Full wwPDB X-ray Structure Validation Report ⓘ

May 4, 2022 – 08:24 PM EDT

PDB ID	:	3E8K
Title	:	Crystal structure of HK97 Prohead II
Authors	:	Gertsman, I.; Speir, J.; Johnson, J.E.
Deposited on	:	2008-08-20
Resolution	:	3.65 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
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

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

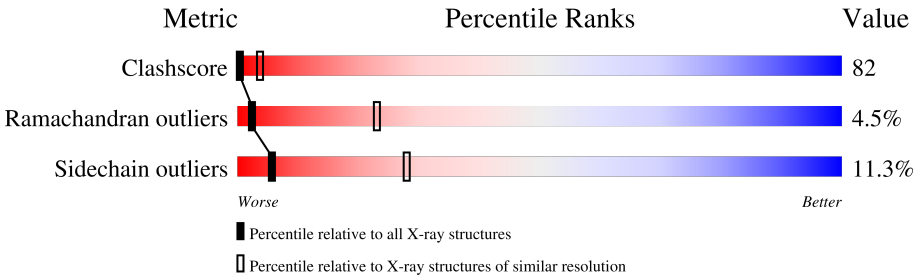
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.28.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.28.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.65 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))
Clashscore	141614	1037 (3.80-3.52)
Ramachandran outliers	138981	1004 (3.80-3.52)
Sidechain outliers	138945	1002 (3.80-3.52)

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 of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5%

Mol	Chain	Length	Quality of chain
1	A	273	30% 52% 11% • 6%
1	B	273	27% 49% 15% 8%
1	C	273	31% 51% 9% • 9%
1	D	273	31% 53% 8% • 7%
1	E	273	25% 56% 12% • 7%
1	F	273	23% 52% 14% • 9%
1	G	273	30% 49% 10% 10%

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 13590 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 Major capsid protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	256	Total	C	N	O	S	0	0	0
			1978	1238	346	384	10			
1	B	250	Total	C	N	O	S	0	0	0
			1934	1209	339	377	9			
1	C	248	Total	C	N	O	S	0	0	0
			1918	1198	337	375	8			
1	D	254	Total	C	N	O	S	0	0	0
			1961	1228	343	381	9			
1	E	255	Total	C	N	O	S	0	0	0
			1970	1233	345	383	9			
1	F	248	Total	C	N	O	S	0	0	0
			1918	1198	337	375	8			
1	G	247	Total	C	N	O	S	0	0	0
			1911	1193	336	374	8			

There are 35 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	159	ALA	-	linker	UNP P49861
A	160	PRO	-	linker	UNP P49861
A	161	GLY	-	linker	UNP P49861
A	162	ASP	-	linker	UNP P49861
A	336	PHE	TRP	engineered mutation	UNP P49861
B	159	ALA	-	linker	UNP P49861
B	160	PRO	-	linker	UNP P49861
B	161	GLY	-	linker	UNP P49861
B	162	ASP	-	linker	UNP P49861
B	336	PHE	TRP	engineered mutation	UNP P49861
C	159	ALA	-	linker	UNP P49861
C	160	PRO	-	linker	UNP P49861
C	161	GLY	-	linker	UNP P49861
C	162	ASP	-	linker	UNP P49861
C	336	PHE	TRP	engineered mutation	UNP P49861

Continued on next page...

Continued from previous page...

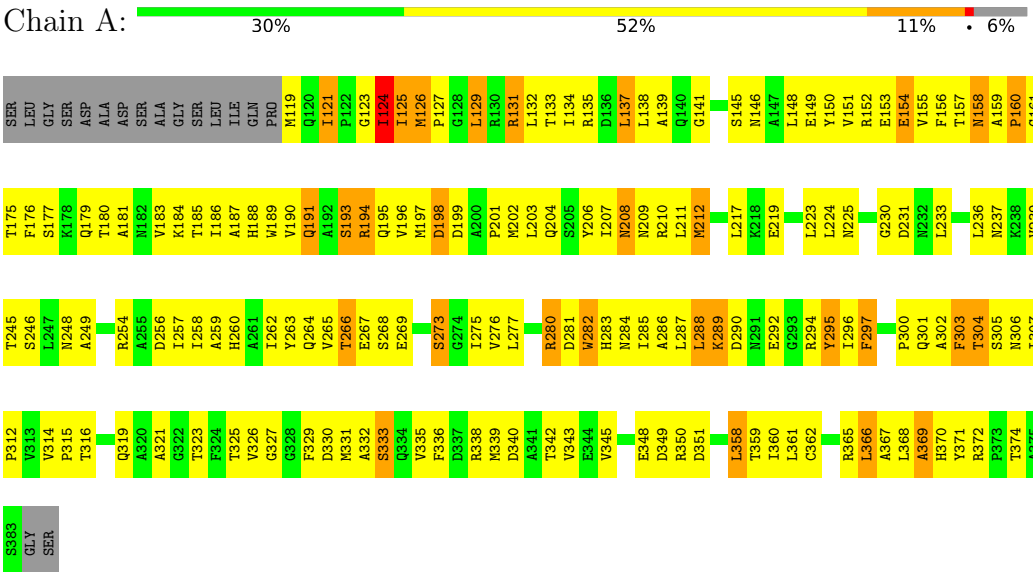
Chain	Residue	Modelled	Actual	Comment	Reference
D	159	ALA	-	linker	UNP P49861
D	160	PRO	-	linker	UNP P49861
D	161	GLY	-	linker	UNP P49861
D	162	ASP	-	linker	UNP P49861
D	336	PHE	TRP	engineered mutation	UNP P49861
E	159	ALA	-	linker	UNP P49861
E	160	PRO	-	linker	UNP P49861
E	161	GLY	-	linker	UNP P49861
E	162	ASP	-	linker	UNP P49861
E	336	PHE	TRP	engineered mutation	UNP P49861
F	159	ALA	-	linker	UNP P49861
F	160	PRO	-	linker	UNP P49861
F	161	GLY	-	linker	UNP P49861
F	162	ASP	-	linker	UNP P49861
F	336	PHE	TRP	engineered mutation	UNP P49861
G	159	ALA	-	linker	UNP P49861
G	160	PRO	-	linker	UNP P49861
G	161	GLY	-	linker	UNP P49861
G	162	ASP	-	linker	UNP P49861
G	336	PHE	TRP	engineered mutation	UNP P49861

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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.

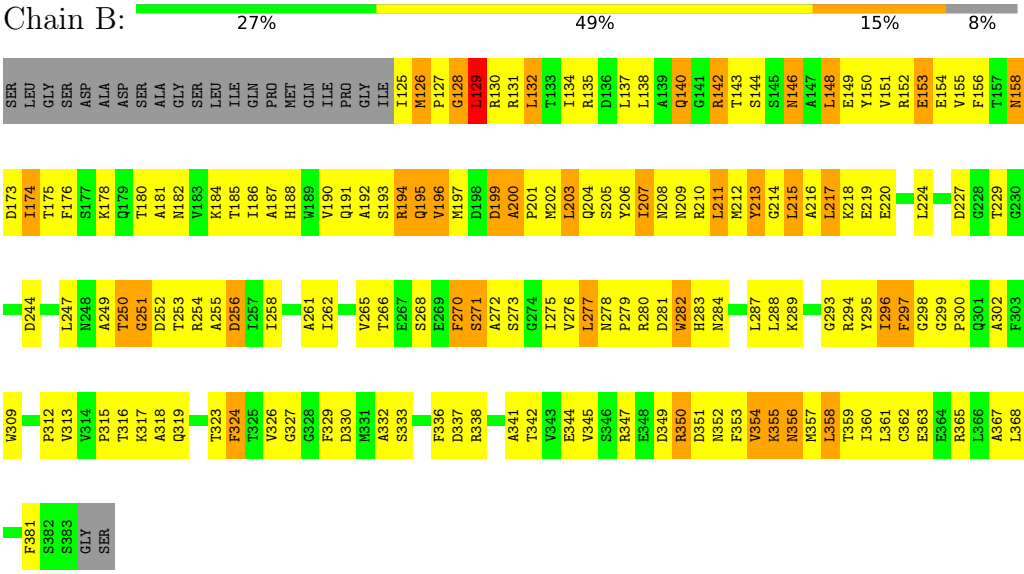
• Molecule 1: Major capsid protein

Chain A:



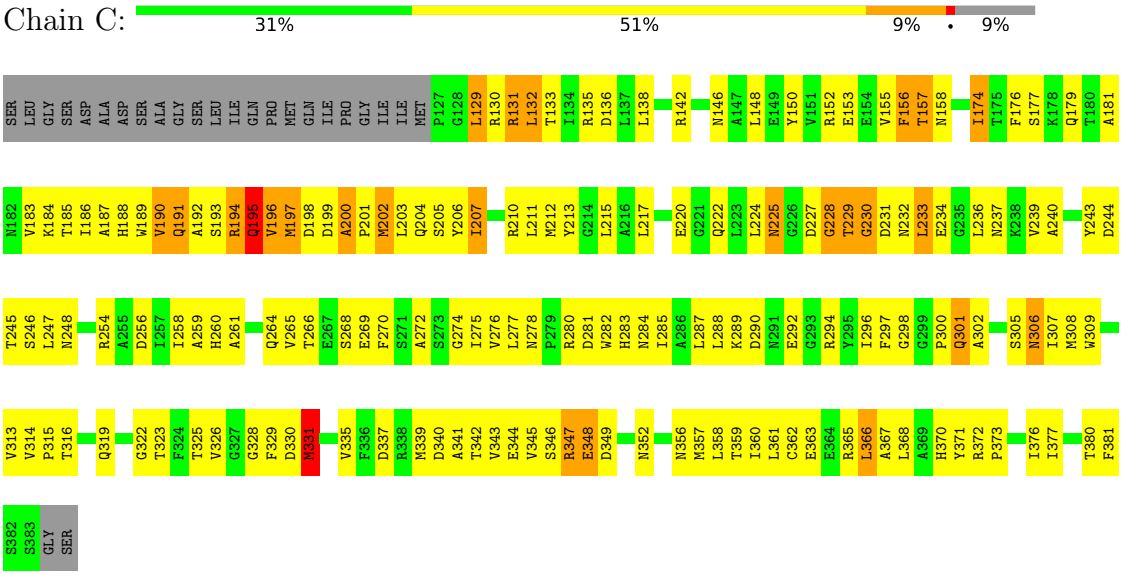
• Molecule 1: Major capsid protein

Chain B:



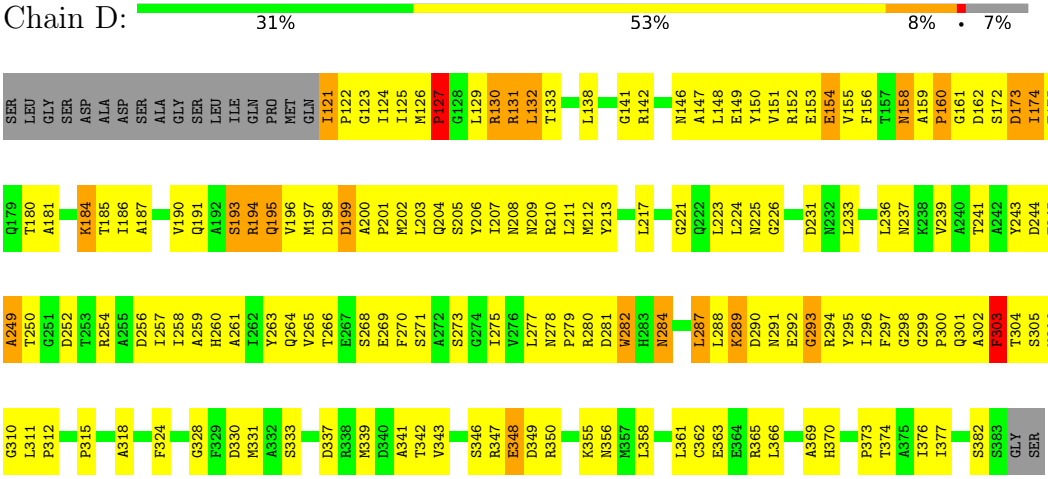
• Molecule 1: Major capsid protein

Chain C:



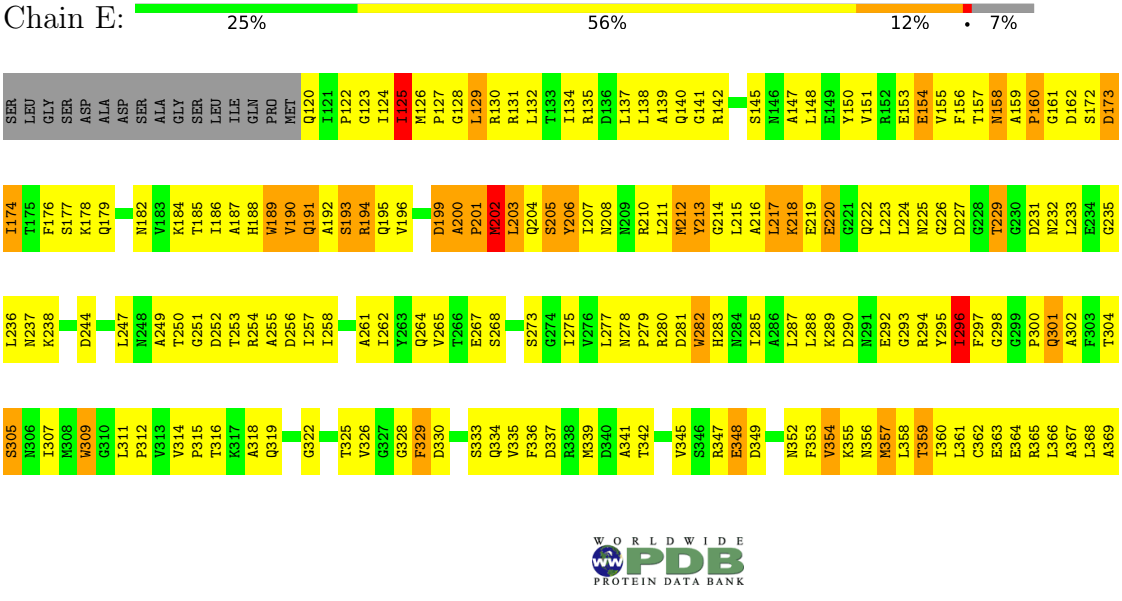
• Molecule 1: Major capsid protein

Chain D:



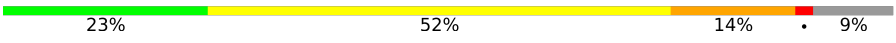
• Molecule 1: Major capsid protein

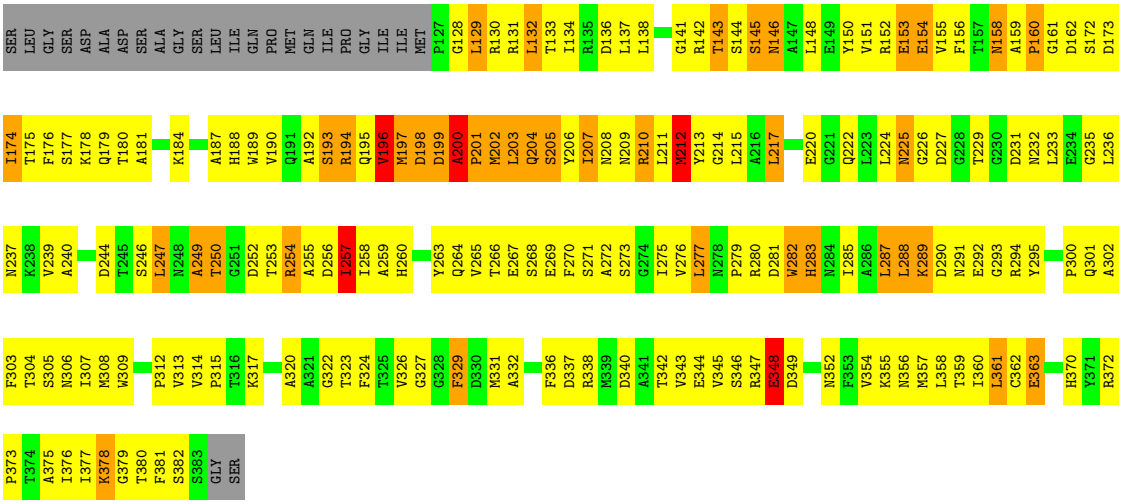
Chain E:



• Molecule 1: Major capsid protein

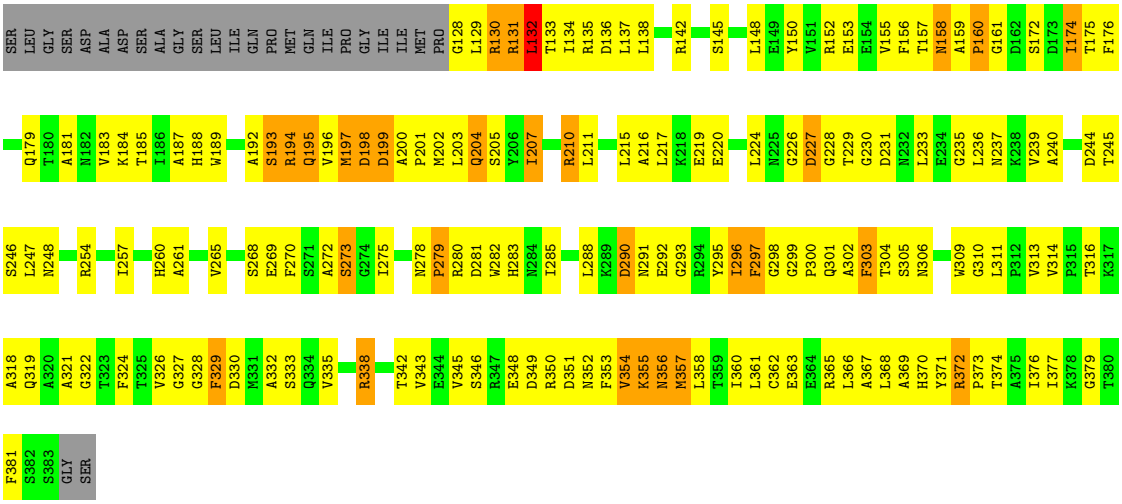
Chain F:





• Molecule 1: Major capsid protein

Chain G:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α, β, γ	553.03Å 574.39Å 587.36Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	35.00 – 3.65 34.99 – 3.65	Depositor EDS
% Data completeness (in resolution range)	64.8 (35.00-3.65) 54.3 (34.99-3.65)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	0.18	Depositor
$< I/\sigma(I) >$ [1]	1.97 (at 3.66Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.366 , (Not available) 0.310 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å^2)	72.5	Xtriage
Anisotropy	0.013	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.25 , -38.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.23$, $< L^2 > = 0.09$	Xtriage
Estimated twinning fraction	0.276 for -h,-l,-k	Xtriage
F_o,F_c correlation	0.75	EDS
Total number of atoms	13590	wwPDB-VP
Average B, all atoms (Å^2)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.58% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	A	0.41	1/2013 (0.0%)	0.68	2/2730 (0.1%)
1	B	0.42	0/1968	0.82	11/2669 (0.4%)
1	C	0.36	0/1952	0.68	2/2647 (0.1%)
1	D	0.37	1/1996 (0.1%)	0.68	5/2708 (0.2%)
1	E	0.40	1/2005 (0.0%)	0.70	5/2720 (0.2%)
1	F	0.42	0/1952	0.83	11/2647 (0.4%)
1	G	0.40	0/1944	0.77	9/2636 (0.3%)
All	All	0.40	3/13830 (0.0%)	0.74	45/18757 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	329	PHE	C-N	-5.66	1.21	1.34
1	A	212	MET	C-N	-5.28	1.21	1.34
1	D	288	LEU	C-N	-5.03	1.22	1.34

All (45) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	F	200	ALA	C-N-CD	-9.66	99.35	120.60
1	G	272	ALA	CB-CA-C	-8.25	97.73	110.10
1	G	228	GLY	N-CA-C	8.21	133.63	113.10
1	D	193	SER	N-CA-CB	-7.66	99.01	110.50
1	G	195	GLN	N-CA-C	-7.24	91.46	111.00
1	F	194	ARG	CB-CA-C	-6.97	96.46	110.40

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	196	VAL	N-CA-C	-6.97	92.19	111.00
1	F	332	ALA	N-CA-CB	-6.81	100.56	110.10
1	B	194	ARG	CB-CA-C	-6.79	96.83	110.40
1	D	226	GLY	N-CA-C	6.75	129.98	113.10
1	B	195	GLN	CB-CA-C	-6.71	96.97	110.40
1	F	272	ALA	CB-CA-C	-6.38	100.53	110.10
1	F	204	GLN	CB-CA-C	-6.19	98.03	110.40
1	F	249	ALA	CB-CA-C	6.18	119.37	110.10
1	B	369	ALA	O-C-N	-6.17	112.82	122.70
1	E	192	ALA	CB-CA-C	-6.17	100.85	110.10
1	A	333	SER	N-CA-CB	6.15	119.72	110.50
1	G	273	SER	N-CA-CB	-5.99	101.51	110.50
1	D	250	THR	N-CA-C	5.96	127.09	111.00
1	G	210	ARG	N-CA-CB	-5.93	99.93	110.60
1	B	251	GLY	N-CA-C	5.89	127.83	113.10
1	G	207	ILE	CB-CA-C	-5.89	99.82	111.60
1	F	250	THR	N-CA-C	-5.88	95.12	111.00
1	B	250	THR	CB-CA-C	-5.81	95.92	111.60
1	A	249	ALA	CB-CA-C	-5.79	101.42	110.10
1	D	249	ALA	CB-CA-C	-5.73	101.51	110.10
1	B	272	ALA	N-CA-CB	-5.64	102.21	110.10
1	G	227	ASP	N-CA-C	5.63	126.19	111.00
1	C	331	MET	N-CA-CB	-5.56	100.60	110.60
1	B	203	LEU	N-CA-C	-5.45	96.30	111.00
1	G	194	ARG	CB-CA-C	-5.42	99.57	110.40
1	B	271	SER	CB-CA-C	-5.38	99.87	110.10
1	E	193	SER	N-CA-C	5.33	125.39	111.00
1	F	212	MET	O-C-N	5.31	131.20	122.70
1	B	128	GLY	N-CA-C	-5.30	99.85	113.10
1	E	202	MET	N-CA-C	5.28	125.27	111.00
1	D	123	GLY	N-CA-C	-5.25	99.97	113.10
1	G	207	ILE	N-CA-C	5.25	125.16	111.00
1	B	250	THR	N-CA-C	5.22	125.09	111.00
1	C	272	ALA	CB-CA-C	-5.21	102.29	110.10
1	F	257	ILE	CB-CA-C	-5.17	101.25	111.60
1	E	203	LEU	N-CA-CB	-5.10	100.19	110.40
1	F	205	SER	N-CA-C	-5.10	97.22	111.00
1	E	218	LYS	CB-CA-C	-5.05	100.29	110.40
1	F	288	LEU	C-N-CA	-5.01	109.18	121.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	369	ALA	Mainchain

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1978	0	1946	311	0
1	B	1934	0	1896	343	0
1	C	1918	0	1878	343	0
1	D	1961	0	1929	330	0
1	E	1970	0	1937	365	0
1	F	1918	0	1878	347	0
1	G	1911	0	1870	285	0
All	All	13590	0	13334	2213	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 82.

All (2213) 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:E:127:PRO:HB2	1:E:213:TYR:CD1	1.32	1.62
1:D:125:ILE:HD11	1:D:208:ASN:CG	1.32	1.49
1:D:125:ILE:HD11	1:D:208:ASN:ND2	1.26	1.45
1:C:196:VAL:HG12	1:C:203:LEU:CD1	1.44	1.45
1:B:201:PRO:O	1:B:204:GLN:CB	1.67	1.41
1:G:197:MET:CE	1:G:358:LEU:HD21	1.56	1.36
1:C:213:TYR:CZ	1:C:217:LEU:HD11	1.64	1.33
1:E:233:LEU:CD1	1:E:366:LEU:HD11	1.56	1.33
1:D:203:LEU:O	1:D:207:ILE:HD13	1.24	1.32
1:E:127:PRO:CB	1:E:213:TYR:HD1	1.44	1.30
1:F:199:ASP:O	1:F:201:PRO:HD2	1.31	1.29
1:E:206:TYR:O	1:E:210:ARG:HB2	1.28	1.29
1:C:196:VAL:CG1	1:C:203:LEU:HD11	1.59	1.29
1:C:194:ARG:O	1:C:196:VAL:N	1.66	1.28
1:F:203:LEU:O	1:F:206:TYR:CB	1.80	1.27
1:F:203:LEU:O	1:F:206:TYR:HB3	1.29	1.26

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:227:ASP:HB3	1:E:229:THR:CG2	1.65	1.26
1:B:211:LEU:HD12	1:B:211:LEU:O	1.28	1.26
1:E:202:MET:O	1:E:205:SER:HB3	1.07	1.25
1:G:197:MET:CE	1:G:358:LEU:CD2	2.13	1.25
1:B:193:SER:O	1:B:196:VAL:CG2	1.87	1.23
1:C:346:SER:O	1:C:359:THR:HG22	1.36	1.23
1:G:278:ASN:OD1	1:G:279:PRO:HD2	1.38	1.22
1:A:287:LEU:C	1:A:288:LEU:HD23	1.58	1.22
1:A:287:LEU:HD12	1:A:287:LEU:O	1.39	1.21
1:D:125:ILE:CD1	1:D:208:ASN:OD1	1.89	1.20
1:A:285:ILE:O	1:A:288:LEU:CD2	1.91	1.19
1:E:202:MET:HE3	1:E:203:LEU:H	1.05	1.18
1:A:285:ILE:O	1:A:288:LEU:HD21	1.02	1.17
1:C:210:ARG:NH2	1:D:153:GLU:CD	1.97	1.17
1:D:247:LEU:HD23	1:D:247:LEU:O	1.45	1.17
1:A:368:LEU:HD21	1:A:370:HIS:NE2	1.60	1.16
1:D:127:PRO:HG3	1:D:212:MET:HE3	1.23	1.16
1:D:190:VAL:HG12	1:D:211:LEU:HD21	1.28	1.16
1:B:215:LEU:C	1:B:215:LEU:CD2	2.12	1.15
1:A:269:GLU:HB3	1:F:217:LEU:HD21	1.22	1.15
1:D:127:PRO:HD3	1:D:212:MET:HE2	1.17	1.15
1:C:129:LEU:HD11	1:D:331:MET:CE	1.75	1.15
1:C:233:LEU:N	1:C:233:LEU:HD23	1.49	1.14
1:D:190:VAL:CG1	1:D:211:LEU:HD21	1.78	1.14
1:E:127:PRO:CB	1:E:213:TYR:CD1	2.23	1.14
1:G:197:MET:HE1	1:G:358:LEU:CD2	1.74	1.14
1:C:129:LEU:HD11	1:D:331:MET:HE1	1.21	1.14
1:B:250:THR:HB	1:B:251:GLY:CA	1.76	1.13
1:C:213:TYR:CE2	1:C:217:LEU:HD11	1.84	1.13
1:C:195:GLN:HE22	1:C:198:ASP:CB	1.60	1.13
1:C:196:VAL:CG1	1:C:203:LEU:HD21	1.78	1.13
1:D:125:ILE:CD1	1:D:208:ASN:CG	2.17	1.13
1:D:127:PRO:HD3	1:D:212:MET:CE	1.76	1.13
1:F:194:ARG:O	1:F:197:MET:HB3	1.48	1.13
1:F:200:ALA:HB3	1:F:201:PRO:HD3	1.20	1.13
1:C:196:VAL:CG1	1:C:203:LEU:CD1	2.22	1.13
1:B:131:ARG:NH2	1:B:220:GLU:OE1	1.81	1.12
1:F:142:ARG:HG3	1:F:337:ASP:HB2	1.16	1.12
1:D:125:ILE:CD1	1:D:208:ASN:ND2	2.12	1.12
1:G:338:ARG:HH11	1:G:338:ARG:CG	1.58	1.12
1:B:201:PRO:C	1:B:204:GLN:H	1.52	1.11

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:215:LEU:C	1:B:215:LEU:HD23	1.65	1.11
1:C:225:ASN:HB3	1:C:237:ASN:HD22	1.08	1.11
1:B:277:LEU:N	1:B:277:LEU:HD23	1.52	1.11
1:E:202:MET:HE3	1:E:203:LEU:N	1.65	1.11
1:F:343:VAL:HG12	1:F:362:CYS:HB3	1.24	1.11
1:G:198:ASP:O	1:G:199:ASP:OD1	1.69	1.10
1:F:203:LEU:C	1:F:203:LEU:CD2	2.18	1.10
1:F:142:ARG:CG	1:F:337:ASP:HB2	1.79	1.10
1:B:193:SER:O	1:B:196:VAL:HG23	1.49	1.10
1:B:212:MET:O	1:B:215:LEU:N	1.83	1.10
1:B:127:PRO:HA	1:B:129:LEU:HD13	1.18	1.09
1:E:215:LEU:O	1:E:218:LYS:HB3	1.52	1.09
1:E:227:ASP:HB3	1:E:229:THR:HG23	1.31	1.09
1:A:125:ILE:CG2	1:A:204:GLN:NE2	2.15	1.09
1:B:201:PRO:O	1:B:204:GLN:HB3	1.44	1.09
1:E:194:ARG:HA	1:E:358:LEU:CD1	1.82	1.09
1:C:287:LEU:HD22	1:C:300:PRO:HB3	1.35	1.09
1:F:203:LEU:C	1:F:203:LEU:HD23	1.68	1.09
1:A:288:LEU:HD23	1:A:288:LEU:N	1.56	1.09
1:B:296:ILE:HD13	1:B:296:ILE:H	1.16	1.08
1:C:196:VAL:HG13	1:C:203:LEU:HD21	1.08	1.08
1:E:202:MET:O	1:E:205:SER:CB	2.01	1.08
1:A:285:ILE:C	1:A:288:LEU:HD21	1.74	1.08
1:F:247:LEU:N	1:F:247:LEU:HD23	1.48	1.08
1:G:129:LEU:CD2	1:G:131:ARG:HB2	1.84	1.08
1:D:127:PRO:CD	1:D:212:MET:HE2	1.82	1.07
1:C:130:ARG:HG3	1:D:271:SER:HB2	1.36	1.07
1:G:158:ASN:OD1	1:G:172:SER:HA	1.53	1.07
1:A:197:MET:SD	1:A:203:LEU:HD13	1.95	1.07
1:A:153:GLU:OE1	1:F:210:ARG:NH2	1.88	1.07
1:C:194:ARG:NH1	1:C:347:ARG:HH22	1.51	1.07
1:D:122:PRO:HG3	1:D:343:VAL:O	1.54	1.06
1:E:203:LEU:O	1:E:206:TYR:N	1.85	1.06
1:D:127:PRO:HG3	1:D:212:MET:CE	1.83	1.06
1:G:129:LEU:HD22	1:G:131:ARG:HB2	1.12	1.06
1:B:250:THR:CB	1:B:251:GLY:HA3	1.78	1.06
1:C:232:ASN:C	1:C:233:LEU:HD23	1.76	1.05
1:C:196:VAL:CG1	1:C:203:LEU:CD2	2.35	1.05
1:D:129:LEU:HD22	1:D:130:ARG:H	1.16	1.05
1:A:202:MET:O	1:A:206:TYR:N	1.88	1.05
1:C:195:GLN:NE2	1:C:198:ASP:HB3	1.70	1.04

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:329:PHE:HA	1:G:332:ALA:HB3	1.39	1.04
1:C:187:ALA:HB2	1:C:363:GLU:HA	1.39	1.04
1:F:324:PHE:HD2	1:F:381:PHE:CE1	1.73	1.04
1:C:203:LEU:O	1:C:206:TYR:N	1.88	1.04
1:D:203:LEU:O	1:D:207:ILE:CD1	2.04	1.04
1:F:246:SER:C	1:F:247:LEU:HD23	1.77	1.04
1:B:201:PRO:O	1:B:204:GLN:CA	2.07	1.03
1:D:249:ALA:O	1:D:252:ASP:OD2	1.75	1.03
1:F:194:ARG:NH1	1:F:347:ARG:NH1	2.06	1.03
1:B:158:ASN:HB2	1:B:172:SER:HA	1.35	1.03
1:C:196:VAL:HG13	1:C:203:LEU:CD2	1.87	1.03
1:G:158:ASN:HD22	1:G:159:ALA:N	1.54	1.03
1:B:201:PRO:O	1:B:204:GLN:N	1.91	1.03
1:A:287:LEU:C	1:A:288:LEU:CD2	2.27	1.03
1:C:195:GLN:HE22	1:C:198:ASP:HB3	0.89	1.03
1:A:127:PRO:HB3	1:A:212:MET:HB3	1.39	1.02
1:B:215:LEU:HD23	1:B:215:LEU:O	1.56	1.02
1:E:233:LEU:HD11	1:E:366:LEU:HD11	1.03	1.02
1:C:201:PRO:O	1:C:204:GLN:HB2	1.59	1.02
1:F:210:ARG:HH11	1:F:210:ARG:HG2	1.20	1.01
1:D:125:ILE:HD11	1:D:208:ASN:HD21	1.26	1.01
1:F:131:ARG:NH2	1:F:220:GLU:OE1	1.93	1.01
1:B:217:LEU:CD1	1:B:217:LEU:C	2.30	1.00
1:B:250:THR:HB	1:B:251:GLY:HA3	1.01	1.00
1:F:203:LEU:HD22	1:F:204:GLN:N	1.74	1.00
1:B:201:PRO:O	1:B:204:GLN:HB2	1.61	1.00
1:G:296:ILE:HG22	1:G:297:PHE:N	1.76	1.00
1:A:125:ILE:CG2	1:A:204:GLN:HE22	1.71	1.00
1:A:368:LEU:CD2	1:A:370:HIS:NE2	2.24	1.00
1:E:194:ARG:HA	1:E:358:LEU:HD13	1.39	1.00
1:E:227:ASP:HB3	1:E:229:THR:HG21	1.41	1.00
1:D:127:PRO:CD	1:D:212:MET:CE	2.36	1.00
1:D:247:LEU:HD23	1:D:247:LEU:C	1.81	1.00
1:F:324:PHE:CD2	1:F:381:PHE:HE1	1.78	1.00
1:G:199:ASP:C	1:G:201:PRO:HD2	1.82	0.99
1:G:338:ARG:HH11	1:G:338:ARG:HG3	0.86	0.99
1:B:217:LEU:C	1:B:217:LEU:HD13	1.77	0.99
1:C:194:ARG:O	1:C:196:VAL:HG23	1.62	0.99
1:G:303:PHE:HD2	1:G:304:THR:H	1.07	0.99
1:B:195:GLN:C	1:B:197:MET:N	2.06	0.99
1:A:125:ILE:HG21	1:A:204:GLN:NE2	1.74	0.99

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:184:LYS:NZ	1:G:230:GLY:O	1.93	0.99
1:A:233:LEU:HD11	1:A:366:LEU:HD11	1.43	0.98
1:E:125:ILE:CD1	1:E:127:PRO:HD3	1.92	0.98
1:D:127:PRO:CG	1:D:212:MET:CE	2.42	0.98
1:F:204:GLN:C	1:F:206:TYR:H	1.63	0.98
1:F:329:PHE:HD1	1:F:329:PHE:N	1.62	0.98
1:C:202:MET:O	1:C:205:SER:N	1.96	0.98
1:C:213:TYR:CE2	1:C:217:LEU:HD21	1.97	0.98
1:G:202:MET:O	1:G:205:SER:OG	1.81	0.97
1:B:249:ALA:HB3	1:B:252:ASP:OD2	1.64	0.97
1:G:227:ASP:OD1	1:G:227:ASP:O	1.82	0.97
1:F:244:ASP:OD2	1:F:247:LEU:HD21	1.63	0.97
1:F:202:MET:O	1:F:205:SER:N	1.97	0.97
1:G:301:GLN:HG3	1:G:302:ALA:H	1.26	0.97
1:E:157:THR:HG22	1:E:267:GLU:HG3	1.45	0.97
1:D:206:TYR:HH	1:E:371:TYR:HE2	1.13	0.96
1:D:127:PRO:CG	1:D:212:MET:HE3	1.95	0.96
1:C:270:PHE:HE2	1:C:331:MET:HG2	1.30	0.96
1:C:201:PRO:O	1:C:204:GLN:N	1.99	0.95
1:C:130:ARG:CG	1:D:271:SER:HB2	1.95	0.95
1:E:233:LEU:HD11	1:E:366:LEU:CD1	1.96	0.95
1:C:287:LEU:HD22	1:C:300:PRO:CB	1.96	0.95
1:A:125:ILE:HG23	1:A:204:GLN:HE22	1.32	0.94
1:D:282:TRP:HE1	1:D:304:THR:HA	1.32	0.94
1:G:129:LEU:HD22	1:G:131:ARG:CB	1.97	0.94
1:F:200:ALA:O	1:F:202:MET:N	2.01	0.94
1:G:301:GLN:HG3	1:G:302:ALA:N	1.82	0.94
1:B:288:LEU:O	1:B:296:ILE:HD11	1.68	0.94
1:E:227:ASP:CB	1:E:229:THR:HG23	1.98	0.94
1:D:125:ILE:CD1	1:D:208:ASN:HD21	1.77	0.93
1:E:157:THR:HG22	1:E:267:GLU:CG	1.98	0.93
1:C:183:VAL:HA	1:C:367:ALA:HB2	1.49	0.93
1:D:125:ILE:HD11	1:D:208:ASN:OD1	1.57	0.93
1:F:203:LEU:O	1:F:203:LEU:HD23	1.66	0.93
1:F:345:VAL:HG13	1:F:358:LEU:HD21	1.50	0.93
1:E:207:ILE:HG13	1:E:208:ASN:H	1.32	0.93
1:A:195:GLN:HG3	1:A:196:VAL:HG23	1.51	0.93
1:B:207:ILE:O	1:B:211:LEU:HB3	1.67	0.93
1:F:197:MET:O	1:F:197:MET:SD	2.27	0.93
1:C:366:LEU:HD22	1:C:367:ALA:H	1.32	0.93
1:G:174:ILE:HD13	1:G:174:ILE:H	1.33	0.93

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:329:PHE:H	1:G:329:PHE:HD2	0.98	0.93
1:A:265:VAL:HG22	1:A:377:ILE:HD13	1.51	0.92
1:B:288:LEU:O	1:B:296:ILE:CD1	2.16	0.92
1:C:213:TYR:HE2	1:C:217:LEU:HD21	1.34	0.92
1:F:253:THR:HG23	1:F:256:ASP:OD1	1.68	0.92
1:B:277:LEU:N	1:B:277:LEU:CD2	2.29	0.92
1:B:195:GLN:C	1:B:197:MET:H	1.66	0.92
1:G:197:MET:HE2	1:G:358:LEU:CD2	1.96	0.92
1:G:197:MET:HE3	1:G:358:LEU:HD21	1.52	0.92
1:E:210:ARG:HH22	1:F:153:GLU:CD	1.73	0.92
1:F:225:ASN:HB3	1:F:237:ASN:HD22	1.33	0.92
1:G:351:ASP:O	1:G:355:LYS:HG2	1.70	0.91
1:F:200:ALA:CB	1:F:201:PRO:HD3	2.00	0.91
1:G:304:THR:HG22	1:G:305:SER:H	1.36	0.91
1:B:211:LEU:HD12	1:B:211:LEU:C	1.72	0.91
1:F:194:ARG:NH1	1:F:347:ARG:HH12	1.64	0.91
1:G:132:LEU:HB2	1:G:136:ASP:HB2	1.52	0.91
1:F:200:ALA:HB3	1:F:201:PRO:CD	1.99	0.91
1:A:174:ILE:H	1:A:174:ILE:HD13	1.33	0.91
1:G:303:PHE:HD2	1:G:304:THR:N	1.69	0.91
1:G:329:PHE:HA	1:G:332:ALA:CB	1.99	0.91
1:A:263:TYR:OH	1:A:267:GLU:OE2	1.87	0.91
1:C:213:TYR:CE1	1:C:217:LEU:HD11	2.05	0.91
1:C:233:LEU:HD11	1:C:366:LEU:CD1	2.01	0.90
1:F:199:ASP:O	1:F:201:PRO:CD	2.18	0.90
1:E:174:ILE:HD13	1:E:174:ILE:H	1.36	0.90
1:D:126:MET:SD	1:D:127:PRO:HD2	2.11	0.90
1:F:202:MET:SD	1:F:203:LEU:N	2.45	0.90
1:C:347:ARG:O	1:C:349:ASP:N	2.05	0.90
1:E:233:LEU:HD13	1:E:366:LEU:HD11	1.53	0.90
1:E:345:VAL:HG22	1:E:360:ILE:HA	1.54	0.90
1:G:197:MET:HE1	1:G:358:LEU:HD21	1.41	0.90
1:G:338:ARG:HG3	1:G:338:ARG:NH1	1.67	0.89
1:F:174:ILE:H	1:F:174:ILE:HD13	1.36	0.89
1:F:211:LEU:HD21	1:F:362:CYS:SG	2.13	0.89
1:B:195:GLN:O	1:B:197:MET:N	2.04	0.89
1:D:194:ARG:HG2	1:D:195:GLN:H	1.37	0.89
1:F:194:ARG:O	1:F:197:MET:CB	2.20	0.89
1:C:206:TYR:OH	1:C:210:ARG:NH1	2.05	0.89
1:E:220:GLU:OE2	1:E:316:THR:CG2	2.21	0.89
1:C:344:GLU:HB2	1:C:361:LEU:HD11	1.55	0.89

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:155:VAL:CG1	1:B:374:THR:HB	2.03	0.89
1:E:206:TYR:O	1:E:210:ARG:CB	2.19	0.89
1:F:354:VAL:HG13	1:F:355:LYS:HG3	1.52	0.89
1:G:327:GLY:O	1:G:329:PHE:CD2	2.25	0.89
1:E:155:VAL:HG23	1:E:174:ILE:HG22	1.53	0.89
1:F:247:LEU:N	1:F:247:LEU:CD2	2.30	0.88
1:C:233:LEU:N	1:C:233:LEU:CD2	2.30	0.88
1:G:200:ALA:O	1:G:204:GLN:N	2.06	0.88
1:D:190:VAL:HG12	1:D:211:LEU:CD2	2.03	0.88
1:D:247:LEU:HD21	1:D:260:HIS:HB3	1.56	0.88
1:F:343:VAL:CG1	1:F:362:CYS:HB3	2.01	0.88
1:B:127:PRO:CA	1:B:129:LEU:HD13	2.02	0.88
1:A:195:GLN:HG3	1:A:196:VAL:H	1.37	0.88
1:G:197:MET:HE2	1:G:358:LEU:HD22	1.55	0.88
1:C:366:LEU:HD22	1:C:367:ALA:N	1.89	0.87
1:E:137:LEU:HD22	1:E:329:PHE:HB2	1.56	0.87
1:F:155:VAL:HG23	1:F:174:ILE:HG22	1.56	0.87
1:F:131:ARG:HD2	1:F:315:PRO:O	1.74	0.87
1:B:185:THR:HG22	1:B:365:ARG:HG2	1.54	0.87
1:B:155:VAL:CG1	1:B:374:THR:CB	2.52	0.87
1:B:345:VAL:HG12	1:B:360:ILE:HA	1.56	0.87
1:E:295:TYR:OH	1:F:256:ASP:OD2	1.91	0.87
1:A:155:VAL:HG23	1:A:174:ILE:HG22	1.54	0.87
1:B:342:THR:O	1:B:362:CYS:HA	1.72	0.87
1:C:194:ARG:CZ	1:C:347:ARG:HH22	1.88	0.87
1:F:361:LEU:HD13	1:F:361:LEU:O	1.75	0.87
1:C:130:ARG:HG3	1:D:271:SER:CB	2.04	0.86
1:A:158:ASN:CG	1:A:172:SER:HA	1.94	0.86
1:C:287:LEU:CD2	1:C:300:PRO:CB	2.52	0.86
1:A:141:GLY:O	1:A:336:PHE:HA	1.74	0.86
1:A:343:VAL:HG12	1:A:362:CYS:HB2	1.54	0.86
1:G:200:ALA:N	1:G:201:PRO:CD	2.38	0.86
1:B:159:ALA:O	1:B:172:SER:HB3	1.73	0.86
1:E:158:ASN:CG	1:E:172:SER:HA	1.95	0.86
1:C:213:TYR:CE2	1:C:217:LEU:CD1	2.58	0.86
1:G:316:THR:HG22	1:G:318:ALA:H	1.37	0.86
1:E:233:LEU:CD1	1:E:366:LEU:CD1	2.51	0.86
1:G:155:VAL:HG11	1:G:374:THR:OG1	1.75	0.86
1:D:122:PRO:HG3	1:D:343:VAL:HG23	1.58	0.86
1:G:199:ASP:HB3	1:G:202:MET:HB3	1.56	0.85
1:C:357:MET:HE1	1:D:178:LYS:HG2	1.59	0.85

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:155:VAL:HG12	1:D:374:THR:OG1	1.76	0.85
1:A:300:PRO:HA	1:A:303:PHE:HB3	1.59	0.85
1:E:207:ILE:HG13	1:E:208:ASN:N	1.91	0.85
1:C:197:MET:SD	1:C:358:LEU:CD1	2.65	0.85
1:G:197:MET:CE	1:G:358:LEU:HD22	2.04	0.85
1:D:207:ILE:HG13	1:D:211:LEU:HD12	1.57	0.85
1:C:203:LEU:O	1:C:206:TYR:CB	2.25	0.85
1:C:258:ILE:HD11	1:C:275:ILE:HG12	1.59	0.85
1:E:202:MET:CE	1:E:203:LEU:N	2.39	0.85
1:G:329:PHE:HD2	1:G:329:PHE:N	1.75	0.84
1:B:194:ARG:NH2	1:B:347:ARG:NH2	2.25	0.84
1:B:215:LEU:C	1:B:215:LEU:HD22	1.96	0.84
1:D:194:ARG:HG2	1:D:195:GLN:N	1.91	0.84
1:B:132:LEU:HD23	1:B:132:LEU:H	1.42	0.84
1:B:127:PRO:C	1:B:129:LEU:H	1.81	0.84
1:B:156:PHE:HB3	1:B:158:ASN:OD1	1.78	0.84
1:E:213:TYR:O	1:E:217:LEU:HB2	1.77	0.84
1:F:203:LEU:CD2	1:F:204:GLN:N	2.38	0.84
1:E:220:GLU:OE2	1:E:316:THR:HG21	1.77	0.83
1:A:296:ILE:HG23	1:A:297:PHE:CD2	2.12	0.83
1:D:158:ASN:CG	1:D:172:SER:HA	1.97	0.83
1:E:355:LYS:O	1:E:357:MET:HG2	1.78	0.83
1:B:296:ILE:H	1:B:296:ILE:CD1	1.91	0.83
1:F:158:ASN:CG	1:F:172:SER:HA	1.98	0.83
1:B:194:ARG:HH22	1:B:347:ARG:HH22	1.23	0.83
1:F:142:ARG:HG2	1:F:337:ASP:O	1.78	0.83
1:G:132:LEU:HB2	1:G:136:ASP:CB	2.08	0.83
1:E:210:ARG:NH2	1:F:153:GLU:OE1	2.10	0.83
1:C:196:VAL:HG12	1:C:203:LEU:CG	2.08	0.83
1:F:202:MET:HG3	1:F:203:LEU:H	1.43	0.83
1:C:233:LEU:CD1	1:C:366:LEU:HD11	2.09	0.82
1:D:132:LEU:HD23	1:D:132:LEU:H	1.41	0.82
1:A:159:ALA:HB1	1:A:160:PRO:HD2	1.62	0.82
1:A:194:ARG:O	1:A:198:ASP:HB2	1.79	0.82
1:B:217:LEU:HD13	1:B:217:LEU:O	1.78	0.82
1:B:316:THR:HG22	1:B:318:ALA:H	1.44	0.82
1:C:210:ARG:NH2	1:D:153:GLU:OE1	2.03	0.82
1:A:275:ILE:HD12	1:A:308:MET:SD	2.20	0.82
1:D:129:LEU:HD22	1:D:130:ARG:N	1.94	0.82
1:F:194:ARG:HH12	1:F:347:ARG:HH12	1.26	0.82
1:B:131:ARG:NH2	1:B:220:GLU:CD	2.32	0.82

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:332:ALA:HB1	1:G:376:ILE:HD11	1.62	0.82
1:E:138:LEU:HD23	1:E:329:PHE:HB3	1.59	0.82
1:G:198:ASP:O	1:G:199:ASP:CG	2.16	0.82
1:A:376:ILE:C	1:A:377:ILE:HD12	1.99	0.81
1:A:129:LEU:HD23	1:A:129:LEU:H	1.45	0.81
1:B:277:LEU:HD23	1:B:277:LEU:H	1.43	0.81
1:C:270:PHE:CE2	1:C:331:MET:HG2	2.14	0.81
1:D:202:MET:HA	1:D:205:SER:OG	1.80	0.81
1:E:132:LEU:HD23	1:E:132:LEU:H	1.43	0.81
1:F:129:LEU:H	1:F:129:LEU:HD12	1.45	0.81
1:F:203:LEU:O	1:F:206:TYR:HB2	1.76	0.81
1:G:138:LEU:HD23	1:G:329:PHE:HB3	1.61	0.81
1:G:158:ASN:ND2	1:G:159:ALA:N	2.29	0.81
1:B:207:ILE:O	1:B:211:LEU:CB	2.28	0.81
1:F:194:ARG:CZ	1:F:347:ARG:NH1	2.44	0.81
1:D:190:VAL:CG1	1:D:211:LEU:CD2	2.59	0.81
1:G:290:ASP:HB3	1:G:292:GLU:HB3	1.63	0.81
1:A:153:GLU:CD	1:F:210:ARG:HH21	1.84	0.81
1:F:287:LEU:HD23	1:F:287:LEU:H	1.46	0.81
1:B:336:PHE:HB2	1:B:367:ALA:HB3	1.63	0.80
1:D:155:VAL:CG1	1:D:374:THR:CB	2.60	0.80
1:D:155:VAL:CG1	1:D:374:THR:OG1	2.29	0.80
1:D:303:PHE:HA	1:D:306:ASN:HB3	1.63	0.80
1:E:211:LEU:HD21	1:E:360:ILE:HD13	1.63	0.80
1:C:207:ILE:HA	1:C:211:LEU:HB3	1.63	0.80
1:E:215:LEU:O	1:E:218:LYS:CB	2.27	0.80
1:E:322:GLY:HA2	1:E:381:PHE:HB2	1.63	0.80
1:F:327:GLY:N	1:F:329:PHE:HE1	1.79	0.80
1:C:366:LEU:C	1:C:366:LEU:HD13	2.01	0.80
1:D:295:TYR:HD1	1:D:299:GLY:HA2	1.46	0.80
1:B:125:ILE:HG12	1:B:127:PRO:HD3	1.64	0.80
1:B:158:ASN:H	1:B:158:ASN:ND2	1.76	0.80
1:C:184:LYS:HD2	1:C:231:ASP:HA	1.64	0.80
1:F:202:MET:CG	1:F:203:LEU:N	2.44	0.80
1:A:266:THR:HG21	1:F:279:PRO:HB3	1.64	0.80
1:C:233:LEU:CD1	1:C:366:LEU:CD1	2.60	0.80
1:G:281:ASP:OD2	1:G:322:GLY:N	2.12	0.80
1:F:204:GLN:C	1:F:206:TYR:N	2.32	0.79
1:G:338:ARG:CG	1:G:338:ARG:NH1	2.30	0.79
1:B:127:PRO:O	1:B:129:LEU:HD22	1.83	0.79
1:C:131:ARG:NH2	1:C:220:GLU:OE1	2.14	0.79

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:349:ASP:OD1	1:D:350:ARG:N	2.16	0.79
1:F:195:GLN:O	1:F:198:ASP:N	2.12	0.79
1:A:195:GLN:O	1:A:199:ASP:CG	2.20	0.79
1:B:159:ALA:HB1	1:B:160:PRO:HD2	1.62	0.79
1:F:244:ASP:OD2	1:F:247:LEU:CD2	2.30	0.79
1:A:123:GLY:O	1:A:124:ILE:HG23	1.81	0.79
1:C:210:ARG:HH22	1:D:153:GLU:CD	1.83	0.79
1:C:194:ARG:HG2	1:C:195:GLN:N	1.97	0.79
1:E:215:LEU:O	1:E:218:LYS:N	2.16	0.79
1:E:342:THR:O	1:E:362:CYS:HA	1.81	0.79
1:D:159:ALA:HB1	1:D:160:PRO:HD2	1.65	0.79
1:B:194:ARG:HH22	1:B:347:ARG:NH2	1.81	0.79
1:D:247:LEU:O	1:D:247:LEU:CD2	2.30	0.79
1:F:288:LEU:HD23	1:F:289:LYS:N	1.98	0.79
1:A:287:LEU:CA	1:A:288:LEU:HD23	2.13	0.78
1:C:225:ASN:HB3	1:C:237:ASN:ND2	1.94	0.78
1:F:282:TRP:HZ3	1:F:308:MET:CE	1.96	0.78
1:B:358:LEU:N	1:B:358:LEU:HD12	1.98	0.78
1:F:253:THR:O	1:F:254:ARG:C	2.21	0.78
1:F:203:LEU:O	1:F:206:TYR:N	2.17	0.78
1:G:156:PHE:CE2	1:G:158:ASN:HB3	2.19	0.78
1:C:201:PRO:O	1:C:204:GLN:CB	2.30	0.78
1:G:366:LEU:C	1:G:366:LEU:HD12	2.03	0.78
1:G:155:VAL:CG1	1:G:374:THR:HG21	2.14	0.78
1:C:343:VAL:HG12	1:C:362:CYS:HB2	1.66	0.78
1:A:190:VAL:HG12	1:A:211:LEU:HD21	1.64	0.78
1:B:193:SER:O	1:B:196:VAL:HG22	1.81	0.78
1:G:224:LEU:HD21	1:G:319:GLN:HB2	1.66	0.78
1:C:197:MET:SD	1:C:358:LEU:HD11	2.23	0.78
1:D:194:ARG:CG	1:D:195:GLN:H	1.94	0.78
1:E:210:ARG:NH2	1:F:153:GLU:CD	2.37	0.77
1:G:156:PHE:CD2	1:G:158:ASN:HB3	2.18	0.77
1:A:269:GLU:HB3	1:F:217:LEU:CD2	2.11	0.77
1:F:324:PHE:CD2	1:F:381:PHE:CE1	2.61	0.77
1:G:138:LEU:CD2	1:G:329:PHE:HB3	2.14	0.77
1:E:190:VAL:N	1:E:360:ILE:HD11	1.98	0.77
1:B:155:VAL:HG11	1:B:374:THR:HB	1.64	0.77
1:E:194:ARG:HG3	1:E:358:LEU:HD11	1.66	0.77
1:F:210:ARG:HG2	1:F:210:ARG:NH1	1.97	0.77
1:A:129:LEU:HD23	1:A:129:LEU:N	2.00	0.77
1:C:346:SER:O	1:C:359:THR:CG2	2.26	0.77

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:129:LEU:HD13	1:D:131:ARG:N	2.00	0.77
1:D:131:ARG:HG2	1:D:132:LEU:N	2.00	0.77
1:D:356:ASN:CG	1:E:178:LYS:HZ1	1.87	0.77
1:G:366:LEU:HD12	1:G:367:ALA:N	2.00	0.76
1:C:202:MET:O	1:C:203:LEU:C	2.23	0.76
1:A:155:VAL:HG11	1:A:374:THR:OG1	1.85	0.76
1:E:207:ILE:HA	1:E:211:LEU:HB2	1.67	0.76
1:E:125:ILE:HD13	1:E:127:PRO:HD3	1.66	0.76
1:F:207:ILE:HD12	1:F:208:ASN:N	2.00	0.76
1:D:158:ASN:ND2	1:D:158:ASN:H	1.82	0.76
1:C:213:TYR:CE2	1:C:217:LEU:CD2	2.68	0.76
1:A:137:LEU:HD22	1:A:329:PHE:HB2	1.68	0.76
1:D:141:GLY:O	1:D:142:ARG:HG2	1.85	0.76
1:E:203:LEU:O	1:E:204:GLN:C	2.23	0.76
1:C:186:ILE:HD13	1:C:222:GLN:HG3	1.66	0.76
1:C:227:ASP:O	1:C:232:ASN:HB2	1.86	0.76
1:A:146:ASN:HD22	1:G:145:SER:HB2	1.50	0.75
1:F:253:THR:CG2	1:F:256:ASP:OD1	2.34	0.75
1:G:183:VAL:HA	1:G:367:ALA:HB2	1.67	0.75
1:D:127:PRO:CG	1:D:212:MET:HE2	2.09	0.75
1:E:296:ILE:HG23	1:E:297:PHE:N	2.02	0.75
1:G:327:GLY:N	1:G:329:PHE:HE2	1.83	0.75
1:B:126:MET:N	1:B:126:MET:SD	2.60	0.75
1:E:125:ILE:HD11	1:E:127:PRO:HD3	1.66	0.75
1:G:145:SER:O	1:G:338:ARG:HD3	1.85	0.75
1:E:189:TRP:HE3	1:E:189:TRP:O	1.70	0.75
1:B:296:ILE:HD13	1:B:296:ILE:N	1.98	0.75
1:A:202:MET:HB2	1:B:336:PHE:HE2	1.52	0.74
1:B:129:LEU:HD23	1:B:129:LEU:C	2.07	0.74
1:D:191:GLN:NE2	1:E:176:PHE:CE2	2.53	0.74
1:F:226:GLY:H	1:F:235:GLY:HA3	1.51	0.74
1:A:176:PHE:HE1	1:F:190:VAL:HG13	1.51	0.74
1:B:158:ASN:HB2	1:B:172:SER:CA	2.16	0.74
1:A:121:ILE:N	1:A:121:ILE:HD12	2.02	0.74
1:B:192:ALA:O	1:B:357:MET:HB2	1.87	0.74
1:C:194:ARG:NH1	1:C:347:ARG:NH2	2.34	0.74
1:F:239:VAL:HG12	1:F:373:PRO:HB3	1.70	0.74
1:G:196:VAL:HG22	1:G:202:MET:CE	2.17	0.74
1:G:199:ASP:C	1:G:201:PRO:CD	2.56	0.74
1:A:287:LEU:O	1:A:287:LEU:CD1	2.30	0.74
1:B:130:ARG:NH2	1:C:330:ASP:OD2	2.20	0.74

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:192:ALA:O	1:C:357:MET:HB3	1.87	0.74
1:G:285:ILE:HA	1:G:288:LEU:HG	1.70	0.74
1:C:187:ALA:CB	1:C:363:GLU:HA	2.15	0.74
1:C:130:ARG:CB	1:D:271:SER:CB	2.66	0.74
1:E:316:THR:HG22	1:E:318:ALA:H	1.53	0.74
1:G:327:GLY:O	1:G:329:PHE:HD2	1.71	0.74
1:B:210:ARG:HH22	1:C:153:GLU:HG3	1.52	0.74
1:E:156:PHE:HD2	1:E:158:ASN:N	1.86	0.74
1:E:216:ALA:C	1:E:218:LYS:N	2.36	0.74
1:C:146:ASN:ND2	1:C:365:ARG:NH2	2.36	0.73
1:G:193:SER:O	1:G:196:VAL:HB	1.87	0.73
1:B:201:PRO:CB	1:B:204:GLN:HB2	2.18	0.73
1:E:123:GLY:C	1:E:124:ILE:HG13	2.07	0.73
1:F:203:LEU:HD22	1:F:204:GLN:CA	2.19	0.73
1:B:258:ILE:H	1:B:258:ILE:HD12	1.54	0.73
1:E:153:GLU:N	1:E:371:TYR:O	2.21	0.73
1:F:158:ASN:ND2	1:F:158:ASN:H	1.83	0.73
1:F:342:THR:O	1:F:362:CYS:HA	1.88	0.73
1:G:203:LEU:O	1:G:205:SER:N	2.21	0.73
1:A:195:GLN:NE2	1:B:149:GLU:OE2	2.21	0.73
1:B:276:VAL:C	1:B:277:LEU:HD23	2.07	0.73
1:G:327:GLY:O	1:G:329:PHE:CE2	2.42	0.73
1:A:284:ASN:O	1:A:288:LEU:HD22	1.88	0.73
1:C:194:ARG:O	1:C:196:VAL:CG2	2.36	0.73
1:B:203:LEU:O	1:B:207:ILE:HG13	1.88	0.73
1:F:200:ALA:O	1:F:201:PRO:C	2.26	0.73
1:G:200:ALA:O	1:G:204:GLN:CB	2.37	0.73
1:E:304:THR:HG21	1:F:309:TRP:O	1.88	0.73
1:F:343:VAL:HG12	1:F:362:CYS:CB	2.11	0.73
1:A:197:MET:SD	1:A:197:MET:C	2.67	0.73
1:B:295:TYR:HB3	1:B:298:GLY:O	1.89	0.73
1:B:296:ILE:O	1:B:298:GLY:N	2.22	0.73
1:C:265:VAL:HG22	1:C:377:ILE:HD13	1.71	0.73
1:A:155:VAL:HG13	1:A:374:THR:HG21	1.71	0.72
1:A:349:ASP:OD1	1:A:350:ARG:HG3	1.89	0.72
1:C:357:MET:CE	1:D:178:LYS:HG2	2.19	0.72
1:E:207:ILE:HG22	1:E:211:LEU:HD22	1.68	0.72
1:C:347:ARG:C	1:C:349:ASP:H	1.88	0.72
1:A:207:ILE:HG13	1:A:211:LEU:HD12	1.71	0.72
1:F:358:LEU:HD23	1:F:359:THR:N	2.04	0.72
1:D:247:LEU:CD2	1:D:260:HIS:HB3	2.20	0.72

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:349:ASP:OD1	1:D:350:ARG:HG3	1.89	0.72
1:E:125:ILE:HG13	1:E:212:MET:HB3	1.70	0.72
1:E:203:LEU:C	1:E:205:SER:N	2.40	0.72
1:G:278:ASN:OD1	1:G:279:PRO:CD	2.30	0.72
1:D:193:SER:O	1:D:194:ARG:HB3	1.89	0.72
1:E:130:ARG:HB3	1:F:271:SER:OG	1.89	0.72
1:C:210:ARG:NH2	1:D:153:GLU:OE2	2.22	0.72
1:A:207:ILE:H	1:A:207:ILE:HD12	1.55	0.72
1:D:156:PHE:HD2	1:D:158:ASN:N	1.88	0.72
1:D:132:LEU:H	1:D:132:LEU:CD2	2.02	0.72
1:B:296:ILE:C	1:B:298:GLY:H	1.91	0.71
1:E:159:ALA:HB1	1:E:160:PRO:HD2	1.70	0.71
1:F:198:ASP:C	1:F:200:ALA:N	2.38	0.71
1:C:195:GLN:O	1:C:196:VAL:C	2.28	0.71
1:G:199:ASP:O	1:G:202:MET:N	2.23	0.71
1:G:200:ALA:N	1:G:201:PRO:HD2	2.04	0.71
1:B:250:THR:CB	1:B:251:GLY:CA	2.49	0.71
1:E:127:PRO:O	1:E:129:LEU:HD22	1.90	0.71
1:G:132:LEU:HB2	1:G:136:ASP:CG	2.11	0.71
1:G:303:PHE:CD2	1:G:304:THR:N	2.57	0.71
1:B:156:PHE:HD2	1:B:158:ASN:N	1.88	0.71
1:E:125:ILE:HG12	1:E:126:MET:N	2.05	0.71
1:E:333:SER:HB2	1:E:369:ALA:O	1.91	0.71
1:G:290:ASP:C	1:G:292:GLU:H	1.92	0.71
1:E:137:LEU:CD2	1:E:329:PHE:HB2	2.20	0.71
1:F:282:TRP:CZ3	1:F:308:MET:CE	2.74	0.71
1:A:153:GLU:CD	1:A:372:ARG:HH21	1.93	0.71
1:A:195:GLN:HG3	1:A:196:VAL:N	2.06	0.71
1:A:366:LEU:HD12	1:A:366:LEU:C	2.11	0.71
1:B:134:ILE:HD13	1:B:220:GLU:HG3	1.72	0.71
1:B:195:GLN:O	1:B:196:VAL:C	2.29	0.71
1:E:123:GLY:O	1:E:124:ILE:HG13	1.91	0.71
1:F:206:TYR:O	1:F:208:ASN:N	2.24	0.71
1:B:158:ASN:ND2	1:B:172:SER:HB2	2.04	0.71
1:E:158:ASN:H	1:E:158:ASN:ND2	1.86	0.71
1:G:297:PHE:H	1:G:297:PHE:HD2	1.38	0.71
1:B:131:ARG:HH21	1:B:220:GLU:CD	1.94	0.71
1:C:146:ASN:HD21	1:C:365:ARG:NH2	1.89	0.71
1:C:195:GLN:O	1:C:198:ASP:N	2.22	0.71
1:F:192:ALA:O	1:F:357:MET:SD	2.49	0.71
1:C:203:LEU:O	1:C:206:TYR:HB3	1.89	0.71

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:282:TRP:CZ3	1:F:308:MET:HE3	2.26	0.71
1:G:203:LEU:C	1:G:205:SER:H	1.93	0.71
1:D:347:ARG:HB2	1:D:358:LEU:HG	1.71	0.70
1:E:142:ARG:HA	1:E:337:ASP:H	1.54	0.70
1:F:206:TYR:HD2	1:F:207:ILE:N	1.89	0.70
1:A:273:SER:OG	1:A:330:ASP:HB2	1.91	0.70
1:G:278:ASN:O	1:G:280:ARG:N	2.24	0.70
1:D:307:ILE:HD12	1:D:307:ILE:O	1.92	0.70
1:B:211:LEU:O	1:B:211:LEU:CD1	2.24	0.70
1:E:126:MET:CE	1:E:129:LEU:HD21	2.21	0.70
1:E:194:ARG:CA	1:E:358:LEU:CD1	2.67	0.70
1:F:329:PHE:HD1	1:F:329:PHE:H	0.82	0.70
1:B:249:ALA:CB	1:B:252:ASP:OD2	2.40	0.70
1:C:196:VAL:HG12	1:C:203:LEU:HD11	0.72	0.70
1:F:327:GLY:N	1:F:329:PHE:CE1	2.59	0.70
1:G:196:VAL:HG22	1:G:202:MET:HE2	1.73	0.70
1:G:200:ALA:O	1:G:204:GLN:HB3	1.92	0.70
1:A:207:ILE:HD12	1:A:207:ILE:N	2.05	0.70
1:B:288:LEU:O	1:B:296:ILE:HD13	1.91	0.70
1:A:194:ARG:HB2	1:A:358:LEU:HD23	1.71	0.70
1:D:122:PRO:CG	1:D:343:VAL:HG23	2.21	0.70
1:G:185:THR:OG1	1:G:365:ARG:HG2	1.90	0.70
1:G:296:ILE:HG22	1:G:297:PHE:H	1.54	0.70
1:D:129:LEU:HD13	1:D:130:ARG:N	2.07	0.70
1:A:125:ILE:HG21	1:A:204:GLN:HE21	1.55	0.69
1:A:194:ARG:O	1:A:198:ASP:CB	2.39	0.69
1:F:275:ILE:HD12	1:F:275:ILE:N	2.06	0.69
1:C:194:ARG:O	1:C:195:GLN:C	2.30	0.69
1:F:159:ALA:HB1	1:F:160:PRO:HD2	1.73	0.69
1:C:292:GLU:HG2	1:C:294:ARG:NE	2.06	0.69
1:F:156:PHE:HD2	1:F:158:ASN:N	1.89	0.69
1:F:329:PHE:N	1:F:329:PHE:CD1	2.35	0.69
1:A:127:PRO:HB3	1:A:212:MET:CB	2.20	0.69
1:B:134:ILE:H	1:B:134:ILE:HD12	1.58	0.69
1:D:209:ASN:O	1:D:213:TYR:CB	2.40	0.69
1:G:296:ILE:CG2	1:G:297:PHE:N	2.48	0.69
1:G:155:VAL:CG1	1:G:374:THR:CG2	2.70	0.69
1:B:155:VAL:CG1	1:B:374:THR:OG1	2.41	0.69
1:B:200:ALA:HB1	1:B:201:PRO:CD	2.23	0.69
1:D:356:ASN:OD1	1:E:178:LYS:NZ	2.19	0.69
1:E:382:SER:O	1:E:383:SER:HB2	1.92	0.69

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:156:PHE:O	1:B:158:ASN:ND2	2.25	0.69
1:E:258:ILE:HD11	1:E:381:PHE:HZ	1.58	0.69
1:C:323:THR:HA	1:C:380:THR:HG22	1.75	0.68
1:G:297:PHE:CG	1:G:298:GLY:N	2.61	0.68
1:A:125:ILE:N	1:A:125:ILE:HD12	2.08	0.68
1:D:148:LEU:HD12	1:D:181:ALA:HB3	1.74	0.68
1:B:125:ILE:HG12	1:B:127:PRO:CD	2.22	0.68
1:B:162:ASP:O	1:B:172:SER:C	2.30	0.68
1:D:247:LEU:C	1:D:247:LEU:CD2	2.60	0.68
1:D:333:SER:HB3	1:D:369:ALA:O	1.92	0.68
1:E:184:LYS:HD2	1:E:231:ASP:HA	1.76	0.68
1:E:203:LEU:O	1:E:205:SER:N	2.27	0.68
1:G:198:ASP:O	1:G:199:ASP:CB	2.40	0.68
1:B:212:MET:O	1:B:213:TYR:C	2.28	0.68
1:C:155:VAL:HG23	1:C:174:ILE:HG22	1.75	0.68
1:C:213:TYR:CZ	1:C:217:LEU:CD1	2.59	0.68
1:F:132:LEU:CD2	1:F:136:ASP:HB2	2.24	0.68
1:A:307:ILE:C	1:A:307:ILE:HD12	2.14	0.68
1:B:275:ILE:HD11	1:B:313:VAL:HG22	1.75	0.68
1:F:202:MET:HG3	1:F:203:LEU:N	2.08	0.68
1:B:296:ILE:C	1:B:298:GLY:N	2.45	0.68
1:B:341:ALA:HA	1:B:363:GLU:O	1.94	0.68
1:C:130:ARG:CB	1:D:271:SER:HB2	2.24	0.68
1:F:142:ARG:NH2	1:F:340:ASP:OD1	2.27	0.68
1:C:153:GLU:OE2	1:C:372:ARG:NH2	2.27	0.68
1:E:220:GLU:HG2	1:E:316:THR:HG21	1.77	0.67
1:A:300:PRO:HA	1:A:303:PHE:CB	2.24	0.67
1:B:201:PRO:C	1:B:204:GLN:N	2.33	0.67
1:B:275:ILE:HG22	1:B:326:VAL:HG22	1.76	0.67
1:G:158:ASN:ND2	1:G:159:ALA:H	1.92	0.67
1:B:131:ARG:NH2	1:B:220:GLU:OE2	2.27	0.67
1:C:131:ARG:HH22	1:C:220:GLU:CD	1.97	0.67
1:C:194:ARG:C	1:C:196:VAL:N	2.41	0.67
1:C:197:MET:SD	1:C:197:MET:N	2.65	0.67
1:G:187:ALA:HB2	1:G:363:GLU:HA	1.76	0.67
1:A:194:ARG:O	1:A:198:ASP:OD2	2.12	0.67
1:C:188:HIS:O	1:C:361:LEU:HA	1.95	0.67
1:F:198:ASP:C	1:F:198:ASP:OD2	2.30	0.67
1:C:192:ALA:HB1	1:D:151:VAL:HG11	1.76	0.67
1:E:219:GLU:OE2	1:E:364:GLU:OE1	2.11	0.67
1:F:282:TRP:HZ3	1:F:308:MET:HE3	1.57	0.67

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:158:ASN:HD22	1:G:159:ALA:H	1.41	0.67
1:E:194:ARG:NH1	1:E:347:ARG:NH2	2.43	0.67
1:E:224:LEU:HD11	1:E:319:GLN:OE1	1.94	0.67
1:F:194:ARG:HB2	1:F:356:ASN:OD1	1.95	0.67
1:C:207:ILE:O	1:C:212:MET:HB2	1.95	0.67
1:C:227:ASP:O	1:C:229:THR:N	2.28	0.67
1:C:361:LEU:HD12	1:C:361:LEU:O	1.95	0.67
1:F:198:ASP:C	1:F:200:ALA:H	1.95	0.67
1:A:280:ARG:HG3	1:A:281:ASP:N	2.07	0.67
1:B:208:ASN:O	1:B:212:MET:HG2	1.95	0.67
1:C:192:ALA:CB	1:D:151:VAL:HG11	2.25	0.67
1:C:244:ASP:H	1:C:264:GLN:HE22	1.42	0.67
1:G:199:ASP:O	1:G:202:MET:HB3	1.94	0.67
1:B:188:HIS:CD2	1:B:214:GLY:HA3	2.30	0.67
1:C:174:ILE:H	1:C:174:ILE:HD13	1.60	0.67
1:D:295:TYR:CD1	1:D:299:GLY:HA2	2.28	0.67
1:G:329:PHE:CD2	1:G:329:PHE:N	2.48	0.67
1:A:345:VAL:HG22	1:A:360:ILE:HA	1.76	0.67
1:D:174:ILE:HG12	1:D:176:PHE:HE2	1.59	0.67
1:D:209:ASN:O	1:D:213:TYR:HB2	1.95	0.67
1:G:200:ALA:HB3	1:G:201:PRO:HD3	1.76	0.66
1:A:195:GLN:CG	1:A:196:VAL:H	2.06	0.66
1:B:125:ILE:C	1:B:127:PRO:HD3	2.14	0.66
1:C:129:LEU:H	1:C:129:LEU:HD22	1.60	0.66
1:D:301:GLN:O	1:D:306:ASN:HB2	1.95	0.66
1:D:339:MET:HB3	1:D:365:ARG:HB2	1.77	0.66
1:E:188:HIS:NE2	1:E:190:VAL:HG13	2.11	0.66
1:F:249:ALA:O	1:F:250:THR:C	2.32	0.66
1:B:199:ASP:OD2	1:B:199:ASP:C	2.34	0.66
1:F:206:TYR:CD2	1:F:207:ILE:N	2.64	0.66
1:B:158:ASN:CB	1:B:172:SER:HA	2.18	0.66
1:C:233:LEU:HD12	1:C:366:LEU:HD11	1.76	0.66
1:C:347:ARG:C	1:C:349:ASP:N	2.43	0.66
1:D:174:ILE:HG12	1:D:176:PHE:CE2	2.30	0.66
1:E:227:ASP:CB	1:E:229:THR:CG2	2.56	0.66
1:A:203:LEU:O	1:A:204:GLN:C	2.32	0.66
1:B:125:ILE:N	1:B:208:ASN:HB3	2.11	0.66
1:C:307:ILE:O	1:C:307:ILE:HG13	1.95	0.66
1:D:184:LYS:HG3	1:D:233:LEU:HD23	1.77	0.66
1:D:187:ALA:HB2	1:D:363:GLU:HB3	1.76	0.66
1:D:270:PHE:HE2	1:D:331:MET:HB3	1.61	0.66

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:227:ASP:OD1	1:G:227:ASP:C	2.34	0.66
1:G:270:PHE:CE1	1:G:372:ARG:CZ	2.78	0.66
1:B:125:ILE:HG12	1:B:127:PRO:CG	2.25	0.66
1:A:191:GLN:H	1:A:191:GLN:HE21	1.41	0.66
1:F:370:HIS:HB3	1:F:373:PRO:HG3	1.78	0.66
1:C:198:ASP:O	1:C:199:ASP:CG	2.34	0.66
1:D:155:VAL:HG11	1:D:374:THR:CB	2.26	0.66
1:E:236:LEU:HD23	1:E:370:HIS:HE1	1.61	0.66
1:F:132:LEU:HD22	1:F:136:ASP:HB2	1.76	0.66
1:A:350:ARG:O	1:A:351:ASP:CG	2.35	0.65
1:B:126:MET:HE3	1:B:212:MET:HG3	1.77	0.65
1:B:199:ASP:O	1:B:200:ALA:HB2	1.95	0.65
1:E:296:ILE:HG23	1:E:297:PHE:H	1.61	0.65
1:F:141:GLY:O	1:F:336:PHE:HA	1.95	0.65
1:C:203:LEU:O	1:C:204:GLN:C	2.33	0.65
1:C:233:LEU:HD11	1:C:366:LEU:HD12	1.78	0.65
1:F:275:ILE:HG23	1:F:326:VAL:HG12	1.78	0.65
1:B:126:MET:N	1:B:127:PRO:HD3	2.11	0.65
1:C:194:ARG:C	1:C:196:VAL:H	1.99	0.65
1:B:194:ARG:HD2	1:B:357:MET:HA	1.78	0.65
1:G:345:VAL:HG11	1:G:358:LEU:HD21	1.78	0.65
1:C:368:LEU:HD21	1:C:370:HIS:NE2	2.12	0.65
1:F:198:ASP:O	1:F:200:ALA:N	2.29	0.65
1:G:279:PRO:O	1:G:282:TRP:HB3	1.96	0.65
1:B:215:LEU:CD2	1:B:215:LEU:O	2.30	0.65
1:C:200:ALA:C	1:C:202:MET:H	2.00	0.65
1:D:125:ILE:HD12	1:D:208:ASN:OD1	1.91	0.65
1:D:127:PRO:CB	1:D:212:MET:HB3	2.26	0.65
1:D:304:THR:OG1	1:D:315:PRO:HG3	1.97	0.65
1:E:212:MET:O	1:E:215:LEU:N	2.30	0.65
1:F:258:ILE:HD11	1:F:275:ILE:HG21	1.77	0.65
1:G:290:ASP:C	1:G:292:GLU:N	2.47	0.65
1:B:194:ARG:HA	1:B:358:LEU:HD11	1.77	0.65
1:D:341:ALA:HA	1:D:363:GLU:O	1.96	0.65
1:E:200:ALA:O	1:E:202:MET:N	2.30	0.65
1:G:194:ARG:C	1:G:197:MET:H	2.00	0.65
1:C:135:ARG:NH2	1:C:337:ASP:OD2	2.29	0.65
1:F:197:MET:SD	1:F:197:MET:C	2.74	0.65
1:G:261:ALA:O	1:G:265:VAL:HG23	1.97	0.65
1:D:129:LEU:HD13	1:D:131:ARG:H	1.61	0.64
1:D:129:LEU:CD1	1:D:131:ARG:H	2.10	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:277:LEU:O	1:D:315:PRO:HA	1.98	0.64
1:D:224:LEU:HD12	1:D:225:ASN:ND2	2.12	0.64
1:G:265:VAL:HG22	1:G:377:ILE:HD13	1.78	0.64
1:A:123:GLY:C	1:A:124:ILE:HG12	2.15	0.64
1:B:155:VAL:HG12	1:B:374:THR:OG1	1.98	0.64
1:C:224:LEU:CD1	1:C:225:ASN:CG	2.66	0.64
1:C:275:ILE:HD12	1:C:275:ILE:N	2.13	0.64
1:D:162:ASP:C	1:D:173:ASP:H	2.01	0.64
1:E:200:ALA:O	1:E:201:PRO:C	2.33	0.64
1:F:200:ALA:CB	1:F:201:PRO:CD	2.57	0.64
1:F:273:SER:O	1:F:312:PRO:HD2	1.98	0.64
1:F:361:LEU:HD13	1:F:361:LEU:C	2.17	0.64
1:B:146:ASN:HD22	1:B:146:ASN:N	1.95	0.64
1:G:159:ALA:HB1	1:G:160:PRO:HD2	1.80	0.64
1:G:345:VAL:HG12	1:G:358:LEU:HD11	1.80	0.64
1:E:258:ILE:HD11	1:E:381:PHE:CZ	2.33	0.64
1:B:216:ALA:O	1:B:217:LEU:C	2.34	0.64
1:F:148:LEU:O	1:F:180:THR:HG23	1.97	0.64
1:C:189:TRP:HA	1:C:360:ILE:O	1.97	0.64
1:C:268:SER:O	1:C:372:ARG:NH1	2.27	0.64
1:E:157:THR:HG22	1:E:267:GLU:HG2	1.80	0.64
1:E:289:LYS:HD3	1:E:293:GLY:HA2	1.77	0.64
1:F:211:LEU:O	1:F:214:GLY:N	2.28	0.64
1:A:275:ILE:HG23	1:A:326:VAL:HG22	1.80	0.64
1:D:193:SER:O	1:D:194:ARG:CB	2.46	0.64
1:D:265:VAL:HG22	1:D:377:ILE:HD13	1.80	0.64
1:D:270:PHE:CE2	1:D:331:MET:HB3	2.33	0.64
1:E:194:ARG:HD2	1:E:347:ARG:CZ	2.28	0.64
1:E:254:ARG:HG2	1:E:381:PHE:HE2	1.63	0.64
1:F:134:ILE:O	1:F:137:LEU:N	2.24	0.64
1:F:327:GLY:C	1:F:329:PHE:CE1	2.72	0.64
1:G:244:ASP:OD2	1:G:246:SER:HB3	1.98	0.64
1:F:224:LEU:HD13	1:F:237:ASN:ND2	2.13	0.63
1:C:195:GLN:NE2	1:C:198:ASP:CB	2.46	0.63
1:E:226:GLY:H	1:E:235:GLY:HA3	1.63	0.63
1:C:341:ALA:HB1	1:C:362:CYS:SG	2.39	0.63
1:F:131:ARG:NH2	1:F:220:GLU:CD	2.51	0.63
1:G:155:VAL:HG22	1:G:156:PHE:N	2.12	0.63
1:B:215:LEU:HD22	1:B:216:ALA:N	2.12	0.63
1:D:129:LEU:HD11	1:D:131:ARG:HD3	1.79	0.63
1:E:229:THR:H	1:E:232:ASN:HB2	1.64	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:301:GLN:HG3	1:F:302:ALA:N	2.13	0.63
1:C:196:VAL:CG1	1:C:203:LEU:CG	2.72	0.63
1:E:127:PRO:HG2	1:E:129:LEU:HD13	1.78	0.63
1:E:216:ALA:C	1:E:218:LYS:H	1.99	0.63
1:B:289:LYS:HD2	1:B:293:GLY:HA2	1.80	0.63
1:C:278:ASN:ND2	1:C:280:ARG:HB3	2.14	0.63
1:C:287:LEU:CD2	1:C:300:PRO:HA	2.29	0.63
1:E:254:ARG:CG	1:E:381:PHE:HE2	2.10	0.63
1:G:134:ILE:HG12	1:G:220:GLU:HG3	1.79	0.63
1:A:237:ASN:HB3	1:A:378:LYS:HD3	1.79	0.63
1:E:244:ASP:OD1	1:E:247:LEU:HG	1.98	0.63
1:F:202:MET:O	1:F:205:SER:HB3	1.97	0.63
1:C:194:ARG:C	1:C:196:VAL:HG23	2.18	0.63
1:E:296:ILE:CG2	1:E:297:PHE:N	2.61	0.63
1:G:199:ASP:CB	1:G:202:MET:HB3	2.29	0.63
1:B:201:PRO:HB3	1:B:204:GLN:HB2	1.79	0.63
1:G:275:ILE:HG23	1:G:326:VAL:HG22	1.79	0.63
1:A:186:ILE:HD12	1:A:186:ILE:N	2.14	0.62
1:D:273:SER:HB3	1:D:328:GLY:HA2	1.81	0.62
1:D:300:PRO:HG2	1:E:301:GLN:HE21	1.64	0.62
1:D:307:ILE:CG2	1:D:312:PRO:HA	2.29	0.62
1:B:195:GLN:HA	1:B:197:MET:HG2	1.80	0.62
1:D:279:PRO:HG3	1:D:315:PRO:HB2	1.81	0.62
1:D:342:THR:O	1:D:362:CYS:HA	1.99	0.62
1:G:135:ARG:NH2	1:G:219:GLU:OE2	2.33	0.62
1:G:145:SER:O	1:G:338:ARG:CD	2.47	0.62
1:G:157:THR:O	1:G:158:ASN:ND2	2.32	0.62
1:A:156:PHE:C	1:A:158:ASN:H	2.03	0.62
1:A:158:ASN:ND2	1:A:172:SER:HA	2.14	0.62
1:A:280:ARG:CG	1:A:281:ASP:N	2.62	0.62
1:B:148:LEU:HD23	1:B:148:LEU:O	1.99	0.62
1:C:287:LEU:CD2	1:C:300:PRO:CA	2.78	0.62
1:F:211:LEU:HD23	1:F:211:LEU:C	2.20	0.62
1:F:345:VAL:CG1	1:F:358:LEU:HD11	2.29	0.62
1:B:201:PRO:C	1:B:204:GLN:HB2	2.20	0.62
1:C:194:ARG:CZ	1:C:347:ARG:NH2	2.62	0.62
1:D:196:VAL:O	1:D:199:ASP:OD1	2.18	0.62
1:G:129:LEU:O	1:G:129:LEU:HD23	1.98	0.62
1:A:349:ASP:OD1	1:A:350:ARG:N	2.33	0.62
1:D:184:LYS:HZ3	1:D:184:LYS:HA	1.65	0.62
1:D:282:TRP:NE1	1:D:304:THR:HA	2.11	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:189:TRP:O	1:E:189:TRP:CE3	2.52	0.62
1:E:268:SER:HB2	1:E:372:ARG:HD3	1.82	0.62
1:F:308:MET:HG2	1:F:309:TRP:CE3	2.35	0.62
1:G:129:LEU:C	1:G:131:ARG:H	2.02	0.62
1:A:156:PHE:O	1:A:158:ASN:ND2	2.33	0.62
1:F:150:TYR:CE1	1:F:179:GLN:HB2	2.35	0.62
1:F:202:MET:SD	1:F:203:LEU:HA	2.40	0.62
1:D:122:PRO:CG	1:D:343:VAL:O	2.39	0.61
1:E:174:ILE:H	1:E:174:ILE:CD1	2.12	0.61
1:G:257:ILE:HA	1:G:260:HIS:HD2	1.65	0.61
1:B:138:LEU:HD23	1:B:329:PHE:HB3	1.80	0.61
1:D:121:ILE:HD13	1:D:121:ILE:C	2.20	0.61
1:E:125:ILE:HG13	1:E:212:MET:CB	2.30	0.61
1:F:203:LEU:O	1:F:206:TYR:CA	2.47	0.61
1:A:134:ILE:HD13	1:A:314:VAL:HG11	1.83	0.61
1:A:240:ALA:HB1	1:A:376:ILE:HG22	1.82	0.61
1:D:303:PHE:N	1:D:303:PHE:CD1	2.67	0.61
1:E:126:MET:HE3	1:E:129:LEU:HD21	1.82	0.61
1:E:233:LEU:HD13	1:E:366:LEU:CD1	2.25	0.61
1:F:194:ARG:NH2	1:G:363:GLU:OE1	2.33	0.61
1:A:207:ILE:H	1:A:207:ILE:CD1	2.12	0.61
1:B:284:ASN:O	1:B:288:LEU:HB2	2.00	0.61
1:C:357:MET:CE	1:D:178:LYS:CG	2.78	0.61
1:D:130:ARG:CZ	1:D:131:ARG:CB	2.79	0.61
1:D:191:GLN:OE1	1:D:191:GLN:N	2.30	0.61
1:D:194:ARG:O	1:D:197:MET:N	2.27	0.61
1:E:296:ILE:HG23	1:E:297:PHE:CD1	2.36	0.61
1:A:332:ALA:O	1:A:371:TYR:HB2	2.00	0.61
1:B:258:ILE:HD12	1:B:258:ILE:N	2.16	0.61
1:D:249:ALA:C	1:D:252:ASP:OD2	2.38	0.61
1:F:177:SER:HB3	1:F:179:GLN:HE21	1.66	0.61
1:F:206:TYR:C	1:F:208:ASN:N	2.52	0.61
1:G:199:ASP:CA	1:G:201:PRO:HD2	2.30	0.61
1:B:173:ASP:OD1	1:B:174:ILE:HD13	2.00	0.61
1:C:194:ARG:O	1:C:196:VAL:CA	2.48	0.61
1:C:213:TYR:CD2	1:C:217:LEU:HD11	2.36	0.61
1:C:277:LEU:O	1:C:315:PRO:HA	2.00	0.61
1:F:210:ARG:O	1:F:210:ARG:HD3	2.00	0.61
1:E:360:ILE:HD12	1:E:360:ILE:O	2.00	0.61
1:F:195:GLN:OE1	1:F:195:GLN:HA	2.01	0.61
1:F:210:ARG:HD3	1:F:210:ARG:C	2.21	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:224:LEU:HD13	1:F:237:ASN:HD21	1.65	0.61
1:G:155:VAL:HG13	1:G:374:THR:HG21	1.82	0.61
1:B:184:LYS:HD2	1:B:231:ASP:HA	1.82	0.61
1:B:209:ASN:O	1:C:331:MET:HE2	2.01	0.61
1:E:134:ILE:H	1:E:134:ILE:HD12	1.64	0.61
1:E:258:ILE:H	1:E:258:ILE:HD12	1.66	0.61
1:G:194:ARG:O	1:G:197:MET:N	2.34	0.61
1:A:191:GLN:OE1	1:A:350:ARG:NH2	2.33	0.61
1:D:275:ILE:HG22	1:D:277:LEU:HD23	1.82	0.61
1:E:207:ILE:HG22	1:E:211:LEU:CD2	2.31	0.61
1:G:158:ASN:ND2	1:G:159:ALA:O	2.34	0.61
1:C:296:ILE:HG23	1:C:297:PHE:CD2	2.36	0.61
1:D:295:TYR:HE1	1:D:300:PRO:HD3	1.66	0.61
1:D:307:ILE:HG21	1:D:312:PRO:HA	1.81	0.61
1:G:368:LEU:H	1:G:368:LEU:HD23	1.66	0.61
1:B:360:ILE:HG22	1:B:361:LEU:N	2.16	0.60
1:F:327:GLY:CA	1:F:329:PHE:HE1	2.14	0.60
1:F:344:GLU:HB2	1:F:361:LEU:HD11	1.82	0.60
1:C:343:VAL:HG12	1:C:362:CYS:CB	2.31	0.60
1:E:278:ASN:HB3	1:E:281:ASP:OD2	2.01	0.60
1:F:225:ASN:HD22	1:F:225:ASN:N	1.97	0.60
1:F:266:THR:HA	1:F:270:PHE:O	2.02	0.60
1:A:133:THR:HG22	1:A:135:ARG:H	1.66	0.60
1:A:296:ILE:HG23	1:A:297:PHE:CE2	2.35	0.60
1:E:258:ILE:HD12	1:E:258:ILE:N	2.15	0.60
1:E:273:SER:N	1:E:328:GLY:HA2	2.15	0.60
1:F:343:VAL:HA	1:F:361:LEU:O	2.01	0.60
1:A:194:ARG:HB2	1:A:358:LEU:CD2	2.30	0.60
1:A:233:LEU:HD11	1:A:366:LEU:CD1	2.26	0.60
1:A:368:LEU:HD23	1:A:370:HIS:NE2	2.12	0.60
1:C:224:LEU:HD12	1:C:225:ASN:ND2	2.16	0.60
1:F:202:MET:SD	1:F:203:LEU:CA	2.88	0.60
1:A:285:ILE:HA	1:A:288:LEU:HD11	1.82	0.60
1:C:192:ALA:HB1	1:D:151:VAL:CG1	2.31	0.60
1:C:239:VAL:HG12	1:C:373:PRO:HB3	1.84	0.60
1:C:275:ILE:HG22	1:C:277:LEU:HD11	1.83	0.60
1:E:131:ARG:NH1	1:E:316:THR:HA	2.16	0.60
1:E:335:VAL:HG22	1:E:368:LEU:HD13	1.83	0.60
1:C:130:ARG:CB	1:D:271:SER:OG	2.50	0.60
1:D:184:LYS:NZ	1:D:231:ASP:HA	2.17	0.60
1:E:199:ASP:CB	1:E:202:MET:HE2	2.31	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:158:ASN:H	1:A:158:ASN:ND2	2.00	0.60
1:A:206:TYR:O	1:A:210:ARG:HB3	2.01	0.60
1:A:297:PHE:CE2	1:A:309:TRP:CZ2	2.89	0.60
1:B:201:PRO:CA	1:B:204:GLN:HB2	2.32	0.60
1:F:203:LEU:HD22	1:F:204:GLN:HA	1.83	0.60
1:A:124:ILE:O	1:A:126:MET:SD	2.59	0.60
1:B:125:ILE:HG12	1:B:127:PRO:HG3	1.84	0.60
1:B:134:ILE:HD12	1:B:134:ILE:N	2.16	0.60
1:D:130:ARG:CZ	1:D:131:ARG:HB2	2.31	0.60
1:E:204:GLN:O	1:E:208:ASN:HB2	2.01	0.60
1:A:146:ASN:ND2	1:G:145:SER:HB2	2.17	0.60
1:C:190:VAL:HG22	1:D:176:PHE:CE1	2.36	0.60
1:D:303:PHE:N	1:D:303:PHE:HD1	1.99	0.60
1:E:194:ARG:HH11	1:E:347:ARG:CZ	2.15	0.60
1:F:327:GLY:O	1:F:329:PHE:CE1	2.53	0.60
1:F:346:SER:HB3	1:F:348:GLU:HG3	1.84	0.60
1:G:376:ILE:HD12	1:G:376:ILE:N	2.16	0.60
1:C:130:ARG:CG	1:D:271:SER:CB	2.69	0.60
1:C:224:LEU:HD13	1:C:237:ASN:ND2	2.16	0.60
1:E:155:VAL:CG1	1:E:374:THR:HB	2.32	0.60
1:A:189:TRP:HB3	1:A:361:LEU:HD13	1.84	0.59
1:B:217:LEU:C	1:B:217:LEU:HD12	2.21	0.59
1:C:155:VAL:CG2	1:C:174:ILE:HG22	2.31	0.59
1:C:247:LEU:HB3	1:C:260:HIS:HD2	1.66	0.59
1:D:261:ALA:O	1:D:265:VAL:HG23	2.02	0.59
1:C:129:LEU:HD22	1:C:129:LEU:N	2.15	0.59
1:D:201:PRO:O	1:D:204:GLN:N	2.34	0.59
1:F:292:GLU:O	1:F:294:ARG:HG2	2.02	0.59
1:G:174:ILE:H	1:G:174:ILE:CD1	2.12	0.59
1:A:285:ILE:O	1:A:288:LEU:CG	2.49	0.59
1:B:194:ARG:HA	1:B:358:LEU:CD1	2.32	0.59
1:D:155:VAL:HG11	1:D:374:THR:HB	1.83	0.59
1:B:236:LEU:HD23	1:B:370:HIS:HE1	1.66	0.59
1:B:341:ALA:HB1	1:B:362:CYS:SG	2.43	0.59
1:D:296:ILE:C	1:D:298:GLY:H	2.06	0.59
1:G:345:VAL:HG22	1:G:360:ILE:HG22	1.84	0.59
1:A:176:PHE:CE1	1:F:190:VAL:HG13	2.37	0.59
1:A:191:GLN:HE21	1:A:191:GLN:N	1.98	0.59
1:C:187:ALA:HB2	1:C:363:GLU:CA	2.23	0.59
1:C:203:LEU:O	1:C:206:TYR:CA	2.50	0.59
1:D:155:VAL:CG1	1:D:374:THR:HG21	2.32	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:289:LYS:N	1:D:289:LYS:HD2	2.17	0.59
1:E:194:ARG:HA	1:E:358:LEU:HD11	1.82	0.59
1:E:300:PRO:HB2	1:F:309:TRP:CE2	2.37	0.59
1:C:330:ASP:OD1	1:C:331:MET:N	2.35	0.59
1:D:241:THR:O	1:D:377:ILE:HA	2.03	0.59
1:E:182:ASN:HB2	1:E:184:LYS:NZ	2.17	0.59
1:E:366:LEU:C	1:E:366:LEU:HD12	2.23	0.59
1:F:202:MET:SD	1:F:202:MET:C	2.80	0.59
1:F:254:ARG:HG2	1:F:381:PHE:CD2	2.38	0.59
1:G:196:VAL:C	1:G:198:ASP:H	2.06	0.59
1:A:155:VAL:CG1	1:A:374:THR:HG21	2.32	0.59
1:A:277:LEU:O	1:A:315:PRO:HA	2.03	0.59
1:B:158:ASN:ND2	1:B:158:ASN:N	2.48	0.59
1:B:180:THR:HG22	1:B:181:ALA:N	2.18	0.59
1:B:194:ARG:CZ	1:B:347:ARG:NH2	2.66	0.59
1:D:186:ILE:HD12	1:D:186:ILE:N	2.17	0.59
1:F:142:ARG:HG3	1:F:337:ASP:CB	2.11	0.59
1:F:227:ASP:O	1:F:232:ASN:HB2	2.03	0.59
1:F:327:GLY:CA	1:F:329:PHE:CE1	2.85	0.59
1:G:351:ASP:O	1:G:355:LYS:CG	2.48	0.59
1:B:262:ILE:H	1:B:262:ILE:HD12	1.66	0.59
1:E:382:SER:O	1:E:383:SER:CB	2.49	0.59
1:A:155:VAL:CG1	1:A:374:THR:OG1	2.50	0.59
1:B:142:ARG:HG3	1:B:337:ASP:HB2	1.85	0.59
1:D:132:LEU:HD23	1:D:132:LEU:N	2.16	0.59
1:E:218:LYS:HG3	1:E:218:LYS:O	2.03	0.59
1:F:175:THR:HG22	1:F:176:PHE:H	1.67	0.59
1:G:155:VAL:HG23	1:G:174:ILE:HG22	1.83	0.59
1:A:224:LEU:HD12	1:A:225:ASN:ND2	2.17	0.59
1:A:265:VAL:HG11	1:A:327:GLY:HA2	1.85	0.59
1:C:347:ARG:O	1:C:352:ASN:HB2	2.02	0.59
1:E:202:MET:SD	1:E:203:LEU:N	2.76	0.59
1:G:189:TRP:HB3	1:G:361:LEU:HD13	1.84	0.59
1:A:183:VAL:HG22	1:A:367:ALA:HB2	1.83	0.58
1:A:187:ALA:HB1	1:A:361:LEU:HD11	1.85	0.58
1:A:237:ASN:ND2	1:A:325:THR:HG21	2.18	0.58
1:A:343:VAL:HG12	1:A:362:CYS:CB	2.31	0.58
1:D:207:ILE:HD12	1:D:207:ILE:N	2.18	0.58
1:E:200:ALA:HB3	1:E:201:PRO:CD	2.33	0.58
1:F:202:MET:O	1:F:205:SER:CB	2.51	0.58
1:G:280:ARG:C	1:G:282:TRP:N	2.56	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:358:LEU:N	1:B:358:LEU:CD1	2.66	0.58
1:C:133:THR:HG22	1:C:135:ARG:H	1.68	0.58
1:C:227:ASP:O	1:C:232:ASN:CB	2.51	0.58
1:C:376:ILE:N	1:C:376:ILE:HD12	2.18	0.58
1:D:358:LEU:N	1:D:358:LEU:HD12	2.18	0.58
1:E:335:VAL:HG22	1:E:368:LEU:CD1	2.33	0.58
1:A:153:GLU:CD	1:F:210:ARG:NH2	2.51	0.58
1:B:368:LEU:HD23	1:B:369:ALA:N	2.18	0.58
1:C:194:ARG:O	1:C:196:VAL:CB	2.52	0.58
1:C:244:ASP:H	1:C:264:GLN:NE2	2.01	0.58
1:F:210:ARG:HH11	1:F:210:ARG:CG	2.02	0.58
1:A:244:ASP:OD2	1:A:246:SER:HB3	2.02	0.58
1:A:345:VAL:HG13	1:A:359:THR:O	2.04	0.58
1:D:244:ASP:O	1:D:247:LEU:HB3	2.03	0.58
1:D:290:ASP:OD2	1:D:294:ARG:HB3	2.03	0.58
1:E:194:ARG:NH1	1:E:347:ARG:CZ	2.67	0.58
1:F:210:ARG:NH1	1:F:210:ARG:CG	2.65	0.58
1:G:150:TYR:HE2	1:G:181:ALA:HB2	1.67	0.58
1:G:285:ILE:HA	1:G:288:LEU:CG	2.34	0.58
1:A:224:LEU:HD21	1:A:276:VAL:HG11	1.84	0.58
1:C:224:LEU:HD12	1:C:225:ASN:CG	2.24	0.58
1:C:344:GLU:H	1:C:361:LEU:HD12	1.69	0.58
1:F:375:ALA:C	1:F:376:ILE:HD12	2.24	0.58
1:F:155:VAL:HG13	1:F:155:VAL:O	2.03	0.58
1:F:195:GLN:OE1	1:F:195:GLN:CA	2.50	0.58
1:F:211:LEU:HD22	1:F:212:MET:HE3	1.85	0.58
1:G:226:GLY:H	1:G:235:GLY:HA3	1.68	0.58
1:G:310:GLY:C	1:G:311:LEU:HD22	2.24	0.58
1:B:253:THR:HG22	1:B:254:ARG:N	2.19	0.58
1:C:201:PRO:O	1:C:204:GLN:CA	2.51	0.58
1:C:207:ILE:H	1:C:207:ILE:HD13	1.68	0.58
1:E:193:SER:O	1:E:195:GLN:N	2.36	0.58
1:E:210:ARG:NH2	1:F:153:GLU:OE2	2.35	0.58
1:F:175:THR:HG22	1:F:176:PHE:N	2.19	0.58
1:G:135:ARG:HH21	1:G:219:GLU:CD	2.06	0.58
1:G:199:ASP:HB3	1:G:202:MET:CB	2.31	0.58
1:A:190:VAL:HG21	1:A:210:ARG:NH1	2.19	0.58
1:C:138:LEU:HD23	1:C:329:PHE:HB3	1.84	0.58
1:E:212:MET:C	1:E:214:GLY:N	2.55	0.58
1:F:331:MET:O	1:F:331:MET:HG2	2.04	0.58
1:G:175:THR:HG22	1:G:176:PHE:N	2.18	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:282:TRP:CZ3	1:F:308:MET:HE1	2.39	0.58
1:C:190:VAL:N	1:C:360:ILE:O	2.31	0.58
1:C:244:ASP:OD2	1:C:247:LEU:HG	2.04	0.58
1:C:306:ASN:HB3	1:C:313:VAL:HB	1.85	0.58
1:D:155:VAL:O	1:D:155:VAL:HG13	2.03	0.58
1:G:354:VAL:O	1:G:356:ASN:N	2.37	0.58
1:A:345:VAL:HA	1:A:359:THR:O	2.05	0.57
1:B:149:GLU:HG2	1:B:180:THR:OG1	2.04	0.57
1:F:153:GLU:CD	1:F:372:ARG:HH21	2.08	0.57
1:A:155:VAL:HG23	1:A:174:ILE:CG2	2.30	0.57
1:C:200:ALA:HB1	1:C:201:PRO:HD2	1.86	0.57
1:F:211:LEU:CD2	1:F:212:MET:HE3	2.34	0.57
1:G:281:ASP:O	1:G:285:ILE:CD1	2.52	0.57
1:B:148:LEU:O	1:B:180:THR:HG23	2.04	0.57
1:C:155:VAL:HA	1:C:174:ILE:HA	1.86	0.57
1:E:158:ASN:N	1:E:158:ASN:ND2	2.50	0.57
1:C:184:LYS:HB2	1:C:233:LEU:HD21	1.86	0.57
1:D:239:VAL:HG12	1:D:373:PRO:HB3	1.86	0.57
1:E:148:LEU:N	1:E:148:LEU:HD23	2.20	0.57
1:E:253:THR:HB	1:E:256:ASP:OD1	2.04	0.57
1:A:174:ILE:H	1:A:174:ILE:CD1	2.11	0.57
1:B:279:PRO:HD3	1:B:316:THR:O	2.04	0.57
1:D:356:ASN:ND2	1:E:178:LYS:NZ	2.53	0.57
1:E:185:THR:HG22	1:E:365:ARG:HG2	1.87	0.57
1:E:207:ILE:CG1	1:E:208:ASN:H	2.12	0.57
1:C:152:ARG:HB3	1:C:177:SER:HB2	1.86	0.57
1:D:158:ASN:ND2	1:D:158:ASN:N	2.48	0.57
1:E:155:VAL:HG23	1:E:174:ILE:CG2	2.32	0.57
1:E:185:THR:O	1:E:186:ILE:HD13	2.03	0.57
1:F:143:THR:OG1	1:F:144:SER:N	2.37	0.57
1:A:191:GLN:N	1:A:191:GLN:NE2	2.53	0.57
1:A:339:MET:HB3	1:A:365:ARG:HB2	1.87	0.57
1:C:184:LYS:HG3	1:C:233:LEU:CD2	2.35	0.57
1:D:125:ILE:HD13	1:D:208:ASN:OD1	1.97	0.57
1:E:273:SER:H	1:E:328:GLY:HA2	1.70	0.57
1:G:175:THR:HG22	1:G:176:PHE:H	1.69	0.57
1:A:183:VAL:HA	1:A:367:ALA:HB2	1.87	0.57
1:A:197:MET:C	1:A:199:ASP:H	2.06	0.57
1:B:162:ASP:C	1:B:173:ASP:N	2.55	0.57
1:C:150:TYR:CE1	1:C:179:GLN:HB2	2.40	0.57
1:C:292:GLU:HG2	1:C:294:ARG:HE	1.66	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:346:SER:O	1:D:347:ARG:HB3	2.05	0.57
1:B:134:ILE:HD13	1:B:220:GLU:CG	2.35	0.57
1:B:342:THR:O	1:B:362:CYS:CA	2.49	0.57
1:B:342:THR:OG1	1:B:363:GLU:HB2	2.05	0.57
1:D:127:PRO:HB3	1:D:212:MET:HB3	1.85	0.57
1:F:174:ILE:HD13	1:F:174:ILE:N	2.14	0.57
1:F:347:ARG:O	1:F:352:ASN:HB2	2.04	0.57
1:G:196:VAL:C	1:G:198:ASP:N	2.58	0.57
1:G:295:TYR:HB2	1:G:298:GLY:O	2.05	0.57
1:B:129:LEU:C	1:B:131:ARG:N	2.57	0.56
1:E:194:ARG:CZ	1:E:347:ARG:NH2	2.68	0.56
1:F:212:MET:HA	1:F:212:MET:CE	2.34	0.56
1:B:127:PRO:C	1:B:129:LEU:N	2.51	0.56
1:B:162:ASP:HB3	1:B:173:ASP:HB2	1.86	0.56
1:C:131:ARG:HB2	1:C:131:ARG:HH11	1.70	0.56
1:C:202:MET:CE	1:C:203:LEU:HD23	2.35	0.56
1:C:266:THR:HA	1:C:270:PHE:O	2.05	0.56
1:D:302:ALA:O	1:D:304:THR:N	2.38	0.56
1:D:309:TRP:HE3	1:D:309:TRP:H	1.53	0.56
1:E:199:ASP:O	1:E:202:MET:CE	2.53	0.56
1:E:206:TYR:C	1:E:206:TYR:CD2	2.75	0.56
1:A:190:VAL:CG1	1:A:211:LEU:HD21	2.35	0.56
1:A:368:LEU:HD21	1:A:370:HIS:CD2	2.36	0.56
1:A:368:LEU:CD2	1:A:370:HIS:CD2	2.89	0.56
1:B:217:LEU:HD12	1:B:218:LYS:N	2.20	0.56
1:B:252:ASP:HB3	1:B:256:ASP:HB2	1.87	0.56
1:C:288:LEU:HD23	1:C:289:LYS:O	2.04	0.56
1:E:151:VAL:HG23	1:E:151:VAL:O	2.06	0.56
1:E:222:GLN:OE1	1:E:232:ASN:HA	2.05	0.56
1:E:261:ALA:O	1:E:265:VAL:HG23	2.06	0.56
1:G:304:THR:HG22	1:G:305:SER:N	2.14	0.56
1:B:126:MET:CE	1:B:212:MET:HG3	2.36	0.56
1:B:134:ILE:H	1:B:134:ILE:CD1	2.19	0.56
1:B:276:VAL:C	1:B:277:LEU:CD2	2.70	0.56
1:C:177:SER:O	1:C:179:GLN:HG2	2.05	0.56
1:D:254:ARG:O	1:D:258:ILE:HD13	2.06	0.56
1:E:134:ILE:HD12	1:E:134:ILE:N	2.21	0.56
1:E:203:LEU:HD12	1:E:206:TYR:HB3	1.87	0.56
1:F:142:ARG:HA	1:F:337:ASP:H	1.71	0.56
1:D:343:VAL:HG12	1:D:362:CYS:SG	2.45	0.56
1:D:358:LEU:H	1:D:358:LEU:CD1	2.19	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:157:THR:CG2	1:E:267:GLU:CG	2.78	0.56
1:E:190:VAL:HG12	1:F:176:PHE:CZ	2.40	0.56
1:E:224:LEU:HD12	1:E:225:ASN:OD1	2.05	0.56
1:F:277:LEU:N	1:F:277:LEU:HD12	2.21	0.56
1:G:311:LEU:HD22	1:G:311:LEU:N	2.20	0.56
1:G:366:LEU:CD1	1:G:367:ALA:N	2.68	0.56
1:A:158:ASN:ND2	1:A:158:ASN:N	2.54	0.56
1:A:240:ALA:CB	1:A:376:ILE:HG22	2.36	0.56
1:A:276:VAL:HB	1:A:325:THR:OG1	2.06	0.56
1:C:276:VAL:HG22	1:C:314:VAL:CG2	2.36	0.56
1:A:129:LEU:N	1:A:129:LEU:CD2	2.69	0.56
1:A:184:LYS:HE3	1:A:230:GLY:O	2.05	0.56
1:A:185:THR:HG22	1:A:365:ARG:HG2	1.88	0.56
1:A:207:ILE:HG23	1:A:211:LEU:HD12	1.86	0.56
1:B:155:VAL:HG13	1:B:374:THR:CB	2.35	0.56
1:B:261:ALA:O	1:B:265:VAL:HG23	2.06	0.56
1:D:377:ILE:HD12	1:D:377:ILE:N	2.21	0.56
1:E:155:VAL:HG13	1:E:155:VAL:O	2.06	0.56
1:E:193:SER:O	1:E:196:VAL:HG23	2.06	0.56
1:E:225:ASN:HA	1:E:235:GLY:HA3	1.88	0.56
1:C:213:TYR:CD2	1:C:217:LEU:CD1	2.89	0.56
1:D:209:ASN:O	1:D:213:TYR:HB3	2.06	0.56
1:G:377:ILE:HD12	1:G:377:ILE:N	2.21	0.56
1:A:275:ILE:CD1	1:A:308:MET:SD	2.94	0.56
1:A:287:LEU:N	1:A:288:LEU:CD2	2.69	0.56
1:B:255:ALA:HA	1:B:258:ILE:HD13	1.88	0.56
1:C:196:VAL:CG1	1:C:203:LEU:HD13	2.32	0.56
1:C:207:ILE:HG22	1:C:211:LEU:HD13	1.87	0.56
1:C:357:MET:HE2	1:D:178:LYS:CG	2.35	0.56
1:E:127:PRO:HG2	1:E:129:LEU:CD1	2.35	0.56
1:F:253:THR:HG23	1:F:256:ASP:CG	2.25	0.56
1:B:202:MET:C	1:B:204:GLN:N	2.50	0.56
1:C:200:ALA:C	1:C:202:MET:N	2.58	0.56
1:E:200:ALA:N	1:E:201:PRO:HD2	2.20	0.56
1:E:202:MET:HE1	1:E:203:LEU:HB2	1.88	0.56
1:F:254:ARG:HB3	1:F:285:ILE:CD1	2.37	0.56
1:G:291:ASN:C	1:G:293:GLY:H	2.09	0.56
1:A:349:ASP:OD1	1:A:350:ARG:CG	2.55	0.55
1:B:194:ARG:O	1:B:195:GLN:HB2	2.06	0.55
1:D:190:VAL:HG11	1:D:211:LEU:HD21	1.84	0.55
1:E:354:VAL:O	1:E:356:ASN:N	2.40	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:196:VAL:O	1:G:198:ASP:N	2.39	0.55
1:D:154:GLU:HB3	1:D:175:THR:HB	1.87	0.55
1:E:135:ARG:NH2	1:E:337:ASP:OD2	2.34	0.55
1:G:152:ARG:HG3	1:G:371:TYR:O	2.06	0.55
1:D:244:ASP:HB2	1:D:264:GLN:NE2	2.21	0.55
1:E:128:GLY:O	1:E:129:LEU:HB2	2.05	0.55
1:E:305:SER:HB2	1:E:307:ILE:HG12	1.87	0.55
1:F:377:ILE:HD12	1:F:377:ILE:N	2.21	0.55
1:B:125:ILE:CD1	1:B:127:PRO:HG3	2.37	0.55
1:B:132:LEU:HD23	1:B:132:LEU:N	2.18	0.55
1:C:284:ASN:O	1:C:288:LEU:HB2	2.07	0.55
1:E:236:LEU:HD23	1:E:370:HIS:CE1	2.41	0.55
1:F:192:ALA:O	1:F:357:MET:HA	2.05	0.55
1:C:268:SER:O	1:C:269:GLU:HB2	2.06	0.55
1:A:297:PHE:HD2	1:A:297:PHE:N	2.04	0.55
1:B:250:THR:HG22	1:B:251:GLY:N	2.18	0.55
1:C:225:ASN:N	1:C:225:ASN:HD22	2.02	0.55
1:C:297:PHE:HE1	1:C:308:MET:HE3	1.71	0.55
1:D:257:ILE:HA	1:D:260:HIS:HD2	1.71	0.55
1:D:295:TYR:CE1	1:D:300:PRO:HD3	2.41	0.55
1:E:227:ASP:O	1:E:229:THR:HG22	2.07	0.55
1:F:203:LEU:HD23	1:F:206:TYR:HB3	1.89	0.55
1:F:376:ILE:HD12	1:F:376:ILE:N	2.22	0.55
1:A:175:THR:HG22	1:A:176:PHE:N	2.22	0.55
1:B:129:LEU:C	1:B:129:LEU:CD2	2.74	0.55
1:D:356:ASN:HD21	1:E:178:LYS:NZ	2.04	0.55
1:E:132:LEU:H	1:E:132:LEU:CD2	2.17	0.55
1:E:297:PHE:CD2	1:E:298:GLY:N	2.75	0.55
1:G:278:ASN:O	1:G:281:ASP:N	2.40	0.55
1:C:157:THR:OG1	1:C:158:ASN:N	2.38	0.55
1:C:357:MET:SD	1:D:178:LYS:HD3	2.47	0.55
1:E:194:ARG:HH11	1:E:347:ARG:NH1	2.04	0.55
1:E:296:ILE:HG22	1:E:298:GLY:H	1.71	0.55
1:F:260:HIS:O	1:F:263:TYR:HB3	2.07	0.55
1:G:335:VAL:HG12	1:G:368:LEU:HB3	1.89	0.55
1:G:372:ARG:HH11	1:G:372:ARG:HG2	1.72	0.55
1:G:372:ARG:HG2	1:G:372:ARG:NH1	2.22	0.55
1:B:148:LEU:C	1:B:180:THR:HG23	2.28	0.55
1:B:296:ILE:O	1:B:296:ILE:HG12	2.06	0.55
1:C:194:ARG:HB2	1:C:358:LEU:HG	1.88	0.55
1:F:376:ILE:C	1:F:377:ILE:HD12	2.27	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:144:SER:HA	1:B:338:ARG:NH1	2.22	0.55
1:E:359:THR:O	1:E:359:THR:HG22	2.07	0.55
1:G:282:TRP:CZ3	1:G:313:VAL:HG21	2.41	0.55
1:B:194:ARG:HD2	1:B:358:LEU:HD12	1.89	0.54
1:C:146:ASN:HD21	1:C:365:ARG:HH22	1.54	0.54
1:C:278:ASN:HD21	1:C:280:ARG:HB3	1.70	0.54
1:F:194:ARG:NH1	1:F:347:ARG:CZ	2.69	0.54
1:F:206:TYR:O	1:F:207:ILE:C	2.45	0.54
1:G:270:PHE:HE1	1:G:372:ARG:CZ	2.19	0.54
1:A:127:PRO:HD3	1:A:212:MET:CE	2.38	0.54
1:C:196:VAL:HG11	1:C:203:LEU:CD1	2.29	0.54
1:D:129:LEU:CD1	1:D:131:ARG:N	2.67	0.54
1:E:215:LEU:O	1:E:218:LYS:CA	2.55	0.54
1:E:262:ILE:N	1:E:262:ILE:HD12	2.22	0.54
1:B:289:LYS:HD2	1:B:293:GLY:CA	2.37	0.54
1:D:343:VAL:HA	1:D:361:LEU:O	2.06	0.54
1:F:207:ILE:HD12	1:F:207:ILE:C	2.28	0.54
1:G:203:LEU:C	1:G:205:SER:N	2.57	0.54
1:B:153:GLU:HB2	1:B:371:TYR:O	2.08	0.54
1:B:258:ILE:H	1:B:258:ILE:CD1	2.20	0.54
1:C:132:LEU:CD2	1:C:136:ASP:HB2	2.38	0.54
1:C:275:ILE:HG13	1:C:326:VAL:HG12	1.89	0.54
1:D:244:ASP:HB2	1:D:264:GLN:HE22	1.72	0.54
1:D:343:VAL:HG12	1:D:362:CYS:HB2	1.89	0.54
1:E:227:ASP:C	1:E:229:THR:HG23	2.28	0.54
1:A:202:MET:CG	1:A:203:LEU:N	2.71	0.54
1:A:377:ILE:HD12	1:A:377:ILE:N	2.22	0.54
1:B:329:PHE:O	1:B:330:ASP:C	2.45	0.54
1:B:368:LEU:HD23	1:B:368:LEU:C	2.28	0.54
1:D:191:GLN:HB2	1:E:151:VAL:HG21	1.88	0.54
1:G:316:THR:HG22	1:G:318:ALA:N	2.17	0.54
1:B:144:SER:HA	1:B:338:ARG:HH11	1.71	0.54
1:B:161:GLY:O	1:B:172:SER:N	2.41	0.54
1:B:344:GLU:N	1:B:361:LEU:O	2.38	0.54
1:F:344:GLU:H	1:F:361:LEU:CD1	2.21	0.54
1:G:355:LYS:O	1:G:356:ASN:C	2.46	0.54
1:A:121:ILE:HG23	1:A:343:VAL:O	2.08	0.54
1:A:297:PHE:CD2	1:A:297:PHE:N	2.74	0.54
1:B:210:ARG:HH22	1:C:153:GLU:CG	2.18	0.54
1:F:281:ASP:O	1:F:285:ILE:HG12	2.08	0.54
1:B:161:GLY:O	1:B:162:ASP:C	2.45	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:278:ASN:HB3	1:B:281:ASP:OD2	2.08	0.54
1:E:191:GLN:HB3	1:E:359:THR:HA	1.90	0.54
1:F:158:ASN:N	1:F:158:ASN:HD22	2.04	0.54
1:F:225:ASN:HA	1:F:235:GLY:HA3	1.88	0.54
1:G:131:ARG:O	1:G:133:THR:N	2.33	0.54
1:E:277:LEU:N	1:E:277:LEU:HD23	2.23	0.54
1:F:211:LEU:CD2	1:F:362:CYS:SG	2.93	0.54
1:G:128:GLY:O	1:G:130:ARG:HG2	2.08	0.54
1:E:155:VAL:CG1	1:E:374:THR:CB	2.85	0.54
1:E:287:LEU:HD12	1:E:295:TYR:HE1	1.73	0.54
1:B:195:GLN:CA	1:B:197:MET:HG2	2.38	0.53
1:B:344:GLU:O	1:B:361:LEU:N	2.42	0.53
1:C:281:ASP:O	1:C:285:ILE:HG12	2.08	0.53
1:D:138:LEU:HD12	1:D:138:LEU:N	2.22	0.53
1:D:148:LEU:HD12	1:D:148:LEU:O	2.06	0.53
1:D:174:ILE:H	1:D:174:ILE:HD13	1.72	0.53
1:F:199:ASP:O	1:F:200:ALA:C	2.47	0.53
1:G:285:ILE:CA	1:G:288:LEU:HG	2.37	0.53
1:C:366:LEU:HD13	1:C:367:ALA:N	2.22	0.53
1:D:174:ILE:O	1:D:174:ILE:CG1	2.56	0.53
1:E:217:LEU:HD11	1:F:269:GLU:HB3	1.89	0.53
1:G:194:ARG:C	1:G:196:VAL:N	2.51	0.53
1:G:278:ASN:O	1:G:279:PRO:C	2.46	0.53
1:C:345:VAL:HG13	1:C:360:ILE:HD13	1.91	0.53
1:E:215:LEU:HD23	1:E:215:LEU:C	2.28	0.53
1:G:281:ASP:O	1:G:285:ILE:HD12	2.07	0.53
1:B:304:THR:HG21	1:C:309:TRP:O	2.07	0.53
1:C:227:ASP:C	1:C:229:THR:N	2.61	0.53
1:D:174:ILE:HG12	1:D:174:ILE:O	2.07	0.53
1:D:247:LEU:HD21	1:D:260:HIS:CB	2.32	0.53
1:E:199:ASP:O	1:E:202:MET:HE3	2.08	0.53
1:F:275:ILE:HG23	1:F:326:VAL:CG1	2.38	0.53
1:G:239:VAL:HG12	1:G:373:PRO:HB3	1.91	0.53
1:A:366:LEU:HD12	1:A:366:LEU:O	2.08	0.53
1:A:366:LEU:C	1:A:366:LEU:CD1	2.76	0.53
1:B:149:GLU:HA	1:B:180:THR:HA	1.91	0.53
1:B:175:THR:HG22	1:B:176:PHE:H	1.73	0.53
1:C:132:LEU:HD23	1:C:136:ASP:OD2	2.09	0.53
1:C:243:TYR:OH	1:C:260:HIS:HB2	2.08	0.53
1:D:301:GLN:O	1:D:302:ALA:C	2.47	0.53
1:D:307:ILE:HB	1:D:311:LEU:O	2.09	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:204:GLN:HA	1:F:207:ILE:HG13	1.90	0.53
1:B:202:MET:O	1:B:203:LEU:C	2.47	0.53
1:C:287:LEU:HD23	1:C:300:PRO:HA	1.89	0.53
1:D:356:ASN:ND2	1:E:178:LYS:HZ1	2.05	0.53
1:E:187:ALA:HB2	1:E:363:GLU:HA	1.90	0.53
1:E:307:ILE:HG22	1:E:312:PRO:HA	1.91	0.53
1:G:200:ALA:O	1:G:204:GLN:CA	2.57	0.53
1:A:125:ILE:CG2	1:A:204:GLN:HE21	2.09	0.53
1:E:157:THR:CG2	1:E:267:GLU:HG2	2.38	0.53
1:E:199:ASP:HB3	1:E:202:MET:HE2	1.91	0.53
1:E:206:TYR:C	1:E:206:TYR:HD2	2.11	0.53
1:F:253:THR:O	1:F:256:ASP:N	2.42	0.53
1:B:153:GLU:OE1	1:B:371:TYR:O	2.27	0.53
1:B:158:ASN:ND2	1:B:172:SER:CB	2.72	0.53
1:C:152:ARG:O	1:C:176:PHE:HA	2.09	0.53
1:D:309:TRP:N	1:D:309:TRP:CE3	2.77	0.53
1:E:252:ASP:HB3	1:E:256:ASP:HB2	1.90	0.53
1:E:282:TRP:HA	1:E:282:TRP:CE3	2.44	0.53
1:F:206:TYR:C	1:F:208:ASN:H	2.10	0.53
1:F:314:VAL:HG23	1:F:314:VAL:O	2.08	0.53
1:B:194:ARG:HG2	1:B:356:ASN:O	2.08	0.53
1:C:194:ARG:HA	1:C:358:LEU:CD1	2.39	0.53
1:D:158:ASN:N	1:D:158:ASN:HD22	2.05	0.53
1:E:158:ASN:N	1:E:158:ASN:HD22	2.06	0.53
1:E:196:VAL:O	1:E:196:VAL:HG12	2.09	0.53
1:E:207:ILE:O	1:E:211:LEU:N	2.39	0.53
1:A:289:LYS:HD2	1:A:289:LYS:N	2.23	0.53
1:B:150:TYR:HE2	1:B:181:ALA:HB2	1.73	0.53
1:D:124:ILE:CG2	1:D:125:ILE:N	2.72	0.53
1:D:356:ASN:CG	1:E:178:LYS:NZ	2.62	0.53
1:E:220:GLU:OE2	1:E:316:THR:OG1	2.22	0.53
1:E:220:GLU:CG	1:E:316:THR:HG21	2.39	0.53
1:F:155:VAL:HG23	1:F:174:ILE:CG2	2.33	0.53
1:F:268:SER:O	1:F:269:GLU:HB2	2.09	0.53
1:G:278:ASN:HD22	1:G:321:ALA:CA	2.22	0.53
1:B:148:LEU:CD2	1:B:181:ALA:HB3	2.40	0.52
1:C:155:VAL:CB	1:C:174:ILE:HG22	2.39	0.52
1:C:202:MET:HE1	1:C:203:LEU:HD23	1.90	0.52
1:E:282:TRP:HA	1:E:282:TRP:HE3	1.74	0.52
1:F:292:GLU:O	1:F:294:ARG:N	2.42	0.52
1:G:137:LEU:HD11	1:G:314:VAL:HG21	1.91	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:240:ALA:HB2	1:A:376:ILE:HG21	1.89	0.52
1:B:155:VAL:HG13	1:B:155:VAL:O	2.09	0.52
1:C:190:VAL:HG22	1:D:176:PHE:CZ	2.44	0.52
1:C:213:TYR:O	1:C:217:LEU:HD13	2.08	0.52
1:E:287:LEU:N	1:E:287:LEU:HD22	2.24	0.52
1:F:342:THR:O	1:F:363:GLU:N	2.42	0.52
1:A:194:ARG:HG2	1:A:195:GLN:N	2.23	0.52
1:B:129:LEU:C	1:B:131:ARG:H	2.12	0.52
1:B:148:LEU:CD2	1:B:148:LEU:N	2.72	0.52
1:C:349:ASP:O	1:C:352:ASN:OD1	2.27	0.52
1:D:210:ARG:NH1	1:E:371:TYR:CE2	2.77	0.52
1:F:156:PHE:HD2	1:F:158:ASN:CA	2.22	0.52
1:B:206:TYR:HD2	1:B:210:ARG:HB2	1.74	0.52
1:D:184:LYS:HA	1:D:184:LYS:NZ	2.25	0.52
1:G:189:TRP:HZ3	1:G:350:ARG:HH22	1.55	0.52
1:A:340:ASP:O	1:A:342:THR:HG23	2.09	0.52
1:E:207:ILE:CA	1:E:211:LEU:HB2	2.38	0.52
1:E:262:ILE:HD12	1:E:262:ILE:H	1.73	0.52
1:F:158:ASN:ND2	1:F:172:SER:HA	2.25	0.52
1:F:327:GLY:C	1:F:329:PHE:CD1	2.83	0.52
1:G:268:SER:O	1:G:269:GLU:CB	2.58	0.52
1:G:268:SER:O	1:G:269:GLU:HB3	2.10	0.52
1:G:280:ARG:O	1:G:283:HIS:N	2.42	0.52
1:B:175:THR:HG22	1:B:176:PHE:N	2.25	0.52
1:C:130:ARG:HB3	1:D:271:SER:OG	2.10	0.52
1:C:287:LEU:HD21	1:C:300:PRO:CB	2.36	0.52
1:E:156:PHE:HD2	1:E:158:ASN:CA	2.22	0.52
1:F:153:GLU:OE2	1:F:372:ARG:NH2	2.42	0.52
1:F:276:VAL:HG22	1:F:314:VAL:CG2	2.40	0.52
1:F:343:VAL:HA	1:F:362:CYS:HA	1.91	0.52
1:G:156:PHE:O	1:G:158:ASN:OD1	2.28	0.52
1:A:304:THR:O	1:A:306:ASN:N	2.43	0.52
1:B:205:SER:O	1:B:206:TYR:C	2.46	0.52
1:B:206:TYR:HE2	1:B:210:ARG:HE	1.58	0.52
1:D:155:VAL:CG1	1:D:374:THR:HB	2.38	0.52
1:D:303:PHE:O	1:D:306:ASN:HB3	2.10	0.52
1:B:329:PHE:HA	1:B:332:ALA:HB3	1.91	0.52
1:C:130:ARG:HB3	1:D:271:SER:CB	2.40	0.52
1:C:287:LEU:HD21	1:C:300:PRO:HB2	1.92	0.52
1:F:188:HIS:O	1:F:361:LEU:HA	2.10	0.52
1:B:204:GLN:OE1	1:B:204:GLN:HA	2.09	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:275:ILE:HG23	1:C:326:VAL:HG12	1.91	0.52
1:D:284:ASN:O	1:D:287:LEU:HD12	2.10	0.52
1:E:135:ARG:HD2	1:E:219:GLU:OE1	2.10	0.52
1:F:202:MET:O	1:F:205:SER:CA	2.57	0.52
1:G:128:GLY:C	1:G:130:ARG:N	2.60	0.52
1:B:156:PHE:HD2	1:B:158:ASN:CA	2.23	0.52
1:B:251:GLY:O	1:B:252:ASP:CG	2.49	0.52
1:G:155:VAL:HA	1:G:174:ILE:HG22	1.90	0.52
1:G:324:PHE:CZ	1:G:379:GLY:HA3	2.45	0.52
1:B:208:ASN:HD22	1:B:208:ASN:N	2.07	0.51
1:B:307:ILE:HG22	1:B:312:PRO:HA	1.91	0.51
1:C:277:LEU:N	1:C:277:LEU:HD12	2.25	0.51
1:D:156:PHE:HD2	1:D:158:ASN:CA	2.23	0.51
1:E:127:PRO:HB2	1:E:213:TYR:CE1	2.25	0.51
1:F:145:SER:O	1:F:338:ARG:HD3	2.09	0.51
1:F:158:ASN:ND2	1:F:158:ASN:N	2.49	0.51
1:A:155:VAL:HG13	1:A:155:VAL:O	2.10	0.51
1:D:224:LEU:O	1:D:237:ASN:OD1	2.29	0.51
1:E:193:SER:C	1:E:195:GLN:H	2.12	0.51
1:F:138:LEU:CD2	1:F:329:PHE:HB3	2.39	0.51
1:F:249:ALA:C	1:F:250:THR:O	2.41	0.51
1:G:150:TYR:CE2	1:G:369:ALA:HB1	2.45	0.51
1:G:376:ILE:C	1:G:377:ILE:HD12	2.30	0.51
1:A:202:MET:CG	1:A:203:LEU:H	2.23	0.51
1:A:331:MET:HE3	1:F:209:ASN:O	2.10	0.51
1:B:317:LYS:HG2	1:B:317:LYS:O	2.11	0.51
1:E:329:PHE:H	1:E:329:PHE:HD1	1.57	0.51
1:G:216:ALA:HA	1:G:219:GLU:HG2	1.91	0.51
1:A:240:ALA:HB2	1:A:376:ILE:CG2	2.40	0.51
1:B:299:GLY:O	1:B:302:ALA:N	2.44	0.51
1:C:296:ILE:C	1:C:297:PHE:HD2	2.13	0.51
1:D:155:VAL:CG1	1:D:374:THR:CG2	2.89	0.51
1:D:293:GLY:H	1:F:294:ARG:HB2	1.75	0.51
1:D:300:PRO:HG2	1:E:301:GLN:NE2	2.25	0.51
1:E:134:ILE:H	1:E:134:ILE:CD1	2.24	0.51
1:B:289:LYS:HD2	1:B:293:GLY:C	2.30	0.51
1:B:308:MET:HG3	1:B:309:TRP:HD1	1.75	0.51
1:C:195:GLN:O	1:C:197:MET:N	2.43	0.51
1:D:210:ARG:NH1	1:E:371:TYR:CD2	2.79	0.51
1:D:290:ASP:CG	1:D:294:ARG:HB3	2.30	0.51
1:F:193:SER:HA	1:F:357:MET:HA	1.92	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:155:VAL:HG22	1:G:156:PHE:H	1.74	0.51
1:G:158:ASN:OD1	1:G:172:SER:CA	2.44	0.51
1:G:343:VAL:HG22	1:G:362:CYS:SG	2.50	0.51
1:A:156:PHE:C	1:A:158:ASN:N	2.64	0.51
1:B:137:LEU:CD2	1:B:329:PHE:HB2	2.40	0.51
1:B:209:ASN:C	1:C:331:MET:CE	2.79	0.51
1:E:150:TYR:CE1	1:E:179:GLN:HB2	2.45	0.51
1:E:199:ASP:HB3	1:E:202:MET:HB3	1.92	0.51
1:G:237:ASN:HD21	1:G:319:GLN:HE22	1.57	0.51
1:A:153:GLU:OE2	1:A:372:ARG:NH2	2.43	0.51
1:A:203:LEU:HD12	1:A:207:ILE:HD11	1.92	0.51
1:D:146:ASN:O	1:D:147:ALA:HB2	2.10	0.51
1:D:175:THR:HG22	1:D:176:PHE:N	2.25	0.51
1:A:254:ARG:O	1:A:258:ILE:HD13	2.11	0.51
1:G:343:VAL:HG13	1:G:361:LEU:O	2.10	0.51
1:A:138:LEU:HD12	1:A:138:LEU:N	2.26	0.51
1:C:132:LEU:HD21	1:C:136:ASP:CB	2.40	0.51
1:E:158:ASN:ND2	1:E:172:SER:HA	2.26	0.51
1:E:190:VAL:HG12	1:F:176:PHE:CE1	2.46	0.51
1:E:224:LEU:HD11	1:E:319:GLN:CD	2.31	0.51
1:E:281:ASP:O	1:E:285:ILE:HG13	2.11	0.51
1:E:349:ASP:O	1:E:352:ASN:OD1	2.29	0.51
1:F:138:LEU:HD23	1:F:329:PHE:HB3	1.93	0.51
1:F:193:SER:O	1:F:196:VAL:HG13	2.11	0.51
1:G:131:ARG:HD3	1:G:306:ASN:HD21	1.76	0.51
1:G:371:TYR:O	1:G:373:PRO:HD3	2.10	0.51
1:A:287:LEU:C	1:A:288:LEU:HD22	2.24	0.50
1:A:308:MET:C	1:A:310:GLY:H	2.14	0.50
1:B:162:ASP:O	1:B:173:ASP:N	2.44	0.50
1:C:129:LEU:CD1	1:D:331:MET:CE	2.69	0.50
1:C:224:LEU:HD13	1:C:225:ASN:CG	2.31	0.50
1:D:349:ASP:OD1	1:D:349:ASP:C	2.49	0.50
1:E:236:LEU:HD13	1:E:329:PHE:HE2	1.75	0.50
1:F:184:LYS:HB2	1:F:233:LEU:HD21	1.92	0.50
1:G:211:LEU:HD21	1:G:362:CYS:HB2	1.93	0.50
1:G:302:ALA:O	1:G:303:PHE:HB2	2.11	0.50
1:B:158:ASN:CB	1:B:172:SER:HB2	2.41	0.50
1:B:212:MET:O	1:B:214:GLY:N	2.45	0.50
1:C:207:ILE:HD13	1:C:207:ILE:N	2.25	0.50
1:D:358:LEU:N	1:D:358:LEU:CD1	2.74	0.50
1:G:301:GLN:CG	1:G:302:ALA:H	2.11	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:285:ILE:C	1:A:288:LEU:CD2	2.62	0.50
1:B:216:ALA:O	1:B:217:LEU:O	2.29	0.50
1:B:289:LYS:HD2	1:B:294:ARG:N	2.26	0.50
1:C:191:GLN:OE1	1:C:191:GLN:O	2.30	0.50
1:C:204:GLN:O	1:C:207:ILE:HD13	2.11	0.50
1:C:366:LEU:CD1	1:C:366:LEU:C	2.75	0.50
1:D:376:ILE:C	1:D:377:ILE:HD12	2.32	0.50
1:E:360:ILE:HD12	1:E:360:ILE:C	2.32	0.50
1:E:361:LEU:HG	1:E:362:CYS:N	2.26	0.50
1:F:142:ARG:HG2	1:F:337:ASP:HB2	1.81	0.50
1:F:195:GLN:C	1:F:197:MET:N	2.65	0.50
1:G:327:GLY:C	1:G:329:PHE:CD2	2.85	0.50
1:G:366:LEU:C	1:G:366:LEU:CD1	2.74	0.50
1:A:131:ARG:HH21	1:A:316:THR:HB	1.75	0.50
1:A:145:SER:H	1:A:338:ARG:HD3	1.77	0.50
1:B:354:VAL:C	1:B:356:ASN:N	2.63	0.50
1:A:151:VAL:HG22	1:A:152:ARG:N	2.27	0.50
1:B:129:LEU:O	1:B:131:ARG:N	2.44	0.50
1:B:258:ILE:HD11	1:B:381:PHE:CZ	2.46	0.50
1:B:282:TRP:HA	1:B:282:TRP:HE3	1.76	0.50
1:C:130:ARG:HB2	1:D:271:SER:OG	2.12	0.50
1:D:303:PHE:CA	1:D:306:ASN:HB3	2.38	0.50
1:E:264:GLN:O	1:E:267:GLU:HB2	2.12	0.50
1:B:188:HIS:O	1:B:361:LEU:HD12	2.12	0.50
1:B:199:ASP:O	1:B:200:ALA:CB	2.59	0.50
1:C:206:TYR:O	1:C:210:ARG:N	2.36	0.50
1:D:129:LEU:CD1	1:D:131:ARG:HD3	2.42	0.50
1:E:126:MET:HE1	1:E:129:LEU:HD21	1.91	0.50
1:E:214:GLY:O	1:E:217:LEU:HB3	2.11	0.50
1:E:226:GLY:N	1:E:235:GLY:HA3	2.27	0.50
1:F:129:LEU:HD12	1:F:129:LEU:N	2.22	0.50
1:A:348:GLU:O	1:A:348:GLU:CG	2.60	0.50
1:B:137:LEU:HD22	1:B:329:PHE:HB2	1.93	0.50
1:B:282:TRP:HA	1:B:282:TRP:CE3	2.47	0.50
1:E:137:LEU:HD22	1:E:329:PHE:CB	2.36	0.50
1:G:134:ILE:CG1	1:G:220:GLU:HG3	2.42	0.50
1:G:352:ASN:O	1:G:355:LYS:O	2.29	0.50
1:A:286:ALA:C	1:A:288:LEU:CD2	2.79	0.50
1:B:158:ASN:CG	1:B:172:SER:O	2.50	0.50
1:C:184:LYS:HB3	1:C:231:ASP:O	2.12	0.50
1:C:276:VAL:C	1:C:277:LEU:HD12	2.32	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:152:ARG:HB3	1:D:177:SER:HB2	1.94	0.50
1:D:266:THR:HA	1:D:270:PHE:O	2.11	0.50
1:E:141:GLY:C	1:E:336:PHE:HA	2.32	0.50
1:F:327:GLY:O	1:F:329:PHE:HE1	1.95	0.50
1:G:174:ILE:O	1:G:174:ILE:HG12	2.12	0.50
1:B:148:LEU:N	1:B:148:LEU:HD22	2.26	0.49
1:B:158:ASN:OD1	1:B:172:SER:O	2.29	0.49
1:B:319:GLN:HE22	1:B:324:PHE:HA	1.76	0.49
1:B:368:LEU:HD21	1:B:370:HIS:CE1	2.46	0.49
1:C:195:GLN:NE2	1:C:198:ASP:O	2.45	0.49
1:C:202:MET:O	1:C:205:SER:CA	2.60	0.49
1:E:307:ILE:HG13	1:E:307:ILE:O	2.12	0.49
1:F:212:MET:HA	1:F:212:MET:HE2	1.94	0.49
1:F:327:GLY:C	1:F:329:PHE:HE1	2.12	0.49
1:A:190:VAL:HG21	1:A:210:ARG:HH12	1.77	0.49
1:A:296:ILE:O	1:A:297:PHE:HB2	2.12	0.49
1:A:309:TRP:HA	1:A:309:TRP:CE3	2.47	0.49
1:D:290:ASP:C	1:D:292:GLU:H	2.15	0.49
1:D:349:ASP:OD1	1:D:350:ARG:CG	2.58	0.49
1:E:206:TYR:HD2	1:E:210:ARG:HB2	1.77	0.49
1:F:129:LEU:O	1:F:130:ARG:HB2	2.11	0.49
1:F:132:LEU:CD2	1:F:136:ASP:CB	2.90	0.49
1:G:244:ASP:CG	1:G:246:SER:HB3	2.33	0.49
1:D:197:MET:CE	1:D:203:LEU:HA	2.42	0.49
1:D:277:LEU:HD13	1:D:324:PHE:HB3	1.93	0.49
1:E:296:ILE:O	1:E:297:PHE:C	2.49	0.49
1:G:192:ALA:O	1:G:357:MET:SD	2.70	0.49
1:B:151:VAL:HG13	1:B:151:VAL:O	2.12	0.49
1:B:268:SER:HB3	1:B:374:THR:HG22	1.93	0.49
1:B:280:ARG:O	1:B:283:HIS:N	2.45	0.49
1:B:288:LEU:C	1:B:296:ILE:HD11	2.30	0.49
1:D:155:VAL:HG13	1:D:374:THR:HG21	1.94	0.49
1:F:200:ALA:O	1:F:203:LEU:N	2.44	0.49
1:F:258:ILE:CD1	1:F:275:ILE:HG21	2.42	0.49
1:F:280:ARG:O	1:F:283:HIS:HB3	2.12	0.49
1:A:267:GLU:OE1	1:F:317:LYS:NZ	2.41	0.49
1:A:286:ALA:C	1:A:288:LEU:HD21	2.33	0.49
1:B:280:ARG:O	1:B:281:ASP:C	2.51	0.49
1:C:343:VAL:HA	1:C:362:CYS:HA	1.95	0.49
1:D:131:ARG:HG2	1:D:132:LEU:O	2.12	0.49
1:E:273:SER:HB2	1:E:330:ASP:OD1	2.12	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:279:PRO:HG3	1:E:315:PRO:O	2.12	0.49
1:E:287:LEU:HD12	1:E:295:TYR:CE1	2.48	0.49
1:G:197:MET:C	1:G:198:ASP:OD1	2.51	0.49
1:G:273:SER:O	1:G:311:LEU:HD12	2.13	0.49
1:E:191:GLN:HE21	1:E:191:GLN:C	2.15	0.49
1:E:300:PRO:HG2	1:F:309:TRP:NE1	2.27	0.49
1:F:212:MET:O	1:F:215:LEU:N	2.46	0.49
1:A:308:MET:C	1:A:310:GLY:N	2.66	0.49
1:C:215:LEU:HD23	1:C:215:LEU:C	2.32	0.49
1:C:217:LEU:HD23	1:D:269:GLU:HB3	1.95	0.49
1:D:162:ASP:OD1	1:D:173:ASP:HB2	2.12	0.49
1:E:184:LYS:HG3	1:E:232:ASN:O	2.12	0.49
1:F:206:TYR:CD2	1:F:206:TYR:C	2.86	0.49
1:F:226:GLY:N	1:F:235:GLY:HA3	2.25	0.49
1:F:327:GLY:O	1:F:329:PHE:CD1	2.66	0.49
1:G:303:PHE:CD2	1:G:304:THR:O	2.66	0.49
1:A:174:ILE:O	1:A:174:ILE:HG12	2.13	0.49
1:A:201:PRO:O	1:A:202:MET:C	2.49	0.49
1:A:263:TYR:CZ	1:A:267:GLU:OE2	2.66	0.49
1:E:125:ILE:CG1	1:E:126:MET:N	2.73	0.49
1:F:225:ASN:N	1:F:225:ASN:ND2	2.60	0.49
1:F:358:LEU:HD23	1:F:358:LEU:C	2.32	0.49
1:G:239:VAL:HG12	1:G:239:VAL:O	2.13	0.49
1:C:155:VAL:HB	1:C:174:ILE:HG22	1.94	0.49
1:C:305:SER:O	1:C:307:ILE:HG23	2.13	0.49
1:D:290:ASP:O	1:D:291:ASN:HB2	2.11	0.49
1:D:343:VAL:HG12	1:D:362:CYS:CB	2.43	0.49
1:E:182:ASN:HB2	1:E:184:LYS:HZ2	1.78	0.49
1:A:254:ARG:HA	1:A:257:ILE:HD12	1.95	0.49
1:A:263:TYR:OH	1:F:280:ARG:NE	2.25	0.49
1:B:360:ILE:CG2	1:B:361:LEU:N	2.75	0.49
1:C:148:LEU:HB2	1:C:181:ALA:HB3	1.94	0.49
1:E:194:ARG:NH1	1:E:347:ARG:NH1	2.61	0.49
1:F:192:ALA:O	1:F:357:MET:CA	2.60	0.49
1:G:210:ARG:O	1:G:211:LEU:C	2.49	0.49
1:A:266:THR:HG21	1:F:279:PRO:CB	2.39	0.48
1:B:135:ARG:HH11	1:B:135:ARG:HG3	1.77	0.48
1:B:153:GLU:OE1	1:B:371:TYR:HB3	2.12	0.48
1:C:129:LEU:HD11	1:D:331:MET:HE3	1.86	0.48
1:C:330:ASP:OD1	1:C:330:ASP:C	2.52	0.48
1:D:199:ASP:OD1	1:D:200:ALA:N	2.46	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:155:VAL:HG11	1:E:374:THR:HB	1.95	0.48
1:G:158:ASN:CG	1:G:172:SER:HA	2.31	0.48
1:A:308:MET:O	1:A:310:GLY:N	2.45	0.48
1:B:155:VAL:HG12	1:B:374:THR:CB	2.39	0.48
1:B:244:ASP:OD1	1:B:247:LEU:HG	2.12	0.48
1:C:131:ARG:HH21	1:C:316:THR:HB	1.78	0.48
1:C:258:ILE:CD1	1:C:275:ILE:HG21	2.42	0.48
1:C:343:VAL:HA	1:C:361:LEU:O	2.13	0.48
1:D:131:ARG:HH21	1:D:133:THR:HG22	1.78	0.48
1:E:134:ILE:HD12	1:E:314:VAL:HG11	1.95	0.48
1:F:146:ASN:N	1:F:146:ASN:OD1	2.46	0.48
1:F:198:ASP:OD2	1:F:198:ASP:O	2.30	0.48
1:F:204:GLN:O	1:F:206:TYR:N	2.45	0.48
1:A:127:PRO:HD3	1:A:212:MET:HE2	1.94	0.48
1:A:202:MET:HG3	1:A:203:LEU:N	2.28	0.48
1:A:302:ALA:HA	1:A:306:ASN:HD22	1.77	0.48
1:B:249:ALA:N	1:B:252:ASP:OD2	2.46	0.48
1:C:342:THR:O	1:C:363:GLU:N	2.43	0.48
1:D:129:LEU:HD13	1:D:129:LEU:C	2.33	0.48
1:D:224:LEU:C	1:D:224:LEU:HD13	2.33	0.48
1:E:191:GLN:C	1:E:191:GLN:NE2	2.66	0.48
1:G:132:LEU:HG	1:G:136:ASP:OD1	2.13	0.48
1:G:142:ARG:HG2	1:G:142:ARG:HH11	1.78	0.48
1:G:199:ASP:O	1:G:203:LEU:N	2.45	0.48
1:A:137:LEU:HD22	1:A:329:PHE:CB	2.40	0.48
1:A:309:TRP:HA	1:A:309:TRP:HE3	1.78	0.48
1:C:245:THR:HA	1:C:248:ASN:ND2	2.28	0.48
1:D:158:ASN:H	1:D:158:ASN:HD22	1.58	0.48
1:E:189:TRP:HA	1:E:360:ILE:HD12	1.95	0.48
1:E:216:ALA:O	1:E:218:LYS:N	2.46	0.48
1:A:258:ILE:N	1:A:258:ILE:HD12	2.29	0.48
1:A:303:PHE:CD2	1:A:304:THR:N	2.82	0.48
1:B:146:ASN:N	1:B:146:ASN:ND2	2.62	0.48
1:B:349:ASP:O	1:B:352:ASN:HB2	2.13	0.48
1:D:194:ARG:HA	1:D:358:LEU:HD22	1.94	0.48
1:D:202:MET:O	1:D:203:LEU:C	2.51	0.48
1:D:302:ALA:O	1:D:305:SER:N	2.46	0.48
1:E:296:ILE:O	1:E:298:GLY:O	2.31	0.48
1:F:195:GLN:O	1:F:197:MET:N	2.47	0.48
1:F:249:ALA:N	1:F:252:ASP:OD2	2.44	0.48
1:B:155:VAL:HG13	1:B:374:THR:OG1	2.13	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:280:ARG:HG2	1:E:280:ARG:HH11	1.79	0.48
1:G:175:THR:C	1:G:176:PHE:HD2	2.16	0.48
1:A:266:THR:C	1:A:268:SER:N	2.67	0.48
1:C:210:ARG:HH21	1:D:153:GLU:CD	1.77	0.48
1:C:345:VAL:HA	1:C:359:THR:O	2.12	0.48
1:D:303:PHE:HA	1:D:306:ASN:CB	2.39	0.48
1:E:154:GLU:OE2	1:E:177:SER:OG	2.23	0.48
1:E:195:GLN:OE1	1:E:195:GLN:HA	2.14	0.48
1:G:343:VAL:HA	1:G:361:LEU:O	2.13	0.48
1:B:262:ILE:HD12	1:B:262:ILE:N	2.27	0.48
1:C:194:ARG:HA	1:C:358:LEU:HD12	1.96	0.48
1:C:339:MET:HG2	1:C:340:ASP:N	2.28	0.48
1:D:125:ILE:CG1	1:D:208:ASN:HD21	2.26	0.48
1:D:201:PRO:O	1:D:202:MET:C	2.52	0.48
1:E:130:ARG:CB	1:F:271:SER:OG	2.59	0.48
1:G:156:PHE:CZ	1:G:158:ASN:HB3	2.49	0.48
1:A:285:ILE:O	1:A:288:LEU:HD11	2.14	0.48
1:A:300:PRO:CA	1:A:303:PHE:HB3	2.39	0.48
1:A:303:PHE:CD2	1:A:303:PHE:C	2.87	0.48
1:B:262:ILE:H	1:B:262:ILE:CD1	2.27	0.48
1:C:129:LEU:CD1	1:D:331:MET:HE1	2.15	0.48
1:C:296:ILE:HG13	1:C:297:PHE:CE2	2.48	0.48
1:D:155:VAL:HG11	1:D:374:THR:HG21	1.95	0.48
1:D:245:THR:C	1:D:247:LEU:H	2.17	0.48
1:D:302:ALA:HB3	1:D:305:SER:OG	2.13	0.48
1:D:355:LYS:O	1:E:178:LYS:NZ	2.45	0.48
1:E:199:ASP:HB2	1:E:202:MET:HE2	1.96	0.48
1:E:224:LEU:HD13	1:E:224:LEU:C	2.33	0.48
1:E:309:TRP:HA	1:E:309:TRP:HE3	1.79	0.48
1:F:222:GLN:HE22	1:F:232:ASN:HB3	1.79	0.48
1:G:148:LEU:HB2	1:G:181:ALA:HB3	1.95	0.48
1:A:283:HIS:HA	1:A:303:PHE:HE1	1.79	0.48
1:B:249:ALA:HB3	1:B:252:ASP:CG	2.33	0.48
1:C:275:ILE:CG2	1:C:277:LEU:HD11	2.43	0.48
1:E:309:TRP:HA	1:E:309:TRP:CE3	2.49	0.48
1:F:265:VAL:HG22	1:F:377:ILE:HD13	1.94	0.48
1:F:361:LEU:O	1:F:361:LEU:CD1	2.55	0.48
1:A:132:LEU:O	1:A:314:VAL:HG13	2.13	0.47
1:A:179:GLN:HG3	1:A:180:THR:N	2.29	0.47
1:B:354:VAL:O	1:B:356:ASN:N	2.47	0.47
1:F:142:ARG:CG	1:F:337:ASP:CB	2.72	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:125:ILE:CG1	1:B:127:PRO:HG3	2.44	0.47
1:B:253:THR:HB	1:B:256:ASP:OD1	2.13	0.47
1:D:158:ASN:ND2	1:D:172:SER:HA	2.29	0.47
1:G:345:VAL:CG2	1:G:360:ILE:HG22	2.43	0.47
1:A:264:GLN:OE1	1:A:377:ILE:HG21	2.14	0.47
1:A:287:LEU:N	1:A:288:LEU:HD23	2.29	0.47
1:B:158:ASN:H	1:B:158:ASN:HD22	1.56	0.47
1:B:158:ASN:CG	1:B:172:SER:HB2	2.35	0.47
1:B:307:ILE:HA	1:B:313:VAL:HG23	1.96	0.47
1:C:132:LEU:HD21	1:C:136:ASP:HB2	1.95	0.47
1:C:174:ILE:HD13	1:C:174:ILE:N	2.28	0.47
1:G:156:PHE:CE2	1:G:158:ASN:CB	2.94	0.47
1:G:280:ARG:C	1:G:282:TRP:H	2.16	0.47
1:G:329:PHE:HA	1:G:332:ALA:HB2	1.90	0.47
1:G:356:ASN:C	1:G:356:ASN:ND2	2.67	0.47
1:A:184:LYS:HD2	1:A:231:ASP:HA	1.97	0.47
1:A:263:TYR:O	1:A:266:THR:HB	2.14	0.47
1:A:266:THR:C	1:A:268:SER:H	2.18	0.47
1:B:194:ARG:NH1	1:B:347:ARG:NH2	2.62	0.47
1:B:204:GLN:O	1:B:207:ILE:HB	2.15	0.47
1:B:212:MET:O	1:B:215:LEU:CA	2.59	0.47
1:B:236:LEU:HD13	1:B:329:PHE:HE2	1.80	0.47
1:C:347:ARG:O	1:C:348:GLU:C	2.51	0.47
1:D:155:VAL:HG12	1:D:374:THR:CB	2.39	0.47
1:D:307:ILE:HD13	1:D:310:GLY:O	2.15	0.47
1:E:162:ASP:OD1	1:E:173:ASP:HB2	2.15	0.47
1:B:128:GLY:O	1:B:213:TYR:OH	2.30	0.47
1:B:140:GLN:OE1	1:B:140:GLN:N	2.47	0.47
1:C:189:TRP:HB3	1:C:361:LEU:HB3	1.96	0.47
1:C:258:ILE:HD12	1:C:275:ILE:HG21	1.97	0.47
1:D:129:LEU:CD2	1:D:130:ARG:H	2.07	0.47
1:E:190:VAL:HG22	1:E:211:LEU:HD11	1.95	0.47
1:G:138:LEU:HD21	1:G:329:PHE:HB3	1.94	0.47
1:G:196:VAL:HG22	1:G:202:MET:HE1	1.93	0.47
1:G:342:THR:O	1:G:363:GLU:N	2.47	0.47
1:A:224:LEU:HD13	1:A:237:ASN:OD1	2.14	0.47
1:B:125:ILE:CD1	1:B:127:PRO:CG	2.93	0.47
1:B:158:ASN:CG	1:B:172:SER:CA	2.83	0.47
1:B:158:ASN:HD22	1:B:172:SER:HB2	1.77	0.47
1:D:142:ARG:HA	1:D:337:ASP:H	1.79	0.47
1:E:193:SER:C	1:E:195:GLN:N	2.68	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:216:ALA:O	1:E:217:LEU:C	2.53	0.47
1:E:249:ALA:O	1:E:250:THR:C	2.51	0.47
1:F:304:THR:HG22	1:F:305:SER:N	2.30	0.47
1:A:245:THR:HG23	1:A:248:ASN:HD21	1.80	0.47
1:A:265:VAL:O	1:A:265:VAL:HG12	2.14	0.47
1:B:156:PHE:HB3	1:B:158:ASN:CG	2.34	0.47
1:B:158:ASN:CG	1:B:172:SER:C	2.74	0.47
1:B:190:VAL:HG23	1:B:190:VAL:O	2.15	0.47
1:B:194:ARG:CD	1:B:357:MET:HA	2.43	0.47
1:C:191:GLN:HA	1:C:358:LEU:O	2.15	0.47
1:C:195:GLN:OE1	1:C:195:GLN:HA	2.15	0.47
1:C:335:VAL:HG13	1:C:366:LEU:CD2	2.45	0.47
1:D:155:VAL:HG11	1:D:374:THR:CG2	2.45	0.47
1:D:197:MET:HE1	1:D:203:LEU:HA	1.95	0.47
1:E:131:ARG:HH12	1:E:316:THR:HA	1.78	0.47
1:E:201:PRO:HG2	1:E:202:MET:H	1.79	0.47
1:E:296:ILE:CG2	1:E:297:PHE:CD1	2.97	0.47
1:E:301:GLN:OE1	1:E:304:THR:HB	2.14	0.47
1:F:189:TRP:HA	1:F:360:ILE:O	2.15	0.47
1:F:301:GLN:O	1:F:302:ALA:C	2.53	0.47
1:G:174:ILE:HD13	1:G:174:ILE:N	2.14	0.47
1:A:150:TYR:HE1	1:A:181:ALA:HB2	1.79	0.47
1:A:179:GLN:HA	1:A:179:GLN:NE2	2.30	0.47
1:A:331:MET:CE	1:F:209:ASN:O	2.63	0.47
1:B:159:ALA:HB1	1:B:160:PRO:CD	2.39	0.47
1:E:130:ARG:HG2	1:F:271:SER:OG	2.15	0.47
1:E:155:VAL:CG2	1:E:174:ILE:HG22	2.35	0.47
1:G:200:ALA:N	1:G:201:PRO:HD3	2.29	0.47
1:G:360:ILE:HG13	1:G:360:ILE:O	2.14	0.47
1:B:156:PHE:CD2	1:B:158:ASN:HB3	2.50	0.47
1:C:146:ASN:ND2	1:C:365:ARG:HH21	2.11	0.47
1:C:225:ASN:ND2	1:C:225:ASN:N	2.62	0.47
1:D:194:ARG:O	1:D:195:GLN:C	2.54	0.47
1:E:186:ILE:HD11	1:E:222:GLN:HG3	1.96	0.47
1:E:329:PHE:CD1	1:E:329:PHE:N	2.82	0.47
1:G:299:GLY:O	1:G:300:PRO:C	2.52	0.47
1:A:155:VAL:CG1	1:A:374:THR:CG2	2.92	0.47
1:C:206:TYR:CE2	1:C:210:ARG:HD3	2.50	0.47
1:C:275:ILE:HG22	1:C:277:LEU:CD1	2.45	0.47
1:C:297:PHE:CD2	1:C:297:PHE:N	2.83	0.47
1:D:124:ILE:O	1:D:125:ILE:HG22	2.15	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:217:LEU:O	1:D:217:LEU:HD23	2.15	0.47
1:E:295:TYR:O	1:E:296:ILE:O	2.33	0.47
1:E:352:ASN:O	1:E:355:LYS:O	2.32	0.47
1:F:322:GLY:O	1:F:380:THR:HG22	2.14	0.47
1:F:361:LEU:C	1:F:361:LEU:CD1	2.83	0.47
1:A:158:ASN:N	1:A:158:ASN:HD22	2.12	0.46
1:B:306:ASN:HD22	1:B:315:PRO:HG2	1.80	0.46
1:D:301:GLN:C	1:D:303:PHE:N	2.66	0.46
1:E:220:GLU:OE2	1:E:316:THR:HG23	2.13	0.46
1:A:202:MET:HB2	1:B:336:PHE:CE2	2.41	0.46
1:A:240:ALA:CB	1:A:376:ILE:CG2	2.93	0.46
1:B:161:GLY:C	1:B:172:SER:N	2.68	0.46
1:B:209:ASN:HB3	1:C:331:MET:CE	2.45	0.46
1:B:211:LEU:HD13	1:B:211:LEU:HA	1.64	0.46
1:C:133:THR:HA	1:C:220:GLU:OE2	2.14	0.46
1:C:200:ALA:O	1:C:202:MET:N	2.48	0.46
1:C:227:ASP:C	1:C:229:THR:H	2.19	0.46
1:C:342:THR:O	1:C:362:CYS:HA	2.16	0.46
1:C:377:ILE:N	1:C:377:ILE:HD12	2.31	0.46
1:E:325:THR:HG22	1:E:329:PHE:HZ	1.79	0.46
1:E:356:ASN:O	1:E:357:MET:HB3	2.16	0.46
1:F:137:LEU:O	1:F:137:LEU:HD23	2.15	0.46
1:A:207:ILE:O	1:A:211:LEU:HB2	2.16	0.46
1:D:174:ILE:H	1:D:174:ILE:CD1	2.27	0.46
1:E:301:GLN:O	1:E:304:THR:N	2.48	0.46
1:G:132:LEU:HG	1:G:136:ASP:CG	2.35	0.46
1:A:196:VAL:O	1:A:199:ASP:HB2	2.16	0.46
1:D:346:SER:O	1:D:348:GLU:HG3	2.16	0.46
1:D:349:ASP:O	1:D:350:ARG:C	2.54	0.46
1:E:128:GLY:N	1:E:213:TYR:CD1	2.81	0.46
1:E:302:ALA:HA	1:E:305:SER:OG	2.16	0.46
1:E:358:LEU:HD12	1:E:358:LEU:N	2.30	0.46
1:F:295:TYR:CE2	1:F:300:PRO:HG3	2.51	0.46
1:A:358:LEU:C	1:A:358:LEU:HD12	2.36	0.46
1:B:148:LEU:HD21	1:B:181:ALA:HB3	1.97	0.46
1:B:354:VAL:C	1:B:356:ASN:H	2.18	0.46
1:D:122:PRO:CB	1:D:343:VAL:HG23	2.45	0.46
1:D:150:TYR:OH	1:D:152:ARG:NH2	2.49	0.46
1:D:224:LEU:HD12	1:D:225:ASN:CG	2.36	0.46
1:F:342:THR:O	1:F:362:CYS:CA	2.62	0.46
1:G:155:VAL:CG2	1:G:156:PHE:N	2.78	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:156:PHE:CG	1:G:158:ASN:HB3	2.49	0.46
1:A:195:GLN:CG	1:A:196:VAL:N	2.69	0.46
1:A:321:ALA:C	1:A:323:THR:H	2.18	0.46
1:C:201:PRO:O	1:C:202:MET:C	2.54	0.46
1:C:211:LEU:HD23	1:C:211:LEU:C	2.35	0.46
1:D:149:GLU:HA	1:D:180:THR:HA	1.98	0.46
1:F:198:ASP:O	1:F:199:ASP:C	2.54	0.46
1:F:202:MET:O	1:F:203:LEU:C	2.53	0.46
1:G:153:GLU:OE1	1:G:372:ARG:NE	2.48	0.46
1:G:217:LEU:HD12	1:G:217:LEU:N	2.31	0.46
1:G:273:SER:H	1:G:328:GLY:HA2	1.81	0.46
1:A:196:VAL:O	1:A:199:ASP:N	2.47	0.46
1:A:256:ASP:O	1:A:259:ALA:HB3	2.16	0.46
1:A:309:TRP:CH2	1:F:301:GLN:HB3	2.51	0.46
1:B:190:VAL:HG12	1:C:176:PHE:HZ	1.79	0.46
1:B:209:ASN:O	1:C:331:MET:CE	2.63	0.46
1:C:184:LYS:CB	1:C:233:LEU:HD21	2.46	0.46
1:C:296:ILE:O	1:C:297:PHE:HD2	1.98	0.46
1:E:300:PRO:HG2	1:F:309:TRP:HE1	1.81	0.46
1:E:302:ALA:HA	1:E:305:SER:HG	1.80	0.46
1:F:151:VAL:O	1:F:151:VAL:HG13	2.16	0.46
1:F:162:ASP:OD1	1:F:173:ASP:CG	2.54	0.46
1:F:292:GLU:HB2	1:F:294:ARG:HD3	1.96	0.46
1:G:152:ARG:HH21	1:G:370:HIS:HB2	1.79	0.46
1:G:197:MET:SD	1:G:197:MET:O	2.73	0.46
1:A:158:ASN:ND2	1:A:172:SER:CA	2.79	0.46
1:A:206:TYR:HB3	1:A:207:ILE:HD12	1.98	0.46
1:A:343:VAL:HA	1:A:361:LEU:O	2.16	0.46
1:B:266:THR:HA	1:B:270:PHE:O	2.16	0.46
1:C:207:ILE:H	1:C:207:ILE:CD1	2.28	0.46
1:D:127:PRO:CD	1:D:212:MET:HE3	2.30	0.46
1:G:217:LEU:HD12	1:G:217:LEU:H	1.80	0.46
1:G:366:LEU:HD12	1:G:367:ALA:CA	2.46	0.46
1:A:155:VAL:CG2	1:A:174:ILE:HG22	2.37	0.46
1:A:289:LYS:HD2	1:A:289:LYS:H	1.80	0.46
1:D:174:ILE:HD13	1:D:174:ILE:O	2.16	0.46
1:D:299:GLY:O	1:D:301:GLN:HG2	2.16	0.46
1:E:174:ILE:O	1:E:174:ILE:HG12	2.15	0.46
1:F:224:LEU:CD1	1:F:237:ASN:HD21	2.29	0.46
1:G:327:GLY:N	1:G:329:PHE:CE2	2.74	0.46
1:A:149:GLU:OE1	1:F:195:GLN:CG	2.64	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:174:ILE:HD13	1:B:174:ILE:O	2.15	0.46
1:D:190:VAL:HG11	1:D:211:LEU:CD2	2.41	0.46
1:F:254:ARG:HG2	1:F:381:PHE:HD2	1.81	0.46
1:G:200:ALA:O	1:G:201:PRO:C	2.53	0.46
1:G:202:MET:HG2	1:G:203:LEU:N	2.31	0.46
1:A:131:ARG:HH21	1:A:316:THR:CB	2.29	0.45
1:A:290:ASP:C	1:A:292:GLU:N	2.69	0.45
1:C:217:LEU:CD2	1:D:269:GLU:HB3	2.46	0.45
1:D:153:GLU:O	1:D:155:VAL:N	2.49	0.45
1:A:263:TYR:CE2	1:F:280:ARG:NE	2.84	0.45
1:G:134:ILE:O	1:G:137:LEU:HB2	2.15	0.45
1:B:158:ASN:OD1	1:B:172:SER:C	2.55	0.45
1:B:180:THR:CG2	1:B:181:ALA:N	2.80	0.45
1:B:299:GLY:O	1:B:300:PRO:C	2.55	0.45
1:C:186:ILE:CD1	1:C:222:GLN:HG3	2.41	0.45
1:C:283:HIS:HE1	1:D:260:HIS:HA	1.81	0.45
1:E:132:LEU:HG	1:E:132:LEU:O	2.15	0.45
1:E:141:GLY:O	1:E:336:PHE:HA	2.17	0.45
1:E:157:THR:HB	1:E:267:GLU:OE1	2.15	0.45
1:E:215:LEU:C	1:E:218:LYS:H	2.17	0.45
1:E:280:ARG:O	1:E:283:HIS:HB3	2.17	0.45
1:A:194:ARG:O	1:A:198:ASP:N	2.44	0.45
1:A:282:TRP:HA	1:A:282:TRP:CE3	2.51	0.45
1:A:286:ALA:CB	1:A:303:PHE:HD1	2.29	0.45
1:B:326:VAL:HG12	1:B:327:GLY:N	2.32	0.45
1:C:130:ARG:O	1:C:131:ARG:O	2.34	0.45
1:C:296:ILE:C	1:C:297:PHE:CD2	2.90	0.45
1:C:361:LEU:HD12	1:C:361:LEU:C	2.36	0.45
1:D:290:ASP:C	1:D:292:GLU:N	2.70	0.45
1:F:290:ASP:CG	1:F:291:ASN:H	2.20	0.45
1:B:158:ASN:N	1:B:158:ASN:HD22	2.13	0.45
1:C:227:ASP:O	1:C:232:ASN:ND2	2.50	0.45
1:D:156:PHE:CD2	1:D:158:ASN:N	2.78	0.45
1:F:153:GLU:O	1:F:155:VAL:N	2.50	0.45
1:F:291:ASN:CG	1:F:292:GLU:H	2.20	0.45
1:A:139:ALA:O	1:A:335:VAL:HG12	2.16	0.45
1:A:307:ILE:C	1:A:307:ILE:CD1	2.82	0.45
1:B:323:THR:HG22	1:B:324:PHE:N	2.32	0.45
1:D:223:LEU:N	1:D:223:LEU:HD12	2.32	0.45
1:E:258:ILE:H	1:E:258:ILE:CD1	2.30	0.45
1:F:192:ALA:O	1:F:357:MET:CB	2.64	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:236:LEU:O	1:F:240:ALA:N	2.50	0.45
1:F:253:THR:O	1:F:255:ALA:N	2.48	0.45
1:F:322:GLY:O	1:F:380:THR:HB	2.17	0.45
1:A:155:VAL:HA	1:A:174:ILE:HG22	1.99	0.45
1:A:267:GLU:OE1	1:F:317:LYS:CE	2.65	0.45
1:A:296:ILE:C	1:A:297:PHE:CD2	2.90	0.45
1:B:227:ASP:O	1:B:229:THR:HG23	2.17	0.45
1:D:194:ARG:HG3	1:D:358:LEU:HD21	1.98	0.45
1:E:227:ASP:C	1:E:229:THR:CG2	2.85	0.45
1:G:129:LEU:O	1:G:130:ARG:HB2	2.17	0.45
1:G:129:LEU:C	1:G:131:ARG:N	2.69	0.45
1:G:197:MET:HE3	1:G:345:VAL:HG11	1.99	0.45
1:A:123:GLY:O	1:A:124:ILE:CG2	2.59	0.45
1:B:209:ASN:C	1:C:331:MET:HE2	2.37	0.45
1:F:275:ILE:HG22	1:F:276:VAL:N	2.32	0.45
1:G:187:ALA:HB1	1:G:362:CYS:O	2.17	0.45
1:A:290:ASP:OD1	1:A:294:ARG:HB3	2.17	0.45
1:E:341:ALA:HA	1:E:363:GLU:O	2.16	0.45
1:G:236:LEU:N	1:G:236:LEU:HD12	2.32	0.45
1:A:197:MET:C	1:A:199:ASP:N	2.70	0.45
1:A:207:ILE:HG22	1:A:212:MET:HG2	1.98	0.45
1:A:219:GLU:O	1:A:223:LEU:HD13	2.17	0.45
1:A:282:TRP:HA	1:A:282:TRP:HE3	1.82	0.45
1:A:361:LEU:HD12	1:A:362:CYS:H	1.82	0.45
1:E:126:MET:HE3	1:E:129:LEU:CD2	2.45	0.45
1:E:194:ARG:HE	1:E:356:ASN:ND2	2.15	0.45
1:E:202:MET:CE	1:E:203:LEU:HB2	2.47	0.45
1:E:290:ASP:C	1:E:292:GLU:H	2.21	0.45
1:F:244:ASP:OD2	1:F:246:SER:HB3	2.17	0.45
1:G:270:PHE:CE1	1:G:372:ARG:NE	2.85	0.45
1:G:329:PHE:O	1:G:330:ASP:C	2.56	0.45
1:A:179:GLN:HA	1:A:179:GLN:HE21	1.82	0.44
1:A:197:MET:SD	1:A:198:ASP:N	2.90	0.44
1:B:289:LYS:HA	1:B:296:ILE:CD1	2.47	0.44
1:D:201:PRO:C	1:D:203:LEU:N	2.68	0.44
1:D:224:LEU:HD13	1:D:237:ASN:OD1	2.17	0.44
1:D:305:SER:O	1:D:307:ILE:N	2.45	0.44
1:E:156:PHE:O	1:E:158:ASN:ND2	2.50	0.44
1:E:191:GLN:HB2	1:E:358:LEU:O	2.17	0.44
1:E:203:LEU:HD12	1:E:206:TYR:CB	2.47	0.44
1:E:206:TYR:O	1:E:206:TYR:HD2	2.00	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:262:ILE:H	1:E:262:ILE:CD1	2.30	0.44
1:E:301:GLN:OE1	1:E:301:GLN:O	2.35	0.44
1:E:347:ARG:C	1:E:349:ASP:H	2.20	0.44
1:F:264:GLN:HA	1:F:267:GLU:HG2	1.98	0.44
1:F:323:THR:HA	1:F:380:THR:HG22	1.98	0.44
1:F:378:LYS:CG	1:F:379:GLY:N	2.79	0.44
1:G:150:TYR:CE1	1:G:179:GLN:HB3	2.52	0.44
1:A:239:VAL:HG21	1:A:370:HIS:HD1	1.82	0.44
1:A:273:SER:O	1:A:312:PRO:HD2	2.17	0.44
1:B:329:PHE:CD1	1:B:329:PHE:N	2.81	0.44
1:B:333:SER:HB2	1:B:369:ALA:O	2.17	0.44
1:C:245:THR:HG23	1:C:248:ASN:HD22	1.81	0.44
1:C:247:LEU:HB3	1:C:260:HIS:CD2	2.51	0.44
1:E:125:ILE:HG23	1:E:126:MET:H	1.82	0.44
1:E:194:ARG:NH1	1:E:347:ARG:HH22	2.12	0.44
1:F:142:ARG:NH2	1:F:340:ASP:CG	2.71	0.44
1:F:174:ILE:H	1:F:174:ILE:CD1	2.17	0.44
1:A:236:LEU:HD23	1:A:370:HIS:CE1	2.53	0.44
1:B:173:ASP:OD1	1:B:174:ILE:N	2.50	0.44
1:C:285:ILE:HG21	1:C:308:MET:HE1	1.99	0.44
1:C:359:THR:O	1:C:359:THR:HG23	2.18	0.44
1:E:211:LEU:HG	1:E:362:CYS:SG	2.56	0.44
1:F:257:ILE:C	1:F:259:ALA:N	2.69	0.44
1:F:275:ILE:CG2	1:F:277:LEU:HD11	2.47	0.44
1:F:347:ARG:O	1:F:349:ASP:N	2.50	0.44
1:C:142:ARG:CB	1:C:337:ASP:O	2.66	0.44
1:C:156:PHE:HD2	1:C:156:PHE:HA	1.72	0.44
1:D:202:MET:CA	1:D:205:SER:OG	2.61	0.44
1:D:247:LEU:HD21	1:D:260:HIS:CG	2.53	0.44
1:F:288:LEU:HD23	1:F:289:LYS:O	2.18	0.44
1:A:188:HIS:O	1:A:361:LEU:HD12	2.17	0.44
1:A:224:LEU:HD12	1:A:225:ASN:CG	2.38	0.44
1:A:295:TYR:HD2	1:A:295:TYR:HA	1.69	0.44
1:A:374:THR:C	1:A:376:ILE:H	2.21	0.44
1:B:129:LEU:HD23	1:B:129:LEU:O	2.17	0.44
1:D:258:ILE:O	1:D:261:ALA:HB3	2.17	0.44
1:C:185:THR:HA	1:C:365:ARG:HA	1.99	0.44
1:C:203:LEU:O	1:C:206:TYR:HB2	2.16	0.44
1:C:234:GLU:O	1:C:368:LEU:HD23	2.18	0.44
1:D:191:GLN:NE2	1:E:176:PHE:CD2	2.85	0.44
1:D:297:PHE:CD2	1:D:308:MET:HB2	2.52	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:254:ARG:HD3	1:G:381:PHE:CE1	2.52	0.44
1:G:290:ASP:O	1:G:292:GLU:N	2.50	0.44
1:A:121:ILE:C	1:A:123:GLY:H	2.20	0.44
1:A:241:THR:O	1:A:377:ILE:HA	2.17	0.44
1:A:269:GLU:CB	1:F:217:LEU:HD21	2.16	0.44
1:B:194:ARG:NH2	1:B:347:ARG:CZ	2.80	0.44
1:B:237:ASN:HD22	1:B:237:ASN:N	2.15	0.44
1:D:280:ARG:HG3	1:E:309:TRP:HB3	2.00	0.44
1:F:349:ASP:O	1:F:352:ASN:OD1	2.35	0.44
1:F:356:ASN:O	1:F:357:MET:HG2	2.18	0.44
1:G:155:VAL:HG11	1:G:374:THR:CG2	2.47	0.44
1:A:330:ASP:OD2	1:F:130:ARG:NH2	2.43	0.44
1:B:224:LEU:HD13	1:B:224:LEU:C	2.38	0.44
1:E:156:PHE:CD2	1:E:158:ASN:N	2.77	0.44
1:F:194:ARG:HH22	1:G:363:GLU:CD	2.22	0.44
1:G:197:MET:HE1	1:G:358:LEU:HD23	1.85	0.44
1:G:327:GLY:H	1:G:329:PHE:HE2	1.63	0.44
1:G:355:LYS:O	1:G:357:MET:HB2	2.17	0.44
1:A:154:GLU:OE2	1:A:177:SER:HB2	2.18	0.44
1:A:217:LEU:C	1:A:217:LEU:HD23	2.38	0.44
1:A:223:LEU:N	1:A:223:LEU:HD12	2.32	0.44
1:B:142:ARG:HG2	1:B:337:ASP:O	2.18	0.44
1:B:200:ALA:HB1	1:B:201:PRO:HD2	1.98	0.44
1:D:161:GLY:O	1:D:162:ASP:C	2.56	0.44
1:D:194:ARG:HB2	1:D:358:LEU:CD1	2.48	0.44
1:D:194:ARG:HB2	1:D:358:LEU:HD13	1.99	0.44
1:E:219:GLU:HG2	1:E:223:LEU:HD11	1.99	0.44
1:E:254:ARG:CG	1:E:381:PHE:CE2	2.98	0.44
1:A:263:TYR:HB2	1:F:303:PHE:CE2	2.53	0.43
1:A:345:VAL:HG22	1:A:360:ILE:HG23	2.00	0.43
1:B:142:ARG:HA	1:B:337:ASP:H	1.83	0.43
1:C:301:GLN:HG2	1:C:302:ALA:N	2.32	0.43
1:E:190:VAL:CG2	1:E:360:ILE:HD11	2.48	0.43
1:E:366:LEU:HD12	1:E:367:ALA:N	2.32	0.43
1:F:324:PHE:HD2	1:F:381:PHE:HE1	0.86	0.43
1:A:194:ARG:CA	1:A:198:ASP:OD2	2.66	0.43
1:B:273:SER:HB2	1:B:330:ASP:H	1.82	0.43
1:C:335:VAL:HG13	1:C:366:LEU:HD21	2.00	0.43
1:E:220:GLU:CD	1:E:316:THR:HG21	2.35	0.43
1:E:254:ARG:HG3	1:E:381:PHE:HE2	1.83	0.43
1:F:204:GLN:O	1:F:208:ASN:HB2	2.18	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:213:TYR:O	1:F:217:LEU:HB2	2.17	0.43
1:G:184:LYS:HD2	1:G:231:ASP:HA	1.98	0.43
1:A:292:GLU:C	1:A:294:ARG:H	2.22	0.43
1:B:208:ASN:N	1:B:208:ASN:ND2	2.66	0.43
1:C:283:HIS:CE1	1:D:260:HIS:HA	2.53	0.43
1:D:195:GLN:OE1	1:D:195:GLN:HA	2.18	0.43
1:D:296:ILE:C	1:D:298:GLY:N	2.70	0.43
1:E:288:LEU:O	1:E:295:TYR:HA	2.18	0.43
1:E:345:VAL:HG13	1:E:359:THR:O	2.18	0.43
1:G:155:VAL:CG1	1:G:374:THR:OG1	2.58	0.43
1:G:288:LEU:HD12	1:G:296:ILE:HD12	2.00	0.43
1:A:329:PHE:HA	1:A:332:ALA:HB3	2.01	0.43
1:B:155:VAL:HG13	1:B:374:THR:HG21	2.00	0.43
1:B:158:ASN:CB	1:B:172:SER:CA	2.86	0.43
1:B:206:TYR:O	1:B:210:ARG:HB2	2.19	0.43
1:B:288:LEU:C	1:B:288:LEU:HD23	2.39	0.43
1:E:186:ILE:CD1	1:E:222:GLN:HG3	2.48	0.43
1:E:258:ILE:O	1:E:261:ALA:HB3	2.18	0.43
1:E:296:ILE:HD13	1:E:296:ILE:HA	1.88	0.43
1:E:311:LEU:HA	1:E:312:PRO:HD3	1.92	0.43
1:F:215:LEU:C	1:F:215:LEU:HD23	2.38	0.43
1:A:148:LEU:O	1:A:180:THR:HG23	2.19	0.43
1:B:194:ARG:HH11	1:B:356:ASN:HD21	1.66	0.43
1:C:345:VAL:HG12	1:C:346:SER:N	2.33	0.43
1:E:191:GLN:CB	1:E:359:THR:HA	2.47	0.43
1:F:174:ILE:O	1:F:174:ILE:HG12	2.18	0.43
1:F:343:VAL:CA	1:F:361:LEU:O	2.66	0.43
1:G:158:ASN:ND2	1:G:172:SER:OG	2.46	0.43
1:G:335:VAL:HA	1:G:368:LEU:HA	2.00	0.43
1:A:202:MET:CB	1:B:336:PHE:HE2	2.25	0.43
1:F:270:PHE:HE1	1:F:372:ARG:NH1	2.15	0.43
1:F:322:GLY:O	1:F:380:THR:CG2	2.67	0.43
1:A:236:LEU:HD23	1:A:370:HIS:NE2	2.34	0.43
1:B:182:ASN:HB2	1:B:184:LYS:NZ	2.33	0.43
1:B:287:LEU:HD22	1:B:287:LEU:N	2.33	0.43
1:C:229:THR:O	1:C:232:ASN:HB2	2.19	0.43
1:D:243:TYR:HE2	1:D:248:ASN:HD21	1.67	0.43
1:F:148:LEU:O	1:F:181:ALA:N	2.46	0.43
1:F:156:PHE:O	1:F:158:ASN:ND2	2.52	0.43
1:G:202:MET:O	1:G:205:SER:N	2.52	0.43
1:C:185:THR:OG1	1:C:365:ARG:HG2	2.18	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:254:ARG:HB3	1:C:381:PHE:CE2	2.54	0.43
1:C:314:VAL:HG23	1:C:314:VAL:O	2.19	0.43
1:C:325:THR:HA	1:C:377:ILE:O	2.18	0.43
1:D:130:ARG:CD	1:D:131:ARG:N	2.82	0.43
1:D:208:ASN:N	1:D:208:ASN:HD22	2.15	0.43
1:D:278:ASN:HB3	1:D:281:ASP:OD2	2.19	0.43
1:E:279:PRO:HD3	1:E:316:THR:O	2.19	0.43
1:F:222:GLN:HA	1:F:222:GLN:HE21	1.84	0.43
1:A:296:ILE:O	1:A:297:PHE:CB	2.67	0.43
1:A:343:VAL:HA	1:A:362:CYS:HA	2.01	0.43
1:B:238:LYS:HD2	1:B:238:LYS:HA	1.73	0.43
1:B:253:THR:HG22	1:B:254:ARG:H	1.83	0.43
1:C:347:ARG:HG2	1:C:348:GLU:N	2.34	0.43
1:E:203:LEU:C	1:E:206:TYR:H	2.09	0.43
1:G:349:ASP:OD2	1:G:350:ARG:HG3	2.18	0.43
1:D:174:ILE:CG1	1:D:176:PHE:HE2	2.28	0.43
1:D:236:LEU:HD23	1:D:370:HIS:CE1	2.54	0.43
1:E:333:SER:HA	1:E:371:TYR:CD1	2.53	0.43
1:F:211:LEU:CD2	1:F:212:MET:CE	2.97	0.43
1:F:306:ASN:HB3	1:F:313:VAL:HB	2.00	0.43
1:F:344:GLU:O	1:F:361:LEU:HD12	2.19	0.43
1:G:282:TRP:CH2	1:G:313:VAL:HG21	2.54	0.43
1:B:194:ARG:HD2	1:B:358:LEU:CD1	2.49	0.42
1:B:215:LEU:HD22	1:B:216:ALA:CA	2.49	0.42
1:B:215:LEU:HD22	1:B:216:ALA:HA	2.00	0.42
1:C:274:GLY:C	1:C:275:ILE:HD12	2.40	0.42
1:C:376:ILE:C	1:C:377:ILE:HD12	2.39	0.42
1:E:194:ARG:NE	1:E:356:ASN:OD1	2.52	0.42
1:G:285:ILE:HA	1:G:288:LEU:CD1	2.49	0.42
1:G:309:TRP:HA	1:G:309:TRP:CE3	2.54	0.42
1:A:124:ILE:O	1:A:126:MET:HE3	2.19	0.42
1:A:137:LEU:HB3	1:A:138:LEU:HD12	2.01	0.42
1:A:203:LEU:CD1	1:A:207:ILE:HD11	2.49	0.42
1:A:345:VAL:HG22	1:A:360:ILE:HG12	2.00	0.42
1:C:195:GLN:C	1:C:197:MET:N	2.71	0.42
1:C:207:ILE:CA	1:C:211:LEU:HB3	2.40	0.42
1:D:280:ARG:HG3	1:E:309:TRP:O	2.19	0.42
1:E:194:ARG:H	1:E:357:MET:HA	1.84	0.42
1:G:233:LEU:HD13	1:G:368:LEU:HD22	2.00	0.42
1:A:203:LEU:O	1:A:206:TYR:N	2.52	0.42
1:A:277:LEU:HD23	1:A:277:LEU:HA	1.52	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:195:GLN:HG3	1:D:196:VAL:N	2.34	0.42
1:D:277:LEU:CD1	1:D:324:PHE:HB3	2.49	0.42
1:F:344:GLU:H	1:F:361:LEU:HD13	1.84	0.42
1:G:244:ASP:OD2	1:G:247:LEU:HG	2.20	0.42
1:G:355:LYS:HB3	1:G:355:LYS:HE2	1.61	0.42
1:A:132:LEU:N	1:A:132:LEU:HD12	2.33	0.42
1:C:183:VAL:CA	1:C:367:ALA:HB2	2.35	0.42
1:C:227:ASP:HB3	1:C:229:THR:HG1	1.85	0.42
1:C:256:ASP:O	1:C:259:ALA:HB3	2.20	0.42
1:C:280:ARG:O	1:C:283:HIS:HB3	2.20	0.42
1:D:236:LEU:HA	1:D:370:HIS:CE1	2.54	0.42
1:D:258:ILE:N	1:D:258:ILE:HD12	2.34	0.42
1:D:258:ILE:HG21	1:D:308:MET:HE2	2.01	0.42
1:E:127:PRO:HA	1:E:213:TYR:HB2	2.01	0.42
1:E:253:THR:HG22	1:E:255:ALA:H	1.84	0.42
1:E:296:ILE:C	1:E:298:GLY:N	2.70	0.42
1:G:194:ARG:O	1:G:195:GLN:C	2.55	0.42
1:A:194:ARG:HA	1:A:198:ASP:OD2	2.20	0.42
1:B:206:TYR:CD2	1:B:210:ARG:HB2	2.55	0.42
1:B:209:ASN:HB3	1:C:331:MET:HE3	2.00	0.42
1:C:202:MET:O	1:C:205:SER:HB3	2.19	0.42
1:D:268:SER:HB3	1:D:374:THR:HG22	2.01	0.42
1:E:158:ASN:H	1:E:158:ASN:HD22	1.61	0.42
1:E:236:LEU:HD13	1:E:329:PHE:CE2	2.54	0.42
1:F:129:LEU:O	1:F:130:ARG:CB	2.66	0.42
1:G:333:SER:HB3	1:G:369:ALA:O	2.18	0.42
1:A:195:GLN:HG3	1:A:196:VAL:CG2	2.35	0.42
1:A:208:ASN:N	1:A:208:ASN:HD22	2.17	0.42
1:B:217:LEU:O	1:B:220:GLU:N	2.53	0.42
1:C:224:LEU:HD13	1:C:237:ASN:HD21	1.82	0.42
1:A:153:GLU:O	1:A:155:VAL:N	2.52	0.42
1:A:349:ASP:OD1	1:A:349:ASP:C	2.57	0.42
1:B:217:LEU:O	1:B:218:LYS:C	2.57	0.42
1:E:275:ILE:HG22	1:E:326:VAL:HG13	2.02	0.42
1:E:301:GLN:O	1:E:302:ALA:C	2.58	0.42
1:E:358:LEU:HB3	1:E:359:THR:H	1.61	0.42
1:F:345:VAL:HG13	1:F:358:LEU:HD11	2.02	0.42
1:G:133:THR:HB	1:G:220:GLU:OE2	2.19	0.42
1:B:125:ILE:HD11	1:B:127:PRO:HG3	2.02	0.42
1:B:152:ARG:O	1:B:154:GLU:N	2.53	0.42
1:B:244:ASP:CG	1:B:247:LEU:HG	2.40	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:190:VAL:HG22	1:D:176:PHE:HE1	1.84	0.42
1:D:173:ASP:OD1	1:D:174:ILE:HD13	2.20	0.42
1:F:222:GLN:HA	1:F:222:GLN:NE2	2.35	0.42
1:G:211:LEU:C	1:G:211:LEU:HD23	2.40	0.42
1:G:299:GLY:O	1:G:303:PHE:HB2	2.20	0.42
1:A:175:THR:HG22	1:A:176:PHE:H	1.84	0.42
1:B:186:ILE:HG22	1:B:187:ALA:N	2.34	0.42
1:B:342:THR:O	1:B:362:CYS:SG	2.77	0.42
1:C:152:ARG:HG3	1:C:371:TYR:O	2.19	0.42
1:C:198:ASP:O	1:C:198:ASP:CG	2.57	0.42
1:C:224:LEU:CD1	1:C:237:ASN:HD21	2.33	0.42
1:D:158:ASN:CG	1:D:172:SER:CA	2.80	0.42
1:D:292:GLU:O	1:D:294:ARG:N	2.53	0.42
1:D:343:VAL:CG1	1:D:362:CYS:SG	3.08	0.42
1:E:125:ILE:HG13	1:E:212:MET:CG	2.49	0.42
1:F:187:ALA:HB2	1:F:363:GLU:HA	2.02	0.42
1:F:195:GLN:O	1:F:196:VAL:C	2.58	0.42
1:F:225:ASN:ND2	1:F:225:ASN:O	2.53	0.42
1:F:227:ASP:C	1:F:229:THR:H	2.23	0.42
1:A:152:ARG:HB3	1:A:177:SER:HB3	2.02	0.42
1:B:156:PHE:CD2	1:B:158:ASN:CA	3.01	0.42
1:C:258:ILE:O	1:C:261:ALA:HB3	2.20	0.42
1:C:278:ASN:HB3	1:C:319:GLN:O	2.20	0.42
1:C:288:LEU:HD23	1:C:288:LEU:C	2.40	0.42
1:C:322:GLY:O	1:C:380:THR:HA	2.20	0.42
1:C:328:GLY:O	1:C:331:MET:N	2.45	0.42
1:D:185:THR:C	1:D:186:ILE:HD12	2.40	0.42
1:D:207:ILE:HG13	1:D:211:LEU:CD1	2.41	0.42
1:E:139:ALA:HB3	1:E:334:GLN:HB3	2.00	0.42
1:E:189:TRP:O	1:E:191:GLN:N	2.53	0.42
1:E:227:ASP:O	1:E:229:THR:CG2	2.67	0.42
1:E:254:ARG:HA	1:E:257:ILE:CD1	2.49	0.42
1:F:227:ASP:C	1:F:229:THR:N	2.73	0.42
1:G:280:ARG:C	1:G:283:HIS:H	2.23	0.42
1:G:352:ASN:O	1:G:353:PHE:C	2.56	0.42
1:A:203:LEU:O	1:A:207:ILE:HD13	2.20	0.41
1:A:210:ARG:HG2	1:A:210:ARG:HH11	1.85	0.41
1:A:329:PHE:H	1:A:329:PHE:HD1	1.66	0.41
1:B:137:LEU:HD23	1:B:137:LEU:O	2.20	0.41
1:B:191:GLN:HA	1:B:359:THR:HA	2.02	0.41
1:B:252:ASP:HB3	1:B:256:ASP:CB	2.49	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:349:ASP:O	1:B:352:ASN:CB	2.67	0.41
1:B:351:ASP:HB3	1:B:355:LYS:HE3	2.02	0.41
1:C:227:ASP:O	1:C:228:GLY:C	2.59	0.41
1:D:125:ILE:CG1	1:D:208:ASN:ND2	2.80	0.41
1:D:173:ASP:OD1	1:D:174:ILE:CD1	2.68	0.41
1:E:125:ILE:HD11	1:E:127:PRO:CD	2.42	0.41
1:A:131:ARG:HB3	1:A:131:ARG:HH11	1.85	0.41
1:A:331:MET:SD	1:F:209:ASN:O	2.78	0.41
1:B:153:GLU:O	1:B:155:VAL:N	2.54	0.41
1:B:187:ALA:HB1	1:B:362:CYS:O	2.20	0.41
1:D:149:GLU:HG2	1:D:180:THR:HG23	2.03	0.41
1:D:187:ALA:HB1	1:D:361:LEU:HD11	2.00	0.41
1:E:202:MET:HE3	1:E:202:MET:HB3	1.73	0.41
1:F:192:ALA:C	1:F:357:MET:SD	2.97	0.41
1:B:296:ILE:O	1:B:297:PHE:CG	2.73	0.41
1:D:206:TYR:O	1:D:210:ARG:HB3	2.20	0.41
1:E:156:PHE:CD2	1:E:158:ASN:CA	3.04	0.41
1:E:190:VAL:HG23	1:E:190:VAL:O	2.20	0.41
1:F:257:ILE:O	1:F:258:ILE:C	2.59	0.41
1:F:338:ARG:HH11	1:F:338:ARG:HG3	1.84	0.41
1:B:216:ALA:O	1:B:219:GLU:HB3	2.20	0.41
1:C:357:MET:CE	1:D:178:LYS:HD3	2.51	0.41
1:D:225:ASN:ND2	1:D:318:ALA:O	2.54	0.41
1:E:190:VAL:N	1:E:360:ILE:CD1	2.78	0.41
1:F:184:LYS:HD2	1:F:231:ASP:HA	2.02	0.41
1:G:199:ASP:O	1:G:200:ALA:C	2.59	0.41
1:A:134:ILE:O	1:A:138:LEU:HD13	2.20	0.41
1:A:245:THR:O	1:A:245:THR:HG22	2.21	0.41
1:A:290:ASP:C	1:A:292:GLU:H	2.23	0.41
1:C:268:SER:HB2	1:C:372:ARG:HD3	2.02	0.41
1:D:221:GLY:O	1:D:225:ASN:N	2.47	0.41
1:E:235:GLY:O	1:E:238:LYS:HB3	2.20	0.41
1:E:300:PRO:CG	1:F:309:TRP:NE1	2.83	0.41
1:F:151:VAL:CG2	1:F:176:PHE:HB3	2.50	0.41
1:F:208:ASN:OD1	1:F:208:ASN:C	2.58	0.41
1:F:348:GLU:H	1:F:348:GLU:HG2	1.55	0.41
1:A:186:ILE:N	1:A:186:ILE:CD1	2.83	0.41
1:A:345:VAL:CG2	1:A:360:ILE:HG12	2.51	0.41
1:D:206:TYR:OH	1:D:210:ARG:NH1	2.53	0.41
1:D:207:ILE:CD1	1:D:207:ILE:N	2.84	0.41
1:G:282:TRP:CE3	1:G:313:VAL:HG11	2.55	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:149:GLU:OE1	1:F:195:GLN:HG2	2.21	0.41
1:A:193:SER:OG	1:A:195:GLN:HG2	2.20	0.41
1:A:266:THR:O	1:A:268:SER:N	2.53	0.41
1:A:316:THR:HG23	1:A:319:GLN:H	1.85	0.41
1:B:125:ILE:CG1	1:B:127:PRO:CG	2.96	0.41
1:D:124:ILE:HG23	1:D:125:ILE:N	2.34	0.41
1:D:217:LEU:HD23	1:D:217:LEU:C	2.40	0.41
1:D:233:LEU:HD11	1:D:366:LEU:HD11	2.03	0.41
1:D:268:SER:O	1:D:270:PHE:HD1	2.04	0.41
1:E:237:ASN:N	1:E:237:ASN:HD22	2.18	0.41
1:E:325:THR:HA	1:E:377:ILE:O	2.21	0.41
1:E:347:ARG:O	1:E:352:ASN:HB2	2.21	0.41
1:F:288:LEU:O	1:F:295:TYR:HA	2.21	0.41
1:F:320:ALA:O	1:F:323:THR:HB	2.20	0.41
1:G:335:VAL:HG12	1:G:368:LEU:CB	2.51	0.41
1:A:125:ILE:N	1:A:125:ILE:CD1	2.74	0.41
1:B:143:THR:OG1	1:B:144:SER:N	2.54	0.41
1:C:207:ILE:CG2	1:C:211:LEU:HD13	2.50	0.41
1:C:277:LEU:HA	1:C:319:GLN:HG2	2.03	0.41
1:D:162:ASP:C	1:D:173:ASP:N	2.70	0.41
1:D:256:ASP:O	1:D:259:ALA:HB3	2.19	0.41
1:F:152:ARG:O	1:F:154:GLU:N	2.54	0.41
1:G:207:ILE:O	1:G:211:LEU:HB3	2.21	0.41
1:G:236:LEU:O	1:G:240:ALA:N	2.54	0.41
1:G:345:VAL:CG1	1:G:358:LEU:HD11	2.48	0.41
1:A:333:SER:HB3	1:A:369:ALA:O	2.21	0.41
1:B:253:THR:CG2	1:B:254:ARG:N	2.83	0.41
1:B:324:PHE:N	1:B:324:PHE:CD1	2.89	0.41
1:C:290:ASP:C	1:C:292:GLU:N	2.74	0.41
1:C:300:PRO:C	1:C:302:ALA:N	2.74	0.41
1:D:196:VAL:HA	1:D:199:ASP:OD1	2.21	0.41
1:D:208:ASN:ND2	1:D:208:ASN:N	2.69	0.41
1:D:309:TRP:HE3	1:D:309:TRP:N	2.17	0.41
1:D:328:GLY:C	1:D:330:ASP:N	2.74	0.41
1:E:154:GLU:OE2	1:E:177:SER:CB	2.69	0.41
1:E:296:ILE:O	1:E:298:GLY:N	2.53	0.41
1:F:178:LYS:HE3	1:F:178:LYS:HB2	1.80	0.41
1:F:193:SER:O	1:F:196:VAL:CG1	2.69	0.41
1:F:275:ILE:HG22	1:F:277:LEU:HD11	2.02	0.41
1:F:331:MET:O	1:F:331:MET:CG	2.69	0.41
1:G:128:GLY:C	1:G:130:ARG:H	2.24	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:306:ASN:OD1	1:G:306:ASN:O	2.39	0.41
1:C:131:ARG:HB2	1:C:131:ARG:NH1	2.34	0.41
1:C:189:TRP:CD2	1:C:189:TRP:O	2.74	0.41
1:C:196:VAL:HG11	1:C:203:LEU:HD13	1.98	0.41
1:C:236:LEU:O	1:C:240:ALA:HB2	2.21	0.41
1:D:236:LEU:HD23	1:D:370:HIS:NE2	2.35	0.41
1:E:145:SER:C	1:E:147:ALA:H	2.23	0.41
1:E:194:ARG:HE	1:E:356:ASN:HD21	1.69	0.41
1:E:211:LEU:HD12	1:E:211:LEU:HA	1.65	0.41
1:F:290:ASP:OD1	1:F:291:ASN:N	2.49	0.41
1:G:142:ARG:HG2	1:G:142:ARG:NH1	2.35	0.41
1:A:152:ARG:O	1:A:154:GLU:N	2.55	0.40
1:A:158:ASN:OD1	1:A:172:SER:HA	2.21	0.40
1:B:148:LEU:HD23	1:B:181:ALA:HB3	2.04	0.40
1:D:131:ARG:NH2	1:D:133:THR:HG22	2.36	0.40
1:E:292:GLU:O	1:E:294:ARG:N	2.50	0.40
1:G:188:HIS:N	1:G:215:LEU:HD13	2.37	0.40
1:G:199:ASP:O	1:G:202:MET:CB	2.67	0.40
1:G:346:SER:O	1:G:358:LEU:HD12	2.20	0.40
1:A:195:GLN:O	1:A:199:ASP:OD2	2.39	0.40
1:A:258:ILE:O	1:A:262:ILE:HG13	2.21	0.40
1:B:196:VAL:HG23	1:B:196:VAL:H	1.68	0.40
1:B:342:THR:O	1:B:363:GLU:N	2.54	0.40
1:C:202:MET:O	1:C:203:LEU:O	2.39	0.40
1:D:127:PRO:HB3	1:D:212:MET:CB	2.49	0.40
1:E:120:GLN:O	1:E:122:PRO:HD3	2.22	0.40
1:E:290:ASP:C	1:E:292:GLU:N	2.74	0.40
1:F:143:THR:HG22	1:F:336:PHE:HB3	2.03	0.40
1:G:204:GLN:HG2	1:G:204:GLN:O	2.21	0.40
1:G:211:LEU:HD12	1:G:360:ILE:HD12	2.03	0.40
1:A:127:PRO:HD3	1:A:212:MET:HE3	2.03	0.40
1:A:183:VAL:HG13	1:A:366:LEU:C	2.41	0.40
1:A:297:PHE:HE1	1:A:308:MET:CE	2.34	0.40
1:B:158:ASN:C	1:B:172:SER:HB2	2.42	0.40
1:C:204:GLN:HA	1:C:207:ILE:CD1	2.51	0.40
1:E:218:LYS:O	1:E:219:GLU:C	2.59	0.40
1:E:289:LYS:HA	1:E:294:ARG:O	2.21	0.40
1:E:339:MET:HB3	1:E:339:MET:HE2	1.94	0.40
1:F:282:TRP:CE3	1:F:282:TRP:HA	2.57	0.40
1:G:155:VAL:CG2	1:G:156:PHE:H	2.35	0.40
1:G:248:ASN:N	1:G:248:ASN:HD22	2.19	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:327:GLY:C	1:G:329:PHE:HD2	2.21	0.40
1:A:260:HIS:O	1:A:263:TYR:HB3	2.21	0.40
1:A:285:ILE:HA	1:A:288:LEU:CD1	2.47	0.40
1:C:184:LYS:HE3	1:C:230:GLY:O	2.22	0.40
1:D:260:HIS:O	1:D:263:TYR:HB3	2.21	0.40
1:D:347:ARG:O	1:D:347:ARG:CG	2.69	0.40
1:E:134:ILE:HD13	1:E:220:GLU:HG3	2.02	0.40
1:E:194:ARG:HD2	1:E:347:ARG:NE	2.36	0.40
1:F:211:LEU:HD23	1:F:212:MET:N	2.37	0.40
1:A:290:ASP:OD2	1:A:292:GLU:O	2.39	0.40
1:B:156:PHE:CD2	1:B:158:ASN:CB	3.05	0.40
1:B:266:THR:C	1:B:268:SER:H	2.24	0.40
1:B:288:LEU:HD23	1:B:289:LYS:N	2.36	0.40
1:B:349:ASP:O	1:B:350:ARG:C	2.60	0.40
1:C:194:ARG:HA	1:C:358:LEU:HG	2.02	0.40
1:C:224:LEU:HD13	1:C:224:LEU:C	2.42	0.40
1:C:224:LEU:O	1:C:237:ASN:ND2	2.55	0.40
1:C:244:ASP:OD2	1:C:246:SER:HB3	2.22	0.40
1:D:296:ILE:HG22	1:D:297:PHE:CD1	2.57	0.40
1:F:142:ARG:HH22	1:F:340:ASP:CG	2.25	0.40
1:F:252:ASP:HB3	1:F:256:ASP:HB2	2.04	0.40
1:F:282:TRP:HA	1:F:282:TRP:HE3	1.86	0.40
1:F:378:LYS:HG3	1:F:379:GLY:N	2.36	0.40
1:G:188:HIS:O	1:G:361:LEU:HD12	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	254/273 (93%)	195 (77%)	49 (19%)	10 (4%)	3 26

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	248/273 (91%)	189 (76%)	48 (19%)	11 (4%)	2	24
1	C	246/273 (90%)	188 (76%)	47 (19%)	11 (4%)	2	23
1	D	252/273 (92%)	209 (83%)	34 (14%)	9 (4%)	3	29
1	E	253/273 (93%)	190 (75%)	49 (19%)	14 (6%)	2	20
1	F	246/273 (90%)	192 (78%)	40 (16%)	14 (6%)	1	19
1	G	245/273 (90%)	199 (81%)	36 (15%)	10 (4%)	3	25
All	All	1744/1911 (91%)	1362 (78%)	303 (17%)	79 (4%)	2	23

All (79) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	124	ILE
1	A	208	ASN
1	B	200	ALA
1	B	297	PHE
1	C	131	ARG
1	C	195	GLN
1	C	306	ASN
1	D	194	ARG
1	D	195	GLN
1	D	303	PHE
1	E	296	ILE
1	F	200	ALA
1	F	201	PRO
1	G	199	ASP
1	G	204	GLN
1	G	279	PRO
1	A	304	THR
1	B	129	LEU
1	B	350	ARG
1	C	157	THR
1	C	196	VAL
1	C	228	GLY
1	C	229	THR
1	D	154	GLU
1	D	293	GLY
1	F	128	GLY
1	F	293	GLY
1	F	348	GLU
1	G	132	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	G	296	ILE
1	G	354	VAL
1	A	154	GLU
1	A	358	LEU
1	B	153	GLU
1	C	200	ALA
1	D	127	PRO
1	D	173	ASP
1	E	161	GLY
1	E	200	ALA
1	E	348	GLU
1	F	153	GLU
1	F	154	GLU
1	F	161	GLY
1	F	382	SER
1	A	309	TRP
1	C	348	GLU
1	D	160	PRO
1	E	194	ARG
1	E	213	TYR
1	E	354	VAL
1	G	197	MET
1	A	160	PRO
1	B	172	SER
1	B	354	VAL
1	B	355	LYS
1	D	382	SER
1	E	125	ILE
1	E	190	VAL
1	E	357	MET
1	F	199	ASP
1	F	207	ILE
1	F	283	HIS
1	G	160	PRO
1	G	348	GLU
1	A	198	ASP
1	A	305	SER
1	B	162	ASP
1	C	230	GLY
1	E	154	GLU
1	E	201	PRO
1	F	160	PRO

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	G	161	GLY
1	A	161	GLY
1	E	160	PRO
1	B	207	ILE
1	C	298	GLY
1	B	159	ALA
1	F	196	VAL
1	E	251	GLY

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	211/223 (95%)	184 (87%)	27 (13%)	4 22
1	B	206/223 (92%)	181 (88%)	25 (12%)	5 24
1	C	204/223 (92%)	184 (90%)	20 (10%)	8 33
1	D	209/223 (94%)	191 (91%)	18 (9%)	10 39
1	E	210/223 (94%)	185 (88%)	25 (12%)	5 25
1	F	204/223 (92%)	173 (85%)	31 (15%)	3 17
1	G	203/223 (91%)	185 (91%)	18 (9%)	9 38
All	All	1447/1561 (93%)	1283 (89%)	164 (11%)	6 28

All (164) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	119	MET
1	A	121	ILE
1	A	124	ILE
1	A	125	ILE
1	A	126	MET
1	A	129	LEU
1	A	131	ARG
1	A	137	LEU
1	A	157	THR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	158	ASN
1	A	174	ILE
1	A	191	GLN
1	A	193	SER
1	A	194	ARG
1	A	209	ASN
1	A	266	THR
1	A	273	SER
1	A	280	ARG
1	A	282	TRP
1	A	288	LEU
1	A	289	LYS
1	A	295	TYR
1	A	297	PHE
1	A	301	GLN
1	A	303	PHE
1	A	309	TRP
1	A	366	LEU
1	B	126	MET
1	B	129	LEU
1	B	132	LEU
1	B	140	GLN
1	B	142	ARG
1	B	146	ASN
1	B	148	LEU
1	B	158	ASN
1	B	174	ILE
1	B	178	LYS
1	B	199	ASP
1	B	211	LEU
1	B	213	TYR
1	B	215	LEU
1	B	217	LEU
1	B	256	ASP
1	B	270	PHE
1	B	271	SER
1	B	277	LEU
1	B	282	TRP
1	B	296	ILE
1	B	324	PHE
1	B	353	PHE
1	B	356	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	358	LEU
1	C	129	LEU
1	C	132	LEU
1	C	156	PHE
1	C	174	ILE
1	C	190	VAL
1	C	191	GLN
1	C	193	SER
1	C	194	ARG
1	C	195	GLN
1	C	197	MET
1	C	202	MET
1	C	207	ILE
1	C	225	ASN
1	C	233	LEU
1	C	282	TRP
1	C	301	GLN
1	C	331	MET
1	C	347	ARG
1	C	356	ASN
1	C	366	LEU
1	D	121	ILE
1	D	127	PRO
1	D	130	ARG
1	D	131	ARG
1	D	132	LEU
1	D	158	ASN
1	D	174	ILE
1	D	184	LYS
1	D	198	ASP
1	D	199	ASP
1	D	247	LEU
1	D	282	TRP
1	D	284	ASN
1	D	287	LEU
1	D	289	LYS
1	D	303	PHE
1	D	309	TRP
1	D	348	GLU
1	E	125	ILE
1	E	129	LEU
1	E	140	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	E	158	ASN
1	E	173	ASP
1	E	174	ILE
1	E	189	TRP
1	E	191	GLN
1	E	199	ASP
1	E	202	MET
1	E	205	SER
1	E	206	TYR
1	E	212	MET
1	E	217	LEU
1	E	220	GLU
1	E	229	THR
1	E	282	TRP
1	E	296	ILE
1	E	301	GLN
1	E	305	SER
1	E	309	TRP
1	E	348	GLU
1	E	353	PHE
1	E	359	THR
1	E	382	SER
1	F	129	LEU
1	F	132	LEU
1	F	133	THR
1	F	143	THR
1	F	145	SER
1	F	146	ASN
1	F	158	ASN
1	F	174	ILE
1	F	193	SER
1	F	196	VAL
1	F	197	MET
1	F	198	ASP
1	F	202	MET
1	F	203	LEU
1	F	210	ARG
1	F	212	MET
1	F	217	LEU
1	F	225	ASN
1	F	247	LEU
1	F	254	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	F	257	ILE
1	F	277	LEU
1	F	282	TRP
1	F	287	LEU
1	F	289	LYS
1	F	307	ILE
1	F	329	PHE
1	F	348	GLU
1	F	361	LEU
1	F	363	GLU
1	F	378	LYS
1	G	130	ARG
1	G	131	ARG
1	G	132	LEU
1	G	158	ASN
1	G	174	ILE
1	G	193	SER
1	G	198	ASP
1	G	229	THR
1	G	245	THR
1	G	290	ASP
1	G	297	PHE
1	G	303	PHE
1	G	329	PHE
1	G	338	ARG
1	G	355	LYS
1	G	356	ASN
1	G	357	MET
1	G	372	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (53) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	146	ASN
1	A	158	ASN
1	A	179	GLN
1	A	204	GLN
1	A	208	ASN
1	A	225	ASN
1	A	334	GLN
1	B	146	ASN
1	B	158	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	208	ASN
1	B	209	ASN
1	B	284	ASN
1	B	319	GLN
1	B	334	GLN
1	B	352	ASN
1	B	356	ASN
1	B	370	HIS
1	C	146	ASN
1	C	191	GLN
1	C	195	GLN
1	C	204	GLN
1	C	222	GLN
1	C	225	ASN
1	C	232	ASN
1	C	237	ASN
1	C	248	ASN
1	C	264	GLN
1	C	278	ASN
1	C	283	HIS
1	C	284	ASN
1	C	301	GLN
1	C	356	ASN
1	D	158	ASN
1	D	208	ASN
1	D	225	ASN
1	D	334	GLN
1	E	158	ASN
1	E	179	GLN
1	E	191	GLN
1	E	232	ASN
1	E	237	ASN
1	E	334	GLN
1	F	140	GLN
1	F	158	ASN
1	F	179	GLN
1	F	222	GLN
1	F	225	ASN
1	F	237	ASN
1	G	158	ASN
1	G	248	ASN
1	G	260	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	G	291	ASN
1	G	356	ASN

5.3.3 RNA

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

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

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers

Unable to reproduce the depositors R factor - this section is therefore empty.