



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 02:31 am GMT

PDB ID : 4FPB
Title : Crystal Structure of Recombinant Human Hexokinase Type I with 1,5-Anhydroglucitol 6-Phosphate
Authors : Shen, L.; Honzatko, R.B.
Deposited on : 2012-06-21
Resolution : 3.00 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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : recalc28949

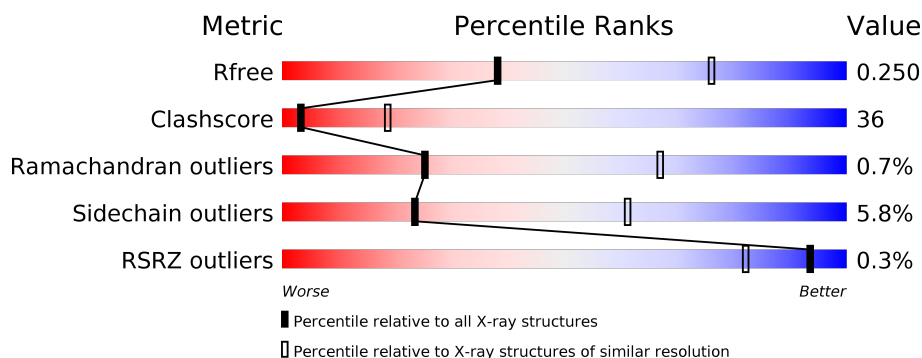
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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}	100719	1692 (3.00-3.00)
Clashscore	112137	2037 (3.00-3.00)
Ramachandran outliers	110173	1973 (3.00-3.00)
Sidechain outliers	110143	1976 (3.00-3.00)
RSRZ outliers	101464	1716 (3.00-3.00)

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	917	
1	B	917	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	BGC	A	1001	-	-	-	X
2	BGC	B	1001	-	-	-	X
2	BGC	B	1003	-	-	-	X
3	0WK	B	1004	-	-	-	X
5	CIT	A	1007	-	-	-	X
5	CIT	B	1007	-	-	-	X

2 Entry composition [i](#)

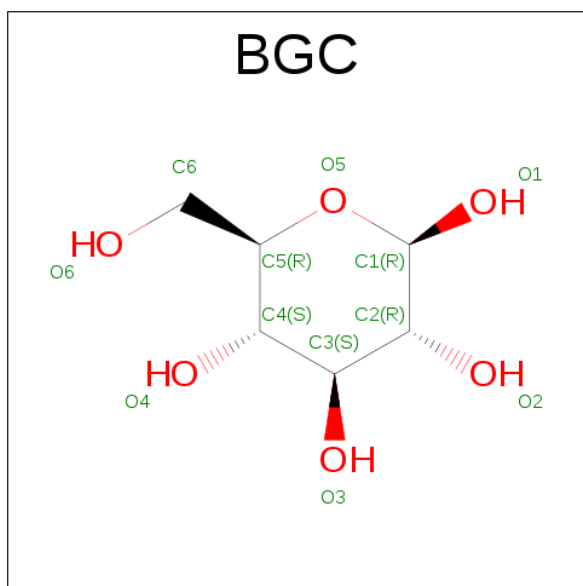
There are 6 unique types of molecules in this entry. The entry contains 14395 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Hexokinase-1.

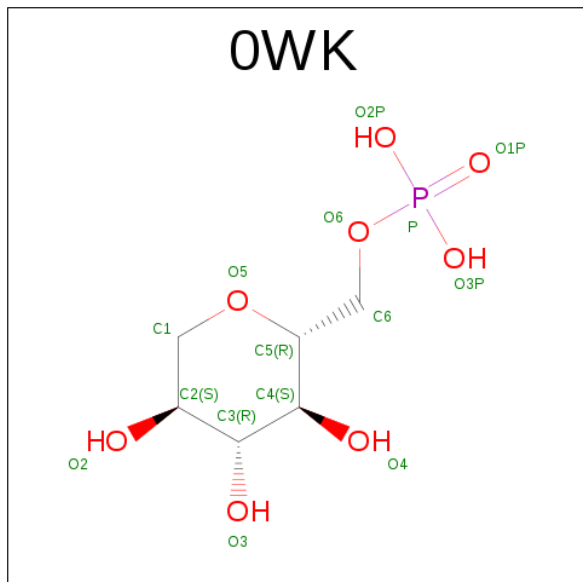
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	899	Total	C	N	O	S	0	0	0
			7032	4407	1240	1332	53			
1	B	899	Total	C	N	O	S	0	0	0
			7032	4407	1240	1332	53			

- Molecule 2 is SUGAR (BETA-D-GLUCOSE) (three-letter code: BGC) (formula: $C_6H_{12}O_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			12	6	6		
2	A	1	Total	C	O	0	0
			12	6	6		
2	B	1	Total	C	O	0	0
			12	6	6		
2	B	1	Total	C	O	0	0
			12	6	6		

- Molecule 3 is 1,5-ANHYDRO-6-O-PHOSPHONO-D-GLUCITOL (three-letter code: 0WK) (formula: $C_6H_{13}O_8P$).

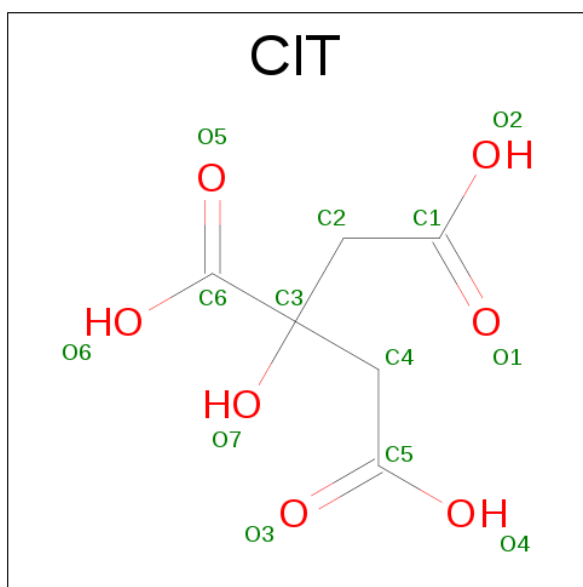


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	O	P	0	0
			15	6	8	1		
3	A	1	Total	C	O	P	0	0
			15	6	8	1		
3	B	1	Total	C	O	P	0	0
			15	6	8	1		
3	B	1	Total	C	O	P	0	0
			15	6	8	1		

- Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	2	Total	Na	0	0
			2	2		
4	A	2	Total	Na	0	0
			2	2		

- Molecule 5 is CITRIC ACID (three-letter code: CIT) (formula: $C_6H_8O_7$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			13	6	7		
5	B	1	Total	C	O	0	0
			13	6	7		

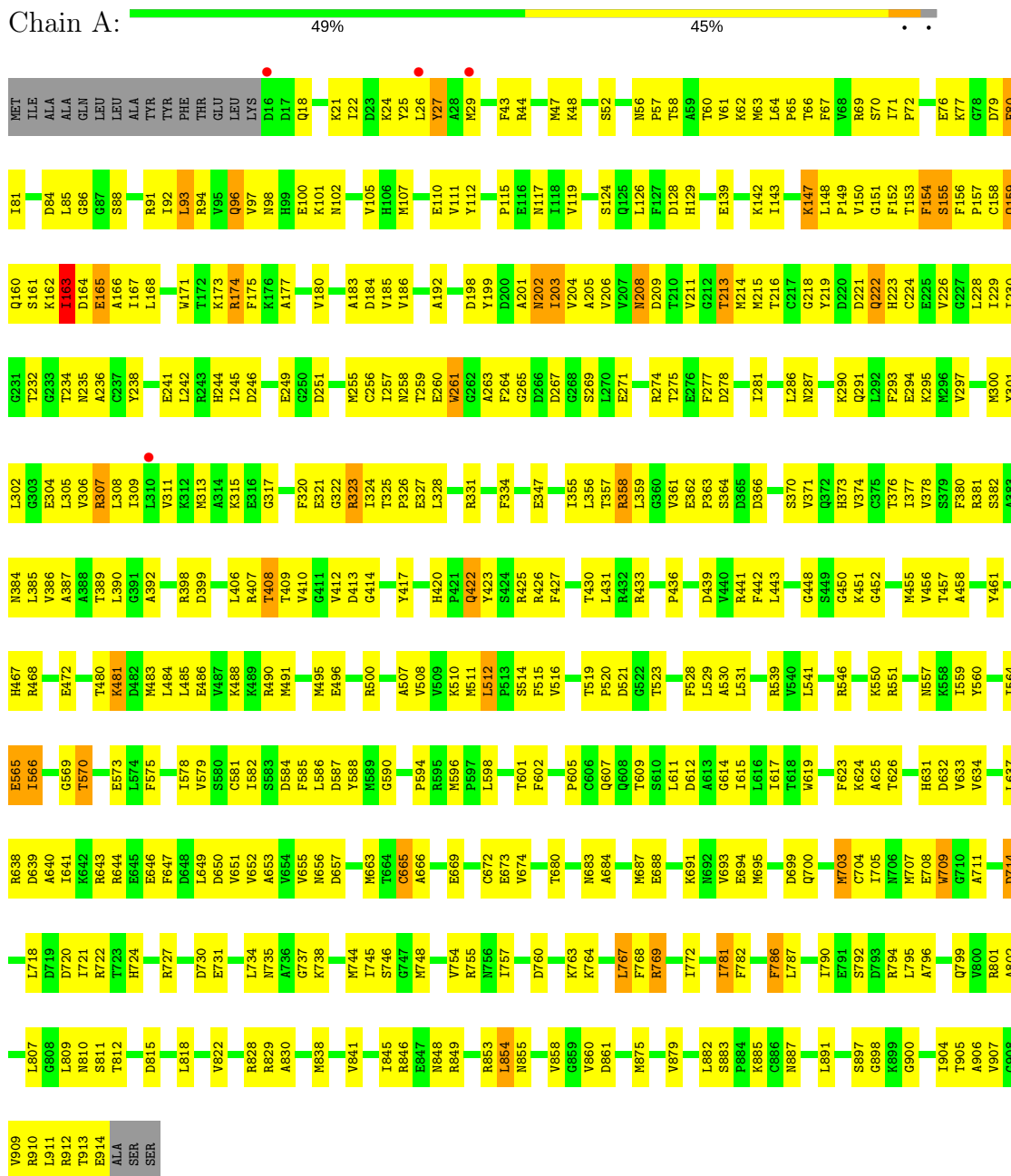
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	94	Total	O	0	0
			94	94		
6	B	99	Total	O	0	0
			99	99		

3 Residue-property plots

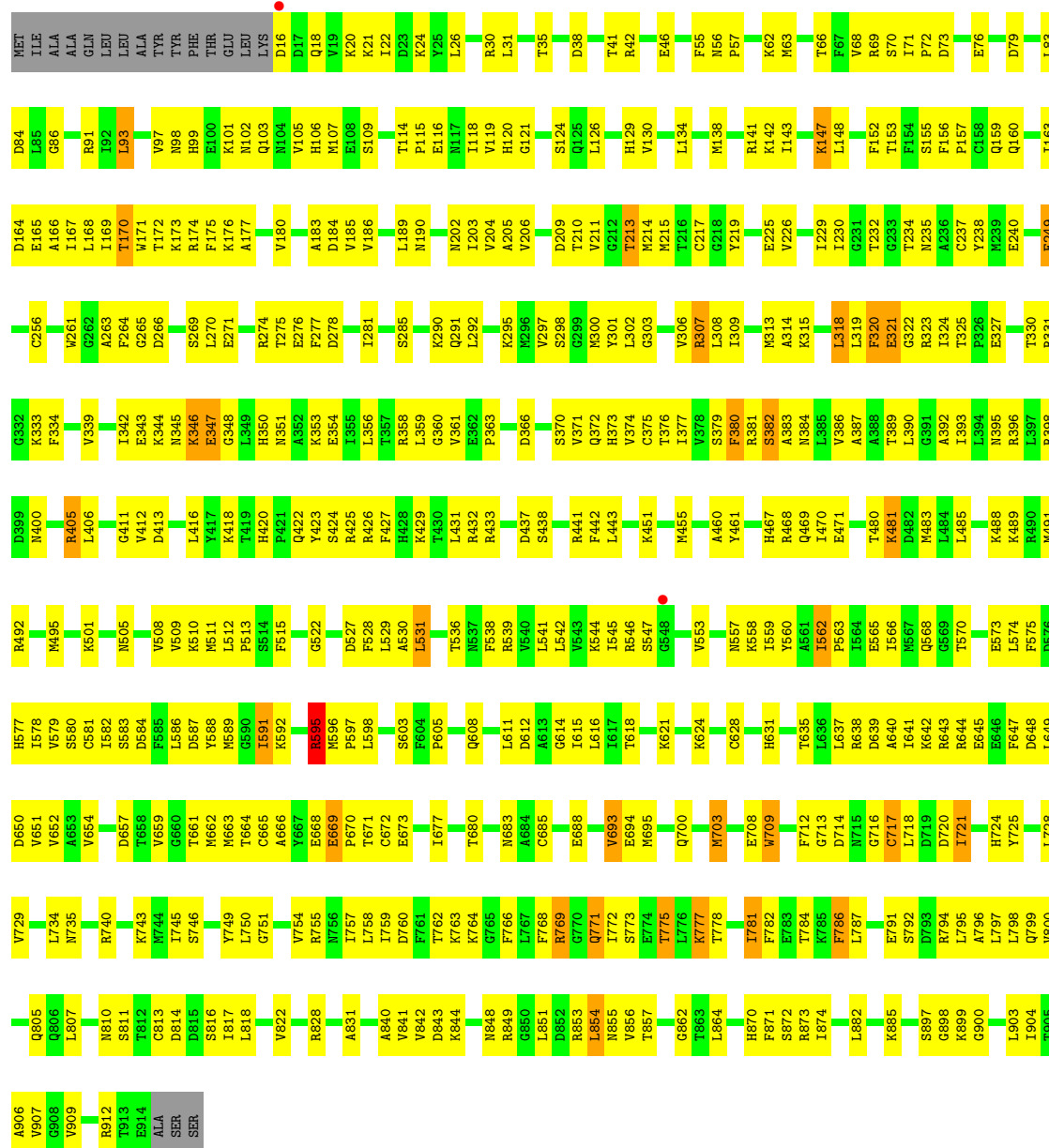
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are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

- Molecule 1: Hexokinase-1



- Molecule 1: Hexokinase-1

Chain B: 49% 46% .



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	82.72Å 121.21Å 120.79Å 90.00° 93.12° 90.00°	Depositor
Resolution (Å)	46.24 – 3.00 46.24 – 3.00	Depositor EDS
% Data completeness (in resolution range)	82.7 (46.24-3.00) 82.7 (46.24-3.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.91 (at 3.01Å)	Xtriage
Refinement program	REFMAC 5.5.0066	Depositor
R, R_{free}	0.229 , 0.256 0.225 , 0.250	Depositor DCC
R_{free} test set	1955 reflections (5.21%)	DCC
Wilson B-factor (Å ²)	71.5	Xtriage
Anisotropy	0.100	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.24 , 19.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	14395	wwPDB-VP
Average B, all atoms (Å ²)	77.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.54% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NA, BGC, 0WK, CIT

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	0.36	1/7138 (0.0%)	0.49	1/9606 (0.0%)
1	B	0.35	2/7138 (0.0%)	0.51	2/9606 (0.0%)
All	All	0.35	3/14276 (0.0%)	0.50	3/19212 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	2
All	All	0	3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	323	ARG	CZ-NH2	14.91	1.52	1.33
1	B	595	ARG	CZ-NH2	12.36	1.49	1.33
1	B	595	ARG	CZ-NH1	9.11	1.44	1.33

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	595	ARG	NE-CZ-NH1	-11.74	114.43	120.30
1	A	323	ARG	NE-CZ-NH1	-5.90	117.35	120.30
1	B	595	ARG	NE-CZ-NH2	5.73	123.16	120.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	154	PHE	Peptide
1	B	595	ARG	Sidechain
1	B	668	GLU	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	7032	0	7090	521	0
1	B	7032	0	7090	508	0
2	A	24	0	24	4	0
2	B	24	0	24	4	0
3	A	30	0	22	2	0
3	B	30	0	22	1	0
4	A	2	0	0	0	0
4	B	2	0	0	0	0
5	A	13	0	5	1	0
5	B	13	0	5	4	0
6	A	94	0	0	10	0
6	B	99	0	0	25	0
All	All	14395	0	14282	1025	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 36.

All (1025) 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:B:319:LEU:HB3	1:B:320:PHE:CE1	1.36	1.56
1:A:320:PHE:CZ	1:A:361:VAL:HG21	1.64	1.31
1:A:570:THR:CG2	1:A:573:GLU:HG3	1.58	1.31
1:A:520:PRO:HD3	1:A:663:MET:CE	1.65	1.25
1:B:319:LEU:CB	1:B:320:PHE:CE1	2.25	1.20
1:A:162:LYS:O	1:A:163:ILE:HG22	1.42	1.20
1:B:319:LEU:HB3	1:B:320:PHE:CD1	1.78	1.18
1:A:93:LEU:HD23	1:A:93:LEU:N	1.64	1.12
1:B:319:LEU:C	1:B:320:PHE:HD1	1.50	1.12

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:507:ALA:O	1:A:510:LYS:HE2	1.50	1.10
1:B:320:PHE:HB3	1:B:323:ARG:HH21	1.14	1.10
1:B:346:LYS:HG3	1:B:347:GLU:OE2	1.52	1.10
1:B:541:LEU:HD23	1:B:557:ASN:HB3	1.34	1.10
1:A:380:PHE:CD2	1:A:426:ARG:HD3	1.87	1.09
1:A:160:GLN:HG2	1:A:165:GLU:O	1.52	1.08
1:B:320:PHE:N	1:B:320:PHE:HD1	1.49	1.08
1:A:663:MET:HG3	1:A:904:ILE:HD11	1.12	1.07
1:B:536:THR:HG22	6:B:1160:HOH:O	1.51	1.07
1:B:319:LEU:C	1:B:320:PHE:CD1	2.28	1.07
1:B:169:ILE:HG22	1:B:170:THR:HG22	1.10	1.07
1:B:854:LEU:HD12	1:B:855:ASN:N	1.69	1.06
1:A:570:THR:HG23	1:A:573:GLU:HG3	1.09	1.06
1:A:480:THR:HG23	1:A:483:MET:HE3	1.38	1.05
1:A:663:MET:HG3	1:A:904:ILE:CD1	1.86	1.05
1:A:520:PRO:HD3	1:A:663:MET:HE1	1.40	1.04
1:A:786:PHE:CE2	1:A:790:ILE:HD11	1.94	1.03
1:B:320:PHE:HB3	1:B:323:ARG:NH2	1.74	1.02
1:B:319:LEU:CB	1:B:320:PHE:HE1	1.64	1.01
1:B:870:HIS:CD2	1:B:873:ARG:HH21	1.78	1.01
1:A:380:PHE:HD2	1:A:426:ARG:HD3	1.20	1.01
1:B:344:LYS:O	1:B:348:GLY:CA	2.11	0.99
1:B:522:GLY:HA3	6:B:1195:HOH:O	1.64	0.98
1:B:320:PHE:HD2	1:B:361:VAL:HB	1.24	0.98
1:A:570:THR:HG23	1:A:573:GLU:CG	1.93	0.98
1:A:564:ILE:HG13	1:A:565:GLU:N	1.76	0.97
1:B:115:PRO:HD2	1:B:118:ILE:HD12	1.48	0.96
1:B:853:ARG:HB3	1:B:853:ARG:HH11	1.28	0.96
1:B:160:GLN:HG2	1:B:165:GLU:O	1.64	0.95
1:B:760:ASP:O	1:B:764:LYS:HG2	1.65	0.95
1:B:853:ARG:HB3	1:B:853:ARG:NH1	1.82	0.95
1:B:320:PHE:CD2	1:B:361:VAL:HB	2.01	0.95
1:B:425:ARG:HH22	5:B:1007:CIT:H22	1.29	0.95
1:A:380:PHE:HE2	1:A:426:ARG:HG2	1.28	0.95
1:A:290:LYS:O	1:A:295:LYS:HE3	1.67	0.94
1:A:422:GLN:OE1	1:A:422:GLN:HA	1.66	0.94
1:B:320:PHE:N	1:B:320:PHE:CD1	2.25	0.93
1:A:663:MET:CG	1:A:904:ILE:HD11	1.99	0.93
1:A:320:PHE:CE2	1:A:361:VAL:HG21	2.03	0.92
1:A:203:ILE:CD1	1:A:203:ILE:N	2.32	0.92
1:A:174:ARG:HH11	1:A:174:ARG:HG3	1.34	0.92

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:320:PHE:CZ	1:A:361:VAL:CG2	2.51	0.92
1:A:486:GLU:HG2	6:A:1119:HOH:O	1.69	0.91
1:A:510:LYS:HB3	1:A:512:LEU:CD1	2.00	0.91
1:A:431:LEU:HD23	1:A:442:PHE:HZ	1.35	0.91
1:A:510:LYS:HB3	1:A:512:LEU:HD11	1.49	0.91
1:A:162:LYS:O	1:A:163:ILE:CG2	2.19	0.90
1:A:520:PRO:HD3	1:A:663:MET:HE3	1.51	0.90
1:B:101:LYS:O	1:B:103:GLN:HG3	1.71	0.90
1:A:760:ASP:OD2	1:A:764:LYS:HE2	1.72	0.90
1:A:564:ILE:HG13	1:A:565:GLU:H	1.32	0.90
1:A:714:ASP:OD2	1:A:738:LYS:HA	1.72	0.89
1:B:313:MET:HE2	1:B:318:LEU:HD12	1.52	0.89
1:B:762:THR:CG2	1:B:772:ILE:HD13	2.03	0.88
1:B:771:GLN:C	1:B:771:GLN:HE21	1.77	0.88
1:A:44:ARG:HG2	1:A:392:ALA:HB1	1.56	0.88
1:A:570:THR:HG21	1:A:573:GLU:HG3	1.54	0.88
1:B:420:HIS:HD2	1:B:423:TYR:H	1.22	0.87
1:B:426:ARG:HH21	5:B:1007:CIT:H41	1.38	0.87
1:B:346:LYS:CG	1:B:347:GLU:OE2	2.22	0.87
1:A:219:TYR:HD2	1:A:451:LYS:HD3	1.37	0.87
1:B:297:VAL:HA	1:B:382:SER:HB2	1.55	0.87
1:A:203:ILE:HD12	1:A:203:ILE:N	1.89	0.86
1:B:173:LYS:HE2	2:B:1001:BGC:O5	1.75	0.86
1:A:97:VAL:HG22	1:A:105:VAL:HA	1.56	0.86
1:B:344:LYS:O	1:B:348:GLY:N	2.09	0.85
1:B:844:LYS:NZ	1:B:848:ASN:HD21	1.74	0.85
1:B:545:ILE:O	1:B:546:ARG:HD3	1.74	0.85
1:A:93:LEU:CD2	1:A:93:LEU:N	2.39	0.85
1:A:795:LEU:HD11	1:A:799:GLN:HG2	1.58	0.85
1:A:62:LYS:HB3	1:A:64:LEU:CD2	2.06	0.85
1:B:319:LEU:CB	1:B:320:PHE:CD1	2.53	0.85
1:B:266:ASP:OD1	1:B:292:LEU:HG	1.75	0.84
1:B:320:PHE:CB	1:B:323:ARG:NH2	2.39	0.84
1:B:870:HIS:HD2	1:B:873:ARG:HH21	1.23	0.84
1:A:900:GLY:O	1:A:904:ILE:HG12	1.78	0.83
1:B:390:LEU:HD12	1:B:390:LEU:O	1.78	0.83
1:B:189:LEU:HD23	1:B:203:ILE:HD11	1.59	0.83
1:B:347:GLU:HB2	1:B:351:ASN:ND2	1.93	0.83
1:A:174:ARG:HG3	1:A:174:ARG:NH1	1.89	0.83
1:B:315:LYS:HG2	1:B:324:ILE:CD1	2.09	0.82
1:B:480:THR:HG23	1:B:483:MET:CE	2.08	0.82

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:93:LEU:HD23	1:A:93:LEU:H	1.42	0.82
1:A:174:ARG:NH2	1:A:300:MET:HG3	1.93	0.82
1:B:265:GLY:HA2	1:B:269:SER:HB3	1.62	0.81
1:A:422:GLN:HG3	1:A:426:ARG:NH2	1.95	0.81
1:A:612:ASP:O	1:A:634:VAL:HG21	1.81	0.81
1:B:98:ASN:O	1:B:103:GLN:O	1.97	0.81
1:B:313:MET:CE	1:B:318:LEU:HD12	2.10	0.81
1:B:356:LEU:HD11	1:B:371:VAL:HG21	1.63	0.81
1:B:390:LEU:HD23	1:B:427:PHE:HZ	1.45	0.81
1:A:520:PRO:CD	1:A:663:MET:CE	2.55	0.81
1:A:202:ASN:C	1:A:203:ILE:HD12	2.02	0.81
1:A:174:ARG:HH11	1:A:174:ARG:CG	1.94	0.80
1:A:174:ARG:HH22	1:A:300:MET:HG3	1.44	0.80
1:B:118:ILE:HD13	1:B:129:HIS:CD2	2.17	0.80
1:B:320:PHE:HE2	1:B:361:VAL:HG21	1.46	0.80
1:B:230:ILE:HD11	1:B:386:VAL:HG11	1.64	0.80
1:B:545:ILE:C	1:B:546:ARG:HD3	2.02	0.80
1:B:541:LEU:HD23	1:B:557:ASN:CB	2.11	0.80
1:A:163:ILE:HD13	1:A:163:ILE:O	1.82	0.80
1:A:66:THR:HG22	1:A:256:CYS:O	1.81	0.80
1:A:315:LYS:HA	1:A:324:ILE:HD11	1.64	0.80
1:A:86:GLY:HA3	1:A:155:SER:OG	1.82	0.79
1:B:762:THR:HG21	1:B:772:ILE:HD13	1.63	0.79
1:A:361:VAL:O	1:A:363:PRO:HD3	1.83	0.79
1:A:422:GLN:HG3	1:A:425:ARG:HH21	1.48	0.78
1:A:380:PHE:CE2	1:A:426:ARG:HG2	2.17	0.78
1:B:782:PHE:HD1	1:B:786:PHE:CE1	2.02	0.78
1:A:229:ILE:HD12	3:A:1002:OWK:H7	1.65	0.78
1:B:563:PRO:HD2	1:B:566:ILE:HD12	1.64	0.78
1:B:680:THR:O	1:B:746:SER:HB2	1.84	0.78
1:B:771:GLN:CA	1:B:771:GLN:HE21	1.96	0.78
1:A:422:GLN:HB3	1:A:426:ARG:CZ	2.14	0.78
1:A:156:PHE:HZ	1:A:175:PHE:CD2	2.02	0.78
1:B:870:HIS:CD2	1:B:873:ARG:NH2	2.51	0.78
1:A:422:GLN:CA	1:A:422:GLN:OE1	2.32	0.78
1:A:58:THR:OG1	1:B:799:GLN:NE2	2.17	0.77
1:B:320:PHE:CA	1:B:323:ARG:NH2	2.46	0.77
1:A:62:LYS:HB3	1:A:64:LEU:HD21	1.64	0.77
1:B:169:ILE:HG22	1:B:170:THR:CG2	2.05	0.77
1:B:189:LEU:HD23	1:B:203:ILE:CD1	2.13	0.77
1:A:66:THR:CG2	1:A:256:CYS:O	2.32	0.77

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:584:ASP:O	1:A:587:ASP:HB2	1.84	0.77
1:B:169:ILE:CG2	1:B:170:THR:HG22	2.05	0.77
1:B:854:LEU:HD12	1:B:855:ASN:H	1.48	0.77
1:A:208:ASN:HD22	1:A:209:ASP:N	1.82	0.77
1:B:382:SER:OG	1:B:423:TYR:HE2	1.67	0.77
1:B:565:GLU:HG2	1:B:566:ILE:H	1.49	0.77
1:B:318:LEU:O	1:B:319:LEU:HD23	1.85	0.77
1:A:66:THR:HG21	1:A:256:CYS:HB3	1.67	0.76
1:A:324:ILE:HG23	1:A:328:LEU:HD23	1.65	0.76
1:A:911:LEU:O	1:A:914:GLU:HB3	1.84	0.76
1:B:595:ARG:NE	1:B:648:ASP:OD2	2.18	0.76
1:B:844:LYS:HZ3	1:B:848:ASN:HD21	1.33	0.76
1:A:202:ASN:OD1	1:A:202:ASN:C	2.23	0.76
1:A:219:TYR:CD2	1:A:451:LYS:HD3	2.20	0.76
1:A:166:ALA:HB3	1:A:185:VAL:CG2	2.15	0.76
1:A:57:PRO:HG2	1:B:799:GLN:HE21	1.51	0.75
1:A:390:LEU:O	1:A:390:LEU:HD12	1.86	0.75
1:B:455:MET:HE2	1:B:455:MET:HA	1.69	0.75
1:B:66:THR:HG22	1:B:256:CYS:O	1.85	0.75
1:A:85:LEU:O	1:A:155:SER:CB	2.35	0.74
1:B:204:VAL:HG12	1:B:460:ALA:HB1	1.69	0.74
1:B:101:LYS:O	1:B:103:GLN:CG	2.35	0.74
1:B:347:GLU:CB	1:B:351:ASN:ND2	2.50	0.74
1:A:218:GLY:HA2	1:A:221:ASP:O	1.87	0.74
1:A:380:PHE:HE2	1:A:426:ARG:CG	2.01	0.74
1:A:520:PRO:CD	1:A:663:MET:HE1	2.17	0.74
1:B:405:ARG:HB3	1:B:405:ARG:HH11	1.51	0.74
1:A:422:GLN:HB3	1:A:426:ARG:NH1	2.03	0.73
1:A:245:ILE:HD13	1:A:257:ILE:HD11	1.69	0.73
1:A:480:THR:HG23	1:A:483:MET:CE	2.17	0.73
1:A:575:PHE:O	1:A:579:VAL:HG23	1.88	0.73
1:A:94:ARG:NE	1:A:96:GLN:OE1	2.22	0.73
1:A:105:VAL:HG21	1:A:219:TYR:HE2	1.53	0.73
1:A:320:PHE:CE1	1:A:361:VAL:CG2	2.71	0.73
1:A:472:GLU:OE1	6:A:1118:HOH:O	2.07	0.73
1:B:664:THR:HG23	1:B:899:LYS:HB3	1.71	0.73
1:A:290:LYS:O	1:A:295:LYS:CE	2.36	0.72
1:A:320:PHE:CE1	1:A:361:VAL:HG21	2.23	0.72
1:A:480:THR:OG1	1:A:483:MET:HG3	1.89	0.72
1:A:222:GLN:OE1	1:A:222:GLN:N	2.22	0.72
1:B:265:GLY:O	1:B:292:LEU:HD12	1.89	0.72

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:422:GLN:CG	1:A:426:ARG:NH2	2.53	0.72
1:B:522:GLY:CA	6:B:1195:HOH:O	2.27	0.72
1:A:93:LEU:CD1	1:A:450:GLY:HA3	2.19	0.72
1:A:431:LEU:HD23	1:A:442:PHE:CZ	2.23	0.72
1:A:93:LEU:HD11	1:A:450:GLY:HA3	1.71	0.72
1:B:390:LEU:HD23	1:B:427:PHE:CZ	2.24	0.71
1:A:507:ALA:O	1:A:510:LYS:CE	2.36	0.71
1:A:85:LEU:O	1:A:155:SER:HB2	1.91	0.71
1:A:691:LYS:HA	1:A:699:ASP:HB2	1.72	0.71
1:A:105:VAL:HG21	1:A:219:TYR:CE2	2.26	0.71
1:A:154:PHE:HA	1:A:155:SER:CB	2.20	0.70
1:A:640:ALA:HA	1:A:643:ARG:HE	1.56	0.70
1:A:26:LEU:HD22	1:A:29:MET:CE	2.20	0.70
1:B:320:PHE:CE2	1:B:361:VAL:HG21	2.26	0.70
1:A:119:VAL:HG13	1:A:175:PHE:CD1	2.27	0.70
1:B:531:LEU:HD11	1:B:582:ILE:HD12	1.73	0.70
1:B:635:THR:HG22	1:B:639:ASP:OD2	1.91	0.69
1:B:657:ASP:OD2	1:B:677:ILE:HD13	1.93	0.69
1:B:315:LYS:HG2	1:B:324:ILE:HD11	1.74	0.69
1:A:235:ASN:HA	1:A:261:TRP:NE1	2.08	0.69
1:A:721:ILE:C	1:A:721:ILE:HD12	2.13	0.69
1:B:320:PHE:HA	1:B:323:ARG:NH2	2.06	0.69
1:B:771:GLN:HE21	1:B:772:ILE:N	1.90	0.69
1:B:56:ASN:N	1:B:57:PRO:HD2	2.08	0.69
1:A:221:ASP:C	1:A:222:GLN:OE1	2.31	0.69
1:B:382:SER:OG	1:B:423:TYR:CE2	2.47	0.68
1:B:529:LEU:HD11	1:B:586:LEU:HD21	1.74	0.68
1:B:347:GLU:HB2	1:B:351:ASN:HD21	1.56	0.68
1:B:597:PRO:HA	1:B:650:ASP:O	1.93	0.68
1:B:441:ARG:NH2	1:B:443:LEU:HD13	2.08	0.68
1:B:579:VAL:HG11	1:B:641:ILE:HA	1.76	0.68
1:B:578:ILE:O	1:B:582:ILE:HG12	1.94	0.68
1:B:118:ILE:HD13	1:B:129:HIS:HD2	1.57	0.68
1:B:166:ALA:HB3	1:B:185:VAL:HG22	1.76	0.67
1:A:420:HIS:CD2	1:A:423:TYR:HB2	2.30	0.67
1:A:854:LEU:HD12	1:A:855:ASN:N	2.09	0.67
1:A:72:PRO:HD3	1:A:215:MET:CE	2.25	0.67
1:A:291:GLN:O	1:A:295:LYS:HG3	1.95	0.67
1:A:91:ARG:HH11	1:A:91:ARG:HB2	1.59	0.67
1:B:347:GLU:CD	1:B:347:GLU:N	2.47	0.67
1:B:624:LYS:HD2	1:B:734:LEU:HB3	1.77	0.67

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:306:VAL:HG11	1:A:334:PHE:CE2	2.29	0.67
1:B:319:LEU:HB3	1:B:320:PHE:HE1	0.87	0.67
1:A:62:LYS:CB	1:A:64:LEU:HD21	2.25	0.67
1:B:230:ILE:HG22	1:B:416:LEU:HD23	1.76	0.66
1:B:469:GLN:NE2	1:B:766:PHE:HZ	1.93	0.66
1:A:184:ASP:OD1	1:A:186:VAL:HB	1.95	0.66
1:B:530:ALA:HB3	1:B:541:LEU:HB2	1.76	0.66
1:B:771:GLN:CA	1:B:771:GLN:NE2	2.56	0.66
1:B:319:LEU:CA	1:B:320:PHE:HD1	2.07	0.66
1:A:139:GLU:OE1	1:A:139:GLU:HA	1.96	0.66
1:A:520:PRO:CD	1:A:663:MET:HE3	2.22	0.66
1:B:539:ARG:CZ	1:B:559:ILE:HD11	2.25	0.66
1:B:382:SER:HG	1:B:423:TYR:HE2	1.43	0.66
1:A:168:LEU:CD2	1:A:180:VAL:HG12	2.25	0.66
1:A:44:ARG:HG2	1:A:392:ALA:CB	2.25	0.66
1:B:666:ALA:HA	1:B:672:CYS:HB3	1.78	0.66
1:A:159:GLN:HB3	1:A:167:ILE:HB	1.77	0.65
1:A:168:LEU:HD23	1:A:180:VAL:HG12	1.78	0.65
1:A:566:ILE:HD13	1:A:566:ILE:H	1.60	0.65
1:A:529:LEU:HD11	1:A:586:LEU:HD21	1.77	0.65
1:A:769:ARG:NH2	1:A:812:THR:HG23	2.11	0.65
1:B:346:LYS:CB	1:B:347:GLU:OE2	2.45	0.65
1:B:769:ARG:NH2	1:B:810:ASN:O	2.30	0.65
1:B:814:ASP:O	6:B:1178:HOH:O	2.15	0.65
1:A:222:GLN:O	1:A:223:HIS:CG	2.50	0.65
1:A:56:ASN:N	1:A:57:PRO:HD2	2.12	0.65
1:B:565:GLU:HG2	1:B:566:ILE:N	2.11	0.65
1:A:162:LYS:HB3	1:A:164:ASP:HB3	1.79	0.65
1:A:347:GLU:OE2	1:A:347:GLU:HA	1.97	0.65
1:A:441:ARG:NH2	1:A:443:LEU:HD13	2.12	0.65
1:A:566:ILE:N	1:A:566:ILE:CD1	2.60	0.65
1:A:62:LYS:HB3	1:A:64:LEU:HD23	1.77	0.65
1:A:154:PHE:HA	1:A:155:SER:HB2	1.79	0.64
1:B:471:GLU:CG	6:B:1129:HOH:O	2.45	0.64
1:A:412:VAL:HG12	1:A:413:ASP:N	2.12	0.64
1:A:691:LYS:HB3	6:A:1132:HOH:O	1.96	0.64
1:B:79:ASP:HB3	1:B:148:LEU:HD22	1.79	0.64
1:A:376:THR:O	1:A:380:PHE:HB2	1.97	0.64
1:A:587:ASP:O	1:A:590:GLY:N	2.28	0.64
1:B:628:CYS:O	1:B:631:HIS:HB2	1.96	0.64
1:A:311:VAL:HG22	1:A:328:LEU:HG	1.79	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:221:ASP:OD1	1:A:222:GLN:O	2.16	0.64
1:A:91:ARG:HB2	1:A:91:ARG:NH1	2.13	0.64
1:A:98:ASN:CG	1:A:101:LYS:HD3	2.18	0.64
1:B:121:GLY:O	1:B:177:ALA:HA	1.98	0.64
1:B:342:ILE:O	1:B:372:GLN:HG3	1.97	0.64
1:B:97:VAL:HG21	1:B:455:MET:HE1	1.79	0.64
1:A:100:GLU:HA	1:A:100:GLU:OE1	1.97	0.64
1:A:163:ILE:CD1	1:A:205:ALA:HB1	2.27	0.64
1:A:530:ALA:O	1:A:531:LEU:HD12	1.98	0.64
1:A:624:LYS:HE3	1:A:734:LEU:HD22	1.78	0.64
1:B:344:LYS:O	1:B:348:GLY:HA2	1.98	0.64
1:A:302:LEU:O	1:A:306:VAL:HG23	1.97	0.63
1:A:94:ARG:NH1	1:A:143:ILE:HG21	2.13	0.63
1:A:570:THR:CG2	1:A:573:GLU:CG	2.55	0.63
1:A:680:THR:O	1:A:746:SER:HB2	1.97	0.63
1:A:875:MET:O	1:A:879:VAL:HG23	1.98	0.63
1:B:164:ASP:HB3	1:B:204:VAL:O	1.99	0.63
1:B:649:LEU:HD12	1:B:649:LEU:O	1.98	0.63
1:B:762:THR:HG22	1:B:772:ILE:HD13	1.80	0.63
1:B:141:ARG:O	1:B:143:ILE:HG23	1.99	0.63
1:A:208:ASN:HD22	1:A:209:ASP:H	1.45	0.63
1:A:209:ASP:OD1	1:A:229:ILE:HG13	1.99	0.63
1:A:829:ARG:HD2	6:A:1101:HOH:O	1.98	0.63
1:B:501:LYS:CB	1:B:695:MET:SD	2.87	0.63
1:A:24:LYS:O	1:A:27:TYR:HB3	1.99	0.63
1:A:786:PHE:CZ	1:A:790:ILE:HG13	2.34	0.62
1:A:665:CYS:SG	1:A:891:LEU:HD23	2.39	0.62
1:B:587:ASP:OD1	1:B:592:LYS:HD2	1.98	0.62
1:B:772:ILE:CG2	1:B:777:LYS:HD2	2.29	0.62
1:A:234:THR:HG22	1:A:294:GLU:HG3	1.81	0.62
1:A:98:ASN:OD1	1:A:100:GLU:HB2	2.00	0.62
1:A:101:LYS:N	1:A:101:LYS:HD2	2.15	0.62
1:A:98:ASN:OD1	1:A:101:LYS:HD3	1.99	0.62
1:A:325:THR:HB	1:A:326:PRO:HD2	1.80	0.62
1:A:380:PHE:CE2	1:A:426:ARG:CG	2.80	0.62
1:B:451:LYS:O	1:B:455:MET:HG2	1.99	0.62
1:B:471:GLU:HG3	6:B:1129:HOH:O	2.00	0.62
1:A:818:LEU:O	1:A:822:VAL:HG23	2.00	0.62
1:B:26:LEU:HD11	1:B:374:VAL:HG13	1.82	0.62
1:B:354:GLU:O	1:B:358:ARG:HG3	2.00	0.62
1:B:663:MET:HG3	1:B:904:ILE:HD11	1.80	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:97:VAL:HG21	1:B:455:MET:CE	2.30	0.62
1:A:644:ARG:NH1	1:A:646:GLU:OE2	2.33	0.61
1:A:640:ALA:HB2	1:A:643:ARG:HH21	1.65	0.61
1:B:797:LEU:HD21	1:B:817:ILE:CD1	2.30	0.61
1:B:35:THR:O	1:B:38:ASP:HB3	2.00	0.61
1:B:786:PHE:CE2	1:B:807:LEU:HD11	2.35	0.61
1:B:91:ARG:NH1	1:B:91:ARG:HB2	2.15	0.61
1:B:79:ASP:HB3	1:B:148:LEU:CD2	2.31	0.61
1:A:828:ARG:HD3	6:A:1183:HOH:O	2.01	0.61
1:B:527:ASP:OD2	1:B:544:LYS:HE2	2.00	0.61
1:B:800:VAL:HG12	1:B:816:SER:HB3	1.83	0.61
1:A:745:ILE:HA	1:A:830:ALA:HB1	1.82	0.61
1:B:165:GLU:HG3	1:B:184:ASP:OD2	2.01	0.61
1:B:380:PHE:CE2	1:B:426:ARG:HD3	2.36	0.61
1:A:578:ILE:O	1:A:582:ILE:HG13	2.01	0.60
1:A:277:PHE:CE1	1:A:309:ILE:HA	2.35	0.60
1:B:539:ARG:HH11	1:B:557:ASN:ND2	1.99	0.60
1:B:638:ARG:O	1:B:642:LYS:HG3	2.01	0.60
1:A:79:ASP:O	1:A:148:LEU:HD22	2.01	0.60
1:A:598:LEU:HD22	1:A:651:VAL:HG22	1.83	0.60
1:A:760:ASP:O	1:A:764:LYS:HG3	2.00	0.60
1:B:163:ILE:HG22	6:B:1153:HOH:O	2.02	0.60
1:A:295:LYS:HA	1:A:301:TYR:CD2	2.37	0.60
1:A:566:ILE:N	1:A:566:ILE:HD13	2.15	0.60
1:B:21:LYS:NZ	1:B:21:LYS:HB3	2.17	0.60
1:B:538:PHE:CD2	1:B:562:ILE:HD11	2.36	0.60
1:B:583:SER:HB2	1:B:647:PHE:HE2	1.66	0.60
1:A:564:ILE:HA	6:A:1164:HOH:O	2.00	0.60
1:A:433:ARG:O	1:A:436:PRO:HD3	2.02	0.60
1:B:106:HIS:ND1	1:B:107:MET:N	2.50	0.60
1:B:420:HIS:CD2	1:B:423:TYR:HB2	2.37	0.60
1:B:105:VAL:HG11	1:B:451:LYS:HG3	1.84	0.60
1:B:483:MET:HG3	6:B:1168:HOH:O	2.01	0.60
1:B:291:GLN:HA	1:B:291:GLN:OE1	2.02	0.60
1:B:319:LEU:CA	1:B:320:PHE:CD1	2.83	0.60
1:B:412:VAL:HG12	1:B:413:ASP:N	2.17	0.60
1:B:320:PHE:HB3	1:B:323:ARG:CZ	2.32	0.59
1:B:71:ILE:HA	1:B:215:MET:SD	2.42	0.59
1:B:232:THR:O	1:B:298:SER:HB2	2.03	0.59
1:B:853:ARG:HH11	1:B:853:ARG:CB	2.08	0.59
1:A:748:MET:HG2	1:A:748:MET:O	2.02	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:649:LEU:HD12	1:B:649:LEU:C	2.22	0.59
1:A:166:ALA:HB3	1:A:185:VAL:HG22	1.83	0.59
1:A:420:HIS:HD2	1:A:423:TYR:HB2	1.65	0.59
1:B:20:LYS:HG3	1:B:24:LYS:HE3	1.83	0.59
1:B:743:LYS:HA	1:B:749:TYR:CD2	2.37	0.59
1:A:162:LYS:O	1:A:163:ILE:CB	2.51	0.59
1:A:579:VAL:HG21	1:A:640:ALA:CB	2.31	0.59
1:B:105:VAL:HG21	1:B:219:TYR:CE2	2.37	0.59
1:B:480:THR:HG23	1:B:483:MET:HE2	1.83	0.59
1:B:644:ARG:O	1:B:645:GLU:HB2	2.02	0.59
1:A:384:ASN:O	1:A:387:ALA:HB3	2.03	0.59
1:B:485:LEU:HD23	1:B:882:LEU:HD22	1.85	0.59
1:A:26:LEU:HD22	1:A:29:MET:HE2	1.83	0.59
1:A:767:LEU:HB3	1:A:768:PHE:CD2	2.37	0.59
1:A:91:ARG:HH11	1:A:91:ARG:CB	2.16	0.59
1:B:652:VAL:HG21	1:B:909:VAL:HG23	1.82	0.59
1:A:422:GLN:CG	1:A:426:ARG:CZ	2.81	0.59
1:B:171:TRP:HB3	1:B:175:PHE:O	2.02	0.59
1:A:297:VAL:O	1:A:297:VAL:HG12	2.03	0.58
1:A:422:GLN:CB	1:A:426:ARG:NH1	2.66	0.58
1:A:665:CYS:SG	1:A:672:CYS:SG	3.00	0.58
1:A:218:GLY:HA2	1:A:224:CYS:HB3	1.85	0.58
1:A:65:PRO:HA	1:A:257:ILE:HD13	1.85	0.58
1:A:431:LEU:CD2	1:A:442:PHE:HZ	2.11	0.58
1:A:735:ASN:HB2	1:A:738:LYS:HE3	1.86	0.58
1:B:152:PHE:HB3	1:B:206:VAL:HG22	1.84	0.58
1:B:347:GLU:OE2	1:B:347:GLU:N	2.35	0.58
1:A:422:GLN:CB	1:A:426:ARG:CZ	2.80	0.58
1:B:295:LYS:HA	1:B:301:TYR:CD2	2.38	0.58
1:B:771:GLN:NE2	1:B:772:ILE:N	2.50	0.58
1:B:786:PHE:C	1:B:786:PHE:CD1	2.76	0.58
1:A:126:LEU:O	1:A:129:HIS:HB3	2.02	0.58
1:A:516:VAL:HG21	1:A:904:ILE:HD12	1.85	0.58
1:A:528:PHE:CE2	1:A:906:ALA:HA	2.38	0.58
1:B:420:HIS:HD2	1:B:423:TYR:N	1.96	0.58
1:B:420:HIS:CD2	1:B:423:TYR:H	2.11	0.58
1:A:198:ASP:OD2	1:A:198:ASP:O	2.22	0.58
1:B:659:VAL:HA	1:B:685:CYS:SG	2.44	0.58
1:B:429:LYS:HE3	1:B:433:ARG:NH1	2.19	0.58
1:B:73:ASP:OD1	1:B:76:GLU:OE2	2.22	0.58
1:A:323:ARG:NH2	1:A:362:GLU:O	2.36	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:650:ASP:O	1:A:652:VAL:HG23	2.04	0.57
1:A:769:ARG:NH2	1:A:815:ASP:OD2	2.37	0.57
1:B:538:PHE:CB	1:B:562:ILE:CD1	2.82	0.57
1:B:615:ILE:HA	1:B:631:HIS:O	2.03	0.57
1:B:26:LEU:HD12	1:B:377:ILE:CD1	2.34	0.57
1:B:66:THR:HG23	1:B:68:VAL:H	1.69	0.57
1:B:184:ASP:OD1	1:B:186:VAL:HG23	2.05	0.57
1:B:320:PHE:CD2	1:B:361:VAL:CB	2.82	0.57
1:A:306:VAL:HG11	1:A:334:PHE:HE2	1.69	0.57
1:A:320:PHE:CG	1:A:361:VAL:HB	2.38	0.57
1:A:80:PHE:CE2	1:A:458:ALA:HA	2.39	0.57
1:A:688:GLU:OE1	1:A:848:ASN:ND2	2.37	0.57
1:A:422:GLN:HG3	1:A:426:ARG:CZ	2.34	0.57
1:A:380:PHE:CE2	1:A:426:ARG:HD3	2.39	0.57
1:B:616:LEU:HD11	1:B:618:THR:O	2.04	0.57
1:B:714:ASP:OD1	1:B:740:ARG:HG2	2.04	0.57
1:B:528:PHE:CZ	1:B:906:ALA:HB2	2.40	0.57
1:A:222:GLN:O	1:A:223:HIS:ND1	2.37	0.57
1:B:541:LEU:HD13	1:B:898:GLY:CA	2.35	0.57
1:A:160:GLN:CG	1:A:165:GLU:O	2.40	0.57
1:A:381:ARG:O	1:A:382:SER:C	2.43	0.57
1:A:786:PHE:CZ	1:A:790:ILE:HD11	2.40	0.57
1:B:66:THR:HG21	1:B:256:CYS:HB3	1.85	0.57
1:B:666:ALA:HA	1:B:669:GLU:O	2.05	0.57
1:A:44:ARG:HA	1:A:47:MET:HE2	1.87	0.56
1:A:530:ALA:HB3	1:A:541:LEU:HB2	1.87	0.56
1:A:786:PHE:C	1:A:786:PHE:CD1	2.78	0.56
1:A:541:LEU:HD22	1:A:898:GLY:HA3	1.87	0.56
1:A:92:ILE:C	1:A:93:LEU:HD23	2.22	0.56
1:B:320:PHE:CB	1:B:323:ARG:CZ	2.83	0.56
1:B:320:PHE:CB	1:B:323:ARG:HH21	1.97	0.56
1:A:198:ASP:OD2	1:A:198:ASP:C	2.44	0.56
1:A:72:PRO:HG3	1:A:455:MET:HB3	1.87	0.56
1:B:541:LEU:HD13	1:B:898:GLY:HA3	1.87	0.56
1:B:688:GLU:OE2	1:B:844:LYS:NZ	2.37	0.56
1:A:204:VAL:HG21	1:A:461:TYR:HD1	1.71	0.56
1:A:531:LEU:O	1:A:601:THR:HB	2.06	0.56
1:B:488:LYS:HG3	1:B:840:ALA:HB2	1.87	0.56
1:B:673:GLU:CD	1:B:849:ARG:HH22	2.08	0.56
1:A:373:HIS:CD2	1:A:377:ILE:HD11	2.41	0.56
1:B:575:PHE:O	1:B:579:VAL:HG23	2.05	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:828:ARG:NH2	1:B:874:ILE:HD13	2.21	0.56
1:A:656:ASN:ND2	2:A:1003:BGC:O3	2.38	0.56
1:A:845:ILE:HG22	1:A:854:LEU:HD21	1.88	0.56
1:B:302:LEU:O	1:B:306:VAL:HG23	2.06	0.56
1:B:320:PHE:O	1:B:323:ARG:HG3	2.05	0.56
1:A:297:VAL:HG13	1:A:382:SER:OG	2.06	0.56
1:B:772:ILE:HG21	1:B:777:LYS:HD2	1.88	0.56
1:A:203:ILE:HD13	1:A:203:ILE:N	2.18	0.55
1:A:309:ILE:O	1:A:313:MET:HG3	2.06	0.55
1:A:325:THR:HB	1:A:326:PRO:CD	2.36	0.55
1:A:579:VAL:HG21	1:A:640:ALA:HB3	1.87	0.55
1:B:210:THR:OG1	1:B:237:CYS:HB3	2.06	0.55
1:B:431:LEU:CD2	1:B:442:PHE:HZ	2.20	0.55
1:A:374:VAL:HA	1:A:377:ILE:HD12	1.88	0.55
1:B:309:ILE:O	1:B:313:MET:HG3	2.06	0.55
1:B:405:ARG:HB3	1:B:405:ARG:NH1	2.20	0.55
1:A:213:THR:HG22	1:A:214:MET:N	2.21	0.55
1:A:115:PRO:HB2	1:A:117:ASN:ND2	2.22	0.55
1:A:320:PHE:O	1:A:323:ARG:HG3	2.06	0.55
1:A:413:ASP:OD2	1:A:448:GLY:HA2	2.07	0.55
1:A:588:TYR:CE2	1:B:331:ARG:HD2	2.42	0.55
1:A:64:LEU:HD13	1:A:158:CYS:O	2.06	0.55
1:B:134:LEU:O	1:B:138:MET:HG3	2.06	0.55
1:B:652:VAL:HG21	1:B:909:VAL:CG2	2.37	0.55
1:B:671:THR:OG1	1:B:857:THR:HG23	2.05	0.55
1:A:167:ILE:HA	1:A:183:ALA:O	2.06	0.55
1:A:222:GLN:O	1:A:223:HIS:CB	2.54	0.55
1:B:320:PHE:O	1:B:321:GLU:HB2	2.06	0.55
1:B:718:LEU:HB2	6:B:1102:HOH:O	2.05	0.55
1:A:912:ARG:C	1:A:914:GLU:H	2.10	0.55
1:B:595:ARG:HG3	1:B:649:LEU:HA	1.88	0.55
1:B:800:VAL:CG1	1:B:816:SER:HB3	2.36	0.55
1:A:245:ILE:CD1	1:A:257:ILE:HD11	2.37	0.55
1:A:425:ARG:HH22	1:A:426:ARG:HE	1.55	0.55
1:A:546:ARG:O	1:A:551:ARG:HA	2.06	0.55
1:A:794:ARG:HH21	1:B:794:ARG:NH2	2.05	0.55
1:A:171:TRP:CZ2	1:A:177:ALA:HB3	2.42	0.55
1:A:152:PHE:HB3	1:A:206:VAL:HG22	1.89	0.55
1:A:297:VAL:CG1	1:A:297:VAL:O	2.55	0.55
1:B:596:MET:O	1:B:649:LEU:HB2	2.06	0.55
1:B:93:LEU:N	1:B:93:LEU:HD12	2.21	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:344:LYS:O	1:B:348:GLY:HA3	2.03	0.54
1:B:429:LYS:HE3	1:B:433:ARG:HH12	1.72	0.54
1:B:605:PRO:HB3	1:B:708:GLU:HG3	1.89	0.54
1:B:553:VAL:O	1:B:553:VAL:HG12	2.06	0.54
1:A:323:ARG:NH2	1:A:362:GLU:HB2	2.21	0.54
1:A:657:ASP:OD2	2:A:1003:BGC:H6C1	2.07	0.54
1:B:565:GLU:CG	1:B:566:ILE:N	2.69	0.54
1:B:754:VAL:HA	1:B:757:ILE:HD12	1.89	0.54
1:A:320:PHE:HZ	1:A:356:LEU:HD22	1.73	0.54
1:A:673:GLU:OE1	1:A:849:ARG:NH2	2.37	0.54
1:B:120:HIS:HA	1:B:176:LYS:O	2.08	0.54
1:B:347:GLU:HB3	1:B:351:ASN:ND2	2.22	0.54
1:B:393:ILE:O	1:B:396:ARG:HB3	2.07	0.54
1:B:587:ASP:OD1	1:B:592:LYS:CD	2.55	0.54
1:B:688:GLU:OE1	1:B:688:GLU:HA	2.08	0.54
1:B:775:THR:O	1:B:778:THR:N	2.36	0.54
1:B:786:PHE:CD2	1:B:807:LEU:HD11	2.42	0.54
1:B:86:GLY:HA3	1:B:155:SER:OG	2.08	0.54
1:B:320:PHE:O	1:B:323:ARG:CZ	2.55	0.54
1:B:26:LEU:HD12	1:B:377:ILE:HD12	1.89	0.54
1:B:644:ARG:HA	1:B:644:ARG:HH11	1.72	0.54
1:B:813:CYS:HB2	6:B:1132:HOH:O	2.06	0.54
1:A:25:TYR:HE2	1:A:313:MET:HG2	1.73	0.54
1:A:564:ILE:CG1	1:A:565:GLU:N	2.61	0.54
1:B:374:VAL:HA	1:B:377:ILE:HD12	1.88	0.54
1:A:110:GLU:HG3	1:A:111:VAL:H	1.72	0.54
1:A:693:VAL:O	1:A:695:MET:N	2.40	0.54
1:B:171:TRP:CZ2	1:B:180:VAL:HG11	2.42	0.54
1:B:380:PHE:CD2	1:B:426:ARG:HD3	2.43	0.54
1:B:508:VAL:O	6:B:1109:HOH:O	2.18	0.54
1:A:578:ILE:HG22	1:A:582:ILE:HD11	1.90	0.53
1:A:721:ILE:C	1:A:721:ILE:CD1	2.76	0.53
1:B:771:GLN:HA	1:B:771:GLN:NE2	2.22	0.53
1:A:327:GLU:N	1:A:327:GLU:OE1	2.40	0.53
1:A:514:SER:OG	1:A:704:CYS:O	2.24	0.53
1:B:56:ASN:N	1:B:57:PRO:CD	2.71	0.53
1:A:163:ILE:HD13	1:A:205:ALA:HB1	1.89	0.53
1:A:560:TYR:CD2	1:A:581:CYS:HB3	2.43	0.53
1:B:209:ASP:OD2	2:B:1001:BGC:H6C1	2.09	0.53
1:B:495:MET:HB3	1:B:511:MET:HE2	1.90	0.53
1:B:204:VAL:HG11	1:B:461:TYR:N	2.22	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:538:PHE:HB3	1:B:562:ILE:CD1	2.39	0.53
1:B:616:LEU:HD11	1:B:618:THR:C	2.29	0.53
1:B:854:LEU:C	1:B:854:LEU:HD12	2.27	0.53
1:B:18:GLN:HE21	1:B:366:ASP:HB3	1.74	0.53
1:B:522:GLY:O	1:B:547:SER:HB2	2.09	0.53
1:B:587:ASP:CG	1:B:592:LYS:HD2	2.29	0.53
1:B:513:PRO:HB2	1:B:703:MET:CE	2.38	0.53
1:A:274:ARG:HH11	1:A:274:ARG:HG2	1.73	0.53
1:A:320:PHE:CE1	1:A:361:VAL:HG23	2.44	0.53
1:A:69:ARG:O	1:A:70:SER:HB3	2.09	0.53
1:B:307:ARG:HG2	1:B:307:ARG:HH11	1.73	0.53
1:B:631:HIS:HE1	6:B:1174:HOH:O	1.91	0.53
1:B:640:ALA:HA	1:B:643:ARG:HE	1.73	0.53
1:A:58:THR:CG2	6:B:1184:HOH:O	2.56	0.53
1:A:605:PRO:HD3	2:A:1003:BGC:O2	2.09	0.53
1:A:485:LEU:HD23	1:A:882:LEU:HD22	1.90	0.53
1:B:271:GLU:OE2	1:B:274:ARG:HD3	2.08	0.53
1:B:93:LEU:HG	1:B:109:SER:CB	2.38	0.53
1:A:86:GLY:HA2	1:A:175:PHE:CE2	2.44	0.53
1:B:654:VAL:HG13	1:B:654:VAL:O	2.08	0.53
1:A:165:GLU:HA	1:A:186:VAL:HG21	1.91	0.53
1:A:539:ARG:CZ	1:A:559:ILE:HD11	2.39	0.53
1:B:303:GLY:HA2	1:B:339:VAL:HG21	1.90	0.53
1:A:84:ASP:HA	1:A:153:THR:HB	1.90	0.53
1:B:501:LYS:HB2	1:B:695:MET:SD	2.47	0.53
1:B:718:LEU:HD22	1:B:721:ILE:HD11	1.90	0.52
1:B:93:LEU:HG	1:B:109:SER:HB2	1.91	0.52
1:B:441:ARG:HH21	1:B:443:LEU:HD13	1.73	0.52
1:B:55:PHE:C	1:B:57:PRO:HD2	2.30	0.52
1:B:66:THR:CG2	1:B:256:CYS:HB3	2.40	0.52
1:B:330:THR:HB	1:B:333:LYS:HG3	1.92	0.52
1:A:786:PHE:CD1	1:A:787:LEU:N	2.77	0.52
1:A:883:SER:HA	6:A:1103:HOH:O	2.09	0.52
1:B:361:VAL:O	1:B:363:PRO:HD3	2.09	0.52
1:B:579:VAL:HG13	1:B:641:ILE:HG12	1.92	0.52
1:A:601:THR:HA	1:A:655:VAL:O	2.10	0.52
1:B:163:ILE:HG13	1:B:205:ALA:HB1	1.90	0.52
1:A:306:VAL:O	1:A:309:ILE:N	2.43	0.52
1:A:398:ARG:NH1	1:A:398:ARG:HB3	2.24	0.52
1:A:693:VAL:C	1:A:695:MET:H	2.13	0.52
1:B:16:ASP:O	1:B:20:LYS:HB2	2.09	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:314:ALA:O	1:B:322:GLY:HA2	2.10	0.52
1:A:154:PHE:CA	1:A:155:SER:CB	2.87	0.52
1:A:275:THR:N	1:A:278:ASP:OD2	2.27	0.52
1:A:93:LEU:HD12	1:A:450:GLY:HA3	1.91	0.52
1:A:611:LEU:HG	1:A:653:ALA:CB	2.40	0.52
1:B:387:ALA:HA	1:B:427:PHE:HE1	1.75	0.52
1:A:110:GLU:HG3	1:A:111:VAL:N	2.25	0.52
1:A:317:GLY:HA2	1:A:322:GLY:CA	2.40	0.52
1:A:356:LEU:O	1:A:359:LEU:HB2	2.10	0.52
1:A:490:ARG:NH2	1:A:720:ASP:OD2	2.32	0.52
1:B:98:ASN:ND2	1:B:101:LYS:HD2	2.24	0.52
1:B:321:GLU:HB2	1:B:323:ARG:NH1	2.25	0.52
1:A:452:GLY:O	1:A:456:VAL:HG23	2.09	0.51
1:A:361:VAL:O	1:A:363:PRO:CD	2.55	0.51
1:A:380:PHE:CD2	1:A:426:ARG:CD	2.78	0.51
1:A:80:PHE:CD1	1:A:80:PHE:N	2.78	0.51
1:B:768:PHE:HE1	1:B:811:SER:HB3	1.75	0.51
1:A:72:PRO:HD3	1:A:215:MET:SD	2.50	0.51
1:A:480:THR:O	1:A:481:LYS:C	2.48	0.51
1:A:512:LEU:CD1	1:A:512:LEU:N	2.73	0.51
1:B:480:THR:HG23	1:B:483:MET:HE3	1.91	0.51
1:A:520:PRO:HD3	1:A:663:MET:SD	2.49	0.51
1:A:523:THR:OG1	1:A:910:ARG:NH1	2.42	0.51
1:A:277:PHE:CZ	1:A:309:ILE:HA	2.46	0.51
1:B:327:GLU:O	1:B:333:LYS:HG3	2.10	0.51
1:A:235:ASN:HA	1:A:261:TRP:CD1	2.46	0.51
1:A:529:LEU:CD1	1:A:586:LEU:HD21	2.40	0.51
1:B:189:LEU:O	1:B:190:ASN:C	2.48	0.51
1:B:306:VAL:O	1:B:308:LEU:N	2.44	0.51
1:B:318:LEU:O	1:B:319:LEU:CD2	2.58	0.51
1:B:538:PHE:HB3	1:B:562:ILE:HD12	1.93	0.51
1:A:86:GLY:CA	1:A:155:SER:OG	2.57	0.50
1:B:560:TYR:CD2	1:B:581:CYS:HB3	2.46	0.50
1:A:500:ARG:HG2	1:A:500:ARG:HH11	1.76	0.50
1:A:845:ILE:HG22	1:A:854:LEU:CD2	2.42	0.50
1:B:119:VAL:CG1	1:B:175:PHE:HA	2.42	0.50
1:B:156:PHE:HB3	1:B:157:PRO:HD2	1.94	0.50
1:B:346:LYS:HB2	1:B:347:GLU:OE2	2.11	0.50
1:B:510:LYS:HB3	1:B:512:LEU:CD2	2.42	0.50
1:B:577:HIS:O	1:B:580:SER:HB3	2.12	0.50
1:A:25:TYR:CE2	1:A:313:MET:HG2	2.46	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:578:ILE:HG22	1:A:582:ILE:CD1	2.41	0.50
1:B:313:MET:CE	1:B:318:LEU:CD1	2.88	0.50
1:A:180:VAL:O	1:A:183:ALA:HB3	2.11	0.50
1:B:320:PHE:CE2	1:B:361:VAL:CG2	2.95	0.50
1:B:495:MET:HE1	1:B:841:VAL:HG22	1.93	0.50
1:A:271:GLU:HA	1:A:271:GLU:OE1	2.12	0.50
1:A:174:ARG:O	1:A:286:LEU:CD1	2.59	0.50
1:A:154:PHE:HA	1:A:155:SER:HB3	1.93	0.50
1:A:683:ASN:HA	1:A:709:TRP:CD1	2.47	0.50
1:A:760:ASP:OD2	1:A:764:LYS:CE	2.53	0.50
1:A:652:VAL:HB	1:A:905:THR:HG23	1.92	0.50
1:B:290:LYS:O	1:B:295:LYS:HE3	2.10	0.50
1:B:574:LEU:O	1:B:577:HIS:HB3	2.11	0.50
1:B:844:LYS:HZ3	1:B:848:ASN:ND2	2.05	0.50
1:A:66:THR:CG2	1:A:256:CYS:HB3	2.39	0.50
1:B:229:ILE:O	1:B:234:THR:HA	2.12	0.50
1:A:512:LEU:N	1:A:512:LEU:HD13	2.27	0.50
1:A:638:ARG:O	1:A:641:ILE:HB	2.12	0.50
1:A:786:PHE:CE1	1:A:790:ILE:HG13	2.47	0.50
1:B:426:ARG:HH21	5:B:1007:CIT:C4	2.18	0.50
1:B:666:ALA:CA	1:B:672:CYS:HB3	2.41	0.50
1:B:513:PRO:HB2	1:B:703:MET:HE3	1.93	0.50
1:B:759:ILE:O	1:B:762:THR:HB	2.12	0.50
1:B:768:PHE:CE1	1:B:811:SER:HB3	2.47	0.50
1:A:799:GLN:O	1:A:802:ALA:HB3	2.11	0.49
1:B:118:ILE:CD1	1:B:129:HIS:HD2	2.25	0.49
1:B:84:ASP:HA	1:B:153:THR:HB	1.93	0.49
1:B:553:VAL:HG11	1:B:899:LYS:HG3	1.94	0.49
1:A:430:THR:HG23	1:A:433:ARG:NH2	2.28	0.49
1:B:98:ASN:C	1:B:103:GLN:O	2.50	0.49
1:B:141:ARG:HD2	1:B:141:ARG:N	2.27	0.49
1:B:325:THR:HG21	1:B:360:GLY:HA3	1.93	0.49
1:B:467:HIS:O	1:B:468:ARG:C	2.50	0.49
1:A:528:PHE:CZ	1:A:906:ALA:HA	2.47	0.49
1:A:408:THR:OG1	1:A:409:THR:N	2.45	0.49
1:B:786:PHE:CD1	1:B:787:LEU:N	2.80	0.49
1:B:307:ARG:HG2	1:B:307:ARG:NH1	2.27	0.49
1:B:529:LEU:O	1:B:598:LEU:HA	2.13	0.49
1:A:221:ASP:OD1	1:A:222:GLN:N	2.46	0.49
1:A:796:ALA:O	1:A:799:GLN:HB3	2.13	0.49
1:B:791:GLU:O	1:B:792:SER:C	2.50	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:389:THR:O	1:A:392:ALA:N	2.46	0.49
1:A:422:GLN:HG3	1:A:425:ARG:NH2	2.22	0.49
1:A:611:LEU:HG	1:A:653:ALA:HB2	1.94	0.49
1:B:350:HIS:O	1:B:353:LYS:HB3	2.13	0.49
1:B:764:LYS:HE2	6:B:1124:HOH:O	2.12	0.49
1:A:510:LYS:HB3	1:A:512:LEU:HD13	1.89	0.48
1:A:711:ALA:O	1:A:714:ASP:HB2	2.12	0.48
1:A:786:PHE:CZ	1:A:790:ILE:CG1	2.96	0.48
1:B:390:LEU:CD2	1:B:427:PHE:HZ	2.22	0.48
1:B:538:PHE:CG	1:B:562:ILE:HD11	2.48	0.48
1:B:598:LEU:HD22	1:B:651:VAL:HG22	1.95	0.48
1:A:22:ILE:HD11	1:A:370:SER:HB3	1.94	0.48
1:A:579:VAL:HA	1:A:582:ILE:HD12	1.95	0.48
1:B:275:THR:O	1:B:278:ASP:N	2.47	0.48
1:B:347:GLU:O	1:B:348:GLY:C	2.52	0.48
1:B:320:PHE:CE2	1:B:361:VAL:CB	2.96	0.48
1:A:361:VAL:HG23	1:A:361:VAL:O	2.13	0.48
1:A:602:PHE:CE2	1:A:633:VAL:HG11	2.48	0.48
1:A:786:PHE:CD2	1:A:807:LEU:HD11	2.48	0.48
1:A:786:PHE:CE2	1:A:790:ILE:CD1	2.83	0.48
1:A:854:LEU:HD12	1:A:854:LEU:C	2.33	0.48
1:B:173:LYS:CE	2:B:1001:BGC:O5	2.53	0.48
1:B:471:GLU:HG2	6:B:1129:HOH:O	2.09	0.48
1:B:818:LEU:O	1:B:822:VAL:HG23	2.13	0.48
1:A:162:LYS:C	1:A:164:ASP:H	2.16	0.48
1:A:520:PRO:CG	1:A:663:MET:HE3	2.43	0.48
1:A:786:PHE:CZ	1:A:790:ILE:CD1	2.96	0.48
1:B:204:VAL:HG12	1:B:460:ALA:CB	2.41	0.48
1:B:320:PHE:CE2	1:B:361:VAL:HG11	2.48	0.48
1:A:637:LEU:O	1:A:641:ILE:HG12	2.14	0.48
1:B:398:ARG:HB2	1:B:406:LEU:HD22	1.96	0.48
1:A:156:PHE:HB3	1:A:157:PRO:CD	2.44	0.48
1:A:496:GLU:O	1:A:500:ARG:HG3	2.14	0.48
1:B:189:LEU:CD2	1:B:203:ILE:HD11	2.35	0.48
1:B:320:PHE:HE2	1:B:361:VAL:CG2	2.21	0.48
1:A:264:PHE:HB3	1:A:293:PHE:CB	2.44	0.48
1:A:623:PHE:N	1:A:623:PHE:CD2	2.80	0.48
1:A:767:LEU:HD22	1:A:768:PHE:CE2	2.48	0.48
1:B:531:LEU:HD22	1:B:598:LEU:HD11	1.95	0.48
1:A:412:VAL:CG1	1:A:413:ASP:N	2.76	0.47
1:B:159:GLN:OE1	1:B:159:GLN:HA	2.13	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:202:ASN:O	1:B:204:VAL:HG23	2.14	0.47
1:A:406:LEU:HG	1:A:408:THR:HG22	1.96	0.47
1:A:56:ASN:N	1:A:57:PRO:CD	2.76	0.47
1:A:781:ILE:HG22	1:A:782:PHE:N	2.28	0.47
1:B:291:GLN:O	1:B:295:LYS:HG3	2.15	0.47
1:B:612:ASP:HB3	1:B:652:VAL:O	2.14	0.47
1:A:66:THR:HG21	1:A:256:CYS:CB	2.40	0.47
1:A:67:PHE:CZ	1:A:161:SER:O	2.67	0.47
1:B:159:GLN:HB3	1:B:167:ILE:HB	1.96	0.47
1:A:261:TRP:O	1:A:264:PHE:HB2	2.15	0.47
1:A:721:ILE:HD12	1:A:722:ARG:N	2.28	0.47
1:A:854:LEU:HD12	1:A:855:ASN:O	2.15	0.47
1:B:235:ASN:HB2	6:B:1136:HOH:O	2.15	0.47
1:A:199:TYR:CE2	1:A:201:ALA:HB2	2.49	0.47
1:A:520:PRO:HG3	1:A:663:MET:HE3	1.96	0.47
1:A:838:MET:O	1:A:841:VAL:N	2.47	0.47
1:B:718:LEU:C	1:B:720:ASP:N	2.68	0.47
1:A:154:PHE:CA	1:A:155:SER:HB2	2.45	0.47
1:A:43:PHE:O	1:A:47:MET:HG3	2.15	0.47
1:B:841:VAL:HG12	1:B:842:VAL:N	2.29	0.47
1:A:101:LYS:N	1:A:101:LYS:CD	2.77	0.47
1:A:287:ASN:O	1:A:295:LYS:NZ	2.45	0.47
1:A:564:ILE:CG1	1:A:565:GLU:H	2.16	0.47
1:B:330:THR:HG21	1:B:333:LYS:HE2	1.96	0.47
1:B:491:MET:O	1:B:495:MET:HG3	2.15	0.47
1:B:69:ARG:O	1:B:70:SER:HB3	2.15	0.47
1:A:693:VAL:HG12	1:A:693:VAL:O	2.15	0.47
1:B:395:ASN:OD1	1:B:398:ARG:NH2	2.48	0.47
1:B:724:HIS:CE1	1:B:728:LEU:HD11	2.49	0.47
1:A:238:TYR:O	1:A:256:CYS:HA	2.15	0.47
1:A:241:GLU:O	1:A:244:HIS:HB2	2.14	0.47
1:A:71:ILE:HA	1:A:215:MET:SD	2.54	0.47
1:B:163:ILE:HG13	1:B:205:ALA:CB	2.44	0.47
1:B:306:VAL:O	1:B:307:ARG:C	2.54	0.47
1:B:628:CYS:HB2	6:B:1123:HOH:O	2.14	0.47
1:B:781:ILE:HG22	1:B:782:PHE:N	2.31	0.46
1:B:505:ASN:HB2	6:B:1111:HOH:O	2.15	0.46
1:B:579:VAL:HG21	1:B:640:ALA:HB3	1.96	0.46
1:B:755:ARG:HD2	1:B:778:THR:O	2.16	0.46
1:B:797:LEU:HD21	1:B:817:ILE:HD13	1.98	0.46
1:B:488:LYS:HE3	1:B:840:ALA:HA	1.97	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:105:VAL:CG2	1:A:219:TYR:OH	2.63	0.46
1:A:511:MET:O	1:A:705:ILE:HD12	2.16	0.46
1:A:718:LEU:C	1:A:720:ASP:N	2.68	0.46
1:B:596:MET:HB3	1:B:597:PRO:HD2	1.97	0.46
1:A:320:PHE:CE2	1:A:361:VAL:HG11	2.51	0.46
1:A:380:PHE:CE2	1:A:426:ARG:CD	2.99	0.46
1:A:76:GLU:HG2	1:A:455:MET:SD	2.56	0.46
1:A:44:ARG:HA	1:A:47:MET:CE	2.45	0.46
1:A:652:VAL:HG21	1:A:909:VAL:CG2	2.46	0.46
1:A:398:ARG:HH11	1:A:398:ARG:HB3	1.80	0.46
1:A:647:PHE:CD1	1:A:647:PHE:N	2.83	0.46
1:B:119:VAL:HG12	1:B:120:HIS:HD2	1.80	0.46
1:B:844:LYS:HZ2	1:B:848:ASN:HD21	1.61	0.46
1:B:616:LEU:HD12	1:B:618:THR:H	1.81	0.46
1:B:83:LEU:HB2	1:B:152:PHE:HD1	1.81	0.46
1:A:52:SER:HA	1:A:246:ASP:OD2	2.16	0.45
1:A:619:TRP:CD1	1:A:624:LYS:HA	2.51	0.45
1:B:105:VAL:HG21	1:B:219:TYR:HE2	1.81	0.45
1:B:147:LYS:HD3	1:B:147:LYS:H	1.81	0.45
1:B:346:LYS:C	1:B:347:GLU:CD	2.74	0.45
1:B:42:ARG:HH11	1:B:270:LEU:HD23	1.80	0.45
1:B:735:ASN:N	1:B:735:ASN:OD1	2.48	0.45
1:B:492:ARG:NE	1:B:844:LYS:HG3	2.32	0.45
1:A:311:VAL:O	1:A:315:LYS:HG3	2.15	0.45
1:A:666:ALA:HA	1:A:669:GLU:O	2.15	0.45
1:B:683:ASN:HA	1:B:709:TRP:CD1	2.51	0.45
1:B:797:LEU:HD13	1:B:813:CYS:HB3	1.98	0.45
1:A:687:MET:SD	1:A:704:CYS:HB2	2.56	0.45
1:B:126:LEU:O	1:B:130:VAL:HG23	2.17	0.45
1:B:30:ARG:HG2	1:B:377:ILE:HG23	1.98	0.45
1:B:666:ALA:HA	1:B:672:CYS:CB	2.45	0.45
1:B:716:GLY:C	1:B:718:LEU:H	2.19	0.45
1:B:718:LEU:C	1:B:720:ASP:H	2.20	0.45
1:B:725:TYR:O	1:B:729:VAL:HG23	2.16	0.45
1:B:772:ILE:HG22	1:B:777:LYS:HD2	1.96	0.45
1:B:862:GLY:HA2	3:B:1004:OWK:O6	2.16	0.45
1:B:513:PRO:CB	1:B:703:MET:HE2	2.46	0.45
1:B:899:LYS:O	1:B:903:LEU:HG	2.17	0.45
1:A:154:PHE:C	1:A:156:PHE:H	2.17	0.45
1:A:58:THR:O	1:A:58:THR:HG22	2.17	0.45
1:A:727:ARG:O	1:A:731:GLU:HB2	2.16	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:508:VAL:HG23	1:B:509:VAL:N	2.32	0.45
1:B:650:ASP:OD2	1:B:912:ARG:NH1	2.41	0.45
1:A:317:GLY:HA2	1:A:322:GLY:HA2	1.99	0.45
1:A:539:ARG:HH11	1:A:557:ASN:ND2	2.15	0.45
1:A:846:ARG:HA	1:A:854:LEU:HD22	1.98	0.45
1:A:156:PHE:CZ	1:A:175:PHE:CD2	2.94	0.45
1:A:357:THR:OG1	1:A:363:PRO:HG2	2.17	0.45
1:A:564:ILE:CA	6:A:1164:HOH:O	2.63	0.45
1:A:569:GLY:O	1:A:626:THR:HG23	2.17	0.45
1:A:652:VAL:O	1:A:652:VAL:HG12	2.16	0.45
1:B:431:LEU:HD22	1:B:442:PHE:HZ	1.82	0.45
1:B:843:ASP:HB3	6:B:1113:HOH:O	2.17	0.45
1:A:88:SER:OG	3:A:1002:OWK:O3P	2.34	0.45
1:A:110:GLU:HG2	1:A:112:TYR:CE1	2.52	0.45
1:A:897:SER:O	1:A:898:GLY:C	2.55	0.45
1:B:509:VAL:HB	6:B:1110:HOH:O	2.16	0.45
1:B:515:PHE:O	1:B:611:LEU:HD13	2.16	0.45
1:A:763:LYS:HG3	1:A:772:ILE:HD11	1.99	0.45
1:A:781:ILE:HA	1:A:781:ILE:HD13	1.75	0.45
1:B:481:LYS:O	1:B:485:LEU:HG	2.16	0.45
1:A:107:MET:HG3	1:A:107:MET:O	2.17	0.45
1:A:166:ALA:O	1:A:184:ASP:HA	2.17	0.45
1:A:26:LEU:HD21	1:A:309:ILE:HG23	1.99	0.45
1:A:579:VAL:HG13	1:A:641:ILE:HD13	1.99	0.45
1:A:913:THR:HG22	1:A:913:THR:O	2.17	0.45
1:A:364:SER:C	1:A:366:ASP:H	2.20	0.44
1:A:390:LEU:HD23	1:A:427:PHE:HZ	1.82	0.44
1:A:691:LYS:HA	1:A:699:ASP:CB	2.44	0.44
1:B:400:ASN:HD22	1:B:400:ASN:N	2.15	0.44
1:A:162:LYS:HD2	1:A:164:ASP:HB3	1.99	0.44
1:A:202:ASN:OD1	1:A:202:ASN:O	2.35	0.44
1:A:801:ARG:HG3	1:A:811:SER:O	2.17	0.44
1:B:608:GLN:HG2	1:B:614:GLY:HA2	2.00	0.44
1:B:642:LYS:C	1:B:644:ARG:H	2.19	0.44
1:A:124:SER:O	1:A:128:ASP:HB2	2.17	0.44
1:A:306:VAL:O	1:A:308:LEU:N	2.51	0.44
1:B:325:THR:OG1	1:B:359:LEU:O	2.34	0.44
1:B:568:GLN:HA	1:B:624:LYS:O	2.16	0.44
1:B:71:ILE:HB	1:B:72:PRO:HD2	1.99	0.44
1:B:797:LEU:HD21	1:B:817:ILE:HD11	1.99	0.44
1:B:828:ARG:NH2	1:B:874:ILE:CD1	2.80	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:754:VAL:HA	1:A:757:ILE:HD12	2.00	0.44
1:A:674:VAL:HB	1:A:858:VAL:HG22	1.99	0.44
1:B:342:ILE:CG2	1:B:372:GLN:HA	2.47	0.44
1:A:657:ASP:N	1:A:657:ASP:OD1	2.50	0.44
1:B:374:VAL:O	1:B:375:CYS:C	2.56	0.44
1:B:870:HIS:C	6:B:1146:HOH:O	2.55	0.44
1:A:128:ASP:HA	1:A:192:ALA:HB1	1.98	0.44
1:A:521:ASP:OD2	1:A:523:THR:HG23	2.17	0.44
1:A:853:ARG:HD3	1:A:885:LYS:O	2.18	0.44
1:B:373:HIS:O	1:B:377:ILE:HG13	2.18	0.44
1:B:542:LEU:HD13	1:B:542:LEU:C	2.38	0.44
1:A:425:ARG:NH2	1:A:426:ARG:NE	2.65	0.44
1:A:149:PRO:HG3	1:A:461:TYR:CE1	2.51	0.44
1:A:709:TRP:C	1:A:709:TRP:CD1	2.90	0.44
1:B:545:ILE:O	1:B:546:ARG:CD	2.57	0.44
1:B:31:LEU:HD11	1:B:381:ARG:HG3	1.99	0.44
1:A:110:GLU:CG	1:A:111:VAL:N	2.80	0.44
1:A:26:LEU:HD21	1:A:309:ILE:CG2	2.48	0.44
1:A:385:LEU:O	1:A:386:VAL:C	2.54	0.44
1:A:510:LYS:CB	1:A:512:LEU:CD1	2.86	0.44
1:A:541:LEU:N	1:A:541:LEU:HD12	2.32	0.44
1:A:67:PHE:CB	1:A:163:ILE:HB	2.47	0.44
1:A:718:LEU:HB2	6:A:1102:HOH:O	2.18	0.44
1:B:285:SER:OG	1:B:295:LYS:NZ	2.51	0.44
1:B:306:VAL:HG11	1:B:334:PHE:CE2	2.53	0.44
1:A:156:PHE:HB3	1:A:157:PRO:HD2	1.99	0.43
1:A:173:LYS:NZ	2:A:1001:BGC:O6	2.50	0.43
1:A:304:GLU:CD	1:A:307:ARG:HE	2.21	0.43
1:B:640:ALA:HA	1:B:643:ARG:NE	2.32	0.43
1:B:661:THR:O	1:B:662:MET:C	2.55	0.43
1:B:762:THR:HG22	1:B:772:ILE:CD1	2.46	0.43
1:A:763:LYS:CG	1:A:772:ILE:HD11	2.48	0.43
1:A:853:ARG:HG2	1:A:853:ARG:HH11	1.82	0.43
1:A:551:ARG:HB2	6:A:1155:HOH:O	2.18	0.43
1:A:652:VAL:HG21	1:A:909:VAL:HG22	2.00	0.43
1:B:508:VAL:HG23	1:B:509:VAL:H	1.82	0.43
1:A:211:VAL:HG22	1:A:256:CYS:SG	2.59	0.43
1:B:851:LEU:HD23	1:B:851:LEU:N	2.34	0.43
1:A:235:ASN:OD1	1:A:236:ALA:N	2.50	0.43
1:B:98:ASN:HD21	1:B:101:LYS:HD2	1.83	0.43
1:B:539:ARG:NH2	1:B:559:ILE:HD11	2.32	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:592:LYS:HB3	1:B:592:LYS:HE2	1.67	0.43
1:B:680:THR:O	1:B:746:SER:CB	2.62	0.43
1:A:245:ILE:HD11	1:A:257:ILE:HG12	1.99	0.43
1:A:320:PHE:CD2	1:A:361:VAL:HG11	2.54	0.43
1:A:491:MET:O	1:A:495:MET:HG3	2.18	0.43
1:A:721:ILE:HD13	1:A:744:MET:HE1	2.00	0.43
1:B:124:SER:N	6:B:1172:HOH:O	2.51	0.43
1:B:186:VAL:HG22	1:B:206:VAL:HG21	2.00	0.43
1:B:510:LYS:HB3	1:B:512:LEU:HD21	2.01	0.43
1:B:598:LEU:C	1:B:598:LEU:HD23	2.39	0.43
1:B:745:ILE:O	1:B:750:LEU:HG	2.19	0.43
1:B:784:THR:CG2	1:B:864:LEU:HA	2.48	0.43
1:A:26:LEU:HD11	1:A:309:ILE:HG21	2.01	0.43
1:A:422:GLN:CG	1:A:425:ARG:HH21	2.23	0.43
1:A:519:THR:O	1:A:520:PRO:C	2.56	0.43
1:A:755:ARG:HH11	1:A:755:ARG:HG2	1.84	0.43
1:A:632:ASP:C	1:A:632:ASP:OD1	2.56	0.43
1:B:142:LYS:HE2	1:B:142:LYS:HA	2.00	0.43
1:B:172:THR:HG21	1:B:291:GLN:HE21	1.83	0.43
1:B:21:LYS:HB3	1:B:21:LYS:HZ2	1.83	0.43
1:B:492:ARG:CZ	1:B:844:LYS:HG3	2.49	0.43
1:B:563:PRO:CD	1:B:566:ILE:HD12	2.40	0.43
1:A:228:LEU:HB3	1:A:412:VAL:HG22	2.01	0.43
1:A:242:LEU:C	1:A:244:HIS:H	2.21	0.43
1:A:60:THR:HB	1:A:263:ALA:O	2.18	0.43
1:B:389:THR:O	1:B:392:ALA:N	2.51	0.43
1:A:18:GLN:OE1	1:A:366:ASP:O	2.37	0.43
1:A:413:ASP:OD1	1:A:414:GLY:N	2.50	0.43
1:A:614:GLY:O	1:A:632:ASP:HA	2.19	0.43
1:A:845:ILE:CG2	1:A:854:LEU:HD21	2.49	0.43
1:B:107:MET:HE1	1:B:451:LYS:HB2	2.01	0.43
1:B:118:ILE:CD1	1:B:129:HIS:CD2	2.94	0.43
1:B:713:GLY:HA2	1:B:717:CYS:SG	2.59	0.43
1:A:371:VAL:O	1:A:374:VAL:N	2.52	0.42
1:A:619:TRP:HZ2	1:A:625:ALA:HB3	1.83	0.42
1:A:860:VAL:HG12	1:A:861:ASP:N	2.34	0.42
1:B:168:LEU:HD23	1:B:180:VAL:HG12	2.01	0.42
1:B:238:TYR:CE2	1:B:240:GLU:HB2	2.53	0.42
1:B:603:SER:HB2	1:B:621:LYS:HZ1	1.84	0.42
1:B:426:ARG:NH2	5:B:1007:CIT:H41	2.19	0.42
1:B:147:LYS:HD3	1:B:147:LYS:N	2.34	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:589:MET:HB3	1:B:591:ILE:HG12	2.00	0.42
1:A:632:ASP:OD1	1:A:634:VAL:N	2.52	0.42
1:B:167:ILE:HA	1:B:183:ALA:O	2.18	0.42
1:B:66:THR:CG2	1:B:256:CYS:O	2.62	0.42
1:B:217:CYS:SG	1:B:411:GLY:CA	3.07	0.42
1:B:412:VAL:CG1	1:B:413:ASP:N	2.82	0.42
1:B:665:CYS:O	1:B:669:GLU:HB3	2.19	0.42
1:B:796:ALA:O	1:B:799:GLN:HB3	2.19	0.42
1:A:168:LEU:HD22	1:A:180:VAL:HG12	1.98	0.42
1:A:355:ILE:O	1:A:358:ARG:HB2	2.20	0.42
1:A:77:LYS:HA	1:A:97:VAL:O	2.20	0.42
1:A:853:ARG:HG2	1:A:853:ARG:NH1	2.34	0.42
1:B:342:ILE:O	1:B:342:ILE:HG22	2.19	0.42
1:A:730:ASP:OD1	1:A:737:GLY:N	2.45	0.42
1:A:97:VAL:HG21	1:A:105:VAL:HG22	2.01	0.42
1:B:405:ARG:NH1	1:B:438:SER:HA	2.34	0.42
1:B:570:THR:OG1	1:B:573:GLU:HG3	2.20	0.42
1:B:763:LYS:HG3	1:B:772:ILE:HD11	2.02	0.42
1:B:782:PHE:CD1	1:B:786:PHE:CE1	2.93	0.42
1:A:199:TYR:HE2	1:A:201:ALA:HB2	1.83	0.42
1:A:216:THR:HG23	1:A:451:LYS:HB3	2.01	0.42
1:A:484:LEU:HB3	1:A:882:LEU:HD11	2.01	0.42
1:A:598:LEU:HD13	1:A:649:LEU:HD13	2.01	0.42
1:A:639:ASP:O	1:A:643:ARG:HG3	2.20	0.42
1:A:684:ALA:O	1:A:707:MET:HB2	2.18	0.42
1:B:266:ASP:HA	1:B:292:LEU:HD12	2.01	0.42
1:B:693:VAL:HG12	1:B:693:VAL:O	2.20	0.42
5:A:1007:CIT:O3	5:A:1007:CIT:O7	2.37	0.42
1:A:61:VAL:HG12	1:A:63:MET:HG2	2.01	0.42
1:B:211:VAL:HA	1:B:237:CYS:SG	2.59	0.42
1:B:275:THR:O	1:B:277:PHE:N	2.53	0.42
1:B:492:ARG:NH2	1:B:844:LYS:HG3	2.34	0.42
1:B:579:VAL:HA	1:B:582:ILE:CG1	2.49	0.42
1:B:639:ASP:O	1:B:643:ARG:HG3	2.19	0.42
1:B:728:LEU:HD23	1:B:728:LEU:HA	1.83	0.42
1:A:168:LEU:CD2	1:A:180:VAL:CG1	2.95	0.42
1:B:758:LEU:O	1:B:759:ILE:C	2.57	0.42
1:A:168:LEU:HD22	1:A:180:VAL:CG1	2.50	0.42
1:A:347:GLU:OE2	1:A:347:GLU:CA	2.65	0.42
1:A:398:ARG:HG3	1:A:406:LEU:HB2	2.01	0.42
1:A:67:PHE:CE2	1:A:161:SER:C	2.93	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:225:GLU:C	1:B:226:VAL:HG23	2.40	0.42
1:B:107:MET:HE2	1:B:451:LYS:HG3	2.00	0.42
1:B:545:ILE:HG23	1:B:553:VAL:HG22	2.00	0.42
1:B:669:GLU:HA	1:B:670:PRO:HD2	1.79	0.42
1:A:171:TRP:NE1	1:A:177:ALA:N	2.56	0.42
1:A:486:GLU:O	1:A:490:ARG:HG3	2.20	0.42
1:B:683:ASN:HB3	2:B:1003:BGC:H5	2.02	0.42
1:B:46:GLU:HG3	1:B:264:PHE:CE1	2.55	0.42
1:B:22:ILE:HD11	1:B:370:SER:HB3	2.02	0.42
1:B:489:LYS:O	1:B:492:ARG:HB3	2.20	0.42
1:B:583:SER:HB2	1:B:647:PHE:CE2	2.51	0.42
1:B:795:LEU:HD11	1:B:799:GLN:HG2	2.01	0.42
1:A:245:ILE:HD11	1:A:257:ILE:CG1	2.50	0.41
1:A:378:VAL:O	1:A:381:ARG:HB3	2.20	0.41
1:A:510:LYS:HD3	1:A:510:LYS:HA	1.61	0.41
1:A:652:VAL:O	1:A:653:ALA:HB2	2.20	0.41
1:A:795:LEU:CD1	1:A:799:GLN:HG2	2.39	0.41
1:B:249:GLU:HB3	1:B:797:LEU:HD12	2.01	0.41
1:B:853:ARG:HA	1:B:885:LYS:O	2.20	0.41
1:A:147:LYS:HG2	1:A:147:LYS:H	1.47	0.41
1:A:615:ILE:HA	1:A:631:HIS:O	2.20	0.41
1:B:119:VAL:CG1	1:B:174:ARG:O	2.68	0.41
1:B:649:LEU:CD1	1:B:649:LEU:C	2.87	0.41
1:B:712:PHE:HE1	1:B:717:CYS:HG	1.63	0.41
1:B:797:LEU:HD11	1:B:817:ILE:HD11	2.01	0.41
1:B:856:VAL:O	1:B:856:VAL:HG13	2.21	0.41
1:B:897:SER:O	1:B:898:GLY:C	2.57	0.41
1:A:81:ILE:HG13	1:A:148:LEU:HD13	2.03	0.41
1:A:230:ILE:HB	1:A:417:TYR:HB2	2.01	0.41
1:A:607:GLN:HB2	1:A:617:ILE:HD11	2.02	0.41
1:A:515:PHE:HA	1:A:703:MET:SD	2.60	0.41
1:A:755:ARG:NH1	1:A:755:ARG:HG2	2.35	0.41
1:A:907:VAL:O	1:A:911:LEU:HG	2.19	0.41
1:B:174:ARG:HG2	1:B:300:MET:CE	2.50	0.41
1:B:263:ALA:O	1:B:266:ASP:CG	2.58	0.41
1:B:315:LYS:HG2	1:B:324:ILE:HD13	1.98	0.41
1:B:539:ARG:HB2	1:B:558:LYS:O	2.20	0.41
1:B:91:ARG:HH11	1:B:91:ARG:HB2	1.84	0.41
1:A:425:ARG:NH2	1:A:426:ARG:HE	2.18	0.41
1:A:407:ARG:HG2	1:A:439:ASP:HB2	2.02	0.41
1:A:693:VAL:C	1:A:695:MET:N	2.73	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:707:MET:O	1:A:708:GLU:HB2	2.21	0.41
1:A:331:ARG:HD2	1:B:588:TYR:CE2	2.55	0.41
1:B:306:VAL:O	1:B:309:ILE:N	2.53	0.41
1:B:384:ASN:HA	1:B:384:ASN:HD22	1.57	0.41
1:B:539:ARG:HH11	1:B:557:ASN:HD21	1.65	0.41
1:B:584:ASP:O	1:B:587:ASP:HB2	2.20	0.41
1:B:813:CYS:O	1:B:814:ASP:C	2.57	0.41
1:B:907:VAL:HG21	6:B:1158:HOH:O	2.20	0.41
1:A:107:MET:HE3	1:A:451:LYS:HE2	2.03	0.41
1:A:258:ASN:OD1	1:A:258:ASN:C	2.59	0.41
1:A:700:GLN:HA	1:A:700:GLN:HE21	1.85	0.41
1:A:790:ILE:H	1:A:790:ILE:HG12	1.74	0.41
1:A:85:LEU:O	1:A:155:SER:OG	2.38	0.41
1:B:700:GLN:HG3	6:B:1161:HOH:O	2.20	0.41
1:A:315:LYS:CA	1:A:324:ILE:HD11	2.42	0.41
1:A:724:HIS:HA	1:A:727:ARG:NH1	2.36	0.41
1:A:786:PHE:HD1	1:A:787:LEU:N	2.18	0.41
1:B:343:GLU:HG3	1:B:420:HIS:HE1	1.86	0.41
1:A:48:LYS:HE3	1:A:48:LYS:HB2	1.77	0.41
1:A:81:ILE:HB	1:A:150:VAL:HG22	2.01	0.41
1:A:912:ARG:HH11	1:A:912:ARG:HG3	1.84	0.41
1:B:217:CYS:SG	1:B:411:GLY:HA3	2.61	0.41
1:B:347:GLU:CB	1:B:351:ASN:HD21	2.22	0.41
1:B:418:LYS:HD2	6:B:1151:HOH:O	2.20	0.41
1:B:595:ARG:CD	1:B:648:ASP:OD2	2.69	0.41
1:B:664:THR:OG1	1:B:900:GLY:N	2.50	0.41
1:A:151:GLY:HA3	1:A:457:THR:OG1	2.21	0.41
1:B:266:ASP:HA	1:B:292:LEU:CD1	2.50	0.41
1:B:342:ILE:HG22	1:B:372:GLN:HG3	2.03	0.41
1:B:501:LYS:HB3	1:B:695:MET:SD	2.60	0.41
1:A:560:TYR:OH	1:A:585:PHE:HB2	2.21	0.41
1:A:619:TRP:CZ2	1:A:625:ALA:HB3	2.55	0.41
1:B:539:ARG:HB3	1:B:559:ILE:HD13	2.03	0.41
1:B:578:ILE:C	1:B:582:ILE:HG12	2.41	0.41
1:A:148:LEU:HD23	1:A:148:LEU:HA	1.81	0.41
1:A:255:MET:HG3	1:A:256:CYS:N	2.36	0.41
1:A:259:THR:O	1:A:260:GLU:HB2	2.20	0.41
1:B:213:THR:HG22	1:B:214:MET:N	2.36	0.41
1:B:376:THR:O	1:B:380:PHE:HB2	2.21	0.41
1:B:383:ALA:HA	1:B:423:TYR:CZ	2.56	0.41
1:A:208:ASN:O	1:A:211:VAL:N	2.54	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:265:GLY:C	1:A:267:ASP:H	2.25	0.40
1:A:93:LEU:HD11	1:A:450:GLY:CA	2.45	0.40
1:B:168:LEU:CD2	1:B:180:VAL:HG12	2.51	0.40
1:B:640:ALA:HB2	1:B:643:ARG:HH21	1.85	0.40
1:B:786:PHE:CE2	1:B:807:LEU:CD1	3.04	0.40
1:A:185:VAL:HG23	1:A:186:VAL:N	2.36	0.40
1:A:203:ILE:H	1:A:203:ILE:HD13	1.87	0.40
1:A:226:VAL:HB	1:A:410:VAL:HG22	2.04	0.40
1:A:480:THR:CG2	1:A:483:MET:CE	2.92	0.40
1:B:579:VAL:HA	1:B:582:ILE:HG12	2.03	0.40
1:B:637:LEU:HD23	1:B:651:VAL:HG21	2.04	0.40
1:A:361:VAL:O	1:A:361:VAL:CG2	2.70	0.40
1:A:80:PHE:HE2	1:A:458:ALA:HA	1.84	0.40
1:A:531:LEU:HD13	1:A:598:LEU:HD11	2.03	0.40
1:B:541:LEU:HD13	1:B:898:GLY:HA2	2.04	0.40
1:B:751:GLY:HA3	1:B:782:PHE:O	2.22	0.40
1:A:683:ASN:OD1	1:A:684:ALA:N	2.51	0.40
1:A:809:LEU:HD23	1:A:809:LEU:HA	1.94	0.40
1:A:912:ARG:C	1:A:914:GLU:N	2.74	0.40
1:B:467:HIS:O	1:B:470:ILE:N	2.55	0.40
1:B:62:LYS:O	1:B:63:MET:HB2	2.21	0.40
1:B:772:ILE:O	1:B:773:SER:C	2.59	0.40
1:B:831:ALA:HA	1:B:871:PHE:CZ	2.55	0.40
1:A:142:LYS:HB3	1:A:142:LYS:HE2	1.90	0.40
1:A:234:THR:H	1:A:294:GLU:HG3	1.86	0.40
1:A:467:HIS:O	1:A:468:ARG:C	2.60	0.40
1:A:488:LYS:O	1:A:491:MET:HB3	2.22	0.40
1:A:691:LYS:CA	1:A:699:ASP:HB2	2.47	0.40
1:B:339:VAL:HG12	1:B:339:VAL:O	2.22	0.40
1:B:230:ILE:CD1	1:B:386:VAL:HG11	2.43	0.40
1:B:422:GLN:HB3	1:B:426:ARG:NE	2.37	0.40
1:B:579:VAL:CG2	1:B:640:ALA:HB3	2.51	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	897/917 (98%)	794 (88%)	97 (11%)	6 (1%)	25	67
1	B	897/917 (98%)	777 (87%)	114 (13%)	6 (1%)	25	67
All	All	1794/1834 (98%)	1571 (88%)	211 (12%)	12 (1%)	25	67

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	163	ILE
1	A	251	ASP
1	A	694	GLU
1	A	307	ARG
1	B	276	GLU
1	B	307	ARG
1	B	781	ILE
1	B	694	GLU
1	B	717	CYS
1	A	155	SER
1	A	594	PRO
1	B	693	VAL

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	774/788 (98%)	726 (94%)	48 (6%)	21	58
1	B	774/788 (98%)	732 (95%)	42 (5%)	26	64
All	All	1548/1576 (98%)	1458 (94%)	90 (6%)	23	61

All (90) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	21	LYS
1	A	27	TYR
1	A	80	PHE
1	A	93	LEU
1	A	96	GLN
1	A	102	ASN
1	A	147	LYS
1	A	159	GLN
1	A	163	ILE
1	A	165	GLU
1	A	174	ARG
1	A	202	ASN
1	A	203	ILE
1	A	208	ASN
1	A	213	THR
1	A	222	GLN
1	A	232	THR
1	A	249	GLU
1	A	261	TRP
1	A	269	SER
1	A	281	ILE
1	A	305	LEU
1	A	321	GLU
1	A	358	ARG
1	A	399	ASP
1	A	408	THR
1	A	422	GLN
1	A	481	LYS
1	A	508	VAL
1	A	512	LEU
1	A	550	LYS
1	A	565	GLU
1	A	566	ILE
1	A	570	THR
1	A	596	MET
1	A	609	THR
1	A	665	CYS
1	A	703	MET
1	A	709	TRP
1	A	714	ASP
1	A	767	LEU
1	A	769	ARG
1	A	781	ILE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	786	PHE
1	A	792	SER
1	A	810	ASN
1	A	854	LEU
1	A	887	ASN
1	B	41	THR
1	B	93	LEU
1	B	99	HIS
1	B	102	ASN
1	B	114	THR
1	B	116	GLU
1	B	147	LYS
1	B	170	THR
1	B	213	THR
1	B	249	GLU
1	B	261	TRP
1	B	281	ILE
1	B	318	LEU
1	B	320	PHE
1	B	321	GLU
1	B	345	ASN
1	B	346	LYS
1	B	347	GLU
1	B	379	SER
1	B	380	PHE
1	B	382	SER
1	B	405	ARG
1	B	424	SER
1	B	432	ARG
1	B	437	ASP
1	B	481	LYS
1	B	531	LEU
1	B	562	ILE
1	B	591	ILE
1	B	669	GLU
1	B	703	MET
1	B	709	TRP
1	B	721	ILE
1	B	769	ARG
1	B	771	GLN
1	B	775	THR
1	B	777	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	786	PHE
1	B	798	LEU
1	B	805	GLN
1	B	854	LEU
1	B	872	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (46) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	99	HIS
1	A	102	ASN
1	A	104	ASN
1	A	125	GLN
1	A	159	GLN
1	A	190	ASN
1	A	208	ASN
1	A	258	ASN
1	A	373	HIS
1	A	384	ASN
1	A	400	ASN
1	A	466	GLN
1	A	506	ASN
1	A	557	ASN
1	A	700	GLN
1	A	771	GLN
1	A	799	GLN
1	A	805	GLN
1	A	806	GLN
1	A	810	ASN
1	A	887	ASN
1	B	18	GLN
1	B	98	ASN
1	B	99	HIS
1	B	120	HIS
1	B	125	GLN
1	B	129	HIS
1	B	202	ASN
1	B	351	ASN
1	B	384	ASN
1	B	400	ASN
1	B	420	HIS
1	B	466	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	469	GLN
1	B	502	GLN
1	B	506	ASN
1	B	557	ASN
1	B	607	GLN
1	B	771	GLN
1	B	799	GLN
1	B	805	GLN
1	B	806	GLN
1	B	832	GLN
1	B	848	ASN
1	B	870	HIS
1	B	887	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 14 ligands modelled in this entry, 4 are monoatomic - leaving 10 for Mogul analysis.

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	$\# Z > 2$
2	BGC	A	1001	-	12,12,12	0.38	0	17,17,17	0.99	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	0WK	A	1002	-	15,15,15	0.45	0	21,22,22	0.92	0
2	BGC	A	1003	-	12,12,12	0.36	0	17,17,17	1.44	2 (11%)
3	0WK	A	1004	-	15,15,15	0.45	0	21,22,22	0.78	0
5	CIT	A	1007	-	3,12,12	1.24	0	3,17,17	1.77	1 (33%)
2	BGC	B	1001	-	12,12,12	0.33	0	17,17,17	0.96	1 (5%)
3	0WK	B	1002	-	15,15,15	0.42	0	21,22,22	0.77	0
2	BGC	B	1003	-	12,12,12	0.46	0	17,17,17	1.37	2 (11%)
3	0WK	B	1004	-	15,15,15	0.41	0	21,22,22	0.84	0
5	CIT	B	1007	-	3,12,12	1.09	0	3,17,17	1.07	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
2	BGC	A	1001	-	-	0/2/22/22	0/1/1/1
3	0WK	A	1002	-	-	0/6/23/23	0/1/1/1
2	BGC	A	1003	-	-	0/2/22/22	0/1/1/1
3	0WK	A	1004	-	-	0/6/23/23	0/1/1/1
5	CIT	A	1007	-	-	0/6/16/16	0/0/0/0
2	BGC	B	1001	-	-	0/2/22/22	0/1/1/1
3	0WK	B	1002	-	-	0/6/23/23	0/1/1/1
2	BGC	B	1003	-	-	0/2/22/22	0/1/1/1
3	0WK	B	1004	-	-	0/6/23/23	0/1/1/1
5	CIT	B	1007	-	-	0/6/16/16	0/0/0/0

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1003	BGC	O5-C1-C2	-3.82	103.70	110.04
2	B	1003	BGC	O5-C1-C2	-3.66	103.96	110.04
2	A	1001	BGC	C6-C5-C4	-3.06	105.83	113.00
5	A	1007	CIT	C3-C4-C5	-3.01	110.25	114.95
2	B	1003	BGC	C1-O5-C5	-2.81	108.32	113.39
2	A	1003	BGC	C6-C5-C4	-2.66	106.78	113.00
2	B	1001	BGC	C1-O5-C5	-2.18	109.46	113.39

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

8 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1001	BGC	1	0
3	A	1002	0WK	2	0
2	A	1003	BGC	3	0
5	A	1007	CIT	1	0
2	B	1001	BGC	3	0
2	B	1003	BGC	1	0
3	B	1004	0WK	1	0
5	B	1007	CIT	4	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	899/917 (98%)	-0.30	4 (0%)	92 77	45, 76, 106, 143	0
1	B	899/917 (98%)	-0.35	2 (0%)	94 85	44, 76, 106, 143	0
All	All	1798/1834 (98%)	-0.32	6 (0%)	93 82	44, 76, 106, 143	0

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	16	ASP	3.6
1	A	29	MET	3.6
1	A	310	LEU	3.3
1	A	26	LEU	2.9
1	A	16	ASP	2.8
1	B	548	GLY	2.0

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

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

6.3 Carbohydrates [i](#)

There are no 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
5	CIT	B	1007	13/13	0.68	0.27	7.02	124,126,127,127	0
2	BGC	B	1001	12/12	0.91	0.31	3.99	78,79,79,80	0
5	CIT	A	1007	13/13	0.73	0.41	3.33	127,127,129,129	0
3	0WK	B	1004	15/15	0.96	0.29	3.07	60,60,62,62	0
2	BGC	A	1001	12/12	0.92	0.50	3.02	80,81,81,82	0
2	BGC	B	1003	12/12	0.92	0.26	2.61	53,55,56,56	0
3	0WK	B	1002	15/15	0.95	0.21	1.24	77,78,78,78	0
2	BGC	A	1003	12/12	0.95	0.21	0.65	51,54,55,56	0
3	0WK	A	1002	15/15	0.94	0.32	0.53	79,80,80,80	0
3	0WK	A	1004	15/15	0.96	0.22	0.40	59,60,61,61	0
4	NA	B	1005	1/1	0.90	0.12	-1.31	77,77,77,77	0
4	NA	B	1006	1/1	0.92	0.08	-1.82	54,54,54,54	0
4	NA	A	1005	1/1	0.89	0.09	-2.44	74,74,74,74	0
4	NA	A	1006	1/1	0.95	0.05	-3.45	55,55,55,55	0

6.5 Other polymers [i](#)

There are no such residues in this entry.