



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 10:11 AM GMT

PDB ID : 3L5N
Title : Staphylococcal Complement Inhibitor (SCIN) in complex with Human Complement Component C3b
Authors : Geisbrecht, B.V.; Garcia, B.L.
Deposited on : 2009-12-22
Resolution : 7.54 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

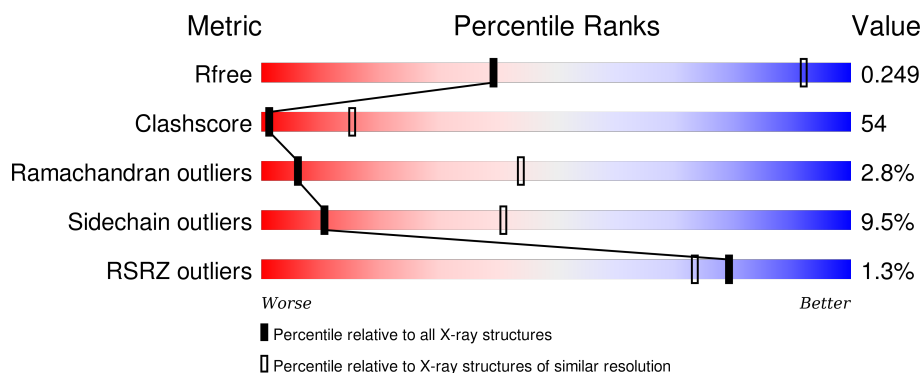
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 7.54 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	1014 (9.50-3.66)
Clashscore	102246	1063 (10.00-3.70)
Ramachandran outliers	100387	1035 (9.50-3.66)
Sidechain outliers	100360	1005 (9.50-3.66)
RSRZ outliers	91569	1013 (9.50-3.66)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	645	<div> <div style="width: 35%; background-color: green;"></div> <div style="width: 55%; background-color: yellow;"></div> <div style="width: 8%; background-color: orange;"></div> <div style="width: 2%; background-color: red;"></div> <div style="width: 0%; background-color: grey;"></div> </div> <div>35% 55% 8% •</div>
2	B	915	<div> <div style="width: 44%; background-color: green;"></div> <div style="width: 47%; background-color: yellow;"></div> <div style="width: 7%; background-color: orange;"></div> <div style="width: 2%; background-color: red;"></div> <div style="width: 0%; background-color: grey;"></div> </div> <div>2% 44% 47% 7% •</div>
3	M	88	<div> <div style="width: 47%; background-color: green;"></div> <div style="width: 45%; background-color: yellow;"></div> <div style="width: 5%; background-color: orange;"></div> <div style="width: 0%; background-color: red;"></div> <div style="width: 0%; background-color: grey;"></div> </div> <div>47% 45% • 5%</div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 12785 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 Complement C3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	634	Total	C	N	O	S	0	0	0
			4932	3143	833	941	15			

- Molecule 2 is a protein called Complement C3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	891	Total	C	N	O	S	1168	0	0
			7118	4512	1195	1373	38			

- Molecule 3 is a protein called Staphylococcal complement inhibitor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	M	84	Total	C	N	O	S	0	0	0
			682	432	111	137	2			

There are 3 discrepancies between the modelled and reference sequences:

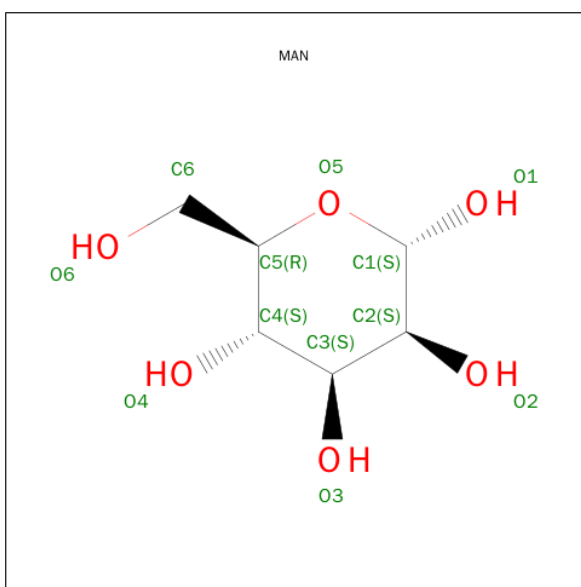
Chain	Residue	Modelled	Actual	Comment	Reference
M	-2	GLY	-	EXPRESSION TAG	UNP Q931M7
M	-1	SER	-	EXPRESSION TAG	UNP Q931M7
M	0	THR	-	EXPRESSION TAG	UNP Q931M7

- Molecule 4 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	A	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 5 is SUGAR (ALPHA-D-MANNOSE) (three-letter code: MAN) (formula: C₆H₁₂O₆).

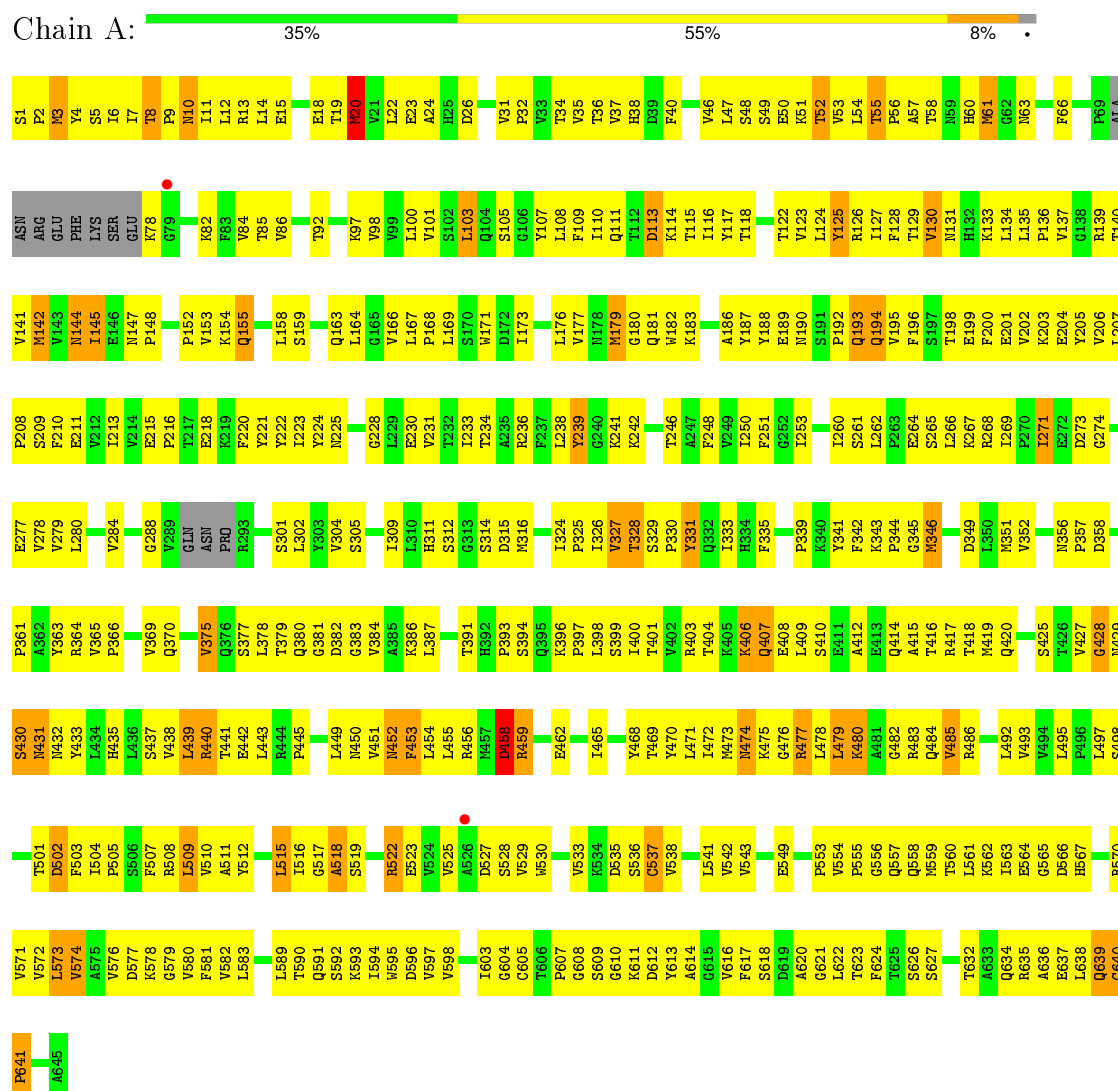


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			11	6	5		

3 Residue-property plots

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

• Molecule 1: Complement C3





4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	128.03 Å 128.03 Å 468.59 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.62 – 7.54 49.51 – 7.52	Depositor EDS
% Data completeness (in resolution range)	86.2 (49.62-7.54) 87.0 (49.51-7.52)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.66 (at 7.37 Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.5_2)	Depositor
R, R_{free}	0.265 , 0.268 0.252 , 0.249	Depositor DCC
R_{free} test set	238 reflections (5.00%)	DCC
Wilson B-factor (Å ²)	427.9	Xtriage
Anisotropy	1.104	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.22 , 189.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Outliers	2 of 5291 reflections (0.038%)	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	12785	wwPDB-VP
Average B, all atoms (Å ²)	172.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.72% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.41	0/5030	0.62	1/6834 (0.0%)
2	B	0.38	1/7257 (0.0%)	0.55	0/9824
3	M	0.33	0/690	0.51	0/923
All	All	0.39	1/12977 (0.0%)	0.58	1/17581 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	976	GLU	CG-CD	5.27	1.59	1.51

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	428	GLY	N-CA-C	-5.02	100.56	113.10

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4932	0	4999	631	0
2	B	7118	0	7041	672	0
3	M	682	0	697	47	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	42	0	39	5	0
5	A	11	0	10	1	0
All	All	12785	0	12786	1261	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 54.

All (1261) 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)
2:B:1269:GLU:O	2:B:1270:LEU:CG	1.69	1.41
1:A:363:TYR:CD1	1:A:364:ARG:HG3	1.60	1.35
1:A:363:TYR:CE1	1:A:364:ARG:HG3	1.60	1.34
2:B:783:LEU:N	2:B:798:PRO:HB3	1.41	1.34
1:A:541:LEU:CG	2:B:796:ALA:HB2	1.62	1.29
1:A:541:LEU:HG	2:B:796:ALA:CB	1.62	1.27
1:A:363:TYR:CA	1:A:379:THR:HG21	1.69	1.21
1:A:516:ILE:HB	1:A:522:ARG:NE	1.56	1.20
1:A:591:GLN:CB	2:B:795:VAL:HG11	1.71	1.19
1:A:380:GLN:NE2	1:A:440:ARG:HH12	1.40	1.18
1:A:363:TYR:HA	1:A:379:THR:CG2	1.72	1.17
2:B:965:VAL:HG13	2:B:1267:HIS:CD2	1.79	1.17
2:B:965:VAL:HG13	2:B:1267:HIS:NE2	1.59	1.15
1:A:363:TYR:CE1	1:A:364:ARG:CG	2.30	1.15
1:A:516:ILE:HB	1:A:522:ARG:CD	1.75	1.15
1:A:591:GLN:HB2	2:B:795:VAL:HG11	1.24	1.14
1:A:515:LEU:O	1:A:515:LEU:HD23	1.49	1.13
2:B:782:ILE:CG2	2:B:783:LEU:H	1.60	1.12
2:B:1361:THR:HB	2:B:1442:HIS:HA	1.32	1.11
2:B:744:GLU:CG	2:B:775:ASP:H	1.65	1.10
2:B:1228:PRO:HB2	2:B:1229:PRO:HD3	1.31	1.10
1:A:591:GLN:HB2	2:B:795:VAL:CG1	1.82	1.09
2:B:782:ILE:C	2:B:798:PRO:CB	2.21	1.09
2:B:782:ILE:HG22	2:B:783:LEU:N	1.59	1.07
2:B:978:LEU:HD21	2:B:981:LEU:HG	1.33	1.06
1:A:380:GLN:HE22	1:A:440:ARG:NH1	1.53	1.06
2:B:744:GLU:HG3	2:B:775:ASP:H	1.15	1.05
1:A:364:ARG:N	1:A:379:THR:HB	1.70	1.05
1:A:610:GLY:HA3	1:A:616:VAL:HG23	1.36	1.05
2:B:782:ILE:C	2:B:798:PRO:HB3	1.76	1.04
1:A:222:TYR:CE1	1:A:328:THR:HG22	1.93	1.04

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:302:LEU:HD11	1:A:326:ILE:HD11	1.06	1.02
2:B:799:PHE:O	2:B:800:GLU:HG3	1.58	1.02
1:A:13:ARG:HH22	1:A:476:GLY:HA3	1.25	1.00
2:B:1458:TYR:HB3	2:B:1466:SER:HB3	1.41	0.99
2:B:783:LEU:N	2:B:798:PRO:CB	2.25	0.99
2:B:1128:SER:HA	2:B:1131:GLU:OE2	1.61	0.99
1:A:363:TYR:CE1	1:A:364:ARG:NH1	2.30	0.99
2:B:964:PRO:HB3	2:B:1270:LEU:HD11	1.45	0.97
1:A:501:THR:O	1:A:538:VAL:HG22	1.64	0.97
1:A:364:ARG:H	1:A:379:THR:HB	1.21	0.97
2:B:917:ASN:HB3	2:B:1325:MET:HE2	1.47	0.96
1:A:341:TYR:HB2	1:A:609:SER:HB2	1.48	0.96
2:B:833:ARG:HG2	2:B:833:ARG:HH11	1.29	0.96
1:A:478:LEU:HD21	1:A:622:LEU:HD21	1.48	0.96
2:B:1269:GLU:O	2:B:1270:LEU:HG	0.78	0.95
1:A:554:VAL:HG12	1:A:555:PRO:HD2	1.47	0.95
2:B:1338:LYS:HA	2:B:1371:ARG:HB2	1.47	0.95
2:B:799:PHE:HD1	2:B:800:GLU:H	1.10	0.95
1:A:516:ILE:HB	1:A:522:ARG:HE	1.18	0.95
1:A:567:HIS:CG	2:B:760:PRO:HG3	2.00	0.95
2:B:1397:LYS:NZ	2:B:1412:LEU:HG	1.80	0.95
1:A:591:GLN:CB	2:B:795:VAL:CG1	2.44	0.95
1:A:589:LEU:HD11	1:A:594:ILE:HD11	1.49	0.94
1:A:590:THR:HB	1:A:593:LYS:HG3	1.48	0.94
2:B:972:ALA:HB1	2:B:1005:TYR:OH	1.66	0.94
1:A:541:LEU:HG	2:B:796:ALA:HB2	0.94	0.94
1:A:302:LEU:CD1	1:A:326:ILE:HD11	1.96	0.94
2:B:914:ILE:HG23	2:B:1328:ALA:HB3	1.49	0.94
1:A:541:LEU:HD22	2:B:786:SER:HB3	1.47	0.94
2:B:965:VAL:CG1	2:B:1267:HIS:NE2	2.30	0.93
1:A:377:SER:OG	1:A:387:LEU:HG	1.68	0.92
2:B:1278:LEU:H	2:B:1281:ARG:HD2	1.34	0.92
2:B:1268:GLN:HG2	2:B:1268:GLN:O	1.69	0.92
1:A:327:VAL:HG21	1:A:357:PRO:HB3	1.47	0.92
2:B:965:VAL:O	2:B:1267:HIS:CD2	2.24	0.91
1:A:36:THR:HG23	1:A:48:SER:HB3	1.50	0.91
1:A:363:TYR:CD1	1:A:364:ARG:CG	2.51	0.91
2:B:799:PHE:CD1	2:B:800:GLU:N	2.37	0.91
2:B:783:LEU:HA	2:B:798:PRO:HD3	1.49	0.91
2:B:1259:GLN:HE22	2:B:1262:LYS:HE2	1.34	0.91
1:A:339:PRO:HA	1:A:608:GLY:HA3	1.52	0.91

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:363:TYR:HA	1:A:379:THR:HG21	0.90	0.90
1:A:430:SER:O	1:A:431:ASN:CG	2.09	0.90
2:B:1055:TRP:CE2	2:B:1108:ILE:HG22	2.07	0.90
2:B:965:VAL:O	2:B:1267:HIS:HD2	1.55	0.90
2:B:745:PHE:N	2:B:746:PRO:HD2	1.87	0.90
1:A:113:ASP:HB2	2:B:751:TRP:CZ3	2.07	0.90
1:A:328:THR:O	1:A:330:PRO:HD3	1.72	0.89
1:A:246:THR:HB	2:B:1425:TYR:OH	1.72	0.89
1:A:522:ARG:CG	1:A:522:ARG:HH11	1.84	0.89
1:A:207:LEU:HD21	2:B:747:GLU:HG2	1.51	0.89
1:A:516:ILE:HD12	1:A:522:ARG:HD3	1.52	0.89
2:B:1269:GLU:C	2:B:1270:LEU:HG	1.92	0.88
2:B:736:GLU:HG2	2:B:891:LYS:HD2	1.55	0.88
2:B:965:VAL:C	2:B:1267:HIS:HD2	1.76	0.88
1:A:220:PHE:CZ	1:A:330:PRO:HB3	2.08	0.88
2:B:1397:LYS:HZ3	2:B:1412:LEU:HG	1.38	0.88
2:B:782:ILE:HG22	2:B:783:LEU:H	0.74	0.88
1:A:515:LEU:C	1:A:515:LEU:HD23	1.93	0.88
2:B:978:LEU:HD11	2:B:981:LEU:HD12	1.55	0.88
1:A:363:TYR:HE1	1:A:364:ARG:HD3	1.38	0.87
2:B:1126:LEU:HD23	2:B:1173:ALA:HB1	1.56	0.87
1:A:543:VAL:HG12	2:B:799:PHE:HE2	1.38	0.86
2:B:744:GLU:HG3	2:B:775:ASP:N	1.90	0.86
2:B:992:ASN:HD21	2:B:1033:GLN:HB2	1.40	0.86
1:A:220:PHE:CG	1:A:357:PRO:HG2	2.10	0.86
1:A:591:GLN:O	1:A:594:ILE:HB	1.75	0.86
1:A:555:PRO:HB3	2:B:775:ASP:HA	1.56	0.86
1:A:459:ARG:HG3	1:A:459:ARG:O	1.74	0.86
2:B:964:PRO:CB	2:B:1270:LEU:HD11	2.06	0.86
2:B:1168:ALA:HA	2:B:1188:PHE:HE1	1.40	0.85
1:A:363:TYR:HE1	1:A:364:ARG:CD	1.87	0.85
2:B:809:ILE:O	2:B:903:VAL:HG21	1.75	0.85
2:B:1055:TRP:CZ2	2:B:1108:ILE:HA	2.12	0.85
2:B:756:LEU:HD13	2:B:765:SER:HB2	1.59	0.84
2:B:783:LEU:HB2	2:B:798:PRO:HG3	1.58	0.84
1:A:537:CYS:HB2	2:B:794:CYS:HA	1.60	0.84
1:A:253:ILE:HB	1:A:260:ILE:HB	1.59	0.84
1:A:364:ARG:N	1:A:379:THR:CB	2.40	0.83
2:B:833:ARG:HH22	2:B:899:ILE:HD11	1.43	0.83
1:A:472:ILE:HG21	1:A:503:PHE:CE1	2.14	0.83
1:A:591:GLN:HG2	2:B:795:VAL:HG12	1.61	0.83

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:223:ILE:HD13	1:A:328:THR:OG1	1.79	0.83
1:A:107:TYR:HB2	1:A:109:PHE:CZ	2.13	0.83
2:B:799:PHE:O	2:B:800:GLU:CG	2.27	0.83
1:A:8:THR:CG2	1:A:20:MET:HB2	2.08	0.82
1:A:410:SER:O	1:A:414:GLN:HG2	1.79	0.82
1:A:477:ARG:CG	1:A:477:ARG:HH11	1.92	0.82
1:A:363:TYR:CE1	1:A:364:ARG:CD	2.61	0.82
1:A:364:ARG:H	1:A:379:THR:CB	1.93	0.82
2:B:733:ILE:HG12	2:B:734:ILE:H	1.43	0.82
2:B:742:ARG:HB2	2:B:903:VAL:HG22	1.59	0.81
1:A:314:SER:HB3	2:B:812:ARG:HD3	1.60	0.81
1:A:370:GLN:HE22	1:A:403:ARG:NE	1.78	0.81
1:A:378:LEU:HD13	1:A:379:THR:N	1.94	0.81
1:A:369:VAL:HG23	1:A:375:VAL:HG11	1.62	0.81
1:A:8:THR:HG23	1:A:20:MET:HB2	1.62	0.81
1:A:516:ILE:HB	1:A:522:ARG:HD2	1.63	0.81
2:B:882:LYS:HE2	2:B:886:GLN:HE22	1.44	0.81
1:A:553:PRO:HB2	2:B:773:LEU:HD12	1.63	0.80
1:A:522:ARG:HG3	1:A:522:ARG:HH11	1.45	0.80
2:B:966:ALA:HA	2:B:1267:HIS:HB3	1.61	0.80
1:A:327:VAL:HG21	1:A:357:PRO:CB	2.11	0.80
1:A:430:SER:O	1:A:431:ASN:CB	2.30	0.80
1:A:363:TYR:CD1	1:A:364:ARG:NH1	2.49	0.80
1:A:440:ARG:O	1:A:440:ARG:HG3	1.81	0.80
2:B:782:ILE:HD12	2:B:799:PHE:CE2	2.16	0.80
2:B:745:PHE:N	2:B:746:PRO:CD	2.44	0.80
2:B:1193:LYS:HD3	2:B:1199:GLU:OE2	1.81	0.80
1:A:591:GLN:HA	1:A:594:ILE:CG1	2.13	0.79
1:A:516:ILE:CB	1:A:522:ARG:CD	2.59	0.79
1:A:522:ARG:NH1	1:A:522:ARG:HG3	1.96	0.79
1:A:591:GLN:HB3	2:B:795:VAL:HG11	1.64	0.79
1:A:469:THR:HB	1:A:512:TYR:CE2	2.18	0.79
1:A:6:ILE:HD11	1:A:20:MET:HG2	1.65	0.79
1:A:97:LYS:HG3	1:A:98:VAL:N	1.98	0.79
1:A:13:ARG:HH22	1:A:476:GLY:CA	1.96	0.78
1:A:624:PHE:HB3	1:A:632:THR:HG23	1.64	0.78
1:A:501:THR:O	1:A:538:VAL:CG2	2.31	0.78
1:A:541:LEU:CD2	2:B:796:ALA:HB2	2.12	0.78
1:A:14:LEU:HD21	1:A:101:VAL:CG1	2.14	0.78
1:A:528:SER:HB3	1:A:616:VAL:HG13	1.65	0.78
2:B:1369:ARG:HD3	2:B:1434:ASP:OD1	1.83	0.78

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1228:PRO:HB2	2:B:1229:PRO:CD	2.12	0.78
1:A:329:SER:OG	1:A:415:ALA:HB2	1.84	0.77
1:A:341:TYR:CE1	1:A:611:LYS:HG3	2.19	0.77
1:A:380:GLN:HE22	1:A:440:ARG:HH12	0.79	0.77
1:A:327:VAL:CG2	1:A:357:PRO:HB3	2.13	0.77
1:A:516:ILE:CB	1:A:522:ARG:HE	1.96	0.77
1:A:501:THR:OG1	1:A:538:VAL:HG13	1.85	0.77
2:B:783:LEU:HA	2:B:798:PRO:CD	2.14	0.77
2:B:1038:ARG:CD	2:B:1077:VAL:HG13	2.15	0.77
2:B:744:GLU:C	2:B:746:PRO:HD2	2.03	0.76
1:A:443:LEU:HD11	1:A:449:LEU:HD22	1.67	0.76
1:A:363:TYR:HE1	1:A:364:ARG:HH11	1.26	0.76
1:A:221:TYR:CE1	1:A:228:GLY:HA2	2.21	0.76
1:A:591:GLN:HB2	2:B:795:VAL:CB	2.15	0.76
2:B:1082:VAL:HG13	2:B:1129:LEU:HD22	1.68	0.76
2:B:1259:GLN:HE22	2:B:1262:LYS:CE	1.97	0.76
2:B:782:ILE:HB	2:B:798:PRO:CB	2.16	0.76
1:A:113:ASP:OD1	1:A:114:LYS:HG3	1.85	0.76
1:A:572:VAL:HG12	2:B:753:VAL:HG22	1.68	0.76
2:B:1086:ILE:HD13	2:B:1142:SER:O	1.86	0.75
1:A:590:THR:HG22	1:A:592:SER:N	2.00	0.75
2:B:1259:GLN:HE22	2:B:1262:LYS:HB2	1.51	0.75
1:A:380:GLN:CD	1:A:384:VAL:O	2.24	0.75
1:A:6:ILE:HD12	1:A:7:ILE:H	1.50	0.75
1:A:131:ASN:HD21	1:A:133:LYS:HD3	1.52	0.75
1:A:142:MET:SD	1:A:189:GLU:HB2	2.28	0.74
2:B:960:LEU:HB2	2:B:1298:ARG:O	1.86	0.74
1:A:220:PHE:CB	1:A:357:PRO:HG2	2.17	0.74
2:B:1396:LEU:HD22	2:B:1407:ILE:CD1	2.17	0.74
2:B:783:LEU:H	2:B:798:PRO:HB3	1.52	0.74
1:A:378:LEU:HD13	1:A:378:LEU:C	2.08	0.74
2:B:957:ARG:HG3	2:B:1301:GLU:CG	2.17	0.74
2:B:1342:LYS:HE3	2:B:1367:CYS:HB3	1.69	0.73
1:A:614:ALA:HB1	1:A:632:THR:HA	1.69	0.73
1:A:610:GLY:HA3	1:A:616:VAL:CG2	2.17	0.73
2:B:1084:TRP:CD1	2:B:1088:GLU:HG3	2.23	0.73
1:A:556:GLY:O	3:M:39:TYR:HB2	1.87	0.73
1:A:451:VAL:HB	1:A:495:LEU:HB3	1.71	0.73
1:A:509:LEU:C	1:A:509:LEU:HD13	2.09	0.73
1:A:248:PHE:HD1	2:B:1378:MET:HE3	1.53	0.73
1:A:562:LYS:O	1:A:563:ILE:HG13	1.88	0.73

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:964:PRO:CG	2:B:1270:LEU:HD11	2.19	0.73
1:A:590:THR:O	1:A:594:ILE:HG12	1.88	0.73
1:A:516:ILE:CB	1:A:522:ARG:HD2	2.19	0.72
2:B:883:THR:HG21	2:B:911:PRO:HG3	1.69	0.72
1:A:404:THR:HG23	1:A:414:GLN:HB3	1.72	0.72
1:A:439:LEU:HD12	1:A:439:LEU:H	1.53	0.72
2:B:852:SER:HB3	2:B:878:ILE:HG22	1.71	0.72
2:B:1277:GLN:C	2:B:1278:LEU:HD12	2.09	0.72
1:A:404:THR:HG23	1:A:414:GLN:HE21	1.52	0.72
2:B:1396:LEU:HD22	2:B:1407:ILE:HD13	1.72	0.72
2:B:978:LEU:HD11	2:B:981:LEU:CD1	2.19	0.72
1:A:114:LYS:HD2	2:B:747:GLU:OE1	1.90	0.72
2:B:833:ARG:CG	2:B:833:ARG:HH11	2.02	0.72
1:A:216:PRO:HG3	1:A:231:VAL:HG22	1.71	0.72
2:B:782:ILE:O	2:B:798:PRO:HG3	1.90	0.71
2:B:744:GLU:HB2	2:B:775:ASP:HB2	1.71	0.71
1:A:19:THR:HG22	1:A:20:MET:H	1.53	0.71
1:A:427:VAL:CG2	1:A:613:TYR:CE2	2.72	0.71
1:A:97:LYS:HG3	1:A:98:VAL:H	1.54	0.71
1:A:470:TYR:C	1:A:471:LEU:HD12	2.10	0.71
1:A:40:PHE:HD1	1:A:85:THR:OG1	1.74	0.71
2:B:782:ILE:O	2:B:783:LEU:HB2	1.90	0.71
2:B:934:GLY:O	2:B:935:VAL:HG22	1.90	0.71
2:B:964:PRO:HB3	2:B:1270:LEU:CD1	2.19	0.71
1:A:530:TRP:CG	1:A:607:PRO:HB3	2.25	0.71
1:A:40:PHE:HD1	1:A:85:THR:HG1	1.38	0.71
2:B:1334:LEU:HD12	2:B:1336:CYS:H	1.56	0.71
3:M:3:SER:O	3:M:4:LEU:HG	1.90	0.71
1:A:504:ILE:HG21	1:A:536:SER:H	1.54	0.71
1:A:312:SER:HB2	2:B:873:SER:HB2	1.71	0.71
1:A:369:VAL:CG2	1:A:375:VAL:HG11	2.21	0.70
1:A:577:ASP:OD1	2:B:778:THR:HG21	1.90	0.70
2:B:964:PRO:HG3	2:B:1270:LEU:HD11	1.74	0.70
1:A:327:VAL:HG21	1:A:357:PRO:CG	2.21	0.70
2:B:1090:GLN:HE22	2:B:1146:SER:HA	1.54	0.70
1:A:251:PHE:HD2	1:A:265:SER:HB2	1.56	0.70
2:B:994:ILE:HG23	2:B:1247:THR:OG1	1.91	0.70
1:A:14:LEU:HD21	1:A:101:VAL:HG13	1.74	0.70
1:A:567:HIS:CD2	2:B:760:PRO:HG3	2.25	0.70
1:A:574:VAL:HB	2:B:751:TRP:CE3	2.27	0.70
1:A:530:TRP:CE3	1:A:607:PRO:HB2	2.27	0.70

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:956:THR:OG1	2:B:1324:THR:HG22	1.91	0.70
2:B:1143:LEU:HB3	2:B:1144:PRO:HD3	1.72	0.70
1:A:179:MET:HG3	1:A:202:VAL:O	1.91	0.70
1:A:26:ASP:OD2	1:A:522:ARG:NH2	2.24	0.70
2:B:740:VAL:HB	3:M:42:ARG:HB2	1.73	0.70
1:A:314:SER:CB	2:B:812:ARG:HD3	2.21	0.70
2:B:749:TRP:CE3	2:B:750:LEU:HB2	2.27	0.70
1:A:339:PRO:CA	1:A:608:GLY:HA3	2.20	0.70
1:A:590:THR:HG22	1:A:592:SER:H	1.55	0.70
2:B:1055:TRP:CD2	2:B:1108:ILE:HG22	2.27	0.70
1:A:125:TYR:OH	1:A:145:ILE:HD11	1.91	0.69
1:A:210:PHE:O	1:A:582:VAL:HG11	1.91	0.69
1:A:221:TYR:HB3	1:A:326:ILE:HD13	1.73	0.69
1:A:114:LYS:HE3	1:A:117:TYR:CD1	2.27	0.69
1:A:7:ILE:HG22	1:A:8:THR:H	1.56	0.69
2:B:744:GLU:CB	2:B:775:ASP:H	2.05	0.69
1:A:309:ILE:HG12	1:A:316:MET:HB2	1.74	0.69
2:B:903:VAL:HG12	2:B:905:LYS:HG3	1.74	0.69
2:B:1411:GLU:HG2	2:B:1422:LEU:HD12	1.75	0.69
2:B:811:LEU:HG	2:B:813:LEU:HD13	1.74	0.69
1:A:147:ASN:HB2	1:A:148:PRO:CD	2.23	0.68
2:B:783:LEU:CB	2:B:798:PRO:HG3	2.22	0.68
2:B:1365:GLU:HG3	2:B:1438:ALA:HB2	1.74	0.68
1:A:471:LEU:O	1:A:509:LEU:CD2	2.41	0.68
2:B:749:TRP:HB2	2:B:774:LYS:HE2	1.75	0.68
1:A:501:THR:HB	1:A:538:VAL:HG22	1.74	0.68
2:B:1416:PHE:HZ	2:B:1442:HIS:HD2	1.41	0.68
1:A:222:TYR:CE1	1:A:328:THR:CG2	2.75	0.68
2:B:996:MET:HE3	2:B:1030:GLY:HA3	1.74	0.68
1:A:158:LEU:HG	1:A:159:SER:H	1.58	0.68
2:B:914:ILE:CG2	2:B:1328:ALA:HB3	2.21	0.68
2:B:1084:TRP:O	2:B:1088:GLU:HB2	1.93	0.68
1:A:5:SER:HA	1:A:626:SER:HA	1.75	0.68
2:B:757:LYS:CE	2:B:757:LYS:HA	2.24	0.68
3:M:50:LYS:HE2	3:M:65:GLU:HG3	1.76	0.68
1:A:168:PRO:O	1:A:169:LEU:HD23	1.93	0.68
2:B:1475:LYS:H	2:B:1475:LYS:HD2	1.59	0.68
2:B:850:PHE:CE1	2:B:886:GLN:HB3	2.28	0.67
2:B:829:LEU:HD23	2:B:840:VAL:HG11	1.75	0.67
4:A:647:NAG:H61	5:A:648:MAN:C1	2.23	0.67
2:B:783:LEU:CA	2:B:798:PRO:HG3	2.25	0.67

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1278:LEU:N	2:B:1281:ARG:HD2	2.09	0.67
2:B:957:ARG:HG3	2:B:1301:GLU:HG3	1.76	0.67
1:A:378:LEU:CD1	1:A:379:THR:O	2.42	0.67
1:A:590:THR:CG2	1:A:592:SER:HB3	2.25	0.67
2:B:1406:TYR:CZ	2:B:1408:SER:HA	2.29	0.67
2:B:809:ILE:HG21	2:B:890:VAL:HG23	1.77	0.67
2:B:866:ILE:HG12	2:B:872:LEU:CD2	2.24	0.67
2:B:750:LEU:HD12	2:B:752:ASN:OD1	1.94	0.67
1:A:592:SER:O	1:A:596:ASP:HB2	1.95	0.67
1:A:10:ASN:HB2	1:A:621:GLY:C	2.15	0.67
2:B:850:PHE:CZ	2:B:886:GLN:HB3	2.30	0.66
2:B:795:VAL:O	2:B:795:VAL:HG13	1.94	0.66
2:B:1259:GLN:NE2	2:B:1262:LYS:HB2	2.09	0.66
2:B:1370:TYR:CG	2:B:1376:ALA:HB2	2.30	0.66
1:A:117:TYR:CZ	1:A:123:VAL:HG13	2.31	0.66
1:A:591:GLN:CG	2:B:795:VAL:CG1	2.74	0.66
2:B:805:GLN:HG2	2:B:806:ASP:H	1.60	0.66
2:B:739:ILE:HG12	2:B:900:SER:HB2	1.78	0.66
2:B:975:ALA:CB	2:B:1006:LEU:HD21	2.26	0.66
1:A:433:TYR:HD2	1:A:456:ARG:HG2	1.60	0.66
2:B:964:PRO:HB2	2:B:1291:TRP:CZ3	2.30	0.66
2:B:964:PRO:HB2	2:B:1291:TRP:HZ3	1.61	0.66
2:B:744:GLU:OE1	2:B:774:LYS:HD2	1.96	0.66
1:A:221:TYR:HE1	1:A:228:GLY:HA2	1.60	0.66
2:B:782:ILE:C	2:B:798:PRO:CG	2.65	0.65
1:A:591:GLN:HA	1:A:594:ILE:HG12	1.78	0.65
2:B:1342:LYS:HB2	2:B:1367:CYS:HB2	1.78	0.65
1:A:370:GLN:HE22	1:A:403:ARG:HE	1.42	0.65
2:B:1219:LEU:HD21	2:B:1227:VAL:HG11	1.78	0.65
2:B:1168:ALA:HA	2:B:1188:PHE:CE1	2.28	0.65
1:A:335:PHE:CE2	1:A:417:ARG:HG3	2.31	0.65
2:B:782:ILE:CB	2:B:798:PRO:HB3	2.25	0.65
2:B:1046:ALA:N	2:B:1056:LEU:HD23	2.10	0.65
1:A:477:ARG:HH11	1:A:477:ARG:HG3	1.62	0.65
1:A:576:VAL:HG11	1:A:581:PHE:CZ	2.31	0.65
1:A:364:ARG:CA	1:A:379:THR:HB	2.27	0.65
1:A:554:VAL:HG12	1:A:555:PRO:CD	2.26	0.65
1:A:222:TYR:HE1	1:A:328:THR:HG22	1.60	0.65
1:A:125:TYR:CE1	1:A:169:LEU:HD13	2.31	0.65
2:B:1259:GLN:NE2	2:B:1262:LYS:HE2	2.11	0.65
1:A:445:PRO:HG3	1:A:504:ILE:HD11	1.77	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1279:PRO:HG2	2:B:1306:GLU:HB3	1.77	0.65
1:A:55:THR:HB	1:A:57:ALA:H	1.62	0.65
2:B:1192:ALA:HB2	2:B:1198:TRP:CH2	2.31	0.65
1:A:224:TYR:HE2	1:A:328:THR:HG21	1.61	0.65
2:B:1277:GLN:HG3	2:B:1281:ARG:HE	1.60	0.65
2:B:1166:THR:HA	2:B:1169:ILE:HG22	1.78	0.65
1:A:378:LEU:HD13	1:A:379:THR:O	1.97	0.64
1:A:590:THR:HB	1:A:593:LYS:CG	2.24	0.64
1:A:129:THR:O	1:A:130:VAL:HG13	1.98	0.64
1:A:472:ILE:HG21	1:A:503:PHE:HE1	1.62	0.64
2:B:757:LYS:HE2	2:B:757:LYS:HA	1.79	0.64
3:M:53:TYR:CD1	3:M:56:LYS:HE2	2.33	0.64
2:B:843:GLU:HB2	2:B:861:GLN:HB3	1.78	0.64
2:B:866:ILE:HG12	2:B:872:LEU:HD23	1.79	0.64
2:B:964:PRO:HB3	2:B:1270:LEU:HD21	1.79	0.64
1:A:386:LYS:HD3	1:A:440:ARG:HD3	1.80	0.64
1:A:471:LEU:O	1:A:509:LEU:HD22	1.98	0.64
1:A:591:GLN:CG	2:B:795:VAL:HG12	2.27	0.64
1:A:13:ARG:O	1:A:14:LEU:HD23	1.98	0.64
2:B:782:ILE:CB	2:B:798:PRO:CB	2.76	0.64
2:B:1387:THR:HG22	2:B:1451:GLN:H	1.61	0.64
1:A:342:PHE:CE1	1:A:391:THR:HG21	2.32	0.64
2:B:1128:SER:O	2:B:1129:LEU:HD23	1.98	0.63
2:B:1180:LEU:O	2:B:1185:LEU:HB2	1.98	0.63
2:B:782:ILE:CD1	2:B:799:PHE:CE2	2.81	0.63
1:A:591:GLN:HA	1:A:594:ILE:HG13	1.80	0.63
2:B:996:MET:CE	2:B:1030:GLY:HA3	2.29	0.63
2:B:954:SER:HB2	2:B:1326:TYR:HB3	1.81	0.63
2:B:813:LEU:HD22	2:B:905:LYS:HB2	1.80	0.63
1:A:380:GLN:CG	1:A:384:VAL:O	2.46	0.63
1:A:591:GLN:HG2	2:B:795:VAL:CG1	2.29	0.63
1:A:605:CYS:O	1:A:607:PRO:HD3	1.98	0.63
2:B:1039:GLN:HE21	2:B:1048:VAL:HA	1.63	0.63
1:A:590:THR:HG21	1:A:592:SER:HB3	1.79	0.62
1:A:504:ILE:HD13	1:A:536:SER:OG	1.98	0.62
2:B:1366:ILE:HD13	2:B:1455:VAL:HG11	1.81	0.62
1:A:135:LEU:HB3	1:A:136:PRO:HD2	1.81	0.62
2:B:957:ARG:HG3	2:B:1301:GLU:HG2	1.79	0.62
2:B:998:PRO:O	2:B:1001:ILE:HG22	1.99	0.62
1:A:6:ILE:HD12	1:A:7:ILE:N	2.14	0.62
2:B:985:PRO:HD2	2:B:1026:LEU:HB3	1.80	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:22:LEU:O	1:A:23:GLU:HG3	2.00	0.62
2:B:1254:PHE:O	2:B:1258:ALA:N	2.32	0.62
2:B:1472:HIS:HB2	2:B:1478:GLY:HA2	1.80	0.62
2:B:782:ILE:CG2	2:B:783:LEU:N	2.34	0.62
2:B:1228:PRO:CB	2:B:1229:PRO:HD3	2.17	0.62
2:B:782:ILE:O	2:B:783:LEU:CB	2.48	0.62
2:B:1039:GLN:HB3	2:B:1040:PRO:HD2	1.80	0.62
2:B:965:VAL:CG1	2:B:1267:HIS:CD2	2.72	0.62
1:A:130:VAL:HG12	1:A:135:LEU:O	1.99	0.62
1:A:187:TYR:HB3	1:A:195:VAL:HG22	1.80	0.62
2:B:1056:LEU:HG	2:B:1056:LEU:O	1.98	0.62
2:B:1237:GLN:OE1	2:B:1237:GLN:HA	2.00	0.62
2:B:782:ILE:CA	2:B:798:PRO:HB2	2.30	0.61
2:B:1227:VAL:N	2:B:1228:PRO:HD2	2.15	0.61
1:A:477:ARG:HG2	1:A:477:ARG:HH11	1.65	0.61
1:A:108:LEU:HB2	1:A:196:PHE:CD1	2.35	0.61
1:A:580:VAL:CG2	2:B:747:GLU:HB3	2.29	0.61
2:B:1342:LYS:HE3	2:B:1367:CYS:CB	2.31	0.61
1:A:216:PRO:HA	1:A:231:VAL:HA	1.82	0.61
2:B:782:ILE:CA	2:B:798:PRO:CB	2.78	0.61
2:B:783:LEU:CA	2:B:798:PRO:CG	2.78	0.61
1:A:186:ALA:O	1:A:195:VAL:HG13	2.00	0.61
2:B:1381:LEU:HD11	2:B:1426:LEU:HD11	1.82	0.61
2:B:1390:ALA:HB2	2:B:1444:TYR:CE2	2.35	0.61
1:A:377:SER:HG	1:A:387:LEU:HG	1.65	0.61
2:B:1219:LEU:CD2	2:B:1227:VAL:HG21	2.30	0.61
2:B:1098:GLU:OE2	2:B:1101:PRO:HA	2.00	0.61
1:A:251:PHE:CD2	1:A:265:SER:HB2	2.35	0.61
3:M:53:TYR:HA	3:M:56:LYS:HG2	1.82	0.61
2:B:1265:PRO:O	2:B:1266:ASP:HB2	2.00	0.61
1:A:137:VAL:HG22	1:A:139:ARG:NH1	2.14	0.61
1:A:222:TYR:HB3	1:A:225:ASN:HB2	1.83	0.61
2:B:1278:LEU:O	2:B:1281:ARG:HD3	2.00	0.61
1:A:158:LEU:HG	1:A:159:SER:N	2.15	0.61
2:B:1205:LEU:HD22	2:B:1249:ALA:CB	2.30	0.61
2:B:819:ARG:O	2:B:820:ASN:HB2	2.01	0.61
2:B:1187:LYS:HG2	2:B:1187:LYS:O	2.01	0.61
1:A:221:TYR:HB3	1:A:326:ILE:CD1	2.31	0.60
2:B:738:ASN:HD22	3:M:45:LYS:HB3	1.65	0.60
2:B:750:LEU:HG	2:B:750:LEU:O	2.01	0.60
1:A:32:PRO:HA	1:A:53:VAL:HG22	1.83	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:224:TYR:CE2	1:A:328:THR:HG21	2.36	0.60
1:A:114:LYS:HB2	1:A:117:TYR:CE1	2.36	0.60
2:B:1396:LEU:O	2:B:1407:ILE:HD12	2.01	0.60
2:B:1047:PHE:HB2	2:B:1050:ARG:HB3	1.82	0.60
1:A:365:VAL:HG12	1:A:379:THR:OG1	2.01	0.60
1:A:365:VAL:HG23	1:A:406:LYS:HB2	1.83	0.60
1:A:543:VAL:HG12	2:B:799:PHE:CE2	2.28	0.60
1:A:325:PRO:HG2	1:A:357:PRO:C	2.21	0.60
1:A:13:ARG:NH2	1:A:476:GLY:HA3	2.08	0.60
1:A:509:LEU:HD22	1:A:510:VAL:N	2.15	0.60
1:A:142:MET:HG3	1:A:187:TYR:CZ	2.36	0.60
1:A:566:ASP:O	2:B:756:LEU:HD12	2.02	0.60
2:B:1192:ALA:CB	2:B:1195:LYS:HA	2.32	0.60
2:B:851:CYS:O	2:B:851:CYS:SG	2.58	0.60
2:B:1012:TRP:CZ3	2:B:1020:ARG:HB2	2.36	0.60
2:B:1370:TYR:CD2	2:B:1376:ALA:HB2	2.37	0.60
1:A:361:PRO:HB2	1:A:383:GLY:HA3	1.84	0.60
1:A:508:ARG:CZ	1:A:604:GLY:HA3	2.31	0.60
2:B:782:ILE:C	2:B:798:PRO:HB2	2.16	0.60
1:A:7:ILE:HG22	1:A:8:THR:N	2.16	0.60
1:A:477:ARG:CZ	1:A:479:LEU:HD13	2.32	0.60
2:B:1259:GLN:HE22	2:B:1262:LYS:CB	2.15	0.59
1:A:147:ASN:HA	1:A:182:TRP:CE3	2.37	0.59
1:A:107:TYR:CB	1:A:109:PHE:CZ	2.84	0.59
2:B:1086:ILE:HG23	2:B:1146:SER:HB2	1.84	0.59
2:B:1338:LYS:CA	2:B:1371:ARG:HB2	2.26	0.59
1:A:78:LYS:HD3	1:A:82:LYS:HE3	1.83	0.59
2:B:1459:ALA:HB1	2:B:1461:TYR:CE2	2.37	0.59
1:A:9:PRO:HG2	1:A:18:GLU:OE1	2.02	0.59
2:B:1192:ALA:HB2	2:B:1198:TRP:CZ2	2.37	0.59
1:A:404:THR:HG22	1:A:415:ALA:O	2.01	0.59
1:A:335:PHE:CD2	1:A:417:ARG:HG3	2.37	0.59
2:B:783:LEU:HA	2:B:798:PRO:CG	2.32	0.59
1:A:591:GLN:O	1:A:594:ILE:CB	2.49	0.59
2:B:1215:LEU:HD11	2:B:1227:VAL:HG13	1.85	0.59
1:A:453:PHE:CD2	1:A:493:VAL:O	2.56	0.59
1:A:15:GLU:OE1	1:A:190:ASN:ND2	2.33	0.59
2:B:1269:GLU:O	2:B:1270:LEU:CB	2.45	0.59
2:B:1038:ARG:O	2:B:1039:GLN:O	2.20	0.59
2:B:1123:ALA:HB1	2:B:1169:ILE:O	2.02	0.59
1:A:407:GLN:O	1:A:408:GLU:HB2	2.02	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1074:ASP:HB3	2:B:1077:VAL:HG23	1.85	0.59
2:B:1038:ARG:NE	2:B:1077:VAL:HG13	2.17	0.59
2:B:1205:LEU:HD22	2:B:1249:ALA:HB1	1.85	0.59
2:B:882:LYS:HE2	2:B:886:GLN:NE2	2.17	0.59
2:B:935:VAL:O	2:B:935:VAL:HG23	2.03	0.59
2:B:1239:TYR:HE2	2:B:1249:ALA:O	1.86	0.59
2:B:1181:LYS:HB2	2:B:1181:LYS:NZ	2.18	0.59
1:A:331:TYR:O	1:A:415:ALA:HB3	2.03	0.58
2:B:956:THR:HA	2:B:1324:THR:HA	1.84	0.58
2:B:974:ASP:HB3	2:B:976:GLU:HB2	1.85	0.58
2:B:1270:LEU:HA	2:B:1316:GLY:HA3	1.85	0.58
1:A:327:VAL:CG2	1:A:357:PRO:CG	2.81	0.58
1:A:427:VAL:C	1:A:429:ASN:H	2.06	0.58
1:A:152:PRO:HB3	1:A:155:GLN:HE22	1.68	0.58
2:B:1416:PHE:CZ	2:B:1442:HIS:HD2	2.22	0.58
1:A:439:LEU:CD1	1:A:439:LEU:H	2.17	0.58
2:B:978:LEU:HD22	2:B:978:LEU:C	2.24	0.58
2:B:850:PHE:CZ	2:B:886:GLN:CB	2.86	0.58
1:A:507:PHE:HE1	1:A:533:VAL:HG23	1.67	0.58
2:B:1087:LEU:HD21	2:B:1142:SER:HB3	1.85	0.58
2:B:1251:PHE:HD1	2:B:1252:MET:SD	2.26	0.58
1:A:250:ILE:HD12	2:B:1460:TYR:OH	2.04	0.58
1:A:341:TYR:N	1:A:609:SER:OG	2.37	0.58
2:B:1338:LYS:HA	2:B:1371:ARG:CB	2.30	0.58
1:A:103:LEU:HG	1:A:193:GLN:HE21	1.69	0.58
2:B:809:ILE:HG21	2:B:890:VAL:CG2	2.34	0.58
1:A:439:LEU:HD12	1:A:439:LEU:N	2.19	0.58
2:B:782:ILE:C	2:B:798:PRO:HG3	2.25	0.57
2:B:1227:VAL:N	2:B:1228:PRO:CD	2.67	0.57
1:A:403:ARG:HA	1:A:416:THR:HG22	1.87	0.57
2:B:1086:ILE:HG21	2:B:1142:SER:O	2.05	0.57
1:A:179:MET:HG2	1:A:203:LYS:HA	1.85	0.57
1:A:154:LYS:HD2	1:A:171:TRP:CD1	2.38	0.57
2:B:974:ASP:C	2:B:976:GLU:N	2.57	0.57
1:A:517:GLY:O	1:A:518:ALA:HB3	2.04	0.57
2:B:1155:GLU:HG3	2:B:1184:LEU:HD21	1.85	0.57
1:A:24:ALA:O	1:A:60:HIS:HB3	2.04	0.57
2:B:908:LYS:O	2:B:910:VAL:HG23	2.05	0.57
1:A:363:TYR:CD2	1:A:381:GLY:HA2	2.39	0.57
2:B:799:PHE:CE1	2:B:801:VAL:HG23	2.40	0.57
2:B:739:ILE:HB	2:B:891:LYS:HD3	1.87	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:133:LYS:HE3	1:A:477:ARG:CD	2.34	0.57
2:B:991:GLN:HE22	2:B:1104:HIS:CE1	2.22	0.57
1:A:363:TYR:C	1:A:379:THR:HG21	2.25	0.57
2:B:984:THR:HG23	2:B:1026:LEU:HD22	1.85	0.57
2:B:828:VAL:HB	2:B:830:TYR:CE2	2.39	0.57
1:A:553:PRO:HB2	2:B:773:LEU:CD1	2.32	0.57
1:A:530:TRP:CB	1:A:607:PRO:HB3	2.35	0.57
2:B:1403:VAL:HG22	2:B:1404:ASP:H	1.70	0.57
1:A:187:TYR:CB	1:A:195:VAL:HG22	2.35	0.57
1:A:471:LEU:O	1:A:509:LEU:HD23	2.04	0.57
2:B:1211:THR:OG1	2:B:1233:TRP:HZ3	1.88	0.57
2:B:742:ARG:HH11	2:B:742:ARG:HB3	1.70	0.57
2:B:811:LEU:HD23	2:B:905:LYS:HB2	1.86	0.57
1:A:168:PRO:O	1:A:169:LEU:CD2	2.53	0.57
1:A:234:THR:HG23	1:A:274:GLY:O	2.05	0.57
1:A:363:TYR:CD1	1:A:364:ARG:CZ	2.87	0.56
1:A:590:THR:CB	1:A:593:LYS:HG3	2.31	0.56
1:A:84:VAL:HG13	1:A:101:VAL:HG21	1.87	0.56
1:A:580:VAL:HG21	2:B:747:GLU:HB3	1.87	0.56
2:B:1341:LEU:HA	2:B:1367:CYS:O	2.05	0.56
2:B:1028:LYS:HB2	2:B:1071:ILE:CG2	2.35	0.56
2:B:799:PHE:HE1	2:B:801:VAL:HG23	1.69	0.56
1:A:541:LEU:CD2	2:B:796:ALA:CB	2.80	0.56
2:B:1416:PHE:HZ	2:B:1442:HIS:CD2	2.20	0.56
2:B:742:ARG:O	2:B:903:VAL:HG13	2.05	0.56
2:B:806:ASP:HB2	2:B:899:ILE:HD13	1.86	0.56
2:B:1259:GLN:HA	2:B:1259:GLN:OE1	2.01	0.56
1:A:430:SER:O	1:A:431:ASN:HB2	2.05	0.56
1:A:127:ILE:HG22	1:A:128:PHE:N	2.20	0.56
1:A:330:PRO:O	1:A:357:PRO:HG3	2.06	0.56
2:B:1128:SER:HA	2:B:1131:GLU:CD	2.25	0.56
1:A:144:ASN:CG	1:A:155:GLN:HE21	2.08	0.56
2:B:1387:THR:HG22	2:B:1451:GLN:N	2.21	0.56
1:A:379:THR:HG22	1:A:380:GLN:O	2.06	0.56
1:A:406:LYS:HD3	1:A:407:GLN:O	2.06	0.56
1:A:327:VAL:CG2	1:A:357:PRO:CB	2.78	0.56
1:A:443:LEU:HB2	1:A:533:VAL:HG22	1.86	0.56
2:B:1192:ALA:HB3	2:B:1195:LYS:HA	1.87	0.56
2:B:991:GLN:HE22	2:B:1104:HIS:HE1	1.50	0.56
1:A:640:CYS:HB3	1:A:641:PRO:HD2	1.88	0.56
1:A:603:ILE:HG13	1:A:621:GLY:HA3	1.88	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:582:VAL:O	1:A:582:VAL:HG12	2.05	0.56
1:A:349:ASP:HB3	1:A:351:MET:CE	2.35	0.56
1:A:180:GLY:O	1:A:201:GLU:HG3	2.04	0.56
1:A:590:THR:HG22	1:A:592:SER:CB	2.35	0.56
2:B:1215:LEU:HA	2:B:1218:LEU:HD12	1.87	0.56
2:B:978:LEU:CD2	2:B:981:LEU:HG	2.21	0.56
1:A:311:HIS:CE1	2:B:1410:TYR:HB3	2.41	0.56
2:B:829:LEU:CD2	2:B:840:VAL:HG11	2.35	0.56
2:B:932:ARG:HG3	2:B:932:ARG:O	2.04	0.56
1:A:554:VAL:CG1	1:A:555:PRO:HD2	2.28	0.56
2:B:833:ARG:CG	2:B:833:ARG:NH1	2.67	0.56
1:A:365:VAL:HG13	1:A:365:VAL:O	2.06	0.56
1:A:13:ARG:C	1:A:14:LEU:HD23	2.25	0.56
2:B:741:SER:OG	2:B:891:LYS:HE2	2.06	0.56
2:B:1222:LYS:HA	2:B:1224:PHE:CZ	2.42	0.55
1:A:343:LYS:HE2	1:A:527:ASP:OD1	2.06	0.55
2:B:744:GLU:HA	2:B:744:GLU:OE2	2.06	0.55
2:B:850:PHE:HZ	2:B:886:GLN:CB	2.19	0.55
1:A:1:SER:N	1:A:2:PRO:HD3	2.21	0.55
2:B:1172:TYR:CD1	2:B:1216:LEU:HB3	2.40	0.55
1:A:591:GLN:CA	1:A:594:ILE:HG12	2.36	0.55
1:A:19:THR:HG22	1:A:20:MET:N	2.21	0.55
1:A:441:THR:O	1:A:443:LEU:N	2.39	0.55
2:B:991:GLN:NE2	2:B:1104:HIS:CE1	2.74	0.55
1:A:468:TYR:OH	1:A:486:ARG:HD2	2.06	0.55
2:B:799:PHE:HD1	2:B:800:GLU:N	1.92	0.55
2:B:811:LEU:O	2:B:905:LYS:HD2	2.06	0.55
2:B:1227:VAL:H	2:B:1228:PRO:HD2	1.71	0.55
2:B:1406:TYR:OH	2:B:1408:SER:HA	2.06	0.55
2:B:1083:LYS:HE3	2:B:1141:ASN:OD1	2.05	0.55
1:A:598:VAL:HG12	1:A:598:VAL:O	2.05	0.55
2:B:833:ARG:HG2	2:B:833:ARG:NH1	2.10	0.55
2:B:1343:VAL:HG11	2:B:1471:TYR:CD2	2.41	0.55
2:B:1128:SER:CA	2:B:1131:GLU:OE2	2.47	0.55
1:A:430:SER:O	1:A:431:ASN:OD1	2.23	0.55
2:B:999:THR:HG21	2:B:1026:LEU:O	2.07	0.55
2:B:1192:ALA:HA	2:B:1197:ARG:O	2.07	0.55
2:B:744:GLU:HG3	2:B:774:LYS:HB3	1.88	0.54
2:B:1296:LEU:HD23	2:B:1298:ARG:NH2	2.22	0.54
1:A:236:ARG:HG3	1:A:236:ARG:O	2.06	0.54
2:B:972:ALA:HB2	2:B:1261:GLN:HE21	1.72	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:885:LEU:HD13	2:B:908:LYS:HG2	1.90	0.54
1:A:364:ARG:H	1:A:379:THR:CG2	2.21	0.54
1:A:453:PHE:N	1:A:453:PHE:CD2	2.76	0.54
2:B:1145:GLY:O	2:B:1149:LYS:HG2	2.07	0.54
1:A:614:ALA:HA	1:A:632:THR:HG22	1.90	0.54
2:B:1370:TYR:HB2	2:B:1429:VAL:HG23	1.89	0.54
2:B:744:GLU:HB2	2:B:775:ASP:CB	2.38	0.54
1:A:220:PHE:HB3	1:A:357:PRO:HG2	1.90	0.54
1:A:127:ILE:CG2	1:A:128:PHE:N	2.70	0.54
2:B:1363:ILE:HG12	2:B:1440:LYS:HG2	1.89	0.54
1:A:380:GLN:HE22	1:A:440:ARG:CZ	2.17	0.54
2:B:782:ILE:O	2:B:798:PRO:CG	2.55	0.54
2:B:958:ILE:HG23	2:B:1322:VAL:HG22	1.90	0.54
2:B:1094:GLY:HA3	2:B:1150:ALA:HA	1.89	0.54
2:B:965:VAL:C	2:B:1267:HIS:CD2	2.68	0.54
2:B:882:LYS:HG3	2:B:886:GLN:NE2	2.22	0.54
1:A:380:GLN:C	1:A:382:ASP:H	2.11	0.54
2:B:742:ARG:NH1	2:B:742:ARG:HB3	2.23	0.54
1:A:107:TYR:HB2	1:A:109:PHE:CE2	2.42	0.54
2:B:1028:LYS:HB2	2:B:1071:ILE:HG21	1.90	0.54
2:B:1338:LYS:HA	2:B:1371:ARG:HD2	1.89	0.53
1:A:342:PHE:CD1	1:A:391:THR:HG21	2.43	0.53
1:A:211:GLU:OE2	1:A:236:ARG:HD2	2.08	0.53
2:B:1094:GLY:HA3	2:B:1150:ALA:N	2.24	0.53
2:B:749:TRP:CB	2:B:774:LYS:HE2	2.38	0.53
2:B:744:GLU:CD	2:B:774:LYS:HD2	2.29	0.53
2:B:1411:GLU:HG2	2:B:1422:LEU:CD1	2.37	0.53
3:M:23:LEU:HD11	3:M:51:ALA:O	2.09	0.53
1:A:230:GLU:HG2	1:A:279:VAL:HG13	1.89	0.53
1:A:541:LEU:HA	1:A:564:GLU:O	2.09	0.53
1:A:133:LYS:O	1:A:134:LEU:HB2	2.09	0.53
2:B:1213:TYR:HA	2:B:1216:LEU:HD12	1.91	0.53
1:A:455:LEU:HD23	1:A:486:ARG:NH2	2.23	0.53
2:B:1263:ASP:O	2:B:1264:ALA:C	2.47	0.53
1:A:61:MET:HE1	1:A:482:GLY:HA2	1.89	0.53
1:A:187:TYR:HB2	1:A:194:GLN:O	2.09	0.53
1:A:637:GLU:HG3	1:A:639:GLN:O	2.08	0.53
1:A:458:ASP:N	1:A:458:ASP:OD1	2.41	0.53
1:A:589:LEU:HD11	1:A:594:ILE:CD1	2.30	0.53
1:A:8:THR:HG22	1:A:20:MET:HB2	1.88	0.53
2:B:1054:THR:OG1	2:B:1089:LYS:HG3	2.08	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1217:ALA:O	2:B:1219:LEU:N	2.42	0.53
2:B:1106:GLU:HA	2:B:1112:ARG:CZ	2.39	0.53
1:A:107:TYR:HB2	1:A:109:PHE:HZ	1.69	0.53
1:A:207:LEU:HD21	1:A:580:VAL:HG22	1.90	0.53
2:B:1047:PHE:CE2	2:B:1103:ILE:HD12	2.44	0.53
1:A:378:LEU:CD1	1:A:378:LEU:C	2.76	0.53
1:A:127:ILE:HD12	1:A:127:ILE:N	2.22	0.53
1:A:470:TYR:C	1:A:470:TYR:CD1	2.81	0.53
1:A:250:ILE:HG22	1:A:305:SER:HB3	1.91	0.53
1:A:468:TYR:CZ	1:A:486:ARG:HD2	2.43	0.53
1:A:264:GLU:O	1:A:284:VAL:HG11	2.09	0.53
3:M:49:GLN:HA	3:M:52:MET:HE2	1.91	0.53
1:A:410:SER:C	1:A:412:ALA:H	2.12	0.53
2:B:783:LEU:N	2:B:798:PRO:CG	2.72	0.53
2:B:978:LEU:HB2	2:B:1240:TYR:HD1	1.74	0.53
1:A:18:GLU:O	1:A:66:PHE:CE2	2.62	0.53
1:A:427:VAL:HG23	1:A:613:TYR:CE2	2.44	0.53
1:A:441:THR:O	1:A:443:LEU:HG	2.09	0.53
2:B:840:VAL:HG12	2:B:841:ARG:N	2.24	0.53
2:B:1056:LEU:O	2:B:1060:VAL:HG23	2.09	0.53
2:B:1384:SER:HB2	2:B:1421:THR:HG22	1.92	0.52
2:B:1095:VAL:HG13	2:B:1122:THR:OG1	2.09	0.52
2:B:1087:LEU:HD21	2:B:1142:SER:CB	2.39	0.52
2:B:1143:LEU:HD11	2:B:1147:ILE:HG13	1.91	0.52
2:B:1183:PRO:HG2	2:B:1184:LEU:HD12	1.91	0.52
2:B:1172:TYR:CE1	2:B:1216:LEU:HB3	2.44	0.52
2:B:1078:LEU:CD2	2:B:1135:ILE:HD13	2.39	0.52
1:A:528:SER:CB	1:A:616:VAL:HG13	2.38	0.52
2:B:985:PRO:HB3	2:B:996:MET:HE3	1.90	0.52
1:A:590:THR:HG22	1:A:592:SER:CA	2.39	0.52
2:B:733:ILE:HG13	2:B:894:VAL:O	2.09	0.52
1:A:509:LEU:O	1:A:509:LEU:HD13	2.09	0.52
1:A:145:ILE:O	1:A:153:VAL:HG22	2.09	0.52
2:B:744:GLU:CB	2:B:775:ASP:N	2.72	0.52
1:A:113:ASP:OD2	2:B:748:SER:CB	2.57	0.52
1:A:78:LYS:HE3	1:A:82:LYS:NZ	2.25	0.52
1:A:380:GLN:NE2	1:A:440:ARG:NH1	2.25	0.52
1:A:541:LEU:HG	2:B:796:ALA:HB1	1.77	0.52
1:A:327:VAL:HG21	1:A:357:PRO:HG3	1.92	0.52
1:A:208:PRO:HD2	1:A:583:LEU:HD11	1.92	0.52
2:B:865:THR:HG22	2:B:865:THR:O	2.08	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:M:73:ILE:HG13	3:M:73:ILE:O	2.09	0.52
1:A:164:LEU:HD23	1:A:570:ARG:HB2	1.92	0.52
1:A:364:ARG:N	1:A:379:THR:CG2	2.73	0.52
1:A:504:ILE:HG23	1:A:535:ASP:HA	1.92	0.52
2:B:1102:VAL:O	2:B:1105:GLN:HG2	2.09	0.52
2:B:1037:PHE:HA	2:B:1048:VAL:CG1	2.40	0.52
1:A:566:ASP:CG	2:B:791:LYS:HG3	2.30	0.52
3:M:47:SER:O	3:M:70:LEU:HD13	2.10	0.52
1:A:380:GLN:HG3	1:A:384:VAL:O	2.09	0.52
2:B:749:TRP:CZ3	2:B:750:LEU:HB2	2.45	0.52
2:B:1062:LYS:HE3	2:B:1124:PHE:CZ	2.45	0.52
1:A:591:GLN:OE1	1:A:594:ILE:HG13	2.10	0.51
2:B:916:MET:O	2:B:1325:MET:HG3	2.09	0.51
2:B:1086:ILE:HG21	2:B:1142:SER:HB2	1.91	0.51
2:B:1074:ASP:C	2:B:1076:GLN:H	2.13	0.51
2:B:777:ILE:HD12	2:B:808:PHE:CB	2.39	0.51
2:B:756:LEU:HD22	2:B:765:SER:HB2	1.91	0.51
1:A:141:VAL:HG12	1:A:142:MET:N	2.25	0.51
2:B:1366:ILE:HG21	2:B:1455:VAL:HG11	1.92	0.51
2:B:819:ARG:HG2	2:B:820:ASN:ND2	2.26	0.51
2:B:1260:TYR:O	2:B:1260:TYR:CG	2.63	0.51
1:A:408:GLU:C	1:A:409:LEU:HD12	2.31	0.51
1:A:613:TYR:O	1:A:617:PHE:CD2	2.64	0.51
2:B:1158:TYR:OH	2:B:1188:PHE:HB2	2.11	0.51
2:B:1392:ASP:C	2:B:1394:ASP:H	2.14	0.51
1:A:37:VAL:O	1:A:46:VAL:HG22	2.10	0.51
2:B:1038:ARG:HD3	2:B:1077:VAL:CG1	2.40	0.51
1:A:541:LEU:CB	2:B:796:ALA:HB2	2.37	0.51
1:A:591:GLN:HB2	2:B:795:VAL:HB	1.90	0.51
1:A:366:PRO:HA	1:A:377:SER:O	2.11	0.51
1:A:439:LEU:CD1	1:A:450:ASN:HB2	2.41	0.51
1:A:209:SER:O	1:A:238:LEU:HG	2.10	0.51
1:A:365:VAL:N	1:A:379:THR:OG1	2.20	0.51
1:A:432:ASN:HB2	1:A:523:GLU:OE1	2.10	0.51
1:A:511:ALA:O	1:A:512:TYR:HB3	2.11	0.51
1:A:617:PHE:HB2	1:A:632:THR:HG21	1.92	0.51
2:B:734:ILE:HD11	2:B:898:PHE:HD2	1.76	0.51
1:A:561:LEU:O	1:A:563:ILE:HD12	2.11	0.51
1:A:530:TRP:CD2	1:A:607:PRO:CB	2.94	0.51
1:A:114:LYS:HB2	1:A:117:TYR:CZ	2.46	0.50
1:A:516:ILE:CG1	1:A:522:ARG:HD2	2.40	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:515:LEU:CD2	1:A:515:LEU:C	2.65	0.50
1:A:179:MET:CG	1:A:203:LYS:HA	2.41	0.50
2:B:1277:GLN:HG3	2:B:1281:ARG:NE	2.26	0.50
1:A:187:TYR:CD1	1:A:192:PRO:HA	2.46	0.50
2:B:842:VAL:HG22	2:B:876:TYR:OH	2.11	0.50
2:B:1255:GLN:HA	2:B:1258:ALA:HB3	1.93	0.50
2:B:903:VAL:HG11	2:B:905:LYS:HE3	1.92	0.50
2:B:1397:LYS:HZ1	2:B:1412:LEU:HG	1.71	0.50
2:B:1026:LEU:HD23	2:B:1029:LYS:HD3	1.93	0.50
2:B:1107:MET:O	2:B:1248:GLN:HG2	2.10	0.50
1:A:147:ASN:HB3	1:A:182:TRP:CZ3	2.46	0.50
2:B:1071:ILE:HD11	2:B:1073:ILE:HD11	1.93	0.50
2:B:1260:TYR:CD2	2:B:1260:TYR:O	2.65	0.50
1:A:239:TYR:HA	2:B:779:THR:OG1	2.11	0.50
1:A:517:GLY:O	1:A:518:ALA:CB	2.60	0.50
2:B:1064:PHE:O	2:B:1068:VAL:HG13	2.11	0.50
1:A:437:SER:OG	1:A:452:ASN:HB2	2.12	0.50
2:B:1457:VAL:HG22	2:B:1467:CYS:O	2.12	0.50
2:B:1035:LEU:HD21	2:B:1077:VAL:HG21	1.94	0.50
1:A:220:PHE:CZ	1:A:330:PRO:CB	2.89	0.50
1:A:221:TYR:HE1	1:A:228:GLY:CA	2.23	0.50
1:A:126:ARG:C	1:A:127:ILE:HD12	2.32	0.50
1:A:507:PHE:HE1	1:A:533:VAL:CG2	2.25	0.50
2:B:1259:GLN:OE1	2:B:1262:LYS:HD3	2.12	0.50
1:A:110:ILE:HG22	1:A:111:GLN:N	2.26	0.50
1:A:109:PHE:HD2	1:A:128:PHE:O	1.95	0.50
1:A:194:GLN:O	1:A:194:GLN:OE1	2.30	0.50
1:A:163:GLN:HG2	1:A:167:LEU:HD23	1.94	0.50
2:B:1053:SER:OG	2:B:1102:VAL:HG13	2.12	0.50
1:A:154:LYS:HG2	1:A:155:GLN:N	2.26	0.50
2:B:1211:THR:OG1	2:B:1233:TRP:CZ3	2.64	0.50
3:M:20:LYS:HD3	3:M:55:LEU:HD21	1.93	0.50
2:B:1276:LEU:O	2:B:1285:ILE:HD12	2.12	0.50
2:B:930:LEU:HD12	2:B:936:GLN:HE22	1.76	0.50
2:B:964:PRO:HB3	2:B:1270:LEU:CG	2.41	0.49
1:A:331:TYR:O	1:A:415:ALA:CB	2.60	0.49
2:B:1269:GLU:OE1	2:B:1269:GLU:O	2.30	0.49
1:A:409:LEU:HB2	1:A:414:GLN:OE1	2.12	0.49
1:A:590:THR:CG2	1:A:592:SER:CB	2.90	0.49
1:A:36:THR:HA	1:A:48:SER:HA	1.94	0.49
1:A:427:VAL:HG22	1:A:613:TYR:CE2	2.47	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:207:LEU:CD2	2:B:747:GLU:HG2	2.34	0.49
2:B:1038:ARG:HD3	2:B:1077:VAL:HG13	1.94	0.49
2:B:974:ASP:C	2:B:976:GLU:H	2.15	0.49
2:B:1340:ASP:O	2:B:1368:THR:HA	2.12	0.49
2:B:758:GLU:H	2:B:758:GLU:CD	2.16	0.49
2:B:1315:LYS:HD2	2:B:1315:LYS:H	1.76	0.49
1:A:580:VAL:HG21	2:B:747:GLU:CB	2.41	0.49
2:B:1341:LEU:HD12	2:B:1367:CYS:O	2.11	0.49
2:B:1399:LEU:HB3	2:B:1405:ARG:NH1	2.28	0.49
2:B:1409:LYS:O	2:B:1409:LYS:HG2	2.11	0.49
1:A:13:ARG:HD2	1:A:18:GLU:OE2	2.11	0.49
2:B:1126:LEU:CD2	2:B:1173:ALA:HB1	2.35	0.49
2:B:1036:ALA:O	2:B:1037:PHE:CG	2.66	0.49
2:B:1120:ALA:HA	2:B:1169:ILE:HD13	1.92	0.49
1:A:369:VAL:H	1:A:375:VAL:CG1	2.26	0.49
1:A:516:ILE:CD1	1:A:522:ARG:HD3	2.34	0.49
2:B:843:GLU:HG2	2:B:845:LEU:HD12	1.93	0.49
2:B:885:LEU:CD1	2:B:908:LYS:HG2	2.42	0.49
1:A:522:ARG:HG2	1:A:522:ARG:HH11	1.71	0.49
2:B:811:LEU:HD13	2:B:890:VAL:HG22	1.94	0.49
1:A:37:VAL:HG13	1:A:86:VAL:HG22	1.94	0.49
2:B:838:LEU:HB3	2:B:894:VAL:HG11	1.94	0.49
1:A:453:PHE:O	1:A:492:LEU:HA	2.13	0.49
2:B:1078:LEU:HD21	2:B:1135:ILE:HD13	1.94	0.49
3:M:26:LEU:HD13	3:M:70:LEU:HD11	1.94	0.49
2:B:1399:LEU:HB3	2:B:1405:ARG:HH11	1.77	0.49
2:B:1000:VAL:HG22	2:B:1027:ILE:HG23	1.94	0.49
2:B:1288:ARG:HD3	2:B:1290:HIS:NE2	2.27	0.49
2:B:1259:GLN:HE22	2:B:1262:LYS:CG	2.26	0.49
1:A:253:ILE:O	1:A:260:ILE:HG12	2.12	0.49
1:A:147:ASN:HB3	1:A:182:TRP:CH2	2.48	0.49
2:B:1403:VAL:HG22	2:B:1404:ASP:N	2.27	0.49
1:A:349:ASP:HB3	1:A:351:MET:HE3	1.94	0.49
2:B:1078:LEU:HD11	2:B:1132:ALA:HB1	1.94	0.49
1:A:559:MET:O	1:A:559:MET:HG3	2.12	0.49
1:A:404:THR:CG2	1:A:414:GLN:HB3	2.41	0.49
2:B:744:GLU:HB2	2:B:775:ASP:CA	2.42	0.49
3:M:65:GLU:HG3	3:M:65:GLU:O	2.12	0.49
1:A:168:PRO:O	1:A:169:LEU:HG	2.13	0.49
2:B:1004:HIS:HB2	2:B:1066:LEU:HD21	1.95	0.49
2:B:742:ARG:HD2	2:B:775:ASP:O	2.13	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:22:LEU:HD13	1:A:52:THR:HG21	1.94	0.49
2:B:1094:GLY:HA3	2:B:1150:ALA:CA	2.42	0.49
1:A:557:GLN:HG2	1:A:558:GLN:N	2.28	0.49
2:B:964:PRO:HB3	2:B:1270:LEU:CD2	2.43	0.49
2:B:782:ILE:HB	2:B:798:PRO:HB2	1.92	0.49
1:A:10:ASN:OD1	1:A:618:SER:HA	2.12	0.49
2:B:866:ILE:HG12	2:B:872:LEU:HD22	1.95	0.49
2:B:974:ASP:HB3	2:B:976:GLU:HG3	1.95	0.49
2:B:1184:LEU:N	2:B:1184:LEU:HD12	2.28	0.49
2:B:1290:HIS:O	2:B:1294:ALA:HB2	2.13	0.49
1:A:501:THR:O	1:A:504:ILE:HD12	2.13	0.48
2:B:1025:GLU:O	2:B:1026:LEU:HD23	2.13	0.48
2:B:734:ILE:HG12	3:M:46:ILE:HG23	1.95	0.48
2:B:1239:TYR:CD2	2:B:1253:VAL:HG11	2.47	0.48
2:B:1172:TYR:CE2	2:B:1216:LEU:HD13	2.48	0.48
1:A:352:VAL:O	1:A:384:VAL:HG22	2.13	0.48
2:B:733:ILE:HG12	2:B:734:ILE:N	2.21	0.48
1:A:386:LYS:NZ	1:A:440:ARG:HG2	2.27	0.48
2:B:1215:LEU:HD13	2:B:1230:VAL:CG1	2.43	0.48
1:A:221:TYR:HD2	1:A:326:ILE:HD12	1.78	0.48
1:A:501:THR:C	1:A:538:VAL:HG22	2.31	0.48
1:A:268:ARG:NE	2:B:1406:TYR:CD2	2.81	0.48
1:A:6:ILE:HD11	1:A:20:MET:CG	2.41	0.48
1:A:556:GLY:C	3:M:39:TYR:HB2	2.33	0.48
1:A:343:LYS:HD2	1:A:343:LYS:N	2.27	0.48
2:B:1113:ASN:HD22	2:B:1163:ARG:NE	2.11	0.48
2:B:1269:GLU:C	2:B:1270:LEU:CG	2.66	0.48
2:B:1457:VAL:HG23	2:B:1457:VAL:O	2.14	0.48
2:B:804:MET:HG2	2:B:805:GLN:H	1.78	0.48
1:A:137:VAL:CG2	1:A:139:ARG:NH1	2.76	0.48
1:A:346:MET:HE1	1:A:454:LEU:HG	1.95	0.48
2:B:1203:LYS:HD2	2:B:1206:TYR:CE2	2.49	0.48
1:A:333:ILE:O	1:A:417:ARG:HG2	2.13	0.48
2:B:782:ILE:HG22	2:B:798:PRO:HB3	1.94	0.48
1:A:509:LEU:O	1:A:529:VAL:HG12	2.13	0.48
2:B:730:ASP:O	3:M:53:TYR:HD1	1.97	0.48
2:B:925:LEU:O	2:B:926:ASP:HB2	2.13	0.48
2:B:1038:ARG:C	2:B:1039:GLN:O	2.51	0.48
2:B:733:ILE:HD11	2:B:893:ALA:O	2.13	0.48
2:B:1253:VAL:O	2:B:1257:LEU:HD12	2.13	0.48
3:M:15:LEU:HG	3:M:63:MET:HB3	1.96	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:898:PHE:HB2	3:M:50:LYS:HE3	1.96	0.48
1:A:145:ILE:HG21	1:A:171:TRP:CE3	2.49	0.48
2:B:1475:LYS:HE2	2:B:1493:GLU:OE2	2.13	0.48
1:A:501:THR:CB	1:A:538:VAL:HG13	2.43	0.48
2:B:841:ARG:HB2	2:B:895:TYR:CE1	2.48	0.48
2:B:1279:PRO:HB2	2:B:1306:GLU:CD	2.34	0.48
1:A:304:VAL:HG12	1:A:305:SER:N	2.28	0.48
2:B:1175:ALA:HB1	2:B:1221:LEU:HD21	1.95	0.48
2:B:1392:ASP:O	2:B:1394:ASP:N	2.46	0.48
1:A:380:GLN:C	1:A:382:ASP:N	2.66	0.47
1:A:465:ILE:HD11	1:A:515:LEU:HB3	1.95	0.47
2:B:1219:LEU:HD23	2:B:1227:VAL:HG21	1.95	0.47
1:A:314:SER:OG	2:B:828:VAL:HG22	2.14	0.47
2:B:1012:TRP:CH2	2:B:1020:ARG:HB2	2.49	0.47
2:B:1172:TYR:CD2	2:B:1216:LEU:HD13	2.49	0.47
1:A:462:GLU:HB2	1:A:486:ARG:HH22	1.79	0.47
3:M:54:ALA:CB	3:M:62:LYS:HB3	2.44	0.47
2:B:1477:ASP:OD2	2:B:1479:LYS:HD3	2.13	0.47
2:B:782:ILE:HD12	2:B:799:PHE:CD2	2.48	0.47
2:B:744:GLU:HB2	2:B:775:ASP:N	2.29	0.47
1:A:12:LEU:O	1:A:13:ARG:HG3	2.14	0.47
1:A:509:LEU:HD22	1:A:510:VAL:H	1.79	0.47
2:B:1047:PHE:HE2	2:B:1103:ILE:HD12	1.78	0.47
3:M:71:GLN:HA	3:M:71:GLN:HE21	1.79	0.47
1:A:571:VAL:HB	2:B:754:GLU:O	2.14	0.47
2:B:1415:ALA:O	2:B:1419:ARG:NH1	2.47	0.47
2:B:1219:LEU:C	2:B:1221:LEU:H	2.17	0.47
1:A:222:TYR:CD1	1:A:328:THR:HA	2.49	0.47
1:A:10:ASN:HB2	1:A:622:LEU:N	2.29	0.47
1:A:246:THR:HG21	2:B:1425:TYR:CE1	2.49	0.47
2:B:1039:GLN:HB3	2:B:1040:PRO:CD	2.44	0.47
1:A:133:LYS:HG2	1:A:477:ARG:HD3	1.95	0.47
1:A:38:HIS:O	1:A:85:THR:HB	2.14	0.47
3:M:26:LEU:HG	3:M:26:LEU:O	2.14	0.47
3:M:71:GLN:HG3	3:M:71:GLN:O	2.15	0.47
1:A:480:LYS:HZ1	1:A:497:LEU:HD13	1.80	0.47
2:B:729:LEU:C	2:B:729:LEU:HD13	2.34	0.47
1:A:541:LEU:HD12	1:A:542:VAL:N	2.30	0.47
2:B:1055:TRP:HE3	2:B:1102:VAL:HG11	1.79	0.47
1:A:114:LYS:HE3	1:A:117:TYR:CE1	2.49	0.47
1:A:508:ARG:HH21	1:A:607:PRO:HG3	1.80	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:433:TYR:CD2	1:A:456:ARG:HG2	2.46	0.47
1:A:345:GLY:C	1:A:346:MET:HG2	2.33	0.47
1:A:515:LEU:CD2	1:A:523:GLU:HB3	2.45	0.47
1:A:108:LEU:HB2	1:A:196:PHE:CE1	2.50	0.47
3:M:20:LYS:HD3	3:M:55:LEU:CD2	2.44	0.47
1:A:397:PRO:HB3	1:A:420:GLN:HE21	1.78	0.47
2:B:1475:LYS:N	2:B:1475:LYS:HD2	2.27	0.47
1:A:469:THR:O	1:A:511:ALA:HA	2.15	0.47
2:B:744:GLU:HG3	2:B:774:LYS:CA	2.44	0.47
2:B:1082:VAL:HG22	2:B:1129:LEU:HD22	1.97	0.47
1:A:188:TYR:HD1	1:A:194:GLN:HE22	1.62	0.47
1:A:239:TYR:HE1	2:B:832:TYR:CZ	2.33	0.47
2:B:920:VAL:CG2	2:B:1324:THR:HG23	2.45	0.47
1:A:145:ILE:HG21	1:A:171:TRP:CZ3	2.50	0.47
1:A:139:ARG:O	1:A:159:SER:OG	2.29	0.47
2:B:991:GLN:OE1	2:B:1104:HIS:CE1	2.67	0.47
2:B:1066:LEU:O	2:B:1066:LEU:HD23	2.14	0.47
3:M:54:ALA:HB1	3:M:62:LYS:HB3	1.97	0.47
1:A:400:ILE:O	1:A:418:THR:HA	2.14	0.47
3:M:43:THR:HG22	3:M:43:THR:O	2.14	0.47
1:A:363:TYR:HD2	1:A:381:GLY:HA2	1.80	0.47
2:B:749:TRP:CD2	2:B:774:LYS:HG2	2.50	0.47
2:B:1278:LEU:O	2:B:1281:ARG:CD	2.62	0.47
2:B:736:GLU:OE2	2:B:845:LEU:HD21	2.15	0.47
1:A:439:LEU:HD13	1:A:450:ASN:HB2	1.96	0.47
1:A:31:VAL:HG11	1:A:54:LEU:HD12	1.97	0.47
1:A:262:LEU:CD2	1:A:288:GLY:HA3	2.45	0.47
1:A:370:GLN:HB2	1:A:401:THR:O	2.15	0.47
1:A:512:TYR:HB2	1:A:525:VAL:O	2.15	0.47
2:B:756:LEU:HD22	2:B:765:SER:CB	2.45	0.47
1:A:168:PRO:O	1:A:169:LEU:CG	2.63	0.47
1:A:468:TYR:CE2	1:A:486:ARG:HD2	2.49	0.47
1:A:58:THR:O	1:A:61:MET:HB2	2.14	0.47
1:A:209:SER:C	1:A:238:LEU:HG	2.36	0.47
2:B:817:VAL:CG2	2:B:907:LEU:HD11	2.45	0.47
2:B:927:PRO:HG2	2:B:1313:GLU:CA	2.44	0.47
2:B:811:LEU:HD22	2:B:903:VAL:O	2.14	0.46
2:B:1281:ARG:O	2:B:1281:ARG:CG	2.63	0.46
1:A:109:PHE:HE2	1:A:130:VAL:CG2	2.27	0.46
1:A:136:PRO:HG3	2:B:789:ASP:HA	1.97	0.46
1:A:268:ARG:HD2	2:B:1425:TYR:CD1	2.50	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:734:ILE:CD1	2:B:898:PHE:HD2	2.27	0.46
1:A:147:ASN:HB2	1:A:148:PRO:HD3	1.96	0.46
3:M:14:LYS:HG2	3:M:14:LYS:O	2.15	0.46
2:B:1410:TYR:O	2:B:1410:TYR:CD2	2.68	0.46
1:A:176:LEU:HD21	2:B:1327:HIS:NE2	2.30	0.46
1:A:555:PRO:HB3	2:B:775:ASP:CA	2.39	0.46
1:A:207:LEU:HG	1:A:579:GLY:O	2.15	0.46
2:B:889:GLU:OE2	2:B:891:LYS:CE	2.64	0.46
1:A:187:TYR:CG	1:A:195:VAL:HG22	2.50	0.46
1:A:269:ILE:HD12	1:A:277:GLU:O	2.15	0.46
2:B:993:MET:HE3	2:B:1063:VAL:HG21	1.98	0.46
2:B:889:GLU:OE2	2:B:891:LYS:HE3	2.16	0.46
1:A:475:LYS:HD2	1:A:598:VAL:HG11	1.98	0.46
2:B:1091:LYS:HB3	2:B:1092:PRO:CD	2.45	0.46
1:A:113:ASP:OD2	2:B:748:SER:HB3	2.14	0.46
1:A:35:VAL:CG1	1:A:36:THR:N	2.79	0.46
2:B:733:ILE:HG23	2:B:734:ILE:N	2.29	0.46
1:A:22:LEU:HD13	1:A:52:THR:CG2	2.46	0.46
2:B:1113:ASN:C	2:B:1115:ASN:H	2.17	0.46
1:A:541:LEU:CD2	2:B:786:SER:HB3	2.33	0.46
1:A:428:GLY:C	1:A:430:SER:N	2.68	0.46
1:A:574:VAL:CB	2:B:751:TRP:CE3	2.98	0.46
1:A:141:VAL:C	1:A:142:MET:SD	2.94	0.46
1:A:339:PRO:HG3	1:A:608:GLY:HA2	1.98	0.46
1:A:238:LEU:HD22	1:A:578:LYS:HB3	1.98	0.46
3:M:6:THR:H	3:M:9:GLU:HB3	1.81	0.46
2:B:838:LEU:HB3	2:B:894:VAL:CG1	2.46	0.46
3:M:72:LYS:O	3:M:76:GLU:HG3	2.16	0.46
2:B:1275:SER:OG	2:B:1311:THR:HB	2.16	0.46
2:B:1219:LEU:HD21	2:B:1227:VAL:HG21	1.97	0.46
1:A:356:ASN:HB3	1:A:357:PRO:CD	2.46	0.46
2:B:1457:VAL:O	2:B:1466:SER:HA	2.16	0.46
1:A:36:THR:HG22	1:A:37:VAL:N	2.31	0.46
1:A:553:PRO:O	2:B:803:VAL:HG13	2.16	0.46
1:A:451:VAL:HG23	1:A:495:LEU:O	2.16	0.46
2:B:1429:VAL:O	2:B:1429:VAL:HG23	2.15	0.46
3:M:53:TYR:O	3:M:56:LYS:HG3	2.16	0.46
1:A:363:TYR:HD1	1:A:364:ARG:CZ	2.30	0.45
2:B:807:PHE:HB3	2:B:899:ILE:HG21	1.97	0.45
2:B:949:VAL:HG23	2:B:1328:ALA:O	2.16	0.45
2:B:1296:LEU:HD23	2:B:1298:ARG:HH22	1.81	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:876:TYR:HA	2:B:1451:GLN:NE2	2.30	0.45
2:B:754:GLU:HG3	2:B:769:MET:SD	2.56	0.45
1:A:335:PHE:HE2	1:A:417:ARG:HG3	1.78	0.45
1:A:428:GLY:O	1:A:429:ASN:HB3	2.16	0.45
1:A:268:ARG:HB3	1:A:268:ARG:CZ	2.44	0.45
2:B:957:ARG:O	2:B:1322:VAL:HG13	2.17	0.45
1:A:530:TRP:HB2	1:A:607:PRO:HB3	1.98	0.45
1:A:173:ILE:HD13	1:A:202:VAL:CG2	2.47	0.45
2:B:1029:LYS:O	2:B:1033:GLN:HG3	2.16	0.45
1:A:20:MET:SD	1:A:20:MET:C	2.95	0.45
1:A:131:ASN:HD21	1:A:133:LYS:CD	2.24	0.45
3:M:50:LYS:HE2	3:M:65:GLU:CG	2.45	0.45
2:B:1033:GLN:O	2:B:1036:ALA:HB3	2.16	0.45
2:B:1289:ILE:HG23	2:B:1294:ALA:HA	1.97	0.45
1:A:560:THR:HA	2:B:769:MET:O	2.17	0.45
1:A:118:THR:HG23	1:A:205:TYR:CE2	2.51	0.45
1:A:484:GLN:HG3	1:A:485:VAL:N	2.30	0.45
3:M:19:LEU:HG	3:M:19:LEU:O	2.16	0.45
2:B:1227:VAL:H	2:B:1228:PRO:CD	2.29	0.45
2:B:981:LEU:HD13	2:B:1002:ALA:HB2	1.97	0.45
1:A:339:PRO:HG3	1:A:608:GLY:CA	2.47	0.45
2:B:1408:SER:C	2:B:1410:TYR:H	2.20	0.45
2:B:1369:ARG:HG3	2:B:1433:GLU:O	2.15	0.45
2:B:778:THR:OG1	2:B:779:THR:N	2.50	0.45
2:B:1370:TYR:CD1	2:B:1376:ALA:HB2	2.51	0.45
1:A:115:THR:HG23	1:A:581:PHE:HE1	1.82	0.45
1:A:116:ILE:HG13	1:A:201:GLU:O	2.16	0.45
1:A:284:VAL:O	1:A:284:VAL:HG12	2.15	0.45
3:M:15:LEU:HD21	3:M:64:SER:HB2	1.98	0.45
1:A:397:PRO:CB	1:A:420:GLN:HE21	2.29	0.45
2:B:993:MET:HE3	2:B:1059:TYR:CE2	2.51	0.45
1:A:451:VAL:O	1:A:453:PHE:CE2	2.70	0.45
1:A:239:TYR:HE1	2:B:832:TYR:CE1	2.34	0.45
2:B:730:ASP:O	3:M:53:TYR:CD1	2.70	0.45
2:B:1387:THR:CG2	2:B:1450:ILE:HA	2.47	0.45
1:A:497:LEU:HD12	1:A:498:SER:H	1.82	0.45
2:B:1431:HIS:H	2:B:1431:HIS:CD2	2.34	0.45
2:B:1219:LEU:C	2:B:1221:LEU:N	2.70	0.45
2:B:1230:VAL:O	2:B:1230:VAL:HG12	2.17	0.45
1:A:109:PHE:O	1:A:127:ILE:HA	2.17	0.45
2:B:791:LYS:O	2:B:792:GLY:C	2.54	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:63:ASN:HD22	4:A:646:NAG:H83	1.81	0.45
2:B:954:SER:HB3	2:B:1326:TYR:CB	2.47	0.45
1:A:61:MET:HE3	1:A:61:MET:HB3	1.53	0.45
1:A:11:ILE:HG12	1:A:100:LEU:HD23	1.98	0.45
2:B:1221:LEU:O	2:B:1222:LYS:CB	2.65	0.45
2:B:1281:ARG:O	2:B:1281:ARG:HG2	2.17	0.45
1:A:507:PHE:CE1	1:A:533:VAL:HG23	2.51	0.45
1:A:248:PHE:CZ	2:B:1380:ILE:HG12	2.52	0.45
2:B:782:ILE:CG2	2:B:798:PRO:HB3	2.47	0.45
1:A:117:TYR:HD2	1:A:200:PHE:CD1	2.34	0.45
2:B:756:LEU:CD1	2:B:765:SER:HB2	2.39	0.45
2:B:956:THR:CG2	2:B:1324:THR:HG22	2.47	0.45
4:A:646:NAG:O4	4:A:647:NAG:C1	2.65	0.45
1:A:516:ILE:HG23	1:A:516:ILE:O	2.16	0.45
1:A:324:ILE:HA	1:A:325:PRO:HD3	1.81	0.45
2:B:954:SER:CB	2:B:1326:TYR:HB3	2.45	0.45
2:B:1239:TYR:HD2	2:B:1253:VAL:HG11	1.81	0.45
1:A:370:GLN:NE2	1:A:403:ARG:NE	2.56	0.44
1:A:605:CYS:C	1:A:607:PRO:HD3	2.37	0.44
1:A:400:ILE:O	1:A:418:THR:HG23	2.17	0.44
2:B:964:PRO:CB	2:B:1270:LEU:HD21	2.45	0.44
2:B:1191:THR:HG22	2:B:1198:TRP:CD1	2.52	0.44
2:B:918:LYS:HE3	2:B:1326:TYR:OH	2.17	0.44
2:B:1113:ASN:C	2:B:1115:ASN:N	2.71	0.44
3:M:67:LYS:HE2	3:M:67:LYS:HB3	1.66	0.44
2:B:1091:LYS:HB3	2:B:1092:PRO:HD2	2.00	0.44
2:B:1232:ARG:O	2:B:1232:ARG:HG2	2.17	0.44
1:A:233:ILE:CG2	1:A:271:ILE:HD11	2.48	0.44
1:A:591:GLN:HA	1:A:591:GLN:OE1	2.17	0.44
2:B:1476:GLU:HG3	2:B:1477:ASP:N	2.32	0.44
2:B:1269:GLU:O	2:B:1270:LEU:CD2	2.57	0.44
1:A:516:ILE:CG1	1:A:522:ARG:CD	2.95	0.44
1:A:573:LEU:HG	2:B:752:ASN:O	2.17	0.44
2:B:805:GLN:HG2	2:B:806:ASP:N	2.30	0.44
1:A:427:VAL:C	1:A:429:ASN:N	2.71	0.44
2:B:1140:VAL:O	2:B:1140:VAL:HG12	2.16	0.44
2:B:1117:LYS:O	2:B:1118:ASP:OD1	2.35	0.44
2:B:964:PRO:CB	2:B:1291:TRP:CZ3	3.01	0.44
2:B:1262:LYS:HE2	2:B:1262:LYS:HB2	1.73	0.44
2:B:1143:LEU:CD1	2:B:1147:ILE:HG13	2.48	0.44
1:A:265:SER:O	1:A:267:LYS:HG2	2.18	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:967:GLN:HB3	2:B:968:MET:H	1.69	0.44
2:B:759:PRO:HA	2:B:760:PRO:HD3	1.87	0.44
1:A:179:MET:CE	1:A:204:GLU:HG3	2.47	0.44
1:A:309:ILE:HD11	1:A:316:MET:SD	2.58	0.44
1:A:3:MET:HG2	1:A:4:TYR:N	2.33	0.44
2:B:744:GLU:CG	2:B:774:LYS:HB3	2.47	0.44
2:B:1230:VAL:O	2:B:1230:VAL:CG1	2.66	0.44
1:A:140:THR:C	1:A:141:VAL:CG2	2.86	0.44
1:A:55:THR:CB	1:A:57:ALA:H	2.29	0.44
2:B:1213:TYR:HD1	2:B:1216:LEU:HD12	1.82	0.44
2:B:754:GLU:HB3	2:B:767:LYS:HE3	1.99	0.44
1:A:34:THR:HG22	1:A:51:LYS:HE3	2.00	0.44
2:B:959:LEU:HD21	2:B:961:GLN:HB2	2.00	0.44
1:A:333:ILE:HD12	1:A:416:THR:HA	2.00	0.44
1:A:10:ASN:HA	1:A:623:THR:HG23	1.99	0.44
2:B:940:ILE:HD12	2:B:1308:PHE:CZ	2.52	0.44
2:B:1120:ALA:HA	2:B:1169:ILE:HG21	1.99	0.44
2:B:948:GLN:NE2	2:B:954:SER:HB3	2.33	0.44
2:B:1063:VAL:HG12	2:B:1063:VAL:O	2.17	0.44
2:B:1448:GLU:O	2:B:1448:GLU:HG3	2.18	0.44
2:B:998:PRO:HA	2:B:1001:ILE:HG22	2.00	0.44
3:M:18:GLU:O	3:M:67:LYS:HG3	2.18	0.44
1:A:565:GLY:O	2:B:764:ILE:HA	2.17	0.44
1:A:451:VAL:O	1:A:453:PHE:HE2	2.01	0.43
1:A:530:TRP:CG	1:A:607:PRO:CB	2.99	0.43
2:B:954:SER:CB	2:B:1326:TYR:CB	2.95	0.43
2:B:1203:LYS:HB2	2:B:1206:TYR:CD2	2.53	0.43
3:M:44:ILE:HD11	3:M:74:TYR:HE1	1.82	0.43
2:B:847:ASN:C	2:B:849:ALA:H	2.21	0.43
2:B:1267:HIS:CG	2:B:1267:HIS:O	2.70	0.43
2:B:1086:ILE:CD1	2:B:1143:LEU:HA	2.48	0.43
1:A:346:MET:SD	1:A:435:HIS:HB2	2.59	0.43
2:B:1310:VAL:HG12	2:B:1311:THR:N	2.33	0.43
1:A:361:PRO:CB	1:A:382:ASP:O	2.66	0.43
1:A:19:THR:O	1:A:20:MET:CB	2.65	0.43
1:A:7:ILE:CG2	1:A:8:THR:H	2.29	0.43
2:B:1462:ASN:HD22	2:B:1462:ASN:HA	1.59	0.43
2:B:782:ILE:HB	2:B:798:PRO:HB3	1.89	0.43
1:A:516:ILE:HD12	1:A:522:ARG:CD	2.35	0.43
2:B:811:LEU:HG	2:B:813:LEU:CD1	2.46	0.43
2:B:1259:GLN:NE2	2:B:1262:LYS:CE	2.72	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:850:PHE:HZ	2:B:886:GLN:HB2	1.83	0.43
2:B:1023:ALA:O	2:B:1027:ILE:HG13	2.18	0.43
2:B:1069:ASN:HD22	2:B:1069:ASN:HA	1.55	0.43
2:B:950:PRO:O	2:B:951:ASP:HB2	2.18	0.43
1:A:541:LEU:CG	2:B:796:ALA:CB	2.47	0.43
1:A:591:GLN:O	1:A:594:ILE:N	2.50	0.43
1:A:617:PHE:CB	1:A:632:THR:HG21	2.47	0.43
1:A:109:PHE:O	1:A:127:ILE:HG23	2.18	0.43
2:B:1143:LEU:HD11	2:B:1147:ILE:CG1	2.49	0.43
1:A:365:VAL:CG1	1:A:379:THR:OG1	2.66	0.43
1:A:35:VAL:HG12	1:A:36:THR:N	2.33	0.43
2:B:1121:LEU:HD12	2:B:1121:LEU:O	2.18	0.43
1:A:358:ASP:OD1	1:A:358:ASP:N	2.52	0.43
2:B:860:HIS:CE1	2:B:862:GLN:HE22	2.36	0.43
1:A:341:TYR:HB2	1:A:609:SER:CB	2.32	0.43
1:A:580:VAL:HG22	2:B:747:GLU:HG2	2.01	0.43
2:B:992:ASN:OD1	2:B:1033:GLN:NE2	2.52	0.43
2:B:963:THR:HG22	2:B:963:THR:O	2.18	0.43
2:B:744:GLU:HG3	2:B:774:LYS:CB	2.48	0.43
1:A:117:TYR:CD2	1:A:200:PHE:CD1	3.07	0.43
2:B:733:ILE:C	2:B:734:ILE:HD12	2.38	0.43
1:A:443:LEU:CD1	1:A:449:LEU:HD22	2.42	0.43
1:A:118:THR:HB	2:B:815:TYR:CE1	2.54	0.43
1:A:363:TYR:CE1	1:A:364:ARG:HD3	2.28	0.43
2:B:981:LEU:HD22	2:B:998:PRO:CB	2.49	0.43
1:A:14:LEU:HD21	1:A:101:VAL:HG11	1.97	0.43
2:B:975:ALA:HB2	2:B:1006:LEU:HD21	1.99	0.43
1:A:473:MET:O	1:A:474:ASN:HB2	2.18	0.43
1:A:206:VAL:O	1:A:208:PRO:HD3	2.19	0.43
1:A:335:PHE:CD2	1:A:419:MET:HB3	2.54	0.43
1:A:541:LEU:HD12	1:A:542:VAL:H	1.83	0.43
1:A:110:ILE:HG12	1:A:127:ILE:HG13	2.01	0.43
2:B:1034:GLN:C	2:B:1036:ALA:H	2.22	0.43
1:A:148:PRO:HB3	1:A:181:GLN:H	1.83	0.43
2:B:738:ASN:HD22	3:M:45:LYS:HE2	1.84	0.43
1:A:103:LEU:CG	1:A:193:GLN:HE21	2.31	0.43
1:A:58:THR:O	1:A:61:MET:N	2.52	0.43
2:B:1122:THR:O	2:B:1122:THR:HG22	2.18	0.43
2:B:847:ASN:HA	2:B:848:PRO:HD2	1.90	0.43
2:B:1153:PHE:CD2	2:B:1154:LEU:HD23	2.53	0.43
1:A:183:LYS:HA	1:A:199:GLU:HG2	2.01	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:744:GLU:CB	2:B:775:ASP:HB2	2.42	0.42
2:B:1227:VAL:O	2:B:1231:VAL:HG23	2.19	0.42
1:A:135:LEU:CB	1:A:136:PRO:HD2	2.49	0.42
2:B:1408:SER:C	2:B:1410:TYR:N	2.72	0.42
1:A:52:THR:HG23	1:A:53:VAL:N	2.34	0.42
2:B:974:ASP:O	2:B:976:GLU:N	2.52	0.42
2:B:799:PHE:C	2:B:800:GLU:HG3	2.33	0.42
1:A:555:PRO:CG	2:B:777:ILE:HG12	2.49	0.42
1:A:567:HIS:CB	2:B:760:PRO:HG3	2.46	0.42
1:A:78:LYS:HE3	1:A:82:LYS:HZ1	1.84	0.42
2:B:944:ASP:O	2:B:945:LEU:C	2.58	0.42
1:A:12:LEU:HD12	1:A:84:VAL:HG21	2.01	0.42
2:B:1126:LEU:HD11	2:B:1177:MET:HE1	2.01	0.42
2:B:1341:LEU:HD23	2:B:1469:ARG:HB2	2.00	0.42
1:A:470:TYR:HA	1:A:510:VAL:O	2.19	0.42
1:A:144:ASN:ND2	1:A:155:GLN:HB3	2.34	0.42
2:B:1054:THR:HG22	2:B:1054:THR:O	2.18	0.42
2:B:927:PRO:HG2	2:B:1313:GLU:N	2.34	0.42
1:A:34:THR:HG22	1:A:51:LYS:CE	2.49	0.42
1:A:404:THR:CG2	1:A:414:GLN:HE21	2.26	0.42
2:B:782:ILE:CA	2:B:798:PRO:HB3	2.39	0.42
1:A:223:ILE:H	1:A:223:ILE:HD12	1.85	0.42
1:A:187:TYR:HB3	1:A:195:VAL:HA	2.00	0.42
2:B:1078:LEU:HD11	2:B:1132:ALA:CB	2.49	0.42
3:M:67:LYS:HG2	3:M:67:LYS:O	2.19	0.42
2:B:1407:ILE:O	2:B:1408:SER:C	2.57	0.42
2:B:882:LYS:HG3	2:B:886:GLN:CD	2.40	0.42
2:B:1306:GLU:OE1	2:B:1306:GLU:HA	2.20	0.42
2:B:819:ARG:O	2:B:820:ASN:CB	2.65	0.42
1:A:126:ARG:HG3	2:B:751:TRP:HZ2	1.84	0.42
2:B:1107:MET:HB2	2:B:1247:THR:HB	2.01	0.42
1:A:280:LEU:HD11	1:A:284:VAL:HB	2.01	0.42
3:M:37:ASN:ND2	3:M:38:THR:H	2.17	0.42
1:A:366:PRO:HG2	1:A:406:LYS:HA	2.01	0.42
1:A:613:TYR:O	1:A:617:PHE:CE2	2.72	0.42
1:A:432:ASN:O	1:A:525:VAL:HG11	2.19	0.42
2:B:749:TRP:CE3	2:B:750:LEU:CB	3.01	0.42
2:B:836:GLN:HG2	2:B:897:HIS:CE1	2.55	0.42
2:B:744:GLU:H	2:B:775:ASP:HB2	1.85	0.42
2:B:740:VAL:CB	3:M:42:ARG:HB2	2.44	0.42
2:B:1193:LYS:O	2:B:1194:ASP:HB2	2.20	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1132:ALA:HA	2:B:1135:ILE:HD12	2.01	0.42
2:B:1113:ASN:O	2:B:1115:ASN:N	2.52	0.42
2:B:1163:ARG:C	2:B:1165:TYR:H	2.23	0.42
2:B:1063:VAL:O	2:B:1063:VAL:CG1	2.68	0.42
1:A:522:ARG:HA	1:A:522:ARG:HD2	1.51	0.42
1:A:555:PRO:O	3:M:42:ARG:NH2	2.52	0.42
1:A:194:GLN:NE2	1:A:196:PHE:HE1	2.18	0.42
1:A:55:THR:C	1:A:57:ALA:H	2.24	0.42
2:B:818:VAL:HG12	2:B:819:ARG:N	2.35	0.42
2:B:1276:LEU:C	2:B:1285:ILE:HD12	2.40	0.42
2:B:1115:ASN:HB3	2:B:1163:ARG:HD2	2.02	0.42
1:A:47:LEU:HD21	1:A:49:SER:OG	2.20	0.42
2:B:774:LYS:HB2	2:B:780:TRP:CZ2	2.54	0.41
2:B:1277:GLN:O	2:B:1308:PHE:HB2	2.20	0.41
1:A:113:ASP:OD2	2:B:748:SER:HB2	2.19	0.41
1:A:574:VAL:HG21	2:B:751:TRP:CZ3	2.54	0.41
2:B:1140:VAL:HG13	2:B:1142:SER:H	1.84	0.41
1:A:103:LEU:HG	1:A:193:GLN:NE2	2.32	0.41
1:A:369:VAL:HG12	1:A:370:GLN:N	2.35	0.41
1:A:375:VAL:HG22	1:A:387:LEU:HD21	2.02	0.41
2:B:981:LEU:CD1	2:B:1002:ALA:HB2	2.50	0.41
2:B:1105:GLN:O	2:B:1112:ARG:NE	2.53	0.41
1:A:580:VAL:CG2	2:B:747:GLU:CB	2.97	0.41
1:A:537:CYS:SG	1:A:537:CYS:O	2.77	0.41
1:A:164:LEU:HD23	1:A:570:ARG:CB	2.50	0.41
2:B:1014:LYS:H	2:B:1014:LYS:HG2	1.64	0.41
1:A:554:VAL:CG1	1:A:555:PRO:CD	2.95	0.41
1:A:603:ILE:O	1:A:635:ARG:NH1	2.40	0.41
1:A:429:ASN:O	1:A:429:ASN:OD1	2.39	0.41
2:B:1086:ILE:CG2	2:B:1142:SER:HB2	2.51	0.41
1:A:530:TRP:CE3	1:A:607:PRO:CB	3.01	0.41
2:B:1437:LEU:O	2:B:1438:ALA:HB2	2.20	0.41
1:A:394:SER:C	1:A:396:LYS:H	2.22	0.41
1:A:370:GLN:HE22	1:A:403:ARG:CZ	2.31	0.41
1:A:221:TYR:CZ	1:A:228:GLY:HA2	2.56	0.41
2:B:1366:ILE:HD13	2:B:1455:VAL:CG1	2.48	0.41
2:B:840:VAL:HG12	2:B:841:ARG:H	1.85	0.41
1:A:55:THR:HG22	1:A:56:PRO:HD2	2.02	0.41
1:A:1:SER:N	1:A:2:PRO:CD	2.82	0.41
1:A:176:LEU:HD22	2:B:915:ARG:CD	2.51	0.41
3:M:44:ILE:HD12	3:M:77:ILE:HD12	2.02	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1274:VAL:HG22	2:B:1312:ALA:HA	2.01	0.41
2:B:1204:GLN:HA	2:B:1207:ASN:ND2	2.35	0.41
1:A:593:LYS:O	1:A:597:VAL:HG23	2.21	0.41
1:A:218:GLU:HB3	1:A:220:PHE:O	2.21	0.41
2:B:1106:GLU:HA	2:B:1112:ARG:NH1	2.35	0.41
1:A:311:HIS:HA	2:B:1423:ILE:HD11	2.02	0.41
1:A:477:ARG:NH1	1:A:479:LEU:HD13	2.35	0.41
1:A:153:VAL:HG21	1:A:171:TRP:CZ2	2.55	0.41
1:A:315:ASP:OD1	1:A:316:MET:N	2.53	0.41
2:B:1192:ALA:HB1	2:B:1195:LYS:HA	2.03	0.41
2:B:1253:VAL:HG22	2:B:1253:VAL:O	2.20	0.41
1:A:100:LEU:HD22	1:A:636:ALA:C	2.40	0.41
1:A:220:PHE:CE1	1:A:330:PRO:HG3	2.56	0.41
2:B:990:GLU:O	2:B:994:ILE:HG13	2.19	0.41
2:B:1161:LEU:HD13	2:B:1166:THR:O	2.20	0.41
1:A:61:MET:HG3	1:A:483:ARG:CZ	2.51	0.41
1:A:269:ILE:HD13	1:A:278:VAL:HB	2.03	0.41
2:B:1446:ASN:O	2:B:1447:VAL:HG23	2.21	0.41
2:B:1061:VAL:HG12	2:B:1061:VAL:O	2.21	0.41
2:B:942:PRO:HG3	2:B:1307:GLY:CA	2.51	0.41
2:B:799:PHE:HE1	2:B:801:VAL:CG2	2.31	0.41
2:B:782:ILE:HD11	2:B:799:PHE:CZ	2.55	0.41
2:B:742:ARG:H	2:B:903:VAL:HA	1.86	0.41
2:B:744:GLU:CA	2:B:746:PRO:HD2	2.50	0.41
1:A:536:SER:O	1:A:595:TRP:CZ2	2.74	0.41
2:B:1408:SER:O	2:B:1410:TYR:N	2.54	0.41
1:A:153:VAL:HG21	1:A:171:TRP:CH2	2.56	0.41
1:A:344:PRO:HD2	1:A:433:TYR:CE1	2.55	0.41
1:A:163:GLN:HB2	1:A:163:GLN:HE21	1.65	0.41
3:M:67:LYS:O	3:M:71:GLN:HB2	2.20	0.41
2:B:817:VAL:HG21	2:B:907:LEU:HD11	2.01	0.41
1:A:549:GLU:HG2	1:A:549:GLU:O	2.21	0.41
1:A:375:VAL:HG22	1:A:387:LEU:CD2	2.51	0.41
1:A:370:GLN:OE1	1:A:403:ARG:NH2	2.54	0.41
2:B:1083:LYS:HD2	2:B:1140:VAL:HG22	2.03	0.41
1:A:468:TYR:HE2	1:A:486:ARG:HB2	1.85	0.41
1:A:4:TYR:O	1:A:627:SER:HB3	2.21	0.41
1:A:213:ILE:HG22	1:A:215:GLU:HG3	2.03	0.41
1:A:612:ASP:OD1	1:A:612:ASP:N	2.54	0.41
1:A:361:PRO:CB	1:A:383:GLY:HA3	2.50	0.40
2:B:1341:LEU:HD11	2:B:1366:ILE:CG2	2.51	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:266:LEU:HG	2:B:1378:MET:HE1	2.03	0.40
2:B:1237:GLN:O	2:B:1238:ARG:C	2.60	0.40
1:A:474:ASN:O	1:A:475:LYS:HB2	2.22	0.40
1:A:166:VAL:O	1:A:167:LEU:HD23	2.21	0.40
3:M:84:LYS:HG3	3:M:84:LYS:O	2.21	0.40
1:A:502:ASP:OD1	1:A:502:ASP:N	2.54	0.40
1:A:142:MET:N	1:A:142:MET:SD	2.94	0.40
1:A:63:ASN:HB3	4:A:646:NAG:C1	2.52	0.40
2:B:975:ALA:HB1	2:B:1006:LEU:HD21	1.98	0.40
1:A:640:CYS:HB3	1:A:641:PRO:CD	2.51	0.40
2:B:1260:TYR:C	2:B:1263:ASP:OD1	2.59	0.40
1:A:50:GLU:C	1:A:51:LYS:HG2	2.41	0.40
2:B:1085:LEU:HD13	2:B:1125:VAL:CG1	2.51	0.40
1:A:242:LYS:HD3	1:A:273:ASP:O	2.21	0.40
1:A:543:VAL:O	2:B:799:PHE:CD2	2.74	0.40
1:A:110:ILE:HD12	1:A:198:THR:HB	2.03	0.40
2:B:985:PRO:CD	2:B:1026:LEU:HB3	2.48	0.40
1:A:124:LEU:HD23	1:A:169:LEU:O	2.20	0.40
1:A:582:VAL:O	1:A:582:VAL:CG1	2.69	0.40
1:A:63:ASN:HB2	4:A:646:NAG:H2	2.03	0.40
2:B:1198:TRP:O	2:B:1210:ALA:HB3	2.21	0.40
2:B:1213:TYR:CD1	2:B:1216:LEU:HD12	2.56	0.40
2:B:1399:LEU:O	2:B:1405:ARG:HB3	2.20	0.40
2:B:1003:VAL:CG1	2:B:1070:LEU:HD22	2.51	0.40
3:M:77:ILE:O	3:M:77:ILE:HG22	2.21	0.40
2:B:855:THR:OG1	2:B:858:ARG:NH1	2.55	0.40
1:A:386:LYS:HD2	1:A:386:LYS:HA	1.69	0.40
1:A:117:TYR:CE2	1:A:123:VAL:HG13	2.57	0.40
2:B:1026:LEU:HA	2:B:1029:LYS:HB3	2.02	0.40
1:A:154:LYS:CD	1:A:171:TRP:CD1	3.03	0.40
2:B:1113:ASN:HD22	2:B:1163:ARG:CZ	2.33	0.40
2:B:1375:ASP:N	2:B:1375:ASP:OD1	2.55	0.40
1:A:363:TYR:CE2	1:A:381:GLY:HA2	2.57	0.40
2:B:1228:PRO:CB	2:B:1229:PRO:CD	2.87	0.40
2:B:1397:LYS:CE	2:B:1412:LEU:HG	2.49	0.40
3:M:50:LYS:CE	3:M:65:GLU:HG3	2.48	0.40
2:B:1141:ASN:O	2:B:1144:PRO:HD2	2.21	0.40
1:A:189:GLU:O	1:A:189:GLU:HG2	2.21	0.40
2:B:1000:VAL:HG13	2:B:1070:LEU:CD1	2.51	0.40
1:A:176:LEU:HD22	2:B:915:ARG:HD3	2.02	0.40
1:A:47:LEU:C	1:A:47:LEU:HD23	2.41	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	628/645 (97%)	524 (83%)	88 (14%)	16 (2%)	7	46
2	B	881/915 (96%)	726 (82%)	126 (14%)	29 (3%)	5	40
3	M	82/88 (93%)	73 (89%)	9 (11%)	0	100	100
All	All	1591/1648 (96%)	1323 (83%)	223 (14%)	45 (3%)	6	44

All (45) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	431	ASN
1	A	505	PRO
1	A	518	ALA
2	B	733	ILE
2	B	783	LEU
2	B	1270	LEU
1	A	20	MET
1	A	241	LYS
1	A	407	GLN
1	A	474	ASN
2	B	792	GLY
2	B	989	GLY
2	B	1039	GLN
2	B	1218	LEU
2	B	1393	THR
2	B	1573	LYS
1	A	442	GLU
1	A	458	ASP
2	B	968	MET
2	B	1149	LYS
2	B	1486	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	620	ALA
1	A	638	LEU
2	B	1222	LYS
2	B	1571	ALA
1	A	271	ILE
1	A	641	PRO
2	B	782	ILE
2	B	820	ASN
2	B	848	PRO
2	B	926	ASP
2	B	954	SER
2	B	1175	ALA
2	B	1409	LYS
1	A	640	CYS
2	B	953	GLU
2	B	1114	ASN
2	B	1238	ARG
2	B	1337	ASN
1	A	145	ILE
2	B	880	PRO
2	B	1453	GLY
1	A	393	PRO
2	B	1016	GLY
2	B	1452	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	557/567 (98%)	502 (90%)	55 (10%)	10	39
2	B	790/810 (98%)	715 (90%)	75 (10%)	11	41
3	M	76/79 (96%)	71 (93%)	5 (7%)	21	57
All	All	1423/1456 (98%)	1288 (90%)	135 (10%)	11	41

All (135) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	MET
1	A	8	THR
1	A	10	ASN
1	A	20	MET
1	A	52	THR
1	A	55	THR
1	A	61	MET
1	A	92	THR
1	A	103	LEU
1	A	105	SER
1	A	113	ASP
1	A	122	THR
1	A	125	TYR
1	A	130	VAL
1	A	142	MET
1	A	144	ASN
1	A	155	GLN
1	A	177	VAL
1	A	179	MET
1	A	193	GLN
1	A	194	GLN
1	A	239	TYR
1	A	261	SER
1	A	301	SER
1	A	327	VAL
1	A	328	THR
1	A	331	TYR
1	A	346	MET
1	A	375	VAL
1	A	398	LEU
1	A	399	SER
1	A	406	LYS
1	A	425	SER
1	A	430	SER
1	A	438	VAL
1	A	439	LEU
1	A	440	ARG
1	A	452	ASN
1	A	453	PHE
1	A	458	ASP
1	A	459	ARG
1	A	477	ARG
1	A	479	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	480	LYS
1	A	485	VAL
1	A	502	ASP
1	A	509	LEU
1	A	515	LEU
1	A	519	SER
1	A	522	ARG
1	A	537	CYS
1	A	573	LEU
1	A	574	VAL
1	A	634	GLN
1	A	639	GLN
2	B	747	GLU
2	B	757	LYS
2	B	758	GLU
2	B	762	ASN
2	B	770	ASN
2	B	776	SER
2	B	789	ASP
2	B	828	VAL
2	B	833	ARG
2	B	834	GLN
2	B	845	LEU
2	B	851	CYS
2	B	907	LEU
2	B	912	GLU
2	B	917	ASN
2	B	932	ARG
2	B	937	LYS
2	B	945	LEU
2	B	951	ASP
2	B	953	GLU
2	B	968	MET
2	B	976	GLU
2	B	977	ARG
2	B	978	LEU
2	B	990	GLU
2	B	1018	GLU
2	B	1050	ARG
2	B	1069	ASN
2	B	1078	LEU
2	B	1099	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	B	1117	LYS
2	B	1136	CYS
2	B	1137	GLU
2	B	1139	GLN
2	B	1141	ASN
2	B	1194	ASP
2	B	1196	ASN
2	B	1259	GLN
2	B	1262	LYS
2	B	1268	GLN
2	B	1269	GLU
2	B	1281	ARG
2	B	1282	SER
2	B	1283	SER
2	B	1284	LYS
2	B	1292	GLU
2	B	1334	LEU
2	B	1337	ASN
2	B	1342	LYS
2	B	1361	THR
2	B	1375	ASP
2	B	1384	SER
2	B	1387	THR
2	B	1393	THR
2	B	1394	ASP
2	B	1396	LEU
2	B	1397	LYS
2	B	1411	GLU
2	B	1412	LEU
2	B	1419	ARG
2	B	1423	ILE
2	B	1433	GLU
2	B	1445	PHE
2	B	1448	GLU
2	B	1462	ASN
2	B	1479	LYS
2	B	1487	GLU
2	B	1488	LEU
2	B	1489	CYS
2	B	1498	ILE
2	B	1503	ASP
2	B	1535	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	B	1536	PHE
2	B	1569	ARG
2	B	1637	PHE
3	M	11	GLN
3	M	23	LEU
3	M	56	LYS
3	M	69	GLN
3	M	71	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (54) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	63	ASN
1	A	87	GLN
1	A	104	GLN
1	A	132	HIS
1	A	144	ASN
1	A	155	GLN
1	A	162	ASN
1	A	163	GLN
1	A	193	GLN
1	A	194	GLN
1	A	318	GLN
1	A	380	GLN
1	A	390	ASN
1	A	414	GLN
1	A	420	GLN
1	A	490	GLN
1	A	558	GLN
1	A	587	ASN
1	A	631	GLN
1	A	634	GLN
1	A	639	GLN
2	B	738	ASN
2	B	770	ASN
2	B	820	ASN
2	B	834	GLN
2	B	847	ASN
2	B	862	GLN
2	B	886	GLN
2	B	897	HIS
2	B	948	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	B	992	ASN
2	B	1033	GLN
2	B	1069	ASN
2	B	1076	GLN
2	B	1090	GLN
2	B	1104	HIS
2	B	1113	ASN
2	B	1115	ASN
2	B	1130	GLN
2	B	1160	ASN
2	B	1204	GLN
2	B	1259	GLN
2	B	1267	HIS
2	B	1277	GLN
2	B	1401	ASN
2	B	1431	HIS
2	B	1442	HIS
2	B	1451	GLN
2	B	1462	ASN
3	M	11	GLN
3	M	37	ASN
3	M	49	GLN
3	M	69	GLN
3	M	71	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

4 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	NAG	A	646	-	14,14,15	0.57	0	15,19,21	1.70	4 (26%)
4	NAG	A	647	-	14,14,15	0.59	0	15,19,21	1.69	3 (20%)
5	MAN	A	648	-	11,11,12	0.68	0	14,15,17	0.54	0
4	NAG	A	649	-	14,14,15	0.61	0	15,19,21	0.91	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	A	646	-	-	0/6/23/26	0/1/1/1
4	NAG	A	647	-	-	0/6/23/26	0/1/1/1
5	MAN	A	648	-	-	0/2/19/22	0/1/1/1
4	NAG	A	649	-	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	647	NAG	C1-O5-C5	-3.02	108.42	112.25
4	A	646	NAG	O7-C7-C8	-2.16	118.11	122.06
4	A	646	NAG	O5-C5-C6	2.80	113.42	107.35
4	A	646	NAG	C8-C7-N2	2.89	121.63	116.11
4	A	647	NAG	C3-C4-C5	3.58	116.44	110.20
4	A	647	NAG	C4-C3-C2	3.84	117.20	111.23
4	A	646	NAG	C2-N2-C7	4.26	128.51	123.04

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	646	NAG	4	0
4	A	647	NAG	2	0
5	A	648	MAN	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	634/645 (98%)	-0.20	2 (0%) 94 92	60, 127, 187, 245	0
2	B	748/915 (81%)	-0.06	17 (2%) 64 59	20, 180, 248, 326	0
3	M	84/88 (95%)	-0.39	0 100 100	165, 204, 265, 298	0
All	All	1466/1648 (88%)	-0.14	19 (1%) 79 73	20, 156, 238, 326	0

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	892	ALA	3.6
2	B	1449	LEU	3.6
2	B	1438	ALA	3.0
2	B	784	ALA	2.8
2	B	877	VAL	2.8
2	B	1381	LEU	2.7
2	B	853	LEU	2.7
2	B	1243	GLY	2.6
2	B	1439	PHE	2.5
2	B	1257	LEU	2.4
2	B	876	TYR	2.4
2	B	1450	ILE	2.4
2	B	1437	LEU	2.3
1	A	526	ALA	2.2
2	B	1424	ILE	2.2
1	A	79	GLY	2.2
2	B	1082	VAL	2.1
2	B	1219	LEU	2.1
2	B	1081	ALA	2.1

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
4	NAG	A	646	14/15	0.78	0.36	0.34	117,151,158,160	0
4	NAG	A	649	14/15	0.37	0.72	-	198,208,218,226	0
5	MAN	A	648	11/12	0.42	0.76	-	211,220,230,239	0
4	NAG	A	647	14/15	0.85	0.27	-	154,188,202,211	0

6.5 Other polymers [i](#)

There are no such residues in this entry.