W O R L D W I D E
wwPDB
P R O T E I N   D A T A   B A N K

Full wwPDB X-ray Structure Validation Report (i)

Aug 27, 2023 – 11:57 AM EDT

PDB ID	:	3HI8
Title	:	Crystal structure of proliferating cell nuclear antigen (PCNA) from Haloferax volcanii
Authors	:	Morgunova, E.; Gray, F.C.; MacNeill, S.A.; Ladenstein, R.
Deposited on	:	2009-05-19
Resolution	:	3.20 Å(reported)

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

|		
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.35
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)	:	2.35

1 Overall quality at a glance ⓘ

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

The reported resolution of this entry is 3.20 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	Percentile Ranks	Value
Rfree		0.266
Clashscore		95
Ramachandran outliers		3.7%
Sidechain outliers		21.7%
RSRZ outliers		3.4%

Worse ——— *Better*

▮ Percentile relative to all X-ray structures
▯ Percentile relative to X-ray structures of similar resolution
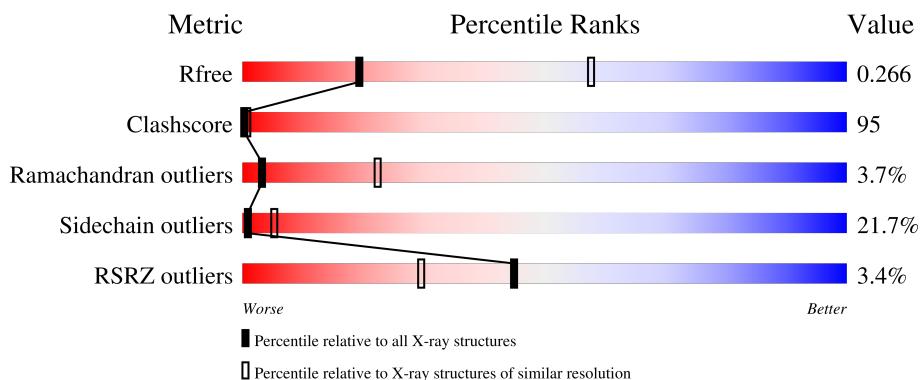
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)

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% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	247	3% 23% 59% 14% •
1	B	247	4% 22% 60% 14% •
1	C	247	4% 22% 60% 14% •
1	D	247	3% 23% 60% 14% •
1	E	247	2% 23% 60% 14% •
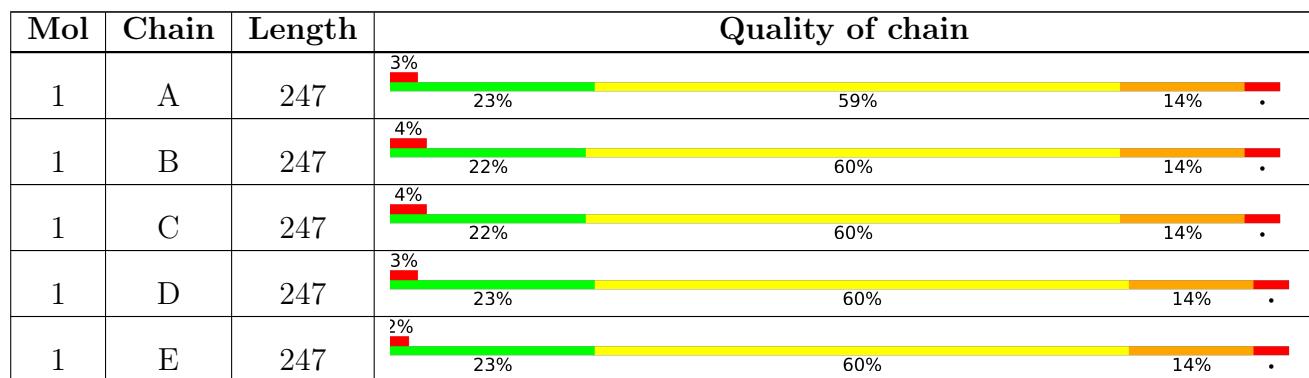
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	247	

2 Entry composition ⓘ

There are 2 unique types of molecules in this entry. The entry contains 11245 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 Proliferating cell nuclear antigen PcnA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	247	Total	C	N	O	S	0	0	0
			1869	1167	308	386	8			
1	B	247	Total	C	N	O	S	0	0	0
			1869	1167	308	386	8			
1	C	247	Total	C	N	O	S	0	0	0
			1869	1167	308	386	8			
1	D	247	Total	C	N	O	S	0	0	0
			1869	1167	308	386	8			
1	E	247	Total	C	N	O	S	0	0	0
			1869	1167	308	386	8			
1	F	247	Total	C	N	O	S	0	0	0
			1869	1167	308	386	8			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	5	Total	O	0	0
			5	5		
2	B	3	Total	O	0	0
			3	3		
2	C	2	Total	O	0	0
			2	2		
2	D	7	Total	O	0	0
			7	7		
2	E	5	Total	O	0	0
			5	5		
2	F	9	Total	O	0	0
			9	9		

WORLDWIDE
PDB
PROTEIN DATA BANK

3 Residue-property plots ⓘ

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 and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Proliferating cell nuclear antigen PcnA
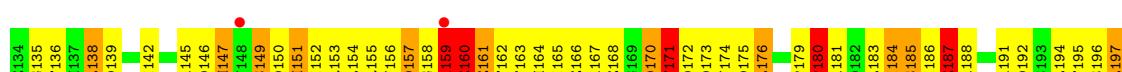
Chain A:

• Molecule 1: Proliferating cell nuclear antigen PcnA

Chain B:

• Molecule 1: Proliferating cell nuclear antigen PcnA

Chain C:

• Molecule 1: Proliferating cell nuclear antigen PcnA

• Molecule 1: Proliferating cell nuclear antigen PcnA

• Molecule 1: Proliferating cell nuclear antigen PcnA

Chain F:
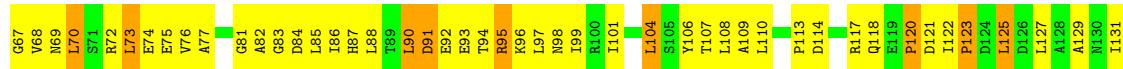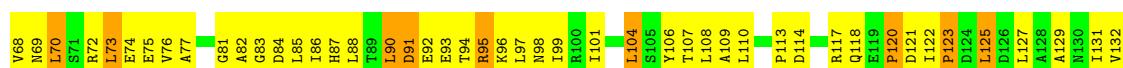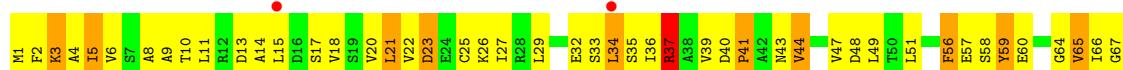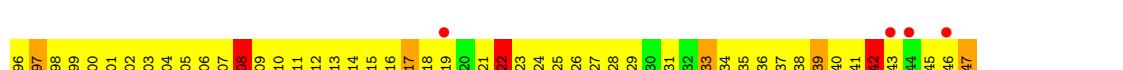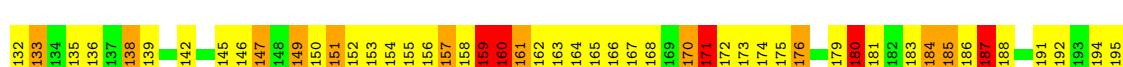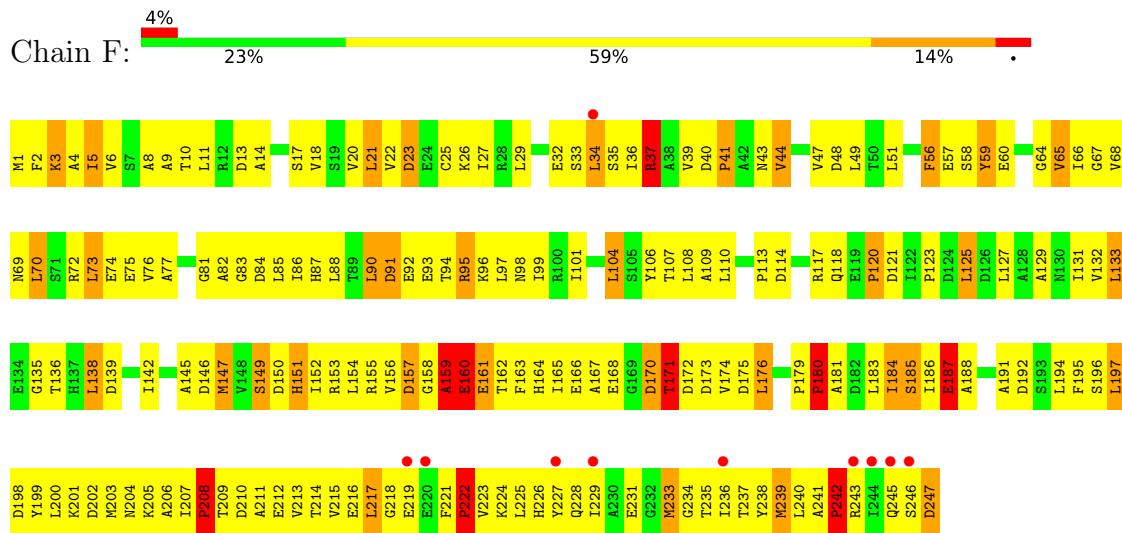
4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	174.44Å 123.24Å 123.26Å 90.00° 135.00° 90.00°	Depositor
Resolution (Å)	32.95 – 3.20 32.96 – 3.20	Depositor EDS
% Data completeness (in resolution range)	86.6 (32.95-3.20) 86.6 (32.96-3.20)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	0.12	Depositor
$< I/\sigma(I) >$ [1]	1.19 (at 3.18Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.237 , 0.250 0.230 , 0.266	Depositor DCC
R_{free} test set	1323 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å^2)	138.1	Xtriage
Anisotropy	0.037	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.22 , 87.0	EDS
L-test for twinning[2]	$< |L| > = 0.34, < L^2 > = 0.17$	Xtriage
Estimated twinning fraction	0.357 for -h-2*l,k,h+l 0.348 for k+l,h+l,-l 0.357 for -k+l,-h-l,-l 0.349 for -h-k-l,l,k 0.349 for -h+k-l,-l,-k 0.347 for -h-k-l,-l,h+l 0.347 for k+l,-h-l,-k 0.348 for -h+k-l,l,h+l 0.349 for -k+l,h+l,k 0.357 for -h,-k,h+l 0.358 for -h-2*l,-k,l	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	11245	wwPDB-VP
Average B, all atoms (Å^2)	139.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.83% 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 ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths RMSZ	Bond lengths #$|Z|$ >5	Bond angles RMSZ	Bond angles #$|Z|$ >5
1	A	0.71	0/1893	1.20	11/2572 (0.4%)
1	B	0.71	0/1893	1.20	11/2572 (0.4%)
1	C	0.71	0/1893	1.20	11/2572 (0.4%)
1	D	0.71	0/1893	1.20	11/2572 (0.4%)
1	E	0.71	0/1893	1.20	11/2572 (0.4%)
1	F	0.71	0/1893	1.20	11/2572 (0.4%)
All	All	0.71	0/11358	1.20	66/15432 (0.4%)

There are no bond length outliers.

All (66) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	180	PRO	CA-N-CD	-14.39	91.35	111.50
1	F	180	PRO	CA-N-CD	-14.37	91.38	111.50
1	C	180	PRO	CA-N-CD	-14.37	91.39	111.50
1	A	180	PRO	CA-N-CD	-14.36	91.39	111.50
1	E	180	PRO	CA-N-CD	-14.35	91.41	111.50
1	B	180	PRO	CA-N-CD	-14.35	91.41	111.50
1	E	120	PRO	CA-N-CD	-13.38	92.77	111.50
1	A	120	PRO	CA-N-CD	-13.36	92.80	111.50
1	F	120	PRO	CA-N-CD	-13.35	92.81	111.50
1	D	120	PRO	CA-N-CD	-13.35	92.81	111.50
1	B	120	PRO	CA-N-CD	-13.35	92.82	111.50
1	C	120	PRO	CA-N-CD	-13.33	92.83	111.50
1	D	242	PRO	CA-N-CD	-10.54	96.75	111.50
1	F	242	PRO	CA-N-CD	-10.53	96.76	111.50
1	E	242	PRO	CA-N-CD	-10.53	96.76	111.50
1	C	242	PRO	CA-N-CD	-10.52	96.78	111.50
1	A	242	PRO	CA-N-CD	-10.51	96.79	111.50
1	B	242	PRO	CA-N-CD	-10.51	96.79	111.50
1	B	171	THR	CA-CB-OG1	10.40	130.84	109.00
1	D	171	THR	CA-CB-OG1	10.40	130.83	109.00
1	C	171	THR	CA-CB-OG1	10.39	130.82	109.00

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	171	THR	CA-CB-OG1	10.38	130.79	109.00
1	F	171	THR	CA-CB-OG1	10.38	130.79	109.00
1	A	171	THR	CA-CB-OG1	10.37	130.77	109.00
1	E	222	PRO	CA-N-CD	-10.13	97.32	111.50
1	B	222	PRO	CA-N-CD	-10.13	97.32	111.50
1	F	222	PRO	CA-N-CD	-10.12	97.33	111.50
1	D	222	PRO	CA-N-CD	-10.10	97.36	111.50
1	A	222	PRO	CA-N-CD	-10.10	97.36	111.50
1	C	222	PRO	CA-N-CD	-10.10	97.36	111.50
1	F	208	PRO	CA-N-CD	-9.94	97.58	111.50
1	D	208	PRO	CA-N-CD	-9.93	97.60	111.50
1	C	208	PRO	CA-N-CD	-9.93	97.60	111.50
1	B	208	PRO	CA-N-CD	-9.92	97.61	111.50
1	A	208	PRO	CA-N-CD	-9.91	97.62	111.50
1	E	208	PRO	CA-N-CD	-9.90	97.64	111.50
1	F	41	PRO	CA-N-CD	-9.85	97.70	111.50
1	E	41	PRO	CA-N-CD	-9.84	97.73	111.50
1	D	41	PRO	CA-N-CD	-9.84	97.73	111.50
1	A	41	PRO	CA-N-CD	-9.83	97.74	111.50
1	C	41	PRO	CA-N-CD	-9.81	97.76	111.50
1	B	41	PRO	CA-N-CD	-9.81	97.76	111.50
1	E	160	GLU	CB-CA-C	7.18	124.76	110.40
1	C	160	GLU	CB-CA-C	7.17	124.74	110.40
1	A	160	GLU	CB-CA-C	7.17	124.73	110.40
1	F	160	GLU	CB-CA-C	7.16	124.73	110.40
1	B	160	GLU	CB-CA-C	7.16	124.72	110.40
1	D	160	GLU	CB-CA-C	7.16	124.72	110.40
1	B	123	PRO	CB-CA-C	5.91	126.78	112.00
1	A	123	PRO	CB-CA-C	5.91	126.77	112.00
1	D	123	PRO	CB-CA-C	5.91	126.77	112.00
1	C	123	PRO	CB-CA-C	5.90	126.76	112.00
1	E	123	PRO	CB-CA-C	5.90	126.76	112.00
1	F	123	PRO	CB-CA-C	5.90	126.74	112.00
1	D	159	ALA	O-C-N	5.53	131.54	122.70
1	A	159	ALA	O-C-N	5.52	131.54	122.70
1	C	159	ALA	O-C-N	5.51	131.52	122.70
1	F	159	ALA	O-C-N	5.51	131.52	122.70
1	E	159	ALA	O-C-N	5.50	131.50	122.70
1	B	159	ALA	O-C-N	5.50	131.49	122.70
1	E	187	GLU	N-CA-C	-5.26	96.80	111.00
1	A	187	GLU	N-CA-C	-5.25	96.82	111.00
1	D	187	GLU	N-CA-C	-5.25	96.82	111.00

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	F	187	GLU	N-CA-C	-5.25	96.83	111.00
1	C	187	GLU	N-CA-C	-5.24	96.84	111.00
1	B	187	GLU	N-CA-C	-5.24	96.86	111.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1869	0	1847	373	0
1	B	1869	0	1847	377	0
1	C	1869	0	1847	372	0
1	D	1869	0	1847	374	0
1	E	1869	0	1847	365	0
1	F	1869	0	1847	358	0
2	A	5	0	0	0	0
2	B	3	0	0	0	0
2	C	2	0	0	0	0
2	D	7	0	0	0	0
2	E	5	0	0	0	0
2	F	9	0	0	0	0
All	All	11245	0	11082	2123	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 95.

All (2123) 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:A:149:SER:CB	1:A:167:ALA:HB1	1.53	1.38
1:B:149:SER:CB	1:B:167:ALA:HB1	1.53	1.37
1:C:149:SER:CB	1:C:167:ALA:HB1	1.53	1.36
1:F:149:SER:CB	1:F:167:ALA:HB1	1.53	1.35
1:E:149:SER:CB	1:E:167:ALA:HB1	1.53	1.35

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:149:SER:CB	1:D:167:ALA:HB1	1.53	1.35
1:D:156:VAL:HB	1:D:191:ALA:O	1.25	1.33
1:A:150:ASP:O	1:A:197:LEU:HD22	1.28	1.32
1:B:150:ASP:O	1:B:197:LEU:HD22	1.28	1.31
1:C:156:VAL:HB	1:C:191:ALA:O	1.25	1.31
1:F:95:ARG:O	1:F:109:ALA:HA	1.29	1.30
1:C:150:ASP:O	1:C:197:LEU:HD22	1.28	1.30
1:F:150:ASP:O	1:F:197:LEU:HD22	1.28	1.29
1:A:156:VAL:HB	1:A:191:ALA:O	1.25	1.29
1:D:8:ALA:HB3	1:D:82:ALA:O	1.32	1.29
1:E:95:ARG:O	1:E:109:ALA:HA	1.29	1.29
1:A:8:ALA:HB3	1:A:82:ALA:O	1.32	1.29
1:E:156:VAL:HB	1:E:191:ALA:O	1.25	1.29
1:A:95:ARG:O	1:A:109:ALA:HA	1.29	1.28
1:D:150:ASP:O	1:D:197:LEU:HD22	1.28	1.28
1:B:156:VAL:HB	1:B:191:ALA:O	1.25	1.27
1:E:8:ALA:HB3	1:E:82:ALA:O	1.33	1.26
1:E:150:ASP:O	1:E:197:LEU:HD22	1.28	1.26
1:D:72:ARG:HH12	1:F:171:THR:CG2	1.48	1.25
1:D:95:ARG:O	1:D:109:ALA:HA	1.29	1.25
1:B:47:VAL:HA	1:B:237:THR:O	1.36	1.25
1:C:8:ALA:HB3	1:C:82:ALA:O	1.32	1.25
1:C:47:VAL:HA	1:C:237:THR:O	1.36	1.25
1:C:95:ARG:O	1:C:109:ALA:HA	1.29	1.25
1:F:8:ALA:HB3	1:F:82:ALA:O	1.32	1.24
1:F:156:VAL:HB	1:F:191:ALA:O	1.25	1.24
1:B:8:ALA:HB3	1:B:82:ALA:O	1.32	1.24
1:B:95:ARG:O	1:B:109:ALA:HA	1.29	1.24
1:D:47:VAL:HA	1:D:237:THR:O	1.36	1.23
1:B:171:THR:CG2	1:C:72:ARG:HH12	1.50	1.22
1:E:47:VAL:HA	1:E:237:THR:O	1.36	1.21
1:E:171:THR:CG2	1:F:72:ARG:HH12	1.54	1.20
1:A:23:ASP:O	1:A:70:LEU:HB3	1.03	1.20
1:F:47:VAL:HA	1:F:237:THR:O	1.36	1.19
1:A:72:ARG:HH12	1:C:171:THR:CG2	1.55	1.18
1:A:47:VAL:HA	1:A:237:THR:O	1.36	1.18
1:B:23:ASP:O	1:B:70:LEU:HB3	1.03	1.18
1:C:23:ASP:O	1:C:70:LEU:HB3	1.03	1.18
1:C:195:PHE:CE2	1:C:242:PRO:HD3	1.79	1.18
1:D:23:ASP:O	1:D:70:LEU:HB3	1.03	1.17
1:E:23:ASP:O	1:E:70:LEU:HB3	1.03	1.17

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:195:PHE:CE2	1:A:242:PRO:HD3	1.79	1.17
1:D:195:PHE:CE2	1:D:242:PRO:HD3	1.79	1.17
1:F:23:ASP:O	1:F:70:LEU:HB3	1.03	1.17
1:A:195:PHE:HE2	1:A:242:PRO:HD3	1.00	1.17
1:F:222:PRO:HD3	1:F:242:PRO:HG2	1.23	1.17
1:A:171:THR:CG2	1:B:72:ARG:HH12	1.57	1.16
1:E:195:PHE:CE2	1:E:242:PRO:HD3	1.79	1.16
1:A:222:PRO:HD3	1:A:242:PRO:CG	1.75	1.16
1:F:195:PHE:CE2	1:F:242:PRO:HD3	1.79	1.16
1:F:222:PRO:HD3	1:F:242:PRO:CG	1.75	1.16
1:D:171:THR:CG2	1:E:72:ARG:HH12	1.57	1.16
1:B:195:PHE:CE2	1:B:242:PRO:HD3	1.79	1.16
1:E:222:PRO:HD3	1:E:242:PRO:CG	1.75	1.16
1:F:8:ALA:HB1	1:F:81:GLY:O	1.46	1.16
1:B:222:PRO:HD3	1:B:242:PRO:CG	1.75	1.15
1:C:222:PRO:HD3	1:C:242:PRO:CG	1.75	1.15
1:A:8:ALA:HB1	1:A:81:GLY:O	1.46	1.15
1:D:222:PRO:HD3	1:D:242:PRO:CG	1.75	1.15
1:E:2:PHE:O	1:E:88:LEU:O	1.66	1.14
1:B:2:PHE:O	1:B:88:LEU:O	1.66	1.14
1:F:2:PHE:O	1:F:88:LEU:O	1.66	1.14
1:C:222:PRO:HD3	1:C:242:PRO:HG2	1.23	1.13
1:E:195:PHE:HE2	1:E:242:PRO:HD3	1.00	1.13
1:B:23:ASP:O	1:B:70:LEU:CB	1.97	1.13
1:C:2:PHE:O	1:C:88:LEU:O	1.66	1.13
1:E:149:SER:HB2	1:E:167:ALA:HB1	1.15	1.13
1:F:23:ASP:O	1:F:70:LEU:CB	1.97	1.13
1:A:23:ASP:O	1:A:70:LEU:CB	1.97	1.13
1:D:23:ASP:O	1:D:70:LEU:CB	1.97	1.13
1:B:8:ALA:HB1	1:B:81:GLY:O	1.46	1.12
1:E:8:ALA:HB1	1:E:81:GLY:O	1.46	1.12
1:C:8:ALA:HB1	1:C:81:GLY:O	1.46	1.12
1:C:23:ASP:O	1:C:70:LEU:CB	1.97	1.12
1:D:222:PRO:HD3	1:D:242:PRO:HG2	1.23	1.12
1:B:149:SER:HB2	1:B:167:ALA:HB1	1.15	1.12
1:D:2:PHE:O	1:D:88:LEU:O	1.66	1.12
1:F:195:PHE:HE2	1:F:242:PRO:HD3	1.00	1.12
1:A:2:PHE:O	1:A:88:LEU:O	1.66	1.12
1:A:149:SER:HB3	1:A:167:ALA:HB1	1.32	1.12
1:B:222:PRO:HD3	1:B:242:PRO:HG2	1.23	1.12
1:C:152:ILE:HG23	1:C:165:ILE:CG2	1.80	1.12

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:8:ALA:HB1	1:D:81:GLY:O	1.46	1.12
1:E:222:PRO:HD3	1:E:242:PRO:HG2	1.23	1.12
1:E:152:ILE:HG23	1:E:165:ILE:CG2	1.80	1.12
1:D:149:SER:HB2	1:D:167:ALA:HB1	1.15	1.11
1:D:27:ILE:N	1:D:66:ILE:O	1.83	1.11
1:B:152:ILE:HG23	1:B:165:ILE:CG2	1.80	1.11
1:E:23:ASP:O	1:E:70:LEU:CB	1.97	1.11
1:C:195:PHE:HE2	1:C:242:PRO:HD3	1.00	1.11
1:C:149:SER:HB2	1:C:167:ALA:HB1	1.15	1.11
1:F:27:ILE:N	1:F:66:ILE:O	1.83	1.11
1:A:152:ILE:HG23	1:A:165:ILE:CG2	1.80	1.10
1:F:152:ILE:HG23	1:F:165:ILE:CG2	1.80	1.10
1:D:152:ILE:HG23	1:D:165:ILE:CG2	1.80	1.10
1:B:195:PHE:HE2	1:B:242:PRO:HD3	1.00	1.10
1:F:149:SER:HB2	1:F:167:ALA:HB1	1.15	1.10
1:A:27:ILE:N	1:A:66:ILE:O	1.83	1.09
1:A:149:SER:HB2	1:A:167:ALA:HB1	1.15	1.09
1:B:27:ILE:N	1:B:66:ILE:O	1.83	1.09
1:B:149:SER:HB3	1:B:167:ALA:HB1	1.32	1.09
1:A:96:LYS:HA	1:A:108:LEU:O	1.52	1.09
1:B:96:LYS:HA	1:B:108:LEU:O	1.53	1.09
1:C:27:ILE:N	1:C:66:ILE:O	1.83	1.09
1:E:27:ILE:N	1:E:66:ILE:O	1.83	1.09
1:D:96:LYS:HA	1:D:108:LEU:O	1.53	1.09
1:F:96:LYS:HA	1:F:108:LEU:O	1.52	1.09
1:D:195:PHE:HE2	1:D:242:PRO:HD3	1.00	1.09
1:A:222:PRO:HD3	1:A:242:PRO:HG2	1.23	1.08
1:C:96:LYS:HA	1:C:108:LEU:O	1.52	1.08
1:E:149:SER:HB3	1:E:167:ALA:HB1	1.32	1.08
1:F:149:SER:HB3	1:F:167:ALA:HB1	1.32	1.08
1:E:96:LYS:HA	1:E:108:LEU:O	1.52	1.07
1:C:149:SER:HB3	1:C:167:ALA:HB1	1.32	1.05
1:C:228:GLN:HA	1:C:234:GLY:O	1.57	1.04
1:A:228:GLN:HA	1:A:234:GLY:O	1.58	1.03
1:D:149:SER:HB3	1:D:167:ALA:HB1	1.32	1.03
1:C:191:ALA:HB1	1:C:218:GLY:C	1.80	1.02
1:D:228:GLN:HA	1:D:234:GLY:O	1.58	1.02
1:E:191:ALA:HB1	1:E:218:GLY:C	1.79	1.02
1:B:191:ALA:HB1	1:B:218:GLY:C	1.79	1.01
1:F:191:ALA:HB1	1:F:218:GLY:C	1.79	1.01
1:A:191:ALA:HB1	1:A:218:GLY:C	1.79	1.01

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:228:GLN:HA	1:B:234:GLY:O	1.58	1.01
1:F:228:GLN:HA	1:F:234:GLY:O	1.58	1.01
1:B:152:ILE:HG23	1:B:165:ILE:HG23	1.41	1.01
1:D:197:LEU:HD23	1:D:198:ASP:N	1.76	1.01
1:E:228:GLN:HA	1:E:234:GLY:O	1.58	1.01
1:B:149:SER:HB2	1:B:167:ALA:CB	1.91	1.01
1:D:191:ALA:HB1	1:D:218:GLY:C	1.79	1.01
1:F:149:SER:HB2	1:F:167:ALA:CB	1.91	1.01
1:B:197:LEU:HD23	1:B:198:ASP:N	1.76	1.00
1:E:149:SER:HB2	1:E:167:ALA:CB	1.91	1.00
1:B:171:THR:HG23	1:C:72:ARG:NH1	1.76	1.00
1:C:197:LEU:HD23	1:C:198:ASP:N	1.76	1.00
1:D:149:SER:HB2	1:D:167:ALA:CB	1.91	1.00
1:D:152:ILE:HG23	1:D:165:ILE:HG23	1.40	1.00
1:A:197:LEU:HD23	1:A:198:ASP:N	1.76	1.00
1:F:152:ILE:HG23	1:F:165:ILE:HG23	1.40	1.00
1:D:72:ARG:HH12	1:F:171:THR:HG23	1.25	0.99
1:C:149:SER:HB2	1:C:167:ALA:CB	1.91	0.99
1:F:197:LEU:HD23	1:F:198:ASP:N	1.76	0.99
1:E:156:VAL:HG21	1:E:217:LEU:HG	1.44	0.99
1:B:165:ILE:O	1:B:176:LEU:HD23	1.63	0.99
1:C:165:ILE:O	1:C:176:LEU:HD23	1.63	0.99
1:C:156:VAL:HG21	1:C:217:LEU:HG	1.44	0.99
1:A:149:SER:HB2	1:A:167:ALA:CB	1.91	0.99
1:D:171:THR:HG23	1:E:72:ARG:HH12	1.27	0.99
1:E:197:LEU:HD23	1:E:198:ASP:N	1.76	0.99
1:E:165:ILE:O	1:E:176:LEU:HD23	1.63	0.99
1:E:152:ILE:HG23	1:E:165:ILE:HG23	1.40	0.98
1:B:156:VAL:HG21	1:B:217:LEU:HG	1.44	0.98
1:A:165:ILE:O	1:A:176:LEU:HD23	1.63	0.98
1:D:165:ILE:O	1:D:176:LEU:HD23	1.63	0.98
1:A:152:ILE:HG23	1:A:165:ILE:HG23	1.40	0.98
1:C:152:ILE:HG23	1:C:165:ILE:HG23	1.40	0.97
1:D:72:ARG:NH1	1:F:171:THR:HG23	1.78	0.97
1:F:156:VAL:HG21	1:F:217:LEU:HG	1.44	0.97
1:B:8:ALA:HB3	1:B:82:ALA:C	1.85	0.97
1:C:8:ALA:HB3	1:C:82:ALA:C	1.85	0.97
1:E:171:THR:HG23	1:F:72:ARG:HH12	1.29	0.97
1:F:165:ILE:O	1:F:176:LEU:HD23	1.63	0.97
1:A:37:ARG:HG2	1:A:37:ARG:O	1.65	0.97
1:B:37:ARG:O	1:B:37:ARG:HG2	1.65	0.97

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:171:THR:CG2	1:C:72:ARG:NH1	2.28	0.97
1:C:156:VAL:CB	1:C:191:ALA:O	2.13	0.97
1:F:8:ALA:HB3	1:F:82:ALA:C	1.85	0.96
1:D:72:ARG:NH1	1:F:171:THR:CG2	2.27	0.96
1:E:8:ALA:HB3	1:E:82:ALA:C	1.85	0.96
1:B:171:THR:HG23	1:C:72:ARG:HH12	1.23	0.96
1:A:156:VAL:CB	1:A:191:ALA:O	2.13	0.96
1:B:156:VAL:CB	1:B:191:ALA:O	2.13	0.96
1:A:8:ALA:HB3	1:A:82:ALA:C	1.85	0.96
1:E:37:ARG:O	1:E:37:ARG:HG2	1.65	0.96
1:C:222:PRO:HD3	1:C:242:PRO:CD	1.95	0.95
1:A:222:PRO:HD3	1:A:242:PRO:CD	1.95	0.95
1:B:222:PRO:HD3	1:B:242:PRO:CD	1.95	0.95
1:D:37:ARG:HG2	1:D:37:ARG:O	1.65	0.95
1:E:156:VAL:CB	1:E:191:ALA:O	2.13	0.95
1:E:222:PRO:HD3	1:E:242:PRO:CD	1.95	0.95
1:F:156:VAL:CB	1:F:191:ALA:O	2.13	0.95
1:D:156:VAL:CB	1:D:191:ALA:O	2.13	0.95
1:D:156:VAL:HG21	1:D:217:LEU:HG	1.44	0.95
1:F:222:PRO:HD3	1:F:242:PRO:CD	1.95	0.95
1:A:156:VAL:HG21	1:A:217:LEU:HG	1.44	0.95
1:F:37:ARG:O	1:F:37:ARG:HG2	1.65	0.95
1:D:8:ALA:HB3	1:D:82:ALA:C	1.85	0.95
1:E:222:PRO:CD	1:E:242:PRO:HG2	1.97	0.94
1:C:37:ARG:O	1:C:37:ARG:HG2	1.65	0.94
1:C:222:PRO:CD	1:C:242:PRO:HG2	1.97	0.94
1:D:222:PRO:HD3	1:D:242:PRO:CD	1.95	0.94
1:A:222:PRO:CD	1:A:242:PRO:HG2	1.97	0.94
1:F:150:ASP:O	1:F:197:LEU:CD2	2.16	0.94
1:E:171:THR:HG23	1:F:72:ARG:NH1	1.82	0.94
1:F:156:VAL:CG2	1:F:217:LEU:HG	1.98	0.94
1:E:133:LEU:HG	1:E:183:LEU:HD11	1.50	0.94
1:F:222:PRO:CD	1:F:242:PRO:HG2	1.97	0.94
1:C:150:ASP:O	1:C:197:LEU:CD2	2.16	0.94
1:B:133:LEU:HG	1:B:183:LEU:HD11	1.50	0.93
1:D:222:PRO:CD	1:D:242:PRO:HG2	1.97	0.93
1:D:156:VAL:CG2	1:D:217:LEU:HG	1.98	0.93
1:C:156:VAL:CG2	1:C:217:LEU:HG	1.98	0.93
1:A:156:VAL:CG2	1:A:217:LEU:HG	1.98	0.93
1:A:72:ARG:NH1	1:C:171:THR:HG23	1.83	0.93
1:B:150:ASP:O	1:B:197:LEU:CD2	2.16	0.93

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:222:PRO:CD	1:B:242:PRO:HG2	1.97	0.93
1:F:194:LEU:HD23	1:F:245:GLN:HG3	1.51	0.93
1:A:133:LEU:HG	1:A:183:LEU:HD11	1.50	0.93
1:D:171:THR:HG23	1:E:72:ARG:NH1	1.83	0.93
1:E:171:THR:CG2	1:F:72:ARG:NH1	2.32	0.93
1:A:72:ARG:NH1	1:C:171:THR:CG2	2.32	0.93
1:A:146:ASP:HA	1:A:197:LEU:HD11	1.51	0.93
1:C:133:LEU:HG	1:C:183:LEU:HD11	1.50	0.93
1:A:150:ASP:O	1:A:197:LEU:CD2	2.16	0.93
1:E:156:VAL:CG2	1:E:217:LEU:HG	1.98	0.93
1:C:194:LEU:HD23	1:C:245:GLN:HG3	1.51	0.92
1:B:227:TYR:O	1:B:235:THR:HA	1.69	0.92
1:C:227:TYR:O	1:C:235:THR:HA	1.69	0.92
1:A:227:TYR:O	1:A:235:THR:HA	1.69	0.92
1:D:227:TYR:O	1:D:235:THR:HA	1.70	0.92
1:A:171:THR:HG23	1:B:72:ARG:HH12	1.33	0.92
1:D:194:LEU:HD23	1:D:245:GLN:HG3	1.51	0.92
1:F:95:ARG:O	1:F:109:ALA:CA	2.18	0.92
1:B:156:VAL:CG2	1:B:217:LEU:HG	1.98	0.92
1:E:95:ARG:O	1:E:109:ALA:CA	2.18	0.92
1:A:72:ARG:HH12	1:C:171:THR:HG23	1.31	0.91
1:A:95:ARG:O	1:A:109:ALA:CA	2.18	0.91
1:E:194:LEU:HD23	1:E:245:GLN:HG3	1.51	0.91
1:F:133:LEU:HG	1:F:183:LEU:HD11	1.50	0.91
1:F:227:TYR:O	1:F:235:THR:HA	1.69	0.91
1:C:95:ARG:O	1:C:109:ALA:CA	2.18	0.91
1:A:194:LEU:HD23	1:A:245:GLN:HG3	1.51	0.91
1:B:194:LEU:HD23	1:B:245:GLN:HG3	1.51	0.91
1:E:150:ASP:O	1:E:197:LEU:CD2	2.16	0.91
1:B:33:SER:CB	1:B:51:LEU:O	2.19	0.91
1:D:146:ASP:HA	1:D:197:LEU:HD11	1.51	0.91
1:D:150:ASP:O	1:D:197:LEU:CD2	2.16	0.91
1:C:33:SER:CB	1:C:51:LEU:O	2.19	0.91
1:C:146:ASP:HA	1:C:197:LEU:HD11	1.51	0.91
1:D:33:SER:CB	1:D:51:LEU:O	2.19	0.91
1:E:146:ASP:HA	1:E:197:LEU:HD11	1.51	0.90
1:E:227:TYR:O	1:E:235:THR:HA	1.69	0.90
1:A:171:THR:HG23	1:B:72:ARG:NH1	1.85	0.90
1:D:21:LEU:HB3	1:D:40:ASP:HB3	1.54	0.90
1:D:133:LEU:HG	1:D:183:LEU:HD11	1.50	0.90
1:E:33:SER:CB	1:E:51:LEU:O	2.19	0.90

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:33:SER:CB	1:A:51:LEU:O	2.19	0.90
1:E:153:ARG:O	1:E:165:ILE:HA	1.72	0.90
1:B:146:ASP:HA	1:B:197:LEU:HD11	1.51	0.90
1:A:108:LEU:HD22	1:A:110:LEU:HD23	1.54	0.90
1:A:153:ARG:O	1:A:165:ILE:HA	1.72	0.90
1:D:133:LEU:HG	1:D:183:LEU:CD1	2.02	0.90
1:B:153:ARG:O	1:B:165:ILE:HA	1.72	0.90
1:C:108:LEU:HD22	1:C:110:LEU:HD23	1.54	0.90
1:A:21:LEU:HB3	1:A:40:ASP:HB3	1.54	0.89
1:E:6:VAL:HG22	1:E:56:PHE:HD2	1.38	0.89
1:F:146:ASP:HA	1:F:197:LEU:HD11	1.51	0.89
1:A:6:VAL:HG22	1:A:56:PHE:HD2	1.37	0.89
1:A:171:THR:CG2	1:B:72:ARG:NH1	2.34	0.89
1:E:21:LEU:HB3	1:E:40:ASP:HB3	1.54	0.89
1:E:133:LEU:HG	1:E:183:LEU:CD1	2.02	0.89
1:F:21:LEU:HB3	1:F:40:ASP:HB3	1.54	0.89
1:F:133:LEU:HG	1:F:183:LEU:CD1	2.02	0.89
1:C:6:VAL:HG22	1:C:56:PHE:HD2	1.37	0.89
1:A:133:LEU:HG	1:A:183:LEU:CD1	2.02	0.89
1:F:33:SER:CB	1:F:51:LEU:O	2.19	0.89
1:F:108:LEU:HD22	1:F:110:LEU:HD23	1.54	0.89
1:D:95:ARG:O	1:D:109:ALA:CA	2.18	0.89
1:D:72:ARG:HH12	1:F:171:THR:HG21	1.35	0.88
1:F:8:ALA:N	1:F:84:ASP:O	2.06	0.88
1:A:173:ASP:HB2	1:B:107:THR:CG2	2.02	0.88
1:C:153:ARG:O	1:C:165:ILE:HA	1.72	0.88
1:B:6:VAL:HG22	1:B:56:PHE:HD2	1.37	0.88
1:C:133:LEU:HG	1:C:183:LEU:CD1	2.02	0.88
1:D:153:ARG:O	1:D:165:ILE:HA	1.72	0.88
1:B:142:ILE:HD13	1:B:152:ILE:HD12	1.56	0.88
1:B:173:ASP:HB2	1:C:107:THR:CG2	2.03	0.88
1:D:171:THR:CG2	1:E:72:ARG:NH1	2.35	0.88
1:F:153:ARG:O	1:F:165:ILE:HA	1.72	0.88
1:B:133:LEU:HG	1:B:183:LEU:CD1	2.02	0.88
1:D:8:ALA:N	1:D:84:ASP:O	2.06	0.88
1:E:108:LEU:HD22	1:E:110:LEU:HD23	1.54	0.88
1:D:6:VAL:HG22	1:D:56:PHE:HD2	1.38	0.88
1:D:170:ASP:O	1:D:171:THR:HG22	1.74	0.88
1:F:213:VAL:HG22	1:F:227:TYR:CZ	2.09	0.88
1:B:8:ALA:N	1:B:84:ASP:O	2.06	0.88
1:C:170:ASP:O	1:C:171:THR:HG22	1.74	0.88

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:213:VAL:HG22	1:C:227:TYR:CZ	2.09	0.88
1:B:21:LEU:HB3	1:B:40:ASP:HB3	1.54	0.87
1:B:95:ARG:O	1:B:109:ALA:CA	2.18	0.87
1:D:108:LEU:HD22	1:D:110:LEU:HD23	1.54	0.87
1:F:142:ILE:HD13	1:F:152:ILE:HD12	1.56	0.87
1:A:107:THR:CG2	1:C:173:ASP:HB2	2.04	0.87
1:A:213:VAL:HG22	1:A:227:TYR:CZ	2.09	0.87
1:A:8:ALA:N	1:A:84:ASP:O	2.06	0.87
1:B:213:VAL:HG22	1:B:227:TYR:CZ	2.09	0.87
1:C:142:ILE:HD13	1:C:152:ILE:HD12	1.56	0.87
1:E:152:ILE:CG2	1:E:165:ILE:HG23	2.05	0.87
1:E:213:VAL:HG22	1:E:227:TYR:CZ	2.09	0.87
1:B:170:ASP:O	1:B:171:THR:HG22	1.74	0.87
1:C:8:ALA:N	1:C:84:ASP:O	2.06	0.87
1:A:170:ASP:O	1:A:171:THR:HG22	1.74	0.87
1:F:152:ILE:CG2	1:F:165:ILE:HG23	2.05	0.87
1:E:8:ALA:N	1:E:84:ASP:O	2.06	0.86
1:C:152:ILE:CG2	1:C:165:ILE:HG23	2.05	0.86
1:D:213:VAL:HG22	1:D:227:TYR:CZ	2.09	0.86
1:E:142:ILE:HD13	1:E:152:ILE:HD12	1.56	0.86
1:E:146:ASP:HA	1:E:197:LEU:CD1	2.05	0.86
1:B:152:ILE:CG2	1:B:165:ILE:HG23	2.05	0.86
1:C:146:ASP:HA	1:C:197:LEU:CD1	2.05	0.86
1:B:108:LEU:HD22	1:B:110:LEU:HD23	1.54	0.86
1:B:146:ASP:HA	1:B:197:LEU:CD1	2.05	0.86
1:A:152:ILE:CG2	1:A:165:ILE:HG23	2.05	0.86
1:D:173:ASP:HB2	1:E:107:THR:CG2	2.05	0.86
1:F:222:PRO:HD3	1:F:242:PRO:HD2	1.58	0.86
1:A:222:PRO:HD3	1:A:242:PRO:HD2	1.58	0.86
1:C:21:LEU:HB3	1:C:40:ASP:HB3	1.54	0.86
1:D:146:ASP:HA	1:D:197:LEU:CD1	2.05	0.86
1:F:6:VAL:HG22	1:F:56:PHE:HD2	1.37	0.86
1:D:152:ILE:CG2	1:D:165:ILE:HG23	2.05	0.86
1:A:146:ASP:HA	1:A:197:LEU:CD1	2.05	0.86
1:C:152:ILE:CG2	1:C:165:ILE:CG2	2.54	0.86
1:F:170:ASP:O	1:F:171:THR:HG22	1.74	0.85
1:C:222:PRO:HD3	1:C:242:PRO:HD2	1.58	0.85
1:B:152:ILE:CG2	1:B:165:ILE:CG2	2.54	0.85
1:E:170:ASP:O	1:E:171:THR:HG22	1.74	0.85
1:D:142:ILE:HD13	1:D:152:ILE:HD12	1.56	0.85
1:D:152:ILE:CG2	1:D:165:ILE:CG2	2.54	0.85

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:146:ASP:HA	1:F:197:LEU:CD1	2.05	0.85
1:E:173:ASP:HB2	1:F:107:THR:CG2	2.06	0.85
1:A:152:ILE:CG2	1:A:165:ILE:CG2	2.54	0.84
1:E:129:ALA:HB1	1:E:156:VAL:HG11	1.59	0.84
1:F:152:ILE:CG2	1:F:165:ILE:CG2	2.54	0.84
1:A:142:ILE:HD13	1:A:152:ILE:HD12	1.56	0.84
1:E:152:ILE:CG2	1:E:165:ILE:CG2	2.54	0.84
1:F:135:GLY:N	1:F:211:ALA:O	2.10	0.84
1:B:129:ALA:HB1	1:B:156:VAL:HG11	1.59	0.84
1:C:135:GLY:N	1:C:211:ALA:O	2.10	0.84
1:E:135:GLY:N	1:E:211:ALA:O	2.10	0.84
1:A:129:ALA:HB1	1:A:156:VAL:HG11	1.59	0.84
1:C:34:LEU:O	1:C:51:LEU:HB2	1.78	0.84
1:A:34:LEU:O	1:A:51:LEU:HB2	1.78	0.84
1:F:34:LEU:O	1:F:51:LEU:HB2	1.78	0.83
1:A:135:GLY:N	1:A:211:ALA:O	2.10	0.83
1:E:222:PRO:HD3	1:E:242:PRO:HD2	1.58	0.83
1:B:222:PRO:HD3	1:B:242:PRO:HD2	1.58	0.83
1:D:8:ALA:CB	1:D:81:GLY:O	2.27	0.83
1:D:34:LEU:O	1:D:51:LEU:HB2	1.78	0.83
1:D:135:GLY:N	1:D:211:ALA:O	2.10	0.83
1:E:33:SER:HB2	1:E:51:LEU:O	1.79	0.83
1:B:135:GLY:N	1:B:211:ALA:O	2.10	0.83
1:A:72:ARG:HH12	1:C:171:THR:HG21	1.42	0.83
1:B:8:ALA:CB	1:B:81:GLY:O	2.27	0.82
1:D:129:ALA:HB1	1:D:156:VAL:HG11	1.59	0.82
1:C:8:ALA:CB	1:C:81:GLY:O	2.27	0.82
1:D:213:VAL:HG22	1:D:227:TYR:OH	1.80	0.82
1:A:213:VAL:HG22	1:A:227:TYR:OH	1.80	0.82
1:B:33:SER:HB2	1:B:51:LEU:O	1.79	0.82
1:D:222:PRO:HD3	1:D:242:PRO:HD2	1.58	0.82
1:E:8:ALA:CB	1:E:81:GLY:O	2.27	0.82
1:C:129:ALA:HB1	1:C:156:VAL:HG11	1.59	0.82
1:F:129:ALA:HB1	1:F:156:VAL:HG11	1.59	0.82
1:A:8:ALA:CB	1:A:81:GLY:O	2.27	0.82
1:E:34:LEU:O	1:E:51:LEU:HB2	1.78	0.82
1:C:213:VAL:HG22	1:C:227:TYR:OH	1.80	0.81
1:B:34:LEU:O	1:B:51:LEU:HB2	1.78	0.81
1:D:9:ALA:HB2	1:D:82:ALA:HB1	1.63	0.81
1:B:222:PRO:HB3	1:B:239:MET:HG2	1.61	0.81
1:C:222:PRO:HB3	1:C:239:MET:HG2	1.61	0.81

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:222:PRO:HB3	1:A:239:MET:HG2	1.61	0.81
1:F:33:SER:HB2	1:F:51:LEU:O	1.79	0.81
1:C:166:GLU:HB3	1:C:175:ASP:HA	1.63	0.81
1:B:213:VAL:HG22	1:B:227:TYR:OH	1.80	0.81
1:F:9:ALA:HB2	1:F:82:ALA:HB1	1.63	0.81
1:F:213:VAL:HG22	1:F:227:TYR:OH	1.80	0.81
1:D:151:HIS:HA	1:D:197:LEU:H	1.46	0.81
1:E:171:THR:HG21	1:F:72:ARG:HH12	1.42	0.81
1:F:166:GLU:HB3	1:F:175:ASP:HA	1.63	0.81
1:A:171:THR:HG21	1:B:72:ARG:HH12	1.46	0.81
1:B:152:ILE:HG23	1:B:165:ILE:HG22	1.63	0.81
1:C:136:THR:HB	1:C:209:THR:HA	1.63	0.81
1:D:33:SER:HB2	1:D:51:LEU:O	1.79	0.81
1:E:222:PRO:HB3	1:E:239:MET:HG2	1.61	0.81
1:F:222:PRO:HB3	1:F:239:MET:HG2	1.61	0.81
1:E:166:GLU:HB3	1:E:175:ASP:HA	1.63	0.80
1:E:213:VAL:HG22	1:E:227:TYR:OH	1.80	0.80
1:C:33:SER:HB2	1:C:51:LEU:O	1.79	0.80
1:D:107:THR:CG2	1:F:173:ASP:HB2	2.12	0.80
1:A:33:SER:HB2	1:A:51:LEU:O	1.79	0.80
1:B:171:THR:HG21	1:C:72:ARG:HH12	1.43	0.80
1:C:229:ILE:HD11	1:C:236:ILE:HD11	1.63	0.80
1:E:152:ILE:HG23	1:E:165:ILE:HG22	1.63	0.80
1:F:152:ILE:HG23	1:F:165:ILE:HG22	1.63	0.80
1:E:136:THR:HB	1:E:209:THR:HA	1.63	0.80
1:D:222:PRO:HB3	1:D:239:MET:HG2	1.61	0.80
1:E:195:PHE:HB3	1:E:240:LEU:HD22	1.64	0.80
1:F:8:ALA:CB	1:F:81:GLY:O	2.27	0.80
1:C:195:PHE:HB3	1:C:240:LEU:HD22	1.64	0.80
1:D:166:GLU:HB3	1:D:175:ASP:HA	1.63	0.80
1:B:9:ALA:HB2	1:B:82:ALA:HB1	1.63	0.79
1:D:195:PHE:HB3	1:D:240:LEU:HD22	1.64	0.79
1:F:229:ILE:HD11	1:F:236:ILE:HD11	1.63	0.79
1:A:229:ILE:HD11	1:A:236:ILE:HD11	1.63	0.79
1:D:152:ILE:HG23	1:D:165:ILE:HG22	1.63	0.79
1:F:4:ALA:O	1:F:87:HIS:HA	1.83	0.79
1:F:195:PHE:HB3	1:F:240:LEU:HD22	1.64	0.79
1:B:136:THR:HB	1:B:209:THR:HA	1.63	0.79
1:B:166:GLU:HB3	1:B:175:ASP:HA	1.63	0.79
1:E:9:ALA:HB2	1:E:82:ALA:HB1	1.63	0.79
1:E:4:ALA:O	1:E:87:HIS:HA	1.83	0.79

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:152:ILE:HG23	1:C:165:ILE:HG22	1.63	0.79
1:A:9:ALA:HB2	1:A:82:ALA:HB1	1.63	0.79
1:A:152:ILE:HG23	1:A:165:ILE:HG22	1.63	0.79
1:C:9:ALA:HB2	1:C:82:ALA:HB1	1.63	0.79
1:D:136:THR:HB	1:D:209:THR:HA	1.63	0.79
1:B:151:HIS:HA	1:B:197:LEU:H	1.46	0.79
1:C:4:ALA:O	1:C:87:HIS:HA	1.83	0.79
1:D:229:ILE:HD11	1:D:236:ILE:HD11	1.63	0.79
1:C:151:HIS:HA	1:C:197:LEU:H	1.46	0.79
1:F:136:THR:HB	1:F:209:THR:HA	1.63	0.79
1:B:4:ALA:O	1:B:87:HIS:HA	1.83	0.78
1:D:4:ALA:O	1:D:87:HIS:HA	1.83	0.78
1:F:151:HIS:HA	1:F:197:LEU:H	1.46	0.78
1:A:4:ALA:O	1:A:87:HIS:HA	1.83	0.78
1:A:151:HIS:HA	1:A:197:LEU:H	1.46	0.78
1:B:204:ASN:HA	1:B:207:ILE:HD13	1.65	0.78
1:A:136:THR:HB	1:A:209:THR:HA	1.63	0.78
1:A:166:GLU:HB3	1:A:175:ASP:HA	1.63	0.78
1:B:229:ILE:HD11	1:B:236:ILE:HD11	1.63	0.78
1:A:195:PHE:HB3	1:A:240:LEU:HD22	1.64	0.78
1:B:195:PHE:HB3	1:B:240:LEU:HD22	1.64	0.78
1:D:171:THR:HG21	1:E:72:ARG:HH12	1.47	0.78
1:B:171:THR:O	1:B:172:ASP:OD1	2.02	0.78
1:D:204:ASN:HA	1:D:207:ILE:HD13	1.66	0.78
1:F:204:ASN:HA	1:F:207:ILE:HD13	1.66	0.78
1:A:171:THR:O	1:A:172:ASP:OD1	2.02	0.78
1:C:149:SER:CB	1:C:167:ALA:CB	2.49	0.78
1:C:171:THR:O	1:C:172:ASP:OD1	2.02	0.78
1:F:171:THR:O	1:F:172:ASP:OD1	2.02	0.78
1:E:1:MET:HG3	1:E:91:ASP:CB	2.14	0.77
1:E:151:HIS:HA	1:E:197:LEU:H	1.46	0.77
1:E:229:ILE:HD11	1:E:236:ILE:HD11	1.63	0.77
1:D:157:ASP:CG	1:D:157:ASP:O	2.23	0.77
1:F:1:MET:HG3	1:F:91:ASP:CB	2.14	0.77
1:A:1:MET:HG3	1:A:91:ASP:CB	2.14	0.77
1:C:204:ASN:HA	1:C:207:ILE:HD13	1.66	0.77
1:D:1:MET:HG3	1:D:91:ASP:CB	2.14	0.77
1:B:1:MET:HG3	1:B:91:ASP:CB	2.14	0.77
1:A:39:VAL:CG1	1:A:43:ASN:HA	2.15	0.77
1:C:1:MET:HG3	1:C:91:ASP:CB	2.14	0.77
1:D:20:VAL:HG13	1:D:202:ASP:HB3	1.67	0.77

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:157:ASP:CG	1:C:157:ASP:O	2.23	0.77
1:A:20:VAL:HG13	1:A:202:ASP:HB3	1.67	0.77
1:C:39:VAL:CG1	1:C:43:ASN:HA	2.15	0.77
1:F:151:HIS:HB3	1:F:196:SER:HA	1.67	0.77
1:E:20:VAL:HG13	1:E:202:ASP:HB3	1.67	0.76
1:E:157:ASP:CG	1:E:157:ASP:O	2.23	0.76
1:D:171:THR:O	1:D:172:ASP:OD1	2.02	0.76
1:E:204:ASN:HA	1:E:207:ILE:HD13	1.66	0.76
1:E:39:VAL:CG1	1:E:43:ASN:HA	2.15	0.76
1:E:171:THR:O	1:E:172:ASP:OD1	2.02	0.76
1:A:8:ALA:CB	1:A:82:ALA:O	2.25	0.76
1:A:151:HIS:HB3	1:A:196:SER:HA	1.67	0.76
1:A:204:ASN:HA	1:A:207:ILE:HD13	1.65	0.76
1:B:3:LYS:O	1:B:58:SER:O	2.04	0.76
1:B:39:VAL:CG1	1:B:43:ASN:HA	2.15	0.76
1:F:3:LYS:O	1:F:58:SER:O	2.04	0.76
1:F:39:VAL:CG1	1:F:43:ASN:HA	2.15	0.76
1:D:39:VAL:CG1	1:D:43:ASN:HA	2.15	0.76
1:F:157:ASP:CG	1:F:157:ASP:O	2.23	0.76
1:B:157:ASP:CG	1:B:157:ASP:O	2.23	0.76
1:E:3:LYS:O	1:E:58:SER:O	2.04	0.76
1:C:3:LYS:O	1:C:58:SER:O	2.04	0.75
1:E:25:CYS:SG	1:E:70:LEU:HG	2.26	0.75
1:E:151:HIS:HB3	1:E:196:SER:HA	1.68	0.75
1:A:25:CYS:SG	1:A:70:LEU:HG	2.26	0.75
1:E:8:ALA:CB	1:E:82:ALA:O	2.26	0.75
1:B:8:ALA:CB	1:B:82:ALA:O	2.25	0.75
1:C:20:VAL:HG13	1:C:202:ASP:HB3	1.67	0.75
1:D:5:ILE:HG22	1:D:85:LEU:HB3	1.68	0.75
1:B:151:HIS:HB3	1:B:196:SER:HA	1.67	0.75
1:F:20:VAL:HG13	1:F:202:ASP:HB3	1.67	0.75
1:C:5:ILE:HG22	1:C:85:LEU:HB3	1.68	0.75
1:C:151:HIS:HB3	1:C:196:SER:HA	1.67	0.75
1:B:20:VAL:HG13	1:B:202:ASP:HB3	1.67	0.75
1:C:214:THR:OG1	1:C:226:HIS:HB2	1.87	0.75
1:F:26:LYS:HE2	1:F:113:PRO:O	1.87	0.75
1:F:191:ALA:CB	1:F:218:GLY:HA2	2.17	0.75
1:A:3:LYS:O	1:A:58:SER:O	2.04	0.75
1:B:5:ILE:HG22	1:B:85:LEU:HB3	1.68	0.75
1:C:29:LEU:HD23	1:C:34:LEU:HD13	1.69	0.75
1:D:240:LEU:HD23	1:D:241:ALA:O	1.87	0.75

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:5:ILE:HG22	1:F:85:LEU:HB3	1.68	0.75
1:F:29:LEU:HD23	1:F:34:LEU:HD13	1.69	0.75
1:A:108:LEU:HD22	1:A:110:LEU:CD2	2.17	0.74
1:B:240:LEU:HD23	1:B:241:ALA:O	1.87	0.74
1:D:3:LYS:O	1:D:58:SER:O	2.04	0.74
1:D:25:CYS:SG	1:D:70:LEU:HG	2.26	0.74
1:D:29:LEU:HD23	1:D:34:LEU:HD13	1.69	0.74
1:F:25:CYS:SG	1:F:70:LEU:HG	2.26	0.74
1:F:214:THR:OG1	1:F:226:HIS:HB2	1.87	0.74
1:C:240:LEU:HD23	1:C:241:ALA:O	1.87	0.74
1:C:26:LYS:HE2	1:C:113:PRO:O	1.87	0.74
1:C:191:ALA:CB	1:C:218:GLY:HA2	2.17	0.74
1:A:157:ASP:CG	1:A:157:ASP:O	2.23	0.74
1:D:214:THR:OG1	1:D:226:HIS:HB2	1.87	0.74
1:D:149:SER:CB	1:D:167:ALA:CB	2.49	0.74
1:E:108:LEU:HD22	1:E:110:LEU:CD2	2.17	0.74
1:E:240:LEU:HD23	1:E:241:ALA:O	1.87	0.74
1:B:25:CYS:SG	1:B:70:LEU:HG	2.26	0.74
1:D:191:ALA:CB	1:D:218:GLY:HA2	2.17	0.74
1:D:197:LEU:HA	1:D:200:LEU:HD12	1.70	0.74
1:E:26:LYS:HE2	1:E:113:PRO:O	1.87	0.74
1:E:29:LEU:HD23	1:E:34:LEU:HD13	1.69	0.74
1:A:96:LYS:CA	1:A:108:LEU:O	2.35	0.74
1:C:25:CYS:SG	1:C:70:LEU:HG	2.26	0.74
1:F:108:LEU:HD22	1:F:110:LEU:CD2	2.17	0.74
1:A:197:LEU:HA	1:A:200:LEU:HD12	1.70	0.74
1:C:6:VAL:HG22	1:C:56:PHE:CD2	2.23	0.74
1:C:197:LEU:HA	1:C:200:LEU:HD12	1.70	0.74
1:F:240:LEU:HD23	1:F:241:ALA:O	1.87	0.74
1:A:29:LEU:HD23	1:A:34:LEU:HD13	1.69	0.74
1:B:108:LEU:HD22	1:B:110:LEU:CD2	2.17	0.74
1:E:214:THR:OG1	1:E:226:HIS:HB2	1.87	0.74
1:D:6:VAL:HG22	1:D:56:PHE:CD2	2.23	0.74
1:D:108:LEU:HD22	1:D:110:LEU:CD2	2.17	0.74
1:A:191:ALA:CB	1:A:218:GLY:HA2	2.17	0.73
1:B:197:LEU:HA	1:B:200:LEU:HD12	1.70	0.73
1:B:214:THR:OG1	1:B:226:HIS:HB2	1.87	0.73
1:B:26:LYS:HE2	1:B:113:PRO:O	1.87	0.73
1:B:191:ALA:CB	1:B:218:GLY:HA2	2.17	0.73
1:D:151:HIS:HB3	1:D:196:SER:HA	1.68	0.73
1:E:5:ILE:HG22	1:E:85:LEU:HB3	1.68	0.73

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:191:ALA:CB	1:E:218:GLY:HA2	2.17	0.73
1:D:26:LYS:HE2	1:D:113:PRO:O	1.87	0.73
1:D:96:LYS:CA	1:D:108:LEU:O	2.35	0.73
1:A:6:VAL:HG22	1:A:56:PHE:CD2	2.23	0.73
1:A:26:LYS:HE2	1:A:113:PRO:O	1.87	0.73
1:E:1:MET:HG3	1:E:91:ASP:HB3	1.70	0.73
1:A:214:THR:OG1	1:A:226:HIS:HB2	1.87	0.73
1:B:1:MET:HG3	1:B:91:ASP:HB3	1.70	0.73
1:C:8:ALA:CB	1:C:82:ALA:O	2.25	0.73
1:D:8:ALA:CB	1:D:82:ALA:O	2.26	0.73
1:A:240:LEU:HD23	1:A:241:ALA:O	1.87	0.72
1:C:108:LEU:HD22	1:C:110:LEU:CD2	2.17	0.72
1:F:8:ALA:CB	1:F:82:ALA:O	2.25	0.72
1:F:197:LEU:HA	1:F:200:LEU:HD12	1.70	0.72
1:E:101:ILE:HD11	1:E:104:LEU:HD12	1.71	0.72
1:E:6:VAL:HG22	1:E:56:PHE:CD2	2.23	0.72
1:E:197:LEU:HA	1:E:200:LEU:HD12	1.70	0.72
1:A:5:ILE:HG22	1:A:85:LEU:HB3	1.68	0.72
1:B:29:LEU:HD23	1:B:34:LEU:HD13	1.69	0.72
1:B:96:LYS:CA	1:B:108:LEU:O	2.35	0.72
1:A:104:LEU:HD21	1:C:174:VAL:HG23	1.72	0.72
1:C:1:MET:HG3	1:C:91:ASP:HB3	1.70	0.72
1:D:101:ILE:HD11	1:D:104:LEU:HD12	1.71	0.72
1:B:101:ILE:HD11	1:B:104:LEU:HD12	1.71	0.72
1:F:96:LYS:CA	1:F:108:LEU:O	2.35	0.72
1:D:1:MET:HG3	1:D:91:ASP:HB3	1.70	0.72
1:A:1:MET:HG3	1:A:91:ASP:HB3	1.70	0.72
1:A:101:ILE:HD11	1:A:104:LEU:HD12	1.71	0.72
1:E:96:LYS:CA	1:E:108:LEU:O	2.35	0.72
1:A:197:LEU:HD23	1:A:198:ASP:H	1.55	0.71
1:B:197:LEU:HD23	1:B:198:ASP:H	1.55	0.71
1:C:104:LEU:HD13	1:C:104:LEU:O	1.90	0.71
1:E:104:LEU:O	1:E:104:LEU:HD13	1.90	0.71
1:C:29:LEU:HA	1:C:34:LEU:HB3	1.73	0.71
1:C:101:ILE:HD11	1:C:104:LEU:HD12	1.71	0.71
1:C:191:ALA:CB	1:C:218:GLY:CA	2.69	0.71
1:F:197:LEU:HD23	1:F:198:ASP:H	1.55	0.71
1:B:142:ILE:HD13	1:B:152:ILE:CD1	2.21	0.71
1:D:29:LEU:HA	1:D:34:LEU:HB3	1.73	0.71
1:D:142:ILE:HD13	1:D:152:ILE:CD1	2.21	0.71
1:B:104:LEU:O	1:B:104:LEU:HD13	1.91	0.71

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:142:ILE:HD13	1:C:152:ILE:CD1	2.21	0.71
1:D:197:LEU:HD23	1:D:198:ASP:H	1.55	0.71
1:F:191:ALA:HB1	1:F:218:GLY:CA	2.21	0.71
1:D:191:ALA:HB1	1:D:218:GLY:CA	2.21	0.71
1:E:191:ALA:HB1	1:E:218:GLY:CA	2.21	0.71
1:F:101:ILE:HD11	1:F:104:LEU:HD12	1.71	0.71
1:A:142:ILE:HD13	1:A:152:ILE:CD1	2.21	0.71
1:B:6:VAL:HG22	1:B:56:PHE:CD2	2.23	0.71
1:B:29:LEU:HA	1:B:34:LEU:HB3	1.73	0.71
1:A:191:ALA:HB1	1:A:218:GLY:CA	2.21	0.71
1:C:229:ILE:HD11	1:C:236:ILE:CD1	2.21	0.71
1:D:191:ALA:CB	1:D:218:GLY:CA	2.69	0.71
1:D:229:ILE:HD11	1:D:236:ILE:CD1	2.21	0.71
1:E:29:LEU:HA	1:E:34:LEU:HB3	1.73	0.71
1:B:155:ARG:HA	1:B:192:ASP:HB2	1.73	0.70
1:B:191:ALA:HB1	1:B:218:GLY:CA	2.21	0.70
1:E:142:ILE:HD13	1:E:152:ILE:CD1	2.21	0.70
1:F:104:LEU:O	1:F:104:LEU:HD13	1.90	0.70
1:F:155:ARG:HA	1:F:192:ASP:HB2	1.73	0.70
1:A:29:LEU:HA	1:A:34:LEU:HB3	1.73	0.70
1:A:104:LEU:O	1:A:104:LEU:HD13	1.90	0.70
1:B:191:ALA:CB	1:B:218:GLY:CA	2.69	0.70
1:C:125:LEU:HD12	1:C:224:LYS:HE3	1.74	0.70
1:F:191:ALA:CB	1:F:218:GLY:CA	2.69	0.70
1:F:229:ILE:HD11	1:F:236:ILE:CD1	2.21	0.70
1:F:142:ILE:HD13	1:F:152:ILE:CD1	2.21	0.70
1:B:229:ILE:HD11	1:B:236:ILE:CD1	2.21	0.70
1:C:155:ARG:HA	1:C:192:ASP:HB2	1.73	0.70
1:A:174:VAL:HG23	1:B:104:LEU:HD21	1.73	0.70
1:A:229:ILE:HD11	1:A:236:ILE:CD1	2.21	0.70
1:D:138:LEU:HG	1:D:213:VAL:HG11	1.74	0.70
1:E:155:ARG:HA	1:E:192:ASP:HB2	1.73	0.70
1:E:191:ALA:CB	1:E:218:GLY:CA	2.69	0.70
1:F:125:LEU:HD12	1:F:224:LYS:HE3	1.73	0.70
1:F:138:LEU:HG	1:F:213:VAL:HG11	1.74	0.70
1:F:1:MET:HG3	1:F:91:ASP:HB3	1.70	0.70
1:D:104:LEU:O	1:D:104:LEU:HD13	1.90	0.70
1:E:229:ILE:HD11	1:E:236:ILE:CD1	2.21	0.70
1:B:138:LEU:HG	1:B:213:VAL:HG11	1.74	0.70
1:F:29:LEU:HA	1:F:34:LEU:HB3	1.73	0.70
1:A:155:ARG:HA	1:A:192:ASP:HB2	1.73	0.70

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:138:LEU:HG	1:C:213:VAL:HG11	1.74	0.70
1:F:6:VAL:HG22	1:F:56:PHE:CD2	2.23	0.70
1:A:125:LEU:HD12	1:A:224:LYS:HE3	1.74	0.69
1:A:191:ALA:CB	1:A:218:GLY:CA	2.69	0.69
1:B:125:LEU:HD12	1:B:224:LYS:HE3	1.74	0.69
1:E:197:LEU:HD23	1:E:198:ASP:H	1.55	0.69
1:A:33:SER:HB3	1:A:51:LEU:O	1.92	0.69
1:B:107:THR:HG23	1:B:107:THR:O	1.92	0.69
1:C:191:ALA:HB1	1:C:218:GLY:CA	2.21	0.69
1:F:25:CYS:O	1:F:67:GLY:HA2	1.93	0.69
1:A:25:CYS:O	1:A:68:VAL:N	2.26	0.69
1:C:33:SER:HB3	1:C:51:LEU:O	1.92	0.69
1:C:197:LEU:HD23	1:C:198:ASP:H	1.55	0.69
1:D:107:THR:HG23	1:D:107:THR:O	1.92	0.69
1:D:155:ARG:HA	1:D:192:ASP:HB2	1.73	0.69
1:E:107:THR:HG23	1:E:107:THR:O	1.92	0.69
1:E:215:VAL:HG12	1:E:223:VAL:HG21	1.75	0.69
1:F:215:VAL:HG12	1:F:223:VAL:HG21	1.75	0.69
1:B:174:VAL:HG23	1:C:104:LEU:HD21	1.75	0.69
1:E:138:LEU:HG	1:E:213:VAL:HG11	1.74	0.69
1:A:25:CYS:O	1:A:67:GLY:HA2	1.93	0.69
1:B:215:VAL:HG12	1:B:223:VAL:HG21	1.75	0.69
1:C:25:CYS:O	1:C:68:VAL:N	2.26	0.69
1:C:107:THR:HG23	1:C:107:THR:O	1.92	0.69
1:D:25:CYS:O	1:D:67:GLY:HA2	1.93	0.69
1:D:104:LEU:HD21	1:F:174:VAL:HG23	1.73	0.69
1:E:33:SER:HB3	1:E:51:LEU:O	1.92	0.69
1:F:107:THR:O	1:F:107:THR:HG23	1.92	0.69
1:A:138:LEU:HG	1:A:213:VAL:HG11	1.73	0.69
1:C:20:VAL:HG21	1:C:202:ASP:O	1.93	0.69
1:E:20:VAL:HG21	1:E:202:ASP:O	1.93	0.69
1:A:20:VAL:HG21	1:A:202:ASP:O	1.93	0.69
1:A:98:ASN:HA	1:A:106:TYR:O	1.93	0.69
1:B:25:CYS:O	1:B:67:GLY:HA2	1.93	0.69
1:F:33:SER:HB3	1:F:51:LEU:O	1.92	0.69
1:F:98:ASN:HA	1:F:106:TYR:O	1.93	0.69
1:A:215:VAL:HG12	1:A:223:VAL:HG21	1.75	0.68
1:C:98:ASN:HA	1:C:106:TYR:O	1.93	0.68
1:E:125:LEU:HD12	1:E:224:LYS:HE3	1.73	0.68
1:F:25:CYS:O	1:F:68:VAL:N	2.26	0.68
1:C:96:LYS:CA	1:C:108:LEU:O	2.35	0.68

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:125:LEU:HD12	1:D:224:LYS:HE3	1.73	0.68
1:D:153:ARG:HG2	1:D:194:LEU:CD2	2.24	0.68
1:D:20:VAL:HG21	1:D:202:ASP:O	1.93	0.68
1:C:25:CYS:O	1:C:67:GLY:HA2	1.93	0.68
1:B:3:LYS:O	1:B:59:TYR:HA	1.94	0.68
1:D:215:VAL:HG12	1:D:223:VAL:HG21	1.75	0.68
1:D:33:SER:HB3	1:D:51:LEU:O	1.92	0.68
1:C:153:ARG:HG2	1:C:194:LEU:CD2	2.24	0.68
1:E:191:ALA:HB1	1:E:218:GLY:O	1.94	0.68
1:F:20:VAL:HG21	1:F:202:ASP:O	1.93	0.68
1:F:191:ALA:HB1	1:F:218:GLY:O	1.94	0.68
1:A:153:ARG:HG2	1:A:194:LEU:CD2	2.24	0.68
1:F:149:SER:CB	1:F:167:ALA:CB	2.49	0.68
1:F:153:ARG:HG2	1:F:194:LEU:CD2	2.24	0.68
1:B:20:VAL:HG21	1:B:202:ASP:O	1.93	0.67
1:E:25:CYS:O	1:E:67:GLY:HA2	1.93	0.67
1:A:3:LYS:O	1:A:59:TYR:HA	1.94	0.67
1:A:107:THR:HG23	1:A:107:THR:O	1.92	0.67
1:C:191:ALA:HB1	1:C:218:GLY:O	1.94	0.67
1:E:25:CYS:O	1:E:68:VAL:N	2.26	0.67
1:C:3:LYS:O	1:C:59:TYR:HA	1.94	0.67
1:D:222:PRO:CD	1:D:242:PRO:CG	2.64	0.67
1:E:3:LYS:O	1:E:59:TYR:HA	1.94	0.67
1:E:174:VAL:HG23	1:F:104:LEU:HD21	1.75	0.67
1:E:153:ARG:HG2	1:E:194:LEU:CD2	2.24	0.67
1:E:161:GLU:HB3	1:E:188:ALA:HB1	1.76	0.67
1:A:191:ALA:HB1	1:A:218:GLY:O	1.94	0.67
1:B:136:THR:HB	1:B:209:THR:HG22	1.77	0.67
1:C:136:THR:HB	1:C:209:THR:HG22	1.77	0.67
1:C:215:VAL:HG12	1:C:223:VAL:HG21	1.75	0.67
1:D:191:ALA:HB1	1:D:218:GLY:O	1.94	0.67
1:A:73:LEU:HD22	1:A:77:ALA:HB2	1.77	0.67
1:B:153:ARG:HG2	1:B:194:LEU:CD2	2.24	0.67
1:A:180:PRO:HA	1:A:186:ILE:HD11	1.77	0.67
1:B:4:ALA:O	1:B:86:ILE:O	2.13	0.67
1:B:191:ALA:HB1	1:B:218:GLY:O	1.94	0.67
1:A:47:VAL:CA	1:A:237:THR:O	2.30	0.67
1:C:161:GLU:HB3	1:C:188:ALA:HB1	1.76	0.67
1:D:98:ASN:HA	1:D:106:TYR:O	1.93	0.67
1:E:136:THR:HB	1:E:209:THR:HG22	1.77	0.67
1:F:3:LYS:O	1:F:59:TYR:HA	1.94	0.67

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:87:HIS:HE1	1:D:185:SER:HA	1.60	0.67
1:D:180:PRO:HA	1:D:186:ILE:HD11	1.77	0.67
1:F:231:GLU:HB2	1:F:233:MET:CE	2.25	0.67
1:A:161:GLU:HB3	1:A:188:ALA:HB1	1.76	0.67
1:B:33:SER:HB3	1:B:51:LEU:O	1.92	0.67
1:E:47:VAL:CA	1:E:237:THR:O	2.30	0.67
1:F:180:PRO:HA	1:F:186:ILE:HD11	1.77	0.67
1:F:207:ILE:HD12	1:F:207:ILE:N	2.10	0.67
1:A:207:ILE:HD12	1:A:207:ILE:N	2.10	0.66
1:D:47:VAL:CA	1:D:237:THR:O	2.30	0.66
1:E:98:ASN:HA	1:E:106:TYR:O	1.93	0.66
1:C:180:PRO:HA	1:C:186:ILE:HD11	1.77	0.66
1:B:39:VAL:HG13	1:B:43:ASN:HA	1.78	0.66
1:B:161:GLU:HB3	1:B:188:ALA:HB1	1.76	0.66
1:B:236:ILE:O	1:B:236:ILE:HG13	1.95	0.66
1:C:236:ILE:HG13	1:C:236:ILE:O	1.95	0.66
1:D:3:LYS:O	1:D:59:TYR:HA	1.94	0.66
1:E:231:GLU:HB2	1:E:233:MET:CE	2.25	0.66
1:F:4:ALA:O	1:F:86:ILE:O	2.13	0.66
1:A:231:GLU:HB2	1:A:233:MET:CE	2.25	0.66
1:B:98:ASN:HA	1:B:106:TYR:O	1.93	0.66
1:B:149:SER:CB	1:B:167:ALA:CB	2.49	0.66
1:D:236:ILE:HG13	1:D:236:ILE:O	1.96	0.66
1:F:236:ILE:HG13	1:F:236:ILE:O	1.96	0.66
1:A:236:ILE:HG13	1:A:236:ILE:O	1.96	0.66
1:D:231:GLU:HB2	1:D:233:MET:CE	2.25	0.66
1:E:180:PRO:HA	1:E:186:ILE:HD11	1.77	0.66
1:A:4:ALA:O	1:A:86:ILE:O	2.13	0.66
1:D:170:ASP:O	1:D:171:THR:CG2	2.44	0.66
1:F:136:THR:HB	1:F:209:THR:HG22	1.77	0.66
1:C:39:VAL:HG13	1:C:43:ASN:HA	1.78	0.66
1:D:161:GLU:HB3	1:D:188:ALA:HB1	1.76	0.66
1:E:207:ILE:N	1:E:207:ILE:HD12	2.10	0.66
1:B:73:LEU:HD22	1:B:77:ALA:HB2	1.77	0.66
1:C:73:LEU:HD22	1:C:77:ALA:HB2	1.77	0.66
1:D:25:CYS:O	1:D:68:VAL:N	2.26	0.66
1:E:39:VAL:HG13	1:E:43:ASN:HA	1.78	0.66
1:D:73:LEU:HD22	1:D:77:ALA:HB2	1.77	0.66
1:D:136:THR:HB	1:D:209:THR:HG22	1.77	0.66
1:B:25:CYS:O	1:B:68:VAL:N	2.26	0.66
1:B:47:VAL:CA	1:B:237:THR:O	2.30	0.66

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:207:ILE:N	1:B:207:ILE:HD12	2.10	0.66
1:C:4:ALA:O	1:C:86:ILE:O	2.13	0.66
1:D:32:GLU:N	1:D:32:GLU:OE1	2.29	0.65
1:B:231:GLU:HB2	1:B:233:MET:CE	2.25	0.65
1:C:231:GLU:HB2	1:C:233:MET:CE	2.25	0.65
1:F:161:GLU:HB3	1:F:188:ALA:HB1	1.76	0.65
1:F:170:ASP:O	1:F:171:THR:CG2	2.44	0.65
1:A:29:LEU:CD2	1:A:34:LEU:HD13	2.26	0.65
1:C:170:ASP:O	1:C:171:THR:CG2	2.44	0.65
1:E:4:ALA:O	1:E:86:ILE:O	2.13	0.65
1:A:39:VAL:HG13	1:A:43:ASN:HA	1.78	0.65
1:C:29:LEU:CD2	1:C:34:LEU:HD13	2.26	0.65
1:C:136:THR:HB	1:C:209:THR:CA	2.27	0.65
1:D:4:ALA:O	1:D:86:ILE:O	2.13	0.65
1:D:207:ILE:HD12	1:D:207:ILE:N	2.10	0.65
1:B:136:THR:HB	1:B:209:THR:CA	2.27	0.65
1:C:207:ILE:HD12	1:C:207:ILE:N	2.10	0.65
1:E:73:LEU:HD22	1:E:77:ALA:HB2	1.77	0.65
1:E:200:LEU:HA	1:E:203:MET:HE2	1.77	0.65
1:F:73:LEU:HD22	1:F:77:ALA:HB2	1.77	0.65
1:A:200:LEU:HA	1:A:203:MET:HE2	1.78	0.65
1:D:29:LEU:CD2	1:D:34:LEU:HD13	2.26	0.65
1:F:39:VAL:HG13	1:F:43:ASN:HA	1.78	0.65
1:A:170:ASP:O	1:A:171:THR:CG2	2.44	0.65
1:B:170:ASP:O	1:B:171:THR:CG2	2.44	0.65
1:B:180:PRO:HA	1:B:186:ILE:HD11	1.77	0.65
1:C:32:GLU:OE1	1:C:32:GLU:N	2.30	0.65
1:D:39:VAL:HG13	1:D:43:ASN:HA	1.77	0.65
1:E:29:LEU:CD2	1:E:34:LEU:HD13	2.26	0.65
1:A:149:SER:CB	1:A:167:ALA:CB	2.49	0.65
1:B:154:LEU:O	1:B:156:VAL:HG23	1.97	0.65
1:C:222:PRO:CD	1:C:242:PRO:CG	2.64	0.65
1:D:154:LEU:O	1:D:156:VAL:HG23	1.97	0.65
1:F:29:LEU:CD2	1:F:34:LEU:HD13	2.26	0.65
1:A:195:PHE:CE2	1:A:240:LEU:O	2.50	0.65
1:B:136:THR:CB	1:B:209:THR:HG22	2.27	0.65
1:B:157:ASP:HA	1:B:160:GLU:O	1.97	0.65
1:D:136:THR:HB	1:D:209:THR:CA	2.27	0.65
1:E:157:ASP:HA	1:E:160:GLU:O	1.97	0.65
1:F:136:THR:HB	1:F:209:THR:CA	2.27	0.65
1:A:136:THR:HB	1:A:209:THR:HG22	1.77	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:87:HIS:CE1	1:D:185:SER:HA	2.31	0.64
1:E:73:LEU:CD2	1:E:77:ALA:HB2	2.27	0.64
1:E:136:THR:CB	1:E:209:THR:HG22	2.28	0.64
1:A:136:THR:CB	1:A:209:THR:HG22	2.28	0.64
1:A:154:LEU:O	1:A:156:VAL:HG23	1.97	0.64
1:D:196:SER:H	1:D:240:LEU:HD21	1.62	0.64
1:E:236:ILE:O	1:E:236:ILE:HG13	1.95	0.64
1:A:73:LEU:CD2	1:A:77:ALA:HB2	2.27	0.64
1:A:136:THR:HB	1:A:209:THR:CA	2.27	0.64
1:C:157:ASP:HA	1:C:160:GLU:O	1.97	0.64
1:D:108:LEU:CD2	1:D:110:LEU:HD23	2.28	0.64
1:B:73:LEU:CD2	1:B:77:ALA:HB2	2.27	0.64
1:E:32:GLU:OE1	1:E:32:GLU:N	2.29	0.64
1:B:215:VAL:HG12	1:B:223:VAL:CG2	2.28	0.64
1:D:195:PHE:CE2	1:D:240:LEU:O	2.50	0.64
1:D:200:LEU:HA	1:D:203:MET:HE2	1.78	0.64
1:F:136:THR:CB	1:F:209:THR:HG22	2.27	0.64
1:F:158:GLY:H	1:F:162:THR:HB	1.62	0.64
1:C:195:PHE:CE2	1:C:240:LEU:O	2.50	0.64
1:C:200:LEU:HA	1:C:203:MET:HE2	1.80	0.64
1:D:157:ASP:HA	1:D:160:GLU:O	1.97	0.64
1:D:215:VAL:HG12	1:D:223:VAL:CG2	2.28	0.64
1:E:136:THR:HB	1:E:209:THR:CB	2.28	0.64
1:E:195:PHE:CE2	1:E:240:LEU:O	2.50	0.64
1:F:32:GLU:OE1	1:F:32:GLU:N	2.30	0.64
1:A:108:LEU:CD2	1:A:110:LEU:HD23	2.28	0.64
1:B:136:THR:HB	1:B:209:THR:CB	2.28	0.64
1:C:73:LEU:CD2	1:C:77:ALA:HB2	2.27	0.64
1:C:136:THR:CB	1:C:209:THR:HG22	2.27	0.64
1:D:73:LEU:CD2	1:D:77:ALA:HB2	2.27	0.64
1:E:136:THR:HB	1:E:209:THR:CA	2.27	0.64
1:A:136:THR:HB	1:A:209:THR:CB	2.28	0.64
1:B:195:PHE:CE2	1:B:240:LEU:O	2.50	0.64
1:E:215:VAL:HG12	1:E:223:VAL:CG2	2.28	0.64
1:F:215:VAL:HG12	1:F:223:VAL:CG2	2.28	0.64
1:A:32:GLU:OE1	1:A:32:GLU:N	2.30	0.64
1:A:215:VAL:HG12	1:A:223:VAL:CG2	2.28	0.64
1:D:158:GLY:H	1:D:162:THR:HB	1.62	0.64
1:E:170:ASP:O	1:E:171:THR:CG2	2.44	0.64
1:F:157:ASP:HA	1:F:160:GLU:O	1.97	0.64
1:A:231:GLU:HB2	1:A:233:MET:HE2	1.80	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:136:THR:CB	1:D:209:THR:HG22	2.27	0.64
1:E:2:PHE:HZ	1:E:64:GLY:HA3	1.64	0.64
1:B:29:LEU:CD2	1:B:34:LEU:HD13	2.26	0.63
1:B:158:GLY:H	1:B:162:THR:HB	1.62	0.63
1:B:196:SER:H	1:B:240:LEU:HD21	1.62	0.63
1:D:174:VAL:HG23	1:E:104:LEU:HD21	1.79	0.63
1:C:158:GLY:O	1:C:159:ALA:HB3	1.98	0.63
1:E:158:GLY:H	1:E:162:THR:HB	1.62	0.63
1:E:196:SER:H	1:E:240:LEU:HD21	1.62	0.63
1:A:157:ASP:HA	1:A:160:GLU:O	1.97	0.63
1:B:158:GLY:O	1:B:159:ALA:HB3	1.98	0.63
1:E:158:GLY:O	1:E:159:ALA:HB3	1.98	0.63
1:F:154:LEU:O	1:F:156:VAL:HG23	1.97	0.63
1:A:158:GLY:H	1:A:162:THR:HB	1.62	0.63
1:D:136:THR:HB	1:D:209:THR:CB	2.28	0.63
1:F:73:LEU:CD2	1:F:77:ALA:HB2	2.27	0.63
1:C:2:PHE:HZ	1:C:64:GLY:HA3	1.64	0.63
1:C:158:GLY:H	1:C:162:THR:HB	1.62	0.63
1:C:215:VAL:HG12	1:C:223:VAL:CG2	2.28	0.63
1:B:32:GLU:OE1	1:B:32:GLU:N	2.29	0.63
1:D:158:GLY:O	1:D:159:ALA:HB3	1.98	0.63
1:E:154:LEU:O	1:E:156:VAL:HG23	1.97	0.63
1:F:47:VAL:CA	1:F:237:THR:O	2.30	0.63
1:F:136:THR:HB	1:F:209:THR:CB	2.28	0.63
1:A:158:GLY:O	1:A:159:ALA:HB3	1.98	0.63
1:C:154:LEU:O	1:C:156:VAL:HG23	1.97	0.63
1:D:231:GLU:HB2	1:D:233:MET:HE3	1.80	0.63
1:F:2:PHE:HZ	1:F:64:GLY:HA3	1.63	0.63
1:F:195:PHE:CE2	1:F:240:LEU:O	2.50	0.63
1:C:136:THR:HB	1:C:209:THR:CB	2.28	0.63
1:C:172:ASP:O	1:C:173:ASP:OD1	2.17	0.63
1:F:94:THR:O	1:F:110:LEU:HB2	1.99	0.63
1:D:2:PHE:HZ	1:D:64:GLY:HA3	1.64	0.62
1:E:149:SER:CB	1:E:167:ALA:CB	2.49	0.62
1:F:158:GLY:O	1:F:159:ALA:HB3	1.98	0.62
1:D:154:LEU:O	1:D:155:ARG:C	2.38	0.62
1:D:172:ASP:O	1:D:173:ASP:OD1	2.17	0.62
1:E:108:LEU:CD2	1:E:110:LEU:HD23	2.28	0.62
1:B:94:THR:O	1:B:110:LEU:HB2	1.99	0.62
1:C:196:SER:H	1:C:240:LEU:HD21	1.62	0.62
1:E:154:LEU:O	1:E:155:ARG:C	2.38	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:97:LEU:HD12	1:B:110:LEU:HD21	1.81	0.62
1:D:73:LEU:HA	1:D:76:VAL:CG1	2.29	0.62
1:F:108:LEU:CD2	1:F:110:LEU:HD23	2.28	0.62
1:F:153:ARG:HG2	1:F:194:LEU:HD21	1.82	0.62
1:B:2:PHE:HZ	1:B:64:GLY:HA3	1.64	0.62
1:F:195:PHE:HZ	1:F:221:PHE:O	1.83	0.62
1:A:196:SER:H	1:A:240:LEU:HD21	1.62	0.62
1:E:195:PHE:HZ	1:E:221:PHE:O	1.83	0.62
1:F:154:LEU:O	1:F:155:ARG:C	2.38	0.62
1:F:196:SER:H	1:F:240:LEU:HD21	1.62	0.62
1:E:73:LEU:HA	1:E:76:VAL:CG1	2.29	0.62
1:E:94:THR:O	1:E:110:LEU:HB2	1.99	0.62
1:F:172:ASP:O	1:F:173:ASP:OD1	2.17	0.62
1:A:154:LEU:O	1:A:155:ARG:C	2.38	0.62
1:C:108:LEU:CD2	1:C:110:LEU:HD23	2.28	0.62
1:A:2:PHE:HZ	1:A:64:GLY:HA3	1.64	0.62
1:A:172:ASP:O	1:A:173:ASP:OD1	2.17	0.62
1:C:73:LEU:HA	1:C:76:VAL:CG1	2.29	0.62
1:C:94:THR:O	1:C:110:LEU:HB2	1.99	0.62
1:D:153:ARG:HG2	1:D:194:LEU:HD21	1.81	0.62
1:A:222:PRO:CD	1:A:242:PRO:CG	2.64	0.62
1:C:153:ARG:HG2	1:C:194:LEU:HD21	1.82	0.62
1:B:73:LEU:HA	1:B:76:VAL:CG1	2.29	0.61
1:B:108:LEU:CD2	1:B:110:LEU:HD23	2.28	0.61
1:E:153:ARG:HG2	1:E:194:LEU:HD21	1.82	0.61
1:A:73:LEU:HA	1:A:76:VAL:CG1	2.29	0.61
1:A:153:ARG:HG2	1:A:194:LEU:HD21	1.82	0.61
1:B:213:VAL:CG2	1:B:227:TYR:OH	2.48	0.61
1:E:172:ASP:O	1:E:173:ASP:OD1	2.17	0.61
1:F:73:LEU:HA	1:F:76:VAL:CG1	2.29	0.61
1:A:195:PHE:HZ	1:A:221:PHE:O	1.83	0.61
1:B:172:ASP:O	1:B:173:ASP:OD1	2.17	0.61
1:D:213:VAL:CG2	1:D:227:TYR:OH	2.48	0.61
1:F:156:VAL:HG21	1:F:217:LEU:CG	2.27	0.61
1:F:200:LEU:HA	1:F:203:MET:HE2	1.80	0.61
1:A:213:VAL:CG2	1:A:227:TYR:OH	2.48	0.61
1:B:176:LEU:HD13	1:C:104:LEU:HB2	1.81	0.61
1:C:154:LEU:O	1:C:155:ARG:C	2.38	0.61
1:C:231:GLU:HB2	1:C:233:MET:HE2	1.82	0.61
1:D:195:PHE:HZ	1:D:221:PHE:O	1.83	0.61
1:F:179:PRO:O	1:F:183:LEU:HD22	2.01	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:195:PHE:HZ	1:B:221:PHE:O	1.83	0.61
1:E:179:PRO:O	1:E:183:LEU:HD22	2.01	0.61
1:C:195:PHE:HZ	1:C:221:PHE:O	1.83	0.61
1:D:94:THR:O	1:D:110:LEU:HB2	1.99	0.61
1:E:97:LEU:HD12	1:E:110:LEU:HD21	1.82	0.61
1:A:94:THR:O	1:A:110:LEU:HB2	1.99	0.61
1:B:185:SER:HA	1:E:87:HIS:CE1	2.35	0.61
1:C:97:LEU:HD12	1:C:110:LEU:HD21	1.82	0.61
1:E:156:VAL:HG23	1:E:217:LEU:HG	1.83	0.61
1:B:153:ARG:HG2	1:B:194:LEU:HD21	1.82	0.61
1:B:154:LEU:O	1:B:155:ARG:C	2.38	0.61
1:B:185:SER:HA	1:E:87:HIS:HE1	1.66	0.61
1:D:8:ALA:HB2	1:D:84:ASP:O	2.01	0.61
1:E:27:ILE:O	1:E:65:VAL:HG23	2.01	0.61
1:F:133:LEU:HG	1:F:183:LEU:HD12	1.83	0.61
1:A:179:PRO:O	1:A:183:LEU:HD22	2.01	0.60
1:B:8:ALA:HB2	1:B:84:ASP:O	2.01	0.60
1:A:97:LEU:HD12	1:A:110:LEU:HD21	1.81	0.60
1:B:179:PRO:O	1:B:183:LEU:HD22	2.01	0.60
1:C:191:ALA:CB	1:C:218:GLY:C	2.66	0.60
1:F:198:ASP:O	1:F:201:LYS:HB2	2.01	0.60
1:B:27:ILE:O	1:B:65:VAL:HG23	2.01	0.60
1:B:156:VAL:HG21	1:B:217:LEU:CG	2.27	0.60
1:C:156:VAL:HG23	1:C:217:LEU:HG	1.83	0.60
1:E:133:LEU:HG	1:E:183:LEU:HD12	1.83	0.60
1:E:198:ASP:O	1:E:201:LYS:HB2	2.01	0.60
1:A:133:LEU:HG	1:A:183:LEU:HD12	1.83	0.60
1:B:133:LEU:HG	1:B:183:LEU:HD12	1.83	0.60
1:B:156:VAL:H	1:B:192:ASP:CB	2.15	0.60
1:D:72:ARG:NH1	1:F:171:THR:HG21	2.08	0.60
1:D:133:LEU:HG	1:D:183:LEU:HD12	1.83	0.60
1:D:156:VAL:H	1:D:192:ASP:CB	2.15	0.60
1:F:213:VAL:CG2	1:F:227:TYR:OH	2.48	0.60
1:F:231:GLU:HB2	1:F:233:MET:HE3	1.83	0.60
1:A:8:ALA:HB2	1:A:84:ASP:O	2.01	0.60
1:A:27:ILE:O	1:A:65:VAL:HG23	2.01	0.60
1:A:156:VAL:H	1:A:192:ASP:CB	2.15	0.60
1:D:27:ILE:O	1:D:65:VAL:HG23	2.01	0.60
1:F:27:ILE:O	1:F:65:VAL:HG23	2.01	0.60
1:B:198:ASP:O	1:B:201:LYS:HB2	2.01	0.60
1:C:47:VAL:CA	1:C:237:THR:O	2.30	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:97:LEU:HD12	1:D:110:LEU:HD21	1.81	0.60
1:E:156:VAL:H	1:E:192:ASP:CB	2.15	0.60
1:C:198:ASP:O	1:C:201:LYS:HB2	2.01	0.60
1:B:161:GLU:O	1:B:162:THR:OG1	2.20	0.60
1:C:179:PRO:O	1:C:183:LEU:HD22	2.01	0.60
1:F:97:LEU:HD12	1:F:110:LEU:HD21	1.81	0.60
1:C:213:VAL:CG2	1:C:227:TYR:OH	2.48	0.60
1:D:179:PRO:O	1:D:183:LEU:HD22	2.01	0.60
1:C:27:ILE:O	1:C:65:VAL:HG23	2.01	0.59
1:F:8:ALA:HB2	1:F:84:ASP:O	2.01	0.59
1:B:179:PRO:HG2	1:D:179:PRO:HG2	1.83	0.59
1:D:198:ASP:O	1:D:201:LYS:HB2	2.01	0.59
1:F:156:VAL:HG23	1:F:217:LEU:HG	1.83	0.59
1:C:8:ALA:HB2	1:C:84:ASP:O	2.01	0.59
1:F:156:VAL:H	1:F:192:ASP:CB	2.15	0.59
1:E:213:VAL:CG2	1:E:227:TYR:OH	2.48	0.59
1:B:175:ASP:O	1:C:104:LEU:HD22	2.03	0.59
1:A:198:ASP:O	1:A:201:LYS:HB2	2.01	0.59
1:B:195:PHE:CB	1:B:240:LEU:HD22	2.33	0.59
1:E:8:ALA:HB2	1:E:84:ASP:O	2.01	0.59
1:F:194:LEU:CD2	1:F:245:GLN:HG3	2.30	0.59
1:A:195:PHE:CB	1:A:240:LEU:HD22	2.33	0.59
1:C:195:PHE:CB	1:C:240:LEU:HD22	2.33	0.59
1:A:156:VAL:HG23	1:A:217:LEU:HG	1.83	0.59
1:A:157:ASP:HB2	1:A:160:GLU:O	2.03	0.59
1:D:87:HIS:O	1:D:99:ILE:HG13	2.03	0.59
1:D:157:ASP:HB2	1:D:160:GLU:O	2.03	0.59
1:D:222:PRO:CD	1:D:242:PRO:HD2	2.32	0.59
1:E:222:PRO:CD	1:E:242:PRO:CG	2.64	0.59
1:E:231:GLU:HB2	1:E:233:MET:HE3	1.85	0.59
1:F:35:SER:O	1:F:36:ILE:HD13	2.03	0.59
1:E:35:SER:O	1:E:36:ILE:HD13	2.03	0.59
1:A:87:HIS:O	1:A:99:ILE:HG13	2.03	0.59
1:B:200:LEU:HA	1:B:203:MET:HE2	1.83	0.59
1:E:157:ASP:HB2	1:E:160:GLU:O	2.03	0.59
1:B:157:ASP:HB2	1:B:160:GLU:O	2.03	0.58
1:C:156:VAL:H	1:C:192:ASP:CB	2.15	0.58
1:F:157:ASP:HB2	1:F:160:GLU:O	2.03	0.58
1:B:101:ILE:CD1	1:B:104:LEU:HD12	2.34	0.58
1:C:216:GLU:OE1	1:C:224:LYS:HD2	2.03	0.58
1:F:216:GLU:OE1	1:F:224:LYS:HD2	2.03	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:101:ILE:CD1	1:A:104:LEU:HD12	2.34	0.58
1:A:216:GLU:OE1	1:A:224:LYS:HD2	2.03	0.58
1:C:6:VAL:CG2	1:C:56:PHE:HD2	2.14	0.58
1:C:73:LEU:HA	1:C:76:VAL:HG12	1.86	0.58
1:C:101:ILE:CD1	1:C:104:LEU:HD12	2.34	0.58
1:C:157:ASP:HB2	1:C:160:GLU:O	2.03	0.58
1:C:222:PRO:CD	1:C:242:PRO:HD2	2.32	0.58
1:D:156:VAL:HG23	1:D:217:LEU:HG	1.83	0.58
1:E:216:GLU:OE1	1:E:224:LYS:HD2	2.03	0.58
1:F:133:LEU:CG	1:F:183:LEU:CD1	2.80	0.58
1:A:191:ALA:CB	1:A:218:GLY:C	2.66	0.58
1:A:73:LEU:HA	1:A:76:VAL:HG12	1.86	0.58
1:A:176:LEU:HD13	1:B:104:LEU:HB2	1.85	0.58
1:D:216:GLU:OE1	1:D:224:LYS:HD2	2.03	0.58
1:E:161:GLU:O	1:E:162:THR:OG1	2.20	0.58
1:B:35:SER:O	1:B:36:ILE:HD13	2.03	0.58
1:B:131:ILE:HD11	1:B:217:LEU:HB2	1.86	0.58
1:E:97:LEU:HB3	1:E:108:LEU:HB3	1.86	0.58
1:C:87:HIS:O	1:C:99:ILE:HG13	2.03	0.58
1:B:87:HIS:O	1:B:99:ILE:HG13	2.03	0.58
1:C:6:VAL:N	1:C:86:ILE:O	2.37	0.58
1:D:35:SER:O	1:D:36:ILE:HD13	2.03	0.58
1:E:195:PHE:CB	1:E:240:LEU:HD22	2.33	0.58
1:A:131:ILE:HD11	1:A:217:LEU:HB2	1.86	0.58
1:E:11:LEU:HD11	1:E:77:ALA:HB1	1.86	0.58
1:E:87:HIS:O	1:E:99:ILE:HG13	2.03	0.58
1:E:191:ALA:CB	1:E:218:GLY:C	2.66	0.58
1:F:87:HIS:O	1:F:99:ILE:HG13	2.03	0.58
1:B:214:THR:O	1:B:225:LEU:HA	2.04	0.57
1:B:216:GLU:OE1	1:B:224:LYS:HD2	2.03	0.57
1:D:73:LEU:HA	1:D:76:VAL:HG12	1.86	0.57
1:D:97:LEU:HB3	1:D:108:LEU:HB3	1.86	0.57
1:E:6:VAL:CG2	1:E:56:PHE:HD2	2.14	0.57
1:E:101:ILE:CD1	1:E:104:LEU:HD12	2.34	0.57
1:E:133:LEU:CG	1:E:183:LEU:CD1	2.80	0.57
1:E:194:LEU:CD2	1:E:245:GLN:HG3	2.30	0.57
1:F:222:PRO:CD	1:F:242:PRO:HD2	2.32	0.57
1:A:35:SER:O	1:A:36:ILE:HD13	2.03	0.57
1:A:186:ILE:HG22	1:A:187:GLU:N	2.19	0.57
1:B:186:ILE:HG22	1:B:187:GLU:N	2.19	0.57
1:B:191:ALA:CB	1:B:218:GLY:C	2.66	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:131:ILE:HD11	1:E:217:LEU:HB2	1.86	0.57
1:F:73:LEU:HA	1:F:76:VAL:HG12	1.86	0.57
1:F:97:LEU:HB3	1:F:108:LEU:HB3	1.86	0.57
1:E:214:THR:O	1:E:225:LEU:HA	2.04	0.57
1:A:214:THR:O	1:A:225:LEU:HA	2.04	0.57
1:C:35:SER:O	1:C:36:ILE:HD13	2.03	0.57
1:D:186:ILE:HG22	1:D:187:GLU:N	2.19	0.57
1:F:214:THR:O	1:F:225:LEU:HA	2.04	0.57
1:B:73:LEU:HA	1:B:76:VAL:HG12	1.86	0.57
1:C:133:LEU:HG	1:C:183:LEU:HD12	1.83	0.57
1:C:214:THR:O	1:C:225:LEU:HA	2.04	0.57
1:D:157:ASP:O	1:D:157:ASP:OD1	2.23	0.57
1:D:195:PHE:CB	1:D:240:LEU:HD22	2.33	0.57
1:E:73:LEU:HA	1:E:76:VAL:HG12	1.86	0.57
1:A:104:LEU:HB2	1:C:176:LEU:HD13	1.87	0.57
1:D:195:PHE:CE1	1:D:223:VAL:HB	2.40	0.57
1:F:6:VAL:N	1:F:86:ILE:O	2.37	0.57
1:F:101:ILE:CD1	1:F:104:LEU:HD12	2.34	0.57
1:B:157:ASP:O	1:B:157:ASP:OD1	2.23	0.57
1:B:195:PHE:CE1	1:B:223:VAL:HB	2.40	0.57
1:C:97:LEU:HB3	1:C:108:LEU:HB3	1.86	0.57
1:C:194:LEU:CD2	1:C:245:GLN:HG3	2.30	0.57
1:E:152:ILE:HG13	1:E:197:LEU:HB2	1.87	0.57
1:F:152:ILE:HG13	1:F:197:LEU:HB2	1.87	0.57
1:A:157:ASP:O	1:A:157:ASP:OD1	2.23	0.57
1:C:145:ALA:O	1:C:197:LEU:CD1	2.53	0.57
1:D:101:ILE:CD1	1:D:104:LEU:HD12	2.34	0.57
1:F:195:PHE:CB	1:F:240:LEU:HD22	2.33	0.57
1:A:11:LEU:HD11	1:A:77:ALA:HB1	1.86	0.57
1:A:194:LEU:CD2	1:A:245:GLN:HG3	2.30	0.57
1:C:11:LEU:HD11	1:C:77:ALA:HB1	1.86	0.57
1:F:186:ILE:HG22	1:F:187:GLU:N	2.19	0.57
1:A:6:VAL:CG2	1:A:56:PHE:HD2	2.14	0.57
1:C:131:ILE:HD11	1:C:217:LEU:HB2	1.86	0.57
1:C:157:ASP:O	1:C:157:ASP:OD1	2.23	0.57
1:B:194:LEU:CD2	1:B:245:GLN:HG3	2.30	0.56
1:A:156:VAL:H	1:A:192:ASP:HB3	1.71	0.56
1:A:222:PRO:CD	1:A:242:PRO:HD2	2.32	0.56
1:C:195:PHE:CE1	1:C:223:VAL:HB	2.40	0.56
1:D:68:VAL:O	1:D:70:LEU:N	2.38	0.56
1:E:186:ILE:HG22	1:E:187:GLU:N	2.19	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:68:VAL:O	1:F:70:LEU:N	2.38	0.56
1:A:70:LEU:O	1:A:74:GLU:HB2	2.06	0.56
1:A:97:LEU:HB3	1:A:108:LEU:HB3	1.86	0.56
1:A:152:ILE:HG13	1:A:197:LEU:HB2	1.87	0.56
1:A:156:VAL:HG21	1:A:217:LEU:CG	2.27	0.56
1:B:70:LEU:O	1:B:74:GLU:HB2	2.06	0.56
1:B:97:LEU:HB3	1:B:108:LEU:HB3	1.86	0.56
1:B:231:GLU:HB2	1:B:233:MET:HE2	1.87	0.56
1:D:92:GLU:O	1:D:93:GLU:HG2	2.05	0.56
1:D:131:ILE:HD11	1:D:217:LEU:HB2	1.86	0.56
1:D:145:ALA:O	1:D:197:LEU:CD1	2.53	0.56
1:D:149:SER:HB3	1:D:167:ALA:CB	2.22	0.56
1:D:156:VAL:H	1:D:192:ASP:HB3	1.71	0.56
1:E:145:ALA:O	1:E:197:LEU:CD1	2.53	0.56
1:F:145:ALA:O	1:F:197:LEU:CD1	2.53	0.56
1:F:195:PHE:CE1	1:F:223:VAL:HB	2.40	0.56
1:B:222:PRO:CB	1:B:239:MET:HG2	2.34	0.56
1:C:133:LEU:CG	1:C:183:LEU:CD1	2.80	0.56
1:C:152:ILE:HG13	1:C:197:LEU:HB2	1.87	0.56
1:C:186:ILE:HG22	1:C:187:GLU:N	2.19	0.56
1:D:214:THR:O	1:D:225:LEU:HA	2.04	0.56
1:E:92:GLU:O	1:E:93:GLU:HG2	2.06	0.56
1:B:11:LEU:HD11	1:B:77:ALA:HB1	1.86	0.56
1:C:222:PRO:CB	1:C:239:MET:HG2	2.34	0.56
1:D:6:VAL:CG2	1:D:56:PHE:HD2	2.14	0.56
1:D:6:VAL:N	1:D:86:ILE:O	2.37	0.56
1:E:157:ASP:O	1:E:157:ASP:OD1	2.23	0.56
1:F:131:ILE:HD11	1:F:217:LEU:HB2	1.86	0.56
1:F:157:ASP:O	1:F:157:ASP:OD1	2.23	0.56
1:A:195:PHE:CE1	1:A:223:VAL:HB	2.40	0.56
1:B:145:ALA:O	1:B:197:LEU:CD1	2.53	0.56
1:B:156:VAL:H	1:B:192:ASP:HB3	1.71	0.56
1:C:201:LYS:O	1:C:205:LYS:HB2	2.06	0.56
1:E:6:VAL:N	1:E:86:ILE:O	2.37	0.56
1:A:145:ALA:O	1:A:197:LEU:CD1	2.53	0.56
1:A:201:LYS:O	1:A:205:LYS:HB2	2.06	0.56
1:B:6:VAL:N	1:B:86:ILE:O	2.37	0.56
1:B:117:ARG:HG3	1:B:118:GLN:N	2.21	0.56
1:B:195:PHE:HE2	1:B:240:LEU:O	1.89	0.56
1:D:200:LEU:HG	1:D:240:LEU:HD13	1.88	0.56
1:E:222:PRO:CD	1:E:242:PRO:HD2	2.33	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:200:LEU:HG	1:B:240:LEU:HD13	1.88	0.56
1:C:161:GLU:O	1:C:162:THR:OG1	2.20	0.56
1:D:127:LEU:HD22	1:D:218:GLY:HA3	1.88	0.56
1:D:161:GLU:O	1:D:162:THR:OG1	2.20	0.56
1:D:201:LYS:O	1:D:205:LYS:HB2	2.06	0.56
1:F:11:LEU:HD11	1:F:77:ALA:HB1	1.86	0.56
1:F:222:PRO:CD	1:F:242:PRO:CG	2.64	0.56
1:B:136:THR:HA	1:B:208:PRO:O	2.06	0.56
1:B:222:PRO:CD	1:B:242:PRO:HD2	2.33	0.56
1:C:70:LEU:O	1:C:74:GLU:HB2	2.06	0.56
1:C:156:VAL:H	1:C:192:ASP:HB3	1.70	0.56
1:E:136:THR:HA	1:E:208:PRO:O	2.06	0.56
1:F:225:LEU:O	1:F:237:THR:HA	2.06	0.56
1:A:200:LEU:HG	1:A:240:LEU:HD13	1.88	0.56
1:B:92:GLU:O	1:B:93:GLU:HG2	2.05	0.56
1:B:231:GLU:HB2	1:B:233:MET:HE3	1.88	0.56
1:C:200:LEU:HG	1:C:240:LEU:HD13	1.88	0.56
1:D:11:LEU:HD11	1:D:77:ALA:HB1	1.86	0.56
1:E:225:LEU:O	1:E:237:THR:HA	2.06	0.56
1:F:201:LYS:O	1:F:205:LYS:HB2	2.06	0.56
1:B:201:LYS:O	1:B:205:LYS:HB2	2.06	0.55
1:C:97:LEU:N	1:C:108:LEU:O	2.40	0.55
1:D:104:LEU:HB2	1:F:176:LEU:HD13	1.88	0.55
1:D:152:ILE:HG13	1:D:197:LEU:HB2	1.87	0.55
1:E:195:PHE:HE2	1:E:240:LEU:O	1.89	0.55
1:E:195:PHE:CE1	1:E:223:VAL:HB	2.40	0.55
1:F:49:LEU:HD21	1:F:236:ILE:HG22	1.88	0.55
1:F:92:GLU:O	1:F:93:GLU:HG2	2.05	0.55
1:F:149:SER:HB3	1:F:167:ALA:CB	2.22	0.55
1:A:92:GLU:O	1:A:93:GLU:HG2	2.05	0.55
1:B:49:LEU:HD21	1:B:236:ILE:HG22	1.88	0.55
1:B:97:LEU:N	1:B:108:LEU:O	2.40	0.55
1:B:152:ILE:HG13	1:B:197:LEU:HB2	1.87	0.55
1:C:136:THR:HA	1:C:208:PRO:O	2.06	0.55
1:E:70:LEU:O	1:E:74:GLU:HB2	2.06	0.55
1:E:222:PRO:CB	1:E:239:MET:HG2	2.34	0.55
1:F:5:ILE:HA	1:F:86:ILE:O	2.07	0.55
1:A:68:VAL:O	1:A:70:LEU:N	2.37	0.55
1:A:97:LEU:N	1:A:108:LEU:O	2.40	0.55
1:D:156:VAL:HG21	1:D:217:LEU:CG	2.27	0.55
1:E:156:VAL:H	1:E:192:ASP:HB3	1.71	0.55

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:201:LYS:O	1:E:205:LYS:HB2	2.06	0.55
1:F:70:LEU:O	1:F:74:GLU:HB2	2.06	0.55
1:F:146:ASP:HA	1:F:197:LEU:HD12	1.87	0.55
1:F:161:GLU:O	1:F:162:THR:OG1	2.20	0.55
1:A:117:ARG:HG3	1:A:118:GLN:N	2.21	0.55
1:A:161:GLU:O	1:A:162:THR:OG1	2.20	0.55
1:A:222:PRO:CB	1:A:239:MET:HG2	2.34	0.55
1:D:136:THR:HA	1:D:208:PRO:O	2.06	0.55
1:E:97:LEU:N	1:E:108:LEU:O	2.40	0.55
1:A:225:LEU:O	1:A:237:THR:HA	2.06	0.55
1:D:176:LEU:HD13	1:E:104:LEU:HB2	1.88	0.55
1:F:8:ALA:CB	1:F:84:ASP:O	2.55	0.55
1:F:97:LEU:N	1:F:108:LEU:O	2.40	0.55
1:F:156:VAL:H	1:F:192:ASP:HB3	1.71	0.55
1:D:1:MET:HG3	1:D:91:ASP:HB2	1.89	0.55
1:F:117:ARG:HG3	1:F:118:GLN:N	2.21	0.55
1:A:127:LEU:HD22	1:A:218:GLY:HA3	1.88	0.55
1:B:127:LEU:HD22	1:B:218:GLY:HA3	1.88	0.55
1:D:70:LEU:O	1:D:74:GLU:HB2	2.06	0.55
1:E:127:LEU:HD22	1:E:218:GLY:HA3	1.88	0.55
1:F:136:THR:HB	1:F:209:THR:CG2	2.37	0.55
1:A:6:VAL:N	1:A:86:ILE:O	2.37	0.55
1:A:49:LEU:HD21	1:A:236:ILE:HG22	1.88	0.55
1:A:136:THR:HA	1:A:208:PRO:O	2.06	0.55
1:B:1:MET:HG3	1:B:91:ASP:HB2	1.89	0.55
1:B:68:VAL:O	1:B:70:LEU:N	2.38	0.55
1:B:138:LEU:HD12	1:B:204:ASN:ND2	2.22	0.55
1:B:156:VAL:HG23	1:B:217:LEU:HG	1.83	0.55
1:D:97:LEU:N	1:D:108:LEU:O	2.40	0.55
1:D:117:ARG:HG3	1:D:118:GLN:N	2.21	0.55
1:E:8:ALA:CB	1:E:84:ASP:O	2.55	0.55
1:E:138:LEU:HD12	1:E:204:ASN:ND2	2.22	0.55
1:A:216:GLU:HB2	1:A:224:LYS:HB2	1.89	0.55
1:C:5:ILE:HA	1:C:86:ILE:O	2.07	0.55
1:C:127:LEU:HD22	1:C:218:GLY:HA3	1.88	0.55
1:C:225:LEU:O	1:C:237:THR:HA	2.06	0.55
1:D:138:LEU:HD12	1:D:204:ASN:ND2	2.22	0.55
1:D:216:GLU:HB2	1:D:224:LYS:HB2	1.89	0.55
1:F:136:THR:HA	1:F:208:PRO:O	2.06	0.55
1:A:5:ILE:HA	1:A:86:ILE:O	2.07	0.55
1:B:20:VAL:CG1	1:B:202:ASP:HB3	2.36	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:5:ILE:HA	1:D:86:ILE:O	2.07	0.55
1:D:8:ALA:CB	1:D:84:ASP:O	2.55	0.55
1:D:49:LEU:HD21	1:D:236:ILE:HG22	1.88	0.55
1:E:20:VAL:CG1	1:E:202:ASP:HB3	2.36	0.55
1:E:49:LEU:HD21	1:E:236:ILE:HG22	1.88	0.55
1:B:8:ALA:CB	1:B:84:ASP:O	2.55	0.54
1:C:8:ALA:CB	1:C:84:ASP:O	2.55	0.54
1:C:195:PHE:HE2	1:C:240:LEU:O	1.89	0.54
1:C:216:GLU:HB2	1:C:224:LYS:HB2	1.89	0.54
1:D:195:PHE:HE2	1:D:240:LEU:O	1.89	0.54
1:A:138:LEU:HD12	1:A:204:ASN:ND2	2.22	0.54
1:C:1:MET:HG3	1:C:91:ASP:HB2	1.89	0.54
1:C:92:GLU:O	1:C:93:GLU:HG2	2.05	0.54
1:D:225:LEU:O	1:D:237:THR:HA	2.06	0.54
1:E:5:ILE:HA	1:E:86:ILE:O	2.07	0.54
1:A:1:MET:HG3	1:A:91:ASP:HB2	1.89	0.54
1:B:20:VAL:HG13	1:B:202:ASP:CB	2.37	0.54
1:B:133:LEU:CG	1:B:183:LEU:HD11	2.32	0.54
1:C:94:THR:O	1:C:94:THR:HG22	2.08	0.54
1:C:136:THR:HB	1:C:209:THR:CG2	2.37	0.54
1:F:138:LEU:HD12	1:F:204:ASN:ND2	2.22	0.54
1:B:136:THR:HB	1:B:209:THR:CG2	2.37	0.54
1:B:149:SER:HB3	1:B:167:ALA:CB	2.22	0.54
1:C:117:ARG:HG3	1:C:118:GLN:N	2.21	0.54
1:A:196:SER:H	1:A:240:LEU:CD2	2.21	0.54
1:B:133:LEU:CG	1:B:183:LEU:CD1	2.80	0.54
1:B:225:LEU:O	1:B:237:THR:HA	2.06	0.54
1:C:146:ASP:HA	1:C:197:LEU:HD12	1.87	0.54
1:D:94:THR:O	1:D:94:THR:HG22	2.08	0.54
1:D:153:ARG:HG2	1:D:194:LEU:HD22	1.90	0.54
1:A:8:ALA:CB	1:A:84:ASP:O	2.55	0.54
1:B:5:ILE:HA	1:B:86:ILE:O	2.07	0.54
1:C:156:VAL:HG21	1:C:217:LEU:CG	2.27	0.54
1:F:216:GLU:HB2	1:F:224:LYS:HB2	1.89	0.54
1:E:20:VAL:HG13	1:E:202:ASP:CB	2.37	0.54
1:E:68:VAL:O	1:E:70:LEU:N	2.37	0.54
1:E:136:THR:HB	1:E:209:THR:CG2	2.37	0.54
1:A:183:LEU:O	1:A:185:SER:N	2.41	0.54
1:B:196:SER:H	1:B:240:LEU:CD2	2.21	0.54
1:D:136:THR:HB	1:D:209:THR:CG2	2.37	0.54
1:E:117:ARG:HG3	1:E:118:GLN:N	2.21	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:127:LEU:HD22	1:F:218:GLY:HA3	1.88	0.54
1:F:183:LEU:O	1:F:185:SER:N	2.41	0.54
1:F:195:PHE:HE2	1:F:240:LEU:O	1.89	0.54
1:B:183:LEU:O	1:B:185:SER:N	2.41	0.54
1:C:49:LEU:HD21	1:C:236:ILE:HG22	1.88	0.54
1:D:37:ARG:HB2	1:D:48:ASP:HA	1.90	0.54
1:E:1:MET:HG3	1:E:91:ASP:HB2	1.89	0.54
1:E:37:ARG:HB2	1:E:48:ASP:HA	1.90	0.54
1:E:200:LEU:HG	1:E:240:LEU:HD13	1.88	0.54
1:F:94:THR:O	1:F:94:THR:HG22	2.08	0.54
1:F:196:SER:H	1:F:240:LEU:CD2	2.21	0.54
1:F:200:LEU:HG	1:F:240:LEU:HD13	1.88	0.54
1:C:138:LEU:HD12	1:C:204:ASN:ND2	2.22	0.54
1:C:183:LEU:O	1:C:185:SER:N	2.41	0.54
1:B:216:GLU:HB2	1:B:224:LYS:HB2	1.89	0.53
1:E:216:GLU:HB2	1:E:224:LYS:HB2	1.89	0.53
1:C:153:ARG:HG2	1:C:194:LEU:HD22	1.90	0.53
1:D:146:ASP:HA	1:D:197:LEU:HD12	1.87	0.53
1:E:156:VAL:HG21	1:E:217:LEU:CG	2.27	0.53
1:E:176:LEU:HD13	1:F:104:LEU:HB2	1.89	0.53
1:A:37:ARG:HB2	1:A:48:ASP:HA	1.90	0.53
1:A:195:PHE:HE2	1:A:240:LEU:O	1.89	0.53
1:A:146:ASP:HA	1:A:197:LEU:HD12	1.87	0.53
1:B:6:VAL:CG2	1:B:56:PHE:HD2	2.14	0.53
1:B:37:ARG:HB2	1:B:48:ASP:HA	1.90	0.53
1:B:146:ASP:HA	1:B:197:LEU:HD12	1.87	0.53
1:E:11:LEU:HD21	1:E:77:ALA:HB1	1.91	0.53
1:E:231:GLU:HB2	1:E:233:MET:HE2	1.90	0.53
1:A:136:THR:HB	1:A:209:THR:CG2	2.37	0.53
1:E:94:THR:O	1:E:94:THR:HG22	2.08	0.53
1:E:153:ARG:HG2	1:E:194:LEU:HD22	1.90	0.53
1:E:183:LEU:O	1:E:185:SER:N	2.41	0.53
1:A:11:LEU:HD21	1:A:77:ALA:HB1	1.91	0.53
1:A:94:THR:O	1:A:94:THR:HG22	2.08	0.53
1:D:191:ALA:CB	1:D:218:GLY:C	2.66	0.53
1:D:215:VAL:CG1	1:D:223:VAL:HG21	2.39	0.53
1:E:146:ASP:HA	1:E:197:LEU:HD12	1.87	0.53
1:F:6:VAL:CG2	1:F:56:PHE:HD2	2.14	0.53
1:A:133:LEU:CG	1:A:183:LEU:CD1	2.80	0.53
1:C:3:LYS:O	1:C:59:TYR:CA	2.57	0.53
1:D:20:VAL:CG1	1:D:202:ASP:HB3	2.36	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:44:VAL:HG12	1:D:241:ALA:HB2	1.91	0.53
1:D:183:LEU:O	1:D:185:SER:N	2.41	0.53
1:E:171:THR:HG21	1:F:72:ARG:NH1	2.13	0.53
1:F:44:VAL:HG12	1:F:241:ALA:HB2	1.91	0.53
1:F:222:PRO:CB	1:F:239:MET:HG2	2.34	0.53
1:B:94:THR:O	1:B:94:THR:HG22	2.08	0.53
1:B:153:ARG:HG2	1:B:194:LEU:HD22	1.90	0.53
1:C:20:VAL:HG13	1:C:202:ASP:CB	2.37	0.53
1:D:196:SER:H	1:D:240:LEU:CD2	2.21	0.53
1:E:44:VAL:HG12	1:E:241:ALA:CB	2.39	0.53
1:E:149:SER:HB3	1:E:167:ALA:CB	2.22	0.53
1:A:197:LEU:HD23	1:A:197:LEU:C	2.29	0.53
1:B:11:LEU:HD21	1:B:77:ALA:HB1	1.91	0.53
1:D:133:LEU:CG	1:D:183:LEU:CD1	2.80	0.53
1:D:194:LEU:CD2	1:D:245:GLN:HG3	2.30	0.53
1:F:11:LEU:HD21	1:F:77:ALA:HB1	1.91	0.53
1:C:196:SER:H	1:C:240:LEU:CD2	2.21	0.53
1:E:133:LEU:CG	1:E:183:LEU:HD11	2.32	0.53
1:F:1:MET:HG3	1:F:91:ASP:HB2	1.89	0.53
1:F:104:LEU:HD13	1:F:104:LEU:C	2.30	0.53
1:B:3:LYS:O	1:B:59:TYR:CA	2.57	0.52
1:B:194:LEU:O	1:B:195:PHE:CG	2.63	0.52
1:C:11:LEU:HD21	1:C:77:ALA:HB1	1.91	0.52
1:C:37:ARG:HB2	1:C:48:ASP:HA	1.90	0.52
1:C:149:SER:OG	1:C:168:GLU:O	2.27	0.52
1:D:44:VAL:HG12	1:D:241:ALA:CB	2.39	0.52
1:F:20:VAL:HG13	1:F:202:ASP:CB	2.37	0.52
1:F:215:VAL:CG1	1:F:223:VAL:HG21	2.39	0.52
1:A:149:SER:OG	1:A:168:GLU:O	2.27	0.52
1:B:215:VAL:CG1	1:B:223:VAL:HG21	2.39	0.52
1:C:131:ILE:CD1	1:C:217:LEU:HB2	2.40	0.52
1:E:131:ILE:CD1	1:E:217:LEU:HB2	2.40	0.52
1:E:196:SER:H	1:E:240:LEU:CD2	2.21	0.52
1:A:194:LEU:O	1:A:195:PHE:CG	2.63	0.52
1:B:149:SER:OG	1:B:168:GLU:O	2.27	0.52
1:C:136:THR:OG1	1:C:209:THR:HG22	2.10	0.52
1:D:136:THR:OG1	1:D:209:THR:HG22	2.10	0.52
1:E:3:LYS:O	1:E:59:TYR:CA	2.57	0.52
1:F:3:LYS:O	1:F:59:TYR:CA	2.57	0.52
1:F:44:VAL:HG12	1:F:241:ALA:CB	2.39	0.52
1:F:131:ILE:CD1	1:F:217:LEU:HB2	2.40	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:139:ASP:OD1	1:F:208:PRO:O	2.28	0.52
1:C:44:VAL:HG12	1:C:241:ALA:CB	2.39	0.52
1:F:37:ARG:HB2	1:F:48:ASP:HA	1.90	0.52
1:F:136:THR:OG1	1:F:209:THR:HG22	2.10	0.52
1:A:139:ASP:OD1	1:A:208:PRO:O	2.28	0.52
1:B:136:THR:OG1	1:B:209:THR:HG22	2.10	0.52
1:C:194:LEU:O	1:C:195:PHE:CG	2.62	0.52
1:C:197:LEU:HD23	1:C:197:LEU:C	2.29	0.52
1:A:104:LEU:HD13	1:A:104:LEU:C	2.30	0.52
1:B:44:VAL:HG12	1:B:241:ALA:CB	2.39	0.52
1:C:139:ASP:OD1	1:C:208:PRO:O	2.28	0.52
1:D:11:LEU:HD21	1:D:77:ALA:HB1	1.91	0.52
1:D:139:ASP:OD1	1:D:208:PRO:O	2.28	0.52
1:E:194:LEU:O	1:E:195:PHE:CG	2.63	0.52
1:F:133:LEU:CG	1:F:183:LEU:HD11	2.32	0.52
1:A:44:VAL:HG12	1:A:241:ALA:CB	2.39	0.52
1:A:153:ARG:HG2	1:A:194:LEU:HD22	1.90	0.52
1:C:133:LEU:CD2	1:C:183:LEU:HD12	2.40	0.52
1:D:175:ASP:O	1:E:104:LEU:HD22	2.09	0.52
1:E:104:LEU:HD13	1:E:104:LEU:C	2.30	0.52
1:F:106:TYR:HE2	1:F:108:LEU:HB2	1.75	0.52
1:C:20:VAL:CG1	1:C:202:ASP:HB3	2.36	0.52
1:C:37:ARG:O	1:C:37:ARG:CG	2.49	0.52
1:D:104:LEU:HD13	1:D:104:LEU:C	2.30	0.52
1:E:44:VAL:HG12	1:E:241:ALA:HB2	1.91	0.52
1:F:197:LEU:HD23	1:F:197:LEU:C	2.29	0.52
1:D:3:LYS:O	1:D:59:TYR:CA	2.57	0.52
1:A:8:ALA:HB3	1:A:84:ASP:H	1.75	0.52
1:A:131:ILE:CD1	1:A:217:LEU:HB2	2.40	0.52
1:B:131:ILE:CD1	1:B:217:LEU:HB2	2.40	0.52
1:B:139:ASP:OD1	1:B:208:PRO:O	2.28	0.52
1:C:66:ILE:HG21	1:C:110:LEU:HD13	1.93	0.52
1:C:133:LEU:CG	1:C:183:LEU:HD11	2.32	0.52
1:D:95:ARG:O	1:D:110:LEU:N	2.43	0.52
1:D:194:LEU:O	1:D:195:PHE:CG	2.63	0.52
1:E:8:ALA:HB3	1:E:84:ASP:H	1.75	0.52
1:F:133:LEU:CD2	1:F:183:LEU:HD12	2.40	0.52
1:A:20:VAL:CG1	1:A:202:ASP:HB3	2.36	0.51
1:B:106:TYR:HE2	1:B:108:LEU:HB2	1.75	0.51
1:B:197:LEU:HD23	1:B:197:LEU:C	2.29	0.51
1:B:222:PRO:CD	1:B:242:PRO:CG	2.64	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:8:ALA:HB3	1:D:84:ASP:H	1.75	0.51
1:A:57:GLU:OE1	1:A:57:GLU:N	2.44	0.51
1:A:106:TYR:HE2	1:A:108:LEU:HB2	1.75	0.51
1:D:133:LEU:CD2	1:D:183:LEU:HD12	2.40	0.51
1:D:222:PRO:CB	1:D:239:MET:HG2	2.34	0.51
1:E:95:ARG:O	1:E:110:LEU:N	2.43	0.51
1:F:20:VAL:CG1	1:F:202:ASP:HB3	2.36	0.51
1:F:194:LEU:O	1:F:195:PHE:CG	2.62	0.51
1:A:20:VAL:HG13	1:A:202:ASP:CB	2.37	0.51
1:B:57:GLU:N	1:B:57:GLU:OE1	2.44	0.51
1:B:133:LEU:CD2	1:B:183:LEU:HD12	2.40	0.51
1:C:8:ALA:HB3	1:C:84:ASP:H	1.75	0.51
1:C:57:GLU:OE1	1:C:57:GLU:N	2.44	0.51
1:E:139:ASP:OD1	1:E:208:PRO:O	2.28	0.51
1:F:8:ALA:HB3	1:F:84:ASP:H	1.75	0.51
1:D:131:ILE:CD1	1:D:217:LEU:HB2	2.40	0.51
1:D:149:SER:OG	1:D:168:GLU:O	2.27	0.51
1:A:3:LYS:O	1:A:59:TYR:CA	2.57	0.51
1:C:104:LEU:HD13	1:C:104:LEU:C	2.30	0.51
1:C:215:VAL:CG1	1:C:223:VAL:HG21	2.39	0.51
1:E:133:LEU:CD2	1:E:183:LEU:HD12	2.40	0.51
1:E:215:VAL:CG1	1:E:223:VAL:HG21	2.39	0.51
1:F:161:GLU:HB3	1:F:188:ALA:CB	2.41	0.51
1:A:136:THR:OG1	1:A:209:THR:HG22	2.10	0.51
1:C:68:VAL:O	1:C:70:LEU:N	2.37	0.51
1:C:106:TYR:HE2	1:C:108:LEU:HB2	1.75	0.51
1:F:231:GLU:HB2	1:F:233:MET:HE2	1.91	0.51
1:A:29:LEU:HD12	1:A:29:LEU:N	2.26	0.51
1:A:44:VAL:HG12	1:A:241:ALA:HB2	1.91	0.51
1:B:44:VAL:HG12	1:B:241:ALA:HB2	1.91	0.51
1:C:95:ARG:O	1:C:110:LEU:N	2.43	0.51
1:D:161:GLU:HB3	1:D:188:ALA:CB	2.41	0.51
1:D:170:ASP:C	1:D:171:THR:HG22	2.31	0.51
1:E:136:THR:OG1	1:E:209:THR:HG22	2.10	0.51
1:A:58:SER:C	1:A:59:TYR:HD2	2.14	0.51
1:B:8:ALA:HB3	1:B:84:ASP:H	1.75	0.51
1:B:95:ARG:O	1:B:110:LEU:N	2.43	0.51
1:E:56:PHE:CD1	1:E:56:PHE:N	2.79	0.51
1:E:149:SER:OG	1:E:168:GLU:O	2.27	0.51
1:B:161:GLU:HB3	1:B:188:ALA:CB	2.41	0.51
1:C:206:ALA:C	1:C:207:ILE:HD12	2.32	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:58:SER:C	1:E:59:TYR:HD2	2.14	0.51
1:A:66:ILE:HG21	1:A:110:LEU:HD13	1.93	0.51
1:B:104:LEU:HD13	1:B:104:LEU:C	2.30	0.51
1:C:44:VAL:HG12	1:C:241:ALA:HB2	1.91	0.51
1:D:20:VAL:HG13	1:D:202:ASP:CB	2.37	0.51
1:D:29:LEU:N	1:D:29:LEU:HD12	2.26	0.51
1:D:197:LEU:HD23	1:D:197:LEU:C	2.29	0.51
1:E:57:GLU:N	1:E:57:GLU:OE1	2.44	0.51
1:E:206:ALA:C	1:E:207:ILE:HD12	2.32	0.51
1:D:57:GLU:OE1	1:D:57:GLU:N	2.44	0.50
1:F:58:SER:C	1:F:59:TYR:HD2	2.14	0.50
1:F:153:ARG:HG2	1:F:194:LEU:HD22	1.90	0.50
1:B:13:ASP:OD2	1:B:14:ALA:N	2.45	0.50
1:C:108:LEU:HD23	1:C:109:ALA:O	2.12	0.50
1:D:66:ILE:HG21	1:D:110:LEU:HD13	1.93	0.50
1:D:106:TYR:HE2	1:D:108:LEU:HB2	1.75	0.50
1:E:66:ILE:HG21	1:E:110:LEU:HD13	1.93	0.50
1:A:95:ARG:O	1:A:110:LEU:N	2.43	0.50
1:A:104:LEU:HD22	1:C:175:ASP:O	2.11	0.50
1:A:107:THR:HG22	1:C:173:ASP:HB2	1.91	0.50
1:D:56:PHE:CD1	1:D:56:PHE:N	2.79	0.50
1:E:161:GLU:HB3	1:E:188:ALA:CB	2.41	0.50
1:F:56:PHE:CD1	1:F:56:PHE:N	2.79	0.50
1:F:108:LEU:HD23	1:F:109:ALA:O	2.12	0.50
1:A:215:VAL:CG1	1:A:223:VAL:HG21	2.39	0.50
1:B:66:ILE:HG21	1:B:110:LEU:HD13	1.92	0.50
1:C:184:ILE:HD13	1:C:212:GLU:OE2	2.12	0.50
1:E:106:TYR:HE2	1:E:108:LEU:HB2	1.75	0.50
1:E:194:LEU:HD23	1:E:245:GLN:CG	2.34	0.50
1:F:95:ARG:O	1:F:110:LEU:N	2.43	0.50
1:B:29:LEU:N	1:B:29:LEU:HD12	2.26	0.50
1:B:184:ILE:HD13	1:B:212:GLU:OE2	2.12	0.50
1:C:8:ALA:CB	1:C:84:ASP:H	2.25	0.50
1:C:58:SER:C	1:C:59:TYR:HD2	2.14	0.50
1:D:13:ASP:OD2	1:D:14:ALA:N	2.45	0.50
1:E:13:ASP:OD2	1:E:14:ALA:N	2.45	0.50
1:F:29:LEU:HD12	1:F:29:LEU:N	2.26	0.50
1:A:13:ASP:OD2	1:A:14:ALA:N	2.45	0.50
1:A:133:LEU:CD2	1:A:183:LEU:HD12	2.40	0.50
1:A:173:ASP:HB2	1:B:107:THR:HG22	1.92	0.50
1:A:206:ALA:C	1:A:207:ILE:HD12	2.32	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:56:PHE:CD1	1:B:56:PHE:N	2.79	0.50
1:B:108:LEU:HD23	1:B:109:ALA:O	2.12	0.50
1:D:184:ILE:HD13	1:D:212:GLU:OE2	2.12	0.50
1:E:8:ALA:CB	1:E:84:ASP:H	2.25	0.50
1:E:153:ARG:CG	1:E:194:LEU:HD21	2.42	0.50
1:A:184:ILE:HD13	1:A:212:GLU:OE2	2.12	0.50
1:D:194:LEU:HD23	1:D:245:GLN:CG	2.34	0.50
1:F:153:ARG:CG	1:F:194:LEU:HD21	2.42	0.50
1:F:184:ILE:HD13	1:F:212:GLU:OE2	2.12	0.50
1:A:153:ARG:CG	1:A:194:LEU:HD21	2.42	0.50
1:C:13:ASP:OD2	1:C:14:ALA:N	2.45	0.50
1:C:29:LEU:HD12	1:C:29:LEU:N	2.26	0.50
1:D:10:THR:HA	1:D:13:ASP:OD1	2.12	0.50
1:D:108:LEU:HD23	1:D:109:ALA:O	2.12	0.50
1:F:8:ALA:CB	1:F:84:ASP:H	2.25	0.50
1:F:13:ASP:OD2	1:F:14:ALA:N	2.45	0.50
1:F:57:GLU:OE1	1:F:57:GLU:N	2.44	0.50
1:A:10:THR:O	1:A:13:ASP:OD2	2.30	0.50
1:B:10:THR:HA	1:B:13:ASP:OD1	2.12	0.50
1:C:153:ARG:CG	1:C:194:LEU:HD21	2.42	0.50
1:D:206:ALA:C	1:D:207:ILE:HD12	2.32	0.50
1:D:231:GLU:HB2	1:D:233:MET:HE2	1.94	0.50
1:F:191:ALA:CB	1:F:218:GLY:C	2.66	0.50
1:D:58:SER:C	1:D:59:TYR:HD2	2.14	0.49
1:D:153:ARG:CG	1:D:194:LEU:HD21	2.42	0.49
1:F:66:ILE:HG21	1:F:110:LEU:HD13	1.93	0.49
1:A:108:LEU:HD23	1:A:109:ALA:O	2.12	0.49
1:E:10:THR:HA	1:E:13:ASP:OD1	2.12	0.49
1:B:8:ALA:CB	1:B:84:ASP:H	2.25	0.49
1:B:58:SER:C	1:B:59:TYR:HD2	2.14	0.49
1:B:153:ARG:CG	1:B:194:LEU:HD21	2.42	0.49
1:C:56:PHE:CD1	1:C:56:PHE:N	2.79	0.49
1:C:194:LEU:HD23	1:C:245:GLN:CG	2.34	0.49
1:E:108:LEU:HD23	1:E:109:ALA:O	2.12	0.49
1:E:170:ASP:C	1:E:171:THR:HG22	2.31	0.49
1:A:8:ALA:CB	1:A:84:ASP:H	2.25	0.49
1:B:10:THR:O	1:B:13:ASP:OD2	2.30	0.49
1:C:170:ASP:C	1:C:171:THR:HG22	2.31	0.49
1:E:29:LEU:HD12	1:E:29:LEU:N	2.26	0.49
1:F:206:ALA:C	1:F:207:ILE:HD12	2.32	0.49
1:A:10:THR:HA	1:A:13: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:B:56:PHE:HE1	1:B:59:TYR:CZ	2.31	0.49
1:C:56:PHE:HE1	1:C:59:TYR:CZ	2.31	0.49
1:E:56:PHE:HE1	1:E:59:TYR:CZ	2.31	0.49
1:F:149:SER:OG	1:F:168:GLU:O	2.27	0.49
1:F:194:LEU:HD23	1:F:245:GLN:CG	2.34	0.49
1:A:194:LEU:HD23	1:A:245:GLN:CG	2.34	0.49
1:D:8:ALA:CB	1:D:84:ASP:H	2.25	0.49
1:C:68:VAL:HG11	1:C:73:LEU:HD12	1.95	0.49
1:C:162:THR:HG22	1:C:163:PHE:N	2.28	0.49
1:C:231:GLU:HB2	1:C:233:MET:HE3	1.92	0.49
1:D:56:PHE:HE1	1:D:59:TYR:CZ	2.31	0.49
1:D:142:ILE:HA	1:D:152:ILE:HD11	1.95	0.49
1:E:10:THR:O	1:E:13:ASP:OD2	2.30	0.49
1:E:68:VAL:HG11	1:E:73:LEU:HD12	1.95	0.49
1:E:184:ILE:HD13	1:E:212:GLU:OE2	2.12	0.49
1:A:231:GLU:HB2	1:A:233:MET:HE3	1.95	0.49
1:B:195:PHE:HD2	1:B:240:LEU:CD2	2.26	0.49
1:C:10:THR:O	1:C:13:ASP:OD2	2.30	0.49
1:C:195:PHE:HD2	1:C:240:LEU:CD2	2.26	0.49
1:D:68:VAL:HG11	1:D:73:LEU:HD12	1.95	0.49
1:B:206:ALA:C	1:B:207:ILE:HD12	2.32	0.49
1:C:10:THR:HA	1:C:13:ASP:OD1	2.12	0.49
1:D:10:THR:O	1:D:13:ASP:OD2	2.30	0.49
1:E:142:ILE:HA	1:E:152:ILE:HD11	1.95	0.49
1:F:10:THR:HA	1:F:13:ASP:OD1	2.12	0.49
1:F:68:VAL:HG11	1:F:73:LEU:HD12	1.95	0.49
1:F:157:ASP:CA	1:F:160:GLU:O	2.61	0.49
1:F:194:LEU:HB3	1:F:243:ARG:HB2	1.95	0.49
1:F:195:PHE:HD2	1:F:240:LEU:CD2	2.26	0.49
1:A:56:PHE:HE1	1:A:59:TYR:CZ	2.31	0.48
1:A:194:LEU:HB3	1:A:243:ARG:HB2	1.95	0.48
1:B:142:ILE:HA	1:B:152:ILE:HD11	1.95	0.48
1:F:10:THR:O	1:F:13:ASP:OD2	2.30	0.48
1:A:161:GLU:HB3	1:A:188:ALA:CB	2.41	0.48
1:B:194:LEU:HB3	1:B:243:ARG:HB2	1.95	0.48
1:D:157:ASP:CA	1:D:160:GLU:O	2.61	0.48
1:E:162:THR:HG22	1:E:163:PHE:N	2.28	0.48
1:A:68:VAL:HG11	1:A:73:LEU:HD12	1.95	0.48
1:C:5:ILE:HD13	1:D:184:ILE:O	2.13	0.48
1:C:107:THR:CG2	1:C:107:THR:O	2.61	0.48
1:C:194:LEU:HB3	1:C:243:ARG:HB2	1.95	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:157:ASP:CA	1:E:160:GLU:O	2.61	0.48
1:A:170:ASP:C	1:A:171:THR:HG22	2.31	0.48
1:B:170:ASP:C	1:B:171:THR:HG22	2.31	0.48
1:C:142:ILE:HA	1:C:152:ILE:HD11	1.95	0.48
1:C:161:GLU:HB3	1:C:188:ALA:CB	2.41	0.48
1:D:107:THR:CG2	1:D:107:THR:O	2.61	0.48
1:A:20:VAL:HG12	1:A:21:LEU:HD23	1.96	0.48
1:A:56:PHE:CD1	1:A:56:PHE:N	2.79	0.48
1:A:142:ILE:HA	1:A:152:ILE:HD11	1.95	0.48
1:A:195:PHE:HD2	1:A:240:LEU:CD2	2.26	0.48
1:B:162:THR:HG22	1:B:163:PHE:N	2.28	0.48
1:C:157:ASP:CA	1:C:160:GLU:O	2.61	0.48
1:D:56:PHE:CD1	1:D:59:TYR:CD2	3.02	0.48
1:D:195:PHE:HD2	1:D:240:LEU:CD2	2.26	0.48
1:F:107:THR:CG2	1:F:107:THR:O	2.61	0.48
1:F:142:ILE:HA	1:F:152:ILE:HD11	1.95	0.48
1:C:56:PHE:CD1	1:C:59:TYR:CD2	3.02	0.48
1:D:20:VAL:HG12	1:D:21:LEU:HD23	1.95	0.48
1:D:104:LEU:HD22	1:F:175:ASP:O	2.12	0.48
1:F:162:THR:HG22	1:F:163:PHE:N	2.28	0.48
1:F:170:ASP:C	1:F:171:THR:HG22	2.31	0.48
1:A:162:THR:HG22	1:A:163:PHE:N	2.28	0.48
1:B:175:ASP:O	1:C:104:LEU:CD2	2.62	0.48
1:E:56:PHE:CD1	1:E:59:TYR:CD2	3.02	0.48
1:E:156:VAL:CG1	1:E:191:ALA:O	2.62	0.48
1:F:56:PHE:HE1	1:F:59:TYR:CZ	2.31	0.48
1:A:152:ILE:HD13	1:A:165:ILE:HG21	1.96	0.48
1:B:47:VAL:HB	1:B:238:TYR:CE2	2.49	0.48
1:C:20:VAL:HG12	1:C:21:LEU:HD23	1.96	0.48
1:C:47:VAL:HB	1:C:238:TYR:CE2	2.49	0.48
1:D:195:PHE:CE2	1:D:242:PRO:CD	2.73	0.48
1:E:195:PHE:CE2	1:E:242:PRO:CD	2.73	0.48
1:F:56:PHE:CD1	1:F:59:TYR:CD2	3.02	0.48
1:F:152:ILE:HD13	1:F:165:ILE:HG21	1.96	0.48
1:B:3:LYS:O	1:B:59:TYR:HB3	2.14	0.48
1:C:149:SER:HB3	1:C:167:ALA:CB	2.22	0.48
1:C:156:VAL:CG1	1:C:191:ALA:O	2.62	0.48
1:D:152:ILE:HD13	1:D:165:ILE:HG21	1.96	0.48
1:E:97:LEU:HB2	1:E:110:LEU:HD21	1.96	0.48
1:F:47:VAL:HB	1:F:238:TYR:CE2	2.49	0.48
1:F:156:VAL:CG1	1:F:191:ALA:O	2.62	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:72:ARG:NH1	1:C:171:THR:HG21	2.13	0.47
1:B:44:VAL:CG1	1:B:241:ALA:HB2	2.44	0.47
1:B:56:PHE:CD1	1:B:59:TYR:CD2	3.02	0.47
1:D:194:LEU:HB3	1:D:243:ARG:HB2	1.95	0.47
1:F:3:LYS:O	1:F:59:TYR:HB3	2.14	0.47
1:C:44:VAL:CG1	1:C:241:ALA:HB2	2.44	0.47
1:C:151:HIS:CB	1:C:195:PHE:O	2.62	0.47
1:D:47:VAL:HB	1:D:238:TYR:CE2	2.49	0.47
1:D:97:LEU:HB2	1:D:110:LEU:HD21	1.96	0.47
1:D:186:ILE:CG2	1:D:187:GLU:N	2.77	0.47
1:A:133:LEU:CG	1:A:183:LEU:HD11	2.32	0.47
1:B:68:VAL:HG11	1:B:73:LEU:HD12	1.95	0.47
1:B:151:HIS:CB	1:B:195:PHE:O	2.62	0.47
1:B:152:ILE:HD13	1:B:165:ILE:HG21	1.96	0.47
1:D:151:HIS:CB	1:D:195:PHE:O	2.62	0.47
1:E:151:HIS:CB	1:E:195:PHE:O	2.62	0.47
1:E:195:PHE:HD2	1:E:240:LEU:CD2	2.26	0.47
1:A:5:ILE:O	1:A:56:PHE:HA	2.15	0.47
1:B:157:ASP:CA	1:B:160:GLU:O	2.61	0.47
1:D:44:VAL:CG1	1:D:241:ALA:HB2	2.44	0.47
1:E:20:VAL:HG12	1:E:21:LEU:HD23	1.95	0.47
1:E:65:VAL:HG22	1:E:113:PRO:CG	2.44	0.47
1:E:186:ILE:CG2	1:E:187:GLU:N	2.78	0.47
1:A:44:VAL:CG1	1:A:241:ALA:HB2	2.44	0.47
1:A:65:VAL:HG22	1:A:113:PRO:CG	2.45	0.47
1:C:97:LEU:HB2	1:C:110:LEU:HD21	1.96	0.47
1:D:162:THR:HG22	1:D:163:PHE:N	2.28	0.47
1:E:152:ILE:HD13	1:E:165:ILE:HG21	1.96	0.47
1:E:175:ASP:O	1:F:104:LEU:HD22	2.14	0.47
1:F:240:LEU:HD23	1:F:241:ALA:N	2.30	0.47
1:A:56:PHE:CD1	1:A:59:TYR:CD2	3.02	0.47
1:B:173:ASP:HB2	1:C:107:THR:HG23	1.90	0.47
1:B:194:LEU:HD23	1:B:245:GLN:CG	2.34	0.47
1:C:133:LEU:O	1:C:213:VAL:N	2.29	0.47
1:D:5:ILE:O	1:D:56:PHE:HA	2.15	0.47
1:E:5:ILE:O	1:E:56:PHE:HA	2.15	0.47
1:E:47:VAL:HB	1:E:238:TYR:CE2	2.49	0.47
1:E:194:LEU:HB3	1:E:243:ARG:HB2	1.95	0.47
1:F:151:HIS:CB	1:F:195:PHE:O	2.62	0.47
1:A:3:LYS:O	1:A:59:TYR:HB3	2.14	0.47
1:A:47:VAL:HB	1:A:238:TYR:CE2	2.49	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:97:LEU:HB2	1:A:110:LEU:HD21	1.96	0.47
1:A:151:HIS:CB	1:A:195:PHE:O	2.62	0.47
1:A:157:ASP:CA	1:A:160:GLU:O	2.61	0.47
1:B:20:VAL:HG12	1:B:21:LEU:HD23	1.96	0.47
1:B:97:LEU:HB2	1:B:110:LEU:HD21	1.96	0.47
1:B:146:ASP:C	1:B:147:MET:HG3	2.35	0.47
1:B:186:ILE:CG2	1:B:187:GLU:N	2.78	0.47
1:C:65:VAL:HG22	1:C:113:PRO:CG	2.45	0.47
1:C:146:ASP:C	1:C:147:MET:HG3	2.35	0.47
1:D:3:LYS:O	1:D:59:TYR:HB3	2.14	0.47
1:D:65:VAL:HG22	1:D:113:PRO:CG	2.44	0.47
1:F:4:ALA:HB1	1:F:56:PHE:CD2	2.50	0.47
1:F:44:VAL:CG1	1:F:241:ALA:HB2	2.44	0.47
1:F:65:VAL:HG22	1:F:113:PRO:CG	2.45	0.47
1:F:133:LEU:HA	1:F:133:LEU:HD23	1.74	0.47
1:A:240:LEU:HD23	1:A:241:ALA:N	2.30	0.47
1:B:4:ALA:HB1	1:B:56:PHE:CD2	2.50	0.47
1:D:240:LEU:HD23	1:D:241:ALA:N	2.30	0.47
1:E:4:ALA:HB1	1:E:56:PHE:CD2	2.50	0.47
1:F:20:VAL:HG12	1:F:21:LEU:HD23	1.96	0.47
1:B:65:VAL:HG22	1:B:113:PRO:CG	2.44	0.47
1:B:195:PHE:CE2	1:B:242:PRO:CD	2.73	0.47
1:B:240:LEU:HD23	1:B:241:ALA:N	2.30	0.47
1:C:3:LYS:O	1:C:59:TYR:HB3	2.14	0.47
1:E:3:LYS:O	1:E:59:TYR:HB3	2.14	0.47
1:E:44:VAL:CG1	1:E:241:ALA:HB2	2.44	0.47
1:A:4:ALA:HB1	1:A:56:PHE:CD2	2.50	0.47
1:C:4:ALA:HB1	1:C:56:PHE:CD2	2.50	0.47
1:C:5:ILE:O	1:C:56:PHE:HA	2.15	0.47
1:F:5:ILE:O	1:F:56:PHE:HA	2.15	0.47
1:F:8:ALA:HB3	1:F:82:ALA:CA	2.45	0.47
1:A:175:ASP:O	1:B:104:LEU:HD22	2.14	0.46
1:C:8:ALA:HB3	1:C:82:ALA:CA	2.45	0.46
1:C:152:ILE:HD13	1:C:165:ILE:HG21	1.96	0.46
1:D:156:VAL:HA	1:D:162:THR:O	2.16	0.46
1:F:158:GLY:O	1:F:159:ALA:CB	2.63	0.46
1:C:240:LEU:HD23	1:C:241:ALA:N	2.30	0.46
1:D:133:LEU:CG	1:D:183:LEU:HD11	2.32	0.46
1:D:146:ASP:C	1:D:147:MET:HG3	2.35	0.46
1:E:107:THR:CG2	1:E:107:THR:O	2.61	0.46
1:F:156:VAL:HA	1:F:162:THR:O	2.16	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:186:ILE:CG2	1:A:187:GLU:N	2.78	0.46
1:B:5:ILE:O	1:B:56:PHE:HA	2.15	0.46
1:B:172:ASP:OD1	1:C:108:LEU:HG	2.15	0.46
1:C:5:ILE:HB	1:C:57:GLU:OE1	2.15	0.46
1:D:4:ALA:HB1	1:D:56:PHE:CD2	2.50	0.46
1:F:146:ASP:C	1:F:147:MET:HG3	2.35	0.46
1:A:146:ASP:C	1:A:147:MET:HG3	2.35	0.46
1:A:173:ASP:HB2	1:B:107:THR:HG23	1.93	0.46
1:B:5:ILE:HB	1:B:57:GLU:OE1	2.15	0.46
1:B:73:LEU:O	1:B:76:VAL:HG12	2.16	0.46
1:E:133:LEU:HD23	1:E:133:LEU:HA	1.74	0.46
1:F:97:LEU:HB2	1:F:110:LEU:HD21	1.96	0.46
1:F:186:ILE:CG2	1:F:187:GLU:N	2.78	0.46
1:B:107:THR:CG2	1:B:107:THR:O	2.61	0.46
1:C:47:VAL:HG13	1:C:47:VAL:O	2.16	0.46
1:C:131:ILE:HD13	1:C:217:LEU:HD23	1.98	0.46
1:E:146:ASP:C	1:E:147:MET:HG3	2.35	0.46
1:E:156:VAL:HA	1:E:162:THR:O	2.16	0.46
1:A:149:SER:HB3	1:A:167:ALA:CB	2.22	0.46
1:A:156:VAL:CG1	1:A:191:ALA:O	2.62	0.46
1:C:8:ALA:HB2	1:C:84:ASP:HB2	1.98	0.46
1:C:186:ILE:CG2	1:C:187:GLU:N	2.78	0.46
1:C:195:PHE:CE2	1:C:242:PRO:CD	2.73	0.46
1:D:47:VAL:O	1:D:47:VAL:HG13	2.16	0.46
1:E:5:ILE:HB	1:E:57:GLU:OE1	2.15	0.46
1:F:5:ILE:HB	1:F:57:GLU:OE1	2.15	0.46
1:F:47:VAL:O	1:F:47:VAL:HG13	2.16	0.46
1:A:133:LEU:CG	1:A:183:LEU:HD12	2.45	0.46
1:B:8:ALA:HB2	1:B:84:ASP:HB2	1.98	0.46
1:B:156:VAL:CG1	1:B:191:ALA:O	2.62	0.46
1:D:5:ILE:HB	1:D:57:GLU:OE1	2.16	0.46
1:A:47:VAL:O	1:A:47:VAL:HG13	2.16	0.46
1:B:65:VAL:HG22	1:B:113:PRO:HG2	1.98	0.46
1:A:8:ALA:HB2	1:A:84:ASP:HB2	1.98	0.46
1:A:107:THR:CG2	1:A:107:THR:O	2.61	0.46
1:B:18:VAL:HB	1:B:22:VAL:HG22	1.98	0.46
1:B:29:LEU:HB3	1:B:34:LEU:HD22	1.98	0.46
1:B:156:VAL:HA	1:B:162:THR:O	2.16	0.46
1:C:133:LEU:CG	1:C:183:LEU:HD12	2.45	0.46
1:D:8:ALA:HB3	1:D:82:ALA:CA	2.45	0.46
1:D:133:LEU:HD23	1:D:133:LEU:HA	1.74	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:131:ILE:HG22	1:E:132:VAL:N	2.31	0.46
1:A:5:ILE:HB	1:A:57:GLU:OE1	2.15	0.46
1:A:18:VAL:HB	1:A:22:VAL:HG22	1.98	0.46
1:B:8:ALA:HB3	1:B:82:ALA:CA	2.45	0.46
1:D:133:LEU:CG	1:D:183:LEU:HD12	2.45	0.46
1:F:131:ILE:HG22	1:F:132:VAL:N	2.31	0.46
1:F:133:LEU:CG	1:F:183:LEU:HD12	2.45	0.46
1:A:8:ALA:HB3	1:A:82:ALA:CA	2.45	0.45
1:A:131:ILE:HG22	1:A:132:VAL:N	2.31	0.45
1:B:47:VAL:HG13	1:B:47:VAL:O	2.16	0.45
1:B:131:ILE:HG22	1:B:132:VAL:N	2.31	0.45
1:C:65:VAL:HG22	1:C:113:PRO:HG2	1.98	0.45
1:C:131:ILE:HG22	1:C:132:VAL:N	2.31	0.45
1:C:156:VAL:HA	1:C:162:THR:O	2.16	0.45
1:D:131:ILE:HD13	1:D:217:LEU:HD23	1.98	0.45
1:D:176:LEU:HD13	1:E:104:LEU:HD23	1.97	0.45
1:F:131:ILE:HD13	1:F:217:LEU:HD23	1.98	0.45
1:F:138:LEU:O	1:F:138:LEU:HD13	2.17	0.45
1:A:69:ASN:HB2	1:A:108:LEU:HD21	1.99	0.45
1:A:180:PRO:O	1:A:183:LEU:CB	2.65	0.45
1:B:131:ILE:HD13	1:B:217:LEU:HD23	1.98	0.45
1:B:173:ASP:HB2	1:C:107:THR:HG22	1.92	0.45
1:C:180:PRO:O	1:C:183:LEU:CB	2.65	0.45
1:E:18:VAL:HB	1:E:22:VAL:HG22	1.98	0.45
1:E:73:LEU:O	1:E:76:VAL:HG12	2.16	0.45
1:E:133:LEU:CG	1:E:183:LEU:HD12	2.45	0.45
1:F:29:LEU:HB3	1:F:34:LEU:HD22	1.98	0.45
1:C:18:VAL:HB	1:C:22:VAL:HG22	1.98	0.45
1:E:47:VAL:HG13	1:E:47:VAL:O	2.16	0.45
1:E:131:ILE:HD13	1:E:217:LEU:HD23	1.98	0.45
1:F:73:LEU:O	1:F:76:VAL:HG12	2.16	0.45
1:D:65:VAL:HG22	1:D:113:PRO:HG2	1.98	0.45
1:D:138:LEU:O	1:D:138:LEU:HD13	2.17	0.45
1:D:240:LEU:CD2	1:D:241:ALA:O	2.62	0.45
1:E:180:PRO:O	1:E:183:LEU:CB	2.65	0.45
1:A:29:LEU:HB3	1:A:34:LEU:HD22	1.98	0.45
1:A:156:VAL:HA	1:A:162:THR:O	2.16	0.45
1:D:73:LEU:O	1:D:76:VAL:HG12	2.16	0.45
1:F:8:ALA:HB2	1:F:84:ASP:HB2	1.98	0.45
1:B:138:LEU:O	1:B:138:LEU:HD13	2.17	0.45
1:B:158:GLY:O	1:B:159:ALA:CB	2.63	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:180:PRO:O	1:B:183:LEU:CB	2.65	0.45
1:C:69:ASN:HB2	1:C:108:LEU:HD21	1.99	0.45
1:C:73:LEU:O	1:C:76:VAL:HG12	2.16	0.45
1:D:49:LEU:CD2	1:D:236:ILE:HG22	2.47	0.45
1:E:29:LEU:HB3	1:E:34:LEU:HD22	1.98	0.45
1:F:65:VAL:HG22	1:F:113:PRO:HG2	1.98	0.45
1:B:176:LEU:HD13	1:C:104:LEU:HD23	1.98	0.45
1:C:29:LEU:HB3	1:C:34:LEU:HD22	1.98	0.45
1:D:155:ARG:O	1:D:163:PHE:HA	2.17	0.45
1:D:180:PRO:O	1:D:183:LEU:CB	2.65	0.45
1:E:155:ARG:O	1:E:163:PHE:HA	2.17	0.45
1:E:240:LEU:HD23	1:E:241:ALA:N	2.30	0.45
1:A:107:THR:HG23	1:C:173:ASP:HB2	1.95	0.45
1:A:108:LEU:HG	1:C:172:ASP:OD1	2.17	0.45
1:B:26:LYS:HA	1:B:67:GLY:HA2	1.99	0.45
1:C:106:TYR:CE2	1:C:108:LEU:HB2	2.52	0.45
1:C:240:LEU:O	1:C:242:PRO:HD3	2.17	0.45
1:F:95:ARG:C	1:F:110:LEU:H	2.20	0.45
1:C:49:LEU:CD2	1:C:236:ILE:HG22	2.47	0.45
1:D:8:ALA:HB2	1:D:84:ASP:HB2	1.98	0.45
1:D:173:ASP:HB2	1:E:107:THR:HG23	1.93	0.45
1:E:69:ASN:HB2	1:E:108:LEU:HD21	1.98	0.45
1:E:138:LEU:O	1:E:138:LEU:HD13	2.17	0.45
1:E:199:TYR:O	1:E:203:MET:HG3	2.17	0.45
1:F:180:PRO:O	1:F:183:LEU:CB	2.65	0.45
1:A:26:LYS:HA	1:A:67:GLY:HA2	1.99	0.45
1:A:49:LEU:CD2	1:A:236:ILE:HG22	2.47	0.45
1:A:155:ARG:O	1:A:163:PHE:HA	2.17	0.45
1:B:240:LEU:O	1:B:242:PRO:HD3	2.17	0.45
1:C:26:LYS:HA	1:C:67:GLY:HA2	1.99	0.45
1:D:133:LEU:O	1:D:213:VAL:N	2.29	0.45
1:F:155:ARG:O	1:F:163:PHE:HA	2.17	0.45
1:A:95:ARG:C	1:A:110:LEU:H	2.20	0.44
1:A:131:ILE:HG12	1:A:163:PHE:CD1	2.52	0.44
1:B:49:LEU:CD2	1:B:236:ILE:HG22	2.47	0.44
1:B:155:ARG:O	1:B:163:PHE:HA	2.17	0.44
1:C:151:HIS:HB3	1:C:195:PHE:O	2.18	0.44
1:C:199:TYR:O	1:C:203:MET:HG3	2.17	0.44
1:D:66:ILE:CD1	1:D:90:LEU:HD13	2.47	0.44
1:D:156:VAL:CG1	1:D:191:ALA:O	2.62	0.44
1:E:65:VAL:HG22	1:E:113:PRO:HG2	1.98	0.44

Continued on next page...

Full wwPDB X-ray Structure Validation Report

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:197:LEU:HD23	1:E:197:LEU:C	2.30	0.44
1:F:240:LEU:O	1:F:242:PRO:HD3	2.17	0.44
1:A:66:ILE:CD1	1:A:90:LEU:HD13	2.47	0.44
1:B:66:ILE:CD1	1:B:90:LEU:HD13	2.47	0.44
1:D:18:VAL:HB	1:D:22:VAL:HG22	1.98	0.44
1:D:106:TYR:CE2	1:D:108:LEU:HB2	2.52	0.44
1:D:131:ILE:HG22	1:D:132:VAL:N	2.31	0.44
1:F:18:VAL:HB	1:F:22:VAL:HG22	1.98	0.44
1:F:106:TYR:CE2	1:F:108:LEU:HB2	2.52	0.44
1:A:73:LEU:O	1:A:76:VAL:HG12	2.16	0.44
1:A:158:GLY:O	1:A:159:ALA:CB	2.63	0.44
1:B:179:PRO:HG2	1:D:179:PRO:CG	2.47	0.44
1:C:95:ARG:C	1:C:110:LEU:H	2.20	0.44
1:C:138:LEU:HD13	1:C:138:LEU:O	2.17	0.44
1:D:240:LEU:O	1:D:242:PRO:HD3	2.17	0.44
1:E:8:ALA:HB2	1:E:84:ASP:HB2	1.98	0.44
1:F:26:LYS:HA	1:F:67:GLY:HA2	1.99	0.44
1:F:66:ILE:CD1	1:F:90:LEU:HD13	2.48	0.44
1:A:138:LEU:O	1:A:138:LEU:HD13	2.17	0.44
1:A:199:TYR:O	1:A:203:MET:HG3	2.17	0.44
1:B:95:ARG:C	1:B:110:LEU:H	2.20	0.44
1:D:29:LEU:HB3	1:D:34:LEU:HD22	1.98	0.44
1:D:69:ASN:HB2	1:D:108:LEU:HD21	1.99	0.44
1:D:131:ILE:HG12	1:D:163:PHE:CD1	2.52	0.44
1:E:106:TYR:CE2	1:E:108:LEU:HB2	2.52	0.44
1:E:158:GLY:O	1:E:159:ALA:CB	2.64	0.44
1:A:65:VAL:HG22	1:A:113:PRO:HG2	1.98	0.44
1:B:151:HIS:HB3	1:B:195:PHE:O	2.18	0.44
1:C:155:ARG:O	1:C:163:PHE:HA	2.17	0.44
1:C:207:ILE:N	1:C:207:ILE:CD1	2.81	0.44
1:D:2:PHE:CD1	1:D:90:LEU:HD12	2.53	0.44
1:D:95:ARG:C	1:D:110:LEU:H	2.20	0.44
1:E:66:ILE:CD1	1:E:90:LEU:HD13	2.48	0.44
1:E:131:ILE:HG12	1:E:163:PHE:CD1	2.52	0.44
1:B:69:ASN:HB2	1:B:108:LEU:HD21	1.98	0.44
1:C:2:PHE:CD1	1:C:90:LEU:HD12	2.53	0.44
1:D:151:HIS:HB3	1:D:195:PHE:O	2.18	0.44
1:E:240:LEU:O	1:E:242:PRO:HD3	2.17	0.44
1:F:69:ASN:HB2	1:F:108:LEU:HD21	1.99	0.44
1:F:151:HIS:HB3	1:F:195:PHE:O	2.18	0.44
1:A:131:ILE:HD13	1:A:217:LEU:HD23	1.98	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:199:TYR:O	1:B:203:MET:HG3	2.17	0.44
1:E:8:ALA:HB3	1:E:82:ALA:CA	2.45	0.44
1:E:95:ARG:C	1:E:110:LEU:H	2.20	0.44
1:F:49:LEU:CD2	1:F:236:ILE:HG22	2.47	0.44
1:A:133:LEU:O	1:A:213:VAL:N	2.28	0.44
1:A:173:ASP:HB2	1:B:107:THR:HG21	1.93	0.44
1:A:240:LEU:O	1:A:242:PRO:HD3	2.17	0.44
1:B:207:ILE:N	1:B:207:ILE:CD1	2.81	0.44
1:C:66:ILE:CD1	1:C:90:LEU:HD13	2.47	0.44
1:D:155:ARG:HB3	1:D:164:HIS:HB2	2.00	0.44
1:D:157:ASP:CB	1:D:160:GLU:O	2.66	0.44
1:E:150:ASP:O	1:E:197:LEU:HB3	2.18	0.44
1:B:131:ILE:HG12	1:B:163:PHE:CD1	2.52	0.44
1:C:150:ASP:O	1:C:197:LEU:HB3	2.18	0.44
1:D:26:LYS:HA	1:D:67:GLY:HA2	1.99	0.44
1:E:207:ILE:N	1:E:207:ILE:CD1	2.81	0.44
1:F:29:LEU:HG	1:F:34:LEU:HB3	2.00	0.44
1:F:195:PHE:CE2	1:F:242:PRO:CD	2.73	0.44
1:A:2:PHE:CD1	1:A:90:LEU:HD12	2.53	0.43
1:A:155:ARG:HB3	1:A:164:HIS:HB2	2.00	0.43
1:A:207:ILE:HG21	1:A:227:TYR:OH	2.18	0.43
1:A:240:LEU:CD2	1:A:241:ALA:O	2.62	0.43
1:B:106:TYR:CE2	1:B:108:LEU:HB2	2.52	0.43
1:C:155:ARG:HB3	1:C:164:HIS:HB2	2.00	0.43
1:D:173:ASP:HB2	1:E:107:THR:HG21	1.96	0.43
1:D:199:TYR:O	1:D:203:MET:HG3	2.17	0.43
1:F:35:SER:HB2	1:F:49:LEU:O	2.18	0.43
1:A:172:ASP:OD1	1:B:108:LEU:HG	2.18	0.43
1:A:195:PHE:CE2	1:A:242:PRO:CD	2.73	0.43
1:B:157:ASP:CB	1:B:160:GLU:O	2.66	0.43
1:C:73:LEU:HD23	1:C:76:VAL:HG13	2.00	0.43
1:C:122:ILE:O	1:C:123:PRO:C	2.56	0.43
1:C:131:ILE:HG12	1:C:163:PHE:CD1	2.52	0.43
1:C:157:ASP:CB	1:C:160:GLU:O	2.66	0.43
1:D:150:ASP:O	1:D:197:LEU:HB3	2.18	0.43
1:E:207:ILE:HG21	1:E:227:TYR:OH	2.18	0.43
1:F:73:LEU:HD23	1:F:76:VAL:HG13	2.00	0.43
1:F:131:ILE:HG12	1:F:163:PHE:CD1	2.52	0.43
1:F:150:ASP:O	1:F:197:LEU:HB3	2.18	0.43
1:F:199:TYR:O	1:F:203:MET:HG3	2.17	0.43
1:A:198:ASP:C	1:A:200:LEU:H	2.22	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:35:SER:HB2	1:B:49:LEU:O	2.18	0.43
1:C:82:ALA:O	1:C:84:ASP:N	2.51	0.43
1:C:207:ILE:HG21	1:C:227:TYR:OH	2.19	0.43
1:A:150:ASP:O	1:A:197:LEU:HB3	2.18	0.43
1:A:235:THR:HG22	1:A:236:ILE:N	2.34	0.43
1:B:82:ALA:O	1:B:84:ASP:N	2.51	0.43
1:D:20:VAL:HG12	1:D:21:LEU:CD2	2.49	0.43
1:D:107:THR:HG22	1:F:173:ASP:HB2	1.98	0.43
1:D:207:ILE:HG21	1:D:227:TYR:OH	2.18	0.43
1:E:20:VAL:HG12	1:E:21:LEU:CD2	2.49	0.43
1:E:49:LEU:CD2	1:E:236:ILE:HG22	2.47	0.43
1:A:176:LEU:HD13	1:B:104:LEU:HD23	2.00	0.43
1:B:2:PHE:CD1	1:B:90:LEU:HD12	2.53	0.43
1:B:184:ILE:O	1:E:5:ILE:HD13	2.18	0.43
1:F:20:VAL:HG12	1:F:21:LEU:CD2	2.49	0.43
1:F:155:ARG:HB3	1:F:164:HIS:HB2	2.00	0.43
1:F:157:ASP:CB	1:F:160:GLU:O	2.66	0.43
1:B:27:ILE:HD12	1:B:68:VAL:HG21	2.01	0.43
1:B:73:LEU:HD23	1:B:76:VAL:HG13	2.00	0.43
1:B:133:LEU:HA	1:B:133:LEU:HD23	1.74	0.43
1:B:155:ARG:HB3	1:B:164:HIS:HB2	2.00	0.43
1:C:20:VAL:HG12	1:C:21:LEU:CD2	2.49	0.43
1:D:171:THR:HG21	1:E:72:ARG:NH1	2.19	0.43
1:E:2:PHE:CD1	1:E:90:LEU:HD12	2.53	0.43
1:E:122:ILE:O	1:E:123:PRO:C	2.56	0.43
1:F:82:ALA:O	1:F:84:ASP:N	2.51	0.43
1:F:145:ALA:O	1:F:197:LEU:HD13	2.19	0.43
1:F:235:THR:HG22	1:F:236:ILE:N	2.34	0.43
1:B:56:PHE:CD1	1:B:59:TYR:CE2	3.07	0.43
1:C:145:ALA:O	1:C:197:LEU:HD13	2.19	0.43
1:C:240:LEU:CD2	1:C:241:ALA:O	2.62	0.43
1:D:73:LEU:CA	1:D:76:VAL:HG12	2.49	0.43
1:E:56:PHE:CD1	1:E:59:TYR:CE2	3.07	0.43
1:E:82:ALA:O	1:E:84:ASP:N	2.51	0.43
1:F:56:PHE:CD1	1:F:59:TYR:CE2	3.07	0.43
1:F:198:ASP:C	1:F:200:LEU:H	2.22	0.43
1:A:20:VAL:HG12	1:A:21:LEU:CD2	2.49	0.43
1:A:151:HIS:HB3	1:A:195:PHE:O	2.18	0.43
1:B:145:ALA:O	1:B:197:LEU:HD13	2.19	0.43
1:C:56:PHE:CD1	1:C:59:TYR:CE2	3.07	0.43
1:D:27:ILE:HD12	1:D:68:VAL:HG21	2.01	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:73:LEU:HD23	1:E:76:VAL:HG13	2.00	0.43
1:E:151:HIS:HB3	1:E:195:PHE:O	2.18	0.43
1:E:235:THR:HG22	1:E:236:ILE:N	2.34	0.43
1:F:73:LEU:CA	1:F:76:VAL:HG12	2.49	0.43
1:A:171:THR:HG21	1:B:72:ARG:NH1	2.16	0.43
1:B:150:ASP:O	1:B:197:LEU:HB3	2.18	0.43
1:B:171:THR:HG21	1:C:72:ARG:NH1	2.13	0.43
1:B:235:THR:HG22	1:B:236:ILE:N	2.34	0.43
1:C:35:SER:HB2	1:C:49:LEU:O	2.19	0.43
1:C:198:ASP:C	1:C:200:LEU:H	2.22	0.43
1:D:73:LEU:HD23	1:D:76:VAL:HG13	2.00	0.43
1:E:70:LEU:O	1:E:70:LEU:HD22	2.19	0.43
1:E:157:ASP:CB	1:E:160:GLU:O	2.66	0.43
1:F:2:PHE:CD1	1:F:90:LEU:HD12	2.53	0.43
1:F:27:ILE:HG23	1:F:36:ILE:HD11	2.01	0.43
1:F:207:ILE:HG21	1:F:227:TYR:OH	2.18	0.43
1:A:27:ILE:HD12	1:A:68:VAL:HG21	2.01	0.43
1:A:73:LEU:HD23	1:A:76:VAL:HG13	2.00	0.43
1:A:109:ALA:HB3	1:C:171:THR:OG1	2.19	0.43
1:A:171:THR:OG1	1:B:109:ALA:HB3	2.19	0.43
1:D:27:ILE:HG23	1:D:36:ILE:HD11	2.01	0.43
1:D:35:SER:HB2	1:D:49:LEU:O	2.18	0.43
1:D:145:ALA:O	1:D:197:LEU:HD13	2.19	0.43
1:E:5:ILE:HD12	1:E:57:GLU:HB2	2.01	0.43
1:E:131:ILE:N	1:E:131:ILE:HD12	2.34	0.43
1:F:133:LEU:O	1:F:213:VAL:N	2.28	0.43
1:B:20:VAL:HG12	1:B:21:LEU:CD2	2.49	0.42
1:B:131:ILE:HD12	1:B:131:ILE:N	2.34	0.42
1:C:70:LEU:O	1:C:70:LEU:HD22	2.19	0.42
1:D:5:ILE:HD12	1:D:57:GLU:HB2	2.01	0.42
1:E:26:LYS:HA	1:E:67:GLY:HA2	1.99	0.42
1:A:35:SER:HB2	1:A:49:LEU:O	2.19	0.42
1:B:207:ILE:HG21	1:B:227:TYR:OH	2.18	0.42
1:C:27:ILE:HD12	1:C:68:VAL:HG21	2.01	0.42
1:E:27:ILE:HD12	1:E:68:VAL:HG21	2.01	0.42
1:E:35:SER:HB2	1:E:49:LEU:O	2.18	0.42
1:A:106:TYR:CE2	1:A:108:LEU:HB2	2.52	0.42
1:D:207:ILE:N	1:D:207:ILE:CD1	2.81	0.42
1:F:82:ALA:C	1:F:84:ASP:H	2.23	0.42
1:A:17:SER:OG	1:A:236:ILE:HG21	2.20	0.42
1:A:145:ALA:O	1:A:197:LEU:HD13	2.19	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:239:MET:HB3	1:A:239:MET:HE2	1.96	0.42
1:C:17:SER:OG	1:C:236:ILE:HG21	2.20	0.42
1:C:43:ASN:HD22	1:C:43:ASN:N	2.18	0.42
1:C:82:ALA:C	1:C:84:ASP:H	2.23	0.42
1:C:131:ILE:N	1:C:131:ILE:HD12	2.34	0.42
1:D:131:ILE:HD12	1:D:131:ILE:N	2.34	0.42
1:D:235:THR:HG22	1:D:236:ILE:N	2.34	0.42
1:F:27:ILE:HD12	1:F:68:VAL:HG21	2.01	0.42
1:F:131:ILE:N	1:F:131:ILE:HD12	2.34	0.42
1:A:29:LEU:HG	1:A:34:LEU:HB3	2.00	0.42
1:C:27:ILE:HG23	1:C:36:ILE:HD11	2.01	0.42
1:E:27:ILE:HG23	1:E:36:ILE:HD11	2.01	0.42
1:A:82:ALA:O	1:A:84:ASP:N	2.51	0.42
1:A:157:ASP:CB	1:A:160:GLU:O	2.66	0.42
1:B:27:ILE:HG23	1:B:36:ILE:HD11	2.01	0.42
1:B:133:LEU:CG	1:B:183:LEU:HD12	2.45	0.42
1:B:198:ASP:C	1:B:200:LEU:H	2.22	0.42
1:C:29:LEU:HG	1:C:34:LEU:HB3	2.00	0.42
1:D:29:LEU:HG	1:D:34:LEU:HB3	2.00	0.42
1:A:56:PHE:CD1	1:A:59:TYR:CE2	3.07	0.42
1:A:73:LEU:CA	1:A:76:VAL:HG12	2.49	0.42
1:B:29:LEU:HG	1:B:34:LEU:HB3	2.00	0.42
1:B:70:LEU:O	1:B:70:LEU:HD22	2.19	0.42
1:D:56:PHE:CD1	1:D:59:TYR:CE2	3.07	0.42
1:E:82:ALA:C	1:E:84:ASP:H	2.23	0.42
1:F:5:ILE:HD12	1:F:57:GLU:HB2	2.01	0.42
1:A:122:ILE:O	1:A:123:PRO:C	2.56	0.42
1:C:25:CYS:O	1:C:67:GLY:CA	2.66	0.42
1:C:49:LEU:HD23	1:C:235:THR:O	2.20	0.42
1:C:73:LEU:CA	1:C:76:VAL:HG12	2.49	0.42
1:D:82:ALA:O	1:D:84:ASP:N	2.51	0.42
1:D:122:ILE:O	1:D:123:PRO:C	2.56	0.42
1:E:17:SER:OG	1:E:236:ILE:HG21	2.20	0.42
1:E:25:CYS:O	1:E:67:GLY:CA	2.66	0.42
1:E:29:LEU:HG	1:E:34:LEU:HB3	2.00	0.42
1:E:73:LEU:CA	1:E:76:VAL:HG12	2.49	0.42
1:E:155:ARG:HB3	1:E:164:HIS:HB2	2.00	0.42
1:A:131:ILE:HD12	1:A:131:ILE:N	2.34	0.42
1:B:122:ILE:O	1:B:123:PRO:C	2.56	0.42
1:D:20:VAL:CG2	1:D:202:ASP:O	2.66	0.42
1:D:70:LEU:O	1:D:70:LEU:HD22	2.19	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:198:ASP:C	1:D:200:LEU:H	2.22	0.42
1:E:172:ASP:OD1	1:F:108:LEU:HG	2.19	0.42
1:F:17:SER:OG	1:F:236:ILE:HG21	2.20	0.42
1:A:246:SER:O	1:A:247:ASP:HB2	2.20	0.42
1:B:43:ASN:N	1:B:43:ASN:HD22	2.18	0.42
1:B:73:LEU:CA	1:B:76:VAL:HG12	2.49	0.42
1:C:5:ILE:CA	1:C:86:ILE:O	2.68	0.42
1:C:235:THR:HG22	1:C:236:ILE:N	2.34	0.42
1:E:173:ASP:HB2	1:F:107:THR:HG22	1.95	0.42
1:F:47:VAL:HB	1:F:238:TYR:CD2	2.55	0.42
1:F:49:LEU:HD23	1:F:235:THR:O	2.20	0.42
1:B:49:LEU:HD23	1:B:235:THR:O	2.20	0.41
1:B:240:LEU:CD2	1:B:241:ALA:O	2.62	0.41
1:C:158:GLY:O	1:C:159:ALA:CB	2.63	0.41
1:D:82:ALA:C	1:D:84:ASP:H	2.23	0.41
1:E:47:VAL:HB	1:E:238:TYR:CD2	2.55	0.41
1:E:240:LEU:CD2	1:E:241:ALA:O	2.62	0.41
1:F:5:ILE:CA	1:F:86:ILE:O	2.68	0.41
1:A:5:ILE:HD12	1:A:57:GLU:HB2	2.01	0.41
1:B:32:GLU:O	1:B:33:SER:OG	2.35	0.41
1:C:86:ILE:HG21	1:C:99:ILE:HD11	2.02	0.41
1:C:246:SER:O	1:C:247:ASP:HB2	2.20	0.41
1:D:17:SER:OG	1:D:236:ILE:HG21	2.20	0.41
1:D:49:LEU:HD23	1:D:235:THR:O	2.20	0.41
1:E:5:ILE:CA	1:E:86:ILE:O	2.68	0.41
1:E:145:ALA:O	1:E:197:LEU:HD13	2.19	0.41
1:A:27:ILE:HG23	1:A:36:ILE:HD11	2.01	0.41
1:A:34:LEU:HD23	1:A:34:LEU:N	2.35	0.41
1:A:70:LEU:O	1:A:70:LEU:HD22	2.19	0.41
1:A:86:ILE:HG21	1:A:99:ILE:HD11	2.02	0.41
1:D:47:VAL:HB	1:D:238:TYR:CD2	2.55	0.41
1:D:123:PRO:HG3	1:D:239:MET:HE1	2.02	0.41
1:D:175:ASP:O	1:E:104:LEU:CD2	2.68	0.41
1:E:198:ASP:C	1:E:200:LEU:H	2.22	0.41
1:A:174:VAL:CG2	1:B:104:LEU:HD21	2.47	0.41
1:A:214:THR:HG1	1:A:226:HIS:HB2	1.82	0.41
1:B:17:SER:OG	1:B:236:ILE:HG21	2.20	0.41
1:D:34:LEU:N	1:D:34:LEU:HD23	2.35	0.41
1:D:158:GLY:O	1:D:159:ALA:CB	2.63	0.41
1:E:49:LEU:HD23	1:E:235:THR:O	2.20	0.41
1:B:179:PRO:CG	1:D:179:PRO:HG2	2.48	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:5:ILE:HD12	1:C:57:GLU:HB2	2.01	0.41
1:C:32:GLU:O	1:C:33:SER:OG	2.35	0.41
1:E:43:ASN:N	1:E:43:ASN:HD22	2.18	0.41
1:F:240:LEU:CD2	1:F:241:ALA:O	2.63	0.41
1:F:246:SER:O	1:F:247:ASP:HB2	2.20	0.41
1:B:76:VAL:HG13	1:B:77:ALA:N	2.36	0.41
1:B:209:THR:O	1:B:210:ASP:HB2	2.21	0.41
1:D:209:THR:O	1:D:210:ASP:HB2	2.21	0.41
1:E:131:ILE:HD11	1:E:156:VAL:HG21	2.03	0.41
1:F:36:ILE:HG22	1:F:37:ARG:N	2.36	0.41
1:A:76:VAL:HG13	1:A:77:ALA:N	2.36	0.41
1:B:82:ALA:C	1:B:84:ASP:H	2.23	0.41
1:D:25:CYS:O	1:D:67:GLY:CA	2.66	0.41
1:E:2:PHE:HA	1:E:60:GLU:O	2.21	0.41
1:F:70:LEU:O	1:F:70:LEU:HD22	2.19	0.41
1:C:47:VAL:HB	1:C:238:TYR:CD2	2.55	0.41
1:D:36:ILE:HG22	1:D:37:ARG:N	2.36	0.41
1:D:37:ARG:O	1:D:37:ARG:CG	2.49	0.41
1:D:86:ILE:HG21	1:D:99:ILE:HD11	2.02	0.41
1:D:176:LEU:HD22	1:D:176:LEU:N	2.36	0.41
1:E:246:SER:O	1:E:247:ASP:HB2	2.20	0.41
1:A:5:ILE:CA	1:A:86:ILE:O	2.68	0.41
1:A:49:LEU:HD23	1:A:235:THR:O	2.20	0.41
1:A:82:ALA:C	1:A:84:ASP:H	2.23	0.41
1:A:123:PRO:HG3	1:A:239:MET:HE1	2.03	0.41
1:A:131:ILE:HD11	1:A:156:VAL:HG21	2.03	0.41
1:A:159:ALA:O	1:A:160:GLU:HB2	2.21	0.41
1:B:36:ILE:HG22	1:B:37:ARG:N	2.36	0.41
1:B:159:ALA:O	1:B:160:GLU:HB2	2.21	0.41
1:C:76:VAL:HG13	1:C:77:ALA:N	2.36	0.41
1:D:199:TYR:HB2	1:D:240:LEU:HD11	2.03	0.41
1:D:246:SER:O	1:D:247:ASP:HB2	2.20	0.41
1:E:176:LEU:HD22	1:E:176:LEU:N	2.36	0.41
1:E:180:PRO:O	1:E:183:LEU:HB2	2.21	0.41
1:E:209:THR:O	1:E:210:ASP:HB2	2.21	0.41
1:F:2:PHE:HA	1:F:60:GLU:O	2.21	0.41
1:F:34:LEU:N	1:F:34:LEU:HD23	2.35	0.41
1:F:176:LEU:HD22	1:F:176:LEU:N	2.36	0.41
1:F:221:PHE:C	1:F:242:PRO:HG3	2.42	0.41
1:A:47:VAL:HB	1:A:238:TYR:CD2	2.55	0.41
1:A:107:THR:HG21	1:C:173:ASP:HB2	1.96	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:180:PRO:O	1:A:183:LEU:HB2	2.21	0.41
1:B:7:SER:HA	1:B:85:LEU:HD23	2.04	0.41
1:B:69:ASN:CG	1:B:108:LEU:HD21	2.42	0.41
1:D:69:ASN:CG	1:D:108:LEU:HD21	2.42	0.41
1:F:69:ASN:CG	1:F:108:LEU:HD21	2.42	0.41
1:F:209:THR:O	1:F:210:ASP:HB2	2.21	0.41
1:A:2:PHE:HA	1:A:60:GLU:O	2.21	0.40
1:A:43:ASN:N	1:A:43:ASN:HD22	2.18	0.40
1:A:104:LEU:CD2	1:C:175:ASP:O	2.69	0.40
1:A:199:TYR:HB2	1:A:240:LEU:HD11	2.03	0.40
1:B:5:ILE:HD12	1:B:57:GLU:HB2	2.01	0.40
1:B:239:MET:HB3	1:B:239:MET:HE2	1.96	0.40
1:C:2:PHE:HA	1:C:60:GLU:O	2.21	0.40
1:C:7:SER:HA	1:C:85:LEU:HD23	2.04	0.40
1:D:5:ILE:CA	1:D:86:ILE:O	2.68	0.40
1:D:104:LEU:CD2	1:F:175:ASP:O	2.69	0.40
1:D:117:ARG:CG	1:D:118:GLN:N	2.84	0.40
1:E:34:LEU:N	1:E:34:LEU:HD23	2.35	0.40
1:E:43:ASN:HD21	1:E:117:ARG:HH22	1.69	0.40
1:F:43:ASN:HD21	1:F:117:ARG:HH22	1.69	0.40
1:F:43:ASN:N	1:F:43:ASN:HD22	2.18	0.40
1:A:36:ILE:HG22	1:A:37:ARG:N	2.36	0.40
1:A:73:LEU:C	1:A:76:VAL:HG12	2.42	0.40
1:A:176:LEU:N	1:A:176:LEU:HD22	2.36	0.40
1:B:34:LEU:HD23	1:B:34:LEU:N	2.35	0.40
1:B:176:LEU:N	1:B:176:LEU:HD22	2.36	0.40
1:C:69:ASN:CG	1:C:108:LEU:HD21	2.42	0.40
1:C:145:ALA:C	1:C:197:LEU:HD12	2.42	0.40
1:D:76:VAL:HG13	1:D:77:ALA:N	2.36	0.40
1:E:69:ASN:CG	1:E:108:LEU:HD21	2.42	0.40
1:E:195:PHE:HD2	1:E:240:LEU:HD23	1.86	0.40
1:F:76:VAL:HG13	1:F:77:ALA:N	2.36	0.40
1:A:69:ASN:CG	1:A:108:LEU:HD21	2.42	0.40
1:B:145:ALA:C	1:B:197:LEU:HD12	2.42	0.40
1:B:195:PHE:HD2	1:B:240:LEU:HD23	1.86	0.40
1:B:246:SER:O	1:B:247:ASP:HB2	2.20	0.40
1:C:176:LEU:N	1:C:176:LEU:HD22	2.36	0.40
1:C:199:TYR:HB2	1:C:240:LEU:HD11	2.03	0.40
1:D:15:LEU:HD23	1:D:15:LEU:N	2.37	0.40
1:D:43:ASN:HD21	1:D:117:ARG:HH22	1.69	0.40
1:D:221:PHE:C	1:D:242:PRO:HG3	2.42	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:7:SER:HA	1:E:85:LEU:HD23	2.04	0.40
1:F:159:ALA:O	1:F:160:GLU:HB2	2.21	0.40
1:A:131:ILE:HD13	1:A:163:PHE:HE1	1.87	0.40
1:B:1:MET:O	1:B:60:GLU:O	2.40	0.40
1:B:15:LEU:N	1:B:15:LEU:HD23	2.37	0.40
1:B:47:VAL:HB	1:B:238:TYR:CD2	2.55	0.40
1:B:131:ILE:HD13	1:B:163:PHE:HE1	1.87	0.40
1:C:34:LEU:HD23	1:C:34:LEU:N	2.35	0.40
1:C:46:MET:HE2	1:C:46:MET:HB3	1.97	0.40
1:C:209:THR:O	1:C:210:ASP:HB2	2.21	0.40
1:D:172:ASP:OD1	1:E:108:LEU:HG	2.22	0.40
1:E:86:ILE:HG21	1:E:99:ILE:HD11	2.02	0.40
1:F:1:MET:O	1:F:60:GLU:O	2.40	0.40
1:A:1:MET:O	1:A:60:GLU:O	2.40	0.40
1:A:43:ASN:HD21	1:A:117:ARG:HH22	1.69	0.40
1:A:221:PHE:C	1:A:242:PRO:HG3	2.42	0.40
1:B:25:CYS:O	1:B:67:GLY:CA	2.66	0.40
1:B:86:ILE:HG21	1:B:99:ILE:HD11	2.02	0.40
1:B:199:TYR:HB2	1:B:240:LEU:HD11	2.03	0.40
1:C:58:SER:C	1:C:59:TYR:CD2	2.94	0.40
1:C:159:ALA:O	1:C:160:GLU:HB2	2.21	0.40
1:D:2:PHE:HA	1:D:60:GLU:O	2.21	0.40
1:D:32:GLU:O	1:D:33:SER:OG	2.35	0.40
1:D:195:PHE:HD2	1:D:240:LEU:HD23	1.86	0.40
1:E:221:PHE:C	1:E:242:PRO:HG3	2.42	0.40
1:F:32:GLU:O	1:F:33:SER:OG	2.35	0.40
1:F:86:ILE:HG21	1:F:99:ILE:HD11	2.02	0.40

There are no symmetry-related clashes.

5.3   Torsion angles ⓘ

5.3.1   Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	245/247 (99%)	206 (84%)	30 (12%)	9 (4%)	3	22
1	B	245/247 (99%)	206 (84%)	30 (12%)	9 (4%)	3	22
1	C	245/247 (99%)	206 (84%)	30 (12%)	9 (4%)	3	22
1	D	245/247 (99%)	206 (84%)	30 (12%)	9 (4%)	3	22
1	E	245/247 (99%)	206 (84%)	30 (12%)	9 (4%)	3	22
1	F	245/247 (99%)	206 (84%)	30 (12%)	9 (4%)	3	22
All	All	1470/1482 (99%)	1236 (84%)	180 (12%)	54 (4%)	3	22

All (54) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	184	ILE
1	A	208	PRO
1	B	184	ILE
1	B	208	PRO
1	C	184	ILE
1	C	208	PRO
1	D	184	ILE
1	D	208	PRO
1	E	184	ILE
1	E	208	PRO
1	F	184	ILE
1	F	208	PRO
1	A	83	GLY
1	A	160	GLU
1	A	180	PRO
1	B	83	GLY
1	B	160	GLU
1	B	180	PRO
1	C	83	GLY
1	C	160	GLU
1	C	180	PRO
1	D	83	GLY
1	D	160	GLU
1	D	180	PRO
1	E	83	GLY
1	E	160	GLU
1	E	180	PRO
1	F	83	GLY
1	F	160	GLU
1	F	180	PRO

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	37	ARG
1	A	159	ALA
1	B	37	ARG
1	B	159	ALA
1	C	37	ARG
1	C	159	ALA
1	D	37	ARG
1	D	159	ALA
1	E	37	ARG
1	F	37	ARG
1	F	159	ALA
1	E	159	ALA
1	A	181	ALA
1	B	181	ALA
1	C	181	ALA
1	D	181	ALA
1	E	181	ALA
1	F	181	ALA
1	A	242	PRO
1	B	242	PRO
1	C	242	PRO
1	D	242	PRO
1	E	242	PRO
1	F	242	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	203/203 (100%)	159 (78%)	44 (22%)	1	5
1	B	203/203 (100%)	159 (78%)	44 (22%)	1	5
1	C	203/203 (100%)	159 (78%)	44 (22%)	1	5
1	D	203/203 (100%)	159 (78%)	44 (22%)	1	5
1	E	203/203 (100%)	159 (78%)	44 (22%)	1	5

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	F	203/203 (100%)	159 (78%)	44 (22%)	1	5
All	All	1218/1218 (100%)	954 (78%)	264 (22%)	1	5

All (264) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	LYS
1	A	5	ILE
1	A	21	LEU
1	A	23	ASP
1	A	34	LEU
1	A	37	ARG
1	A	41	PRO
1	A	44	VAL
1	A	56	PHE
1	A	59	TYR
1	A	65	VAL
1	A	70	LEU
1	A	73	LEU
1	A	75	GLU
1	A	90	LEU
1	A	91	ASP
1	A	95	ARG
1	A	104	LEU
1	A	114	ASP
1	A	120	PRO
1	A	121	ASP
1	A	125	LEU
1	A	133	LEU
1	A	138	LEU
1	A	147	MET
1	A	149	SER
1	A	151	HIS
1	A	157	ASP
1	A	161	GLU
1	A	170	ASP
1	A	171	THR
1	A	176	LEU
1	A	180	PRO
1	A	185	SER
1	A	187	GLU
1	A	197	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	208	PRO
1	A	217	LEU
1	A	219	GLU
1	A	222	PRO
1	A	233	MET
1	A	239	MET
1	A	242	PRO
1	A	247	ASP
1	B	3	LYS
1	B	5	ILE
1	B	21	LEU
1	B	23	ASP
1	B	34	LEU
1	B	37	ARG
1	B	41	PRO
1	B	44	VAL
1	B	56	PHE
1	B	59	TYR
1	B	65	VAL
1	B	70	LEU
1	B	73	LEU
1	B	75	GLU
1	B	90	LEU
1	B	91	ASP
1	B	95	ARG
1	B	104	LEU
1	B	114	ASP
1	B	120	PRO
1	B	121	ASP
1	B	125	LEU
1	B	133	LEU
1	B	138	LEU
1	B	147	MET
1	B	149	SER
1	B	151	HIS
1	B	157	ASP
1	B	161	GLU
1	B	170	ASP
1	B	171	THR
1	B	176	LEU
1	B	180	PRO
1	B	185	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	187	GLU
1	B	197	LEU
1	B	208	PRO
1	B	217	LEU
1	B	219	GLU
1	B	222	PRO
1	B	233	MET
1	B	239	MET
1	B	242	PRO
1	B	247	ASP
1	C	3	LYS
1	C	5	ILE
1	C	21	LEU
1	C	23	ASP
1	C	34	LEU
1	C	37	ARG
1	C	41	PRO
1	C	44	VAL
1	C	56	PHE
1	C	59	TYR
1	C	65	VAL
1	C	70	LEU
1	C	73	LEU
1	C	75	GLU
1	C	90	LEU
1	C	91	ASP
1	C	95	ARG
1	C	104	LEU
1	C	114	ASP
1	C	120	PRO
1	C	121	ASP
1	C	125	LEU
1	C	133	LEU
1	C	138	LEU
1	C	147	MET
1	C	149	SER
1	C	151	HIS
1	C	157	ASP
1	C	161	GLU
1	C	170	ASP
1	C	171	THR
1	C	176	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	180	PRO
1	C	185	SER
1	C	187	GLU
1	C	197	LEU
1	C	208	PRO
1	C	217	LEU
1	C	219	GLU
1	C	222	PRO
1	C	233	MET
1	C	239	MET
1	C	242	PRO
1	C	247	ASP
1	D	3	LYS
1	D	5	ILE
1	D	21	LEU
1	D	23	ASP
1	D	34	LEU
1	D	37	ARG
1	D	41	PRO
1	D	44	VAL
1	D	56	PHE
1	D	59	TYR
1	D	65	VAL
1	D	70	LEU
1	D	73	LEU
1	D	75	GLU
1	D	90	LEU
1	D	91	ASP
1	D	95	ARG
1	D	104	LEU
1	D	114	ASP
1	D	120	PRO
1	D	121	ASP
1	D	125	LEU
1	D	133	LEU
1	D	138	LEU
1	D	147	MET
1	D	149	SER
1	D	151	HIS
1	D	157	ASP
1	D	161	GLU
1	D	170	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	171	THR
1	D	176	LEU
1	D	180	PRO
1	D	185	SER
1	D	187	GLU
1	D	197	LEU
1	D	208	PRO
1	D	217	LEU
1	D	219	GLU
1	D	222	PRO
1	D	233	MET
1	D	239	MET
1	D	242	PRO
1	D	247	ASP
1	E	3	LYS
1	E	5	ILE
1	E	21	LEU
1	E	23	ASP
1	E	34	LEU
1	E	37	ARG
1	E	41	PRO
1	E	44	VAL
1	E	56	PHE
1	E	59	TYR
1	E	65	VAL
1	E	70	LEU
1	E	73	LEU
1	E	75	GLU
1	E	90	LEU
1	E	91	ASP
1	E	95	ARG
1	E	104	LEU
1	E	114	ASP
1	E	120	PRO
1	E	121	ASP
1	E	125	LEU
1	E	133	LEU
1	E	138	LEU
1	E	147	MET
1	E	149	SER
1	E	151	HIS
1	E	157	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	E	161	GLU
1	E	170	ASP
1	E	171	THR
1	E	176	LEU
1	E	180	PRO
1	E	185	SER
1	E	187	GLU
1	E	197	LEU
1	E	208	PRO
1	E	217	LEU
1	E	219	GLU
1	E	222	PRO
1	E	233	MET
1	E	239	MET
1	E	242	PRO
1	E	247	ASP
1	F	3	LYS
1	F	5	ILE
1	F	21	LEU
1	F	23	ASP
1	F	34	LEU
1	F	37	ARG
1	F	41	PRO
1	F	44	VAL
1	F	56	PHE
1	F	59	TYR
1	F	65	VAL
1	F	70	LEU
1	F	73	LEU
1	F	75	GLU
1	F	90	LEU
1	F	91	ASP
1	F	95	ARG
1	F	104	LEU
1	F	114	ASP
1	F	120	PRO
1	F	121	ASP
1	F	125	LEU
1	F	133	LEU
1	F	138	LEU
1	F	147	MET
1	F	149	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	F	151	HIS
1	F	157	ASP
1	F	161	GLU
1	F	170	ASP
1	F	171	THR
1	F	176	LEU
1	F	180	PRO
1	F	185	SER
1	F	187	GLU
1	F	197	LEU
1	F	208	PRO
1	F	217	LEU
1	F	219	GLU
1	F	222	PRO
1	F	233	MET
1	F	239	MET
1	F	242	PRO
1	F	247	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	43	ASN
1	B	43	ASN
1	C	43	ASN
1	C	87	HIS
1	D	43	ASN
1	E	43	ASN
1	E	87	HIS
1	F	43	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 ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	247/247 (100%)	-0.44	8 (3%)	47	31	93, 138, 172, 203	0
1	B	247/247 (100%)	-0.38	9 (3%)	42	27	94, 139, 172, 204	0
1	C	247/247 (100%)	-0.39	9 (3%)	42	27	94, 139, 172, 203	0
1	D	247/247 (100%)	-0.42	8 (3%)	47	31	94, 138, 173, 204	0
1	E	247/247 (100%)	-0.45	6 (2%)	59	44	94, 139, 172, 203	0
1	F	247/247 (100%)	-0.34	10 (4%)	38	25	94, 139, 172, 205	0
All	All	1482/1482 (100%)	-0.40	50 (3%)	45	29	93, 139, 175, 205	0

All (50) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	246	SER	5.3
1	C	244	ILE	4.8
1	F	244	ILE	4.8
1	B	246	SER	4.8
1	D	244	ILE	4.3
1	B	245	GLN	4.2
1	B	244	ILE	4.0
1	A	244	ILE	4.0
1	A	148	VAL	3.9
1	A	246	SER	3.8
1	C	246	SER	3.6
1	D	246	SER	3.5
1	C	243	ARG	3.4
1	B	220	GLU	3.3
1	E	244	ILE	3.1
1	C	245	GLN	3.1
1	E	246	SER	3.1
1	C	15	LEU	3.0
1	F	243	ARG	3.0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	D	15	LEU	3.0
1	A	220	GLU	3.0
1	B	148	VAL	3.0
1	D	243	ARG	2.9
1	C	148	VAL	2.8
1	A	245	GLN	2.7
1	F	245	GLN	2.7
1	D	220	GLU	2.7
1	F	219	GLU	2.7
1	A	219	GLU	2.6
1	A	159	ALA	2.6
1	E	61	ALA	2.5
1	E	102	ASP	2.5
1	D	236	ILE	2.5
1	F	220	GLU	2.4
1	D	34	LEU	2.4
1	C	229	ILE	2.4
1	E	219	GLU	2.4
1	C	220	GLU	2.3
1	C	236	ILE	2.3
1	F	34	LEU	2.2
1	F	227	TYR	2.2
1	B	94	THR	2.1
1	A	243	ARG	2.1
1	D	245	GLN	2.1
1	F	236	ILE	2.1
1	F	229	ILE	2.0
1	E	243	ARG	2.0
1	B	229	ILE	2.0
1	B	243	ARG	2.0
1	B	219	GLU	2.0

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

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

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.