



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 03:45 PM UTC

PDB ID : 1NR1 / pdb_00001nr1
Title : Crystal structure of the R463A mutant of human Glutamate dehydrogenase
Authors : Banerjee, S.; Schmidt, T.; Fang, J.; Stanley, C.A.; Smith, T.J.
Deposited on : 2003-01-23
Resolution : 3.30 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4-5-2 with Phenix2.0
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

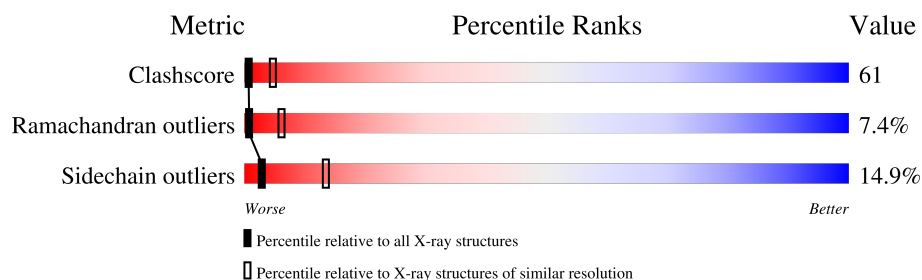
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.30 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	190562	1209 (3.32-3.28)
Ramachandran outliers	187476	1188 (3.32-3.28)
Sidechain outliers	187428	1187 (3.32-3.28)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	496	
1	B	496	
1	C	496	
1	D	496	
1	E	496	
1	F	496	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 23208 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 Glutamate dehydrogenase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	496	Total	C	N	O	S	0	0	0
			3868	2447	676	726	19			
1	B	496	Total	C	N	O	S	0	0	0
			3868	2447	676	726	19			
1	C	496	Total	C	N	O	S	0	0	0
			3868	2447	676	726	19			
1	D	496	Total	C	N	O	S	0	0	0
			3868	2447	676	726	19			
1	E	496	Total	C	N	O	S	0	0	0
			3868	2447	676	726	19			
1	F	496	Total	C	N	O	S	0	0	0
			3868	2447	676	726	19			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	88	GLN	HIS	conflict	UNP P00367
A	89	HIS	GLN	conflict	UNP P00367
A	463	ALA	ARG	engineered mutation	UNP P00367
B	88	GLN	HIS	conflict	UNP P00367
B	89	HIS	GLN	conflict	UNP P00367
B	463	ALA	ARG	engineered mutation	UNP P00367
C	88	GLN	HIS	conflict	UNP P00367
C	89	HIS	GLN	conflict	UNP P00367
C	463	ALA	ARG	engineered mutation	UNP P00367
D	88	GLN	HIS	conflict	UNP P00367
D	89	HIS	GLN	conflict	UNP P00367
D	463	ALA	ARG	engineered mutation	UNP P00367
E	88	GLN	HIS	conflict	UNP P00367
E	89	HIS	GLN	conflict	UNP P00367
E	463	ALA	ARG	engineered mutation	UNP P00367
F	88	GLN	HIS	conflict	UNP P00367
F	89	HIS	GLN	conflict	UNP P00367

Continued on next page...

Continued from previous page...

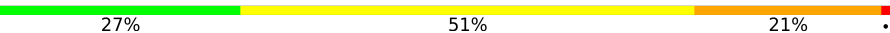
Chain	Residue	Modelled	Actual	Comment	Reference
F	463	ALA	ARG	engineered mutation	UNP P00367

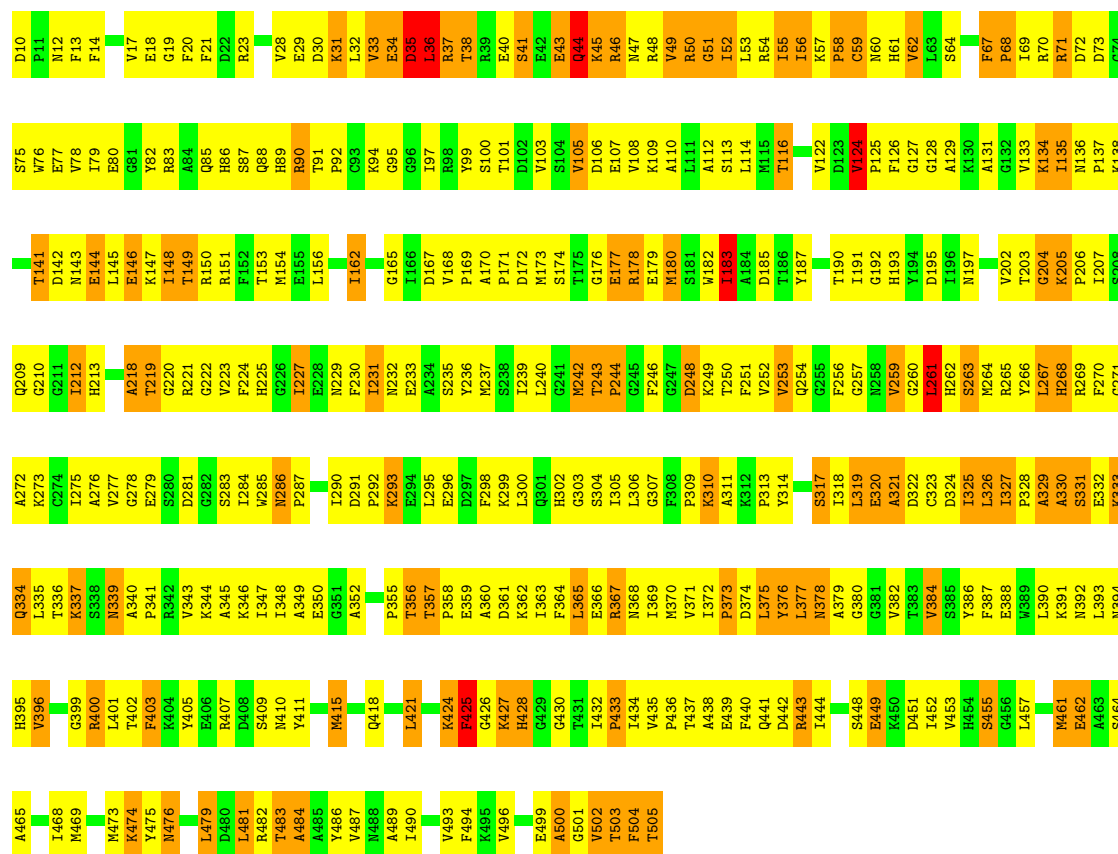
3 Residue-property plots

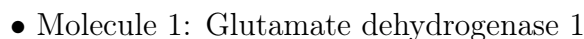
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded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

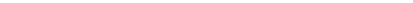
Note EDS was not executed.

• Molecule 1: Glutamate dehydrogenase 1

Chain A: 

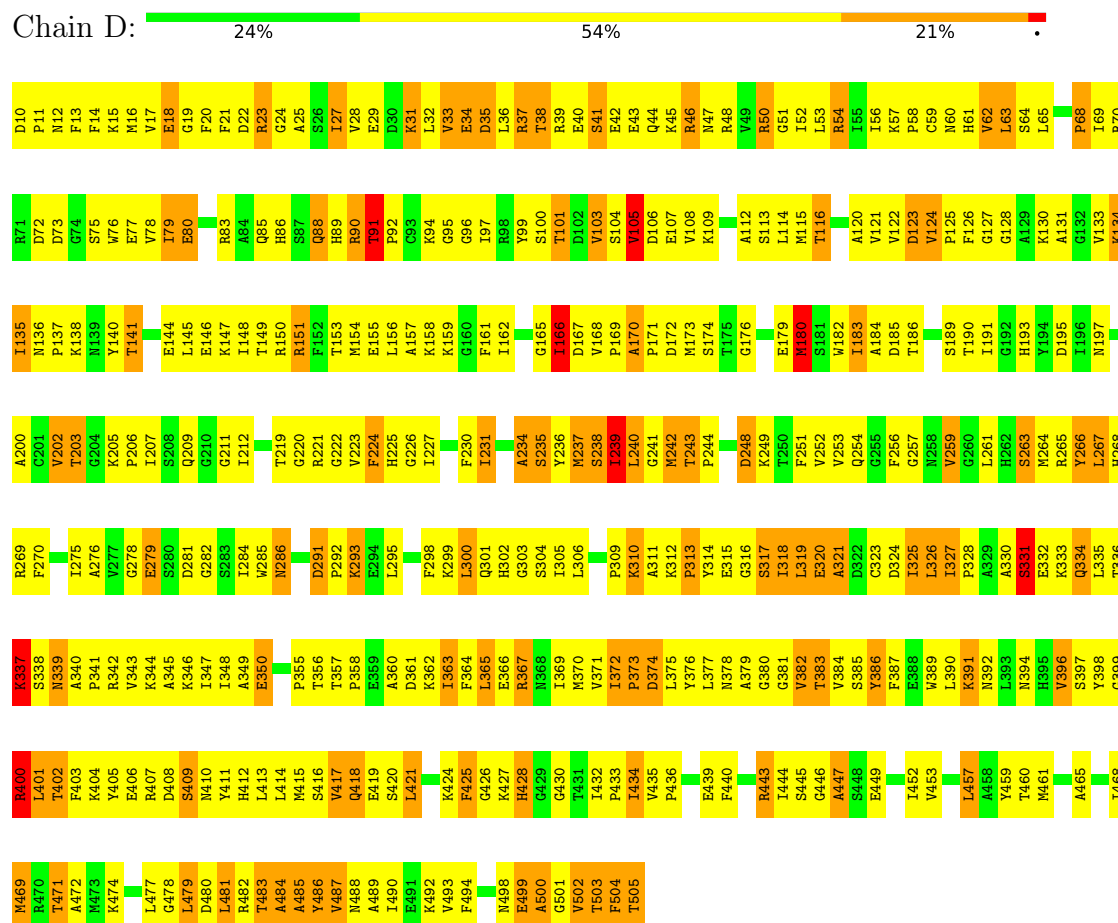


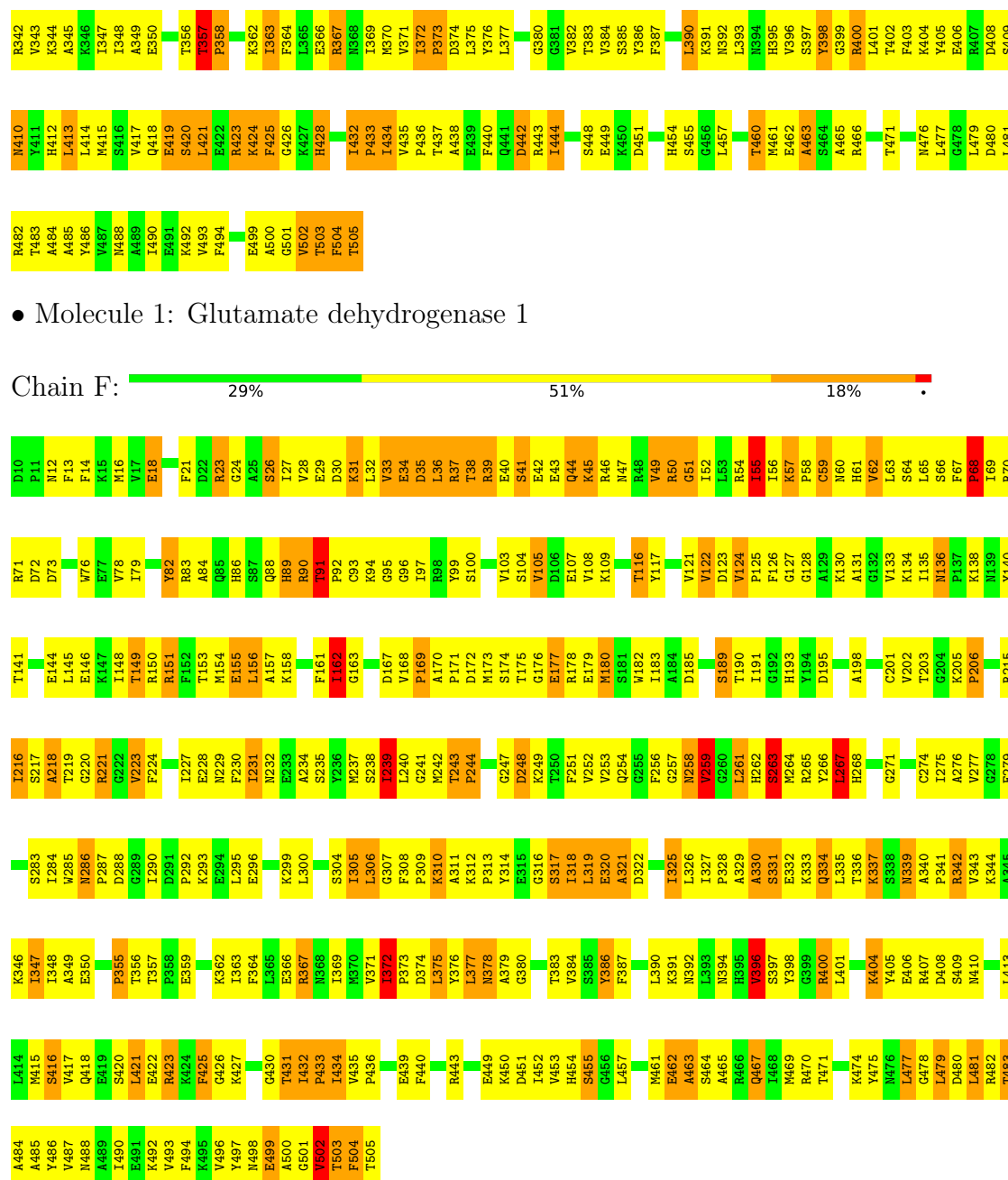


Chain C:  33% 47% 18%



• Molecule 1: Glutamate dehydrogenase 1





• Molecule 1: Glutamate dehydrogenase 1

4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	96.92Å 98.64Å 124.26Å 86.48° 69.69° 60.87°	Depositor
Resolution (Å)	19.99 – 3.30	Depositor
% Data completeness (in resolution range)	90.9 (19.99-3.30)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.222 , 0.284	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	23208	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

5 Model quality i

5.1 Standard geometry i

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.81	5/3952 (0.1%)	1.29	44/5333 (0.8%)
1	B	0.82	2/3952 (0.1%)	1.32	53/5333 (1.0%)
1	C	0.83	1/3952 (0.0%)	1.36	53/5333 (1.0%)
1	D	0.83	4/3952 (0.1%)	1.28	44/5333 (0.8%)
1	E	0.81	1/3952 (0.0%)	1.30	46/5333 (0.9%)
1	F	0.77	1/3952 (0.0%)	1.31	48/5333 (0.9%)
All	All	0.81	14/23712 (0.1%)	1.31	288/31998 (0.9%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	D	0	2
1	E	0	2
All	All	0	4

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	243	THR	CA-CB	11.47	1.60	1.52
1	D	469	MET	SD-CE	6.04	1.94	1.79
1	F	180	MET	SD-CE	-6.02	1.64	1.79
1	D	180	MET	SD-CE	-5.84	1.65	1.79
1	A	207	ILE	CA-CB	5.78	1.63	1.54
1	A	183	ILE	CA-CB	5.63	1.60	1.54
1	D	183	ILE	CA-CB	5.40	1.60	1.54
1	A	149	THR	CA-CB	5.40	1.61	1.53
1	D	243	THR	CA-CB	5.27	1.61	1.53
1	A	384	VAL	CA-CB	5.19	1.60	1.54
1	A	59	CYS	CB-SG	5.18	1.98	1.81
1	B	327	ILE	CA-CB	5.12	1.59	1.53

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	243	THR	CA-CB	5.07	1.57	1.52
1	C	180	MET	SD-CE	-5.01	1.67	1.79

All (288) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	503	THR	N-CA-C	-17.49	94.68	114.62
1	B	91	THR	CA-C-N	-13.38	105.55	119.99
1	B	91	THR	C-N-CA	-13.38	105.55	119.99
1	E	39	ARG	N-CA-C	-13.37	97.43	113.88
1	B	382	VAL	N-CA-C	-13.27	97.94	110.42
1	A	504	PHE	N-CA-C	-12.82	94.47	110.88
1	F	503	THR	N-CA-C	-12.79	97.81	114.31
1	D	504	PHE	N-CA-C	-12.57	94.79	110.88
1	C	504	PHE	N-CA-C	-11.98	95.13	111.55
1	E	503	THR	N-CA-C	-11.86	97.19	114.39
1	B	504	PHE	N-CA-C	-11.38	95.02	111.30
1	B	39	ARG	N-CA-C	-11.30	99.99	113.88
1	D	417	VAL	N-CA-C	-11.15	99.94	110.42
1	F	60	ASN	N-CA-C	10.81	123.06	111.28
1	E	504	PHE	N-CA-C	-10.38	95.83	111.81
1	A	46	ARG	N-CA-C	-10.30	99.02	111.69
1	F	163	GLY	CA-C-N	10.11	130.27	119.05
1	F	163	GLY	C-N-CA	10.11	130.27	119.05
1	C	60	ASN	N-CA-C	9.82	121.58	111.07
1	A	156	LEU	N-CA-C	-9.81	99.63	112.68
1	E	423	ARG	N-CA-C	-9.75	100.57	114.12
1	C	405	TYR	N-CA-C	-9.73	100.23	111.03
1	B	503	THR	N-CA-C	-9.72	98.53	113.89
1	D	503	THR	N-CA-C	-9.71	97.84	113.19
1	C	124	VAL	CA-C-N	9.62	131.86	119.84
1	C	124	VAL	C-N-CA	9.62	131.86	119.84
1	A	503	THR	N-CA-C	-9.54	97.76	113.50
1	D	484	ALA	N-CA-C	-9.40	100.59	111.03
1	C	221	ARG	N-CA-C	-9.30	100.72	112.90
1	C	91	THR	CA-C-N	-9.22	110.22	119.90
1	C	91	THR	C-N-CA	-9.22	110.22	119.90
1	F	57	LYS	CA-C-N	9.06	130.49	119.98
1	F	57	LYS	C-N-CA	9.06	130.49	119.98
1	A	484	ALA	N-CA-C	-9.00	100.42	111.40
1	E	45	LYS	N-CA-C	-8.97	102.50	112.72
1	C	372	ILE	CA-C-N	8.85	130.90	119.84

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	372	ILE	C-N-CA	8.85	130.90	119.84
1	A	89	HIS	N-CA-C	-8.63	101.81	111.82
1	F	504	PHE	N-CA-C	-8.62	98.54	111.81
1	A	291	ASP	CA-C-N	8.54	127.85	118.97
1	A	291	ASP	C-N-CA	8.54	127.85	118.97
1	C	243	THR	CA-C-N	8.51	128.94	120.52
1	C	243	THR	C-N-CA	8.51	128.94	120.52
1	A	246	PHE	N-CA-C	-8.41	104.16	114.75
1	A	50	ARG	N-CA-C	-8.37	102.97	113.02
1	D	383	THR	N-CA-C	-8.33	100.72	112.13
1	D	238	SER	N-CA-C	-8.32	100.72	112.13
1	C	152	PHE	N-CA-C	-8.29	101.66	112.68
1	B	57	LYS	CA-C-N	8.28	130.19	119.84
1	B	57	LYS	C-N-CA	8.28	130.19	119.84
1	D	487	VAL	N-CA-C	-8.24	102.67	110.42
1	F	479	LEU	N-CA-C	-8.11	101.22	112.25
1	C	66	SER	N-CA-C	-8.01	94.71	107.93
1	F	417	VAL	N-CA-C	-8.01	102.89	110.42
1	B	89	HIS	N-CA-C	-7.90	103.64	113.28
1	B	372	ILE	CA-C-N	7.88	127.94	119.90
1	B	372	ILE	C-N-CA	7.88	127.94	119.90
1	A	146	GLU	N-CA-C	-7.79	101.20	111.24
1	A	227	ILE	N-CA-C	-7.65	103.23	110.42
1	C	259	VAL	N-CA-C	7.64	117.76	110.42
1	C	136	ASN	CA-C-N	7.60	129.34	119.84
1	C	136	ASN	C-N-CA	7.60	129.34	119.84
1	E	479	LEU	N-CA-C	-7.59	102.25	112.26
1	E	151	ARG	N-CA-C	-7.46	102.84	110.97
1	B	243	THR	N-CA-C	-7.41	95.93	112.23
1	D	386	TYR	N-CA-C	-7.39	103.16	111.07
1	B	259	VAL	N-CA-C	7.36	118.12	110.62
1	C	45	LYS	N-CA-C	-7.34	104.06	113.16
1	A	51	GLY	N-CA-C	-7.33	103.93	112.73
1	A	382	VAL	CB-CA-C	-7.25	102.69	111.97
1	E	60	ASN	N-CA-C	7.24	119.86	111.02
1	D	168	VAL	CA-C-N	7.23	128.88	119.84
1	D	168	VAL	C-N-CA	7.23	128.88	119.84
1	E	91	THR	CA-C-N	-7.23	111.97	120.13
1	E	91	THR	C-N-CA	-7.23	111.97	120.13
1	B	136	ASN	CA-C-N	7.18	128.81	119.84
1	B	136	ASN	C-N-CA	7.18	128.81	119.84
1	E	442	ASP	N-CA-C	-7.16	103.17	110.97

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	89	HIS	N-CA-C	-7.14	104.44	113.01
1	D	479	LEU	N-CA-C	-7.14	102.54	112.25
1	E	271	GLY	N-CA-C	7.13	123.17	114.69
1	C	377	LEU	N-CA-C	7.10	119.92	111.33
1	B	484	ALA	N-CA-C	-7.07	103.65	111.36
1	F	51	GLY	N-CA-C	-7.03	105.65	114.16
1	F	259	VAL	N-CA-C	7.03	118.63	110.62
1	C	291	ASP	CA-C-N	7.02	128.62	119.84
1	C	291	ASP	C-N-CA	7.02	128.62	119.84
1	F	45	LYS	N-CA-C	-7.02	104.28	112.92
1	D	35	ASP	N-CA-C	6.94	121.37	112.34
1	B	468	ILE	N-CA-C	-6.93	103.58	110.30
1	E	243	THR	CA-C-N	6.91	128.48	119.84
1	E	243	THR	C-N-CA	6.91	128.48	119.84
1	F	484	ALA	N-CA-C	-6.88	103.89	112.90
1	F	66	SER	N-CA-C	-6.87	96.31	108.13
1	A	205	LYS	CA-C-N	6.85	126.61	119.76
1	A	205	LYS	C-N-CA	6.85	126.61	119.76
1	F	89	HIS	N-CA-C	-6.82	104.22	112.54
1	E	243	THR	CB-CA-C	6.80	116.03	111.20
1	B	479	LEU	N-CA-C	-6.79	105.41	113.21
1	D	91	THR	CA-C-N	-6.78	111.98	120.79
1	D	91	THR	C-N-CA	-6.78	111.98	120.79
1	A	479	LEU	N-CA-C	-6.77	103.33	112.26
1	B	45	LYS	N-CA-C	-6.75	104.62	112.92
1	A	442	ASP	N-CA-C	-6.72	103.64	110.97
1	C	246	PHE	N-CA-C	-6.72	106.03	114.56
1	C	316	GLY	N-CA-C	-6.71	97.27	113.18
1	B	423	ARG	N-CA-C	-6.70	104.32	113.30
1	A	424	LYS	N-CA-C	-6.69	100.38	109.54
1	D	127	GLY	N-CA-C	-6.63	103.67	112.82
1	C	44	GLN	N-CA-C	-6.60	104.53	112.58
1	E	372	ILE	CA-C-N	6.58	126.53	119.76
1	E	372	ILE	C-N-CA	6.58	126.53	119.76
1	D	88	GLN	N-CA-C	-6.53	103.42	112.30
1	F	477	LEU	N-CA-C	-6.52	100.56	110.14
1	C	59	CYS	CB-CA-C	6.51	119.11	110.06
1	F	423	ARG	N-CA-C	-6.49	103.97	112.41
1	B	27	ILE	CB-CA-C	-6.47	103.40	112.14
1	C	57	LYS	CA-C-N	6.46	128.17	120.23
1	C	57	LYS	C-N-CA	6.46	128.17	120.23
1	D	291	ASP	CA-C-N	6.44	126.20	119.05

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	291	ASP	C-N-CA	6.44	126.20	119.05
1	E	113	SER	N-CA-C	-6.39	104.00	110.97
1	C	395	HIS	N-CA-C	6.37	120.20	111.54
1	A	110	ALA	N-CA-C	6.35	118.20	111.28
1	D	243	THR	CA-C-N	6.29	127.52	120.66
1	D	243	THR	C-N-CA	6.29	127.52	120.66
1	C	50	ARG	N-CA-C	-6.26	105.62	113.20
1	E	438	ALA	N-CA-C	-6.25	104.39	111.14
1	D	46	ARG	N-CA-C	-6.25	105.14	112.89
1	D	27	ILE	CB-CA-C	-6.24	103.86	112.04
1	C	79	ILE	CB-CA-C	-6.24	103.02	111.63
1	C	386	TYR	N-CA-C	-6.24	104.39	111.07
1	F	453	VAL	N-CA-C	-6.24	105.07	110.74
1	D	477	LEU	N-CA-C	-6.20	100.06	109.85
1	E	51	GLY	N-CA-C	-6.19	105.13	113.24
1	E	133	VAL	N-CA-C	-6.19	98.61	107.77
1	B	59	CYS	N-CA-C	-6.18	101.40	110.42
1	F	243	THR	CA-C-N	6.17	127.58	120.98
1	F	243	THR	C-N-CA	6.17	127.58	120.98
1	D	18	GLU	N-CA-C	-6.16	104.48	111.14
1	B	316	GLY	N-CA-C	-6.16	98.58	113.18
1	A	178	ARG	N-CA-C	-6.16	103.30	111.24
1	F	151	ARG	N-CA-C	-6.12	104.53	111.14
1	D	468	ILE	N-CA-C	-6.11	104.38	110.30
1	D	60	ASN	N-CA-C	6.08	121.35	111.37
1	D	240	LEU	N-CA-C	-6.06	105.61	114.39
1	F	50	ARG	N-CA-C	-6.05	106.25	113.21
1	B	47	ASN	N-CA-C	-6.04	104.78	111.36
1	A	257	GLY	N-CA-C	-6.00	103.91	112.55
1	F	39	ARG	N-CA-C	-6.00	104.67	112.23
1	F	404	LYS	N-CA-C	-5.97	104.41	111.03
1	F	396	VAL	CB-CA-C	-5.95	101.53	111.29
1	C	55	ILE	CB-CA-C	-5.91	104.49	111.94
1	D	50	ARG	N-CA-C	-5.89	106.05	113.18
1	D	401	LEU	N-CA-C	5.89	120.46	113.28
1	F	375	LEU	N-CA-C	-5.86	105.39	112.54
1	F	96	GLY	N-CA-C	5.85	122.12	112.30
1	B	65	LEU	N-CA-C	5.84	118.98	109.06
1	B	127	GLY	N-CA-C	-5.82	100.28	112.04
1	C	89	HIS	N-CA-C	-5.82	105.44	112.54
1	A	148	ILE	N-CA-C	5.81	117.24	110.62
1	D	374	ASP	N-CA-C	-5.80	104.38	112.45

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	373	PRO	N-CA-C	5.80	119.72	110.21
1	F	91	THR	CA-C-N	-5.77	113.84	119.90
1	F	91	THR	C-N-CA	-5.77	113.84	119.90
1	B	276	ALA	N-CA-C	5.76	118.86	109.24
1	B	243	THR	CB-CA-C	5.75	116.00	111.00
1	E	286	ASN	CA-C-N	5.74	127.01	119.84
1	E	286	ASN	C-N-CA	5.74	127.01	119.84
1	A	377	LEU	N-CA-C	5.72	118.25	111.33
1	B	327	ILE	CA-C-N	5.72	126.99	119.84
1	B	327	ILE	C-N-CA	5.72	126.99	119.84
1	C	148	ILE	CB-CA-C	-5.70	104.51	111.87
1	C	56	ILE	CB-CA-C	-5.67	104.71	111.97
1	F	124	VAL	CA-C-N	5.67	126.93	119.84
1	F	124	VAL	C-N-CA	5.67	126.93	119.84
1	B	67	PHE	CA-C-N	5.67	126.92	119.84
1	B	67	PHE	C-N-CA	5.67	126.92	119.84
1	C	205	LYS	CA-C-N	5.67	126.11	119.99
1	C	205	LYS	C-N-CA	5.67	126.11	119.99
1	A	35	ASP	N-CA-C	5.66	122.86	110.80
1	D	166	ILE	N-CA-C	5.66	116.09	111.62
1	E	91	THR	N-CA-C	5.66	122.31	109.81
1	A	365	LEU	N-CA-C	-5.65	104.81	110.97
1	B	393	LEU	N-CA-C	-5.65	102.92	111.56
1	C	67	PHE	CA-C-N	-5.65	112.78	119.84
1	C	67	PHE	C-N-CA	-5.65	112.78	119.84
1	E	420	SER	N-CA-C	5.64	117.43	111.28
1	F	377	LEU	N-CA-C	5.63	118.14	111.33
1	A	449	GLU	N-CA-C	5.62	118.13	111.33
1	A	45	LYS	N-CA-C	-5.60	103.74	111.81
1	C	127	GLY	N-CA-C	-5.60	105.09	112.82
1	F	59	CYS	N-CA-C	-5.60	101.62	109.96
1	B	243	THR	CA-C-N	5.59	126.83	119.84
1	B	243	THR	C-N-CA	5.59	126.83	119.84
1	B	327	ILE	N-CA-C	5.59	113.58	107.60
1	E	476	ASN	N-CA-C	5.58	119.09	111.39
1	E	393	LEU	N-CA-C	-5.58	104.83	111.69
1	A	329	ALA	N-CA-C	5.58	117.68	110.65
1	A	44	GLN	N-CA-C	-5.58	106.86	113.38
1	C	215	ARG	N-CA-C	5.58	118.55	111.69
1	D	243	THR	N-CA-C	-5.58	97.49	109.81
1	F	372	ILE	N-CA-C	-5.58	102.49	107.56
1	B	442	ASP	N-CA-C	-5.56	104.86	111.03

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	57	LYS	N-CA-C	5.54	122.05	109.81
1	F	263	SER	N-CA-C	-5.53	105.17	111.14
1	E	291	ASP	CA-C-N	5.50	124.69	118.97
1	E	291	ASP	C-N-CA	5.50	124.69	118.97
1	E	242	MET	N-CA-C	5.50	117.83	109.63
1	D	103	VAL	N-CA-C	-5.50	104.00	110.21
1	E	263	SER	N-CA-C	-5.49	104.33	111.02
1	B	60	ASN	N-CA-C	5.48	117.06	111.14
1	F	105	VAL	N-CA-C	-5.48	105.02	111.00
1	E	390	LEU	N-CA-C	-5.48	104.95	111.03
1	A	36	LEU	N-CA-C	-5.47	106.53	113.43
1	B	410	ASN	N-CA-C	-5.47	104.95	111.03
1	C	59	CYS	N-CA-C	-5.47	102.10	110.30
1	F	18	GLU	N-CA-C	-5.46	105.01	110.97
1	A	124	VAL	CA-C-N	5.46	126.67	119.84
1	A	124	VAL	C-N-CA	5.46	126.67	119.84
1	F	455	SER	N-CA-C	-5.45	104.98	111.03
1	A	259	VAL	N-CA-C	5.45	116.08	110.36
1	D	372	ILE	CA-C-N	5.44	126.64	119.84
1	D	372	ILE	C-N-CA	5.44	126.64	119.84
1	D	183	ILE	N-CA-C	-5.44	105.03	110.30
1	F	55	ILE	N-CA-C	-5.43	105.55	110.82
1	B	221	ARG	N-CA-C	-5.43	105.36	111.28
1	A	58	PRO	N-CA-C	5.42	119.73	110.95
1	E	18	GLU	N-CA-C	-5.42	104.91	112.45
1	B	56	ILE	N-CA-C	5.42	115.56	110.30
1	E	437	THR	N-CA-C	-5.41	103.75	110.41
1	D	379	ALA	N-CA-C	-5.41	106.53	113.02
1	E	96	GLY	N-CA-C	5.40	119.45	112.54
1	D	257	GLY	N-CA-C	-5.39	104.32	112.41
1	A	55	ILE	CB-CA-C	-5.39	104.98	111.88
1	E	373	PRO	N-CA-C	5.38	119.54	111.14
1	D	170	ALA	CA-C-N	5.38	125.85	120.52
1	D	170	ALA	C-N-CA	5.38	125.85	120.52
1	E	36	LEU	N-CA-C	5.38	117.84	111.33
1	E	357	THR	CA-C-N	5.37	126.55	119.84
1	E	357	THR	C-N-CA	5.37	126.55	119.84
1	B	146	GLU	N-CA-C	-5.36	105.08	111.03
1	F	127	GLY	N-CA-C	-5.36	105.69	112.54
1	B	377	LEU	N-CA-C	5.35	122.19	110.80
1	A	56	ILE	N-CA-C	5.35	115.55	110.42
1	B	166	ILE	CB-CA-C	-5.34	107.17	111.71

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	243	THR	N-CA-C	-5.34	99.90	111.53
1	F	136	ASN	CA-C-N	5.33	126.51	119.84
1	F	136	ASN	C-N-CA	5.33	126.51	119.84
1	C	196	ILE	N-CA-C	-5.32	105.78	113.07
1	B	453	VAL	CB-CA-C	-5.31	105.17	111.81
1	C	449	GLU	N-CA-C	5.31	117.75	111.33
1	F	244	PRO	N-CA-C	5.29	118.92	110.40
1	C	407	ARG	N-CA-C	-5.27	105.44	111.14
1	B	23	ARG	N-CA-C	-5.27	105.22	110.97
1	F	386	TYR	N-CA-C	-5.26	105.63	111.36
1	B	51	GLY	N-CA-C	-5.26	107.26	113.99
1	C	447	ALA	N-CA-C	-5.26	102.61	110.23
1	B	59	CYS	CB-CA-C	5.24	116.99	109.71
1	E	444	ILE	CB-CA-C	-5.23	105.19	111.88
1	C	17	VAL	N-CA-C	-5.23	104.43	111.44
1	A	204	GLY	N-CA-C	-5.23	107.83	115.72
1	C	146	GLU	N-CA-C	-5.22	105.28	110.97
1	C	244	PRO	N-CA-C	5.21	118.90	111.13
1	E	182	TRP	N-CA-C	-5.21	105.51	111.14
1	A	276	ALA	N-CA-C	5.20	117.83	108.48
1	D	472	ALA	N-CA-C	-5.19	104.69	111.02
1	A	243	THR	CA-C-N	5.18	126.32	119.84
1	A	243	THR	C-N-CA	5.18	126.32	119.84
1	F	347	ILE	N-CA-C	5.18	115.44	107.77
1	C	58	PRO	N-CA-C	5.17	118.61	110.50
1	B	417	VAL	N-CA-C	-5.16	105.37	111.00
1	B	181	SER	N-CA-C	-5.16	105.57	111.14
1	B	257	GLY	N-CA-C	-5.16	105.12	112.55
1	F	267	LEU	N-CA-C	-5.15	104.74	111.02
1	E	200	ALA	N-CA-C	-5.14	106.41	113.30
1	D	195	ASP	N-CA-C	5.13	116.62	108.67
1	B	253	VAL	N-CA-C	5.12	115.42	107.28
1	E	392	ASN	N-CA-C	5.12	117.60	111.71
1	C	110	ALA	N-CA-C	5.12	116.55	111.07
1	D	166	ILE	N-CA-CB	-5.10	107.46	111.64
1	C	90	ARG	N-CA-C	-5.10	101.09	109.40
1	F	44	GLN	N-CA-C	-5.09	105.72	112.24
1	F	288	ASP	N-CA-C	-5.08	105.39	112.45
1	E	89	HIS	N-CA-C	-5.04	107.08	113.18
1	A	144	GLU	N-CA-C	-5.04	105.25	111.40
1	B	113	SER	N-CA-C	-5.02	105.72	111.14
1	A	148	ILE	CB-CA-C	-5.01	105.47	112.04

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	266	TYR	Sidechain
1	D	459	TYR	Sidechain
1	E	187	TYR	Sidechain
1	E	398	TYR	Sidechain

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	3868	0	3833	556	0
1	B	3868	0	3833	466	0
1	C	3868	0	3833	449	0
1	D	3868	0	3833	538	0
1	E	3868	0	3833	442	0
1	F	3868	0	3833	519	0
All	All	23208	0	22998	2797	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 61.

All (2797) 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:C:337:LYS:HE3	1:C:359:GLU:HG3	1.26	1.16
1:E:190:THR:HG22	1:E:191:ILE:H	1.09	1.15
1:A:251:PHE:HB3	1:A:325:ILE:HG13	1.29	1.14
1:A:71:ARG:HB3	1:A:71:ARG:HH11	1.07	1.13
1:D:86:HIS:CD2	1:D:116:THR:HG21	1.83	1.11
1:E:116:THR:HG22	1:E:128:GLY:N	1.66	1.10
1:D:99:TYR:OH	1:D:149:THR:HG22	1.49	1.10
1:C:327:ILE:HG22	1:C:349:ALA:HB3	1.33	1.09
1:F:277:VAL:HB	1:F:284:ILE:HD12	1.27	1.09
1:A:37:ARG:HB2	1:A:37:ARG:HH11	0.99	1.08
1:E:116:THR:HG22	1:E:128:GLY:H	0.95	1.08

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:37:ARG:HH21	1:C:49:VAL:HG11	1.14	1.07
1:A:10:ASP:HB2	1:A:333:LYS:HE2	1.31	1.07
1:E:38:THR:HG23	1:E:41:SER:HB3	1.38	1.06
1:B:190:THR:HG22	1:B:191:ILE:H	1.17	1.05
1:F:251:PHE:HB3	1:F:325:ILE:HG13	1.37	1.05
1:A:71:ARG:HB3	1:A:71:ARG:NH1	1.72	1.05
1:C:99:TYR:OH	1:C:149:THR:HG22	1.56	1.04
1:E:284:ILE:HG23	1:E:311:ALA:HB1	1.38	1.03
1:D:325:ILE:HG22	1:D:347:ILE:HB	1.40	1.03
1:F:86:HIS:CD2	1:F:116:THR:HG21	1.93	1.02
1:F:333:LYS:HE3	1:F:357:THR:HG22	1.40	1.02
1:C:325:ILE:HG22	1:C:347:ILE:HB	1.42	1.02
1:D:348:ILE:HB	1:D:371:VAL:HG22	1.36	1.02
1:E:190:THR:HG22	1:E:191:ILE:N	1.74	1.02
1:E:34:GLU:HA	1:E:38:THR:HB	1.39	1.01
1:D:284:ILE:HG23	1:D:311:ALA:HB1	1.41	1.01
1:A:185:ASP:OD1	1:F:505:THR:HG23	1.61	1.01
1:A:37:ARG:HB2	1:A:37:ARG:NH1	1.75	1.01
1:E:320:GLU:HG2	1:E:342:ARG:HG2	1.43	1.01
1:F:38:THR:HG23	1:F:41:SER:HB3	1.37	1.01
1:F:327:ILE:HG22	1:F:349:ALA:HB3	1.40	1.01
1:F:486:TYR:O	1:F:490:ILE:HG12	1.62	1.00
1:B:37:ARG:HH11	1:B:37:ARG:HB2	1.22	1.00
1:B:116:THR:HG22	1:B:128:GLY:H	1.25	1.00
1:F:334:GLN:HA	1:F:334:GLN:HE21	1.23	0.99
1:A:99:TYR:OH	1:A:149:THR:HG22	1.62	0.99
1:D:37:ARG:HB2	1:D:37:ARG:HH11	1.24	0.99
1:C:141:THR:HG23	1:C:144:GLU:HG3	1.45	0.99
1:F:43:GLU:HB3	1:F:45:LYS:HG3	1.44	0.99
1:B:505:THR:HG23	1:F:185:ASP:OD1	1.62	0.98
1:B:37:ARG:HB2	1:B:37:ARG:NH1	1.79	0.98
1:A:116:THR:HG22	1:A:128:GLY:HA3	1.45	0.98
1:A:237:MET:HE1	1:A:347:ILE:HD11	1.45	0.98
1:C:71:ARG:HB3	1:C:71:ARG:HH11	1.23	0.97
1:E:37:ARG:NH1	1:E:37:ARG:HB2	1.79	0.97
1:B:116:THR:HG22	1:B:128:GLY:N	1.80	0.97
1:C:83:ARG:HD3	1:C:131:ALA:HB2	1.46	0.97
1:E:418:GLN:HB2	1:E:433:PRO:HD2	1.47	0.97
1:C:185:ASP:OD1	1:E:505:THR:HG23	1.65	0.96
1:B:418:GLN:HB2	1:B:433:PRO:HD2	1.46	0.95
1:D:86:HIS:HD2	1:D:116:THR:HG21	1.22	0.95

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:372:ILE:HG21	1:D:377:LEU:HD13	1.47	0.95
1:A:91:THR:HB	1:A:92:PRO:HD3	1.49	0.95
1:F:243:THR:N	1:F:244:PRO:HD3	1.80	0.94
1:C:284:ILE:HG13	1:C:311:ALA:HB1	1.47	0.94
1:B:327:ILE:HG22	1:B:349:ALA:HB3	1.50	0.94
1:F:86:HIS:HD2	1:F:116:THR:HG21	1.23	0.94
1:A:86:HIS:CD2	1:A:116:THR:HG21	2.02	0.94
1:A:13:PHE:HD1	1:A:14:PHE:H	1.13	0.93
1:E:327:ILE:HG22	1:E:349:ALA:HB3	1.47	0.93
1:D:41:SER:HA	1:D:46:ARG:HE	1.31	0.93
1:B:343:VAL:HG21	1:B:364:PHE:HE1	1.34	0.93
1:A:61:HIS:HD2	1:A:88:GLN:HE22	1.17	0.93
1:A:23:ARG:HE	1:A:483:THR:HG21	1.32	0.92
1:C:243:THR:N	1:C:244:PRO:HD3	1.84	0.92
1:A:284:ILE:HG23	1:A:311:ALA:HB1	1.48	0.92
1:B:100:SER:O	1:B:103:VAL:HG13	1.69	0.92
1:C:396:VAL:HG13	1:E:386:TYR:OH	1.70	0.92
1:F:264:MET:HE3	1:F:292:PRO:HA	1.52	0.92
1:C:221:ARG:HH11	1:C:221:ARG:HG2	1.34	0.92
1:E:86:HIS:CD2	1:E:116:THR:HG21	2.05	0.92
1:F:61:HIS:HD2	1:F:88:GLN:HE22	1.12	0.92
1:C:252:VAL:HG13	1:C:276:ALA:HB3	1.50	0.92
1:A:319:LEU:H	1:A:319:LEU:HD12	1.35	0.92
1:F:24:GLY:O	1:F:28:VAL:HG23	1.70	0.91
1:E:99:TYR:OH	1:E:149:THR:HG22	1.69	0.91
1:A:243:THR:N	1:A:244:PRO:HD3	1.85	0.91
1:C:145:LEU:O	1:C:149:THR:HG23	1.71	0.91
1:C:86:HIS:CD2	1:C:116:THR:HG21	2.05	0.90
1:C:144:GLU:O	1:C:148:ILE:HG13	1.72	0.90
1:B:76:TRP:HE1	1:D:502:VAL:HG11	1.37	0.90
1:B:190:THR:HG22	1:B:191:ILE:N	1.81	0.90
1:D:83:ARG:HD2	1:D:131:ALA:HB2	1.52	0.90
1:D:427:LYS:HD3	1:D:430:GLY:HA3	1.52	0.90
1:E:336:THR:H	1:E:339:ASN:HD21	1.15	0.90
1:D:154:MET:SD	1:D:190:THR:HG21	2.11	0.90
1:B:281:ASP:HB2	1:B:306:LEU:HD11	1.54	0.89
1:F:325:ILE:HG22	1:F:347:ILE:HB	1.55	0.89
1:B:116:THR:HG22	1:B:128:GLY:CA	2.03	0.89
1:B:251:PHE:HB3	1:B:325:ILE:HG13	1.55	0.89
1:D:505:THR:HG23	1:E:185:ASP:OD1	1.73	0.89
1:F:251:PHE:CB	1:F:325:ILE:HG13	2.03	0.89

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:343:VAL:HG21	1:F:364:PHE:HE1	1.37	0.88
1:B:264:MET:HE3	1:B:292:PRO:HA	1.55	0.88
1:A:83:ARG:HD3	1:A:131:ALA:HB2	1.53	0.88
1:A:37:ARG:HH11	1:A:37:ARG:CB	1.84	0.88
1:D:251:PHE:HB3	1:D:325:ILE:HG12	1.54	0.88
1:E:71:ARG:HB3	1:E:71:ARG:HH11	1.37	0.88
1:B:86:HIS:CD2	1:B:116:THR:HG21	2.08	0.88
1:C:333:LYS:HD3	1:C:357:THR:HG22	1.54	0.87
1:E:41:SER:HA	1:E:46:ARG:HD2	1.56	0.87
1:B:43:GLU:HB3	1:B:45:LYS:HG3	1.55	0.87
1:C:169:PRO:O	1:C:202:VAL:HG23	1.74	0.87
1:A:116:THR:HG22	1:A:128:GLY:CA	2.03	0.87
1:D:91:THR:HB	1:D:92:PRO:HD3	1.53	0.87
1:A:54:ARG:O	1:A:58:PRO:HD2	1.75	0.87
1:D:227:ILE:HD11	1:D:349:ALA:HB2	1.55	0.87
1:C:116:THR:HG22	1:C:128:GLY:HA3	1.56	0.87
1:A:502:VAL:HG11	1:E:76:TRP:NE1	1.90	0.87
1:C:13:PHE:CZ	1:C:107:GLU:HG3	2.10	0.87
1:F:146:GLU:O	1:F:150:ARG:HG3	1.73	0.86
1:E:100:SER:O	1:E:103:VAL:HG13	1.75	0.86
1:D:243:THR:N	1:D:244:PRO:HD3	1.89	0.86
1:D:34:GLU:HA	1:D:38:THR:HB	1.56	0.86
1:D:97:ILE:HD13	1:D:131:ALA:HB3	1.56	0.86
1:D:425:PHE:CE1	1:D:427:LYS:HE2	2.10	0.86
1:E:135:ILE:HD11	1:E:140:TYR:OH	1.75	0.86
1:F:332:GLU:HG2	1:F:333:LYS:HG3	1.57	0.86
1:C:229:ASN:ND2	1:C:462:GLU:HA	1.90	0.85
1:F:91:THR:HB	1:F:92:PRO:HD3	1.59	0.85
1:A:103:VAL:HA	1:A:107:GLU:OE2	1.77	0.85
1:C:433:PRO:O	1:C:435:VAL:N	2.09	0.85
1:D:63:LEU:HD21	1:D:65:LEU:HD21	1.56	0.85
1:F:83:ARG:HD2	1:F:131:ALA:HB2	1.58	0.85
1:F:61:HIS:CD2	1:F:88:GLN:HE22	1.94	0.85
1:A:285:TRP:HB2	1:A:314:TYR:HB2	1.57	0.85
1:E:206:PRO:HD2	1:E:209:GLN:HB2	1.59	0.85
1:F:135:ILE:HD11	1:F:140:TYR:OH	1.76	0.85
1:E:433:PRO:O	1:E:435:VAL:N	2.09	0.84
1:B:362:LYS:O	1:B:366:GLU:HG3	1.77	0.84
1:C:505:THR:HG23	1:D:185:ASP:OD1	1.77	0.84
1:E:72:ASP:OD1	1:E:144:GLU:HG3	1.77	0.84
1:C:254:GLN:HE22	1:C:334:GLN:HG2	1.40	0.84

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:285:TRP:HB2	1:D:314:TYR:HB2	1.57	0.84
1:B:146:GLU:O	1:B:150:ARG:HG3	1.78	0.84
1:B:205:LYS:NZ	1:B:392:ASN:HD21	1.75	0.83
1:D:105:VAL:O	1:D:109:LYS:HG3	1.79	0.83
1:D:502:VAL:HG23	1:D:503:THR:H	1.44	0.83
1:A:410:ASN:ND2	1:B:413:LEU:HD21	1.93	0.83
1:C:76:TRP:HE1	1:F:502:VAL:HG11	1.43	0.83
1:A:71:ARG:HH11	1:A:71:ARG:CB	1.91	0.82
1:A:171:PRO:HG3	1:A:180:MET:SD	2.20	0.82
1:A:504:PHE:HE1	1:E:151:ARG:NH2	1.76	0.82
1:D:327:ILE:HD13	1:D:327:ILE:N	1.94	0.82
1:A:146:GLU:O	1:A:150:ARG:HG3	1.78	0.82
1:E:466:ARG:HH11	1:E:466:ARG:HG3	1.44	0.82
1:F:319:LEU:H	1:F:319:LEU:HD12	1.43	0.82
1:C:97:ILE:CD1	1:C:131:ALA:HB3	2.09	0.82
1:F:13:PHE:HD1	1:F:14:PHE:N	1.77	0.82
1:F:433:PRO:O	1:F:435:VAL:N	2.12	0.82
1:D:483:THR:O	1:D:487:VAL:HG23	1.79	0.82
1:A:122:VAL:HG11	1:A:379:ALA:HB1	1.60	0.82
1:B:244:PRO:HG2	1:B:248:ASP:N	1.94	0.82
1:D:43:GLU:HB3	1:D:45:LYS:HG3	1.62	0.81
1:E:147:LYS:O	1:E:151:ARG:HG3	1.80	0.81
1:A:319:LEU:H	1:A:319:LEU:CD1	1.93	0.81
1:E:146:GLU:O	1:E:150:ARG:HG3	1.80	0.81
1:A:502:VAL:HG23	1:A:503:THR:H	1.44	0.81
1:C:325:ILE:HG22	1:C:347:ILE:CB	2.10	0.81
1:A:23:ARG:NE	1:A:483:THR:HG21	1.95	0.81
1:B:502:VAL:HG23	1:B:503:THR:H	1.43	0.81
1:F:350:GLU:HG2	1:F:355:PRO:HG3	1.62	0.81
1:A:318:ILE:HD12	1:A:319:LEU:N	1.96	0.81
1:C:86:HIS:HD2	1:C:116:THR:HG21	1.45	0.81
1:C:337:LYS:CE	1:C:359:GLU:HG3	2.09	0.81
1:F:94:LYS:HD3	1:F:126:PHE:CE1	2.15	0.81
1:A:505:THR:HG23	1:B:185:ASP:OD1	1.81	0.81
1:D:227:ILE:HD11	1:D:349:ALA:CB	2.10	0.81
1:E:264:MET:HE3	1:E:292:PRO:HA	1.61	0.81
1:F:50:ARG:HG3	1:F:50:ARG:O	1.79	0.81
1:F:398:TYR:HB2	1:F:449:GLU:HG3	1.63	0.81
1:C:339:ASN:HD22	1:C:340:ALA:N	1.80	0.80
1:B:172:ASP:O	1:B:174:SER:N	2.14	0.80
1:E:343:VAL:HG21	1:E:364:PHE:HE1	1.47	0.80

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:57:LYS:N	1:F:58:PRO:HD2	1.97	0.80
1:F:350:GLU:OE1	1:F:373:PRO:HA	1.80	0.80
1:A:264:MET:HE3	1:A:292:PRO:HA	1.64	0.80
1:A:503:THR:HG21	1:E:151:ARG:HD3	1.63	0.80
1:B:339:ASN:HD22	1:B:339:ASN:H	1.28	0.80
1:D:172:ASP:O	1:D:174:SER:N	2.15	0.80
1:C:77:GLU:HA	1:F:54:ARG:NH2	1.96	0.80
1:B:76:TRP:NE1	1:D:502:VAL:HG11	1.97	0.80
1:B:11:PRO:O	1:B:333:LYS:HE2	1.80	0.79
1:E:418:GLN:OE1	1:E:432:ILE:HA	1.82	0.79
1:E:61:HIS:HD2	1:E:88:GLN:HE22	1.29	0.79
1:F:340:ALA:HB3	1:F:341:PRO:HD3	1.64	0.79
1:A:34:GLU:HA	1:A:38:THR:HB	1.63	0.79
1:C:34:GLU:HA	1:C:38:THR:HB	1.63	0.79
1:D:324:ASP:HB2	1:D:325:ILE:HD13	1.64	0.79
1:C:486:TYR:O	1:C:490:ILE:HG12	1.81	0.79
1:D:38:THR:HG23	1:D:41:SER:HB3	1.64	0.79
1:D:326:LEU:HD12	1:D:348:ILE:CD1	2.13	0.79
1:E:243:THR:N	1:E:244:PRO:HD3	1.95	0.79
1:D:326:LEU:HD12	1:D:348:ILE:HD12	1.63	0.79
1:D:350:GLU:CD	1:D:482:ARG:HH22	1.90	0.79
1:A:143:ASN:HD21	1:C:70:ARG:HH22	1.29	0.79
1:E:400:ARG:HH11	1:E:400:ARG:HG3	1.48	0.79
1:F:350:GLU:OE2	1:F:355:PRO:HD2	1.83	0.79
1:A:86:HIS:HD2	1:A:116:THR:HG21	1.47	0.79
1:C:190:THR:HG22	1:C:191:ILE:N	1.97	0.79
1:A:281:ASP:HB2	1:A:306:LEU:HD11	1.62	0.78
1:B:243:THR:N	1:B:244:PRO:HD3	1.97	0.78
1:F:29:GLU:O	1:F:33:VAL:HG23	1.82	0.78
1:B:34:GLU:HA	1:B:38:THR:HB	1.64	0.78
1:D:37:ARG:HB2	1:D:37:ARG:NH1	1.97	0.78
1:A:38:THR:HG23	1:A:41:SER:HB3	1.66	0.78
1:E:400:ARG:HH11	1:E:400:ARG:CG	1.96	0.78
1:D:252:VAL:HG22	1:D:275:ILE:CG2	2.14	0.78
1:F:240:LEU:HB3	1:F:346:LYS:HD2	1.66	0.78
1:C:237:MET:HE1	1:C:347:ILE:HD11	1.65	0.78
1:F:418:GLN:HB2	1:F:433:PRO:HD2	1.66	0.78
1:A:168:VAL:HG13	1:A:202:VAL:HA	1.64	0.78
1:B:502:VAL:HG11	1:D:76:TRP:HE1	1.49	0.78
1:C:141:THR:HG23	1:C:144:GLU:CG	2.13	0.78
1:D:348:ILE:CB	1:D:371:VAL:HG22	2.14	0.78

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:179:GLU:O	1:F:183:ILE:HG13	1.84	0.78
1:A:76:TRP:NE1	1:E:502:VAL:HG11	1.98	0.77
1:B:69:ILE:HA	1:B:151:ARG:NH1	1.98	0.77
1:D:145:LEU:O	1:D:149:THR:HG23	1.85	0.77
1:A:61:HIS:CD2	1:A:88:GLN:HE22	2.03	0.77
1:C:378:ASN:C	1:C:378:ASN:HD22	1.93	0.77
1:F:253:VAL:HG13	1:F:277:VAL:HG13	1.66	0.77
1:F:355:PRO:HG2	1:F:356:THR:HG23	1.66	0.77
1:D:394:ASN:O	1:D:396:VAL:HG23	1.84	0.77
1:F:37:ARG:HB2	1:F:37:ARG:HH11	1.47	0.77
1:F:409:SER:O	1:F:413:LEU:HD23	1.84	0.77
1:A:284:ILE:HD12	1:A:305:ILE:HD12	1.67	0.77
1:A:427:LYS:HE2	1:A:427:LYS:HA	1.65	0.77
1:B:116:THR:HG22	1:B:128:GLY:HA3	1.67	0.77
1:F:61:HIS:HD2	1:F:88:GLN:NE2	1.82	0.77
1:F:285:TRP:CD1	1:F:287:PRO:HD3	2.20	0.77
1:A:352:ALA:O	1:A:355:PRO:HD3	1.85	0.77
1:D:327:ILE:HD13	1:D:327:ILE:H	1.50	0.77
1:E:502:VAL:HG23	1:E:503:THR:H	1.48	0.77
1:A:370:MET:HB2	1:A:479:LEU:HD23	1.67	0.77
1:A:440:PHE:CD2	1:B:412:HIS:HB3	2.20	0.77
1:D:116:THR:HG22	1:D:128:GLY:HA3	1.66	0.77
1:F:334:GLN:HE21	1:F:334:GLN:CA	1.95	0.77
1:D:337:LYS:HB3	1:D:337:LYS:NZ	1.98	0.77
1:F:23:ARG:HE	1:F:27:ILE:HD11	1.48	0.77
1:F:180:MET:HE3	1:F:202:VAL:HG21	1.65	0.77
1:F:180:MET:HE3	1:F:202:VAL:CG2	2.14	0.77
1:A:40:GLU:HG3	1:A:46:ARG:HH12	1.49	0.76
1:A:190:THR:HG22	1:A:191:ILE:N	2.00	0.76
1:E:47:ASN:O	1:E:50:ARG:HG2	1.86	0.76
1:E:340:ALA:HB3	1:E:341:PRO:HD3	1.66	0.76
1:C:254:GLN:OE1	1:C:319:LEU:HD11	1.85	0.76
1:C:502:VAL:HG11	1:F:76:TRP:NE1	1.99	0.76
1:A:281:ASP:HB3	1:A:306:LEU:HD21	1.65	0.76
1:B:99:TYR:OH	1:B:149:THR:HG22	1.86	0.76
1:F:69:ILE:HA	1:F:151:ARG:CZ	2.15	0.76
1:A:360:ALA:HB1	1:A:364:PHE:HE2	1.47	0.76
1:C:222:GLY:HA2	1:C:457:LEU:HD21	1.68	0.76
1:C:502:VAL:HG23	1:C:503:THR:H	1.50	0.76
1:D:223:VAL:HG13	1:D:377:LEU:HD21	1.68	0.76
1:D:323:CYS:O	1:D:345:ALA:HA	1.85	0.76

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:372:ILE:HG22	1:A:377:LEU:HB2	1.67	0.76
1:A:145:LEU:O	1:A:149:THR:HG23	1.85	0.76
1:B:180:MET:N	1:B:180:MET:HE3	2.01	0.76
1:E:71:ARG:HB3	1:E:71:ARG:NH1	2.01	0.76
1:B:293:LYS:HE2	1:B:293:LYS:HA	1.66	0.76
1:D:432:ILE:O	1:D:432:ILE:HG13	1.85	0.76
1:E:434:ILE:O	1:E:436:PRO:HD3	1.86	0.76
1:E:172:ASP:O	1:E:174:SER:N	2.19	0.75
1:F:343:VAL:HG21	1:F:364:PHE:CE1	2.21	0.75
1:B:104:SER:O	1:B:107:GLU:N	2.19	0.75
1:D:331:SER:HB2	1:D:334:GLN:OE1	1.86	0.75
1:F:28:VAL:HG22	1:F:487:VAL:HG13	1.68	0.75
1:F:93:CYS:HB2	1:F:167:ASP:OD1	1.86	0.75
1:A:340:ALA:HB3	1:A:341:PRO:HD3	1.69	0.75
1:B:34:GLU:HG3	1:B:35:ASP:OD2	1.86	0.75
1:B:154:MET:SD	1:B:190:THR:HG21	2.26	0.75
1:E:486:TYR:O	1:E:490:ILE:HG12	1.84	0.75
1:B:365:LEU:HD23	1:B:366:GLU:N	2.00	0.75
1:C:61:HIS:CD2	1:C:88:GLN:HE22	2.05	0.75
1:C:157:ALA:HB1	1:C:191:ILE:HG21	1.68	0.75
1:A:348:ILE:HD11	1:A:364:PHE:CE1	2.22	0.75
1:E:83:ARG:HG2	1:E:161:PHE:HD1	1.52	0.75
1:A:325:ILE:HG22	1:A:347:ILE:CG2	2.17	0.75
1:C:190:THR:HG22	1:C:191:ILE:H	1.52	0.75
1:D:320:GLU:HG3	1:D:342:ARG:HG2	1.69	0.75
1:C:78:VAL:H	1:F:54:ARG:HH22	1.33	0.75
1:D:23:ARG:HH11	1:D:23:ARG:HG3	1.49	0.75
1:A:122:VAL:HG11	1:A:379:ALA:CB	2.16	0.75
1:F:91:THR:CB	1:F:92:PRO:HD3	2.17	0.75
1:D:252:VAL:HG23	1:D:323:CYS:SG	2.26	0.74
1:F:363:ILE:O	1:F:367:ARG:HG2	1.86	0.74
1:B:325:ILE:HG22	1:B:347:ILE:CG2	2.17	0.74
1:D:29:GLU:O	1:D:33:VAL:HG23	1.86	0.74
1:D:501:GLY:N	1:D:505:THR:HA	2.02	0.74
1:E:501:GLY:N	1:E:505:THR:HA	2.02	0.74
1:B:505:THR:OXT	1:F:150:ARG:NH2	2.18	0.74
1:D:251:PHE:CB	1:D:325:ILE:HG12	2.18	0.74
1:A:363:ILE:HG23	1:A:367:ARG:HD3	1.69	0.74
1:D:252:VAL:HG22	1:D:275:ILE:HG23	1.70	0.74
1:D:337:LYS:HB3	1:D:337:LYS:HZ3	1.53	0.74
1:B:502:VAL:N	1:B:505:THR:HB	2.02	0.74

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:69:ILE:HA	1:C:151:ARG:NH1	2.03	0.74
1:E:86:HIS:HD2	1:E:116:THR:HG21	1.53	0.74
1:A:57:LYS:HB3	1:A:58:PRO:CD	2.18	0.73
1:B:52:ILE:HD12	1:B:497:TYR:HB3	1.70	0.73
1:E:96:GLY:O	1:E:130:LYS:HD2	1.89	0.73
1:F:13:PHE:CZ	1:F:107:GLU:HA	2.22	0.73
1:F:34:GLU:HA	1:F:38:THR:HB	1.69	0.73
1:F:284:ILE:HG23	1:F:311:ALA:HB1	1.70	0.73
1:A:336:THR:HG22	1:A:357:THR:HG21	1.70	0.73
1:F:501:GLY:N	1:F:505:THR:HA	2.03	0.73
1:E:190:THR:CG2	1:E:191:ILE:N	2.48	0.73
1:C:242:MET:HE1	1:C:324:ASP:OD2	1.88	0.73
1:D:275:ILE:HG23	1:D:276:ALA:H	1.53	0.73
1:E:418:GLN:CB	1:E:433:PRO:HD2	2.18	0.73
1:B:483:THR:O	1:B:487:VAL:HG23	1.88	0.73
1:F:154:MET:SD	1:F:190:THR:HG21	2.28	0.73
1:A:13:PHE:HD1	1:A:14:PHE:N	1.86	0.73
1:C:38:THR:HG23	1:C:41:SER:HB3	1.69	0.73
1:C:436:PRO:HB3	1:C:440:PHE:HD1	1.53	0.73
1:E:37:ARG:HB2	1:E:37:ARG:HH11	1.53	0.73
1:E:480:ASP:OD1	1:E:483:THR:HG22	1.89	0.73
1:B:259:VAL:O	1:B:263:SER:HB2	1.88	0.73
1:C:79:ILE:HD12	1:C:135:ILE:HD11	1.70	0.73
1:D:264:MET:CE	1:D:292:PRO:HA	2.19	0.73
1:E:116:THR:CG2	1:E:128:GLY:H	1.89	0.73
1:F:135:ILE:HD11	1:F:140:TYR:CZ	2.24	0.73
1:F:223:VAL:HG11	1:F:263:SER:OG	1.88	0.73
1:C:502:VAL:HG11	1:F:76:TRP:HE1	1.53	0.72
1:D:360:ALA:O	1:D:364:PHE:CD2	2.42	0.72
1:E:335:LEU:HB2	1:E:356:THR:HG22	1.71	0.72
1:F:243:THR:N	1:F:244:PRO:CD	2.50	0.72
1:A:10:ASP:HB2	1:A:333:LYS:CE	2.15	0.72
1:A:348:ILE:HB	1:A:371:VAL:HG22	1.71	0.72
1:A:386:TYR:OH	1:B:396:VAL:HG13	1.89	0.72
1:E:23:ARG:HH11	1:E:23:ARG:HG3	1.52	0.72
1:F:251:PHE:HB3	1:F:325:ILE:CG1	2.16	0.72
1:B:86:HIS:HD2	1:B:116:THR:HG21	1.53	0.72
1:D:350:GLU:CD	1:D:482:ARG:NH2	2.48	0.72
1:C:71:ARG:HH11	1:C:71:ARG:CB	1.99	0.72
1:F:307:GLY:O	1:F:309:PRO:HD3	1.90	0.72
1:B:500:ALA:C	1:B:505:THR:HA	2.14	0.72

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:94:LYS:HB2	1:D:126:PHE:CD1	2.25	0.72
1:E:154:MET:SD	1:E:190:THR:HG21	2.28	0.72
1:E:339:ASN:HD22	1:E:339:ASN:H	1.35	0.72
1:F:432:ILE:N	1:F:432:ILE:HD13	2.05	0.72
1:A:150:ARG:NH1	1:F:505:THR:OXT	2.23	0.72
1:B:319:LEU:HD12	1:B:319:LEU:N	2.03	0.72
1:D:37:ARG:HD3	1:D:37:ARG:C	2.13	0.72
1:F:334:GLN:HA	1:F:334:GLN:NE2	1.99	0.72
1:A:333:LYS:HA	1:A:355:PRO:O	1.89	0.72
1:F:57:LYS:O	1:F:86:HIS:HE1	1.72	0.72
1:F:501:GLY:CA	1:F:505:THR:HA	2.20	0.72
1:A:254:GLN:HB2	1:A:318:ILE:HD11	1.72	0.72
1:C:501:GLY:CA	1:C:505:THR:HA	2.20	0.72
1:D:99:TYR:HH	1:D:149:THR:HG22	1.55	0.72
1:B:309:PRO:O	1:B:310:LYS:HB2	1.90	0.72
1:D:304:SER:HB3	1:D:306:LEU:HD13	1.72	0.72
1:A:69:ILE:HG12	1:A:79:ILE:HD11	1.72	0.71
1:A:427:LYS:HG3	1:A:428:HIS:H	1.54	0.71
1:B:339:ASN:H	1:B:339:ASN:ND2	1.88	0.71
1:B:416:SER:O	1:B:420:SER:HB2	1.90	0.71
1:B:480:ASP:OD1	1:B:483:THR:HG23	1.91	0.71
1:F:243:THR:H	1:F:244:PRO:HD3	1.54	0.71
1:A:319:LEU:HD12	1:A:319:LEU:N	2.06	0.71
1:A:359:GLU:HA	1:A:362:LYS:HD3	1.72	0.71
1:B:151:ARG:HD3	1:D:503:THR:HG21	1.70	0.71
1:D:415:MET:HE1	1:D:419:GLU:HG3	1.72	0.71
1:F:427:LYS:HZ1	1:F:430:GLY:HA2	1.54	0.71
1:E:13:PHE:HD1	1:E:14:PHE:N	1.88	0.71
1:F:500:ALA:C	1:F:505:THR:HA	2.15	0.71
1:C:76:TRP:NE1	1:F:502:VAL:HG11	2.06	0.71
1:B:221:ARG:HG2	1:B:225:HIS:HE1	1.56	0.71
1:B:319:LEU:CD1	1:B:319:LEU:H	2.04	0.71
1:C:172:ASP:O	1:C:174:SER:N	2.23	0.71
1:A:378:ASN:HD22	1:A:378:ASN:H	1.38	0.71
1:A:501:GLY:N	1:A:505:THR:HA	2.06	0.70
1:C:168:VAL:HG13	1:C:202:VAL:HA	1.72	0.70
1:C:180:MET:HE2	1:C:183:ILE:HD12	1.72	0.70
1:C:264:MET:HE3	1:C:292:PRO:HG3	1.71	0.70
1:C:436:PRO:HA	1:D:416:SER:HB3	1.73	0.70
1:C:501:GLY:N	1:C:505:THR:HA	2.06	0.70
1:C:404:LYS:NZ	1:C:407:ARG:HH21	1.90	0.70

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:158:LYS:HD3	1:F:193:HIS:CE1	2.26	0.70
1:A:72:ASP:OD1	1:A:144:GLU:HG3	1.91	0.70
1:A:150:ARG:NH2	1:F:505:THR:OXT	2.23	0.70
1:B:143:ASN:HD21	1:E:70:ARG:HH12	1.37	0.70
1:A:154:MET:SD	1:A:190:THR:HG21	2.32	0.70
1:C:77:GLU:HA	1:F:54:ARG:HH22	1.55	0.70
1:D:275:ILE:HG23	1:D:276:ALA:N	2.06	0.70
1:D:372:ILE:HG22	1:D:377:LEU:HB2	1.73	0.70
1:E:398:TYR:HB2	1:E:449:GLU:HG3	1.73	0.70
1:E:462:GLU:O	1:E:463:ALA:C	2.31	0.70
1:A:279:GLU:HG3	1:A:305:ILE:HG12	1.73	0.70
1:B:248:ASP:OD2	1:B:249:LYS:HG3	1.90	0.70
1:B:378:ASN:H	1:B:378:ASN:HD22	1.38	0.70
1:C:393:LEU:O	1:C:395:HIS:HD2	1.74	0.70
1:F:144:GLU:O	1:F:148:ILE:HG13	1.91	0.70
1:B:104:SER:O	1:B:106:ASP:N	2.24	0.70
1:C:502:VAL:N	1:C:505:THR:HB	2.06	0.70
1:F:176:GLY:O	1:F:180:MET:HG2	1.90	0.70
1:F:237:MET:HE1	1:F:347:ILE:HD11	1.71	0.70
1:C:243:THR:N	1:C:244:PRO:CD	2.54	0.70
1:E:13:PHE:HD1	1:E:14:PHE:H	1.38	0.70
1:C:205:LYS:HD2	1:C:209:GLN:O	1.91	0.70
1:D:94:LYS:HD3	1:D:126:PHE:CE1	2.27	0.70
1:D:325:ILE:HD13	1:D:325:ILE:N	2.05	0.70
1:E:59:CYS:SG	1:E:109:LYS:O	2.50	0.70
1:E:428:HIS:CD2	1:E:428:HIS:N	2.60	0.70
1:A:374:ASP:O	1:A:378:ASN:ND2	2.25	0.69
1:B:93:CYS:HB2	1:B:167:ASP:OD1	1.91	0.69
1:C:350:GLU:CD	1:C:482:ARG:HH22	1.99	0.69
1:D:325:ILE:CG2	1:D:347:ILE:HB	2.20	0.69
1:F:256:PHE:CE2	1:F:295:LEU:HG	2.26	0.69
1:B:51:GLY:HA2	1:B:54:ARG:HG3	1.72	0.69
1:E:61:HIS:CD2	1:E:88:GLN:HE22	2.10	0.69
1:A:427:LYS:HG3	1:A:428:HIS:N	2.06	0.69
1:D:243:THR:H	1:D:244:PRO:HD3	1.55	0.69
1:F:13:PHE:CD1	1:F:14:PHE:N	2.58	0.69
1:F:284:ILE:HG22	1:F:285:TRP:N	2.08	0.69
1:A:343:VAL:HG21	1:A:364:PHE:HE1	1.58	0.69
1:B:116:THR:CG2	1:B:128:GLY:H	2.04	0.69
1:B:440:PHE:HE2	1:B:444:ILE:HD11	1.57	0.69
1:D:34:GLU:HA	1:D:38:THR:CB	2.23	0.69

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:190:THR:HG22	1:D:191:ILE:N	2.08	0.69
1:E:221:ARG:HE	1:E:454:HIS:CE1	2.10	0.69
1:F:68:PRO:O	1:F:151:ARG:NH1	2.25	0.69
1:B:335:LEU:CD1	1:B:348:ILE:HD13	2.23	0.69
1:A:240:LEU:HA	1:A:346:LYS:NZ	2.08	0.69
1:A:251:PHE:CB	1:A:325:ILE:HG13	2.17	0.69
1:C:12:ASN:ND2	1:C:14:PHE:HB3	2.08	0.69
1:C:28:VAL:HG13	1:C:32:LEU:HD22	1.75	0.69
1:C:136:ASN:OD1	1:C:138:LYS:HB2	1.92	0.69
1:D:418:GLN:HB2	1:D:433:PRO:HD2	1.73	0.69
1:E:122:VAL:HG23	1:E:124:VAL:HG23	1.73	0.69
1:A:461:MET:HA	1:A:461:MET:HE3	1.74	0.69
1:F:400:ARG:O	1:F:400:ARG:HD2	1.92	0.69
1:A:57:LYS:HB3	1:A:58:PRO:HD3	1.74	0.69
1:A:64:SER:HB2	1:E:62:VAL:CG1	2.23	0.69
1:D:61:HIS:HD2	1:D:88:GLN:HE22	1.37	0.69
1:E:252:VAL:HG22	1:E:275:ILE:HG22	1.73	0.69
1:A:76:TRP:HZ3	1:E:49:VAL:HG23	1.58	0.68
1:A:418:GLN:HB2	1:A:433:PRO:HD2	1.74	0.68
1:B:264:MET:HG2	1:B:292:PRO:HG3	1.75	0.68
1:D:281:ASP:HB2	1:D:306:LEU:HD11	1.75	0.68
1:A:281:ASP:CB	1:A:306:LEU:HD21	2.23	0.68
1:B:62:VAL:HG11	1:B:109:LYS:NZ	2.07	0.68
1:C:243:THR:HG23	1:C:243:THR:O	1.93	0.68
1:C:501:GLY:HA3	1:C:504:PHE:O	1.92	0.68
1:E:367:ARG:HB3	1:E:367:ARG:HH11	1.56	0.68
1:A:243:THR:N	1:A:244:PRO:CD	2.56	0.68
1:E:339:ASN:H	1:E:339:ASN:ND2	1.89	0.68
1:D:325:ILE:HD13	1:D:325:ILE:H	1.59	0.68
1:E:362:LYS:O	1:E:366:GLU:HG3	1.93	0.68
1:C:460:THR:HG23	1:D:400:ARG:HH21	1.58	0.68
1:D:264:MET:HE3	1:D:292:PRO:HA	1.75	0.68
1:E:336:THR:N	1:E:339:ASN:HD21	1.89	0.68
1:F:335:LEU:HB2	1:F:356:THR:HG22	1.76	0.68
1:A:230:PHE:CD2	1:A:469:MET:HE2	2.28	0.68
1:C:116:THR:HG22	1:C:128:GLY:CA	2.22	0.68
1:D:263:SER:O	1:D:267:LEU:HD23	1.94	0.68
1:F:348:ILE:HB	1:F:371:VAL:HG22	1.75	0.68
1:A:133:VAL:O	1:A:135:ILE:N	2.26	0.68
1:D:242:MET:HA	1:D:244:PRO:HG3	1.76	0.68
1:D:500:ALA:C	1:D:505:THR:HA	2.19	0.68

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:34:GLU:HA	1:E:38:THR:CB	2.22	0.68
1:A:337:LYS:HE3	1:A:359:GLU:HG3	1.75	0.68
1:C:436:PRO:HB3	1:C:440:PHE:CD1	2.28	0.68
1:E:153:THR:OG1	1:E:183:ILE:HG23	1.93	0.68
1:E:281:ASP:HB2	1:E:306:LEU:HD11	1.75	0.68
1:A:427:LYS:HG2	1:A:430:GLY:HA3	1.76	0.68
1:B:10:ASP:O	1:B:10:ASP:OD2	2.12	0.68
1:F:317:SER:HB2	1:F:319:LEU:HD13	1.75	0.68
1:B:23:ARG:HE	1:B:483:THR:HG21	1.59	0.67
1:C:29:GLU:O	1:C:33:VAL:HG23	1.94	0.67
1:D:332:GLU:HG2	1:D:333:LYS:HG2	1.74	0.67
1:F:38:THR:O	1:F:38:THR:HG22	1.93	0.67
1:A:221:ARG:O	1:A:224:PHE:HB3	1.95	0.67
1:B:205:LYS:HZ1	1:B:392:ASN:ND2	1.93	0.67
1:C:319:LEU:HD23	1:C:335:LEU:HD23	1.76	0.67
1:D:28:VAL:HG22	1:D:487:VAL:HG13	1.75	0.67
1:F:90:ARG:HG3	1:F:125:PRO:C	2.20	0.67
1:F:314:TYR:HE2	1:F:318:ILE:HA	1.59	0.67
1:F:427:LYS:HG2	1:F:430:GLY:HA3	1.77	0.67
1:B:427:LYS:HG3	1:B:428:HIS:H	1.58	0.67
1:D:91:THR:HB	1:D:92:PRO:CD	2.24	0.67
1:F:285:TRP:HB2	1:F:314:TYR:HB2	1.76	0.67
1:A:14:PHE:O	1:A:18:GLU:HB2	1.94	0.67
1:A:332:GLU:HG2	1:A:333:LYS:HG2	1.74	0.67
1:B:122:VAL:HB	1:B:460:THR:HG21	1.75	0.67
1:B:319:LEU:HD12	1:B:319:LEU:H	1.59	0.67
1:B:103:VAL:HA	1:B:107:GLU:OE2	1.94	0.67
1:B:190:THR:CG2	1:B:191:ILE:N	2.54	0.67
1:B:264:MET:HE3	1:B:292:PRO:CA	2.23	0.67
1:B:501:GLY:N	1:B:505:THR:HA	2.09	0.67
1:E:37:ARG:HB2	1:E:37:ARG:CZ	2.24	0.67
1:B:332:GLU:HG2	1:B:333:LYS:HG2	1.77	0.67
1:E:34:GLU:CA	1:E:38:THR:HB	2.22	0.67
1:F:436:PRO:HB3	1:F:440:PHE:CD1	2.29	0.67
1:F:86:HIS:CD2	1:F:116:THR:CG2	2.76	0.67
1:F:91:THR:HB	1:F:92:PRO:CD	2.24	0.67
1:F:436:PRO:HB3	1:F:440:PHE:HD1	1.60	0.67
1:B:146:GLU:HA	1:B:182:TRP:CE3	2.30	0.67
1:C:34:GLU:HA	1:C:38:THR:CB	2.24	0.67
1:C:439:GLU:H	1:C:439:GLU:CD	2.03	0.67
1:D:252:VAL:HG13	1:D:276:ALA:HB3	1.76	0.67

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:501:GLY:CA	1:D:505:THR:HA	2.25	0.67
1:A:436:PRO:HB3	1:A:440:PHE:HD1	1.60	0.66
1:A:464:SER:O	1:A:468:ILE:HG12	1.95	0.66
1:B:13:PHE:HD1	1:B:14:PHE:N	1.92	0.66
1:B:251:PHE:CB	1:B:325:ILE:HG13	2.25	0.66
1:B:372:ILE:HG21	1:B:377:LEU:HD13	1.77	0.66
1:D:433:PRO:O	1:D:435:VAL:N	2.28	0.66
1:F:319:LEU:HD23	1:F:335:LEU:HD23	1.77	0.66
1:F:431:THR:C	1:F:432:ILE:HD13	2.20	0.66
1:D:59:CYS:SG	1:D:109:LYS:O	2.45	0.66
1:D:327:ILE:CG2	1:D:349:ALA:HB3	2.26	0.66
1:E:33:VAL:O	1:E:34:GLU:O	2.14	0.66
1:F:172:ASP:O	1:F:174:SER:N	2.28	0.66
1:A:76:TRP:HE1	1:E:502:VAL:HG11	1.60	0.66
1:B:243:THR:HG23	1:B:243:THR:O	1.94	0.66
1:D:190:THR:HG23	1:F:190:THR:HG23	1.76	0.66
1:F:350:GLU:C	1:F:377:LEU:HD23	2.21	0.66
1:B:221:ARG:HG2	1:B:225:HIS:CE1	2.29	0.66
1:B:95:GLY:O	1:B:169:PRO:HA	1.95	0.66
1:B:169:PRO:HB2	1:B:202:VAL:HG23	1.75	0.66
1:C:374:ASP:OD2	1:C:375:LEU:N	2.28	0.66
1:B:38:THR:HG23	1:B:41:SER:HB3	1.76	0.66
1:A:69:ILE:HG12	1:A:79:ILE:CD1	2.26	0.66
1:A:243:THR:O	1:A:243:THR:HG23	1.95	0.66
1:C:279:GLU:HG3	1:C:305:ILE:HG12	1.77	0.66
1:E:501:GLY:CA	1:E:505:THR:HA	2.25	0.66
1:F:223:VAL:HG22	1:F:377:LEU:HG	1.77	0.66
1:F:326:LEU:HD12	1:F:348:ILE:HD12	1.76	0.66
1:B:374:ASP:O	1:B:378:ASN:ND2	2.29	0.66
1:D:336:THR:C	1:D:338:SER:H	2.03	0.66
1:D:360:ALA:O	1:D:364:PHE:HD2	1.78	0.66
1:D:502:VAL:N	1:D:505:THR:HB	2.11	0.66
1:A:78:VAL:HG23	1:A:78:VAL:O	1.95	0.66
1:A:367:ARG:O	1:A:369:ILE:HG12	1.95	0.66
1:D:100:SER:O	1:D:103:VAL:HG13	1.95	0.66
1:D:103:VAL:HG23	1:D:134:LYS:HE2	1.76	0.66
1:A:97:ILE:HD13	1:A:131:ALA:HB3	1.78	0.65
1:C:50:ARG:HD2	1:C:50:ARG:O	1.96	0.65
1:C:221:ARG:HH11	1:C:221:ARG:CG	2.08	0.65
1:D:345:ALA:O	1:D:369:ILE:HD12	1.96	0.65
1:D:418:GLN:OE1	1:D:434:ILE:HG12	1.97	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:206:PRO:HD2	1:E:209:GLN:CB	2.25	0.65
1:C:154:MET:SD	1:C:190:THR:HG21	2.36	0.65
1:A:125:PRO:O	1:A:126:PHE:CD2	2.49	0.65
1:C:50:ARG:HD2	1:C:50:ARG:C	2.22	0.65
1:C:327:ILE:H	1:C:327:ILE:HD13	1.61	0.65
1:E:33:VAL:O	1:E:37:ARG:HG3	1.97	0.65
1:F:259:VAL:O	1:F:263:SER:HB2	1.97	0.65
1:F:427:LYS:NZ	1:F:430:GLY:HA2	2.10	0.65
1:F:475:TYR:O	1:F:477:LEU:HD23	1.96	0.65
1:A:64:SER:HB2	1:E:62:VAL:HG12	1.77	0.65
1:A:146:GLU:HG2	1:A:150:ARG:HD2	1.76	0.65
1:B:59:CYS:SG	1:B:109:LYS:O	2.45	0.65
1:B:145:LEU:O	1:B:149:THR:HG23	1.97	0.65
1:C:505:THR:O	1:D:185:ASP:CG	2.40	0.65
1:E:116:THR:HG22	1:E:128:GLY:CA	2.26	0.65
1:A:47:ASN:HD21	1:A:50:ARG:CZ	2.09	0.65
1:F:239:ILE:HG22	1:F:239:ILE:O	1.97	0.65
1:F:285:TRP:HB2	1:F:314:TYR:CB	2.27	0.65
1:C:202:VAL:O	1:C:205:LYS:NZ	2.29	0.65
1:D:390:LEU:HD13	1:E:396:VAL:HG21	1.78	0.65
1:E:480:ASP:CG	1:E:483:THR:HG22	2.21	0.65
1:F:327:ILE:CG2	1:F:349:ALA:HB3	2.21	0.65
1:F:376:TYR:OH	1:F:465:ALA:HB2	1.96	0.65
1:A:17:VAL:CG2	1:A:114:LEU:HD13	2.27	0.65
1:E:243:THR:HG23	1:E:243:THR:O	1.95	0.65
1:F:63:LEU:HD22	1:F:161:PHE:CE2	2.32	0.65
1:D:362:LYS:O	1:D:366:GLU:HG3	1.97	0.65
1:F:217:SER:HA	1:F:262:HIS:CD2	2.31	0.65
1:F:261:LEU:HD12	1:F:261:LEU:O	1.97	0.65
1:B:231:ILE:HD13	1:B:237:MET:SD	2.36	0.65
1:E:67:PHE:CE1	1:E:79:ILE:HB	2.32	0.65
1:F:177:GLU:HB2	1:F:206:PRO:HG3	1.77	0.65
1:A:79:ILE:HD12	1:A:79:ILE:N	2.11	0.65
1:A:179:GLU:HA	1:A:182:TRP:CE3	2.31	0.65
1:B:332:GLU:O	1:B:334:GLN:NE2	2.30	0.65
1:C:404:LYS:HZ3	1:C:407:ARG:HH21	1.45	0.65
1:E:55:ILE:O	1:E:58:PRO:HD2	1.98	0.65
1:B:501:GLY:CA	1:B:505:THR:HA	2.27	0.64
1:C:43:GLU:HB3	1:C:45:LYS:HG3	1.78	0.64
1:C:390:LEU:O	1:C:393:LEU:N	2.29	0.64
1:E:500:ALA:HB1	1:E:505:THR:C	2.23	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:49:VAL:O	1:F:52:ILE:HG12	1.96	0.64
1:F:362:LYS:O	1:F:366:GLU:HG3	1.97	0.64
1:A:317:SER:HB2	1:A:319:LEU:HD13	1.79	0.64
1:A:500:ALA:CA	1:A:505:THR:O	2.45	0.64
1:C:251:PHE:HB3	1:C:325:ILE:HG13	1.79	0.64
1:E:325:ILE:HG23	1:E:347:ILE:CG2	2.27	0.64
1:E:502:VAL:N	1:E:505:THR:HB	2.13	0.64
1:A:146:GLU:HG2	1:A:150:ARG:HH11	1.60	0.64
1:B:93:CYS:CB	1:B:167:ASP:OD1	2.45	0.64
1:B:418:GLN:CB	1:B:433:PRO:HD2	2.23	0.64
1:D:404:LYS:CE	1:D:407:ARG:HH21	2.10	0.64
1:A:72:ASP:CG	1:A:141:THR:HG21	2.23	0.64
1:A:502:VAL:HG23	1:A:503:THR:N	2.13	0.64
1:C:92:PRO:HG2	1:C:389:TRP:CZ2	2.32	0.64
1:D:256:PHE:HE2	1:D:264:MET:HE2	1.62	0.64
1:D:320:GLU:O	1:D:321:ALA:O	2.14	0.64
1:A:292:PRO:O	1:A:296:GLU:HB2	1.98	0.64
1:E:435:VAL:O	1:E:435:VAL:HG13	1.98	0.64
1:F:418:GLN:CB	1:F:433:PRO:HD2	2.28	0.64
1:A:343:VAL:HG21	1:A:364:PHE:CE1	2.32	0.64
1:B:28:VAL:HG23	1:B:487:VAL:HG13	1.80	0.64
1:B:205:LYS:HZ3	1:B:392:ASN:HD21	1.44	0.64
1:B:264:MET:CE	1:B:292:PRO:HA	2.28	0.64
1:C:97:ILE:HD12	1:C:131:ALA:HB3	1.78	0.64
1:D:227:ILE:HD13	1:D:372:ILE:HD12	1.80	0.64
1:D:350:GLU:OE1	1:D:482:ARG:NH2	2.31	0.64
1:E:349:ALA:HB1	1:E:377:LEU:HD21	1.79	0.64
1:A:249:LYS:HD2	1:A:271:GLY:O	1.98	0.64
1:A:327:ILE:HG23	1:A:349:ALA:HB3	1.77	0.64
1:C:76:TRP:HE1	1:F:502:VAL:CG1	2.09	0.64
1:C:285:TRP:CB	1:C:314:TYR:HB2	2.27	0.64
1:F:205:LYS:NZ	1:F:392:ASN:HD21	1.95	0.64
1:A:133:VAL:O	1:A:135:ILE:HB	1.97	0.64
1:A:259:VAL:HG13	1:A:260:GLY:N	2.13	0.64
1:B:150:ARG:O	1:B:153:THR:N	2.30	0.64
1:C:151:ARG:CD	1:F:503:THR:HG21	2.27	0.64
1:D:243:THR:N	1:D:244:PRO:CD	2.54	0.64
1:F:205:LYS:HZ1	1:F:392:ASN:ND2	1.96	0.64
1:A:205:LYS:NZ	1:A:392:ASN:HD21	1.96	0.64
1:B:77:GLU:HA	1:D:54:ARG:NH1	2.12	0.64
1:C:79:ILE:HD12	1:C:135:ILE:CD1	2.28	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:330:ALA:O	1:C:331:SER:O	2.15	0.64
1:C:474:LYS:HD3	1:C:475:TYR:CE2	2.33	0.64
1:E:242:MET:HE1	1:E:324:ASP:OD2	1.97	0.64
1:E:343:VAL:HG21	1:E:364:PHE:CE1	2.32	0.64
1:F:253:VAL:HA	1:F:327:ILE:HG13	1.80	0.64
1:A:240:LEU:HB3	1:A:346:LYS:HD2	1.79	0.64
1:A:427:LYS:NZ	1:A:428:HIS:H	1.96	0.64
1:B:61:HIS:ND1	1:D:159:LYS:HE3	2.13	0.64
1:F:108:VAL:HG23	1:F:109:LYS:N	2.13	0.64
1:F:261:LEU:HD12	1:F:261:LEU:C	2.22	0.64
1:B:237:MET:HE2	1:B:237:MET:HA	1.81	0.63
1:C:229:ASN:HD21	1:C:462:GLU:HA	1.59	0.63
1:C:362:LYS:O	1:C:366:GLU:HG3	1.98	0.63
1:D:343:VAL:HG21	1:D:364:PHE:HE1	1.62	0.63
1:D:502:VAL:HG23	1:D:503:THR:N	2.11	0.63
1:C:95:GLY:O	1:C:169:PRO:HA	1.97	0.63
1:C:427:LYS:HG2	1:C:430:GLY:HA3	1.80	0.63
1:F:501:GLY:HA3	1:F:505:THR:HA	1.80	0.63
1:D:242:MET:O	1:D:243:THR:HG22	1.98	0.63
1:F:243:THR:HG23	1:F:243:THR:O	1.97	0.63
1:D:237:MET:HE1	1:D:347:ILE:HD11	1.80	0.63
1:D:411:TYR:O	1:D:415:MET:HB2	1.98	0.63
1:E:376:TYR:OH	1:E:465:ALA:HB2	1.98	0.63
1:A:205:LYS:NZ	1:A:392:ASN:ND2	2.46	0.63
1:A:295:LEU:HD11	1:A:305:ILE:HB	1.81	0.63
1:B:145:LEU:HA	1:B:148:ILE:HD12	1.80	0.63
1:B:204:GLY:HA2	1:B:215:ARG:HD2	1.79	0.63
1:B:295:LEU:HD11	1:B:305:ILE:HG22	1.79	0.63
1:B:393:LEU:O	1:B:395:HIS:CD2	2.51	0.63
1:A:205:LYS:HZ1	1:A:392:ASN:ND2	1.97	0.63
1:C:61:HIS:CD2	1:C:88:GLN:NE2	2.66	0.63
1:D:224:PHE:CD2	1:D:266:TYR:HB3	2.33	0.63
1:D:337:LYS:HG2	1:D:337:LYS:O	1.97	0.63
1:E:221:ARG:NE	1:E:454:HIS:CE1	2.67	0.63
1:A:285:TRP:O	1:A:286:ASN:HB2	1.98	0.63
1:A:394:ASN:O	1:A:396:VAL:HG23	1.98	0.63
1:B:427:LYS:HG2	1:B:430:GLY:HA3	1.79	0.63
1:C:284:ILE:HG13	1:C:311:ALA:CB	2.24	0.63
1:C:340:ALA:HB3	1:C:341:PRO:HD3	1.79	0.63
1:D:433:PRO:O	1:D:434:ILE:C	2.41	0.63
1:E:72:ASP:CG	1:E:141:THR:HG21	2.23	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:440:PHE:O	1:E:444:ILE:HG13	1.99	0.63
1:F:249:LYS:HD2	1:F:271:GLY:O	1.98	0.63
1:A:47:ASN:ND2	1:A:50:ARG:CZ	2.61	0.63
1:C:393:LEU:O	1:C:395:HIS:CD2	2.52	0.63
1:F:483:THR:O	1:F:487:VAL:HG23	1.99	0.63
1:A:172:ASP:O	1:A:174:SER:N	2.32	0.63
1:B:261:LEU:C	1:B:261:LEU:HD12	2.24	0.63
1:D:16:MET:HE1	1:D:333:LYS:HE3	1.81	0.63
1:D:205:LYS:HZ1	1:D:392:ASN:HD21	1.45	0.63
1:D:284:ILE:HG23	1:D:311:ALA:CB	2.25	0.63
1:E:73:ASP:O	1:E:73:ASP:OD1	2.17	0.63
1:F:285:TRP:NE1	1:F:287:PRO:HD3	2.13	0.63
1:B:168:VAL:HG13	1:B:201:CYS:C	2.25	0.62
1:B:391:LYS:HD2	1:B:449:GLU:OE2	1.98	0.62
1:B:477:LEU:HD12	1:B:484:ALA:HB2	1.81	0.62
1:C:223:VAL:HA	1:C:377:LEU:CD1	2.29	0.62
1:D:133:VAL:O	1:D:133:VAL:HG12	1.99	0.62
1:E:168:VAL:HG13	1:E:201:CYS:C	2.24	0.62
1:A:259:VAL:HG13	1:A:260:GLY:H	1.65	0.62
1:F:51:GLY:HA2	1:F:54:ARG:HG2	1.81	0.62
1:B:146:GLU:HA	1:B:182:TRP:CZ3	2.33	0.62
1:C:223:VAL:HA	1:C:377:LEU:HD11	1.82	0.62
1:C:264:MET:HE3	1:C:292:PRO:HA	1.81	0.62
1:C:418:GLN:OE1	1:C:433:PRO:HD2	1.99	0.62
1:C:438:ALA:O	1:C:439:GLU:C	2.43	0.62
1:D:95:GLY:O	1:D:169:PRO:HA	2.00	0.62
1:E:336:THR:HA	1:E:357:THR:HG23	1.81	0.62
1:F:168:VAL:HG13	1:F:201:CYS:O	1.99	0.62
1:F:242:MET:O	1:F:243:THR:HG22	2.00	0.62
1:F:274:CYS:O	1:F:290:ILE:HD12	2.00	0.62
1:A:314:TYR:HE2	1:A:318:ILE:HA	1.65	0.62
1:B:243:THR:N	1:B:244:PRO:CD	2.63	0.62
1:B:284:ILE:HG23	1:B:311:ALA:HB1	1.81	0.62
1:C:221:ARG:HD2	1:C:225:HIS:CE1	2.35	0.62
1:D:370:MET:HG3	1:D:479:LEU:HB3	1.81	0.62
1:D:480:ASP:OD2	1:D:483:THR:HG23	2.00	0.62
1:A:304:SER:OG	1:A:305:ILE:N	2.25	0.62
1:B:90:ARG:HB3	1:B:125:PRO:O	1.99	0.62
1:D:281:ASP:HB3	1:D:306:LEU:HD21	1.80	0.62
1:E:73:ASP:O	1:E:75:SER:N	2.33	0.62
1:F:242:MET:HA	1:F:244:PRO:HG3	1.82	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:242:MET:HA	1:F:242:MET:HE2	1.81	0.62
1:A:224:PHE:CD1	1:A:225:HIS:N	2.68	0.62
1:A:325:ILE:HG22	1:A:347:ILE:HB	1.81	0.62
1:B:69:ILE:HG12	1:B:79:ILE:HD11	1.82	0.62
1:C:390:LEU:O	1:C:392:ASN:N	2.32	0.62
1:E:500:ALA:C	1:E:505:THR:HA	2.25	0.62
1:F:23:ARG:NE	1:F:27:ILE:HD11	2.12	0.62
1:F:350:GLU:HG2	1:F:355:PRO:CG	2.28	0.62
1:A:94:LYS:HD3	1:A:126:PHE:CE1	2.35	0.62
1:C:502:VAL:HG23	1:C:503:THR:N	2.14	0.62
1:D:21:PHE:CE2	1:D:57:LYS:HB2	2.34	0.62
1:D:63:LEU:HD22	1:D:161:PHE:CD2	2.35	0.62
1:F:238:SER:C	1:F:240:LEU:H	2.07	0.62
1:A:268:HIS:CD2	1:A:292:PRO:HD3	2.35	0.62
1:A:376:TYR:C	1:A:376:TYR:CD1	2.78	0.62
1:B:238:SER:O	1:B:241:GLY:N	2.31	0.62
1:C:57:LYS:HB3	1:C:58:PRO:HD3	1.80	0.62
1:D:86:HIS:CG	1:D:116:THR:HG21	2.35	0.62
1:D:116:THR:HG22	1:D:128:GLY:CA	2.29	0.62
1:B:54:ARG:NH1	1:B:54:ARG:HB3	2.15	0.62
1:D:443:ARG:HH11	1:D:443:ARG:HG3	1.63	0.62
1:E:248:ASP:OD2	1:E:249:LYS:HG3	1.99	0.62
1:F:202:VAL:HG22	1:F:203:THR:N	2.15	0.62
1:A:443:ARG:HH21	1:B:409:SER:CB	2.12	0.62
1:F:435:VAL:HG13	1:F:435:VAL:O	2.00	0.62
1:C:421:LEU:HD11	1:E:421:LEU:CD2	2.28	0.61
1:D:34:GLU:CA	1:D:38:THR:HB	2.29	0.61
1:E:264:MET:CE	1:E:292:PRO:HA	2.29	0.61
1:E:400:ARG:HG3	1:E:400:ARG:NH1	2.14	0.61
1:B:34:GLU:CA	1:B:38:THR:HB	2.31	0.61
1:D:34:GLU:O	1:D:38:THR:HB	2.00	0.61
1:D:52:ILE:O	1:D:56:ILE:HG13	1.99	0.61
1:D:205:LYS:NZ	1:D:392:ASN:HD21	1.98	0.61
1:D:239:ILE:O	1:D:239:ILE:HG22	1.99	0.61
1:F:23:ARG:O	1:F:27:ILE:HG13	2.00	0.61
1:A:57:LYS:O	1:A:86:HIS:HE1	1.83	0.61
1:A:501:GLY:CA	1:A:505:THR:HA	2.30	0.61
1:D:243:THR:O	1:D:243:THR:HG23	2.00	0.61
1:A:337:LYS:HE3	1:A:359:GLU:CD	2.25	0.61
1:B:404:LYS:HZ3	1:B:407:ARG:HH21	1.47	0.61
1:C:78:VAL:N	1:F:54:ARG:HH22	1.97	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:343:VAL:HG21	1:C:364:PHE:CE1	2.36	0.61
1:D:224:PHE:CD1	1:D:225:HIS:N	2.68	0.61
1:D:224:PHE:HD1	1:D:225:HIS:N	1.98	0.61
1:B:122:VAL:HB	1:B:460:THR:CG2	2.31	0.61
1:B:376:TYR:OH	1:B:465:ALA:HB2	2.00	0.61
1:D:376:TYR:C	1:D:376:TYR:CD1	2.78	0.61
1:F:330:ALA:O	1:F:331:SER:O	2.19	0.61
1:A:262:HIS:HA	1:A:265:ARG:HG3	1.83	0.61
1:A:284:ILE:CD1	1:A:305:ILE:HD12	2.29	0.61
1:C:37:ARG:NH2	1:C:49:VAL:HG11	2.00	0.61
1:C:242:MET:HA	1:C:244:PRO:HG3	1.81	0.61
1:E:21:PHE:CE2	1:E:57:LYS:HB2	2.36	0.61
1:A:91:THR:HB	1:A:92:PRO:CD	2.26	0.61
1:A:259:VAL:O	1:A:263:SER:HB2	2.00	0.61
1:B:318:ILE:HD13	1:B:318:ILE:H	1.64	0.61
1:C:334:GLN:CA	1:C:334:GLN:HE21	2.12	0.61
1:D:318:ILE:C	1:D:318:ILE:HD12	2.25	0.61
1:E:65:LEU:HD12	1:E:152:PHE:CE1	2.36	0.61
1:F:71:ARG:NH1	1:F:71:ARG:HB3	2.16	0.61
1:A:372:ILE:CG2	1:A:377:LEU:HB2	2.31	0.61
1:B:31:LYS:HG3	1:B:475:TYR:HE1	1.66	0.61
1:B:285:TRP:HB2	1:B:314:TYR:HB2	1.83	0.61
1:C:337:LYS:HE3	1:C:359:GLU:CG	2.18	0.61
1:D:238:SER:C	1:D:240:LEU:H	2.09	0.61
1:F:242:MET:HE2	1:F:244:PRO:CG	2.31	0.61
1:A:30:ASP:O	1:A:34:GLU:HG2	2.00	0.61
1:A:70:ARG:HH12	1:C:143:ASN:ND2	1.99	0.61
1:A:427:LYS:CG	1:A:430:GLY:H	2.14	0.61
1:B:179:GLU:O	1:B:183:ILE:HD13	2.00	0.61
1:C:505:THR:O	1:D:185:ASP:OD1	2.19	0.61
1:D:240:LEU:HD23	1:D:479:LEU:HD21	1.81	0.61
1:E:367:ARG:HB3	1:E:367:ARG:NH1	2.15	0.61
1:F:21:PHE:CE1	1:F:490:ILE:HD12	2.36	0.61
1:F:374:ASP:O	1:F:378:ASN:ND2	2.34	0.61
1:C:503:THR:HG21	1:F:151:ARG:CD	2.31	0.61
1:D:319:LEU:H	1:D:319:LEU:HD12	1.66	0.61
1:D:371:VAL:HG11	1:D:482:ARG:HH21	1.65	0.61
1:E:336:THR:H	1:E:339:ASN:ND2	1.95	0.61
1:A:323:CYS:O	1:A:345:ALA:HA	2.01	0.60
1:B:180:MET:HG2	1:B:203:THR:O	2.01	0.60
1:B:425:PHE:CD1	1:B:427:LYS:HB2	2.36	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:72:ASP:OD1	1:C:144:GLU:CG	2.49	0.60
1:C:325:ILE:HG22	1:C:347:ILE:CG2	2.31	0.60
1:D:54:ARG:O	1:D:58:PRO:HD2	2.01	0.60
1:F:268:HIS:CD2	1:F:292:PRO:HD3	2.36	0.60
1:A:248:ASP:OD2	1:A:249:LYS:HG3	2.02	0.60
1:D:421:LEU:CD2	1:E:421:LEU:HD11	2.31	0.60
1:E:168:VAL:HG13	1:E:201:CYS:O	2.02	0.60
1:D:12:ASN:HD21	1:D:14:PHE:HB3	1.66	0.60
1:D:443:ARG:HG3	1:D:443:ARG:NH1	2.17	0.60
1:E:243:THR:N	1:E:244:PRO:CD	2.64	0.60
1:E:375:LEU:HD23	1:E:485:ALA:HB1	1.83	0.60
1:F:285:TRP:CB	1:F:314:TYR:HB2	2.30	0.60
1:A:51:GLY:O	1:A:54:ARG:N	2.35	0.60
1:A:425:PHE:CD1	1:A:425:PHE:C	2.80	0.60
1:B:42:GLU:HB2	1:B:46:ARG:HH22	1.65	0.60
1:E:319:LEU:HD23	1:E:335:LEU:HD23	1.83	0.60
1:F:502:VAL:HG23	1:F:503:THR:H	1.65	0.60
1:A:143:ASN:ND2	1:C:70:ARG:HH22	1.99	0.60
1:A:346:LYS:O	1:A:347:ILE:HG13	2.00	0.60
1:C:261:LEU:HD12	1:C:261:LEU:O	2.01	0.60
1:D:193:HIS:CE1	1:F:158:LYS:HD3	2.36	0.60
1:D:343:VAL:HG21	1:D:364:PHE:CE1	2.36	0.60
1:D:348:ILE:HB	1:D:371:VAL:CG2	2.22	0.60
1:A:384:VAL:O	1:A:387:PHE:HB2	2.02	0.60
1:B:147:LYS:HE3	1:D:504:PHE:CZ	2.37	0.60
1:B:343:VAL:HG21	1:B:364:PHE:CE1	2.25	0.60
1:C:72:ASP:OD1	1:C:144:GLU:HG3	2.02	0.60
1:C:151:ARG:HD3	1:F:503:THR:HG21	1.84	0.60
1:C:263:SER:O	1:C:267:LEU:HD23	2.01	0.60
1:D:327:ILE:HG22	1:D:349:ALA:HB3	1.83	0.60
1:F:279:GLU:HG3	1:F:305:ILE:HG12	1.83	0.60
1:A:240:LEU:HA	1:A:346:LYS:HZ1	1.66	0.60
1:A:318:ILE:HD12	1:A:318:ILE:C	2.26	0.60
1:A:375:LEU:HD22	1:A:486:TYR:CE2	2.36	0.60
1:E:348:ILE:HB	1:E:371:VAL:HG22	1.84	0.60
1:E:466:ARG:HG3	1:E:466:ARG:NH1	2.15	0.60
1:B:242:MET:O	1:B:243:THR:HG22	2.00	0.60
1:B:256:PHE:HE2	1:B:264:MET:CE	2.14	0.60
1:C:83:ARG:CD	1:C:131:ALA:HB2	2.28	0.60
1:C:264:MET:HE3	1:C:292:PRO:CB	2.32	0.60
1:C:362:LYS:HA	1:C:362:LYS:HE3	1.84	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:32:LEU:HD11	1:D:494:PHE:CE2	2.37	0.60
1:D:342:ARG:HB2	1:D:342:ARG:HH11	1.67	0.60
1:F:339:ASN:HD22	1:F:339:ASN:C	2.09	0.60
1:D:133:VAL:O	1:D:135:ILE:N	2.34	0.60
1:F:56:ILE:HD13	1:F:493:VAL:CG1	2.32	0.60
1:A:473:MET:O	1:A:476:ASN:N	2.29	0.60
1:D:410:ASN:ND2	1:E:413:LEU:HD21	2.17	0.60
1:E:316:GLY:O	1:E:317:SER:C	2.45	0.60
1:A:168:VAL:HG13	1:A:202:VAL:CA	2.31	0.59
1:A:411:TYR:O	1:A:415:MET:HB2	2.02	0.59
1:B:71:ARG:HB3	1:B:71:ARG:NH1	2.17	0.59
1:C:264:MET:CE	1:C:292:PRO:HA	2.32	0.59
1:C:409:SER:O	1:C:410:ASN:C	2.44	0.59
1:D:370:MET:HB2	1:D:479:LEU:HD23	1.84	0.59
1:A:337:LYS:HE3	1:A:359:GLU:CG	2.31	0.59
1:C:13:PHE:O	1:C:17:VAL:HG23	2.01	0.59
1:C:312:LYS:HG3	1:C:312:LYS:O	2.01	0.59
1:C:437:THR:HG23	1:D:416:SER:HA	1.83	0.59
1:C:465:ALA:O	1:C:469:MET:HG3	2.02	0.59
1:C:501:GLY:HA3	1:C:505:THR:HA	1.84	0.59
1:D:500:ALA:HB1	1:D:505:THR:OG1	2.03	0.59
1:A:285:TRP:CB	1:A:314:TYR:HB2	2.32	0.59
1:C:350:GLU:OE2	1:C:356:THR:HG23	2.01	0.59
1:D:382:VAL:O	1:D:382:VAL:HG12	2.02	0.59
1:A:483:THR:O	1:A:487:VAL:HG23	2.02	0.59
1:B:60:ASN:HB3	1:B:61:HIS:HD2	1.65	0.59
1:B:168:VAL:HG13	1:B:201:CYS:O	2.02	0.59
1:E:285:TRP:HB2	1:E:314:TYR:HB2	1.85	0.59
1:B:319:LEU:N	1:B:319:LEU:CD1	2.64	0.59
1:B:372:ILE:CG2	1:B:377:LEU:HD13	2.32	0.59
1:D:240:LEU:HD12	1:D:242:MET:HG3	1.84	0.59
1:D:312:LYS:HD2	1:D:313:PRO:HD2	1.84	0.59
1:E:339:ASN:HD22	1:E:339:ASN:N	1.94	0.59
1:A:343:VAL:HG22	1:A:367:ARG:NH2	2.17	0.59
1:A:378:ASN:HD22	1:A:378:ASN:N	1.95	0.59
1:B:62:VAL:HG11	1:B:109:LYS:HZ2	1.68	0.59
1:B:249:LYS:HD2	1:B:271:GLY:O	2.02	0.59
1:B:252:VAL:HG23	1:B:323:CYS:SG	2.42	0.59
1:B:367:ARG:O	1:B:369:ILE:HG12	2.03	0.59
1:B:502:VAL:HG23	1:B:503:THR:N	2.17	0.59
1:C:61:HIS:HE1	1:F:155:GLU:HG3	1.68	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:278:GLY:HA3	1:C:318:ILE:HD13	1.85	0.59
1:C:421:LEU:HD11	1:E:421:LEU:HD21	1.83	0.59
1:D:136:ASN:O	1:D:138:LYS:N	2.36	0.59
1:D:238:SER:O	1:D:241:GLY:N	2.29	0.59
1:D:251:PHE:HB3	1:D:325:ILE:CG1	2.31	0.59
1:E:110:ALA:O	1:E:113:SER:HB3	2.03	0.59
1:F:238:SER:O	1:F:241:GLY:N	2.25	0.59
1:A:190:THR:HG22	1:A:191:ILE:H	1.65	0.59
1:B:14:PHE:O	1:B:18:GLU:HB2	2.02	0.59
1:C:98:ARG:NH2	1:C:107:GLU:OE1	2.36	0.59
1:C:248:ASP:OD2	1:C:249:LYS:HG3	2.03	0.59
1:B:30:ASP:O	1:B:34:GLU:HG2	2.03	0.59
1:B:58:PRO:O	1:B:59:CYS:C	2.46	0.59
1:B:94:LYS:HB2	1:B:126:PHE:CD1	2.37	0.59
1:B:151:ARG:CD	1:D:503:THR:HG21	2.33	0.59
1:E:91:THR:CB	1:E:92:PRO:HD3	2.33	0.59
1:E:424:LYS:NZ	1:E:424:LYS:HB3	2.16	0.59
1:F:57:LYS:N	1:F:58:PRO:CD	2.66	0.59
1:D:169:PRO:HB2	1:D:202:VAL:HG23	1.85	0.59
1:E:129:ALA:O	1:E:130:LYS:HB2	2.03	0.59
1:F:14:PHE:O	1:F:18:GLU:HB2	2.03	0.59
1:F:205:LYS:NZ	1:F:392:ASN:ND2	2.50	0.59
1:F:257:GLY:O	1:F:258:ASN:C	2.46	0.59
1:F:433:PRO:O	1:F:434:ILE:C	2.45	0.59
1:B:94:LYS:NZ	1:B:203:THR:OG1	2.29	0.58
1:E:339:ASN:HD22	1:E:340:ALA:N	2.01	0.58
1:B:63:LEU:HG	1:B:65:LEU:HD23	1.85	0.58
1:C:264:MET:HE3	1:C:292:PRO:CG	2.32	0.58
1:D:505:THR:O	1:E:185:ASP:OD1	2.21	0.58
1:D:339:ASN:H	1:D:339:ASN:HD22	1.50	0.58
1:E:103:VAL:HG23	1:E:103:VAL:O	2.03	0.58
1:E:151:ARG:O	1:E:154:MET:HB2	2.03	0.58
1:F:205:LYS:HZ3	1:F:392:ASN:HD21	1.52	0.58
1:A:32:LEU:HD21	1:A:494:PHE:CD1	2.37	0.58
1:A:40:GLU:HG3	1:A:46:ARG:NH1	2.18	0.58
1:A:378:ASN:H	1:A:378:ASN:ND2	1.99	0.58
1:A:500:ALA:HA	1:A:505:THR:O	2.03	0.58
1:E:336:THR:HG22	1:E:357:THR:HG21	1.84	0.58
1:F:23:ARG:HH11	1:F:23:ARG:HG3	1.67	0.58
1:F:217:SER:OG	1:F:454:HIS:NE2	2.25	0.58
1:F:439:GLU:H	1:F:439:GLU:CD	2.12	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:170:ALA:C	1:A:180:MET:HE2	2.28	0.58
1:B:77:GLU:HA	1:D:54:ARG:HH12	1.68	0.58
1:E:370:MET:HE3	1:E:372:ILE:HG12	1.86	0.58
1:F:384:VAL:O	1:F:387:PHE:N	2.37	0.58
1:B:180:MET:HE3	1:B:180:MET:CA	2.33	0.58
1:B:430:GLY:O	1:B:432:ILE:HG13	2.03	0.58
1:B:505:THR:OXT	1:F:185:ASP:OD1	2.22	0.58
1:E:284:ILE:CG2	1:E:311:ALA:HB1	2.25	0.58
1:F:72:ASP:OD1	1:F:144:GLU:HG2	2.03	0.58
1:A:418:GLN:HB2	1:A:433:PRO:CD	2.34	0.58
1:C:264:MET:HE3	1:C:292:PRO:CA	2.34	0.58
1:D:41:SER:HA	1:D:46:ARG:NE	2.12	0.58
1:D:78:VAL:HG23	1:D:78:VAL:O	2.03	0.58
1:D:284:ILE:HG13	1:D:305:ILE:HD12	1.86	0.58
1:D:293:LYS:HE2	1:D:293:LYS:HA	1.84	0.58
1:D:480:ASP:CG	1:D:483:THR:HG23	2.29	0.58
1:B:243:THR:H	1:B:244:PRO:HD3	1.69	0.58
1:B:414:LEU:HB3	1:B:434:ILE:HA	1.86	0.58
1:D:253:VAL:HA	1:D:327:ILE:HG12	1.84	0.58
1:E:23:ARG:HG3	1:E:23:ARG:NH1	2.19	0.58
1:E:349:ALA:HB1	1:E:377:LEU:CD2	2.34	0.58
1:A:264:MET:HE3	1:A:292:PRO:CA	2.32	0.58
1:A:293:LYS:HE2	1:A:293:LYS:HA	1.85	0.58
1:D:86:HIS:CD2	1:D:116:THR:CG2	2.74	0.58
1:D:206:PRO:HD2	1:D:209:GLN:HB2	1.86	0.58
1:E:213:HIS:HB2	1:E:449:GLU:HB3	1.86	0.58
1:F:99:TYR:OH	1:F:149:THR:HB	2.04	0.58
1:B:233:GLU:HG2	1:B:236:TYR:HD1	1.69	0.58
1:C:185:ASP:OD1	1:E:505:THR:CG2	2.47	0.58
1:C:179:GLU:OE2	1:C:179:GLU:N	2.33	0.57
1:C:477:LEU:HD12	1:C:484:ALA:HB2	1.85	0.57
1:E:384:VAL:O	1:E:387:PHE:HB2	2.03	0.57
1:F:56:ILE:HD13	1:F:493:VAL:HG12	1.86	0.57
1:F:238:SER:O	1:F:240:LEU:N	2.36	0.57
1:A:336:THR:HG22	1:A:357:THR:CG2	2.34	0.57
1:B:252:VAL:HG13	1:B:276:ALA:O	2.04	0.57
1:D:346:LYS:HA	1:D:369:ILE:HD13	1.86	0.57
1:D:375:LEU:HD23	1:D:485:ALA:HB1	1.84	0.57
1:E:86:HIS:ND1	1:E:113:SER:HA	2.19	0.57
1:A:70:ARG:HH12	1:C:143:ASN:HD21	1.52	0.57
1:A:90:ARG:NH1	1:A:496:VAL:HG21	2.19	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:367:ARG:O	1:C:369:ILE:HG12	2.04	0.57
1:D:319:LEU:HD12	1:D:319:LEU:N	2.19	0.57
1:C:90:ARG:HG2	1:C:125:PRO:HA	1.86	0.57
1:D:227:ILE:HD13	1:D:372:ILE:CD1	2.34	0.57
1:E:339:ASN:HD22	1:E:340:ALA:H	1.53	0.57
1:A:13:PHE:CD1	1:A:14:PHE:N	2.67	0.57
1:A:218:ALA:O	1:A:219:THR:C	2.48	0.57
1:A:449:GLU:O	1:A:453:VAL:HG23	2.04	0.57
1:B:23:ARG:HH11	1:B:23:ARG:HG3	1.70	0.57
1:B:336:THR:HG22	1:B:357:THR:CG2	2.35	0.57
1:B:337:LYS:O	1:B:337:LYS:HG2	2.04	0.57
1:C:212:ILE:HB	1:C:388:GLU:HG3	1.86	0.57
1:C:327:ILE:HD13	1:C:327:ILE:N	2.19	0.57
1:D:77:GLU:HG2	1:D:79:ILE:HD13	1.86	0.57
1:D:146:GLU:O	1:D:150:ARG:HG3	2.04	0.57
1:D:427:LYS:CD	1:D:430:GLY:HA3	2.28	0.57
1:F:156:LEU:HB3	1:F:162:ILE:HB	1.87	0.57
1:F:190:THR:HG22	1:F:191:ILE:N	2.19	0.57
1:F:336:THR:HG22	1:F:357:THR:CG2	2.34	0.57
1:B:321:ALA:O	1:B:344:LYS:HB2	2.04	0.57
1:E:108:VAL:HG23	1:E:109:LYS:H	1.69	0.57
1:F:462:GLU:O	1:F:464:SER:N	2.37	0.57
1:A:205:LYS:HZ3	1:A:392:ASN:HD21	1.50	0.57
1:B:350:GLU:OE2	1:B:356:THR:HG23	2.05	0.57
1:B:404:LYS:NZ	1:B:408:ASP:OD2	2.33	0.57
1:C:30:ASP:O	1:C:34:GLU:HG2	2.04	0.57
1:F:170:ALA:HA	1:F:180:MET:CE	2.34	0.57
1:A:359:GLU:O	1:A:362:LYS:HB2	2.04	0.57
1:B:339:ASN:HD22	1:B:339:ASN:N	1.92	0.57
1:B:348:ILE:HB	1:B:371:VAL:HG13	1.85	0.57
1:C:500:ALA:C	1:C:505:THR:HA	2.29	0.57
1:D:200:ALA:HA	1:D:392:ASN:HD22	1.70	0.57
1:D:333:LYS:HA	1:D:355:PRO:O	2.05	0.57
1:E:482:ARG:HH11	1:E:482:ARG:HG3	1.69	0.57
1:A:47:ASN:HD21	1:A:50:ARG:NH2	2.03	0.57
1:A:76:TRP:CZ3	1:E:49:VAL:HG23	2.38	0.57
1:A:116:THR:HG22	1:A:128:GLY:N	2.20	0.57
1:A:223:VAL:O	1:A:377:LEU:HD11	2.04	0.57
1:A:237:MET:HE2	1:A:237:MET:HA	1.86	0.57
1:A:432:ILE:O	1:A:432:ILE:HG13	2.05	0.57
1:D:14:PHE:O	1:D:18:GLU:HB2	2.05	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:21:PHE:CE1	1:E:490:ILE:HD12	2.39	0.57
1:A:67:PHE:N	1:A:67:PHE:CD2	2.73	0.57
1:A:136:ASN:OD1	1:A:138:LYS:HB2	2.03	0.57
1:A:427:LYS:C	1:A:428:HIS:HD1	2.13	0.57
1:B:150:ARG:O	1:B:152:PHE:N	2.38	0.57
1:B:275:ILE:HD12	1:B:287:PRO:HA	1.86	0.57
1:C:383:THR:O	1:C:386:TYR:HB3	2.05	0.57
1:D:234:ALA:O	1:D:235:SER:C	2.48	0.57
1:E:284:ILE:HG22	1:E:285:TRP:N	2.19	0.57
1:F:230:PHE:CE2	1:F:481:LEU:HD21	2.40	0.57
1:F:427:LYS:NZ	1:F:430:GLY:CA	2.68	0.57
1:A:400:ARG:O	1:A:400:ARG:HD2	2.04	0.56
1:E:32:LEU:HD11	1:E:494:PHE:CE2	2.39	0.56
1:F:326:LEU:HB3	1:F:348:ILE:HD13	1.87	0.56
1:A:99:TYR:CZ	1:A:149:THR:HG22	2.41	0.56
1:B:309:PRO:O	1:B:310:LYS:CB	2.53	0.56
1:D:54:ARG:O	1:D:58:PRO:CD	2.53	0.56
1:F:13:PHE:CE1	1:F:107:GLU:HA	2.40	0.56
1:A:149:THR:HB	1:A:183:ILE:HD11	1.87	0.56
1:A:248:ASP:CG	1:A:249:LYS:HG3	2.29	0.56
1:A:304:SER:OG	1:A:306:LEU:HD13	2.05	0.56
1:A:336:THR:O	1:A:340:ALA:HB2	2.05	0.56
1:A:504:PHE:CE1	1:E:151:ARG:NH2	2.66	0.56
1:B:237:MET:HE2	1:B:237:MET:N	2.21	0.56
1:C:28:VAL:HG12	1:C:29:GLU:N	2.20	0.56
1:C:441:GLN:HG3	1:C:441:GLN:O	2.05	0.56
1:D:161:PHE:O	1:D:167:ASP:HB3	2.03	0.56
1:D:223:VAL:HA	1:D:377:LEU:HG	1.86	0.56
1:D:336:THR:HG22	1:D:357:THR:HG21	1.87	0.56
1:D:350:GLU:OE1	1:D:373:PRO:HA	2.04	0.56
1:E:141:THR:HG22	1:E:144:GLU:CD	2.30	0.56
1:F:103:VAL:HA	1:F:107:GLU:OE1	2.06	0.56
1:A:146:GLU:HG3	1:A:182:TRP:CE2	2.40	0.56
1:A:393:LEU:O	1:A:395:HIS:HD2	1.88	0.56
1:A:418:GLN:HA	1:A:433:PRO:HG2	1.88	0.56
1:A:427:LYS:C	1:A:428:HIS:ND1	2.63	0.56
1:B:79:ILE:N	1:B:79:ILE:HD12	2.20	0.56
1:B:256:PHE:CZ	1:B:261:LEU:HD13	2.41	0.56
1:C:73:ASP:OD1	1:C:75:SER:N	2.36	0.56
1:C:180:MET:HG3	1:C:202:VAL:HG21	1.87	0.56
1:C:400:ARG:HD2	1:C:400:ARG:O	2.05	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:24:GLY:O	1:D:28:VAL:HG23	2.05	0.56
1:E:43:GLU:HB3	1:E:45:LYS:HG3	1.87	0.56
1:B:275:ILE:HG22	1:B:276:ALA:N	2.20	0.56
1:B:295:LEU:HD11	1:B:305:ILE:CG2	2.36	0.56
1:C:281:ASP:HB2	1:C:306:LEU:HD11	1.87	0.56
1:D:106:ASP:HA	1:D:109:LYS:HD3	1.87	0.56
1:D:440:PHE:CE2	1:D:444:ILE:HD11	2.40	0.56
1:F:170:ALA:HA	1:F:180:MET:HE2	1.86	0.56
1:A:337:LYS:CE	1:A:359:GLU:HG3	2.35	0.56
1:A:433:PRO:HD2	1:A:434:ILE:H	1.70	0.56
1:B:436:PRO:HA	1:F:416:SER:OG	2.04	0.56
1:C:77:GLU:HA	1:F:54:ARG:CZ	2.35	0.56
1:A:60:ASN:HA	1:E:66:SER:OG	2.05	0.56
1:A:69:ILE:HA	1:A:151:ARG:NH1	2.21	0.56
1:A:348:ILE:CD1	1:A:364:PHE:CE1	2.88	0.56
1:C:437:THR:CG2	1:D:416:SER:HA	2.35	0.56
1:D:365:LEU:HD23	1:D:365:LEU:C	2.31	0.56
1:D:416:SER:O	1:D:420:SER:HB2	2.06	0.56
1:A:231:ILE:HG22	1:A:232:ASN:N	2.20	0.56
1:C:254:GLN:NE2	1:C:334:GLN:HG2	2.14	0.56
1:C:285:TRP:HB2	1:C:314:TYR:HB2	1.86	0.56
1:D:92:PRO:HG2	1:D:389:TRP:CZ2	2.40	0.56
1:F:367:ARG:CB	1:F:367:ARG:HH11	2.19	0.56
1:A:265:ARG:HG3	1:A:265:ARG:HH11	1.70	0.56
1:A:327:ILE:CG2	1:A:349:ALA:HB3	2.36	0.56
1:B:205:LYS:NZ	1:B:392:ASN:ND2	2.49	0.56
1:C:41:SER:HA	1:C:46:ARG:HD2	1.88	0.56
1:C:146:GLU:OE1	1:E:504:PHE:HB3	2.05	0.56
1:C:333:LYS:HZ2	1:C:357:THR:HA	1.71	0.56
1:D:34:GLU:C	1:D:38:THR:HB	2.31	0.56
1:D:339:ASN:HD22	1:D:339:ASN:N	2.01	0.56
1:D:350:GLU:HG2	1:D:355:PRO:CG	2.35	0.56
1:D:355:PRO:HG2	1:D:356:THR:HG23	1.88	0.56
1:D:384:VAL:HG22	1:D:453:VAL:HG12	1.88	0.56
1:E:410:ASN:HD22	1:E:410:ASN:N	2.02	0.56
1:A:17:VAL:HG22	1:A:114:LEU:HD13	1.88	0.56
1:D:32:LEU:HD12	1:D:32:LEU:O	2.06	0.56
1:E:46:ARG:O	1:E:49:VAL:HG12	2.05	0.56
1:E:135:ILE:HD11	1:E:140:TYR:CZ	2.40	0.56
1:E:136:ASN:OD1	1:E:138:LYS:HG2	2.06	0.56
1:E:433:PRO:O	1:E:434:ILE:C	2.49	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:205:LYS:HE2	1:A:210:GLY:O	2.06	0.55
1:A:278:GLY:O	1:A:279:GLU:HG2	2.07	0.55
1:A:325:ILE:HG22	1:A:347:ILE:HG21	1.87	0.55
1:B:21:PHE:C	1:B:21:PHE:CD2	2.85	0.55
1:C:179:GLU:O	1:C:183:ILE:HG13	2.06	0.55
1:C:304:SER:HB3	1:C:306:LEU:HD13	1.88	0.55
1:D:314:TYR:HE2	1:D:318:ILE:HA	1.71	0.55
1:E:185:ASP:O	1:E:189:SER:OG	2.23	0.55
1:A:170:ALA:CA	1:A:180:MET:HE2	2.35	0.55
1:A:325:ILE:HG22	1:A:347:ILE:CB	2.37	0.55
1:B:162:ILE:HG23	1:B:162:ILE:O	2.04	0.55
1:B:502:VAL:CG1	1:D:76:TRP:HE1	2.19	0.55
1:C:339:ASN:HD22	1:C:340:ALA:H	1.54	0.55
1:F:13:PHE:HA	1:F:16:MET:HE3	1.89	0.55
1:F:295:LEU:HD11	1:F:305:ILE:CG2	2.36	0.55
1:A:179:GLU:O	1:A:183:ILE:HD13	2.06	0.55
1:A:443:ARG:HH21	1:B:409:SER:HB2	1.71	0.55
1:E:175:THR:HG22	1:E:179:GLU:HG2	1.87	0.55
1:E:259:VAL:HG22	1:E:260:GLY:N	2.21	0.55
1:E:309:PRO:O	1:E:310:LYS:HB2	2.06	0.55
1:A:363:ILE:O	1:A:367:ARG:HG2	2.06	0.55
1:A:386:TYR:HE2	1:A:390:LEU:HD21	1.71	0.55
1:A:418:GLN:CA	1:A:433:PRO:HG2	2.37	0.55
1:B:92:PRO:HG2	1:B:389:TRP:CZ2	2.41	0.55
1:B:190:THR:CG2	1:B:191:ILE:H	1.94	0.55
1:B:268:HIS:ND1	1:B:292:PRO:HD2	2.21	0.55
1:E:264:MET:HE3	1:E:292:PRO:CA	2.33	0.55
1:F:37:ARG:C	1:F:39:ARG:H	2.15	0.55
1:A:125:PRO:O	1:A:126:PHE:HD2	1.88	0.55
1:A:213:HIS:O	1:A:453:VAL:HG21	2.06	0.55
1:A:500:ALA:C	1:A:505:THR:HA	2.31	0.55
1:D:264:MET:HE3	1:D:292:PRO:CA	2.37	0.55
1:A:256:PHE:CZ	1:A:261:LEU:HD13	2.42	0.55
1:A:320:GLU:O	1:A:344:LYS:HG2	2.07	0.55
1:C:433:PRO:O	1:C:434:ILE:C	2.49	0.55
1:D:390:LEU:CD2	1:E:396:VAL:HG23	2.37	0.55
1:E:14:PHE:O	1:E:18:GLU:HB2	2.07	0.55
1:E:72:ASP:OD2	1:E:141:THR:HG21	2.07	0.55
1:E:284:ILE:HG12	1:E:305:ILE:HD12	1.89	0.55
1:F:319:LEU:HD23	1:F:335:LEU:CD2	2.36	0.55
1:B:31:LYS:HG3	1:B:475:TYR:CE1	2.41	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:237:MET:HE2	1:B:237:MET:CA	2.36	0.55
1:D:240:LEU:CD2	1:D:479:LEU:HD21	2.36	0.55
1:D:264:MET:HE3	1:D:292:PRO:HB3	1.89	0.55
1:D:325:ILE:HG22	1:D:347:ILE:CB	2.26	0.55
1:E:501:GLY:HA3	1:E:504:PHE:O	2.05	0.55
1:F:83:ARG:HH21	1:F:167:ASP:CG	2.14	0.55
1:A:224:PHE:CD2	1:A:266:TYR:HB3	2.42	0.55
1:B:376:TYR:C	1:B:376:TYR:CD2	2.84	0.55
1:D:224:PHE:CD1	1:D:224:PHE:C	2.84	0.55
1:D:238:SER:O	1:D:240:LEU:N	2.40	0.55
1:D:242:MET:HE2	1:D:244:PRO:CG	2.37	0.55
1:D:251:PHE:CE1	1:D:267:LEU:HB3	2.42	0.55
1:E:350:GLU:OE1	1:E:373:PRO:HA	2.06	0.55
1:F:180:MET:CE	1:F:202:VAL:HG21	2.36	0.55
1:A:251:PHE:CZ	1:A:267:LEU:HB3	2.42	0.55
1:A:253:VAL:HG13	1:A:277:VAL:HG22	1.89	0.55
1:A:440:PHE:CD2	1:B:412:HIS:CB	2.89	0.55
1:C:503:THR:HG21	1:F:151:ARG:HD3	1.88	0.55
1:D:157:ALA:HA	1:D:162:ILE:HG22	1.89	0.55
1:E:29:GLU:O	1:E:33:VAL:HG23	2.06	0.55
1:E:122:VAL:HG23	1:E:122:VAL:O	2.06	0.55
1:F:162:ILE:O	1:F:162:ILE:HD13	2.06	0.55
1:A:94:LYS:HD3	1:A:126:PHE:CD1	2.42	0.55
1:C:251:PHE:HB3	1:C:325:ILE:CG1	2.37	0.55
1:D:17:VAL:HA	1:D:20:PHE:CD1	2.42	0.55
1:F:295:LEU:HD11	1:F:305:ILE:HG22	1.89	0.55
1:B:501:GLY:HA3	1:B:504:PHE:O	2.07	0.54
1:C:141:THR:HG23	1:C:144:GLU:CD	2.32	0.54
1:C:278:GLY:HA3	1:C:318:ILE:CD1	2.37	0.54
1:E:94:LYS:HG2	1:E:126:PHE:CD1	2.42	0.54
1:E:141:THR:HG23	1:E:144:GLU:H	1.72	0.54
1:F:38:THR:HG23	1:F:41:SER:CB	2.25	0.54
1:A:87:SER:O	1:A:127:GLY:HA3	2.07	0.54
1:A:252:VAL:HG23	1:A:323:CYS:SG	2.47	0.54
1:C:298:PHE:O	1:C:300:LEU:N	2.40	0.54
1:D:404:LYS:HE3	1:D:407:ARG:HH21	1.71	0.54
1:D:435:VAL:HG13	1:E:420:SER:OG	2.07	0.54
1:F:502:VAL:N	1:F:505:THR:HB	2.21	0.54
1:A:34:GLU:CA	1:A:38:THR:HB	2.36	0.54
1:A:49:VAL:O	1:A:52:ILE:HG12	2.06	0.54
1:A:355:PRO:HG2	1:A:356:THR:HG23	1.90	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:386:TYR:CE2	1:A:390:LEU:HD21	2.42	0.54
1:A:425:PHE:C	1:A:425:PHE:HD1	2.15	0.54
1:B:110:ALA:O	1:B:113:SER:HB3	2.07	0.54
1:B:179:GLU:H	1:B:179:GLU:CD	2.15	0.54
1:B:254:GLN:HE22	1:B:334:GLN:HG2	1.72	0.54
1:C:153:THR:HG22	1:C:154:MET:N	2.22	0.54
1:C:430:GLY:O	1:C:432:ILE:HG12	2.07	0.54
1:E:45:LYS:HE2	1:E:48:ARG:HH11	1.72	0.54
1:E:363:ILE:HG22	1:E:364:PHE:N	2.22	0.54
1:F:16:MET:SD	1:F:333:LYS:NZ	2.80	0.54
1:F:242:MET:HE2	1:F:244:PRO:HG3	1.90	0.54
1:A:251:PHE:HB3	1:A:325:ILE:CG1	2.21	0.54
1:A:331:SER:HB2	1:A:334:GLN:NE2	2.22	0.54
1:A:360:ALA:HB1	1:A:364:PHE:CE2	2.36	0.54
1:A:360:ALA:O	1:A:361:ASP:C	2.51	0.54
1:A:418:GLN:OE1	1:A:433:PRO:HD2	2.07	0.54
1:A:502:VAL:CG2	1:A:503:THR:H	2.19	0.54
1:B:350:GLU:CD	1:B:482:ARG:HH22	2.14	0.54
1:D:226:GLY:HA3	1:D:377:LEU:HD12	1.89	0.54
1:D:240:LEU:CD2	1:D:479:LEU:CD2	2.86	0.54
1:F:253:VAL:CG1	1:F:277:VAL:HG13	2.37	0.54
1:F:431:THR:O	1:F:433:PRO:HD3	2.08	0.54
1:B:323:CYS:O	1:B:345:ALA:HA	2.08	0.54
1:B:387:PHE:CD2	1:B:387:PHE:N	2.75	0.54
1:B:400:ARG:HG2	1:B:400:ARG:HH11	1.73	0.54
1:C:390:LEU:O	1:C:391:LYS:C	2.48	0.54
1:E:418:GLN:O	1:E:419:GLU:C	2.47	0.54
1:F:373:PRO:CD	1:F:481:LEU:HB3	2.36	0.54
1:C:480:ASP:CG	1:C:483:THR:HG23	2.32	0.54
1:E:13:PHE:CD1	1:E:14:PHE:N	2.72	0.54
1:A:108:VAL:O	1:A:109:LYS:C	2.47	0.54
1:A:146:GLU:CG	1:A:150:ARG:HH11	2.20	0.54
1:A:347:ILE:HG12	1:A:370:MET:HE2	1.90	0.54
1:A:395:HIS:O	1:A:396:VAL:HG22	2.08	0.54
1:B:28:VAL:O	1:B:29:GLU:C	2.50	0.54
1:C:133:VAL:O	1:C:135:ILE:N	2.41	0.54
1:C:316:GLY:O	1:C:317:SER:C	2.50	0.54
1:D:79:ILE:HD13	1:D:79:ILE:N	2.23	0.54
1:D:237:MET:HE1	1:D:347:ILE:CD1	2.38	0.54
1:D:363:ILE:HD13	1:D:363:ILE:N	2.23	0.54
1:F:33:VAL:O	1:F:34:GLU:O	2.25	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:113:SER:O	1:A:116:THR:HG23	2.08	0.54
1:B:57:LYS:N	1:B:58:PRO:HD2	2.23	0.54
1:B:404:LYS:NZ	1:B:407:ARG:HH21	2.06	0.54
1:D:17:VAL:HA	1:D:20:PHE:HD1	1.72	0.54
1:D:158:LYS:HD3	1:F:193:HIS:ND1	2.23	0.54
1:D:501:GLY:HA3	1:D:505:THR:HA	1.89	0.54
1:E:69:ILE:HA	1:E:151:ARG:CZ	2.38	0.54
1:E:237:MET:N	1:E:237:MET:HE2	2.23	0.54
1:E:396:VAL:HG12	1:E:397:SER:N	2.22	0.54
1:F:78:VAL:C	1:F:79:ILE:HD12	2.33	0.54
1:F:108:VAL:HG23	1:F:109:LYS:H	1.71	0.54
1:F:256:PHE:HZ	1:F:296:GLU:HA	1.72	0.54
1:A:23:ARG:HE	1:A:483:THR:CG2	2.15	0.54
1:A:62:VAL:HG13	1:E:64:SER:HB2	1.90	0.54
1:A:372:ILE:HD12	1:A:372:ILE:N	2.23	0.54
1:B:501:GLY:HA3	1:B:505:THR:HA	1.89	0.54
1:C:285:TRP:HB3	1:C:314:TYR:HB2	1.89	0.54
1:D:44:GLN:C	1:D:46:ARG:H	2.16	0.54
1:D:424:LYS:O	1:D:425:PHE:HB2	2.08	0.54
1:E:79:ILE:N	1:E:79:ILE:HD12	2.22	0.54
1:E:91:THR:OG1	1:E:92:PRO:HD3	2.07	0.54
1:E:145:LEU:O	1:E:149:THR:HG23	2.08	0.54
1:F:145:LEU:O	1:F:149:THR:CG2	2.55	0.54
1:A:17:VAL:HA	1:A:20:PHE:CD1	2.43	0.54
1:C:57:LYS:HB3	1:C:58:PRO:CD	2.37	0.54
1:C:57:LYS:N	1:C:58:PRO:HD2	2.23	0.54
1:C:108:VAL:O	1:C:109:LYS:C	2.48	0.54
1:C:162:ILE:HG23	1:C:162:ILE:O	2.07	0.54
1:C:252:VAL:O	1:C:327:ILE:HD13	2.07	0.54
1:D:136:ASN:C	1:D:138:LYS:H	2.16	0.54
1:D:418:GLN:CB	1:D:433:PRO:HD2	2.38	0.54
1:F:261:LEU:HD11	1:F:296:GLU:OE1	2.08	0.54
1:F:457:LEU:HD23	1:F:461:MET:HG2	1.90	0.54
1:B:434:ILE:O	1:B:436:PRO:HD3	2.08	0.53
1:C:221:ARG:CD	1:C:225:HIS:CE1	2.92	0.53
1:D:254:GLN:OE1	1:D:334:GLN:HG2	2.09	0.53
1:E:21:PHE:O	1:E:25:ALA:HB2	2.08	0.53
1:F:336:THR:HG22	1:F:357:THR:HG21	1.90	0.53
1:F:500:ALA:CA	1:F:505:THR:O	2.56	0.53
1:C:16:MET:HE1	1:C:333:LYS:HE2	1.90	0.53
1:D:502:VAL:CG2	1:D:503:THR:H	2.20	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:45:LYS:HE2	1:E:48:ARG:NH1	2.23	0.53
1:E:65:LEU:HD12	1:E:152:PHE:HE1	1.73	0.53
1:F:155:GLU:OE1	1:F:155:GLU:HA	2.08	0.53
1:F:261:LEU:O	1:F:265:ARG:HG2	2.07	0.53
1:F:350:GLU:O	1:F:377:LEU:HD23	2.08	0.53
1:F:410:ASN:O	1:F:413:LEU:HB2	2.08	0.53
1:A:95:GLY:O	1:A:169:PRO:HA	2.07	0.53
1:A:285:TRP:NE1	1:A:287:PRO:HD3	2.23	0.53
1:A:437:THR:HG23	1:B:416:SER:HA	1.90	0.53
1:B:14:PHE:HD1	1:B:110:ALA:HB2	1.73	0.53
1:C:71:ARG:HB3	1:C:71:ARG:NH1	2.08	0.53
1:C:143:ASN:O	1:C:147:LYS:HG3	2.09	0.53
1:E:221:ARG:HG2	1:E:221:ARG:HH11	1.72	0.53
1:A:105:VAL:O	1:A:109:LYS:HG3	2.08	0.53
1:A:150:ARG:CZ	1:F:505:THR:OXT	2.56	0.53
1:A:183:ILE:HD13	1:A:183:ILE:N	2.23	0.53
1:B:42:GLU:HB2	1:B:46:ARG:NH2	2.22	0.53
1:B:383:THR:O	1:B:386:TYR:HB3	2.08	0.53
1:D:336:THR:H	1:D:339:ASN:HD21	1.54	0.53
1:D:485:ALA:O	1:D:488:ASN:N	2.41	0.53
1:F:251:PHE:CE1	1:F:267:LEU:HB3	2.43	0.53
1:B:13:PHE:HD1	1:B:14:PHE:H	1.57	0.53
1:B:341:PRO:HG3	1:B:363:ILE:HG21	1.91	0.53
1:C:384:VAL:HG23	1:C:457:LEU:HD12	1.90	0.53
1:D:135:ILE:CD1	1:D:148:ILE:HD13	2.38	0.53
1:E:423:ARG:HH11	1:E:423:ARG:HG3	1.74	0.53
1:F:231:ILE:HG23	1:F:232:ASN:ND2	2.24	0.53
1:F:256:PHE:CE1	1:F:299:LYS:HG2	2.43	0.53
1:F:285:TRP:O	1:F:286:ASN:HB2	2.07	0.53
1:F:378:ASN:C	1:F:378:ASN:HD22	2.15	0.53
1:A:32:LEU:HD21	1:A:494:PHE:CE1	2.44	0.53
1:B:335:LEU:HD11	1:B:348:ILE:HD13	1.89	0.53
1:C:293:LYS:HE2	1:C:297:ASP:OD2	2.09	0.53
1:C:350:GLU:HG2	1:C:355:PRO:HG2	1.89	0.53
1:C:423:ARG:HH21	1:E:435:VAL:HG11	1.74	0.53
1:E:410:ASN:N	1:E:410:ASN:ND2	2.53	0.53
1:F:122:VAL:O	1:F:124:VAL:HG23	2.08	0.53
1:F:418:GLN:CG	1:F:433:PRO:HD2	2.39	0.53
1:A:264:MET:CE	1:A:292:PRO:HA	2.36	0.53
1:A:363:ILE:HG22	1:A:364:PHE:N	2.23	0.53
1:A:433:PRO:HA	1:B:420:SER:OG	2.08	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:105:VAL:O	1:B:109:LYS:HG3	2.08	0.53
1:B:285:TRP:CB	1:B:314:TYR:HB2	2.38	0.53
1:C:180:MET:HG3	1:C:202:VAL:CG2	2.39	0.53
1:C:203:THR:HA	1:C:388:GLU:OE1	2.09	0.53
1:D:115:MET:O	1:D:116:THR:C	2.49	0.53
1:D:254:GLN:HE22	1:D:334:GLN:CD	2.17	0.53
1:D:300:LEU:HD13	1:D:301:GLN:N	2.23	0.53
1:D:410:ASN:O	1:D:414:LEU:HG	2.08	0.53
1:E:224:PHE:HD2	1:E:267:LEU:HD22	1.73	0.53
1:F:217:SER:OG	1:F:218:ALA:N	2.40	0.53
1:F:421:LEU:C	1:F:423:ARG:H	2.17	0.53
1:F:502:VAL:HG23	1:F:504:PHE:H	1.74	0.53
1:A:47:ASN:O	1:A:50:ARG:CG	2.57	0.53
1:A:212:ILE:HD11	1:A:453:VAL:HG22	1.91	0.53
1:A:239:ILE:O	1:A:239:ILE:HG22	2.07	0.53
1:A:339:ASN:ND2	1:A:339:ASN:H	2.07	0.53
1:A:424:LYS:O	1:A:424:LYS:NZ	2.35	0.53
1:A:500:ALA:HB1	1:A:505:THR:O	2.08	0.53
1:B:150:ARG:O	1:B:151:ARG:C	2.52	0.53
1:C:78:VAL:HG23	1:C:78:VAL:O	2.08	0.53
1:D:23:ARG:HG3	1:D:23:ARG:NH1	2.22	0.53
1:F:469:MET:O	1:F:470:ARG:C	2.51	0.53
1:A:133:VAL:O	1:A:133:VAL:HG12	2.07	0.53
1:A:251:PHE:CE1	1:A:267:LEU:HB3	2.44	0.53
1:B:29:GLU:O	1:B:30:ASP:C	2.52	0.53
1:D:68:PRO:O	1:D:151:ARG:HD2	2.07	0.53
1:D:170:ALA:CA	1:D:180:MET:HE2	2.39	0.53
1:D:251:PHE:HD2	1:D:327:ILE:HD11	1.74	0.53
1:D:275:ILE:CG2	1:D:276:ALA:H	2.21	0.53
1:D:331:SER:HB2	1:D:334:GLN:CD	2.34	0.53
1:D:400:ARG:HG3	1:D:400:ARG:HH11	1.74	0.53
1:E:295:LEU:HD11	1:E:305:ILE:HB	1.90	0.53
1:E:296:GLU:HG2	1:E:296:GLU:O	2.09	0.53
1:F:122:VAL:HG11	1:F:379:ALA:HB3	1.91	0.53
1:F:329:ALA:O	1:F:330:ALA:HB2	2.08	0.53
1:F:404:LYS:O	1:F:405:TYR:C	2.50	0.53
1:F:427:LYS:HE2	1:F:430:GLY:N	2.24	0.53
1:B:13:PHE:CZ	1:B:107:GLU:HG3	2.43	0.53
1:B:50:ARG:HG3	1:B:50:ARG:O	2.09	0.53
1:C:34:GLU:O	1:C:36:LEU:N	2.41	0.53
1:D:281:ASP:CB	1:D:306:LEU:HD21	2.38	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:72:ASP:OD1	1:E:141:THR:HG21	2.08	0.53
1:E:72:ASP:OD1	1:E:144:GLU:CG	2.54	0.53
1:F:35:ASP:CG	1:F:36:LEU:H	2.16	0.53
1:A:73:ASP:OD1	1:A:75:SER:OG	2.25	0.52
1:A:373:PRO:HG3	1:A:482:ARG:N	2.24	0.52
1:B:243:THR:O	1:B:243:THR:CG2	2.55	0.52
1:C:293:LYS:O	1:C:293:LYS:HG3	2.09	0.52
1:D:23:ARG:O	1:D:27:ILE:HG12	2.08	0.52
1:D:314:TYR:HD2	1:D:318:ILE:HG22	1.74	0.52
1:D:317:SER:HB2	1:D:319:LEU:HD13	1.91	0.52
1:E:23:ARG:O	1:E:27:ILE:HG13	2.10	0.52
1:F:32:LEU:HD21	1:F:494:PHE:CG	2.44	0.52
1:A:85:GLN:NE2	1:A:167:ASP:HB2	2.24	0.52
1:A:146:GLU:O	1:A:147:LYS:C	2.52	0.52
1:A:501:GLY:O	1:A:502:VAL:HG13	2.09	0.52
1:B:500:ALA:CA	1:B:505:THR:O	2.58	0.52
1:D:424:LYS:O	1:D:425:PHE:CB	2.57	0.52
1:F:117:TYR:O	1:F:121:VAL:HG23	2.08	0.52
1:F:309:PRO:O	1:F:310:LYS:HB2	2.09	0.52
1:A:17:VAL:HG21	1:A:114:LEU:HD13	1.91	0.52
1:A:240:LEU:HD21	1:A:479:LEU:HD21	1.91	0.52
1:A:501:GLY:HA3	1:A:504:PHE:O	2.10	0.52
1:B:435:VAL:O	1:B:435:VAL:HG13	2.09	0.52
1:C:195:ASP:HB3	1:C:198:ALA:HB2	1.91	0.52
1:E:285:TRP:CB	1:E:314:TYR:HB2	2.38	0.52
1:F:363:ILE:CG2	1:F:367:ARG:HD3	2.39	0.52
1:F:367:ARG:HH11	1:F:367:ARG:HB2	1.73	0.52
1:B:108:VAL:O	1:B:109:LYS:C	2.51	0.52
1:B:335:LEU:HD13	1:B:348:ILE:HD13	1.91	0.52
1:C:71:ARG:NH1	1:C:144:GLU:OE2	2.42	0.52
1:D:170:ALA:C	1:D:180:MET:HE2	2.34	0.52
1:D:481:LEU:O	1:D:482:ARG:C	2.53	0.52
1:F:195:ASP:HB3	1:F:198:ALA:HB2	1.90	0.52
1:F:264:MET:CE	1:F:292:PRO:HA	2.34	0.52
1:A:69:ILE:HD13	1:A:148:ILE:HG12	1.92	0.52
1:A:99:TYR:OH	1:A:149:THR:CG2	2.46	0.52
1:A:350:GLU:OE2	1:A:356:THR:HG23	2.09	0.52
1:A:362:LYS:O	1:A:365:LEU:HB3	2.10	0.52
1:B:283:SER:O	1:B:284:ILE:HD12	2.10	0.52
1:B:364:PHE:O	1:B:365:LEU:C	2.52	0.52
1:C:231:ILE:HD12	1:C:237:MET:SD	2.49	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:334:GLN:CA	1:C:334:GLN:NE2	2.71	0.52
1:C:433:PRO:C	1:C:435:VAL:N	2.68	0.52
1:E:180:MET:HG2	1:E:203:THR:O	2.09	0.52
1:F:105:VAL:O	1:F:108:VAL:HG22	2.10	0.52
1:F:146:GLU:HG2	1:F:150:ARG:HD2	1.91	0.52
1:F:349:ALA:HA	1:F:372:ILE:HG13	1.90	0.52
1:B:28:VAL:CG1	1:B:32:LEU:HD22	2.39	0.52
1:B:179:GLU:C	1:B:183:ILE:HD13	2.33	0.52
1:B:400:ARG:HG2	1:B:400:ARG:NH1	2.24	0.52
1:B:425:PHE:HD1	1:B:427:LYS:HB2	1.74	0.52
1:B:427:LYS:HG3	1:B:428:HIS:N	2.24	0.52
1:B:501:GLY:C	1:B:505:THR:HB	2.34	0.52
1:D:12:ASN:OD1	1:D:15:LYS:HG2	2.10	0.52
1:D:83:ARG:HG2	1:D:161:PHE:HB3	1.91	0.52
1:D:372:ILE:CG2	1:D:377:LEU:HD13	2.30	0.52
1:B:299:LYS:HD2	1:B:304:SER:HA	1.92	0.52
1:B:440:PHE:CE2	1:B:444:ILE:HD11	2.42	0.52
1:C:61:HIS:CE1	1:F:155:GLU:HG3	2.45	0.52
1:C:336:THR:OG1	1:C:338:SER:HB3	2.10	0.52
1:C:500:ALA:C	1:C:505:THR:OXT	2.52	0.52
1:D:505:THR:C	1:E:150:ARG:HH22	2.17	0.52
1:A:183:ILE:HD13	1:A:183:ILE:H	1.75	0.52
1:A:285:TRP:CD1	1:A:286:ASN:N	2.78	0.52
1:C:86:HIS:CD2	1:C:116:THR:CG2	2.88	0.52
1:C:221:ARG:CG	1:C:221:ARG:NH1	2.70	0.52
1:D:350:GLU:HG2	1:D:355:PRO:HG2	1.92	0.52
1:E:284:ILE:HG23	1:E:311:ALA:CB	2.26	0.52
1:F:464:SER:O	1:F:465:ALA:C	2.52	0.52
1:A:122:VAL:O	1:A:122:VAL:HG23	2.10	0.52
1:B:95:GLY:HA3	1:B:129:ALA:O	2.09	0.52
1:C:187:TYR:CE1	1:C:191:ILE:HG22	2.45	0.52
1:C:231:ILE:O	1:C:237:MET:HG3	2.09	0.52
1:C:409:SER:O	1:C:411:TYR:N	2.43	0.52
1:D:399:GLY:HA3	1:D:403:PHE:CE1	2.44	0.52
1:A:37:ARG:HD3	1:A:37:ARG:C	2.35	0.52
1:A:237:MET:CE	1:A:240:LEU:HD12	2.39	0.52
1:A:481:LEU:CD1	1:A:481:LEU:H	2.23	0.52
1:B:65:LEU:O	1:B:80:GLU:HA	2.10	0.52
1:B:363:ILE:O	1:B:367:ARG:HG2	2.10	0.52
1:C:475:TYR:OH	1:C:491:GLU:OE2	2.26	0.52
1:D:105:VAL:O	1:D:108:VAL:HG22	2.09	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:332:GLU:HG2	1:E:333:LYS:HG2	1.92	0.52
1:F:145:LEU:O	1:F:149:THR:HG22	2.10	0.52
1:F:349:ALA:HB1	1:F:377:LEU:HD21	1.91	0.52
1:A:34:GLU:O	1:A:36:LEU:N	2.39	0.51
1:A:265:ARG:HG3	1:A:265:ARG:NH1	2.25	0.51
1:A:341:PRO:HA	1:A:367:ARG:HE	1.74	0.51
1:B:488:ASN:O	1:B:492:LYS:HG3	2.10	0.51
1:C:401:LEU:HD13	1:E:398:TYR:CE2	2.44	0.51
1:D:96:GLY:HA2	1:D:170:ALA:O	2.10	0.51
1:D:197:ASN:O	1:D:200:ALA:HB3	2.10	0.51
1:D:501:GLY:HA3	1:D:504:PHE:O	2.10	0.51
1:E:51:GLY:O	1:E:54:ARG:HG2	2.09	0.51
1:E:428:HIS:N	1:E:428:HIS:HD2	2.07	0.51
1:F:265:ARG:HG3	1:F:265:ARG:HH11	1.75	0.51
1:F:319:LEU:H	1:F:319:LEU:CD1	2.19	0.51
1:A:53:LEU:CD1	1:A:494:PHE:HD1	2.23	0.51
1:A:326:LEU:O	1:A:328:PRO:HD3	2.10	0.51
1:C:38:THR:O	1:C:38:THR:HG22	2.10	0.51
1:C:101:THR:HG22	1:C:101:THR:O	2.09	0.51
1:C:418:GLN:OE1	1:C:432:ILE:HA	2.09	0.51
1:D:268:HIS:O	1:D:270:PHE:N	2.43	0.51
1:E:224:PHE:CZ	1:E:270:PHE:CD2	2.99	0.51
1:F:94:LYS:HD3	1:F:126:PHE:CD1	2.44	0.51
1:F:284:ILE:HG13	1:F:305:ILE:HD12	1.91	0.51
1:F:326:LEU:HB3	1:F:348:ILE:CD1	2.39	0.51
1:A:47:ASN:O	1:A:50:ARG:HG2	2.11	0.51
1:A:284:ILE:HG23	1:A:311:ALA:CB	2.31	0.51
1:B:63:LEU:HG	1:B:65:LEU:CD2	2.40	0.51
1:B:398:TYR:HB2	1:B:449:GLU:HG3	1.93	0.51
1:C:22:ASP:O	1:C:23:ARG:C	2.53	0.51
1:D:256:PHE:CE2	1:D:264:MET:HE2	2.44	0.51
1:D:440:PHE:CZ	1:D:444:ILE:HD11	2.45	0.51
1:F:359:GLU:O	1:F:362:LYS:HB2	2.09	0.51
1:F:425:PHE:CE1	1:F:427:LYS:HB2	2.46	0.51
1:A:136:ASN:O	1:A:137:PRO:C	2.52	0.51
1:A:223:VAL:HG11	1:A:263:SER:OG	2.11	0.51
1:B:104:SER:O	1:B:105:VAL:C	2.52	0.51
1:C:170:ALA:HB1	1:C:171:PRO:CD	2.40	0.51
1:E:32:LEU:HD21	1:E:494:PHE:CD1	2.45	0.51
1:E:501:GLY:HA3	1:E:505:THR:HA	1.92	0.51
1:A:178:ARG:HB3	1:A:179:GLU:OE2	2.10	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:220:GLY:O	1:A:221:ARG:C	2.53	0.51
1:A:285:TRP:HB2	1:A:314:TYR:CB	2.35	0.51
1:B:242:MET:HE2	1:B:244:PRO:HG3	1.92	0.51
1:C:13:PHE:HD1	1:C:14:PHE:N	2.08	0.51
1:D:171:PRO:HG3	1:D:180:MET:SD	2.51	0.51
1:E:293:LYS:NZ	1:E:297:ASP:OD1	2.44	0.51
1:F:224:PHE:CD2	1:F:266:TYR:HB3	2.45	0.51
1:A:285:TRP:CD1	1:A:287:PRO:HD3	2.46	0.51
1:A:396:VAL:CG2	1:F:390:LEU:CD2	2.88	0.51
1:D:77:GLU:HG2	1:D:79:ILE:CD1	2.41	0.51
1:D:309:PRO:O	1:D:310:LYS:CB	2.58	0.51
1:D:404:LYS:HE3	1:D:407:ARG:NH2	2.25	0.51
1:F:37:ARG:NE	1:F:46:ARG:HD3	2.25	0.51
1:F:46:ARG:NE	1:F:46:ARG:HA	2.26	0.51
1:F:55:ILE:O	1:F:58:PRO:HD2	2.10	0.51
1:F:252:VAL:HG22	1:F:276:ALA:HB3	1.91	0.51
1:A:440:PHE:CE1	1:A:444:ILE:HD11	2.45	0.51
1:B:38:THR:HG22	1:B:38:THR:O	2.10	0.51
1:B:46:ARG:O	1:B:49:VAL:HG12	2.10	0.51
1:B:69:ILE:HG12	1:B:79:ILE:CD1	2.40	0.51
1:B:400:ARG:HG3	1:B:401:LEU:HD12	1.92	0.51
1:C:42:GLU:O	1:C:43:GLU:HB2	2.10	0.51
1:D:146:GLU:CD	1:D:150:ARG:HH11	2.19	0.51
1:E:242:MET:O	1:E:243:THR:C	2.54	0.51
1:E:316:GLY:O	1:E:317:SER:O	2.29	0.51
1:E:466:ARG:NH1	1:E:466:ARG:CG	2.74	0.51
1:A:21:PHE:CE2	1:A:57:LYS:HB2	2.46	0.51
1:A:43:GLU:C	1:A:45:LYS:H	2.18	0.51
1:A:227:ILE:HD11	1:A:349:ALA:CB	2.41	0.51
1:B:502:VAL:HG11	1:D:76:TRP:NE1	2.20	0.51
1:E:400:ARG:CG	1:E:400:ARG:NH1	2.65	0.51
1:A:29:GLU:O	1:A:33:VAL:HG23	2.10	0.51
1:B:378:ASN:HD22	1:B:378:ASN:N	2.04	0.51
1:D:336:THR:HG22	1:D:357:THR:CG2	2.41	0.51
1:D:363:ILE:O	1:D:367:ARG:HG2	2.10	0.51
1:F:21:PHE:CE2	1:F:57:LYS:HB2	2.46	0.51
1:F:350:GLU:OE2	1:F:482:ARG:NH2	2.44	0.51
1:A:48:ARG:C	1:A:50:ARG:H	2.17	0.51
1:A:149:THR:HG21	1:A:179:GLU:HG3	1.91	0.51
1:A:224:PHE:CD1	1:A:224:PHE:C	2.88	0.51
1:B:57:LYS:HB3	1:B:58:PRO:HD3	1.93	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:309:PRO:O	1:D:310:LYS:HB2	2.11	0.51
1:D:321:ALA:O	1:D:344:LYS:HB2	2.11	0.51
1:D:324:ASP:HB2	1:D:325:ILE:CD1	2.39	0.51
1:D:374:ASP:OD2	1:D:375:LEU:N	2.44	0.51
1:F:157:ALA:HB2	1:F:162:ILE:HG21	1.93	0.51
1:F:180:MET:CE	1:F:202:VAL:CG2	2.87	0.51
1:A:38:THR:O	1:A:38:THR:CG2	2.59	0.50
1:A:86:HIS:CG	1:A:116:THR:HG21	2.44	0.50
1:A:106:ASP:O	1:A:107:GLU:C	2.54	0.50
1:A:190:THR:CG2	1:A:191:ILE:N	2.67	0.50
1:A:268:HIS:CD2	1:A:292:PRO:CD	2.94	0.50
1:A:309:PRO:O	1:A:310:LYS:HB2	2.12	0.50
1:A:349:ALA:HA	1:A:372:ILE:HB	1.93	0.50
1:B:478:GLY:C	1:B:480:ASP:H	2.17	0.50
1:C:86:HIS:HB3	1:C:116:THR:HG21	1.94	0.50
1:C:153:THR:HG21	1:C:186:THR:HB	1.93	0.50
1:C:298:PHE:CZ	1:C:302:HIS:HE1	2.29	0.50
1:C:502:VAL:CG2	1:C:503:THR:H	2.23	0.50
1:E:108:VAL:HG23	1:E:109:LYS:N	2.26	0.50
1:A:407:ARG:NH1	1:A:411:TYR:CD2	2.79	0.50
1:B:94:LYS:HZ3	1:B:203:THR:HG23	1.76	0.50
1:C:237:MET:O	1:C:242:MET:N	2.36	0.50
1:C:417:VAL:HG21	1:E:417:VAL:HG21	1.93	0.50
1:D:327:ILE:HG23	1:D:349:ALA:HB3	1.92	0.50
1:E:56:ILE:C	1:E:58:PRO:HD2	2.36	0.50
1:F:318:ILE:HD12	1:F:319:LEU:HD12	1.92	0.50
1:F:500:ALA:HB1	1:F:505:THR:OG1	2.11	0.50
1:B:84:ALA:O	1:B:129:ALA:HB1	2.10	0.50
1:B:86:HIS:CD2	1:B:116:THR:CG2	2.88	0.50
1:B:318:ILE:HD13	1:B:318:ILE:N	2.26	0.50
1:C:168:VAL:CG1	1:C:202:VAL:HA	2.40	0.50
1:D:83:ARG:NH2	1:D:167:ASP:OD1	2.44	0.50
1:E:254:GLN:OE1	1:E:319:LEU:HD11	2.11	0.50
1:A:327:ILE:HD13	1:A:327:ILE:N	2.27	0.50
1:A:343:VAL:HG22	1:A:367:ARG:HH21	1.77	0.50
1:C:206:PRO:HD2	1:C:209:GLN:HB2	1.93	0.50
1:D:47:ASN:O	1:D:50:ARG:HG2	2.11	0.50
1:D:172:ASP:C	1:D:172:ASP:OD1	2.53	0.50
1:E:96:GLY:HA2	1:E:170:ALA:O	2.12	0.50
1:E:108:VAL:O	1:E:109:LYS:C	2.55	0.50
1:E:146:GLU:CG	1:E:150:ARG:HH11	2.23	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:178:ARG:O	1:E:179:GLU:C	2.53	0.50
1:E:279:GLU:OE1	1:E:299:LYS:NZ	2.44	0.50
1:F:32:LEU:HD21	1:F:494:PHE:CD2	2.47	0.50
1:C:86:HIS:CG	1:C:116:THR:HG21	2.45	0.50
1:C:146:GLU:HG2	1:C:150:ARG:HD2	1.93	0.50
1:C:251:PHE:CB	1:C:325:ILE:HG13	2.41	0.50
1:C:505:THR:C	1:D:150:ARG:HH22	2.19	0.50
1:D:144:GLU:O	1:D:148:ILE:HG13	2.11	0.50
1:D:242:MET:HE2	1:D:244:PRO:HG2	1.93	0.50
1:E:141:THR:HG22	1:E:144:GLU:OE1	2.11	0.50
1:A:302:HIS:ND1	1:A:302:HIS:O	2.45	0.50
1:A:331:SER:HB2	1:A:334:GLN:HE22	1.76	0.50
1:B:23:ARG:HE	1:B:483:THR:CG2	2.25	0.50
1:C:100:SER:O	1:C:134:LYS:HA	2.11	0.50
1:D:460:THR:O	1:D:461:MET:C	2.55	0.50
1:E:116:THR:CG2	1:E:128:GLY:HA3	2.42	0.50
1:E:118:LYS:HD3	1:E:382:VAL:HG21	1.94	0.50
1:E:175:THR:CG2	1:E:179:GLU:HG2	2.42	0.50
1:F:47:ASN:O	1:F:50:ARG:HG2	2.11	0.50
1:A:503:THR:CA	1:A:505:THR:HG22	2.42	0.50
1:B:325:ILE:HG22	1:B:347:ILE:HG22	1.94	0.50
1:C:409:SER:O	1:C:412:HIS:N	2.43	0.50
1:C:462:GLU:O	1:C:463:ALA:C	2.52	0.50
1:D:176:GLY:N	1:D:179:GLU:OE1	2.30	0.50
1:D:318:ILE:HD12	1:D:319:LEU:N	2.27	0.50
1:D:485:ALA:O	1:D:487:VAL:N	2.44	0.50
1:E:256:PHE:HE2	1:E:264:MET:HE2	1.77	0.50
1:F:157:ALA:HA	1:F:162:ILE:HG22	1.93	0.50
1:A:46:ARG:O	1:A:49:VAL:HG12	2.11	0.50
1:A:47:ASN:O	1:A:50:ARG:CD	2.59	0.50
1:A:505:THR:OXT	1:B:150:ARG:NH2	2.44	0.50
1:B:29:GLU:HG2	1:B:30:ASP:N	2.26	0.50
1:B:474:LYS:NZ	1:B:491:GLU:OE2	2.43	0.50
1:C:418:GLN:OE1	1:C:433:PRO:CD	2.60	0.50
1:D:43:GLU:C	1:D:45:LYS:H	2.18	0.50
1:D:320:GLU:O	1:D:321:ALA:C	2.54	0.50
1:D:390:LEU:HD22	1:E:396:VAL:HG23	1.93	0.50
1:D:413:LEU:O	1:D:417:VAL:HG23	2.11	0.50
1:E:183:ILE:O	1:E:184:ALA:C	2.52	0.50
1:E:256:PHE:CZ	1:E:261:LEU:HD13	2.46	0.50
1:F:349:ALA:HB1	1:F:377:LEU:CD2	2.42	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:364:PHE:HB3	1:F:369:ILE:HB	1.92	0.50
1:A:433:PRO:CD	1:A:434:ILE:H	2.22	0.50
1:B:146:GLU:HG3	1:B:182:TRP:CE2	2.46	0.50
1:B:248:ASP:CG	1:B:249:LYS:N	2.69	0.50
1:B:335:LEU:HD13	1:B:364:PHE:CZ	2.47	0.50
1:C:77:GLU:CA	1:F:54:ARG:HH22	2.25	0.50
1:D:153:THR:HG23	1:D:162:ILE:HD13	1.94	0.50
1:E:190:THR:CG2	1:E:191:ILE:H	1.91	0.50
1:E:396:VAL:CG1	1:E:397:SER:N	2.75	0.50
1:A:79:ILE:CD1	1:A:79:ILE:N	2.74	0.49
1:A:240:LEU:HD21	1:A:479:LEU:CD2	2.42	0.49
1:A:502:VAL:HG11	1:E:76:TRP:HE1	1.71	0.49
1:A:502:VAL:N	1:A:505:THR:HB	2.27	0.49
1:B:306:LEU:CD1	1:B:306:LEU:H	2.25	0.49
1:B:427:LYS:HG3	1:B:430:GLY:H	1.77	0.49
1:C:97:ILE:HD13	1:C:131:ALA:HB3	1.92	0.49
1:C:252:VAL:HB	1:C:326:LEU:HD23	1.93	0.49
1:E:336:THR:HG22	1:E:357:THR:CG2	2.41	0.49
1:E:462:GLU:O	1:E:463:ALA:O	2.29	0.49
1:E:502:VAL:O	1:E:505:THR:CG2	2.60	0.49
1:F:56:ILE:CD1	1:F:493:VAL:HG12	2.42	0.49
1:F:284:ILE:HG22	1:F:285:TRP:H	1.76	0.49
1:F:339:ASN:C	1:F:339:ASN:ND2	2.69	0.49
1:B:340:ALA:O	1:B:343:VAL:HG22	2.12	0.49
1:C:339:ASN:HD22	1:C:339:ASN:C	2.18	0.49
1:D:43:GLU:C	1:D:45:LYS:N	2.68	0.49
1:D:418:GLN:O	1:D:419:GLU:C	2.54	0.49
1:F:67:PHE:CE1	1:F:79:ILE:HB	2.47	0.49
1:F:171:PRO:HG3	1:F:180:MET:HG3	1.94	0.49
1:F:309:PRO:O	1:F:310:LYS:CB	2.60	0.49
1:A:190:THR:CG2	1:A:191:ILE:H	2.24	0.49
1:A:386:TYR:CE2	1:A:390:LEU:HD11	2.47	0.49
1:C:26:SER:O	1:C:27:ILE:C	2.55	0.49
1:C:28:VAL:HG13	1:C:32:LEU:CD2	2.40	0.49
1:C:266:TYR:O	1:C:267:LEU:C	2.54	0.49
1:C:308:PHE:C	1:C:309:PRO:O	2.55	0.49
1:C:494:PHE:C	1:C:494:PHE:CD2	2.90	0.49
1:D:337:LYS:NZ	1:D:337:LYS:CB	2.72	0.49
1:D:381:GLY:C	1:D:383:THR:H	2.20	0.49
1:F:51:GLY:O	1:F:54:ARG:HG2	2.12	0.49
1:A:54:ARG:NH1	1:E:78:VAL:HG13	2.27	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:307:GLY:O	1:A:309:PRO:HD3	2.13	0.49
1:A:331:SER:CB	1:A:334:GLN:HE22	2.25	0.49
1:A:337:LYS:NZ	1:A:359:GLU:HG3	2.27	0.49
1:B:34:GLU:O	1:B:38:THR:HB	2.11	0.49
1:B:339:ASN:ND2	1:B:339:ASN:N	2.52	0.49
1:D:12:ASN:ND2	1:D:14:PHE:HB3	2.27	0.49
1:F:239:ILE:O	1:F:239:ILE:CG2	2.60	0.49
1:F:343:VAL:CG2	1:F:364:PHE:HE1	2.19	0.49
1:A:427:LYS:CG	1:A:428:HIS:H	2.25	0.49
1:B:256:PHE:HE2	1:B:264:MET:HE1	1.78	0.49
1:C:21:PHE:CE1	1:C:490:ILE:HD12	2.47	0.49
1:C:37:ARG:HH21	1:C:49:VAL:CG1	2.04	0.49
1:F:149:THR:O	1:F:153:THR:OG1	2.27	0.49
1:A:31:LYS:HD3	1:A:35:ASP:OD2	2.13	0.49
1:A:203:THR:HB	1:A:388:GLU:OE2	2.13	0.49
1:A:233:GLU:HG2	1:A:236:TYR:CD1	2.47	0.49
1:A:387:PHE:N	1:A:387:PHE:CD2	2.80	0.49
1:C:23:ARG:HG3	1:C:23:ARG:HH11	1.76	0.49
1:C:217:SER:O	1:C:218:ALA:C	2.56	0.49
1:F:220:GLY:O	1:F:223:VAL:N	2.45	0.49
1:F:418:GLN:HG3	1:F:431:THR:O	2.13	0.49
1:A:349:ALA:HB1	1:A:377:LEU:CD2	2.42	0.49
1:A:418:GLN:OE1	1:A:433:PRO:CD	2.60	0.49
1:B:108:VAL:O	1:B:110:ALA:N	2.45	0.49
1:B:425:PHE:O	1:B:427:LYS:N	2.46	0.49
1:C:94:LYS:HD3	1:C:126:PHE:CE1	2.47	0.49
1:C:482:ARG:O	1:C:485:ALA:N	2.44	0.49
1:D:73:ASP:OD2	1:D:75:SER:N	2.33	0.49
1:F:171:PRO:HB3	1:F:175:THR:O	2.12	0.49
1:F:227:ILE:O	1:F:231:ILE:HB	2.13	0.49
1:F:449:GLU:O	1:F:450:LYS:C	2.56	0.49
1:B:52:ILE:HG21	1:B:494:PHE:CD1	2.48	0.49
1:B:292:PRO:O	1:B:293:LYS:C	2.55	0.49
1:B:487:VAL:O	1:B:491:GLU:HG3	2.13	0.49
1:C:418:GLN:O	1:C:419:GLU:C	2.55	0.49
1:D:314:TYR:CD2	1:D:318:ILE:HG22	2.48	0.49
1:E:92:PRO:HA	1:E:166:ILE:O	2.12	0.49
1:E:115:MET:HB3	1:E:128:GLY:HA2	1.94	0.49
1:E:408:ASP:O	1:E:412:HIS:HD2	1.96	0.49
1:F:116:THR:HG22	1:F:128:GLY:HA3	1.94	0.49
1:A:72:ASP:OD1	1:A:144:GLU:OE2	2.30	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:396:VAL:HG22	1:F:390:LEU:HD11	1.95	0.49
1:B:64:SER:HB2	1:D:62:VAL:HG13	1.94	0.49
1:B:433:PRO:HA	1:F:420:SER:HB3	1.93	0.49
1:C:68:PRO:O	1:C:151:ARG:NH1	2.40	0.49
1:C:151:ARG:CZ	1:F:503:THR:OG1	2.60	0.49
1:D:251:PHE:O	1:D:275:ILE:HG22	2.13	0.49
1:F:12:ASN:O	1:F:13:PHE:C	2.55	0.49
1:F:215:ARG:O	1:F:218:ALA:HB3	2.13	0.49
1:F:266:TYR:O	1:F:267:LEU:C	2.56	0.49
1:F:284:ILE:CG2	1:F:285:TRP:N	2.75	0.49
1:F:322:ASP:OD1	1:F:344:LYS:HB3	2.13	0.49
1:F:477:LEU:HD13	1:F:480:ASP:OD2	2.12	0.49
1:A:350:GLU:CD	1:A:482:ARG:HH22	2.20	0.49
1:B:28:VAL:O	1:B:29:GLU:O	2.31	0.49
1:C:284:ILE:HG23	1:C:285:TRP:N	2.28	0.49
1:C:432:ILE:HG22	1:C:434:ILE:CG1	2.43	0.49
1:D:386:TYR:CE2	1:D:390:LEU:HD11	2.48	0.49
1:E:480:ASP:CG	1:E:483:THR:CG2	2.86	0.49
1:F:319:LEU:HD21	1:F:334:GLN:HG3	1.95	0.49
1:A:177:GLU:HB2	1:A:206:PRO:HG3	1.94	0.48
1:A:273:LYS:HD3	1:A:287:PRO:O	2.12	0.48
1:B:320:GLU:HG2	1:B:342:ARG:O	2.13	0.48
1:B:398:TYR:CE2	1:F:401:LEU:HD13	2.47	0.48
1:B:407:ARG:NH1	1:B:411:TYR:CE2	2.81	0.48
1:B:495:LYS:O	1:B:496:VAL:C	2.55	0.48
1:C:168:VAL:HG13	1:C:202:VAL:CA	2.40	0.48
1:D:51:GLY:O	1:D:54:ARG:HG2	2.13	0.48
1:D:331:SER:HB2	1:D:334:GLN:NE2	2.28	0.48
1:D:390:LEU:CD2	1:E:396:VAL:CG2	2.91	0.48
1:D:480:ASP:OD1	1:D:483:THR:HG23	2.13	0.48
1:F:30:ASP:O	1:F:34:GLU:HG2	2.13	0.48
1:B:298:PHE:CZ	1:B:302:HIS:HE1	2.30	0.48
1:C:33:VAL:O	1:C:34:GLU:O	2.31	0.48
1:C:91:THR:CB	1:C:92:PRO:HD3	2.43	0.48
1:C:222:GLY:CA	1:C:457:LEU:HD21	2.40	0.48
1:D:28:VAL:O	1:D:32:LEU:HB3	2.13	0.48
1:D:298:PHE:CE1	1:D:309:PRO:HD3	2.48	0.48
1:D:331:SER:HB2	1:D:334:GLN:HE22	1.78	0.48
1:D:487:VAL:O	1:D:488:ASN:C	2.56	0.48
1:E:95:GLY:O	1:E:169:PRO:HA	2.13	0.48
1:E:146:GLU:HG2	1:E:150:ARG:HD2	1.93	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:116:THR:HB	1:F:128:GLY:H	1.78	0.48
1:A:43:GLU:C	1:A:45:LYS:N	2.70	0.48
1:A:51:GLY:O	1:A:52:ILE:C	2.56	0.48
1:A:427:LYS:HG3	1:A:430:GLY:H	1.78	0.48
1:B:215:ARG:O	1:B:216:ILE:C	2.57	0.48
1:B:219:THR:O	1:B:223:VAL:HG23	2.13	0.48
1:B:440:PHE:CE1	1:F:413:LEU:HD22	2.49	0.48
1:D:85:GLN:OE1	1:D:88:GLN:NE2	2.46	0.48
1:D:439:GLU:CD	1:D:439:GLU:H	2.21	0.48
1:F:202:VAL:CG2	1:F:203:THR:N	2.76	0.48
1:F:336:THR:O	1:F:337:LYS:C	2.57	0.48
1:A:34:GLU:HA	1:A:38:THR:CB	2.39	0.48
1:A:339:ASN:H	1:A:339:ASN:HD22	1.61	0.48
1:A:399:GLY:HA3	1:A:403:PHE:CE1	2.49	0.48
1:A:494:PHE:C	1:A:494:PHE:CD2	2.91	0.48
1:A:501:GLY:HA3	1:A:505:THR:HA	1.96	0.48
1:B:49:VAL:C	1:B:51:GLY:H	2.18	0.48
1:D:10:ASP:O	1:D:10:ASP:CG	2.56	0.48
1:D:317:SER:C	1:D:319:LEU:H	2.21	0.48
1:D:336:THR:C	1:D:338:SER:N	2.71	0.48
1:E:244:PRO:HB2	1:E:248:ASP:H	1.77	0.48
1:E:254:GLN:OE1	1:E:334:GLN:HG2	2.13	0.48
1:F:153:THR:CG2	1:F:183:ILE:HG23	2.43	0.48
1:A:443:ARG:NH2	1:B:409:SER:HB2	2.28	0.48
1:B:21:PHE:HD1	1:B:117:TYR:CZ	2.32	0.48
1:D:91:THR:HG22	1:D:165:GLY:O	2.13	0.48
1:E:317:SER:OG	1:E:320:GLU:OE1	2.30	0.48
1:F:68:PRO:O	1:F:151:ARG:HD2	2.14	0.48
1:F:326:LEU:HD13	1:F:328:PRO:HD3	1.95	0.48
1:A:44:GLN:C	1:A:46:ARG:H	2.20	0.48
1:B:146:GLU:CA	1:B:182:TRP:CZ3	2.97	0.48
1:D:16:MET:CE	1:D:333:LYS:HE3	2.43	0.48
1:D:104:SER:O	1:D:105:VAL:C	2.57	0.48
1:D:390:LEU:CD1	1:E:396:VAL:HG21	2.42	0.48
1:E:323:CYS:O	1:E:345:ALA:HA	2.13	0.48
1:E:383:THR:O	1:E:386:TYR:HB3	2.13	0.48
1:E:428:HIS:HD2	1:E:428:HIS:H	1.61	0.48
1:F:105:VAL:O	1:F:108:VAL:CG2	2.62	0.48
1:F:218:ALA:O	1:F:219:THR:C	2.54	0.48
1:A:170:ALA:C	1:A:180:MET:CE	2.87	0.48
1:A:435:VAL:HG12	1:B:420:SER:OG	2.13	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:135:ILE:HG12	1:B:140:TYR:CE2	2.49	0.48
1:B:175:THR:HG22	1:B:179:GLU:HG2	1.96	0.48
1:C:99:TYR:HB2	1:C:174:SER:HB2	1.96	0.48
1:C:122:VAL:HG11	1:C:379:ALA:HB3	1.96	0.48
1:E:23:ARG:C	1:E:23:ARG:HD3	2.38	0.48
1:F:21:PHE:CD1	1:F:490:ILE:HD12	2.49	0.48
1:F:21:PHE:HE1	1:F:490:ILE:HD12	1.78	0.48
1:F:37:ARG:C	1:F:37:ARG:HD3	2.38	0.48
1:F:46:ARG:HE	1:F:46:ARG:N	2.12	0.48
1:F:380:GLY:O	1:F:383:THR:HB	2.13	0.48
1:A:185:ASP:OD1	1:F:505:THR:CG2	2.46	0.48
1:A:231:ILE:O	1:A:237:MET:HG3	2.13	0.48
1:B:267:LEU:O	1:B:272:ALA:HB3	2.14	0.48
1:B:300:LEU:O	1:B:301:GLN:C	2.56	0.48
1:C:86:HIS:HB3	1:C:116:THR:CG2	2.44	0.48
1:D:220:GLY:C	1:D:222:GLY:N	2.71	0.48
1:F:231:ILE:CG2	1:F:232:ASN:ND2	2.77	0.48
1:F:242:MET:HE2	1:F:244:PRO:HG2	1.96	0.48
1:A:12:ASN:ND2	1:A:14:PHE:HB3	2.29	0.48
1:B:223:VAL:HG13	1:B:377:LEU:HD21	1.96	0.48
1:B:238:SER:O	1:B:240:LEU:N	2.46	0.48
1:C:152:PHE:CE2	1:C:156:LEU:HD21	2.48	0.48
1:C:223:VAL:HG11	1:C:263:SER:OG	2.13	0.48
1:C:349:ALA:HB1	1:C:377:LEU:CD2	2.43	0.48
1:D:166:ILE:HG22	1:D:167:ASP:N	2.28	0.48
1:F:122:VAL:HG23	1:F:124:VAL:HG23	1.95	0.48
1:A:55:ILE:CD1	1:A:55:ILE:H	2.27	0.48
1:A:179:GLU:O	1:A:182:TRP:HB2	2.14	0.48
1:B:500:ALA:C	1:B:505:THR:O	2.57	0.48
1:C:33:VAL:C	1:C:38:THR:HG1	2.22	0.48
1:C:264:MET:HG2	1:C:292:PRO:HG3	1.95	0.48
1:D:33:VAL:HG12	1:D:38:THR:OG1	2.13	0.48
1:D:275:ILE:CG2	1:D:276:ALA:N	2.74	0.48
1:D:421:LEU:HD21	1:E:421:LEU:HD11	1.96	0.48
1:F:215:ARG:O	1:F:218:ALA:CB	2.61	0.48
1:A:204:GLY:N	1:A:388:GLU:OE2	2.40	0.47
1:A:433:PRO:HA	1:B:420:SER:CB	2.44	0.47
1:B:147:LYS:HE3	1:D:504:PHE:HZ	1.77	0.47
1:F:49:VAL:C	1:F:51:GLY:H	2.21	0.47
1:F:94:LYS:HB2	1:F:126:PHE:CD1	2.48	0.47
1:F:502:VAL:O	1:F:505:THR:CG2	2.62	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:57:LYS:CB	1:A:58:PRO:CD	2.88	0.47
1:A:82:TYR:O	1:A:131:ALA:HA	2.14	0.47
1:A:309:PRO:O	1:A:310:LYS:CB	2.62	0.47
1:A:387:PHE:N	1:A:387:PHE:HD2	2.11	0.47
1:B:293:LYS:HZ3	1:B:297:ASP:CG	2.21	0.47
1:C:281:ASP:CB	1:C:306:LEU:HD21	2.44	0.47
1:C:500:ALA:CA	1:C:505:THR:OXT	2.62	0.47
1:D:150:ARG:O	1:D:153:THR:N	2.47	0.47
1:D:183:ILE:O	1:D:184:ALA:C	2.56	0.47
1:D:278:GLY:O	1:D:279:GLU:HG2	2.13	0.47
1:E:12:ASN:O	1:E:13:PHE:C	2.57	0.47
1:E:151:ARG:O	1:E:152:PHE:C	2.57	0.47
1:F:97:ILE:CD1	1:F:131:ALA:HB3	2.45	0.47
1:F:467:GLN:HG3	1:F:470:ARG:HH12	1.79	0.47
1:A:94:LYS:HB2	1:A:126:PHE:CD1	2.50	0.47
1:A:149:THR:HG1	1:A:182:TRP:HE3	1.59	0.47
1:A:193:HIS:CE1	1:C:158:LYS:HG2	2.50	0.47
1:B:325:ILE:HG22	1:B:347:ILE:HB	1.96	0.47
1:C:51:GLY:HA2	1:C:54:ARG:HG2	1.95	0.47
1:C:281:ASP:HB3	1:C:306:LEU:HD21	1.96	0.47
1:D:409:SER:O	1:D:413:LEU:HD23	2.15	0.47
1:D:481:LEU:O	1:D:484:ALA:N	2.47	0.47
1:E:34:GLU:O	1:E:35:ASP:C	2.57	0.47
1:E:122:VAL:HB	1:E:460:THR:CG2	2.43	0.47
1:F:406:GLU:O	1:F:407:ARG:C	2.57	0.47
1:A:28:VAL:HG23	1:A:487:VAL:HG13	1.97	0.47
1:A:69:ILE:HD13	1:A:148:ILE:CG1	2.43	0.47
1:A:108:VAL:HG23	1:A:109:LYS:N	2.28	0.47
1:A:153:THR:HG23	1:A:162:ILE:HD13	1.96	0.47
1:A:378:ASN:ND2	1:A:378:ASN:N	2.60	0.47
1:C:242:MET:HE1	1:C:324:ASP:CG	2.39	0.47
1:C:243:THR:H	1:C:244:PRO:HD3	1.73	0.47
1:D:112:ALA:O	1:D:115:MET:HB2	2.14	0.47
1:D:136:ASN:C	1:D:138:LYS:N	2.72	0.47
1:D:248:ASP:C	1:D:249:LYS:HG3	2.38	0.47
1:D:428:HIS:ND1	1:D:428:HIS:N	2.62	0.47
1:E:238:SER:O	1:E:241:GLY:N	2.47	0.47
1:E:284:ILE:CG2	1:E:285:TRP:N	2.77	0.47
1:E:330:ALA:O	1:E:331:SER:O	2.32	0.47
1:E:460:THR:O	1:E:461:MET:C	2.56	0.47
1:F:256:PHE:O	1:F:256:PHE:HD1	1.95	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:415:MET:SD	1:F:434:ILE:CG2	3.02	0.47
1:A:179:GLU:CD	1:A:179:GLU:H	2.21	0.47
1:A:242:MET:O	1:A:243:THR:HG22	2.14	0.47
1:B:168:VAL:HG13	1:B:202:VAL:HA	1.96	0.47
1:B:198:ALA:C	1:B:200:ALA:H	2.22	0.47
1:B:253:VAL:O	1:B:253:VAL:HG22	2.13	0.47
1:C:252:VAL:HG23	1:C:323:CYS:SG	2.54	0.47
1:C:350:GLU:HG2	1:C:355:PRO:CG	2.43	0.47
1:D:320:GLU:O	1:D:344:LYS:HB2	2.15	0.47
1:D:350:GLU:OE2	1:D:355:PRO:HD2	2.13	0.47
1:E:91:THR:HB	1:E:92:PRO:HD3	1.95	0.47
1:E:410:ASN:ND2	1:E:410:ASN:H	2.12	0.47
1:F:334:GLN:CA	1:F:334:GLN:NE2	2.69	0.47
1:A:277:VAL:HG23	1:A:290:ILE:HD12	1.96	0.47
1:B:13:PHE:CD1	1:B:14:PHE:N	2.79	0.47
1:B:264:MET:HE3	1:B:292:PRO:CB	2.44	0.47
1:B:275:ILE:CD1	1:B:287:PRO:HA	2.44	0.47
1:C:347:ILE:HG12	1:C:370:MET:HE2	1.96	0.47
1:D:70:ARG:O	1:D:147:LYS:NZ	2.38	0.47
1:E:180:MET:HG3	1:E:202:VAL:CG2	2.45	0.47
1:E:321:ALA:O	1:E:344:LYS:HB2	2.13	0.47
1:A:28:VAL:O	1:A:32:LEU:CB	2.62	0.47
1:B:393:LEU:O	1:B:395:HIS:HD2	1.95	0.47
1:B:433:PRO:O	1:B:435:VAL:N	2.47	0.47
1:B:449:GLU:O	1:B:450:LYS:C	2.55	0.47
1:C:243:THR:O	1:C:243:THR:CG2	2.62	0.47
1:C:378:ASN:C	1:C:378:ASN:ND2	2.64	0.47
1:C:425:PHE:HD1	1:C:427:LYS:HB2	1.80	0.47
1:D:94:LYS:CB	1:D:126:PHE:CD1	2.95	0.47
1:D:254:GLN:HE22	1:D:334:GLN:HG2	1.78	0.47
1:D:327:ILE:N	1:D:327:ILE:CD1	2.66	0.47
1:D:346:LYS:HA	1:D:369:ILE:CD1	2.45	0.47
1:D:446:GLY:O	1:D:447:ALA:C	2.57	0.47
1:E:33:VAL:HG12	1:E:38:THR:OG1	2.14	0.47
1:E:69:ILE:HA	1:E:151:ARG:NH1	2.30	0.47
1:E:135:ILE:HD12	1:E:135:ILE:HA	1.62	0.47
1:E:136:ASN:O	1:E:140:TYR:HD2	1.98	0.47
1:E:234:ALA:O	1:E:235:SER:C	2.56	0.47
1:F:433:PRO:C	1:F:435:VAL:N	2.73	0.47
1:A:396:VAL:CG2	1:F:390:LEU:HD21	2.45	0.47
1:B:223:VAL:HG13	1:B:377:LEU:CD2	2.45	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:365:LEU:HD23	1:C:365:LEU:O	2.14	0.47
1:C:460:THR:CG2	1:D:400:ARG:HH21	2.26	0.47
1:D:48:ARG:C	1:D:50:ARG:H	2.21	0.47
1:E:433:PRO:C	1:E:435:VAL:N	2.71	0.47
1:F:350:GLU:O	1:F:377:LEU:HB3	2.14	0.47
1:A:237:MET:O	1:A:242:MET:N	2.43	0.47
1:B:116:THR:CG2	1:B:128:GLY:HA3	2.39	0.47
1:B:349:ALA:HB1	1:B:377:LEU:CD2	2.45	0.47
1:F:256:PHE:O	1:F:256:PHE:CD1	2.68	0.47
1:A:407:ARG:NH1	1:A:411:TYR:CE2	2.83	0.47
1:B:54:ARG:HB3	1:B:54:ARG:CZ	2.45	0.47
1:B:133:VAL:HG12	1:B:135:ILE:HB	1.97	0.47
1:B:145:LEU:HD23	1:B:148:ILE:HD12	1.97	0.47
1:C:46:ARG:O	1:C:49:VAL:HG12	2.14	0.47
1:C:135:ILE:HD13	1:C:148:ILE:HD13	1.96	0.47
1:C:212:ILE:HD12	1:C:388:GLU:HA	1.96	0.47
1:C:221:ARG:HG2	1:C:221:ARG:NH1	2.13	0.47
1:C:221:ARG:HE	1:C:225:HIS:CE1	2.33	0.47
1:C:420:SER:HB3	1:E:433:PRO:HA	1.97	0.47
1:D:38:THR:O	1:D:38:THR:CG2	2.62	0.47
1:E:56:ILE:CD1	1:E:493:VAL:HG12	2.45	0.47
1:A:77:GLU:HA	1:E:54:ARG:NH1	2.30	0.46
1:A:395:HIS:C	1:A:396:VAL:CG2	2.87	0.46
1:C:223:VAL:HG22	1:C:377:LEU:HG	1.97	0.46
1:C:405:TYR:CE1	1:E:443:ARG:NH2	2.83	0.46
1:C:431:THR:C	1:C:432:ILE:HG12	2.38	0.46
1:D:259:VAL:O	1:D:263:SER:HB2	2.15	0.46
1:D:339:ASN:N	1:D:339:ASN:ND2	2.63	0.46
1:D:342:ARG:HB2	1:D:342:ARG:NH1	2.29	0.46
1:E:49:VAL:C	1:E:51:GLY:H	2.23	0.46
1:E:141:THR:HG23	1:E:144:GLU:HB2	1.96	0.46
1:E:243:THR:O	1:E:243:THR:CG2	2.63	0.46
1:E:503:THR:CA	1:E:505:THR:HG22	2.45	0.46
1:F:367:ARG:HB2	1:F:367:ARG:NH1	2.29	0.46
1:A:262:HIS:CD2	1:A:265:ARG:HH12	2.33	0.46
1:A:358:PRO:O	1:A:361:ASP:HB2	2.15	0.46
1:A:401:LEU:HD21	1:F:387:PHE:CE2	2.50	0.46
1:A:401:LEU:HD13	1:F:398:TYR:CE2	2.50	0.46
1:B:326:LEU:O	1:B:328:PRO:HD3	2.16	0.46
1:B:407:ARG:HH11	1:B:407:ARG:HG2	1.80	0.46
1:D:264:MET:HE3	1:D:292:PRO:CB	2.45	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:505:THR:O	1:E:185:ASP:CG	2.58	0.46
1:E:29:GLU:O	1:E:30:ASP:C	2.58	0.46
1:E:250:THR:O	1:E:323:CYS:HB2	2.15	0.46
1:A:254:GLN:HB2	1:A:318:ILE:CD1	2.43	0.46
1:A:322:ASP:HA	1:A:344:LYS:HB2	1.96	0.46
1:A:486:TYR:O	1:A:490:ILE:HG13	2.15	0.46
1:B:54:ARG:O	1:B:58:PRO:CD	2.63	0.46
1:C:150:ARG:O	1:C:153:THR:HB	2.15	0.46
1:C:151:ARG:HD3	1:F:503:THR:CG2	2.45	0.46
1:D:86:HIS:HD2	1:D:116:THR:CG2	2.10	0.46
1:D:125:PRO:O	1:D:126:PHE:CD2	2.67	0.46
1:E:153:THR:O	1:E:154:MET:C	2.58	0.46
1:F:391:LYS:HE3	1:F:397:SER:HA	1.97	0.46
1:F:407:ARG:O	1:F:408:ASP:C	2.56	0.46
1:A:103:VAL:HG21	1:A:134:LYS:N	2.30	0.46
1:A:124:VAL:HG22	1:A:386:TYR:CD1	2.51	0.46
1:A:233:GLU:HG2	1:A:236:TYR:HD1	1.79	0.46
1:A:283:SER:HB2	1:A:314:TYR:O	2.16	0.46
1:A:372:ILE:HA	1:A:481:LEU:HD23	1.98	0.46
1:B:407:ARG:NH1	1:B:407:ARG:HG2	2.30	0.46
1:C:69:ILE:HD13	1:C:148:ILE:HG12	1.96	0.46
1:C:306:LEU:N	1:C:306:LEU:HD12	2.31	0.46
1:D:146:GLU:HG3	1:D:182:TRP:CE2	2.50	0.46
1:E:152:PHE:CE2	1:E:156:LEU:HD21	2.50	0.46
1:E:252:VAL:HG13	1:E:276:ALA:HB3	1.97	0.46
1:E:336:THR:HA	1:E:357:THR:CG2	2.43	0.46
1:F:42:GLU:O	1:F:43:GLU:HB2	2.14	0.46
1:F:51:GLY:CA	1:F:54:ARG:HG2	2.45	0.46
1:F:238:SER:C	1:F:240:LEU:N	2.73	0.46
1:F:394:ASN:O	1:F:396:VAL:HG22	2.15	0.46
1:F:457:LEU:CD2	1:F:461:MET:HG2	2.45	0.46
1:A:47:ASN:ND2	1:A:50:ARG:NH2	2.64	0.46
1:A:401:LEU:HD21	1:F:387:PHE:CD2	2.51	0.46
1:A:451:ASP:O	1:A:455:SER:OG	2.32	0.46
1:B:96:GLY:O	1:B:130:LYS:HD2	2.15	0.46
1:B:384:VAL:O	1:B:387:PHE:HB2	2.16	0.46
1:C:168:VAL:HG13	1:C:201:CYS:C	2.39	0.46
1:C:298:PHE:O	1:C:299:LYS:C	2.57	0.46
1:C:435:VAL:O	1:C:435:VAL:HG12	2.15	0.46
1:D:25:ALA:HB1	1:D:53:LEU:HD23	1.98	0.46
1:D:133:VAL:HG12	1:D:135:ILE:HB	1.97	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:78:VAL:C	1:E:79:ILE:HD12	2.41	0.46
1:E:94:LYS:HD2	1:E:94:LYS:HA	1.76	0.46
1:E:500:ALA:C	1:E:505:THR:OXT	2.58	0.46
1:F:69:ILE:HG23	1:F:79:ILE:HD13	1.96	0.46
1:A:54:ARG:CZ	1:A:54:ARG:HB2	2.45	0.46
1:C:78:VAL:H	1:F:54:ARG:NH2	2.07	0.46
1:C:339:ASN:O	1:C:340:ALA:C	2.58	0.46
1:D:179:GLU:HA	1:D:182:TRP:CE3	2.51	0.46
1:E:94:LYS:HB2	1:E:126:PHE:HB3	1.97	0.46
1:F:51:GLY:O	1:F:54:ARG:CG	2.64	0.46
1:F:71:ARG:HB3	1:F:71:ARG:HH11	1.79	0.46
1:F:95:GLY:O	1:F:169:PRO:HA	2.16	0.46
1:A:267:LEU:HA	1:A:267:LEU:HD13	1.68	0.46
1:B:94:LYS:HD2	1:B:168:VAL:O	2.14	0.46
1:B:196:ILE:O	1:B:395:HIS:CE1	2.68	0.46
1:B:424:LYS:O	1:B:425:PHE:CB	2.63	0.46
1:B:502:VAL:O	1:B:505:THR:CG2	2.63	0.46
1:E:325:ILE:HG23	1:E:347:ILE:HG21	1.96	0.46
1:F:46:ARG:NE	1:F:46:ARG:CA	2.79	0.46
1:F:231:ILE:O	1:F:237:MET:HG3	2.16	0.46
1:B:193:HIS:O	1:B:193:HIS:CG	2.69	0.46
1:B:425:PHE:CD1	1:B:425:PHE:O	2.69	0.46
1:C:349:ALA:HB1	1:C:377:LEU:HD21	1.98	0.46
1:D:28:VAL:CG2	1:D:487:VAL:HG13	2.44	0.46
1:D:306:LEU:HD12	1:D:306:LEU:N	2.31	0.46
1:E:218:ALA:CB	1:E:384:VAL:HG21	2.46	0.46
1:F:38:THR:O	1:F:38:THR:CG2	2.62	0.46
1:F:171:PRO:HG3	1:F:180:MET:CG	2.46	0.46
1:F:416:SER:O	1:F:420:SER:OG	2.24	0.46
1:A:249:LYS:HB2	1:A:272:ALA:HA	1.97	0.46
1:A:427:LYS:HG2	1:A:430:GLY:CA	2.43	0.46
1:A:438:ALA:O	1:A:439:GLU:C	2.58	0.46
1:C:332:GLU:O	1:C:333:LYS:C	2.59	0.46
1:C:408:ASP:O	1:C:409:SER:O	2.34	0.46
1:C:500:ALA:HB1	1:C:505:THR:C	2.41	0.46
1:D:236:TYR:C	1:D:238:SER:H	2.24	0.46
1:E:428:HIS:CD2	1:E:428:HIS:H	2.33	0.46
1:F:91:THR:CB	1:F:92:PRO:CD	2.84	0.46
1:A:72:ASP:OD2	1:A:141:THR:HG21	2.16	0.46
1:A:237:MET:HE1	1:A:240:LEU:HD12	1.97	0.46
1:A:339:ASN:HD22	1:A:339:ASN:N	2.14	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:182:TRP:O	1:B:183:ILE:C	2.58	0.46
1:B:304:SER:OG	1:B:305:ILE:N	2.47	0.46
1:C:153:THR:O	1:C:154:MET:C	2.59	0.46
1:D:73:ASP:OD2	1:D:73:ASP:C	2.57	0.46
1:E:85:GLN:NE2	1:E:167:ASP:OD2	2.49	0.46
1:F:304:SER:OG	1:F:305:ILE:N	2.49	0.46
1:F:409:SER:O	1:F:410:ASN:C	2.57	0.46
1:A:52:ILE:O	1:A:56:ILE:HG13	2.16	0.45
1:A:112:ALA:O	1:A:113:SER:C	2.59	0.45
1:A:265:ARG:O	1:A:268:HIS:HB3	2.16	0.45
1:A:373:PRO:O	1:A:374:ASP:C	2.59	0.45
1:A:500:ALA:CB	1:A:505:THR:O	2.64	0.45
1:B:349:ALA:HB1	1:B:377:LEU:HD21	1.97	0.45
1:C:146:GLU:O	1:C:150:ARG:HG3	2.17	0.45
1:D:18:GLU:O	1:D:19:GLY:C	2.59	0.45
1:D:319:LEU:H	1:D:319:LEU:CD1	2.28	0.45
1:E:169:PRO:C	1:E:202:VAL:HG23	2.41	0.45
1:E:382:VAL:O	1:E:385:SER:OG	2.31	0.45
1:F:268:HIS:C	1:F:268:HIS:ND1	2.73	0.45
1:F:418:GLN:HA	1:F:433:PRO:HG2	1.98	0.45
1:A:162:ILE:HG23	1:A:162:ILE:O	2.16	0.45
1:A:221:ARG:O	1:A:222:GLY:C	2.56	0.45
1:A:421:LEU:HD21	1:B:421:LEU:HD21	1.97	0.45
1:A:427:LYS:HG2	1:A:430:GLY:H	1.80	0.45
1:C:256:PHE:CZ	1:C:295:LEU:HD23	2.52	0.45
1:D:42:GLU:O	1:D:43:GLU:HB2	2.15	0.45
1:E:67:PHE:C	1:E:67:PHE:CD1	2.94	0.45
1:E:220:GLY:O	1:E:221:ARG:C	2.58	0.45
1:F:104:SER:HG	1:F:107:GLU:H	1.61	0.45
1:A:54:ARG:O	1:A:58:PRO:CD	2.57	0.45
1:A:402:THR:O	1:A:405:TYR:N	2.49	0.45
1:A:484:ALA:O	1:A:487:VAL:HB	2.16	0.45
1:B:13:PHE:CE1	1:B:107:GLU:HA	2.51	0.45
1:B:256:PHE:HB3	1:B:279:GLU:OE1	2.17	0.45
1:D:56:ILE:O	1:D:86:HIS:CE1	2.70	0.45
1:E:52:ILE:O	1:E:55:ILE:HB	2.15	0.45
1:E:61:HIS:CD2	1:E:88:GLN:NE2	2.81	0.45
1:E:482:ARG:O	1:E:485:ALA:HB3	2.16	0.45
1:F:306:LEU:H	1:F:306:LEU:HD12	1.82	0.45
1:F:314:TYR:CE2	1:F:318:ILE:HA	2.44	0.45
1:A:253:VAL:HA	1:A:327:ILE:HG12	1.97	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:350:GLU:OE2	1:A:482:ARG:NH2	2.40	0.45
1:B:302:HIS:O	1:B:303:GLY:C	2.59	0.45
1:B:336:THR:HG22	1:B:357:THR:HG21	1.99	0.45
1:C:77:GLU:CA	1:F:54:ARG:HH12	2.30	0.45
1:C:108:VAL:HG23	1:C:109:LYS:N	2.32	0.45
1:C:334:GLN:NE2	1:C:334:GLN:HA	2.31	0.45
1:D:12:ASN:O	1:D:13:PHE:C	2.59	0.45
1:D:32:LEU:HD12	1:D:32:LEU:C	2.42	0.45
1:E:150:ARG:O	1:E:154:MET:HG2	2.16	0.45
1:A:227:ILE:CD1	1:A:349:ALA:HB2	2.47	0.45
1:A:427:LYS:CG	1:A:428:HIS:N	2.78	0.45
1:B:146:GLU:HG3	1:B:182:TRP:CD2	2.51	0.45
1:B:402:THR:O	1:B:403:PHE:C	2.59	0.45
1:C:190:THR:CG2	1:C:191:ILE:H	2.16	0.45
1:C:477:LEU:HD12	1:C:484:ALA:CB	2.46	0.45
1:D:31:LYS:HD3	1:D:35:ASP:OD2	2.15	0.45
1:D:488:ASN:O	1:D:492:LYS:HG2	2.17	0.45
1:E:169:PRO:O	1:E:202:VAL:HG23	2.16	0.45
1:F:73:ASP:C	1:F:73:ASP:OD2	2.59	0.45
1:F:415:MET:HE3	1:F:415:MET:O	2.16	0.45
1:F:500:ALA:C	1:F:505:THR:O	2.59	0.45
1:A:33:VAL:O	1:A:34:GLU:O	2.34	0.45
1:A:253:VAL:O	1:A:253:VAL:HG22	2.17	0.45
1:B:320:GLU:HG2	1:B:342:ARG:HG2	1.98	0.45
1:C:284:ILE:HD12	1:C:284:ILE:HA	1.70	0.45
1:C:293:LYS:HE2	1:C:293:LYS:O	2.16	0.45
1:C:433:PRO:HA	1:D:420:SER:OG	2.17	0.45
1:D:207:ILE:HD11	1:D:212:ILE:O	2.16	0.45
1:E:281:ASP:HB2	1:E:306:LEU:CD1	2.45	0.45
1:E:293:LYS:NZ	1:E:297:ASP:CG	2.74	0.45
1:F:318:ILE:O	1:F:321:ALA:N	2.49	0.45
1:A:71:ARG:HD2	1:A:77:GLU:OE2	2.16	0.45
1:A:86:HIS:CD2	1:A:116:THR:CG2	2.90	0.45
1:A:224:PHE:HD1	1:A:225:HIS:N	2.12	0.45
1:A:224:PHE:CE2	1:A:270:PHE:CD2	3.05	0.45
1:A:390:LEU:O	1:A:394:ASN:ND2	2.49	0.45
1:B:237:MET:HA	1:B:237:MET:CE	2.43	0.45
1:B:325:ILE:HG22	1:B:347:ILE:CB	2.47	0.45
1:C:13:PHE:CE1	1:C:107:GLU:HA	2.52	0.45
1:D:284:ILE:CG1	1:D:305:ILE:HD12	2.47	0.45
1:D:440:PHE:CE1	1:E:413:LEU:HD22	2.51	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:101:THR:HA	1:E:134:LYS:HG3	1.99	0.45
1:E:135:ILE:HG13	1:E:140:TYR:CE2	2.51	0.45
1:F:243:THR:O	1:F:243:THR:CG2	2.63	0.45
1:F:333:LYS:HA	1:F:355:PRO:O	2.17	0.45
1:F:418:GLN:OE1	1:F:434:ILE:HG12	2.17	0.45
1:F:492:LYS:O	1:F:493:VAL:C	2.60	0.45
1:A:62:VAL:CG1	1:E:64:SER:HB2	2.46	0.45
1:A:101:THR:O	1:A:101:THR:HG22	2.17	0.45
1:A:143:ASN:ND2	1:C:70:ARG:NH2	2.65	0.45
1:A:231:ILE:HG22	1:A:232:ASN:OD1	2.17	0.45
1:A:335:LEU:HD13	1:A:348:ILE:HD13	1.98	0.45
1:B:34:GLU:C	1:B:38:THR:HB	2.41	0.45
1:B:387:PHE:N	1:B:387:PHE:HD2	2.15	0.45
1:C:159:LYS:HD2	1:F:161:PHE:CZ	2.52	0.45
1:C:468:ILE:O	1:C:468:ILE:HG22	2.15	0.45
1:D:23:ARG:HD2	1:D:483:THR:HB	1.98	0.45
1:E:28:VAL:O	1:E:29:GLU:C	2.59	0.45
1:F:23:ARG:O	1:F:26:SER:OG	2.35	0.45
1:F:343:VAL:HG11	1:F:364:PHE:CE1	2.52	0.45
1:A:370:MET:CB	1:A:479:LEU:HD23	2.43	0.45
1:A:433:PRO:C	1:A:435:VAL:H	2.25	0.45
1:A:489:ALA:O	1:A:493:VAL:HG23	2.16	0.45
1:B:10:ASP:OD2	1:B:10:ASP:C	2.60	0.45
1:B:502:VAL:O	1:B:505:THR:HG21	2.17	0.45
1:C:229:ASN:HD21	1:C:462:GLU:CA	2.28	0.45
1:D:31:LYS:HD2	1:D:36:LEU:HD11	1.98	0.45
1:D:37:ARG:HH11	1:D:37:ARG:CB	2.11	0.45
1:D:40:GLU:O	1:D:42:GLU:N	2.50	0.45
1:D:51:GLY:HA2	1:D:54:ARG:HG2	1.98	0.45
1:D:104:SER:O	1:D:107:GLU:N	2.49	0.45
1:E:409:SER:O	1:E:410:ASN:C	2.57	0.45
1:A:242:MET:O	1:A:243:THR:C	2.61	0.45
1:A:396:VAL:HG22	1:F:390:LEU:HD21	1.98	0.45
1:B:51:GLY:O	1:B:55:ILE:HG13	2.18	0.45
1:B:254:GLN:HG3	1:B:318:ILE:HD11	2.00	0.45
1:B:385:SER:O	1:B:386:TYR:C	2.60	0.45
1:C:146:GLU:HA	1:C:182:TRP:CE3	2.52	0.45
1:D:399:GLY:O	1:D:400:ARG:C	2.60	0.45
1:E:261:LEU:C	1:E:261:LEU:HD12	2.42	0.45
1:F:375:LEU:HD23	1:F:485:ALA:HB1	1.99	0.45
1:F:501:GLY:HA3	1:F:504:PHE:O	2.16	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:320:GLU:O	1:A:321:ALA:C	2.60	0.44
1:A:341:PRO:HA	1:A:367:ARG:NE	2.32	0.44
1:B:71:ARG:NE	1:B:77:GLU:OE2	2.49	0.44
1:B:156:LEU:HD12	1:B:156:LEU:HA	1.78	0.44
1:C:23:ARG:HE	1:C:483:THR:HG21	1.82	0.44
1:C:180:MET:CA	1:C:180:MET:HE3	2.47	0.44
1:C:206:PRO:O	1:C:207:ILE:C	2.57	0.44
1:C:432:ILE:HG22	1:C:434:ILE:HD11	1.99	0.44
1:D:112:ALA:O	1:D:115:MET:N	2.50	0.44
1:D:390:LEU:HD22	1:E:396:VAL:CG2	2.48	0.44
1:D:433:PRO:C	1:D:435:VAL:N	2.75	0.44
1:F:220:GLY:O	1:F:223:VAL:HB	2.17	0.44
1:F:450:LYS:O	1:F:451:ASP:C	2.60	0.44
1:A:144:GLU:O	1:A:147:LYS:HB2	2.17	0.44
1:A:350:GLU:HG2	1:A:355:PRO:CG	2.48	0.44
1:B:49:VAL:C	1:B:51:GLY:N	2.76	0.44
1:B:407:ARG:NH1	1:B:411:TYR:CD2	2.85	0.44
1:B:431:THR:HG22	1:B:433:PRO:HD3	1.99	0.44
1:C:27:ILE:HG22	1:C:475:TYR:CD1	2.52	0.44
1:C:259:VAL:HG21	1:C:351:GLY:O	2.17	0.44
1:D:180:MET:HE3	1:D:183:ILE:HD12	1.99	0.44
1:D:398:TYR:CE2	1:E:401:LEU:HD22	2.52	0.44
1:D:457:LEU:HD22	1:D:461:MET:HG2	1.98	0.44
1:E:28:VAL:CG1	1:E:32:LEU:HD22	2.48	0.44
1:E:71:ARG:HH11	1:E:71:ARG:CB	2.18	0.44
1:F:285:TRP:HE1	1:F:287:PRO:CG	2.29	0.44
1:A:40:GLU:HG3	1:A:40:GLU:O	2.16	0.44
1:A:55:ILE:HD12	1:A:55:ILE:N	2.32	0.44
1:A:206:PRO:HD2	1:A:209:GLN:HB2	1.99	0.44
1:A:251:PHE:HE1	1:A:272:ALA:CB	2.31	0.44
1:A:348:ILE:O	1:A:371:VAL:HG13	2.17	0.44
1:A:452:ILE:HD12	1:A:452:ILE:N	2.32	0.44
1:B:151:ARG:O	1:B:155:GLU:HG2	2.17	0.44
1:B:300:LEU:HD13	1:B:300:LEU:C	2.42	0.44
1:C:212:ILE:O	1:C:212:ILE:HG23	2.16	0.44
1:D:185:ASP:O	1:D:186:THR:C	2.60	0.44
1:D:226:GLY:HA3	1:D:377:LEU:CD1	2.47	0.44
1:D:317:SER:O	1:D:319:LEU:N	2.50	0.44
1:D:415:MET:CE	1:D:419:GLU:HG3	2.45	0.44
1:E:339:ASN:O	1:E:340:ALA:C	2.60	0.44
1:F:23:ARG:HD3	1:F:23:ARG:C	2.43	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:500:ALA:HA	1:F:505:THR:O	2.16	0.44
1:A:209:GLN:NE2	1:F:496:VAL:O	2.51	0.44
1:B:24:GLY:O	1:B:27:ILE:N	2.49	0.44
1:B:157:ALA:HA	1:B:162:ILE:HG22	1.99	0.44
1:B:293:LYS:NZ	1:B:297:ASP:OD2	2.48	0.44
1:D:125:PRO:O	1:D:126:PHE:HD2	2.01	0.44
1:D:435:VAL:HG13	1:D:435:VAL:O	2.16	0.44
1:E:46:ARG:HA	1:E:46:ARG:HE	1.82	0.44
1:E:62:VAL:O	1:E:62:VAL:HG13	2.16	0.44
1:E:186:THR:O	1:E:190:THR:HB	2.18	0.44
1:F:55:ILE:HG22	1:F:56:ILE:N	2.32	0.44
1:F:168:VAL:O	1:F:169:PRO:O	2.35	0.44
1:F:223:VAL:O	1:F:224:PHE:C	2.60	0.44
1:A:169:PRO:HD2	1:A:202:VAL:HG23	1.99	0.44
1:B:427:LYS:C	1:B:428:HIS:ND1	2.76	0.44
1:D:116:THR:H	1:D:128:GLY:HA3	1.83	0.44
1:D:380:GLY:O	1:D:383:THR:HB	2.17	0.44
1:D:402:THR:O	1:D:403:PHE:C	2.58	0.44
1:F:170:ALA:CA	1:F:180:MET:CE	2.96	0.44
1:F:322:ASP:HA	1:F:344:LYS:HB2	1.99	0.44
1:F:474:LYS:NZ	1:F:475:TYR:CE2	2.85	0.44
1:A:299:LYS:HB2	1:A:305:ILE:HG22	2.00	0.44
1:A:317:SER:OG	1:A:320:GLU:OE2	2.36	0.44
1:A:388:GLU:O	1:A:391:LYS:HB3	2.17	0.44
1:B:298:PHE:CZ	1:B:302:HIS:CE1	3.05	0.44
1:B:418:GLN:OE1	1:B:432:ILE:HA	2.18	0.44
1:C:38:THR:O	1:C:38:THR:CG2	2.65	0.44
1:C:340:ALA:HB1	1:C:363:ILE:HG21	2.00	0.44
1:D:79:ILE:HG22	1:D:80:GLU:N	2.31	0.44
1:D:190:THR:HG22	1:D:191:ILE:H	1.79	0.44
1:D:264:MET:HG2	1:D:292:PRO:HG3	2.00	0.44
1:D:265:ARG:HG2	1:D:292:PRO:HB3	1.99	0.44
1:D:386:TYR:OH	1:E:396:VAL:HG22	2.17	0.44
1:E:336:THR:C	1:E:338:SER:H	2.25	0.44
1:F:13:PHE:HD1	1:F:14:PHE:H	1.44	0.44
1:F:34:GLU:HA	1:F:38:THR:CB	2.44	0.44
1:F:89:HIS:HD2	1:F:496:VAL:HG21	1.83	0.44
1:F:130:LYS:HG3	1:F:131:ALA:N	2.32	0.44
1:F:141:THR:OG1	1:F:144:GLU:HG3	2.18	0.44
1:B:51:GLY:CA	1:B:54:ARG:HG3	2.47	0.44
1:B:229:ASN:ND2	1:B:462:GLU:HA	2.33	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:237:MET:O	1:B:242:MET:N	2.50	0.44
1:B:244:PRO:O	1:B:248:ASP:HA	2.18	0.44
1:B:316:GLY:O	1:B:317:SER:C	2.61	0.44
1:B:433:PRO:HA	1:F:420:SER:CB	2.48	0.44
1:C:47:ASN:O	1:C:50:ARG:CG	2.65	0.44
1:C:72:ASP:OD1	1:C:144:GLU:HG2	2.17	0.44
1:C:221:ARG:HE	1:C:225:HIS:HE1	1.65	0.44
1:C:438:ALA:O	1:C:441:GLN:N	2.48	0.44
1:D:72:ASP:OD2	1:D:141:THR:HG21	2.18	0.44
1:D:291:ASP:HA	1:D:292:PRO:HD3	1.80	0.44
1:D:345:ALA:O	1:D:369:ILE:CD1	2.64	0.44
1:D:374:ASP:C	1:D:376:TYR:N	2.75	0.44
1:D:377:LEU:HG	1:D:377:LEU:O	2.17	0.44
1:D:489:ALA:O	1:D:493:VAL:HG23	2.17	0.44
1:F:285:TRP:NE1	1:F:287:PRO:CD	2.81	0.44
1:A:204:GLY:H	1:A:388:GLU:CD	2.25	0.44
1:B:32:LEU:HD21	1:B:494:PHE:CG	2.52	0.44
1:B:168:VAL:CG1	1:B:202:VAL:HA	2.47	0.44
1:D:339:ASN:HD22	1:D:340:ALA:N	2.16	0.44
1:D:440:PHE:CG	1:E:412:HIS:HB3	2.53	0.44
1:E:180:MET:HG3	1:E:202:VAL:HG22	1.99	0.44
1:F:234:ALA:O	1:F:235:SER:C	2.61	0.44
1:F:316:GLY:O	1:F:317:SER:C	2.60	0.44
1:F:383:THR:O	1:F:386:TYR:HB3	2.17	0.44
1:F:418:GLN:HG3	1:F:433:PRO:CD	2.47	0.44
1:A:332:GLU:O	1:A:333:LYS:C	2.61	0.44
1:A:402:THR:O	1:A:403:PHE:C	2.61	0.44
1:B:91:THR:OG1	1:B:92:PRO:HD3	2.18	0.44
1:B:427:LYS:HG2	1:B:430:GLY:CA	2.48	0.44
1:C:47:ASN:O	1:C:50:ARG:HG3	2.18	0.44
1:D:88:GLN:C	1:D:90:ARG:N	2.72	0.44
1:D:135:ILE:HD13	1:D:140:TYR:CE2	2.53	0.44
1:D:326:LEU:O	1:D:328:PRO:HD3	2.18	0.44
1:E:477:LEU:HD13	1:E:483:THR:HG23	2.00	0.44
1:F:27:ILE:HG22	1:F:475:TYR:CD1	2.53	0.44
1:F:146:GLU:HA	1:F:182:TRP:CE3	2.53	0.44
1:F:228:GLU:O	1:F:231:ILE:HG22	2.18	0.44
1:F:320:GLU:OE1	1:F:342:ARG:HB3	2.18	0.44
1:A:38:THR:O	1:A:38:THR:HG22	2.17	0.43
1:B:183:ILE:N	1:B:183:ILE:HD12	2.33	0.43
1:B:231:ILE:O	1:B:231:ILE:HG23	2.17	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:336:THR:C	1:B:338:SER:N	2.74	0.43
1:C:21:PHE:O	1:C:22:ASP:C	2.61	0.43
1:C:57:LYS:O	1:C:86:HIS:HE1	2.01	0.43
1:C:71:ARG:HH11	1:C:71:ARG:CG	2.31	0.43
1:C:78:VAL:O	1:C:78:VAL:CG2	2.66	0.43
1:C:162:ILE:O	1:C:162:ILE:HG12	2.17	0.43
1:D:114:LEU:HD12	1:D:114:LEU:HA	1.80	0.43
1:D:256:PHE:HD1	1:D:299:LYS:HG2	1.83	0.43
1:D:340:ALA:O	1:D:343:VAL:HG22	2.18	0.43
1:D:340:ALA:HB3	1:D:341:PRO:HD3	2.00	0.43
1:D:373:PRO:HD3	1:D:481:LEU:HB2	2.00	0.43
1:E:168:VAL:HA	1:E:201:CYS:O	2.18	0.43
1:E:285:TRP:O	1:E:286:ASN:HB2	2.18	0.43
1:F:63:LEU:HD22	1:F:161:PHE:CD2	2.53	0.43
1:F:97:ILE:HD13	1:F:131:ALA:HB3	2.00	0.43
1:B:91:THR:CB	1:B:92:PRO:HD3	2.48	0.43
1:B:418:GLN:HG2	1:B:422:GLU:OE2	2.18	0.43
1:C:10:ASP:HA	1:C:11:PRO:HD3	1.76	0.43
1:D:306:LEU:CD1	1:D:306:LEU:H	2.32	0.43
1:E:10:ASP:HA	1:E:11:PRO:HD3	1.75	0.43
1:E:69:ILE:HD13	1:E:148:ILE:CG1	2.48	0.43
1:E:380:GLY:O	1:E:384:VAL:HG23	2.18	0.43
1:E:414:LEU:HB3	1:E:434:ILE:HA	1.99	0.43
1:F:33:VAL:C	1:F:38:THR:OG1	2.61	0.43
1:F:46:ARG:HE	1:F:46:ARG:CA	2.30	0.43
1:F:223:VAL:HG11	1:F:263:SER:HG	1.80	0.43
1:A:32:LEU:HD21	1:A:494:PHE:CG	2.53	0.43
1:A:376:TYR:CD1	1:A:377:LEU:N	2.86	0.43
1:A:503:THR:OG1	1:E:151:ARG:CZ	2.66	0.43
1:B:254:GLN:OE1	1:B:319:LEU:HD11	2.19	0.43
1:C:91:THR:OG1	1:C:92:PRO:HD3	2.18	0.43
1:C:157:ALA:N	1:C:162:ILE:HG22	2.33	0.43
1:C:261:LEU:HD12	1:C:261:LEU:C	2.43	0.43
1:C:372:ILE:HA	1:C:373:PRO:HD3	1.61	0.43
1:D:284:ILE:HD12	1:D:311:ALA:CB	2.48	0.43
1:D:465:ALA:O	1:D:469:MET:HG3	2.18	0.43
1:E:86:HIS:CD2	1:E:116:THR:CG2	2.90	0.43
1:E:223:VAL:HG12	1:E:224:PHE:N	2.33	0.43
1:F:34:GLU:CA	1:F:38:THR:HB	2.44	0.43
1:F:59:CYS:SG	1:F:109:LYS:O	2.63	0.43
1:F:153:THR:HG23	1:F:183:ILE:HG23	1.99	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:256:PHE:CZ	1:F:296:GLU:HA	2.51	0.43
1:A:112:ALA:HB1	1:A:129:ALA:HA	2.00	0.43
1:A:334:GLN:N	1:A:355:PRO:O	2.51	0.43
1:A:372:ILE:HG21	1:A:377:LEU:HD13	2.00	0.43
1:B:94:LYS:CB	1:B:126:PHE:CD1	3.01	0.43
1:B:427:LYS:CG	1:B:430:GLY:H	2.31	0.43
1:C:136:ASN:HA	1:C:137:PRO:HD3	1.76	0.43
1:C:336:THR:C	1:C:338:SER:N	2.72	0.43
1:D:231:ILE:O	1:D:237:MET:HG3	2.16	0.43
1:D:268:HIS:C	1:D:270:PHE:N	2.77	0.43
1:D:387:PHE:HD1	1:D:453:VAL:HG13	1.83	0.43
1:D:484:ALA:O	1:D:487:VAL:HB	2.19	0.43
1:E:86:HIS:CD2	1:E:86:HIS:C	2.97	0.43
1:E:136:ASN:C	1:E:138:LYS:H	2.25	0.43
1:E:449:GLU:O	1:E:451:ASP:N	2.51	0.43
1:F:256:PHE:CD1	1:F:299:LYS:HG2	2.53	0.43
1:A:56:ILE:O	1:A:86:HIS:CE1	2.71	0.43
1:A:374:ASP:O	1:A:376:TYR:N	2.52	0.43
1:B:86:HIS:HB3	1:B:116:THR:CG2	2.49	0.43
1:B:169:PRO:HB2	1:B:202:VAL:CG2	2.45	0.43
1:B:171:PRO:HB2	1:B:175:THR:O	2.19	0.43
1:B:256:PHE:CE2	1:B:264:MET:HE1	2.53	0.43
1:C:116:THR:HG22	1:C:128:GLY:N	2.33	0.43
1:C:162:ILE:HA	1:C:167:ASP:O	2.19	0.43
1:C:308:PHE:O	1:C:309:PRO:C	2.62	0.43
1:D:112:ALA:O	1:D:113:SER:C	2.60	0.43
1:D:150:ARG:O	1:D:151:ARG:C	2.61	0.43
1:D:207:ILE:HD11	1:D:212:ILE:C	2.43	0.43
1:D:478:GLY:C	1:D:480:ASP:H	2.24	0.43
1:E:55:ILE:C	1:E:58:PRO:HD2	2.43	0.43
1:E:320:GLU:OE2	1:E:342:ARG:NE	2.51	0.43
1:F:480:ASP:OD2	1:F:483:THR:HG23	2.18	0.43
1:F:503:THR:C	1:F:505:THR:H	2.25	0.43
1:A:90:ARG:HG2	1:A:125:PRO:HA	2.01	0.43
1:A:116:THR:HG22	1:A:128:GLY:H	1.81	0.43
1:A:170:ALA:HA	1:A:180:MET:HE2	2.00	0.43
1:A:176:GLY:O	1:A:178:ARG:N	2.52	0.43
1:B:94:LYS:HB2	1:B:126:PHE:CG	2.52	0.43
1:B:147:LYS:O	1:B:151:ARG:HG3	2.18	0.43
1:C:76:TRP:CD1	1:F:502:VAL:HG11	2.53	0.43
1:C:90:ARG:HG2	1:C:125:PRO:C	2.43	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:386:TYR:O	1:C:390:LEU:HG	2.19	0.43
1:C:440:PHE:CD2	1:D:412:HIS:HB3	2.54	0.43
1:D:130:LYS:HG3	1:D:131:ALA:N	2.32	0.43
1:D:383:THR:O	1:D:386:TYR:HB3	2.18	0.43
1:E:136:ASN:OD1	1:E:138:LYS:CB	2.66	0.43
1:E:146:GLU:HA	1:E:182:TRP:CE3	2.53	0.43
1:E:298:PHE:CZ	1:E:302:HIS:HE1	2.37	0.43
1:E:410:ASN:O	1:E:413:LEU:HB2	2.19	0.43
1:F:224:PHE:CE2	1:F:266:TYR:O	2.71	0.43
1:F:286:ASN:ND2	1:F:310:LYS:O	2.50	0.43
1:F:474:LYS:NZ	1:F:475:TYR:CZ	2.85	0.43
1:A:212:ILE:CG1	1:A:449:GLU:OE1	2.67	0.43
1:A:254:GLN:O	1:A:254:GLN:HG2	2.17	0.43
1:B:63:LEU:HD21	1:B:65:LEU:CD2	2.49	0.43
1:B:365:LEU:O	1:B:366:GLU:C	2.62	0.43
1:C:229:ASN:OD1	1:C:466:ARG:NH1	2.51	0.43
1:C:503:THR:CG2	1:F:151:ARG:HD3	2.48	0.43
1:D:38:THR:O	1:D:39:ARG:C	2.61	0.43
1:D:63:LEU:CD2	1:D:65:LEU:HD21	2.39	0.43
1:D:400:ARG:HB3	1:D:401:LEU:HD12	2.01	0.43
1:D:410:ASN:CG	1:E:413:LEU:HD21	2.44	0.43
1:E:38:THR:HG22	1:E:38:THR:O	2.18	0.43
1:E:116:THR:CG2	1:E:128:GLY:CA	2.96	0.43
1:E:319:LEU:N	1:E:319:LEU:CD1	2.81	0.43
1:E:402:THR:O	1:E:403:PHE:C	2.61	0.43
1:F:221:ARG:HD3	1:F:454:HIS:CG	2.53	0.43
1:A:17:VAL:HG22	1:A:114:LEU:CD1	2.49	0.43
1:A:229:ASN:ND2	1:A:462:GLU:HA	2.33	0.43
1:A:365:LEU:HD23	1:A:365:LEU:C	2.44	0.43
1:B:177:GLU:HB2	1:B:206:PRO:HG3	2.00	0.43
1:B:234:ALA:O	1:B:235:SER:C	2.62	0.43
1:C:94:LYS:HB3	1:C:115:MET:HE1	2.01	0.43
1:C:113:SER:O	1:C:114:LEU:C	2.61	0.43
1:C:151:ARG:NH2	1:F:504:PHE:CE1	2.87	0.43
1:C:334:GLN:HE21	1:C:334:GLN:N	2.16	0.43
1:C:503:THR:C	1:C:505:THR:H	2.26	0.43
1:D:57:LYS:HB3	1:D:58:PRO:HD3	2.00	0.43
1:D:180:MET:HG2	1:D:203:THR:O	2.18	0.43
1:D:243:THR:O	1:D:243:THR:CG2	2.65	0.43
1:D:268:HIS:ND1	1:D:292:PRO:CD	2.82	0.43
1:D:295:LEU:HD11	1:D:305:ILE:HB	2.00	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:43:GLU:O	1:E:44:GLN:C	2.62	0.43
1:A:436:PRO:HB3	1:A:440:PHE:CD1	2.46	0.43
1:B:33:VAL:O	1:B:37:ARG:HG3	2.18	0.43
1:B:122:VAL:O	1:B:124:VAL:HG23	2.19	0.43
1:B:376:TYR:O	1:B:378:ASN:N	2.50	0.43
1:C:21:PHE:CE2	1:C:57:LYS:HB2	2.54	0.43
1:C:396:VAL:CG1	1:E:386:TYR:OH	2.55	0.43
1:C:432:ILE:CG2	1:C:434:ILE:HD11	2.48	0.43
1:D:251:PHE:CD2	1:D:327:ILE:HD11	2.52	0.43
1:E:168:VAL:HG13	1:E:202:VAL:HA	2.00	0.43
1:E:425:PHE:CD1	1:E:425:PHE:C	2.96	0.43
1:F:13:PHE:O	1:F:14:PHE:C	2.61	0.43
1:F:83:ARG:HD2	1:F:131:ALA:CB	2.40	0.43
1:F:180:MET:HE3	1:F:202:VAL:HG22	1.98	0.43
1:F:485:ALA:O	1:F:488:ASN:HB3	2.18	0.43
1:A:37:ARG:NH1	1:A:37:ARG:O	2.52	0.43
1:A:142:ASP:O	1:A:145:LEU:HB2	2.19	0.43
1:A:376:TYR:HD1	1:A:377:LEU:N	2.16	0.43
1:B:93:CYS:HB3	1:B:167:ASP:OD1	2.19	0.43
1:B:133:VAL:O	1:B:135:ILE:N	2.52	0.43
1:C:10:ASP:N	1:C:10:ASP:OD1	2.52	0.43
1:C:151:ARG:NH2	1:F:503:THR:OG1	2.52	0.43
1:C:213:HIS:HB2	1:C:449:GLU:HG2	2.01	0.43
1:C:435:VAL:HA	1:C:436:PRO:HD3	1.78	0.43
1:D:358:PRO:O	1:D:361:ASP:HB2	2.19	0.43
1:E:44:GLN:O	1:E:44:GLN:CD	2.61	0.43
1:E:69:ILE:HD13	1:E:148:ILE:HG12	2.01	0.43
1:F:108:VAL:CG2	1:F:109:LYS:N	2.82	0.43
1:A:78:VAL:O	1:A:78:VAL:CG2	2.66	0.42
1:A:242:MET:HA	1:A:244:PRO:HG3	2.00	0.42
1:A:390:LEU:HD22	1:B:396:VAL:HG22	2.00	0.42
1:B:183:ILE:O	1:B:184:ALA:C	2.62	0.42
1:B:505:THR:C	1:F:150:ARG:HH12	2.27	0.42
1:C:436:PRO:HA	1:D:416:SER:CB	2.47	0.42
1:D:151:ARG:O	1:D:155:GLU:HG2	2.19	0.42
1:D:240:LEU:HD21	1:D:479:LEU:CD2	2.48	0.42
1:D:373:PRO:HG3	1:D:482:ARG:HA	2.01	0.42
1:E:223:VAL:HG22	1:E:377:LEU:HG	2.01	0.42
1:E:390:LEU:O	1:E:391:LYS:C	2.61	0.42
1:E:399:GLY:O	1:E:400:ARG:C	2.60	0.42
1:E:418:GLN:CG	1:E:433:PRO:HD2	2.49	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:69:ILE:HA	1:F:151:ARG:NH1	2.34	0.42
1:A:53:LEU:HD13	1:A:494:PHE:HD1	1.84	0.42
1:B:285:TRP:NE1	1:B:287:PRO:HG3	2.34	0.42
1:B:332:GLU:O	1:B:333:LYS:C	2.62	0.42
1:B:425:PHE:HE1	1:B:427:LYS:HD3	1.84	0.42
1:C:117:TYR:CE1	1:C:490:ILE:HD13	2.53	0.42
1:C:327:ILE:O	1:C:327:ILE:HG12	2.19	0.42
1:C:359:GLU:O	1:C:363:ILE:HD13	2.19	0.42
1:C:425:PHE:CD1	1:C:427:LYS:HB2	2.54	0.42
1:D:221:ARG:NH2	1:D:266:TYR:OH	2.52	0.42
1:D:254:GLN:NE2	1:D:334:GLN:HG2	2.34	0.42
1:D:444:ILE:O	1:D:444:ILE:HG22	2.19	0.42
1:D:471:THR:O	1:D:474:LYS:HB3	2.19	0.42
1:E:144:GLU:O	1:E:148:ILE:HG13	2.19	0.42
1:E:168:VAL:CG1	1:E:202:VAL:HA	2.50	0.42
1:E:293:LYS:HZ2	1:E:297:ASP:CG	2.27	0.42
1:E:448:SER:O	1:E:451:ASP:HB2	2.19	0.42
1:E:502:VAL:O	1:E:505:THR:HG21	2.19	0.42
1:A:195:ASP:O	1:A:197:ASN:N	2.52	0.42
1:B:86:HIS:CD2	1:B:87:SER:HB2	2.55	0.42
1:B:374:ASP:O	1:B:375:LEU:C	2.62	0.42
1:C:124:VAL:HA	1:C:125:PRO:HD2	1.52	0.42
1:C:170:ALA:HB1	1:C:171:PRO:HD3	2.00	0.42
1:C:300:LEU:HD13	1:C:300:LEU:HA	1.92	0.42
1:C:413:LEU:H	1:C:413:LEU:CD2	2.32	0.42
1:C:418:GLN:HB2	1:C:433:PRO:HD2	2.01	0.42
1:C:502:VAL:HG23	1:C:504:PHE:H	1.85	0.42
1:D:135:ILE:HG23	1:D:136:ASN:N	2.33	0.42
1:D:376:TYR:OH	1:D:465:ALA:HB2	2.19	0.42
1:D:500:ALA:HB1	1:D:505:THR:C	2.44	0.42
1:E:71:ARG:NH1	1:E:144:GLU:OE2	2.52	0.42
1:E:179:GLU:O	1:E:183:ILE:HG13	2.19	0.42
1:F:217:SER:O	1:F:218:ALA:C	2.62	0.42
1:F:462:GLU:HB3	1:F:463:ALA:H	1.71	0.42
1:A:135:ILE:HG23	1:A:136:ASN:N	2.33	0.42
1:A:243:THR:O	1:A:243:THR:CG2	2.64	0.42
1:A:360:ALA:O	1:A:364:PHE:HD2	2.03	0.42
1:A:502:VAL:HG11	1:E:76:TRP:CE2	2.54	0.42
1:B:233:GLU:HG2	1:B:236:TYR:CD1	2.53	0.42
1:C:82:TYR:O	1:C:131:ALA:HB1	2.19	0.42
1:C:396:VAL:HG13	1:E:386:TYR:CZ	2.53	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:115:MET:HE1	1:D:382:VAL:HG22	2.00	0.42
1:D:317:SER:C	1:D:319:LEU:N	2.76	0.42
1:D:482:ARG:HE	1:D:482:ARG:HB2	1.60	0.42
1:D:485:ALA:O	1:D:486:TYR:C	2.62	0.42
1:E:21:PHE:CD2	1:E:21:PHE:C	2.98	0.42
1:E:105:VAL:O	1:E:109:LYS:HG3	2.19	0.42
1:E:196:ILE:O	1:E:395:HIS:CE1	2.72	0.42
1:E:252:VAL:CG2	1:E:275:ILE:HG22	2.45	0.42
1:F:82:TYR:CD1	1:F:82:TYR:N	2.87	0.42
1:F:83:ARG:HG2	1:F:161:PHE:HB3	2.00	0.42
1:F:253:VAL:HB	1:F:327:ILE:HD11	2.00	0.42
1:F:285:TRP:NE1	1:F:287:PRO:CG	2.82	0.42
1:F:318:ILE:O	1:F:319:LEU:C	2.62	0.42
1:A:143:ASN:HD21	1:C:70:ARG:NH2	2.06	0.42
1:B:464:SER:O	1:B:468:ILE:HG12	2.20	0.42
1:C:168:VAL:HG13	1:C:201:CYS:O	2.20	0.42
1:C:435:VAL:O	1:C:435:VAL:CG1	2.63	0.42
1:D:57:LYS:N	1:D:58:PRO:HD2	2.35	0.42
1:D:94:LYS:HE3	1:D:385:SER:HB2	2.01	0.42
1:D:387:PHE:N	1:D:387:PHE:CD2	2.86	0.42
1:E:99:TYR:HB3	1:E:137:PRO:HG3	2.02	0.42
1:E:136:ASN:OD1	1:E:138:LYS:HB2	2.19	0.42
1:E:206:PRO:HD2	1:E:209:GLN:CG	2.48	0.42
1:E:221:ARG:HG2	1:E:221:ARG:NH1	2.34	0.42
1:E:282:GLY:H	1:E:306:LEU:HD11	1.84	0.42
1:F:223:VAL:CG1	1:F:263:SER:OG	2.62	0.42
1:F:384:VAL:HA	1:F:387:PHE:CD1	2.54	0.42
1:A:187:TYR:CE2	1:A:192:GLY:HA3	2.55	0.42
1:A:261:LEU:O	1:A:262:HIS:C	2.62	0.42
1:B:24:GLY:O	1:B:25:ALA:C	2.63	0.42
1:B:33:VAL:HG12	1:B:34:GLU:N	2.35	0.42
1:B:62:VAL:HG11	1:B:109:LYS:HZ3	1.84	0.42
1:B:157:ALA:HA	1:B:162:ILE:CG2	2.49	0.42
1:B:437:THR:O	1:B:438:ALA:C	2.62	0.42
1:C:464:SER:O	1:C:465:ALA:C	2.63	0.42
1:C:504:PHE:CB	1:F:70:ARG:HH22	2.32	0.42
1:D:242:MET:HE2	1:D:244:PRO:HG3	2.01	0.42
1:D:342:ARG:NH1	1:D:342:ARG:CB	2.82	0.42
1:E:89:HIS:CE1	1:E:493:VAL:HG22	2.55	0.42
1:E:336:THR:C	1:E:338:SER:N	2.76	0.42
1:E:386:TYR:CE2	1:E:390:LEU:HD11	2.54	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:397:SER:O	1:E:400:ARG:HB2	2.19	0.42
1:E:477:LEU:HD22	1:E:483:THR:HG21	2.02	0.42
1:F:149:THR:HG21	1:F:182:TRP:HE3	1.84	0.42
1:F:316:GLY:O	1:F:317:SER:O	2.37	0.42
1:A:195:ASP:C	1:A:197:ASN:N	2.77	0.42
1:A:314:TYR:CE2	1:A:318:ILE:HA	2.52	0.42
1:B:336:THR:C	1:B:338:SER:H	2.28	0.42
1:C:71:ARG:HD2	1:C:77:GLU:HB2	2.02	0.42
1:C:83:ARG:HD3	1:C:131:ALA:CB	2.33	0.42
1:C:409:SER:OG	1:E:443:ARG:NH2	2.53	0.42
1:C:482:ARG:O	1:C:483:THR:C	2.63	0.42
1:D:120:ALA:O	1:D:492:LYS:NZ	2.37	0.42
1:D:154:MET:O	1:D:158:LYS:HG3	2.20	0.42
1:D:230:PHE:CD2	1:D:469:MET:HE2	2.55	0.42
1:D:371:VAL:CG1	1:D:482:ARG:HH21	2.31	0.42
1:E:374:ASP:OD2	1:E:375:LEU:N	2.53	0.42
1:F:100:SER:O	1:F:103:VAL:HG13	2.19	0.42
1:F:133:VAL:O	1:F:135:ILE:N	2.53	0.42
1:F:136:ASN:C	1:F:138:LYS:N	2.76	0.42
1:F:185:ASP:O	1:F:189:SER:OG	2.36	0.42
1:F:283:SER:HB2	1:F:314:TYR:O	2.20	0.42
1:A:433:PRO:C	1:A:435:VAL:N	2.78	0.42
1:A:500:ALA:C	1:A:505:THR:O	2.63	0.42
1:B:158:LYS:HD3	1:E:193:HIS:CE1	2.55	0.42
1:B:285:TRP:CD1	1:B:286:ASN:N	2.87	0.42
1:B:403:PHE:CD2	1:B:447:ALA:HB1	2.54	0.42
1:B:475:TYR:CE2	1:B:487:VAL:HG11	2.55	0.42
1:B:502:VAL:CG2	1:B:503:THR:H	2.23	0.42
1:C:225:HIS:CE1	1:C:458:ALA:HB2	2.55	0.42
1:C:242:MET:O	1:C:243:THR:C	2.63	0.42
1:C:262:HIS:O	1:C:263:SER:C	2.62	0.42
1:C:413:LEU:HD22	1:C:413:LEU:N	2.34	0.42
1:D:364:PHE:CD1	1:D:369:ILE:HG21	2.55	0.42
1:E:23:ARG:O	1:E:23:ARG:HD3	2.20	0.42
1:E:67:PHE:HE2	1:E:152:PHE:HD1	1.67	0.42
1:F:168:VAL:HG13	1:F:202:VAL:HA	2.02	0.42
1:F:462:GLU:O	1:F:465:ALA:N	2.52	0.42
1:F:480:ASP:OD1	1:F:483:THR:HG23	2.20	0.42
1:A:240:LEU:CD2	1:A:479:LEU:HD21	2.50	0.42
1:A:367:ARG:HG2	1:A:367:ARG:H	1.68	0.42
1:B:33:VAL:O	1:B:34:GLU:O	2.38	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:19:GLY:O	1:D:20:PHE:C	2.63	0.42
1:D:51:GLY:O	1:D:54:ARG:CG	2.68	0.42
1:D:108:VAL:HG23	1:D:109:LYS:N	2.34	0.42
1:D:335:LEU:HD12	1:D:356:THR:HG22	2.02	0.42
1:E:367:ARG:NH1	1:E:367:ARG:CB	2.82	0.42
1:F:90:ARG:HD2	1:F:90:ARG:HA	1.93	0.42
1:F:220:GLY:O	1:F:221:ARG:C	2.62	0.42
1:F:480:ASP:CG	1:F:483:THR:HG23	2.45	0.42
1:A:250:THR:HB	1:A:324:ASP:OD1	2.20	0.42
1:A:329:ALA:O	1:A:330:ALA:HB2	2.20	0.42
1:A:371:VAL:O	1:A:481:LEU:HD22	2.20	0.42
1:A:433:PRO:CD	1:A:434:ILE:N	2.83	0.42
1:B:178:ARG:O	1:B:179:GLU:C	2.62	0.42
1:B:398:TYR:HB3	1:B:452:ILE:HD12	2.01	0.42
1:D:94:LYS:NZ	1:D:170:ALA:HB2	2.35	0.42
1:D:122:VAL:O	1:D:123:ASP:C	2.62	0.42
1:D:340:ALA:N	1:D:341:PRO:CD	2.83	0.42
1:D:343:VAL:HG23	1:D:367:ARG:NH2	2.35	0.42
1:E:93:CYS:HA	1:E:127:GLY:O	2.20	0.42
1:E:224:PHE:CD2	1:E:267:LEU:HD22	2.55	0.42
1:E:488:ASN:O	1:E:492:LYS:HG3	2.20	0.42
1:E:502:VAL:HG23	1:E:504:PHE:H	1.85	0.42
1:F:34:GLU:O	1:F:35:ASP:C	2.63	0.42
1:F:62:VAL:HG23	1:F:84:ALA:HB2	2.01	0.42
1:F:177:GLU:O	1:F:178:ARG:C	2.63	0.42
1:F:251:PHE:HB2	1:F:325:ILE:O	2.19	0.42
1:A:91:THR:HG22	1:A:165:GLY:O	2.20	0.41
1:A:320:GLU:O	1:A:321:ALA:O	2.37	0.41
1:B:52:ILE:HD13	1:B:52:ILE:HA	1.90	0.41
1:B:193:HIS:CE1	1:E:158:LYS:HD3	2.55	0.41
1:B:393:LEU:C	1:B:395:HIS:N	2.77	0.41
1:C:242:MET:O	1:C:243:THR:HG22	2.20	0.41
1:C:377:LEU:HD12	1:C:377:LEU:O	2.20	0.41
1:C:398:TYR:CZ	1:D:401:LEU:CD2	3.03	0.41
1:C:432:ILE:O	1:D:420:SER:OG	2.38	0.41
1:D:165:GLY:HA3	1:E:196:ILE:HG13	2.02	0.41
1:D:240:LEU:CD2	1:D:479:LEU:HD23	2.50	0.41
1:D:254:GLN:HE22	1:D:334:GLN:CG	2.33	0.41
1:E:302:HIS:O	1:E:303:GLY:C	2.61	0.41
1:F:31:LYS:O	1:F:34:GLU:HG2	2.20	0.41
1:F:145:LEU:O	1:F:149:THR:HG23	2.19	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:171:PRO:HD3	1:F:180:MET:HE2	2.02	0.41
1:A:356:THR:OG1	1:A:482:ARG:NH2	2.54	0.41
1:A:440:PHE:CG	1:B:412:HIS:HB3	2.54	0.41
1:B:37:ARG:HH11	1:B:37:ARG:CB	2.12	0.41
1:B:59:CYS:HA	1:B:86:HIS:HA	2.02	0.41
1:B:399:GLY:O	1:B:400:ARG:C	2.62	0.41
1:C:32:LEU:HD21	1:C:494:PHE:CG	2.55	0.41
1:C:46:ARG:HA	1:C:46:ARG:HE	1.84	0.41
1:C:321:ALA:O	1:C:344:LYS:HB2	2.20	0.41
1:C:500:ALA:HA	1:C:505:THR:OXT	2.20	0.41
1:D:370:MET:HE2	1:D:370:MET:HB3	1.86	0.41
1:E:72:ASP:OD1	1:E:141:THR:CG2	2.68	0.41
1:E:221:ARG:HG3	1:E:266:TYR:CE2	2.55	0.41
1:E:442:ASP:O	1:E:443:ARG:C	2.62	0.41
1:F:44:GLN:HG3	1:F:44:GLN:O	2.20	0.41
1:F:229:ASN:OD1	1:F:462:GLU:HG3	2.19	0.41
1:F:333:LYS:HE3	1:F:357:THR:CG2	2.29	0.41
1:F:343:VAL:HG11	1:F:364:PHE:CZ	2.55	0.41
1:A:116:THR:CG2	1:A:128:GLY:H	2.32	0.41
1:A:170:ALA:HB1	1:A:171:PRO:CD	2.50	0.41
1:B:267:LEU:HA	1:B:267:LEU:HD13	1.81	0.41
1:C:23:ARG:O	1:C:27:ILE:HG13	2.20	0.41
1:C:323:CYS:SG	1:C:345:ALA:HB2	2.60	0.41
1:D:50:ARG:C	1:D:52:ILE:N	2.76	0.41
1:D:227:ILE:HD11	1:D:349:ALA:HB1	1.97	0.41
1:D:281:ASP:HB2	1:D:282:GLY:H	1.62	0.41
1:D:318:ILE:C	1:D:318:ILE:CD1	2.93	0.41
1:D:416:SER:O	1:D:420:SER:CB	2.68	0.41
1:F:378:ASN:ND2	1:F:378:ASN:C	2.78	0.41
1:A:43:GLU:HB3	1:A:45:LYS:HG3	2.02	0.41
1:A:49:VAL:O	1:A:49:VAL:HG22	2.20	0.41
1:A:374:ASP:C	1:A:376:TYR:N	2.77	0.41
1:A:479:LEU:N	1:A:479:LEU:HD12	2.35	0.41
1:B:34:GLU:O	1:B:38:THR:N	2.49	0.41
1:B:145:LEU:HA	1:B:145:LEU:HD23	1.76	0.41
1:B:365:LEU:HD23	1:B:365:LEU:C	2.44	0.41
1:B:435:VAL:HG11	1:F:423:ARG:HH21	1.85	0.41
1:C:502:VAL:HG11	1:F:76:TRP:CD1	2.55	0.41
1:D:252:VAL:CG1	1:D:276:ALA:HB3	2.47	0.41
1:D:486:TYR:O	1:D:490:ILE:HG13	2.20	0.41
1:D:498:ASN:C	1:D:500:ALA:H	2.29	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:122:VAL:HG23	1:E:124:VAL:CG2	2.46	0.41
1:E:152:PHE:O	1:E:156:LEU:HD13	2.21	0.41
1:E:345:ALA:O	1:E:369:ILE:CD1	2.68	0.41
1:E:414:LEU:HA	1:E:414:LEU:HD23	1.75	0.41
1:F:31:LYS:O	1:F:32:LEU:C	2.64	0.41
1:F:168:VAL:HG13	1:F:201:CYS:C	2.45	0.41
1:F:170:ALA:CA	1:F:180:MET:HE1	2.51	0.41
1:F:224:PHE:C	1:F:224:PHE:CD1	2.99	0.41
1:A:298:PHE:CD2	1:A:305:ILE:HA	2.56	0.41
1:B:43:GLU:C	1:B:45:LYS:N	2.77	0.41
1:B:261:LEU:HD12	1:B:261:LEU:O	2.20	0.41
1:C:437:THR:HG23	1:D:416:SER:CA	2.48	0.41
1:D:382:VAL:HA	1:D:385:SER:OG	2.21	0.41
1:D:418:GLN:OE1	1:D:434:ILE:HG23	2.21	0.41
1:D:499:GLU:OE1	1:E:208:SER:OG	2.30	0.41
1:E:43:GLU:C	1:E:45:LYS:N	2.75	0.41
1:E:70:ARG:O	1:E:71:ARG:C	2.62	0.41
1:E:136:ASN:C	1:E:138:LYS:N	2.78	0.41
1:E:226:GLY:O	1:E:227:ILE:C	2.62	0.41
1:F:195:ASP:OD2	1:F:195:ASP:C	2.64	0.41
1:F:498:ASN:C	1:F:500:ALA:H	2.28	0.41
1:A:256:PHE:HE2	1:A:264:MET:HE1	1.85	0.41
1:A:374:ASP:O	1:A:375:LEU:C	2.63	0.41
1:B:53:LEU:O	1:B:54:ARG:C	2.63	0.41
1:B:86:HIS:CG	1:B:116:THR:HG21	2.54	0.41
1:B:290:ILE:HG23	1:B:308:PHE:HE2	1.85	0.41
1:B:298:PHE:CE2	1:B:302:HIS:HE1	2.37	0.41
1:B:319:LEU:HD23	1:B:335:LEU:HD23	2.03	0.41
1:B:400:ARG:HD2	1:B:400:ARG:O	2.20	0.41
1:C:94:LYS:HB3	1:C:115:MET:CE	2.51	0.41
1:C:312:LYS:O	1:C:313:PRO:C	2.63	0.41
1:C:343:VAL:HG21	1:C:364:PHE:HE1	1.84	0.41
1:D:99:TYR:CZ	1:D:149:THR:HG22	2.46	0.41
1:D:238:SER:C	1:D:240:LEU:N	2.70	0.41
1:D:401:LEU:HD12	1:D:401:LEU:N	2.36	0.41
1:D:427:LYS:C	1:D:428:HIS:ND1	2.78	0.41
1:E:314:TYR:HE2	1:E:318:ILE:HA	1.85	0.41
1:F:55:ILE:O	1:F:58:PRO:CG	2.69	0.41
1:F:348:ILE:HG22	1:F:371:VAL:HG13	2.02	0.41
1:F:348:ILE:O	1:F:372:ILE:HG13	2.20	0.41
1:F:384:VAL:O	1:F:387:PHE:HB2	2.20	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:21:PHE:CD2	1:A:57:LYS:HG3	2.55	0.41
1:A:169:PRO:O	1:A:202:VAL:CG2	2.69	0.41
1:A:261:LEU:C	1:A:261:LEU:HD12	2.45	0.41
1:A:473:MET:O	1:A:475:TYR:N	2.53	0.41
1:B:71:ARG:HB3	1:B:71:ARG:HH11	1.86	0.41
1:B:244:PRO:HG2	1:B:248:ASP:H	1.76	0.41
1:B:404:LYS:NZ	1:B:407:ARG:NH2	2.68	0.41
1:C:265:ARG:HG2	1:C:292:PRO:HB3	2.03	0.41
1:D:334:GLN:N	1:D:355:PRO:O	2.54	0.41
1:D:343:VAL:HG22	1:D:367:ARG:HH21	1.85	0.41
1:D:373:PRO:HG3	1:D:482:ARG:N	2.35	0.41
1:D:421:LEU:HD23	1:E:421:LEU:HD11	2.01	0.41
1:D:425:PHE:C	1:D:425:PHE:CD2	2.95	0.41
1:E:57:LYS:N	1:E:58:PRO:CD	2.83	0.41
1:E:404:LYS:O	1:E:405:TYR:C	2.60	0.41
1:F:52:ILE:HG13	1:F:494:PHE:CE1	2.56	0.41
1:F:247:GLY:O	1:F:248:ASP:C	2.63	0.41
1:F:284:ILE:CG1	1:F:305:ILE:HD12	2.51	0.41
1:F:479:LEU:N	1:F:479:LEU:HD12	2.36	0.41
1:A:52:ILE:O	1:A:55:ILE:HB	2.21	0.41
1:A:230:PHE:CE2	1:A:469:MET:HE2	2.56	0.41
1:A:418:GLN:OE1	1:A:434:ILE:HG23	2.20	0.41
1:B:180:MET:CA	1:B:180:MET:CE	2.99	0.41
1:B:207:ILE:HG12	1:B:213:HIS:CD2	2.56	0.41
1:B:284:ILE:HG13	1:B:311:ALA:HB1	2.03	0.41
1:C:91:THR:HB	1:C:92:PRO:HD3	2.02	0.41
1:D:43:GLU:CB	1:D:45:LYS:HG3	2.43	0.41
1:D:396:VAL:HG12	1:D:397:SER:H	1.85	0.41
1:D:407:ARG:O	1:D:408:ASP:C	2.64	0.41
1:E:38:THR:HG23	1:E:41:SER:CB	2.29	0.41
1:E:336:THR:O	1:E:339:ASN:ND2	2.54	0.41
1:F:37:ARG:HE	1:F:46:ARG:HD3	1.86	0.41
1:F:349:ALA:HB2	1:F:372:ILE:HD12	2.01	0.41
1:F:350:GLU:HB3	1:F:374:ASP:HB3	2.02	0.41
1:A:54:ARG:HH12	1:E:78:VAL:HG13	1.86	0.41
1:A:72:ASP:OD1	1:A:144:GLU:CG	2.66	0.41
1:A:350:GLU:CD	1:A:482:ARG:NH2	2.79	0.41
1:A:375:LEU:HD22	1:A:486:TYR:CD2	2.55	0.41
1:A:378:ASN:C	1:A:380:GLY:H	2.29	0.41
1:A:438:ALA:O	1:A:441:GLN:N	2.54	0.41
1:B:21:PHE:CD1	1:B:117:TYR:OH	2.68	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:180:MET:HE3	1:B:180:MET:HA	2.03	0.41
1:C:23:ARG:HG3	1:C:23:ARG:NH1	2.36	0.41
1:C:77:GLU:HA	1:F:54:ARG:NH1	2.35	0.41
1:C:108:VAL:HG23	1:C:109:LYS:H	1.84	0.41
1:C:117:TYR:CE1	1:C:490:ILE:CD1	3.04	0.41
1:C:432:ILE:HG22	1:C:434:ILE:HG12	2.03	0.41
1:C:437:THR:O	1:C:438:ALA:C	2.64	0.41
1:D:19:GLY:O	1:D:22:ASP:N	2.54	0.41
1:D:256:PHE:HE2	1:D:264:MET:CE	2.33	0.41
1:D:306:LEU:N	1:D:306:LEU:CD1	2.84	0.41
1:D:390:LEU:HD21	1:E:396:VAL:HG23	2.03	0.41
1:D:435:VAL:HA	1:D:436:PRO:HD3	1.84	0.41
1:D:440:PHE:HE1	1:E:413:LEU:HD22	1.85	0.41
1:D:452:ILE:HD13	1:E:405:TYR:CD1	2.56	0.41
1:E:113:SER:O	1:E:114:LEU:C	2.63	0.41
1:F:29:GLU:OE2	1:F:50:ARG:HD2	2.21	0.41
1:F:63:LEU:HG	1:F:65:LEU:HD21	2.02	0.41
1:F:136:ASN:O	1:F:138:LYS:N	2.54	0.41
1:F:254:GLN:HE22	1:F:334:GLN:HG2	1.86	0.41
1:F:254:GLN:HB3	1:F:328:PRO:HA	2.02	0.41
1:F:432:ILE:N	1:F:432:ILE:CD1	2.64	0.41
1:F:500:ALA:HB1	1:F:505:THR:O	2.21	0.41
1:A:133:VAL:O	1:A:134:LYS:C	2.64	0.41
1:C:50:ARG:C	1:C:52:ILE:N	2.79	0.41
1:C:126:PHE:HZ	1:C:389:TRP:CE3	2.39	0.41
1:C:239:ILE:HG22	1:C:239:ILE:O	2.19	0.41
1:C:252:VAL:HG13	1:C:276:ALA:CB	2.36	0.41
1:D:211:GLY:O	1:D:391:LYS:HE2	2.21	0.41
1:E:13:PHE:CE1	1:E:107:GLU:HA	2.56	0.41
1:E:330:ALA:O	1:E:331:SER:C	2.63	0.41
1:E:339:ASN:ND2	1:E:340:ALA:N	2.67	0.41
1:E:340:ALA:O	1:E:343:VAL:HG22	2.21	0.41
1:E:492:LYS:O	1:E:493:VAL:C	2.64	0.41
1:F:35:ASP:CG	1:F:36:LEU:N	2.78	0.41
1:F:217:SER:HA	1:F:262:HIS:HD2	1.84	0.41
1:F:227:ILE:HD11	1:F:349:ALA:CB	2.50	0.41
1:F:425:PHE:CD1	1:F:427:LYS:HB2	2.56	0.41
1:A:124:VAL:HA	1:A:125:PRO:HD3	1.89	0.40
1:B:143:ASN:HD21	1:E:70:ARG:NH1	2.13	0.40
1:B:211:GLY:HA2	1:B:388:GLU:OE1	2.21	0.40
1:B:268:HIS:O	1:B:270:PHE:N	2.54	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:363:ILE:HG22	1:B:367:ARG:HD3	2.04	0.40
1:C:157:ALA:O	1:C:159:LYS:N	2.55	0.40
1:C:367:ARG:O	1:C:368:ASN:C	2.63	0.40
1:D:449:GLU:O	1:D:453:VAL:HG23	2.21	0.40
1:E:63:LEU:O	1:E:82:TYR:HA	2.21	0.40
1:E:89:HIS:NE2	1:E:493:VAL:HG22	2.36	0.40
1:E:350:GLU:OE1	1:E:374:ASP:N	2.49	0.40
1:E:460:THR:HG22	1:E:461:MET:N	2.34	0.40
1:F:79:ILE:HD12	1:F:79:ILE:N	2.36	0.40
1:A:12:ASN:O	1:A:13:PHE:C	2.64	0.40
1:A:367:ARG:HB2	1:A:367:ARG:HH11	1.87	0.40
1:B:281:ASP:HB2	1:B:282:GLY:H	1.55	0.40
1:B:424:LYS:O	1:B:425:PHE:HB2	2.20	0.40
1:B:433:PRO:C	1:B:435:VAL:N	2.80	0.40
1:C:87:SER:O	1:C:127:GLY:HA3	2.21	0.40
1:D:16:MET:CE	1:D:333:LYS:CE	2.99	0.40
1:D:124:VAL:HA	1:D:125:PRO:HD2	1.93	0.40
1:D:240:LEU:HD23	1:D:479:LEU:CD2	2.48	0.40
1:E:327:ILE:HA	1:E:328:PRO:HD3	1.86	0.40
1:E:363:ILE:O	1:E:367:ARG:HG3	2.21	0.40
1:F:33:VAL:C	1:F:38:THR:HG1	2.29	0.40
1:A:227:ILE:CD1	1:A:349:ALA:CB	3.00	0.40
1:A:448:SER:O	1:A:451:ASP:HB2	2.22	0.40
1:A:474:LYS:HD3	1:A:475:TYR:CE2	2.56	0.40
1:B:10:ASP:HA	1:B:11:PRO:HD3	1.76	0.40
1:B:32:LEU:HD21	1:B:494:PHE:CD2	2.57	0.40
1:B:71:ARG:HD2	1:B:77:GLU:OE2	2.21	0.40
1:B:78:VAL:O	1:B:78:VAL:CG2	2.69	0.40
1:B:141:THR:O	1:B:142:ASP:C	2.63	0.40
1:B:206:PRO:HD2	1:B:209:GLN:HB2	2.03	0.40
1:B:244:PRO:HG2	1:B:247:GLY:C	2.43	0.40
1:B:249:LYS:HB2	1:B:272:ALA:HA	2.02	0.40
1:B:293:LYS:NZ	1:B:297:ASP:CG	2.79	0.40
1:B:318:ILE:CD1	1:B:319:LEU:HD12	2.52	0.40
1:B:342:ARG:O	1:B:342:ARG:HG2	2.21	0.40
1:C:152:PHE:O	1:C:156:LEU:HD22	2.22	0.40
1:C:177:GLU:HB2	1:C:206:PRO:HG3	2.02	0.40
1:C:180:MET:HE3	1:C:180:MET:HA	2.02	0.40
1:D:13:PHE:HD1	1:D:14:PHE:H	1.69	0.40
1:D:22:ASP:O	1:D:23:ARG:C	2.65	0.40
1:D:97:ILE:CD1	1:D:131:ALA:HB3	2.40	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:336:THR:N	1:D:339:ASN:HD21	2.17	0.40
1:E:231:ILE:CG2	1:E:232:ASN:N	2.82	0.40
1:E:377:LEU:HA	1:E:377:LEU:HD12	1.83	0.40
1:F:215:ARG:O	1:F:216:ILE:C	2.64	0.40
1:A:28:VAL:CG1	1:A:32:LEU:HD22	2.52	0.40
1:A:90:ARG:HD2	1:A:90:ARG:HA	1.74	0.40
1:A:240:LEU:O	1:A:346:LYS:HE3	2.21	0.40
1:C:13:PHE:CE2	1:C:107:GLU:HG3	2.53	0.40
1:C:196:ILE:O	1:C:395:HIS:CE1	2.74	0.40
1:C:395:HIS:C	1:C:396:VAL:HG22	2.47	0.40
1:C:406:GLU:OE1	1:D:405:TYR:HE2	2.05	0.40
1:C:440:PHE:HB2	1:D:412:HIS:ND1	2.36	0.40
1:D:90:ARG:HG2	1:D:125:PRO:HA	2.04	0.40
1:D:285:TRP:O	1:D:286:ASN:HB2	2.20	0.40
1:D:373:PRO:HG3	1:D:482:ARG:CA	2.51	0.40
1:D:505:THR:CG2	1:E:185:ASP:OD1	2.58	0.40
1:F:56:ILE:HG12	1:F:497:TYR:CE2	2.56	0.40
1:F:83:ARG:CD	1:F:131:ALA:HB2	2.40	0.40
1:F:308:PHE:O	1:F:311:ALA:HB3	2.21	0.40
1:F:336:THR:HG22	1:F:357:THR:HG23	2.03	0.40
1:A:19:GLY:O	1:A:20:PHE:C	2.63	0.40
1:A:224:PHE:CE2	1:A:270:PHE:HD2	2.40	0.40
1:A:465:ALA:O	1:A:469:MET:HG3	2.21	0.40
1:B:179:GLU:O	1:B:182:TRP:HB2	2.22	0.40
1:B:420:SER:O	1:B:423:ARG:HB2	2.21	0.40
1:B:432:ILE:HG22	1:B:434:ILE:HD11	2.02	0.40
1:B:435:VAL:CG1	1:F:423:ARG:HH21	2.34	0.40
1:C:38:THR:O	1:C:39:ARG:C	2.63	0.40
1:C:228:GLU:O	1:C:231:ILE:HG22	2.22	0.40
1:E:32:LEU:HD21	1:E:494:PHE:CG	2.57	0.40
1:E:218:ALA:HB1	1:E:384:VAL:HG21	2.02	0.40
1:E:242:MET:O	1:E:243:THR:HG22	2.22	0.40
1:E:273:LYS:HD3	1:E:288:ASP:O	2.22	0.40
1:E:483:THR:HG23	1:E:484:ALA:N	2.36	0.40
1:F:136:ASN:C	1:F:138:LYS:H	2.29	0.40
1:F:263:SER:O	1:F:267:LEU:HD22	2.21	0.40
1:F:349:ALA:CB	1:F:372:ILE:HD12	2.52	0.40
1:F:350:GLU:OE2	1:F:355:PRO:CD	2.60	0.40
1:F:478:GLY:C	1:F:480:ASP:H	2.28	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	494/496 (100%)	350 (71%)	105 (21%)	39 (8%)	1	5
1	B	494/496 (100%)	366 (74%)	86 (17%)	42 (8%)	0	4
1	C	494/496 (100%)	386 (78%)	76 (15%)	32 (6%)	1	8
1	D	494/496 (100%)	374 (76%)	76 (15%)	44 (9%)	0	4
1	E	494/496 (100%)	382 (77%)	87 (18%)	25 (5%)	1	11
1	F	494/496 (100%)	358 (72%)	100 (20%)	36 (7%)	1	6
All	All	2964/2976 (100%)	2216 (75%)	530 (18%)	218 (7%)	1	6

All (218) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	34	GLU
1	A	35	ASP
1	A	134	LYS
1	A	173	MET
1	A	248	ASP
1	A	310	LYS
1	A	317	SER
1	A	321	ALA
1	A	331	SER
1	A	425	PHE
1	A	474	LYS
1	A	502	VAL
1	B	29	GLU
1	B	34	GLU
1	B	41	SER
1	B	105	VAL
1	B	173	MET
1	B	310	LYS
1	B	377	LEU
1	B	425	PHE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	34	GLU
1	C	35	ASP
1	C	134	LYS
1	C	162	ILE
1	C	173	MET
1	C	218	ALA
1	C	331	SER
1	C	391	LYS
1	C	409	SER
1	C	410	ASN
1	C	425	PHE
1	C	434	ILE
1	C	500	ALA
1	D	34	GLU
1	D	41	SER
1	D	91	THR
1	D	134	LYS
1	D	173	MET
1	D	269	ARG
1	D	310	LYS
1	D	321	ALA
1	D	425	PHE
1	D	485	ALA
1	E	29	GLU
1	E	34	GLU
1	E	35	ASP
1	E	74	GLY
1	E	173	MET
1	E	317	SER
1	E	331	SER
1	E	425	PHE
1	E	434	ILE
1	F	33	VAL
1	F	34	GLU
1	F	91	THR
1	F	173	MET
1	F	218	ALA
1	F	239	ILE
1	F	248	ASP
1	F	310	LYS
1	F	317	SER
1	F	331	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	F	425	PHE
1	F	434	ILE
1	F	463	ALA
1	F	502	VAL
1	A	162	ILE
1	A	235	SER
1	A	269	ARG
1	A	303	GLY
1	A	333	LYS
1	A	368	ASN
1	A	481	LEU
1	B	33	VAL
1	B	109	LYS
1	B	134	LYS
1	B	151	ARG
1	B	216	ILE
1	B	239	ILE
1	B	269	ARG
1	B	303	GLY
1	B	330	ALA
1	B	333	LYS
1	B	368	ASN
1	B	426	GLY
1	B	430	GLY
1	B	434	ILE
1	C	33	VAL
1	C	91	THR
1	C	281	ASP
1	C	298	PHE
1	C	299	LYS
1	C	333	LYS
1	C	368	ASN
1	C	426	GLY
1	C	430	GLY
1	D	11	PRO
1	D	239	ILE
1	D	302	HIS
1	D	317	SER
1	D	330	ALA
1	D	337	LYS
1	D	350	GLU
1	D	400	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	426	GLY
1	D	434	ILE
1	D	447	ALA
1	D	486	TYR
1	E	33	VAL
1	E	101	THR
1	E	303	GLY
1	E	426	GLY
1	E	502	VAL
1	F	35	ASP
1	F	123	ASP
1	F	134	LYS
1	F	162	ILE
1	F	169	PRO
1	F	321	ALA
1	F	400	ARG
1	F	422	GLU
1	F	426	GLY
1	F	462	GLU
1	A	52	ILE
1	A	218	ALA
1	A	261	LEU
1	A	286	ASN
1	A	375	LEU
1	A	500	ALA
1	B	13	PHE
1	B	72	ASP
1	B	123	ASP
1	B	234	ALA
1	B	248	ASP
1	B	500	ALA
1	C	125	PRO
1	C	158	LYS
1	C	248	ASP
1	C	439	GLU
1	D	101	THR
1	D	137	PRO
1	D	224	PHE
1	D	237	MET
1	D	248	ASP
1	D	313	PRO
1	D	318	ILE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	E	463	ALA
1	F	38	THR
1	F	41	SER
1	F	305	ILE
1	F	330	ALA
1	A	33	VAL
1	A	177	GLU
1	A	400	ARG
1	A	426	GLY
1	A	462	GLU
1	B	30	ASP
1	B	235	SER
1	B	242	MET
1	B	281	ASP
1	B	306	LEU
1	B	313	PRO
1	B	403	PHE
1	C	390	LEU
1	C	482	ARG
1	D	235	SER
1	D	279	GLU
1	D	331	SER
1	D	418	GLN
1	E	30	ASP
1	F	258	ASN
1	F	286	ASN
1	A	41	SER
1	A	68	PRO
1	A	330	ALA
1	A	403	PHE
1	A	433	PRO
1	B	177	GLU
1	C	68	PRO
1	C	269	ARG
1	C	338	SER
1	D	234	ALA
1	E	13	PHE
1	E	71	ARG
1	E	91	THR
1	E	130	LYS
1	E	248	ASP
1	F	313	PRO

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	268	HIS
1	B	301	GLN
1	B	447	ALA
1	D	123	ASP
1	D	500	ALA
1	F	216	ILE
1	F	433	PRO
1	F	499	GLU
1	A	49	VAL
1	A	313	PRO
1	C	303	GLY
1	D	105	VAL
1	D	286	ASN
1	D	303	GLY
1	B	183	ILE
1	D	33	VAL
1	D	502	VAL
1	B	108	VAL
1	B	169	PRO
1	D	373	PRO
1	D	382	VAL
1	E	68	PRO
1	E	358	PRO
1	E	433	PRO
1	F	68	PRO
1	F	122	VAL
1	A	244	PRO
1	D	316	GLY
1	E	239	ILE
1	B	275	ILE

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	412/412 (100%)	351 (85%)	61 (15%)	3 13

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	412/412 (100%)	351 (85%)	61 (15%)	3	13
1	C	412/412 (100%)	354 (86%)	58 (14%)	3	14
1	D	412/412 (100%)	344 (84%)	68 (16%)	2	11
1	E	412/412 (100%)	353 (86%)	59 (14%)	3	14
1	F	412/412 (100%)	351 (85%)	61 (15%)	3	13
All	All	2472/2472 (100%)	2104 (85%)	368 (15%)	3	13

All (368) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	31	LYS
1	A	36	LEU
1	A	37	ARG
1	A	38	THR
1	A	43	GLU
1	A	44	GLN
1	A	59	CYS
1	A	62	VAL
1	A	67	PHE
1	A	68	PRO
1	A	71	ARG
1	A	80	GLU
1	A	90	ARG
1	A	100	SER
1	A	105	VAL
1	A	116	THR
1	A	124	VAL
1	A	135	ILE
1	A	141	THR
1	A	180	MET
1	A	183	ILE
1	A	212	ILE
1	A	219	THR
1	A	231	ILE
1	A	242	MET
1	A	253	VAL
1	A	261	LEU
1	A	263	SER
1	A	267	LEU
1	A	275	ILE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	293	LYS
1	A	300	LEU
1	A	319	LEU
1	A	320	GLU
1	A	325	ILE
1	A	326	LEU
1	A	327	ILE
1	A	334	GLN
1	A	337	LYS
1	A	339	ASN
1	A	356	THR
1	A	357	THR
1	A	366	GLU
1	A	367	ARG
1	A	376	TYR
1	A	378	ASN
1	A	396	VAL
1	A	409	SER
1	A	415	MET
1	A	421	LEU
1	A	425	PHE
1	A	427	LYS
1	A	428	HIS
1	A	443	ARG
1	A	455	SER
1	A	457	LEU
1	A	461	MET
1	A	476	ASN
1	A	483	THR
1	A	499	GLU
1	A	505	THR
1	B	13	PHE
1	B	28	VAL
1	B	37	ARG
1	B	53	LEU
1	B	62	VAL
1	B	65	LEU
1	B	68	PRO
1	B	91	THR
1	B	108	VAL
1	B	115	MET
1	B	116	THR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	135	ILE
1	B	141	THR
1	B	156	LEU
1	B	166	ILE
1	B	180	MET
1	B	196	ILE
1	B	207	ILE
1	B	219	THR
1	B	231	ILE
1	B	240	LEU
1	B	242	MET
1	B	243	THR
1	B	253	VAL
1	B	259	VAL
1	B	261	LEU
1	B	263	SER
1	B	267	LEU
1	B	281	ASP
1	B	284	ILE
1	B	293	LYS
1	B	318	ILE
1	B	319	LEU
1	B	324	ASP
1	B	325	ILE
1	B	326	LEU
1	B	327	ILE
1	B	333	LYS
1	B	334	GLN
1	B	337	LYS
1	B	339	ASN
1	B	357	THR
1	B	367	ARG
1	B	369	ILE
1	B	371	VAL
1	B	378	ASN
1	B	396	VAL
1	B	406	GLU
1	B	409	SER
1	B	413	LEU
1	B	415	MET
1	B	420	SER
1	B	421	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	428	HIS
1	B	432	ILE
1	B	457	LEU
1	B	471	THR
1	B	477	LEU
1	B	479	LEU
1	B	481	LEU
1	B	498	ASN
1	C	13	PHE
1	C	16	MET
1	C	28	VAL
1	C	37	ARG
1	C	64	SER
1	C	68	PRO
1	C	70	ARG
1	C	71	ARG
1	C	87	SER
1	C	91	THR
1	C	98	ARG
1	C	104	SER
1	C	116	THR
1	C	135	ILE
1	C	141	THR
1	C	153	THR
1	C	156	LEU
1	C	180	MET
1	C	191	ILE
1	C	207	ILE
1	C	217	SER
1	C	221	ARG
1	C	235	SER
1	C	259	VAL
1	C	261	LEU
1	C	263	SER
1	C	265	ARG
1	C	275	ILE
1	C	281	ASP
1	C	284	ILE
1	C	292	PRO
1	C	293	LYS
1	C	312	LYS
1	C	318	ILE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	325	ILE
1	C	326	LEU
1	C	327	ILE
1	C	334	GLN
1	C	337	LYS
1	C	338	SER
1	C	339	ASN
1	C	356	THR
1	C	359	GLU
1	C	362	LYS
1	C	367	ARG
1	C	378	ASN
1	C	396	VAL
1	C	409	SER
1	C	415	MET
1	C	421	LEU
1	C	431	THR
1	C	432	ILE
1	C	435	VAL
1	C	471	THR
1	C	473	MET
1	C	476	ASN
1	C	483	THR
1	C	487	VAL
1	D	23	ARG
1	D	31	LYS
1	D	37	ARG
1	D	38	THR
1	D	54	ARG
1	D	62	VAL
1	D	63	LEU
1	D	64	SER
1	D	68	PRO
1	D	69	ILE
1	D	79	ILE
1	D	80	GLU
1	D	90	ARG
1	D	91	THR
1	D	101	THR
1	D	105	VAL
1	D	116	THR
1	D	121	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	124	VAL
1	D	135	ILE
1	D	141	THR
1	D	151	ARG
1	D	156	LEU
1	D	166	ILE
1	D	180	MET
1	D	189	SER
1	D	202	VAL
1	D	203	THR
1	D	219	THR
1	D	231	ILE
1	D	239	ILE
1	D	242	MET
1	D	259	VAL
1	D	261	LEU
1	D	263	SER
1	D	267	LEU
1	D	293	LYS
1	D	300	LEU
1	D	315	GLU
1	D	319	LEU
1	D	320	GLU
1	D	325	ILE
1	D	326	LEU
1	D	327	ILE
1	D	331	SER
1	D	334	GLN
1	D	337	LYS
1	D	339	ASN
1	D	363	ILE
1	D	365	LEU
1	D	367	ARG
1	D	378	ASN
1	D	391	LYS
1	D	396	VAL
1	D	400	ARG
1	D	402	THR
1	D	406	GLU
1	D	409	SER
1	D	421	LEU
1	D	428	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	443	ARG
1	D	445	SER
1	D	457	LEU
1	D	471	THR
1	D	481	LEU
1	D	483	THR
1	D	499	GLU
1	D	505	THR
1	E	23	ARG
1	E	37	ARG
1	E	42	GLU
1	E	44	GLN
1	E	68	PRO
1	E	76	TRP
1	E	91	THR
1	E	94	LYS
1	E	101	THR
1	E	108	VAL
1	E	135	ILE
1	E	141	THR
1	E	149	THR
1	E	177	GLU
1	E	180	MET
1	E	189	SER
1	E	196	ILE
1	E	219	THR
1	E	221	ARG
1	E	223	VAL
1	E	231	ILE
1	E	235	SER
1	E	253	VAL
1	E	258	ASN
1	E	259	VAL
1	E	261	LEU
1	E	267	LEU
1	E	275	ILE
1	E	293	LYS
1	E	300	LEU
1	E	305	ILE
1	E	320	GLU
1	E	325	ILE
1	E	326	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	E	327	ILE
1	E	334	GLN
1	E	337	LYS
1	E	339	ASN
1	E	357	THR
1	E	358	PRO
1	E	363	ILE
1	E	367	ARG
1	E	400	ARG
1	E	406	GLU
1	E	410	ASN
1	E	413	LEU
1	E	415	MET
1	E	419	GLU
1	E	421	LEU
1	E	424	LYS
1	E	428	HIS
1	E	432	ILE
1	E	455	SER
1	E	457	LEU
1	E	460	THR
1	E	471	THR
1	E	481	LEU
1	E	499	GLU
1	E	505	THR
1	F	23	ARG
1	F	26	SER
1	F	31	LYS
1	F	36	LEU
1	F	37	ARG
1	F	40	GLU
1	F	49	VAL
1	F	55	ILE
1	F	62	VAL
1	F	64	SER
1	F	68	PRO
1	F	82	TYR
1	F	90	ARG
1	F	91	THR
1	F	116	THR
1	F	149	THR
1	F	155	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	F	156	LEU
1	F	162	ILE
1	F	177	GLU
1	F	189	SER
1	F	206	PRO
1	F	221	ARG
1	F	223	VAL
1	F	231	ILE
1	F	239	ILE
1	F	259	VAL
1	F	261	LEU
1	F	263	SER
1	F	267	LEU
1	F	275	ILE
1	F	293	LYS
1	F	300	LEU
1	F	306	LEU
1	F	312	LYS
1	F	318	ILE
1	F	319	LEU
1	F	320	GLU
1	F	325	ILE
1	F	334	GLN
1	F	337	LYS
1	F	339	ASN
1	F	342	ARG
1	F	355	PRO
1	F	367	ARG
1	F	372	ILE
1	F	378	ASN
1	F	396	VAL
1	F	416	SER
1	F	421	LEU
1	F	431	THR
1	F	432	ILE
1	F	443	ARG
1	F	452	ILE
1	F	455	SER
1	F	467	GLN
1	F	471	THR
1	F	481	LEU
1	F	483	THR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	F	499	GLU
1	F	502	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (93) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	44	GLN
1	A	47	ASN
1	A	61	HIS
1	A	85	GLN
1	A	86	HIS
1	A	139	ASN
1	A	143	ASN
1	A	268	HIS
1	A	334	GLN
1	A	339	ASN
1	A	353	ASN
1	A	368	ASN
1	A	378	ASN
1	A	392	ASN
1	A	394	ASN
1	A	410	ASN
1	A	454	HIS
1	A	498	ASN
1	B	86	HIS
1	B	139	ASN
1	B	143	ASN
1	B	197	ASN
1	B	213	HIS
1	B	232	ASN
1	B	302	HIS
1	B	334	GLN
1	B	339	ASN
1	B	353	ASN
1	B	378	ASN
1	B	392	ASN
1	B	395	HIS
1	B	410	ASN
1	B	441	GLN
1	C	47	ASN
1	C	60	ASN
1	C	61	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	86	HIS
1	C	143	ASN
1	C	199	HIS
1	C	225	HIS
1	C	232	ASN
1	C	254	GLN
1	C	262	HIS
1	C	334	GLN
1	C	339	ASN
1	C	368	ASN
1	C	378	ASN
1	C	395	HIS
1	C	410	ASN
1	D	61	HIS
1	D	86	HIS
1	D	143	ASN
1	D	193	HIS
1	D	213	HIS
1	D	232	ASN
1	D	254	GLN
1	D	339	ASN
1	D	368	ASN
1	D	392	ASN
1	D	395	HIS
1	D	410	ASN
1	D	441	GLN
1	D	467	GLN
1	D	476	ASN
1	D	498	ASN
1	E	60	ASN
1	E	61	HIS
1	E	86	HIS
1	E	197	ASN
1	E	232	ASN
1	E	301	GLN
1	E	302	HIS
1	E	334	GLN
1	E	339	ASN
1	E	392	ASN
1	E	395	HIS
1	E	410	ASN
1	E	412	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	E	428	HIS
1	E	498	ASN
1	F	60	ASN
1	F	61	HIS
1	F	86	HIS
1	F	88	GLN
1	F	232	ASN
1	F	258	ASN
1	F	334	GLN
1	F	339	ASN
1	F	353	ASN
1	F	378	ASN
1	F	392	ASN
1	F	395	HIS
1	F	498	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.