA:166:LEU:CD1	2.57	0.66
1:BW:130:ASP:HB2	1:CW:100:GLN:NE2	2.11	0.66
1:BV:101:ARG:CZ	1:BV:166:LEU:CD1	2.74	0.66
1:AB:98:ILE:HG23	1:BY:91:ARG:NH1	2.10	0.66
1:BK:91:ARG:NH1	1:AS:98:ILE:HG23	2.08	0.66
1:BB:139:ASP:HA	1:BB:142:GLN:HG2	1.79	0.66
1:AQ:119:THR:HG23	1:AQ:193:ASP:HB2	1.76	0.66
1:BT:139:ASP:HA	1:BT:142:GLN:HG2	1.76	0.66
1:AP:119:THR:O	1:AP:192:THR:HB	1.96	0.66
1:AA:302:ASP:CB	1:AA:305:ASN:CG	2.64	0.66
1:CT:80:VAL:HG12	1:CT:185:LEU:CB	2.23	0.66
1:BC:98:ILE:HG22	1:AM:91:ARG:NH2	214.40	0.66
1:BG:98:ILE:HG22	1:AP:91:ARG:HE	1.60	0.66
1:BU:101:ARG:CZ	1:BU:166:LEU:CD1	2.73	0.66
1:BD:101:ARG:NH1	1:BD:166:LEU:HD12	2.13	0.66
1:BF:101:ARG:HB3	1:BF:166:LEU:HD11	1.76	0.66
1:CO:63:ILE:HD11	1:CO:89:LEU:HD23	1.76	0.66
1:AP:119:THR:HG23	1:AP:193:ASP:HB2	1.76	0.66
1:BV:72:THR:O	1:BV:191:ASN:ND2	2.27	0.66
1:BU:318:GLU:OE2	1:BU:318:GLU:N	2.28	0.66
1:BV:139:ASP:HA	1:BV:142:GLN:HG2	1.78	0.66
1:AC:253:ASP:CG	1:AC:285:PHE:HA	2.15	0.66
1:AX:302:ASP:CB	1:AX:305:ASN:CG	2.64	0.66
1:AN:302:ASP:CB	1:AN:305:ASN:CG	2.64	0.66
1:AA:91:ARG:NE	1:BV:98:ILE:HG22	2.09	0.66
1:BC:98:ILE:HG22	1:AM:91:ARG:NE	216.64	0.66
1:BC:98:ILE:HG22	1:AY:91:ARG:NE	2.10	0.66
1:CP:99:PHE:CA	1:CP:209:VAL:O	2.43	0.66
1:CY:100:GLN:HG3	1:CY:211:SER:OG	1.96	0.66
1:CB:43:SER:HA	1:CF:112:GLN:NE2	2.11	0.66
1:CK:63:ILE:HD11	1:CK:89:LEU:HD23	1.77	0.66

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CM:63:ILE:HD12	1:CM:88:LEU:HG	1.76	0.66
1:CL:63:ILE:HD11	1:CL:89:LEU:HD23	1.77	0.66
1:AB:253:ASP:CG	1:AB:285:PHE:HA	2.15	0.66
1:AC:302:ASP:CB	1:AC:305:ASN:CG	2.65	0.66
1:AP:302:ASP:CB	1:AP:305:ASN:CG	2.64	0.66
1:AJ:302:ASP:CB	1:AJ:305:ASN:CG	2.64	0.66
1:CL:122:GLY:O	1:CL:188:VAL:N	2.28	0.66
1:CU:141:LEU:CD2	1:CU:184:ILE:HD11	2.19	0.66
1:AG:314:TYR:CE1	1:AG:316:SER:N	2.62	0.66
1:AD:314:TYR:CE1	1:AD:316:SER:N	2.64	0.66
1:AV:106:THR:HA	1:AV:162:TYR:OH	1.95	0.66
1:BQ:68:LEU:HD23	1:BQ:195:VAL:HG22	1.76	0.66
1:AM:68:LEU:HB2	1:AM:195:VAL:HG22	1.76	0.66
1:AC:68:LEU:HB2	1:AC:195:VAL:HG22	1.79	0.66
1:BW:318:GLU:OE2	1:BW:318:GLU:N	2.29	0.66
1:CA:199:VAL:HG13	1:CA:199:VAL:O	1.95	0.66
1:AM:253:ASP:CG	1:AM:285:PHE:HA	2.15	0.66
1:AK:302:ASP:CB	1:AK:305:ASN:CG	2.64	0.66
1:AD:302:ASP:CB	1:AD:305:ASN:CG	2.64	0.66
1:AO:302:ASP:CB	1:AO:305:ASN:CG	2.64	0.66
1:AV:302:ASP:CB	1:AV:305:ASN:CG	2.64	0.66
1:AL:302:ASP:HB3	1:AL:305:ASN:CG	2.14	0.66
1:AP:314:TYR:CE1	1:AP:316:SER:N	2.63	0.66
1:BH:101:ARG:NH1	1:BH:166:LEU:HD12	2.10	0.66
1:CK:99:PHE:CA	1:CK:209:VAL:O	2.44	0.66
1:CW:99:PHE:CA	1:CW:209:VAL:O	2.43	0.66
1:AF:68:LEU:HB2	1:AF:195:VAL:CG2	2.26	0.66
1:AN:68:LEU:HB2	1:AN:195:VAL:CG2	2.26	0.66
1:CJ:63:ILE:HD12	1:CJ:88:LEU:HG	1.76	0.66
1:CH:63:ILE:HD12	1:CH:88:LEU:HG	1.76	0.66
1:BC:72:THR:O	1:BC:191:ASN:ND2	2.29	0.66
1:BW:139:ASP:HA	1:BW:142:GLN:HG2	1.76	0.66
1:AQ:68:LEU:HB2	1:AQ:195:VAL:HG22	1.77	0.66
1:AG:302:ASP:CB	1:AG:305:ASN:CG	2.64	0.66
1:AQ:302:ASP:CB	1:AQ:305:ASN:CG	2.64	0.66
1:CC:80:VAL:HG12	1:CC:185:LEU:CB	2.26	0.66
1:CV:99:PHE:CA	1:CV:209:VAL:O	2.43	0.66
1:CI:63:ILE:HD11	1:CI:89:LEU:HD23	1.78	0.66
1:AV:68:LEU:HB2	1:AV:195:VAL:HG22	1.76	0.66
1:BM:318:GLU:OE2	1:BM:318:GLU:N	2.28	0.66
1:AN:253:ASP:CG	1:AN:285:PHE:HA	2.15	0.66

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AB:302:ASP:CB	1:AB:305:ASN:CG	2.65	0.66
1:CL:80:VAL:HG12	1:CL:185:LEU:CB	2.22	0.66
1:AT:314:TYR:CE1	1:AT:316:SER:N	2.64	0.66
1:CN:99:PHE:CA	1:CN:209:VAL:O	2.43	0.66
1:CG:99:PHE:CA	1:CG:209:VAL:O	2.43	0.66
1:BC:101:ARG:NH1	1:BC:166:LEU:HD12	2.10	0.66
1:BF:101:ARG:CZ	1:BF:166:LEU:CD1	2.73	0.66
1:CP:63:ILE:HD11	1:CP:89:LEU:HD23	1.77	0.66
1:AU:119:THR:HG23	1:AU:193:ASP:HB2	1.78	0.66
1:CD:45:VAL:HG23	1:CW:200:LEU:HD13	37.30	0.66
1:BB:316:SER:HB2	1:BB:319:GLN:OE1	1.95	0.66
1:BC:58:SER:HB3	1:BC:204:SER:HB3	1.80	0.66
1:AF:253:ASP:CG	1:AF:285:PHE:HA	2.16	0.66
1:AT:302:ASP:CB	1:AT:305:ASN:CG	2.64	0.66
1:AR:302:ASP:CB	1:AR:305:ASN:CG	2.64	0.66
1:AZ:302:ASP:CB	1:AZ:305:ASN:CG	2.65	0.66
1:AX:141:LEU:O	1:AX:144:THR:CG2	2.37	0.66
1:AN:141:LEU:O	1:AN:144:THR:CG2	2.41	0.66
1:BH:101:ARG:CZ	1:BH:166:LEU:CD1	2.72	0.66
1:BU:101:ARG:NH1	1:BU:166:LEU:HD12	2.09	0.66
1:BD:101:ARG:CZ	1:BD:166:LEU:CD1	2.73	0.66
1:BD:91:ARG:NH1	1:AW:98:ILE:HG23	2.10	0.66
1:BH:139:ASP:HA	1:BH:142:GLN:HG2	1.77	0.66
1:AO:68:LEU:HB2	1:AO:195:VAL:CG2	2.26	0.66
1:AI:119:THR:HG23	1:AI:193:ASP:HB2	1.77	0.66
1:CC:109:PHE:HB2	1:CC:158:VAL:CG1	2.26	0.66
1:AF:302:ASP:CB	1:AF:305:ASN:CG	2.64	0.65
1:CB:141:LEU:HD23	1:CB:141:LEU:N	2.14	0.65
1:AF:314:TYR:CE1	1:AF:316:SER:N	2.62	0.65
1:BI:101:ARG:NH1	1:BI:166:LEU:HD12	2.11	0.65
1:BL:101:ARG:NH1	1:BL:166:LEU:HD12	2.10	0.65
1:AB:106:THR:HA	1:AB:162:TYR:OH	1.97	0.65
1:CA:58:SER:HA	1:CA:203:TRP:CZ3	2.35	0.65
1:CZ:63:ILE:HD11	1:CZ:89:LEU:HD23	1.78	0.65
1:BL:318:GLU:N	1:BL:318:GLU:OE2	2.29	0.65
1:AU:302:ASP:CB	1:AU:305:ASN:CG	2.64	0.65
1:AY:302:ASP:CB	1:AY:305:ASN:CG	2.64	0.65
1:CM:122:GLY:O	1:CM:188:VAL:HB	1.97	0.65
1:CP:141:LEU:HD23	1:CP:141:LEU:N	2.10	0.65
1:CC:122:GLY:O	1:CC:188:VAL:HB	2.01	0.65
1:BD:98:ILE:HG22	1:AG:91:ARG:NE	89.84	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CC:99:PHE:CA	1:CC:209:VAL:O	2.42	0.65
1:CN:80:VAL:HG12	1:CN:185:LEU:CB	2.26	0.65
1:AA:106:THR:HA	1:AA:162:TYR:OH	1.99	0.65
1:AM:68:LEU:HB2	1:AM:195:VAL:CG2	2.26	0.65
1:BR:139:ASP:HA	1:BR:142:GLN:HG2	1.76	0.65
1:AE:68:LEU:HB2	1:AE:195:VAL:HG22	1.76	0.65
1:AK:265:ILE:CG2	1:AK:313:ALA:O	2.44	0.65
1:BP:318:GLU:OE2	1:BP:318:GLU:N	2.29	0.65
1:AS:302:ASP:CB	1:AS:305:ASN:CG	2.64	0.65
1:CB:122:GLY:HA3	1:BO:114:MET:SD	140.11	0.65
1:CV:141:LEU:HD23	1:CV:141:LEU:N	2.10	0.65
1:CF:122:GLY:O	1:CF:188:VAL:HB	1.95	0.65
1:AL:314:TYR:CE1	1:AL:316:SER:N	2.65	0.65
1:BZ:101:ARG:NH1	1:BZ:166:LEU:HD12	2.11	0.65
1:AD:106:THR:HA	1:AD:162:TYR:OH	1.98	0.65
1:CV:43:SER:HA	1:CZ:112:GLN:NE2	2.11	0.65
1:CL:63:ILE:HD12	1:CL:88:LEU:HG	1.78	0.65
1:BX:139:ASP:HA	1:BX:142:GLN:HG2	1.78	0.65
1:BY:176:ARG:HD2	1:CY:168:TRP:CE2	2.31	0.65
1:AH:302:ASP:CB	1:AH:305:ASN:CG	2.65	0.65
1:CD:122:GLY:O	1:CD:188:VAL:HB	1.97	0.65
1:CK:122:GLY:O	1:CK:188:VAL:N	2.28	0.65
1:BQ:101:ARG:CZ	1:BQ:166:LEU:CD1	2.75	0.65
1:BQ:101:ARG:NH1	1:BQ:166:LEU:CD1	2.60	0.65
1:BV:111:ILE:HG21	1:BV:123:TYR:OH	1.96	0.65
1:AA:68:LEU:HB2	1:AA:195:VAL:CG2	2.29	0.65
1:AT:68:LEU:HB2	1:AT:195:VAL:CG2	2.25	0.65
1:BO:316:SER:HB2	1:BO:319:GLN:OE1	1.95	0.65
1:AW:68:LEU:HB2	1:AW:195:VAL:HG22	1.77	0.65
1:CB:199:VAL:O	1:CB:199:VAL:HG13	1.96	0.65
1:BR:318:GLU:OE2	1:BR:318:GLU:N	2.28	0.65
1:AH:68:LEU:HB2	1:AH:195:VAL:HG22	1.76	0.65
1:AU:314:TYR:HE1	1:AU:316:SER:HA	1.61	0.65
1:BS:101:ARG:NH1	1:BS:166:LEU:HD12	2.12	0.65
1:BB:91:ARG:NH1	1:AK:98:ILE:HG23	2.10	0.65
1:AM:106:THR:HA	1:AM:162:TYR:OH	1.96	0.65
1:AZ:106:THR:HA	1:AZ:162:TYR:OH	1.95	0.65
1:AC:116:PRO:HB3	1:AS:118:ASN:O	1.96	0.65
1:AV:68:LEU:HB2	1:AV:195:VAL:CG2	2.25	0.65
1:CT:199:VAL:HG13	1:CT:199:VAL:O	1.96	0.65
1:AD:253:ASP:CG	1:AD:285:PHE:HA	2.15	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AM:302:ASP:CB	1:AM:305:ASN:CG	2.64	0.65
1:CI:141:LEU:HD23	1:CI:141:LEU:N	2.10	0.65
1:CQ:141:LEU:N	1:CQ:141:LEU:HD23	2.12	0.65
1:AM:141:LEU:O	1:AM:144:THR:CG2	2.41	0.65
1:BD:98:ILE:HG22	1:AG:91:ARG:HE	89.16	0.65
1:CM:99:PHE:CA	1:CM:209:VAL:O	2.45	0.65
1:CF:80:VAL:HG12	1:CF:185:LEU:CB	2.25	0.65
1:BY:101:ARG:NH1	1:BY:166:LEU:HD12	2.11	0.65
1:BB:101:ARG:CZ	1:BB:166:LEU:CD1	2.75	0.65
1:BO:101:ARG:CZ	1:BO:166:LEU:CD1	2.74	0.65
1:CS:63:ILE:HD11	1:CS:89:LEU:HD23	1.78	0.65
1:BU:139:ASP:HA	1:BU:142:GLN:HG2	1.77	0.65
1:AQ:253:ASP:CG	1:AQ:285:PHE:HA	2.14	0.65
1:CQ:122:GLY:C	1:CQ:188:VAL:HB	2.16	0.65
1:AZ:314:TYR:CE1	1:AZ:316:SER:N	2.65	0.65
1:BL:130:ASP:HB2	1:CL:100:GLN:NE2	2.12	0.65
1:BX:101:ARG:CZ	1:BX:166:LEU:CD1	2.74	0.65
1:AW:106:THR:HA	1:AW:162:TYR:OH	1.97	0.65
1:CB:34:ARG:HD3	1:CL:43:SER:O	24.03	0.65
1:BC:139:ASP:HA	1:BC:142:GLN:HG2	1.78	0.65
1:AB:118:ASN:O	1:AK:116:PRO:HB3	1.96	0.65
1:CY:63:ILE:HD11	1:CY:89:LEU:HD23	1.77	0.65
1:BK:139:ASP:HA	1:BK:142:GLN:HG2	1.78	0.65
1:BO:61:SER:CB	1:BO:90:PRO:HD2	2.22	0.65
1:BC:101:ARG:NH1	1:BC:166:LEU:CD1	2.60	0.65
1:AY:119:THR:O	1:AY:192:THR:HB	1.97	0.65
1:AI:68:LEU:HB2	1:AI:195:VAL:HG22	1.78	0.65
1:CT:58:SER:HA	1:CT:203:TRP:CZ3	2.32	0.65
1:CA:109:PHE:HB2	1:CA:158:VAL:CG1	2.27	0.65
1:AV:253:ASP:CG	1:AV:285:PHE:HA	2.15	0.65
1:AL:302:ASP:CB	1:AL:305:ASN:CG	2.65	0.65
1:CJ:141:LEU:N	1:CJ:141:LEU:HD23	2.10	0.65
1:AB:314:TYR:HE1	1:AB:316:SER:HA	1.61	0.65
1:BL:101:ARG:NH1	1:BL:166:LEU:CD1	2.60	0.65
1:CK:112:GLN:NE2	1:CL:43:SER:HA	2.11	0.65
1:CJ:58:SER:HA	1:CJ:203:TRP:CZ3	2.32	0.65
1:BI:72:THR:O	1:BI:191:ASN:ND2	2.29	0.65
1:BG:139:ASP:HA	1:BG:142:GLN:HG2	1.78	0.65
1:BD:58:SER:HB3	1:BD:204:SER:HB3	1.79	0.65
1:AP:63:ILE:HB	1:AP:199:VAL:HG13	1.79	0.65
1:CP:111:ILE:O	1:CP:198:SER:O	2.15	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AI:302:ASP:CB	1:AI:305:ASN:ND2	2.60	0.65
1:AL:144:THR:HG23	1:AL:147:ALA:HB2	1.79	0.65
1:AO:314:TYR:HE1	1:AO:316:SER:HA	1.61	0.65
1:AC:314:TYR:HE1	1:AC:316:SER:HA	1.63	0.65
1:BR:101:ARG:NH1	1:BR:166:LEU:HD12	2.11	0.65
1:BA:80:VAL:HG13	1:BA:185:LEU:HB3	1.83	0.65
1:BD:176:ARG:HD2	1:CD:168:TRP:CE2	2.32	0.65
1:BL:72:THR:O	1:BL:191:ASN:ND2	2.29	0.65
1:CA:111:ILE:O	1:CA:198:SER:O	2.19	0.65
1:AL:253:ASP:CG	1:AL:285:PHE:HA	2.16	0.64
1:AI:302:ASP:CB	1:AI:305:ASN:CG	2.65	0.64
1:CU:141:LEU:N	1:CU:141:LEU:HD23	2.09	0.64
1:CA:122:GLY:C	1:CA:188:VAL:HB	2.17	0.64
1:AM:314:TYR:CD1	1:AM:315:TYR:C	2.70	0.64
1:AX:314:TYR:CD1	1:AX:315:TYR:C	2.70	0.64
1:AQ:314:TYR:HE1	1:AQ:316:SER:HA	1.62	0.64
1:CB:99:PHE:CA	1:CB:209:VAL:O	2.44	0.64
1:BE:101:ARG:NH1	1:BE:166:LEU:HD12	2.12	0.64
1:AA:119:THR:O	1:AA:192:THR:HB	2.07	0.64
1:CH:63:ILE:HD11	1:CH:89:LEU:HD23	1.78	0.64
1:BU:72:THR:O	1:BU:191:ASN:ND2	2.31	0.64
1:CI:163:THR:HG21	1:CI:167:LEU:HD11	1.79	0.64
1:BT:130:ASP:HB2	1:CT:100:GLN:NE2	2.12	0.64
1:AH:106:THR:HA	1:AH:162:TYR:OH	1.97	0.64
1:AR:106:THR:HA	1:AR:162:TYR:OH	1.98	0.64
1:AQ:106:THR:HA	1:AQ:162:TYR:OH	1.97	0.64
1:AR:68:LEU:HB2	1:AR:195:VAL:CG2	2.28	0.64
1:AE:119:THR:O	1:AE:192:THR:HB	1.97	0.64
1:CX:111:ILE:O	1:CX:198:SER:O	2.15	0.64
1:BG:316:SER:HB2	1:BG:319:GLN:OE1	1.98	0.64
1:BJ:58:SER:HB3	1:BJ:204:SER:HB3	1.80	0.64
1:AA:253:ASP:CG	1:AA:285:PHE:HA	2.15	0.64
1:AD:302:ASP:CB	1:AD:305:ASN:ND2	2.61	0.64
1:CW:122:GLY:O	1:CW:188:VAL:HB	1.97	0.64
1:CE:141:LEU:N	1:CE:141:LEU:HD23	2.11	0.64
1:BP:101:ARG:NH1	1:BP:166:LEU:HD12	2.10	0.64
1:CD:34:ARG:CD	1:CD:43:SER:O	21.94	0.64
1:CZ:63:ILE:HD12	1:CZ:88:LEU:HG	1.77	0.64
1:BN:139:ASP:HA	1:BN:142:GLN:HG2	1.78	0.64
1:AU:68:LEU:HB2	1:AU:195:VAL:HG22	1.78	0.64
1:CQ:111:ILE:O	1:CQ:198:SER:O	2.16	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BS:139:ASP:HA	1:BS:142:GLN:HG2	1.78	0.64
1:AF:62:ARG:HH11	1:AF:62:ARG:HG2	1.63	0.64
1:CF:199:VAL:O	1:CF:199:VAL:HG13	1.96	0.64
1:BA:139:ASP:HA	1:BA:142:GLN:HG2	1.78	0.64
1:CD:111:ILE:O	1:CD:198:SER:O	2.22	0.64
1:CM:111:ILE:O	1:CM:198:SER:O	2.15	0.64
1:AJ:253:ASP:CG	1:AJ:285:PHE:HA	2.15	0.64
1:AY:302:ASP:CB	1:AY:305:ASN:ND2	2.60	0.64
1:AD:91:ARG:HE	1:BF:98:ILE:HG22	1.62	0.64
1:AV:314:TYR:CE1	1:AV:316:SER:N	2.64	0.64
1:BB:130:ASP:HB2	1:CB:100:GLN:NE2	2.13	0.64
1:CF:99:PHE:CA	1:CF:209:VAL:O	2.45	0.64
1:CE:99:PHE:CA	1:CE:209:VAL:O	2.44	0.64
1:BP:101:ARG:CZ	1:BP:166:LEU:CD1	2.74	0.64
1:AY:106:THR:HA	1:AY:162:TYR:OH	1.98	0.64
1:AU:106:THR:HA	1:AU:162:TYR:OH	1.98	0.64
1:CO:111:ILE:O	1:CO:198:SER:O	2.15	0.64
1:AY:62:ARG:HH11	1:AY:62:ARG:HG2	1.62	0.64
1:CX:199:VAL:HG13	1:CX:199:VAL:O	1.97	0.64
1:AR:119:THR:HG23	1:AR:193:ASP:HB2	1.80	0.64
1:AR:253:ASP:CG	1:AR:285:PHE:HA	2.16	0.64
1:AP:302:ASP:CB	1:AP:305:ASN:ND2	2.60	0.64
1:BR:130:ASP:HB2	1:CR:100:GLN:NE2	2.13	0.64
1:CI:99:PHE:CA	1:CI:209:VAL:O	2.45	0.64
1:AB:314:TYR:CD1	1:AB:315:TYR:C	2.71	0.64
1:BJ:101:ARG:NH1	1:BJ:166:LEU:CD1	2.60	0.64
1:AT:106:THR:HA	1:AT:162:TYR:OH	1.98	0.64
1:AC:106:THR:HA	1:AC:162:TYR:OH	1.98	0.64
1:AS:106:THR:HA	1:AS:162:TYR:OH	1.97	0.64
1:AM:302:ASP:CB	1:AM:305:ASN:ND2	2.60	0.64
1:CH:141:LEU:HD23	1:CH:141:LEU:N	2.11	0.64
1:CJ:122:GLY:HA3	1:BR:114:MET:SD	2.38	0.64
1:BZ:130:ASP:HB2	1:CZ:100:GLN:NE2	2.13	0.64
1:BJ:101:ARG:NH1	1:BJ:166:LEU:HD12	2.12	0.64
1:AN:62:ARG:HH11	1:AN:62:ARG:HG2	1.62	0.64
1:AK:302:ASP:CB	1:AK:305:ASN:ND2	2.61	0.64
1:CA:122:GLY:HA3	1:BI:114:MET:SD	121.52	0.64
1:AA:314:TYR:CD1	1:AA:315:TYR:C	2.71	0.64
1:CS:80:VAL:HG12	1:CS:185:LEU:CB	2.26	0.64
1:AI:314:TYR:CD1	1:AI:315:TYR:C	2.71	0.64
1:AN:314:TYR:HE1	1:AN:316:SER:HA	1.62	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BR:101:ARG:CZ	1:BR:166:LEU:CD1	2.75	0.64
1:BM:101:ARG:CZ	1:BM:166:LEU:CD1	2.75	0.64
1:CC:43:SER:HA	1:CJ:112:GLN:NE2	2.12	0.64
1:AK:106:THR:HA	1:AK:162:TYR:OH	1.97	0.64
1:CD:38:PRO:O	1:CW:117:ALA:HB2	8.67	0.64
1:BY:72:THR:O	1:BY:191:ASN:ND2	2.30	0.64
1:AS:253:ASP:CG	1:AS:285:PHE:HA	2.15	0.64
1:AG:302:ASP:CB	1:AG:305:ASN:ND2	2.60	0.64
1:CS:141:LEU:CD2	1:CS:184:ILE:HD11	2.20	0.64
1:BD:130:ASP:HB2	1:CD:100:GLN:NE2	2.13	0.64
1:BH:101:ARG:NH1	1:BH:166:LEU:CD1	2.60	0.64
1:BU:101:ARG:NH1	1:BU:166:LEU:CD1	2.61	0.64
1:BP:101:ARG:NH1	1:BP:166:LEU:CD1	2.60	0.64
1:BB:101:ARG:NH1	1:BB:166:LEU:CD1	2.61	0.64
1:BZ:101:ARG:CZ	1:BZ:166:LEU:CD1	2.75	0.64
1:CK:58:SER:HA	1:CK:203:TRP:CZ3	2.32	0.64
1:CB:58:SER:HA	1:CB:203:TRP:CZ3	2.33	0.64
1:BJ:139:ASP:HA	1:BJ:142:GLN:HG2	1.80	0.64
1:CD:199:VAL:O	1:CD:199:VAL:HG13	2.03	0.64
1:BM:316:SER:HB2	1:BM:319:GLN:OE1	1.98	0.64
1:AA:302:ASP:CB	1:AA:305:ASN:ND2	2.60	0.64
1:AH:302:ASP:CB	1:AH:305:ASN:ND2	2.60	0.64
1:CT:141:LEU:N	1:CT:141:LEU:HD23	2.12	0.64
1:BD:98:ILE:CG2	1:AW:91:ARG:NE	2.60	0.64
1:AM:314:TYR:HE1	1:AM:316:SER:HA	1.61	0.64
1:AA:314:TYR:HE1	1:AA:316:SER:HA	1.62	0.64
1:BI:101:ARG:NH1	1:BI:166:LEU:CD1	2.60	0.64
1:BN:101:ARG:NH1	1:BN:166:LEU:HD12	2.13	0.64
1:AA:98:ILE:HG23	1:BI:91:ARG:NH1	79.21	0.64
1:AE:106:THR:HA	1:AE:162:TYR:OH	1.98	0.64
1:CR:63:ILE:HD11	1:CR:89:LEU:HD23	1.78	0.64
1:CH:199:VAL:O	1:CH:199:VAL:HG13	1.97	0.64
1:BH:72:THR:O	1:BH:191:ASN:ND2	2.31	0.64
1:AP:253:ASP:CG	1:AP:285:PHE:HA	2.18	0.64
1:CH:79:VAL:CG1	1:CH:185:LEU:O	2.46	0.64
1:AG:314:TYR:HE1	1:AG:316:SER:HA	1.63	0.64
1:CU:99:PHE:CA	1:CU:209:VAL:O	2.46	0.64
1:AZ:314:TYR:HE1	1:AZ:316:SER:HA	1.63	0.64
1:BA:111:ILE:HG21	1:BA:123:TYR:OH	2.07	0.64
1:CH:58:SER:HA	1:CH:203:TRP:CZ3	2.33	0.64
1:CO:109:PHE:HB2	1:CO:158:VAL:CG1	2.28	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AL:68:LEU:HB2	1:AL:195:VAL:HG22	1.80	0.64
1:CN:151:LYS:NZ	1:BP:153:TRP:O	2.31	0.64
1:CB:111:ILE:O	1:CB:198:SER:O	2.16	0.64
1:CJ:199:VAL:O	1:CJ:199:VAL:HG13	1.98	0.64
1:BI:318:GLU:OE2	1:BI:318:GLU:N	2.31	0.64
1:AP:68:LEU:HB2	1:AP:195:VAL:HG22	1.78	0.64
1:AP:62:ARG:HH11	1:AP:62:ARG:HG2	1.63	0.64
1:AK:299:GLY:CA	1:AK:310:ASP:O	2.45	0.63
1:CI:122:GLY:C	1:CI:188:VAL:HB	2.18	0.63
1:AU:314:TYR:CD1	1:AU:315:TYR:C	2.71	0.63
1:CV:80:VAL:HG12	1:CV:185:LEU:CB	2.27	0.63
1:AD:314:TYR:HE1	1:AD:316:SER:HA	1.64	0.63
1:AT:314:TYR:HE1	1:AT:316:SER:HA	1.63	0.63
1:BG:101:ARG:NH1	1:BG:166:LEU:HD12	2.12	0.63
1:BV:130:ASP:HB2	1:CV:100:GLN:NE2	2.13	0.63
1:BB:101:ARG:NH1	1:BB:166:LEU:HD12	2.13	0.63
1:BW:316:SER:HB2	1:BW:319:GLN:OE1	1.97	0.63
1:BE:139:ASP:HA	1:BE:142:GLN:HG2	1.80	0.63
1:BP:80:VAL:HG13	1:BP:185:LEU:HB3	1.80	0.63
1:CX:163:THR:HG21	1:CX:167:LEU:HD11	1.80	0.63
1:AG:253:ASP:CG	1:AG:285:PHE:HA	2.16	0.63
1:AO:302:ASP:CB	1:AO:305:ASN:ND2	2.60	0.63
1:CZ:79:VAL:CG1	1:CZ:185:LEU:O	2.47	0.63
1:BT:98:ILE:HG22	1:AV:91:ARG:NE	2.14	0.63
1:CO:99:PHE:CA	1:CO:209:VAL:O	2.46	0.63
1:BG:91:ARG:NH1	1:AP:98:ILE:HG23	2.13	0.63
1:AX:106:THR:HA	1:AX:162:TYR:OH	1.98	0.63
1:CD:43:SER:HA	1:CW:112:GLN:NE2	24.18	0.63
1:BC:75:ASP:OD2	1:CJ:62:ARG:NH1	2.26	0.63
1:CT:63:ILE:HD11	1:CT:89:LEU:HD23	1.79	0.63
1:BM:253:ASP:HB2	1:BM:286:ALA:HB2	1.81	0.63
1:BR:127:PHE:HB3	1:BR:160:PRO:HB3	1.79	0.63
1:CO:199:VAL:O	1:CO:199:VAL:HG13	1.98	0.63
1:BX:72:THR:O	1:BX:191:ASN:ND2	2.29	0.63
1:BP:68:LEU:HD23	1:BP:195:VAL:HG22	1.80	0.63
1:AW:302:ASP:CB	1:AW:305:ASN:ND2	2.60	0.63
1:BB:98:ILE:HG22	1:AF:91:ARG:NE	89.11	0.63
1:AX:314:TYR:CZ	1:AX:315:TYR:O	2.52	0.63
1:CJ:122:GLY:O	1:CJ:188:VAL:HB	1.99	0.63
1:AH:63:ILE:HB	1:AH:199:VAL:HG13	1.79	0.63
1:BT:68:LEU:HD23	1:BT:195:VAL:HG22	1.81	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CI:109:PHE:HB2	1:CI:158:VAL:CG1	2.28	0.63
1:AS:68:LEU:HB2	1:AS:195:VAL:HG22	1.79	0.63
1:AT:253:ASP:CG	1:AT:285:PHE:HA	2.16	0.63
1:AM:144:THR:HG23	1:AM:147:ALA:HB2	1.81	0.63
1:BB:98:ILE:HG22	1:AF:91:ARG:HE	89.13	0.63
1:BU:98:ILE:HG22	1:AX:91:ARG:NE	2.13	0.63
1:AO:91:ARG:HE	1:BW:98:ILE:HG22	1.64	0.63
1:AW:314:TYR:HE1	1:AW:316:SER:HA	1.64	0.63
1:BJ:130:ASP:HB2	1:CJ:100:GLN:NE2	2.14	0.63
1:CS:99:PHE:CA	1:CS:209:VAL:O	2.47	0.63
1:AJ:106:THR:HA	1:AJ:162:TYR:OH	1.99	0.63
1:CO:58:SER:HA	1:CO:203:TRP:CZ3	2.34	0.63
1:AK:119:THR:HG23	1:AK:193:ASP:HB2	1.79	0.63
1:CQ:58:SER:HA	1:CQ:203:TRP:CZ3	2.33	0.63
1:BF:139:ASP:HA	1:BF:142:GLN:HG2	1.80	0.63
1:BU:316:SER:HB2	1:BU:319:GLN:OE1	1.98	0.63
1:BA:176:ARG:HD2	1:CA:168:TRP:CE2	2.36	0.63
1:AC:302:ASP:CB	1:AC:305:ASN:ND2	2.61	0.63
1:AF:302:ASP:CB	1:AF:305:ASN:ND2	2.60	0.63
1:CP:122:GLY:O	1:CP:188:VAL:HB	1.98	0.63
1:CD:79:VAL:CG1	1:CD:185:LEU:O	2.47	0.63
1:AO:314:TYR:CD1	1:AO:315:TYR:C	2.70	0.63
1:AS:314:TYR:HE1	1:AS:316:SER:HA	1.63	0.63
1:AR:314:TYR:CE1	1:AR:316:SER:N	2.66	0.63
1:BO:101:ARG:NH1	1:BO:166:LEU:HD12	2.14	0.63
1:BS:68:LEU:HD23	1:BS:195:VAL:HG22	1.79	0.63
1:AT:62:ARG:HH11	1:AT:62:ARG:HG2	1.64	0.63
1:AE:111:ILE:HG22	1:AE:113:PRO:HD3	1.78	0.63
1:AW:265:ILE:CG2	1:AW:313:ALA:O	2.46	0.63
1:CV:79:VAL:CG1	1:CV:185:LEU:O	2.45	0.63
1:CJ:99:PHE:CA	1:CJ:209:VAL:O	2.47	0.63
1:BN:101:ARG:NH1	1:BN:166:LEU:CD1	2.62	0.63
1:AF:106:THR:HA	1:AF:162:TYR:OH	1.98	0.63
1:BA:68:LEU:HD23	1:BA:195:VAL:HG22	1.79	0.63
1:BP:253:ASP:HB2	1:BP:286:ALA:HB2	1.81	0.63
1:AZ:253:ASP:CG	1:AZ:285:PHE:HA	2.15	0.63
1:AY:253:ASP:CG	1:AY:285:PHE:HA	2.16	0.63
1:AQ:302:ASP:CB	1:AQ:305:ASN:ND2	2.61	0.63
1:CG:141:LEU:N	1:CG:141:LEU:HD23	2.14	0.63
1:AN:91:ARG:NE	1:BP:98:ILE:HG22	2.14	0.63
1:AB:91:ARG:NE	1:BO:98:ILE:HG22	133.56	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CH:122:GLY:O	1:CH:188:VAL:HB	1.98	0.63
1:BG:98:ILE:HG22	1:AP:91:ARG:NE	2.14	0.63
1:BR:101:ARG:NH1	1:BR:166:LEU:CD1	2.61	0.63
1:CW:63:ILE:HD11	1:CW:89:LEU:HD23	1.80	0.63
1:BA:316:SER:HB2	1:BA:319:GLN:OE1	1.99	0.63
1:BZ:127:PHE:HB3	1:BZ:160:PRO:HB3	1.80	0.63
1:AE:114:MET:SD	1:AM:122:GLY:HA3	2.38	0.63
1:CS:199:VAL:HG13	1:CS:199:VAL:O	1.99	0.63
1:AH:114:MET:SD	1:AN:122:GLY:HA3	2.39	0.63
1:AX:302:ASP:CB	1:AX:305:ASN:ND2	2.61	0.63
1:AR:302:ASP:CB	1:AR:305:ASN:ND2	2.61	0.63
1:BQ:114:MET:SD	1:CZ:122:GLY:HA3	2.38	0.63
1:AD:144:THR:HG23	1:AD:147:ALA:HB2	1.80	0.63
1:BI:130:ASP:HB2	1:CI:100:GLN:NE2	2.13	0.63
1:CR:79:VAL:CG1	1:CR:185:LEU:O	2.47	0.63
1:AW:314:TYR:CE1	1:AW:316:SER:N	2.65	0.63
1:BV:101:ARG:NH1	1:BV:166:LEU:HD12	2.14	0.63
1:AG:106:THR:HA	1:AG:162:TYR:OH	1.99	0.63
1:BD:111:ILE:HG21	1:BD:123:TYR:OH	1.99	0.63
1:CD:58:SER:HA	1:CD:203:TRP:CZ3	2.34	0.63
1:BA:75:ASP:OD2	1:CG:62:ARG:NH1	2.27	0.63
1:AJ:62:ARG:HG2	1:AJ:62:ARG:HH11	1.64	0.63
1:BM:176:ARG:HD2	1:CM:168:TRP:CE2	2.34	0.63
1:AL:62:ARG:HG2	1:AL:62:ARG:HH11	1.62	0.63
1:BS:316:SER:HB2	1:BS:319:GLN:OE1	1.99	0.63
1:AE:302:ASP:CB	1:AE:305:ASN:ND2	2.60	0.63
1:AY:144:THR:HG23	1:AY:147:ALA:HB2	1.81	0.63
1:CF:95:ALA:O	1:CF:98:ILE:HG12	1.98	0.63
1:AF:314:TYR:CD1	1:AF:315:TYR:C	2.73	0.63
1:BZ:101:ARG:NH1	1:BZ:166:LEU:CD1	2.61	0.63
1:BW:80:VAL:HG13	1:BW:185:LEU:HB3	1.81	0.63
1:AE:68:LEU:HB2	1:AE:195:VAL:CG2	2.29	0.63
1:AS:68:LEU:HB2	1:AS:195:VAL:CG2	2.28	0.63
1:CB:62:ARG:NH1	1:BF:75:ASP:OD2	2.29	0.63
1:CX:109:PHE:HB2	1:CX:158:VAL:CG1	2.29	0.63
1:BI:68:LEU:HD23	1:BI:195:VAL:HG22	1.81	0.63
1:BH:316:SER:HB2	1:BH:319:GLN:OE1	1.99	0.63
1:AW:62:ARG:HG2	1:AW:62:ARG:HH11	1.64	0.63
1:CK:111:ILE:O	1:CK:198:SER:O	2.17	0.63
1:AO:62:ARG:HH11	1:AO:62:ARG:HG2	1.64	0.63
1:BC:68:LEU:HD23	1:BC:195:VAL:HG22	1.85	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BV:58:SER:HB3	1:BV:204:SER:HB3	1.80	0.63
1:BA:253:ASP:HB2	1:BA:286:ALA:HB2	1.83	0.63
1:AU:144:THR:HG23	1:AU:147:ALA:HB2	1.80	0.62
1:AO:91:ARG:NE	1:BW:98:ILE:HG22	2.14	0.62
1:AV:314:TYR:CD1	1:AV:315:TYR:C	2.72	0.62
1:AF:314:TYR:HE1	1:AF:316:SER:HA	1.64	0.62
1:AD:98:ILE:HG23	1:BF:91:ARG:NH1	2.14	0.62
1:BB:176:ARG:HD2	1:CB:168:TRP:CE2	2.40	0.62
1:BH:58:SER:HB3	1:BH:204:SER:HB3	1.81	0.62
1:BI:58:SER:HB3	1:BI:204:SER:HB3	1.81	0.62
1:BY:139:ASP:HA	1:BY:142:GLN:HG2	1.79	0.62
1:BE:58:SER:HB3	1:BE:204:SER:HB3	1.81	0.62
1:BB:253:ASP:HB2	1:BB:286:ALA:HB2	1.81	0.62
1:AT:302:ASP:CB	1:AT:305:ASN:ND2	2.60	0.62
1:CB:122:GLY:O	1:CB:188:VAL:HB	1.99	0.62
1:AV:314:TYR:HE1	1:AV:316:SER:HA	1.63	0.62
1:BU:130:ASP:HB2	1:CU:100:GLN:NE2	2.13	0.62
1:AH:314:TYR:HE1	1:AH:316:SER:HA	1.63	0.62
1:AK:314:TYR:CE1	1:AK:316:SER:N	2.67	0.62
1:BT:101:ARG:NH1	1:BT:166:LEU:HD12	2.13	0.62
1:BY:101:ARG:NH1	1:BY:166:LEU:CD1	2.62	0.62
1:BS:101:ARG:NH1	1:BS:166:LEU:CD1	2.62	0.62
1:CN:58:SER:HA	1:CN:203:TRP:CZ3	2.33	0.62
1:BX:316:SER:HB2	1:BX:319:GLN:OE1	1.99	0.62
1:BI:316:SER:HB2	1:BI:319:GLN:OE1	1.99	0.62
1:BT:58:SER:HB3	1:BT:204:SER:HB3	1.80	0.62
1:AX:68:LEU:HB2	1:AX:195:VAL:HG22	1.81	0.62
1:CZ:199:VAL:HG13	1:CZ:199:VAL:O	1.99	0.62
1:AB:302:ASP:CB	1:AB:305:ASN:ND2	2.61	0.62
1:AU:302:ASP:CB	1:AU:305:ASN:ND2	2.60	0.62
1:AS:302:ASP:CB	1:AS:305:ASN:ND2	2.61	0.62
1:CP:122:GLY:C	1:CP:188:VAL:HB	2.19	0.62
1:AW:144:THR:HG23	1:AW:147:ALA:HB2	1.81	0.62
1:AN:314:TYR:CD1	1:AN:315:TYR:C	2.71	0.62
1:AE:314:TYR:CD1	1:AE:315:TYR:C	2.72	0.62
1:BK:130:ASP:HB2	1:CK:100:GLN:NE2	2.14	0.62
1:BD:101:ARG:NH1	1:BD:166:LEU:CD1	2.62	0.62
1:AP:106:THR:HA	1:AP:162:TYR:OH	1.99	0.62
1:BV:80:VAL:HG13	1:BV:185:LEU:HB3	1.81	0.62
1:CP:58:SER:HA	1:CP:203:TRP:CZ3	2.32	0.62
1:CL:58:SER:HA	1:CL:203:TRP:CZ3	2.34	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CQ:109:PHE:HB2	1:CQ:158:VAL:CG1	2.28	0.62
1:BO:176:ARG:HD2	1:CO:168:TRP:CE2	2.34	0.62
1:BD:68:LEU:HD23	1:BD:195:VAL:HG22	1.81	0.62
1:CD:141:LEU:HD23	1:CD:141:LEU:N	2.15	0.62
1:BD:114:MET:SD	1:CG:122:GLY:HA3	34.84	0.62
1:AD:141:LEU:O	1:AD:144:THR:CG2	2.44	0.62
1:AC:141:LEU:O	1:AC:144:THR:CG2	2.42	0.62
1:AE:144:THR:HG23	1:AE:147:ALA:HB2	1.81	0.62
1:BC:98:ILE:HG22	1:AM:91:ARG:HE	216.51	0.62
1:CC:163:THR:HG21	1:CC:167:LEU:HD11	1.82	0.62
1:CR:141:LEU:HD23	1:CR:141:LEU:N	2.13	0.62
1:AG:314:TYR:CD1	1:AG:315:TYR:C	2.72	0.62
1:AT:314:TYR:CD1	1:AT:315:TYR:C	2.73	0.62
1:BS:101:ARG:CZ	1:BS:166:LEU:CD1	2.76	0.62
1:BC:80:VAL:HG13	1:BC:185:LEU:HB3	1.81	0.62
1:CR:58:SER:HA	1:CR:203:TRP:CZ3	2.34	0.62
1:CE:63:ILE:HD11	1:CE:89:LEU:HD23	1.79	0.62
1:BN:316:SER:HB2	1:BN:319:GLN:OE1	2.00	0.62
1:CG:58:SER:HA	1:CG:203:TRP:CZ3	2.34	0.62
1:BC:176:ARG:HD2	1:CC:168:TRP:CE2	2.34	0.62
1:BZ:316:SER:HB2	1:BZ:319:GLN:OE1	1.99	0.62
1:AD:62:ARG:CZ	1:AH:138:PHE:CE2	139.44	0.62
1:AH:62:ARG:HG2	1:AH:62:ARG:HH11	1.64	0.62
1:AI:253:ASP:CG	1:AI:285:PHE:HA	2.16	0.62
1:CO:141:LEU:N	1:CO:141:LEU:HD23	2.14	0.62
1:AD:91:ARG:HG2	1:BH:98:ILE:HG23	132.59	0.62
1:AB:314:TYR:CZ	1:AB:315:TYR:O	2.53	0.62
1:AS:314:TYR:CD1	1:AS:315:TYR:C	2.72	0.62
1:AE:314:TYR:HE1	1:AE:316:SER:HA	1.62	0.62
1:AB:63:ILE:HB	1:AB:199:VAL:HG13	1.85	0.62
1:AO:106:THR:HA	1:AO:162:TYR:OH	1.99	0.62
1:CR:112:GLN:NE2	1:CT:43:SER:HA	2.14	0.62
1:AZ:119:THR:O	1:AZ:192:THR:HB	2.00	0.62
1:CV:62:ARG:NH1	1:BZ:75:ASP:OD2	2.29	0.62
1:BI:253:ASP:HB2	1:BI:286:ALA:HB2	1.80	0.62
1:BW:58:SER:HB3	1:BW:204:SER:HB3	1.82	0.62
1:BC:61:SER:CB	1:BC:90:PRO:HD2	2.28	0.62
1:AT:141:LEU:O	1:AT:144:THR:CG2	2.41	0.62
1:AB:144:THR:HG23	1:AB:147:ALA:HB2	1.82	0.62
1:AO:314:TYR:CZ	1:AO:315:TYR:O	2.52	0.62
1:AG:61:SER:CB	1:AG:90:PRO:HD2	2.28	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CX:122:GLY:O	1:CX:188:VAL:HB	2.00	0.62
1:AD:314:TYR:CD1	1:AD:315:TYR:C	2.73	0.62
1:CJ:122:GLY:C	1:CJ:188:VAL:HB	2.19	0.62
1:BC:116:PRO:CB	1:CM:118:ASN:HA	221.59	0.62
1:BV:253:ASP:HB2	1:BV:286:ALA:HB2	1.81	0.62
1:AQ:62:ARG:HH11	1:AQ:62:ARG:HG2	1.64	0.62
1:BK:316:SER:HB2	1:BK:319:GLN:OE1	1.99	0.62
1:CG:163:THR:HG21	1:CG:167:LEU:HD11	1.81	0.62
1:CY:141:LEU:HD23	1:CY:141:LEU:N	2.14	0.62
1:AC:144:THR:HG23	1:AC:147:ALA:HB2	1.84	0.62
1:AG:63:ILE:HB	1:AG:199:VAL:HG13	1.82	0.62
1:AH:314:TYR:CD1	1:AH:315:TYR:C	2.72	0.62
1:CV:122:GLY:O	1:CV:188:VAL:HB	2.00	0.62
1:AC:314:TYR:HE1	1:AC:316:SER:N	2.00	0.62
1:BM:130:ASP:HB2	1:CM:100:GLN:NE2	2.14	0.62
1:BN:130:ASP:HB2	1:CN:100:GLN:NE2	2.15	0.62
1:BX:130:ASP:HB2	1:CX:100:GLN:NE2	2.14	0.62
1:BT:111:ILE:HG21	1:BT:123:TYR:OH	2.00	0.62
1:BA:153:TRP:O	1:CI:151:LYS:NZ	2.31	0.62
1:CC:58:SER:HA	1:CC:203:TRP:CZ3	2.36	0.62
1:AL:68:LEU:HB2	1:AL:195:VAL:CG2	2.30	0.62
1:BL:58:SER:HB3	1:BL:204:SER:HB3	1.82	0.62
1:CT:109:PHE:HB2	1:CT:158:VAL:CG1	2.30	0.62
1:BS:58:SER:HB3	1:BS:204:SER:HB3	1.81	0.62
1:BA:127:PHE:HB3	1:BA:160:PRO:HB3	1.82	0.62
1:CG:79:VAL:CG1	1:CG:185:LEU:O	2.48	0.62
1:BS:61:SER:CB	1:BS:90:PRO:HD2	2.23	0.62
1:AU:266:ASP:O	1:AU:314:TYR:HA	2.00	0.62
1:AJ:314:TYR:HE1	1:AJ:316:SER:HA	1.63	0.62
1:AL:314:TYR:HE1	1:AL:316:SER:HA	1.63	0.62
1:AZ:314:TYR:CD1	1:AZ:315:TYR:C	2.72	0.62
1:BG:130:ASP:HB2	1:CG:100:GLN:NE2	2.14	0.62
1:AL:106:THR:HA	1:AL:162:TYR:OH	1.99	0.62
1:CM:58:SER:HA	1:CM:203:TRP:CZ3	2.35	0.62
1:BB:58:SER:HB3	1:BB:204:SER:HB3	1.81	0.62
1:AB:114:MET:SD	1:AO:122:GLY:HA3	146.76	0.62
1:CP:191:ASN:N	1:CP:191:ASN:OD1	2.32	0.62
1:AR:62:ARG:HG2	1:AR:62:ARG:HH11	1.65	0.62
1:AD:320:PRO:O	1:AD:322:GLN:HG3	2.03	0.62
1:BV:316:SER:HB2	1:BV:319:GLN:OE1	2.00	0.62
1:AX:144:THR:HG23	1:AX:147:ALA:HB2	1.81	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BK:98:ILE:CG2	1:AS:91:ARG:NE	2.63	0.62
1:AR:144:THR:HG23	1:AR:147:ALA:HB2	1.80	0.62
1:AC:314:TYR:CD1	1:AC:315:TYR:C	2.73	0.62
1:BG:101:ARG:CZ	1:BG:166:LEU:CD1	2.76	0.62
1:BW:101:ARG:NH1	1:BW:166:LEU:CD1	2.63	0.62
1:CS:58:SER:HA	1:CS:203:TRP:CZ3	2.35	0.62
1:BN:80:VAL:HG13	1:BN:185:LEU:HB3	1.81	0.62
1:CJ:111:ILE:O	1:CJ:198:SER:O	2.17	0.62
1:BD:316:SER:HB2	1:BD:319:GLN:OE1	2.01	0.62
1:AO:314:TYR:HE1	1:AO:316:SER:N	1.98	0.61
1:AQ:314:TYR:CD1	1:AQ:315:TYR:C	2.72	0.61
1:CB:95:ALA:O	1:CB:98:ILE:HG12	2.00	0.61
1:BK:114:MET:SD	1:CS:122:GLY:HA3	2.40	0.61
1:BA:166:LEU:C	1:BA:166:LEU:HD13	2.21	0.61
1:BA:130:ASP:HB2	1:CA:100:GLN:NE2	2.15	0.61
1:CJ:80:VAL:HG12	1:CJ:185:LEU:CB	2.26	0.61
1:AY:63:ILE:HB	1:AY:199:VAL:HG13	1.82	0.61
1:BK:101:ARG:NH1	1:BK:166:LEU:HD12	2.14	0.61
1:AK:63:ILE:HB	1:AK:199:VAL:HG13	1.82	0.61
1:AZ:63:ILE:HB	1:AZ:199:VAL:HG13	1.81	0.61
1:BE:101:ARG:CZ	1:BE:166:LEU:CD1	2.77	0.61
1:BW:68:LEU:HD23	1:BW:195:VAL:HG22	1.81	0.61
1:CV:45:VAL:HG23	1:CZ:200:LEU:HD13	1.82	0.61
1:BV:68:LEU:HD23	1:BV:195:VAL:HG22	1.81	0.61
1:CN:199:VAL:O	1:CN:199:VAL:HG13	1.99	0.61
1:AY:68:LEU:HB2	1:AY:195:VAL:HG22	1.82	0.61
1:BH:176:ARG:HD2	1:CH:168:TRP:CE2	2.35	0.61
1:BG:68:LEU:HD23	1:BG:195:VAL:HG22	1.81	0.61
1:BE:68:LEU:HD23	1:BE:195:VAL:HG22	1.82	0.61
1:AQ:144:THR:HG23	1:AQ:147:ALA:HB2	1.82	0.61
1:AB:141:LEU:O	1:AB:144:THR:CG2	2.43	0.61
1:AZ:144:THR:HG23	1:AZ:147:ALA:HB2	1.82	0.61
1:BL:98:ILE:CG2	1:AU:91:ARG:NE	2.63	0.61
1:BA:98:ILE:CG2	1:AT:91:ARG:NE	58.14	0.61
1:CF:122:GLY:C	1:CF:188:VAL:HB	2.21	0.61
1:AP:314:TYR:CD1	1:AP:315:TYR:C	2.73	0.61
1:AI:68:LEU:HB2	1:AI:195:VAL:CG2	2.30	0.61
1:CC:122:GLY:C	1:CC:188:VAL:HB	2.23	0.61
1:AE:91:ARG:HE	1:BM:98:ILE:HG22	1.65	0.61
1:AB:91:ARG:HE	1:BO:98:ILE:HG22	133.82	0.61
1:AM:314:TYR:CZ	1:AM:315:TYR:O	2.52	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CV:122:GLY:C	1:CV:188:VAL:HB	2.19	0.61
1:AI:314:TYR:HE1	1:AI:316:SER:N	1.98	0.61
1:CE:95:ALA:O	1:CE:98:ILE:HG12	1.99	0.61
1:CV:317:ASP:HB3	1:CV:319:GLN:CD	2.21	0.61
1:BG:101:ARG:NH1	1:BG:166:LEU:CD1	2.63	0.61
1:BE:101:ARG:NH1	1:BE:166:LEU:CD1	2.63	0.61
1:AF:111:ILE:O	1:AF:198:SER:O	2.18	0.61
1:AW:68:LEU:HB2	1:AW:195:VAL:CG2	2.30	0.61
1:BW:176:ARG:HD2	1:CW:168:TRP:CE2	2.35	0.61
1:CQ:199:VAL:O	1:CQ:199:VAL:HG13	2.01	0.61
1:CP:163:THR:HG21	1:CP:167:LEU:HD11	1.82	0.61
1:AW:320:PRO:O	1:AW:322:GLN:HG3	2.00	0.61
1:AJ:302:ASP:CB	1:AJ:305:ASN:ND2	2.60	0.61
1:CT:122:GLY:C	1:CT:188:VAL:HB	2.20	0.61
1:AU:314:TYR:CZ	1:AU:315:TYR:O	2.53	0.61
1:BO:130:ASP:HB2	1:CO:100:GLN:NE2	2.15	0.61
1:CA:317:ASP:HB3	1:CA:319:GLN:CD	2.21	0.61
1:CS:317:ASP:HB3	1:CS:319:GLN:CD	2.21	0.61
1:CT:95:ALA:O	1:CT:98:ILE:HG12	2.00	0.61
1:BM:101:ARG:NH1	1:BM:166:LEU:CD1	2.64	0.61
1:BJ:111:ILE:HG21	1:BJ:123:TYR:OH	2.00	0.61
1:BJ:80:VAL:HG13	1:BJ:185:LEU:HB3	1.83	0.61
1:AZ:62:ARG:HG2	1:AZ:62:ARG:HH11	1.64	0.61
1:CL:191:ASN:OD1	1:CL:191:ASN:N	2.33	0.61
1:AL:302:ASP:CB	1:AL:305:ASN:ND2	2.62	0.61
1:AI:144:THR:HG23	1:AI:147:ALA:HB2	1.83	0.61
1:CD:122:GLY:C	1:CD:188:VAL:HB	2.20	0.61
1:AK:141:LEU:O	1:AK:144:THR:CG2	2.42	0.61
1:AO:144:THR:HG23	1:AO:147:ALA:HB2	1.80	0.61
1:BC:130:ASP:HB2	1:CC:100:GLN:NE2	2.18	0.61
1:AB:266:ASP:O	1:AB:314:TYR:HA	2.02	0.61
1:AY:314:TYR:CD1	1:AY:315:TYR:C	2.74	0.61
1:CC:317:ASP:HB3	1:CC:319:GLN:CD	2.20	0.61
1:BA:91:ARG:NH1	1:AT:98:ILE:HG23	78.73	0.61
1:BY:68:LEU:HD23	1:BY:195:VAL:HG22	1.82	0.61
1:CR:163:THR:HG21	1:CR:167:LEU:HD11	1.83	0.61
1:CZ:122:GLY:C	1:CZ:188:VAL:HB	2.20	0.61
1:BK:98:ILE:C	1:BK:211:SER:O	2.39	0.61
1:CH:122:GLY:C	1:CH:188:VAL:HB	2.21	0.61
1:CO:317:ASP:HB3	1:CO:319:GLN:CD	2.21	0.61
1:AC:63:ILE:HB	1:AC:199:VAL:HG13	1.86	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AN:106:THR:HA	1:AN:162:TYR:OH	1.99	0.61
1:BJ:58:SER:HB3	1:BJ:204:SER:CB	2.31	0.61
1:CD:38:PRO:O	1:CW:117:ALA:CB	8.77	0.61
1:AW:168:TRP:CE2	1:CW:176:ARG:HG2	2.36	0.61
1:AV:61:SER:CB	1:AV:90:PRO:HD2	2.27	0.61
1:CT:317:ASP:HB3	1:CT:319:GLN:CD	2.21	0.61
1:CN:122:GLY:C	1:CN:188:VAL:HB	2.21	0.61
1:CP:317:ASP:HB3	1:CP:319:GLN:CD	2.21	0.61
1:BK:101:ARG:NH1	1:BK:166:LEU:CD1	2.63	0.61
1:BF:101:ARG:NH1	1:BF:166:LEU:HD12	2.16	0.61
1:BC:153:TRP:O	1:CY:151:LYS:NZ	2.33	0.61
1:CK:191:ASN:OD1	1:CK:191:ASN:N	2.31	0.61
1:AL:320:PRO:O	1:AL:322:GLN:HG3	2.00	0.61
1:CX:141:LEU:HD23	1:CX:141:LEU:N	2.15	0.61
1:AR:141:LEU:O	1:AR:144:THR:CG2	2.44	0.61
1:BC:98:ILE:CG2	1:AY:91:ARG:NE	2.64	0.61
1:AU:314:TYR:HE1	1:AU:316:SER:N	1.98	0.61
1:AL:314:TYR:CD1	1:AL:315:TYR:C	2.73	0.61
1:BE:130:ASP:HB2	1:CE:100:GLN:NE2	2.15	0.61
1:BT:101:ARG:NH1	1:BT:166:LEU:CD1	2.63	0.61
1:AB:119:THR:O	1:AB:192:THR:HB	2.02	0.61
1:CX:58:SER:HA	1:CX:203:TRP:CZ3	2.36	0.61
1:AH:68:LEU:HB2	1:AH:195:VAL:CG2	2.31	0.61
1:CD:111:ILE:HG22	1:CD:113:PRO:HD3	1.90	0.61
1:BU:253:ASP:HB2	1:BU:286:ALA:HB2	1.82	0.61
1:CB:109:PHE:HB2	1:CB:158:VAL:CG1	2.31	0.61
1:BS:253:ASP:HB2	1:BS:286:ALA:HB2	1.82	0.61
1:AZ:302:ASP:CB	1:AZ:305:ASN:ND2	2.61	0.61
1:CL:101:ARG:NH1	1:CL:166:LEU:CD1	2.62	0.61
1:BC:98:ILE:O	1:BC:211:SER:C	2.42	0.61
1:AI:314:TYR:CZ	1:AI:315:TYR:O	2.53	0.61
1:AN:266:ASP:O	1:AN:314:TYR:HA	2.01	0.61
1:AN:314:TYR:CZ	1:AN:315:TYR:O	2.54	0.61
1:AJ:314:TYR:CD1	1:AJ:315:TYR:C	2.74	0.61
1:BX:101:ARG:NH1	1:BX:166:LEU:HD12	2.15	0.61
1:BV:101:ARG:NH1	1:BV:166:LEU:CD1	2.64	0.61
1:BW:101:ARG:NH1	1:BW:166:LEU:HD12	2.15	0.61
1:BO:101:ARG:NH1	1:BO:166:LEU:CD1	2.64	0.61
1:AT:119:THR:O	1:AT:192:THR:HB	2.01	0.61
1:BQ:68:LEU:HD23	1:BQ:195:VAL:CG2	2.31	0.61
1:BW:68:LEU:HD23	1:BW:195:VAL:CG2	2.30	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AR:320:PRO:O	1:AR:322:GLN:HG3	2.01	0.61
1:AK:168:TRP:CE2	1:CK:176:ARG:HG2	2.36	0.61
1:BI:176:ARG:HD2	1:CI:168:TRP:CE2	2.36	0.61
1:BM:58:SER:HB3	1:BM:204:SER:HB3	1.83	0.61
1:AA:303:ASN:N	1:AA:305:ASN:OD1	2.34	0.61
1:AD:303:ASN:N	1:AD:305:ASN:OD1	2.35	0.61
1:CM:141:LEU:HD23	1:CM:141:LEU:N	2.16	0.61
1:CT:122:GLY:O	1:CT:188:VAL:HB	2.00	0.61
1:AM:314:TYR:HE1	1:AM:316:SER:N	1.98	0.61
1:CY:317:ASP:HB3	1:CY:319:GLN:CD	2.22	0.61
1:AW:63:ILE:HB	1:AW:199:VAL:HG13	1.81	0.61
1:BO:80:VAL:HG13	1:BO:185:LEU:HB3	1.82	0.61
1:AC:68:LEU:HB2	1:AC:195:VAL:CG2	2.32	0.61
1:AQ:68:LEU:HB2	1:AQ:195:VAL:CG2	2.30	0.61
1:BC:58:SER:HB3	1:BC:204:SER:CB	2.33	0.61
1:CB:151:LYS:NZ	1:BY:153:TRP:O	2.34	0.61
1:BO:253:ASP:HB2	1:BO:286:ALA:HB2	1.82	0.61
1:CE:163:THR:HG21	1:CE:167:LEU:HD11	1.83	0.61
1:CM:191:ASN:OD1	1:CM:191:ASN:N	2.34	0.61
1:CL:111:ILE:O	1:CL:198:SER:O	2.19	0.61
1:AV:302:ASP:CB	1:AV:305:ASN:ND2	2.61	0.60
1:AW:303:ASN:N	1:AW:305:ASN:OD1	2.34	0.60
1:CW:75:ASP:OD1	1:CW:188:VAL:C	2.40	0.60
1:CR:122:GLY:O	1:CR:188:VAL:HB	2.01	0.60
1:AI:106:THR:HA	1:AI:162:TYR:OH	2.01	0.60
1:BM:101:ARG:NH1	1:BM:166:LEU:HD12	2.16	0.60
1:BY:80:VAL:HG13	1:BY:185:LEU:HB3	1.83	0.60
1:CE:58:SER:HA	1:CE:203:TRP:CZ3	2.35	0.60
1:CI:58:SER:HA	1:CI:203:TRP:CZ3	2.36	0.60
1:BA:68:LEU:HD23	1:BA:195:VAL:CG2	2.32	0.60
1:BJ:68:LEU:HD23	1:BJ:195:VAL:HG22	1.82	0.60
1:BP:316:SER:HB2	1:BP:319:GLN:OE1	2.01	0.60
1:CM:199:VAL:O	1:CM:199:VAL:HG13	2.01	0.60
1:AP:303:ASN:N	1:AP:305:ASN:OD1	2.34	0.60
1:AY:303:ASN:N	1:AY:305:ASN:OD1	2.34	0.60
1:AN:302:ASP:CB	1:AN:305:ASN:ND2	2.60	0.60
1:CM:75:ASP:OD1	1:CM:188:VAL:C	2.40	0.60
1:CS:141:LEU:N	1:CS:141:LEU:HD23	2.15	0.60
1:BP:98:ILE:C	1:BP:211:SER:O	2.39	0.60
1:BP:98:ILE:O	1:BP:211:SER:CA	2.49	0.60
1:AD:91:ARG:NE	1:BH:98:ILE:CG2	131.15	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CC:95:ALA:O	1:CC:98:ILE:HG12	2.04	0.60
1:AB:314:TYR:HE1	1:AB:316:SER:N	1.99	0.60
1:BQ:130:ASP:HB2	1:CQ:100:GLN:NE2	2.15	0.60
1:AE:314:TYR:HE1	1:AE:316:SER:N	1.99	0.60
1:BP:130:ASP:HB2	1:CP:100:GLN:NE2	2.16	0.60
1:AK:111:ILE:O	1:AK:198:SER:O	2.18	0.60
1:AK:119:THR:O	1:AK:192:THR:HB	2.00	0.60
1:AB:114:MET:SD	1:AY:122:GLY:HA3	2.41	0.60
1:AK:320:PRO:O	1:AK:322:GLN:HG3	2.00	0.60
1:BA:58:SER:HB3	1:BA:204:SER:HB3	1.85	0.60
1:CD:163:THR:HG21	1:CD:167:LEU:HD11	1.84	0.60
1:AA:91:ARG:NE	1:BI:98:ILE:CG2	58.37	0.60
1:AQ:314:TYR:CZ	1:AQ:315:TYR:O	2.54	0.60
1:AH:314:TYR:CZ	1:AH:315:TYR:O	2.54	0.60
1:CU:317:ASP:HB3	1:CU:319:GLN:CD	2.22	0.60
1:CG:317:ASP:HB3	1:CG:319:GLN:CD	2.21	0.60
1:AW:119:THR:O	1:AW:192:THR:HB	2.02	0.60
1:AP:68:LEU:HB2	1:AP:195:VAL:CG2	2.30	0.60
1:AE:111:ILE:O	1:AE:198:SER:O	2.19	0.60
1:BP:58:SER:HB3	1:BP:204:SER:HB3	1.84	0.60
1:CU:163:THR:HG21	1:CU:167:LEU:HD11	1.83	0.60
1:BG:253:ASP:HB2	1:BG:286:ALA:HB2	1.83	0.60
1:AH:253:ASP:CG	1:AH:285:PHE:HA	2.15	0.60
1:AK:303:ASN:N	1:AK:305:ASN:OD1	2.32	0.60
1:AR:303:ASN:N	1:AR:305:ASN:OD1	2.34	0.60
1:CW:122:GLY:C	1:CW:188:VAL:HB	2.21	0.60
1:CB:122:GLY:C	1:CB:188:VAL:HB	2.22	0.60
1:AK:144:THR:HG23	1:AK:147:ALA:HB2	1.83	0.60
1:AP:144:THR:HG23	1:AP:147:ALA:HB2	1.83	0.60
1:BM:98:ILE:O	1:BM:211:SER:C	2.39	0.60
1:CA:79:VAL:CG1	1:CA:185:LEU:O	2.49	0.60
1:BQ:98:ILE:CG2	1:AZ:91:ARG:NE	2.63	0.60
1:AR:314:TYR:CD1	1:AR:315:TYR:C	2.74	0.60
1:CN:317:ASP:HB3	1:CN:319:GLN:CD	2.21	0.60
1:BT:91:ARG:NH1	1:AV:98:ILE:HG23	2.15	0.60
1:AC:119:THR:O	1:AC:192:THR:HB	2.03	0.60
1:AR:119:THR:O	1:AR:192:THR:HB	2.01	0.60
1:AD:62:ARG:HG2	1:AD:62:ARG:HH11	1.66	0.60
1:AR:168:TRP:CE2	1:CR:176:ARG:HG2	2.36	0.60
1:BG:58:SER:HB3	1:BG:204:SER:HB3	1.83	0.60
1:AQ:63:ILE:HB	1:AQ:199:VAL:HG13	1.83	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CZ:141:LEU:N	1:CZ:141:LEU:HD23	2.16	0.60
1:AJ:144:THR:HG23	1:AJ:147:ALA:HB2	1.84	0.60
1:BK:98:ILE:O	1:BK:211:SER:C	2.40	0.60
1:BB:98:ILE:O	1:BB:211:SER:C	2.40	0.60
1:AA:266:ASP:O	1:AA:314:TYR:HA	2.01	0.60
1:AI:314:TYR:HE1	1:AI:316:SER:HA	1.65	0.60
1:AY:314:TYR:HE1	1:AY:316:SER:HA	1.65	0.60
1:AK:314:TYR:CD1	1:AK:315:TYR:C	2.75	0.60
1:BF:101:ARG:NH1	1:BF:166:LEU:CD1	2.65	0.60
1:BD:80:VAL:HG13	1:BD:185:LEU:HB3	1.83	0.60
1:CF:58:SER:HA	1:CF:203:TRP:CZ3	2.36	0.60
1:BB:68:LEU:HD23	1:BB:195:VAL:HG22	1.84	0.60
1:CZ:111:ILE:O	1:CZ:198:SER:O	2.19	0.60
1:CW:199:VAL:O	1:CW:199:VAL:HG13	2.00	0.60
1:BL:316:SER:HB2	1:BL:319:GLN:OE1	2.01	0.60
1:BH:253:ASP:HB2	1:BH:286:ALA:HB2	1.82	0.60
1:BY:58:SER:HB3	1:BY:204:SER:HB3	1.82	0.60
1:CG:122:GLY:C	1:CG:188:VAL:HB	2.21	0.60
1:BF:98:ILE:C	1:BF:211:SER:O	2.40	0.60
1:CA:75:ASP:OD1	1:CA:188:VAL:C	2.42	0.60
1:AA:314:TYR:CZ	1:AA:315:TYR:O	2.54	0.60
1:AW:314:TYR:CD1	1:AW:315:TYR:C	2.74	0.60
1:CF:317:ASP:HB3	1:CF:319:GLN:CD	2.20	0.60
1:CJ:79:VAL:CG1	1:CJ:185:LEU:O	2.49	0.60
1:BN:101:ARG:NH2	1:BN:166:LEU:HD12	2.16	0.60
1:CW:58:SER:HA	1:CW:203:TRP:CZ3	2.36	0.60
1:AG:119:THR:O	1:AG:192:THR:HB	2.01	0.60
1:AX:119:THR:O	1:AX:192:THR:HB	2.00	0.60
1:BS:58:SER:HB3	1:BS:204:SER:CB	2.32	0.60
1:BH:68:LEU:HD23	1:BH:195:VAL:HG22	1.84	0.60
1:BK:176:ARG:HD2	1:CK:168:TRP:CE2	2.37	0.60
1:BQ:58:SER:HB3	1:BQ:204:SER:HB3	1.84	0.60
1:CT:111:ILE:O	1:CT:198:SER:O	2.19	0.60
1:CQ:191:ASN:OD1	1:CQ:191:ASN:N	2.34	0.60
1:BZ:176:ARG:HD2	1:CZ:168:TRP:CE2	2.36	0.60
1:AC:303:ASN:N	1:AC:305:ASN:OD1	2.34	0.60
1:AA:144:THR:HG23	1:AA:147:ALA:HB2	1.83	0.60
1:BJ:98:ILE:O	1:BJ:211:SER:C	2.40	0.60
1:CP:101:ARG:NH1	1:CP:166:LEU:CD1	2.64	0.60
1:BT:98:ILE:C	1:BT:211:SER:O	2.40	0.60
1:AH:266:ASP:O	1:AH:314:TYR:HA	2.02	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BI:80:VAL:HG13	1:BI:185:LEU:HB3	1.83	0.60
1:AU:111:ILE:O	1:AU:198:SER:O	2.20	0.60
1:AH:119:THR:O	1:AH:192:THR:HB	2.01	0.60
1:AU:68:LEU:HB2	1:AU:195:VAL:CG2	2.31	0.60
1:BH:58:SER:HB3	1:BH:204:SER:CB	2.32	0.60
1:AJ:80:VAL:CG1	1:AJ:185:LEU:HB3	2.32	0.60
1:AD:114:MET:SD	1:AH:122:GLY:HA3	146.91	0.60
1:AQ:122:GLY:HA3	1:AZ:114:MET:SD	2.41	0.60
1:AV:303:ASN:N	1:AV:305:ASN:OD1	2.35	0.60
1:BC:114:MET:SD	1:CM:122:GLY:HA3	217.76	0.60
1:AS:144:THR:HG23	1:AS:147:ALA:HB2	1.82	0.60
1:BD:98:ILE:O	1:BD:211:SER:C	2.41	0.60
1:AE:91:ARG:NE	1:BM:98:ILE:HG22	2.17	0.60
1:CK:79:VAL:CG1	1:CK:185:LEU:O	2.49	0.60
1:AV:314:TYR:CZ	1:AV:315:TYR:O	2.55	0.60
1:CR:111:ILE:O	1:CR:198:SER:O	2.18	0.60
1:CB:317:ASP:HB3	1:CB:319:GLN:CD	2.22	0.60
1:CH:317:ASP:HB3	1:CH:319:GLN:CD	2.21	0.60
1:AE:266:ASP:O	1:AE:314:TYR:HA	2.02	0.60
1:BA:101:ARG:NH2	1:BA:166:LEU:HD12	2.16	0.60
1:AO:98:ILE:HG23	1:BW:91:ARG:NH1	2.16	0.60
1:BC:111:ILE:HG23	1:BC:113:PRO:HD3	1.90	0.60
1:AW:111:ILE:O	1:AW:198:SER:O	2.20	0.60
1:CY:58:SER:HA	1:CY:203:TRP:CZ3	2.37	0.60
1:BD:68:LEU:HD23	1:BD:195:VAL:CG2	2.32	0.60
1:CF:111:ILE:O	1:CF:198:SER:O	2.20	0.60
1:BU:111:ILE:HG22	1:BU:156:ARG:H	1.66	0.60
1:BD:127:PHE:HB3	1:BD:160:PRO:HB3	1.89	0.60
1:AD:122:GLY:HA3	1:AW:114:MET:SD	2.42	0.60
1:AT:168:TRP:CE2	1:CT:176:ARG:HG2	2.36	0.60
1:BU:68:LEU:HD23	1:BU:195:VAL:HG22	1.84	0.60
1:BS:176:ARG:HD2	1:CS:168:TRP:CE2	2.36	0.60
1:AI:303:ASN:N	1:AI:305:ASN:OD1	2.34	0.60
1:CM:122:GLY:C	1:CM:188:VAL:HB	2.21	0.60
1:BE:61:SER:CB	1:BE:90:PRO:HD2	2.25	0.60
1:AK:314:TYR:HE1	1:AK:316:SER:HA	1.66	0.60
1:AR:314:TYR:HE1	1:AR:316:SER:HA	1.64	0.60
1:CE:317:ASP:HB3	1:CE:319:GLN:CD	2.21	0.60
1:AH:98:ILE:HG23	1:BN:91:ARG:NH1	2.16	0.60
1:BM:80:VAL:HG13	1:BM:185:LEU:HB3	1.84	0.60
1:CC:112:GLN:NE2	1:CJ:43:SER:HA	2.17	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AD:119:THR:O	1:AD:192:THR:HB	2.02	0.60
1:AX:68:LEU:HB2	1:AX:195:VAL:CG2	2.30	0.60
1:AY:68:LEU:HB2	1:AY:195:VAL:CG2	2.32	0.60
1:BG:176:ARG:HD2	1:CG:168:TRP:CE2	2.36	0.60
1:CY:111:ILE:O	1:CY:198:SER:O	2.20	0.60
1:BN:253:ASP:HB2	1:BN:286:ALA:HB2	1.82	0.60
1:CN:163:THR:HG21	1:CN:167:LEU:HD11	1.83	0.60
1:BJ:316:SER:HB2	1:BJ:319:GLN:OE1	2.02	0.60
1:BC:316:SER:HB2	1:BC:319:GLN:OE1	2.05	0.60
1:AL:168:TRP:CE2	1:CL:176:ARG:HG2	2.37	0.60
1:CS:109:PHE:HB2	1:CS:158:VAL:CG1	2.32	0.60
1:AM:303:ASN:N	1:AM:305:ASN:OD1	2.35	0.60
1:CY:122:GLY:O	1:CY:188:VAL:HB	2.00	0.60
1:AN:91:ARG:HE	1:BP:98:ILE:HG22	1.67	0.60
1:BB:98:ILE:C	1:BB:211:SER:O	2.41	0.60
1:BC:98:ILE:HG22	1:AM:91:ARG:HH21	214.31	0.60
1:CX:317:ASP:HB3	1:CX:319:GLN:CD	2.22	0.60
1:BQ:80:VAL:HG13	1:BQ:185:LEU:HB3	1.84	0.60
1:AM:119:THR:O	1:AM:192:THR:HB	2.02	0.60
1:BT:68:LEU:HD23	1:BT:195:VAL:CG2	2.31	0.60
1:BU:80:VAL:HG13	1:BU:185:LEU:HB3	1.84	0.60
1:CY:109:PHE:HB2	1:CY:158:VAL:CG1	2.31	0.60
1:BV:176:ARG:HD2	1:CV:168:TRP:CE2	2.37	0.60
1:CQ:163:THR:HG21	1:CQ:167:LEU:HD11	1.84	0.60
1:AG:122:GLY:HA3	1:AP:114:MET:SD	2.42	0.60
1:BP:98:ILE:O	1:BP:211:SER:C	2.40	0.59
1:AG:314:TYR:CZ	1:AG:315:TYR:O	2.54	0.59
1:AZ:314:TYR:CZ	1:AZ:315:TYR:O	2.55	0.59
1:AU:63:ILE:HB	1:AU:199:VAL:HG13	1.84	0.59
1:CW:95:ALA:O	1:CW:98:ILE:HG12	2.02	0.59
1:BJ:166:LEU:C	1:BJ:166:LEU:HD13	2.23	0.59
1:BF:80:VAL:HG13	1:BF:185:LEU:HB3	1.84	0.59
1:AV:111:ILE:O	1:AV:198:SER:O	2.19	0.59
1:AD:122:GLY:HA3	1:AG:114:MET:SD	128.72	0.59
1:BC:253:ASP:HB2	1:BC:286:ALA:HB2	1.83	0.59
1:CH:111:ILE:O	1:CH:198:SER:O	2.20	0.59
1:CW:163:THR:HG21	1:CW:167:LEU:HD11	1.83	0.59
1:BR:253:ASP:HB2	1:BR:286:ALA:HB2	1.84	0.59
1:CD:109:PHE:HB2	1:CD:158:VAL:CG1	2.32	0.59
1:AU:303:ASN:N	1:AU:305:ASN:OD1	2.35	0.59
1:CB:79:VAL:CG1	1:CB:185:LEU:O	2.48	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CE:122:GLY:O	1:CE:188:VAL:HB	2.02	0.59
1:BD:98:ILE:C	1:BD:211:SER:O	2.41	0.59
1:CO:79:VAL:CG1	1:CO:185:LEU:O	2.50	0.59
1:AP:314:TYR:HE1	1:AP:316:SER:HA	1.63	0.59
1:AA:63:ILE:HB	1:AA:199:VAL:HG13	1.85	0.59
1:AG:111:ILE:O	1:AG:198:SER:O	2.20	0.59
1:AI:119:THR:O	1:AI:192:THR:HB	2.03	0.59
1:BR:68:LEU:HD23	1:BR:195:VAL:HG22	1.84	0.59
1:BU:58:SER:HB3	1:BU:204:SER:HB3	1.83	0.59
1:BK:68:LEU:HD23	1:BK:195:VAL:HG22	1.83	0.59
1:BE:253:ASP:HB2	1:BE:286:ALA:HB2	1.84	0.59
1:AO:109:PHE:HB2	1:AO:158:VAL:CG1	2.32	0.59
1:BO:58:SER:HB3	1:BO:204:SER:HB3	1.83	0.59
1:AJ:303:ASN:N	1:AJ:305:ASN:OD1	2.35	0.59
1:AF:303:ASN:N	1:AF:305:ASN:OD1	2.35	0.59
1:CN:141:LEU:N	1:CN:141:LEU:HD23	2.16	0.59
1:BC:98:ILE:C	1:BC:211:SER:O	2.42	0.59
1:CS:79:VAL:CG1	1:CS:185:LEU:O	2.48	0.59
1:AT:314:TYR:CZ	1:AT:315:TYR:O	2.56	0.59
1:BC:156:ARG:NH2	1:CO:34:ARG:HG3	199.74	0.59
1:CP:112:GLN:NE2	1:CQ:43:SER:HA	2.16	0.59
1:CD:62:ARG:NH1	1:BI:75:ASP:OD2	2.31	0.59
1:CZ:58:SER:HA	1:CZ:203:TRP:CZ3	2.36	0.59
1:CS:111:ILE:O	1:CS:198:SER:O	2.20	0.59
1:CI:111:ILE:O	1:CI:198:SER:O	2.19	0.59
1:BZ:253:ASP:HB2	1:BZ:286:ALA:HB2	1.84	0.59
1:BL:127:PHE:HB3	1:BL:160:PRO:HB3	1.84	0.59
1:CZ:109:PHE:HB2	1:CZ:158:VAL:CG1	2.32	0.59
1:BT:127:PHE:HB3	1:BT:160:PRO:HB3	1.83	0.59
1:AO:303:ASN:N	1:AO:305:ASN:OD1	2.35	0.59
1:AV:141:LEU:O	1:AV:144:THR:CG2	2.42	0.59
1:BF:130:ASP:HB2	1:CF:100:GLN:NE2	2.17	0.59
1:AS:314:TYR:HE1	1:AS:316:SER:N	2.00	0.59
1:AD:314:TYR:HE1	1:AD:316:SER:N	2.01	0.59
1:AO:63:ILE:HB	1:AO:199:VAL:HG13	1.84	0.59
1:CJ:317:ASP:HB3	1:CJ:319:GLN:CD	2.22	0.59
1:AI:63:ILE:HB	1:AI:199:VAL:HG13	1.84	0.59
1:CK:43:SER:HA	1:CL:112:GLN:NE2	2.17	0.59
1:AQ:111:ILE:O	1:AQ:198:SER:O	2.20	0.59
1:AF:119:THR:O	1:AF:192:THR:HB	2.02	0.59
1:CL:199:VAL:O	1:CL:199:VAL:HG13	2.02	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BF:58:SER:HB3	1:BF:204:SER:HB3	1.84	0.59
1:CG:109:PHE:HB2	1:CG:158:VAL:CG1	2.32	0.59
1:AE:303:ASN:N	1:AE:305:ASN:OD1	2.36	0.59
1:CY:79:VAL:CG1	1:CY:185:LEU:O	2.47	0.59
1:CR:101:ARG:NH1	1:CR:166:LEU:CD1	2.66	0.59
1:AB:91:ARG:NE	1:BY:98:ILE:CG2	2.65	0.59
1:BN:98:ILE:O	1:BN:211:SER:CA	2.51	0.59
1:BN:98:ILE:O	1:BN:211:SER:C	2.41	0.59
1:BA:98:ILE:O	1:BA:211:SER:C	2.41	0.59
1:BB:114:MET:SD	1:CF:122:GLY:HA3	32.49	0.59
1:CS:95:ALA:O	1:CS:98:ILE:HG12	2.03	0.59
1:CX:95:ALA:O	1:CX:98:ILE:HG12	2.02	0.59
1:CI:317:ASP:HB3	1:CI:319:GLN:CD	2.23	0.59
1:BR:166:LEU:HD13	1:BR:166:LEU:C	2.23	0.59
1:BA:112:GLN:HB2	1:BA:198:SER:O	2.02	0.59
1:BT:111:ILE:HG22	1:BT:156:ARG:H	1.68	0.59
1:CR:43:SER:HA	1:CT:112:GLN:NE2	2.18	0.59
1:AC:111:ILE:O	1:AC:198:SER:O	2.24	0.59
1:CA:62:ARG:NH1	1:BY:75:ASP:OD2	138.57	0.59
1:BK:68:LEU:HD23	1:BK:195:VAL:CG2	2.33	0.59
1:AA:80:VAL:CG1	1:AA:185:LEU:HB3	2.40	0.59
1:BF:176:ARG:HD2	1:CF:168:TRP:CE2	2.37	0.59
1:BM:68:LEU:HD23	1:BM:195:VAL:HG22	1.85	0.59
1:CD:80:VAL:CG1	1:CD:185:LEU:HB2	2.33	0.59
1:AT:144:THR:HG23	1:AT:147:ALA:HB2	1.84	0.59
1:BV:98:ILE:C	1:BV:211:SER:O	2.40	0.59
1:BX:98:ILE:C	1:BX:211:SER:O	2.40	0.59
1:BC:98:ILE:HG22	1:AM:91:ARG:CZ	215.60	0.59
1:BC:98:ILE:CG2	1:AM:91:ARG:NE	216.94	0.59
1:CS:79:VAL:HG13	1:CS:80:VAL:N	2.16	0.59
1:AC:266:ASP:O	1:AC:314:TYR:HA	2.03	0.59
1:AY:314:TYR:HE1	1:AY:316:SER:N	2.00	0.59
1:CN:95:ALA:O	1:CN:98:ILE:HG12	2.03	0.59
1:CP:95:ALA:O	1:CP:98:ILE:HG12	2.03	0.59
1:CC:43:SER:O	1:CO:34:ARG:HD3	203.64	0.59
1:BV:111:ILE:HG22	1:BV:156:ARG:H	1.68	0.59
1:BZ:80:VAL:HG13	1:BZ:185:LEU:HB3	1.85	0.59
1:BS:80:VAL:HG13	1:BS:185:LEU:HB3	1.85	0.59
1:BB:111:ILE:HG23	1:BB:113:PRO:HD3	1.85	0.59
1:AO:111:ILE:O	1:AO:198:SER:O	2.20	0.59
1:CB:62:ARG:NH1	1:BU:75:ASP:OD2	118.60	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BV:127:PHE:HB3	1:BV:160:PRO:HB3	1.84	0.59
1:AO:168:TRP:CE2	1:CO:176:ARG:HG2	2.38	0.59
1:BL:253:ASP:HB2	1:BL:286:ALA:HB2	1.85	0.59
1:AJ:268:SER:HB3	1:AJ:273:ASP:O	2.03	0.59
1:BU:98:ILE:C	1:BU:211:SER:O	2.41	0.59
1:AS:266:ASP:O	1:AS:314:TYR:HA	2.03	0.59
1:CM:317:ASP:HB3	1:CM:319:GLN:CD	2.22	0.59
1:AE:314:TYR:CZ	1:AE:315:TYR:O	2.55	0.59
1:AO:61:SER:CB	1:AO:90:PRO:HD2	2.30	0.59
1:BX:101:ARG:NH1	1:BX:166:LEU:CD1	2.66	0.59
1:AD:111:ILE:O	1:AD:198:SER:O	2.20	0.59
1:BI:58:SER:HB3	1:BI:204:SER:CB	2.32	0.59
1:AO:320:PRO:O	1:AO:322:GLN:HG3	2.03	0.59
1:CB:163:THR:HG21	1:CB:167:LEU:HD11	1.84	0.59
1:AC:62:ARG:HG2	1:AC:62:ARG:HH11	1.69	0.59
1:AK:62:ARG:HG2	1:AK:62:ARG:HH11	1.68	0.59
1:AS:62:ARG:HH11	1:AS:62:ARG:HG2	1.67	0.59
1:BT:316:SER:HB2	1:BT:319:GLN:OE1	2.03	0.59
1:BY:253:ASP:HB2	1:BY:286:ALA:HB2	1.84	0.59
1:BN:112:GLN:HB2	1:BN:198:SER:O	2.02	0.59
1:AO:80:VAL:CG1	1:AO:185:LEU:HB3	2.33	0.59
1:CW:141:LEU:HD23	1:CW:141:LEU:N	2.18	0.59
1:BV:61:SER:CB	1:BV:90:PRO:HD2	2.24	0.59
1:BM:98:ILE:C	1:BM:211:SER:O	2.39	0.59
1:CO:122:GLY:C	1:CO:188:VAL:HB	2.23	0.59
1:AQ:314:TYR:HE1	1:AQ:316:SER:N	1.99	0.59
1:AA:314:TYR:HE1	1:AA:316:SER:N	1.99	0.59
1:AS:314:TYR:CZ	1:AS:315:TYR:O	2.55	0.59
1:CK:101:ARG:NH1	1:CK:166:LEU:CD1	2.65	0.59
1:BE:111:ILE:HG23	1:BE:113:PRO:HD3	1.85	0.59
1:BB:111:ILE:HG22	1:BB:156:ARG:H	1.67	0.59
1:BL:112:GLN:HB2	1:BL:198:SER:O	2.03	0.59
1:BC:127:PHE:HB3	1:BC:160:PRO:HB3	1.86	0.59
1:AC:80:VAL:CG1	1:AC:185:LEU:HB3	2.41	0.59
1:CV:163:THR:HG21	1:CV:167:LEU:HD11	1.84	0.59
1:AY:168:TRP:CE2	1:CY:176:ARG:HG2	2.38	0.59
1:BR:316:SER:HB2	1:BR:319:GLN:OE1	2.02	0.59
1:CU:58:SER:HA	1:CU:203:TRP:CZ3	2.37	0.59
1:AG:303:ASN:N	1:AG:305:ASN:OD1	2.34	0.59
1:CF:141:LEU:N	1:CF:141:LEU:HD23	2.17	0.59
1:CT:79:VAL:CG1	1:CT:185:LEU:O	2.49	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:91:ARG:NE	1:BV:98:ILE:CG2	2.66	0.59
1:BB:98:ILE:O	1:BB:211:SER:CA	2.51	0.59
1:CK:185:LEU:C	1:CK:186:LEU:HD23	2.23	0.59
1:AX:314:TYR:HE1	1:AX:316:SER:N	1.98	0.59
1:AG:266:ASP:O	1:AG:314:TYR:HA	2.03	0.59
1:AG:314:TYR:HE1	1:AG:316:SER:N	1.99	0.59
1:AC:314:TYR:CZ	1:AC:315:TYR:O	2.55	0.59
1:AJ:314:TYR:HE1	1:AJ:316:SER:N	1.99	0.59
1:CD:317:ASP:HB3	1:CD:319:GLN:CD	2.25	0.59
1:BQ:166:LEU:C	1:BQ:166:LEU:HD13	2.24	0.59
1:BD:112:GLN:HB2	1:BD:198:SER:O	2.03	0.59
1:BP:68:LEU:HD23	1:BP:195:VAL:CG2	2.33	0.59
1:BG:68:LEU:HD23	1:BG:195:VAL:CG2	2.33	0.59
1:CA:163:THR:HG21	1:CA:167:LEU:HD11	1.87	0.59
1:BF:316:SER:HB2	1:BF:319:GLN:OE1	2.03	0.59
1:BG:127:PHE:HB3	1:BG:160:PRO:HB3	1.85	0.59
1:CH:109:PHE:HB2	1:CH:158:VAL:CG1	2.32	0.59
1:AF:168:TRP:CE2	1:CF:176:ARG:HG2	2.38	0.59
1:BP:176:ARG:HD2	1:CP:168:TRP:CE2	2.38	0.59
1:CE:199:VAL:O	1:CE:199:VAL:HG13	2.02	0.59
1:BT:253:ASP:HB2	1:BT:286:ALA:HB2	1.83	0.59
1:AQ:303:ASN:N	1:AQ:305:ASN:OD1	2.35	0.59
1:AS:303:ASN:N	1:AS:305:ASN:OD1	2.35	0.59
1:CG:79:VAL:HG13	1:CG:80:VAL:N	2.18	0.59
1:AN:144:THR:HG23	1:AN:147:ALA:HB2	1.84	0.59
1:CD:101:ARG:NH1	1:CD:166:LEU:CD1	2.70	0.59
1:BN:98:ILE:C	1:BN:211:SER:O	2.41	0.59
1:AV:266:ASP:O	1:AV:314:TYR:HA	2.03	0.59
1:CR:122:GLY:C	1:CR:188:VAL:HB	2.23	0.59
1:AH:314:TYR:HE1	1:AH:316:SER:N	1.99	0.59
1:CR:317:ASP:HB3	1:CR:319:GLN:CD	2.24	0.59
1:AJ:63:ILE:HB	1:AJ:199:VAL:HG13	1.84	0.59
1:BT:80:VAL:HG13	1:BT:185:LEU:HB3	1.84	0.59
1:BS:68:LEU:HD23	1:BS:195:VAL:CG2	2.33	0.59
1:BH:112:GLN:HB2	1:BH:198:SER:O	2.03	0.59
1:AB:168:TRP:CE2	1:CB:176:ARG:HG2	2.38	0.59
1:BD:253:ASP:HB2	1:BD:286:ALA:HB2	1.83	0.59
1:AA:320:PRO:O	1:AA:322:GLN:HG3	2.02	0.59
1:CZ:85:VAL:HG13	1:CZ:86:PRO:HD2	1.85	0.59
1:AE:62:ARG:HH11	1:AE:62:ARG:HG2	1.68	0.59
1:CI:199:VAL:HG13	1:CI:199:VAL:O	2.02	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AX:303:ASN:N	1:AX:305:ASN:OD1	2.35	0.58
1:BD:98:ILE:O	1:BD:211:SER:CA	2.52	0.58
1:BC:98:ILE:O	1:BC:211:SER:CA	2.53	0.58
1:AH:91:ARG:NH2	1:BN:210:PRO:HB3	2.18	0.58
1:AV:314:TYR:HE1	1:AV:316:SER:N	2.01	0.58
1:AD:314:TYR:CZ	1:AD:315:TYR:O	2.56	0.58
1:BH:130:ASP:HB2	1:CH:100:GLN:NE2	2.15	0.58
1:CP:112:GLN:HE21	1:CQ:44:THR:H	1.51	0.58
1:BS:111:ILE:HG22	1:BS:156:ARG:H	1.68	0.58
1:BH:80:VAL:HG13	1:BH:185:LEU:HB3	1.85	0.58
1:CV:58:SER:HA	1:CV:203:TRP:CZ3	2.38	0.58
1:BP:111:ILE:HG21	1:BP:123:TYR:OH	2.03	0.58
1:BE:316:SER:HB2	1:BE:319:GLN:OE1	2.03	0.58
1:BZ:112:GLN:HB2	1:BZ:198:SER:O	2.03	0.58
1:BU:153:TRP:O	1:CX:151:LYS:NZ	2.36	0.58
1:CY:199:VAL:O	1:CY:199:VAL:HG13	2.03	0.58
1:AC:320:PRO:O	1:AC:322:GLN:HG3	2.04	0.58
1:AY:141:LEU:O	1:AY:144:THR:CG2	2.42	0.58
1:AF:144:THR:HG23	1:AF:147:ALA:HB2	1.84	0.58
1:AS:141:LEU:O	1:AS:144:THR:CG2	2.44	0.58
1:BI:98:ILE:C	1:BI:211:SER:O	2.42	0.58
1:BF:98:ILE:O	1:BF:211:SER:C	2.41	0.58
1:BA:98:ILE:C	1:BA:211:SER:O	2.41	0.58
1:BG:98:ILE:O	1:BG:211:SER:C	2.42	0.58
1:CQ:317:ASP:HB3	1:CQ:319:GLN:CD	2.22	0.58
1:BR:80:VAL:HG13	1:BR:185:LEU:HB3	1.85	0.58
1:BV:68:LEU:HD23	1:BV:195:VAL:CG2	2.33	0.58
1:BB:68:LEU:HD23	1:BB:195:VAL:CG2	2.36	0.58
1:AB:303:ASN:N	1:AB:305:ASN:OD1	2.35	0.58
1:CY:79:VAL:HG13	1:CY:80:VAL:N	2.17	0.58
1:CI:79:VAL:CG1	1:CI:185:LEU:O	2.51	0.58
1:BY:98:ILE:O	1:BY:211:SER:CA	2.50	0.58
1:AO:266:ASP:O	1:AO:314:TYR:HA	2.03	0.58
1:AF:314:TYR:HE1	1:AF:316:SER:N	1.99	0.58
1:BB:80:VAL:HG13	1:BB:185:LEU:HB3	1.84	0.58
1:BD:75:ASP:OD2	1:CI:62:ARG:NH1	2.33	0.58
1:BL:176:ARG:HD2	1:CL:168:TRP:CE2	2.38	0.58
1:BN:127:PHE:HB3	1:BN:160:PRO:HB3	1.85	0.58
1:BN:176:ARG:HD2	1:CN:168:TRP:CE2	2.38	0.58
1:CF:109:PHE:HB2	1:CF:158:VAL:CG1	2.34	0.58
1:AZ:168:TRP:CE2	1:CZ:176:ARG:HG2	2.37	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BA:115:CYS:HB2	1:BA:116:PRO:HD2	1.93	0.58
1:BX:176:ARG:HD2	1:CX:168:TRP:CE2	2.38	0.58
1:CN:111:ILE:O	1:CN:198:SER:O	2.21	0.58
1:AN:303:ASN:N	1:AN:305:ASN:OD1	2.35	0.58
1:CE:122:GLY:C	1:CE:188:VAL:HB	2.23	0.58
1:AU:141:LEU:O	1:AU:144:THR:CG2	2.42	0.58
1:CU:122:GLY:O	1:CU:188:VAL:HB	2.04	0.58
1:BX:98:ILE:O	1:BX:211:SER:C	2.42	0.58
1:CO:122:GLY:O	1:CO:188:VAL:HB	2.03	0.58
1:AM:266:ASP:O	1:AM:314:TYR:HA	2.03	0.58
1:AP:314:TYR:CZ	1:AP:315:TYR:O	2.55	0.58
1:AL:314:TYR:CZ	1:AL:315:TYR:O	2.56	0.58
1:AF:63:ILE:HB	1:AF:199:VAL:HG13	1.84	0.58
1:BM:111:ILE:HG22	1:BM:156:ARG:H	1.68	0.58
1:BC:111:ILE:HG21	1:BC:123:TYR:OH	2.08	0.58
1:BB:112:GLN:HB2	1:BB:198:SER:O	2.03	0.58
1:AN:119:THR:O	1:AN:192:THR:HB	2.03	0.58
1:BY:68:LEU:HD23	1:BY:195:VAL:CG2	2.33	0.58
1:CL:111:ILE:HG22	1:CL:113:PRO:HD3	1.84	0.58
1:BK:58:SER:HB3	1:BK:204:SER:HB3	1.84	0.58
1:BE:176:ARG:HD2	1:CE:168:TRP:CE2	2.38	0.58
1:AV:62:ARG:HG2	1:AV:62:ARG:HH11	1.68	0.58
1:CY:163:THR:HG21	1:CY:167:LEU:HD11	1.84	0.58
1:BS:98:ILE:C	1:BS:211:SER:O	2.42	0.58
1:BJ:98:ILE:O	1:BJ:211:SER:CA	2.51	0.58
1:CL:317:ASP:HB3	1:CL:319:GLN:CD	2.24	0.58
1:BY:130:ASP:HB2	1:CY:100:GLN:NE2	2.18	0.58
1:BI:101:ARG:NH2	1:BI:166:LEU:HD12	2.18	0.58
1:BJ:101:ARG:NH2	1:BJ:166:LEU:HD12	2.18	0.58
1:BM:166:LEU:HD13	1:BM:166:LEU:C	2.23	0.58
1:BS:111:ILE:HG21	1:BS:123:TYR:OH	2.04	0.58
1:CP:111:ILE:HG22	1:CP:113:PRO:HD3	1.84	0.58
1:BL:58:SER:HB3	1:BL:204:SER:CB	2.34	0.58
1:BT:176:ARG:HD2	1:CT:168:TRP:CE2	2.38	0.58
1:CP:109:PHE:HB2	1:CP:158:VAL:CG1	2.33	0.58
1:AN:168:TRP:CE2	1:CN:176:ARG:HG2	2.39	0.58
1:CM:109:PHE:HB2	1:CM:158:VAL:CG1	2.34	0.58
1:BP:127:PHE:HB3	1:BP:160:PRO:HB3	1.85	0.58
1:CV:191:ASN:OD1	1:CV:191:ASN:N	2.34	0.58
1:AG:62:ARG:HG2	1:AG:62:ARG:HH11	1.68	0.58
1:AT:122:GLY:HA3	1:AV:114:MET:SD	2.44	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BI:127:PHE:HB3	1:BI:160:PRO:HB3	1.85	0.58
1:AT:303:ASN:N	1:AT:305:ASN:OD1	2.34	0.58
1:BM:98:ILE:O	1:BM:211:SER:CA	2.51	0.58
1:BZ:98:ILE:O	1:BZ:211:SER:CA	2.52	0.58
1:BW:98:ILE:O	1:BW:211:SER:C	2.42	0.58
1:AF:314:TYR:CZ	1:AF:315:TYR:O	2.56	0.58
1:AD:266:ASP:O	1:AD:314:TYR:HA	2.03	0.58
1:AZ:314:TYR:HE1	1:AZ:316:SER:N	2.02	0.58
1:BC:166:LEU:C	1:BC:166:LEU:HD13	2.24	0.58
1:BC:111:ILE:HG22	1:BC:156:ARG:H	1.72	0.58
1:BY:111:ILE:HG23	1:BY:113:PRO:HD3	1.85	0.58
1:CI:43:SER:O	1:CY:34:ARG:HD3	2.03	0.58
1:AY:111:ILE:O	1:AY:198:SER:O	2.22	0.58
1:BC:68:LEU:HD23	1:BC:195:VAL:CG2	2.37	0.58
1:AV:168:TRP:CE2	1:CV:176:ARG:HG2	2.39	0.58
1:BA:183:LEU:HD12	1:BA:183:LEU:C	2.30	0.58
1:BX:253:ASP:HB2	1:BX:286:ALA:HB2	1.84	0.58
1:BX:68:LEU:HD23	1:BX:195:VAL:CG2	2.34	0.58
1:AL:303:ASN:N	1:AL:305:ASN:OD1	2.34	0.58
1:BK:98:ILE:O	1:BK:211:SER:CA	2.51	0.58
1:BD:98:ILE:CG2	1:AG:91:ARG:NE	89.09	0.58
1:BV:98:ILE:O	1:BV:211:SER:C	2.41	0.58
1:AF:266:ASP:O	1:AF:314:TYR:HA	2.03	0.58
1:CK:317:ASP:HB3	1:CK:319:GLN:CD	2.23	0.58
1:CA:95:ALA:O	1:CA:98:ILE:HG12	2.04	0.58
1:AN:63:ILE:HB	1:AN:199:VAL:HG13	1.84	0.58
1:BO:127:PHE:HB3	1:BO:160:PRO:HB3	1.84	0.58
1:BU:176:ARG:HD2	1:CU:168:TRP:CE2	2.37	0.58
1:AB:62:ARG:HG2	1:AB:62:ARG:HH11	1.68	0.58
1:BF:253:ASP:HB2	1:BF:286:ALA:HB2	1.86	0.58
1:CC:111:ILE:O	1:CC:198:SER:O	2.21	0.58
1:AM:320:PRO:O	1:AM:322:GLN:HG3	2.03	0.58
1:CZ:80:VAL:CG1	1:CZ:185:LEU:HB2	2.33	0.58
1:CL:75:ASP:OD1	1:CL:188:VAL:C	2.40	0.58
1:AD:91:ARG:NE	1:BF:98:ILE:CG2	2.67	0.58
1:BE:98:ILE:O	1:BE:211:SER:CA	2.52	0.58
1:BA:98:ILE:O	1:BA:211:SER:CA	2.52	0.58
1:BG:210:PRO:HB3	1:AP:91:ARG:NH2	2.19	0.58
1:CD:95:ALA:O	1:CD:98:ILE:HG12	2.04	0.58
1:CX:80:VAL:HG12	1:CX:185:LEU:CB	2.29	0.58
1:AP:314:TYR:HE1	1:AP:316:SER:N	2.01	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BC:101:ARG:NH2	1:BC:166:LEU:HD12	2.18	0.58
1:BP:166:LEU:C	1:BP:166:LEU:HD13	2.24	0.58
1:BG:111:ILE:HG21	1:BG:123:TYR:OH	2.03	0.58
1:BY:111:ILE:HG22	1:BY:156:ARG:H	1.68	0.58
1:BF:111:ILE:HG22	1:BF:156:ARG:H	1.68	0.58
1:AP:111:ILE:O	1:AP:198:SER:O	2.21	0.58
1:AF:320:PRO:O	1:AF:322:GLN:HG3	2.04	0.58
1:CT:163:THR:HG21	1:CT:167:LEU:HD11	1.85	0.58
1:AI:320:PRO:O	1:AI:322:GLN:HG3	2.04	0.58
1:BN:58:SER:HB3	1:BN:204:SER:HB3	1.85	0.58
1:CH:163:THR:HG21	1:CH:167:LEU:HD11	1.85	0.58
1:BB:98:ILE:CG2	1:AK:91:ARG:NE	2.67	0.58
1:BO:98:ILE:O	1:BO:211:SER:C	2.42	0.58
1:BO:98:ILE:O	1:BO:211:SER:CA	2.52	0.58
1:CF:75:ASP:OD1	1:CF:188:VAL:C	2.41	0.58
1:CK:80:VAL:CG1	1:CK:185:LEU:HB2	2.34	0.58
1:AI:266:ASP:O	1:AI:314:TYR:HA	2.03	0.58
1:BT:101:ARG:NH2	1:BT:166:LEU:HD12	2.18	0.58
1:BM:112:GLN:HB2	1:BM:198:SER:O	2.04	0.58
1:BC:112:GLN:HB2	1:BC:198:SER:O	2.05	0.58
1:BK:80:VAL:HG13	1:BK:185:LEU:HB3	1.84	0.58
1:AH:111:ILE:O	1:AH:198:SER:O	2.21	0.58
1:BJ:68:LEU:HD23	1:BJ:195:VAL:CG2	2.34	0.58
1:CT:111:ILE:HD11	1:CT:125:ALA:CB	2.34	0.58
1:CO:151:LYS:NZ	1:BW:153:TRP:O	2.37	0.58
1:BR:176:ARG:HD2	1:CR:168:TRP:CE2	2.39	0.58
1:CQ:185:LEU:C	1:CQ:186:LEU:HD23	2.24	0.58
1:BZ:98:ILE:O	1:BZ:211:SER:C	2.42	0.58
1:CX:122:GLY:C	1:CX:188:VAL:HB	2.24	0.58
1:AL:63:ILE:HB	1:AL:199:VAL:HG13	1.85	0.58
1:BJ:111:ILE:HG22	1:BJ:156:ARG:H	1.69	0.58
1:BI:112:GLN:HB2	1:BI:198:SER:O	2.03	0.58
1:BE:58:SER:HB3	1:BE:204:SER:CB	2.33	0.58
1:AQ:124:VAL:HG11	1:AQ:138:PHE:HD1	1.68	0.58
1:CY:191:ASN:OD1	1:CY:191:ASN:N	2.37	0.58
1:CV:109:PHE:HB2	1:CV:158:VAL:CG1	2.33	0.58
1:CZ:163:THR:HG21	1:CZ:167:LEU:HD11	1.85	0.58
1:CF:191:ASN:N	1:CF:191:ASN:OD1	2.34	0.58
1:BZ:68:LEU:HD23	1:BZ:195:VAL:HG22	1.86	0.58
1:BN:68:LEU:HD23	1:BN:195:VAL:HG22	1.85	0.58
1:BJ:176:ARG:HD2	1:CJ:168:TRP:CE2	2.38	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AG:144:THR:HG23	1:AG:147:ALA:HB2	1.85	0.57
1:CC:101:ARG:NH1	1:CC:166:LEU:CD1	2.68	0.57
1:AZ:141:LEU:O	1:AZ:144:THR:CG2	2.45	0.57
1:BT:98:ILE:HA	1:BT:211:SER:O	2.04	0.57
1:AP:266:ASP:O	1:AP:314:TYR:HA	2.04	0.57
1:BQ:111:ILE:HG22	1:BQ:156:ARG:H	1.68	0.57
1:BJ:111:ILE:HG23	1:BJ:113:PRO:HD3	1.86	0.57
1:BI:111:ILE:HG22	1:BI:156:ARG:H	1.69	0.57
1:AV:119:THR:O	1:AV:192:THR:HB	2.04	0.57
1:AB:138:PHE:CE2	1:AK:62:ARG:CZ	2.87	0.57
1:BZ:58:SER:HB3	1:BZ:204:SER:HB3	1.86	0.57
1:AY:320:PRO:O	1:AY:322:GLN:HG3	2.03	0.57
1:BQ:127:PHE:HB3	1:BQ:160:PRO:HB3	1.86	0.57
1:AC:114:MET:SD	1:AS:122:GLY:HA3	2.44	0.57
1:BT:115:CYS:HB2	1:BT:116:PRO:HD2	1.86	0.57
1:BO:68:LEU:HD23	1:BO:195:VAL:HG22	1.86	0.57
1:AU:320:PRO:O	1:AU:322:GLN:HG3	2.04	0.57
1:AS:168:TRP:CE2	1:CS:176:ARG:HG2	2.39	0.57
1:BQ:176:ARG:HD2	1:CQ:168:TRP:CE2	2.38	0.57
1:BQ:253:ASP:HB2	1:BQ:286:ALA:HB2	1.85	0.57
1:AH:303:ASN:N	1:AH:305:ASN:OD1	2.35	0.57
1:CY:122:GLY:C	1:CY:188:VAL:HB	2.23	0.57
1:CL:122:GLY:O	1:CL:188:VAL:HB	2.03	0.57
1:CI:75:ASP:OD1	1:CI:188:VAL:C	2.41	0.57
1:BH:98:ILE:O	1:BH:211:SER:CA	2.51	0.57
1:BH:98:ILE:O	1:BH:211:SER:C	2.41	0.57
1:BB:210:PRO:HB3	1:AK:91:ARG:NH2	2.19	0.57
1:AH:91:ARG:HE	1:BN:98:ILE:HG22	1.69	0.57
1:BZ:98:ILE:HA	1:BZ:211:SER:O	2.04	0.57
1:AR:314:TYR:CZ	1:AR:315:TYR:O	2.57	0.57
1:CZ:317:ASP:HB3	1:CZ:319:GLN:CD	2.23	0.57
1:AA:111:ILE:O	1:AA:198:SER:O	2.22	0.57
1:BX:127:PHE:HB3	1:BX:160:PRO:HB3	1.85	0.57
1:AK:109:PHE:HB2	1:AK:158:VAL:CG1	2.34	0.57
1:BR:58:SER:HB3	1:BR:204:SER:HB3	1.86	0.57
1:CN:109:PHE:HB2	1:CN:158:VAL:CG1	2.34	0.57
1:AD:168:TRP:CE2	1:CD:176:ARG:HG2	2.42	0.57
1:CF:163:THR:HG21	1:CF:167:LEU:HD11	1.86	0.57
1:BJ:98:ILE:C	1:BJ:211:SER:O	2.42	0.57
1:BU:98:ILE:O	1:BU:211:SER:C	2.43	0.57
1:BT:98:ILE:HG22	1:AV:91:ARG:HE	1.69	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AV:63:ILE:HB	1:AV:199:VAL:HG13	1.86	0.57
1:BQ:98:ILE:O	1:BQ:211:SER:C	2.43	0.57
1:AK:314:TYR:CZ	1:AK:315:TYR:O	2.58	0.57
1:BB:166:LEU:HD13	1:BB:166:LEU:C	2.26	0.57
1:AL:111:ILE:O	1:AL:198:SER:O	2.22	0.57
1:BB:58:SER:HB3	1:BB:204:SER:CB	2.34	0.57
1:BG:58:SER:HB3	1:BG:204:SER:CB	2.33	0.57
1:CR:109:PHE:HB2	1:CR:158:VAL:CG1	2.34	0.57
1:CS:191:ASN:N	1:CS:191:ASN:OD1	2.34	0.57
1:CU:199:VAL:O	1:CU:199:VAL:HG13	2.03	0.57
1:CU:109:PHE:HB2	1:CU:158:VAL:CG1	2.35	0.57
1:AA:168:TRP:CE2	1:CA:176:ARG:HG2	2.41	0.57
1:BX:58:SER:HB3	1:BX:204:SER:HB3	1.85	0.57
1:AZ:303:ASN:N	1:AZ:305:ASN:OD1	2.35	0.57
1:CD:75:ASP:OD1	1:CD:188:VAL:C	2.42	0.57
1:AH:141:LEU:O	1:AH:144:THR:CG2	2.45	0.57
1:BI:98:ILE:O	1:BI:211:SER:CA	2.52	0.57
1:BL:98:ILE:O	1:BL:211:SER:C	2.42	0.57
1:CQ:101:ARG:NH1	1:CQ:166:LEU:CD1	2.68	0.57
1:AZ:266:ASP:O	1:AZ:314:TYR:HA	2.03	0.57
1:AT:314:TYR:HE1	1:AT:316:SER:N	2.01	0.57
1:CJ:75:ASP:OD1	1:CJ:188:VAL:C	2.42	0.57
1:AD:63:ILE:HB	1:AD:199:VAL:HG13	1.86	0.57
1:AJ:98:ILE:CG2	1:BR:91:ARG:NH1	2.67	0.57
1:CA:112:GLN:NE2	1:CG:43:SER:HA	2.20	0.57
1:BE:111:ILE:HG22	1:BE:156:ARG:H	1.70	0.57
1:BD:58:SER:HB3	1:BD:204:SER:CB	2.34	0.57
1:BX:68:LEU:HD23	1:BX:195:VAL:HG22	1.85	0.57
1:CJ:163:THR:HG21	1:CJ:167:LEU:HD11	1.85	0.57
1:BJ:253:ASP:HB2	1:BJ:286:ALA:HB2	1.87	0.57
1:BQ:316:SER:HB2	1:BQ:319:GLN:OE1	2.03	0.57
1:BW:115:CYS:HB2	1:BW:116:PRO:HD2	1.86	0.57
1:CB:75:ASP:OD1	1:CB:188:VAL:C	2.43	0.57
1:BW:98:ILE:C	1:BW:211:SER:O	2.42	0.57
1:CX:185:LEU:C	1:CX:186:LEU:HD23	2.24	0.57
1:CS:122:GLY:O	1:CS:188:VAL:HB	2.04	0.57
1:AY:314:TYR:CZ	1:AY:315:TYR:O	2.57	0.57
1:BA:111:ILE:HG23	1:BA:113:PRO:HD3	1.91	0.57
1:AX:111:ILE:O	1:AX:198:SER:O	2.22	0.57
1:AO:119:THR:O	1:AO:192:THR:HB	2.05	0.57
1:AT:320:PRO:O	1:AT:322:GLN:HG3	2.04	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AC:168:TRP:CE2	1:CC:176:ARG:HG2	2.40	0.57
1:AU:168:TRP:CE2	1:CU:176:ARG:HG2	2.40	0.57
1:CC:191:ASN:N	1:CC:191:ASN:OD1	2.37	0.57
1:CW:79:VAL:CG1	1:CW:185:LEU:O	2.52	0.57
1:CP:79:VAL:CG1	1:CP:185:LEU:O	2.50	0.57
1:CC:75:ASP:OD1	1:CC:188:VAL:C	2.43	0.57
1:AP:141:LEU:O	1:AP:144:THR:CG2	2.45	0.57
1:CI:185:LEU:C	1:CI:186:LEU:HD23	2.24	0.57
1:CQ:95:ALA:O	1:CQ:98:ILE:HG12	2.04	0.57
1:AR:266:ASP:O	1:AR:314:TYR:HA	2.05	0.57
1:AZ:111:ILE:O	1:AZ:198:SER:O	2.22	0.57
1:AS:119:THR:O	1:AS:192:THR:HB	2.05	0.57
1:CD:85:VAL:HG13	1:CD:86:PRO:HD2	1.95	0.57
1:BH:127:PHE:HB3	1:BH:160:PRO:HB3	1.86	0.57
1:CM:163:THR:HG21	1:CM:167:LEU:HD11	1.86	0.57
1:BG:112:GLN:HB2	1:BG:198:SER:O	2.05	0.57
1:CB:118:ASN:HA	1:BY:116:PRO:CB	2.34	0.57
1:AV:144:THR:HG23	1:AV:147:ALA:HB2	1.86	0.57
1:CR:95:ALA:O	1:CR:98:ILE:HG12	2.04	0.57
1:CV:101:ARG:NH1	1:CV:166:LEU:CD1	2.67	0.57
1:BS:130:ASP:HB2	1:CS:100:GLN:NE2	2.17	0.57
1:AT:63:ILE:HB	1:AT:199:VAL:HG13	1.86	0.57
1:BN:166:LEU:HD13	1:BN:166:LEU:C	2.25	0.57
1:BX:111:ILE:HG21	1:BX:123:TYR:OH	2.04	0.57
1:CP:43:SER:HA	1:CQ:112:GLN:NE2	2.19	0.57
1:AK:115:CYS:HB2	1:AK:116:PRO:HD2	1.86	0.57
1:AL:119:THR:O	1:AL:192:THR:HB	2.04	0.57
1:CC:62:ARG:NH1	1:BX:75:ASP:OD2	228.22	0.57
1:CH:111:ILE:HG22	1:CH:113:PRO:HD3	1.86	0.57
1:AT:80:VAL:CG1	1:AT:185:LEU:HB3	2.35	0.57
1:BU:112:GLN:HB2	1:BU:198:SER:O	2.05	0.57
1:BY:316:SER:HB2	1:BY:319:GLN:OE1	2.04	0.57
1:CR:199:VAL:O	1:CR:199:VAL:HG13	2.04	0.57
1:BC:62:ARG:NH2	1:CM:138:PHE:CD2	218.77	0.57
1:AE:320:PRO:O	1:AE:322:GLN:HG3	2.04	0.57
1:CW:80:VAL:CG1	1:CW:185:LEU:HB2	2.35	0.57
1:BR:98:ILE:O	1:BR:211:SER:CA	2.53	0.57
1:CO:101:ARG:NH1	1:CO:166:LEU:CD1	2.67	0.57
1:CD:112:GLN:NE2	1:CI:43:SER:HA	2.19	0.57
1:AX:320:PRO:O	1:AX:322:GLN:HG3	2.05	0.57
1:BN:115:CYS:HB2	1:BN:116:PRO:HD2	1.87	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CY:75:ASP:OD1	1:CY:188:VAL:C	2.43	0.57
1:CC:79:VAL:CG1	1:CC:185:LEU:O	2.51	0.57
1:AX:266:ASP:O	1:AX:314:TYR:HA	2.04	0.57
1:BR:98:ILE:O	1:BR:211:SER:C	2.44	0.57
1:BG:98:ILE:O	1:BG:211:SER:CA	2.53	0.57
1:BX:101:ARG:NH2	1:BX:166:LEU:HD12	2.20	0.57
1:CL:112:GLN:NE2	1:CL:155:SER:OG	2.38	0.57
1:AI:111:ILE:O	1:AI:198:SER:O	2.23	0.57
1:CA:111:ILE:HG22	1:CA:113:PRO:HD3	1.86	0.57
1:BR:68:LEU:HD23	1:BR:195:VAL:CG2	2.35	0.57
1:BO:58:SER:HB3	1:BO:204:SER:CB	2.35	0.57
1:CW:111:ILE:O	1:CW:198:SER:O	2.23	0.57
1:AZ:320:PRO:O	1:AZ:322:GLN:HG3	2.04	0.57
1:CE:111:ILE:O	1:CE:198:SER:O	2.23	0.57
1:CZ:101:ARG:NH1	1:CZ:166:LEU:CD1	2.68	0.57
1:BH:98:ILE:C	1:BH:211:SER:O	2.43	0.57
1:CU:101:ARG:NH1	1:CU:166:LEU:CD1	2.67	0.57
1:CB:101:ARG:NH1	1:CB:166:LEU:CD1	2.67	0.57
1:BY:98:ILE:HA	1:BY:211:SER:O	2.05	0.57
1:AE:63:ILE:HB	1:AE:199:VAL:HG13	1.86	0.57
1:BI:166:LEU:HD13	1:BI:166:LEU:C	2.26	0.57
1:BD:163:THR:OG1	1:BD:165:THR:CG2	2.53	0.57
1:AS:63:ILE:HB	1:AS:199:VAL:HG13	1.87	0.57
1:BT:58:SER:HB3	1:BT:204:SER:CB	2.35	0.57
1:CE:202:ARG:HH12	1:CH:46:THR:HB	1.70	0.57
1:BW:127:PHE:HB3	1:BW:160:PRO:HB3	1.86	0.57
1:AX:62:ARG:HG2	1:AX:62:ARG:HH11	1.69	0.57
1:AH:80:VAL:CG1	1:AH:185:LEU:HB3	2.35	0.57
1:CT:191:ASN:OD1	1:CT:191:ASN:N	2.37	0.57
1:BL:68:LEU:HD23	1:BL:195:VAL:HG22	1.87	0.57
1:CD:191:ASN:OD1	1:CD:191:ASN:N	2.34	0.57
1:AN:320:PRO:O	1:AN:322:GLN:HG3	2.05	0.57
1:BW:253:ASP:HB2	1:BW:286:ALA:HB2	1.86	0.57
1:BO:98:ILE:C	1:BO:211:SER:O	2.43	0.56
1:BY:98:ILE:C	1:BY:211:SER:O	2.43	0.56
1:BY:98:ILE:O	1:BY:211:SER:C	2.42	0.56
1:BK:163:THR:OG1	1:BK:165:THR:CG2	2.53	0.56
1:BQ:91:ARG:NH1	1:AZ:98:ILE:HG23	2.20	0.56
1:BG:111:ILE:HG22	1:BG:156:ARG:H	1.69	0.56
1:BG:111:ILE:HG23	1:BG:113:PRO:HD3	1.86	0.56
1:AN:111:ILE:O	1:AN:198:SER:O	2.23	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AU:119:THR:O	1:AU:192:THR:HB	2.05	0.56
1:CM:111:ILE:HG22	1:CM:113:PRO:HD3	1.87	0.56
1:AD:138:PHE:CE2	1:AW:62:ARG:CZ	2.87	0.56
1:BW:58:SER:HB3	1:BW:204:SER:CB	2.35	0.56
1:CH:85:VAL:HG13	1:CH:86:PRO:HD2	1.87	0.56
1:AW:142:GLN:O	1:AW:142:GLN:NE2	2.38	0.56
1:AV:320:PRO:O	1:AV:322:GLN:HG3	2.04	0.56
1:CP:185:LEU:C	1:CP:186:LEU:HD23	2.25	0.56
1:CD:185:LEU:C	1:CD:186:LEU:HD23	2.25	0.56
1:CE:80:VAL:HG12	1:CE:185:LEU:CB	2.25	0.56
1:AJ:141:LEU:O	1:AJ:144:THR:CG2	2.45	0.56
1:BU:61:SER:CB	1:BU:90:PRO:HD2	2.26	0.56
1:CT:75:ASP:OD1	1:CT:188:VAL:C	2.44	0.56
1:AN:91:ARG:NH2	1:BP:98:ILE:HG22	2.20	0.56
1:BI:98:ILE:O	1:BI:211:SER:C	2.42	0.56
1:BA:98:ILE:CG2	1:AI:91:ARG:NE	2.68	0.56
1:BT:98:ILE:O	1:BT:211:SER:C	2.43	0.56
1:CR:75:ASP:OD1	1:CR:188:VAL:C	2.44	0.56
1:BK:165:THR:OG1	1:BK:166:LEU:N	2.38	0.56
1:BW:101:ARG:NH2	1:BW:166:LEU:HD12	2.19	0.56
1:BO:111:ILE:HG22	1:BO:156:ARG:H	1.69	0.56
1:BZ:111:ILE:HG21	1:BZ:123:TYR:OH	2.05	0.56
1:AQ:115:CYS:HB2	1:AQ:116:PRO:HD2	1.86	0.56
1:CM:111:ILE:HD11	1:CM:125:ALA:CB	2.35	0.56
1:BI:68:LEU:HD23	1:BI:195:VAL:CG2	2.35	0.56
1:BV:58:SER:HB3	1:BV:204:SER:CB	2.35	0.56
1:CH:191:ASN:N	1:CH:191:ASN:OD1	2.36	0.56
1:AC:268:SER:HB3	1:AC:273:ASP:O	2.08	0.56
1:AR:115:CYS:HB2	1:AR:116:PRO:HD2	1.88	0.56
1:AQ:80:VAL:CG1	1:AQ:185:LEU:HB3	2.35	0.56
1:AH:320:PRO:O	1:AH:322:GLN:HG3	2.05	0.56
1:BR:112:GLN:HB2	1:BR:198:SER:O	2.04	0.56
1:AJ:320:PRO:O	1:AJ:322:GLN:HG3	2.05	0.56
1:AW:281:HIS:CE1	1:AW:301:TRP:HB3	2.40	0.56
1:BQ:112:GLN:HB2	1:BQ:198:SER:O	2.06	0.56
1:CU:122:GLY:C	1:CU:188:VAL:HB	2.24	0.56
1:BV:98:ILE:O	1:BV:211:SER:CA	2.52	0.56
1:BL:98:ILE:C	1:BL:211:SER:O	2.43	0.56
1:BA:98:ILE:HA	1:BA:211:SER:O	2.05	0.56
1:BZ:98:ILE:C	1:BZ:211:SER:O	2.42	0.56
1:AO:91:ARG:NE	1:BW:98:ILE:CG2	2.68	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BQ:98:ILE:O	1:BQ:211:SER:CA	2.53	0.56
1:AU:314:TYR:CE1	1:AU:316:SER:CA	2.85	0.56
1:AJ:314:TYR:CZ	1:AJ:315:TYR:O	2.59	0.56
1:AC:61:SER:CB	1:AC:90:PRO:HD2	2.37	0.56
1:CY:95:ALA:O	1:CY:98:ILE:HG12	2.05	0.56
1:BU:166:LEU:C	1:BU:166:LEU:HD13	2.26	0.56
1:CV:98:ILE:HD11	1:CV:99:PHE:CE2	2.40	0.56
1:BB:165:THR:OG1	1:BB:166:LEU:N	2.44	0.56
1:BS:166:LEU:C	1:BS:166:LEU:HD13	2.25	0.56
1:BX:111:ILE:HG22	1:BX:156:ARG:H	1.70	0.56
1:BB:111:ILE:HG21	1:BB:123:TYR:OH	2.07	0.56
1:BW:111:ILE:HG22	1:BW:156:ARG:H	1.69	0.56
1:AQ:119:THR:O	1:AQ:192:THR:HB	2.06	0.56
1:BP:111:ILE:HG22	1:BP:156:ARG:H	1.69	0.56
1:CS:163:THR:HG21	1:CS:167:LEU:HD11	1.87	0.56
1:BR:325:LEU:HD22	1:BR:329:THR:HG21	1.86	0.56
1:CL:163:THR:HG21	1:CL:167:LEU:HD11	1.87	0.56
1:BK:253:ASP:HB2	1:BK:286:ALA:HB2	1.86	0.56
1:CU:111:ILE:HG22	1:CU:113:PRO:HD3	1.88	0.56
1:CU:111:ILE:HD11	1:CU:125:ALA:CB	2.35	0.56
1:CU:111:ILE:O	1:CU:198:SER:O	2.22	0.56
1:BL:74:THR:HA	1:BL:190:ASN:ND2	2.20	0.56
1:BF:68:LEU:HD23	1:BF:195:VAL:HG22	1.87	0.56
1:CD:120:GLY:HA3	1:BH:116:PRO:HD3	151.13	0.56
1:AJ:168:TRP:CE2	1:CJ:176:ARG:HG2	2.40	0.56
1:AG:168:TRP:CE2	1:CG:176:ARG:HG2	2.38	0.56
1:CZ:75:ASP:OD1	1:CZ:188:VAL:C	2.43	0.56
1:CA:185:LEU:C	1:CA:186:LEU:HD23	2.28	0.56
1:BE:98:ILE:O	1:BE:211:SER:C	2.44	0.56
1:BG:98:ILE:C	1:BG:211:SER:O	2.43	0.56
1:CA:101:ARG:NH1	1:CA:166:LEU:CD1	2.69	0.56
1:AR:314:TYR:HE1	1:AR:316:SER:N	2.03	0.56
1:BK:166:LEU:HD13	1:BK:166:LEU:C	2.26	0.56
1:BZ:166:LEU:HD13	1:BZ:166:LEU:C	2.26	0.56
1:AA:115:CYS:HB2	1:AA:116:PRO:HD2	1.89	0.56
1:AM:111:ILE:O	1:AM:198:SER:O	2.23	0.56
1:AG:138:PHE:CE2	1:AP:62:ARG:CZ	2.89	0.56
1:CN:111:ILE:HG22	1:CN:113:PRO:HD3	1.87	0.56
1:AM:80:VAL:CG1	1:AM:185:LEU:HB3	2.35	0.56
1:AB:320:PRO:O	1:AB:322:GLN:HG3	2.05	0.56
1:CE:79:VAL:HG13	1:CE:80:VAL:N	2.21	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CX:101:ARG:NH1	1:CX:166:LEU:CD1	2.67	0.56
1:CI:101:ARG:NH1	1:CI:166:LEU:CD1	2.68	0.56
1:CN:101:ARG:NH1	1:CN:166:LEU:CD1	2.67	0.56
1:AT:61:SER:CB	1:AT:90:PRO:HD2	2.32	0.56
1:BD:166:LEU:HD13	1:BD:166:LEU:C	2.25	0.56
1:AI:168:TRP:CE2	1:CI:176:ARG:HG2	2.40	0.56
1:AP:281:HIS:CE1	1:AP:301:TRP:HB3	2.41	0.56
1:CR:191:ASN:OD1	1:CR:191:ASN:N	2.33	0.56
1:BS:325:LEU:HD22	1:BS:329:THR:HG21	1.87	0.56
1:BW:112:GLN:HB2	1:BW:198:SER:O	2.06	0.56
1:BJ:127:PHE:HB3	1:BJ:160:PRO:HB3	1.87	0.56
1:BW:74:THR:HA	1:BW:190:ASN:ND2	2.21	0.56
1:BF:98:ILE:O	1:BF:211:SER:CA	2.53	0.56
1:AW:314:TYR:CZ	1:AW:315:TYR:O	2.59	0.56
1:BJ:133:ASP:OD2	1:CJ:100:GLN:OE1	2.24	0.56
1:CG:95:ALA:O	1:CG:98:ILE:HG12	2.05	0.56
1:CA:43:SER:O	1:CD:34:ARG:HD3	2.05	0.56
1:BR:111:ILE:HG23	1:BR:113:PRO:HD3	1.88	0.56
1:BC:115:CYS:HB2	1:BC:116:PRO:HD2	1.93	0.56
1:BU:111:ILE:HG21	1:BU:123:TYR:OH	2.05	0.56
1:BU:68:LEU:HD23	1:BU:195:VAL:CG2	2.36	0.56
1:CH:111:ILE:HD11	1:CH:125:ALA:CB	2.35	0.56
1:AT:138:PHE:CE2	1:AV:62:ARG:CZ	2.89	0.56
1:BY:115:CYS:HB2	1:BY:116:PRO:HD2	1.88	0.56
1:CK:163:THR:OG1	1:CK:165:THR:HG23	2.04	0.56
1:AU:281:HIS:CE1	1:AU:301:TRP:HB3	2.41	0.56
1:AB:80:VAL:CG1	1:AB:185:LEU:HB3	2.36	0.56
1:CA:191:ASN:OD1	1:CA:191:ASN:N	2.38	0.56
1:AX:109:PHE:HB2	1:AX:158:VAL:CG1	2.35	0.56
1:AN:80:VAL:CG1	1:AN:185:LEU:HB3	2.36	0.56
1:BB:127:PHE:HB3	1:BB:160:PRO:HB3	1.88	0.56
1:BF:115:CYS:HB2	1:BF:116:PRO:HD2	1.88	0.56
1:CG:191:ASN:OD1	1:CG:191:ASN:N	2.39	0.56
1:CE:79:VAL:CG1	1:CE:185:LEU:O	2.52	0.56
1:AQ:141:LEU:O	1:AQ:144:THR:CG2	2.41	0.56
1:BD:98:ILE:HA	1:BD:211:SER:O	2.06	0.56
1:CQ:75:ASP:OD1	1:CQ:188:VAL:C	2.42	0.56
1:BE:98:ILE:C	1:BE:211:SER:O	2.43	0.56
1:CW:317:ASP:HB3	1:CW:319:GLN:CD	2.24	0.56
1:CN:185:LEU:C	1:CN:186:LEU:HD23	2.26	0.56
1:BX:80:VAL:HG13	1:BX:185:LEU:HB3	1.87	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BH:111:ILE:HG21	1:BH:123:TYR:OH	2.06	0.56
1:BO:115:CYS:HB2	1:BO:116:PRO:HD2	1.87	0.56
1:AQ:320:PRO:O	1:AQ:322:GLN:HG3	2.04	0.56
1:CV:111:ILE:HG22	1:CV:113:PRO:HD3	1.86	0.56
1:CV:111:ILE:O	1:CV:198:SER:O	2.23	0.56
1:BU:325:LEU:HD22	1:BU:329:THR:HG21	1.87	0.56
1:AW:109:PHE:HB2	1:AW:158:VAL:CG1	2.35	0.56
1:BK:127:PHE:HB3	1:BK:160:PRO:HB3	1.86	0.56
1:CM:79:VAL:CG1	1:CM:185:LEU:O	2.50	0.56
1:CC:79:VAL:HG13	1:CC:80:VAL:N	2.20	0.56
1:CK:75:ASP:OD1	1:CK:188:VAL:C	2.43	0.56
1:AQ:266:ASP:O	1:AQ:314:TYR:HA	2.04	0.56
1:CS:101:ARG:NH1	1:CS:166:LEU:CD1	2.67	0.56
1:CN:79:VAL:CG1	1:CN:185:LEU:O	2.51	0.56
1:CA:34:ARG:HD3	1:CC:43:SER:O	159.00	0.56
1:BA:111:ILE:HG22	1:BA:156:ARG:H	1.72	0.56
1:AB:111:ILE:O	1:AB:198:SER:O	2.24	0.56
1:BF:127:PHE:HB3	1:BF:160:PRO:HB3	1.86	0.56
1:AG:320:PRO:O	1:AG:322:GLN:HG3	2.06	0.56
1:CG:111:ILE:O	1:CG:198:SER:O	2.23	0.56
1:AE:168:TRP:CE2	1:CE:176:ARG:HG2	2.41	0.56
1:BS:127:PHE:HB3	1:BS:160:PRO:HB3	1.88	0.56
1:CO:163:THR:HG21	1:CO:167:LEU:HD11	1.88	0.56
1:BO:112:GLN:HB2	1:BO:198:SER:O	2.06	0.56
1:AB:310:ASP:HB3	1:AB:312:VAL:HG22	1.90	0.56
1:CL:79:VAL:CG1	1:CL:185:LEU:O	2.52	0.56
1:CU:185:LEU:C	1:CU:186:LEU:HD23	2.27	0.56
1:CY:101:ARG:NH1	1:CY:166:LEU:CD1	2.68	0.56
1:BT:165:THR:OG1	1:BT:166:LEU:N	2.38	0.56
1:CK:95:ALA:O	1:CK:98:ILE:HG12	2.06	0.56
1:BL:91:ARG:NH1	1:AU:98:ILE:CG2	2.68	0.56
1:AF:111:ILE:HG21	1:AF:123:TYR:CZ	2.41	0.56
1:CE:43:SER:HA	1:CH:112:GLN:NE2	2.21	0.56
1:CB:111:ILE:HD11	1:CB:125:ALA:CB	2.37	0.56
1:BA:75:ASP:OD2	1:CY:62:ARG:NH1	138.09	0.56
1:CE:111:ILE:HG22	1:CE:113:PRO:HD3	1.87	0.56
1:BY:127:PHE:HB3	1:BY:160:PRO:HB3	1.86	0.56
1:AB:122:GLY:HA3	1:AK:114:MET:SD	2.46	0.56
1:CU:191:ASN:OD1	1:CU:191:ASN:N	2.39	0.56
1:BY:183:LEU:HD12	1:BY:183:LEU:C	2.26	0.56
1:AW:141:LEU:O	1:AW:144:THR:CG2	2.45	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BF:98:ILE:HA	1:BF:211:SER:O	2.06	0.56
1:BB:98:ILE:CG2	1:AF:91:ARG:NE	88.99	0.56
1:CH:101:ARG:NH1	1:CH:166:LEU:CD1	2.68	0.56
1:CO:185:LEU:C	1:CO:186:LEU:HD23	2.25	0.56
1:CO:75:ASP:OD1	1:CO:188:VAL:C	2.43	0.56
1:AH:91:ARG:NE	1:BN:98:ILE:HG22	2.20	0.56
1:BT:210:PRO:HB3	1:AV:91:ARG:NH2	2.21	0.56
1:CV:95:ALA:O	1:CV:98:ILE:HG12	2.06	0.56
1:AI:62:ARG:HG2	1:AI:62:ARG:HH11	1.70	0.56
1:BY:58:SER:HB3	1:BY:204:SER:CB	2.36	0.56
1:BF:68:LEU:HD23	1:BF:195:VAL:CG2	2.36	0.56
1:AA:122:GLY:HA3	1:AT:114:MET:SD	30.58	0.56
1:AH:109:PHE:HB2	1:AH:158:VAL:CG1	2.36	0.56
1:BV:112:GLN:HB2	1:BV:198:SER:O	2.06	0.56
1:AW:80:VAL:CG1	1:AW:185:LEU:HB3	2.36	0.56
1:AB:268:SER:HB3	1:AB:273:ASP:O	2.06	0.56
1:CL:185:LEU:C	1:CL:186:LEU:HD23	2.25	0.55
1:CM:95:ALA:O	1:CM:98:ILE:HG12	2.07	0.55
1:BD:101:ARG:NH2	1:BD:166:LEU:HD12	2.20	0.55
1:BE:166:LEU:C	1:BE:166:LEU:HD13	2.27	0.55
1:CO:111:ILE:HD11	1:CO:125:ALA:CB	2.36	0.55
1:BR:58:SER:HB3	1:BR:204:SER:CB	2.36	0.55
1:AB:122:GLY:HA3	1:AF:114:MET:SD	126.48	0.55
1:AP:320:PRO:O	1:AP:322:GLN:HG3	2.05	0.55
1:AF:80:VAL:CG1	1:AF:185:LEU:HB3	2.37	0.55
1:BL:183:LEU:HD12	1:BL:183:LEU:C	2.27	0.55
1:CP:79:VAL:HG13	1:CP:80:VAL:N	2.21	0.55
1:CB:79:VAL:HG13	1:CB:80:VAL:N	2.23	0.55
1:CE:75:ASP:OD1	1:CE:188:VAL:C	2.43	0.55
1:BQ:98:ILE:C	1:BQ:211:SER:O	2.44	0.55
1:BG:98:ILE:HA	1:BG:211:SER:O	2.06	0.55
1:AR:111:ILE:O	1:AR:198:SER:O	2.25	0.55
1:BU:58:SER:HB3	1:BU:204:SER:CB	2.37	0.55
1:CC:111:ILE:HG22	1:CC:113:PRO:HD3	1.89	0.55
1:BQ:115:CYS:HB2	1:BQ:116:PRO:HD2	1.87	0.55
1:AN:268:SER:HB3	1:AN:273:ASP:O	2.06	0.55
1:CL:124:VAL:O	1:CL:124:VAL:HG13	2.06	0.55
1:BC:183:LEU:C	1:BC:183:LEU:HD12	2.26	0.55
1:AI:142:GLN:O	1:AI:142:GLN:NE2	2.39	0.55
1:AY:101:ARG:CZ	1:AY:166:LEU:HD23	2.36	0.55
1:CC:185:LEU:C	1:CC:186:LEU:HD23	2.27	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AF:141:LEU:O	1:AF:144:THR:CG2	2.45	0.55
1:BD:98:ILE:HG22	1:AG:91:ARG:NH2	88.50	0.55
1:BW:98:ILE:O	1:BW:211:SER:CA	2.53	0.55
1:CH:75:ASP:OD1	1:CH:188:VAL:C	2.45	0.55
1:AE:314:TYR:CE1	1:AE:316:SER:CA	2.87	0.55
1:BG:166:LEU:HD13	1:BG:166:LEU:C	2.27	0.55
1:BB:153:TRP:O	1:CF:151:LYS:NZ	21.22	0.55
1:BM:111:ILE:HG21	1:BM:123:TYR:OH	2.06	0.55
1:BS:111:ILE:HG23	1:BS:113:PRO:HD3	1.87	0.55
1:BM:68:LEU:HD23	1:BM:195:VAL:CG2	2.36	0.55
1:AA:109:PHE:HB2	1:AA:158:VAL:CG1	2.38	0.55
1:CO:191:ASN:OD1	1:CO:191:ASN:N	2.40	0.55
1:AA:114:MET:SD	1:AV:122:GLY:HA3	2.46	0.55
1:CG:75:ASP:OD1	1:CG:188:VAL:C	2.45	0.55
1:BV:98:ILE:HA	1:BV:211:SER:O	2.07	0.55
1:BS:98:ILE:O	1:BS:211:SER:C	2.44	0.55
1:BL:98:ILE:O	1:BL:211:SER:CA	2.54	0.55
1:BU:98:ILE:O	1:BU:211:SER:CA	2.55	0.55
1:BE:98:ILE:HA	1:BE:211:SER:O	2.06	0.55
1:CX:75:ASP:OD1	1:CX:188:VAL:C	2.44	0.55
1:CR:111:ILE:HD11	1:CR:125:ALA:CB	2.37	0.55
1:AY:266:ASP:O	1:AY:314:TYR:HA	2.06	0.55
1:BW:163:THR:OG1	1:BW:165:THR:CG2	2.55	0.55
1:BZ:101:ARG:NH2	1:BZ:166:LEU:HD12	2.22	0.55
1:BD:111:ILE:HG23	1:BD:113:PRO:HD3	1.92	0.55
1:AS:111:ILE:O	1:AS:198:SER:O	2.25	0.55
1:AC:281:HIS:CE1	1:AC:301:TRP:HB3	2.42	0.55
1:CL:109:PHE:HB2	1:CL:158:VAL:CG1	2.36	0.55
1:AU:109:PHE:HB2	1:AU:158:VAL:CG1	2.37	0.55
1:AS:310:ASP:HB3	1:AS:312:VAL:HG22	1.86	0.55
1:BN:61:SER:CB	1:BN:90:PRO:HD2	2.25	0.55
1:BM:98:ILE:HA	1:BM:211:SER:O	2.06	0.55
1:CV:75:ASP:OD1	1:CV:188:VAL:C	2.45	0.55
1:BY:166:LEU:HD13	1:BY:166:LEU:C	2.26	0.55
1:BA:80:VAL:CG1	1:BA:185:LEU:HB3	2.38	0.55
1:AE:115:CYS:HB2	1:AE:116:PRO:HD2	1.87	0.55
1:CA:111:ILE:HD11	1:CA:125:ALA:CB	2.37	0.55
1:BK:58:SER:HB3	1:BK:204:SER:CB	2.37	0.55
1:CC:111:ILE:HD11	1:CC:125:ALA:CB	2.37	0.55
1:AY:268:SER:HB3	1:AY:273:ASP:O	2.07	0.55
1:BB:281:HIS:ND1	1:BB:301:TRP:HB3	2.22	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BK:115:CYS:HB2	1:BK:116:PRO:HD2	1.89	0.55
1:AC:143:ALA:HB1	1:AM:91:ARG:HD2	220.17	0.55
1:CC:100:GLN:HA	1:CC:213:GLU:OE2	2.11	0.55
1:AB:314:TYR:CE1	1:AB:316:SER:CA	2.85	0.55
1:AL:314:TYR:HE1	1:AL:316:SER:N	2.02	0.55
1:BU:101:ARG:NH2	1:BU:166:LEU:HD12	2.21	0.55
1:CC:43:SER:O	1:CO:34:ARG:CD	202.74	0.55
1:BO:111:ILE:HG21	1:BO:123:TYR:OH	2.06	0.55
1:BZ:111:ILE:HG22	1:BZ:156:ARG:H	1.71	0.55
1:CR:112:GLN:HE21	1:CT:44:THR:H	1.55	0.55
1:BQ:58:SER:HB3	1:BQ:204:SER:CB	2.37	0.55
1:BF:58:SER:HB3	1:BF:204:SER:CB	2.37	0.55
1:AB:281:HIS:CE1	1:AB:301:TRP:HB3	2.42	0.55
1:AS:109:PHE:HB2	1:AS:158:VAL:CG1	2.37	0.55
1:BK:183:LEU:HD12	1:BK:183:LEU:C	2.27	0.55
1:BL:111:ILE:HG23	1:BL:113:PRO:HD3	1.89	0.55
1:AQ:281:HIS:CE1	1:AQ:301:TRP:HB3	2.41	0.55
1:BP:112:GLN:HB2	1:BP:198:SER:O	2.06	0.55
1:AQ:168:TRP:CE2	1:CQ:176:ARG:HG2	2.41	0.55
1:AQ:109:PHE:HB2	1:AQ:158:VAL:CG1	2.36	0.55
1:CL:122:GLY:C	1:CL:188:VAL:HB	2.26	0.55
1:BC:98:ILE:CG2	1:AM:91:ARG:CZ	215.90	0.55
1:AX:314:TYR:CE1	1:AX:316:SER:HA	2.42	0.55
1:CR:79:VAL:HG13	1:CR:80:VAL:N	2.22	0.55
1:AN:314:TYR:HE1	1:AN:316:SER:N	1.99	0.55
1:CJ:79:VAL:HG13	1:CJ:80:VAL:N	2.21	0.55
1:BS:101:ARG:NH2	1:BS:166:LEU:HD12	2.21	0.55
1:CP:44:THR:H	1:CQ:112:GLN:HE21	1.55	0.55
1:CX:163:THR:OG1	1:CX:165:THR:HG23	2.06	0.55
1:BL:80:VAL:HG13	1:BL:185:LEU:HB3	1.88	0.55
1:CB:191:ASN:OD1	1:CB:191:ASN:N	2.38	0.55
1:BR:115:CYS:HB2	1:BR:116:PRO:HD2	1.88	0.55
1:BI:325:LEU:HD22	1:BI:329:THR:HG21	1.89	0.55
1:BM:75:ASP:OD2	1:CO:62:ARG:NH1	2.31	0.55
1:AF:281:HIS:CE1	1:AF:301:TRP:HB3	2.42	0.55
1:AH:168:TRP:CE2	1:CH:176:ARG:HG2	2.42	0.55
1:BL:153:TRP:O	1:CU:151:LYS:NZ	2.40	0.55
1:CP:75:ASP:OD1	1:CP:188:VAL:C	2.44	0.55
1:CB:185:LEU:C	1:CB:186:LEU:HD23	2.26	0.55
1:AH:144:THR:HG23	1:AH:147:ALA:HB2	1.89	0.55
1:AG:141:LEU:O	1:AG:144:THR:CG2	2.44	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AN:91:ARG:NE	1:BP:98:ILE:CG2	2.69	0.55
1:AL:141:LEU:O	1:AL:144:THR:CG2	2.46	0.55
1:BL:98:ILE:HG22	1:AU:91:ARG:NH2	2.22	0.55
1:CO:95:ALA:O	1:CO:98:ILE:HG12	2.07	0.55
1:AL:266:ASP:O	1:AL:314:TYR:HA	2.07	0.55
1:AK:314:TYR:HE1	1:AK:316:SER:N	2.04	0.55
1:CA:98:ILE:HD11	1:CA:99:PHE:CE2	2.42	0.55
1:BH:166:LEU:C	1:BH:166:LEU:HD13	2.27	0.55
1:BH:101:ARG:NH2	1:BH:166:LEU:HD12	2.21	0.55
1:BG:80:VAL:HG13	1:BG:185:LEU:HB3	1.88	0.55
1:BD:156:ARG:NH2	1:CD:34:ARG:HG3	23.45	0.55
1:BT:74:THR:HA	1:BT:190:ASN:ND2	2.22	0.55
1:AE:111:ILE:HG21	1:AE:123:TYR:CZ	2.42	0.55
1:BM:58:SER:HB3	1:BM:204:SER:CB	2.37	0.55
1:BI:281:HIS:ND1	1:BI:301:TRP:HB3	2.22	0.55
1:AD:109:PHE:HB2	1:AD:158:VAL:CG1	2.37	0.55
1:AD:253:ASP:OD1	1:AD:285:PHE:N	2.42	0.55
1:CW:185:LEU:C	1:CW:186:LEU:HD23	2.26	0.55
1:CT:79:VAL:HG13	1:CT:80:VAL:N	2.21	0.55
1:BT:61:SER:CB	1:BT:90:PRO:HD2	2.28	0.55
1:AD:91:ARG:NH2	1:BH:210:PRO:HB3	131.89	0.55
1:BU:98:ILE:CG2	1:AX:91:ARG:NE	2.70	0.55
1:CF:101:ARG:NH1	1:CF:166:LEU:CD1	2.67	0.55
1:CR:185:LEU:C	1:CR:186:LEU:HD23	2.27	0.55
1:AW:314:TYR:HE1	1:AW:316:SER:N	2.02	0.55
1:CF:79:VAL:HG13	1:CF:80:VAL:N	2.21	0.55
1:BF:163:THR:OG1	1:BF:165:THR:CG2	2.55	0.55
1:AS:80:VAL:CG1	1:AS:185:LEU:HB3	2.37	0.55
1:CW:112:GLN:NE2	1:CW:155:SER:OG	2.40	0.55
1:AT:111:ILE:O	1:AT:198:SER:O	2.25	0.55
1:CK:163:THR:HG21	1:CK:167:LEU:HD11	1.88	0.55
1:BP:75:ASP:OD2	1:CQ:62:ARG:NH1	2.31	0.55
1:AJ:109:PHE:HB2	1:AJ:158:VAL:CG1	2.37	0.55
1:AX:168:TRP:CE2	1:CX:176:ARG:HG2	2.42	0.55
1:BB:115:CYS:HB2	1:BB:116:PRO:HD2	1.89	0.55
1:AS:320:PRO:O	1:AS:322:GLN:HG3	2.06	0.55
1:AO:281:HIS:CE1	1:AO:301:TRP:HB3	2.42	0.55
1:CU:124:VAL:O	1:CU:124:VAL:HG13	2.07	0.55
1:CI:191:ASN:N	1:CI:191:ASN:OD1	2.39	0.55
1:BU:281:HIS:ND1	1:BU:301:TRP:HB3	2.21	0.55
1:CI:80:VAL:CG1	1:CI:185:LEU:HB2	2.36	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BX:98:ILE:O	1:BX:211:SER:CA	2.54	0.55
1:CO:80:VAL:CG1	1:CO:185:LEU:HB2	2.37	0.55
1:CJ:101:ARG:NH1	1:CJ:166:LEU:CD1	2.70	0.55
1:CW:101:ARG:NH1	1:CW:166:LEU:CD1	2.68	0.55
1:CS:122:GLY:C	1:CS:188:VAL:HB	2.26	0.55
1:BA:163:THR:OG1	1:BA:165:THR:CG2	2.57	0.55
1:CL:95:ALA:O	1:CL:98:ILE:HG12	2.07	0.55
1:BW:111:ILE:HG21	1:BW:123:TYR:OH	2.06	0.55
1:AY:119:THR:HG23	1:AY:193:ASP:CB	2.37	0.55
1:CO:111:ILE:HG22	1:CO:113:PRO:HD3	1.89	0.55
1:BN:111:ILE:HG23	1:BN:113:PRO:HD3	1.89	0.55
1:BN:80:VAL:CG1	1:BN:185:LEU:HB3	2.36	0.55
1:BH:68:LEU:HD23	1:BH:195:VAL:CG2	2.37	0.55
1:CW:109:PHE:HB2	1:CW:158:VAL:CG1	2.37	0.55
1:AF:268:SER:HB3	1:AF:273:ASP:O	2.07	0.55
1:BK:74:THR:HA	1:BK:190:ASN:ND2	2.22	0.55
1:AT:109:PHE:HB2	1:AT:158:VAL:CG1	2.37	0.55
1:CE:109:PHE:HB2	1:CE:158:VAL:CG1	2.37	0.55
1:AI:310:ASP:HB3	1:AI:312:VAL:HG22	1.89	0.54
1:AC:310:ASP:HB3	1:AC:312:VAL:HG22	1.93	0.54
1:BC:98:ILE:HA	1:BC:211:SER:O	2.07	0.54
1:BT:166:LEU:C	1:BT:166:LEU:HD13	2.27	0.54
1:CB:111:ILE:HG22	1:CB:113:PRO:HD3	1.90	0.54
1:BA:58:SER:HB3	1:BA:204:SER:CB	2.39	0.54
1:CI:111:ILE:HG22	1:CI:113:PRO:HD3	1.88	0.54
1:BN:68:LEU:HD23	1:BN:195:VAL:CG2	2.37	0.54
1:BN:325:LEU:HD22	1:BN:329:THR:HG21	1.88	0.54
1:AY:109:PHE:HB2	1:AY:158:VAL:CG1	2.37	0.54
1:AX:281:HIS:CE1	1:AX:301:TRP:HB3	2.42	0.54
1:AP:142:GLN:O	1:AP:142:GLN:NE2	2.40	0.54
1:AY:80:VAL:CG1	1:AY:185:LEU:HB3	2.37	0.54
1:AF:124:VAL:HG11	1:AF:138:PHE:HD1	1.72	0.54
1:CG:185:LEU:C	1:CG:186:LEU:HD23	2.27	0.54
1:AR:279:TYR:CE2	1:AR:311:GLY:O	2.60	0.54
1:AB:314:TYR:CE1	1:AB:316:SER:HA	2.41	0.54
1:BF:101:ARG:NH2	1:BF:166:LEU:HD12	2.22	0.54
1:BD:150:ALA:HB2	1:BD:156:ARG:HD3	1.90	0.54
1:AG:115:CYS:HB2	1:AG:116:PRO:HD2	1.89	0.54
1:AC:124:VAL:HG11	1:AC:138:PHE:HD1	1.73	0.54
1:BP:80:VAL:CG1	1:BP:185:LEU:HB3	2.37	0.54
1:BN:111:ILE:HG22	1:BN:156:ARG:H	1.71	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BA:281:HIS:ND1	1:BA:301:TRP:HB3	2.23	0.54
1:CL:190:ASN:N	1:CL:190:ASN:HD22	2.04	0.54
1:BX:112:GLN:HB2	1:BX:198:SER:O	2.07	0.54
1:AJ:114:MET:SD	1:AR:122:GLY:HA3	2.48	0.54
1:CD:79:VAL:HG13	1:CD:80:VAL:N	2.22	0.54
1:CU:79:VAL:CG1	1:CU:185:LEU:O	2.53	0.54
1:CU:79:VAL:HG13	1:CU:80:VAL:N	2.21	0.54
1:AB:91:ARG:NE	1:BO:98:ILE:CG2	133.58	0.54
1:CU:95:ALA:O	1:CU:98:ILE:HG12	2.08	0.54
1:BK:101:ARG:NH2	1:BK:166:LEU:HD12	2.21	0.54
1:CF:79:VAL:CG1	1:CF:185:LEU:O	2.52	0.54
1:BV:101:ARG:NH2	1:BV:166:LEU:HD12	2.21	0.54
1:BF:112:GLN:HB2	1:BF:198:SER:O	2.06	0.54
1:AB:115:CYS:HB2	1:AB:116:PRO:HD2	1.91	0.54
1:AG:119:THR:HG23	1:AG:193:ASP:CB	2.37	0.54
1:AZ:115:CYS:HB2	1:AZ:116:PRO:HD2	1.88	0.54
1:BE:68:LEU:HD23	1:BE:195:VAL:CG2	2.38	0.54
1:CY:111:ILE:HG22	1:CY:113:PRO:HD3	1.89	0.54
1:CL:163:THR:OG1	1:CL:165:THR:HG23	2.06	0.54
1:BM:74:THR:HA	1:BM:190:ASN:ND2	2.22	0.54
1:AP:80:VAL:CG1	1:AP:185:LEU:HB3	2.37	0.54
1:AZ:109:PHE:HB2	1:AZ:158:VAL:CG1	2.36	0.54
1:CW:124:VAL:O	1:CW:124:VAL:HG13	2.06	0.54
1:BO:281:HIS:ND1	1:BO:301:TRP:HB3	2.22	0.54
1:AE:109:PHE:HB2	1:AE:158:VAL:CG1	2.38	0.54
1:BS:168:TRP:CE2	1:AS:176:ARG:HD2	2.43	0.54
1:BE:127:PHE:HB3	1:BE:160:PRO:HB3	1.89	0.54
1:BU:98:ILE:HA	1:BU:211:SER:O	2.08	0.54
1:BA:210:PRO:HB3	1:AI:91:ARG:NH2	2.23	0.54
1:BT:98:ILE:O	1:BT:211:SER:CA	2.54	0.54
1:AM:314:TYR:CE1	1:AM:316:SER:HA	2.41	0.54
1:CI:95:ALA:O	1:CI:98:ILE:HG12	2.06	0.54
1:AJ:266:ASP:O	1:AJ:314:TYR:HA	2.08	0.54
1:AJ:61:SER:CB	1:AJ:90:PRO:HD2	2.35	0.54
1:BF:165:THR:OG1	1:BF:166:LEU:N	2.39	0.54
1:BZ:163:THR:OG1	1:BZ:165:THR:CG2	2.54	0.54
1:CM:112:GLN:NE2	1:CO:43:SER:HA	2.22	0.54
1:BQ:111:ILE:HG21	1:BQ:123:TYR:OH	2.07	0.54
1:BE:80:VAL:HG13	1:BE:185:LEU:HB3	1.88	0.54
1:CQ:111:ILE:HG22	1:CQ:113:PRO:HD3	1.89	0.54
1:CK:111:ILE:HG22	1:CK:113:PRO:HD3	1.88	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CZ:111:ILE:HG22	1:CZ:113:PRO:HD3	1.89	0.54
1:CQ:163:THR:OG1	1:CQ:165:THR:HG23	2.08	0.54
1:CS:111:ILE:HD11	1:CS:125:ALA:CB	2.38	0.54
1:BE:325:LEU:HD22	1:BE:329:THR:HG21	1.89	0.54
1:BO:325:LEU:HD22	1:BO:329:THR:HG21	1.88	0.54
1:CE:46:THR:HB	1:CH:202:ARG:HH12	1.72	0.54
1:BE:112:GLN:HB2	1:BE:198:SER:O	2.08	0.54
1:BM:85:VAL:HG23	1:BM:86:PRO:HD2	1.89	0.54
1:AP:124:VAL:HG11	1:AP:138:PHE:HD1	1.72	0.54
1:AE:310:ASP:HB3	1:AE:312:VAL:HG22	1.90	0.54
1:AI:253:ASP:OD1	1:AI:285:PHE:N	2.41	0.54
1:BX:61:SER:CB	1:BX:90:PRO:HD2	2.27	0.54
1:BN:98:ILE:HA	1:BN:211:SER:O	2.07	0.54
1:CH:79:VAL:HG13	1:CH:80:VAL:N	2.22	0.54
1:CS:75:ASP:OD1	1:CS:188:VAL:C	2.45	0.54
1:AQ:61:SER:CB	1:AQ:90:PRO:HD2	2.34	0.54
1:AK:61:SER:CB	1:AK:90:PRO:HD2	2.32	0.54
1:BJ:165:THR:OG1	1:BJ:166:LEU:N	2.40	0.54
1:BW:166:LEU:C	1:BW:166:LEU:HD13	2.27	0.54
1:BO:165:THR:OG1	1:BO:166:LEU:N	2.41	0.54
1:BM:101:ARG:NH2	1:BM:166:LEU:HD12	2.22	0.54
1:BR:111:ILE:HG22	1:BR:156:ARG:H	1.73	0.54
1:CX:111:ILE:HG22	1:CX:113:PRO:HD3	1.88	0.54
1:BU:80:VAL:CG1	1:BU:185:LEU:HB3	2.37	0.54
1:BL:68:LEU:HD23	1:BL:195:VAL:CG2	2.37	0.54
1:AD:281:HIS:CE1	1:AD:301:TRP:HB3	2.45	0.54
1:BH:325:LEU:HD22	1:BH:329:THR:HG21	1.89	0.54
1:AX:268:SER:HB3	1:AX:273:ASP:O	2.07	0.54
1:BP:168:TRP:CE2	1:AP:176:ARG:HD2	2.43	0.54
1:AQ:268:SER:HB3	1:AQ:273:ASP:O	2.08	0.54
1:AH:281:HIS:CE1	1:AH:301:TRP:HB3	2.42	0.54
1:AM:109:PHE:HB2	1:AM:158:VAL:CG1	2.38	0.54
1:CD:101:ARG:CZ	1:CD:166:LEU:CD1	2.91	0.54
1:CE:101:ARG:NH1	1:CE:166:LEU:CD1	2.69	0.54
1:CR:111:ILE:HG22	1:CR:113:PRO:HD3	1.90	0.54
1:CJ:95:ALA:O	1:CJ:98:ILE:HG12	2.07	0.54
1:AD:61:SER:CB	1:AD:90:PRO:HD2	2.34	0.54
1:BV:166:LEU:C	1:BV:166:LEU:HD13	2.28	0.54
1:BM:163:THR:OG1	1:BM:165:THR:CG2	2.56	0.54
1:CA:34:ARG:HD3	1:CD:43:SER:O	23.90	0.54
1:BF:111:ILE:HG21	1:BF:123:TYR:OH	2.08	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CE:112:GLN:NE2	1:CH:43:SER:HA	2.23	0.54
1:AJ:119:THR:HG23	1:AJ:193:ASP:CB	2.38	0.54
1:AJ:281:HIS:CE1	1:AJ:301:TRP:HB3	2.42	0.54
1:AC:101:ARG:CZ	1:AC:166:LEU:HD23	2.40	0.54
1:AG:268:SER:HB3	1:AG:273:ASP:O	2.08	0.54
1:BP:281:HIS:ND1	1:BP:301:TRP:HB3	2.23	0.54
1:CC:85:VAL:HG13	1:CC:86:PRO:HD2	1.91	0.54
1:AA:281:HIS:CE1	1:AA:301:TRP:HB3	2.43	0.54
1:CZ:80:VAL:HG11	1:CZ:185:LEU:HB2	1.90	0.54
1:BP:61:SER:CB	1:BP:90:PRO:HD2	2.27	0.54
1:CX:79:VAL:HG13	1:CX:80:VAL:N	2.22	0.54
1:CB:98:ILE:HD11	1:CB:99:PHE:CE2	2.43	0.54
1:BI:165:THR:OG1	1:BI:166:LEU:N	2.39	0.54
1:CF:185:LEU:C	1:CF:186:LEU:HD23	2.27	0.54
1:AN:61:SER:HB2	1:AN:89:LEU:HD22	1.90	0.54
1:BY:101:ARG:NH2	1:BY:166:LEU:HD12	2.22	0.54
1:BO:166:LEU:C	1:BO:166:LEU:HD13	2.28	0.54
1:CA:43:SER:HA	1:CY:112:GLN:NE2	135.76	0.54
1:CD:43:SER:HA	1:CI:112:GLN:NE2	2.22	0.54
1:BK:111:ILE:HG22	1:BK:156:ARG:H	1.73	0.54
1:BW:80:VAL:CG1	1:BW:185:LEU:HB3	2.38	0.54
1:BP:115:CYS:HB2	1:BP:116:PRO:HD2	1.90	0.54
1:AL:281:HIS:CE1	1:AL:301:TRP:HB3	2.42	0.54
1:AV:80:VAL:CG1	1:AV:185:LEU:HB3	2.38	0.54
1:CD:46:THR:HB	1:CI:202:ARG:HH12	1.73	0.54
1:BR:99:PHE:CD1	1:BR:99:PHE:N	2.76	0.54
1:BN:74:THR:HA	1:BN:190:ASN:ND2	2.23	0.54
1:BN:281:HIS:ND1	1:BN:301:TRP:HB3	2.22	0.54
1:AM:314:TYR:CG	1:AM:315:TYR:N	2.76	0.54
1:AA:314:TYR:CE1	1:AA:316:SER:HA	2.43	0.54
1:AF:314:TYR:CG	1:AF:315:TYR:N	2.76	0.54
1:BN:163:THR:OG1	1:BN:165:THR:CG2	2.56	0.54
1:BY:123:TYR:HB2	1:BY:185:LEU:HD11	1.90	0.54
1:BK:111:ILE:HG21	1:BK:123:TYR:OH	2.06	0.54
1:CV:112:GLN:NE2	1:CZ:43:SER:HA	2.22	0.54
1:AD:124:VAL:HG11	1:AD:138:PHE:HD1	1.75	0.54
1:AM:268:SER:HB3	1:AM:273:ASP:O	2.07	0.54
1:BA:325:LEU:HD22	1:BA:329:THR:HG21	1.89	0.54
1:AG:80:VAL:CG1	1:AG:185:LEU:HB3	2.37	0.54
1:BD:183:LEU:HD12	1:BD:183:LEU:C	2.28	0.54
1:BB:325:LEU:HD22	1:BB:329:THR:HG21	1.90	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AP:168:TRP:CE2	1:CP:176:ARG:HG2	2.42	0.54
1:AI:281:HIS:CE1	1:AI:301:TRP:HB3	2.42	0.54
1:AC:279:TYR:CE2	1:AC:311:GLY:O	2.60	0.54
1:AI:279:TYR:CE2	1:AI:311:GLY:O	2.60	0.54
1:BB:98:ILE:HG23	1:AK:91:ARG:HG2	1.90	0.54
1:BJ:98:ILE:HA	1:BJ:211:SER:O	2.08	0.54
1:AQ:314:TYR:CE1	1:AQ:316:SER:HA	2.43	0.54
1:BC:163:THR:OG1	1:BC:165:THR:CG2	2.58	0.54
1:CN:79:VAL:HG13	1:CN:80:VAL:N	2.23	0.54
1:BK:111:ILE:HG23	1:BK:113:PRO:HD3	1.89	0.54
1:AU:80:VAL:CG1	1:AU:185:LEU:HB3	2.38	0.54
1:BP:58:SER:HB3	1:BP:204:SER:CB	2.37	0.54
1:BF:183:LEU:C	1:BF:183:LEU:HD12	2.28	0.54
1:CN:191:ASN:OD1	1:CN:191:ASN:N	2.37	0.54
1:AE:281:HIS:CE1	1:AE:301:TRP:HB3	2.43	0.54
1:BM:281:HIS:ND1	1:BM:301:TRP:HB3	2.23	0.54
1:BX:115:CYS:HB2	1:BX:116:PRO:HD2	1.90	0.54
1:CW:191:ASN:OD1	1:CW:191:ASN:N	2.37	0.54
1:CM:185:LEU:C	1:CM:186:LEU:HD23	2.28	0.54
1:CZ:79:VAL:HG13	1:CZ:80:VAL:N	2.23	0.54
1:AM:279:TYR:CE2	1:AM:311:GLY:O	2.61	0.54
1:CA:80:VAL:CG1	1:CA:185:LEU:HB2	2.40	0.54
1:AH:314:TYR:CE1	1:AH:316:SER:CA	2.87	0.54
1:CJ:185:LEU:C	1:CJ:186:LEU:HD23	2.28	0.54
1:BL:163:THR:OG1	1:BL:165:THR:CG2	2.56	0.54
1:AE:98:ILE:HG23	1:BM:91:ARG:NH1	2.23	0.54
1:AZ:162:TYR:N	1:AZ:162:TYR:CD1	2.76	0.54
1:BF:111:ILE:HG23	1:BF:113:PRO:HD3	1.89	0.54
1:BS:112:GLN:HB2	1:BS:198:SER:O	2.07	0.54
1:BI:111:ILE:HG23	1:BI:113:PRO:HD3	1.89	0.54
1:BN:58:SER:HB3	1:BN:204:SER:CB	2.38	0.54
1:CV:111:ILE:HD11	1:CV:125:ALA:CB	2.38	0.54
1:AM:101:ARG:CZ	1:AM:166:LEU:HD23	2.37	0.54
1:AT:281:HIS:CE1	1:AT:301:TRP:HB3	2.43	0.54
1:CZ:191:ASN:N	1:CZ:191:ASN:OD1	2.37	0.54
1:AG:281:HIS:CE1	1:AG:301:TRP:HB3	2.43	0.54
1:CD:124:VAL:HG13	1:CD:124:VAL:O	2.10	0.54
1:BC:325:LEU:HD22	1:BC:329:THR:HG21	1.90	0.54
1:AA:253:ASP:OD1	1:AA:285:PHE:N	2.42	0.53
1:CD:80:VAL:HG11	1:CD:185:LEU:HB2	1.91	0.53
1:CT:185:LEU:C	1:CT:186:LEU:HD23	2.29	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CV:185:LEU:C	1:CV:186:LEU:HD23	2.29	0.53
1:BU:163:THR:OG1	1:BU:165:THR:CG2	2.56	0.53
1:BF:166:LEU:C	1:BF:166:LEU:HD13	2.27	0.53
1:BE:163:THR:OG1	1:BE:165:THR:CG2	2.55	0.53
1:BO:80:VAL:CG1	1:BO:185:LEU:HB3	2.37	0.53
1:CM:34:ARG:CD	1:CW:43:SER:O	2.56	0.53
1:CC:112:GLN:HE21	1:CJ:44:THR:H	1.55	0.53
1:AC:62:ARG:CZ	1:AS:138:PHE:CE2	2.91	0.53
1:AT:124:VAL:HG11	1:AT:138:PHE:HD1	1.74	0.53
1:CK:190:ASN:HD22	1:CK:190:ASN:N	2.06	0.53
1:BL:99:PHE:N	1:BL:99:PHE:CD1	2.75	0.53
1:AA:314:TYR:CE1	1:AA:316:SER:CA	2.88	0.53
1:BR:101:ARG:NH2	1:BR:166:LEU:HD12	2.23	0.53
1:BH:111:ILE:HG22	1:BH:156:ARG:H	1.74	0.53
1:CD:63:ILE:HD12	1:CD:88:LEU:CD1	2.46	0.53
1:CL:111:ILE:HD11	1:CL:125:ALA:CB	2.38	0.53
1:CY:111:ILE:HD11	1:CY:125:ALA:CB	2.38	0.53
1:BZ:58:SER:HB3	1:BZ:204:SER:CB	2.37	0.53
1:BX:58:SER:HB3	1:BX:204:SER:CB	2.38	0.53
1:AU:268:SER:HB3	1:AU:273:ASP:O	2.08	0.53
1:AS:101:ARG:CZ	1:AS:166:LEU:HD23	2.38	0.53
1:BS:281:HIS:ND1	1:BS:301:TRP:HB3	2.23	0.53
1:AS:281:HIS:CE1	1:AS:301:TRP:HB3	2.44	0.53
1:AV:281:HIS:CE1	1:AV:301:TRP:HB3	2.43	0.53
1:BC:281:HIS:ND1	1:BC:301:TRP:HB3	2.24	0.53
1:BD:281:HIS:ND1	1:BD:301:TRP:HB3	2.23	0.53
1:AM:63:ILE:HB	1:AM:199:VAL:HG13	1.89	0.53
1:AU:124:VAL:HG11	1:AU:138:PHE:HD1	1.74	0.53
1:CC:124:VAL:O	1:CC:124:VAL:HG13	2.07	0.53
1:AT:101:ARG:CZ	1:AT:166:LEU:HD23	2.38	0.53
1:AF:305:ASN:N	1:AF:305:ASN:OD1	2.42	0.53
1:AC:91:ARG:NH2	1:BS:210:PRO:HB3	2.22	0.53
1:BR:98:ILE:HA	1:BR:211:SER:O	2.08	0.53
1:BQ:98:ILE:HA	1:BQ:211:SER:O	2.09	0.53
1:AQ:314:TYR:CG	1:AQ:315:TYR:N	2.76	0.53
1:CH:95:ALA:O	1:CH:98:ILE:HG12	2.08	0.53
1:CX:98:ILE:HD11	1:CX:99:PHE:CE2	2.43	0.53
1:BP:101:ARG:NH2	1:BP:166:LEU:HD12	2.24	0.53
1:BB:101:ARG:NH2	1:BB:166:LEU:HD12	2.25	0.53
1:BO:163:THR:OG1	1:BO:165:THR:CG2	2.56	0.53
1:CB:44:THR:H	1:CU:112:GLN:HE21	27.27	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CD:112:GLN:NE2	1:CD:155:SER:OG	2.40	0.53
1:AA:119:THR:HG23	1:AA:193:ASP:CB	2.36	0.53
1:CA:109:PHE:HB2	1:CA:158:VAL:HG12	1.90	0.53
1:CN:111:ILE:HD11	1:CN:125:ALA:CB	2.38	0.53
1:CU:130:ASP:OD2	1:CU:176:ARG:NH2	2.41	0.53
1:AM:168:TRP:CE2	1:CM:176:ARG:HG2	2.44	0.53
1:BI:115:CYS:HB2	1:BI:116:PRO:HD2	1.90	0.53
1:BJ:115:CYS:HB2	1:BJ:116:PRO:HD2	1.89	0.53
1:CV:199:VAL:HG13	1:CV:199:VAL:O	2.08	0.53
1:AZ:268:SER:HB3	1:AZ:273:ASP:O	2.08	0.53
1:BM:99:PHE:CD1	1:BM:99:PHE:N	2.77	0.53
1:AD:310:ASP:HB3	1:AD:312:VAL:HG22	1.90	0.53
1:CE:185:LEU:C	1:CE:186:LEU:HD23	2.28	0.53
1:BA:61:SER:CB	1:BA:90:PRO:HD2	2.28	0.53
1:BP:98:ILE:HA	1:BP:211:SER:O	2.08	0.53
1:CM:91:ARG:HD2	1:CO:98:ILE:HB	1.91	0.53
1:BA:166:LEU:HD13	1:BA:167:LEU:N	2.24	0.53
1:AD:98:ILE:O	1:BH:91:ARG:NH1	119.94	0.53
1:CC:34:ARG:HD3	1:CR:43:SER:O	2.08	0.53
1:CK:44:THR:H	1:CL:112:GLN:HE21	1.57	0.53
1:AD:119:THR:HG23	1:AD:193:ASP:CB	2.37	0.53
1:AF:119:THR:HG23	1:AF:193:ASP:CB	2.39	0.53
1:AA:138:PHE:CE2	1:AI:62:ARG:CZ	2.91	0.53
1:BU:127:PHE:HB3	1:BU:160:PRO:HB3	1.90	0.53
1:BD:115:CYS:HB2	1:BD:116:PRO:HD2	1.91	0.53
1:AM:281:HIS:CE1	1:AM:301:TRP:HB3	2.43	0.53
1:AN:281:HIS:CE1	1:AN:301:TRP:HB3	2.43	0.53
1:AV:109:PHE:HB2	1:AV:158:VAL:CG1	2.39	0.53
1:CE:191:ASN:OD1	1:CE:191:ASN:N	2.38	0.53
1:BZ:183:LEU:C	1:BZ:183:LEU:HD12	2.29	0.53
1:AD:80:VAL:CG1	1:AD:185:LEU:HB3	2.38	0.53
1:AI:268:SER:HB3	1:AI:273:ASP:O	2.09	0.53
1:CJ:109:PHE:HB2	1:CJ:158:VAL:CG1	2.37	0.53
1:AX:124:VAL:HG11	1:AX:138:PHE:HD1	1.73	0.53
1:AM:253:ASP:OD1	1:AM:285:PHE:N	2.41	0.53
1:AB:253:ASP:OD1	1:AB:285:PHE:N	2.41	0.53
1:AU:253:ASP:OD1	1:AU:285:PHE:N	2.42	0.53
1:AZ:253:ASP:OD1	1:AZ:285:PHE:N	2.42	0.53
1:BJ:61:SER:CB	1:BJ:90:PRO:HD2	2.26	0.53
1:BW:98:ILE:HA	1:BW:211:SER:O	2.09	0.53
1:AO:314:TYR:CE1	1:AO:316:SER:HA	2.42	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AT:266:ASP:O	1:AT:314:TYR:HA	2.07	0.53
1:AX:61:SER:CB	1:AX:90:PRO:HD2	2.35	0.53
1:BV:80:VAL:CG1	1:BV:185:LEU:HB3	2.38	0.53
1:BT:111:ILE:HG23	1:BT:113:PRO:HD3	1.89	0.53
1:AB:162:TYR:N	1:AB:162:TYR:CD1	2.77	0.53
1:BY:111:ILE:HG21	1:BY:123:TYR:OH	2.08	0.53
1:AC:115:CYS:HB2	1:AC:116:PRO:HD2	1.91	0.53
1:AM:111:ILE:HG21	1:AM:123:TYR:CZ	2.44	0.53
1:AZ:119:THR:HG23	1:AZ:193:ASP:CB	2.39	0.53
1:BP:111:ILE:HG23	1:BP:113:PRO:HD3	1.90	0.53
1:BY:112:GLN:HB2	1:BY:198:SER:O	2.08	0.53
1:BZ:99:PHE:N	1:BZ:99:PHE:CD1	2.77	0.53
1:BH:281:HIS:ND1	1:BH:301:TRP:HB3	2.23	0.53
1:BF:168:TRP:CE2	1:AF:176:ARG:HD2	2.43	0.53
1:AU:62:ARG:HH11	1:AU:62:ARG:HG2	1.72	0.53
1:BX:281:HIS:ND1	1:BX:301:TRP:HB3	2.23	0.53
1:BE:281:HIS:ND1	1:BE:301:TRP:HB3	2.24	0.53
1:AV:253:ASP:OD1	1:AV:285:PHE:N	2.42	0.53
1:BZ:61:SER:CB	1:BZ:90:PRO:HD2	2.26	0.53
1:AA:279:TYR:CE2	1:AA:311:GLY:O	2.61	0.53
1:BX:98:ILE:HA	1:BX:211:SER:O	2.09	0.53
1:AQ:314:TYR:CE1	1:AQ:316:SER:CA	2.87	0.53
1:AA:314:TYR:CG	1:AA:315:TYR:N	2.76	0.53
1:CU:98:ILE:HD11	1:CU:99:PHE:CE2	2.44	0.53
1:AN:314:TYR:CE1	1:AN:316:SER:HA	2.43	0.53
1:AF:314:TYR:CE1	1:AF:316:SER:HA	2.44	0.53
1:BH:165:THR:OG1	1:BH:166:LEU:N	2.42	0.53
1:BC:74:THR:HA	1:BC:190:ASN:ND2	2.24	0.53
1:AH:115:CYS:HB2	1:AH:116:PRO:HD2	1.89	0.53
1:CJ:163:THR:OG1	1:CJ:165:THR:HG23	2.08	0.53
1:AT:268:SER:HB3	1:AT:273:ASP:O	2.09	0.53
1:BA:99:PHE:CD1	1:BA:99:PHE:N	2.77	0.53
1:AM:142:GLN:O	1:AM:142:GLN:NE2	2.41	0.53
1:BC:85:VAL:HG23	1:BC:86:PRO:HD2	1.94	0.53
1:AI:80:VAL:CG1	1:AI:185:LEU:HB3	2.39	0.53
1:CM:80:VAL:CG1	1:CM:185:LEU:HB2	2.37	0.53
1:BB:98:ILE:HA	1:BB:211:SER:O	2.08	0.53
1:AE:314:TYR:CG	1:AE:315:TYR:N	2.77	0.53
1:CA:100:GLN:HA	1:CA:213:GLU:OE2	2.09	0.53
1:CE:91:ARG:HD2	1:CH:98:ILE:HB	1.91	0.53
1:CZ:95:ALA:O	1:CZ:98:ILE:HG12	2.09	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AI:162:TYR:N	1:AI:162:TYR:CD1	2.76	0.53
1:AR:162:TYR:N	1:AR:162:TYR:CD1	2.76	0.53
1:CQ:43:SER:O	1:CV:34:ARG:HD3	2.09	0.53
1:AS:119:THR:HG23	1:AS:193:ASP:CB	2.38	0.53
1:AO:115:CYS:HB2	1:AO:116:PRO:HD2	1.91	0.53
1:CW:163:THR:OG1	1:CW:165:THR:HG23	2.08	0.53
1:CG:111:ILE:HD11	1:CG:125:ALA:CB	2.38	0.53
1:AA:114:MET:SD	1:AI:122:GLY:HA3	29.24	0.53
1:BZ:115:CYS:HB2	1:BZ:116:PRO:HD2	1.91	0.53
1:AA:110:GLU:HG2	1:AA:112:GLN:HG2	1.91	0.53
1:BX:325:LEU:HD22	1:BX:329:THR:HG21	1.91	0.53
1:BG:99:PHE:N	1:BG:99:PHE:CD1	2.76	0.53
1:AE:268:SER:HB3	1:AE:273:ASP:O	2.09	0.53
1:AB:109:PHE:HB2	1:AB:158:VAL:CG1	2.39	0.53
1:AQ:101:ARG:CZ	1:AQ:166:LEU:HD23	2.39	0.53
1:AJ:101:ARG:CZ	1:AJ:166:LEU:HD23	2.39	0.53
1:BV:115:CYS:HB2	1:BV:116:PRO:HD2	1.90	0.53
1:AS:268:SER:HB3	1:AS:273:ASP:O	2.08	0.53
1:AK:253:ASP:OD1	1:AK:285:PHE:N	2.41	0.53
1:AT:305:ASN:N	1:AT:305:ASN:OD1	2.42	0.53
1:AI:305:ASN:N	1:AI:305:ASN:OD1	2.42	0.53
1:BK:98:ILE:HA	1:BK:211:SER:O	2.09	0.53
1:BR:98:ILE:C	1:BR:211:SER:O	2.46	0.53
1:BC:165:THR:OG1	1:BC:166:LEU:N	2.42	0.53
1:AH:162:TYR:N	1:AH:162:TYR:CD1	2.76	0.53
1:BV:111:ILE:HG23	1:BV:113:PRO:HD3	1.89	0.53
1:AW:119:THR:HG23	1:AW:193:ASP:CB	2.39	0.53
1:AJ:111:ILE:O	1:AJ:198:SER:O	2.27	0.53
1:AB:111:ILE:HG21	1:AB:123:TYR:CZ	2.46	0.53
1:AA:118:ASN:O	1:AT:116:PRO:HB3	15.04	0.53
1:BC:116:PRO:HB3	1:CM:118:ASN:HA	221.53	0.53
1:BN:111:ILE:HG21	1:BN:123:TYR:OH	2.08	0.53
1:AK:80:VAL:CG1	1:AK:185:LEU:HB3	2.39	0.53
1:AR:109:PHE:HB2	1:AR:158:VAL:CG1	2.39	0.53
1:BZ:325:LEU:HD22	1:BZ:329:THR:HG21	1.90	0.53
1:AK:142:GLN:O	1:AK:142:GLN:NE2	2.42	0.53
1:AA:268:SER:HB3	1:AA:273:ASP:O	2.08	0.53
1:AA:310:ASP:HB3	1:AA:312:VAL:HG22	1.91	0.53
1:AL:253:ASP:OD1	1:AL:285:PHE:N	2.42	0.53
1:CI:79:VAL:HG13	1:CI:80:VAL:N	2.22	0.53
1:AA:91:ARG:CZ	1:BI:98:ILE:HG22	57.03	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:79:VAL:HG13	1:CA:80:VAL:N	2.23	0.53
1:AO:314:TYR:CG	1:AO:315:TYR:N	2.77	0.53
1:AU:314:TYR:CG	1:AU:315:TYR:N	2.77	0.53
1:CF:100:GLN:HA	1:CF:213:GLU:OE2	2.09	0.53
1:BI:163:THR:OG1	1:BI:165:THR:CG2	2.57	0.53
1:AR:63:ILE:HB	1:AR:199:VAL:HG13	1.89	0.53
1:AL:111:ILE:HG21	1:AL:123:TYR:CZ	2.43	0.53
1:CS:63:ILE:HD12	1:CS:88:LEU:CD1	2.39	0.53
1:CD:120:GLY:HA2	1:BH:115:CYS:C	148.86	0.53
1:AJ:115:CYS:HB2	1:AJ:116:PRO:HD2	1.90	0.53
1:AR:80:VAL:CG1	1:AR:185:LEU:HB3	2.38	0.53
1:BR:75:ASP:OD2	1:CT:62:ARG:NH1	2.37	0.53
1:BT:183:LEU:HD12	1:BT:183:LEU:C	2.29	0.53
1:CJ:191:ASN:N	1:CJ:191:ASN:OD1	2.36	0.53
1:AP:101:ARG:CZ	1:AP:166:LEU:HD23	2.39	0.53
1:BN:85:VAL:HG23	1:BN:86:PRO:HD2	1.91	0.53
1:AT:253:ASP:OD1	1:AT:285:PHE:N	2.42	0.53
1:AS:253:ASP:OD1	1:AS:285:PHE:N	2.42	0.53
1:AX:253:ASP:OD1	1:AX:285:PHE:N	2.42	0.53
1:CL:80:VAL:CG1	1:CL:185:LEU:HB2	2.38	0.53
1:AB:314:TYR:CG	1:AB:315:TYR:N	2.78	0.53
1:CR:80:VAL:CG1	1:CR:185:LEU:HB2	2.38	0.53
1:AA:61:SER:CB	1:AA:90:PRO:HD2	2.32	0.53
1:BT:163:THR:OG1	1:BT:165:THR:CG2	2.57	0.53
1:BJ:163:THR:OG1	1:BJ:165:THR:CG2	2.57	0.53
1:BO:123:TYR:HB2	1:BO:185:LEU:HD11	1.91	0.53
1:AJ:162:TYR:CD1	1:AJ:162:TYR:N	2.77	0.53
1:BJ:80:VAL:CG1	1:BJ:185:LEU:HB3	2.39	0.53
1:BH:80:VAL:CG1	1:BH:185:LEU:HB3	2.39	0.53
1:BB:80:VAL:CG1	1:BB:185:LEU:HB3	2.39	0.53
1:CP:63:ILE:HD12	1:CP:88:LEU:CG	2.39	0.53
1:AT:115:CYS:HB2	1:AT:116:PRO:HD2	1.89	0.53
1:BV:74:THR:HA	1:BV:190:ASN:ND2	2.24	0.53
1:CT:111:ILE:HG22	1:CT:113:PRO:HD3	1.90	0.53
1:AY:124:VAL:HG11	1:AY:138:PHE:HD1	1.74	0.53
1:BL:123:TYR:HB2	1:BL:185:LEU:HD11	1.91	0.53
1:CQ:85:VAL:HG13	1:CQ:86:PRO:HD2	1.91	0.53
1:BS:99:PHE:N	1:BS:99:PHE:CD1	2.76	0.53
1:AY:142:GLN:NE2	1:AY:142:GLN:O	2.42	0.53
1:AN:115:CYS:HB2	1:AN:116:PRO:HD2	1.90	0.53
1:BK:153:TRP:O	1:CS:151:LYS:NZ	2.41	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AN:253:ASP:OD1	1:AN:285:PHE:N	2.41	0.52
1:AR:302:ASP:C	1:AR:305:ASN:ND2	2.63	0.52
1:BQ:61:SER:CB	1:BQ:90:PRO:HD2	2.27	0.52
1:AN:91:ARG:CZ	1:BP:98:ILE:HG22	2.38	0.52
1:CP:101:ARG:CZ	1:CP:166:LEU:CD1	2.87	0.52
1:AG:314:TYR:CE1	1:AG:316:SER:CA	2.88	0.52
1:AH:314:TYR:CE1	1:AH:316:SER:HA	2.43	0.52
1:AC:314:TYR:CG	1:AC:315:TYR:N	2.79	0.52
1:AS:314:TYR:CE1	1:AS:316:SER:HA	2.43	0.52
1:BO:101:ARG:NH2	1:BO:166:LEU:HD12	2.22	0.52
1:AA:162:TYR:CD1	1:AA:162:TYR:N	2.77	0.52
1:BM:111:ILE:HG23	1:BM:113:PRO:HD3	1.90	0.52
1:BC:156:ARG:HH22	1:CO:34:ARG:CD	199.65	0.52
1:AY:111:ILE:HG21	1:AY:123:TYR:CZ	2.43	0.52
1:AQ:124:VAL:HG11	1:AQ:138:PHE:CD1	2.43	0.52
1:BC:99:PHE:N	1:BC:99:PHE:CD1	2.79	0.52
1:AO:101:ARG:CZ	1:AO:166:LEU:HD23	2.38	0.52
1:BH:99:PHE:N	1:BH:99:PHE:CD1	2.77	0.52
1:BA:85:VAL:HG23	1:BA:86:PRO:HD2	1.91	0.52
1:AG:142:GLN:O	1:AG:142:GLN:NE2	2.41	0.52
1:AG:110:GLU:HG2	1:AG:112:GLN:HG2	1.91	0.52
1:AH:305:ASN:N	1:AH:305:ASN:OD1	2.42	0.52
1:AN:305:ASN:OD1	1:AN:305:ASN:N	2.42	0.52
1:AC:91:ARG:NE	1:BS:98:ILE:CG2	2.71	0.52
1:AO:91:ARG:NH2	1:BW:98:ILE:HG22	2.24	0.52
1:AM:314:TYR:CE1	1:AM:316:SER:CA	2.85	0.52
1:AX:314:TYR:CG	1:AX:315:TYR:N	2.77	0.52
1:CU:100:GLN:HA	1:CU:213:GLU:OE2	2.10	0.52
1:BE:101:ARG:NH2	1:BE:166:LEU:HD12	2.24	0.52
1:AX:162:TYR:CD1	1:AX:162:TYR:N	2.77	0.52
1:BQ:111:ILE:HG23	1:BQ:113:PRO:HD3	1.91	0.52
1:CB:43:SER:HA	1:CU:112:GLN:NE2	26.40	0.52
1:CT:43:SER:O	1:CZ:34:ARG:HD3	2.09	0.52
1:BM:115:CYS:HB2	1:BM:116:PRO:HD2	1.91	0.52
1:BM:325:LEU:HD22	1:BM:329:THR:HG21	1.89	0.52
1:AL:85:VAL:HG22	1:AL:86:PRO:HD2	1.91	0.52
1:CM:85:VAL:HG13	1:CM:86:PRO:HD2	1.92	0.52
1:BJ:112:GLN:HB2	1:BJ:198:SER:O	2.10	0.52
1:AU:142:GLN:O	1:AU:142:GLN:NE2	2.42	0.52
1:AS:142:GLN:NE2	1:AS:142:GLN:O	2.42	0.52
1:BD:99:PHE:CD1	1:BD:99:PHE:N	2.77	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BT:325:LEU:HD22	1:BT:329:THR:HG21	1.92	0.52
1:AX:80:VAL:CG1	1:AX:185:LEU:HB3	2.39	0.52
1:AJ:310:ASP:HB3	1:AJ:312:VAL:HG22	1.90	0.52
1:AP:305:ASN:OD1	1:AP:305:ASN:N	2.42	0.52
1:AH:279:TYR:CE2	1:AH:311:GLY:O	2.61	0.52
1:BI:98:ILE:HA	1:BI:211:SER:O	2.08	0.52
1:BH:98:ILE:HA	1:BH:211:SER:O	2.09	0.52
1:CQ:79:VAL:HG13	1:CQ:80:VAL:N	2.24	0.52
1:CK:122:GLY:C	1:CK:188:VAL:HB	2.29	0.52
1:CS:80:VAL:CG1	1:CS:185:LEU:HB2	2.39	0.52
1:AC:314:TYR:CE1	1:AC:316:SER:HA	2.45	0.52
1:AI:314:TYR:CE1	1:AI:316:SER:CA	2.87	0.52
1:AN:314:TYR:CG	1:AN:315:TYR:N	2.77	0.52
1:AX:63:ILE:HB	1:AX:199:VAL:HG13	1.90	0.52
1:BG:101:ARG:NH2	1:BG:166:LEU:HD12	2.23	0.52
1:AF:61:SER:CB	1:AF:90:PRO:HD2	2.37	0.52
1:AN:98:ILE:HG23	1:BP:91:ARG:NH1	2.25	0.52
1:AN:162:TYR:N	1:AN:162:TYR:CD1	2.76	0.52
1:AB:119:THR:HG23	1:AB:193:ASP:CB	2.38	0.52
1:BB:85:VAL:HG23	1:BB:86:PRO:HD2	1.92	0.52
1:BF:281:HIS:ND1	1:BF:301:TRP:HB3	2.23	0.52
1:CK:109:PHE:HB2	1:CK:158:VAL:CG1	2.40	0.52
1:CB:85:VAL:HG13	1:CB:86:PRO:HD2	1.96	0.52
1:AO:253:ASP:OD1	1:AO:285:PHE:N	2.42	0.52
1:AC:253:ASP:OD1	1:AC:285:PHE:N	2.42	0.52
1:AK:302:ASP:C	1:AK:305:ASN:ND2	2.62	0.52
1:AG:305:ASN:N	1:AG:305:ASN:OD1	2.42	0.52
1:AD:302:ASP:C	1:AD:305:ASN:ND2	2.63	0.52
1:AV:305:ASN:OD1	1:AV:305:ASN:N	2.42	0.52
1:AP:279:TYR:CE2	1:AP:311:GLY:O	2.61	0.52
1:CR:100:GLN:HA	1:CR:213:GLU:OE2	2.10	0.52
1:AE:314:TYR:CE1	1:AE:316:SER:HA	2.42	0.52
1:CN:75:ASP:OD1	1:CN:188:VAL:C	2.46	0.52
1:BR:163:THR:OG1	1:BR:165:THR:CG2	2.57	0.52
1:AT:162:TYR:N	1:AT:162:TYR:CD1	2.78	0.52
1:CA:43:SER:O	1:CR:34:ARG:HD3	129.31	0.52
1:BQ:123:TYR:HB2	1:BQ:185:LEU:HD11	1.91	0.52
1:AD:111:ILE:HG21	1:AD:123:TYR:CZ	2.48	0.52
1:AC:119:THR:HG23	1:AC:193:ASP:CB	2.40	0.52
1:AR:111:ILE:HG21	1:AR:123:TYR:CZ	2.44	0.52
1:CP:63:ILE:HD12	1:CP:88:LEU:CD1	2.39	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AE:80:VAL:CG1	1:AE:185:LEU:HB3	2.40	0.52
1:CF:111:ILE:HD11	1:CF:125:ALA:CB	2.38	0.52
1:BZ:68:LEU:HD23	1:BZ:195:VAL:CG2	2.39	0.52
1:CW:111:ILE:HD11	1:CW:125:ALA:CB	2.40	0.52
1:CW:111:ILE:HG22	1:CW:113:PRO:HD3	1.90	0.52
1:AI:101:ARG:CZ	1:AI:166:LEU:HD23	2.40	0.52
1:BT:112:GLN:HB2	1:BT:198:SER:O	2.09	0.52
1:AH:268:SER:HB3	1:AH:273:ASP:O	2.09	0.52
1:CP:190:ASN:HD22	1:CP:190:ASN:N	2.06	0.52
1:BV:183:LEU:C	1:BV:183:LEU:HD12	2.29	0.52
1:BG:281:HIS:ND1	1:BG:301:TRP:HB3	2.24	0.52
1:AH:253:ASP:OD1	1:AH:285:PHE:N	2.42	0.52
1:AM:253:ASP:CG	1:AM:285:PHE:CA	2.78	0.52
1:AN:253:ASP:CG	1:AN:285:PHE:CA	2.78	0.52
1:AK:305:ASN:OD1	1:AK:305:ASN:N	2.43	0.52
1:AA:305:ASN:N	1:AA:305:ASN:OD1	2.43	0.52
1:AJ:305:ASN:N	1:AJ:305:ASN:OD1	2.42	0.52
1:AB:305:ASN:OD1	1:AB:305:ASN:N	2.42	0.52
1:AO:305:ASN:N	1:AO:305:ASN:OD1	2.42	0.52
1:AE:305:ASN:OD1	1:AE:305:ASN:N	2.42	0.52
1:AR:305:ASN:OD1	1:AR:305:ASN:N	2.43	0.52
1:CH:80:VAL:CG1	1:CH:185:LEU:HB2	2.40	0.52
1:AW:314:TYR:CG	1:AW:315:TYR:N	2.78	0.52
1:CS:63:ILE:HD12	1:CS:88:LEU:CG	2.40	0.52
1:CG:111:ILE:HG22	1:CG:113:PRO:HD3	1.90	0.52
1:BK:281:HIS:ND1	1:BK:301:TRP:HB3	2.25	0.52
1:AO:268:SER:HB3	1:AO:273:ASP:O	2.08	0.52
1:AH:142:GLN:O	1:AH:142:GLN:NE2	2.43	0.52
1:AN:109:PHE:HB2	1:AN:158:VAL:CG1	2.40	0.52
1:BO:205:VAL:HG22	1:BO:206:ARG:N	2.25	0.52
1:BD:325:LEU:HD22	1:BD:329:THR:HG21	1.92	0.52
1:AU:310:ASP:HB3	1:AU:312:VAL:HG22	1.91	0.52
1:AJ:302:ASP:C	1:AJ:305:ASN:ND2	2.63	0.52
1:AQ:305:ASN:OD1	1:AQ:305:ASN:N	2.43	0.52
1:AY:305:ASN:OD1	1:AY:305:ASN:N	2.42	0.52
1:CW:80:VAL:HG11	1:CW:185:LEU:HB2	1.91	0.52
1:CZ:185:LEU:C	1:CZ:186:LEU:HD23	2.29	0.52
1:BL:98:ILE:CG2	1:AU:91:ARG:CZ	2.88	0.52
1:CB:91:ARG:HD2	1:CU:98:ILE:HB	86.60	0.52
1:AW:266:ASP:O	1:AW:314:TYR:HA	2.09	0.52
1:AK:266:ASP:O	1:AK:314:TYR:HA	2.10	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BL:101:ARG:NH2	1:BL:166:LEU:HD12	2.23	0.52
1:AM:162:TYR:N	1:AM:162:TYR:CD1	2.78	0.52
1:AV:119:THR:HG23	1:AV:193:ASP:CB	2.40	0.52
1:AA:118:ASN:O	1:AI:116:PRO:HB3	2.09	0.52
1:BL:115:CYS:HB2	1:BL:116:PRO:HD2	1.90	0.52
1:AR:281:HIS:CE1	1:AR:301:TRP:HB3	2.45	0.52
1:AT:142:GLN:NE2	1:AT:142:GLN:O	2.43	0.52
1:BI:183:LEU:HD12	1:BI:183:LEU:C	2.30	0.52
1:BV:281:HIS:ND1	1:BV:301:TRP:HB3	2.25	0.52
1:AH:310:ASP:HB3	1:AH:312:VAL:HG22	1.90	0.52
1:AC:305:ASN:N	1:AC:305:ASN:OD1	2.42	0.52
1:AA:302:ASP:C	1:AA:305:ASN:ND2	2.63	0.52
1:AD:305:ASN:OD1	1:AD:305:ASN:N	2.42	0.52
1:AQ:302:ASP:C	1:AQ:305:ASN:ND2	2.63	0.52
1:AM:302:ASP:C	1:AM:305:ASN:ND2	2.63	0.52
1:CE:81:ASP:OD2	1:CE:136:HIS:NE2	2.41	0.52
1:CT:80:VAL:CG1	1:CT:185:LEU:HB2	2.39	0.52
1:CX:101:ARG:CZ	1:CX:166:LEU:CD1	2.88	0.52
1:CQ:79:VAL:CG1	1:CQ:185:LEU:O	2.56	0.52
1:CT:101:ARG:NH1	1:CT:166:LEU:CD1	2.71	0.52
1:CH:185:LEU:C	1:CH:186:LEU:HD23	2.30	0.52
1:CV:79:VAL:HG13	1:CV:80:VAL:N	2.24	0.52
1:AS:314:TYR:CG	1:AS:315:TYR:N	2.77	0.52
1:CF:63:ILE:HD12	1:CF:88:LEU:CD1	2.39	0.52
1:AF:115:CYS:HB2	1:AF:116:PRO:HD2	1.92	0.52
1:AN:119:THR:HG23	1:AN:193:ASP:CB	2.40	0.52
1:BZ:74:THR:HA	1:BZ:190:ASN:ND2	2.24	0.52
1:CZ:111:ILE:HD11	1:CZ:125:ALA:CB	2.40	0.52
1:BT:281:HIS:ND1	1:BT:301:TRP:HB3	2.25	0.52
1:AW:124:VAL:HG11	1:AW:138:PHE:HD1	1.74	0.52
1:AF:310:ASP:HB3	1:AF:312:VAL:HG22	1.91	0.52
1:AJ:253:ASP:OD1	1:AJ:285:PHE:N	2.43	0.52
1:AD:253:ASP:CG	1:AD:285:PHE:CA	2.78	0.52
1:AL:253:ASP:CG	1:AL:285:PHE:CA	2.78	0.52
1:AX:305:ASN:N	1:AX:305:ASN:OD1	2.42	0.52
1:AN:302:ASP:C	1:AN:305:ASN:ND2	2.63	0.52
1:AL:302:ASP:C	1:AL:305:ASN:ND2	2.63	0.52
1:BC:98:ILE:CG2	1:AM:91:ARG:NH2	214.71	0.52
1:CM:101:ARG:NH1	1:CM:166:LEU:CD1	2.73	0.52
1:AD:314:TYR:CG	1:AD:315:TYR:N	2.77	0.52
1:BV:163:THR:OG1	1:BV:165:THR:CG2	2.58	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BR:165:THR:OG1	1:BR:166:LEU:N	2.43	0.52
1:CB:112:GLN:NE2	1:CB:155:SER:OG	2.48	0.52
1:BW:111:ILE:HG23	1:BW:113:PRO:HD3	1.92	0.52
1:AW:111:ILE:HG21	1:AW:123:TYR:CZ	2.45	0.52
1:CF:63:ILE:HD12	1:CF:88:LEU:CG	2.38	0.52
1:BB:75:ASP:OD2	1:CU:62:ARG:NH1	45.48	0.52
1:CC:190:ASN:N	1:CC:190:ASN:HD22	2.08	0.52
1:AY:310:ASP:HB3	1:AY:312:VAL:HG22	1.92	0.52
1:AQ:310:ASP:HB3	1:AQ:312:VAL:HG22	1.91	0.52
1:AR:253:ASP:CG	1:AR:285:PHE:CA	2.78	0.52
1:AT:302:ASP:C	1:AT:305:ASN:ND2	2.63	0.52
1:AB:302:ASP:C	1:AB:305:ASN:ND2	2.63	0.52
1:AV:302:ASP:C	1:AV:305:ASN:ND2	2.63	0.52
1:BK:98:ILE:HG22	1:AS:91:ARG:NH2	2.24	0.52
1:CD:100:GLN:HA	1:CD:213:GLU:OE2	2.11	0.52
1:AI:314:TYR:CG	1:AI:315:TYR:N	2.78	0.52
1:AJ:314:TYR:CG	1:AJ:315:TYR:N	2.77	0.52
1:AZ:314:TYR:CG	1:AZ:315:TYR:N	2.78	0.52
1:BX:165:THR:OG1	1:BX:166:LEU:N	2.42	0.52
1:BC:80:VAL:CG1	1:BC:185:LEU:HB3	2.39	0.52
1:BO:111:ILE:HG23	1:BO:113:PRO:HD3	1.92	0.52
1:BO:123:TYR:HB2	1:BO:185:LEU:CD1	2.40	0.52
1:BX:123:TYR:HB2	1:BX:185:LEU:HD11	1.92	0.52
1:CF:57:LEU:HD23	1:CF:203:TRP:CH2	2.45	0.52
1:CP:62:ARG:NH1	1:BQ:75:ASP:OD2	2.35	0.52
1:AQ:118:ASN:O	1:AZ:116:PRO:HB3	2.09	0.52
1:AE:116:PRO:HB3	1:AM:118:ASN:O	2.10	0.52
1:AH:124:VAL:HG11	1:AH:138:PHE:HD1	1.75	0.52
1:CJ:111:ILE:HG22	1:CJ:113:PRO:HD3	1.92	0.52
1:CI:111:ILE:HD11	1:CI:125:ALA:CB	2.40	0.52
1:AS:124:VAL:HG11	1:AS:138:PHE:HD1	1.75	0.52
1:BO:68:LEU:HD23	1:BO:195:VAL:CG2	2.40	0.52
1:BM:127:PHE:HB3	1:BM:160:PRO:HB3	1.91	0.52
1:AV:268:SER:HB3	1:AV:273:ASP:O	2.10	0.52
1:AG:109:PHE:HB2	1:AG:158:VAL:CG1	2.40	0.52
1:AP:109:PHE:HB2	1:AP:158:VAL:CG1	2.39	0.52
1:AJ:124:VAL:HG11	1:AJ:138:PHE:HD1	1.75	0.52
1:CO:190:ASN:HD22	1:CO:190:ASN:N	2.08	0.52
1:CQ:190:ASN:HD22	1:CQ:190:ASN:N	2.08	0.52
1:AM:124:VAL:HG11	1:AM:138:PHE:HD1	1.74	0.52
1:CU:85:VAL:HG13	1:CU:86:PRO:HD2	1.92	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AW:253:ASP:OD1	1:AW:285:PHE:N	2.42	0.52
1:AC:253:ASP:CG	1:AC:285:PHE:CA	2.78	0.52
1:CG:80:VAL:CG1	1:CG:185:LEU:HB2	2.39	0.52
1:CY:80:VAL:CG1	1:CY:185:LEU:HB2	2.40	0.52
1:BD:98:ILE:HG22	1:AG:91:ARG:CZ	89.68	0.52
1:AA:91:ARG:NH2	1:BI:98:ILE:HG22	57.73	0.52
1:BL:98:ILE:HA	1:BL:211:SER:O	2.09	0.52
1:CO:122:GLY:HA3	1:BW:114:MET:SD	2.50	0.52
1:AU:314:TYR:CE1	1:AU:316:SER:HA	2.41	0.52
1:AG:61:SER:HB2	1:AG:89:LEU:HD22	1.92	0.52
1:AG:314:TYR:CG	1:AG:315:TYR:N	2.78	0.52
1:CQ:99:PHE:CB	1:CQ:209:VAL:O	2.59	0.52
1:AB:61:SER:CB	1:AB:90:PRO:HD2	2.38	0.52
1:AO:162:TYR:N	1:AO:162:TYR:CD1	2.78	0.52
1:AG:162:TYR:N	1:AG:162:TYR:CD1	2.77	0.52
1:AJ:111:ILE:HG21	1:AJ:123:TYR:CZ	2.45	0.52
1:CC:109:PHE:HB2	1:CC:158:VAL:HG12	1.92	0.52
1:CC:62:ARG:NH1	1:BJ:75:ASP:OD2	2.36	0.52
1:BN:123:TYR:HB2	1:BN:185:LEU:HD11	1.92	0.52
1:BG:115:CYS:HB2	1:BG:116:PRO:HD2	1.92	0.52
1:BP:325:LEU:HD22	1:BP:329:THR:HG21	1.92	0.52
1:BH:183:LEU:C	1:BH:183:LEU:HD12	2.31	0.52
1:BQ:183:LEU:HD12	1:BQ:183:LEU:C	2.30	0.52
1:AV:142:GLN:O	1:AV:142:GLN:NE2	2.43	0.52
1:CZ:288:ASN:N	1:CZ:288:ASN:OD1	2.44	0.52
1:AX:101:ARG:CZ	1:AX:166:LEU:HD23	2.39	0.52
1:CH:151:LYS:NZ	1:BN:153:TRP:O	2.43	0.52
1:AP:310:ASP:HB3	1:AP:312:VAL:HG22	1.92	0.51
1:AV:253:ASP:CG	1:AV:285:PHE:CA	2.78	0.51
1:AR:253:ASP:OD1	1:AR:285:PHE:N	2.42	0.51
1:BS:98:ILE:O	1:BS:211:SER:CA	2.58	0.51
1:AV:314:TYR:CE1	1:AV:316:SER:HA	2.44	0.51
1:AK:315:TYR:CE2	1:AK:317:ASP:OD2	2.63	0.51
1:CH:98:ILE:HD11	1:CH:99:PHE:CE2	2.45	0.51
1:AC:162:TYR:N	1:AC:162:TYR:CD1	2.77	0.51
1:CO:43:SER:O	1:CU:34:ARG:HD3	2.10	0.51
1:BY:80:VAL:CG1	1:BY:185:LEU:HB3	2.39	0.51
1:CH:43:SER:O	1:CW:34:ARG:HD3	2.09	0.51
1:BJ:150:ALA:HB2	1:BJ:156:ARG:HD3	1.92	0.51
1:BE:123:TYR:HB2	1:BE:185:LEU:HD11	1.92	0.51
1:BI:80:VAL:CG1	1:BI:185:LEU:HB3	2.39	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CC:112:GLN:NE2	1:CX:43:SER:HA	209.41	0.51
1:AM:115:CYS:HB2	1:AM:116:PRO:HD2	1.90	0.51
1:CW:85:VAL:HG13	1:CW:86:PRO:HD2	1.92	0.51
1:BH:205:VAL:HG22	1:BH:206:ARG:N	2.25	0.51
1:CM:237:ASP:HB3	1:CM:297:ARG:HG2	1.92	0.51
1:BR:161:GLN:NE2	1:CR:210:PRO:HD2	2.26	0.51
1:BP:183:LEU:HD12	1:BP:183:LEU:C	2.31	0.51
1:AC:142:GLN:O	1:AC:142:GLN:NE2	2.45	0.51
1:AY:115:CYS:HB2	1:AY:116:PRO:HD2	1.91	0.51
1:CB:237:ASP:HB3	1:CB:297:ARG:HG2	1.92	0.51
1:AP:253:ASP:OD1	1:AP:285:PHE:N	2.43	0.51
1:AI:302:ASP:C	1:AI:305:ASN:ND2	2.63	0.51
1:AM:305:ASN:OD1	1:AM:305:ASN:N	2.42	0.51
1:AZ:305:ASN:N	1:AZ:305:ASN:OD1	2.43	0.51
1:BI:254:GLY:CA	1:BI:283:LYS:HE3	2.27	0.51
1:CU:75:ASP:OD1	1:CU:188:VAL:C	2.49	0.51
1:AH:314:TYR:CG	1:AH:315:TYR:N	2.77	0.51
1:AJ:314:TYR:CE1	1:AJ:316:SER:HA	2.45	0.51
1:AR:314:TYR:CE1	1:AR:316:SER:CA	2.90	0.51
1:CF:80:VAL:CG1	1:CF:185:LEU:HB2	2.40	0.51
1:AN:61:SER:CB	1:AN:90:PRO:HD2	2.33	0.51
1:BJ:166:LEU:HD13	1:BJ:167:LEU:N	2.25	0.51
1:AO:119:THR:HG23	1:AO:193:ASP:CB	2.40	0.51
1:CQ:109:PHE:HB2	1:CQ:158:VAL:HG12	1.92	0.51
1:CS:163:THR:OG1	1:CS:165:THR:HG23	2.10	0.51
1:CO:163:THR:OG1	1:CO:165:THR:HG23	2.10	0.51
1:AD:101:ARG:CZ	1:AD:166:LEU:HD23	2.40	0.51
1:BP:99:PHE:CD1	1:BP:99:PHE:N	2.78	0.51
1:AK:281:HIS:CE1	1:AK:301:TRP:HB3	2.45	0.51
1:AD:268:SER:HB3	1:AD:273:ASP:O	2.10	0.51
1:BZ:281:HIS:ND1	1:BZ:301:TRP:HB3	2.25	0.51
1:BQ:325:LEU:HD22	1:BQ:329:THR:HG21	1.91	0.51
1:CF:124:VAL:HG13	1:CF:124:VAL:O	2.10	0.51
1:CZ:124:VAL:O	1:CZ:124:VAL:HG13	2.11	0.51
1:AV:115:CYS:HB2	1:AV:116:PRO:HD2	1.92	0.51
1:AO:310:ASP:HB3	1:AO:312:VAL:HG22	1.92	0.51
1:AU:253:ASP:CG	1:AU:285:PHE:CA	2.78	0.51
1:AC:302:ASP:C	1:AC:305:ASN:ND2	2.63	0.51
1:AH:302:ASP:C	1:AH:305:ASN:ND2	2.63	0.51
1:AS:305:ASN:OD1	1:AS:305:ASN:N	2.42	0.51
1:CB:81:ASP:OD2	1:CB:136:HIS:NE2	2.40	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CU:80:VAL:CG1	1:CU:185:LEU:HB2	2.39	0.51
1:BK:98:ILE:HG22	1:AS:91:ARG:CZ	2.40	0.51
1:AE:91:ARG:NE	1:BM:98:ILE:CG2	2.74	0.51
1:BS:98:ILE:HA	1:BS:211:SER:O	2.09	0.51
1:CO:79:VAL:HG13	1:CO:80:VAL:N	2.25	0.51
1:CX:99:PHE:CB	1:CX:209:VAL:O	2.58	0.51
1:AV:162:TYR:CD1	1:AV:162:TYR:N	2.78	0.51
1:AZ:80:VAL:CG1	1:AZ:185:LEU:HB3	2.39	0.51
1:AI:111:ILE:HG21	1:AI:123:TYR:CZ	2.45	0.51
1:AX:119:THR:HG23	1:AX:193:ASP:CB	2.41	0.51
1:AH:119:THR:HG23	1:AH:193:ASP:CB	2.40	0.51
1:BD:116:PRO:HD3	1:CW:120:GLY:HA3	1.92	0.51
1:BJ:325:LEU:HD22	1:BJ:329:THR:HG21	1.92	0.51
1:BQ:281:HIS:ND1	1:BQ:301:TRP:HB3	2.25	0.51
1:CL:79:VAL:HG13	1:CL:80:VAL:N	2.24	0.51
1:AV:279:TYR:CE2	1:AV:311:GLY:O	2.63	0.51
1:BO:98:ILE:HA	1:BO:211:SER:O	2.09	0.51
1:CQ:80:VAL:CG1	1:CQ:185:LEU:HB2	2.40	0.51
1:AC:314:TYR:CE1	1:AC:316:SER:CA	2.89	0.51
1:AY:314:TYR:CG	1:AY:315:TYR:N	2.79	0.51
1:CH:100:GLN:HA	1:CH:213:GLU:OE2	2.11	0.51
1:AY:61:SER:CB	1:AY:90:PRO:HD2	2.35	0.51
1:BG:165:THR:OG1	1:BG:166:LEU:N	2.44	0.51
1:AT:118:ASN:O	1:AV:116:PRO:HB3	2.10	0.51
1:AG:101:ARG:CZ	1:AG:166:LEU:HD23	2.40	0.51
1:AC:110:GLU:HG2	1:AC:112:GLN:HG2	1.90	0.51
1:BA:124:VAL:HG11	1:BA:138:PHE:CD2	2.46	0.51
1:AZ:142:GLN:O	1:AZ:142:GLN:NE2	2.43	0.51
1:BP:276:ARG:O	1:AP:276:ARG:NH2	2.44	0.51
1:AW:253:ASP:CG	1:AW:285:PHE:CA	2.78	0.51
1:AQ:253:ASP:CG	1:AQ:285:PHE:CA	2.78	0.51
1:AF:253:ASP:OD1	1:AF:285:PHE:N	2.43	0.51
1:AF:279:TYR:CE2	1:AF:311:GLY:O	2.63	0.51
1:AA:91:ARG:NH2	1:BI:210:PRO:HB3	54.11	0.51
1:CD:98:ILE:HD11	1:CD:99:PHE:CE2	2.45	0.51
1:AP:314:TYR:CG	1:AP:315:TYR:N	2.78	0.51
1:BM:80:VAL:CG1	1:BM:185:LEU:HB3	2.40	0.51
1:BG:123:TYR:HB2	1:BG:185:LEU:HD11	1.92	0.51
1:BX:80:VAL:CG1	1:BX:185:LEU:HB3	2.40	0.51
1:CV:57:LEU:HD23	1:CV:203:TRP:CH2	2.45	0.51
1:BL:150:ALA:HB2	1:BL:156:ARG:HD3	1.92	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BR:281:HIS:ND1	1:BR:301:TRP:HB3	2.25	0.51
1:AP:246:THR:N	1:AP:247:PRO:CD	2.74	0.51
1:BI:99:PHE:N	1:BI:99:PHE:CD1	2.79	0.51
1:BW:161:GLN:NE2	1:CW:210:PRO:HD2	2.25	0.51
1:AD:110:GLU:HG2	1:AD:112:GLN:HG2	1.93	0.51
1:BO:183:LEU:HD12	1:BO:183:LEU:C	2.31	0.51
1:CB:124:VAL:HG13	1:CB:124:VAL:O	2.15	0.51
1:AN:110:GLU:HG2	1:AN:112:GLN:HG2	1.92	0.51
1:AB:101:ARG:CZ	1:AB:166:LEU:HD23	2.41	0.51
1:CX:191:ASN:OD1	1:CX:191:ASN:N	2.41	0.51
1:CD:78:VAL:HG13	1:CD:78:VAL:O	2.18	0.51
1:CC:80:VAL:CG1	1:CC:185:LEU:HB2	2.41	0.51
1:AO:141:LEU:O	1:AO:144:THR:CG2	2.45	0.51
1:BL:98:ILE:HG22	1:AU:91:ARG:HH21	1.75	0.51
1:BY:163:THR:OG1	1:BY:165:THR:CG2	2.59	0.51
1:BX:166:LEU:C	1:BX:166:LEU:HD13	2.31	0.51
1:BL:166:LEU:HD13	1:BL:166:LEU:C	2.31	0.51
1:CC:43:SER:HA	1:CX:112:GLN:NE2	209.61	0.51
1:CM:112:GLN:NE2	1:CM:155:SER:OG	2.43	0.51
1:BZ:111:ILE:HG23	1:BZ:113:PRO:HD3	1.92	0.51
1:BR:111:ILE:HG21	1:BR:123:TYR:OH	2.10	0.51
1:AK:111:ILE:HG21	1:AK:123:TYR:CZ	2.46	0.51
1:AT:111:ILE:HG21	1:AT:123:TYR:CZ	2.46	0.51
1:CB:130:ASP:OD2	1:CB:176:ARG:NH2	2.47	0.51
1:CM:163:THR:OG1	1:CM:165:THR:HG23	2.11	0.51
1:CE:111:ILE:HD11	1:CE:125:ALA:CB	2.41	0.51
1:CQ:62:ARG:HA	1:CQ:200:LEU:HD23	1.93	0.51
1:AX:64:SER:OG	1:AX:80:VAL:HG21	2.11	0.51
1:CX:85:VAL:HG13	1:CX:86:PRO:HD2	1.92	0.51
1:BG:325:LEU:HD22	1:BG:329:THR:HG21	1.91	0.51
1:AL:115:CYS:HB2	1:AL:116:PRO:HD2	1.91	0.51
1:BG:183:LEU:HD12	1:BG:183:LEU:C	2.31	0.51
1:CW:190:ASN:HD22	1:CW:190:ASN:N	2.09	0.51
1:CS:190:ASN:N	1:CS:190:ASN:HD22	2.09	0.51
1:AZ:281:HIS:CE1	1:AZ:301:TRP:HB3	2.45	0.51
1:BK:325:LEU:HD22	1:BK:329:THR:HG21	1.93	0.51
1:BV:85:VAL:HG23	1:BV:86:PRO:HD2	1.91	0.51
1:AA:253:ASP:CG	1:AA:285:PHE:CA	2.78	0.51
1:AG:302:ASP:C	1:AG:305:ASN:ND2	2.63	0.51
1:AU:305:ASN:N	1:AU:305:ASN:OD1	2.42	0.51
1:AQ:279:TYR:CE2	1:AQ:311:GLY:O	2.63	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AD:91:ARG:CZ	1:BF:98:ILE:HG22	2.41	0.51
1:AR:314:TYR:CG	1:AR:315:TYR:N	2.78	0.51
1:CS:98:ILE:HD11	1:CS:99:PHE:CE2	2.46	0.51
1:AE:61:SER:CB	1:AE:90:PRO:HD2	2.35	0.51
1:BQ:163:THR:OG1	1:BQ:165:THR:CG2	2.59	0.51
1:BQ:156:ARG:NH2	1:CV:34:ARG:HG3	2.26	0.51
1:BS:123:TYR:HB2	1:BS:185:LEU:HD11	1.93	0.51
1:CC:63:ILE:HD12	1:CC:88:LEU:CD1	2.41	0.51
1:CV:112:GLN:NE2	1:CV:155:SER:OG	2.44	0.51
1:CG:62:ARG:HA	1:CG:200:LEU:HD23	1.91	0.51
1:BU:74:THR:O	1:BU:75:ASP:C	2.49	0.51
1:CJ:111:ILE:HD11	1:CJ:125:ALA:CB	2.40	0.51
1:CS:111:ILE:HG22	1:CS:113:PRO:HD3	1.93	0.51
1:BL:74:THR:O	1:BL:75:ASP:C	2.49	0.51
1:AW:101:ARG:CZ	1:AW:166:LEU:HD23	2.41	0.51
1:BX:168:TRP:CE2	1:AX:176:ARG:HD2	2.46	0.51
1:BQ:168:TRP:CE2	1:AQ:176:ARG:HD2	2.46	0.51
1:CA:124:VAL:HG13	1:CA:124:VAL:O	2.15	0.51
1:BE:183:LEU:HD12	1:BE:183:LEU:C	2.30	0.51
1:CI:124:VAL:O	1:CI:124:VAL:HG13	2.09	0.51
1:BY:281:HIS:ND1	1:BY:301:TRP:HB3	2.26	0.51
1:AL:109:PHE:HB2	1:AL:158:VAL:CG1	2.40	0.51
1:AO:124:VAL:HG11	1:AO:138:PHE:HD1	1.74	0.51
1:AM:310:ASP:HB3	1:AM:312:VAL:HG22	1.92	0.51
1:AP:302:ASP:C	1:AP:305:ASN:ND2	2.63	0.51
1:AL:305:ASN:N	1:AL:305:ASN:OD1	2.44	0.51
1:CC:101:ARG:CZ	1:CC:166:LEU:CD1	2.91	0.51
1:CL:101:ARG:CZ	1:CL:166:LEU:CD1	2.89	0.51
1:BL:98:ILE:HG22	1:AU:91:ARG:CZ	2.40	0.51
1:CW:101:ARG:CZ	1:CW:166:LEU:CD1	2.89	0.51
1:BT:98:ILE:CA	1:BT:211:SER:O	2.59	0.51
1:BG:98:ILE:CG2	1:AP:91:ARG:NE	2.74	0.51
1:CB:100:GLN:HA	1:CB:213:GLU:OE2	2.11	0.51
1:AI:314:TYR:CE1	1:AI:316:SER:HA	2.45	0.51
1:AZ:314:TYR:CE1	1:AZ:316:SER:HA	2.44	0.51
1:BN:165:THR:OG1	1:BN:166:LEU:N	2.44	0.51
1:BP:166:LEU:HD13	1:BP:167:LEU:N	2.25	0.51
1:BM:166:LEU:HD13	1:BM:167:LEU:N	2.26	0.51
1:AD:162:TYR:CD1	1:AD:162:TYR:N	2.79	0.51
1:AQ:162:TYR:CD1	1:AQ:162:TYR:N	2.78	0.51
1:BS:80:VAL:CG1	1:BS:185:LEU:HB3	2.41	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AC:111:ILE:HG21	1:AC:123:TYR:CZ	2.50	0.51
1:AR:124:VAL:HG11	1:AR:138:PHE:HD1	1.75	0.51
1:BN:74:THR:O	1:BN:75:ASP:C	2.49	0.51
1:CH:237:ASP:HB3	1:CH:297:ARG:HG2	1.91	0.51
1:CE:85:VAL:HG13	1:CE:86:PRO:HD2	1.93	0.51
1:BK:112:GLN:HB2	1:BK:198:SER:O	2.11	0.51
1:BQ:85:VAL:HG23	1:BQ:86:PRO:HD2	1.93	0.51
1:CX:190:ASN:HD22	1:CX:190:ASN:N	2.09	0.51
1:CA:85:VAL:HG13	1:CA:86:PRO:HD2	1.93	0.51
1:AK:101:ARG:CZ	1:AK:166:LEU:HD23	2.40	0.51
1:AR:310:ASP:HB3	1:AR:312:VAL:HG22	1.93	0.51
1:AG:253:ASP:OD1	1:AG:285:PHE:N	2.42	0.51
1:AZ:302:ASP:C	1:AZ:305:ASN:ND2	2.63	0.51
1:CM:79:VAL:HG13	1:CM:80:VAL:N	2.25	0.51
1:CQ:101:ARG:CZ	1:CQ:166:LEU:CD1	2.89	0.51
1:BX:111:ILE:HG23	1:BX:113:PRO:HD3	1.91	0.51
1:CF:34:ARG:CD	1:CY:43:SER:O	2.59	0.51
1:CE:112:GLN:HE21	1:CH:44:THR:H	1.58	0.51
1:BH:111:ILE:HG23	1:BH:113:PRO:HD3	1.91	0.51
1:CC:63:ILE:HD12	1:CC:88:LEU:CG	2.41	0.51
1:AM:119:THR:HG23	1:AM:193:ASP:CB	2.39	0.51
1:BA:74:THR:HA	1:BA:190:ASN:ND2	2.26	0.51
1:CK:111:ILE:HD11	1:CK:125:ALA:CB	2.41	0.51
1:AN:124:VAL:HG11	1:AN:138:PHE:HD1	1.76	0.51
1:BL:111:ILE:HG22	1:BL:156:ARG:H	1.75	0.51
1:BL:276:ARG:O	1:AL:276:ARG:NH2	2.44	0.51
1:CZ:237:ASP:HB3	1:CZ:297:ARG:HG2	1.93	0.51
1:CP:85:VAL:HG13	1:CP:86:PRO:HD2	1.92	0.51
1:AV:110:GLU:HG2	1:AV:112:GLN:HG2	1.93	0.51
1:BS:205:VAL:HG22	1:BS:206:ARG:N	2.26	0.51
1:AY:281:HIS:CE1	1:AY:301:TRP:HB3	2.46	0.51
1:AD:142:GLN:NE2	1:AD:142:GLN:O	2.43	0.51
1:CJ:190:ASN:HD22	1:CJ:190:ASN:N	2.09	0.51
1:AR:268:SER:HB3	1:AR:273:ASP:O	2.10	0.51
1:BE:99:PHE:CD1	1:BE:99:PHE:N	2.78	0.51
1:AG:310:ASP:HB3	1:AG:312:VAL:HG22	1.92	0.51
1:AH:253:ASP:CG	1:AH:285:PHE:CA	2.79	0.51
1:CE:80:VAL:CG1	1:CE:185:LEU:HB2	2.40	0.51
1:AM:315:TYR:CE2	1:AM:317:ASP:OD2	2.64	0.51
1:AG:314:TYR:CE1	1:AG:316:SER:HA	2.44	0.51
1:AL:315:TYR:CE2	1:AL:317:ASP:OD2	2.64	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BD:80:VAL:CG1	1:BD:185:LEU:HB3	2.40	0.51
1:CI:112:GLN:NE2	1:CI:155:SER:OG	2.44	0.51
1:CY:112:GLN:NE2	1:CY:155:SER:OG	2.44	0.51
1:CB:112:GLN:NE2	1:CU:43:SER:HA	125.15	0.51
1:AW:115:CYS:HB2	1:AW:116:PRO:HD2	1.92	0.51
1:BB:74:THR:O	1:BB:75:ASP:C	2.50	0.51
1:CD:111:ILE:HD11	1:CD:125:ALA:CB	2.42	0.51
1:CC:163:THR:OG1	1:CC:165:THR:HG23	2.12	0.51
1:BW:85:VAL:HG23	1:BW:86:PRO:HD2	1.93	0.51
1:AZ:124:VAL:HG11	1:AZ:138:PHE:HD1	1.76	0.51
1:BF:325:LEU:HD22	1:BF:329:THR:HG21	1.92	0.51
1:AS:110:GLU:HG2	1:AS:112:GLN:HG2	1.93	0.51
1:BP:124:VAL:HG11	1:BP:138:PHE:CD2	2.46	0.51
1:BN:168:TRP:CE2	1:AN:176:ARG:HD2	2.46	0.51
1:AV:101:ARG:CZ	1:AV:166:LEU:HD23	2.41	0.51
1:AB:142:GLN:O	1:AB:142:GLN:NE2	2.44	0.51
1:BX:183:LEU:HD12	1:BX:183:LEU:C	2.31	0.51
1:AD:85:VAL:HG22	1:AD:86:PRO:HD2	1.96	0.51
1:AA:246:THR:N	1:AA:247:PRO:CD	2.74	0.51
1:CB:80:VAL:CG1	1:CB:185:LEU:HB2	2.40	0.50
1:CK:122:GLY:O	1:CK:188:VAL:HB	2.10	0.50
1:AA:314:TYR:HE1	1:AA:316:SER:HG	1.64	0.50
1:CM:103:ALA:HB2	1:CM:166:LEU:HB3	1.92	0.50
1:CA:101:ARG:CZ	1:CA:166:LEU:CD1	2.89	0.50
1:AT:314:TYR:CE1	1:AT:316:SER:HA	2.45	0.50
1:CA:99:PHE:CB	1:CA:209:VAL:O	2.61	0.50
1:CA:99:PHE:HB3	1:CA:209:VAL:O	2.14	0.50
1:CT:99:PHE:CB	1:CT:209:VAL:O	2.59	0.50
1:BC:166:LEU:HD13	1:BC:167:LEU:N	2.27	0.50
1:BV:165:THR:OG1	1:BV:166:LEU:N	2.44	0.50
1:BQ:166:LEU:HD13	1:BQ:167:LEU:N	2.27	0.50
1:CB:112:GLN:HE21	1:CF:44:THR:H	1.59	0.50
1:CB:57:LEU:HD23	1:CB:203:TRP:CH2	2.46	0.50
1:BJ:281:HIS:ND1	1:BJ:301:TRP:HB3	2.26	0.50
1:AM:110:GLU:HG2	1:AM:112:GLN:HG2	1.94	0.50
1:CN:133:ASP:O	1:CN:182:ARG:NH2	2.45	0.50
1:BB:214:ASN:HD22	1:BB:215:PRO:HD2	1.79	0.50
1:BN:99:PHE:CD1	1:BN:99:PHE:N	2.78	0.50
1:CI:80:VAL:HG11	1:CI:185:LEU:HB2	1.93	0.50
1:CK:80:VAL:HG11	1:CK:185:LEU:HB2	1.92	0.50
1:CS:185:LEU:C	1:CS:186:LEU:HD23	2.31	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CV:80:VAL:CG1	1:CV:185:LEU:HB2	2.41	0.50
1:AY:315:TYR:CE2	1:AY:317:ASP:OD2	2.65	0.50
1:BA:165:THR:OG1	1:BA:166:LEU:N	2.44	0.50
1:BD:165:THR:OG1	1:BD:166:LEU:N	2.46	0.50
1:AF:162:TYR:CD1	1:AF:162:TYR:N	2.79	0.50
1:AQ:111:ILE:HG21	1:AQ:123:TYR:CZ	2.47	0.50
1:AC:188:VAL:HG23	1:AM:114:MET:SD	242.20	0.50
1:AT:119:THR:HG23	1:AT:193:ASP:CB	2.39	0.50
1:AQ:119:THR:HG23	1:AQ:193:ASP:CB	2.40	0.50
1:BP:85:VAL:HG23	1:BP:86:PRO:HD2	1.93	0.50
1:CR:117:ALA:HB2	1:CT:38:PRO:O	2.11	0.50
1:CF:237:ASP:HB3	1:CF:297:ARG:HG2	1.92	0.50
1:BU:99:PHE:CD1	1:BU:99:PHE:N	2.78	0.50
1:AX:310:ASP:HB3	1:AX:312:VAL:HG22	1.93	0.50
1:AX:302:ASP:C	1:AX:305:ASN:ND2	2.64	0.50
1:AU:279:TYR:CE2	1:AU:311:GLY:O	2.63	0.50
1:AS:314:TYR:CE1	1:AS:316:SER:CA	2.87	0.50
1:AD:315:TYR:CE2	1:AD:317:ASP:OD2	2.67	0.50
1:AT:314:TYR:CG	1:AT:315:TYR:N	2.79	0.50
1:CJ:100:GLN:HA	1:CJ:213:GLU:OE2	2.11	0.50
1:CY:99:PHE:CB	1:CY:209:VAL:O	2.59	0.50
1:BI:166:LEU:HD13	1:BI:167:LEU:N	2.26	0.50
1:BS:166:LEU:HD13	1:BS:167:LEU:N	2.27	0.50
1:AS:61:SER:CB	1:AS:90:PRO:HD2	2.36	0.50
1:BD:123:TYR:HB2	1:BD:185:LEU:HD11	1.93	0.50
1:AX:115:CYS:HB2	1:AX:116:PRO:HD2	1.92	0.50
1:AA:124:VAL:HG11	1:AA:138:PHE:HD1	1.77	0.50
1:BV:325:LEU:HD22	1:BV:329:THR:HG21	1.94	0.50
1:CP:237:ASP:HB3	1:CP:297:ARG:HG2	1.93	0.50
1:CY:288:ASN:N	1:CY:288:ASN:OD1	2.45	0.50
1:AF:142:GLN:O	1:AF:142:GLN:NE2	2.44	0.50
1:CR:190:ASN:N	1:CR:190:ASN:HD22	2.09	0.50
1:CI:237:ASP:HB3	1:CI:297:ARG:HG2	1.93	0.50
1:BA:276:ARG:O	1:AA:276:ARG:NH2	2.44	0.50
1:BN:124:VAL:HG11	1:BN:138:PHE:CD2	2.46	0.50
1:AD:302:ASP:CA	1:AD:305:ASN:ND2	2.77	0.50
1:AF:302:ASP:C	1:AF:305:ASN:ND2	2.64	0.50
1:CY:185:LEU:C	1:CY:186:LEU:HD23	2.32	0.50
1:BL:114:MET:SD	1:CU:122:GLY:HA3	2.52	0.50
1:AD:279:TYR:CE2	1:AD:311:GLY:O	2.63	0.50
1:AZ:279:TYR:CE2	1:AZ:311:GLY:O	2.62	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AD:91:ARG:NH2	1:BF:98:ILE:HG22	2.26	0.50
1:BT:98:ILE:CG2	1:AV:91:ARG:NE	2.74	0.50
1:CR:123:TYR:CD1	1:CR:185:LEU:HD21	2.47	0.50
1:AH:315:TYR:CE2	1:AH:317:ASP:OD2	2.64	0.50
1:AL:314:TYR:CG	1:AL:315:TYR:N	2.79	0.50
1:BQ:101:ARG:NH2	1:BQ:166:LEU:HD12	2.25	0.50
1:AS:162:TYR:CD1	1:AS:162:TYR:N	2.80	0.50
1:AY:162:TYR:CD1	1:AY:162:TYR:N	2.79	0.50
1:AE:162:TYR:N	1:AE:162:TYR:CD1	2.80	0.50
1:BC:74:THR:O	1:BC:75:ASP:C	2.49	0.50
1:CP:199:VAL:CG1	1:CP:199:VAL:O	2.60	0.50
1:CX:111:ILE:HD11	1:CX:125:ALA:CB	2.41	0.50
1:BR:74:THR:HA	1:BR:190:ASN:ND2	2.26	0.50
1:AL:80:VAL:CG1	1:AL:185:LEU:HB3	2.41	0.50
1:BM:168:TRP:CE2	1:AM:176:ARG:HD2	2.46	0.50
1:CD:190:ASN:N	1:CD:190:ASN:HD22	2.10	0.50
1:AX:142:GLN:O	1:AX:142:GLN:NE2	2.44	0.50
1:CH:124:VAL:HG13	1:CH:124:VAL:O	2.11	0.50
1:AV:85:VAL:HG22	1:AV:86:PRO:HD2	1.94	0.50
1:BV:99:PHE:CD1	1:BV:99:PHE:N	2.80	0.50
1:BE:124:VAL:HG11	1:BE:138:PHE:CD2	2.46	0.50
1:AS:253:ASP:CG	1:AS:285:PHE:CA	2.79	0.50
1:AK:302:ASP:CA	1:AK:305:ASN:ND2	2.74	0.50
1:AU:302:ASP:C	1:AU:305:ASN:ND2	2.63	0.50
1:BH:61:SER:CB	1:BH:90:PRO:HD2	2.25	0.50
1:AJ:91:ARG:CZ	1:BR:98:ILE:HG22	2.41	0.50
1:AL:314:TYR:CE1	1:AL:316:SER:HA	2.45	0.50
1:CX:100:GLN:HA	1:CX:213:GLU:OE2	2.11	0.50
1:BL:165:THR:OG1	1:BL:166:LEU:N	2.45	0.50
1:BZ:166:LEU:HD13	1:BZ:167:LEU:N	2.27	0.50
1:BE:166:LEU:HD13	1:BE:167:LEU:N	2.27	0.50
1:BD:111:ILE:HG22	1:BD:156:ARG:H	1.76	0.50
1:AD:115:CYS:HB2	1:AD:116:PRO:HD2	1.94	0.50
1:AK:119:THR:HG23	1:AK:193:ASP:CB	2.41	0.50
1:CP:111:ILE:HD11	1:CP:125:ALA:CB	2.41	0.50
1:BF:74:THR:HA	1:BF:190:ASN:ND2	2.27	0.50
1:BF:74:THR:O	1:BF:75:ASP:C	2.50	0.50
1:AD:114:MET:SD	1:AF:122:GLY:HA3	2.51	0.50
1:CF:111:ILE:HG22	1:CF:113:PRO:HD3	1.94	0.50
1:CB:163:THR:OG1	1:CB:165:THR:HG23	2.17	0.50
1:BM:74:THR:O	1:BM:75:ASP:C	2.50	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AC:118:ASN:O	1:AM:116:PRO:HB3	253.39	0.50
1:AF:109:PHE:HB2	1:AF:158:VAL:CG1	2.41	0.50
1:AS:115:CYS:HB2	1:AS:116:PRO:HD2	1.93	0.50
1:AQ:246:THR:N	1:AQ:247:PRO:CD	2.74	0.50
1:CY:237:ASP:HB3	1:CY:297:ARG:HG2	1.94	0.50
1:BT:85:VAL:HG23	1:BT:86:PRO:HD2	1.92	0.50
1:CQ:288:ASN:OD1	1:CQ:288:ASN:N	2.45	0.50
1:AK:310:ASP:HB3	1:AK:312:VAL:HG22	1.94	0.50
1:AY:253:ASP:OD1	1:AY:285:PHE:N	2.44	0.50
1:CP:80:VAL:CG1	1:CP:185:LEU:HB2	2.42	0.50
1:BM:61:SER:CB	1:BM:90:PRO:HD2	2.27	0.50
1:BA:98:ILE:CA	1:BA:211:SER:O	2.60	0.50
1:CC:99:PHE:CB	1:CC:209:VAL:O	2.62	0.50
1:AB:314:TYR:HE1	1:AB:316:SER:HG	1.58	0.50
1:AV:314:TYR:CG	1:AV:315:TYR:N	2.79	0.50
1:CR:80:VAL:HG11	1:CR:185:LEU:HB2	1.94	0.50
1:AF:314:TYR:CE1	1:AF:316:SER:CA	2.87	0.50
1:CK:101:ARG:CZ	1:CK:166:LEU:CD1	2.90	0.50
1:CT:100:GLN:HA	1:CT:213:GLU:OE2	2.11	0.50
1:CA:112:GLN:NE2	1:CA:155:SER:OG	2.45	0.50
1:BI:74:THR:HA	1:BI:190:ASN:ND2	2.27	0.50
1:BO:74:THR:O	1:BO:75:ASP:C	2.50	0.50
1:BQ:74:THR:O	1:BQ:75:ASP:C	2.50	0.50
1:AL:119:THR:HG23	1:AL:193:ASP:CB	2.41	0.50
1:BA:74:THR:O	1:BA:75:ASP:C	2.50	0.50
1:BR:74:THR:O	1:BR:75:ASP:C	2.49	0.50
1:BM:183:LEU:HD12	1:BM:183:LEU:C	2.32	0.50
1:CK:85:VAL:HG13	1:CK:86:PRO:HD2	1.92	0.50
1:AL:310:ASP:HB3	1:AL:312:VAL:HG22	1.93	0.50
1:AY:302:ASP:C	1:AY:305:ASN:ND2	2.63	0.50
1:AW:302:ASP:C	1:AW:305:ASN:ND2	2.63	0.50
1:CM:81:ASP:HA	1:CM:184:ILE:HG22	1.94	0.50
1:CH:81:ASP:OD2	1:CH:136:HIS:NE2	2.43	0.50
1:BM:98:ILE:CA	1:BM:211:SER:O	2.59	0.50
1:CR:99:PHE:CD2	1:CR:207:LEU:HB3	2.47	0.50
1:CF:98:ILE:HD11	1:CF:99:PHE:CE2	2.47	0.50
1:CY:101:ARG:CZ	1:CY:166:LEU:CD1	2.90	0.50
1:AP:314:TYR:CE1	1:AP:316:SER:HA	2.44	0.50
1:CX:99:PHE:HB3	1:CX:209:VAL:O	2.11	0.50
1:BG:166:LEU:HD13	1:BG:167:LEU:N	2.26	0.50
1:CH:34:ARG:HD3	1:CM:43:SER:O	2.12	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CZ:63:ILE:HD12	1:CZ:88:LEU:CD1	2.41	0.50
1:AR:119:THR:HG23	1:AR:193:ASP:CB	2.42	0.50
1:CB:151:LYS:NZ	1:BO:153:TRP:O	144.26	0.50
1:BU:111:ILE:HG23	1:BU:113:PRO:HD3	1.94	0.50
1:AJ:268:SER:CB	1:AJ:273:ASP:O	2.60	0.50
1:AK:124:VAL:HG11	1:AK:138:PHE:HD1	1.76	0.50
1:CT:163:THR:OG1	1:CT:165:THR:HG23	2.12	0.50
1:AH:80:VAL:HG13	1:AH:185:LEU:HB3	1.93	0.50
1:AF:124:VAL:HG11	1:AF:138:PHE:CD1	2.47	0.50
1:CR:45:VAL:HG23	1:CT:200:LEU:HD13	1.93	0.50
1:BF:161:GLN:NE2	1:CF:210:PRO:HD2	2.26	0.50
1:BJ:99:PHE:N	1:BJ:99:PHE:CD1	2.79	0.50
1:BB:99:PHE:N	1:BB:99:PHE:CD1	2.80	0.50
1:CZ:190:ASN:HD22	1:CZ:190:ASN:N	2.10	0.50
1:BU:183:LEU:HD12	1:BU:183:LEU:C	2.32	0.50
1:AF:101:ARG:CZ	1:AF:166:LEU:HD23	2.42	0.50
1:BT:161:GLN:NE2	1:CT:210:PRO:HD2	2.27	0.50
1:AQ:253:ASP:OD1	1:AQ:285:PHE:N	2.43	0.50
1:AE:302:ASP:C	1:AE:305:ASN:ND2	2.64	0.50
1:CU:81:ASP:HA	1:CU:184:ILE:HG22	1.94	0.50
1:AJ:279:TYR:CE2	1:AJ:311:GLY:O	2.65	0.50
1:AT:279:TYR:CE2	1:AT:311:GLY:O	2.63	0.50
1:CR:101:ARG:CZ	1:CR:166:LEU:CD1	2.90	0.50
1:CX:79:VAL:CG1	1:CX:185:LEU:O	2.53	0.50
1:AK:314:TYR:CG	1:AK:315:TYR:N	2.79	0.50
1:CN:101:ARG:CZ	1:CN:166:LEU:CD1	2.90	0.50
1:CE:98:ILE:HD11	1:CE:99:PHE:CE2	2.47	0.50
1:CG:100:GLN:HA	1:CG:213:GLU:OE2	2.12	0.50
1:BM:165:THR:OG1	1:BM:166:LEU:N	2.43	0.50
1:CD:62:ARG:HA	1:CD:200:LEU:HD23	1.94	0.50
1:CJ:62:ARG:HA	1:CJ:200:LEU:HD23	1.94	0.50
1:CX:63:ILE:HD12	1:CX:88:LEU:CG	2.41	0.50
1:CA:62:ARG:NH1	1:BG:75:ASP:OD2	2.42	0.50
1:CN:163:THR:OG1	1:CN:165:THR:HG23	2.12	0.50
1:CP:45:VAL:HG23	1:CQ:200:LEU:HD13	1.94	0.50
1:BX:85:VAL:HG23	1:BX:86:PRO:HD2	1.94	0.50
1:BJ:85:VAL:HG23	1:BJ:86:PRO:HD2	1.93	0.50
1:BJ:183:LEU:C	1:BJ:183:LEU:HD12	2.31	0.50
1:AA:142:GLN:O	1:AA:142:GLN:NE2	2.46	0.50
1:AJ:142:GLN:NE2	1:AJ:142:GLN:O	2.44	0.50
1:BT:99:PHE:CD1	1:BT:99:PHE:N	2.79	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AC:109:PHE:HB2	1:AC:158:VAL:CG1	2.47	0.50
1:BL:325:LEU:HD22	1:BL:329:THR:HG21	1.94	0.50
1:BK:161:GLN:NE2	1:CK:210:PRO:HD2	2.27	0.50
1:AV:310:ASP:HB3	1:AV:312:VAL:HG22	1.94	0.50
1:AW:310:ASP:HB3	1:AW:312:VAL:HG22	1.93	0.50
1:AB:253:ASP:CG	1:AB:285:PHE:CA	2.78	0.50
1:CI:101:ARG:CZ	1:CI:166:LEU:CD1	2.90	0.50
1:CE:101:ARG:CZ	1:CE:166:LEU:CD1	2.90	0.50
1:BS:165:THR:OG1	1:BS:166:LEU:N	2.45	0.50
1:CK:63:ILE:HD12	1:CK:88:LEU:CG	2.40	0.50
1:CC:199:VAL:CG1	1:CC:199:VAL:O	2.60	0.50
1:AE:119:THR:HG23	1:AE:193:ASP:CB	2.41	0.50
1:AC:188:VAL:CG2	1:AM:114:MET:SD	242.01	0.50
1:CL:63:ILE:HD12	1:CL:88:LEU:CD1	2.42	0.50
1:CA:163:THR:OG1	1:CA:165:THR:HG23	2.15	0.50
1:AJ:246:THR:N	1:AJ:247:PRO:CD	2.75	0.50
1:AE:101:ARG:CZ	1:AE:166:LEU:HD23	2.41	0.50
1:AY:246:THR:N	1:AY:247:PRO:CD	2.74	0.50
1:CM:190:ASN:N	1:CM:190:ASN:HD22	2.10	0.50
1:BT:214:ASN:HD22	1:BT:215:PRO:HD2	1.77	0.50
1:CW:79:VAL:HG13	1:CW:80:VAL:N	2.27	0.49
1:BD:98:ILE:HG23	1:AW:91:ARG:HG2	1.94	0.49
1:AW:279:TYR:CE2	1:AW:311:GLY:O	2.63	0.49
1:AB:91:ARG:NH2	1:BO:210:PRO:HB3	129.91	0.49
1:CK:79:VAL:HG13	1:CK:80:VAL:N	2.26	0.49
1:AC:315:TYR:CE2	1:AC:317:ASP:OD2	2.65	0.49
1:CM:98:ILE:HB	1:CO:91:ARG:HD2	1.93	0.49
1:AH:61:SER:CB	1:AH:90:PRO:HD2	2.34	0.49
1:BA:150:ALA:HB2	1:BA:156:ARG:HD3	1.95	0.49
1:BW:123:TYR:HB2	1:BW:185:LEU:HD11	1.92	0.49
1:CO:57:LEU:HD23	1:CO:203:TRP:CH2	2.47	0.49
1:CQ:111:ILE:HD11	1:CQ:125:ALA:CB	2.41	0.49
1:CH:163:THR:OG1	1:CH:165:THR:HG23	2.12	0.49
1:BC:168:TRP:CE2	1:AC:176:ARG:HD2	2.47	0.49
1:AI:110:GLU:HG2	1:AI:112:GLN:HG2	1.94	0.49
1:BI:205:VAL:HG22	1:BI:206:ARG:N	2.27	0.49
1:BY:325:LEU:HD22	1:BY:329:THR:HG21	1.92	0.49
1:BR:85:VAL:HG23	1:BR:86:PRO:HD2	1.93	0.49
1:AR:246:THR:N	1:AR:247:PRO:CD	2.75	0.49
1:BY:276:ARG:O	1:AY:276:ARG:NH2	2.45	0.49
1:CE:288:ASN:OD1	1:CE:288:ASN:N	2.45	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CG:288:ASN:N	1:CG:288:ASN:OD1	2.45	0.49
1:AK:246:THR:N	1:AK:247:PRO:CD	2.74	0.49
1:AN:310:ASP:HB3	1:AN:312:VAL:HG22	1.93	0.49
1:AO:253:ASP:CG	1:AO:285:PHE:CA	2.78	0.49
1:AF:253:ASP:CG	1:AF:285:PHE:CA	2.80	0.49
1:AW:305:ASN:OD1	1:AW:305:ASN:N	2.43	0.49
1:BD:98:ILE:HG22	1:AG:91:ARG:HH21	87.83	0.49
1:CE:100:GLN:HA	1:CE:213:GLU:OE2	2.12	0.49
1:CY:99:PHE:HB3	1:CY:209:VAL:O	2.12	0.49
1:BK:166:LEU:HD13	1:BK:167:LEU:N	2.27	0.49
1:BB:163:THR:OG1	1:BB:165:THR:CG2	2.61	0.49
1:BR:166:LEU:HD13	1:BR:167:LEU:N	2.27	0.49
1:AU:111:ILE:HG21	1:AU:123:TYR:CZ	2.47	0.49
1:AA:116:PRO:HB3	1:AI:118:ASN:O	13.72	0.49
1:AS:111:ILE:HG21	1:AS:123:TYR:CZ	2.48	0.49
1:CF:199:VAL:CG1	1:CF:199:VAL:O	2.61	0.49
1:CU:163:THR:OG1	1:CU:165:THR:HG23	2.11	0.49
1:AR:122:GLY:C	1:AR:188:VAL:HG22	2.32	0.49
1:AN:246:THR:N	1:AN:247:PRO:CD	2.75	0.49
1:AL:122:GLY:HA3	1:AU:114:MET:SD	2.52	0.49
1:BU:276:ARG:O	1:AU:276:ARG:NH2	2.45	0.49
1:CX:237:ASP:HB3	1:CX:297:ARG:HG2	1.95	0.49
1:BH:168:TRP:CE2	1:AH:176:ARG:HD2	2.47	0.49
1:BG:161:GLN:NE2	1:CG:210:PRO:HD2	2.28	0.49
1:CV:46:THR:HB	1:CZ:202:ARG:HH12	1.76	0.49
1:CA:288:ASN:N	1:CA:288:ASN:OD1	2.47	0.49
1:BL:85:VAL:HG23	1:BL:86:PRO:HD2	1.94	0.49
1:AO:85:VAL:HG22	1:AO:86:PRO:HD2	1.92	0.49
1:BF:99:PHE:CD1	1:BF:99:PHE:N	2.80	0.49
1:AZ:298:TRP:NE1	1:AZ:312:VAL:CB	2.75	0.49
1:CD:81:ASP:HA	1:CD:184:ILE:HG22	1.94	0.49
1:AS:302:ASP:C	1:AS:305:ASN:ND2	2.63	0.49
1:CL:80:VAL:HG22	1:CL:81:ASP:N	2.26	0.49
1:AN:91:ARG:NH2	1:BP:210:PRO:HB3	2.27	0.49
1:CM:98:ILE:HD11	1:CM:99:PHE:CE2	2.48	0.49
1:BH:166:LEU:HD13	1:BH:167:LEU:N	2.26	0.49
1:BW:166:LEU:HD13	1:BW:167:LEU:N	2.26	0.49
1:BS:163:THR:OG1	1:BS:165:THR:CG2	2.60	0.49
1:BE:111:ILE:HG21	1:BE:123:TYR:OH	2.13	0.49
1:CG:34:ARG:HD3	1:CV:43:SER:O	2.12	0.49
1:CG:63:ILE:HD12	1:CG:88:LEU:CG	2.42	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BN:123:TYR:HB2	1:BN:185:LEU:CD1	2.42	0.49
1:AI:109:PHE:HB2	1:AI:158:VAL:CG1	2.41	0.49
1:BA:161:GLN:NE2	1:CA:210:PRO:HD2	2.32	0.49
1:AL:110:GLU:HG2	1:AL:112:GLN:HG2	1.95	0.49
1:BP:161:GLN:NE2	1:CP:210:PRO:HD2	2.27	0.49
1:CS:288:ASN:OD1	1:CS:288:ASN:N	2.45	0.49
1:BJ:168:TRP:CE2	1:AJ:176:ARG:HD2	2.47	0.49
1:CR:85:VAL:HG13	1:CR:86:PRO:HD2	1.94	0.49
1:BX:99:PHE:N	1:BX:99:PHE:CD1	2.80	0.49
1:BE:85:VAL:HG23	1:BE:86:PRO:HD2	1.93	0.49
1:AF:298:TRP:NE1	1:AF:312:VAL:CB	2.76	0.49
1:AZ:310:ASP:HB3	1:AZ:312:VAL:HG22	1.94	0.49
1:AT:302:ASP:CA	1:AT:305:ASN:ND2	2.76	0.49
1:BA:254:GLY:CA	1:BA:283:LYS:HE3	2.28	0.49
1:BF:98:ILE:CA	1:BF:211:SER:O	2.61	0.49
1:BZ:98:ILE:CA	1:BZ:211:SER:O	2.60	0.49
1:BQ:98:ILE:HG22	1:AZ:91:ARG:CZ	2.43	0.49
1:CS:101:ARG:CZ	1:CS:166:LEU:CD1	2.90	0.49
1:CG:101:ARG:NH1	1:CG:166:LEU:CD1	2.74	0.49
1:CQ:99:PHE:HB3	1:CQ:209:VAL:O	2.12	0.49
1:BU:165:THR:OG1	1:BU:166:LEU:N	2.44	0.49
1:AP:61:SER:HB2	1:AP:89:LEU:HD22	1.94	0.49
1:BR:123:TYR:HB2	1:BR:185:LEU:HD11	1.95	0.49
1:BC:142:GLN:HB2	1:CC:48:PHE:CE1	2.48	0.49
1:CK:63:ILE:HD12	1:CK:88:LEU:CD1	2.42	0.49
1:AD:118:ASN:O	1:AW:116:PRO:HB3	2.12	0.49
1:BH:74:THR:O	1:BH:75:ASP:C	2.50	0.49
1:BW:142:GLN:HB2	1:CW:48:PHE:HE1	1.78	0.49
1:AI:115:CYS:HB2	1:AI:116:PRO:HD2	1.94	0.49
1:CD:163:THR:OG1	1:CD:165:THR:HG23	2.12	0.49
1:AB:124:VAL:HG11	1:AB:138:PHE:HD1	1.77	0.49
1:AC:64:SER:OG	1:AC:80:VAL:HG21	2.13	0.49
1:BW:74:THR:O	1:BW:75:ASP:C	2.50	0.49
1:CC:237:ASP:HB3	1:CC:297:ARG:HG2	1.98	0.49
1:BV:168:TRP:CE2	1:AV:176:ARG:HD2	2.47	0.49
1:CP:133:ASP:O	1:CP:182:ARG:NH2	2.45	0.49
1:BI:85:VAL:HG23	1:BI:86:PRO:HD2	1.93	0.49
1:CD:60:MET:HE1	1:CW:47:GLY:H	105.86	0.49
1:CL:85:VAL:HG13	1:CL:86:PRO:HD2	1.93	0.49
1:BN:214:ASN:HD22	1:BN:215:PRO:HD2	1.76	0.49
1:BV:98:ILE:CA	1:BV:211:SER:O	2.60	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AO:279:TYR:CE2	1:AO:311:GLY:O	2.63	0.49
1:CV:101:ARG:CZ	1:CV:166:LEU:CD1	2.90	0.49
1:AD:314:TYR:CE1	1:AD:316:SER:HA	2.45	0.49
1:AR:314:TYR:CE1	1:AR:316:SER:HA	2.46	0.49
1:AD:61:SER:HB2	1:AD:89:LEU:HD22	1.96	0.49
1:CN:80:VAL:CG1	1:CN:185:LEU:HB2	2.42	0.49
1:BD:153:TRP:O	1:CG:151:LYS:NZ	23.72	0.49
1:BC:150:ALA:HB2	1:BC:156:ARG:HD3	1.97	0.49
1:BT:80:VAL:CG1	1:BT:185:LEU:HB3	2.42	0.49
1:BH:74:THR:HA	1:BH:190:ASN:ND2	2.27	0.49
1:BT:74:THR:O	1:BT:75:ASP:C	2.50	0.49
1:BD:74:THR:HA	1:BD:190:ASN:ND2	2.27	0.49
1:BY:74:THR:O	1:BY:75:ASP:C	2.51	0.49
1:BP:74:THR:O	1:BP:75:ASP:C	2.50	0.49
1:BF:85:VAL:HG23	1:BF:86:PRO:HD2	1.94	0.49
1:BO:85:VAL:HG23	1:BO:86:PRO:HD2	1.94	0.49
1:BC:276:ARG:O	1:AC:276:ARG:NH2	2.49	0.49
1:BG:85:VAL:HG23	1:BG:86:PRO:HD2	1.94	0.49
1:BI:214:ASN:HD22	1:BI:215:PRO:HD2	1.76	0.49
1:CV:288:ASN:N	1:CV:288:ASN:OD1	2.45	0.49
1:CD:237:ASP:HB3	1:CD:297:ARG:HG2	1.93	0.49
1:AO:110:GLU:HG2	1:AO:112:GLN:HG2	1.93	0.49
1:CT:85:VAL:HG13	1:CT:86:PRO:HD2	1.94	0.49
1:AW:298:TRP:NE1	1:AW:312:VAL:CB	2.75	0.49
1:AP:253:ASP:CG	1:AP:285:PHE:CA	2.80	0.49
1:AA:302:ASP:CA	1:AA:305:ASN:ND2	2.76	0.49
1:CM:80:VAL:HG11	1:CM:185:LEU:HB2	1.94	0.49
1:AI:263:LEU:HB3	1:AI:279:TYR:O	2.12	0.49
1:AP:315:TYR:CE2	1:AP:317:ASP:OD2	2.66	0.49
1:BU:166:LEU:HD13	1:BU:167:LEU:N	2.27	0.49
1:BT:123:TYR:HB2	1:BT:185:LEU:HD11	1.95	0.49
1:BZ:123:TYR:HB2	1:BZ:185:LEU:HD11	1.95	0.49
1:BI:111:ILE:HG21	1:BI:123:TYR:OH	2.13	0.49
1:AG:111:ILE:HG21	1:AG:123:TYR:CZ	2.48	0.49
1:CX:57:LEU:HD23	1:CX:203:TRP:CH2	2.48	0.49
1:CI:57:LEU:HD23	1:CI:203:TRP:CH2	2.47	0.49
1:CF:163:THR:OG1	1:CF:165:THR:HG23	2.13	0.49
1:AN:101:ARG:CZ	1:AN:166:LEU:HD23	2.42	0.49
1:BQ:99:PHE:N	1:BQ:99:PHE:CD1	2.80	0.49
1:BW:109:PHE:HB2	1:BW:158:VAL:CG1	2.42	0.49
1:BG:124:VAL:HG11	1:BG:138:PHE:CD2	2.47	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AP:268:SER:HB3	1:AP:273:ASP:O	2.11	0.49
1:BA:214:ASN:HD22	1:BA:215:PRO:HD2	1.78	0.49
1:CO:288:ASN:OD1	1:CO:288:ASN:N	2.45	0.49
1:BW:99:PHE:CD1	1:BW:99:PHE:N	2.80	0.49
1:CS:85:VAL:HG13	1:CS:86:PRO:HD2	1.94	0.49
1:BO:99:PHE:CD1	1:BO:99:PHE:N	2.79	0.49
1:CP:81:ASP:OD2	1:CP:136:HIS:NE2	2.45	0.49
1:BY:61:SER:CB	1:BY:90:PRO:HD2	2.28	0.49
1:BD:98:ILE:CA	1:BD:211:SER:O	2.61	0.49
1:AU:315:TYR:CE2	1:AU:317:ASP:OD2	2.66	0.49
1:CD:99:PHE:CB	1:CD:209:VAL:O	2.61	0.49
1:BT:166:LEU:HD13	1:BT:167:LEU:N	2.28	0.49
1:BP:165:THR:OG1	1:BP:166:LEU:N	2.44	0.49
1:AP:61:SER:CB	1:AP:90:PRO:HD2	2.37	0.49
1:CK:112:GLN:HE21	1:CL:44:THR:N	2.10	0.49
1:AX:111:ILE:HG21	1:AX:123:TYR:CZ	2.48	0.49
1:BQ:74:THR:HA	1:BQ:190:ASN:ND2	2.28	0.49
1:AC:124:VAL:HG11	1:AC:138:PHE:CD1	2.48	0.49
1:AC:122:GLY:HA3	1:AY:114:MET:SD	2.52	0.49
1:BJ:74:THR:O	1:BJ:75:ASP:C	2.50	0.49
1:AO:80:VAL:HG13	1:AO:185:LEU:HB3	1.95	0.49
1:AT:124:VAL:HG11	1:AT:138:PHE:CD1	2.48	0.49
1:AX:124:VAL:HG11	1:AX:138:PHE:CD1	2.48	0.49
1:BC:161:GLN:NE2	1:CC:210:PRO:HD2	2.32	0.49
1:BK:205:VAL:HG22	1:BK:206:ARG:N	2.28	0.49
1:AU:122:GLY:HA3	1:AX:114:MET:SD	2.52	0.49
1:CS:124:VAL:HG13	1:CS:124:VAL:O	2.12	0.49
1:CN:288:ASN:N	1:CN:288:ASN:OD1	2.45	0.49
1:CF:190:ASN:HD22	1:CF:190:ASN:N	2.10	0.49
1:CJ:151:LYS:NZ	1:BR:153:TRP:O	2.46	0.49
1:CY:124:VAL:HG13	1:CY:124:VAL:O	2.12	0.49
1:CB:288:ASN:OD1	1:CB:288:ASN:N	2.46	0.49
1:CC:288:ASN:OD1	1:CC:288:ASN:N	2.48	0.49
1:AE:279:TYR:CE2	1:AE:311:GLY:O	2.64	0.49
1:CO:80:VAL:HG11	1:CO:185:LEU:HB2	1.94	0.49
1:AQ:315:TYR:CE2	1:AQ:317:ASP:OD2	2.66	0.49
1:AA:315:TYR:CE2	1:AA:317:ASP:OD2	2.66	0.49
1:CQ:100:GLN:HA	1:CQ:213:GLU:OE2	2.13	0.49
1:CT:99:PHE:HB3	1:CT:209:VAL:O	2.13	0.49
1:CJ:123:TYR:HA	1:CJ:188:VAL:HG23	1.95	0.49
1:AR:61:SER:CB	1:AR:90:PRO:HD2	2.34	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CW:99:PHE:CB	1:CW:209:VAL:O	2.60	0.49
1:CM:43:SER:HA	1:CO:112:GLN:NE2	2.28	0.49
1:BZ:80:VAL:CG1	1:BZ:185:LEU:HB3	2.43	0.49
1:BI:74:THR:O	1:BI:75:ASP:C	2.50	0.49
1:BI:150:ALA:HB2	1:BI:156:ARG:HD3	1.95	0.49
1:BC:142:GLN:HB2	1:CC:48:PHE:HE1	1.77	0.49
1:AA:111:ILE:HG21	1:AA:123:TYR:CZ	2.47	0.49
1:CJ:63:ILE:HD12	1:CJ:88:LEU:CD1	2.42	0.49
1:BR:142:GLN:HB2	1:CR:48:PHE:HE1	1.77	0.49
1:CC:200:LEU:HD13	1:CJ:45:VAL:HG23	1.94	0.49
1:CB:62:ARG:HA	1:CB:200:LEU:HD23	1.95	0.49
1:BV:74:THR:O	1:BV:75:ASP:C	2.51	0.49
1:CO:85:VAL:HG13	1:CO:86:PRO:HD2	1.95	0.49
1:BE:276:ARG:O	1:AE:276:ARG:NH2	2.45	0.49
1:AU:101:ARG:CZ	1:AU:166:LEU:HD23	2.43	0.49
1:BW:276:ARG:O	1:AW:276:ARG:NH2	2.46	0.49
1:BS:183:LEU:HD12	1:BS:183:LEU:C	2.32	0.49
1:BB:183:LEU:C	1:BB:183:LEU:HD12	2.34	0.49
1:CJ:288:ASN:OD1	1:CJ:288:ASN:N	2.45	0.49
1:BV:205:VAL:HG22	1:BV:206:ARG:N	2.27	0.49
1:CT:237:ASP:HB3	1:CT:297:ARG:HG2	1.94	0.49
1:AH:110:GLU:HG2	1:AH:112:GLN:HG2	1.95	0.49
1:AC:298:TRP:NE1	1:AC:312:VAL:HA	2.28	0.49
1:AR:298:TRP:NE1	1:AR:312:VAL:CB	2.76	0.49
1:CZ:81:ASP:HA	1:CZ:184:ILE:HG22	1.95	0.49
1:CQ:81:ASP:OD2	1:CQ:136:HIS:NE2	2.45	0.49
1:AB:279:TYR:CE2	1:AB:311:GLY:O	2.62	0.49
1:BA:98:ILE:HG22	1:AT:91:ARG:CZ	57.54	0.49
1:CF:123:TYR:HA	1:CF:188:VAL:HG23	1.95	0.49
1:CL:98:ILE:HD11	1:CL:99:PHE:CE2	2.48	0.49
1:BC:156:ARG:NH2	1:CO:34:ARG:CG	199.49	0.49
1:CV:44:THR:H	1:CZ:112:GLN:HE21	1.59	0.49
1:CC:112:GLN:NE2	1:CC:155:SER:OG	2.46	0.49
1:CD:63:ILE:HD12	1:CD:88:LEU:CG	2.47	0.49
1:CO:63:ILE:HD12	1:CO:88:LEU:CG	2.41	0.49
1:AQ:188:VAL:CG2	1:AZ:114:MET:SD	3.01	0.49
1:BQ:116:PRO:CB	1:CZ:118:ASN:HA	2.43	0.49
1:BC:205:VAL:HG22	1:BC:206:ARG:N	2.28	0.49
1:AF:246:THR:N	1:AF:247:PRO:CD	2.75	0.49
1:AU:110:GLU:HG2	1:AU:112:GLN:HG2	1.95	0.49
1:AZ:101:ARG:CZ	1:AZ:166:LEU:HD23	2.42	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CM:288:ASN:N	1:CM:288:ASN:OD1	2.46	0.49
1:CN:190:ASN:HD22	1:CN:190:ASN:N	2.10	0.49
1:CH:288:ASN:N	1:CH:288:ASN:OD1	2.45	0.49
1:AA:101:ARG:CZ	1:AA:166:LEU:HD23	2.42	0.49
1:AX:110:GLU:HG2	1:AX:112:GLN:HG2	1.94	0.49
1:CK:133:ASP:O	1:CK:182:ARG:NH2	2.46	0.49
1:BD:85:VAL:HG23	1:BD:86:PRO:HD2	1.95	0.49
1:AG:118:ASN:O	1:AP:116:PRO:HB3	2.12	0.49
1:BX:205:VAL:HG22	1:BX:206:ARG:N	2.28	0.49
1:AC:302:ASP:CA	1:AC:305:ASN:ND2	2.76	0.49
1:AL:302:ASP:CA	1:AL:305:ASN:ND2	2.76	0.49
1:CU:101:ARG:CZ	1:CU:166:LEU:CD1	2.91	0.49
1:BE:98:ILE:CA	1:BE:211:SER:O	2.61	0.49
1:CJ:101:ARG:CZ	1:CJ:166:LEU:CD1	2.90	0.49
1:AP:314:TYR:CE1	1:AP:316:SER:CA	2.88	0.49
1:CE:99:PHE:CB	1:CE:209:VAL:O	2.61	0.49
1:AC:63:ILE:CD1	1:AC:89:LEU:HD21	2.48	0.49
1:CV:99:PHE:CB	1:CV:209:VAL:O	2.61	0.49
1:CA:112:GLN:HE21	1:CG:44:THR:H	1.61	0.49
1:BE:150:ALA:HB2	1:BE:156:ARG:HD3	1.95	0.49
1:CA:130:ASP:OD2	1:CA:176:ARG:NH2	2.49	0.49
1:BL:80:VAL:CG1	1:BL:185:LEU:HB3	2.43	0.49
1:CD:138:PHE:CE1	1:BH:62:ARG:HB2	136.84	0.49
1:BS:85:VAL:HG23	1:BS:86:PRO:HD2	1.94	0.49
1:CV:133:ASP:O	1:CV:182:ARG:NH2	2.46	0.49
1:CK:124:VAL:O	1:CK:124:VAL:HG13	2.13	0.49
1:CQ:124:VAL:HG13	1:CQ:124:VAL:O	2.13	0.49
1:BH:276:ARG:O	1:AH:276:ARG:NH2	2.46	0.49
1:BB:168:TRP:CE2	1:AB:176:ARG:HD2	2.50	0.49
1:AR:101:ARG:CZ	1:AR:166:LEU:HD23	2.42	0.49
1:AC:298:TRP:NE1	1:AC:312:VAL:CB	2.75	0.48
1:AR:302:ASP:CA	1:AR:305:ASN:ND2	2.75	0.48
1:AN:91:ARG:HH21	1:BP:98:ILE:HG22	1.77	0.48
1:BP:98:ILE:CA	1:BP:211:SER:O	2.61	0.48
1:CH:101:ARG:CZ	1:CH:166:LEU:CD1	2.90	0.48
1:AV:61:SER:HB2	1:AV:89:LEU:HD22	1.95	0.48
1:CZ:98:ILE:HD11	1:CZ:99:PHE:CE2	2.48	0.48
1:AE:61:SER:HB2	1:AE:89:LEU:HD22	1.95	0.48
1:BY:166:LEU:HD13	1:BY:167:LEU:N	2.28	0.48
1:CV:100:GLN:HA	1:CV:213:GLU:OE2	2.12	0.48
1:BG:150:ALA:HB2	1:BG:156:ARG:HD3	1.95	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BE:80:VAL:CG1	1:BE:185:LEU:HB3	2.42	0.48
1:BI:123:TYR:HB2	1:BI:185:LEU:HD11	1.95	0.48
1:AK:162:TYR:N	1:AK:162:TYR:CD1	2.80	0.48
1:CT:109:PHE:HB2	1:CT:158:VAL:HG12	1.94	0.48
1:CD:158:VAL:O	1:CD:158:VAL:HG13	2.13	0.48
1:BW:74:THR:HA	1:BW:190:ASN:HD22	1.76	0.48
1:BK:74:THR:HA	1:BK:190:ASN:HD22	1.77	0.48
1:BM:234:SER:HB3	1:BM:237:ASP:OD1	2.13	0.48
1:AE:246:THR:N	1:AE:247:PRO:CD	2.76	0.48
1:BL:260:ASP:HA	1:AL:261:ARG:NH2	2.28	0.48
1:BW:168:TRP:CE2	1:AW:176:ARG:HD2	2.48	0.48
1:AB:110:GLU:HG2	1:AB:112:GLN:HG2	1.96	0.48
1:BJ:205:VAL:HG22	1:BJ:206:ARG:N	2.28	0.48
1:BY:168:TRP:CE2	1:AY:176:ARG:HD2	2.48	0.48
1:CW:288:ASN:N	1:CW:288:ASN:OD1	2.46	0.48
1:CX:288:ASN:N	1:CX:288:ASN:OD1	2.45	0.48
1:CN:124:VAL:O	1:CN:124:VAL:HG13	2.13	0.48
1:CR:288:ASN:N	1:CR:288:ASN:OD1	2.46	0.48
1:CT:190:ASN:N	1:CT:190:ASN:HD22	2.11	0.48
1:BN:183:LEU:HD12	1:BN:183:LEU:C	2.34	0.48
1:CU:288:ASN:N	1:CU:288:ASN:OD1	2.45	0.48
1:BD:214:ASN:HD22	1:BD:215:PRO:HD2	1.78	0.48
1:AC:246:THR:N	1:AC:247:PRO:CD	2.77	0.48
1:BE:214:ASN:HD22	1:BE:215:PRO:HD2	1.78	0.48
1:AG:253:ASP:CG	1:AG:285:PHE:CA	2.79	0.48
1:AN:302:ASP:CA	1:AN:305:ASN:ND2	2.76	0.48
1:CX:81:ASP:OD2	1:CX:136:HIS:NE2	2.44	0.48
1:CF:81:ASP:OD2	1:CF:136:HIS:NE2	2.44	0.48
1:AN:279:TYR:CE2	1:AN:311:GLY:O	2.63	0.48
1:CB:103:ALA:HB2	1:CB:166:LEU:HB3	1.95	0.48
1:BY:98:ILE:CA	1:BY:211:SER:O	2.61	0.48
1:AO:91:ARG:CZ	1:BW:98:ILE:CG2	2.91	0.48
1:BB:166:LEU:HD13	1:BB:167:LEU:N	2.29	0.48
1:AP:162:TYR:CD1	1:AP:162:TYR:N	2.81	0.48
1:CB:112:GLN:HE21	1:CU:44:THR:H	122.28	0.48
1:BQ:142:GLN:HB2	1:CQ:48:PHE:HE1	1.78	0.48
1:BD:117:ALA:HB2	1:CW:117:ALA:HB1	1.95	0.48
1:AG:124:VAL:HG11	1:AG:138:PHE:HD1	1.77	0.48
1:CX:109:PHE:HB2	1:CX:158:VAL:HG12	1.96	0.48
1:AU:124:VAL:HG11	1:AU:138:PHE:CD1	2.48	0.48
1:AJ:116:PRO:HB3	1:AR:118:ASN:O	2.13	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CV:237:ASP:HB3	1:CV:297:ARG:HG2	1.94	0.48
1:BO:168:TRP:CE2	1:AO:176:ARG:HD2	2.48	0.48
1:BR:183:LEU:C	1:BR:183:LEU:HD12	2.33	0.48
1:CK:288:ASN:N	1:CK:288:ASN:OD1	2.46	0.48
1:AW:110:GLU:HG2	1:AW:112:GLN:HG2	1.95	0.48
1:AL:246:THR:N	1:AL:247:PRO:CD	2.75	0.48
1:CA:237:ASP:HB3	1:CA:297:ARG:HG2	1.94	0.48
1:AU:246:THR:N	1:AU:247:PRO:CD	2.76	0.48
1:CE:237:ASP:HB3	1:CE:297:ARG:HG2	1.94	0.48
1:BS:276:ARG:O	1:AS:276:ARG:NH2	2.46	0.48
1:AH:101:ARG:CZ	1:AH:166:LEU:HD23	2.43	0.48
1:AI:302:ASP:CA	1:AI:305:ASN:ND2	2.76	0.48
1:CG:80:VAL:HG11	1:CG:185:LEU:HB2	1.95	0.48
1:CW:123:TYR:CD1	1:CW:185:LEU:HD21	2.49	0.48
1:CO:81:ASP:HA	1:CO:184:ILE:HG22	1.96	0.48
1:CA:81:ASP:HA	1:CA:184:ILE:HG22	1.98	0.48
1:BK:98:ILE:CG2	1:AS:91:ARG:CZ	2.92	0.48
1:BB:98:ILE:CA	1:BB:211:SER:O	2.61	0.48
1:CO:101:ARG:CZ	1:CO:166:LEU:CD1	2.90	0.48
1:CJ:99:PHE:HB3	1:CJ:209:VAL:O	2.13	0.48
1:AU:162:TYR:CD1	1:AU:162:TYR:N	2.81	0.48
1:CF:43:SER:O	1:CI:34:ARG:HD3	2.12	0.48
1:BQ:123:TYR:HB2	1:BQ:185:LEU:CD1	2.43	0.48
1:CK:199:VAL:O	1:CK:199:VAL:CG1	2.61	0.48
1:BW:142:GLN:HB2	1:CW:48:PHE:CE1	2.48	0.48
1:BD:74:THR:O	1:BD:75:ASP:C	2.50	0.48
1:AP:124:VAL:HG11	1:AP:138:PHE:CD1	2.47	0.48
1:AP:115:CYS:HB2	1:AP:116:PRO:HD2	1.95	0.48
1:BY:99:PHE:CD1	1:BY:99:PHE:N	2.81	0.48
1:BL:281:HIS:ND1	1:BL:301:TRP:HB3	2.28	0.48
1:BH:234:SER:HB3	1:BH:237:ASP:OD1	2.12	0.48
1:BQ:276:ARG:O	1:AQ:276:ARG:NH2	2.46	0.48
1:BM:205:VAL:HG22	1:BM:206:ARG:N	2.28	0.48
1:BR:276:ARG:O	1:AR:276:ARG:NH2	2.46	0.48
1:BB:276:ARG:O	1:AB:276:ARG:NH2	2.46	0.48
1:AG:302:ASP:CA	1:AG:305:ASN:ND2	2.76	0.48
1:AE:302:ASP:CA	1:AE:305:ASN:ND2	2.77	0.48
1:CH:81:ASP:HA	1:CH:184:ILE:HG22	1.95	0.48
1:CI:122:GLY:O	1:CI:188:VAL:CB	2.62	0.48
1:AN:91:ARG:CZ	1:BP:98:ILE:CG2	2.91	0.48
1:BT:98:ILE:HG22	1:AV:91:ARG:CZ	2.43	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AT:315:TYR:CE2	1:AT:317:ASP:OD2	2.67	0.48
1:CZ:100:GLN:HA	1:CZ:213:GLU:OE2	2.13	0.48
1:AY:63:ILE:CD1	1:AY:89:LEU:HD21	2.42	0.48
1:BH:163:THR:OG1	1:BH:165:THR:CG2	2.62	0.48
1:BG:123:TYR:HB2	1:BG:185:LEU:CD1	2.43	0.48
1:BF:80:VAL:CG1	1:BF:185:LEU:HB3	2.43	0.48
1:BQ:150:ALA:HB2	1:BQ:156:ARG:HD3	1.96	0.48
1:BB:123:TYR:HB2	1:BB:185:LEU:HD11	1.97	0.48
1:CK:112:GLN:HE21	1:CL:44:THR:H	1.61	0.48
1:AD:124:VAL:HG11	1:AD:138:PHE:CD1	2.50	0.48
1:CF:109:PHE:HB2	1:CF:158:VAL:HG12	1.95	0.48
1:CJ:130:ASP:OD2	1:CJ:176:ARG:NH2	2.47	0.48
1:BL:111:ILE:HG21	1:BL:123:TYR:OH	2.13	0.48
1:AQ:110:GLU:HG2	1:AQ:112:GLN:HG2	1.95	0.48
1:BW:325:LEU:HD22	1:BW:329:THR:HG21	1.95	0.48
1:CN:85:VAL:HG13	1:CN:86:PRO:HD2	1.95	0.48
1:BI:234:SER:HB3	1:BI:237:ASP:OD1	2.13	0.48
1:AG:246:THR:N	1:AG:247:PRO:CD	2.77	0.48
1:AT:110:GLU:HG2	1:AT:112:GLN:HG2	1.95	0.48
1:BH:161:GLN:NE2	1:CH:210:PRO:HD2	2.28	0.48
1:AN:142:GLN:NE2	1:AN:142:GLN:O	2.46	0.48
1:AR:142:GLN:NE2	1:AR:142:GLN:O	2.46	0.48
1:AP:298:TRP:NE1	1:AP:312:VAL:CB	2.75	0.48
1:AP:302:ASP:CA	1:AP:305:ASN:ND2	2.76	0.48
1:CR:81:ASP:OD2	1:CR:136:HIS:NE2	2.43	0.48
1:AV:302:ASP:CA	1:AV:305:ASN:ND2	2.77	0.48
1:CS:81:ASP:HA	1:CS:184:ILE:HG22	1.95	0.48
1:BW:61:SER:CB	1:BW:90:PRO:HD2	2.28	0.48
1:BN:98:ILE:CA	1:BN:211:SER:O	2.62	0.48
1:AO:91:ARG:CZ	1:BW:98:ILE:HG22	2.43	0.48
1:AO:314:TYR:CE1	1:AO:316:SER:CA	2.86	0.48
1:CI:100:GLN:HA	1:CI:213:GLU:OE2	2.13	0.48
1:CQ:98:ILE:HD11	1:CQ:99:PHE:CE2	2.48	0.48
1:AD:314:TYR:CE1	1:AD:316:SER:CA	2.89	0.48
1:AW:314:TYR:CE1	1:AW:316:SER:HA	2.46	0.48
1:CP:100:GLN:HA	1:CP:213:GLU:OE2	2.13	0.48
1:CG:98:ILE:HD11	1:CG:99:PHE:CE2	2.49	0.48
1:AD:98:ILE:CG2	1:BH:91:ARG:NH1	120.13	0.48
1:AW:162:TYR:CD1	1:AW:162:TYR:N	2.82	0.48
1:BY:123:TYR:HB2	1:BY:185:LEU:CD1	2.43	0.48
1:AN:111:ILE:HG21	1:AN:123:TYR:CZ	2.48	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CP:200:LEU:HD13	1:CQ:45:VAL:HG23	1.96	0.48
1:CR:62:ARG:NH1	1:BT:75:ASP:OD2	2.40	0.48
1:AU:119:THR:HG23	1:AU:193:ASP:CB	2.42	0.48
1:CP:163:THR:OG1	1:CP:165:THR:HG23	2.13	0.48
1:BU:123:TYR:HB2	1:BU:185:LEU:HD11	1.94	0.48
1:AQ:64:SER:OG	1:AQ:80:VAL:HG21	2.13	0.48
1:CQ:130:ASP:OD2	1:CQ:176:ARG:NH2	2.47	0.48
1:BK:74:THR:O	1:BK:75:ASP:C	2.51	0.48
1:BL:205:VAL:HG22	1:BL:206:ARG:N	2.29	0.48
1:BN:161:GLN:NE2	1:CN:210:PRO:HD2	2.28	0.48
1:AL:268:SER:HB3	1:AL:273:ASP:O	2.13	0.48
1:BS:74:THR:O	1:BS:75:ASP:C	2.51	0.48
1:BO:161:GLN:NE2	1:CO:210:PRO:HD2	2.28	0.48
1:CN:112:GLN:NE2	1:CN:155:SER:OG	2.47	0.48
1:BO:276:ARG:O	1:AO:276:ARG:NH2	2.47	0.48
1:CG:237:ASP:HB3	1:CG:297:ARG:HG2	1.94	0.48
1:BA:234:SER:HB3	1:BA:237:ASP:OD1	2.13	0.48
1:CF:288:ASN:N	1:CF:288:ASN:OD1	2.46	0.48
1:CI:288:ASN:N	1:CI:288:ASN:OD1	2.46	0.48
1:AQ:142:GLN:NE2	1:AQ:142:GLN:O	2.46	0.48
1:CA:190:ASN:HD22	1:CA:190:ASN:N	2.11	0.48
1:CB:190:ASN:N	1:CB:190:ASN:HD22	2.11	0.48
1:BW:183:LEU:C	1:BW:183:LEU:HD12	2.33	0.48
1:BL:214:ASN:HD22	1:BL:215:PRO:HD2	1.77	0.48
1:BB:232:SER:HB3	1:BB:242:LEU:HD11	1.98	0.48
1:AP:110:GLU:HG2	1:AP:112:GLN:HG2	1.96	0.48
1:AY:110:GLU:HG2	1:AY:112:GLN:HG2	1.95	0.48
1:BT:260:ASP:HA	1:AT:261:ARG:NH2	2.29	0.48
1:BI:276:ARG:O	1:AI:276:ARG:NH2	2.46	0.48
1:AZ:298:TRP:NE1	1:AZ:312:VAL:HA	2.28	0.48
1:AH:302:ASP:CA	1:AH:305:ASN:ND2	2.77	0.48
1:CD:123:TYR:HB2	1:CD:185:LEU:HD21	2.01	0.48
1:CU:123:TYR:HA	1:CU:188:VAL:HG23	1.95	0.48
1:CZ:101:ARG:CZ	1:CZ:166:LEU:CD1	2.92	0.48
1:CT:80:VAL:HG11	1:CT:185:LEU:HB2	1.95	0.48
1:AG:279:TYR:CE2	1:AG:311:GLY:O	2.63	0.48
1:AG:315:TYR:CE2	1:AG:317:ASP:OD2	2.66	0.48
1:CY:103:ALA:HB2	1:CY:166:LEU:HB3	1.96	0.48
1:CA:103:ALA:HB2	1:CA:166:LEU:HB3	1.95	0.48
1:AR:315:TYR:CE2	1:AR:317:ASP:OD2	2.66	0.48
1:CN:103:ALA:HB2	1:CN:166:LEU:HB3	1.96	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BN:166:LEU:HD13	1:BN:167:LEU:N	2.28	0.48
1:AI:63:ILE:CD1	1:AI:89:LEU:HD21	2.44	0.48
1:BH:123:TYR:HB2	1:BH:185:LEU:HD11	1.96	0.48
1:CR:63:ILE:HD12	1:CR:88:LEU:CD1	2.43	0.48
1:BE:74:THR:O	1:BE:75:ASP:C	2.50	0.48
1:AH:111:ILE:HG21	1:AH:123:TYR:CZ	2.49	0.48
1:BZ:74:THR:O	1:BZ:75:ASP:C	2.50	0.48
1:CI:109:PHE:HB2	1:CI:158:VAL:HG12	1.94	0.48
1:BU:150:ALA:HB2	1:BU:156:ARG:HD3	1.95	0.48
1:BH:115:CYS:HB2	1:BH:116:PRO:HD2	1.94	0.48
1:CQ:237:ASP:HB3	1:CQ:297:ARG:HG2	1.95	0.48
1:BX:234:SER:HB3	1:BX:237:ASP:OD1	2.14	0.48
1:CN:237:ASP:HB3	1:CN:297:ARG:HG2	1.96	0.48
1:AL:101:ARG:CZ	1:AL:166:LEU:HD23	2.43	0.48
1:BS:161:GLN:NE2	1:CS:210:PRO:HD2	2.28	0.48
1:CC:46:THR:HB	1:CJ:202:ARG:HH12	1.78	0.48
1:CD:288:ASN:OD1	1:CD:288:ASN:N	2.46	0.48
1:AE:142:GLN:NE2	1:AE:142:GLN:O	2.46	0.48
1:CP:288:ASN:N	1:CP:288:ASN:OD1	2.46	0.48
1:CR:78:VAL:HG13	1:CR:78:VAL:O	2.13	0.48
1:BB:161:GLN:NE2	1:CB:210:PRO:HD2	2.33	0.48
1:AC:85:VAL:HG22	1:AC:86:PRO:HD2	1.95	0.48
1:BW:281:HIS:ND1	1:BW:301:TRP:HB3	2.27	0.48
1:AD:246:THR:N	1:AD:247:PRO:CD	2.79	0.48
1:AX:85:VAL:HG22	1:AX:86:PRO:HD2	1.95	0.48
1:AV:298:TRP:NE1	1:AV:312:VAL:HA	2.28	0.48
1:AM:302:ASP:CA	1:AM:305:ASN:ND2	2.77	0.48
1:AW:302:ASP:CA	1:AW:305:ASN:ND2	2.76	0.48
1:CZ:79:VAL:HG13	1:CZ:80:VAL:HG12	1.94	0.48
1:CA:80:VAL:HG11	1:CA:185:LEU:HB2	1.97	0.48
1:CC:99:PHE:HB3	1:CC:209:VAL:O	2.17	0.48
1:BG:98:ILE:CA	1:BG:211:SER:O	2.61	0.48
1:CJ:99:PHE:CB	1:CJ:209:VAL:O	2.62	0.48
1:CH:99:PHE:CB	1:CH:209:VAL:O	2.62	0.48
1:CY:100:GLN:HA	1:CY:213:GLU:OE2	2.14	0.48
1:CW:99:PHE:HB3	1:CW:209:VAL:O	2.13	0.48
1:BK:80:VAL:CG1	1:BK:185:LEU:HB3	2.44	0.48
1:CK:112:GLN:NE2	1:CK:155:SER:OG	2.46	0.48
1:CR:112:GLN:NE2	1:CR:155:SER:OG	2.47	0.48
1:CJ:63:ILE:HD12	1:CJ:88:LEU:CG	2.42	0.48
1:CH:57:LEU:HD23	1:CH:203:TRP:CH2	2.49	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BR:142:GLN:HB2	1:CR:48:PHE:CE1	2.48	0.48
1:AA:80:VAL:HG13	1:AA:185:LEU:HB3	2.02	0.48
1:CV:109:PHE:HB2	1:CV:158:VAL:HG12	1.95	0.48
1:AZ:110:GLU:HG2	1:AZ:112:GLN:HG2	1.95	0.48
1:BL:168:TRP:CE2	1:AL:176:ARG:HD2	2.48	0.48
1:BD:168:TRP:CE2	1:AD:176:ARG:HD2	2.48	0.48
1:BZ:85:VAL:HG23	1:BZ:86:PRO:HD2	1.96	0.48
1:BI:225:GLN:HG3	1:BI:244:GLY:O	2.14	0.48
1:CD:54:ASP:N	1:CD:54:ASP:OD1	2.46	0.48
1:BB:250:ILE:HG22	1:BB:250:ILE:O	2.15	0.48
1:AN:298:TRP:NE1	1:AN:312:VAL:CB	2.77	0.48
1:AT:298:TRP:NE1	1:AT:312:VAL:CB	2.75	0.48
1:AT:310:ASP:HB3	1:AT:312:VAL:HG22	1.95	0.48
1:AU:302:ASP:CA	1:AU:305:ASN:ND2	2.76	0.48
1:CC:79:VAL:HG13	1:CC:80:VAL:HG12	1.96	0.48
1:BI:61:SER:CB	1:BI:90:PRO:HD2	2.26	0.48
1:BD:61:SER:CB	1:BD:90:PRO:HD2	2.29	0.48
1:BC:98:ILE:CA	1:BC:211:SER:O	2.63	0.48
1:CQ:80:VAL:HG11	1:CQ:185:LEU:HB2	1.96	0.48
1:CO:100:GLN:HA	1:CO:213:GLU:OE2	2.13	0.48
1:CJ:80:VAL:CG1	1:CJ:185:LEU:HB2	2.42	0.48
1:BV:123:TYR:HB2	1:BV:185:LEU:CD1	2.44	0.48
1:BA:123:TYR:HB2	1:BA:185:LEU:HD11	1.96	0.48
1:CA:112:GLN:NE2	1:CY:43:SER:HA	131.74	0.48
1:CB:112:GLN:NE2	1:CF:43:SER:HA	2.28	0.48
1:BS:150:ALA:HB2	1:BS:156:ARG:HD3	1.96	0.48
1:CA:63:ILE:HD12	1:CA:88:LEU:CG	2.43	0.48
1:CA:63:ILE:HD12	1:CA:88:LEU:CD1	2.44	0.48
1:BG:142:GLN:HB2	1:CG:48:PHE:HE1	1.79	0.48
1:CI:163:THR:OG1	1:CI:165:THR:HG23	2.14	0.48
1:BY:74:THR:HA	1:BY:190:ASN:ND2	2.28	0.48
1:AN:268:SER:CB	1:AN:273:ASP:O	2.61	0.48
1:AG:268:SER:CB	1:AG:273:ASP:O	2.62	0.48
1:CW:133:ASP:O	1:CW:182:ARG:NH2	2.46	0.48
1:BD:276:ARG:O	1:AD:276:ARG:NH2	2.46	0.48
1:CY:85:VAL:HG13	1:CY:86:PRO:HD2	1.95	0.48
1:CC:39:VAL:HG21	1:CO:39:VAL:HA	213.40	0.48
1:BJ:184:ILE:N	1:BJ:184:ILE:HD13	2.28	0.48
1:CO:124:VAL:HG13	1:CO:124:VAL:O	2.13	0.48
1:CX:124:VAL:HG13	1:CX:124:VAL:O	2.13	0.48
1:CL:288:ASN:N	1:CL:288:ASN:OD1	2.46	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AE:124:VAL:HG11	1:AE:138:PHE:HD1	1.79	0.48
1:BE:115:CYS:HB2	1:BE:116:PRO:HD2	1.94	0.48
1:AC:298:TRP:HE1	1:AC:312:VAL:HA	1.79	0.48
1:AB:302:ASP:CA	1:AB:305:ASN:ND2	2.77	0.48
1:CN:81:ASP:HA	1:CN:184:ILE:HG22	1.94	0.48
1:CD:79:VAL:HG13	1:CD:80:VAL:HG12	1.98	0.48
1:BM:254:GLY:CA	1:BM:283:LYS:HE3	2.30	0.48
1:AO:91:ARG:HH21	1:BW:98:ILE:HG22	1.79	0.48
1:AM:314:TYR:HE1	1:AM:316:SER:HG	1.61	0.48
1:AJ:91:ARG:CZ	1:BR:98:ILE:CG2	2.91	0.48
1:AV:315:TYR:CE2	1:AV:317:ASP:OD2	2.67	0.48
1:AH:314:TYR:HE1	1:AH:316:SER:HG	1.62	0.48
1:BG:163:THR:OG1	1:BG:165:THR:CG2	2.61	0.48
1:BB:150:ALA:HB2	1:BB:156:ARG:HD3	1.98	0.48
1:AI:119:THR:HG23	1:AI:193:ASP:CB	2.42	0.48
1:BG:142:GLN:HB2	1:CG:48:PHE:CE1	2.49	0.48
1:BG:74:THR:O	1:BG:75:ASP:C	2.51	0.48
1:AJ:64:SER:OG	1:AJ:80:VAL:HG21	2.14	0.48
1:BL:74:THR:HA	1:BL:190:ASN:HD22	1.77	0.48
1:AB:268:SER:CB	1:AB:273:ASP:O	2.62	0.48
1:BK:75:ASP:OD2	1:CL:62:ARG:NH1	2.42	0.48
1:BO:214:ASN:HD22	1:BO:215:PRO:HD2	1.78	0.48
1:BL:161:GLN:NE2	1:CL:210:PRO:HD2	2.29	0.48
1:BU:115:CYS:HB2	1:BU:116:PRO:HD2	1.94	0.48
1:BV:276:ARG:O	1:AV:276:ARG:NH2	2.47	0.48
1:CB:46:THR:HB	1:CU:202:ARG:HH12	35.36	0.48
1:AK:85:VAL:HG22	1:AK:86:PRO:HD2	1.95	0.48
1:CH:190:ASN:HD22	1:CH:190:ASN:N	2.11	0.48
1:BU:214:ASN:HD22	1:BU:215:PRO:HD2	1.79	0.48
1:AD:298:TRP:NE1	1:AD:312:VAL:CB	2.76	0.48
1:AZ:302:ASP:CA	1:AZ:305:ASN:ND2	2.77	0.48
1:BL:98:ILE:CG2	1:AU:91:ARG:NH2	2.77	0.48
1:AE:315:TYR:CE2	1:AE:317:ASP:OD2	2.67	0.48
1:CS:99:PHE:CB	1:CS:209:VAL:O	2.62	0.48
1:AW:61:SER:CB	1:AW:90:PRO:HD2	2.35	0.48
1:BE:165:THR:OG1	1:BE:166:LEU:N	2.46	0.48
1:BF:150:ALA:HB2	1:BF:156:ARG:HD3	1.95	0.48
1:CQ:112:GLN:NE2	1:CQ:155:SER:OG	2.47	0.48
1:AI:124:VAL:HG11	1:AI:138:PHE:HD1	1.78	0.48
1:BP:142:GLN:HB2	1:CP:48:PHE:CE1	2.49	0.48
1:BU:74:THR:HA	1:BU:190:ASN:ND2	2.29	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:64:SER:OG	1:AA:80:VAL:HG21	2.13	0.48
1:AZ:268:SER:CB	1:AZ:273:ASP:O	2.62	0.48
1:BE:168:TRP:CE2	1:AE:176:ARG:HD2	2.48	0.48
1:AW:268:SER:HB3	1:AW:273:ASP:O	2.13	0.48
1:CT:78:VAL:O	1:CT:78:VAL:HG13	2.13	0.48
1:CE:45:VAL:HG13	1:CE:45:VAL:O	2.14	0.48
1:CU:190:ASN:HD22	1:CU:190:ASN:N	2.12	0.48
1:BJ:124:VAL:HG11	1:BJ:138:PHE:CD2	2.48	0.48
1:CS:237:ASP:HB3	1:CS:297:ARG:HG2	1.94	0.48
1:AR:298:TRP:NE1	1:AR:312:VAL:HA	2.29	0.47
1:AT:298:TRP:NE1	1:AT:312:VAL:HA	2.29	0.47
1:AS:302:ASP:CA	1:AS:305:ASN:ND2	2.77	0.47
1:AY:302:ASP:CA	1:AY:305:ASN:ND2	2.76	0.47
1:CC:98:ILE:HD11	1:CC:99:PHE:CE2	2.51	0.47
1:AB:315:TYR:CE2	1:AB:317:ASP:OD2	2.66	0.47
1:CB:99:PHE:HB3	1:CB:209:VAL:O	2.16	0.47
1:CR:79:VAL:HG13	1:CR:80:VAL:HG12	1.95	0.47
1:AY:314:TYR:CE1	1:AY:316:SER:CA	2.89	0.47
1:AA:61:SER:HB2	1:AA:89:LEU:HD22	1.98	0.47
1:CZ:99:PHE:CB	1:CZ:209:VAL:O	2.61	0.47
1:AC:61:SER:HB2	1:AC:89:LEU:HD22	2.05	0.47
1:AB:63:ILE:CD1	1:AB:89:LEU:HD21	2.48	0.47
1:BP:163:THR:OG1	1:BP:165:THR:CG2	2.62	0.47
1:CO:112:GLN:NE2	1:CO:155:SER:OG	2.47	0.47
1:CG:43:SER:O	1:CQ:34:ARG:HD3	2.14	0.47
1:BQ:80:VAL:CG1	1:BQ:185:LEU:HB3	2.43	0.47
1:CO:89:LEU:HD13	1:CO:203:TRP:CG	2.49	0.47
1:BD:142:GLN:HB2	1:CD:48:PHE:HE1	1.82	0.47
1:BJ:74:THR:HA	1:BJ:190:ASN:ND2	2.30	0.47
1:CD:199:VAL:CG1	1:CD:199:VAL:O	2.67	0.47
1:BP:74:THR:HA	1:BP:190:ASN:ND2	2.29	0.47
1:CV:85:VAL:HG13	1:CV:86:PRO:HD2	1.96	0.47
1:BK:260:ASP:HA	1:AK:261:ARG:NH2	2.29	0.47
1:BM:276:ARG:O	1:AM:276:ARG:NH2	2.47	0.47
1:BF:276:ARG:O	1:AF:276:ARG:NH2	2.47	0.47
1:BG:168:TRP:CE2	1:AG:176:ARG:HD2	2.48	0.47
1:CV:190:ASN:N	1:CV:190:ASN:HD22	2.12	0.47
1:CC:250:ILE:HG22	1:CC:250:ILE:O	2.13	0.47
1:AE:85:VAL:HG22	1:AE:86:PRO:HD2	1.95	0.47
1:BE:205:VAL:HG22	1:BE:206:ARG:N	2.29	0.47
1:AJ:302:ASP:CA	1:AJ:305:ASN:ND2	2.77	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AF:302:ASP:CA	1:AF:305:ASN:ND2	2.77	0.47
1:CI:81:ASP:OD2	1:CI:136:HIS:NE2	2.45	0.47
1:CQ:123:TYR:HB2	1:CQ:185:LEU:HD21	1.95	0.47
1:CO:98:ILE:HD11	1:CO:99:PHE:CE2	2.49	0.47
1:CM:100:GLN:HA	1:CM:213:GLU:OE2	2.13	0.47
1:CW:100:GLN:HA	1:CW:213:GLU:OE2	2.15	0.47
1:BD:166:LEU:HD13	1:BD:167:LEU:N	2.29	0.47
1:BA:91:ARG:NH1	1:AI:98:ILE:CG2	2.75	0.47
1:BD:123:TYR:HB2	1:BD:185:LEU:CD1	2.46	0.47
1:BF:123:TYR:HB2	1:BF:185:LEU:HD11	1.96	0.47
1:BF:156:ARG:NH2	1:CI:34:ARG:HG3	2.29	0.47
1:AP:119:THR:HG23	1:AP:193:ASP:CB	2.41	0.47
1:CN:109:PHE:HB2	1:CN:158:VAL:HG12	1.96	0.47
1:AT:64:SER:OG	1:AT:80:VAL:HG21	2.14	0.47
1:AF:64:SER:OG	1:AF:80:VAL:HG21	2.15	0.47
1:BD:161:GLN:NE2	1:CD:210:PRO:HD2	2.29	0.47
1:BP:234:SER:HB3	1:BP:237:ASP:OD1	2.14	0.47
1:BQ:225:GLN:HG3	1:BQ:244:GLY:O	2.13	0.47
1:CW:54:ASP:OD1	1:CW:54:ASP:N	2.46	0.47
1:CS:54:ASP:N	1:CS:54:ASP:OD1	2.47	0.47
1:BB:225:GLN:HG3	1:BB:244:GLY:O	2.15	0.47
1:BG:276:ARG:O	1:AG:276:ARG:NH2	2.47	0.47
1:BJ:276:ARG:O	1:AJ:276:ARG:NH2	2.47	0.47
1:CP:79:VAL:HG13	1:CP:80:VAL:HG12	1.97	0.47
1:CL:80:VAL:HG11	1:CL:185:LEU:HB2	1.95	0.47
1:CV:81:ASP:OD1	1:CV:81:ASP:C	2.53	0.47
1:CQ:81:ASP:HA	1:CQ:184:ILE:HG22	1.96	0.47
1:BB:61:SER:CB	1:BB:90:PRO:HD2	2.30	0.47
1:BA:98:ILE:HG22	1:AT:91:ARG:NH2	57.95	0.47
1:CE:99:PHE:HB3	1:CE:209:VAL:O	2.14	0.47
1:BG:80:VAL:CG1	1:BG:185:LEU:HB3	2.44	0.47
1:CA:43:SER:HA	1:CG:112:GLN:NE2	2.28	0.47
1:CT:112:GLN:NE2	1:CT:155:SER:OG	2.48	0.47
1:BL:142:GLN:HB2	1:CL:48:PHE:CE1	2.50	0.47
1:CW:58:SER:HB3	1:CW:204:SER:HB2	1.96	0.47
1:BO:142:GLN:HB2	1:CO:48:PHE:HE1	1.80	0.47
1:CF:62:ARG:HA	1:CF:200:LEU:HD23	1.96	0.47
1:AH:116:PRO:HB3	1:AN:118:ASN:O	2.14	0.47
1:BT:74:THR:HA	1:BT:190:ASN:HD22	1.79	0.47
1:AJ:80:VAL:HG13	1:AJ:185:LEU:HB3	1.96	0.47
1:CU:158:VAL:HG13	1:CU:158:VAL:O	2.15	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AV:64:SER:OG	1:AV:80:VAL:HG21	2.14	0.47
1:AM:268:SER:CB	1:AM:273:ASP:O	2.62	0.47
1:AD:64:SER:OG	1:AD:80:VAL:HG21	2.18	0.47
1:AT:268:SER:CB	1:AT:273:ASP:O	2.62	0.47
1:AU:85:VAL:HG22	1:AU:86:PRO:HD2	1.95	0.47
1:AP:224:THR:HG22	1:AP:329:THR:N	2.30	0.47
1:CF:85:VAL:HG13	1:CF:86:PRO:HD2	1.97	0.47
1:BK:234:SER:HB3	1:BK:237:ASP:OD1	2.14	0.47
1:BM:161:GLN:NE2	1:CM:210:PRO:HD2	2.29	0.47
1:AP:298:TRP:NE1	1:AP:312:VAL:HA	2.30	0.47
1:AQ:302:ASP:CA	1:AQ:305:ASN:ND2	2.77	0.47
1:CX:81:ASP:HA	1:CX:184:ILE:HG22	1.96	0.47
1:CB:81:ASP:HA	1:CB:184:ILE:HG22	2.00	0.47
1:CC:123:TYR:HA	1:CC:188:VAL:HG23	1.97	0.47
1:BD:98:ILE:HG22	1:AW:91:ARG:CZ	2.43	0.47
1:BU:210:PRO:HB3	1:AX:91:ARG:NH2	2.29	0.47
1:BU:98:ILE:CA	1:BU:211:SER:O	2.61	0.47
1:BA:98:ILE:HG23	1:AI:91:ARG:HG2	1.97	0.47
1:CX:123:TYR:HB2	1:CX:185:LEU:HD21	1.95	0.47
1:CN:99:PHE:CB	1:CN:209:VAL:O	2.61	0.47
1:CN:99:PHE:HB3	1:CN:209:VAL:O	2.14	0.47
1:CP:99:PHE:CB	1:CP:209:VAL:O	2.62	0.47
1:CG:99:PHE:CB	1:CG:209:VAL:O	2.63	0.47
1:CG:112:GLN:NE2	1:CG:155:SER:OG	2.47	0.47
1:BV:150:ALA:HB2	1:BV:156:ARG:HD3	1.96	0.47
1:BV:123:TYR:HB2	1:BV:185:LEU:HD11	1.96	0.47
1:CO:63:ILE:HD12	1:CO:88:LEU:CD1	2.44	0.47
1:BO:74:THR:HA	1:BO:190:ASN:ND2	2.29	0.47
1:CT:63:ILE:HD12	1:CT:88:LEU:CD1	2.44	0.47
1:BD:75:ASP:OD2	1:CW:62:ARG:NH1	44.19	0.47
1:CT:199:VAL:O	1:CT:199:VAL:CG1	2.62	0.47
1:BS:115:CYS:HB2	1:BS:116:PRO:HD2	1.96	0.47
1:BV:75:ASP:OD2	1:CZ:62:ARG:NH1	2.42	0.47
1:CY:109:PHE:HB2	1:CY:158:VAL:HG12	1.96	0.47
1:AC:268:SER:CB	1:AC:273:ASP:O	2.62	0.47
1:BX:276:ARG:O	1:AX:276:ARG:NH2	2.47	0.47
1:BI:124:VAL:HG11	1:BI:138:PHE:CD2	2.49	0.47
1:BZ:161:GLN:NE2	1:CZ:210:PRO:HD2	2.29	0.47
1:BK:99:PHE:N	1:BK:99:PHE:CD1	2.81	0.47
1:BO:254:GLY:CA	1:BO:283:LYS:HE3	2.30	0.47
1:AA:91:ARG:CZ	1:BV:98:ILE:HG22	2.44	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:122:GLY:O	1:CA:188:VAL:CB	2.61	0.47
1:AP:314:TYR:HE1	1:AP:316:SER:HG	1.60	0.47
1:AU:61:SER:CB	1:AU:90:PRO:HD2	2.33	0.47
1:CL:99:PHE:CB	1:CL:209:VAL:O	2.62	0.47
1:BO:166:LEU:HD13	1:BO:167:LEU:N	2.29	0.47
1:CF:34:ARG:HG3	1:BY:156:ARG:NH2	2.29	0.47
1:BI:123:TYR:HB2	1:BI:185:LEU:CD1	2.44	0.47
1:AP:111:ILE:HG21	1:AP:123:TYR:CZ	2.50	0.47
1:CY:63:ILE:HD12	1:CY:88:LEU:CG	2.43	0.47
1:CG:199:VAL:O	1:CG:199:VAL:CG1	2.60	0.47
1:CZ:63:ILE:HD12	1:CZ:88:LEU:CG	2.43	0.47
1:BX:74:THR:O	1:BX:75:ASP:C	2.50	0.47
1:CU:109:PHE:HB2	1:CU:158:VAL:HG12	1.96	0.47
1:BN:234:SER:HB3	1:BN:237:ASP:OD1	2.15	0.47
1:AO:246:THR:N	1:AO:247:PRO:CD	2.77	0.47
1:BY:85:VAL:HG23	1:BY:86:PRO:HD2	1.96	0.47
1:BR:225:GLN:HG3	1:BR:244:GLY:O	2.14	0.47
1:BI:161:GLN:NE2	1:CI:210:PRO:HD2	2.29	0.47
1:CJ:124:VAL:HG13	1:CJ:124:VAL:O	2.13	0.47
1:CP:250:ILE:O	1:CP:250:ILE:HG22	2.13	0.47
1:AE:110:GLU:HG2	1:AE:112:GLN:HG2	1.96	0.47
1:CH:138:PHE:CD1	1:CH:138:PHE:C	2.88	0.47
1:AD:224:THR:HG22	1:AD:329:THR:N	2.32	0.47
1:AV:124:VAL:HG11	1:AV:138:PHE:HD1	1.79	0.47
1:BZ:168:TRP:CE2	1:AZ:176:ARG:HD2	2.50	0.47
1:AV:298:TRP:NE1	1:AV:312:VAL:CB	2.75	0.47
1:AX:302:ASP:CA	1:AX:305:ASN:ND2	2.77	0.47
1:CY:123:TYR:HA	1:CY:188:VAL:HG23	1.97	0.47
1:CP:123:TYR:HB2	1:CP:185:LEU:HD21	1.96	0.47
1:CL:123:TYR:HB2	1:CL:185:LEU:HD21	1.97	0.47
1:AY:279:TYR:CE2	1:AY:311:GLY:O	2.66	0.47
1:AB:91:ARG:NH2	1:BY:98:ILE:HG22	2.29	0.47
1:BJ:98:ILE:CA	1:BJ:211:SER:O	2.63	0.47
1:BG:98:ILE:HG23	1:AP:91:ARG:HG2	1.97	0.47
1:CF:101:ARG:CZ	1:CF:166:LEU:CD1	2.92	0.47
1:CB:99:PHE:CB	1:CB:209:VAL:O	2.62	0.47
1:CS:80:VAL:HG11	1:CS:185:LEU:HB2	1.95	0.47
1:AN:315:TYR:CE2	1:AN:317:ASP:OD2	2.68	0.47
1:CN:98:ILE:HD11	1:CN:99:PHE:CE2	2.50	0.47
1:AB:98:ILE:CG2	1:BY:91:ARG:NH1	2.77	0.47
1:AZ:111:ILE:HG21	1:AZ:123:TYR:CZ	2.50	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CR:63:ILE:HD12	1:CR:88:LEU:CG	2.42	0.47
1:BB:74:THR:HA	1:BB:190:ASN:ND2	2.30	0.47
1:CI:89:LEU:HD13	1:CI:203:TRP:CG	2.49	0.47
1:CT:57:LEU:HD23	1:CT:203:TRP:CH2	2.49	0.47
1:BA:74:THR:HA	1:BA:190:ASN:HD22	1.82	0.47
1:AK:64:SER:OG	1:AK:80:VAL:HG21	2.14	0.47
1:CD:77:TYR:C	1:CD:77:TYR:CD1	2.91	0.47
1:CM:46:THR:HB	1:CO:202:ARG:HH12	1.80	0.47
1:BT:276:ARG:O	1:AT:276:ARG:NH2	2.47	0.47
1:BU:136:HIS:O	1:BU:186:LEU:HD11	2.14	0.47
1:BG:234:SER:HB3	1:BG:237:ASP:OD1	2.15	0.47
1:AY:100:GLN:HA	1:AY:169:THR:OG1	2.15	0.47
1:BO:260:ASP:HA	1:AO:261:ARG:NH2	2.30	0.47
1:BK:85:VAL:HG23	1:BK:86:PRO:HD2	1.96	0.47
1:CP:124:VAL:O	1:CP:124:VAL:HG13	2.14	0.47
1:AB:298:TRP:NE1	1:AB:312:VAL:CB	2.77	0.47
1:BG:61:SER:CB	1:BG:90:PRO:HD2	2.26	0.47
1:BL:61:SER:CB	1:BL:90:PRO:HD2	2.28	0.47
1:BP:254:GLY:CA	1:BP:283:LYS:HE3	2.30	0.47
1:BX:98:ILE:CA	1:BX:211:SER:O	2.63	0.47
1:CX:79:VAL:HG13	1:CX:80:VAL:HG12	1.96	0.47
1:AI:315:TYR:CE2	1:AI:317:ASP:OD2	2.68	0.47
1:AZ:315:TYR:CE2	1:AZ:317:ASP:OD2	2.67	0.47
1:AW:315:TYR:CE2	1:AW:317:ASP:OD2	2.67	0.47
1:CZ:99:PHE:HB3	1:CZ:209:VAL:O	2.15	0.47
1:CN:80:VAL:HG11	1:CN:185:LEU:HB2	1.97	0.47
1:AC:98:ILE:CG2	1:BS:91:ARG:NH1	2.75	0.47
1:BC:91:ARG:NH1	1:AY:98:ILE:CG2	2.76	0.47
1:BE:123:TYR:HB2	1:BE:185:LEU:CD1	2.44	0.47
1:CA:57:LEU:HD23	1:CA:203:TRP:CH2	2.51	0.47
1:BM:142:GLN:HB2	1:CM:48:PHE:CE1	2.50	0.47
1:BM:142:GLN:HB2	1:CM:48:PHE:HE1	1.79	0.47
1:CE:63:ILE:HD12	1:CE:88:LEU:CG	2.44	0.47
1:CI:63:ILE:HD12	1:CI:88:LEU:CD1	2.45	0.47
1:CB:199:VAL:O	1:CB:199:VAL:CG1	2.62	0.47
1:AQ:63:ILE:CD1	1:AQ:89:LEU:HD21	2.45	0.47
1:AU:268:SER:CB	1:AU:273:ASP:O	2.63	0.47
1:AW:124:VAL:HG11	1:AW:138:PHE:CD1	2.48	0.47
1:CR:117:ALA:CB	1:CT:38:PRO:O	2.63	0.47
1:AS:246:THR:N	1:AS:247:PRO:CD	2.77	0.47
1:BO:232:SER:HB3	1:BO:242:LEU:HD11	1.97	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:46:THR:HB	1:CY:202:ARG:HH12	126.72	0.47
1:CJ:78:VAL:HG13	1:CJ:78:VAL:O	2.14	0.47
1:BW:205:VAL:HG22	1:BW:206:ARG:N	2.30	0.47
1:BU:161:GLN:NE2	1:CU:210:PRO:HD2	2.29	0.47
1:AF:85:VAL:HG22	1:AF:86:PRO:HD2	1.96	0.47
1:AP:85:VAL:HG22	1:AP:86:PRO:HD2	1.96	0.47
1:BU:168:TRP:CE2	1:AU:176:ARG:HD2	2.50	0.47
1:AZ:122:GLY:C	1:AZ:188:VAL:HG22	2.35	0.47
1:BH:124:VAL:HG11	1:BH:138:PHE:CD2	2.49	0.47
1:AI:85:VAL:HG22	1:AI:86:PRO:HD2	1.97	0.47
1:BQ:161:GLN:NE2	1:CQ:210:PRO:HD2	2.29	0.47
1:CO:237:ASP:HB3	1:CO:297:ARG:HG2	1.95	0.47
1:AL:124:VAL:HG11	1:AL:138:PHE:HD1	1.79	0.47
1:BX:161:GLN:NE2	1:CX:210:PRO:HD2	2.29	0.47
1:BS:214:ASN:HD22	1:BS:215:PRO:HD2	1.79	0.47
1:BZ:276:ARG:O	1:AZ:276:ARG:NH2	2.48	0.47
1:BU:124:VAL:HG11	1:BU:138:PHE:CD2	2.50	0.47
1:CT:133:ASP:O	1:CT:182:ARG:NH2	2.48	0.47
1:BA:168:TRP:CE2	1:AA:176:ARG:HD2	2.50	0.47
1:BK:98:ILE:CA	1:BK:211:SER:O	2.62	0.47
1:BK:98:ILE:HG22	1:AS:91:ARG:HH21	1.79	0.47
1:CB:101:ARG:CZ	1:CB:166:LEU:CD1	2.92	0.47
1:AB:91:ARG:CZ	1:BY:98:ILE:HG22	2.45	0.47
1:CR:99:PHE:CB	1:CR:209:VAL:O	2.63	0.47
1:AN:314:TYR:CE1	1:AN:316:SER:CA	2.87	0.47
1:AZ:314:TYR:CE1	1:AZ:316:SER:CA	2.89	0.47
1:CM:99:PHE:CD2	1:CM:207:LEU:HB3	2.50	0.47
1:CS:100:GLN:HA	1:CS:213:GLU:OE2	2.14	0.47
1:CP:98:ILE:HD11	1:CP:99:PHE:CE2	2.49	0.47
1:AI:61:SER:HB2	1:AI:89:LEU:HD22	1.97	0.47
1:BF:166:LEU:HD13	1:BF:167:LEU:N	2.30	0.47
1:BZ:165:THR:OG1	1:BZ:166:LEU:N	2.48	0.47
1:CU:112:GLN:NE2	1:CU:155:SER:OG	2.48	0.47
1:BW:123:TYR:HB2	1:BW:185:LEU:CD1	2.44	0.47
1:AO:111:ILE:HG21	1:AO:123:TYR:CZ	2.49	0.47
1:CM:63:ILE:HD12	1:CM:88:LEU:CG	2.44	0.47
1:BF:142:GLN:HB2	1:CF:48:PHE:HE1	1.79	0.47
1:CY:62:ARG:HA	1:CY:200:LEU:HD23	1.97	0.47
1:AC:80:VAL:HG13	1:AC:185:LEU:HB3	2.02	0.47
1:AF:268:SER:CB	1:AF:273:ASP:O	2.63	0.47
1:AS:268:SER:CB	1:AS:273:ASP:O	2.63	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:268:SER:CB	1:AA:273:ASP:O	2.64	0.47
1:AO:268:SER:CB	1:AO:273:ASP:O	2.63	0.47
1:AJ:110:GLU:HG2	1:AJ:112:GLN:HG2	1.97	0.47
1:CJ:54:ASP:N	1:CJ:54:ASP:OD1	2.46	0.47
1:AO:114:MET:SD	1:AW:122:GLY:HA3	2.55	0.47
1:BC:124:VAL:HG11	1:BC:138:PHE:CD2	2.56	0.47
1:BK:168:TRP:CE2	1:AK:176:ARG:HD2	2.49	0.47
1:AP:298:TRP:HE1	1:AP:312:VAL:HA	1.80	0.47
1:CB:123:TYR:HA	1:CB:188:VAL:HG23	1.96	0.47
1:CB:81:ASP:C	1:CB:81:ASP:OD1	2.53	0.47
1:CN:81:ASP:C	1:CN:81:ASP:OD1	2.53	0.47
1:CC:122:GLY:O	1:CC:188:VAL:CB	2.68	0.47
1:CU:80:VAL:HG11	1:CU:185:LEU:HB2	1.97	0.47
1:AA:263:LEU:HB3	1:AA:279:TYR:O	2.14	0.47
1:AB:263:LEU:HB3	1:AB:279:TYR:O	2.17	0.47
1:CT:79:VAL:HG13	1:CT:80:VAL:HG12	1.97	0.47
1:BA:98:ILE:CG2	1:AT:91:ARG:CZ	57.94	0.47
1:CV:103:ALA:HB2	1:CV:166:LEU:HB3	1.97	0.47
1:AY:314:TYR:CE1	1:AY:316:SER:HA	2.46	0.47
1:BC:91:ARG:NH1	1:AM:98:ILE:HG23	206.27	0.47
1:BS:123:TYR:HB2	1:BS:185:LEU:CD1	2.45	0.47
1:BH:123:TYR:HB2	1:BH:185:LEU:CD1	2.45	0.47
1:CX:199:VAL:CG1	1:CX:199:VAL:O	2.63	0.47
1:AZ:103:ALA:HB2	1:AZ:166:LEU:HA	1.97	0.47
1:AY:85:VAL:HG22	1:AY:86:PRO:HD2	1.96	0.47
1:BW:234:SER:HB3	1:BW:237:ASP:OD1	2.14	0.47
1:CA:133:ASP:O	1:CA:182:ARG:NH2	2.52	0.47
1:BY:124:VAL:HG11	1:BY:138:PHE:CD2	2.50	0.47
1:AZ:246:THR:N	1:AZ:247:PRO:CD	2.78	0.47
1:BM:250:ILE:O	1:BM:250:ILE:HG22	2.14	0.47
1:CM:250:ILE:O	1:CM:250:ILE:HG22	2.15	0.47
1:CT:288:ASN:OD1	1:CT:288:ASN:N	2.47	0.47
1:CR:124:VAL:HG13	1:CR:124:VAL:O	2.15	0.47
1:BI:168:TRP:CE2	1:AI:176:ARG:HD2	2.50	0.47
1:AF:110:GLU:HG2	1:AF:112:GLN:HG2	1.96	0.47
1:BC:234:SER:HB3	1:BC:237:ASP:OD1	2.18	0.47
1:AZ:298:TRP:HE1	1:AZ:312:VAL:HA	1.79	0.47
1:CY:79:VAL:HG13	1:CY:80:VAL:HG12	1.96	0.47
1:CB:80:VAL:HG11	1:CB:185:LEU:HB2	1.97	0.47
1:CB:79:VAL:HG13	1:CB:80:VAL:HG12	1.97	0.47
1:CU:103:ALA:HB2	1:CU:166:LEU:HB3	1.97	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CJ:101:ARG:HB2	1:CJ:208:SER:HG	1.76	0.47
1:AX:314:TYR:CE1	1:AX:316:SER:CA	2.86	0.47
1:CL:99:PHE:CD2	1:CL:207:LEU:HB3	2.50	0.47
1:AR:61:SER:HB2	1:AR:89:LEU:HD22	1.96	0.47
1:BX:163:THR:OG1	1:BX:165:THR:CG2	2.62	0.47
1:AW:61:SER:HB2	1:AW:89:LEU:HD22	1.96	0.47
1:BQ:165:THR:OG1	1:BQ:166:LEU:N	2.48	0.47
1:BC:123:TYR:HB2	1:BC:185:LEU:HD11	1.97	0.47
1:CX:89:LEU:HD13	1:CX:203:TRP:CG	2.50	0.47
1:BD:142:GLN:HB2	1:CD:48:PHE:CE1	2.52	0.47
1:CA:199:VAL:CG1	1:CA:199:VAL:O	2.63	0.47
1:CR:163:THR:OG1	1:CR:165:THR:HG23	2.15	0.47
1:CK:130:ASP:OD2	1:CK:176:ARG:NH2	2.48	0.47
1:CS:109:PHE:HB2	1:CS:158:VAL:HG12	1.97	0.47
1:CZ:109:PHE:HB2	1:CZ:158:VAL:HG12	1.97	0.47
1:CC:130:ASP:OD2	1:CC:176:ARG:NH2	2.54	0.47
1:AY:268:SER:CB	1:AY:273:ASP:O	2.63	0.47
1:AR:110:GLU:HG2	1:AR:112:GLN:HG2	1.96	0.47
1:BH:225:GLN:HG3	1:BH:244:GLY:O	2.15	0.47
1:BA:205:VAL:HG22	1:BA:206:ARG:N	2.31	0.47
1:BQ:232:SER:HB3	1:BQ:242:LEU:HD11	1.97	0.47
1:AU:115:CYS:HB2	1:AU:116:PRO:HD2	1.96	0.47
1:AB:85:VAL:HG22	1:AB:86:PRO:HD2	2.02	0.47
1:BH:184:ILE:HD13	1:BH:184:ILE:N	2.29	0.47
1:BG:250:ILE:HG22	1:BG:250:ILE:O	2.15	0.47
1:CK:77:TYR:CD1	1:CK:77:TYR:C	2.86	0.47
1:AW:224:THR:HG22	1:AW:329:THR:N	2.30	0.47
1:BV:161:GLN:NE2	1:CV:210:PRO:HD2	2.30	0.47
1:CD:81:ASP:C	1:CD:81:ASP:OD1	2.52	0.46
1:CL:79:VAL:HG13	1:CL:80:VAL:HG12	1.97	0.46
1:CC:81:ASP:OD1	1:CC:81:ASP:C	2.54	0.46
1:AH:263:LEU:HB3	1:AH:279:TYR:O	2.15	0.46
1:AA:91:ARG:CZ	1:BI:98:ILE:CG2	57.86	0.46
1:AD:91:ARG:NH2	1:BF:210:PRO:HB3	2.29	0.46
1:AX:315:TYR:CE2	1:AX:317:ASP:OD2	2.68	0.46
1:CS:79:VAL:HG13	1:CS:80:VAL:HG12	1.96	0.46
1:CK:99:PHE:CB	1:CK:209:VAL:O	2.63	0.46
1:CX:62:ARG:HA	1:CX:200:LEU:HD23	1.95	0.46
1:CC:57:LEU:HD23	1:CC:203:TRP:CH2	2.50	0.46
1:CA:89:LEU:HD13	1:CA:203:TRP:CG	2.50	0.46
1:CT:63:ILE:HD12	1:CT:88:LEU:CG	2.43	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CI:63:ILE:HD12	1:CI:88:LEU:CG	2.43	0.46
1:BZ:142:GLN:HB2	1:CZ:48:PHE:CE1	2.50	0.46
1:BK:142:GLN:HB2	1:CK:48:PHE:CE1	2.50	0.46
1:BK:142:GLN:HB2	1:CK:48:PHE:HE1	1.80	0.46
1:CA:200:LEU:HD13	1:CG:45:VAL:HG23	1.96	0.46
1:CZ:163:THR:OG1	1:CZ:165:THR:HG23	2.14	0.46
1:AX:268:SER:CB	1:AX:273:ASP:O	2.63	0.46
1:BS:74:THR:HA	1:BS:190:ASN:ND2	2.29	0.46
1:CC:46:THR:HB	1:CX:202:ARG:HH12	198.54	0.46
1:BY:205:VAL:HG22	1:BY:206:ARG:N	2.30	0.46
1:CU:237:ASP:HB3	1:CU:297:ARG:HG2	1.96	0.46
1:BY:214:ASN:HD22	1:BY:215:PRO:HD2	1.79	0.46
1:CG:85:VAL:HG13	1:CG:86:PRO:HD2	1.96	0.46
1:BH:85:VAL:HG23	1:BH:86:PRO:HD2	1.97	0.46
1:BG:232:SER:HB3	1:BG:242:LEU:HD11	1.96	0.46
1:CC:54:ASP:OD1	1:CC:54:ASP:N	2.51	0.46
1:CI:190:ASN:N	1:CI:190:ASN:HD22	2.13	0.46
1:CJ:85:VAL:O	1:CJ:86:PRO:C	2.54	0.46
1:BU:85:VAL:HG23	1:BU:86:PRO:HD2	1.95	0.46
1:CS:112:GLN:NE2	1:CS:155:SER:OG	2.48	0.46
1:AG:298:TRP:NE1	1:AG:312:VAL:CB	2.77	0.46
1:CL:123:TYR:CD1	1:CL:185:LEU:HD21	2.50	0.46
1:CE:123:TYR:HA	1:CE:188:VAL:HG23	1.97	0.46
1:AL:279:TYR:CE2	1:AL:311:GLY:O	2.64	0.46
1:CB:98:ILE:HB	1:CU:91:ARG:HD2	66.54	0.46
1:AU:63:ILE:CD1	1:AU:89:LEU:HD21	2.45	0.46
1:AZ:61:SER:HB2	1:AZ:89:LEU:HD22	1.97	0.46
1:CA:44:THR:H	1:CY:112:GLN:HE21	135.51	0.46
1:BV:123:TYR:N	1:BV:188:VAL:HG22	2.30	0.46
1:BR:123:TYR:HB2	1:BR:185:LEU:CD1	2.45	0.46
1:CD:112:GLN:HE21	1:CW:44:THR:N	121.12	0.46
1:CM:89:LEU:HD13	1:CM:203:TRP:CG	2.50	0.46
1:BO:142:GLN:HB2	1:CO:48:PHE:CE1	2.49	0.46
1:CU:63:ILE:HD12	1:CU:88:LEU:CD1	2.45	0.46
1:BP:142:GLN:HB2	1:CP:48:PHE:HE1	1.80	0.46
1:AQ:116:PRO:HG2	1:AQ:119:THR:OG1	2.15	0.46
1:CC:62:ARG:HA	1:CC:200:LEU:HD23	1.99	0.46
1:AR:124:VAL:HG11	1:AR:138:PHE:CD1	2.50	0.46
1:BA:116:PRO:CB	1:CT:118:ASN:HA	143.46	0.46
1:AM:80:VAL:HG13	1:AM:185:LEU:HB3	1.97	0.46
1:AM:124:VAL:HG11	1:AM:138:PHE:CD1	2.50	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BW:136:HIS:O	1:BW:186:LEU:HD11	2.15	0.46
1:BM:232:SER:HB3	1:BM:242:LEU:HD11	1.97	0.46
1:CR:46:THR:HB	1:CT:202:ARG:HH12	1.80	0.46
1:BZ:214:ASN:HD22	1:BZ:215:PRO:HD2	1.81	0.46
1:CF:39:VAL:HA	1:CY:39:VAL:HG21	1.97	0.46
1:AA:298:TRP:NE1	1:AA:312:VAL:HA	2.30	0.46
1:AH:298:TRP:NE1	1:AH:312:VAL:HA	2.30	0.46
1:CW:79:VAL:HG13	1:CW:80:VAL:HG12	1.98	0.46
1:CE:80:VAL:HG11	1:CE:185:LEU:HB2	1.97	0.46
1:CF:81:ASP:HA	1:CF:184:ILE:HG22	1.97	0.46
1:AA:91:ARG:NH2	1:BV:98:ILE:HG22	2.31	0.46
1:CQ:122:GLY:O	1:CQ:188:VAL:CB	2.62	0.46
1:AJ:91:ARG:HG2	1:BR:98:ILE:HG23	1.97	0.46
1:CF:99:PHE:CB	1:CF:209:VAL:O	2.63	0.46
1:AJ:61:SER:HB2	1:AJ:89:LEU:HD22	1.97	0.46
1:AL:63:ILE:CD1	1:AL:89:LEU:HD21	2.45	0.46
1:AF:63:ILE:CD1	1:AF:89:LEU:HD21	2.46	0.46
1:BC:123:TYR:HB2	1:BC:185:LEU:CD1	2.48	0.46
1:AL:162:TYR:N	1:AL:162:TYR:CD1	2.84	0.46
1:CB:34:ARG:HD3	1:CB:43:SER:O	22.19	0.46
1:CD:112:GLN:HE21	1:CW:44:THR:H	121.31	0.46
1:CC:112:GLN:HE21	1:CX:44:THR:H	208.21	0.46
1:CE:34:ARG:HD3	1:CN:43:SER:O	2.15	0.46
1:AZ:80:VAL:HG13	1:AZ:185:LEU:HB3	1.98	0.46
1:BP:150:ALA:HB2	1:BP:156:ARG:HD3	1.98	0.46
1:AW:246:THR:N	1:AW:247:PRO:CD	2.79	0.46
1:AK:234:SER:HB3	1:AK:237:ASP:O	2.15	0.46
1:CR:237:ASP:HB3	1:CR:297:ARG:HG2	1.96	0.46
1:BA:225:GLN:HG3	1:BA:244:GLY:O	2.15	0.46
1:CQ:250:ILE:O	1:CQ:250:ILE:HG22	2.16	0.46
1:BS:250:ILE:HG22	1:BS:250:ILE:O	2.15	0.46
1:CF:78:VAL:O	1:CF:78:VAL:HG13	2.15	0.46
1:AM:85:VAL:HG22	1:AM:86:PRO:HD2	1.97	0.46
1:BK:214:ASN:HD22	1:BK:215:PRO:HD2	1.79	0.46
1:BT:168:TRP:CE2	1:AT:176:ARG:HD2	2.51	0.46
1:AO:302:ASP:CA	1:AO:305:ASN:ND2	2.78	0.46
1:CY:80:VAL:HG11	1:CY:185:LEU:HB2	1.96	0.46
1:CE:81:ASP:HA	1:CE:184:ILE:HG22	1.98	0.46
1:BL:98:ILE:CA	1:BL:211:SER:O	2.63	0.46
1:CF:122:GLY:O	1:CF:188:VAL:CB	2.63	0.46
1:CI:98:ILE:HD11	1:CI:99:PHE:CE2	2.50	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CJ:98:ILE:HD11	1:CJ:99:PHE:CE2	2.50	0.46
1:CW:98:ILE:HD11	1:CW:99:PHE:CE2	2.51	0.46
1:BY:150:ALA:HB2	1:BY:156:ARG:HD3	1.97	0.46
1:CB:44:THR:H	1:CF:112:GLN:HE21	1.62	0.46
1:CZ:112:GLN:NE2	1:CZ:155:SER:OG	2.49	0.46
1:CB:89:LEU:HD13	1:CB:203:TRP:CG	2.55	0.46
1:BV:142:GLN:HB2	1:CV:48:PHE:CE1	2.50	0.46
1:CH:63:ILE:HD12	1:CH:88:LEU:CD1	2.45	0.46
1:CI:62:ARG:HA	1:CI:200:LEU:HD23	1.97	0.46
1:AA:138:PHE:CE2	1:AT:62:ARG:CZ	45.59	0.46
1:CZ:199:VAL:CG1	1:CZ:199:VAL:O	2.64	0.46
1:CI:113:PRO:HA	1:CI:197:VAL:HA	1.97	0.46
1:AD:268:SER:CB	1:AD:273:ASP:O	2.64	0.46
1:BE:232:SER:HB3	1:BE:242:LEU:HD11	1.97	0.46
1:AS:85:VAL:HG22	1:AS:86:PRO:HD2	1.97	0.46
1:CS:62:ARG:HA	1:CS:200:LEU:HD23	1.98	0.46
1:BA:232:SER:HB3	1:BA:242:LEU:HD11	1.98	0.46
1:CD:202:ARG:HH12	1:CI:46:THR:HB	1.80	0.46
1:CI:85:VAL:HG13	1:CI:86:PRO:HD2	1.97	0.46
1:BD:234:SER:HB3	1:BD:237:ASP:OD1	2.18	0.46
1:AB:298:TRP:NE1	1:AB:312:VAL:HA	2.30	0.46
1:CG:122:GLY:O	1:CG:188:VAL:CB	2.61	0.46
1:BD:98:ILE:CG2	1:AG:91:ARG:CZ	88.94	0.46
1:CI:123:TYR:HA	1:CI:188:VAL:HG23	1.98	0.46
1:CT:123:TYR:HA	1:CT:188:VAL:HG23	1.98	0.46
1:BH:98:ILE:CA	1:BH:211:SER:O	2.64	0.46
1:BQ:98:ILE:HG22	1:AZ:91:ARG:NH2	2.31	0.46
1:CH:80:VAL:HG11	1:CH:185:LEU:HB2	1.96	0.46
1:CD:99:PHE:HB3	1:CD:209:VAL:O	2.15	0.46
1:CG:101:ARG:CZ	1:CG:166:LEU:CD1	2.94	0.46
1:AJ:315:TYR:CE2	1:AJ:317:ASP:OD2	2.69	0.46
1:CE:98:ILE:HB	1:CH:91:ARG:HD2	1.96	0.46
1:CS:99:PHE:HB3	1:CS:209:VAL:O	2.15	0.46
1:BG:123:TYR:N	1:BG:188:VAL:HG22	2.31	0.46
1:AE:253:ASP:CG	1:AE:285:PHE:CA	2.78	0.46
1:BC:156:ARG:HH22	1:CO:34:ARG:CG	199.61	0.46
1:BO:150:ALA:HB2	1:BO:156:ARG:HD3	1.96	0.46
1:CE:112:GLN:NE2	1:CE:155:SER:OG	2.48	0.46
1:CM:63:ILE:HD12	1:CM:88:LEU:CD1	2.46	0.46
1:CE:57:LEU:HD23	1:CE:203:TRP:CH2	2.51	0.46
1:BA:142:GLN:HB2	1:CA:48:PHE:CE1	2.50	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CJ:199:VAL:O	1:CJ:199:VAL:CG1	2.62	0.46
1:CD:120:GLY:CA	1:BH:115:CYS:C	149.32	0.46
1:AR:85:VAL:HG22	1:AR:86:PRO:HD2	1.98	0.46
1:AK:110:GLU:HG2	1:AK:112:GLN:HG2	1.97	0.46
1:BB:205:VAL:HG22	1:BB:206:ARG:N	2.31	0.46
1:BH:232:SER:HB3	1:BH:242:LEU:HD11	1.96	0.46
1:BS:234:SER:HB3	1:BS:237:ASP:OD1	2.16	0.46
1:BT:136:HIS:O	1:BT:186:LEU:HD11	2.15	0.46
1:BT:234:SER:HB3	1:BT:237:ASP:OD1	2.14	0.46
1:AK:298:TRP:NE1	1:AK:312:VAL:CB	2.78	0.46
1:AF:298:TRP:NE1	1:AF:312:VAL:HA	2.30	0.46
1:CZ:122:GLY:O	1:CZ:188:VAL:CB	2.63	0.46
1:CY:81:ASP:HA	1:CY:184:ILE:HG22	1.96	0.46
1:AH:91:ARG:NE	1:BN:98:ILE:CG2	2.79	0.46
1:BW:98:ILE:CA	1:BW:211:SER:O	2.63	0.46
1:CT:98:ILE:HD11	1:CT:99:PHE:CE2	2.50	0.46
1:CN:100:GLN:HA	1:CN:213:GLU:OE2	2.15	0.46
1:BK:123:TYR:HB2	1:BK:185:LEU:HD11	1.98	0.46
1:BB:156:ARG:NH2	1:CB:34:ARG:HG3	23.46	0.46
1:CD:112:GLN:HE21	1:CI:44:THR:H	1.63	0.46
1:BQ:142:GLN:HB2	1:CQ:48:PHE:CE1	2.50	0.46
1:CS:199:VAL:O	1:CS:199:VAL:CG1	2.63	0.46
1:CD:109:PHE:HB2	1:CD:158:VAL:HG12	1.96	0.46
1:AA:122:GLY:HA3	1:AI:114:MET:SD	2.55	0.46
1:AA:122:GLY:C	1:AA:188:VAL:HG22	2.36	0.46
1:AI:268:SER:CB	1:AI:273:ASP:O	2.64	0.46
1:AQ:85:VAL:HG22	1:AQ:86:PRO:HD2	1.96	0.46
1:BN:276:ARG:O	1:AN:276:ARG:NH2	2.48	0.46
1:CY:190:ASN:N	1:CY:190:ASN:HD22	2.13	0.46
1:AO:142:GLN:O	1:AO:142:GLN:NE2	2.49	0.46
1:CE:124:VAL:O	1:CE:124:VAL:HG13	2.16	0.46
1:CG:124:VAL:O	1:CG:124:VAL:HG13	2.16	0.46
1:AN:85:VAL:HG22	1:AN:86:PRO:HD2	1.97	0.46
1:AD:298:TRP:NE1	1:AD:312:VAL:HA	2.31	0.46
1:AL:298:TRP:NE1	1:AL:312:VAL:CB	2.76	0.46
1:CM:81:ASP:OD2	1:CM:136:HIS:NE2	2.43	0.46
1:CA:81:ASP:OD1	1:CA:81:ASP:C	2.54	0.46
1:BI:98:ILE:CA	1:BI:211:SER:O	2.63	0.46
1:CI:103:ALA:HB2	1:CI:166:LEU:HB3	1.98	0.46
1:CE:103:ALA:HB2	1:CE:166:LEU:HB3	1.98	0.46
1:CX:80:VAL:CG1	1:CX:185:LEU:HB2	2.43	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CU:99:PHE:CB	1:CU:209:VAL:O	2.64	0.46
1:CK:98:ILE:HD11	1:CK:99:PHE:CE2	2.51	0.46
1:AZ:61:SER:CB	1:AZ:90:PRO:HD2	2.39	0.46
1:BX:123:TYR:HB2	1:BX:185:LEU:CD1	2.45	0.46
1:BJ:123:TYR:HB2	1:BJ:185:LEU:HD11	1.97	0.46
1:BB:156:ARG:HH22	1:CB:34:ARG:CD	24.20	0.46
1:BW:150:ALA:HB2	1:BW:156:ARG:HD3	1.97	0.46
1:CK:44:THR:N	1:CL:112:GLN:HE21	2.12	0.46
1:AV:111:ILE:HG21	1:AV:123:TYR:CZ	2.50	0.46
1:CA:113:PRO:HA	1:CA:197:VAL:HA	2.05	0.46
1:BN:142:GLN:HB2	1:CN:48:PHE:CE1	2.50	0.46
1:CU:72:THR:O	1:CU:191:ASN:OD1	2.34	0.46
1:BL:123:TYR:HB2	1:BL:185:LEU:CD1	2.46	0.46
1:AV:268:SER:CB	1:AV:273:ASP:O	2.64	0.46
1:BX:214:ASN:HD22	1:BX:215:PRO:HD2	1.79	0.46
1:BO:136:HIS:O	1:BO:186:LEU:HD11	2.16	0.46
1:BG:214:ASN:HD22	1:BG:215:PRO:HD2	1.81	0.46
1:BN:232:SER:HB3	1:BN:242:LEU:HD11	1.97	0.46
1:AZ:224:THR:HG22	1:AZ:329:THR:N	2.30	0.46
1:CF:250:ILE:HG22	1:CF:250:ILE:O	2.16	0.46
1:CA:250:ILE:HG22	1:CA:250:ILE:O	2.15	0.46
1:BL:225:GLN:HG3	1:BL:244:GLY:O	2.16	0.46
1:BN:205:VAL:HG22	1:BN:206:ARG:N	2.30	0.46
1:BU:234:SER:HB3	1:BU:237:ASP:OD1	2.16	0.46
1:BU:232:SER:HB3	1:BU:242:LEU:HD11	1.98	0.46
1:AJ:298:TRP:NE1	1:AJ:312:VAL:HA	2.31	0.46
1:AO:302:ASP:C	1:AO:305:ASN:ND2	2.64	0.46
1:CP:81:ASP:HA	1:CP:184:ILE:HG22	1.98	0.46
1:CC:103:ALA:HB2	1:CC:166:LEU:HB3	2.02	0.46
1:AE:91:ARG:HD2	1:AM:143:ALA:HB1	1.98	0.46
1:CL:100:GLN:N	1:CL:209:VAL:O	2.49	0.46
1:AD:63:ILE:HG23	1:AD:88:LEU:HD11	1.98	0.46
1:CW:63:ILE:HD12	1:CW:88:LEU:CG	2.43	0.46
1:CY:89:LEU:HD13	1:CY:203:TRP:CG	2.51	0.46
1:CU:62:ARG:HA	1:CU:200:LEU:HD23	1.98	0.46
1:CE:163:THR:OG1	1:CE:165:THR:HG23	2.15	0.46
1:AY:124:VAL:HG11	1:AY:138:PHE:CD1	2.50	0.46
1:AB:80:VAL:HG13	1:AB:185:LEU:HB3	1.99	0.46
1:AY:80:VAL:HG13	1:AY:185:LEU:HB3	1.96	0.46
1:AE:268:SER:CB	1:AE:273:ASP:O	2.64	0.46
1:AH:268:SER:CB	1:AH:273:ASP:O	2.63	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AL:64:SER:OG	1:AL:80:VAL:HG21	2.15	0.46
1:AK:268:SER:HB3	1:AK:273:ASP:O	2.15	0.46
1:BE:225:GLN:HG3	1:BE:244:GLY:O	2.16	0.46
1:BY:260:ASP:HA	1:AY:261:ARG:NH2	2.31	0.46
1:BA:109:PHE:HB2	1:BA:158:VAL:CG1	2.47	0.46
1:BS:109:PHE:HB2	1:BS:158:VAL:CG1	2.46	0.46
1:BP:232:SER:HB3	1:BP:242:LEU:HD11	1.98	0.46
1:AR:298:TRP:HE1	1:AR:312:VAL:HA	1.81	0.46
1:CJ:81:ASP:OD2	1:CJ:136:HIS:NE2	2.44	0.46
1:AD:91:ARG:CZ	1:BF:98:ILE:CG2	2.94	0.46
1:AS:279:TYR:CE2	1:AS:311:GLY:O	2.64	0.46
1:CH:103:ALA:HB2	1:CH:166:LEU:HB3	1.97	0.46
1:BO:98:ILE:CA	1:BO:211:SER:O	2.64	0.46
1:AX:279:TYR:CE2	1:AX:311:GLY:O	2.65	0.46
1:CT:101:ARG:CZ	1:CT:166:LEU:CD1	2.94	0.46
1:AK:314:TYR:CE1	1:AK:316:SER:HA	2.48	0.46
1:CY:98:ILE:HD11	1:CY:99:PHE:CE2	2.51	0.46
1:CN:79:VAL:HG13	1:CN:80:VAL:HG12	1.98	0.46
1:CF:80:VAL:HG11	1:CF:185:LEU:HB2	1.98	0.46
1:AJ:98:ILE:HG12	1:BR:91:ARG:HG2	1.98	0.46
1:CH:34:ARG:CD	1:BM:156:ARG:HH22	2.28	0.46
1:BT:123:TYR:HB2	1:BT:185:LEU:CD1	2.46	0.46
1:BE:74:THR:HA	1:BE:190:ASN:ND2	2.30	0.46
1:CY:63:ILE:HD12	1:CY:88:LEU:CD1	2.46	0.46
1:CE:63:ILE:HD12	1:CE:88:LEU:CD1	2.46	0.46
1:CV:200:LEU:HD13	1:CZ:45:VAL:HG23	1.97	0.46
1:BZ:142:GLN:HB2	1:CZ:48:PHE:HE1	1.80	0.46
1:CL:89:LEU:HD13	1:CL:203:TRP:CG	2.51	0.46
1:BX:74:THR:HA	1:BX:190:ASN:ND2	2.31	0.46
1:BA:142:GLN:HB2	1:CA:48:PHE:HE1	1.80	0.46
1:BF:142:GLN:HB2	1:CF:48:PHE:CE1	2.51	0.46
1:AH:124:VAL:HG11	1:AH:138:PHE:CD1	2.51	0.46
1:AB:103:ALA:HB2	1:AB:166:LEU:HA	1.97	0.46
1:CF:39:VAL:HA	1:CY:39:VAL:CG2	2.45	0.46
1:CT:69:PRO:O	1:CT:72:THR:OG1	2.27	0.46
1:CA:202:ARG:HH12	1:CG:46:THR:HB	1.81	0.46
1:CA:54:ASP:OD1	1:CA:54:ASP:N	2.48	0.46
1:AB:246:THR:N	1:AB:247:PRO:CD	2.80	0.46
1:AW:85:VAL:HG22	1:AW:86:PRO:HD2	1.97	0.46
1:BL:234:SER:HB3	1:BL:237:ASP:OD1	2.15	0.46
1:BW:214:ASN:HD22	1:BW:215:PRO:HD2	1.81	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AV:246:THR:N	1:AV:247:PRO:CD	2.79	0.46
1:CD:81:ASP:OD2	1:CD:136:HIS:NE2	2.45	0.46
1:CL:103:ALA:HB2	1:CL:166:LEU:HB3	1.97	0.46
1:AB:91:ARG:CZ	1:BO:98:ILE:HG22	132.58	0.46
1:CA:79:VAL:HG13	1:CA:80:VAL:HG12	1.97	0.46
1:BT:98:ILE:HG22	1:AV:91:ARG:NH2	2.31	0.46
1:CX:123:TYR:HA	1:CX:188:VAL:HG23	1.98	0.46
1:AH:63:ILE:HG23	1:AH:88:LEU:HD11	1.98	0.46
1:AD:98:ILE:HG12	1:BH:91:ARG:HG2	125.13	0.46
1:AI:162:TYR:CE2	1:AI:164:ARG:HG2	2.51	0.46
1:AA:98:ILE:CG2	1:BV:91:ARG:NH1	2.79	0.46
1:BM:123:TYR:N	1:BM:188:VAL:HG22	2.31	0.46
1:AJ:162:TYR:CE2	1:AJ:164:ARG:HG2	2.51	0.46
1:CK:155:SER:O	1:CK:156:ARG:HD3	2.16	0.46
1:CR:57:LEU:HD23	1:CR:203:TRP:CH2	2.50	0.46
1:CE:44:THR:H	1:CH:112:GLN:HE21	1.62	0.46
1:BS:142:GLN:HB2	1:CS:48:PHE:HE1	1.81	0.46
1:AN:124:VAL:HG11	1:AN:138:PHE:CD1	2.51	0.46
1:AG:188:VAL:CG2	1:AP:114:MET:SD	3.05	0.46
1:BN:74:THR:HA	1:BN:190:ASN:HD22	1.81	0.46
1:AD:80:VAL:HG13	1:AD:185:LEU:HB3	1.98	0.46
1:AR:268:SER:CB	1:AR:273:ASP:O	2.64	0.46
1:CD:138:PHE:HE1	1:BH:62:ARG:HB2	136.56	0.46
1:AW:268:SER:CB	1:AW:273:ASP:O	2.64	0.46
1:BW:260:ASP:HA	1:AW:261:ARG:NH2	2.31	0.46
1:AG:100:GLN:HA	1:AG:169:THR:OG1	2.16	0.46
1:CA:77:TYR:CD1	1:CA:77:TYR:C	2.89	0.46
1:BU:250:ILE:O	1:BU:250:ILE:HG22	2.16	0.46
1:CD:250:ILE:HG22	1:CD:250:ILE:O	2.16	0.46
1:CW:250:ILE:O	1:CW:250:ILE:HG22	2.15	0.46
1:BU:184:ILE:N	1:BU:184:ILE:HD13	2.31	0.46
1:BB:124:VAL:HG11	1:BB:138:PHE:CD2	2.53	0.46
1:AU:298:TRP:NE1	1:AU:312:VAL:CB	2.78	0.45
1:CW:81:ASP:OD1	1:CW:81:ASP:C	2.55	0.45
1:CZ:81:ASP:OD2	1:CZ:136:HIS:NE2	2.43	0.45
1:BB:100:GLN:O	1:BB:169:THR:N	2.45	0.45
1:BA:100:GLN:NE2	1:BA:211:SER:CB	2.80	0.45
1:CT:103:ALA:HB2	1:CT:166:LEU:HB3	1.98	0.45
1:BQ:98:ILE:CG2	1:AZ:91:ARG:CZ	2.94	0.45
1:CA:91:ARG:HD2	1:CY:98:ILE:HB	128.27	0.45
1:AX:61:SER:HB2	1:AX:89:LEU:HD22	1.98	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AS:61:SER:HB2	1:AS:89:LEU:HD22	1.99	0.45
1:BZ:123:TYR:HB2	1:BZ:185:LEU:CD1	2.45	0.45
1:AB:116:PRO:HB3	1:AY:118:ASN:O	2.16	0.45
1:AA:116:PRO:HG2	1:AA:119:THR:OG1	2.17	0.45
1:BV:142:GLN:HB2	1:CV:48:PHE:HE1	1.80	0.45
1:BN:142:GLN:HB2	1:CN:48:PHE:HE1	1.80	0.45
1:CB:111:ILE:HD11	1:CB:125:ALA:HB3	1.98	0.45
1:CG:57:LEU:HD23	1:CG:203:TRP:CH2	2.51	0.45
1:CN:199:VAL:O	1:CN:199:VAL:CG1	2.64	0.45
1:AQ:138:PHE:CE2	1:AZ:62:ARG:CZ	2.99	0.45
1:BQ:116:PRO:HD3	1:CZ:120:GLY:HA3	1.97	0.45
1:CO:62:ARG:HA	1:CO:200:LEU:HD23	1.97	0.45
1:AT:103:ALA:HB2	1:AT:166:LEU:HA	1.97	0.45
1:AJ:124:VAL:HG11	1:AJ:138:PHE:CD1	2.50	0.45
1:BH:109:PHE:HB2	1:BH:158:VAL:CG1	2.46	0.45
1:BQ:214:ASN:HD22	1:BQ:215:PRO:HD2	1.81	0.45
1:BR:205:VAL:HG22	1:BR:206:ARG:N	2.30	0.45
1:CE:151:LYS:NZ	1:BM:153:TRP:O	2.49	0.45
1:AA:85:VAL:HG22	1:AA:86:PRO:HD2	2.01	0.45
1:BU:109:PHE:HB2	1:BU:158:VAL:CG1	2.46	0.45
1:CI:250:ILE:HG22	1:CI:250:ILE:O	2.16	0.45
1:CO:54:ASP:OD1	1:CO:54:ASP:N	2.49	0.45
1:CK:237:ASP:HB3	1:CK:297:ARG:HG2	1.97	0.45
1:AN:137:THR:HG23	1:AN:140:ALA:CB	2.45	0.45
1:AA:298:TRP:NE1	1:AA:312:VAL:CB	2.77	0.45
1:AH:298:TRP:HE1	1:AH:312:VAL:HA	1.82	0.45
1:AW:298:TRP:NE1	1:AW:312:VAL:HA	2.31	0.45
1:CW:123:TYR:HB2	1:CW:185:LEU:HD21	1.99	0.45
1:CJ:81:ASP:HA	1:CJ:184:ILE:HG22	1.98	0.45
1:CG:81:ASP:HA	1:CG:184:ILE:HG22	1.98	0.45
1:AD:143:ALA:HB1	1:AG:91:ARG:HD2	96.00	0.45
1:AC:91:ARG:HG2	1:BS:98:ILE:HG23	1.97	0.45
1:CI:99:PHE:CB	1:CI:209:VAL:O	2.64	0.45
1:AC:314:TYR:HE1	1:AC:316:SER:HG	1.63	0.45
1:CL:100:GLN:HA	1:CL:213:GLU:OE2	2.16	0.45
1:BG:130:ASP:HB3	1:BG:133:ASP:HB2	1.98	0.45
1:BK:91:ARG:HG2	1:AS:98:ILE:HG12	1.98	0.45
1:BD:123:TYR:N	1:BD:188:VAL:HG22	2.30	0.45
1:BF:123:TYR:HB2	1:BF:185:LEU:CD1	2.47	0.45
1:BH:150:ALA:HB2	1:BH:156:ARG:HD3	1.97	0.45
1:BB:123:TYR:HB2	1:BB:185:LEU:CD1	2.45	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AU:80:VAL:HG13	1:AU:185:LEU:HB3	1.98	0.45
1:CX:63:ILE:HD12	1:CX:88:LEU:CD1	2.47	0.45
1:CM:57:LEU:HD23	1:CM:203:TRP:CH2	2.51	0.45
1:CG:63:ILE:HD12	1:CG:88:LEU:CD1	2.46	0.45
1:CV:112:GLN:HE21	1:CZ:44:THR:H	1.64	0.45
1:CP:89:LEU:HD13	1:CP:203:TRP:CG	2.52	0.45
1:CV:89:LEU:HD13	1:CV:203:TRP:CG	2.51	0.45
1:CA:45:VAL:O	1:CA:45:VAL:HG13	2.20	0.45
1:CK:113:PRO:HA	1:CK:197:VAL:HA	1.99	0.45
1:AH:62:ARG:CZ	1:AN:138:PHE:CE2	3.00	0.45
1:AQ:188:VAL:HG23	1:AZ:114:MET:SD	2.56	0.45
1:BU:123:TYR:HB2	1:BU:185:LEU:CD1	2.46	0.45
1:AS:124:VAL:HG11	1:AS:138:PHE:CD1	2.50	0.45
1:CH:69:PRO:O	1:CH:72:THR:OG1	2.23	0.45
1:AP:268:SER:CB	1:AP:273:ASP:O	2.65	0.45
1:CK:78:VAL:HG13	1:CK:78:VAL:O	2.16	0.45
1:AL:142:GLN:O	1:AL:142:GLN:NE2	2.50	0.45
1:CH:250:ILE:O	1:CH:250:ILE:HG22	2.17	0.45
1:BR:184:ILE:N	1:BR:184:ILE:HD13	2.31	0.45
1:CU:250:ILE:HG22	1:CU:250:ILE:O	2.16	0.45
1:CZ:78:VAL:O	1:CZ:78:VAL:HG13	2.15	0.45
1:BS:232:SER:HB3	1:BS:242:LEU:HD11	1.97	0.45
1:CT:121:GLY:C	1:CT:152:TRP:CD1	2.89	0.45
1:BM:214:ASN:HD22	1:BM:215:PRO:HD2	1.80	0.45
1:BV:214:ASN:HD22	1:BV:215:PRO:HD2	1.80	0.45
1:BD:232:SER:HB3	1:BD:242:LEU:HD11	1.98	0.45
1:AV:298:TRP:HE1	1:AV:312:VAL:HA	1.81	0.45
1:AY:298:TRP:NE1	1:AY:312:VAL:CB	2.76	0.45
1:CP:81:ASP:C	1:CP:81:ASP:OD1	2.55	0.45
1:BD:210:PRO:HB3	1:AW:91:ARG:NH2	2.31	0.45
1:AO:315:TYR:CE2	1:AO:317:ASP:OD2	2.69	0.45
1:CO:99:PHE:CD2	1:CO:207:LEU:HB3	2.51	0.45
1:CM:99:PHE:CB	1:CM:209:VAL:O	2.64	0.45
1:AH:61:SER:HB2	1:AH:89:LEU:HD22	1.97	0.45
1:BX:166:LEU:HD13	1:BX:167:LEU:N	2.32	0.45
1:CV:99:PHE:HB3	1:CV:209:VAL:O	2.15	0.45
1:CH:34:ARG:HG3	1:BM:156:ARG:NH2	2.31	0.45
1:BA:123:TYR:HB2	1:BA:185:LEU:CD1	2.46	0.45
1:BX:150:ALA:HB2	1:BX:156:ARG:HD3	1.98	0.45
1:CD:200:LEU:HD13	1:CI:45:VAL:HG23	1.99	0.45
1:CD:92:LEU:HB2	1:CD:203:TRP:CH2	2.61	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CW:63:ILE:HD12	1:CW:88:LEU:CD1	2.45	0.45
1:BZ:74:THR:HA	1:BZ:190:ASN:HD22	1.82	0.45
1:CZ:57:LEU:HD23	1:CZ:203:TRP:CH2	2.52	0.45
1:CG:163:THR:OG1	1:CG:165:THR:HG23	2.17	0.45
1:CH:109:PHE:HB2	1:CH:158:VAL:HG12	1.97	0.45
1:AA:103:ALA:HB2	1:AA:166:LEU:HA	2.02	0.45
1:CJ:85:VAL:HG13	1:CJ:86:PRO:HD2	1.97	0.45
1:BX:225:GLN:HG3	1:BX:244:GLY:O	2.15	0.45
1:AJ:85:VAL:HG22	1:AJ:86:PRO:HD2	1.97	0.45
1:AT:85:VAL:HG22	1:AT:86:PRO:HD2	1.99	0.45
1:CZ:54:ASP:OD1	1:CZ:54:ASP:N	2.50	0.45
1:BC:184:ILE:N	1:BC:184:ILE:HD13	2.35	0.45
1:CV:250:ILE:HG22	1:CV:250:ILE:O	2.16	0.45
1:BP:250:ILE:HG22	1:BP:250:ILE:O	2.16	0.45
1:BC:232:SER:HB3	1:BC:242:LEU:HD11	1.98	0.45
1:AJ:298:TRP:NE1	1:AJ:312:VAL:CB	2.76	0.45
1:AJ:298:TRP:HE1	1:AJ:312:VAL:HA	1.82	0.45
1:AW:298:TRP:HE1	1:AW:312:VAL:HA	1.82	0.45
1:CG:79:VAL:HG13	1:CG:80:VAL:HG12	1.99	0.45
1:CN:81:ASP:OD2	1:CN:136:HIS:NE2	2.44	0.45
1:CD:123:TYR:HB2	1:CD:185:LEU:CD2	2.51	0.45
1:CZ:103:ALA:HB2	1:CZ:166:LEU:HB3	1.97	0.45
1:AA:91:ARG:HH21	1:BI:98:ILE:HG22	58.50	0.45
1:BS:98:ILE:CA	1:BS:211:SER:O	2.64	0.45
1:CX:103:ALA:HB2	1:CX:166:LEU:HB3	1.99	0.45
1:BA:210:PRO:HB3	1:AT:91:ARG:NH2	55.10	0.45
1:CK:79:VAL:HG13	1:CK:80:VAL:HG12	1.98	0.45
1:CW:103:ALA:HB2	1:CW:166:LEU:HB3	1.97	0.45
1:AO:314:TYR:HE1	1:AO:316:SER:HG	1.62	0.45
1:CR:98:ILE:HD11	1:CR:99:PHE:CE2	2.52	0.45
1:CG:103:ALA:HB2	1:CG:166:LEU:HB3	1.97	0.45
1:AF:315:TYR:CE2	1:AF:317:ASP:OD2	2.69	0.45
1:AD:314:TYR:C	1:AD:314:TYR:CD1	2.92	0.45
1:BM:123:TYR:HB2	1:BM:185:LEU:HD11	1.98	0.45
1:BZ:150:ALA:HB2	1:BZ:156:ARG:HD3	1.98	0.45
1:CC:155:SER:O	1:CC:156:ARG:HD3	2.17	0.45
1:BH:74:THR:HA	1:BH:190:ASN:HD22	1.81	0.45
1:CN:57:LEU:HD23	1:CN:203:TRP:CH2	2.51	0.45
1:BJ:142:GLN:HB2	1:CJ:48:PHE:HE1	1.80	0.45
1:BV:74:THR:HA	1:BV:190:ASN:HD22	1.79	0.45
1:AG:188:VAL:HG23	1:AP:114:MET:SD	2.57	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CR:109:PHE:HB2	1:CR:158:VAL:HG12	1.97	0.45
1:AC:281:HIS:ND1	1:AC:301:TRP:HB3	2.31	0.45
1:AO:124:VAL:HG11	1:AO:138:PHE:CD1	2.49	0.45
1:AY:264:SER:OG	1:AY:276:ARG:NH1	2.50	0.45
1:AX:246:THR:N	1:AX:247:PRO:CD	2.79	0.45
1:BJ:214:ASN:HD22	1:BJ:215:PRO:HD2	1.80	0.45
1:AA:224:THR:HG22	1:AA:329:THR:N	2.36	0.45
1:CV:78:VAL:HG13	1:CV:78:VAL:O	2.17	0.45
1:CI:78:VAL:HG13	1:CI:78:VAL:O	2.16	0.45
1:CU:102:TYR:HD2	1:CU:205:VAL:HG21	1.81	0.45
1:AH:298:TRP:NE1	1:AH:312:VAL:CB	2.76	0.45
1:CS:81:ASP:OD1	1:CS:81:ASP:C	2.55	0.45
1:AS:315:TYR:CE2	1:AS:317:ASP:OD2	2.68	0.45
1:AA:63:ILE:CD1	1:AA:89:LEU:HD21	2.47	0.45
1:CH:99:PHE:HB3	1:CH:209:VAL:O	2.17	0.45
1:CP:99:PHE:HB3	1:CP:209:VAL:O	2.17	0.45
1:CK:99:PHE:HB3	1:CK:209:VAL:O	2.17	0.45
1:CJ:112:GLN:NE2	1:CJ:155:SER:OG	2.50	0.45
1:CQ:63:ILE:HD12	1:CQ:88:LEU:CD1	2.47	0.45
1:CH:112:GLN:NE2	1:CH:155:SER:OG	2.49	0.45
1:BP:123:TYR:HB2	1:BP:185:LEU:HD11	1.98	0.45
1:CU:58:SER:HB3	1:CU:204:SER:HB2	1.99	0.45
1:CP:109:PHE:HB2	1:CP:158:VAL:HG12	1.98	0.45
1:CD:72:THR:O	1:CD:191:ASN:OD1	2.37	0.45
1:CG:130:ASP:OD2	1:CG:176:ARG:NH2	2.49	0.45
1:AV:122:GLY:C	1:AV:188:VAL:HG22	2.37	0.45
1:BM:85:VAL:CG2	1:BM:86:PRO:HD2	2.47	0.45
1:BU:128:LEU:HD12	1:BU:184:ILE:HD11	1.98	0.45
1:AN:226:GLY:N	1:AN:243:LEU:O	2.49	0.45
1:AF:226:GLY:N	1:AF:243:LEU:O	2.47	0.45
1:BI:250:ILE:O	1:BI:250:ILE:HG22	2.16	0.45
1:CS:250:ILE:HG22	1:CS:250:ILE:O	2.17	0.45
1:AA:100:GLN:HA	1:AA:169:THR:OG1	2.20	0.45
1:AI:298:TRP:NE1	1:AI:312:VAL:CB	2.78	0.45
1:AI:298:TRP:NE1	1:AI:312:VAL:HA	2.32	0.45
1:CU:81:ASP:OD1	1:CU:81:ASP:C	2.54	0.45
1:CO:79:VAL:HG13	1:CO:80:VAL:HG12	1.98	0.45
1:CQ:123:TYR:HB2	1:CQ:185:LEU:CD2	2.47	0.45
1:CM:101:ARG:CZ	1:CM:166:LEU:CD1	2.94	0.45
1:CA:98:ILE:HB	1:CY:91:ARG:HD2	119.40	0.45
1:AT:61:SER:HB2	1:AT:89:LEU:HD22	1.97	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BA:123:TYR:N	1:BA:188:VAL:HG22	2.31	0.45
1:BI:74:THR:HA	1:BI:190:ASN:HD22	1.80	0.45
1:CR:112:GLN:HE21	1:CT:44:THR:N	2.14	0.45
1:CQ:89:LEU:HD13	1:CQ:203:TRP:CG	2.52	0.45
1:BB:142:GLN:HB2	1:CB:48:PHE:HE1	1.81	0.45
1:BT:142:GLN:HB2	1:CT:48:PHE:HE1	1.81	0.45
1:CL:57:LEU:HD23	1:CL:203:TRP:CH2	2.52	0.45
1:CB:109:PHE:HB2	1:CB:158:VAL:HG12	1.97	0.45
1:CG:109:PHE:HB2	1:CG:158:VAL:HG12	1.98	0.45
1:AK:124:VAL:HG11	1:AK:138:PHE:CD1	2.52	0.45
1:CI:130:ASP:OD2	1:CI:176:ARG:NH2	2.50	0.45
1:AG:85:VAL:HG22	1:AG:86:PRO:HD2	1.98	0.45
1:BQ:205:VAL:HG22	1:BQ:206:ARG:N	2.32	0.45
1:BF:232:SER:HB3	1:BF:242:LEU:HD11	1.99	0.45
1:BZ:124:VAL:HG11	1:BZ:138:PHE:CD2	2.52	0.45
1:BQ:184:ILE:N	1:BQ:184:ILE:HD13	2.32	0.45
1:BB:234:SER:HB3	1:BB:237:ASP:OD1	2.17	0.45
1:AV:234:SER:HB3	1:AV:237:ASP:O	2.17	0.45
1:AA:226:GLY:N	1:AA:243:LEU:O	2.49	0.45
1:AQ:298:TRP:NE1	1:AQ:312:VAL:HA	2.32	0.45
1:AE:298:TRP:NE1	1:AE:312:VAL:HA	2.32	0.45
1:CO:81:ASP:C	1:CO:81:ASP:OD1	2.55	0.45
1:CA:81:ASP:OD2	1:CA:136:HIS:NE2	2.45	0.45
1:CY:81:ASP:OD2	1:CY:136:HIS:NE2	2.46	0.45
1:CC:81:ASP:HA	1:CC:184:ILE:HG22	2.00	0.45
1:BD:254:GLY:CA	1:BD:283:LYS:HE3	2.28	0.45
1:AA:91:ARG:NH2	1:BV:210:PRO:HB3	2.32	0.45
1:BC:98:ILE:HG22	1:AY:91:ARG:CZ	2.47	0.45
1:AB:91:ARG:HD2	1:AY:143:ALA:HB1	1.98	0.45
1:CR:99:PHE:HB3	1:CR:209:VAL:O	2.17	0.45
1:AM:61:SER:CB	1:AM:90:PRO:HD2	2.36	0.45
1:AF:98:ILE:HG22	1:AF:99:PHE:CD2	2.51	0.45
1:CD:44:THR:H	1:CI:112:GLN:HE21	1.63	0.45
1:CM:34:ARG:HG3	1:BW:156:ARG:NH2	2.31	0.45
1:CM:62:ARG:HA	1:CM:200:LEU:HD23	1.98	0.45
1:CY:57:LEU:HD23	1:CY:203:TRP:CH2	2.52	0.45
1:CU:63:ILE:HD12	1:CU:88:LEU:CG	2.44	0.45
1:AU:118:ASN:O	1:AX:116:PRO:HB3	2.16	0.45
1:CO:109:PHE:HB2	1:CO:158:VAL:HG12	1.96	0.45
1:AA:124:VAL:HG11	1:AA:138:PHE:CD1	2.52	0.45
1:AJ:62:ARG:CZ	1:AR:138:PHE:CE2	3.00	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CY:113:PRO:HA	1:CY:197:VAL:HA	1.99	0.45
1:AP:281:HIS:ND1	1:AP:301:TRP:HB3	2.32	0.45
1:CD:118:ASN:HA	1:BF:116:PRO:CB	2.47	0.45
1:AQ:268:SER:CB	1:AQ:273:ASP:O	2.64	0.45
1:CD:46:THR:HB	1:CW:202:ARG:HH12	33.52	0.45
1:CP:130:ASP:OD2	1:CP:176:ARG:NH2	2.50	0.45
1:CA:202:ARG:HH12	1:CY:46:THR:HB	117.34	0.45
1:BV:234:SER:HB3	1:BV:237:ASP:OD1	2.16	0.45
1:BW:225:GLN:HG3	1:BW:244:GLY:O	2.17	0.45
1:BB:128:LEU:HD12	1:BB:184:ILE:HD11	1.98	0.45
1:BM:128:LEU:HD12	1:BM:184:ILE:HD11	1.99	0.45
1:CO:250:ILE:HG22	1:CO:250:ILE:O	2.16	0.45
1:CX:250:ILE:HG22	1:CX:250:ILE:O	2.16	0.45
1:CU:119:THR:O	1:CU:120:GLY:C	2.55	0.45
1:CJ:237:ASP:HB3	1:CJ:297:ARG:HG2	1.97	0.45
1:CB:138:PHE:C	1:CB:138:PHE:CD1	2.91	0.45
1:AM:246:THR:N	1:AM:247:PRO:CD	2.79	0.45
1:CL:133:ASP:O	1:CL:182:ARG:NH2	2.49	0.45
1:AY:253:ASP:CG	1:AY:285:PHE:CA	2.80	0.45
1:CL:123:TYR:HB2	1:CL:185:LEU:CD2	2.47	0.45
1:CC:80:VAL:HG11	1:CC:185:LEU:HB2	1.99	0.45
1:AK:279:TYR:CE2	1:AK:311:GLY:O	2.65	0.45
1:CH:79:VAL:HG13	1:CH:80:VAL:HG12	1.99	0.45
1:AK:314:TYR:CE1	1:AK:316:SER:CA	2.93	0.45
1:CG:99:PHE:HB3	1:CG:209:VAL:O	2.17	0.45
1:BV:166:LEU:HD13	1:BV:167:LEU:N	2.32	0.45
1:CO:155:SER:O	1:CO:156:ARG:HD3	2.17	0.45
1:BX:123:TYR:N	1:BX:188:VAL:HG22	2.31	0.45
1:AE:162:TYR:CE2	1:AE:164:ARG:HG2	2.52	0.45
1:BJ:123:TYR:HB2	1:BJ:185:LEU:CD1	2.47	0.45
1:BR:150:ALA:HB2	1:BR:156:ARG:HD3	1.98	0.45
1:CR:155:SER:O	1:CR:156:ARG:HD3	2.17	0.45
1:CS:57:LEU:HD23	1:CS:203:TRP:CH2	2.51	0.45
1:CN:63:ILE:HD12	1:CN:88:LEU:CG	2.45	0.45
1:CJ:57:LEU:HD23	1:CJ:203:TRP:CH2	2.51	0.45
1:CQ:199:VAL:O	1:CQ:199:VAL:CG1	2.65	0.45
1:BC:62:ARG:NH2	1:CM:138:PHE:CE2	217.77	0.45
1:CA:69:PRO:O	1:CA:72:THR:OG1	2.28	0.45
1:AI:122:GLY:C	1:AI:188:VAL:HG22	2.37	0.45
1:AA:114:MET:SD	1:AI:188:VAL:HG23	31.44	0.45
1:AZ:264:SER:OG	1:AZ:276:ARG:NH1	2.48	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CL:237:ASP:HB3	1:CL:297:ARG:HG2	1.98	0.45
1:BZ:205:VAL:HG22	1:BZ:206:ARG:N	2.32	0.45
1:CB:202:ARG:HH12	1:CU:46:THR:HB	108.55	0.45
1:CL:54:ASP:N	1:CL:54:ASP:OD1	2.50	0.45
1:CB:77:TYR:CD1	1:CB:77:TYR:C	2.89	0.45
1:CC:202:ARG:HH12	1:CJ:46:THR:HB	1.80	0.45
1:CC:202:ARG:HH12	1:CX:46:THR:HB	198.28	0.45
1:CL:214:ASN:HA	1:CL:215:PRO:HD3	1.84	0.45
1:BD:225:GLN:HG3	1:BD:244:GLY:O	2.17	0.45
1:BV:136:HIS:O	1:BV:186:LEU:HD11	2.17	0.45
1:CC:133:ASP:O	1:CC:182:ARG:NH2	2.49	0.45
1:AC:298:TRP:O	1:AC:310:ASP:O	2.35	0.45
1:AO:298:TRP:NE1	1:AO:312:VAL:CB	2.76	0.45
1:CM:79:VAL:HG13	1:CM:80:VAL:HG12	1.97	0.45
1:CZ:80:VAL:HG11	1:CZ:185:LEU:CB	2.45	0.45
1:CI:99:PHE:CD2	1:CI:207:LEU:HB3	2.52	0.45
1:AJ:314:TYR:HE1	1:AJ:316:SER:HG	1.64	0.45
1:CM:44:THR:H	1:CO:112:GLN:HE21	1.63	0.45
1:AL:162:TYR:CE2	1:AL:164:ARG:HG2	2.52	0.45
1:CC:45:VAL:HG13	1:CC:45:VAL:O	2.17	0.45
1:BB:142:GLN:HB2	1:CB:48:PHE:CE1	2.51	0.45
1:CZ:58:SER:HB3	1:CZ:204:SER:HB2	1.98	0.45
1:CO:199:VAL:O	1:CO:199:VAL:CG1	2.64	0.45
1:CW:199:VAL:CG1	1:CW:199:VAL:O	2.65	0.45
1:CS:130:ASP:OD2	1:CS:176:ARG:NH2	2.49	0.45
1:BY:86:PRO:HB3	1:BY:92:LEU:HD22	1.99	0.45
1:BA:136:HIS:O	1:BA:186:LEU:HD11	2.17	0.45
1:BU:205:VAL:HG22	1:BU:206:ARG:N	2.32	0.45
1:CB:264:SER:HB2	1:CB:324:LEU:HD22	2.02	0.45
1:AT:224:THR:HG22	1:AT:329:THR:N	2.32	0.45
1:CB:250:ILE:HG22	1:CB:250:ILE:O	2.17	0.45
1:BJ:260:ASP:HA	1:AJ:261:ARG:NH2	2.31	0.45
1:BC:136:HIS:O	1:BC:186:LEU:HD11	2.18	0.45
1:BL:232:SER:HB3	1:BL:242:LEU:HD11	1.99	0.45
1:AO:298:TRP:NE1	1:AO:312:VAL:HA	2.32	0.45
1:CW:123:TYR:HB2	1:CW:185:LEU:CD2	2.47	0.45
1:AA:91:ARG:CZ	1:BV:98:ILE:CG2	2.95	0.45
1:BC:98:ILE:HG22	1:AY:91:ARG:NH2	2.31	0.45
1:AW:314:TYR:CE1	1:AW:316:SER:CA	2.91	0.45
1:CP:99:PHE:CD2	1:CP:207:LEU:HB3	2.52	0.45
1:BY:165:THR:OG1	1:BY:166:LEU:N	2.49	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AS:63:ILE:CD1	1:AS:89:LEU:HD21	2.47	0.45
1:AR:98:ILE:HG22	1:AR:99:PHE:CD2	2.52	0.45
1:AO:162:TYR:CE2	1:AO:164:ARG:HG2	2.52	0.45
1:AB:162:TYR:CE2	1:AB:164:ARG:HG2	2.52	0.45
1:BQ:156:ARG:HH22	1:CV:34:ARG:CD	2.30	0.45
1:CF:112:GLN:NE2	1:CF:155:SER:OG	2.50	0.45
1:BR:80:VAL:CG1	1:BR:185:LEU:HB3	2.46	0.45
1:CD:89:LEU:HD13	1:CD:203:TRP:CG	2.54	0.45
1:CM:62:ARG:H	1:BO:142:GLN:NE2	2.15	0.45
1:AQ:122:GLY:C	1:AQ:188:VAL:HG22	2.37	0.45
1:CC:113:PRO:HA	1:CC:197:VAL:HA	1.99	0.45
1:CD:119:THR:O	1:CD:120:GLY:C	2.63	0.45
1:CN:118:ASN:HA	1:BP:116:PRO:CB	2.47	0.45
1:BD:260:ASP:HA	1:AD:261:ARG:NH2	2.32	0.45
1:BX:124:VAL:HG11	1:BX:138:PHE:CD2	2.52	0.45
1:BZ:234:SER:HB3	1:BZ:237:ASP:OD1	2.17	0.45
1:CC:77:TYR:CD1	1:CC:77:TYR:C	2.89	0.45
1:CP:78:VAL:O	1:CP:78:VAL:HG13	2.17	0.45
1:CQ:78:VAL:HG13	1:CQ:78:VAL:O	2.17	0.45
1:BR:168:TRP:CE2	1:AR:176:ARG:HD2	2.52	0.45
1:CK:91:ARG:NH1	1:CL:52:THR:O	2.50	0.45
1:BC:109:PHE:HB2	1:BC:158:VAL:CG1	2.47	0.45
1:AA:298:TRP:HE1	1:AA:312:VAL:HA	1.82	0.44
1:AM:298:TRP:NE1	1:AM:312:VAL:HA	2.32	0.44
1:AY:298:TRP:NE1	1:AY:312:VAL:HA	2.31	0.44
1:CA:123:TYR:HA	1:CA:188:VAL:HG23	2.00	0.44
1:AT:143:ALA:HB1	1:AV:91:ARG:HD2	1.99	0.44
1:BR:98:ILE:CA	1:BR:211:SER:O	2.65	0.44
1:AD:98:ILE:HG22	1:AD:99:PHE:CD2	2.51	0.44
1:AF:61:SER:HB2	1:AF:89:LEU:HD22	1.99	0.44
1:AS:98:ILE:HG22	1:AS:99:PHE:CD2	2.52	0.44
1:BL:91:ARG:HG2	1:AU:98:ILE:HG12	1.98	0.44
1:BT:142:GLN:HB2	1:CT:48:PHE:CE1	2.51	0.44
1:CH:199:VAL:CG1	1:CH:199:VAL:O	2.63	0.44
1:BY:142:GLN:HB2	1:CY:48:PHE:CE1	2.52	0.44
1:AD:122:GLY:C	1:AD:188:VAL:HG22	2.37	0.44
1:BQ:124:VAL:HG11	1:BQ:138:PHE:CD2	2.52	0.44
1:AM:238:PHE:CZ	1:AM:296:PHE:HB2	2.52	0.44
1:BD:205:VAL:HG22	1:BD:206:ARG:N	2.34	0.44
1:CL:69:PRO:O	1:CL:72:THR:OG1	2.28	0.44
1:BU:225:GLN:HG3	1:BU:244:GLY:O	2.18	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BY:109:PHE:HB2	1:BY:158:VAL:CG1	2.47	0.44
1:AX:298:TRP:NE1	1:AX:312:VAL:CB	2.77	0.44
1:AT:298:TRP:HE1	1:AT:312:VAL:HA	1.82	0.44
1:AT:302:ASP:OD2	1:AT:305:ASN:CB	2.60	0.44
1:CK:123:TYR:CD1	1:CK:185:LEU:HD21	2.52	0.44
1:CK:186:LEU:HD23	1:CK:186:LEU:N	2.32	0.44
1:CH:123:TYR:HA	1:CH:188:VAL:HG23	1.99	0.44
1:CJ:99:PHE:CD2	1:CJ:207:LEU:HB3	2.52	0.44
1:AB:98:ILE:HG22	1:AB:99:PHE:CD2	2.60	0.44
1:BU:91:ARG:NH1	1:AX:98:ILE:CG2	2.80	0.44
1:CP:112:GLN:NE2	1:CP:155:SER:OG	2.50	0.44
1:BJ:123:TYR:N	1:BJ:188:VAL:HG22	2.32	0.44
1:AQ:69:PRO:C	1:AQ:72:THR:HG1	2.21	0.44
1:CW:57:LEU:HD23	1:CW:203:TRP:CH2	2.52	0.44
1:CM:199:VAL:O	1:CM:199:VAL:CG1	2.65	0.44
1:CR:130:ASP:OD2	1:CR:176:ARG:NH2	2.51	0.44
1:AM:64:SER:OG	1:AM:80:VAL:HG21	2.16	0.44
1:BM:74:THR:HA	1:BM:190:ASN:HD22	1.82	0.44
1:BU:281:HIS:CE1	1:BU:301:TRP:HB3	2.52	0.44
1:AY:64:SER:OG	1:AY:80:VAL:HG21	2.17	0.44
1:AZ:124:VAL:HG11	1:AZ:138:PHE:CD1	2.52	0.44
1:BP:136:HIS:O	1:BP:186:LEU:HD11	2.17	0.44
1:BF:260:ASP:HA	1:AF:261:ARG:NH2	2.32	0.44
1:CI:214:ASN:HA	1:CI:215:PRO:HD3	1.85	0.44
1:CE:133:ASP:O	1:CE:182:ARG:NH2	2.50	0.44
1:CJ:77:TYR:C	1:CJ:77:TYR:CD1	2.91	0.44
1:CB:78:VAL:HG13	1:CB:78:VAL:O	2.21	0.44
1:CE:190:ASN:HD22	1:CE:190:ASN:N	2.15	0.44
1:BX:250:ILE:O	1:BX:250:ILE:HG22	2.16	0.44
1:AT:246:THR:N	1:AT:247:PRO:CD	2.80	0.44
1:AQ:298:TRP:NE1	1:AQ:312:VAL:CB	2.76	0.44
1:CZ:81:ASP:OD1	1:CZ:81:ASP:C	2.54	0.44
1:CP:123:TYR:CD1	1:CP:185:LEU:HD21	2.53	0.44
1:CP:80:VAL:HG11	1:CP:185:LEU:HB2	1.99	0.44
1:CD:123:TYR:HA	1:CD:188:VAL:HG23	1.98	0.44
1:AM:263:LEU:HB3	1:AM:279:TYR:O	2.17	0.44
1:AD:263:LEU:HB3	1:AD:279:TYR:O	2.17	0.44
1:AB:91:ARG:CZ	1:BY:98:ILE:CG2	2.95	0.44
1:BA:100:GLN:O	1:BA:169:THR:N	2.45	0.44
1:BQ:98:ILE:CA	1:BQ:211:SER:O	2.65	0.44
1:CF:99:PHE:CD2	1:CF:207:LEU:HB3	2.53	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AW:314:TYR:C	1:AW:314:TYR:CD1	2.91	0.44
1:CL:99:PHE:HB3	1:CL:209:VAL:O	2.17	0.44
1:BL:166:LEU:HD13	1:BL:167:LEU:N	2.32	0.44
1:BW:165:THR:OG1	1:BW:166:LEU:N	2.49	0.44
1:AA:98:ILE:HG12	1:BI:91:ARG:HG2	80.03	0.44
1:AY:162:TYR:CE2	1:AY:164:ARG:HG2	2.52	0.44
1:BI:123:TYR:N	1:BI:188:VAL:HG22	2.32	0.44
1:CC:45:VAL:HG23	1:CJ:200:LEU:HD13	2.00	0.44
1:BL:142:GLN:HB2	1:CL:48:PHE:HE1	1.80	0.44
1:BE:74:THR:HA	1:BE:190:ASN:HD22	1.83	0.44
1:BU:142:GLN:HB2	1:CU:48:PHE:CE1	2.52	0.44
1:BN:111:ILE:HG22	1:BN:155:SER:HA	1.99	0.44
1:AQ:63:ILE:HG23	1:AQ:88:LEU:HD11	1.99	0.44
1:AD:188:VAL:CG2	1:AW:114:MET:SD	3.05	0.44
1:CR:158:VAL:O	1:CR:158:VAL:HG13	2.18	0.44
1:AB:281:HIS:ND1	1:AB:301:TRP:HB3	2.33	0.44
1:AQ:281:HIS:ND1	1:AQ:301:TRP:HB3	2.32	0.44
1:CH:130:ASP:OD2	1:CH:176:ARG:NH2	2.50	0.44
1:CX:130:ASP:OD2	1:CX:176:ARG:NH2	2.50	0.44
1:AI:80:VAL:HG13	1:AI:185:LEU:HB3	1.97	0.44
1:AC:264:SER:OG	1:AC:276:ARG:NH1	2.47	0.44
1:AW:122:GLY:C	1:AW:188:VAL:HG22	2.38	0.44
1:BW:124:VAL:HG11	1:BW:138:PHE:CD2	2.53	0.44
1:BA:184:ILE:N	1:BA:184:ILE:HD13	2.37	0.44
1:CP:202:ARG:HH12	1:CQ:46:THR:HB	1.83	0.44
1:CR:133:ASP:O	1:CR:182:ARG:NH2	2.50	0.44
1:BV:260:ASP:HA	1:AV:261:ARG:NH2	2.32	0.44
1:BV:109:PHE:HB2	1:BV:158:VAL:CG1	2.47	0.44
1:CK:46:THR:HB	1:CL:202:ARG:HH12	1.82	0.44
1:BI:136:HIS:O	1:BI:186:LEU:HD11	2.16	0.44
1:AA:234:SER:HB3	1:AA:237:ASP:O	2.19	0.44
1:BY:161:GLN:NE2	1:CY:210:PRO:HD2	2.32	0.44
1:CJ:250:ILE:O	1:CJ:250:ILE:HG22	2.18	0.44
1:CE:250:ILE:O	1:CE:250:ILE:HG22	2.18	0.44
1:BD:124:VAL:HG11	1:BD:138:PHE:CD2	2.52	0.44
1:BR:260:ASP:HA	1:AR:261:ARG:NH2	2.31	0.44
1:BM:136:HIS:O	1:BM:186:LEU:HD11	2.18	0.44
1:CP:123:TYR:HB2	1:CP:185:LEU:CD2	2.48	0.44
1:CK:81:ASP:C	1:CK:81:ASP:OD1	2.56	0.44
1:AF:263:LEU:HB3	1:AF:279:TYR:O	2.17	0.44
1:CI:80:VAL:HG11	1:CI:185:LEU:CB	2.45	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BQ:254:GLY:CA	1:BQ:283:LYS:HE3	2.30	0.44
1:BB:98:ILE:HG22	1:AF:91:ARG:CZ	88.45	0.44
1:CX:123:TYR:HB2	1:CX:185:LEU:CD2	2.47	0.44
1:BB:130:ASP:HB3	1:BB:133:ASP:HB2	2.05	0.44
1:CC:317:ASP:HB3	1:CC:319:GLN:NE2	2.34	0.44
1:CE:99:PHE:CD2	1:CE:207:LEU:HB3	2.53	0.44
1:AY:61:SER:HB2	1:AY:89:LEU:HD22	2.00	0.44
1:AD:63:ILE:CD1	1:AD:89:LEU:HD21	2.48	0.44
1:AM:61:SER:HB2	1:AM:89:LEU:HD22	1.99	0.44
1:BC:123:TYR:N	1:BC:188:VAL:HG22	2.34	0.44
1:CC:44:THR:H	1:CJ:112:GLN:HE21	1.65	0.44
1:CB:43:SER:O	1:CL:34:ARG:HD3	2.17	0.44
1:CD:57:LEU:HD23	1:CD:203:TRP:CH2	2.53	0.44
1:CE:62:ARG:H	1:BH:142:GLN:NE2	2.15	0.44
1:CP:57:LEU:HD23	1:CP:203:TRP:CH2	2.51	0.44
1:BS:142:GLN:HB2	1:CS:48:PHE:CE1	2.52	0.44
1:CA:62:ARG:HA	1:CA:200:LEU:HD23	2.02	0.44
1:BY:142:GLN:HB2	1:CY:48:PHE:HE1	1.82	0.44
1:BN:150:ALA:HB2	1:BN:156:ARG:HD3	2.00	0.44
1:BM:281:HIS:CE1	1:BM:301:TRP:HB3	2.53	0.44
1:BD:281:HIS:CE1	1:BD:301:TRP:HB3	2.53	0.44
1:BW:232:SER:HB3	1:BW:242:LEU:HD11	1.99	0.44
1:CN:54:ASP:N	1:CN:54:ASP:OD1	2.51	0.44
1:CG:190:ASN:HD22	1:CG:190:ASN:N	2.16	0.44
1:BC:250:ILE:O	1:BC:250:ILE:HG22	2.23	0.44
1:CH:54:ASP:OD1	1:CH:54:ASP:N	2.50	0.44
1:CG:77:TYR:CD1	1:CG:77:TYR:C	2.91	0.44
1:AM:298:TRP:NE1	1:AM:312:VAL:CB	2.77	0.44
1:AE:298:TRP:NE1	1:AE:312:VAL:CB	2.77	0.44
1:AA:302:ASP:OD2	1:AA:305:ASN:CB	2.62	0.44
1:CG:123:TYR:HA	1:CG:188:VAL:HG23	1.99	0.44
1:CD:123:TYR:CD1	1:CD:185:LEU:HD21	2.58	0.44
1:CQ:81:ASP:C	1:CQ:81:ASP:OD1	2.55	0.44
1:BK:61:SER:CB	1:BK:90:PRO:HD2	2.30	0.44
1:AO:91:ARG:NH2	1:BW:98:ILE:CG2	2.81	0.44
1:AH:63:ILE:CD1	1:AH:89:LEU:HD21	2.48	0.44
1:AO:61:SER:HB2	1:AO:89:LEU:HD22	2.00	0.44
1:BC:163:THR:C	1:BC:165:THR:HG22	2.38	0.44
1:BC:163:THR:O	1:BC:165:THR:HG22	2.17	0.44
1:AB:98:ILE:CG2	1:BO:91:ARG:NH1	122.57	0.44
1:CD:44:THR:H	1:CW:112:GLN:HE21	26.03	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BO:123:TYR:N	1:BO:188:VAL:HG22	2.33	0.44
1:BA:122:GLY:C	1:BA:188:VAL:CG2	2.83	0.44
1:CE:62:ARG:HA	1:CE:200:LEU:HD23	2.00	0.44
1:CR:62:ARG:HA	1:CR:200:LEU:HD23	1.99	0.44
1:CT:113:PRO:HA	1:CT:197:VAL:HA	2.00	0.44
1:AB:124:VAL:HG11	1:AB:138:PHE:CD1	2.52	0.44
1:CE:199:VAL:O	1:CE:199:VAL:CG1	2.66	0.44
1:AB:122:GLY:C	1:AB:188:VAL:HG22	2.38	0.44
1:AI:264:SER:OG	1:AI:276:ARG:NH1	2.50	0.44
1:BU:260:ASP:HA	1:AU:261:ARG:NH2	2.33	0.44
1:AD:183:LEU:HG	1:AD:184:ILE:N	2.32	0.44
1:BN:260:ASP:HA	1:AN:261:ARG:NH2	2.33	0.44
1:CM:78:VAL:HG13	1:CM:78:VAL:O	2.18	0.44
1:CF:119:THR:O	1:CF:119:THR:HG22	2.18	0.44
1:CB:54:ASP:OD1	1:CB:54:ASP:N	2.51	0.44
1:BQ:260:ASP:HA	1:AQ:261:ARG:NH2	2.33	0.44
1:AL:224:THR:HG22	1:AL:329:THR:N	2.32	0.44
1:AV:224:THR:HG22	1:AV:329:THR:N	2.33	0.44
1:AY:298:TRP:HE1	1:AY:312:VAL:HA	1.83	0.44
1:CS:81:ASP:OD2	1:CS:136:HIS:NE2	2.44	0.44
1:BB:98:ILE:HG22	1:AF:91:ARG:NH2	87.80	0.44
1:BL:98:ILE:HB	1:BL:99:PHE:CD1	2.53	0.44
1:CK:80:VAL:HG13	1:CK:185:LEU:N	2.33	0.44
1:CO:103:ALA:HB2	1:CO:166:LEU:HB3	2.00	0.44
1:CX:80:VAL:HG11	1:CX:185:LEU:HB2	1.99	0.44
1:CV:80:VAL:HG11	1:CV:185:LEU:HB2	1.98	0.44
1:AB:61:SER:HB2	1:AB:89:LEU:HD22	1.99	0.44
1:BS:163:THR:C	1:BS:165:THR:HG22	2.38	0.44
1:CC:89:LEU:HD13	1:CC:203:TRP:CG	2.52	0.44
1:CQ:63:ILE:HD12	1:CQ:88:LEU:CG	2.45	0.44
1:BJ:142:GLN:HB2	1:CJ:48:PHE:CE1	2.52	0.44
1:AB:62:ARG:CZ	1:AY:138:PHE:CE2	3.01	0.44
1:CD:77:TYR:CD1	1:CD:78:VAL:N	2.96	0.44
1:AQ:264:SER:OG	1:AQ:276:ARG:NH1	2.50	0.44
1:AL:103:ALA:HB2	1:AL:166:LEU:HA	2.00	0.44
1:AD:100:GLN:HA	1:AD:169:THR:OG1	2.20	0.44
1:BG:136:HIS:O	1:BG:186:LEU:HD11	2.16	0.44
1:AI:224:THR:HG22	1:AI:329:THR:N	2.33	0.44
1:BR:214:ASN:HD22	1:BR:215:PRO:HD2	1.82	0.44
1:BH:250:ILE:HG22	1:BH:250:ILE:O	2.16	0.44
1:CN:250:ILE:O	1:CN:250:ILE:HG22	2.17	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AS:256:VAL:HB	1:AS:335:ASP:HB3	1.99	0.44
1:AC:137:THR:HG23	1:AC:140:ALA:CB	2.52	0.44
1:CB:214:ASN:HA	1:CB:215:PRO:HD3	1.85	0.44
1:AC:226:GLY:N	1:AC:243:LEU:O	2.48	0.44
1:CB:123:TYR:HB2	1:CB:185:LEU:HD21	2.06	0.44
1:CL:81:ASP:HA	1:CL:184:ILE:HG22	1.98	0.44
1:CV:81:ASP:OD2	1:CV:136:HIS:NE2	2.45	0.44
1:AE:91:ARG:NH2	1:BM:98:ILE:HG22	2.32	0.44
1:CO:123:TYR:HB2	1:CO:185:LEU:HD21	1.99	0.44
1:AL:314:TYR:CD1	1:AL:314:TYR:C	2.91	0.44
1:AK:63:ILE:CD1	1:AK:89:LEU:HD21	2.48	0.44
1:AA:98:ILE:CG2	1:BI:91:ARG:NH1	78.28	0.44
1:AR:162:TYR:CE2	1:AR:164:ARG:HG2	2.53	0.44
1:CI:45:VAL:O	1:CI:45:VAL:HG13	2.17	0.44
1:BI:142:GLN:HB2	1:CI:48:PHE:HE1	1.83	0.44
1:CB:63:ILE:HD12	1:CB:88:LEU:CG	2.47	0.44
1:CE:89:LEU:HD13	1:CE:203:TRP:CG	2.53	0.44
1:CA:158:VAL:HG13	1:CA:158:VAL:O	2.17	0.44
1:AN:122:GLY:C	1:AN:188:VAL:HG22	2.38	0.44
1:AJ:80:VAL:HG12	1:AJ:185:LEU:HB3	1.99	0.44
1:CM:109:PHE:HB2	1:CM:158:VAL:HG12	1.98	0.44
1:AP:80:VAL:HG13	1:AP:185:LEU:HB3	1.98	0.44
1:CC:85:VAL:O	1:CC:86:PRO:C	2.63	0.44
1:BN:85:VAL:CG2	1:BN:86:PRO:HD2	2.47	0.44
1:BO:300:ILE:HG23	1:AO:323:ILE:CD1	2.48	0.44
1:AB:137:THR:HG23	1:AB:140:ALA:CB	2.48	0.44
1:BE:161:GLN:NE2	1:CE:210:PRO:HD2	2.32	0.44
1:BF:225:GLN:HG3	1:BF:244:GLY:O	2.18	0.44
1:AT:238:PHE:CZ	1:AT:296:PHE:HB2	2.53	0.44
1:BM:260:ASP:HA	1:AM:261:ARG:NH2	2.33	0.44
1:BX:232:SER:HB3	1:BX:242:LEU:HD11	2.00	0.44
1:BG:260:ASP:HA	1:AG:261:ARG:NH2	2.32	0.44
1:CA:78:VAL:O	1:CA:78:VAL:HG13	2.18	0.44
1:BC:214:ASN:HD22	1:BC:215:PRO:HD2	1.82	0.44
1:AC:234:SER:HB3	1:AC:237:ASP:O	2.17	0.44
1:CK:121:GLY:C	1:CK:152:TRP:CD1	2.91	0.44
1:BJ:232:SER:HB3	1:BJ:242:LEU:HD11	2.00	0.44
1:AT:100:GLN:HA	1:AT:169:THR:OG1	2.18	0.44
1:AL:298:TRP:NE1	1:AL:312:VAL:HA	2.33	0.44
1:AF:298:TRP:HE1	1:AF:312:VAL:HA	1.82	0.44
1:CM:123:TYR:CD1	1:CM:185:LEU:HD21	2.52	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CY:123:TYR:HB2	1:CY:185:LEU:HD21	2.00	0.44
1:AA:63:ILE:HG23	1:AA:88:LEU:HD11	2.05	0.44
1:CH:99:PHE:CD2	1:CH:207:LEU:HB3	2.53	0.44
1:CN:99:PHE:CD2	1:CN:207:LEU:HB3	2.53	0.44
1:AX:63:ILE:HG23	1:AX:88:LEU:HD11	2.00	0.44
1:AN:98:ILE:HG22	1:AN:99:PHE:CD2	2.53	0.44
1:AH:98:ILE:HG22	1:AH:99:PHE:CD2	2.53	0.44
1:BD:156:ARG:HH22	1:CD:34:ARG:CD	24.20	0.44
1:BR:123:TYR:N	1:BR:188:VAL:HG22	2.33	0.44
1:CC:62:ARG:H	1:BJ:142:GLN:NE2	2.16	0.44
1:BU:142:GLN:HB2	1:CU:48:PHE:HE1	1.82	0.44
1:BC:118:ASN:ND2	1:CM:118:ASN:OD1	223.58	0.44
1:CB:158:VAL:O	1:CB:158:VAL:HG13	2.18	0.44
1:AT:80:VAL:HG13	1:AT:185:LEU:HB3	1.99	0.44
1:AI:64:SER:OG	1:AI:80:VAL:HG21	2.17	0.44
1:AX:264:SER:OG	1:AX:276:ARG:NH1	2.50	0.44
1:BF:136:HIS:O	1:BF:186:LEU:HD11	2.18	0.44
1:AH:85:VAL:HG22	1:AH:86:PRO:HD2	2.00	0.44
1:BD:109:PHE:HB2	1:BD:158:VAL:CG1	2.48	0.44
1:CW:237:ASP:HB3	1:CW:297:ARG:HG2	2.00	0.44
1:CJ:119:THR:O	1:CJ:120:GLY:C	2.56	0.44
1:AH:246:THR:N	1:AH:247:PRO:CD	2.80	0.44
1:CV:138:PHE:C	1:CV:138:PHE:CD1	2.92	0.44
1:BN:184:ILE:N	1:BN:184:ILE:HD13	2.32	0.44
1:AF:100:GLN:HA	1:AF:169:THR:OG1	2.17	0.44
1:BA:260:ASP:HA	1:AA:261:ARG:NH2	2.32	0.44
1:BR:234:SER:HB3	1:BR:237:ASP:OD1	2.18	0.44
1:AQ:298:TRP:HE1	1:AQ:312:VAL:HA	1.83	0.44
1:CW:123:TYR:HA	1:CW:188:VAL:HG23	2.00	0.44
1:CC:123:TYR:HB2	1:CC:185:LEU:HD21	2.00	0.44
1:BB:254:GLY:CA	1:BB:283:LYS:HE3	2.30	0.44
1:CI:123:TYR:HB2	1:CI:185:LEU:HD21	2.00	0.44
1:AD:91:ARG:CZ	1:BH:210:PRO:HB3	131.69	0.44
1:BB:100:GLN:NE2	1:BB:211:SER:CB	2.84	0.44
1:BQ:210:PRO:HB3	1:AZ:91:ARG:NH2	2.32	0.44
1:CC:99:PHE:CD2	1:CC:207:LEU:HB3	2.53	0.44
1:CJ:122:GLY:O	1:CJ:188:VAL:CB	2.65	0.44
1:BD:91:ARG:NH1	1:AW:98:ILE:CG2	2.80	0.44
1:AA:162:TYR:CE2	1:AA:164:ARG:HG2	2.53	0.44
1:AM:162:TYR:CE2	1:AM:164:ARG:HG2	2.53	0.44
1:AD:162:TYR:CE2	1:AD:164:ARG:HG2	2.53	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CL:63:ILE:HD12	1:CL:88:LEU:CG	2.47	0.44
1:BD:74:THR:HA	1:BD:190:ASN:HD22	1.84	0.44
1:CD:45:VAL:O	1:CD:45:VAL:HG13	2.17	0.44
1:AG:124:VAL:HG11	1:AG:138:PHE:CD1	2.53	0.44
1:AM:122:GLY:C	1:AM:188:VAL:HG22	2.38	0.44
1:CZ:62:ARG:HA	1:CZ:200:LEU:HD23	1.99	0.44
1:CN:130:ASP:OD2	1:CN:176:ARG:NH2	2.51	0.44
1:CB:118:ASN:HA	1:BO:116:PRO:CB	150.76	0.44
1:AW:64:SER:OG	1:AW:80:VAL:HG21	2.17	0.44
1:AH:281:HIS:ND1	1:AH:301:TRP:HB3	2.33	0.44
1:BP:281:HIS:CE1	1:BP:301:TRP:HB3	2.53	0.44
1:BD:99:PHE:HA	1:BD:209:VAL:O	2.18	0.44
1:AK:103:ALA:HB2	1:AK:166:LEU:HA	1.99	0.44
1:CB:202:ARG:HH12	1:CF:46:THR:HB	1.83	0.44
1:AZ:85:VAL:HG22	1:AZ:86:PRO:HD2	2.00	0.44
1:AY:224:THR:HG22	1:AY:329:THR:N	2.33	0.44
1:BX:260:ASP:HA	1:AX:261:ARG:NH2	2.33	0.44
1:CG:250:ILE:HG22	1:CG:250:ILE:O	2.17	0.44
1:CO:78:VAL:O	1:CO:78:VAL:HG13	2.17	0.44
1:CX:78:VAL:O	1:CX:78:VAL:HG13	2.17	0.44
1:BE:250:ILE:O	1:BE:250:ILE:HG22	2.17	0.44
1:CY:138:PHE:C	1:CY:138:PHE:CD1	2.92	0.44
1:CI:77:TYR:C	1:CI:77:TYR:CD1	2.90	0.44
1:BD:184:ILE:N	1:BD:184:ILE:HD13	2.33	0.44
1:AW:137:THR:HG23	1:AW:140:ALA:CB	2.48	0.44
1:BM:228:LEU:HD13	1:BM:238:PHE:CD2	2.53	0.44
1:AD:298:TRP:HE1	1:AD:312:VAL:HA	1.83	0.43
1:AB:298:TRP:O	1:AB:310:ASP:O	2.38	0.43
1:CS:103:ALA:O	1:CS:205:VAL:HG23	2.17	0.43
1:AV:314:TYR:HE1	1:AV:316:SER:HG	1.64	0.43
1:CU:99:PHE:HB3	1:CU:209:VAL:O	2.18	0.43
1:AK:314:TYR:CD1	1:AK:314:TYR:C	2.91	0.43
1:AT:63:ILE:CD1	1:AT:89:LEU:HD21	2.48	0.43
1:AJ:63:ILE:CD1	1:AJ:89:LEU:HD21	2.48	0.43
1:BB:163:THR:O	1:BB:165:THR:HG22	2.23	0.43
1:AM:98:ILE:HG22	1:AM:99:PHE:CD2	2.53	0.43
1:BK:123:TYR:N	1:BK:188:VAL:HG22	2.32	0.43
1:CH:63:ILE:HD12	1:CH:88:LEU:CG	2.45	0.43
1:AC:80:VAL:HG12	1:AC:185:LEU:HB3	2.10	0.43
1:CD:85:VAL:O	1:CD:86:PRO:C	2.57	0.43
1:AU:281:HIS:ND1	1:AU:301:TRP:HB3	2.33	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AN:80:VAL:HG13	1:AN:185:LEU:HB3	1.99	0.43
1:CW:69:PRO:O	1:CW:72:THR:OG1	2.25	0.43
1:CM:130:ASP:OD2	1:CM:176:ARG:NH2	2.50	0.43
1:BA:99:PHE:HA	1:BA:209:VAL:O	2.19	0.43
1:BC:85:VAL:CG2	1:BC:86:PRO:HD2	2.52	0.43
1:AJ:103:ALA:HB2	1:AJ:166:LEU:HA	2.00	0.43
1:CT:62:ARG:HA	1:CT:200:LEU:HD23	1.99	0.43
1:BI:99:PHE:HA	1:BI:209:VAL:O	2.18	0.43
1:AO:226:GLY:N	1:AO:243:LEU:O	2.50	0.43
1:AP:137:THR:HG23	1:AP:140:ALA:CB	2.47	0.43
1:CT:124:VAL:O	1:CT:124:VAL:HG13	2.18	0.43
1:CC:78:VAL:HG13	1:CC:78:VAL:O	2.18	0.43
1:CL:78:VAL:HG13	1:CL:78:VAL:O	2.18	0.43
1:CU:77:TYR:CD1	1:CU:77:TYR:C	2.90	0.43
1:CM:77:TYR:CD1	1:CM:77:TYR:C	2.90	0.43
1:BN:250:ILE:HG22	1:BN:250:ILE:O	2.18	0.43
1:BB:228:LEU:HD13	1:BB:238:PHE:CD2	2.56	0.43
1:BZ:260:ASP:HA	1:AZ:261:ARG:NH2	2.33	0.43
1:AA:256:VAL:HB	1:AA:335:ASP:HB3	2.00	0.43
1:BF:205:VAL:HG22	1:BF:206:ARG:N	2.33	0.43
1:AP:302:ASP:OD2	1:AP:305:ASN:CB	2.59	0.43
1:CX:81:ASP:OD1	1:CX:81:ASP:C	2.56	0.43
1:CW:81:ASP:HA	1:CW:184:ILE:HG22	1.99	0.43
1:CV:81:ASP:HA	1:CV:184:ILE:HG22	1.99	0.43
1:BB:283:LYS:HG2	1:BB:285:PHE:CE1	2.54	0.43
1:BD:98:ILE:CG2	1:AW:91:ARG:CZ	2.97	0.43
1:CT:80:VAL:HG22	1:CT:81:ASP:N	2.32	0.43
1:CH:122:GLY:O	1:CH:188:VAL:CB	2.65	0.43
1:CO:99:PHE:CB	1:CO:209:VAL:O	2.65	0.43
1:CS:123:TYR:HA	1:CS:188:VAL:HG23	1.99	0.43
1:CT:99:PHE:CD2	1:CT:207:LEU:HB3	2.53	0.43
1:CM:99:PHE:HB3	1:CM:209:VAL:O	2.19	0.43
1:BU:163:THR:O	1:BU:165:THR:HG22	2.17	0.43
1:CF:79:VAL:HG13	1:CF:80:VAL:HG12	1.99	0.43
1:BM:123:TYR:HB2	1:BM:185:LEU:CD1	2.48	0.43
1:CX:112:GLN:NE2	1:CX:155:SER:OG	2.51	0.43
1:BF:111:ILE:CG2	1:BF:112:GLN:N	2.82	0.43
1:CP:62:ARG:HA	1:CP:200:LEU:HD23	2.00	0.43
1:CB:63:ILE:HD12	1:CB:88:LEU:CD1	2.50	0.43
1:CN:63:ILE:HD12	1:CN:88:LEU:CD1	2.47	0.43
1:CD:113:PRO:HA	1:CD:197:VAL:HA	2.01	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CL:199:VAL:CG1	1:CL:199:VAL:O	2.65	0.43
1:AK:109:PHE:HB2	1:AK:158:VAL:HG12	1.99	0.43
1:CC:72:THR:O	1:CC:191:ASN:OD1	2.36	0.43
1:AQ:80:VAL:HG12	1:AQ:185:LEU:HB3	2.00	0.43
1:AX:281:HIS:ND1	1:AX:301:TRP:HB3	2.33	0.43
1:BA:281:HIS:CE1	1:BA:301:TRP:HB3	2.56	0.43
1:AG:64:SER:OG	1:AG:80:VAL:HG21	2.18	0.43
1:AV:281:HIS:ND1	1:AV:301:TRP:HB3	2.33	0.43
1:AL:268:SER:CB	1:AL:273:ASP:O	2.65	0.43
1:CA:60:MET:CE	1:CA:202:ARG:HB3	2.48	0.43
1:BV:232:SER:HB3	1:BV:242:LEU:HD11	2.00	0.43
1:BP:205:VAL:HG22	1:BP:206:ARG:N	2.33	0.43
1:AQ:224:THR:HG22	1:AQ:329:THR:N	2.33	0.43
1:BW:246:THR:N	1:BW:247:PRO:CD	2.81	0.43
1:BO:234:SER:HB3	1:BO:237:ASP:OD1	2.18	0.43
1:AD:288:ASN:O	1:AD:289:ALA:C	2.56	0.43
1:CH:119:THR:O	1:CH:120:GLY:C	2.56	0.43
1:CO:278:VAL:O	1:CO:278:VAL:HG13	2.19	0.43
1:CZ:250:ILE:O	1:CZ:250:ILE:HG22	2.17	0.43
1:CY:119:THR:HG22	1:CY:119:THR:O	2.18	0.43
1:CZ:77:TYR:C	1:CZ:77:TYR:CD1	2.90	0.43
1:BF:250:ILE:O	1:BF:250:ILE:HG22	2.17	0.43
1:BK:124:VAL:HG11	1:BK:138:PHE:CD2	2.53	0.43
1:AJ:122:GLY:C	1:AJ:188:VAL:HG22	2.38	0.43
1:AC:308:PHE:CE2	1:AC:310:ASP:HA	2.53	0.43
1:AG:298:TRP:O	1:AG:310:ASP:O	2.37	0.43
1:AE:298:TRP:O	1:AE:310:ASP:O	2.36	0.43
1:AX:253:ASP:CG	1:AX:285:PHE:CA	2.79	0.43
1:AU:302:ASP:OD2	1:AU:305:ASN:CB	2.61	0.43
1:CY:81:ASP:C	1:CY:81:ASP:OD1	2.57	0.43
1:BD:210:PRO:HB3	1:AG:91:ARG:NH2	90.40	0.43
1:AG:263:LEU:HB3	1:AG:279:TYR:O	2.19	0.43
1:AX:263:LEU:HB3	1:AX:279:TYR:O	2.18	0.43
1:CK:123:TYR:HB2	1:CK:185:LEU:CD2	2.49	0.43
1:AA:314:TYR:CD1	1:AA:314:TYR:C	2.92	0.43
1:CF:99:PHE:HB3	1:CF:209:VAL:O	2.17	0.43
1:CE:317:ASP:HB3	1:CE:319:GLN:NE2	2.34	0.43
1:AR:63:ILE:HG23	1:AR:88:LEU:HD11	2.00	0.43
1:AL:61:SER:CB	1:AL:90:PRO:HD2	2.38	0.43
1:AC:162:TYR:CE2	1:AC:164:ARG:HG2	2.53	0.43
1:CV:62:ARG:HA	1:CV:200:LEU:HD23	2.01	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CW:62:ARG:HA	1:CW:200:LEU:HD23	1.99	0.43
1:CL:130:ASP:OD2	1:CL:176:ARG:NH2	2.50	0.43
1:AP:64:SER:OG	1:AP:80:VAL:HG21	2.18	0.43
1:AK:122:GLY:C	1:AK:188:VAL:HG22	2.39	0.43
1:BB:260:ASP:HA	1:AB:261:ARG:NH2	2.34	0.43
1:CD:133:ASP:O	1:CD:182:ARG:NH2	2.52	0.43
1:BO:225:GLN:HG3	1:BO:244:GLY:O	2.18	0.43
1:AK:137:THR:HG23	1:AK:140:ALA:CB	2.49	0.43
1:CA:102:TYR:HD2	1:CA:205:VAL:HG21	1.83	0.43
1:CO:121:GLY:C	1:CO:152:TRP:CD1	2.92	0.43
1:AI:246:THR:N	1:AI:247:PRO:CD	2.81	0.43
1:BI:232:SER:HB3	1:BI:242:LEU:HD11	1.99	0.43
1:BO:250:ILE:HG22	1:BO:250:ILE:O	2.17	0.43
1:BK:109:PHE:HB2	1:BK:158:VAL:CG1	2.49	0.43
1:BL:246:THR:N	1:BL:247:PRO:CD	2.81	0.43
1:AA:308:PHE:CE2	1:AA:310:ASP:HA	2.53	0.43
1:AS:298:TRP:HE1	1:AS:312:VAL:HA	1.84	0.43
1:AS:298:TRP:NE1	1:AS:312:VAL:HA	2.33	0.43
1:CO:81:ASP:OD2	1:CO:136:HIS:NE2	2.44	0.43
1:CC:81:ASP:OD2	1:CC:136:HIS:NE2	2.47	0.43
1:CT:81:ASP:OD2	1:CT:136:HIS:NE2	2.46	0.43
1:BC:98:ILE:HG22	1:AY:91:ARG:HH21	1.84	0.43
1:AB:91:ARG:NH2	1:BY:210:PRO:HB3	2.34	0.43
1:CD:103:ALA:HB2	1:CD:166:LEU:HB3	2.00	0.43
1:BE:100:GLN:NE2	1:BE:211:SER:CB	2.81	0.43
1:AG:63:ILE:CD1	1:AG:89:LEU:HD21	2.49	0.43
1:AL:314:TYR:HE1	1:AL:316:SER:HG	1.65	0.43
1:BA:130:ASP:HB3	1:BA:133:ASP:HB2	2.03	0.43
1:CJ:80:VAL:HG11	1:CJ:185:LEU:HB2	2.00	0.43
1:CY:99:PHE:CD2	1:CY:207:LEU:HB3	2.53	0.43
1:AD:98:ILE:CG2	1:BF:91:ARG:NH1	2.81	0.43
1:BZ:123:TYR:N	1:BZ:188:VAL:HG22	2.34	0.43
1:BB:142:GLN:NE2	1:CF:62:ARG:H	2.17	0.43
1:CV:63:ILE:HD12	1:CV:88:LEU:CD1	2.49	0.43
1:BP:123:TYR:HB2	1:BP:185:LEU:CD1	2.48	0.43
1:CK:72:THR:O	1:CK:191:ASN:OD1	2.36	0.43
1:AH:122:GLY:C	1:AH:188:VAL:HG22	2.39	0.43
1:AB:109:PHE:CE2	1:AB:127:PHE:CD1	3.06	0.43
1:AR:80:VAL:HG13	1:AR:185:LEU:HB3	1.99	0.43
1:CK:109:PHE:HB2	1:CK:158:VAL:HG12	2.00	0.43
1:BJ:281:HIS:CE1	1:BJ:301:TRP:HB3	2.53	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BL:281:HIS:CE1	1:BL:301:TRP:HB3	2.53	0.43
1:BB:184:ILE:HD13	1:BB:184:ILE:N	2.37	0.43
1:BA:128:LEU:HD12	1:BA:184:ILE:HD11	2.03	0.43
1:CV:264:SER:HB2	1:CV:324:LEU:HD22	2.00	0.43
1:AO:100:GLN:HA	1:AO:169:THR:OG1	2.18	0.43
1:AS:137:THR:HG23	1:AS:140:ALA:CB	2.49	0.43
1:CT:77:TYR:CD1	1:CT:77:TYR:C	2.90	0.43
1:CH:45:VAL:O	1:CH:45:VAL:HG13	2.19	0.43
1:CL:119:THR:O	1:CL:120:GLY:C	2.57	0.43
1:CC:214:ASN:HA	1:CC:215:PRO:HD3	1.85	0.43
1:AX:298:TRP:NE1	1:AX:312:VAL:HA	2.33	0.43
1:AG:308:PHE:CE2	1:AG:310:ASP:HA	2.53	0.43
1:AP:298:TRP:O	1:AP:310:ASP:O	2.36	0.43
1:CW:141:LEU:O	1:CW:144:THR:N	2.48	0.43
1:CB:123:TYR:HB2	1:CB:185:LEU:CD2	2.58	0.43
1:CL:80:VAL:HG11	1:CL:185:LEU:CB	2.49	0.43
1:CD:186:LEU:N	1:CD:186:LEU:HD23	2.34	0.43
1:CU:79:VAL:HG13	1:CU:80:VAL:HG12	2.00	0.43
1:AB:91:ARG:HH21	1:BY:98:ILE:HG22	1.83	0.43
1:BR:163:THR:O	1:BR:165:THR:HG22	2.18	0.43
1:AZ:63:ILE:CD1	1:AZ:89:LEU:HD21	2.47	0.43
1:BC:142:GLN:NE2	1:CJ:62:ARG:H	2.17	0.43
1:CF:89:LEU:HD13	1:CF:203:TRP:CG	2.52	0.43
1:AA:69:PRO:C	1:AA:72:THR:HG1	2.21	0.43
1:AD:116:PRO:HG2	1:AD:119:THR:OG1	2.19	0.43
1:AW:116:PRO:HG2	1:AW:119:THR:OG1	2.19	0.43
1:BH:142:GLN:HB2	1:CH:48:PHE:HE1	1.83	0.43
1:CV:63:ILE:HD12	1:CV:88:LEU:CG	2.46	0.43
1:CK:39:VAL:O	1:CL:117:ALA:N	2.30	0.43
1:CH:89:LEU:HD13	1:CH:203:TRP:CG	2.54	0.43
1:CC:62:ARG:H	1:BX:142:GLN:NE2	217.33	0.43
1:AH:64:SER:OG	1:AH:80:VAL:HG21	2.19	0.43
1:CL:163:THR:HG23	1:CL:164:ARG:N	2.33	0.43
1:AO:281:HIS:ND1	1:AO:301:TRP:HB3	2.33	0.43
1:BO:281:HIS:CE1	1:BO:301:TRP:HB3	2.54	0.43
1:AS:281:HIS:ND1	1:AS:301:TRP:HB3	2.34	0.43
1:BB:85:VAL:CG2	1:BB:86:PRO:HD2	2.50	0.43
1:CI:133:ASP:O	1:CI:182:ARG:NH2	2.52	0.43
1:CX:102:TYR:HD2	1:CX:205:VAL:HG21	1.82	0.43
1:BK:276:ARG:O	1:AK:276:ARG:NH2	2.51	0.43
1:BF:234:SER:HB3	1:BF:237:ASP:OD1	2.19	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AT:234:SER:HB3	1:AT:237:ASP:O	2.19	0.43
1:BH:300:ILE:HG23	1:AH:323:ILE:CD1	2.49	0.43
1:CF:264:SER:HB2	1:CF:324:LEU:HD22	1.99	0.43
1:CU:133:ASP:O	1:CU:182:ARG:NH2	2.52	0.43
1:CS:214:ASN:HA	1:CS:215:PRO:HD3	1.85	0.43
1:AE:238:PHE:CZ	1:AE:296:PHE:HB2	2.54	0.43
1:BZ:232:SER:HB3	1:BZ:242:LEU:HD11	2.00	0.43
1:CA:119:THR:O	1:CA:119:THR:HG22	2.25	0.43
1:CS:138:PHE:C	1:CS:138:PHE:CD1	2.91	0.43
1:CE:77:TYR:CD1	1:CE:77:TYR:C	2.90	0.43
1:AC:274:VAL:HG13	1:AC:274:VAL:O	2.18	0.43
1:BB:300:ILE:HG23	1:AB:323:ILE:CD1	2.49	0.43
1:AM:234:SER:HB3	1:AM:237:ASP:O	2.18	0.43
1:AH:238:PHE:CZ	1:AH:296:PHE:HB2	2.53	0.43
1:AI:308:PHE:CE2	1:AI:310:ASP:HA	2.54	0.43
1:AB:298:TRP:HE1	1:AB:312:VAL:HA	1.83	0.43
1:AU:298:TRP:NE1	1:AU:312:VAL:HA	2.33	0.43
1:AL:298:TRP:HE1	1:AL:312:VAL:HA	1.84	0.43
1:AH:298:TRP:O	1:AH:310:ASP:O	2.36	0.43
1:AW:298:TRP:O	1:AW:310:ASP:O	2.36	0.43
1:AQ:302:ASP:OD2	1:AQ:305:ASN:CB	2.61	0.43
1:CI:79:VAL:HG13	1:CI:80:VAL:HG12	2.00	0.43
1:AD:91:ARG:HH21	1:BF:98:ILE:HG22	1.83	0.43
1:AL:143:ALA:HB1	1:AU:91:ARG:HD2	2.01	0.43
1:CQ:79:VAL:HG13	1:CQ:80:VAL:HG12	2.01	0.43
1:AJ:91:ARG:NH2	1:BR:98:ILE:HG22	2.34	0.43
1:CH:80:VAL:HG11	1:CH:185:LEU:CB	2.49	0.43
1:AI:63:ILE:HG23	1:AI:88:LEU:HD11	2.01	0.43
1:AM:89:LEU:HD21	1:AM:201:CYS:HB3	2.01	0.43
1:AZ:63:ILE:HG23	1:AZ:88:LEU:HD11	2.01	0.43
1:AK:98:ILE:HG22	1:AK:99:PHE:CD2	2.54	0.43
1:AT:106:THR:O	1:AT:203:TRP:HA	2.18	0.43
1:BM:150:ALA:HB2	1:BM:156:ARG:HD3	2.00	0.43
1:CW:89:LEU:HD13	1:CW:203:TRP:CG	2.54	0.43
1:CS:89:LEU:HD13	1:CS:203:TRP:CG	2.54	0.43
1:BG:74:THR:HA	1:BG:190:ASN:ND2	2.34	0.43
1:CW:130:ASP:OD2	1:CW:176:ARG:NH2	2.52	0.43
1:AO:109:PHE:HB2	1:AO:158:VAL:HG12	2.00	0.43
1:CY:130:ASP:OD2	1:CY:176:ARG:NH2	2.50	0.43
1:BI:281:HIS:CE1	1:BI:301:TRP:HB3	2.54	0.43
1:CB:85:VAL:O	1:CB:86:PRO:C	2.57	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BW:281:HIS:CE1	1:BW:301:TRP:HB3	2.53	0.43
1:CB:121:GLY:C	1:CB:152:TRP:CD1	2.92	0.43
1:CM:133:ASP:O	1:CM:182:ARG:NH2	2.50	0.43
1:BF:124:VAL:HG11	1:BF:138:PHE:CD2	2.54	0.43
1:AI:226:GLY:N	1:AI:243:LEU:O	2.50	0.43
1:CL:77:TYR:C	1:CL:77:TYR:CD1	2.89	0.43
1:CL:138:PHE:C	1:CL:138:PHE:CD1	2.92	0.43
1:CP:54:ASP:N	1:CP:54:ASP:OD1	2.51	0.43
1:CF:77:TYR:CD1	1:CF:77:TYR:C	2.91	0.43
1:BJ:126:GLY:HA3	1:BJ:141:LEU:HD22	2.00	0.43
1:CK:54:ASP:OD1	1:CK:54:ASP:N	2.51	0.43
1:BS:225:GLN:HG3	1:BS:244:GLY:O	2.18	0.43
1:CH:133:ASP:O	1:CH:182:ARG:NH2	2.51	0.43
1:AM:298:TRP:O	1:AM:310:ASP:O	2.37	0.43
1:AM:298:TRP:HE1	1:AM:312:VAL:HA	1.83	0.43
1:AK:253:ASP:CG	1:AK:285:PHE:CA	2.76	0.43
1:CI:81:ASP:C	1:CI:81:ASP:OD1	2.57	0.43
1:CI:81:ASP:HA	1:CI:184:ILE:HG22	2.00	0.43
1:CD:122:GLY:O	1:CD:188:VAL:CB	2.65	0.43
1:AT:263:LEU:HB3	1:AT:279:TYR:O	2.19	0.43
1:AE:91:ARG:CZ	1:BM:98:ILE:HG22	2.48	0.43
1:BY:100:GLN:NE2	1:BY:211:SER:CB	2.81	0.43
1:AG:89:LEU:HD21	1:AG:201:CYS:HB3	2.00	0.43
1:AN:162:TYR:CE2	1:AN:164:ARG:HG2	2.53	0.43
1:BC:111:ILE:HG22	1:BC:155:SER:HA	2.01	0.43
1:BO:111:ILE:HG22	1:BO:155:SER:HA	2.00	0.43
1:BT:123:TYR:N	1:BT:188:VAL:HG22	2.33	0.43
1:CB:155:SER:O	1:CB:156:ARG:HD3	2.18	0.43
1:AF:69:PRO:C	1:AF:72:THR:HG1	2.21	0.43
1:CA:58:SER:HA	1:CA:203:TRP:CE3	2.58	0.43
1:AZ:64:SER:OG	1:AZ:80:VAL:HG21	2.19	0.43
1:CB:45:VAL:O	1:CB:45:VAL:HG13	2.19	0.43
1:CN:89:LEU:HD13	1:CN:203:TRP:CG	2.54	0.43
1:AC:122:GLY:C	1:AC:188:VAL:HG22	2.39	0.43
1:CB:113:PRO:HA	1:CB:197:VAL:HA	2.00	0.43
1:CN:111:ILE:HD11	1:CN:125:ALA:HB3	2.01	0.43
1:CB:46:THR:HB	1:CF:202:ARG:HH12	1.84	0.43
1:AM:264:SER:OG	1:AM:276:ARG:NH1	2.48	0.43
1:BM:184:ILE:HD13	1:BM:184:ILE:N	2.34	0.43
1:AR:57:LEU:O	1:AR:204:SER:HA	2.18	0.43
1:BE:260:ASP:HA	1:AE:261:ARG:NH2	2.34	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AO:256:VAL:HB	1:AO:335:ASP:HB3	2.01	0.43
1:AC:238:PHE:CZ	1:AC:296:PHE:HB2	2.54	0.43
1:AZ:234:SER:HB3	1:AZ:237:ASP:O	2.19	0.43
1:BY:234:SER:HB3	1:BY:237:ASP:OD1	2.19	0.43
1:BP:260:ASP:HA	1:AP:261:ARG:NH2	2.34	0.43
1:CV:54:ASP:OD1	1:CV:54:ASP:N	2.51	0.43
1:CG:78:VAL:HG13	1:CG:78:VAL:O	2.17	0.43
1:AZ:183:LEU:HG	1:AZ:184:ILE:N	2.33	0.43
1:BJ:225:GLN:HG3	1:BJ:244:GLY:O	2.18	0.43
1:BY:136:HIS:O	1:BY:186:LEU:HD11	2.19	0.43
1:CJ:81:ASP:OD1	1:CJ:81:ASP:C	2.57	0.43
1:CE:81:ASP:C	1:CE:81:ASP:OD1	2.57	0.43
1:AW:263:LEU:HB3	1:AW:279:TYR:O	2.19	0.43
1:BH:100:GLN:NE2	1:BH:211:SER:CB	2.82	0.43
1:CO:123:TYR:HA	1:CO:188:VAL:HG23	2.00	0.43
1:CK:123:TYR:HB2	1:CK:185:LEU:HD21	2.00	0.43
1:CV:79:VAL:HG13	1:CV:80:VAL:HG12	1.99	0.43
1:CZ:99:PHE:CD2	1:CZ:207:LEU:HB3	2.54	0.43
1:CX:98:ILE:HG13	1:CX:99:PHE:CD2	2.54	0.43
1:AE:63:ILE:HG23	1:AE:88:LEU:HD11	1.99	0.43
1:BK:111:ILE:HG22	1:BK:155:SER:HA	1.99	0.43
1:CD:155:SER:O	1:CD:156:ARG:HD3	2.19	0.43
1:AH:69:PRO:C	1:AH:72:THR:HG1	2.21	0.43
1:AI:124:VAL:HG11	1:AI:138:PHE:CD1	2.54	0.43
1:CD:36:ASP:HB3	1:CD:38:PRO:CB	6.43	0.43
1:CD:163:THR:HG23	1:CD:164:ARG:N	2.40	0.43
1:CU:111:ILE:HD11	1:CU:125:ALA:HB3	1.99	0.43
1:BT:99:PHE:HA	1:BT:209:VAL:O	2.19	0.43
1:AN:103:ALA:HB2	1:AN:166:LEU:HA	2.01	0.43
1:BO:124:VAL:HG11	1:BO:138:PHE:CD2	2.54	0.43
1:AC:224:THR:HG22	1:AC:329:THR:N	2.34	0.43
1:CP:46:THR:HB	1:CQ:202:ARG:HH12	1.84	0.43
1:AN:238:PHE:CZ	1:AN:296:PHE:HB2	2.53	0.43
1:AY:88:LEU:O	1:AY:88:LEU:HD13	2.19	0.43
1:CW:77:TYR:CD1	1:CW:77:TYR:C	2.91	0.43
1:CK:250:ILE:HG22	1:CK:250:ILE:O	2.18	0.43
1:CQ:54:ASP:OD1	1:CQ:54:ASP:N	2.51	0.43
1:CP:77:TYR:C	1:CP:77:TYR:CD1	2.89	0.43
1:CY:78:VAL:HG13	1:CY:78:VAL:O	2.19	0.43
1:BW:184:ILE:HD13	1:BW:184:ILE:N	2.34	0.43
1:CT:54:ASP:OD1	1:CT:54:ASP:N	2.51	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AM:224:THR:HG22	1:AM:329:THR:N	2.34	0.43
1:BA:246:THR:N	1:BA:247:PRO:CD	2.83	0.43
1:CC:102:TYR:HD2	1:CC:205:VAL:HG21	1.85	0.43
1:BC:225:GLN:HG3	1:BC:244:GLY:O	2.21	0.43
1:BJ:161:GLN:NE2	1:CJ:210:PRO:HD2	2.32	0.43
1:BK:184:ILE:N	1:BK:184:ILE:HD13	2.33	0.43
1:AI:298:TRP:HE1	1:AI:312:VAL:HA	1.84	0.43
1:AB:308:PHE:CE2	1:AB:310:ASP:HA	2.54	0.43
1:AO:298:TRP:HE1	1:AO:312:VAL:HA	1.83	0.43
1:AM:308:PHE:CE2	1:AM:310:ASP:HA	2.53	0.43
1:AE:308:PHE:CE2	1:AE:310:ASP:HA	2.54	0.43
1:AD:302:ASP:OD2	1:AD:305:ASN:CB	2.62	0.43
1:CH:81:ASP:OD1	1:CH:81:ASP:C	2.57	0.43
1:CR:103:ALA:HB2	1:CR:166:LEU:HB3	2.01	0.43
1:CI:99:PHE:HB3	1:CI:209:VAL:O	2.17	0.43
1:AJ:314:TYR:C	1:AJ:314:TYR:CD1	2.91	0.43
1:CG:99:PHE:CD2	1:CG:207:LEU:HB3	2.54	0.43
1:BI:142:GLN:HB2	1:CI:48:PHE:CE1	2.53	0.43
1:CZ:45:VAL:O	1:CZ:45:VAL:HG13	2.19	0.43
1:CD:45:VAL:HG23	1:CI:200:LEU:HD13	1.99	0.43
1:BU:74:THR:HA	1:BU:190:ASN:HD22	1.83	0.43
1:CQ:158:VAL:O	1:CQ:158:VAL:HG13	2.18	0.43
1:CT:111:ILE:HD11	1:CT:125:ALA:HB3	2.00	0.43
1:BS:281:HIS:CE1	1:BS:301:TRP:HB3	2.54	0.43
1:CD:202:ARG:HH12	1:CW:46:THR:HB	106.75	0.43
1:AV:100:GLN:HA	1:AV:169:THR:OG1	2.19	0.43
1:BO:184:ILE:HD13	1:BO:184:ILE:N	2.34	0.43
1:CW:214:ASN:HA	1:CW:215:PRO:HD3	1.82	0.43
1:CC:264:SER:HB2	1:CC:324:LEU:HD22	2.00	0.43
1:AH:226:GLY:N	1:AH:243:LEU:O	2.49	0.43
1:BT:205:VAL:HG22	1:BT:206:ARG:N	2.33	0.43
1:CU:54:ASP:N	1:CU:54:ASP:OD1	2.51	0.43
1:CR:250:ILE:O	1:CR:250:ILE:HG22	2.19	0.43
1:CC:138:PHE:CD1	1:CC:138:PHE:C	2.96	0.43
1:CU:138:PHE:CD1	1:CU:138:PHE:C	2.92	0.43
1:CE:138:PHE:CD1	1:CE:138:PHE:C	2.92	0.43
1:CO:264:SER:HB2	1:CO:324:LEU:HD22	2.01	0.43
1:BK:225:GLN:HG3	1:BK:244:GLY:O	2.18	0.43
1:BS:228:LEU:HD13	1:BS:238:PHE:CD2	2.54	0.43
1:BV:300:ILE:HD13	1:AV:321:ARG:HD2	2.01	0.43
1:AU:100:GLN:HA	1:AU:169:THR:OG1	2.19	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AQ:298:TRP:O	1:AQ:310:ASP:O	2.36	0.43
1:AG:298:TRP:NE1	1:AG:312:VAL:HA	2.33	0.43
1:AR:298:TRP:O	1:AR:310:ASP:O	2.36	0.43
1:AO:302:ASP:OD2	1:AO:305:ASN:CB	2.63	0.43
1:CZ:80:VAL:HG13	1:CZ:185:LEU:N	2.34	0.43
1:CG:81:ASP:OD2	1:CG:136:HIS:NE2	2.44	0.43
1:AN:91:ARG:HD2	1:AP:143:ALA:HB1	1.99	0.43
1:AB:91:ARG:NH2	1:BO:98:ILE:HG22	132.07	0.43
1:AV:314:TYR:C	1:AV:314:TYR:CD1	2.92	0.43
1:AE:314:TYR:HE1	1:AE:316:SER:HG	1.61	0.43
1:AT:314:TYR:CD1	1:AT:314:TYR:C	2.93	0.43
1:CF:317:ASP:HB3	1:CF:319:GLN:NE2	2.33	0.43
1:AU:61:SER:HB2	1:AU:89:LEU:HD22	2.00	0.43
1:AX:63:ILE:CD1	1:AX:89:LEU:HD21	2.49	0.43
1:AS:80:VAL:HG13	1:AS:185:LEU:HB3	2.00	0.43
1:AV:98:ILE:HG22	1:AV:99:PHE:CD2	2.53	0.43
1:CX:155:SER:O	1:CX:156:ARG:HD3	2.18	0.43
1:BB:117:ALA:HB2	1:CK:117:ALA:HB1	2.01	0.43
1:CJ:89:LEU:HD13	1:CJ:203:TRP:CG	2.54	0.43
1:CB:163:THR:HG23	1:CB:164:ARG:N	2.37	0.43
1:CD:69:PRO:O	1:CD:72:THR:OG1	2.25	0.43
1:CA:72:THR:O	1:CA:191:ASN:OD1	2.40	0.43
1:BX:281:HIS:CE1	1:BX:301:TRP:HB3	2.54	0.43
1:BA:85:VAL:CG2	1:BA:86:PRO:HD2	2.51	0.43
1:BU:99:PHE:HA	1:BU:209:VAL:O	2.19	0.43
1:BJ:86:PRO:HB3	1:BJ:92:LEU:HD22	2.01	0.43
1:CY:250:ILE:O	1:CY:250:ILE:HG22	2.18	0.43
1:BP:184:ILE:HD13	1:BP:184:ILE:N	2.34	0.43
1:CV:77:TYR:C	1:CV:77:TYR:CD1	2.89	0.43
1:CI:54:ASP:N	1:CI:54:ASP:OD1	2.51	0.43
1:CR:77:TYR:C	1:CR:77:TYR:CD1	2.90	0.43
1:BI:260:ASP:HA	1:AI:261:ARG:NH2	2.33	0.43
1:CL:102:TYR:HD2	1:CL:205:VAL:HG21	1.84	0.43
1:CU:214:ASN:HA	1:CU:215:PRO:HD3	1.84	0.43
1:AD:298:TRP:O	1:AD:310:ASP:O	2.36	0.42
1:AS:298:TRP:NE1	1:AS:312:VAL:CB	2.79	0.42
1:AS:298:TRP:O	1:AS:310:ASP:O	2.36	0.42
1:AV:298:TRP:O	1:AV:310:ASP:O	2.37	0.42
1:CR:81:ASP:OD1	1:CR:81:ASP:C	2.58	0.42
1:AN:302:ASP:C	1:AN:305:ASN:HD21	2.23	0.42
1:CM:81:ASP:C	1:CM:81:ASP:OD1	2.57	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CL:81:ASP:C	1:CL:81:ASP:OD1	2.58	0.42
1:CG:81:ASP:C	1:CG:81:ASP:OD1	2.58	0.42
1:CE:79:VAL:HG13	1:CE:80:VAL:HG12	2.00	0.42
1:AN:91:ARG:NH2	1:BP:98:ILE:CG2	2.82	0.42
1:BC:98:ILE:CG2	1:AY:91:ARG:CZ	2.97	0.42
1:CA:80:VAL:HG11	1:CA:185:LEU:CB	2.49	0.42
1:CQ:103:ALA:HB2	1:CQ:166:LEU:HB3	2.00	0.42
1:CH:123:TYR:HB2	1:CH:185:LEU:HD21	2.00	0.42
1:CF:103:ALA:HB2	1:CF:166:LEU:HB3	2.01	0.42
1:AE:314:TYR:CD1	1:AE:314:TYR:C	2.93	0.42
1:AJ:63:ILE:HG23	1:AJ:88:LEU:HD11	2.01	0.42
1:BV:130:ASP:HB3	1:BV:133:ASP:HB2	2.01	0.42
1:BA:111:ILE:CG2	1:BA:112:GLN:N	2.82	0.42
1:CK:89:LEU:HD13	1:CK:203:TRP:CG	2.54	0.42
1:AY:69:PRO:C	1:AY:72:THR:HG1	2.21	0.42
1:AK:116:PRO:HG2	1:AK:119:THR:OG1	2.19	0.42
1:CQ:57:LEU:HD23	1:CQ:203:TRP:CH2	2.53	0.42
1:AD:188:VAL:HG23	1:AW:114:MET:SD	2.58	0.42
1:AA:109:PHE:HB2	1:AA:158:VAL:HG12	2.03	0.42
1:AM:109:PHE:CE2	1:AM:127:PHE:CD1	3.07	0.42
1:BV:281:HIS:CE1	1:BV:301:TRP:HB3	2.54	0.42
1:AL:122:GLY:C	1:AL:188:VAL:HG22	2.39	0.42
1:AO:264:SER:OG	1:AO:276:ARG:NH1	2.49	0.42
1:AT:264:SER:OG	1:AT:276:ARG:NH1	2.51	0.42
1:BK:128:LEU:HD12	1:BK:184:ILE:HD11	2.01	0.42
1:BE:234:SER:HB3	1:BE:237:ASP:OD1	2.19	0.42
1:BY:232:SER:HB3	1:BY:242:LEU:HD11	2.00	0.42
1:BR:136:HIS:O	1:BR:186:LEU:HD11	2.19	0.42
1:CK:128:LEU:HA	1:CK:129:PRO:HD3	1.91	0.42
1:CD:102:TYR:HD2	1:CD:205:VAL:HG21	1.84	0.42
1:CD:214:ASN:HA	1:CD:215:PRO:HD3	1.84	0.42
1:BM:321:ARG:HD2	1:CM:300:ILE:HD13	2.02	0.42
1:AN:308:PHE:CE2	1:AN:310:ASP:HA	2.54	0.42
1:AG:298:TRP:HE1	1:AG:312:VAL:HA	1.83	0.42
1:CB:122:GLY:O	1:CB:188:VAL:CB	2.67	0.42
1:CQ:123:TYR:HA	1:CQ:188:VAL:HG23	2.00	0.42
1:AC:314:TYR:CD1	1:AC:314:TYR:C	2.93	0.42
1:AT:63:ILE:HG23	1:AT:88:LEU:HD11	2.01	0.42
1:AE:89:LEU:HD21	1:AE:201:CYS:HB3	1.99	0.42
1:CW:99:PHE:CD2	1:CW:207:LEU:HB3	2.54	0.42
1:BJ:163:THR:O	1:BJ:165:THR:HG22	2.18	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BQ:123:TYR:N	1:BQ:188:VAL:HG22	2.34	0.42
1:BB:111:ILE:CG2	1:BB:112:GLN:N	2.82	0.42
1:CK:58:SER:HA	1:CK:203:TRP:CE3	2.54	0.42
1:AF:116:PRO:HG2	1:AF:119:THR:OG1	2.19	0.42
1:CV:57:LEU:HD23	1:CV:203:TRP:HH2	1.84	0.42
1:CN:58:SER:HB3	1:CN:204:SER:HB2	2.01	0.42
1:BB:253:ASP:CB	1:BB:286:ALA:HB2	2.49	0.42
1:AF:122:GLY:C	1:AF:188:VAL:HG22	2.40	0.42
1:CH:111:ILE:HD11	1:CH:125:ALA:HB3	2.01	0.42
1:CF:130:ASP:OD2	1:CF:176:ARG:NH2	2.52	0.42
1:CR:45:VAL:O	1:CR:45:VAL:HG13	2.19	0.42
1:BB:86:PRO:HB3	1:BB:92:LEU:HD22	2.01	0.42
1:BW:86:PRO:HB3	1:BW:92:LEU:HD22	2.00	0.42
1:BO:99:PHE:HA	1:BO:209:VAL:O	2.19	0.42
1:AG:264:SER:OG	1:AG:276:ARG:NH1	2.50	0.42
1:BF:300:ILE:HD13	1:AF:321:ARG:HD2	2.02	0.42
1:BT:128:LEU:HD12	1:BT:184:ILE:HD11	2.01	0.42
1:AO:238:PHE:CZ	1:AO:296:PHE:HB2	2.54	0.42
1:AX:137:THR:HG23	1:AX:140:ALA:CB	2.49	0.42
1:BB:136:HIS:O	1:BB:186:LEU:HD11	2.22	0.42
1:AP:234:SER:HB3	1:AP:237:ASP:O	2.19	0.42
1:CG:102:TYR:HD2	1:CG:205:VAL:HG21	1.84	0.42
1:BH:214:ASN:HD22	1:BH:215:PRO:HD2	1.83	0.42
1:CD:246:THR:N	1:CD:247:PRO:CD	2.88	0.42
1:BP:126:GLY:HA2	1:BP:158:VAL:HG21	2.01	0.42
1:BX:184:ILE:N	1:BX:184:ILE:HD13	2.34	0.42
1:CN:138:PHE:CD1	1:CN:138:PHE:C	2.93	0.42
1:CL:250:ILE:O	1:CL:250:ILE:HG22	2.18	0.42
1:CR:54:ASP:N	1:CR:54:ASP:OD1	2.52	0.42
1:CH:77:TYR:CD1	1:CH:77:TYR:C	2.93	0.42
1:BV:184:ILE:N	1:BV:184:ILE:HD13	2.33	0.42
1:CI:119:THR:HG22	1:CI:119:THR:O	2.19	0.42
1:CR:119:THR:O	1:CR:119:THR:HG22	2.19	0.42
1:AM:226:GLY:N	1:AM:243:LEU:O	2.51	0.42
1:AL:298:TRP:CG	1:AL:312:VAL:HG13	2.48	0.42
1:AZ:253:ASP:CG	1:AZ:285:PHE:CA	2.78	0.42
1:CM:123:TYR:HA	1:CM:188:VAL:HG23	2.01	0.42
1:CM:80:VAL:HG22	1:CM:81:ASP:N	2.34	0.42
1:CI:123:TYR:HB2	1:CI:185:LEU:CD2	2.50	0.42
1:CR:80:VAL:HG13	1:CR:185:LEU:N	2.34	0.42
1:CU:99:PHE:CD2	1:CU:207:LEU:HB3	2.54	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AS:314:TYR:CD1	1:AS:314:TYR:C	2.92	0.42
1:AN:314:TYR:C	1:AN:314:TYR:CD1	2.93	0.42
1:AF:314:TYR:C	1:AF:314:TYR:CD1	2.92	0.42
1:CU:317:ASP:HB3	1:CU:319:GLN:NE2	2.35	0.42
1:BK:123:TYR:HB2	1:BK:185:LEU:CD1	2.49	0.42
1:BB:123:TYR:N	1:BB:188:VAL:HG22	2.36	0.42
1:CB:34:ARG:CD	1:CL:43:SER:O	23.65	0.42
1:CJ:58:SER:HB3	1:CJ:204:SER:HB2	2.01	0.42
1:AO:122:GLY:C	1:AO:188:VAL:HG22	2.40	0.42
1:CZ:113:PRO:HA	1:CZ:197:VAL:HA	2.01	0.42
1:CH:113:PRO:HA	1:CH:197:VAL:HA	2.00	0.42
1:AO:64:SER:OG	1:AO:80:VAL:HG21	2.19	0.42
1:AF:281:HIS:ND1	1:AF:301:TRP:HB3	2.33	0.42
1:BB:116:PRO:HD3	1:CK:120:GLY:HA3	2.00	0.42
1:AM:281:HIS:ND1	1:AM:301:TRP:HB3	2.34	0.42
1:CQ:85:VAL:O	1:CQ:86:PRO:C	2.58	0.42
1:AN:109:PHE:CE2	1:AN:127:PHE:CD1	3.07	0.42
1:AW:103:ALA:HB2	1:AW:166:LEU:HA	2.00	0.42
1:BV:99:PHE:HA	1:BV:209:VAL:O	2.20	0.42
1:BQ:99:PHE:HA	1:BQ:209:VAL:O	2.19	0.42
1:BS:184:ILE:N	1:BS:184:ILE:HD13	2.34	0.42
1:AX:234:SER:HB3	1:AX:237:ASP:O	2.19	0.42
1:AB:238:PHE:CZ	1:AB:296:PHE:HB2	2.55	0.42
1:AC:57:LEU:O	1:AC:204:SER:HA	2.23	0.42
1:BI:184:ILE:N	1:BI:184:ILE:HD13	2.35	0.42
1:CV:124:VAL:O	1:CV:124:VAL:HG13	2.19	0.42
1:CQ:77:TYR:C	1:CQ:77:TYR:CD1	2.92	0.42
1:BS:260:ASP:HA	1:AS:261:ARG:NH2	2.34	0.42
1:BM:300:ILE:HG23	1:AM:323:ILE:CD1	2.50	0.42
1:AL:226:GLY:N	1:AL:243:LEU:O	2.46	0.42
1:AE:137:THR:HG23	1:AE:140:ALA:CB	2.49	0.42
1:AN:298:TRP:NE1	1:AN:312:VAL:HA	2.33	0.42
1:AX:308:PHE:CE2	1:AX:310:ASP:HA	2.54	0.42
1:AQ:127:PHE:O	1:AQ:144:THR:OG1	2.30	0.42
1:BS:89:LEU:HA	1:BS:90:PRO:HD3	1.93	0.42
1:BI:130:ASP:HB3	1:BI:133:ASP:HB2	2.00	0.42
1:AI:314:TYR:CD1	1:AI:314:TYR:C	2.92	0.42
1:AJ:314:TYR:CE1	1:AJ:316:SER:CA	2.88	0.42
1:AD:314:TYR:HE1	1:AD:316:SER:HG	1.64	0.42
1:CG:317:ASP:HB3	1:CG:319:GLN:NE2	2.34	0.42
1:CY:317:ASP:HB3	1:CY:319:GLN:NE2	2.35	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BS:163:THR:O	1:BS:165:THR:HG22	2.19	0.42
1:AZ:89:LEU:HD21	1:AZ:201:CYS:HB3	2.01	0.42
1:BM:122:GLY:O	1:BM:188:VAL:HG22	2.19	0.42
1:CJ:34:ARG:HD3	1:CS:43:SER:O	2.19	0.42
1:AL:69:PRO:C	1:AL:72:THR:HG1	2.22	0.42
1:CK:163:THR:HG23	1:CK:164:ARG:N	2.34	0.42
1:AW:80:VAL:HG13	1:AW:185:LEU:HB3	2.00	0.42
1:AG:80:VAL:HG13	1:AG:185:LEU:HB3	2.01	0.42
1:BH:281:HIS:CE1	1:BH:301:TRP:HB3	2.54	0.42
1:BP:99:PHE:HA	1:BP:209:VAL:O	2.19	0.42
1:BV:85:VAL:CG2	1:BV:86:PRO:HD2	2.50	0.42
1:BB:99:PHE:HA	1:BB:209:VAL:O	2.19	0.42
1:CC:39:VAL:HG23	1:CO:38:PRO:C	211.53	0.42
1:AV:264:SER:OG	1:AV:276:ARG:NH1	2.50	0.42
1:AV:124:VAL:HG11	1:AV:138:PHE:CD1	2.54	0.42
1:CH:119:THR:O	1:CH:119:THR:HG22	2.20	0.42
1:CO:119:THR:O	1:CO:120:GLY:C	2.57	0.42
1:AG:226:GLY:N	1:AG:243:LEU:O	2.51	0.42
1:AD:57:LEU:O	1:AD:204:SER:HA	2.24	0.42
1:CI:264:SER:HB2	1:CI:324:LEU:HD22	2.02	0.42
1:CL:121:GLY:C	1:CL:152:TRP:CD1	2.93	0.42
1:CB:80:VAL:HG22	1:CB:81:ASP:N	2.35	0.42
1:AU:314:TYR:HE1	1:AU:316:SER:HG	1.64	0.42
1:AG:314:TYR:HE1	1:AG:316:SER:HG	1.62	0.42
1:CB:98:ILE:HB	1:CF:91:ARG:HD2	2.00	0.42
1:CR:123:TYR:HB2	1:CR:185:LEU:HD21	2.02	0.42
1:AZ:98:ILE:HG22	1:AZ:99:PHE:CD2	2.55	0.42
1:AZ:162:TYR:CE2	1:AZ:164:ARG:HG2	2.54	0.42
1:CQ:43:SER:O	1:CV:34:ARG:CD	2.68	0.42
1:BE:111:ILE:HG22	1:BE:155:SER:HA	2.01	0.42
1:AT:188:VAL:CG2	1:AV:114:MET:SD	3.08	0.42
1:BB:281:HIS:CE1	1:BB:301:TRP:HB3	2.55	0.42
1:CE:109:PHE:HB2	1:CE:158:VAL:HG12	2.01	0.42
1:AE:281:HIS:ND1	1:AE:301:TRP:HB3	2.34	0.42
1:CW:72:THR:O	1:CW:191:ASN:OD1	2.37	0.42
1:CE:264:SER:HB2	1:CE:324:LEU:HD22	2.01	0.42
1:BZ:225:GLN:HG3	1:BZ:244:GLY:O	2.19	0.42
1:BG:246:THR:N	1:BG:247:PRO:CD	2.82	0.42
1:BG:109:PHE:HB2	1:BG:158:VAL:CG1	2.50	0.42
1:BN:136:HIS:O	1:BN:186:LEU:HD11	2.19	0.42
1:CA:138:PHE:CD1	1:CA:138:PHE:C	2.95	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BR:232:SER:HB3	1:BR:242:LEU:HD11	2.00	0.42
1:CG:138:PHE:CD1	1:CG:138:PHE:C	2.92	0.42
1:BK:136:HIS:O	1:BK:186:LEU:HD11	2.19	0.42
1:AB:226:GLY:N	1:AB:243:LEU:O	2.51	0.42
1:BM:124:VAL:HG11	1:BM:138:PHE:CD2	2.54	0.42
1:AI:256:VAL:HB	1:AI:335:ASP:HB3	2.01	0.42
1:CL:128:LEU:HA	1:CL:129:PRO:HD3	1.91	0.42
1:AF:298:TRP:O	1:AF:310:ASP:O	2.37	0.42
1:AE:298:TRP:HE1	1:AE:312:VAL:HA	1.84	0.42
1:CW:122:GLY:O	1:CW:188:VAL:CB	2.66	0.42
1:AJ:127:PHE:O	1:AJ:144:THR:OG1	2.33	0.42
1:BF:100:GLN:NE2	1:BF:211:SER:CB	2.82	0.42
1:AP:314:TYR:C	1:AP:314:TYR:CD1	2.92	0.42
1:BA:163:THR:C	1:BA:165:THR:HG22	2.39	0.42
1:AG:98:ILE:HG22	1:AG:99:PHE:CD2	2.54	0.42
1:AW:98:ILE:HG22	1:AW:99:PHE:CD2	2.54	0.42
1:AS:64:SER:OG	1:AS:80:VAL:HG21	2.20	0.42
1:AQ:98:ILE:HG22	1:AQ:99:PHE:CD2	2.54	0.42
1:CM:112:GLN:HE21	1:CO:44:THR:H	1.66	0.42
1:BF:123:TYR:N	1:BF:188:VAL:HG22	2.34	0.42
1:AK:69:PRO:C	1:AK:72:THR:HG1	2.23	0.42
1:CD:58:SER:HB3	1:CD:204:SER:HB2	2.01	0.42
1:BO:74:THR:HA	1:BO:190:ASN:HD22	1.85	0.42
1:AB:64:SER:OG	1:AB:80:VAL:HG21	2.20	0.42
1:AN:281:HIS:ND1	1:AN:301:TRP:HB3	2.34	0.42
1:BR:281:HIS:CE1	1:BR:301:TRP:HB3	2.54	0.42
1:CC:39:VAL:CG2	1:CO:39:VAL:HA	213.68	0.42
1:CC:39:VAL:HA	1:CU:39:VAL:CG2	213.77	0.42
1:AK:268:SER:CB	1:AK:273:ASP:O	2.67	0.42
1:CA:119:THR:O	1:CA:120:GLY:C	2.58	0.42
1:BC:260:ASP:HA	1:AC:261:ARG:NH2	2.34	0.42
1:BV:225:GLN:HG3	1:BV:244:GLY:O	2.19	0.42
1:BG:321:ARG:HD2	1:CG:300:ILE:HD13	2.02	0.42
1:BK:100:GLN:O	1:BK:169:THR:N	2.44	0.42
1:BB:62:ARG:HB2	1:CK:138:PHE:CE1	2.54	0.42
1:AQ:100:GLN:HA	1:AQ:169:THR:OG1	2.19	0.42
1:BH:246:THR:N	1:BH:247:PRO:CD	2.83	0.42
1:AD:137:THR:HG23	1:AD:140:ALA:CB	2.49	0.42
1:BS:124:VAL:HG11	1:BS:138:PHE:CD2	2.54	0.42
1:AU:308:PHE:CE2	1:AU:310:ASP:HA	2.55	0.42
1:AT:308:PHE:CE2	1:AT:310:ASP:HA	2.55	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AI:302:ASP:C	1:AI:305:ASN:HD21	2.22	0.42
1:AS:302:ASP:OD2	1:AS:305:ASN:CB	2.63	0.42
1:CZ:123:TYR:HA	1:CZ:188:VAL:HG23	2.00	0.42
1:CU:123:TYR:HB2	1:CU:185:LEU:HD21	2.01	0.42
1:CI:186:LEU:N	1:CI:186:LEU:HD23	2.34	0.42
1:CT:80:VAL:HG11	1:CT:185:LEU:CB	2.47	0.42
1:CP:103:ALA:HB2	1:CP:166:LEU:HB3	2.00	0.42
1:BZ:100:GLN:NE2	1:BZ:211:SER:CB	2.82	0.42
1:AM:314:TYR:C	1:AM:314:TYR:CD1	2.92	0.42
1:CC:98:ILE:HB	1:CJ:91:ARG:HD2	2.02	0.42
1:CV:123:TYR:HA	1:CV:188:VAL:HG23	2.00	0.42
1:AL:314:TYR:CE1	1:AL:316:SER:CA	2.89	0.42
1:CO:317:ASP:HB3	1:CO:319:GLN:NE2	2.33	0.42
1:AH:89:LEU:HD21	1:AH:201:CYS:HB3	2.01	0.42
1:CC:91:ARG:HD2	1:CJ:98:ILE:HB	2.02	0.42
1:AT:89:LEU:HD21	1:AT:201:CYS:HB3	2.01	0.42
1:AT:98:ILE:HG22	1:AT:99:PHE:CD2	2.54	0.42
1:BB:91:ARG:NH1	1:AF:98:ILE:CG2	67.92	0.42
1:AP:106:THR:O	1:AP:203:TRP:HA	2.19	0.42
1:BG:122:GLY:C	1:BG:188:VAL:CG2	2.82	0.42
1:AC:138:PHE:HE2	1:AM:62:ARG:HB2	231.35	0.42
1:BM:253:ASP:CB	1:BM:286:ALA:HB2	2.47	0.42
1:CF:111:ILE:HD11	1:CF:125:ALA:HB3	2.02	0.42
1:CU:113:PRO:HA	1:CU:197:VAL:HA	2.01	0.42
1:CL:109:PHE:HB2	1:CL:158:VAL:HG12	2.01	0.42
1:AL:281:HIS:ND1	1:AL:301:TRP:HB3	2.35	0.42
1:BN:281:HIS:CE1	1:BN:301:TRP:HB3	2.55	0.42
1:CZ:72:THR:O	1:CZ:191:ASN:OD1	2.38	0.42
1:AG:281:HIS:ND1	1:AG:301:TRP:HB3	2.34	0.42
1:AF:103:ALA:HB2	1:AF:166:LEU:HA	2.02	0.42
1:BE:86:PRO:HB3	1:BE:92:LEU:HD22	2.01	0.42
1:AC:246:THR:O	1:AC:250:ILE:HG12	2.19	0.42
1:CK:246:THR:N	1:CK:247:PRO:CD	2.83	0.42
1:AO:234:SER:HB3	1:AO:237:ASP:O	2.20	0.42
1:AG:137:THR:HG23	1:AG:140:ALA:CB	2.49	0.42
1:BG:228:LEU:HD13	1:BG:238:PHE:CD2	2.55	0.42
1:CX:264:SER:HB2	1:CX:324:LEU:HD22	2.00	0.42
1:BS:300:ILE:HD13	1:AS:321:ARG:HD2	2.02	0.42
1:AJ:234:SER:HB3	1:AJ:237:ASP:O	2.20	0.42
1:CR:138:PHE:C	1:CR:138:PHE:CD1	2.92	0.42
1:BA:228:LEU:HD13	1:BA:238:PHE:CD2	2.54	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BK:228:LEU:HD13	1:BK:238:PHE:CD2	2.55	0.42
1:BZ:184:ILE:HD13	1:BZ:184:ILE:N	2.34	0.42
1:BD:228:LEU:HD13	1:BD:238:PHE:CD2	2.55	0.42
1:AL:100:GLN:HA	1:AL:169:THR:OG1	2.19	0.42
1:AH:308:PHE:CE2	1:AH:310:ASP:HA	2.55	0.42
1:CG:123:TYR:CD1	1:CG:185:LEU:HD21	2.55	0.42
1:CP:123:TYR:HA	1:CP:188:VAL:HG23	2.01	0.42
1:CD:188:VAL:HG11	1:BH:114:MET:CE	138.39	0.42
1:CD:80:VAL:HG11	1:CD:185:LEU:CB	2.49	0.42
1:BD:100:GLN:O	1:BD:169:THR:N	2.45	0.42
1:BL:100:GLN:NE2	1:BL:211:SER:CB	2.82	0.42
1:CA:123:TYR:CD1	1:CA:185:LEU:HD21	2.54	0.42
1:CJ:103:ALA:HB2	1:CJ:166:LEU:HB3	2.00	0.42
1:CB:99:PHE:CD2	1:CB:207:LEU:HB3	2.55	0.42
1:CA:317:ASP:HB3	1:CA:319:GLN:NE2	2.34	0.42
1:AK:314:TYR:HE1	1:AK:316:SER:HG	1.63	0.42
1:CN:317:ASP:HB3	1:CN:319:GLN:NE2	2.35	0.42
1:CV:317:ASP:HB3	1:CV:319:GLN:NE2	2.35	0.42
1:CJ:317:ASP:HB3	1:CJ:319:GLN:NE2	2.35	0.42
1:BK:163:THR:O	1:BK:165:THR:HG22	2.20	0.42
1:CK:100:GLN:HA	1:CK:213:GLU:OE2	2.19	0.42
1:AS:63:ILE:HG23	1:AS:88:LEU:HD11	2.02	0.42
1:BO:156:ARG:NH2	1:CU:34:ARG:HG3	2.35	0.42
1:BE:123:TYR:N	1:BE:188:VAL:HG22	2.34	0.42
1:CB:44:THR:OG1	1:CF:110:GLU:OE1	2.28	0.42
1:BC:74:THR:HA	1:BC:190:ASN:HD22	1.84	0.42
1:AZ:123:TYR:HB2	1:AZ:185:LEU:HD11	2.01	0.42
1:AE:116:PRO:HG2	1:AE:119:THR:OG1	2.20	0.42
1:BX:142:GLN:HB2	1:CX:48:PHE:CE1	2.55	0.42
1:BP:253:ASP:CB	1:BP:286:ALA:HB2	2.49	0.42
1:AD:188:VAL:HG23	1:AG:114:MET:SD	126.97	0.42
1:BZ:253:ASP:CB	1:BZ:286:ALA:HB2	2.50	0.42
1:CI:199:VAL:O	1:CI:199:VAL:CG1	2.66	0.42
1:CB:118:ASN:HA	1:BY:116:PRO:HB3	2.02	0.42
1:CH:72:THR:O	1:CH:191:ASN:OD1	2.38	0.42
1:AW:281:HIS:ND1	1:AW:301:TRP:HB3	2.35	0.42
1:BC:86:PRO:HB3	1:BC:92:LEU:HD22	2.01	0.42
1:AO:103:ALA:HB2	1:AO:166:LEU:HA	2.01	0.42
1:CX:72:THR:O	1:CX:191:ASN:OD1	2.37	0.42
1:BQ:85:VAL:CG2	1:BQ:86:PRO:HD2	2.50	0.42
1:BE:99:PHE:HA	1:BE:209:VAL:O	2.19	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BG:205:VAL:HG22	1:BG:206:ARG:N	2.35	0.42
1:CP:102:TYR:HD2	1:CP:205:VAL:HG21	1.85	0.42
1:AP:256:VAL:HB	1:AP:335:ASP:HB3	2.01	0.42
1:AT:57:LEU:O	1:AT:204:SER:HA	2.20	0.42
1:AG:256:VAL:HB	1:AG:335:ASP:HB3	2.01	0.42
1:CH:214:ASN:HA	1:CH:215:PRO:HD3	1.83	0.42
1:CY:264:SER:HB2	1:CY:324:LEU:HD22	2.01	0.42
1:BJ:234:SER:HB3	1:BJ:237:ASP:OD1	2.20	0.42
1:BC:300:ILE:HD13	1:AC:321:ARG:HD2	2.02	0.42
1:BT:124:VAL:HG11	1:BT:138:PHE:CD2	2.55	0.42
1:BB:321:ARG:HD2	1:CB:300:ILE:HD13	2.01	0.42
1:BS:136:HIS:O	1:BS:186:LEU:HD11	2.20	0.42
1:AE:224:THR:HG22	1:AE:329:THR:N	2.34	0.42
1:CN:62:ARG:HA	1:CN:200:LEU:HD23	2.02	0.42
1:AY:298:TRP:O	1:AY:310:ASP:O	2.38	0.42
1:AQ:308:PHE:CE2	1:AQ:310:ASP:HA	2.55	0.42
1:BK:98:ILE:CG2	1:AS:91:ARG:HE	2.24	0.42
1:AP:263:LEU:HB3	1:AP:279:TYR:O	2.20	0.42
1:AV:263:LEU:HB3	1:AV:279:TYR:O	2.20	0.42
1:CD:91:ARG:HD2	1:CI:98:ILE:HB	2.02	0.42
1:CK:102:TYR:HD2	1:CK:205:VAL:HG21	1.85	0.42
1:AU:63:ILE:HG23	1:AU:88:LEU:HD11	2.00	0.42
1:BQ:163:THR:O	1:BQ:165:THR:HG22	2.20	0.42
1:AP:162:TYR:CE2	1:AP:164:ARG:HG2	2.55	0.42
1:CA:43:SER:O	1:CR:34:ARG:CD	129.11	0.42
1:CR:44:THR:H	1:CT:112:GLN:HE21	1.67	0.42
1:CR:58:SER:HB3	1:CR:204:SER:HB2	2.01	0.42
1:BH:142:GLN:HB2	1:CH:48:PHE:CE1	2.55	0.42
1:BB:149:VAL:HG23	1:CB:48:PHE:HE2	1.85	0.42
1:BD:149:VAL:HG23	1:CD:48:PHE:CE2	2.57	0.42
1:BS:149:VAL:HG23	1:CS:48:PHE:HE2	1.85	0.42
1:BY:74:THR:HA	1:BY:190:ASN:HD22	1.85	0.42
1:CD:119:THR:HG22	1:CD:119:THR:O	2.20	0.42
1:AH:109:PHE:HB2	1:AH:158:VAL:HG12	2.02	0.42
1:BP:74:THR:HA	1:BP:190:ASN:HD22	1.85	0.42
1:CW:109:PHE:HB2	1:CW:158:VAL:HG12	2.00	0.42
1:BM:86:PRO:HB3	1:BM:92:LEU:HD22	2.02	0.42
1:AV:80:VAL:HG13	1:AV:185:LEU:HB3	2.01	0.42
1:AT:281:HIS:ND1	1:AT:301:TRP:HB3	2.35	0.42
1:BG:99:PHE:HA	1:BG:209:VAL:O	2.20	0.42
1:BC:99:PHE:HA	1:BC:209:VAL:O	2.19	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AD:103:ALA:HB2	1:AD:166:LEU:HA	2.02	0.42
1:AG:101:ARG:NH1	1:AG:166:LEU:HD23	2.35	0.42
1:AN:264:SER:OG	1:AN:276:ARG:NH1	2.52	0.42
1:BE:136:HIS:O	1:BE:186:LEU:HD11	2.19	0.42
1:CX:128:LEU:HA	1:CX:129:PRO:HD3	1.93	0.42
1:AO:102:TYR:O	1:AO:167:LEU:HB2	2.19	0.42
1:AH:137:THR:HG23	1:AH:140:ALA:CB	2.49	0.42
1:CV:38:PRO:O	1:CZ:117:ALA:HB2	2.19	0.42
1:BJ:300:ILE:HD13	1:AJ:321:ARG:HD2	2.02	0.42
1:CE:54:ASP:N	1:CE:54:ASP:OD1	2.53	0.42
1:CY:45:VAL:O	1:CY:45:VAL:HG13	2.20	0.42
1:BJ:79:VAL:O	1:BJ:79:VAL:CG2	2.67	0.42
1:AT:226:GLY:N	1:AT:243:LEU:O	2.49	0.42
1:CM:202:ARG:HH12	1:CO:46:THR:HB	1.84	0.42
1:AL:302:ASP:OD2	1:AL:305:ASN:CB	2.62	0.42
1:CB:141:LEU:O	1:CB:142:GLN:C	2.56	0.42
1:BG:89:LEU:HA	1:BG:90:PRO:HD3	1.95	0.42
1:BX:254:GLY:CA	1:BX:283:LYS:HE3	2.31	0.42
1:AV:63:ILE:HG23	1:AV:88:LEU:HD11	2.02	0.42
1:AQ:314:TYR:CD1	1:AQ:314:TYR:C	2.93	0.42
1:CD:99:PHE:CD2	1:CD:207:LEU:HB3	2.57	0.42
1:AZ:314:TYR:C	1:AZ:314:TYR:CD1	2.93	0.42
1:CP:317:ASP:HB3	1:CP:319:GLN:NE2	2.35	0.42
1:CK:99:PHE:CD2	1:CK:207:LEU:HB3	2.55	0.42
1:AU:162:TYR:CE2	1:AU:164:ARG:HG2	2.55	0.42
1:CF:57:LEU:HD23	1:CF:203:TRP:HH2	1.84	0.42
1:BE:191:ASN:HD22	1:BE:191:ASN:H	1.68	0.42
1:CD:58:SER:HA	1:CD:203:TRP:CE3	2.55	0.42
1:CN:58:SER:HA	1:CN:203:TRP:CE3	2.55	0.42
1:CT:45:VAL:HG13	1:CT:45:VAL:O	2.20	0.42
1:CV:62:ARG:H	1:BZ:142:GLN:NE2	2.18	0.42
1:CD:120:GLY:HA2	1:BH:115:CYS:CA	149.84	0.42
1:CE:130:ASP:OD2	1:CE:176:ARG:NH2	2.52	0.42
1:CJ:109:PHE:HB2	1:CJ:158:VAL:HG12	2.02	0.42
1:BM:300:ILE:HD13	1:AM:321:ARG:HD2	2.02	0.42
1:BZ:128:LEU:HD12	1:BZ:184:ILE:HD11	2.01	0.42
1:BN:225:GLN:HG3	1:BN:244:GLY:O	2.20	0.42
1:CU:264:SER:HB2	1:CU:324:LEU:HD22	2.02	0.42
1:BP:225:GLN:HG3	1:BP:244:GLY:O	2.20	0.42
1:BH:126:GLY:HA3	1:BH:141:LEU:HD22	2.02	0.42
1:CA:284:LYS:HD3	1:CA:296:PHE:CZ	2.57	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AJ:137:THR:HG23	1:AJ:140:ALA:CB	2.50	0.42
1:CM:264:SER:HB2	1:CM:324:LEU:HD22	2.01	0.42
1:BC:100:GLN:O	1:BC:169:THR:N	2.51	0.42
1:CB:102:TYR:HD2	1:CB:205:VAL:HG21	1.88	0.42
1:BR:321:ARG:HD2	1:CR:300:ILE:HD13	2.02	0.42
1:CF:278:VAL:O	1:CF:278:VAL:HG13	2.20	0.42
1:CO:77:TYR:C	1:CO:77:TYR:CD1	2.93	0.42
1:CF:138:PHE:C	1:CF:138:PHE:CD1	2.93	0.42
1:AU:137:THR:HG23	1:AU:140:ALA:CB	2.49	0.42
1:AW:300:ILE:HB	1:AW:309:THR:OG1	2.20	0.42
1:CA:93:GLY:O	1:CA:97:ARG:NH1	2.53	0.42
1:AJ:288:ASN:O	1:AJ:289:ALA:C	2.59	0.42
1:AZ:298:TRP:O	1:AZ:310:ASP:O	2.37	0.41
1:AK:302:ASP:OD2	1:AK:305:ASN:CB	2.61	0.41
1:AW:302:ASP:OD2	1:AW:305:ASN:CB	2.62	0.41
1:AE:91:ARG:NH2	1:BM:210:PRO:HB3	2.34	0.41
1:CT:81:ASP:C	1:CT:81:ASP:OD1	2.58	0.41
1:CX:122:GLY:O	1:CX:188:VAL:CB	2.68	0.41
1:CR:123:TYR:HA	1:CR:188:VAL:HG23	2.01	0.41
1:CT:317:ASP:HB3	1:CT:319:GLN:NE2	2.34	0.41
1:CS:80:VAL:HG11	1:CS:185:LEU:CB	2.50	0.41
1:CK:103:ALA:HB2	1:CK:166:LEU:HB3	2.01	0.41
1:AC:63:ILE:HG23	1:AC:88:LEU:HD11	2.02	0.41
1:AD:89:LEU:HD21	1:AD:201:CYS:HB3	2.03	0.41
1:BK:163:THR:C	1:BK:165:THR:HG22	2.40	0.41
1:AN:89:LEU:HD21	1:AN:201:CYS:HB3	2.02	0.41
1:AC:98:ILE:HG12	1:BS:91:ARG:HG2	2.01	0.41
1:BO:122:GLY:C	1:BO:188:VAL:CG2	2.84	0.41
1:BY:111:ILE:HG22	1:BY:155:SER:HA	2.01	0.41
1:BK:150:ALA:HB2	1:BK:156:ARG:HD3	2.01	0.41
1:CK:62:ARG:HA	1:CK:200:LEU:HD23	2.01	0.41
1:CY:92:LEU:HB2	1:CY:203:TRP:CH2	2.55	0.41
1:AG:116:PRO:HG2	1:AG:119:THR:OG1	2.20	0.41
1:BW:149:VAL:HG23	1:CW:48:PHE:HE2	1.85	0.41
1:CU:57:LEU:HD23	1:CU:203:TRP:CH2	2.54	0.41
1:CN:113:PRO:HA	1:CN:197:VAL:HA	2.02	0.41
1:CV:130:ASP:OD2	1:CV:176:ARG:NH2	2.53	0.41
1:BK:281:HIS:CE1	1:BK:301:TRP:HB3	2.55	0.41
1:AZ:281:HIS:ND1	1:AZ:301:TRP:HB3	2.35	0.41
1:BW:85:VAL:CG2	1:BW:86:PRO:HD2	2.50	0.41
1:BE:85:VAL:CG2	1:BE:86:PRO:HD2	2.50	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BD:85:VAL:CG2	1:BD:86:PRO:HD2	2.52	0.41
1:AR:103:ALA:HB2	1:AR:166:LEU:HA	2.01	0.41
1:CY:85:VAL:O	1:CY:86:PRO:C	2.59	0.41
1:BE:246:THR:N	1:BE:247:PRO:CD	2.83	0.41
1:BP:228:LEU:HD13	1:BP:238:PHE:CD2	2.55	0.41
1:AX:238:PHE:CZ	1:AX:296:PHE:HB2	2.55	0.41
1:BG:225:GLN:HG3	1:BG:244:GLY:O	2.20	0.41
1:AP:288:ASN:O	1:AP:289:ALA:C	2.58	0.41
1:CN:77:TYR:CD1	1:CN:77:TYR:C	2.91	0.41
1:CZ:119:THR:O	1:CZ:119:THR:HG22	2.19	0.41
1:CH:78:VAL:HG13	1:CH:78:VAL:O	2.20	0.41
1:CS:93:GLY:O	1:CS:97:ARG:NH1	2.53	0.41
1:CS:264:SER:HB2	1:CS:324:LEU:HD22	2.01	0.41
1:BL:321:ARG:HD2	1:CL:300:ILE:HD13	2.01	0.41
1:AO:298:TRP:O	1:AO:310:ASP:O	2.38	0.41
1:AN:298:TRP:HE1	1:AN:312:VAL:HA	1.85	0.41
1:AC:302:ASP:C	1:AC:305:ASN:HD21	2.23	0.41
1:AJ:305:ASN:ND2	1:AJ:307:THR:H	2.18	0.41
1:AY:302:ASP:OD2	1:AY:305:ASN:CB	2.62	0.41
1:CG:80:VAL:HG11	1:CG:185:LEU:CB	2.48	0.41
1:CG:80:VAL:HG13	1:CG:185:LEU:N	2.35	0.41
1:CC:80:VAL:HG22	1:CC:81:ASP:N	2.35	0.41
1:AS:263:LEU:HB3	1:AS:279:TYR:O	2.21	0.41
1:CQ:123:TYR:CD1	1:CQ:185:LEU:HD21	2.55	0.41
1:CC:100:GLN:HG2	1:CC:211:SER:HG	1.81	0.41
1:CO:99:PHE:HB3	1:CO:209:VAL:O	2.20	0.41
1:CH:317:ASP:HB3	1:CH:319:GLN:NE2	2.34	0.41
1:AF:314:TYR:HE1	1:AF:316:SER:HG	1.65	0.41
1:CC:317:ASP:CB	1:CC:319:GLN:NE2	2.84	0.41
1:CJ:123:TYR:HB2	1:CJ:185:LEU:HD21	2.02	0.41
1:CI:317:ASP:HB3	1:CI:319:GLN:NE2	2.35	0.41
1:AR:89:LEU:HD21	1:AR:201:CYS:HB3	2.02	0.41
1:BK:130:ASP:HB3	1:BK:133:ASP:HB2	2.00	0.41
1:AI:89:LEU:HD21	1:AI:201:CYS:HB3	2.01	0.41
1:BT:122:GLY:O	1:BT:188:VAL:HG22	2.20	0.41
1:BJ:111:ILE:HG22	1:BJ:155:SER:HA	2.02	0.41
1:BH:123:TYR:N	1:BH:188:VAL:HG22	2.35	0.41
1:AA:265:ILE:HG21	1:AA:313:ALA:O	2.20	0.41
1:CL:45:VAL:O	1:CL:45:VAL:HG13	2.20	0.41
1:AD:116:PRO:HB3	1:AF:118:ASN:O	2.20	0.41
1:AI:116:PRO:HG2	1:AI:119:THR:OG1	2.20	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BY:176:ARG:HD2	1:CY:168:TRP:CZ2	2.55	0.41
1:CM:111:ILE:HD11	1:CM:125:ALA:HB3	2.02	0.41
1:AQ:188:VAL:HG21	1:AZ:114:MET:SD	2.60	0.41
1:CF:113:PRO:HA	1:CF:197:VAL:HA	2.02	0.41
1:BJ:319:GLN:C	1:BJ:319:GLN:HE21	2.23	0.41
1:CY:158:VAL:HG13	1:CY:158:VAL:O	2.20	0.41
1:CS:113:PRO:HA	1:CS:197:VAL:HA	2.02	0.41
1:CV:113:PRO:HA	1:CV:197:VAL:HA	2.00	0.41
1:AA:281:HIS:ND1	1:AA:301:TRP:HB3	2.35	0.41
1:AM:103:ALA:HB2	1:AM:166:LEU:HA	2.01	0.41
1:BC:281:HIS:CE1	1:BC:301:TRP:HB3	2.56	0.41
1:BZ:99:PHE:HA	1:BZ:209:VAL:O	2.21	0.41
1:BN:99:PHE:HA	1:BN:209:VAL:O	2.20	0.41
1:BP:86:PRO:HB3	1:BP:92:LEU:HD22	2.03	0.41
1:AR:100:GLN:HA	1:AR:169:THR:OG1	2.21	0.41
1:BG:300:ILE:HG23	1:AG:323:ILE:CD1	2.51	0.41
1:CO:214:ASN:HA	1:CO:215:PRO:HD3	1.83	0.41
1:AZ:137:THR:HG23	1:AZ:140:ALA:CB	2.50	0.41
1:BZ:300:ILE:HD13	1:AZ:321:ARG:HD2	2.02	0.41
1:CD:121:GLY:C	1:CD:152:TRP:CD1	2.94	0.41
1:CP:214:ASN:HA	1:CP:215:PRO:HD3	1.83	0.41
1:BB:109:PHE:HB2	1:BB:158:VAL:CG1	2.56	0.41
1:BQ:246:THR:N	1:BQ:247:PRO:CD	2.83	0.41
1:CX:77:TYR:CD1	1:CX:77:TYR:C	2.91	0.41
1:BD:250:ILE:HG22	1:BD:250:ILE:O	2.20	0.41
1:BE:184:ILE:HD13	1:BE:184:ILE:N	2.34	0.41
1:BH:260:ASP:HA	1:AH:261:ARG:NH2	2.35	0.41
1:AB:256:VAL:HB	1:AB:335:ASP:HB3	2.02	0.41
1:AU:256:VAL:HB	1:AU:335:ASP:HB3	2.02	0.41
1:AA:298:TRP:O	1:AA:310:ASP:O	2.38	0.41
1:AO:308:PHE:CE2	1:AO:310:ASP:HA	2.55	0.41
1:AJ:298:TRP:O	1:AJ:310:ASP:O	2.37	0.41
1:AX:298:TRP:HE1	1:AX:312:VAL:HA	1.85	0.41
1:AX:302:ASP:OD2	1:AX:305:ASN:CB	2.61	0.41
1:CZ:141:LEU:O	1:CZ:142:GLN:C	2.59	0.41
1:CI:123:TYR:CD1	1:CI:185:LEU:HD21	2.55	0.41
1:CT:123:TYR:CD1	1:CT:185:LEU:HD21	2.55	0.41
1:BV:100:GLN:NE2	1:BV:211:SER:CB	2.84	0.41
1:AO:263:LEU:HB3	1:AO:279:TYR:O	2.20	0.41
1:CO:123:TYR:HB2	1:CO:185:LEU:CD2	2.51	0.41
1:BG:100:GLN:NE2	1:BG:211:SER:CB	2.83	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BT:130:ASP:HB3	1:BT:133:ASP:HB2	2.02	0.41
1:AO:63:ILE:HG23	1:AO:88:LEU:HD11	2.03	0.41
1:BU:163:THR:C	1:BU:165:THR:HG22	2.40	0.41
1:AK:61:SER:HB2	1:AK:89:LEU:HD22	2.02	0.41
1:BD:91:ARG:NH1	1:AG:98:ILE:CG2	67.11	0.41
1:AX:162:TYR:CE2	1:AX:164:ARG:HG2	2.55	0.41
1:BD:122:GLY:O	1:BD:188:VAL:HG22	2.24	0.41
1:AK:162:TYR:CE2	1:AK:164:ARG:HG2	2.55	0.41
1:BQ:149:VAL:HG23	1:CQ:48:PHE:HE2	1.85	0.41
1:BD:149:VAL:HG23	1:CD:48:PHE:HE2	1.87	0.41
1:BT:149:VAL:HG23	1:CT:48:PHE:HE2	1.85	0.41
1:CQ:113:PRO:HA	1:CQ:197:VAL:HA	2.01	0.41
1:BU:253:ASP:CB	1:BU:286:ALA:HB2	2.49	0.41
1:CB:167:LEU:N	1:CB:167:LEU:HD12	2.35	0.41
1:CD:130:ASP:OD2	1:CD:176:ARG:NH2	2.54	0.41
1:AT:80:VAL:HG12	1:AT:185:LEU:HB3	2.02	0.41
1:BY:319:GLN:HE21	1:BY:319:GLN:C	2.24	0.41
1:AS:101:ARG:NH1	1:AS:166:LEU:HD23	2.35	0.41
1:AX:80:VAL:HG13	1:AX:185:LEU:HB3	2.01	0.41
1:BT:281:HIS:CE1	1:BT:301:TRP:HB3	2.55	0.41
1:CX:85:VAL:O	1:CX:86:PRO:C	2.58	0.41
1:BT:85:VAL:CG2	1:BT:86:PRO:HD2	2.50	0.41
1:AD:264:SER:OG	1:AD:276:ARG:NH1	2.53	0.41
1:BP:109:PHE:HB2	1:BP:158:VAL:CG1	2.51	0.41
1:AC:267:TYR:CE2	1:CC:320:PRO:HD3	2.58	0.41
1:AM:100:GLN:HA	1:AM:169:THR:OG1	2.21	0.41
1:AR:300:ILE:HB	1:AR:309:THR:OG1	2.20	0.41
1:CH:102:TYR:HD2	1:CH:205:VAL:HG21	1.84	0.41
1:CD:219:THR:HG21	1:CD:333:ARG:O	2.24	0.41
1:BY:126:GLY:HA3	1:BY:141:LEU:HD22	2.02	0.41
1:CR:202:ARG:HH12	1:CT:46:THR:HB	1.85	0.41
1:CR:214:ASN:HA	1:CR:215:PRO:HD3	1.84	0.41
1:AD:81:ASP:OD1	1:AD:81:ASP:C	2.61	0.41
1:CB:119:THR:O	1:CB:119:THR:HG22	2.21	0.41
1:CY:278:VAL:O	1:CY:278:VAL:HG13	2.20	0.41
1:CM:124:VAL:HG13	1:CM:124:VAL:O	2.20	0.41
1:AH:183:LEU:HG	1:AH:184:ILE:N	2.34	0.41
1:AG:238:PHE:CZ	1:AG:296:PHE:HB2	2.55	0.41
1:AQ:238:PHE:CZ	1:AQ:296:PHE:HB2	2.55	0.41
1:BK:232:SER:HB3	1:BK:242:LEU:HD11	2.01	0.41
1:CA:219:THR:HG21	1:CA:333:ARG:O	2.19	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AK:305:ASN:ND2	1:AK:307:THR:H	2.19	0.41
1:AM:302:ASP:OD2	1:AM:305:ASN:CB	2.61	0.41
1:BD:100:GLN:NE2	1:BD:211:SER:CB	2.84	0.41
1:AN:263:LEU:HB3	1:AN:279:TYR:O	2.19	0.41
1:BX:100:GLN:NE2	1:BX:211:SER:CB	2.83	0.41
1:AG:63:ILE:HG23	1:AG:88:LEU:HD11	2.02	0.41
1:CS:79:VAL:CG1	1:CS:80:VAL:N	2.83	0.41
1:AI:314:TYR:HE1	1:AI:316:SER:HG	1.66	0.41
1:AW:314:TYR:HE1	1:AW:316:SER:HG	1.66	0.41
1:CS:317:ASP:HB3	1:CS:319:GLN:NE2	2.34	0.41
1:CJ:79:VAL:HG13	1:CJ:80:VAL:HG12	2.01	0.41
1:AO:63:ILE:CD1	1:AO:89:LEU:HD21	2.50	0.41
1:BH:130:ASP:HB3	1:BH:133:ASP:HB2	2.01	0.41
1:AI:98:ILE:HG22	1:AI:99:PHE:CD2	2.55	0.41
1:AU:98:ILE:HG22	1:AU:99:PHE:CD2	2.55	0.41
1:AS:162:TYR:CE2	1:AS:164:ARG:HG2	2.55	0.41
1:BV:111:ILE:HG22	1:BV:155:SER:HA	2.03	0.41
1:BX:122:GLY:C	1:BX:188:VAL:CG2	2.83	0.41
1:BF:156:ARG:HH22	1:CI:34:ARG:CD	2.33	0.41
1:BB:111:ILE:HG22	1:BB:155:SER:HA	2.03	0.41
1:CF:155:SER:O	1:CF:156:ARG:HD3	2.19	0.41
1:CF:58:SER:HB3	1:CF:204:SER:HB2	2.02	0.41
1:AB:116:PRO:HG2	1:AB:119:THR:OG1	2.21	0.41
1:AZ:116:PRO:HG2	1:AZ:119:THR:OG1	2.20	0.41
1:CU:63:ILE:HA	1:CU:63:ILE:HD13	1.87	0.41
1:AH:116:PRO:HG2	1:AH:119:THR:OG1	2.20	0.41
1:BC:191:ASN:HD22	1:BC:191:ASN:H	1.69	0.41
1:AP:63:ILE:HG23	1:AP:88:LEU:HD11	2.03	0.41
1:BV:253:ASP:CB	1:BV:286:ALA:HB2	2.50	0.41
1:CE:111:ILE:HD11	1:CE:125:ALA:HB3	2.02	0.41
1:BL:111:ILE:HG22	1:BL:155:SER:HA	2.03	0.41
1:AJ:114:MET:SD	1:AR:188:VAL:HG23	2.61	0.41
1:AI:281:HIS:ND1	1:AI:301:TRP:HB3	2.34	0.41
1:AI:103:ALA:HB2	1:AI:166:LEU:HA	2.01	0.41
1:AG:103:ALA:HB2	1:AG:166:LEU:HA	2.02	0.41
1:BV:86:PRO:HB3	1:BV:92:LEU:HD22	2.02	0.41
1:CF:85:VAL:O	1:CF:86:PRO:C	2.59	0.41
1:BF:214:ASN:HD22	1:BF:215:PRO:HD2	1.85	0.41
1:BF:128:LEU:HD12	1:BF:184:ILE:HD11	2.02	0.41
1:AU:267:TYR:CE2	1:CU:320:PRO:HD3	2.56	0.41
1:BX:300:ILE:HD13	1:AX:321:ARG:HD2	2.03	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AO:224:THR:HG22	1:AO:329:THR:N	2.35	0.41
1:BO:228:LEU:HD13	1:BO:238:PHE:CD2	2.54	0.41
1:AX:256:VAL:HB	1:AX:335:ASP:HB3	2.02	0.41
1:AE:183:LEU:HG	1:AE:184:ILE:N	2.35	0.41
1:BQ:234:SER:HB3	1:BQ:237:ASP:OD1	2.19	0.41
1:BI:228:LEU:HD13	1:BI:238:PHE:CD2	2.55	0.41
1:CG:264:SER:HB2	1:CG:324:LEU:HD22	2.01	0.41
1:CN:278:VAL:HG13	1:CN:278:VAL:O	2.20	0.41
1:CF:54:ASP:N	1:CF:54:ASP:OD1	2.53	0.41
1:CT:250:ILE:HG22	1:CT:250:ILE:O	2.20	0.41
1:AN:57:LEU:HA	1:AN:57:LEU:HD23	1.95	0.41
1:AL:256:VAL:HB	1:AL:335:ASP:HB3	2.03	0.41
1:BT:109:PHE:HB2	1:BT:158:VAL:CG1	2.50	0.41
1:AK:298:TRP:O	1:AK:310:ASP:O	2.37	0.41
1:CG:123:TYR:HB2	1:CG:185:LEU:HD21	2.00	0.41
1:CB:123:TYR:CD1	1:CB:185:LEU:HD21	2.62	0.41
1:BE:89:LEU:HA	1:BE:90:PRO:HD3	1.94	0.41
1:BB:98:ILE:CG2	1:AF:91:ARG:CZ	88.33	0.41
1:AX:314:TYR:C	1:AX:314:TYR:CD1	2.93	0.41
1:AU:314:TYR:CD1	1:AU:314:TYR:C	2.93	0.41
1:BD:130:ASP:HB3	1:BD:133:ASP:HB2	2.04	0.41
1:AG:314:TYR:C	1:AG:314:TYR:CD1	2.93	0.41
1:CB:317:ASP:HB3	1:CB:319:GLN:NE2	2.35	0.41
1:CV:122:GLY:O	1:CV:188:VAL:CB	2.68	0.41
1:CN:122:GLY:O	1:CN:188:VAL:CB	2.66	0.41
1:CK:317:ASP:HB3	1:CK:319:GLN:NE2	2.36	0.41
1:CX:317:ASP:HB3	1:CX:319:GLN:NE2	2.35	0.41
1:CA:99:PHE:CD2	1:CA:207:LEU:HB3	2.56	0.41
1:BD:163:THR:O	1:BD:165:THR:HG22	2.21	0.41
1:AE:98:ILE:HG22	1:AE:99:PHE:CD2	2.55	0.41
1:BD:91:ARG:HG2	1:AW:98:ILE:HG12	2.01	0.41
1:AU:69:PRO:C	1:AU:72:THR:HG1	2.23	0.41
1:CB:45:VAL:HG23	1:CF:200:LEU:HD13	2.01	0.41
1:AA:62:ARG:CZ	1:AI:138:PHE:CE2	44.41	0.41
1:BS:115:CYS:HB3	1:BS:195:VAL:HG12	2.03	0.41
1:CA:62:ARG:H	1:BY:142:GLN:NE2	128.65	0.41
1:CC:163:THR:HG23	1:CC:164:ARG:N	2.35	0.41
1:AN:64:SER:OG	1:AN:80:VAL:HG21	2.21	0.41
1:AM:126:GLY:HA2	1:AM:158:VAL:HG21	2.03	0.41
1:BB:214:ASN:ND2	1:BB:215:PRO:HD2	2.41	0.41
1:AE:226:GLY:N	1:AE:243:LEU:O	2.52	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AZ:300:ILE:HB	1:AZ:309:THR:OG1	2.21	0.41
1:CY:102:TYR:HD2	1:CY:205:VAL:HG21	1.85	0.41
1:AR:224:THR:HG22	1:AR:329:THR:N	2.36	0.41
1:AW:288:ASN:O	1:AW:289:ALA:C	2.58	0.41
1:CF:45:VAL:O	1:CF:45:VAL:HG13	2.20	0.41
1:AS:57:LEU:HD23	1:AS:57:LEU:HA	1.95	0.41
1:BT:199:VAL:O	1:BT:199:VAL:HG13	2.19	0.41
1:BZ:136:HIS:O	1:BZ:186:LEU:HD11	2.21	0.41
1:CV:119:THR:O	1:CV:120:GLY:C	2.59	0.41
1:AD:226:GLY:N	1:AD:243:LEU:O	2.52	0.41
1:AP:308:PHE:CE2	1:AP:310:ASP:HA	2.55	0.41
1:AE:298:TRP:CG	1:AE:312:VAL:HG13	2.51	0.41
1:AW:302:ASP:C	1:AW:305:ASN:HD21	2.23	0.41
1:CK:81:ASP:HA	1:CK:184:ILE:HG22	2.01	0.41
1:CE:80:VAL:HG22	1:CE:81:ASP:N	2.34	0.41
1:BY:254:GLY:CA	1:BY:283:LYS:HE3	2.30	0.41
1:CI:80:VAL:HG13	1:CI:185:LEU:N	2.36	0.41
1:BE:100:GLN:NE2	1:BE:211:SER:OG	2.54	0.41
1:AV:63:ILE:CD1	1:AV:89:LEU:HD21	2.51	0.41
1:CC:98:ILE:HB	1:CX:91:ARG:HD2	211.98	0.41
1:CV:123:TYR:CD1	1:CV:185:LEU:HD21	2.55	0.41
1:CM:317:ASP:HB3	1:CM:319:GLN:NE2	2.36	0.41
1:AY:314:TYR:HE1	1:AY:316:SER:HG	1.66	0.41
1:CS:98:ILE:HG13	1:CS:99:PHE:CD2	2.55	0.41
1:AY:63:ILE:HD11	1:AY:89:LEU:HD21	2.02	0.41
1:AR:63:ILE:CD1	1:AR:89:LEU:HD21	2.51	0.41
1:BB:163:THR:C	1:BB:165:THR:HG22	2.42	0.41
1:AS:64:SER:O	1:AS:199:VAL:HG12	2.21	0.41
1:AA:98:ILE:HG22	1:AA:99:PHE:CD2	2.58	0.41
1:AJ:98:ILE:HG22	1:AJ:99:PHE:CD2	2.55	0.41
1:AW:162:TYR:CE2	1:AW:164:ARG:HG2	2.56	0.41
1:BT:150:ALA:HB2	1:BT:156:ARG:HD3	2.03	0.41
1:BS:123:TYR:N	1:BS:188:VAL:HG22	2.34	0.41
1:BI:111:ILE:CG2	1:BI:112:GLN:N	2.83	0.41
1:AO:69:PRO:C	1:AO:72:THR:HG1	2.22	0.41
1:CJ:45:VAL:HG13	1:CJ:45:VAL:O	2.21	0.41
1:CX:113:PRO:HA	1:CX:197:VAL:HA	2.01	0.41
1:AE:64:SER:OG	1:AE:80:VAL:HG21	2.20	0.41
1:CT:158:VAL:O	1:CT:158:VAL:HG13	2.21	0.41
1:AY:122:GLY:C	1:AY:188:VAL:HG22	2.41	0.41
1:CJ:113:PRO:HA	1:CJ:197:VAL:HA	2.02	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AK:138:PHE:CE2	1:AS:62:ARG:CZ	3.04	0.41
1:CV:163:THR:OG1	1:CV:165:THR:HG23	2.21	0.41
1:AY:109:PHE:HB2	1:AY:158:VAL:HG12	2.03	0.41
1:AJ:114:MET:SD	1:AR:188:VAL:CG2	3.08	0.41
1:AB:109:PHE:HE2	1:AB:127:PHE:CD1	2.38	0.41
1:BG:281:HIS:CE1	1:BG:301:TRP:HB3	2.55	0.41
1:BX:99:PHE:HA	1:BX:209:VAL:O	2.21	0.41
1:CD:138:PHE:HZ	1:BH:200:LEU:HD21	135.38	0.41
1:AL:124:VAL:HG11	1:AL:138:PHE:CD1	2.55	0.41
1:CK:77:TYR:CD1	1:CK:78:VAL:N	2.88	0.41
1:CE:219:THR:HG21	1:CE:333:ARG:O	2.20	0.41
1:AH:224:THR:HG22	1:AH:329:THR:N	2.35	0.41
1:AV:238:PHE:CZ	1:AV:296:PHE:HB2	2.56	0.41
1:BA:300:ILE:HD13	1:AA:321:ARG:HD2	2.01	0.41
1:AR:256:VAL:HB	1:AR:335:ASP:HB3	2.02	0.41
1:CK:60:MET:HE1	1:CL:47:GLY:H	1.86	0.41
1:AR:212:LEU:HD12	1:AR:212:LEU:C	2.41	0.41
1:BE:109:PHE:HB2	1:BE:158:VAL:CG1	2.51	0.41
1:AV:137:THR:HG23	1:AV:140:ALA:CB	2.51	0.41
1:BC:321:ARG:HD2	1:CC:300:ILE:HD13	2.04	0.41
1:CZ:264:SER:HB2	1:CZ:324:LEU:HD22	2.02	0.41
1:BM:225:GLN:HG3	1:BM:244:GLY:O	2.20	0.41
1:CH:264:SER:HB2	1:CH:324:LEU:HD22	2.02	0.41
1:AS:308:PHE:CE2	1:AS:310:ASP:HA	2.55	0.41
1:AX:298:TRP:O	1:AX:310:ASP:O	2.38	0.41
1:AT:298:TRP:O	1:AT:310:ASP:O	2.38	0.41
1:AJ:302:ASP:C	1:AJ:305:ASN:HD21	2.23	0.41
1:CY:79:VAL:CG1	1:CY:80:VAL:N	2.83	0.41
1:CD:80:VAL:HG13	1:CD:185:LEU:N	2.38	0.41
1:BH:100:GLN:NE2	1:BH:211:SER:OG	2.54	0.41
1:CA:186:LEU:N	1:CA:186:LEU:HD23	2.38	0.41
1:BN:163:THR:O	1:BN:165:THR:HG22	2.21	0.41
1:AI:61:SER:CB	1:AI:90:PRO:HD2	2.37	0.41
1:BV:163:THR:C	1:BV:165:THR:HG22	2.41	0.41
1:BA:91:ARG:HG2	1:AI:98:ILE:HG12	2.02	0.41
1:AO:98:ILE:HG22	1:AO:99:PHE:CD2	2.56	0.41
1:CD:117:ALA:HB1	1:BH:117:ALA:HB2	147.86	0.41
1:AQ:162:TYR:CE2	1:AQ:164:ARG:HG2	2.55	0.41
1:AC:116:PRO:HG2	1:AC:119:THR:OG1	2.21	0.41
1:CM:200:LEU:HD13	1:CO:45:VAL:HG23	2.03	0.41
1:CZ:89:LEU:HD13	1:CZ:203:TRP:CG	2.56	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CP:113:PRO:HA	1:CP:197:VAL:HA	2.02	0.41
1:CI:158:VAL:HG13	1:CI:158:VAL:O	2.21	0.41
1:CT:130:ASP:OD2	1:CT:176:ARG:NH2	2.54	0.41
1:CO:130:ASP:OD2	1:CO:176:ARG:NH2	2.54	0.41
1:BD:253:ASP:CB	1:BD:286:ALA:HB2	2.50	0.41
1:BA:116:PRO:HD3	1:CT:120:GLY:HA3	138.50	0.41
1:CY:163:THR:OG1	1:CY:165:THR:HG23	2.21	0.41
1:CE:60:MET:CE	1:CE:202:ARG:HB3	2.49	0.41
1:CG:113:PRO:HA	1:CG:197:VAL:HA	2.02	0.41
1:AD:109:PHE:HB2	1:AD:158:VAL:HG12	2.03	0.41
1:CP:45:VAL:O	1:CP:45:VAL:HG13	2.20	0.41
1:AT:109:PHE:CE2	1:AT:127:PHE:CD1	3.09	0.41
1:BM:99:PHE:HA	1:BM:209:VAL:O	2.21	0.41
1:AI:109:PHE:CE2	1:AI:127:PHE:CD1	3.08	0.41
1:BH:86:PRO:HB3	1:BH:92:LEU:HD22	2.01	0.41
1:CZ:133:ASP:O	1:CZ:182:ARG:NH2	2.54	0.41
1:AI:102:TYR:HD2	1:AI:205:VAL:HG21	1.86	0.41
1:CV:121:GLY:C	1:CV:152:TRP:CD1	2.94	0.41
1:BI:300:ILE:HD13	1:AI:321:ARG:HD2	2.02	0.41
1:AR:137:THR:HG23	1:AR:140:ALA:CB	2.51	0.41
1:CD:264:SER:HB2	1:CD:324:LEU:HD22	2.03	0.41
1:BA:321:ARG:HD2	1:CA:300:ILE:HD13	2.06	0.41
1:CS:78:VAL:O	1:CS:78:VAL:HG13	2.21	0.41
1:BS:169:THR:H	1:BS:169:THR:HG1	1.65	0.41
1:BS:321:ARG:HD2	1:CS:300:ILE:HD13	2.01	0.41
1:AI:183:LEU:HG	1:AI:184:ILE:N	2.36	0.41
1:BU:228:LEU:HD13	1:BU:238:PHE:CD2	2.56	0.41
1:BD:321:ARG:HD2	1:CD:300:ILE:HD13	2.03	0.41
1:AN:234:SER:HB3	1:AN:237:ASP:O	2.19	0.41
1:AU:298:TRP:O	1:AU:310:ASP:O	2.39	0.41
1:AU:298:TRP:HE1	1:AU:312:VAL:HA	1.85	0.41
1:AF:308:PHE:CE2	1:AF:310:ASP:HA	2.55	0.41
1:CY:122:GLY:O	1:CY:188:VAL:CB	2.68	0.41
1:BH:254:GLY:CA	1:BH:283:LYS:HE3	2.28	0.41
1:BB:98:ILE:HG23	1:AF:91:ARG:HG2	89.20	0.41
1:AB:91:ARG:CZ	1:BO:98:ILE:CG2	132.61	0.41
1:AJ:91:ARG:NH2	1:BR:210:PRO:HB3	2.36	0.41
1:CK:103:ALA:O	1:CK:205:VAL:HG23	2.21	0.41
1:BM:130:ASP:HB3	1:BM:133:ASP:HB2	2.02	0.41
1:CQ:317:ASP:HB3	1:CQ:319:GLN:NE2	2.35	0.41
1:AY:89:LEU:HD21	1:AY:201:CYS:HB3	2.02	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BW:130:ASP:HB3	1:BW:133:ASP:HB2	2.02	0.41
1:AY:98:ILE:HG22	1:AY:99:PHE:CD2	2.56	0.41
1:BS:111:ILE:CG2	1:BS:112:GLN:N	2.82	0.41
1:AU:64:SER:OG	1:AU:80:VAL:HG21	2.19	0.41
1:AW:69:PRO:C	1:AW:72:THR:HG1	2.23	0.41
1:CX:63:ILE:HG23	1:CX:88:LEU:HD21	2.03	0.41
1:AO:116:PRO:HG2	1:AO:119:THR:OG1	2.21	0.41
1:AA:80:VAL:HG12	1:AA:185:LEU:HB3	2.09	0.41
1:AY:101:ARG:NH1	1:AY:166:LEU:HD23	2.36	0.41
1:AD:281:HIS:ND1	1:AD:301:TRP:HB3	2.36	0.41
1:AJ:281:HIS:ND1	1:AJ:301:TRP:HB3	2.36	0.41
1:BE:281:HIS:CE1	1:BE:301:TRP:HB3	2.56	0.41
1:BG:86:PRO:HB3	1:BG:92:LEU:HD22	2.03	0.41
1:AH:264:SER:OG	1:AH:276:ARG:NH1	2.51	0.41
1:CN:155:SER:O	1:CN:156:ARG:HD3	2.21	0.41
1:CL:119:THR:HG22	1:CL:119:THR:O	2.20	0.41
1:BH:300:ILE:HD13	1:AH:321:ARG:HD2	2.02	0.41
1:BX:228:LEU:HD13	1:BX:238:PHE:CD2	2.55	0.41
1:CO:128:LEU:HA	1:CO:129:PRO:HD3	1.94	0.41
1:BO:321:ARG:HD2	1:CO:300:ILE:HD13	2.02	0.41
1:BB:263:LEU:CD2	1:BB:298:TRP:HB3	2.51	0.41
1:BH:228:LEU:HD13	1:BH:238:PHE:CD2	2.56	0.41
1:AI:234:SER:HB3	1:AI:237:ASP:O	2.20	0.41
1:BQ:321:ARG:HD2	1:CQ:300:ILE:HD13	2.03	0.41
1:AF:183:LEU:HG	1:AF:184:ILE:N	2.35	0.41
1:AZ:100:GLN:HA	1:AZ:169:THR:OG1	2.20	0.41
1:AG:183:LEU:HG	1:AG:184:ILE:N	2.35	0.41
1:BG:184:ILE:HD13	1:BG:184:ILE:N	2.35	0.41
1:CM:54:ASP:N	1:CM:54:ASP:OD1	2.54	0.41
1:CG:278:VAL:HG13	1:CG:278:VAL:O	2.20	0.41
1:CQ:278:VAL:O	1:CQ:278:VAL:HG13	2.20	0.41
1:AH:81:ASP:C	1:AH:81:ASP:OD1	2.58	0.41
1:CP:119:THR:HG22	1:CP:119:THR:O	2.19	0.41
1:CM:278:VAL:O	1:CM:278:VAL:HG13	2.21	0.41
1:AJ:100:GLN:HA	1:AJ:169:THR:OG1	2.21	0.41
1:BL:128:LEU:HD12	1:BL:184:ILE:HD11	2.02	0.41
1:AB:100:GLN:HA	1:AB:169:THR:OG1	2.22	0.41
1:BT:232:SER:HB3	1:BT:242:LEU:HD11	2.02	0.41
1:CM:128:LEU:HA	1:CM:129:PRO:HD3	1.97	0.41
1:AS:288:ASN:O	1:AS:289:ALA:C	2.59	0.41
1:AB:183:LEU:HG	1:AB:184:ILE:N	2.38	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AL:298:TRP:O	1:AL:310:ASP:O	2.39	0.41
1:AH:302:ASP:OD2	1:AH:305:ASN:CB	2.62	0.41
1:CG:123:TYR:HB2	1:CG:185:LEU:CD2	2.51	0.41
1:CW:80:VAL:HG22	1:CW:81:ASP:N	2.36	0.41
1:CM:122:GLY:O	1:CM:188:VAL:CB	2.66	0.41
1:CZ:123:TYR:CD1	1:CZ:185:LEU:HD21	2.56	0.41
1:CC:123:TYR:HB2	1:CC:185:LEU:CD2	2.51	0.41
1:BI:283:LYS:HG2	1:BI:285:PHE:CE1	2.56	0.41
1:CU:80:VAL:HG22	1:CU:81:ASP:N	2.35	0.41
1:AC:263:LEU:HB3	1:AC:279:TYR:O	2.21	0.41
1:BB:210:PRO:HB3	1:AK:91:ARG:CZ	2.50	0.41
1:BU:100:GLN:NE2	1:BU:211:SER:CB	2.84	0.41
1:CQ:80:VAL:HG11	1:CQ:185:LEU:CB	2.47	0.41
1:BT:100:GLN:NE2	1:BT:211:SER:CB	2.84	0.41
1:AO:91:ARG:HD2	1:AW:143:ALA:HB1	2.02	0.41
1:CB:98:ILE:HG13	1:CB:99:PHE:CD2	2.56	0.41
1:CS:123:TYR:HB2	1:CS:185:LEU:HD21	2.03	0.41
1:CQ:99:PHE:CD2	1:CQ:207:LEU:HB3	2.56	0.41
1:AY:314:TYR:C	1:AY:314:TYR:CD1	2.94	0.41
1:BA:166:LEU:C	1:BA:166:LEU:CD1	2.89	0.41
1:AR:314:TYR:C	1:AR:314:TYR:CD1	2.93	0.41
1:CO:317:ASP:CB	1:CO:319:GLN:NE2	2.84	0.41
1:CE:98:ILE:O	1:CH:91:ARG:NH2	2.54	0.41
1:CE:317:ASP:CB	1:CE:319:GLN:NE2	2.84	0.41
1:AC:88:LEU:C	1:AC:88:LEU:HD13	2.41	0.41
1:CZ:317:ASP:HB3	1:CZ:319:GLN:NE2	2.35	0.41
1:CV:98:ILE:HG13	1:CV:99:PHE:CD2	2.56	0.41
1:AT:162:TYR:CE2	1:AT:164:ARG:HG2	2.56	0.41
1:BM:163:THR:C	1:BM:165:THR:HG22	2.41	0.41
1:BM:111:ILE:CG2	1:BM:112:GLN:N	2.84	0.41
1:CM:155:SER:O	1:CM:156:ARG:HD3	2.21	0.41
1:BA:111:ILE:HG22	1:BA:155:SER:HA	2.02	0.41
1:BB:156:ARG:HH22	1:CB:34:ARG:CG	22.81	0.41
1:CK:57:LEU:HD23	1:CK:203:TRP:CH2	2.56	0.41
1:CR:89:LEU:HD13	1:CR:203:TRP:CG	2.56	0.41
1:BM:149:VAL:HG23	1:CM:48:PHE:HE2	1.86	0.41
1:CQ:45:VAL:O	1:CQ:45:VAL:HG13	2.20	0.41
1:CP:58:SER:HA	1:CP:203:TRP:CE3	2.56	0.41
1:BR:149:VAL:HG23	1:CR:48:PHE:HE2	1.86	0.41
1:BJ:74:THR:HA	1:BJ:190:ASN:HD22	1.86	0.41
1:BX:142:GLN:HB2	1:CX:48:PHE:HE1	1.86	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AE:123:TYR:HB2	1:AE:185:LEU:HD11	2.02	0.41
1:BF:74:THR:HA	1:BF:190:ASN:HD22	1.85	0.41
1:CX:158:VAL:HG13	1:CX:158:VAL:O	2.21	0.41
1:BH:253:ASP:CB	1:BH:286:ALA:HB2	2.50	0.41
1:CS:158:VAL:O	1:CS:158:VAL:HG13	2.20	0.41
1:AG:122:GLY:C	1:AG:188:VAL:HG22	2.41	0.41
1:BG:84:ILE:HG13	1:BG:127:PHE:HE2	1.86	0.41
1:CH:85:VAL:O	1:CH:86:PRO:C	2.58	0.41
1:CG:69:PRO:O	1:CG:72:THR:OG1	2.26	0.41
1:CG:111:ILE:HD11	1:CG:125:ALA:HB3	2.01	0.41
1:AA:126:GLY:HA2	1:AA:158:VAL:HG21	2.03	0.41
1:AS:101:ARG:CZ	1:AS:166:LEU:CD2	2.99	0.41
1:AB:126:GLY:HA2	1:AB:158:VAL:HG21	2.03	0.41
1:BF:281:HIS:CE1	1:BF:301:TRP:HB3	2.55	0.41
1:AG:109:PHE:CE2	1:AG:127:PHE:CD1	3.09	0.41
1:CU:85:VAL:O	1:CU:86:PRO:C	2.59	0.41
1:BY:281:HIS:CE1	1:BY:301:TRP:HB3	2.55	0.41
1:BJ:99:PHE:HA	1:BJ:209:VAL:O	2.21	0.41
1:BX:85:VAL:CG2	1:BX:86:PRO:HD2	2.51	0.41
1:AK:246:THR:N	1:AK:247:PRO:HD2	2.36	0.41
1:BF:99:PHE:HA	1:BF:209:VAL:O	2.20	0.41
1:AE:264:SER:OG	1:AE:276:ARG:NH1	2.52	0.41
1:AJ:264:SER:OG	1:AJ:276:ARG:NH1	2.53	0.41
1:CB:138:PHE:CD2	1:BY:62:ARG:NH2	2.89	0.41
1:CB:121:GLY:HA3	1:CB:152:TRP:HD1	1.85	0.41
1:BO:128:LEU:HD12	1:BO:184:ILE:HD11	2.02	0.41
1:CO:119:THR:HG22	1:CO:119:THR:O	2.21	0.41
1:CK:306:LYS:HE3	1:CK:336:SER:HB2	2.03	0.41
1:AF:137:THR:HG23	1:AF:140:ALA:CB	2.51	0.41
1:CX:214:ASN:HA	1:CX:215:PRO:HD3	1.83	0.41
1:AS:224:THR:HG22	1:AS:329:THR:N	2.36	0.41
1:BZ:321:ARG:HD2	1:CZ:300:ILE:HD13	2.03	0.41
1:CY:54:ASP:N	1:CY:54:ASP:OD1	2.52	0.41
1:AS:212:LEU:C	1:AS:212:LEU:HD12	2.41	0.41
1:BD:62:ARG:NH2	1:CW:138:PHE:CD2	2.89	0.41
1:AU:234:SER:HB3	1:AU:237:ASP:O	2.21	0.41
1:AE:300:ILE:HB	1:AE:309:THR:OG1	2.21	0.41
1:AX:224:THR:HG22	1:AX:329:THR:N	2.36	0.41
1:AK:183:LEU:HG	1:AK:184:ILE:N	2.36	0.41
1:CL:264:SER:HB2	1:CL:324:LEU:HD22	2.03	0.41
1:CH:284:LYS:HD3	1:CH:296:PHE:CZ	2.55	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AS:234:SER:HB3	1:AS:237:ASP:O	2.20	0.41
1:AL:300:ILE:HB	1:AL:309:THR:OG1	2.21	0.41
1:BQ:250:ILE:O	1:BQ:250:ILE:HG22	2.20	0.41
1:CB:278:VAL:O	1:CB:278:VAL:HG13	2.21	0.41
1:BJ:246:THR:N	1:BJ:247:PRO:CD	2.84	0.41
1:AC:100:GLN:HA	1:AC:169:THR:OG1	2.21	0.41
1:BV:124:VAL:HG11	1:BV:138:PHE:CD2	2.56	0.41
1:CT:264:SER:HB2	1:CT:324:LEU:HD22	2.02	0.41
1:AV:302:ASP:C	1:AV:305:ASN:HD21	2.23	0.41
1:AF:302:ASP:C	1:AF:305:ASN:HD21	2.23	0.41
1:CH:141:LEU:O	1:CH:142:GLN:C	2.58	0.41
1:AB:91:ARG:HE	1:BY:98:ILE:CG2	2.28	0.41
1:CK:123:TYR:HA	1:CK:188:VAL:HG23	2.03	0.41
1:BT:98:ILE:CG2	1:AV:91:ARG:CZ	2.99	0.41
1:BQ:100:GLN:NE2	1:BQ:211:SER:CB	2.84	0.41
1:CT:317:ASP:CB	1:CT:319:GLN:NE2	2.84	0.41
1:CQ:98:ILE:C	1:CQ:211:SER:O	2.56	0.41
1:CA:317:ASP:CB	1:CA:319:GLN:NE2	2.84	0.41
1:CR:317:ASP:HB3	1:CR:319:GLN:NE2	2.36	0.41
1:CW:317:ASP:HB3	1:CW:319:GLN:NE2	2.36	0.41
1:BA:103:ALA:HB2	1:BA:166:LEU:HD22	2.03	0.41
1:CF:317:ASP:CB	1:CF:319:GLN:NE2	2.83	0.41
1:BT:163:THR:C	1:BT:165:THR:HG22	2.41	0.41
1:BB:91:ARG:NH1	1:AK:98:ILE:O	2.54	0.41
1:AH:162:TYR:CE2	1:AH:164:ARG:HG2	2.55	0.41
1:BG:111:ILE:HG22	1:BG:155:SER:HA	2.02	0.41
1:AG:69:PRO:C	1:AG:72:THR:HG1	2.23	0.41
1:AD:69:PRO:C	1:AD:72:THR:HG1	2.26	0.41
1:BA:191:ASN:H	1:BA:191:ASN:HD22	1.72	0.41
1:CY:58:SER:HA	1:CY:203:TRP:CE3	2.56	0.41
1:CB:58:SER:HA	1:CB:203:TRP:CE3	2.56	0.41
1:AK:68:LEU:HB2	1:AK:195:VAL:HG23	2.03	0.41
1:CA:45:VAL:HG23	1:CY:200:LEU:HD13	130.90	0.41
1:CG:58:SER:HB3	1:CG:204:SER:HB2	2.03	0.41
1:AD:188:VAL:CG2	1:AG:114:MET:SD	126.43	0.41
1:BM:115:CYS:HB3	1:BM:195:VAL:HG12	2.03	0.41
1:AA:114:MET:SD	1:AI:188:VAL:CG2	31.86	0.41
1:CL:158:VAL:O	1:CL:158:VAL:HG13	2.20	0.41
1:AP:246:THR:N	1:AP:247:PRO:HD2	2.36	0.41
1:BR:85:VAL:CG2	1:BR:86:PRO:HD2	2.51	0.41
1:AH:103:ALA:HB2	1:AH:166:LEU:HA	2.03	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BY:99:PHE:HA	1:BY:209:VAL:O	2.20	0.41
1:CB:119:THR:O	1:CB:120:GLY:C	2.64	0.41
1:CK:219:THR:HG21	1:CK:333:ARG:O	2.21	0.41
1:BP:300:ILE:HD13	1:AP:321:ARG:HD2	2.03	0.41
1:AW:100:GLN:HA	1:AW:169:THR:OG1	2.20	0.41
1:CQ:284:LYS:HD3	1:CQ:296:PHE:CZ	2.56	0.41
1:AU:238:PHE:CZ	1:AU:296:PHE:HB2	2.55	0.41
1:BF:246:THR:N	1:BF:247:PRO:CD	2.84	0.41
1:BM:109:PHE:HB2	1:BM:158:VAL:CG1	2.50	0.41
1:BH:136:HIS:O	1:BH:186:LEU:HD11	2.20	0.41
1:AO:267:TYR:CE2	1:CO:320:PRO:HD3	2.55	0.41
1:CY:133:ASP:O	1:CY:182:ARG:NH2	2.54	0.41
1:AO:57:LEU:O	1:AO:204:SER:HA	2.20	0.41
1:BZ:250:ILE:HG22	1:BZ:250:ILE:O	2.20	0.41
1:CJ:138:PHE:C	1:CJ:138:PHE:CD1	2.94	0.41
1:AP:81:ASP:C	1:AP:81:ASP:OD1	2.60	0.41
1:CX:138:PHE:CD1	1:CX:138:PHE:C	2.95	0.41
1:CB:219:THR:HG21	1:CB:333:ARG:O	2.21	0.41
1:AH:288:ASN:O	1:AH:289:ALA:C	2.60	0.41
1:CI:219:THR:HG21	1:CI:333:ARG:O	2.21	0.41
1:CA:246:THR:N	1:CA:247:PRO:CD	2.84	0.41
1:AI:298:TRP:O	1:AI:310:ASP:O	2.38	0.40
1:AS:302:ASP:C	1:AS:305:ASN:HD21	2.23	0.40
1:AV:302:ASP:OD2	1:AV:305:ASN:CB	2.62	0.40
1:CP:80:VAL:HG22	1:CP:81:ASP:N	2.35	0.40
1:AC:91:ARG:CZ	1:BS:98:ILE:HG22	2.51	0.40
1:BT:98:ILE:HG23	1:AV:91:ARG:HG2	2.03	0.40
1:CS:103:ALA:HB2	1:CS:166:LEU:HB3	2.03	0.40
1:AB:314:TYR:CD1	1:AB:314:TYR:C	2.94	0.40
1:CP:91:ARG:HD2	1:CQ:98:ILE:HB	2.03	0.40
1:BS:130:ASP:HB3	1:BS:133:ASP:HB2	2.03	0.40
1:AI:60:MET:HA	1:AI:201:CYS:O	2.21	0.40
1:AW:63:ILE:CD1	1:AW:89:LEU:HD21	2.51	0.40
1:CD:44:THR:N	1:CW:112:GLN:HE21	25.50	0.40
1:AU:123:TYR:HB2	1:AU:185:LEU:HD11	2.03	0.40
1:AN:69:PRO:C	1:AN:72:THR:HG1	2.25	0.40
1:BB:149:VAL:HG23	1:CB:48:PHE:CE2	2.56	0.40
1:AX:116:PRO:HG2	1:AX:119:THR:OG1	2.21	0.40
1:BS:149:VAL:HG23	1:CS:48:PHE:CE2	2.55	0.40
1:CZ:130:ASP:OD2	1:CZ:176:ARG:NH2	2.54	0.40
1:AW:80:VAL:HG12	1:AW:185:LEU:HB3	2.03	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CB:72:THR:O	1:CB:191:ASN:OD1	2.39	0.40
1:BB:116:PRO:CB	1:CF:118:ASN:HA	14.16	0.40
1:CL:190:ASN:N	1:CL:190:ASN:ND2	2.69	0.40
1:BH:99:PHE:HA	1:BH:209:VAL:O	2.21	0.40
1:BO:141:LEU:HD21	1:BO:184:ILE:HG12	2.03	0.40
1:AQ:267:TYR:CE2	1:CQ:320:PRO:HD3	2.56	0.40
1:AD:74:THR:O	1:AD:75:ASP:C	2.59	0.40
1:BD:246:THR:N	1:BD:247:PRO:CD	2.84	0.40
1:CA:264:SER:HB2	1:CA:324:LEU:HD22	2.01	0.40
1:CD:93:GLY:O	1:CD:97:ARG:NH1	2.57	0.40
1:BP:214:ASN:HD22	1:BP:215:PRO:HD2	1.86	0.40
1:AC:288:ASN:O	1:AC:289:ALA:C	2.59	0.40
1:CU:284:LYS:HD3	1:CU:296:PHE:CZ	2.56	0.40
1:BL:280:TRP:CD2	1:AL:326:PRO:HG3	2.56	0.40
1:AU:224:THR:HG22	1:AU:329:THR:N	2.36	0.40
1:AJ:224:THR:HG22	1:AJ:329:THR:N	2.37	0.40
1:CT:284:LYS:HD3	1:CT:296:PHE:CZ	2.56	0.40
1:AX:288:ASN:O	1:AX:289:ALA:C	2.60	0.40
1:BJ:199:VAL:HG13	1:BJ:199:VAL:O	2.21	0.40
1:AJ:81:ASP:C	1:AJ:81:ASP:OD1	2.59	0.40
1:CP:138:PHE:C	1:CP:138:PHE:CD1	2.95	0.40
1:AN:74:THR:O	1:AN:75:ASP:C	2.60	0.40
1:BB:222:ILE:HG21	1:BB:248:LEU:HG	2.03	0.40
1:AB:302:ASP:OD2	1:AB:305:ASN:CB	2.64	0.40
1:CE:123:TYR:HB2	1:CE:185:LEU:HD21	2.02	0.40
1:BZ:100:GLN:O	1:BZ:169:THR:N	2.43	0.40
1:CB:91:ARG:HD2	1:CF:98:ILE:HB	2.03	0.40
1:CH:317:ASP:CB	1:CH:319:GLN:NE2	2.84	0.40
1:BE:130:ASP:HB3	1:BE:133:ASP:HB2	2.03	0.40
1:AC:89:LEU:HD21	1:AC:201:CYS:HB3	2.05	0.40
1:CP:317:ASP:CB	1:CP:319:GLN:NE2	2.84	0.40
1:AN:63:ILE:HG23	1:AN:88:LEU:HD11	2.04	0.40
1:AG:162:TYR:CE2	1:AG:164:ARG:HG2	2.55	0.40
1:BV:122:GLY:C	1:BV:188:VAL:CG2	2.84	0.40
1:CF:34:ARG:CG	1:BY:156:ARG:HH22	2.34	0.40
1:CB:57:LEU:HD23	1:CB:203:TRP:HH2	1.85	0.40
1:AE:80:VAL:HG13	1:AE:185:LEU:HB3	2.02	0.40
1:BR:319:GLN:C	1:BR:319:GLN:HE21	2.24	0.40
1:AQ:109:PHE:HB2	1:AQ:158:VAL:HG12	2.03	0.40
1:CB:69:PRO:O	1:CB:72:THR:OG1	2.28	0.40
1:CW:85:VAL:O	1:CW:86:PRO:C	2.60	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AE:101:ARG:CZ	1:AE:166:LEU:CD2	2.99	0.40
1:AE:124:VAL:HG11	1:AE:138:PHE:CD1	2.56	0.40
1:AV:100:GLN:NE2	1:CV:129:PRO:HB2	2.36	0.40
1:CR:60:MET:HE2	1:CR:202:ARG:HB3	2.02	0.40
1:AF:224:THR:HG22	1:AF:329:THR:N	2.36	0.40
1:CX:119:THR:O	1:CX:120:GLY:C	2.59	0.40
1:BY:300:ILE:HD13	1:AY:321:ARG:HD2	2.03	0.40
1:AQ:226:GLY:N	1:AQ:243:LEU:O	2.53	0.40
1:AB:300:ILE:HB	1:AB:309:THR:OG1	2.24	0.40
1:BA:250:ILE:O	1:BA:250:ILE:HG22	2.21	0.40
1:BT:250:ILE:HG22	1:BT:250:ILE:O	2.21	0.40
1:CQ:138:PHE:CD1	1:CQ:138:PHE:C	2.94	0.40
1:AK:226:GLY:N	1:AK:243:LEU:O	2.50	0.40
1:BU:300:ILE:HD13	1:AU:321:ARG:HD2	2.03	0.40
1:CN:284:LYS:HD3	1:CN:296:PHE:CZ	2.57	0.40
1:BL:124:VAL:HG11	1:BL:138:PHE:CD2	2.56	0.40
1:CX:284:LYS:HD3	1:CX:296:PHE:CZ	2.57	0.40
1:BT:246:THR:N	1:BT:247:PRO:CD	2.83	0.40
1:AN:114:MET:SD	1:AP:122:GLY:HA3	2.61	0.40
1:CD:141:LEU:O	1:CD:144:THR:N	2.50	0.40
1:AA:91:ARG:HD2	1:AI:143:ALA:HB1	53.80	0.40
1:CC:98:ILE:HG13	1:CC:99:PHE:CD2	2.59	0.40
1:CR:111:ILE:HG21	1:CR:123:TYR:CE1	2.56	0.40
1:AE:63:ILE:CD1	1:AE:89:LEU:HD21	2.52	0.40
1:AB:89:LEU:HD21	1:AB:201:CYS:HB3	2.06	0.40
1:BD:163:THR:C	1:BD:165:THR:HG22	2.47	0.40
1:BC:111:ILE:CG2	1:BC:112:GLN:N	2.85	0.40
1:AB:118:ASN:O	1:AF:116:PRO:HB3	145.29	0.40
1:CP:62:ARG:H	1:BQ:142:GLN:NE2	2.19	0.40
1:CV:89:LEU:HD22	1:CV:203:TRP:CD1	2.56	0.40
1:CJ:58:SER:HA	1:CJ:203:TRP:CE3	2.56	0.40
1:BE:142:GLN:HB2	1:CE:48:PHE:CE1	2.57	0.40
1:CS:197:VAL:HG22	1:CS:198:SER:N	2.36	0.40
1:CF:72:THR:O	1:CF:191:ASN:OD1	2.39	0.40
1:CR:199:VAL:O	1:CR:199:VAL:CG1	2.68	0.40
1:CM:138:PHE:C	1:CM:138:PHE:CD1	2.93	0.40
1:AJ:109:PHE:HB2	1:AJ:158:VAL:HG12	2.03	0.40
1:BJ:85:VAL:CG2	1:BJ:86:PRO:HD2	2.50	0.40
1:AU:264:SER:OG	1:AU:276:ARG:NH1	2.51	0.40
1:AU:103:ALA:HB2	1:AU:166:LEU:HA	2.03	0.40
1:AG:100:GLN:NE2	1:CG:129:PRO:HB2	2.37	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CJ:119:THR:HG22	1:CJ:119:THR:O	2.21	0.40
1:CN:264:SER:HB2	1:CN:324:LEU:HD22	2.03	0.40
1:BK:300:ILE:HG23	1:AK:323:ILE:CD1	2.51	0.40
1:BQ:109:PHE:HB2	1:BQ:158:VAL:CG1	2.52	0.40
1:AQ:234:SER:HB3	1:AQ:237:ASP:O	2.21	0.40
1:CA:214:ASN:HA	1:CA:215:PRO:HD3	1.85	0.40
1:CY:214:ASN:HA	1:CY:215:PRO:HD3	1.86	0.40
1:CB:284:LYS:HD3	1:CB:296:PHE:CZ	2.58	0.40
1:BL:109:PHE:HB2	1:BL:158:VAL:CG1	2.51	0.40
1:CS:45:VAL:HG13	1:CS:45:VAL:O	2.21	0.40
1:CZ:138:PHE:CD1	1:CZ:138:PHE:C	2.94	0.40
1:CQ:264:SER:HB2	1:CQ:324:LEU:HD22	2.02	0.40
1:BN:300:ILE:HD13	1:AN:321:ARG:HD2	2.03	0.40
1:AZ:102:TYR:O	1:AZ:167:LEU:HB2	2.20	0.40
1:AM:256:VAL:HB	1:AM:335:ASP:HB3	2.02	0.40
1:AA:288:ASN:O	1:AA:289:ALA:C	2.59	0.40
1:AG:300:ILE:HB	1:AG:309:THR:OG1	2.21	0.40
1:CE:102:TYR:HD2	1:CE:205:VAL:HG21	1.86	0.40
1:CR:81:ASP:HA	1:CR:184:ILE:HG22	2.04	0.40
1:CZ:80:VAL:HG22	1:CZ:81:ASP:N	2.37	0.40
1:CL:186:LEU:N	1:CL:186:LEU:HD23	2.36	0.40
1:CC:186:LEU:HD23	1:CC:186:LEU:N	2.37	0.40
1:CU:81:ASP:OD2	1:CU:136:HIS:NE2	2.46	0.40
1:CT:122:GLY:O	1:CT:188:VAL:CB	2.67	0.40
1:BO:100:GLN:NE2	1:BO:211:SER:CB	2.84	0.40
1:CJ:102:TYR:HD2	1:CJ:205:VAL:HG21	1.87	0.40
1:CJ:103:ALA:O	1:CJ:205:VAL:HG23	2.21	0.40
1:CH:123:TYR:HB2	1:CH:185:LEU:CD2	2.52	0.40
1:CR:123:TYR:HB2	1:CR:185:LEU:CD2	2.51	0.40
1:CR:113:PRO:HA	1:CR:197:VAL:HA	2.04	0.40
1:BF:130:ASP:HB3	1:BF:133:ASP:HB2	2.03	0.40
1:CN:123:TYR:HA	1:CN:188:VAL:HG23	2.04	0.40
1:AN:63:ILE:CD1	1:AN:89:LEU:HD21	2.52	0.40
1:BW:163:THR:O	1:BW:165:THR:HG22	2.21	0.40
1:AV:162:TYR:CE2	1:AV:164:ARG:HG2	2.56	0.40
1:BD:111:ILE:CG2	1:BD:112:GLN:N	2.87	0.40
1:AW:113:PRO:HA	1:AW:197:VAL:HA	2.03	0.40
1:BK:191:ASN:HD22	1:BK:191:ASN:H	1.69	0.40
1:AC:69:PRO:C	1:AC:72:THR:HG1	2.24	0.40
1:CQ:58:SER:HA	1:CQ:203:TRP:CE3	2.57	0.40
1:BI:139:ASP:O	1:BI:142:GLN:HG3	2.21	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BE:142:GLN:HB2	1:CE:48:PHE:HE1	1.86	0.40
1:AT:188:VAL:HG23	1:AV:114:MET:SD	2.62	0.40
1:CE:113:PRO:HA	1:CE:197:VAL:HA	2.04	0.40
1:CE:85:VAL:O	1:CE:86:PRO:C	2.60	0.40
1:BO:85:VAL:CG2	1:BO:86:PRO:HD2	2.51	0.40
1:BO:214:ASN:ND2	1:BO:215:PRO:HD2	2.37	0.40
1:CS:155:SER:O	1:CS:156:ARG:HD3	2.21	0.40
1:BM:141:LEU:HD21	1:BM:184:ILE:HG12	2.03	0.40
1:BT:184:ILE:HD13	1:BT:184:ILE:N	2.36	0.40
1:BS:141:LEU:HD21	1:BS:184:ILE:HG12	2.04	0.40
1:BP:300:ILE:HG23	1:AP:323:ILE:CD1	2.51	0.40
1:CP:284:LYS:HD3	1:CP:296:PHE:CZ	2.57	0.40
1:BW:321:ARG:HD2	1:CW:300:ILE:HD13	2.04	0.40
1:CC:219:THR:HG21	1:CC:333:ARG:O	2.20	0.40
1:CL:219:THR:HG21	1:CL:333:ARG:O	2.22	0.40
1:CB:133:ASP:O	1:CB:182:ARG:NH2	2.55	0.40
1:CQ:119:THR:O	1:CQ:120:GLY:C	2.59	0.40
1:AR:234:SER:HB3	1:AR:237:ASP:O	2.21	0.40
1:CQ:306:LYS:HE3	1:CQ:336:SER:HB2	2.03	0.40
1:AD:102:TYR:HD2	1:AD:205:VAL:HG21	1.85	0.40
1:CF:306:LYS:HE3	1:CF:336:SER:HB2	2.03	0.40
1:CA:114:MET:O	1:CA:115:CYS:HB3	2.22	0.40
1:CM:45:VAL:O	1:CM:45:VAL:HG13	2.21	0.40
1:CY:77:TYR:C	1:CY:77:TYR:CD1	2.93	0.40
1:BA:117:ALA:HB2	1:CT:117:ALA:HB1	141.43	0.40
1:CI:93:GLY:O	1:CI:97:ARG:NH1	2.53	0.40
1:BL:300:ILE:HG23	1:AL:323:ILE:CD1	2.52	0.40
1:BJ:109:PHE:HB2	1:BJ:158:VAL:CG1	2.52	0.40
1:BB:246:THR:N	1:BB:247:PRO:CD	2.85	0.40
1:BK:246:THR:N	1:BK:247:PRO:CD	2.84	0.40
1:AR:308:PHE:CE2	1:AR:310:ASP:HA	2.56	0.40
1:AR:305:ASN:ND2	1:AR:307:THR:H	2.19	0.40
1:CL:123:TYR:HA	1:CL:188:VAL:HG23	2.04	0.40
1:CL:74:THR:O	1:CL:75:ASP:C	2.59	0.40
1:CG:141:LEU:O	1:CG:144:THR:N	2.48	0.40
1:AE:263:LEU:HB3	1:AE:279:TYR:O	2.21	0.40
1:BI:100:GLN:NE2	1:BI:211:SER:CB	2.85	0.40
1:AB:143:ALA:HB1	1:AF:91:ARG:HD2	94.65	0.40
1:BW:100:GLN:NE2	1:BW:211:SER:CB	2.84	0.40
1:AB:63:ILE:HG23	1:AB:88:LEU:HD11	2.04	0.40
1:BN:163:THR:C	1:BN:165:THR:HG22	2.42	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AL:61:SER:HB2	1:AL:89:LEU:HD22	2.04	0.40
1:BM:163:THR:O	1:BM:165:THR:HG22	2.21	0.40
1:BV:122:GLY:O	1:BV:188:VAL:HG22	2.20	0.40
1:AD:106:THR:O	1:AD:203:TRP:HA	2.30	0.40
1:AX:98:ILE:HG22	1:AX:99:PHE:CD2	2.57	0.40
1:BX:111:ILE:HG22	1:BX:155:SER:HA	2.04	0.40
1:BY:123:TYR:N	1:BY:188:VAL:HG22	2.33	0.40
1:CA:112:GLN:HE21	1:CY:44:THR:H	129.31	0.40
1:AF:106:THR:O	1:AF:203:TRP:HA	2.21	0.40
1:BB:156:ARG:NH2	1:CB:34:ARG:CG	23.34	0.40
1:AI:69:PRO:C	1:AI:72:THR:HG1	2.25	0.40
1:AB:69:PRO:C	1:AB:72:THR:HG1	2.29	0.40
1:CF:58:SER:HA	1:CF:203:TRP:CE3	2.57	0.40
1:CQ:155:SER:O	1:CQ:156:ARG:HD3	2.22	0.40
1:BN:253:ASP:CB	1:BN:286:ALA:HB2	2.49	0.40
1:CM:163:THR:HG23	1:CM:164:ARG:N	2.37	0.40
1:CG:72:THR:O	1:CG:191:ASN:OD1	2.39	0.40
1:AF:80:VAL:HG13	1:AF:185:LEU:HB3	2.01	0.40
1:AD:109:PHE:CE2	1:AD:127:PHE:CD1	3.12	0.40
1:AT:101:ARG:CZ	1:AT:166:LEU:CD2	3.00	0.40
1:AQ:103:ALA:HB2	1:AQ:166:LEU:HA	2.03	0.40
1:AQ:101:ARG:NH1	1:AQ:166:LEU:HD23	2.37	0.40
1:AO:101:ARG:NH1	1:AO:166:LEU:HD23	2.37	0.40
1:CT:85:VAL:O	1:CT:86:PRO:C	2.59	0.40
1:BK:99:PHE:HA	1:BK:209:VAL:O	2.22	0.40
1:AN:137:THR:HG23	1:AN:140:ALA:HB3	2.04	0.40
1:BD:128:LEU:HD12	1:BD:184:ILE:HD11	2.05	0.40
1:CO:121:GLY:HA3	1:CO:152:TRP:HD1	1.87	0.40
1:BS:300:ILE:HG23	1:AS:323:ILE:CD1	2.52	0.40
1:BZ:300:ILE:HG23	1:AZ:323:ILE:CD1	2.52	0.40
1:BU:246:THR:N	1:BU:247:PRO:CD	2.85	0.40
1:BE:228:LEU:HD13	1:BE:238:PHE:CD2	2.56	0.40
1:AN:256:VAL:HB	1:AN:335:ASP:HB3	2.03	0.40
1:AA:238:PHE:CZ	1:AA:296:PHE:HB2	2.59	0.40
1:BN:321:ARG:HD2	1:CN:300:ILE:HD13	2.02	0.40
1:BG:126:GLY:HA3	1:BG:141:LEU:HD22	2.02	0.40
1:BX:321:ARG:HD2	1:CX:300:ILE:HD13	2.04	0.40
1:BQ:300:ILE:HG23	1:AQ:323:ILE:CD1	2.51	0.40
1:AI:137:THR:HG23	1:AI:140:ALA:CB	2.52	0.40
1:AE:288:ASN:O	1:AE:289:ALA:C	2.59	0.40
1:AS:238:PHE:CZ	1:AS:296:PHE:HB2	2.56	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BJ:321:ARG:HD2	1:CJ:300:ILE:HD13	2.03	0.40
1:BF:169:THR:HG1	1:BF:169:THR:H	1.65	0.40
1:AY:183:LEU:HG	1:AY:184:ILE:N	2.36	0.40
1:AN:100:GLN:HA	1:AN:169:THR:OG1	2.21	0.40
1:BQ:136:HIS:O	1:BQ:186:LEU:HD11	2.21	0.40
1:AZ:238:PHE:CZ	1:AZ:296:PHE:HB2	2.57	0.40
1:AR:288:ASN:O	1:AR:289:ALA:C	2.59	0.40
1:AH:100:GLN:HA	1:AH:169:THR:OG1	2.22	0.40
1:AI:238:PHE:CZ	1:AI:296:PHE:HB2	2.56	0.40
1:CV:214:ASN:HA	1:CV:215:PRO:HD3	1.82	0.40

All (71) 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:BL:297:ARG:CZ	1:CD:271:THR:OG1[4_546]	0.58	1.62
1:AC:318:GLU:CD	1:CZ:235:THR:CA[4_545]	0.93	1.27
1:BI:318:GLU:OE1	1:BI:318:GLU:OE2[2_656]	1.02	1.18
1:CQ:271:THR:O	1:Ba:290:GLY:O[4_555]	1.05	1.15
1:AC:318:GLU:CG	1:CZ:235:THR:CA[4_545]	1.06	1.14
1:CQ:271:THR:CA	1:Ba:290:GLY:CA[4_555]	1.07	1.13
1:CK:271:THR:OG1	1:BW:297:ARG:CZ[4_546]	1.16	1.04
1:BI:318:GLU:CD	1:BI:318:GLU:OE1[2_656]	1.20	1.00
1:BL:297:ARG:NE	1:CD:271:THR:OG1[4_546]	1.37	0.83
1:AC:318:GLU:CG	1:CZ:235:THR:C[4_545]	1.37	0.83
1:BL:297:ARG:NH1	1:CD:271:THR:OG1[4_546]	1.40	0.80
1:AC:318:GLU:CG	1:CZ:235:THR:N[4_545]	1.41	0.79
1:BC:271:THR:OG1	1:CZ:295:TRP:CE2[4_545]	1.41	0.79
1:BI:318:GLU:CD	1:BI:318:GLU:OE2[2_656]	1.41	0.79
1:AC:318:GLU:CD	1:CZ:235:THR:N[4_545]	1.44	0.76
1:AC:318:GLU:CB	1:CZ:235:THR:N[4_545]	1.48	0.72
1:BI:318:GLU:CG	1:BI:318:GLU:CD[2_656]	1.55	0.65
1:CQ:270:GLY:O	1:Ba:290:GLY:N[4_555]	1.56	0.64
1:AC:318:GLU:OE1	1:CZ:235:THR:N[4_545]	1.56	0.64
1:BI:318:GLU:CG	1:BI:318:GLU:CG[2_656]	1.57	0.63
1:BL:297:ARG:NH2	1:CD:271:THR:OG1[4_546]	1.59	0.61
1:CQ:271:THR:C	1:Ba:290:GLY:O[4_555]	1.60	0.60
1:BC:271:THR:OG1	1:CZ:295:TRP:CZ2[4_545]	1.62	0.58
1:CK:271:THR:OG1	1:BW:297:ARG:NH2[4_546]	1.64	0.56
1:AC:318:GLU:CG	1:CZ:236:ASN:N[4_545]	1.71	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BC:271:THR:OG1	1:CZ:295:TRP:CD2[4_545]	1.72	0.48
1:CK:271:THR:OG1	1:BW:297:ARG:NE[4_546]	1.75	0.45
1:BC:315:TYR:OH	1:CZ:290:GLY:CA[4_545]	1.78	0.42
1:CQ:271:THR:CA	1:Ba:290:GLY:C[4_555]	1.79	0.41
1:CQ:271:THR:C	1:Ba:290:GLY:C[4_555]	1.80	0.40
1:BI:318:GLU:OE1	1:BI:318:GLU:OE1[2_656]	1.80	0.40
1:AC:318:GLU:OE1	1:CZ:235:THR:CA[4_545]	1.81	0.39
1:AC:318:GLU:OE2	1:CZ:235:THR:CA[4_545]	1.84	0.36
1:CQ:271:THR:N	1:Ba:290:GLY:CA[4_555]	1.84	0.36
1:BC:269:LEU:O	1:CZ:295:TRP:NE1[4_545]	1.86	0.34
1:CK:271:THR:OG1	1:BW:297:ARG:NH1[4_546]	1.86	0.34
1:AP:297:ARG:NH2	1:BR:315:TYR:OH[4_555]	1.88	0.32
1:CK:270:GLY:O	1:BW:237:ASP:OD2[4_546]	1.88	0.32
1:BI:318:GLU:CG	1:BI:318:GLU:OE2[2_656]	1.92	0.28
1:Be:236:ASN:ND2	1:Be:270:GLY:O[2_556]	1.94	0.26
1:CQ:271:THR:O	1:Ba:290:GLY:C[4_555]	1.96	0.24
1:BC:315:TYR:OH	1:CZ:290:GLY:N[4_545]	1.96	0.24
1:BC:315:TYR:OH	1:CZ:291:THR:N[4_545]	1.96	0.24
1:BC:271:THR:OG1	1:CZ:295:TRP:CH2[4_545]	1.96	0.24
1:CQ:271:THR:C	1:Ba:290:GLY:CA[4_555]	1.98	0.22
1:CP:271:THR:OG1	1:CT:288:ASN:ND2[4_555]	1.98	0.22
1:BL:237:ASP:CB	1:Cd:270:GLY:O[4_546]	1.99	0.21
1:CK:270:GLY:O	1:BW:237:ASP:CG[4_546]	1.99	0.21
1:BL:297:ARG:CZ	1:Cd:271:THR:CB[4_546]	2.00	0.20
1:BJ:153:TRP:O	1:CL:151:LYS:NZ[2_555]	2.02	0.18
1:CP:270:GLY:O	1:CT:288:ASN:CB[4_555]	2.04	0.16
1:AC:318:GLU:CD	1:CZ:235:THR:C[4_545]	2.04	0.16
1:BC:269:LEU:O	1:CZ:295:TRP:CD1[4_545]	2.05	0.15
1:BL:237:ASP:CG	1:Cd:270:GLY:O[4_546]	2.05	0.15
1:BC:269:LEU:C	1:CZ:295:TRP:NE1[4_545]	2.05	0.15
1:CA:288:ASN:ND2	1:AJ:273:ASP:OD1[4_555]	2.06	0.14
1:BC:271:THR:OG1	1:CZ:295:TRP:CE3[4_545]	2.08	0.12
1:CR:151:LYS:NZ	1:BX:153:TRP:O[2_555]	2.08	0.12
1:CQ:271:THR:CA	1:Ba:290:GLY:O[4_555]	2.08	0.12
1:BC:315:TYR:OH	1:CZ:290:GLY:C[4_545]	2.08	0.12
1:BI:318:GLU:CB	1:BI:318:GLU:CG[2_656]	2.09	0.11
1:AC:318:GLU:CD	1:CZ:234:SER:C[4_545]	2.10	0.10
1:AC:318:GLU:OE2	1:CZ:314:TYR:CB[4_545]	2.12	0.08
1:CQ:271:THR:CG2	1:Ba:290:GLY:O[4_555]	2.13	0.07
1:AC:318:GLU:N	1:CZ:235:THR:CB[4_545]	2.14	0.06
1:AC:318:GLU:CG	1:CZ:235:THR:CB[4_545]	2.16	0.04

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AC:318:GLU:OE2	1:CZ:235:THR:C[4_545]	2.16	0.04
1:BC:271:THR:OG1	1:CZ:295:TRP:CZ3[4_545]	2.16	0.04
1:AC:318:GLU:CG	1:CZ:234:SER:C[4_545]	2.17	0.03
1:AC:318:GLU:OE2	1:CZ:235:THR:O[4_545]	2.17	0.03
1:AC:318:GLU:CA	1:CZ:235:THR:OG1[4_545]	2.18	0.02

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 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	AA	285/338 (84%)	277 (97%)	8 (3%)	0	100	100
1	AB	285/338 (84%)	278 (98%)	7 (2%)	0	100	100
1	AC	285/338 (84%)	277 (97%)	8 (3%)	0	100	100
1	AD	285/338 (84%)	276 (97%)	9 (3%)	0	100	100
1	AE	285/338 (84%)	277 (97%)	8 (3%)	0	100	100
1	AF	285/338 (84%)	278 (98%)	7 (2%)	0	100	100
1	AG	285/338 (84%)	276 (97%)	9 (3%)	0	100	100
1	AH	285/338 (84%)	277 (97%)	8 (3%)	0	100	100
1	AI	285/338 (84%)	278 (98%)	7 (2%)	0	100	100
1	AJ	285/338 (84%)	277 (97%)	8 (3%)	0	100	100
1	AK	285/338 (84%)	277 (97%)	8 (3%)	0	100	100
1	AL	285/338 (84%)	275 (96%)	10 (4%)	0	100	100
1	AM	285/338 (84%)	279 (98%)	6 (2%)	0	100	100
1	AN	285/338 (84%)	276 (97%)	9 (3%)	0	100	100
1	AO	285/338 (84%)	277 (97%)	8 (3%)	0	100	100
1	AP	285/338 (84%)	277 (97%)	8 (3%)	0	100	100
1	AQ	285/338 (84%)	276 (97%)	9 (3%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AR	285/338 (84%)	278 (98%)	7 (2%)	0	100	100
1	AS	285/338 (84%)	276 (97%)	9 (3%)	0	100	100
1	AT	285/338 (84%)	278 (98%)	7 (2%)	0	100	100
1	AU	285/338 (84%)	276 (97%)	9 (3%)	0	100	100
1	AV	285/338 (84%)	276 (97%)	9 (3%)	0	100	100
1	AW	285/338 (84%)	275 (96%)	10 (4%)	0	100	100
1	AX	285/338 (84%)	278 (98%)	7 (2%)	0	100	100
1	AY	285/338 (84%)	276 (97%)	9 (3%)	0	100	100
1	AZ	285/338 (84%)	279 (98%)	6 (2%)	0	100	100
1	Aa	285/338 (84%)	278 (98%)	7 (2%)	0	100	100
1	Ab	285/338 (84%)	277 (97%)	8 (3%)	0	100	100
1	Ac	285/338 (84%)	276 (97%)	9 (3%)	0	100	100
1	Ad	285/338 (84%)	276 (97%)	9 (3%)	0	100	100
1	BA	284/338 (84%)	281 (99%)	3 (1%)	0	100	100
1	BB	284/338 (84%)	280 (99%)	4 (1%)	0	100	100
1	BC	284/338 (84%)	281 (99%)	3 (1%)	0	100	100
1	BD	284/338 (84%)	282 (99%)	2 (1%)	0	100	100
1	BE	284/338 (84%)	282 (99%)	2 (1%)	0	100	100
1	BF	284/338 (84%)	280 (99%)	4 (1%)	0	100	100
1	BG	284/338 (84%)	281 (99%)	3 (1%)	0	100	100
1	BH	284/338 (84%)	282 (99%)	2 (1%)	0	100	100
1	BI	284/338 (84%)	281 (99%)	3 (1%)	0	100	100
1	BJ	284/338 (84%)	280 (99%)	4 (1%)	0	100	100
1	BK	284/338 (84%)	280 (99%)	4 (1%)	0	100	100
1	BL	284/338 (84%)	281 (99%)	3 (1%)	0	100	100
1	BM	284/338 (84%)	280 (99%)	4 (1%)	0	100	100
1	BN	284/338 (84%)	282 (99%)	2 (1%)	0	100	100
1	BO	284/338 (84%)	281 (99%)	3 (1%)	0	100	100
1	BP	284/338 (84%)	279 (98%)	5 (2%)	0	100	100
1	BQ	284/338 (84%)	281 (99%)	3 (1%)	0	100	100
1	BR	284/338 (84%)	278 (98%)	6 (2%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	BS	284/338 (84%)	282 (99%)	2 (1%)	0	100	100
1	BT	284/338 (84%)	281 (99%)	3 (1%)	0	100	100
1	BU	284/338 (84%)	282 (99%)	2 (1%)	0	100	100
1	BV	284/338 (84%)	283 (100%)	1 (0%)	0	100	100
1	BW	284/338 (84%)	281 (99%)	3 (1%)	0	100	100
1	BX	284/338 (84%)	282 (99%)	2 (1%)	0	100	100
1	BY	284/338 (84%)	282 (99%)	2 (1%)	0	100	100
1	BZ	284/338 (84%)	280 (99%)	4 (1%)	0	100	100
1	Ba	284/338 (84%)	279 (98%)	5 (2%)	0	100	100
1	Bb	284/338 (84%)	282 (99%)	2 (1%)	0	100	100
1	Bc	284/338 (84%)	281 (99%)	3 (1%)	0	100	100
1	Bd	284/338 (84%)	281 (99%)	3 (1%)	0	100	100
1	CA	302/338 (89%)	288 (95%)	14 (5%)	0	100	100
1	CB	302/338 (89%)	287 (95%)	15 (5%)	0	100	100
1	CC	302/338 (89%)	288 (95%)	14 (5%)	0	100	100
1	CD	302/338 (89%)	288 (95%)	14 (5%)	0	100	100
1	CE	302/338 (89%)	288 (95%)	14 (5%)	0	100	100
1	CF	302/338 (89%)	287 (95%)	15 (5%)	0	100	100
1	CG	302/338 (89%)	288 (95%)	14 (5%)	0	100	100
1	CH	302/338 (89%)	288 (95%)	14 (5%)	0	100	100
1	CI	302/338 (89%)	287 (95%)	15 (5%)	0	100	100
1	CJ	302/338 (89%)	289 (96%)	13 (4%)	0	100	100
1	CK	302/338 (89%)	286 (95%)	16 (5%)	0	100	100
1	CL	302/338 (89%)	287 (95%)	15 (5%)	0	100	100
1	CM	302/338 (89%)	287 (95%)	15 (5%)	0	100	100
1	CN	302/338 (89%)	287 (95%)	15 (5%)	0	100	100
1	CO	302/338 (89%)	288 (95%)	14 (5%)	0	100	100
1	CP	302/338 (89%)	287 (95%)	15 (5%)	0	100	100
1	CQ	302/338 (89%)	287 (95%)	15 (5%)	0	100	100
1	CR	302/338 (89%)	287 (95%)	15 (5%)	0	100	100
1	CS	302/338 (89%)	290 (96%)	12 (4%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	CT	302/338 (89%)	285 (94%)	17 (6%)	0	100	100
1	CU	302/338 (89%)	285 (94%)	17 (6%)	0	100	100
1	CV	302/338 (89%)	286 (95%)	16 (5%)	0	100	100
1	CW	302/338 (89%)	286 (95%)	16 (5%)	0	100	100
1	CX	302/338 (89%)	289 (96%)	13 (4%)	0	100	100
1	CY	302/338 (89%)	287 (95%)	15 (5%)	0	100	100
1	CZ	302/338 (89%)	286 (95%)	16 (5%)	0	100	100
1	Ca	302/338 (89%)	287 (95%)	15 (5%)	0	100	100
1	Cb	302/338 (89%)	287 (95%)	15 (5%)	0	100	100
1	Cc	302/338 (89%)	290 (96%)	12 (4%)	0	100	100
1	Cd	302/338 (89%)	289 (96%)	13 (4%)	0	100	100
All	All	26130/30420 (86%)	25356 (97%)	774 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	AA	242/283 (86%)	209 (86%)	33 (14%)	5	29
1	AB	242/283 (86%)	206 (85%)	36 (15%)	4	25
1	AC	242/283 (86%)	207 (86%)	35 (14%)	4	26
1	AD	242/283 (86%)	208 (86%)	34 (14%)	4	28
1	AE	242/283 (86%)	206 (85%)	36 (15%)	4	25
1	AF	242/283 (86%)	208 (86%)	34 (14%)	4	28
1	AG	242/283 (86%)	208 (86%)	34 (14%)	4	28
1	AH	242/283 (86%)	209 (86%)	33 (14%)	5	29
1	AI	242/283 (86%)	206 (85%)	36 (15%)	4	25
1	AJ	242/283 (86%)	209 (86%)	33 (14%)	5	29

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AK	242/283 (86%)	209 (86%)	33 (14%)	5	29
1	AL	242/283 (86%)	207 (86%)	35 (14%)	4	26
1	AM	242/283 (86%)	211 (87%)	31 (13%)	5	31
1	AN	242/283 (86%)	209 (86%)	33 (14%)	5	29
1	AO	242/283 (86%)	209 (86%)	33 (14%)	5	29
1	AP	242/283 (86%)	210 (87%)	32 (13%)	5	30
1	AQ	242/283 (86%)	208 (86%)	34 (14%)	4	28
1	AR	242/283 (86%)	205 (85%)	37 (15%)	3	24
1	AS	242/283 (86%)	207 (86%)	35 (14%)	4	26
1	AT	242/283 (86%)	208 (86%)	34 (14%)	4	28
1	AU	242/283 (86%)	207 (86%)	35 (14%)	4	26
1	AV	242/283 (86%)	207 (86%)	35 (14%)	4	26
1	AW	242/283 (86%)	208 (86%)	34 (14%)	4	28
1	AX	242/283 (86%)	208 (86%)	34 (14%)	4	28
1	AY	242/283 (86%)	210 (87%)	32 (13%)	5	30
1	AZ	242/283 (86%)	210 (87%)	32 (13%)	5	30
1	Aa	242/283 (86%)	208 (86%)	34 (14%)	4	28
1	Ab	242/283 (86%)	206 (85%)	36 (15%)	4	25
1	Ac	242/283 (86%)	208 (86%)	34 (14%)	4	28
1	Ad	242/283 (86%)	209 (86%)	33 (14%)	5	29
1	BA	242/283 (86%)	213 (88%)	29 (12%)	6	33
1	BB	242/283 (86%)	212 (88%)	30 (12%)	6	32
1	BC	242/283 (86%)	214 (88%)	28 (12%)	7	36
1	BD	242/283 (86%)	215 (89%)	27 (11%)	7	38
1	BE	242/283 (86%)	215 (89%)	27 (11%)	7	38
1	BF	242/283 (86%)	214 (88%)	28 (12%)	7	36
1	BG	242/283 (86%)	214 (88%)	28 (12%)	7	36
1	BH	242/283 (86%)	216 (89%)	26 (11%)	8	40
1	BI	242/283 (86%)	213 (88%)	29 (12%)	6	33
1	BJ	242/283 (86%)	215 (89%)	27 (11%)	7	38
1	BK	242/283 (86%)	215 (89%)	27 (11%)	7	38

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	BL	242/283 (86%)	214 (88%)	28 (12%)	7	36
1	BM	242/283 (86%)	214 (88%)	28 (12%)	7	36
1	BN	242/283 (86%)	214 (88%)	28 (12%)	7	36
1	BO	242/283 (86%)	214 (88%)	28 (12%)	7	36
1	BP	242/283 (86%)	214 (88%)	28 (12%)	7	36
1	BQ	242/283 (86%)	215 (89%)	27 (11%)	7	38
1	BR	242/283 (86%)	215 (89%)	27 (11%)	7	38
1	BS	242/283 (86%)	215 (89%)	27 (11%)	7	38
1	BT	242/283 (86%)	214 (88%)	28 (12%)	7	36
1	BU	242/283 (86%)	214 (88%)	28 (12%)	7	36
1	BV	242/283 (86%)	215 (89%)	27 (11%)	7	38
1	BW	242/283 (86%)	216 (89%)	26 (11%)	8	40
1	BX	242/283 (86%)	215 (89%)	27 (11%)	7	38
1	BY	242/283 (86%)	215 (89%)	27 (11%)	7	38
1	BZ	242/283 (86%)	214 (88%)	28 (12%)	7	36
1	Ba	242/283 (86%)	215 (89%)	27 (11%)	7	38
1	Bb	242/283 (86%)	214 (88%)	28 (12%)	7	36
1	Bc	242/283 (86%)	213 (88%)	29 (12%)	6	33
1	Bd	242/283 (86%)	213 (88%)	29 (12%)	6	33
1	CA	255/283 (90%)	229 (90%)	26 (10%)	9	42
1	CB	255/283 (90%)	230 (90%)	25 (10%)	10	44
1	CC	255/283 (90%)	229 (90%)	26 (10%)	9	42
1	CD	255/283 (90%)	229 (90%)	26 (10%)	9	42
1	CE	255/283 (90%)	227 (89%)	28 (11%)	8	39
1	CF	255/283 (90%)	230 (90%)	25 (10%)	10	44
1	CG	255/283 (90%)	226 (89%)	29 (11%)	7	36
1	CH	255/283 (90%)	229 (90%)	26 (10%)	9	42
1	CI	255/283 (90%)	228 (89%)	27 (11%)	8	40
1	CJ	255/283 (90%)	229 (90%)	26 (10%)	9	42
1	CK	255/283 (90%)	228 (89%)	27 (11%)	8	40
1	CL	255/283 (90%)	231 (91%)	24 (9%)	11	47

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	CM	255/283 (90%)	229 (90%)	26 (10%)	9	42
1	CN	255/283 (90%)	228 (89%)	27 (11%)	8	40
1	CO	255/283 (90%)	230 (90%)	25 (10%)	10	44
1	CP	255/283 (90%)	230 (90%)	25 (10%)	10	44
1	CQ	255/283 (90%)	229 (90%)	26 (10%)	9	42
1	CR	255/283 (90%)	230 (90%)	25 (10%)	10	44
1	CS	255/283 (90%)	228 (89%)	27 (11%)	8	40
1	CT	255/283 (90%)	230 (90%)	25 (10%)	10	44
1	CU	255/283 (90%)	228 (89%)	27 (11%)	8	40
1	CV	255/283 (90%)	227 (89%)	28 (11%)	8	39
1	CW	255/283 (90%)	228 (89%)	27 (11%)	8	40
1	CX	255/283 (90%)	228 (89%)	27 (11%)	8	40
1	CY	255/283 (90%)	228 (89%)	27 (11%)	8	40
1	CZ	255/283 (90%)	228 (89%)	27 (11%)	8	40
1	Ca	255/283 (90%)	228 (89%)	27 (11%)	8	40
1	Cb	255/283 (90%)	229 (90%)	26 (10%)	9	42
1	Cc	255/283 (90%)	228 (89%)	27 (11%)	8	40
1	Cd	255/283 (90%)	231 (91%)	24 (9%)	11	47
All	All	22170/25470 (87%)	19531 (88%)	2639 (12%)	6	34

All (2639) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	BA	57	LEU
1	BA	58	SER
1	BA	63	ILE
1	BA	67	VAL
1	BA	68	LEU
1	BA	78	VAL
1	BA	79	VAL
1	BA	88	LEU
1	BA	92	LEU
1	BA	100	GLN
1	BA	104	VAL
1	BA	105	GLU
1	BA	134	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	BA	142	GLN
1	BA	145	ARG
1	BA	156	ARG
1	BA	165	THR
1	BA	167	LEU
1	BA	183	LEU
1	BA	184	ILE
1	BA	191	ASN
1	BA	193	ASP
1	BA	196	ASN
1	BA	198	SER
1	BA	207	LEU
1	BA	212	LEU
1	BA	225	GLN
1	BA	271	THR
1	BA	319	GLN
1	AA	54	ASP
1	AA	62	ARG
1	AA	72	THR
1	AA	74	THR
1	AA	75	ASP
1	AA	87	ASP
1	AA	118	ASN
1	AA	124	VAL
1	AA	128	LEU
1	AA	137	THR
1	AA	141	LEU
1	AA	142	GLN
1	AA	149	VAL
1	AA	159	ARG
1	AA	162	TYR
1	AA	163	THR
1	AA	165	THR
1	AA	167	LEU
1	AA	170	SER
1	AA	176	ARG
1	AA	183	LEU
1	AA	196	ASN
1	AA	208	SER
1	AA	211	SER
1	AA	225	GLN
1	AA	236	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	AA	253	ASP
1	AA	264	SER
1	AA	271	THR
1	AA	304	PHE
1	AA	312	VAL
1	AA	315	TYR
1	AA	317	ASP
1	CA	35	THR
1	CA	43	SER
1	CA	48	PHE
1	CA	72	THR
1	CA	74	THR
1	CA	75	ASP
1	CA	77	TYR
1	CA	87	ASP
1	CA	101	ARG
1	CA	112	GLN
1	CA	114	MET
1	CA	137	THR
1	CA	141	LEU
1	CA	151	LYS
1	CA	156	ARG
1	CA	175	GLN
1	CA	176	ARG
1	CA	177	LEU
1	CA	185	LEU
1	CA	198	SER
1	CA	204	SER
1	CA	208	SER
1	CA	231	ASP
1	CA	288	ASN
1	CA	316	SER
1	CA	337	GLU
1	BB	57	LEU
1	BB	58	SER
1	BB	63	ILE
1	BB	67	VAL
1	BB	68	LEU
1	BB	78	VAL
1	BB	79	VAL
1	BB	88	LEU
1	BB	92	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	BB	100	GLN
1	BB	104	VAL
1	BB	105	GLU
1	BB	134	ASN
1	BB	139	ASP
1	BB	142	GLN
1	BB	145	ARG
1	BB	156	ARG
1	BB	165	THR
1	BB	167	LEU
1	BB	183	LEU
1	BB	184	ILE
1	BB	191	ASN
1	BB	196	ASN
1	BB	198	SER
1	BB	202	ARG
1	BB	207	LEU
1	BB	212	LEU
1	BB	271	THR
1	BB	310	ASP
1	BB	319	GLN
1	AB	54	ASP
1	AB	58	SER
1	AB	62	ARG
1	AB	72	THR
1	AB	74	THR
1	AB	75	ASP
1	AB	83	THR
1	AB	87	ASP
1	AB	128	LEU
1	AB	137	THR
1	AB	141	LEU
1	AB	142	GLN
1	AB	144	THR
1	AB	149	VAL
1	AB	157	THR
1	AB	159	ARG
1	AB	162	TYR
1	AB	163	THR
1	AB	165	THR
1	AB	167	LEU
1	AB	170	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	AB	176	ARG
1	AB	183	LEU
1	AB	196	ASN
1	AB	208	SER
1	AB	211	SER
1	AB	212	LEU
1	AB	225	GLN
1	AB	236	ASN
1	AB	253	ASP
1	AB	264	SER
1	AB	271	THR
1	AB	304	PHE
1	AB	312	VAL
1	AB	315	TYR
1	AB	317	ASP
1	CB	35	THR
1	CB	43	SER
1	CB	48	PHE
1	CB	72	THR
1	CB	74	THR
1	CB	75	ASP
1	CB	77	TYR
1	CB	87	ASP
1	CB	101	ARG
1	CB	112	GLN
1	CB	114	MET
1	CB	137	THR
1	CB	141	LEU
1	CB	151	LYS
1	CB	156	ARG
1	CB	175	GLN
1	CB	176	ARG
1	CB	177	LEU
1	CB	185	LEU
1	CB	198	SER
1	CB	204	SER
1	CB	231	ASP
1	CB	288	ASN
1	CB	316	SER
1	CB	337	GLU
1	BC	57	LEU
1	BC	58	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	BC	63	ILE
1	BC	67	VAL
1	BC	68	LEU
1	BC	78	VAL
1	BC	79	VAL
1	BC	88	LEU
1	BC	92	LEU
1	BC	100	GLN
1	BC	104	VAL
1	BC	105	GLU
1	BC	134	ASN
1	BC	145	ARG
1	BC	156	ARG
1	BC	165	THR
1	BC	167	LEU
1	BC	183	LEU
1	BC	184	ILE
1	BC	191	ASN
1	BC	193	ASP
1	BC	196	ASN
1	BC	198	SER
1	BC	202	ARG
1	BC	207	LEU
1	BC	212	LEU
1	BC	271	THR
1	BC	319	GLN
1	AC	54	ASP
1	AC	58	SER
1	AC	62	ARG
1	AC	72	THR
1	AC	74	THR
1	AC	75	ASP
1	AC	87	ASP
1	AC	101	ARG
1	AC	118	ASN
1	AC	124	VAL
1	AC	128	LEU
1	AC	137	THR
1	AC	141	LEU
1	AC	142	GLN
1	AC	149	VAL
1	AC	159	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	AC	162	TYR
1	AC	163	THR
1	AC	165	THR
1	AC	167	LEU
1	AC	170	SER
1	AC	176	ARG
1	AC	183	LEU
1	AC	196	ASN
1	AC	208	SER
1	AC	211	SER
1	AC	225	GLN
1	AC	236	ASN
1	AC	253	ASP
1	AC	264	SER
1	AC	271	THR
1	AC	304	PHE
1	AC	312	VAL
1	AC	315	TYR
1	AC	317	ASP
1	CC	35	THR
1	CC	43	SER
1	CC	48	PHE
1	CC	54	ASP
1	CC	72	THR
1	CC	74	THR
1	CC	75	ASP
1	CC	77	TYR
1	CC	87	ASP
1	CC	101	ARG
1	CC	112	GLN
1	CC	114	MET
1	CC	137	THR
1	CC	141	LEU
1	CC	151	LYS
1	CC	156	ARG
1	CC	175	GLN
1	CC	176	ARG
1	CC	177	LEU
1	CC	185	LEU
1	CC	198	SER
1	CC	204	SER
1	CC	231	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	CC	288	ASN
1	CC	316	SER
1	CC	337	GLU
1	BD	57	LEU
1	BD	58	SER
1	BD	63	ILE
1	BD	67	VAL
1	BD	68	LEU
1	BD	78	VAL
1	BD	79	VAL
1	BD	88	LEU
1	BD	92	LEU
1	BD	100	GLN
1	BD	104	VAL
1	BD	105	GLU
1	BD	134	ASN
1	BD	145	ARG
1	BD	156	ARG
1	BD	165	THR
1	BD	167	LEU
1	BD	183	LEU
1	BD	184	ILE
1	BD	191	ASN
1	BD	193	ASP
1	BD	196	ASN
1	BD	198	SER
1	BD	207	LEU
1	BD	212	LEU
1	BD	271	THR
1	BD	319	GLN
1	AD	54	ASP
1	AD	58	SER
1	AD	62	ARG
1	AD	72	THR
1	AD	74	THR
1	AD	75	ASP
1	AD	87	ASP
1	AD	124	VAL
1	AD	128	LEU
1	AD	137	THR
1	AD	141	LEU
1	AD	142	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	AD	144	THR
1	AD	149	VAL
1	AD	159	ARG
1	AD	162	TYR
1	AD	163	THR
1	AD	165	THR
1	AD	167	LEU
1	AD	170	SER
1	AD	176	ARG
1	AD	183	LEU
1	AD	196	ASN
1	AD	208	SER
1	AD	211	SER
1	AD	225	GLN
1	AD	236	ASN
1	AD	253	ASP
1	AD	264	SER
1	AD	271	THR
1	AD	304	PHE
1	AD	312	VAL
1	AD	315	TYR
1	AD	317	ASP
1	CD	35	THR
1	CD	43	SER
1	CD	54	ASP
1	CD	72	THR
1	CD	74	THR
1	CD	75	ASP
1	CD	77	TYR
1	CD	87	ASP
1	CD	101	ARG
1	CD	112	GLN
1	CD	114	MET
1	CD	137	THR
1	CD	141	LEU
1	CD	151	LYS
1	CD	156	ARG
1	CD	175	GLN
1	CD	176	ARG
1	CD	177	LEU
1	CD	185	LEU
1	CD	198	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	CD	204	SER
1	CD	208	SER
1	CD	231	ASP
1	CD	288	ASN
1	CD	316	SER
1	CD	337	GLU
1	BE	57	LEU
1	BE	58	SER
1	BE	63	ILE
1	BE	67	VAL
1	BE	68	LEU
1	BE	78	VAL
1	BE	79	VAL
1	BE	88	LEU
1	BE	92	LEU
1	BE	100	GLN
1	BE	104	VAL
1	BE	105	GLU
1	BE	134	ASN
1	BE	145	ARG
1	BE	156	ARG
1	BE	165	THR
1	BE	167	LEU
1	BE	183	LEU
1	BE	184	ILE
1	BE	191	ASN
1	BE	193	ASP
1	BE	196	ASN
1	BE	198	SER
1	BE	207	LEU
1	BE	212	LEU
1	BE	271	THR
1	BE	319	GLN
1	AE	54	ASP
1	AE	58	SER
1	AE	62	ARG
1	AE	72	THR
1	AE	74	THR
1	AE	75	ASP
1	AE	87	ASP
1	AE	101	ARG
1	AE	118	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	AE	128	LEU
1	AE	137	THR
1	AE	141	LEU
1	AE	142	GLN
1	AE	144	THR
1	AE	149	VAL
1	AE	157	THR
1	AE	159	ARG
1	AE	162	TYR
1	AE	163	THR
1	AE	165	THR
1	AE	167	LEU
1	AE	170	SER
1	AE	176	ARG
1	AE	183	LEU
1	AE	196	ASN
1	AE	208	SER
1	AE	211	SER
1	AE	225	GLN
1	AE	236	ASN
1	AE	253	ASP
1	AE	264	SER
1	AE	271	THR
1	AE	304	PHE
1	AE	312	VAL
1	AE	315	TYR
1	AE	317	ASP
1	CE	35	THR
1	CE	43	SER
1	CE	48	PHE
1	CE	72	THR
1	CE	74	THR
1	CE	75	ASP
1	CE	77	TYR
1	CE	87	ASP
1	CE	101	ARG
1	CE	106	THR
1	CE	112	GLN
1	CE	114	MET
1	CE	137	THR
1	CE	141	LEU
1	CE	151	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	CE	156	ARG
1	CE	175	GLN
1	CE	176	ARG
1	CE	177	LEU
1	CE	185	LEU
1	CE	186	LEU
1	CE	198	SER
1	CE	204	SER
1	CE	208	SER
1	CE	231	ASP
1	CE	288	ASN
1	CE	316	SER
1	CE	337	GLU
1	BF	57	LEU
1	BF	58	SER
1	BF	63	ILE
1	BF	67	VAL
1	BF	68	LEU
1	BF	78	VAL
1	BF	79	VAL
1	BF	88	LEU
1	BF	92	LEU
1	BF	100	GLN
1	BF	104	VAL
1	BF	105	GLU
1	BF	134	ASN
1	BF	145	ARG
1	BF	156	ARG
1	BF	165	THR
1	BF	167	LEU
1	BF	183	LEU
1	BF	184	ILE
1	BF	191	ASN
1	BF	193	ASP
1	BF	196	ASN
1	BF	198	SER
1	BF	202	ARG
1	BF	207	LEU
1	BF	212	LEU
1	BF	271	THR
1	BF	319	GLN
1	AF	54	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	AF	58	SER
1	AF	62	ARG
1	AF	72	THR
1	AF	74	THR
1	AF	75	ASP
1	AF	87	ASP
1	AF	118	ASN
1	AF	124	VAL
1	AF	128	LEU
1	AF	137	THR
1	AF	141	LEU
1	AF	142	GLN
1	AF	149	VAL
1	AF	159	ARG
1	AF	162	TYR
1	AF	163	THR
1	AF	165	THR
1	AF	167	LEU
1	AF	170	SER
1	AF	176	ARG
1	AF	183	LEU
1	AF	196	ASN
1	AF	208	SER
1	AF	211	SER
1	AF	225	GLN
1	AF	236	ASN
1	AF	253	ASP
1	AF	264	SER
1	AF	271	THR
1	AF	304	PHE
1	AF	312	VAL
1	AF	315	TYR
1	AF	317	ASP
1	CF	35	THR
1	CF	43	SER
1	CF	48	PHE
1	CF	72	THR
1	CF	74	THR
1	CF	75	ASP
1	CF	77	TYR
1	CF	87	ASP
1	CF	101	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	CF	112	GLN
1	CF	114	MET
1	CF	137	THR
1	CF	141	LEU
1	CF	151	LYS
1	CF	156	ARG
1	CF	175	GLN
1	CF	176	ARG
1	CF	177	LEU
1	CF	185	LEU
1	CF	198	SER
1	CF	204	SER
1	CF	231	ASP
1	CF	288	ASN
1	CF	316	SER
1	CF	337	GLU
1	BG	57	LEU
1	BG	58	SER
1	BG	63	ILE
1	BG	67	VAL
1	BG	68	LEU
1	BG	78	VAL
1	BG	79	VAL
1	BG	88	LEU
1	BG	92	LEU
1	BG	100	GLN
1	BG	104	VAL
1	BG	105	GLU
1	BG	134	ASN
1	BG	145	ARG
1	BG	156	ARG
1	BG	165	THR
1	BG	167	LEU
1	BG	183	LEU
1	BG	184	ILE
1	BG	191	ASN
1	BG	193	ASP
1	BG	196	ASN
1	BG	198	SER
1	BG	202	ARG
1	BG	207	LEU
1	BG	212	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	BG	271	THR
1	BG	319	GLN
1	AG	54	ASP
1	AG	58	SER
1	AG	62	ARG
1	AG	72	THR
1	AG	74	THR
1	AG	75	ASP
1	AG	83	THR
1	AG	87	ASP
1	AG	128	LEU
1	AG	137	THR
1	AG	141	LEU
1	AG	142	GLN
1	AG	149	VAL
1	AG	159	ARG
1	AG	162	TYR
1	AG	163	THR
1	AG	165	THR
1	AG	167	LEU
1	AG	170	SER
1	AG	176	ARG
1	AG	183	LEU
1	AG	196	ASN
1	AG	208	SER
1	AG	211	SER
1	AG	212	LEU
1	AG	225	GLN
1	AG	236	ASN
1	AG	253	ASP
1	AG	264	SER
1	AG	271	THR
1	AG	304	PHE
1	AG	312	VAL
1	AG	315	TYR
1	AG	317	ASP
1	CG	35	THR
1	CG	43	SER
1	CG	48	PHE
1	CG	54	ASP
1	CG	72	THR
1	CG	74	THR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	CG	75	ASP
1	CG	77	TYR
1	CG	87	ASP
1	CG	101	ARG
1	CG	106	THR
1	CG	112	GLN
1	CG	114	MET
1	CG	137	THR
1	CG	141	LEU
1	CG	151	LYS
1	CG	156	ARG
1	CG	175	GLN
1	CG	176	ARG
1	CG	177	LEU
1	CG	185	LEU
1	CG	186	LEU
1	CG	198	SER
1	CG	204	SER
1	CG	208	SER
1	CG	231	ASP
1	CG	288	ASN
1	CG	316	SER
1	CG	337	GLU
1	BH	57	LEU
1	BH	58	SER
1	BH	63	ILE
1	BH	67	VAL
1	BH	68	LEU
1	BH	78	VAL
1	BH	79	VAL
1	BH	88	LEU
1	BH	92	LEU
1	BH	100	GLN
1	BH	104	VAL
1	BH	105	GLU
1	BH	134	ASN
1	BH	145	ARG
1	BH	156	ARG
1	BH	165	THR
1	BH	167	LEU
1	BH	183	LEU
1	BH	184	ILE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	BH	191	ASN
1	BH	196	ASN
1	BH	198	SER
1	BH	207	LEU
1	BH	212	LEU
1	BH	271	THR
1	BH	319	GLN
1	AH	54	ASP
1	AH	58	SER
1	AH	62	ARG
1	AH	72	THR
1	AH	74	THR
1	AH	75	ASP
1	AH	87	ASP
1	AH	128	LEU
1	AH	137	THR
1	AH	141	LEU
1	AH	142	GLN
1	AH	144	THR
1	AH	149	VAL
1	AH	159	ARG
1	AH	162	TYR
1	AH	163	THR
1	AH	165	THR
1	AH	167	LEU
1	AH	170	SER
1	AH	176	ARG
1	AH	183	LEU
1	AH	196	ASN
1	AH	208	SER
1	AH	211	SER
1	AH	225	GLN
1	AH	236	ASN
1	AH	253	ASP
1	AH	264	SER
1	AH	271	THR
1	AH	304	PHE
1	AH	312	VAL
1	AH	315	TYR
1	AH	317	ASP
1	CH	35	THR
1	CH	43	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	CH	48	PHE
1	CH	72	THR
1	CH	74	THR
1	CH	75	ASP
1	CH	77	TYR
1	CH	87	ASP
1	CH	101	ARG
1	CH	112	GLN
1	CH	114	MET
1	CH	137	THR
1	CH	141	LEU
1	CH	151	LYS
1	CH	156	ARG
1	CH	175	GLN
1	CH	176	ARG
1	CH	177	LEU
1	CH	185	LEU
1	CH	198	SER
1	CH	204	SER
1	CH	208	SER
1	CH	231	ASP
1	CH	288	ASN
1	CH	316	SER
1	CH	337	GLU
1	BI	57	LEU
1	BI	58	SER
1	BI	63	ILE
1	BI	67	VAL
1	BI	68	LEU
1	BI	78	VAL
1	BI	79	VAL
1	BI	88	LEU
1	BI	92	LEU
1	BI	100	GLN
1	BI	104	VAL
1	BI	105	GLU
1	BI	134	ASN
1	BI	139	ASP
1	BI	145	ARG
1	BI	156	ARG
1	BI	165	THR
1	BI	167	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	BI	183	LEU
1	BI	184	ILE
1	BI	191	ASN
1	BI	193	ASP
1	BI	196	ASN
1	BI	198	SER
1	BI	202	ARG
1	BI	207	LEU
1	BI	212	LEU
1	BI	271	THR
1	BI	319	GLN
1	AI	54	ASP
1	AI	58	SER
1	AI	62	ARG
1	AI	72	THR
1	AI	74	THR
1	AI	75	ASP
1	AI	87	ASP
1	AI	124	VAL
1	AI	128	LEU
1	AI	130	ASP
1	AI	137	THR
1	AI	141	LEU
1	AI	142	GLN
1	AI	144	THR
1	AI	149	VAL
1	AI	157	THR
1	AI	159	ARG
1	AI	162	TYR
1	AI	163	THR
1	AI	165	THR
1	AI	167	LEU
1	AI	170	SER
1	AI	176	ARG
1	AI	183	LEU
1	AI	196	ASN
1	AI	208	SER
1	AI	211	SER
1	AI	225	GLN
1	AI	236	ASN
1	AI	253	ASP
1	AI	264	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	AI	271	THR
1	AI	304	PHE
1	AI	312	VAL
1	AI	315	TYR
1	AI	317	ASP
1	CI	35	THR
1	CI	43	SER
1	CI	48	PHE
1	CI	54	ASP
1	CI	72	THR
1	CI	74	THR
1	CI	75	ASP
1	CI	77	TYR
1	CI	87	ASP
1	CI	101	ARG
1	CI	112	GLN
1	CI	114	MET
1	CI	137	THR
1	CI	141	LEU
1	CI	151	LYS
1	CI	156	ARG
1	CI	175	GLN
1	CI	176	ARG
1	CI	177	LEU
1	CI	185	LEU
1	CI	198	SER
1	CI	204	SER
1	CI	208	SER
1	CI	231	ASP
1	CI	288	ASN
1	CI	316	SER
1	CI	337	GLU
1	BJ	57	LEU
1	BJ	58	SER
1	BJ	63	ILE
1	BJ	67	VAL
1	BJ	68	LEU
1	BJ	78	VAL
1	BJ	79	VAL
1	BJ	88	LEU
1	BJ	92	LEU
1	BJ	100	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	BJ	104	VAL
1	BJ	105	GLU
1	BJ	134	ASN
1	BJ	145	ARG
1	BJ	156	ARG
1	BJ	165	THR
1	BJ	167	LEU
1	BJ	183	LEU
1	BJ	184	ILE
1	BJ	191	ASN
1	BJ	193	ASP
1	BJ	196	ASN
1	BJ	198	SER
1	BJ	207	LEU
1	BJ	212	LEU
1	BJ	271	THR
1	BJ	319	GLN
1	AJ	54	ASP
1	AJ	62	ARG
1	AJ	72	THR
1	AJ	74	THR
1	AJ	75	ASP
1	AJ	83	THR
1	AJ	87	ASP
1	AJ	128	LEU
1	AJ	137	THR
1	AJ	141	LEU
1	AJ	142	GLN
1	AJ	144	THR
1	AJ	149	VAL
1	AJ	159	ARG
1	AJ	162	TYR
1	AJ	163	THR
1	AJ	165	THR
1	AJ	167	LEU
1	AJ	170	SER
1	AJ	176	ARG
1	AJ	183	LEU
1	AJ	196	ASN
1	AJ	208	SER
1	AJ	211	SER
1	AJ	225	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	AJ	236	ASN
1	AJ	253	ASP
1	AJ	264	SER
1	AJ	271	THR
1	AJ	304	PHE
1	AJ	312	VAL
1	AJ	315	TYR
1	AJ	317	ASP
1	CJ	35	THR
1	CJ	43	SER
1	CJ	48	PHE
1	CJ	72	THR
1	CJ	74	THR
1	CJ	75	ASP
1	CJ	77	TYR
1	CJ	87	ASP
1	CJ	101	ARG
1	CJ	112	GLN
1	CJ	114	MET
1	CJ	137	THR
1	CJ	141	LEU
1	CJ	151	LYS
1	CJ	156	ARG
1	CJ	175	GLN
1	CJ	176	ARG
1	CJ	177	LEU
1	CJ	185	LEU
1	CJ	198	SER
1	CJ	204	SER
1	CJ	208	SER
1	CJ	231	ASP
1	CJ	288	ASN
1	CJ	316	SER
1	CJ	337	GLU
1	BK	57	LEU
1	BK	58	SER
1	BK	63	ILE
1	BK	67	VAL
1	BK	68	LEU
1	BK	78	VAL
1	BK	79	VAL
1	BK	88	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	BK	92	LEU
1	BK	100	GLN
1	BK	104	VAL
1	BK	105	GLU
1	BK	134	ASN
1	BK	145	ARG
1	BK	156	ARG
1	BK	165	THR
1	BK	167	LEU
1	BK	183	LEU
1	BK	184	ILE
1	BK	191	ASN
1	BK	196	ASN
1	BK	198	SER
1	BK	202	ARG
1	BK	207	LEU
1	BK	212	LEU
1	BK	271	THR
1	BK	319	GLN
1	AK	54	ASP
1	AK	62	ARG
1	AK	72	THR
1	AK	74	THR
1	AK	75	ASP
1	AK	83	THR
1	AK	87	ASP
1	AK	128	LEU
1	AK	137	THR
1	AK	141	LEU
1	AK	142	GLN
1	AK	144	THR
1	AK	149	VAL
1	AK	159	ARG
1	AK	162	TYR
1	AK	163	THR
1	AK	165	THR
1	AK	167	LEU
1	AK	170	SER
1	AK	176	ARG
1	AK	183	LEU
1	AK	196	ASN
1	AK	208	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	AK	211	SER
1	AK	225	GLN
1	AK	236	ASN
1	AK	253	ASP
1	AK	264	SER
1	AK	271	THR
1	AK	304	PHE
1	AK	312	VAL
1	AK	315	TYR
1	AK	317	ASP
1	CK	35	THR
1	CK	43	SER
1	CK	72	THR
1	CK	74	THR
1	CK	75	ASP
1	CK	77	TYR
1	CK	81	ASP
1	CK	87	ASP
1	CK	101	ARG
1	CK	112	GLN
1	CK	114	MET
1	CK	137	THR
1	CK	141	LEU
1	CK	151	LYS
1	CK	156	ARG
1	CK	175	GLN
1	CK	176	ARG
1	CK	177	LEU
1	CK	185	LEU
1	CK	198	SER
1	CK	204	SER
1	CK	208	SER
1	CK	231	ASP
1	CK	288	ASN
1	CK	296	PHE
1	CK	316	SER
1	CK	337	GLU
1	BL	57	LEU
1	BL	58	SER
1	BL	63	ILE
1	BL	67	VAL
1	BL	68	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	BL	78	VAL
1	BL	79	VAL
1	BL	88	LEU
1	BL	92	LEU
1	BL	100	GLN
1	BL	104	VAL
1	BL	105	GLU
1	BL	134	ASN
1	BL	142	GLN
1	BL	145	ARG
1	BL	156	ARG
1	BL	165	THR
1	BL	167	LEU
1	BL	183	LEU
1	BL	184	ILE
1	BL	191	ASN
1	BL	193	ASP
1	BL	196	ASN
1	BL	198	SER
1	BL	207	LEU
1	BL	212	LEU
1	BL	271	THR
1	BL	319	GLN
1	AL	54	ASP
1	AL	58	SER
1	AL	62	ARG
1	AL	72	THR
1	AL	74	THR
1	AL	75	ASP
1	AL	87	ASP
1	AL	118	ASN
1	AL	124	VAL
1	AL	128	LEU
1	AL	137	THR
1	AL	141	LEU
1	AL	142	GLN
1	AL	144	THR
1	AL	149	VAL
1	AL	157	THR
1	AL	159	ARG
1	AL	163	THR
1	AL	165	THR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	AL	167	LEU
1	AL	170	SER
1	AL	176	ARG
1	AL	183	LEU
1	AL	196	ASN
1	AL	208	SER
1	AL	211	SER
1	AL	225	GLN
1	AL	236	ASN
1	AL	253	ASP
1	AL	264	SER
1	AL	271	THR
1	AL	304	PHE
1	AL	312	VAL
1	AL	315	TYR
1	AL	317	ASP
1	CL	35	THR
1	CL	43	SER
1	CL	72	THR
1	CL	74	THR
1	CL	75	ASP
1	CL	77	TYR
1	CL	87	ASP
1	CL	101	ARG
1	CL	112	GLN
1	CL	114	MET
1	CL	137	THR
1	CL	141	LEU
1	CL	151	LYS
1	CL	156	ARG
1	CL	175	GLN
1	CL	176	ARG
1	CL	177	LEU
1	CL	185	LEU
1	CL	204	SER
1	CL	208	SER
1	CL	231	ASP
1	CL	288	ASN
1	CL	316	SER
1	CL	337	GLU
1	BM	57	LEU
1	BM	58	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	BM	63	ILE
1	BM	67	VAL
1	BM	68	LEU
1	BM	78	VAL
1	BM	79	VAL
1	BM	88	LEU
1	BM	92	LEU
1	BM	100	GLN
1	BM	104	VAL
1	BM	105	GLU
1	BM	134	ASN
1	BM	145	ARG
1	BM	156	ARG
1	BM	165	THR
1	BM	167	LEU
1	BM	183	LEU
1	BM	184	ILE
1	BM	191	ASN
1	BM	193	ASP
1	BM	196	ASN
1	BM	198	SER
1	BM	202	ARG
1	BM	207	LEU
1	BM	212	LEU
1	BM	271	THR
1	BM	319	GLN
1	AM	54	ASP
1	AM	62	ARG
1	AM	72	THR
1	AM	74	THR
1	AM	75	ASP
1	AM	87	ASP
1	AM	128	LEU
1	AM	137	THR
1	AM	141	LEU
1	AM	142	GLN
1	AM	149	VAL
1	AM	159	ARG
1	AM	162	TYR
1	AM	163	THR
1	AM	165	THR
1	AM	167	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	AM	170	SER
1	AM	176	ARG
1	AM	183	LEU
1	AM	196	ASN
1	AM	208	SER
1	AM	211	SER
1	AM	225	GLN
1	AM	236	ASN
1	AM	253	ASP
1	AM	264	SER
1	AM	271	THR
1	AM	304	PHE
1	AM	312	VAL
1	AM	315	TYR
1	AM	317	ASP
1	CM	35	THR
1	CM	43	SER
1	CM	48	PHE
1	CM	72	THR
1	CM	74	THR
1	CM	75	ASP
1	CM	77	TYR
1	CM	87	ASP
1	CM	101	ARG
1	CM	112	GLN
1	CM	114	MET
1	CM	137	THR
1	CM	141	LEU
1	CM	151	LYS
1	CM	156	ARG
1	CM	175	GLN
1	CM	176	ARG
1	CM	177	LEU
1	CM	185	LEU
1	CM	198	SER
1	CM	204	SER
1	CM	208	SER
1	CM	231	ASP
1	CM	288	ASN
1	CM	316	SER
1	CM	337	GLU
1	BN	57	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	BN	58	SER
1	BN	63	ILE
1	BN	67	VAL
1	BN	68	LEU
1	BN	78	VAL
1	BN	79	VAL
1	BN	88	LEU
1	BN	92	LEU
1	BN	100	GLN
1	BN	104	VAL
1	BN	105	GLU
1	BN	134	ASN
1	BN	142	GLN
1	BN	145	ARG
1	BN	156	ARG
1	BN	165	THR
1	BN	167	LEU
1	BN	183	LEU
1	BN	184	ILE
1	BN	191	ASN
1	BN	193	ASP
1	BN	196	ASN
1	BN	198	SER
1	BN	207	LEU
1	BN	212	LEU
1	BN	271	THR
1	BN	319	GLN
1	AN	54	ASP
1	AN	62	ARG
1	AN	72	THR
1	AN	74	THR
1	AN	75	ASP
1	AN	87	ASP
1	AN	124	VAL
1	AN	128	LEU
1	AN	137	THR
1	AN	141	LEU
1	AN	142	GLN
1	AN	144	THR
1	AN	149	VAL
1	AN	159	ARG
1	AN	162	TYR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	AN	163	THR
1	AN	165	THR
1	AN	167	LEU
1	AN	170	SER
1	AN	176	ARG
1	AN	183	LEU
1	AN	196	ASN
1	AN	208	SER
1	AN	211	SER
1	AN	225	GLN
1	AN	236	ASN
1	AN	253	ASP
1	AN	264	SER
1	AN	271	THR
1	AN	304	PHE
1	AN	312	VAL
1	AN	315	TYR
1	AN	317	ASP
1	CN	35	THR
1	CN	43	SER
1	CN	48	PHE
1	CN	72	THR
1	CN	74	THR
1	CN	75	ASP
1	CN	77	TYR
1	CN	87	ASP
1	CN	101	ARG
1	CN	112	GLN
1	CN	114	MET
1	CN	137	THR
1	CN	141	LEU
1	CN	151	LYS
1	CN	156	ARG
1	CN	175	GLN
1	CN	176	ARG
1	CN	177	LEU
1	CN	185	LEU
1	CN	186	LEU
1	CN	198	SER
1	CN	204	SER
1	CN	208	SER
1	CN	231	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	CN	288	ASN
1	CN	316	SER
1	CN	337	GLU
1	BO	57	LEU
1	BO	58	SER
1	BO	63	ILE
1	BO	67	VAL
1	BO	68	LEU
1	BO	78	VAL
1	BO	79	VAL
1	BO	88	LEU
1	BO	92	LEU
1	BO	100	GLN
1	BO	104	VAL
1	BO	105	GLU
1	BO	134	ASN
1	BO	142	GLN
1	BO	145	ARG
1	BO	156	ARG
1	BO	165	THR
1	BO	167	LEU
1	BO	183	LEU
1	BO	184	ILE
1	BO	191	ASN
1	BO	193	ASP
1	BO	196	ASN
1	BO	198	SER
1	BO	207	LEU
1	BO	212	LEU
1	BO	271	THR
1	BO	319	GLN
1	AO	54	ASP
1	AO	62	ARG
1	AO	72	THR
1	AO	74	THR
1	AO	75	ASP
1	AO	87	ASP
1	AO	118	ASN
1	AO	124	VAL
1	AO	128	LEU
1	AO	137	THR
1	AO	141	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	AO	142	GLN
1	AO	149	VAL
1	AO	159	ARG
1	AO	162	TYR
1	AO	163	THR
1	AO	165	THR
1	AO	167	LEU
1	AO	170	SER
1	AO	176	ARG
1	AO	183	LEU
1	AO	196	ASN
1	AO	208	SER
1	AO	211	SER
1	AO	225	GLN
1	AO	236	ASN
1	AO	253	ASP
1	AO	264	SER
1	AO	271	THR
1	AO	304	PHE
1	AO	312	VAL
1	AO	315	TYR
1	AO	317	ASP
1	CO	35	THR
1	CO	43	SER
1	CO	48	PHE
1	CO	72	THR
1	CO	74	THR
1	CO	75	ASP
1	CO	77	TYR
1	CO	87	ASP
1	CO	101	ARG
1	CO	112	GLN
1	CO	114	MET
1	CO	141	LEU
1	CO	151	LYS
1	CO	156	ARG
1	CO	175	GLN
1	CO	176	ARG
1	CO	177	LEU
1	CO	185	LEU
1	CO	198	SER
1	CO	204	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	CO	208	SER
1	CO	231	ASP
1	CO	288	ASN
1	CO	316	SER
1	CO	337	GLU
1	BP	57	LEU
1	BP	58	SER
1	BP	63	ILE
1	BP	67	VAL
1	BP	68	LEU
1	BP	78	VAL
1	BP	79	VAL
1	BP	88	LEU
1	BP	92	LEU
1	BP	100	GLN
1	BP	104	VAL
1	BP	105	GLU
1	BP	134	ASN
1	BP	142	GLN
1	BP	145	ARG
1	BP	156	ARG
1	BP	165	THR
1	BP	167	LEU
1	BP	183	LEU
1	BP	184	ILE
1	BP	191	ASN
1	BP	193	ASP
1	BP	196	ASN
1	BP	198	SER
1	BP	207	LEU
1	BP	212	LEU
1	BP	271	THR
1	BP	319	GLN
1	AP	54	ASP
1	AP	62	ARG
1	AP	72	THR
1	AP	74	THR
1	AP	75	ASP
1	AP	87	ASP
1	AP	128	LEU
1	AP	137	THR
1	AP	141	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	AP	142	GLN
1	AP	144	THR
1	AP	149	VAL
1	AP	159	ARG
1	AP	162	TYR
1	AP	163	THR
1	AP	165	THR
1	AP	167	LEU
1	AP	170	SER
1	AP	176	ARG
1	AP	183	LEU
1	AP	196	ASN
1	AP	208	SER
1	AP	211	SER
1	AP	225	GLN
1	AP	236	ASN
1	AP	253	ASP
1	AP	264	SER
1	AP	271	THR
1	AP	304	PHE
1	AP	312	VAL
1	AP	315	TYR
1	AP	317	ASP
1	CP	35	THR
1	CP	43	SER
1	CP	48	PHE
1	CP	72	THR
1	CP	74	THR
1	CP	75	ASP
1	CP	77	TYR
1	CP	87	ASP
1	CP	101	ARG
1	CP	112	GLN
1	CP	114	MET
1	CP	137	THR
1	CP	141	LEU
1	CP	151	LYS
1	CP	156	ARG
1	CP	175	GLN
1	CP	176	ARG
1	CP	177	LEU
1	CP	185	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	CP	198	SER
1	CP	204	SER
1	CP	231	ASP
1	CP	288	ASN
1	CP	316	SER
1	CP	337	GLU
1	BQ	57	LEU
1	BQ	58	SER
1	BQ	63	ILE
1	BQ	67	VAL
1	BQ	68	LEU
1	BQ	78	VAL
1	BQ	79	VAL
1	BQ	86	PRO
1	BQ	88	LEU
1	BQ	92	LEU
1	BQ	100	GLN
1	BQ	104	VAL
1	BQ	105	GLU
1	BQ	134	ASN
1	BQ	145	ARG
1	BQ	156	ARG
1	BQ	165	THR
1	BQ	167	LEU
1	BQ	183	LEU
1	BQ	184	ILE
1	BQ	191	ASN
1	BQ	196	ASN
1	BQ	198	SER
1	BQ	207	LEU
1	BQ	212	LEU
1	BQ	271	THR
1	BQ	319	GLN
1	AQ	54	ASP
1	AQ	58	SER
1	AQ	62	ARG
1	AQ	72	THR
1	AQ	74	THR
1	AQ	75	ASP
1	AQ	87	ASP
1	AQ	124	VAL
1	AQ	128	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	AQ	137	THR
1	AQ	141	LEU
1	AQ	142	GLN
1	AQ	144	THR
1	AQ	149	VAL
1	AQ	159	ARG
1	AQ	162	TYR
1	AQ	163	THR
1	AQ	165	THR
1	AQ	167	LEU
1	AQ	170	SER
1	AQ	176	ARG
1	AQ	183	LEU
1	AQ	196	ASN
1	AQ	208	SER
1	AQ	211	SER
1	AQ	225	GLN
1	AQ	236	ASN
1	AQ	253	ASP
1	AQ	264	SER
1	AQ	271	THR
1	AQ	304	PHE
1	AQ	312	VAL
1	AQ	315	TYR
1	AQ	317	ASP
1	CQ	35	THR
1	CQ	43	SER
1	CQ	48	PHE
1	CQ	72	THR
1	CQ	74	THR
1	CQ	75	ASP
1	CQ	77	TYR
1	CQ	87	ASP
1	CQ	101	ARG
1	CQ	106	THR
1	CQ	112	GLN
1	CQ	114	MET
1	CQ	137	THR
1	CQ	141	LEU
1	CQ	151	LYS
1	CQ	156	ARG
1	CQ	175	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	CQ	176	ARG
1	CQ	177	LEU
1	CQ	185	LEU
1	CQ	198	SER
1	CQ	204	SER
1	CQ	231	ASP
1	CQ	288	ASN
1	CQ	316	SER
1	CQ	337	GLU
1	BR	57	LEU
1	BR	58	SER
1	BR	63	ILE
1	BR	67	VAL
1	BR	68	LEU
1	BR	78	VAL
1	BR	79	VAL
1	BR	88	LEU
1	BR	92	LEU
1	BR	100	GLN
1	BR	104	VAL
1	BR	105	GLU
1	BR	134	ASN
1	BR	145	ARG
1	BR	156	ARG
1	BR	165	THR
1	BR	167	LEU
1	BR	183	LEU
1	BR	184	ILE
1	BR	191	ASN
1	BR	193	ASP
1	BR	196	ASN
1	BR	198	SER
1	BR	207	LEU
1	BR	212	LEU
1	BR	271	THR
1	BR	319	GLN
1	AR	54	ASP
1	AR	62	ARG
1	AR	72	THR
1	AR	74	THR
1	AR	75	ASP
1	AR	87	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	AR	118	ASN
1	AR	128	LEU
1	AR	130	ASP
1	AR	137	THR
1	AR	141	LEU
1	AR	142	GLN
1	AR	144	THR
1	AR	149	VAL
1	AR	157	THR
1	AR	159	ARG
1	AR	162	TYR
1	AR	163	THR
1	AR	165	THR
1	AR	167	LEU
1	AR	170	SER
1	AR	176	ARG
1	AR	183	LEU
1	AR	186	LEU
1	AR	196	ASN
1	AR	208	SER
1	AR	211	SER
1	AR	212	LEU
1	AR	225	GLN
1	AR	236	ASN
1	AR	253	ASP
1	AR	264	SER
1	AR	271	THR
1	AR	304	PHE
1	AR	312	VAL
1	AR	315	TYR
1	AR	317	ASP
1	CR	35	THR
1	CR	43	SER
1	CR	72	THR
1	CR	74	THR
1	CR	75	ASP
1	CR	77	TYR
1	CR	87	ASP
1	CR	101	ARG
1	CR	112	GLN
1	CR	114	MET
1	CR	137	THR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	CR	141	LEU
1	CR	151	LYS
1	CR	156	ARG
1	CR	175	GLN
1	CR	176	ARG
1	CR	177	LEU
1	CR	185	LEU
1	CR	198	SER
1	CR	204	SER
1	CR	208	SER
1	CR	231	ASP
1	CR	288	ASN
1	CR	316	SER
1	CR	337	GLU
1	BS	57	LEU
1	BS	58	SER
1	BS	63	ILE
1	BS	67	VAL
1	BS	68	LEU
1	BS	78	VAL
1	BS	79	VAL
1	BS	88	LEU
1	BS	92	LEU
1	BS	100	GLN
1	BS	104	VAL
1	BS	105	GLU
1	BS	134	ASN
1	BS	145	ARG
1	BS	156	ARG
1	BS	165	THR
1	BS	167	LEU
1	BS	183	LEU
1	BS	184	ILE
1	BS	191	ASN
1	BS	193	ASP
1	BS	196	ASN
1	BS	198	SER
1	BS	207	LEU
1	BS	212	LEU
1	BS	271	THR
1	BS	319	GLN
1	AS	54	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	AS	58	SER
1	AS	62	ARG
1	AS	72	THR
1	AS	74	THR
1	AS	75	ASP
1	AS	87	ASP
1	AS	101	ARG
1	AS	118	ASN
1	AS	128	LEU
1	AS	137	THR
1	AS	141	LEU
1	AS	142	GLN
1	AS	144	THR
1	AS	149	VAL
1	AS	159	ARG
1	AS	162	TYR
1	AS	163	THR
1	AS	165	THR
1	AS	167	LEU
1	AS	170	SER
1	AS	176	ARG
1	AS	183	LEU
1	AS	196	ASN
1	AS	208	SER
1	AS	211	SER
1	AS	225	GLN
1	AS	236	ASN
1	AS	253	ASP
1	AS	264	SER
1	AS	271	THR
1	AS	304	PHE
1	AS	312	VAL
1	AS	315	TYR
1	AS	317	ASP
1	CS	35	THR
1	CS	43	SER
1	CS	48	PHE
1	CS	54	ASP
1	CS	72	THR
1	CS	74	THR
1	CS	75	ASP
1	CS	77	TYR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	CS	87	ASP
1	CS	101	ARG
1	CS	112	GLN
1	CS	114	MET
1	CS	137	THR
1	CS	151	LYS
1	CS	156	ARG
1	CS	175	GLN
1	CS	176	ARG
1	CS	177	LEU
1	CS	185	LEU
1	CS	186	LEU
1	CS	198	SER
1	CS	204	SER
1	CS	208	SER
1	CS	231	ASP
1	CS	288	ASN
1	CS	316	SER
1	CS	337	GLU
1	BT	57	LEU
1	BT	58	SER
1	BT	63	ILE
1	BT	67	VAL
1	BT	68	LEU
1	BT	78	VAL
1	BT	79	VAL
1	BT	88	LEU
1	BT	92	LEU
1	BT	100	GLN
1	BT	104	VAL
1	BT	105	GLU
1	BT	134	ASN
1	BT	142	GLN
1	BT	145	ARG
1	BT	156	ARG
1	BT	165	THR
1	BT	167	LEU
1	BT	183	LEU
1	BT	184	ILE
1	BT	191	ASN
1	BT	193	ASP
1	BT	196	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	BT	198	SER
1	BT	207	LEU
1	BT	212	LEU
1	BT	271	THR
1	BT	319	GLN
1	AT	54	ASP
1	AT	62	ARG
1	AT	72	THR
1	AT	74	THR
1	AT	75	ASP
1	AT	83	THR
1	AT	87	ASP
1	AT	128	LEU
1	AT	137	THR
1	AT	141	LEU
1	AT	142	GLN
1	AT	144	THR
1	AT	149	VAL
1	AT	157	THR
1	AT	159	ARG
1	AT	162	TYR
1	AT	163	THR
1	AT	165	THR
1	AT	167	LEU
1	AT	170	SER
1	AT	176	ARG
1	AT	183	LEU
1	AT	196	ASN
1	AT	208	SER
1	AT	211	SER
1	AT	225	GLN
1	AT	236	ASN
1	AT	253	ASP
1	AT	264	SER
1	AT	271	THR
1	AT	304	PHE
1	AT	312	VAL
1	AT	315	TYR
1	AT	317	ASP
1	CT	35	THR
1	CT	43	SER
1	CT	48	PHE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	CT	72	THR
1	CT	74	THR
1	CT	75	ASP
1	CT	77	TYR
1	CT	87	ASP
1	CT	101	ARG
1	CT	112	GLN
1	CT	114	MET
1	CT	137	THR
1	CT	141	LEU
1	CT	151	LYS
1	CT	156	ARG
1	CT	175	GLN
1	CT	176	ARG
1	CT	177	LEU
1	CT	185	LEU
1	CT	198	SER
1	CT	204	SER
1	CT	231	ASP
1	CT	288	ASN
1	CT	316	SER
1	CT	337	GLU
1	BU	57	LEU
1	BU	58	SER
1	BU	63	ILE
1	BU	67	VAL
1	BU	68	LEU
1	BU	78	VAL
1	BU	79	VAL
1	BU	88	LEU
1	BU	92	LEU
1	BU	100	GLN
1	BU	104	VAL
1	BU	105	GLU
1	BU	134	ASN
1	BU	142	GLN
1	BU	145	ARG
1	BU	156	ARG
1	BU	165	THR
1	BU	167	LEU
1	BU	183	LEU
1	BU	184	ILE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	BU	191	ASN
1	BU	193	ASP
1	BU	196	ASN
1	BU	198	SER
1	BU	207	LEU
1	BU	212	LEU
1	BU	271	THR
1	BU	319	GLN
1	AU	54	ASP
1	AU	58	SER
1	AU	62	ARG
1	AU	72	THR
1	AU	74	THR
1	AU	75	ASP
1	AU	87	ASP
1	AU	101	ARG
1	AU	118	ASN
1	AU	124	VAL
1	AU	128	LEU
1	AU	137	THR
1	AU	141	LEU
1	AU	142	GLN
1	AU	149	VAL
1	AU	157	THR
1	AU	159	ARG
1	AU	163	THR
1	AU	165	THR
1	AU	167	LEU
1	AU	170	SER
1	AU	176	ARG
1	AU	183	LEU
1	AU	196	ASN
1	AU	208	SER
1	AU	211	SER
1	AU	225	GLN
1	AU	236	ASN
1	AU	253	ASP
1	AU	264	SER
1	AU	271	THR
1	AU	304	PHE
1	AU	312	VAL
1	AU	315	TYR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	AU	317	ASP
1	CU	35	THR
1	CU	43	SER
1	CU	48	PHE
1	CU	72	THR
1	CU	74	THR
1	CU	75	ASP
1	CU	77	TYR
1	CU	87	ASP
1	CU	101	ARG
1	CU	112	GLN
1	CU	114	MET
1	CU	137	THR
1	CU	141	LEU
1	CU	151	LYS
1	CU	156	ARG
1	CU	175	GLN
1	CU	176	ARG
1	CU	177	LEU
1	CU	185	LEU
1	CU	186	LEU
1	CU	198	SER
1	CU	204	SER
1	CU	208	SER
1	CU	231	ASP
1	CU	288	ASN
1	CU	316	SER
1	CU	337	GLU
1	BV	57	LEU
1	BV	58	SER
1	BV	63	ILE
1	BV	67	VAL
1	BV	68	LEU
1	BV	78	VAL
1	BV	79	VAL
1	BV	88	LEU
1	BV	92	LEU
1	BV	100	GLN
1	BV	104	VAL
1	BV	105	GLU
1	BV	134	ASN
1	BV	145	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	BV	156	ARG
1	BV	165	THR
1	BV	167	LEU
1	BV	183	LEU
1	BV	184	ILE
1	BV	191	ASN
1	BV	193	ASP
1	BV	196	ASN
1	BV	198	SER
1	BV	207	LEU
1	BV	212	LEU
1	BV	271	THR
1	BV	319	GLN
1	AV	54	ASP
1	AV	58	SER
1	AV	62	ARG
1	AV	72	THR
1	AV	74	THR
1	AV	75	ASP
1	AV	87	ASP
1	AV	124	VAL
1	AV	128	LEU
1	AV	137	THR
1	AV	141	LEU
1	AV	142	GLN
1	AV	144	THR
1	AV	149	VAL
1	AV	157	THR
1	AV	159	ARG
1	AV	162	TYR
1	AV	163	THR
1	AV	165	THR
1	AV	167	LEU
1	AV	170	SER
1	AV	176	ARG
1	AV	183	LEU
1	AV	196	ASN
1	AV	208	SER
1	AV	211	SER
1	AV	225	GLN
1	AV	236	ASN
1	AV	253	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	AV	264	SER
1	AV	271	THR
1	AV	304	PHE
1	AV	312	VAL
1	AV	315	TYR
1	AV	317	ASP
1	CV	35	THR
1	CV	43	SER
1	CV	48	PHE
1	CV	72	THR
1	CV	74	THR
1	CV	75	ASP
1	CV	77	TYR
1	CV	87	ASP
1	CV	101	ARG
1	CV	112	GLN
1	CV	114	MET
1	CV	137	THR
1	CV	141	LEU
1	CV	151	LYS
1	CV	156	ARG
1	CV	175	GLN
1	CV	176	ARG
1	CV	177	LEU
1	CV	185	LEU
1	CV	186	LEU
1	CV	198	SER
1	CV	204	SER
1	CV	208	SER
1	CV	231	ASP
1	CV	288	ASN
1	CV	316	SER
1	CV	331	CYS
1	CV	337	GLU
1	BW	57	LEU
1	BW	58	SER
1	BW	63	ILE
1	BW	67	VAL
1	BW	68	LEU
1	BW	78	VAL
1	BW	79	VAL
1	BW	88	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	BW	92	LEU
1	BW	100	GLN
1	BW	104	VAL
1	BW	105	GLU
1	BW	134	ASN
1	BW	145	ARG
1	BW	156	ARG
1	BW	165	THR
1	BW	167	LEU
1	BW	183	LEU
1	BW	184	ILE
1	BW	191	ASN
1	BW	196	ASN
1	BW	198	SER
1	BW	207	LEU
1	BW	212	LEU
1	BW	271	THR
1	BW	319	GLN
1	AW	54	ASP
1	AW	58	SER
1	AW	62	ARG
1	AW	72	THR
1	AW	74	THR
1	AW	75	ASP
1	AW	87	ASP
1	AW	118	ASN
1	AW	124	VAL
1	AW	128	LEU
1	AW	137	THR
1	AW	141	LEU
1	AW	142	GLN
1	AW	149	VAL
1	AW	159	ARG
1	AW	162	TYR
1	AW	163	THR
1	AW	165	THR
1	AW	167	LEU
1	AW	170	SER
1	AW	176	ARG
1	AW	183	LEU
1	AW	196	ASN
1	AW	208	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	AW	211	SER
1	AW	225	GLN
1	AW	236	ASN
1	AW	253	ASP
1	AW	264	SER
1	AW	271	THR
1	AW	304	PHE
1	AW	312	VAL
1	AW	315	TYR
1	AW	317	ASP
1	CW	35	THR
1	CW	43	SER
1	CW	48	PHE
1	CW	72	THR
1	CW	74	THR
1	CW	75	ASP
1	CW	77	TYR
1	CW	87	ASP
1	CW	101	ARG
1	CW	106	THR
1	CW	112	GLN
1	CW	114	MET
1	CW	137	THR
1	CW	141	LEU
1	CW	151	LYS
1	CW	156	ARG
1	CW	175	GLN
1	CW	176	ARG
1	CW	177	LEU
1	CW	185	LEU
1	CW	198	SER
1	CW	204	SER
1	CW	208	SER
1	CW	231	ASP
1	CW	288	ASN
1	CW	316	SER
1	CW	337	GLU
1	BX	57	LEU
1	BX	58	SER
1	BX	63	ILE
1	BX	67	VAL
1	BX	68	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	BX	78	VAL
1	BX	79	VAL
1	BX	88	LEU
1	BX	92	LEU
1	BX	100	GLN
1	BX	104	VAL
1	BX	105	GLU
1	BX	134	ASN
1	BX	142	GLN
1	BX	145	ARG
1	BX	156	ARG
1	BX	165	THR
1	BX	167	LEU
1	BX	183	LEU
1	BX	184	ILE
1	BX	191	ASN
1	BX	196	ASN
1	BX	198	SER
1	BX	207	LEU
1	BX	212	LEU
1	BX	271	THR
1	BX	319	GLN
1	AX	54	ASP
1	AX	62	ARG
1	AX	72	THR
1	AX	74	THR
1	AX	75	ASP
1	AX	87	ASP
1	AX	118	ASN
1	AX	124	VAL
1	AX	128	LEU
1	AX	137	THR
1	AX	141	LEU
1	AX	142	GLN
1	AX	144	THR
1	AX	149	VAL
1	AX	159	ARG
1	AX	162	TYR
1	AX	163	THR
1	AX	165	THR
1	AX	167	LEU
1	AX	170	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	AX	176	ARG
1	AX	183	LEU
1	AX	196	ASN
1	AX	208	SER
1	AX	211	SER
1	AX	225	GLN
1	AX	236	ASN
1	AX	253	ASP
1	AX	264	SER
1	AX	271	THR
1	AX	304	PHE
1	AX	312	VAL
1	AX	315	TYR
1	AX	317	ASP
1	CX	35	THR
1	CX	43	SER
1	CX	48	PHE
1	CX	72	THR
1	CX	74	THR
1	CX	75	ASP
1	CX	77	TYR
1	CX	87	ASP
1	CX	101	ARG
1	CX	106	THR
1	CX	112	GLN
1	CX	114	MET
1	CX	137	THR
1	CX	141	LEU
1	CX	151	LYS
1	CX	156	ARG
1	CX	175	GLN
1	CX	176	ARG
1	CX	177	LEU
1	CX	185	LEU
1	CX	198	SER
1	CX	204	SER
1	CX	208	SER
1	CX	231	ASP
1	CX	288	ASN
1	CX	316	SER
1	CX	337	GLU
1	BY	57	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	BY	58	SER
1	BY	63	ILE
1	BY	67	VAL
1	BY	68	LEU
1	BY	78	VAL
1	BY	79	VAL
1	BY	88	LEU
1	BY	92	LEU
1	BY	100	GLN
1	BY	104	VAL
1	BY	105	GLU
1	BY	134	ASN
1	BY	145	ARG
1	BY	156	ARG
1	BY	165	THR
1	BY	167	LEU
1	BY	183	LEU
1	BY	184	ILE
1	BY	191	ASN
1	BY	193	ASP
1	BY	196	ASN
1	BY	198	SER
1	BY	207	LEU
1	BY	212	LEU
1	BY	271	THR
1	BY	319	GLN
1	AY	54	ASP
1	AY	58	SER
1	AY	62	ARG
1	AY	72	THR
1	AY	74	THR
1	AY	75	ASP
1	AY	87	ASP
1	AY	128	LEU
1	AY	137	THR
1	AY	141	LEU
1	AY	142	GLN
1	AY	149	VAL
1	AY	159	ARG
1	AY	162	TYR
1	AY	163	THR
1	AY	165	THR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	AY	167	LEU
1	AY	170	SER
1	AY	176	ARG
1	AY	183	LEU
1	AY	196	ASN
1	AY	208	SER
1	AY	211	SER
1	AY	225	GLN
1	AY	236	ASN
1	AY	253	ASP
1	AY	264	SER
1	AY	271	THR
1	AY	304	PHE
1	AY	312	VAL
1	AY	315	TYR
1	AY	317	ASP
1	CY	35	THR
1	CY	43	SER
1	CY	48	PHE
1	CY	72	THR
1	CY	74	THR
1	CY	75	ASP
1	CY	77	TYR
1	CY	87	ASP
1	CY	101	ARG
1	CY	106	THR
1	CY	112	GLN
1	CY	114	MET
1	CY	137	THR
1	CY	141	LEU
1	CY	151	LYS
1	CY	156	ARG
1	CY	175	GLN
1	CY	176	ARG
1	CY	177	LEU
1	CY	185	LEU
1	CY	198	SER
1	CY	204	SER
1	CY	208	SER
1	CY	231	ASP
1	CY	288	ASN
1	CY	316	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	CY	337	GLU
1	BZ	57	LEU
1	BZ	58	SER
1	BZ	63	ILE
1	BZ	67	VAL
1	BZ	68	LEU
1	BZ	78	VAL
1	BZ	79	VAL
1	BZ	88	LEU
1	BZ	92	LEU
1	BZ	100	GLN
1	BZ	104	VAL
1	BZ	105	GLU
1	BZ	134	ASN
1	BZ	145	ARG
1	BZ	156	ARG
1	BZ	165	THR
1	BZ	167	LEU
1	BZ	183	LEU
1	BZ	184	ILE
1	BZ	191	ASN
1	BZ	193	ASP
1	BZ	196	ASN
1	BZ	198	SER
1	BZ	202	ARG
1	BZ	207	LEU
1	BZ	212	LEU
1	BZ	271	THR
1	BZ	319	GLN
1	AZ	54	ASP
1	AZ	62	ARG
1	AZ	72	THR
1	AZ	74	THR
1	AZ	75	ASP
1	AZ	87	ASP
1	AZ	124	VAL
1	AZ	128	LEU
1	AZ	137	THR
1	AZ	141	LEU
1	AZ	142	GLN
1	AZ	144	THR
1	AZ	149	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	AZ	159	ARG
1	AZ	163	THR
1	AZ	165	THR
1	AZ	167	LEU
1	AZ	170	SER
1	AZ	176	ARG
1	AZ	183	LEU
1	AZ	196	ASN
1	AZ	208	SER
1	AZ	211	SER
1	AZ	225	GLN
1	AZ	236	ASN
1	AZ	253	ASP
1	AZ	264	SER
1	AZ	271	THR
1	AZ	304	PHE
1	AZ	312	VAL
1	AZ	315	TYR
1	AZ	317	ASP
1	CZ	35	THR
1	CZ	43	SER
1	CZ	48	PHE
1	CZ	54	ASP
1	CZ	72	THR
1	CZ	74	THR
1	CZ	75	ASP
1	CZ	77	TYR
1	CZ	87	ASP
1	CZ	101	ARG
1	CZ	112	GLN
1	CZ	114	MET
1	CZ	137	THR
1	CZ	141	LEU
1	CZ	151	LYS
1	CZ	156	ARG
1	CZ	175	GLN
1	CZ	176	ARG
1	CZ	177	LEU
1	CZ	185	LEU
1	CZ	198	SER
1	CZ	204	SER
1	CZ	208	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	CZ	231	ASP
1	CZ	288	ASN
1	CZ	316	SER
1	CZ	337	GLU
1	Ba	57	LEU
1	Ba	58	SER
1	Ba	63	ILE
1	Ba	67	VAL
1	Ba	68	LEU
1	Ba	78	VAL
1	Ba	79	VAL
1	Ba	88	LEU
1	Ba	92	LEU
1	Ba	100	GLN
1	Ba	104	VAL
1	Ba	105	GLU
1	Ba	134	ASN
1	Ba	145	ARG
1	Ba	156	ARG
1	Ba	165	THR
1	Ba	167	LEU
1	Ba	183	LEU
1	Ba	184	ILE
1	Ba	191	ASN
1	Ba	193	ASP
1	Ba	196	ASN
1	Ba	198	SER
1	Ba	207	LEU
1	Ba	212	LEU
1	Ba	271	THR
1	Ba	319	GLN
1	Aa	54	ASP
1	Aa	58	SER
1	Aa	62	ARG
1	Aa	72	THR
1	Aa	74	THR
1	Aa	75	ASP
1	Aa	83	THR
1	Aa	87	ASP
1	Aa	128	LEU
1	Aa	137	THR
1	Aa	141	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	Aa	142	GLN
1	Aa	149	VAL
1	Aa	157	THR
1	Aa	159	ARG
1	Aa	162	TYR
1	Aa	163	THR
1	Aa	165	THR
1	Aa	167	LEU
1	Aa	170	SER
1	Aa	176	ARG
1	Aa	183	LEU
1	Aa	196	ASN
1	Aa	208	SER
1	Aa	211	SER
1	Aa	225	GLN
1	Aa	236	ASN
1	Aa	253	ASP
1	Aa	264	SER
1	Aa	271	THR
1	Aa	304	PHE
1	Aa	312	VAL
1	Aa	315	TYR
1	Aa	317	ASP
1	Ca	35	THR
1	Ca	43	SER
1	Ca	48	PHE
1	Ca	72	THR
1	Ca	74	THR
1	Ca	75	ASP
1	Ca	77	TYR
1	Ca	87	ASP
1	Ca	101	ARG
1	Ca	112	GLN
1	Ca	114	MET
1	Ca	137	THR
1	Ca	141	LEU
1	Ca	151	LYS
1	Ca	156	ARG
1	Ca	175	GLN
1	Ca	176	ARG
1	Ca	177	LEU
1	Ca	185	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	Ca	186	LEU
1	Ca	198	SER
1	Ca	204	SER
1	Ca	208	SER
1	Ca	231	ASP
1	Ca	288	ASN
1	Ca	316	SER
1	Ca	337	GLU
1	Bb	57	LEU
1	Bb	58	SER
1	Bb	63	ILE
1	Bb	67	VAL
1	Bb	68	LEU
1	Bb	78	VAL
1	Bb	79	VAL
1	Bb	88	LEU
1	Bb	92	LEU
1	Bb	100	GLN
1	Bb	104	VAL
1	Bb	105	GLU
1	Bb	134	ASN
1	Bb	145	ARG
1	Bb	156	ARG
1	Bb	165	THR
1	Bb	167	LEU
1	Bb	183	LEU
1	Bb	184	ILE
1	Bb	191	ASN
1	Bb	193	ASP
1	Bb	196	ASN
1	Bb	198	SER
1	Bb	202	ARG
1	Bb	207	LEU
1	Bb	212	LEU
1	Bb	271	THR
1	Bb	319	GLN
1	Ab	54	ASP
1	Ab	58	SER
1	Ab	62	ARG
1	Ab	72	THR
1	Ab	74	THR
1	Ab	75	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	Ab	83	THR
1	Ab	87	ASP
1	Ab	124	VAL
1	Ab	128	LEU
1	Ab	137	THR
1	Ab	141	LEU
1	Ab	142	GLN
1	Ab	144	THR
1	Ab	149	VAL
1	Ab	159	ARG
1	Ab	162	TYR
1	Ab	163	THR
1	Ab	165	THR
1	Ab	167	LEU
1	Ab	170	SER
1	Ab	176	ARG
1	Ab	183	LEU
1	Ab	196	ASN
1	Ab	208	SER
1	Ab	211	SER
1	Ab	212	LEU
1	Ab	225	GLN
1	Ab	236	ASN
1	Ab	253	ASP
1	Ab	264	SER
1	Ab	271	THR
1	Ab	304	PHE
1	Ab	312	VAL
1	Ab	315	TYR
1	Ab	317	ASP
1	Cb	35	THR
1	Cb	43	SER
1	Cb	48	PHE
1	Cb	72	THR
1	Cb	74	THR
1	Cb	75	ASP
1	Cb	77	TYR
1	Cb	87	ASP
1	Cb	101	ARG
1	Cb	112	GLN
1	Cb	114	MET
1	Cb	137	THR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	Cb	141	LEU
1	Cb	151	LYS
1	Cb	156	ARG
1	Cb	175	GLN
1	Cb	176	ARG
1	Cb	177	LEU
1	Cb	185	LEU
1	Cb	198	SER
1	Cb	204	SER
1	Cb	208	SER
1	Cb	231	ASP
1	Cb	288	ASN
1	Cb	316	SER
1	Cb	337	GLU
1	Bc	57	LEU
1	Bc	58	SER
1	Bc	63	ILE
1	Bc	67	VAL
1	Bc	68	LEU
1	Bc	78	VAL
1	Bc	79	VAL
1	Bc	88	LEU
1	Bc	92	LEU
1	Bc	100	GLN
1	Bc	104	VAL
1	Bc	105	GLU
1	Bc	134	ASN
1	Bc	145	ARG
1	Bc	156	ARG
1	Bc	165	THR
1	Bc	167	LEU
1	Bc	183	LEU
1	Bc	184	ILE
1	Bc	191	ASN
1	Bc	193	ASP
1	Bc	196	ASN
1	Bc	198	SER
1	Bc	202	ARG
1	Bc	207	LEU
1	Bc	212	LEU
1	Bc	271	THR
1	Bc	310	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	Bc	319	GLN
1	Ac	54	ASP
1	Ac	58	SER
1	Ac	62	ARG
1	Ac	72	THR
1	Ac	74	THR
1	Ac	75	ASP
1	Ac	87	ASP
1	Ac	119	THR
1	Ac	124	VAL
1	Ac	128	LEU
1	Ac	137	THR
1	Ac	141	LEU
1	Ac	142	GLN
1	Ac	149	VAL
1	Ac	159	ARG
1	Ac	162	TYR
1	Ac	163	THR
1	Ac	165	THR
1	Ac	167	LEU
1	Ac	170	SER
1	Ac	176	ARG
1	Ac	183	LEU
1	Ac	196	ASN
1	Ac	208	SER
1	Ac	211	SER
1	Ac	225	GLN
1	Ac	236	ASN
1	Ac	253	ASP
1	Ac	264	SER
1	Ac	271	THR
1	Ac	304	PHE
1	Ac	312	VAL
1	Ac	315	TYR
1	Ac	317	ASP
1	Cc	35	THR
1	Cc	43	SER
1	Cc	48	PHE
1	Cc	54	ASP
1	Cc	72	THR
1	Cc	74	THR
1	Cc	75	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	Cc	77	TYR
1	Cc	87	ASP
1	Cc	101	ARG
1	Cc	112	GLN
1	Cc	114	MET
1	Cc	137	THR
1	Cc	141	LEU
1	Cc	151	LYS
1	Cc	156	ARG
1	Cc	175	GLN
1	Cc	176	ARG
1	Cc	177	LEU
1	Cc	185	LEU
1	Cc	198	SER
1	Cc	204	SER
1	Cc	208	SER
1	Cc	231	ASP
1	Cc	288	ASN
1	Cc	316	SER
1	Cc	337	GLU
1	Bd	57	LEU
1	Bd	58	SER
1	Bd	63	ILE
1	Bd	67	VAL
1	Bd	68	LEU
1	Bd	78	VAL
1	Bd	79	VAL
1	Bd	88	LEU
1	Bd	92	LEU
1	Bd	100	GLN
1	Bd	104	VAL
1	Bd	105	GLU
1	Bd	134	ASN
1	Bd	142	GLN
1	Bd	145	ARG
1	Bd	156	ARG
1	Bd	165	THR
1	Bd	167	LEU
1	Bd	183	LEU
1	Bd	184	ILE
1	Bd	191	ASN
1	Bd	193	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	Bd	196	ASN
1	Bd	198	SER
1	Bd	207	LEU
1	Bd	212	LEU
1	Bd	225	GLN
1	Bd	271	THR
1	Bd	319	GLN
1	Ad	54	ASP
1	Ad	62	ARG
1	Ad	72	THR
1	Ad	74	THR
1	Ad	75	ASP
1	Ad	87	ASP
1	Ad	124	VAL
1	Ad	128	LEU
1	Ad	137	THR
1	Ad	141	LEU
1	Ad	142	GLN
1	Ad	149	VAL
1	Ad	159	ARG
1	Ad	162	TYR
1	Ad	163	THR
1	Ad	165	THR
1	Ad	167	LEU
1	Ad	170	SER
1	Ad	176	ARG
1	Ad	183	LEU
1	Ad	186	LEU
1	Ad	196	ASN
1	Ad	208	SER
1	Ad	211	SER
1	Ad	225	GLN
1	Ad	236	ASN
1	Ad	253	ASP
1	Ad	264	SER
1	Ad	271	THR
1	Ad	304	PHE
1	Ad	312	VAL
1	Ad	315	TYR
1	Ad	317	ASP
1	Cd	35	THR
1	Cd	43	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	Cd	48	PHE
1	Cd	72	THR
1	Cd	74	THR
1	Cd	75	ASP
1	Cd	77	TYR
1	Cd	87	ASP
1	Cd	101	ARG
1	Cd	112	GLN
1	Cd	114	MET
1	Cd	137	THR
1	Cd	141	LEU
1	Cd	151	LYS
1	Cd	175	GLN
1	Cd	176	ARG
1	Cd	177	LEU
1	Cd	185	LEU
1	Cd	198	SER
1	Cd	204	SER
1	Cd	231	ASP
1	Cd	288	ASN
1	Cd	316	SER
1	Cd	337	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (487) such sidechains are listed below:

Mol	Chain	Res	Type
1	BA	100	GLN
1	BA	142	GLN
1	BA	190	ASN
1	BA	191	ASN
1	BA	196	ASN
1	BA	214	ASN
1	AA	65	GLN
1	AA	118	ASN
1	AA	134	ASN
1	AA	142	GLN
1	AA	191	ASN
1	AA	196	ASN
1	AA	225	GLN
1	AA	236	ASN
1	AA	258	GLN
1	CA	56	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	CA	112	GLN
1	CA	190	ASN
1	BB	100	GLN
1	BB	142	GLN
1	BB	190	ASN
1	BB	191	ASN
1	BB	196	ASN
1	AB	65	GLN
1	AB	118	ASN
1	AB	134	ASN
1	AB	142	GLN
1	AB	196	ASN
1	AB	236	ASN
1	AB	258	GLN
1	CB	56	HIS
1	CB	112	GLN
1	CB	190	ASN
1	BC	142	GLN
1	BC	190	ASN
1	BC	191	ASN
1	BC	196	ASN
1	AC	65	GLN
1	AC	118	ASN
1	AC	134	ASN
1	AC	142	GLN
1	AC	191	ASN
1	AC	196	ASN
1	AC	225	GLN
1	AC	236	ASN
1	AC	258	GLN
1	CC	56	HIS
1	CC	112	GLN
1	CC	190	ASN
1	BD	65	GLN
1	BD	100	GLN
1	BD	142	GLN
1	BD	190	ASN
1	BD	191	ASN
1	BD	196	ASN
1	AD	65	GLN
1	AD	118	ASN
1	AD	134	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	AD	142	GLN
1	AD	191	ASN
1	AD	196	ASN
1	AD	225	GLN
1	AD	236	ASN
1	AD	258	GLN
1	CD	56	HIS
1	CD	112	GLN
1	CD	190	ASN
1	BE	100	GLN
1	BE	142	GLN
1	BE	190	ASN
1	BE	191	ASN
1	BE	196	ASN
1	AE	65	GLN
1	AE	118	ASN
1	AE	134	ASN
1	AE	142	GLN
1	AE	196	ASN
1	AE	225	GLN
1	AE	236	ASN
1	AE	258	GLN
1	CE	56	HIS
1	CE	112	GLN
1	CE	190	ASN
1	BF	100	GLN
1	BF	142	GLN
1	BF	190	ASN
1	BF	191	ASN
1	BF	196	ASN
1	AF	65	GLN
1	AF	118	ASN
1	AF	134	ASN
1	AF	142	GLN
1	AF	191	ASN
1	AF	196	ASN
1	AF	225	GLN
1	AF	236	ASN
1	AF	258	GLN
1	CF	56	HIS
1	CF	112	GLN
1	CF	190	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	BG	100	GLN
1	BG	142	GLN
1	BG	190	ASN
1	BG	191	ASN
1	BG	196	ASN
1	AG	65	GLN
1	AG	118	ASN
1	AG	134	ASN
1	AG	142	GLN
1	AG	191	ASN
1	AG	196	ASN
1	AG	225	GLN
1	AG	236	ASN
1	AG	258	GLN
1	CG	56	HIS
1	CG	112	GLN
1	CG	190	ASN
1	BH	94	HIS
1	BH	100	GLN
1	BH	142	GLN
1	BH	190	ASN
1	BH	191	ASN
1	BH	196	ASN
1	AH	65	GLN
1	AH	134	ASN
1	AH	142	GLN
1	AH	191	ASN
1	AH	196	ASN
1	AH	225	GLN
1	AH	236	ASN
1	AH	258	GLN
1	CH	56	HIS
1	CH	94	HIS
1	CH	112	GLN
1	CH	190	ASN
1	BI	100	GLN
1	BI	142	GLN
1	BI	190	ASN
1	BI	191	ASN
1	BI	196	ASN
1	BI	214	ASN
1	AI	65	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	AI	118	ASN
1	AI	134	ASN
1	AI	142	GLN
1	AI	196	ASN
1	AI	225	GLN
1	AI	236	ASN
1	AI	258	GLN
1	CI	56	HIS
1	CI	112	GLN
1	CI	190	ASN
1	BJ	100	GLN
1	BJ	142	GLN
1	BJ	190	ASN
1	BJ	191	ASN
1	BJ	196	ASN
1	AJ	65	GLN
1	AJ	118	ASN
1	AJ	134	ASN
1	AJ	142	GLN
1	AJ	196	ASN
1	AJ	225	GLN
1	AJ	236	ASN
1	CJ	56	HIS
1	CJ	94	HIS
1	CJ	112	GLN
1	CJ	190	ASN
1	BK	100	GLN
1	BK	190	ASN
1	BK	191	ASN
1	BK	196	ASN
1	AK	65	GLN
1	AK	118	ASN
1	AK	134	ASN
1	AK	142	GLN
1	AK	191	ASN
1	AK	196	ASN
1	AK	225	GLN
1	AK	236	ASN
1	AK	258	GLN
1	CK	56	HIS
1	CK	112	GLN
1	CK	190	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	BL	100	GLN
1	BL	190	ASN
1	BL	191	ASN
1	BL	196	ASN
1	BL	214	ASN
1	AL	65	GLN
1	AL	134	ASN
1	AL	142	GLN
1	AL	196	ASN
1	AL	225	GLN
1	AL	236	ASN
1	AL	258	GLN
1	CL	56	HIS
1	CL	112	GLN
1	CL	190	ASN
1	BM	100	GLN
1	BM	142	GLN
1	BM	190	ASN
1	BM	191	ASN
1	BM	196	ASN
1	AM	65	GLN
1	AM	118	ASN
1	AM	134	ASN
1	AM	142	GLN
1	AM	196	ASN
1	AM	225	GLN
1	AM	236	ASN
1	AM	258	GLN
1	CM	56	HIS
1	CM	112	GLN
1	CM	190	ASN
1	BN	100	GLN
1	BN	190	ASN
1	BN	191	ASN
1	BN	196	ASN
1	AN	65	GLN
1	AN	118	ASN
1	AN	134	ASN
1	AN	142	GLN
1	AN	196	ASN
1	AN	225	GLN
1	AN	236	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	AN	258	GLN
1	CN	56	HIS
1	CN	112	GLN
1	CN	190	ASN
1	BO	100	GLN
1	BO	142	GLN
1	BO	190	ASN
1	BO	191	ASN
1	BO	196	ASN
1	AO	65	GLN
1	AO	134	ASN
1	AO	142	GLN
1	AO	191	ASN
1	AO	196	ASN
1	AO	225	GLN
1	AO	236	ASN
1	AO	258	GLN
1	CO	56	HIS
1	CO	112	GLN
1	CO	190	ASN
1	BP	100	GLN
1	BP	142	GLN
1	BP	190	ASN
1	BP	191	ASN
1	BP	196	ASN
1	AP	65	GLN
1	AP	118	ASN
1	AP	134	ASN
1	AP	142	GLN
1	AP	196	ASN
1	AP	225	GLN
1	AP	236	ASN
1	AP	258	GLN
1	CP	56	HIS
1	CP	112	GLN
1	CP	190	ASN
1	BQ	142	GLN
1	BQ	190	ASN
1	BQ	191	ASN
1	BQ	196	ASN
1	BQ	214	ASN
1	AQ	65	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	AQ	118	ASN
1	AQ	134	ASN
1	AQ	142	GLN
1	AQ	196	ASN
1	AQ	225	GLN
1	AQ	236	ASN
1	AQ	258	GLN
1	CQ	56	HIS
1	CQ	112	GLN
1	CQ	190	ASN
1	BR	100	GLN
1	BR	190	ASN
1	BR	191	ASN
1	BR	196	ASN
1	AR	65	GLN
1	AR	118	ASN
1	AR	134	ASN
1	AR	142	GLN
1	AR	196	ASN
1	AR	225	GLN
1	AR	236	ASN
1	AR	258	GLN
1	CR	56	HIS
1	CR	112	GLN
1	CR	190	ASN
1	BS	100	GLN
1	BS	190	ASN
1	BS	191	ASN
1	BS	196	ASN
1	AS	65	GLN
1	AS	118	ASN
1	AS	134	ASN
1	AS	142	GLN
1	AS	196	ASN
1	AS	225	GLN
1	AS	236	ASN
1	AS	258	GLN
1	CS	56	HIS
1	CS	112	GLN
1	CS	190	ASN
1	BT	100	GLN
1	BT	190	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	BT	191	ASN
1	BT	196	ASN
1	BT	214	ASN
1	AT	65	GLN
1	AT	118	ASN
1	AT	134	ASN
1	AT	142	GLN
1	AT	196	ASN
1	AT	225	GLN
1	AT	236	ASN
1	AT	258	GLN
1	CT	56	HIS
1	CT	112	GLN
1	CT	190	ASN
1	BU	100	GLN
1	BU	142	GLN
1	BU	190	ASN
1	BU	191	ASN
1	BU	196	ASN
1	AU	65	GLN
1	AU	134	ASN
1	AU	142	GLN
1	AU	191	ASN
1	AU	196	ASN
1	AU	225	GLN
1	AU	236	ASN
1	AU	258	GLN
1	CU	56	HIS
1	CU	112	GLN
1	CU	190	ASN
1	BV	142	GLN
1	BV	190	ASN
1	BV	191	ASN
1	BV	196	ASN
1	BV	214	ASN
1	AV	65	GLN
1	AV	118	ASN
1	AV	134	ASN
1	AV	142	GLN
1	AV	196	ASN
1	AV	225	GLN
1	AV	236	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	AV	258	GLN
1	CV	56	HIS
1	CV	112	GLN
1	CV	190	ASN
1	BW	100	GLN
1	BW	190	ASN
1	BW	191	ASN
1	BW	196	ASN
1	BW	214	ASN
1	AW	65	GLN
1	AW	118	ASN
1	AW	134	ASN
1	AW	142	GLN
1	AW	196	ASN
1	AW	225	GLN
1	AW	236	ASN
1	AW	258	GLN
1	CW	56	HIS
1	CW	112	GLN
1	CW	190	ASN
1	BX	100	GLN
1	BX	142	GLN
1	BX	190	ASN
1	BX	191	ASN
1	BX	196	ASN
1	AX	65	GLN
1	AX	134	ASN
1	AX	142	GLN
1	AX	196	ASN
1	AX	225	GLN
1	AX	236	ASN
1	AX	258	GLN
1	CX	56	HIS
1	CX	112	GLN
1	CX	190	ASN
1	BY	100	GLN
1	BY	142	GLN
1	BY	190	ASN
1	BY	191	ASN
1	BY	196	ASN
1	BY	214	ASN
1	AY	65	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	AY	118	ASN
1	AY	134	ASN
1	AY	142	GLN
1	AY	191	ASN
1	AY	196	ASN
1	AY	225	GLN
1	AY	236	ASN
1	AY	258	GLN
1	CY	56	HIS
1	CY	112	GLN
1	CY	190	ASN
1	BZ	100	GLN
1	BZ	142	GLN
1	BZ	190	ASN
1	BZ	191	ASN
1	BZ	196	ASN
1	BZ	214	ASN
1	AZ	65	GLN
1	AZ	118	ASN
1	AZ	134	ASN
1	AZ	142	GLN
1	AZ	191	ASN
1	AZ	196	ASN
1	AZ	225	GLN
1	AZ	258	GLN
1	CZ	56	HIS
1	CZ	112	GLN
1	CZ	190	ASN
1	Ba	100	GLN
1	Ba	142	GLN
1	Ba	190	ASN
1	Ba	191	ASN
1	Ba	196	ASN
1	Aa	65	GLN
1	Aa	118	ASN
1	Aa	134	ASN
1	Aa	142	GLN
1	Aa	196	ASN
1	Aa	225	GLN
1	Aa	236	ASN
1	Aa	258	GLN
1	Ca	56	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	Ca	94	HIS
1	Ca	112	GLN
1	Ca	190	ASN
1	Bb	100	GLN
1	Bb	142	GLN
1	Bb	190	ASN
1	Bb	191	ASN
1	Bb	196	ASN
1	Ab	65	GLN
1	Ab	118	ASN
1	Ab	134	ASN
1	Ab	142	GLN
1	Ab	196	ASN
1	Ab	225	GLN
1	Ab	236	ASN
1	Ab	258	GLN
1	Cb	56	HIS
1	Cb	112	GLN
1	Cb	190	ASN
1	Bc	100	GLN
1	Bc	142	GLN
1	Bc	190	ASN
1	Bc	191	ASN
1	Bc	196	ASN
1	Ac	65	GLN
1	Ac	118	ASN
1	Ac	134	ASN
1	Ac	142	GLN
1	Ac	196	ASN
1	Ac	225	GLN
1	Ac	236	ASN
1	Ac	258	GLN
1	Cc	56	HIS
1	Cc	112	GLN
1	Cc	190	ASN
1	Bd	100	GLN
1	Bd	190	ASN
1	Bd	191	ASN
1	Bd	196	ASN
1	Ad	65	GLN
1	Ad	118	ASN
1	Ad	134	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	Ad	142	GLN
1	Ad	191	ASN
1	Ad	196	ASN
1	Ad	225	GLN
1	Ad	258	GLN
1	Cd	56	HIS
1	Cd	112	GLN
1	Cd	190	ASN
1	Cd	196	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 90 ligands modelled in this entry, 90 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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, 95th 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 ²)	Q<0.9
1	AA	287/338 (84%)	-0.02	1 (0%) 94 90	44, 93, 184, 235	0
1	AB	287/338 (84%)	1.14	61 (21%) 1 1	31, 79, 239, 363	0
1	AC	287/338 (84%)	0.35	26 (9%) 11 8	32, 75, 244, 339	0
1	AD	287/338 (84%)	0.37	16 (5%) 28 19	40, 82, 155, 215	0
1	AE	287/338 (84%)	0.23	6 (2%) 67 52	44, 88, 179, 251	0
1	AF	287/338 (84%)	0.37	20 (6%) 19 13	37, 80, 176, 225	0
1	AG	287/338 (84%)	0.65	36 (12%) 5 5	42, 89, 208, 293	0
1	AH	287/338 (84%)	0.65	38 (13%) 4 4	39, 86, 244, 334	0
1	AI	287/338 (84%)	0.38	23 (8%) 15 10	38, 93, 255, 333	0
1	AJ	287/338 (84%)	0.04	5 (1%) 73 59	36, 75, 146, 223	0
1	AK	287/338 (84%)	0.01	2 (0%) 89 81	31, 63, 120, 191	0
1	AL	287/338 (84%)	0.05	1 (0%) 94 90	32, 69, 138, 194	0
1	AM	287/338 (84%)	1.06	51 (17%) 2 2	41, 91, 249, 306	0
1	AN	287/338 (84%)	-0.16	4 (1%) 78 65	41, 85, 200, 285	0
1	AO	287/338 (84%)	0.50	21 (7%) 18 12	36, 83, 203, 294	0
1	AP	287/338 (84%)	0.10	9 (3%) 52 38	41, 81, 187, 253	0
1	AQ	287/338 (84%)	0.07	8 (2%) 56 42	46, 83, 172, 212	0
1	AR	287/338 (84%)	-0.08	0 100 100	40, 77, 141, 197	0
1	AS	287/338 (84%)	-0.07	7 (2%) 62 47	28, 78, 171, 271	0
1	AT	287/338 (84%)	0.17	3 (1%) 84 73	46, 89, 169, 226	0
1	AU	287/338 (84%)	0.71	33 (11%) 6 6	32, 86, 200, 301	0
1	AV	287/338 (84%)	0.38	19 (6%) 22 14	45, 90, 183, 234	0
1	AW	287/338 (84%)	0.07	2 (0%) 89 81	37, 72, 129, 194	0
1	AX	287/338 (84%)	0.47	26 (9%) 11 8	37, 79, 185, 294	0

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	AY	287/338 (84%)	0.12	7 (2%) 62 47	37, 77, 153, 206	0
1	AZ	287/338 (84%)	0.16	8 (2%) 56 42	39, 84, 178, 279	0
1	Aa	287/338 (84%)	0.02	7 (2%) 62 47	41, 90, 182, 222	0
1	Ab	287/338 (84%)	1.24	56 (19%) 1 1	38, 81, 245, 357	0
1	Ac	287/338 (84%)	0.30	16 (5%) 28 19	45, 82, 169, 236	0
1	Ad	287/338 (84%)	0.31	11 (3%) 44 32	43, 77, 141, 218	0
1	BA	286/338 (84%)	0.28	17 (5%) 26 17	37, 88, 199, 239	0
1	BB	286/338 (84%)	0.80	39 (13%) 4 4	25, 71, 229, 336	0
1	BC	286/338 (84%)	0.86	48 (16%) 2 2	30, 79, 265, 341	0
1	BD	286/338 (84%)	0.04	5 (1%) 73 59	34, 79, 172, 283	0
1	BE	286/338 (84%)	0.36	17 (5%) 26 17	41, 81, 199, 285	0
1	BF	286/338 (84%)	0.32	24 (8%) 14 10	32, 75, 188, 271	0
1	BG	286/338 (84%)	0.84	37 (12%) 5 4	39, 81, 215, 307	0
1	BH	286/338 (84%)	0.84	45 (15%) 3 2	36, 78, 245, 329	0
1	BI	286/338 (84%)	0.38	27 (9%) 11 8	35, 82, 280, 360	0
1	BJ	286/338 (84%)	0.05	3 (1%) 84 73	24, 67, 162, 275	0
1	BK	286/338 (84%)	0.19	4 (1%) 78 65	27, 62, 144, 203	0
1	BL	286/338 (84%)	-0.00	0 100 100	29, 66, 129, 190	0
1	BM	286/338 (84%)	1.13	57 (19%) 1 1	32, 79, 256, 365	0
1	BN	286/338 (84%)	0.15	16 (5%) 28 19	37, 80, 201, 324	0
1	BO	286/338 (84%)	1.22	69 (24%) 1 1	29, 76, 223, 315	0
1	BP	286/338 (84%)	0.18	13 (4%) 37 26	37, 81, 198, 270	0
1	BQ	286/338 (84%)	-0.00	2 (0%) 89 81	35, 78, 180, 295	0
1	BR	286/338 (84%)	0.29	7 (2%) 62 47	37, 80, 149, 225	0
1	BS	286/338 (84%)	0.08	7 (2%) 62 47	27, 67, 180, 308	0
1	BT	286/338 (84%)	0.17	5 (1%) 73 59	38, 84, 176, 270	0
1	BU	286/338 (84%)	0.64	36 (12%) 5 5	32, 75, 209, 323	0
1	BV	286/338 (84%)	0.01	4 (1%) 78 65	38, 86, 183, 243	0
1	BW	286/338 (84%)	-0.06	1 (0%) 94 90	33, 66, 123, 203	0
1	BX	286/338 (84%)	0.39	20 (6%) 19 13	35, 80, 198, 263	0
1	BY	286/338 (84%)	0.53	20 (6%) 19 13	35, 78, 150, 213	0

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	BZ	286/338 (84%)	0.22	11 (3%) 44 32	38, 83, 195, 246	0
1	Ba	286/338 (84%)	0.06	5 (1%) 73 59	34, 81, 197, 330	0
1	Bb	286/338 (84%)	0.76	43 (15%) 3 3	30, 69, 249, 342	0
1	Bc	286/338 (84%)	0.27	13 (4%) 37 26	33, 79, 214, 279	0
1	Bd	286/338 (84%)	0.51	23 (8%) 15 10	37, 79, 168, 230	0
1	CA	304/338 (89%)	0.30	24 (7%) 15 10	40, 78, 206, 252	0
1	CB	304/338 (89%)	1.66	91 (29%) 1 1	29, 75, 282, 357	0
1	CC	304/338 (89%)	0.59	45 (14%) 3 3	28, 72, 269, 370	0
1	CD	304/338 (89%)	0.10	13 (4%) 39 27	38, 76, 190, 273	0
1	CE	304/338 (89%)	0.71	49 (16%) 3 2	34, 76, 239, 323	0
1	CF	304/338 (89%)	0.79	51 (16%) 2 2	34, 72, 234, 326	0
1	CG	304/338 (89%)	1.95	90 (29%) 1 1	39, 83, 269, 342	0
1	CH	304/338 (89%)	1.96	94 (30%) 1 1	37, 79, 323, 403	0
1	CI	304/338 (89%)	0.73	51 (16%) 2 2	34, 81, 284, 396	0
1	CJ	304/338 (89%)	0.12	12 (3%) 43 31	26, 70, 200, 287	0
1	CK	304/338 (89%)	0.13	2 (0%) 89 81	28, 64, 113, 174	0
1	CL	304/338 (89%)	0.03	2 (0%) 89 81	26, 66, 129, 190	0
1	CM	304/338 (89%)	1.37	76 (25%) 1 1	33, 75, 306, 389	0
1	CN	304/338 (89%)	0.43	33 (10%) 7 6	39, 77, 229, 320	0
1	CO	304/338 (89%)	0.91	53 (17%) 2 2	30, 74, 258, 396	0
1	CP	304/338 (89%)	0.33	24 (7%) 15 10	33, 81, 201, 288	0
1	CQ	304/338 (89%)	0.22	16 (5%) 30 21	39, 80, 187, 294	0
1	CR	304/338 (89%)	0.12	7 (2%) 64 48	34, 79, 153, 209	0
1	CS	304/338 (89%)	0.34	24 (7%) 15 10	28, 66, 226, 306	0
1	CT	304/338 (89%)	0.10	7 (2%) 64 48	37, 76, 186, 299	0
1	CU	304/338 (89%)	1.15	68 (22%) 1 1	31, 70, 249, 303	0
1	CV	304/338 (89%)	0.24	13 (4%) 39 27	41, 80, 196, 237	0
1	CW	304/338 (89%)	0.00	6 (1%) 68 54	30, 75, 137, 176	0
1	CX	304/338 (89%)	0.07	16 (5%) 30 21	39, 78, 244, 302	0
1	CY	304/338 (89%)	0.53	29 (9%) 10 8	33, 73, 176, 256	0
1	CZ	304/338 (89%)	0.38	32 (10%) 8 6	43, 82, 187, 293	0

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	Ca	304/338 (89%)	0.68	40 (13%) 4 4	35, 78, 209, 267	0
1	Cb	304/338 (89%)	1.89	84 (27%) 1 1	30, 73, 298, 419	0
1	Cc	304/338 (89%)	0.64	47 (15%) 3 2	38, 80, 263, 325	0
1	Cd	304/338 (89%)	0.21	13 (4%) 39 27	35, 75, 137, 221	0
All	All	26310/30420 (86%)	0.45	2253 (8%) 13 10	24, 78, 223, 419	0

All (2253) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	Cb	232	SER	28.1
1	CG	265	ILE	22.5
1	CH	337	GLU	21.4
1	Cb	227	SER	20.3
1	BG	317	ASP	20.0
1	Cb	231	ASP	19.6
1	CB	265	ILE	19.4
1	CH	265	ILE	18.7
1	Cb	265	ILE	17.4
1	BM	264	SER	16.9
1	CH	282	LEU	16.9
1	CH	293	ALA	16.6
1	Bb	318	GLU	16.5
1	CM	282	LEU	16.3
1	CH	286	ALA	16.0
1	CF	293	ALA	15.7
1	CM	265	ILE	15.4
1	Ab	306	LYS	15.4
1	BH	327	VAL	15.3
1	CM	245	SER	15.1
1	Cb	249	ASP	15.1
1	Ab	270	GLY	15.0
1	CO	265	ILE	15.0
1	CB	282	LEU	14.8
1	CG	253	ASP	14.7
1	Bb	317	ASP	14.5
1	Cc	274	VAL	14.4
1	Cb	282	LEU	14.2
1	CH	336	SER	14.2
1	Cb	294	GLY	14.2
1	CH	288	ASN	14.0
1	CM	328	GLY	13.9

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	CB	250	ILE	13.7
1	CU	265	ILE	13.5
1	CG	247	PRO	13.4
1	BC	263	LEU	13.3
1	CG	286	ALA	13.2
1	CG	246	THR	13.2
1	Cb	241	ILE	13.1
1	CH	294	GLY	13.1
1	CB	232	SER	13.0
1	CM	246	THR	12.9
1	Cb	288	ASN	12.9
1	Ab	273	ASP	12.9
1	BM	318	GLU	12.6
1	CO	282	LEU	12.6
1	Cb	250	ILE	12.6
1	Ac	269	LEU	12.5
1	Cb	255	ALA	12.3
1	CN	265	ILE	12.3
1	BC	264	SER	12.2
1	Cb	286	ALA	12.1
1	BB	317	ASP	12.0
1	CH	257	PHE	12.0
1	CU	232	SER	12.0
1	CI	263	LEU	11.9
1	CG	289	ALA	11.9
1	BG	318	GLU	11.7
1	CM	256	VAL	11.5
1	BB	264	SER	11.5
1	BB	318	GLU	11.4
1	Ab	337	GLU	11.4
1	CG	282	LEU	11.4
1	CN	282	LEU	11.3
1	CG	232	SER	11.2
1	Ca	293	ALA	11.2
1	CH	263	LEU	11.2
1	CB	257	PHE	11.1
1	CB	288	ASN	11.1
1	CO	286	ALA	11.1
1	CG	293	ALA	11.1
1	CF	265	ILE	11.1
1	CO	289	ALA	10.9
1	BM	239	LYS	10.9

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	CU	282	LEU	10.9
1	AB	230	ASN	10.9
1	Cb	321	ARG	10.9
1	CO	288	ASN	10.8
1	CH	289	ALA	10.8
1	CM	247	PRO	10.8
1	AI	230	ASN	10.7
1	Bc	318	GLU	10.7
1	Cb	291	THR	10.7
1	CH	262	PRO	10.7
1	Cb	242	LEU	10.6
1	Ca	290	GLY	10.6
1	BO	239	LYS	10.6
1	CM	257	PHE	10.5
1	CB	321	ARG	10.5
1	CE	265	ILE	10.5
1	CG	249	ASP	10.3
1	CH	250	ILE	10.2
1	CG	274	VAL	10.2
1	CB	289	ALA	10.2
1	CG	250	ILE	10.1
1	Ab	268	SER	10.1
1	AB	306	LYS	10.1
1	Cb	263	LEU	10.1
1	BC	268	SER	10.1
1	Cb	279	TYR	10.0
1	Cb	293	ALA	10.0
1	CG	288	ASN	10.0
1	CM	240	SER	10.0
1	BO	315	TYR	10.0
1	CI	265	ILE	9.9
1	BO	264	SER	9.9
1	Cc	289	ALA	9.9
1	CB	263	LEU	9.8
1	BH	318	GLU	9.8
1	BO	318	GLU	9.8
1	CH	225	GLN	9.8
1	Ab	303	ASN	9.7
1	Cb	289	ALA	9.7
1	BO	296	PHE	9.7
1	CU	293	ALA	9.7
1	BO	292	PRO	9.7

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	Ca	282	LEU	9.7
1	CH	253	ASP	9.7
1	Ab	304	PHE	9.7
1	BH	264	SER	9.7
1	CG	318	GLU	9.6
1	CI	249	ASP	9.6
1	Cc	232	SER	9.6
1	CH	291	THR	9.6
1	BG	312	VAL	9.5
1	Ab	269	LEU	9.4
1	CG	294	GLY	9.4
1	BH	328	GLY	9.4
1	CO	291	THR	9.4
1	BO	291	THR	9.3
1	CB	223	MET	9.3
1	CM	227	SER	9.2
1	Cb	239	LYS	9.2
1	CH	232	SER	9.2
1	BC	278	VAL	9.2
1	CB	291	THR	9.1
1	AM	306	LYS	9.1
1	CG	279	TYR	9.1
1	CM	279	TYR	8.9
1	CM	294	GLY	8.9
1	Ab	271	THR	8.9
1	Cb	223	MET	8.9
1	Cc	293	ALA	8.9
1	AB	236	ASN	8.8
1	BB	326	PRO	8.8
1	BM	238	PHE	8.8
1	CG	233	LEU	8.8
1	CH	287	GLY	8.8
1	AH	230	ASN	8.8
1	CE	282	LEU	8.8
1	BG	298	TRP	8.8
1	Cb	287	GLY	8.8
1	Cb	290	GLY	8.8
1	CG	245	SER	8.8
1	CG	252	PRO	8.7
1	Cb	240	SER	8.7
1	CI	220	ALA	8.7
1	CG	242	LEU	8.7

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	AB	322	GLN	8.7
1	CB	262	PRO	8.7
1	CB	251	ALA	8.7
1	CH	333	ARG	8.7
1	CP	265	ILE	8.7
1	CH	300	ILE	8.7
1	CH	249	ASP	8.7
1	BC	317	ASP	8.6
1	BM	298	TRP	8.6
1	CX	282	LEU	8.4
1	AF	269	LEU	8.4
1	Cb	222	ILE	8.4
1	CM	249	ASP	8.4
1	BG	264	SER	8.4
1	BO	278	VAL	8.4
1	AI	318	GLU	8.3
1	CM	223	MET	8.3
1	BU	318	GLU	8.3
1	BG	276	ARG	8.3
1	Ab	336	SER	8.3
1	CG	255	ALA	8.3
1	CB	256	VAL	8.3
1	AB	268	SER	8.3
1	CB	233	LEU	8.2
1	CF	282	LEU	8.2
1	BH	326	PRO	8.2
1	CO	250	ILE	8.2
1	CH	335	ASP	8.2
1	CB	270	GLY	8.1
1	CG	285	PHE	8.1
1	BH	278	VAL	8.1
1	BG	296	PHE	8.0
1	BE	317	ASP	8.0
1	BO	237	ASP	8.0
1	CO	279	TYR	7.9
1	Bb	264	SER	7.9
1	BH	317	ASP	7.9
1	CH	327	VAL	7.9
1	BO	298	TRP	7.9
1	BM	317	ASP	7.9
1	AG	268	SER	7.9
1	CM	232	SER	7.9

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	CH	251	ALA	7.9
1	AB	273	ASP	7.8
1	CH	223	MET	7.8
1	BG	315	TYR	7.8
1	CB	249	ASP	7.7
1	CB	227	SER	7.7
1	CC	279	TYR	7.7
1	BO	238	PHE	7.7
1	BE	318	GLU	7.6
1	BI	262	PRO	7.6
1	CM	253	ASP	7.6
1	CU	227	SER	7.6
1	Ab	265	ILE	7.6
1	CI	257	PHE	7.6
1	CM	330	VAL	7.5
1	BO	312	VAL	7.5
1	CO	257	PHE	7.5
1	CO	249	ASP	7.5
1	CO	287	GLY	7.5
1	Ab	308	PHE	7.5
1	Cb	246	THR	7.5
1	Cb	247	PRO	7.5
1	Cb	253	ASP	7.5
1	CG	241	ILE	7.5
1	CB	255	ALA	7.5
1	CM	241	ILE	7.5
1	Cb	281	HIS	7.4
1	BB	327	VAL	7.4
1	BC	269	LEU	7.4
1	CU	286	ALA	7.4
1	Cb	233	LEU	7.4
1	CG	321	ARG	7.4
1	BI	296	PHE	7.4
1	AM	269	LEU	7.4
1	BN	264	SER	7.3
1	CM	244	GLY	7.3
1	CG	257	PHE	7.3
1	CU	263	LEU	7.3
1	Cb	274	VAL	7.3
1	CH	221	PRO	7.3
1	CE	293	ALA	7.3
1	CH	270	GLY	7.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	CB	317	ASP	7.3
1	BB	262	PRO	7.2
1	Ab	272	GLY	7.2
1	CU	250	ILE	7.2
1	CU	292	PRO	7.2
1	CF	319	GLN	7.2
1	CM	327	VAL	7.2
1	CO	255	ALA	7.2
1	BM	315	TYR	7.2
1	BM	276	ARG	7.2
1	CO	256	VAL	7.2
1	Ac	265	ILE	7.1
1	Cb	226	GLY	7.1
1	Cb	252	PRO	7.1
1	CB	287	GLY	7.1
1	CU	317	ASP	7.1
1	Ab	333	ARG	7.1
1	BB	228	LEU	7.1
1	CB	245	SER	7.1
1	CF	257	PHE	7.0
1	AI	266	ASP	7.0
1	BN	317	ASP	7.0
1	CG	287	GLY	7.0
1	CB	240	SER	7.0
1	CG	231	ASP	7.0
1	AM	260	ASP	7.0
1	CH	264	SER	7.0
1	CB	225	GLN	7.0
1	CH	290	GLY	7.0
1	CO	253	ASP	6.9
1	CH	247	PRO	6.9
1	CX	265	ILE	6.9
1	BH	296	PHE	6.9
1	AM	325	LEU	6.9
1	CG	331	CYS	6.9
1	BS	317	ASP	6.9
1	AB	271	THR	6.9
1	AO	324	LEU	6.9
1	CE	337	GLU	6.8
1	CB	234	SER	6.8
1	BB	328	GLY	6.8
1	CG	270	GLY	6.8

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	Cb	327	VAL	6.8
1	CA	282	LEU	6.8
1	BM	277	ALA	6.8
1	BM	237	ASP	6.8
1	CM	263	LEU	6.8
1	CY	232	SER	6.8
1	CO	290	GLY	6.8
1	CI	218	THR	6.8
1	CF	266	ASP	6.7
1	BH	238	PHE	6.7
1	CI	282	LEU	6.7
1	Cc	282	LEU	6.7
1	Cb	318	GLU	6.7
1	AB	303	ASN	6.7
1	Cb	292	PRO	6.7
1	CU	262	PRO	6.7
1	Cb	333	ARG	6.7
1	CB	290	GLY	6.7
1	AH	325	LEU	6.7
1	BU	239	LYS	6.7
1	Bc	317	ASP	6.7
1	CM	289	ALA	6.6
1	CI	255	ALA	6.6
1	AF	236	ASN	6.6
1	CU	321	ARG	6.6
1	CI	294	GLY	6.6
1	Ab	305	ASN	6.6
1	BO	262	PRO	6.6
1	AB	260	ASP	6.6
1	CM	293	ALA	6.6
1	CH	279	TYR	6.6
1	BO	317	ASP	6.6
1	Ca	292	PRO	6.6
1	CH	330	VAL	6.6
1	AC	282	LEU	6.5
1	Bb	239	LYS	6.5
1	BB	296	PHE	6.5
1	CB	231	ASP	6.5
1	CG	330	VAL	6.5
1	Bb	315	TYR	6.5
1	CO	263	LEU	6.5
1	BH	227	SER	6.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	CI	254	GLY	6.5
1	CU	255	ALA	6.4
1	CF	294	GLY	6.4
1	CU	241	ILE	6.4
1	Bb	298	TRP	6.4
1	BB	227	SER	6.4
1	CM	250	ILE	6.4
1	BO	236	ASN	6.4
1	CG	244	GLY	6.4
1	AM	324	LEU	6.4
1	CF	291	THR	6.4
1	Ab	218	THR	6.4
1	BN	318	GLU	6.4
1	CI	279	TYR	6.4
1	BB	278	VAL	6.4
1	Cc	246	THR	6.3
1	CG	227	SER	6.3
1	Ab	325	LEU	6.3
1	CH	252	PRO	6.3
1	Ca	257	PHE	6.3
1	CG	263	LEU	6.3
1	AB	304	PHE	6.3
1	CF	337	GLU	6.2
1	CG	290	GLY	6.2
1	CN	293	ALA	6.2
1	Cb	307	THR	6.2
1	CE	286	ALA	6.2
1	BI	264	SER	6.2
1	CI	221	PRO	6.2
1	AM	236	ASN	6.2
1	BB	277	ALA	6.2
1	BY	317	ASP	6.2
1	CI	288	ASN	6.2
1	CH	245	SER	6.2
1	AX	337	GLU	6.2
1	AI	228	LEU	6.2
1	CM	307	THR	6.2
1	BH	239	LYS	6.2
1	CG	240	SER	6.1
1	CH	317	ASP	6.1
1	CG	333	ARG	6.1
1	CO	316	SER	6.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	Ca	249	ASP	6.1
1	Ca	291	THR	6.1
1	CB	337	GLU	6.1
1	BH	262	PRO	6.1
1	CF	286	ALA	6.1
1	CG	310	ASP	6.1
1	CH	227	SER	6.1
1	AB	307	THR	6.0
1	BM	278	VAL	6.0
1	CO	293	ALA	6.0
1	Cc	292	PRO	6.0
1	CC	317	ASP	6.0
1	CB	316	SER	6.0
1	Cc	264	SER	6.0
1	CB	247	PRO	6.0
1	BM	292	PRO	6.0
1	CY	264	SER	6.0
1	CU	290	GLY	6.0
1	CE	289	ALA	6.0
1	BP	317	ASP	6.0
1	AI	270	GLY	5.9
1	CB	318	GLU	5.9
1	AH	322	GLN	5.9
1	AO	269	LEU	5.9
1	CH	240	SER	5.9
1	CH	231	ASP	5.9
1	Ba	317	ASP	5.9
1	CE	287	GLY	5.9
1	CI	219	THR	5.9
1	BC	266	ASP	5.9
1	Cb	317	ASP	5.9
1	Bb	327	VAL	5.9
1	CM	335	ASP	5.9
1	BO	309	THR	5.9
1	BI	317	ASP	5.9
1	CG	292	PRO	5.9
1	CI	318	GLU	5.9
1	CN	232	SER	5.9
1	CG	262	PRO	5.9
1	AE	337	GLU	5.8
1	Ac	268	SER	5.8
1	BC	249	ASP	5.8

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	BU	238	PHE	5.8
1	CB	294	GLY	5.8
1	BU	317	ASP	5.8
1	CI	277	ALA	5.8
1	CE	266	ASP	5.8
1	Cb	276	ARG	5.8
1	CF	264	SER	5.8
1	BO	297	ARG	5.8
1	Cb	225	GLN	5.7
1	BS	315	TYR	5.7
1	CF	333	ARG	5.7
1	CO	251	ALA	5.7
1	AB	305	ASN	5.7
1	CO	264	SER	5.7
1	CB	333	ARG	5.7
1	CS	255	ALA	5.7
1	Bb	292	PRO	5.7
1	BB	238	PHE	5.7
1	CF	287	GLY	5.7
1	CU	242	LEU	5.7
1	Cb	251	ALA	5.7
1	Ab	260	ASP	5.7
1	CJ	286	ALA	5.7
1	CE	249	ASP	5.7
1	AC	298	TRP	5.7
1	CI	248	LEU	5.7
1	Cb	257	PHE	5.7
1	CA	249	ASP	5.6
1	Ab	281	HIS	5.6
1	CG	335	ASP	5.6
1	Cb	244	GLY	5.6
1	Ca	255	ALA	5.6
1	Cb	245	SER	5.6
1	AG	307	THR	5.6
1	BO	327	VAL	5.6
1	CB	286	ALA	5.6
1	AO	325	LEU	5.6
1	Ab	307	THR	5.6
1	Cb	256	VAL	5.6
1	Bd	287	GLY	5.6
1	BB	298	TRP	5.6
1	CF	255	ALA	5.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	CH	233	LEU	5.5
1	BF	239	LYS	5.5
1	BU	264	SER	5.5
1	CU	287	GLY	5.5
1	CS	282	LEU	5.5
1	CU	327	VAL	5.5
1	BX	264	SER	5.5
1	CC	258	GLN	5.5
1	CN	257	PHE	5.5
1	CH	283	LYS	5.5
1	CG	317	ASP	5.5
1	CH	285	PHE	5.5
1	CB	244	GLY	5.5
1	BM	296	PHE	5.5
1	CP	317	ASP	5.4
1	CB	281	HIS	5.4
1	AO	230	ASN	5.4
1	CH	281	HIS	5.4
1	CM	252	PRO	5.4
1	CG	328	GLY	5.4
1	AH	260	ASP	5.4
1	AM	273	ASP	5.4
1	CO	292	PRO	5.4
1	CU	256	VAL	5.4
1	CB	271	THR	5.4
1	AF	337	GLU	5.4
1	BI	318	GLU	5.4
1	CI	269	LEU	5.4
1	CM	323	ILE	5.4
1	CB	226	GLY	5.4
1	CM	281	HIS	5.4
1	CG	319	GLN	5.4
1	Ca	289	ALA	5.4
1	Bb	276	ARG	5.4
1	BX	317	ASP	5.4
1	Cb	328	GLY	5.4
1	BD	317	ASP	5.4
1	AM	281	HIS	5.4
1	CG	223	MET	5.4
1	CH	284	LYS	5.4
1	CB	279	TYR	5.4
1	AO	273	ASP	5.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	BU	296	PHE	5.4
1	CU	257	PHE	5.4
1	CU	333	ARG	5.4
1	CF	263	LEU	5.4
1	AB	232	SER	5.3
1	CE	272	GLY	5.3
1	BM	328	GLY	5.3
1	Bd	289	ALA	5.3
1	CS	293	ALA	5.3
1	AG	230	ASN	5.3
1	CB	293	ALA	5.3
1	CU	231	ASP	5.3
1	CN	233	LEU	5.3
1	CU	316	SER	5.3
1	CH	222	ILE	5.3
1	BI	227	SER	5.3
1	CH	328	GLY	5.3
1	CB	246	THR	5.3
1	AU	281	HIS	5.3
1	BE	315	TYR	5.3
1	CZ	333	ARG	5.2
1	AM	337	GLU	5.2
1	AG	306	LYS	5.2
1	CF	318	GLU	5.2
1	BM	297	ARG	5.2
1	AM	230	ASN	5.2
1	CU	328	GLY	5.2
1	BC	276	ARG	5.2
1	CD	282	LEU	5.2
1	AU	337	GLU	5.2
1	CE	270	GLY	5.2
1	Cb	319	GLN	5.1
1	CE	288	ASN	5.1
1	CH	255	ALA	5.1
1	Ab	277	ALA	5.1
1	CG	239	LYS	5.1
1	CM	333	ARG	5.1
1	BX	318	GLU	5.1
1	Cc	250	ILE	5.1
1	CO	247	PRO	5.1
1	BC	224	THR	5.1
1	AB	308	PHE	5.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	CU	221	PRO	5.1
1	Ca	288	ASN	5.1
1	BF	315	TYR	5.1
1	Ba	318	GLU	5.1
1	BH	277	ALA	5.1
1	Cd	254	GLY	5.1
1	AX	265	ILE	5.1
1	AB	269	LEU	5.1
1	AB	301	TRP	5.1
1	BX	278	VAL	5.1
1	AM	228	LEU	5.1
1	CH	234	SER	5.1
1	BM	236	ASN	5.1
1	CI	289	ALA	5.1
1	AD	269	LEU	5.1
1	BM	291	THR	5.1
1	CO	252	PRO	5.1
1	BO	279	TYR	5.1
1	CB	274	VAL	5.1
1	BU	277	ALA	5.1
1	CH	274	VAL	5.1
1	Ab	335	ASP	5.0
1	CH	218	THR	5.0
1	CO	232	SER	5.0
1	CB	253	ASP	5.0
1	AG	236	ASN	5.0
1	CU	252	PRO	5.0
1	AB	270	GLY	5.0
1	AM	297	ARG	5.0
1	Cb	323	ILE	5.0
1	CI	293	ALA	5.0
1	CQ	282	LEU	5.0
1	CG	264	SER	5.0
1	Ab	230	ASN	5.0
1	Ab	228	LEU	5.0
1	Aa	269	LEU	5.0
1	Cb	221	PRO	5.0
1	AX	268	SER	5.0
1	Bb	291	THR	5.0
1	BA	239	LYS	5.0
1	CB	323	ILE	5.0
1	BS	318	GLU	5.0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	BC	325	LEU	5.0
1	CJ	289	ALA	5.0
1	CO	245	SER	5.0
1	Ca	250	ILE	5.0
1	BB	312	VAL	5.0
1	CH	241	ILE	5.0
1	CH	244	GLY	5.0
1	CB	327	VAL	4.9
1	AG	266	ASP	4.9
1	Ac	273	ASP	4.9
1	CC	243	LEU	4.9
1	BO	277	ALA	4.9
1	CN	250	ILE	4.9
1	AB	318	GLU	4.9
1	CH	224	THR	4.9
1	CT	337	GLU	4.9
1	CM	248	LEU	4.9
1	BC	277	ALA	4.9
1	CG	251	ALA	4.9
1	Cb	277	ALA	4.9
1	AB	217	GLU	4.9
1	BU	328	GLY	4.9
1	CF	232	SER	4.9
1	AB	257	PHE	4.9
1	Bb	238	PHE	4.9
1	BC	262	PRO	4.8
1	Ab	324	LEU	4.8
1	AM	271	THR	4.8
1	CN	255	ALA	4.8
1	AB	325	LEU	4.8
1	CB	335	ASP	4.8
1	CO	317	ASP	4.8
1	AO	320	PRO	4.8
1	CI	239	LYS	4.8
1	AC	278	VAL	4.8
1	AO	322	GLN	4.8
1	BH	298	TRP	4.8
1	BX	298	TRP	4.8
1	AC	264	SER	4.7
1	CB	336	SER	4.7
1	BO	290	GLY	4.7
1	BG	229	TYR	4.7

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	AB	297	ARG	4.7
1	BP	318	GLU	4.7
1	CM	288	ASN	4.7
1	AB	218	THR	4.7
1	CB	239	LYS	4.7
1	BU	262	PRO	4.7
1	CF	316	SER	4.7
1	Cb	262	PRO	4.7
1	AH	228	LEU	4.7
1	Cc	296	PHE	4.7
1	BY	323	ILE	4.7
1	CL	269	LEU	4.7
1	BB	239	LYS	4.7
1	BH	315	TYR	4.7
1	CA	256	VAL	4.7
1	CU	289	ALA	4.6
1	Cc	265	ILE	4.6
1	CH	307	THR	4.6
1	CM	255	ALA	4.6
1	AX	270	GLY	4.6
1	CG	221	PRO	4.6
1	AS	306	LYS	4.6
1	BF	312	VAL	4.6
1	AU	306	LYS	4.6
1	CH	316	SER	4.6
1	CF	249	ASP	4.6
1	CH	235	THR	4.6
1	CP	263	LEU	4.6
1	AU	271	THR	4.6
1	Bb	262	PRO	4.6
1	AF	268	SER	4.6
1	BO	255	ALA	4.6
1	Ab	278	VAL	4.6
1	CB	221	PRO	4.6
1	AC	232	SER	4.6
1	AD	337	GLU	4.6
1	CU	240	SER	4.6
1	BF	317	ASP	4.6
1	CI	241	ILE	4.6
1	BH	228	LEU	4.6
1	CX	247	PRO	4.6
1	AB	240	SER	4.6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	CO	333	ARG	4.6
1	BB	281	HIS	4.6
1	Ca	240	SER	4.6
1	BB	315	TYR	4.6
1	BC	218	THR	4.6
1	CB	292	PRO	4.5
1	AG	269	LEU	4.5
1	BG	275	ASP	4.5
1	CC	264	SER	4.5
1	BO	311	GLY	4.5
1	CM	262	PRO	4.5
1	CC	274	VAL	4.5
1	CE	253	ASP	4.5
1	CC	218	THR	4.5
1	CG	291	THR	4.5
1	CU	291	THR	4.5
1	Ac	306	LYS	4.5
1	BO	276	ARG	4.5
1	CF	292	PRO	4.5
1	BU	327	VAL	4.5
1	BX	262	PRO	4.5
1	AF	271	THR	4.5
1	AH	281	HIS	4.5
1	BF	318	GLU	4.5
1	CH	332	THR	4.5
1	BX	291	THR	4.5
1	BO	284	LYS	4.5
1	AH	333	ARG	4.5
1	Bd	288	ASN	4.5
1	AG	260	ASP	4.5
1	AH	307	THR	4.5
1	CU	253	ASP	4.5
1	Ab	320	PRO	4.5
1	Bb	319	GLN	4.5
1	Ad	322	GLN	4.5
1	BG	231	ASP	4.5
1	Bb	326	PRO	4.5
1	AG	277	ALA	4.5
1	CU	264	SER	4.5
1	Ab	322	GLN	4.4
1	BM	255	ALA	4.4
1	CG	295	TRP	4.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	BC	265	ILE	4.4
1	CM	318	GLU	4.4
1	Cb	332	THR	4.4
1	CN	256	VAL	4.4
1	CB	307	THR	4.4
1	BH	237	ASP	4.4
1	CM	303	ASN	4.4
1	CC	240	SER	4.4
1	CN	286	ALA	4.4
1	AU	268	SER	4.4
1	BH	321	ARG	4.4
1	BM	327	VAL	4.4
1	BG	239	LYS	4.4
1	CD	249	ASP	4.4
1	AB	228	LEU	4.4
1	AM	220	ALA	4.4
1	CF	274	VAL	4.3
1	AC	283	LYS	4.3
1	CM	251	ALA	4.3
1	BG	238	PHE	4.3
1	CA	281	HIS	4.3
1	BO	227	SER	4.3
1	Bd	303	ASN	4.3
1	CQ	249	ASP	4.3
1	Bb	296	PHE	4.3
1	BI	237	ASP	4.3
1	AI	271	THR	4.3
1	CE	316	SER	4.3
1	BF	227	SER	4.3
1	BV	263	LEU	4.3
1	AH	337	GLU	4.3
1	Ab	236	ASN	4.3
1	CG	332	THR	4.3
1	BU	298	TRP	4.3
1	AO	228	LEU	4.3
1	CH	323	ILE	4.3
1	BG	277	ALA	4.3
1	CG	271	THR	4.3
1	Cb	285	PHE	4.3
1	CF	290	GLY	4.3
1	BH	276	ARG	4.3
1	CI	240	SER	4.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	Ca	294	GLY	4.3
1	AM	258	GLN	4.3
1	CU	247	PRO	4.3
1	AX	322	GLN	4.3
1	CC	231	ASP	4.3
1	AH	303	ASN	4.3
1	CR	289	ALA	4.3
1	CM	225	GLN	4.3
1	CU	337	GLU	4.3
1	CP	282	LEU	4.3
1	CU	251	ALA	4.3
1	CF	256	VAL	4.2
1	BG	326	PRO	4.2
1	CM	321	ARG	4.2
1	CP	279	TYR	4.2
1	CS	274	VAL	4.2
1	AI	218	THR	4.2
1	CS	265	ILE	4.2
1	AU	230	ASN	4.2
1	AG	297	ARG	4.2
1	Ab	217	GLU	4.2
1	Cc	321	ARG	4.2
1	AH	279	TYR	4.2
1	CI	256	VAL	4.2
1	CM	274	VAL	4.2
1	AJ	337	GLU	4.2
1	CC	228	LEU	4.2
1	CF	279	TYR	4.2
1	CP	274	VAL	4.2
1	AB	337	GLU	4.2
1	CN	249	ASP	4.2
1	AH	273	ASP	4.2
1	Cc	291	THR	4.2
1	BF	298	TRP	4.2
1	Cc	333	ARG	4.2
1	CC	259	LEU	4.2
1	Ca	256	VAL	4.2
1	CF	321	ARG	4.2
1	AG	276	ARG	4.2
1	AO	308	PHE	4.2
1	CE	274	VAL	4.2
1	CO	328	GLY	4.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	AX	228	LEU	4.2
1	Bb	278	VAL	4.2
1	CB	264	SER	4.2
1	CI	253	ASP	4.2
1	CS	227	SER	4.2
1	BX	315	TYR	4.2
1	AQ	337	GLU	4.1
1	BB	237	ASP	4.1
1	CU	335	ASP	4.1
1	BX	277	ALA	4.1
1	BI	292	PRO	4.1
1	BO	301	TRP	4.1
1	CI	251	ALA	4.1
1	CU	249	ASP	4.1
1	BB	263	LEU	4.1
1	CB	284	LYS	4.1
1	CU	288	ASN	4.1
1	CM	239	LYS	4.1
1	AU	270	GLY	4.1
1	CX	279	TYR	4.1
1	Cb	303	ASN	4.1
1	CM	286	ALA	4.1
1	BU	315	TYR	4.1
1	AI	281	HIS	4.1
1	BY	318	GLU	4.1
1	CC	332	THR	4.1
1	AU	308	PHE	4.1
1	AG	337	GLU	4.1
1	CC	319	GLN	4.1
1	CG	284	LYS	4.1
1	CF	335	ASP	4.0
1	AC	263	LEU	4.0
1	Aa	337	GLU	4.0
1	AF	270	GLY	4.0
1	CA	318	GLU	4.0
1	AX	269	LEU	4.0
1	CB	229	TYR	4.0
1	BE	238	PHE	4.0
1	AG	322	GLN	4.0
1	Cc	257	PHE	4.0
1	CM	221	PRO	4.0
1	CP	268	SER	4.0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	AB	266	ASP	4.0
1	CB	218	THR	4.0
1	AM	270	GLY	4.0
1	CU	266	ASP	4.0
1	AU	297	ARG	4.0
1	BU	309	THR	4.0
1	CM	261	ARG	4.0
1	CP	264	SER	4.0
1	AC	238	PHE	4.0
1	Cb	330	VAL	4.0
1	CJ	293	ALA	4.0
1	BR	331	CYS	4.0
1	Ad	321	ARG	4.0
1	BP	277	ALA	4.0
1	CE	336	SER	4.0
1	BI	297	ARG	4.0
1	AY	269	LEU	4.0
1	CY	274	VAL	4.0
1	AG	273	ASP	4.0
1	CG	273	ASP	4.0
1	CH	271	THR	4.0
1	CM	337	GLU	4.0
1	CO	240	SER	4.0
1	BM	312	VAL	4.0
1	Bb	229	TYR	4.0
1	AG	304	PHE	4.0
1	CG	298	TRP	4.0
1	BO	328	GLY	4.0
1	CH	219	THR	4.0
1	CG	336	SER	4.0
1	CG	222	ILE	4.0
1	CH	319	GLN	4.0
1	AB	237	ASP	3.9
1	CG	225	GLN	3.9
1	Ab	254	GLY	3.9
1	CB	222	ILE	3.9
1	Ca	284	LYS	3.9
1	CM	332	THR	3.9
1	AB	324	LEU	3.9
1	CH	239	LYS	3.9
1	CA	337	GLU	3.9
1	Cc	316	SER	3.9

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	CB	220	ALA	3.9
1	AU	269	LEU	3.9
1	AG	51	GLY	3.9
1	CA	307	THR	3.9
1	Cc	270	GLY	3.9
1	CB	241	ILE	3.9
1	Cc	286	ALA	3.9
1	CI	290	GLY	3.9
1	Cc	240	SER	3.9
1	CE	255	ALA	3.9
1	BO	257	PHE	3.9
1	AC	242	LEU	3.9
1	CG	235	THR	3.9
1	CF	253	ASP	3.9
1	AH	304	PHE	3.9
1	CH	318	GLU	3.9
1	CM	317	ASP	3.9
1	BM	262	PRO	3.9
1	CU	285	PHE	3.9
1	AG	265	ILE	3.9
1	CA	233	LEU	3.9
1	AB	281	HIS	3.9
1	Cc	263	LEU	3.9
1	AU	280	TRP	3.9
1	BH	322	GLN	3.9
1	Cb	322	GLN	3.9
1	Ca	269	LEU	3.9
1	CY	290	GLY	3.8
1	AB	238	PHE	3.8
1	BA	227	SER	3.8
1	BI	315	TYR	3.8
1	Bb	275	ASP	3.8
1	CG	266	ASP	3.8
1	AH	263	LEU	3.8
1	CF	289	ALA	3.8
1	CE	267	TYR	3.8
1	BX	276	ARG	3.8
1	AX	271	THR	3.8
1	CU	233	LEU	3.8
1	CY	337	GLU	3.8
1	AB	276	ARG	3.8
1	CE	257	PHE	3.8

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	Ca	333	ARG	3.8
1	CC	325	LEU	3.8
1	BF	262	PRO	3.8
1	CO	270	GLY	3.8
1	Ab	257	PHE	3.8
1	AM	264	SER	3.8
1	AO	337	GLU	3.8
1	AH	265	ILE	3.8
1	Ab	233	LEU	3.8
1	BB	311	GLY	3.8
1	AI	232	SER	3.8
1	Cc	288	ASN	3.8
1	CG	281	HIS	3.8
1	BM	322	GLN	3.8
1	AB	320	PRO	3.8
1	Bb	290	GLY	3.8
1	BY	291	THR	3.8
1	BF	275	ASP	3.8
1	Cc	310	ASP	3.8
1	BA	264	SER	3.8
1	CE	250	ILE	3.8
1	CC	260	ASP	3.8
1	AB	252	PRO	3.8
1	BO	326	PRO	3.8
1	AF	275	ASP	3.8
1	CQ	317	ASP	3.8
1	Ba	315	TYR	3.8
1	CB	224	THR	3.7
1	CE	263	LEU	3.7
1	Bc	299	GLY	3.7
1	AO	263	LEU	3.7
1	CO	281	HIS	3.7
1	Bb	231	ASP	3.7
1	Cb	229	TYR	3.7
1	Ca	252	PRO	3.7
1	CA	305	ASN	3.7
1	CO	332	THR	3.7
1	CE	221	PRO	3.7
1	BI	239	LYS	3.7
1	CA	257	PHE	3.7
1	Ca	253	ASP	3.7
1	CY	282	LEU	3.7

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	AG	303	ASN	3.7
1	CM	277	ALA	3.7
1	Bb	255	ALA	3.7
1	BG	278	VAL	3.7
1	AU	325	LEU	3.7
1	Ab	263	LEU	3.7
1	CG	234	SER	3.7
1	BP	229	TYR	3.7
1	AU	218	THR	3.7
1	Ab	279	TYR	3.7
1	AM	322	GLN	3.7
1	CC	283	LYS	3.7
1	CC	313	ALA	3.7
1	BH	226	GLY	3.7
1	CH	256	VAL	3.7
1	BO	242	LEU	3.7
1	BH	291	THR	3.7
1	CB	230	ASN	3.7
1	BH	319	GLN	3.7
1	BM	260	ASP	3.7
1	CT	282	LEU	3.7
1	CZ	278	VAL	3.7
1	BB	301	TRP	3.7
1	CN	263	LEU	3.7
1	AV	296	PHE	3.7
1	BB	267	TYR	3.7
1	CX	257	PHE	3.7
1	AI	217	GLU	3.7
1	AX	296	PHE	3.6
1	Bb	311	GLY	3.6
1	CI	281	HIS	3.6
1	AM	266	ASP	3.6
1	AB	258	GLN	3.6
1	AE	336	SER	3.6
1	CB	252	PRO	3.6
1	CM	287	GLY	3.6
1	BO	232	SER	3.6
1	BU	242	LEU	3.6
1	BU	278	VAL	3.6
1	Ab	258	GLN	3.6
1	AM	308	PHE	3.6
1	Cb	270	GLY	3.6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	CC	248	LEU	3.6
1	AH	306	LYS	3.6
1	CB	272	GLY	3.6
1	CE	318	GLU	3.6
1	CW	337	GLU	3.6
1	Ac	267	TYR	3.6
1	Ab	275	ASP	3.6
1	Cd	269	LEU	3.6
1	CU	323	ILE	3.6
1	AI	236	ASN	3.6
1	Ad	164	ARG	3.6
1	AH	280	TRP	3.6
1	CQ	318	GLU	3.6
1	AM	164	ARG	3.6
1	Ca	286	ALA	3.6
1	BO	275	ASP	3.6
1	AH	268	SER	3.6
1	Cb	283	LYS	3.6
1	CF	244	GLY	3.6
1	BU	237	ASP	3.6
1	AM	180	PRO	3.5
1	CG	327	VAL	3.5
1	CB	280	TRP	3.5
1	CH	266	ASP	3.5
1	AS	337	GLU	3.5
1	BZ	328	GLY	3.5
1	Cc	273	ASP	3.5
1	BU	326	PRO	3.5
1	CZ	255	ALA	3.5
1	BB	319	GLN	3.5
1	AM	218	THR	3.5
1	Cc	290	GLY	3.5
1	Cc	284	LYS	3.5
1	Cc	332	THR	3.5
1	CC	275	ASP	3.5
1	BG	230	ASN	3.5
1	CN	241	ILE	3.5
1	BC	320	PRO	3.5
1	BH	282	LEU	3.5
1	AU	228	LEU	3.5
1	BX	239	LYS	3.5
1	AH	324	LEU	3.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	CS	307	THR	3.5
1	CO	337	GLU	3.5
1	CZ	279	TYR	3.5
1	BY	288	ASN	3.5
1	Ab	280	TRP	3.5
1	Cb	264	SER	3.5
1	CE	335	ASP	3.5
1	CI	252	PRO	3.5
1	CG	256	VAL	3.5
1	BG	232	SER	3.5
1	AZ	232	SER	3.5
1	CP	337	GLU	3.5
1	CU	279	TYR	3.5
1	AB	310	ASP	3.5
1	CZ	239	LYS	3.5
1	Bb	280	TRP	3.5
1	CP	318	GLU	3.5
1	BF	264	SER	3.5
1	BH	255	ALA	3.5
1	CG	307	THR	3.5
1	CI	278	VAL	3.5
1	Ac	278	VAL	3.5
1	BC	273	ASP	3.5
1	CU	336	SER	3.5
1	CI	271	THR	3.5
1	CJ	282	LEU	3.5
1	AX	297	ARG	3.5
1	AX	324	LEU	3.5
1	Ab	262	PRO	3.5
1	Cb	298	TRP	3.5
1	CE	285	PHE	3.5
1	CE	290	GLY	3.5
1	BK	287	GLY	3.5
1	BO	265	ILE	3.4
1	BN	298	TRP	3.4
1	BG	248	LEU	3.4
1	BM	227	SER	3.4
1	AX	336	SER	3.4
1	CH	292	PRO	3.4
1	BI	298	TRP	3.4
1	CC	268	SER	3.4
1	AD	236	ASN	3.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	CO	303	ASN	3.4
1	Aa	236	ASN	3.4
1	AM	332	THR	3.4
1	CJ	255	ALA	3.4
1	CE	292	PRO	3.4
1	BE	239	LYS	3.4
1	Bb	237	ASP	3.4
1	CP	319	GLN	3.4
1	CU	222	ILE	3.4
1	BB	329	THR	3.4
1	CB	310	ASP	3.4
1	BY	321	ARG	3.4
1	AM	318	GLU	3.4
1	CU	261	ARG	3.4
1	AF	324	LEU	3.4
1	BH	263	LEU	3.4
1	BO	249	ASP	3.4
1	CB	277	ALA	3.4
1	CM	224	THR	3.4
1	BZ	265	ILE	3.4
1	Bd	279	TYR	3.4
1	BN	296	PHE	3.4
1	AQ	322	GLN	3.4
1	CE	294	GLY	3.4
1	BH	301	TRP	3.4
1	Cb	320	PRO	3.4
1	Cc	227	SER	3.4
1	CH	267	TYR	3.4
1	BO	263	LEU	3.4
1	AC	255	ALA	3.4
1	BP	262	PRO	3.4
1	CG	315	TYR	3.4
1	AI	260	ASP	3.4
1	Cc	231	ASP	3.4
1	Bd	277	ALA	3.4
1	Ab	297	ARG	3.4
1	CZ	242	LEU	3.3
1	BC	232	SER	3.3
1	CO	227	SER	3.3
1	AB	333	ARG	3.3
1	Ab	266	ASP	3.3
1	Ac	275	ASP	3.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	BC	229	TYR	3.3
1	AH	277	ALA	3.3
1	CG	276	ARG	3.3
1	BU	227	SER	3.3
1	AG	325	LEU	3.3
1	BR	318	GLU	3.3
1	Ab	240	SER	3.3
1	CS	289	ALA	3.3
1	AU	333	ARG	3.3
1	BF	296	PHE	3.3
1	Cc	245	SER	3.3
1	BH	281	HIS	3.3
1	AH	269	LEU	3.3
1	AD	325	LEU	3.3
1	Ac	263	LEU	3.3
1	CC	276	ARG	3.3
1	AC	312	VAL	3.3
1	CC	262	PRO	3.3
1	AE	322	GLN	3.3
1	BO	337	GLU	3.3
1	Ab	301	TRP	3.3
1	Cb	308	PHE	3.3
1	Cb	228	LEU	3.3
1	AC	276	ARG	3.3
1	BC	289	ALA	3.3
1	CH	303	ASN	3.3
1	CU	283	LYS	3.3
1	AF	322	GLN	3.3
1	BI	238	PHE	3.3
1	AU	264	SER	3.3
1	BB	236	ASN	3.3
1	CS	288	ASN	3.3
1	CB	276	ARG	3.3
1	Cc	244	GLY	3.3
1	Bc	298	TRP	3.3
1	BG	291	THR	3.3
1	Bb	328	GLY	3.3
1	Cc	272	GLY	3.3
1	AM	257	PHE	3.3
1	BO	280	TRP	3.3
1	CF	233	LEU	3.3
1	CN	223	MET	3.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	AM	296	PHE	3.3
1	BB	260	ASP	3.3
1	AX	273	ASP	3.3
1	Bb	322	GLN	3.3
1	Cc	253	ASP	3.3
1	BH	229	TYR	3.3
1	BY	315	TYR	3.3
1	BD	52	THR	3.3
1	CI	266	ASP	3.3
1	CN	288	ASN	3.3
1	BC	270	GLY	3.3
1	CS	232	SER	3.3
1	AG	332	THR	3.3
1	AH	271	THR	3.3
1	BX	296	PHE	3.3
1	BC	324	LEU	3.2
1	CT	293	ALA	3.2
1	AE	306	LYS	3.2
1	Bd	315	TYR	3.2
1	Aa	268	SER	3.2
1	BI	282	LEU	3.2
1	AP	271	THR	3.2
1	CZ	243	LEU	3.2
1	CU	322	GLN	3.2
1	BM	305	ASN	3.2
1	AP	337	GLU	3.2
1	AQ	217	GLU	3.2
1	AM	263	LEU	3.2
1	AM	280	TRP	3.2
1	Bb	227	SER	3.2
1	CD	286	ALA	3.2
1	CG	218	THR	3.2
1	Cd	313	ALA	3.2
1	CH	217	GLU	3.2
1	BO	253	ASP	3.2
1	Ca	283	LYS	3.2
1	Cb	234	SER	3.2
1	CM	217	GLU	3.2
1	Bc	312	VAL	3.2
1	BB	261	ARG	3.2
1	CU	229	TYR	3.2
1	CE	256	VAL	3.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	CF	276	ARG	3.2
1	AX	257	PHE	3.2
1	CH	246	THR	3.2
1	AU	320	PRO	3.2
1	CC	282	LEU	3.2
1	AC	280	TRP	3.2
1	CS	257	PHE	3.2
1	AG	237	ASP	3.2
1	AX	236	ASN	3.2
1	CM	218	THR	3.2
1	CI	270	GLY	3.2
1	CU	274	VAL	3.2
1	BA	315	TYR	3.2
1	Bb	267	TYR	3.2
1	AH	270	GLY	3.2
1	BP	263	LEU	3.2
1	BU	292	PRO	3.2
1	CB	269	LEU	3.2
1	BM	282	LEU	3.2
1	CE	231	ASP	3.2
1	AU	262	PRO	3.2
1	BF	238	PHE	3.2
1	CP	249	ASP	3.2
1	AV	53	ASN	3.2
1	CI	309	THR	3.2
1	CM	300	ILE	3.2
1	AO	268	SER	3.2
1	CN	294	GLY	3.2
1	CU	276	ARG	3.2
1	CV	337	GLU	3.2
1	CZ	337	GLU	3.2
1	Bb	309	THR	3.2
1	Ac	308	PHE	3.2
1	AS	268	SER	3.1
1	CF	250	ILE	3.1
1	AH	336	SER	3.1
1	CQ	240	SER	3.1
1	Ca	265	ILE	3.1
1	BH	236	ASN	3.1
1	AP	269	LEU	3.1
1	CP	269	LEU	3.1
1	CH	295	TRP	3.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	CH	275	ASP	3.1
1	Aa	336	SER	3.1
1	AY	276	ARG	3.1
1	BS	298	TRP	3.1
1	BC	230	ASN	3.1
1	CB	273	ASP	3.1
1	AC	310	ASP	3.1
1	CY	269	LEU	3.1
1	CM	336	SER	3.1
1	CO	237	ASP	3.1
1	Bc	273	ASP	3.1
1	CB	261	ARG	3.1
1	BC	327	VAL	3.1
1	BX	238	PHE	3.1
1	CN	333	ARG	3.1
1	Cb	309	THR	3.1
1	CF	262	PRO	3.1
1	BO	283	LYS	3.1
1	BZ	315	TYR	3.1
1	BF	278	VAL	3.1
1	BM	280	TRP	3.1
1	CM	231	ASP	3.1
1	CO	276	ARG	3.1
1	AJ	269	LEU	3.1
1	BO	319	GLN	3.1
1	CX	263	LEU	3.1
1	AT	265	ILE	3.1
1	Bc	315	TYR	3.1
1	CA	228	LEU	3.1
1	CB	275	ASP	3.1
1	BS	239	LYS	3.1
1	AU	263	LEU	3.1
1	CZ	249	ASP	3.1
1	Cc	249	ASP	3.1
1	CZ	318	GLU	3.1
1	CH	273	ASP	3.1
1	CC	303	ASN	3.1
1	CE	333	ARG	3.1
1	BM	311	GLY	3.1
1	CI	317	ASP	3.1
1	AM	333	ARG	3.1
1	CI	264	SER	3.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	AV	298	TRP	3.1
1	CH	321	ARG	3.0
1	AE	236	ASN	3.0
1	CN	291	THR	3.0
1	CU	284	LYS	3.0
1	CY	249	ASP	3.0
1	BB	271	THR	3.0
1	AH	257	PHE	3.0
1	CF	272	GLY	3.0
1	CS	290	GLY	3.0
1	AU	260	ASP	3.0
1	AC	297	ARG	3.0
1	CU	330	VAL	3.0
1	CY	265	ILE	3.0
1	AH	266	ASP	3.0
1	BM	231	ASP	3.0
1	CH	277	ALA	3.0
1	BM	309	THR	3.0
1	CM	291	THR	3.0
1	Ab	267	TYR	3.0
1	CU	223	MET	3.0
1	AB	233	LEU	3.0
1	BI	291	THR	3.0
1	CN	287	GLY	3.0
1	AV	235	THR	3.0
1	CW	269	LEU	3.0
1	Bd	52	THR	3.0
1	CG	267	TYR	3.0
1	CE	321	ARG	3.0
1	BG	297	ARG	3.0
1	CJ	264	SER	3.0
1	BY	322	GLN	3.0
1	BB	282	LEU	3.0
1	BO	282	LEU	3.0
1	BZ	229	TYR	3.0
1	BF	276	ARG	3.0
1	BN	327	VAL	3.0
1	AZ	336	SER	3.0
1	BG	233	LEU	3.0
1	CM	226	GLY	3.0
1	BH	292	PRO	3.0
1	AD	164	ARG	3.0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	AB	227	SER	3.0
1	AG	336	SER	3.0
1	CA	248	LEU	3.0
1	BC	247	PRO	3.0
1	BG	262	PRO	3.0
1	CM	270	GLY	3.0
1	Ca	337	GLU	3.0
1	BC	291	THR	3.0
1	AH	301	TRP	3.0
1	AI	243	LEU	3.0
1	CN	290	GLY	3.0
1	AB	302	ASP	3.0
1	CO	233	LEU	3.0
1	CC	267	TYR	3.0
1	AQ	271	THR	3.0
1	CV	257	PHE	3.0
1	AI	331	CYS	3.0
1	AB	336	SER	3.0
1	AC	257	PHE	3.0
1	AO	297	ARG	3.0
1	BG	309	THR	3.0
1	BG	314	TYR	3.0
1	BO	302	ASP	3.0
1	Bb	297	ARG	3.0
1	AV	264	SER	2.9
1	CN	307	THR	2.9
1	BX	323	ILE	2.9
1	BP	315	TYR	2.9
1	BO	310	ASP	2.9
1	BP	278	VAL	2.9
1	AP	278	VAL	2.9
1	Cd	317	ASP	2.9
1	AB	239	LYS	2.9
1	BI	276	ARG	2.9
1	CG	296	PHE	2.9
1	CV	279	TYR	2.9
1	AC	322	GLN	2.9
1	CX	321	ARG	2.9
1	CM	319	GLN	2.9
1	AU	322	GLN	2.9
1	AM	217	GLU	2.9
1	Cc	276	ARG	2.9

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	Ca	263	LEU	2.9
1	BM	303	ASN	2.9
1	BC	253	ASP	2.9
1	CT	257	PHE	2.9
1	Bc	320	PRO	2.9
1	CE	284	LYS	2.9
1	AO	271	THR	2.9
1	CB	242	LEU	2.9
1	CG	337	GLU	2.9
1	BA	292	PRO	2.9
1	CK	315	TYR	2.9
1	CP	231	ASP	2.9
1	AG	324	LEU	2.9
1	Cb	301	TRP	2.9
1	AM	320	PRO	2.9
1	CM	283	LYS	2.9
1	CC	316	SER	2.9
1	CF	245	SER	2.9
1	CP	270	GLY	2.9
1	CP	277	ALA	2.9
1	AU	273	ASP	2.9
1	Cc	255	ALA	2.9
1	CU	319	GLN	2.9
1	BA	325	LEU	2.9
1	BZ	228	LEU	2.9
1	BI	278	VAL	2.9
1	BU	52	THR	2.9
1	CM	264	SER	2.9
1	AY	266	ASP	2.9
1	AH	218	THR	2.9
1	CO	319	GLN	2.9
1	CG	254	GLY	2.9
1	AH	233	LEU	2.9
1	AU	324	LEU	2.9
1	AC	227	SER	2.9
1	BO	256	VAL	2.9
1	CB	319	GLN	2.9
1	AD	315	TYR	2.9
1	CH	261	ARG	2.9
1	Cb	273	ASP	2.9
1	CJ	296	PHE	2.9
1	BU	263	LEU	2.9

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	CY	244	GLY	2.9
1	Cb	218	THR	2.9
1	Bb	312	VAL	2.9
1	CU	303	ASN	2.9
1	CC	226	GLY	2.8
1	Ab	296	PHE	2.9
1	CD	257	PHE	2.8
1	CF	310	ASP	2.8
1	AU	265	ILE	2.8
1	AY	275	ASP	2.8
1	CB	330	VAL	2.8
1	BO	267	TYR	2.8
1	AB	265	ILE	2.8
1	AF	264	SER	2.8
1	BM	310	ASP	2.8
1	AM	303	ASN	2.8
1	Cd	249	ASP	2.8
1	CM	242	LEU	2.8
1	BG	327	VAL	2.8
1	Cb	272	GLY	2.8
1	BY	276	ARG	2.8
1	CB	306	LYS	2.8
1	CH	269	LEU	2.8
1	AI	332	THR	2.8
1	BM	301	TRP	2.8
1	AS	269	LEU	2.8
1	BX	235	THR	2.8
1	Ca	281	HIS	2.8
1	Bb	281	HIS	2.8
1	Ad	276	ARG	2.8
1	CH	334	VAL	2.8
1	CH	278	VAL	2.8
1	BB	309	THR	2.8
1	CG	277	ALA	2.8
1	AM	163	THR	2.8
1	AC	228	LEU	2.8
1	Bc	249	ASP	2.8
1	AM	304	PHE	2.8
1	BZ	263	LEU	2.8
1	CU	244	GLY	2.8
1	BE	309	THR	2.8
1	CG	303	ASN	2.8

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	CO	336	SER	2.8
1	AY	265	ILE	2.8
1	CC	280	TRP	2.8
1	Ca	245	SER	2.8
1	AM	181	GLY	2.8
1	BX	326	PRO	2.8
1	Ca	287	GLY	2.8
1	CM	260	ASP	2.8
1	AN	268	SER	2.8
1	BH	320	PRO	2.8
1	BI	248	LEU	2.8
1	BM	302	ASP	2.8
1	CZ	282	LEU	2.8
1	AM	331	CYS	2.8
1	BU	291	THR	2.8
1	BY	239	LYS	2.8
1	BH	260	ASP	2.8
1	CG	309	THR	2.8
1	AV	239	LYS	2.8
1	AU	282	LEU	2.8
1	CY	263	LEU	2.8
1	AB	267	TYR	2.8
1	AB	220	ALA	2.8
1	Bb	224	THR	2.8
1	Cc	287	GLY	2.8
1	BC	322	GLN	2.7
1	BO	322	GLN	2.7
1	CS	253	ASP	2.7
1	Bd	267	TYR	2.7
1	AG	257	PHE	2.7
1	CO	218	THR	2.7
1	CQ	265	ILE	2.7
1	CZ	334	VAL	2.7
1	CH	280	TRP	2.7
1	CU	220	ALA	2.7
1	AV	238	PHE	2.7
1	CR	337	GLU	2.7
1	CU	245	SER	2.7
1	AH	237	ASP	2.7
1	AH	258	GLN	2.7
1	BY	293	ALA	2.7
1	CZ	317	ASP	2.7

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	AM	265	ILE	2.7
1	CI	232	SER	2.7
1	BM	235	THR	2.7
1	AX	281	HIS	2.7
1	AB	272	GLY	2.7
1	AB	335	ASP	2.7
1	Cc	275	ASP	2.7
1	CH	315	TYR	2.7
1	CI	245	SER	2.7
1	Cd	318	GLU	2.7
1	BO	303	ASN	2.7
1	AV	269	LEU	2.7
1	CC	312	VAL	2.7
1	BG	311	GLY	2.7
1	CY	293	ALA	2.7
1	CO	323	ILE	2.7
1	BC	231	ASP	2.7
1	AC	266	ASP	2.7
1	CC	281	HIS	2.7
1	CP	240	SER	2.7
1	CS	263	LEU	2.7
1	Ca	264	SER	2.7
1	CT	286	ALA	2.7
1	CU	318	GLU	2.7
1	Aa	275	ASP	2.7
1	Cb	310	ASP	2.7
1	CV	289	ALA	2.7
1	BU	260	ASP	2.7
1	CG	316	SER	2.7
1	CH	230	ASN	2.7
1	BO	248	LEU	2.7
1	AB	277	ALA	2.7
1	CM	220	ALA	2.7
1	BH	329	THR	2.7
1	CU	246	THR	2.7
1	BO	314	TYR	2.7
1	CC	266	ASP	2.7
1	CI	250	ILE	2.7
1	CR	268	SER	2.7
1	CX	281	HIS	2.7
1	BB	303	ASN	2.7
1	BM	256	VAL	2.7

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	AI	220	ALA	2.7
1	CA	317	ASP	2.7
1	CE	247	PRO	2.7
1	BO	261	ARG	2.7
1	Cd	319	GLN	2.7
1	BI	236	ASN	2.7
1	CB	266	ASP	2.7
1	BE	320	PRO	2.7
1	BE	264	SER	2.7
1	CM	276	ARG	2.7
1	CD	250	ILE	2.7
1	AM	53	ASN	2.7
1	BO	306	LYS	2.7
1	AF	325	LEU	2.7
1	CG	248	LEU	2.7
1	Cc	247	PRO	2.7
1	Bd	275	ASP	2.7
1	CF	270	GLY	2.7
1	AO	306	LYS	2.7
1	CA	302	ASP	2.6
1	AC	317	ASP	2.6
1	Ac	264	SER	2.6
1	CE	218	THR	2.6
1	CR	290	GLY	2.6
1	BH	297	ARG	2.6
1	CO	321	ARG	2.6
1	CB	320	PRO	2.6
1	AV	162	TYR	2.6
1	Bd	337	GLU	2.6
1	AF	237	ASP	2.6
1	CJ	265	ILE	2.6
1	Ca	241	ILE	2.6
1	BI	281	HIS	2.6
1	BM	248	LEU	2.6
1	CJ	274	VAL	2.6
1	CZ	295	TRP	2.6
1	CE	252	PRO	2.6
1	AO	236	ASN	2.6
1	BH	275	ASP	2.6
1	BM	275	ASP	2.6
1	Cb	275	ASP	2.6
1	BC	330	VAL	2.6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	Cb	271	THR	2.6
1	BP	279	TYR	2.6
1	AU	105	GLU	2.6
1	BC	288	ASN	2.6
1	CS	250	ILE	2.6
1	CH	268	SER	2.6
1	AM	268	SER	2.6
1	BO	294	GLY	2.6
1	Cb	261	ARG	2.6
1	BR	278	VAL	2.6
1	AG	315	TYR	2.6
1	Ad	318	GLU	2.6
1	CD	255	ALA	2.6
1	CE	233	LEU	2.6
1	CZ	272	GLY	2.6
1	AU	266	ASP	2.6
1	AG	320	PRO	2.6
1	CG	308	PHE	2.6
1	BM	257	PHE	2.6
1	BM	326	PRO	2.6
1	CY	289	ALA	2.6
1	CB	278	VAL	2.6
1	CF	315	TYR	2.6
1	CJ	337	GLU	2.6
1	Cc	266	ASP	2.6
1	BM	52	THR	2.6
1	CC	255	ALA	2.6
1	CZ	230	ASN	2.6
1	Ad	227	SER	2.6
1	AI	273	ASP	2.6
1	BN	276	ARG	2.6
1	Cc	241	ILE	2.6
1	BM	242	LEU	2.6
1	CN	277	ALA	2.6
1	Ad	320	PRO	2.6
1	CR	283	LYS	2.6
1	AX	306	LYS	2.6
1	AB	53	ASN	2.6
1	AB	162	TYR	2.6
1	AS	230	ASN	2.6
1	AB	275	ASP	2.6
1	CP	275	ASP	2.6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	Bb	325	LEU	2.6
1	Bc	237	ASP	2.6
1	BR	270	GLY	2.6
1	Bd	331	CYS	2.6
1	AM	286	ALA	2.6
1	AV	337	GLU	2.6
1	BG	316	SER	2.6
1	BE	281	HIS	2.6
1	CF	317	ASP	2.6
1	AD	105	GLU	2.6
1	CI	305	ASN	2.6
1	Ab	332	THR	2.6
1	CE	315	TYR	2.6
1	BU	225	GLN	2.6
1	CG	224	THR	2.6
1	CM	271	THR	2.6
1	CN	337	GLU	2.6
1	Ca	251	ALA	2.6
1	BG	282	LEU	2.6
1	AB	256	VAL	2.6
1	AG	271	THR	2.6
1	CG	229	TYR	2.6
1	AN	228	LEU	2.6
1	BO	269	LEU	2.6
1	BM	330	VAL	2.6
1	BZ	322	GLN	2.6
1	AS	236	ASN	2.5
1	BF	327	VAL	2.5
1	BC	251	ALA	2.5
1	CI	300	ILE	2.5
1	CM	234	SER	2.5
1	BU	233	LEU	2.5
1	Ca	222	ILE	2.5
1	Cb	248	LEU	2.5
1	CQ	56	HIS	2.5
1	CY	253	ASP	2.5
1	AP	270	GLY	2.5
1	CS	332	THR	2.5
1	CE	240	SER	2.5
1	BI	228	LEU	2.5
1	CI	242	LEU	2.5
1	CA	262	PRO	2.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	CG	220	ALA	2.5
1	BT	296	PHE	2.5
1	BV	277	ALA	2.5
1	BO	300	ILE	2.5
1	BM	281	HIS	2.5
1	BO	287	GLY	2.5
1	BU	303	ASN	2.5
1	CY	266	ASP	2.5
1	AZ	304	PHE	2.5
1	CZ	303	ASN	2.5
1	BX	309	THR	2.5
1	CZ	228	LEU	2.5
1	Cc	233	LEU	2.5
1	CZ	232	SER	2.5
1	CM	301	TRP	2.5
1	BN	239	LYS	2.5
1	BC	334	VAL	2.5
1	CD	274	VAL	2.5
1	BU	276	ARG	2.5
1	BU	337	GLU	2.5
1	AF	336	SER	2.5
1	BE	298	TRP	2.5
1	CN	252	PRO	2.5
1	CN	292	PRO	2.5
1	CZ	238	PHE	2.5
1	Cb	220	ALA	2.5
1	Cb	295	TRP	2.5
1	AG	278	VAL	2.5
1	AU	236	ASN	2.5
1	AB	279	TYR	2.5
1	AM	307	THR	2.5
1	BQ	296	PHE	2.5
1	BB	242	LEU	2.5
1	CU	277	ALA	2.5
1	CY	242	LEU	2.5
1	BA	236	ASN	2.5
1	CH	310	ASP	2.5
1	CU	297	ARG	2.5
1	AY	337	GLU	2.5
1	BM	283	LYS	2.5
1	CA	227	SER	2.5
1	AD	268	SER	2.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	BP	264	SER	2.5
1	CE	281	HIS	2.5
1	CF	275	ASP	2.5
1	CM	275	ASP	2.5
1	CZ	231	ASP	2.5
1	Bd	306	LYS	2.5
1	CC	277	ALA	2.5
1	BI	277	ALA	2.5
1	AI	240	SER	2.5
1	AN	325	LEU	2.5
1	CV	282	LEU	2.5
1	CA	319	GLN	2.5
1	CC	105	GLU	2.5
1	AJ	275	ASP	2.5
1	BP	275	ASP	2.5
1	BB	297	ARG	2.5
1	Ab	232	SER	2.5
1	CG	272	GLY	2.5
1	CA	309	THR	2.5
1	BD	303	ASN	2.5
1	BT	52	THR	2.5
1	Cd	256	VAL	2.5
1	CQ	316	SER	2.5
1	AH	318	GLU	2.5
1	CA	254	GLY	2.5
1	CG	278	VAL	2.5
1	Cb	278	VAL	2.5
1	AF	288	ASN	2.5
1	Bc	291	THR	2.5
1	CO	234	SER	2.5
1	Ca	279	TYR	2.5
1	BF	321	ARG	2.5
1	CV	256	VAL	2.5
1	CD	262	PRO	2.5
1	BE	235	THR	2.5
1	AG	308	PHE	2.5
1	AI	322	GLN	2.5
1	CN	240	SER	2.5
1	CP	278	VAL	2.5
1	Ad	229	TYR	2.4
1	CB	258	GLN	2.4
1	CZ	322	GLN	2.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	BO	281	HIS	2.4
1	BY	275	ASP	2.4
1	AB	319	GLN	2.4
1	BG	319	GLN	2.4
1	AL	227	SER	2.4
1	BM	323	ILE	2.4
1	CT	336	SER	2.4
1	AX	333	ARG	2.4
1	CC	333	ARG	2.4
1	AN	324	LEU	2.4
1	CB	300	ILE	2.4
1	AX	227	SER	2.4
1	Cc	323	ILE	2.4
1	BB	280	TRP	2.4
1	BD	296	PHE	2.4
1	Ca	296	PHE	2.4
1	BB	279	TYR	2.4
1	BN	315	TYR	2.4
1	CI	332	THR	2.4
1	CQ	257	PHE	2.4
1	AX	232	SER	2.4
1	BG	269	LEU	2.4
1	BE	312	VAL	2.4
1	CH	229	TYR	2.4
1	CU	281	HIS	2.4
1	AB	208	SER	2.4
1	BC	271	THR	2.4
1	BC	336	SER	2.4
1	CH	302	ASP	2.4
1	AU	257	PHE	2.4
1	CY	255	ALA	2.4
1	BV	325	LEU	2.4
1	Ca	297	ARG	2.4
1	BE	300	ILE	2.4
1	CV	290	GLY	2.4
1	CF	320	PRO	2.4
1	AD	324	LEU	2.4
1	BF	235	THR	2.4
1	AG	233	LEU	2.4
1	CM	298	TRP	2.4
1	BY	233	LEU	2.4
1	Ca	330	VAL	2.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	BC	323	ILE	2.4
1	CQ	252	PRO	2.4
1	BI	327	VAL	2.4
1	CO	335	ASP	2.4
1	Ac	279	TYR	2.4
1	AZ	303	ASN	2.4
1	CG	283	LYS	2.4
1	CH	326	PRO	2.4
1	CL	284	LYS	2.4
1	AP	322	GLN	2.4
1	CE	232	SER	2.4
1	CG	323	ILE	2.4
1	AM	84	ILE	2.4
1	AV	323	ILE	2.4
1	CM	290	GLY	2.4
1	CU	225	GLN	2.4
1	BZ	325	LEU	2.4
1	CZ	248	LEU	2.4
1	Cc	298	TRP	2.4
1	BN	238	PHE	2.4
1	Cc	308	PHE	2.4
1	CA	334	VAL	2.4
1	BJ	315	TYR	2.4
1	AH	296	PHE	2.4
1	CW	257	PHE	2.4
1	Ac	270	GLY	2.4
1	BE	271	THR	2.4
1	AH	297	ARG	2.4
1	Bd	274	VAL	2.4
1	CX	250	ILE	2.4
1	CB	260	ASP	2.4
1	BG	237	ASP	2.4
1	BI	275	ASP	2.4
1	CI	246	THR	2.4
1	CM	278	VAL	2.4
1	CO	231	ASP	2.4
1	CO	330	VAL	2.4
1	AU	310	ASP	2.4
1	Bb	282	LEU	2.4
1	Ad	266	ASP	2.4
1	AH	262	PRO	2.4
1	AM	305	ASN	2.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	CF	283	LYS	2.4
1	BY	295	TRP	2.4
1	AB	263	LEU	2.4
1	AI	235	THR	2.4
1	CJ	249	ASP	2.4
1	CB	322	GLN	2.4
1	CC	314	TYR	2.4
1	Ab	247	PRO	2.4
1	BN	223	MET	2.4
1	CE	264	SER	2.4
1	AW	208	SER	2.4
1	CN	335	ASP	2.4
1	CQ	332	THR	2.4
1	BS	52	THR	2.4
1	CU	218	THR	2.4
1	CC	318	GLU	2.3
1	CH	320	PRO	2.3
1	CS	337	GLU	2.3
1	CC	242	LEU	2.3
1	CQ	255	ALA	2.3
1	AI	317	ASP	2.3
1	BF	320	PRO	2.3
1	BG	320	PRO	2.3
1	CO	262	PRO	2.3
1	Bd	333	ARG	2.3
1	CI	287	GLY	2.3
1	CN	253	ASP	2.3
1	CZ	218	THR	2.3
1	CB	285	PHE	2.3
1	BO	323	ILE	2.3
1	BA	262	PRO	2.3
1	AY	317	ASP	2.3
1	CA	323	ILE	2.3
1	CZ	281	HIS	2.3
1	BN	282	LEU	2.3
1	BT	263	LEU	2.3
1	BN	52	THR	2.3
1	BO	273	ASP	2.3
1	Cc	279	TYR	2.3
1	AB	105	GLU	2.3
1	CI	217	GLU	2.3
1	CB	328	GLY	2.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	BH	280	TRP	2.3
1	AJ	51	GLY	2.3
1	BF	326	PRO	2.3
1	BI	326	PRO	2.3
1	CN	251	ALA	2.3
1	BP	296	PHE	2.3
1	BT	277	ALA	2.3
1	AE	206	ARG	2.3
1	BR	275	ASP	2.3
1	CY	333	ARG	2.3
1	BM	230	ASN	2.3
1	CS	264	SER	2.3
1	AV	301	TRP	2.3
1	Cd	230	ASN	2.3
1	CB	308	PHE	2.3
1	BC	257	PHE	2.3
1	BG	292	PRO	2.3
1	AH	238	PHE	2.3
1	Bb	234	SER	2.3
1	CD	291	THR	2.3
1	CW	315	TYR	2.3
1	CC	278	VAL	2.3
1	CV	281	HIS	2.3
1	CV	284	LYS	2.3
1	CP	230	ASN	2.3
1	Bc	238	PHE	2.3
1	BC	318	GLU	2.3
1	Ca	246	THR	2.3
1	CZ	296	PHE	2.3
1	BO	240	SER	2.3
1	CY	321	ARG	2.3
1	AS	265	ILE	2.3
1	AC	324	LEU	2.3
1	CX	274	VAL	2.3
1	BZ	242	LEU	2.3
1	AO	270	GLY	2.3
1	AO	321	ARG	2.3
1	BM	229	TYR	2.3
1	Cb	325	LEU	2.3
1	BB	276	ARG	2.3
1	BO	270	GLY	2.3
1	CT	333	ARG	2.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	BC	248	LEU	2.3
1	CS	327	VAL	2.3
1	CA	335	ASP	2.3
1	CC	265	ILE	2.3
1	BZ	323	ILE	2.3
1	Ba	239	LYS	2.3
1	CB	267	TYR	2.3
1	AX	229	TYR	2.3
1	Bd	263	LEU	2.3
1	CF	288	ASN	2.3
1	Bd	318	GLU	2.3
1	AG	220	ALA	2.3
1	CC	256	VAL	2.3
1	BM	263	LEU	2.3
1	AX	237	ASP	2.3
1	Ab	237	ASP	2.3
1	AG	267	TYR	2.3
1	BC	331	CYS	2.3
1	CX	255	ALA	2.3
1	CZ	280	TRP	2.3
1	BC	310	ASP	2.3
1	BU	271	THR	2.3
1	CA	336	SER	2.2
1	AM	240	SER	2.2
1	Cc	328	GLY	2.2
1	AC	230	ASN	2.2
1	BZ	327	VAL	2.2
1	Ab	334	VAL	2.2
1	Ad	134	ASN	2.2
1	CB	332	THR	2.2
1	CI	231	ASP	2.2
1	BO	285	PHE	2.2
1	BO	332	THR	2.2
1	AA	336	SER	2.2
1	BO	252	PRO	2.2
1	AU	336	SER	2.2
1	CQ	263	LEU	2.2
1	AM	229	TYR	2.2
1	BK	135	ASP	2.2
1	CM	302	ASP	2.2
1	AX	266	ASP	2.2
1	Ca	270	GLY	2.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	AB	243	LEU	2.2
1	CX	232	SER	2.2
1	BY	331	CYS	2.2
1	CH	301	TRP	2.2
1	Ac	336	SER	2.2
1	BA	238	PHE	2.2
1	CI	229	TYR	2.2
1	AP	279	TYR	2.2
1	BA	237	ASP	2.2
1	AF	260	ASP	2.2
1	CY	284	LYS	2.2
1	BO	299	GLY	2.2
1	CS	247	PRO	2.2
1	BE	296	PHE	2.2
1	CN	285	PHE	2.2
1	Bd	284	LYS	2.2
1	BM	307	THR	2.2
1	AM	310	ASP	2.2
1	CS	286	ALA	2.2
1	BF	234	SER	2.2
1	CH	297	ARG	2.2
1	BB	231	ASP	2.2
1	BG	273	ASP	2.2
1	AC	281	HIS	2.2
1	CC	297	ARG	2.2
1	BH	309	THR	2.2
1	Cd	268	SER	2.2
1	CE	297	ARG	2.2
1	BM	223	MET	2.2
1	AO	277	ALA	2.2
1	CE	332	THR	2.2
1	AV	206	ARG	2.2
1	Ab	302	ASP	2.2
1	CF	336	SER	2.2
1	BK	240	SER	2.2
1	CM	233	LEU	2.2
1	BW	323	ILE	2.2
1	Ca	259	LEU	2.2
1	CR	284	LYS	2.2
1	CY	257	PHE	2.2
1	BY	298	TRP	2.2
1	BO	268	SER	2.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	CS	256	VAL	2.2
1	BD	277	ALA	2.2
1	BH	223	MET	2.2
1	CS	333	ARG	2.2
1	BO	225	GLN	2.2
1	CV	258	GLN	2.2
1	BJ	323	ILE	2.2
1	BN	248	LEU	2.2
1	CP	242	LEU	2.2
1	BV	278	VAL	2.2
1	CB	243	LEU	2.2
1	AF	273	ASP	2.2
1	AG	53	ASN	2.2
1	BU	236	ASN	2.2
1	Bd	256	VAL	2.2
1	BC	234	SER	2.2
1	CO	294	GLY	2.2
1	BF	277	ALA	2.2
1	BS	296	PHE	2.2
1	BC	315	TYR	2.2
1	CN	242	LEU	2.2
1	AO	262	PRO	2.2
1	BH	302	ASP	2.2
1	CY	303	ASN	2.2
1	Ab	163	THR	2.2
1	CH	220	ALA	2.2
1	AP	336	SER	2.2
1	BY	234	SER	2.2
1	CI	267	TYR	2.2
1	BA	263	LEU	2.2
1	BA	282	LEU	2.2
1	CO	239	LYS	2.2
1	AZ	296	PHE	2.2
1	AZ	337	GLU	2.2
1	CE	307	THR	2.2
1	BQ	317	ASP	2.2
1	CQ	286	ALA	2.2
1	AK	105	GLU	2.2
1	AV	318	GLU	2.2
1	CY	270	GLY	2.2
1	CZ	226	GLY	2.2
1	BO	251	ALA	2.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	CG	325	LEU	2.2
1	CP	34	ARG	2.2
1	BU	248	LEU	2.2
1	AX	315	TYR	2.2
1	AB	298	TRP	2.2
1	AD	265	ILE	2.2
1	BA	234	SER	2.1
1	CS	336	SER	2.1
1	Bd	301	TRP	2.1
1	AB	294	GLY	2.1
1	BF	228	LEU	2.1
1	BH	325	LEU	2.1
1	CC	253	ASP	2.1
1	BI	309	THR	2.1
1	BN	265	ILE	2.1
1	CX	303	ASN	2.1
1	CX	323	ILE	2.1
1	CZ	335	ASP	2.1
1	Ab	238	PHE	2.1
1	Bd	265	ILE	2.1
1	BM	254	GLY	2.1
1	Ab	255	ALA	2.1
1	AF	263	LEU	2.1
1	AT	164	ARG	2.1
1	BX	263	LEU	2.1
1	AX	280	TRP	2.1
1	CZ	240	SER	2.1
1	AC	262	PRO	2.1
1	BE	314	TYR	2.1
1	AG	228	LEU	2.1
1	AV	324	LEU	2.1
1	BC	235	THR	2.1
1	CG	268	SER	2.1
1	BH	231	ASP	2.1
1	AH	264	SER	2.1
1	AW	318	GLU	2.1
1	AD	263	LEU	2.1
1	BR	263	LEU	2.1
1	BU	330	VAL	2.1
1	CY	277	ALA	2.1
1	AC	265	ILE	2.1
1	CR	257	PHE	2.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	BA	240	SER	2.1
1	CG	311	GLY	2.1
1	AV	51	GLY	2.1
1	BM	321	ARG	2.1
1	AO	266	ASP	2.1
1	BT	233	LEU	2.1
1	CW	278	VAL	2.1
1	BX	292	PRO	2.1
1	CZ	257	PHE	2.1
1	Cc	252	PRO	2.1
1	Cb	337	GLU	2.1
1	BC	242	LEU	2.1
1	CG	243	LEU	2.1
1	BH	224	THR	2.1
1	AI	297	ARG	2.1
1	AQ	277	ALA	2.1
1	BU	281	HIS	2.1
1	CV	255	ALA	2.1
1	BY	136	HIS	2.1
1	Bd	276	ARG	2.1
1	AD	229	TYR	2.1
1	CY	331	CYS	2.1
1	CF	222	ILE	2.1
1	CU	298	TRP	2.1
1	BA	228	LEU	2.1
1	BI	225	GLN	2.1
1	AV	282	LEU	2.1
1	BY	235	THR	2.1
1	AZ	266	ASP	2.1
1	AD	206	ARG	2.1
1	AH	299	GLY	2.1
1	Ab	274	VAL	2.1
1	CF	240	SER	2.1
1	Bb	258	GLN	2.1
1	BC	275	ASP	2.1
1	BG	260	ASP	2.1
1	BH	52	THR	2.1
1	BK	275	ASP	2.1
1	BC	337	GLU	2.1
1	CP	321	ARG	2.1
1	AQ	97	ARG	2.1
1	Bb	230	ASN	2.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	Bb	248	LEU	2.1
1	CH	296	PHE	2.1
1	BG	322	GLN	2.1
1	CB	217	GLU	2.1
1	AU	276	ARG	2.1
1	CE	269	LEU	2.1
1	CF	298	TRP	2.1
1	BR	257	PHE	2.1
1	CB	254	GLY	2.1
1	CF	332	THR	2.1
1	AM	262	PRO	2.1
1	BU	312	VAL	2.1
1	CY	310	ASP	2.1
1	AZ	318	GLU	2.1
1	Cb	224	THR	2.1
1	Ac	282	LEU	2.1
1	AB	293	ALA	2.1
1	CV	283	LYS	2.1
1	Ca	239	LYS	2.1
1	AD	163	THR	2.1
1	CD	269	LEU	2.1
1	BM	243	LEU	2.1
1	AM	166	LEU	2.1
1	CY	262	PRO	2.1
1	Cb	316	SER	2.1
1	BN	235	THR	2.1
1	CW	249	ASP	2.1
1	BM	284	LYS	2.1
1	Bb	236	ASN	2.1
1	CD	256	VAL	2.1
1	CN	336	SER	2.1
1	AP	304	PHE	2.1
1	CP	262	PRO	2.1
1	AQ	262	PRO	2.1
1	AU	217	GLU	2.1
1	BX	227	SER	2.1
1	Bc	296	PHE	2.1
1	CB	302	ASP	2.1
1	CE	273	ASP	2.1
1	CG	219	THR	2.1
1	CK	249	ASP	2.1
1	CU	307	THR	2.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	BF	267	TYR	2.1
1	AF	265	ILE	2.1
1	BH	279	TYR	2.1
1	CM	267	TYR	2.1
1	AT	53	ASN	2.1
1	CQ	256	VAL	2.1
1	CZ	258	GLN	2.1
1	BF	311	GLY	2.1
1	BC	252	PRO	2.0
1	CN	281	HIS	2.0
1	BU	240	SER	2.0
1	CC	273	ASP	2.0
1	AG	275	ASP	2.0
1	CH	260	ASP	2.0
1	CO	246	THR	2.0
1	AV	331	CYS	2.0
1	CX	266	ASP	2.0
1	AV	322	GLN	2.0
1	AX	230	ASN	2.0
1	CA	283	LYS	2.0
1	AD	217	GLU	2.0
1	AG	238	PHE	2.0
1	AD	262	PRO	2.0
1	CE	56	HIS	2.0
1	CV	227	SER	2.0
1	Bd	208	SER	2.0
1	Ad	264	SER	2.0
1	BB	325	LEU	2.0
1	CD	266	ASP	2.0
1	CF	327	VAL	2.0
1	CO	269	LEU	2.0
1	BP	274	VAL	2.0
1	BY	266	ASP	2.0
1	CD	270	GLY	2.0
1	Bb	254	GLY	2.0
1	Cd	336	SER	2.0
1	BJ	52	THR	2.0
1	AJ	52	THR	2.0
1	BM	332	THR	2.0
1	Bb	228	LEU	2.0
1	Cd	235	THR	2.0
1	BA	296	PHE	2.0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	AI	306	LYS	2.0
1	CJ	105	GLU	2.0
1	CY	319	GLN	2.0
1	AF	277	ALA	2.0
1	CQ	293	ALA	2.0
1	CF	328	GLY	2.0
1	CO	266	ASP	2.0
1	BE	321	ARG	2.0
1	AK	164	ARG	2.0
1	AM	250	ILE	2.0
1	Bb	261	ARG	2.0
1	CB	283	LYS	2.0
1	CF	281	HIS	2.0
1	Ca	308	PHE	2.0
1	AF	317	ASP	2.0
1	CH	276	ARG	2.0
1	CH	309	THR	2.0
1	CI	276	ARG	2.0
1	AM	237	ASP	2.0
1	CM	299	GLY	2.0
1	CY	318	GLU	2.0
1	Cb	235	THR	2.0
1	Ac	310	ASP	2.0
1	CE	239	LYS	2.0
1	CU	234	SER	2.0
1	CX	336	SER	2.0
1	Ab	136	HIS	2.0
1	CI	286	ALA	2.0
1	BM	225	GLN	2.0
1	BO	293	ALA	2.0
1	AQ	265	ILE	2.0
1	BA	229	TYR	2.0
1	Aa	228	LEU	2.0
1	Cd	324	LEU	2.0
1	CC	261	ARG	2.0
1	BU	297	ARG	2.0
1	Ba	328	GLY	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 [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	CA	AE	401	1/1	0.96	0.18	-0.53	38,38,38,38	0
2	CA	BS	401	1/1	0.99	0.20	-0.58	23,23,23,23	0
2	CA	AF	401	1/1	0.99	0.18	-0.62	50,50,50,50	0
2	CA	AZ	401	1/1	0.99	0.18	-0.65	36,36,36,36	0
2	CA	Ba	401	1/1	0.98	0.19	-0.67	53,53,53,53	0
2	CA	Aa	401	1/1	0.98	0.15	-0.69	45,45,45,45	0
2	CA	AK	401	1/1	0.98	0.19	-0.74	36,36,36,36	0
2	CA	AN	401	1/1	0.99	0.17	-0.85	42,42,42,42	0
2	CA	BA	401	1/1	0.99	0.16	-0.88	35,35,35,35	0
2	CA	AC	401	1/1	0.98	0.18	-0.89	28,28,28,28	0
2	CA	AW	401	1/1	0.99	0.17	-0.90	39,39,39,39	0
2	CA	AI	401	1/1	0.98	0.17	-1.00	43,43,43,43	0
2	CA	AO	401	1/1	0.99	0.16	-1.03	47,47,47,47	0
2	CA	BT	401	1/1	0.98	0.16	-1.04	19,19,19,19	0
2	CA	AR	401	1/1	0.99	0.14	-1.07	40,40,40,40	0
2	CA	AV	401	1/1	0.99	0.15	-1.10	39,39,39,39	0
2	CA	BE	401	1/1	0.99	0.15	-1.14	35,35,35,35	0
2	CA	Bc	401	1/1	0.98	0.14	-1.16	29,29,29,29	0
2	CA	BP	402	1/1	0.98	0.13	-1.19	35,35,35,35	0
2	CA	BE	402	1/1	0.99	0.18	-1.19	33,33,33,33	0
2	CA	Ac	401	1/1	0.99	0.15	-1.20	48,48,48,48	0
2	CA	AA	401	1/1	0.99	0.14	-1.22	57,57,57,57	0
2	CA	Bc	402	1/1	1.00	0.16	-1.23	43,43,43,43	0
2	CA	BJ	401	1/1	0.97	0.16	-1.28	27,27,27,27	0
2	CA	BP	401	1/1	0.98	0.17	-1.32	33,33,33,33	0
2	CA	BI	401	1/1	0.94	0.15	-1.33	43,43,43,43	0
2	CA	AH	401	1/1	0.98	0.13	-1.35	34,34,34,34	0
2	CA	AS	401	1/1	0.99	0.16	-1.35	27,27,27,27	0
2	CA	BO	401	1/1	0.98	0.18	-1.37	34,34,34,34	0
2	CA	BN	401	1/1	0.98	0.17	-1.38	39,39,39,39	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	CA	AB	401	1/1	0.99	0.14	-1.40	40,40,40,40	0
2	CA	BC	402	1/1	0.98	0.14	-1.42	38,38,38,38	0
2	CA	BU	402	1/1	0.98	0.15	-1.45	29,29,29,29	0
2	CA	AD	401	1/1	0.99	0.14	-1.45	36,36,36,36	0
2	CA	AY	401	1/1	0.99	0.14	-1.46	30,30,30,30	0
2	CA	BC	401	1/1	0.98	0.16	-1.47	22,22,22,22	0
2	CA	Ad	401	1/1	0.99	0.15	-1.49	42,42,42,42	0
2	CA	BA	402	1/1	0.98	0.13	-1.52	41,41,41,41	0
2	CA	AG	401	1/1	0.99	0.11	-1.52	44,44,44,44	0
2	CA	Bb	401	1/1	0.97	0.17	-1.55	24,24,24,24	0
2	CA	BH	401	1/1	0.99	0.12	-1.58	34,34,34,34	0
2	CA	BK	401	1/1	0.98	0.16	-1.59	22,22,22,22	0
2	CA	BX	402	1/1	0.99	0.12	-1.60	31,31,31,31	0
2	CA	BF	401	1/1	0.98	0.16	-1.60	27,27,27,27	0
2	CA	BI	402	1/1	0.98	0.14	-1.64	54,54,54,54	0
2	CA	Bd	402	1/1	0.98	0.12	-1.65	48,48,48,48	0
2	CA	BS	402	1/1	0.99	0.16	-1.68	36,36,36,36	0
2	CA	AM	401	1/1	0.99	0.12	-1.70	45,45,45,45	0
2	CA	BL	402	1/1	0.98	0.14	-1.74	34,34,34,34	0
2	CA	BW	401	1/1	0.99	0.14	-1.75	25,25,25,25	0
2	CA	BF	402	1/1	0.99	0.14	-1.79	36,36,36,36	0
2	CA	BL	401	1/1	0.98	0.15	-1.81	24,24,24,24	0
2	CA	AX	401	1/1	0.99	0.13	-1.81	38,38,38,38	0
2	CA	BO	402	1/1	0.91	0.14	-1.85	52,52,52,52	0
2	CA	BQ	402	1/1	0.96	0.12	-1.86	43,43,43,43	0
2	CA	AJ	401	1/1	0.99	0.14	-1.86	38,38,38,38	0
2	CA	BH	402	1/1	0.98	0.11	-1.86	41,41,41,41	0
2	CA	BZ	401	1/1	0.97	0.14	-1.88	36,36,36,36	0
2	CA	AP	401	1/1	0.98	0.12	-1.88	42,42,42,42	0
2	CA	AL	401	1/1	0.99	0.15	-1.93	41,41,41,41	0
2	CA	BB	402	1/1	0.96	0.12	-1.95	35,35,35,35	0
2	CA	BY	402	1/1	0.95	0.12	-1.95	33,33,33,33	0
2	CA	BV	402	1/1	0.95	0.12	-1.99	57,57,57,57	0
2	CA	BX	401	1/1	0.97	0.14	-2.01	35,35,35,35	0
2	CA	BG	402	1/1	0.98	0.13	-2.04	54,54,54,54	0
2	CA	BV	401	1/1	0.96	0.12	-2.04	36,36,36,36	0
2	CA	AQ	401	1/1	0.99	0.11	-2.05	57,57,57,57	0
2	CA	BD	401	1/1	0.95	0.14	-2.07	36,36,36,36	0
2	CA	Ab	401	1/1	0.98	0.10	-2.09	38,38,38,38	0
2	CA	AT	401	1/1	0.98	0.12	-2.10	36,36,36,36	0
2	CA	Ba	402	1/1	0.95	0.10	-2.13	42,42,42,42	0
2	CA	BJ	402	1/1	0.99	0.12	-2.15	29,29,29,29	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	CA	BD	402	1/1	0.99	0.14	-2.16	44,44,44,44	0
2	CA	BU	401	1/1	0.98	0.13	-2.16	32,32,32,32	0
2	CA	BW	402	1/1	0.99	0.16	-2.17	42,42,42,42	0
2	CA	BR	401	1/1	0.98	0.13	-2.18	26,26,26,26	0
2	CA	BZ	402	1/1	0.98	0.10	-2.24	57,57,57,57	0
2	CA	BM	402	1/1	0.99	0.12	-2.26	33,33,33,33	0
2	CA	BY	401	1/1	0.99	0.12	-2.27	31,31,31,31	0
2	CA	BR	402	1/1	0.99	0.10	-2.30	53,53,53,53	0
2	CA	BN	402	1/1	0.95	0.11	-2.30	50,50,50,50	0
2	CA	BQ	401	1/1	0.96	0.14	-2.35	32,32,32,32	0
2	CA	Bd	401	1/1	0.99	0.13	-2.37	37,37,37,37	0
2	CA	AU	401	1/1	0.97	0.12	-2.41	30,30,30,30	0
2	CA	Bb	402	1/1	0.99	0.16	-2.41	33,33,33,33	0
2	CA	BK	402	1/1	0.99	0.12	-2.52	31,31,31,31	0
2	CA	BB	401	1/1	0.97	0.12	-2.53	26,26,26,26	0
2	CA	BM	401	1/1	0.96	0.08	-2.77	39,39,39,39	0
2	CA	BG	401	1/1	0.98	0.11	-3.20	38,38,38,38	0
2	CA	BT	402	1/1	0.99	0.13	-3.25	42,42,42,42	0

6.5 Other polymers [i](#)

There are no such residues in this entry.