



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 12:22 AM GMT

PDB ID : 2A01
Title : Crystal Structure of Lipid-free Human Apolipoprotein A-I
Authors : Ajees, A.A.; Anantharamaiah, G.M.; Mishra, V.K.; Hussain, M.M.; Murthy, K.H.M.
Deposited on : 2005-06-15
Resolution : 2.40 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

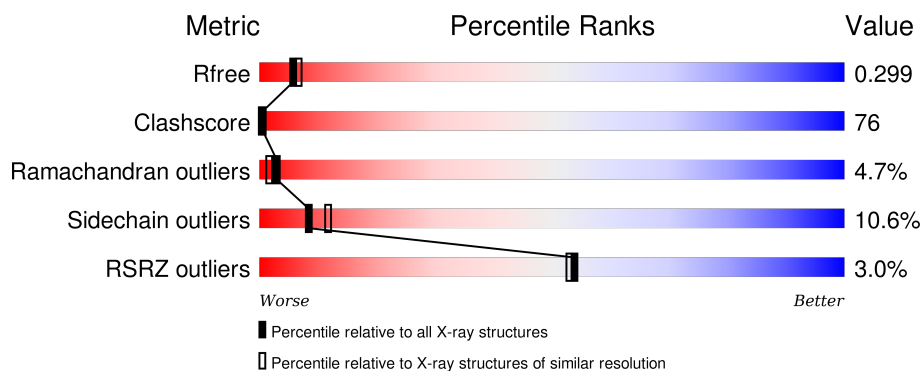
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	2919 (2.40-2.40)
Clashscore	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (2.40-2.40)
RSRZ outliers	91569	2928 (2.40-2.40)

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	243	<div> <div>3%</div> <div>61%</div> <div>32%</div> <div>5%</div> </div>
1	B	243	<div> <div>3%</div> <div>28%</div> <div>58%</div> <div>13%</div> </div>
1	C	243	<div> <div>2%</div> <div>33%</div> <div>49%</div> <div>15%</div> </div>

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	AC9	B	603	-	-	X	-
2	AC9	B	604	-	-	X	-
2	AC9	C	606	-	-	X	-
2	AC9	C	607	-	-	X	-

2 Entry composition [i](#)

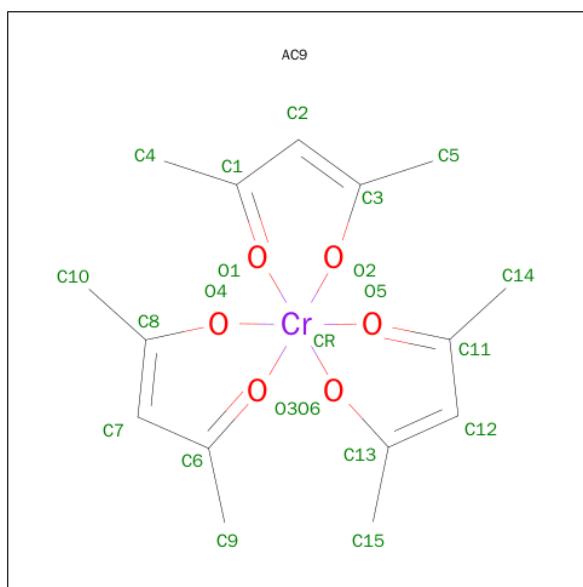
There are 3 unique types of molecules in this entry. The entry contains 6628 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Apolipoprotein A-I.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	243	Total	C	N	O	S	0	0	0
			1979	1241	347	388	3			
1	B	243	Total	C	N	O	S	0	0	0
			1979	1241	347	388	3			
1	C	243	Total	C	N	O	S	0	0	0
			1979	1241	347	388	3			

- Molecule 2 is TRISACETYLACETONATOCHROMIUM(III) (three-letter code: AC9) (formula: $C_{15}H_{21}CrO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	Cr	O	0	0
			22	15	1	6		
2	A	1	Total	C	Cr	O	0	0
			22	15	1	6		
2	B	1	Total	C	Cr	O	0	0
			22	15	1	6		

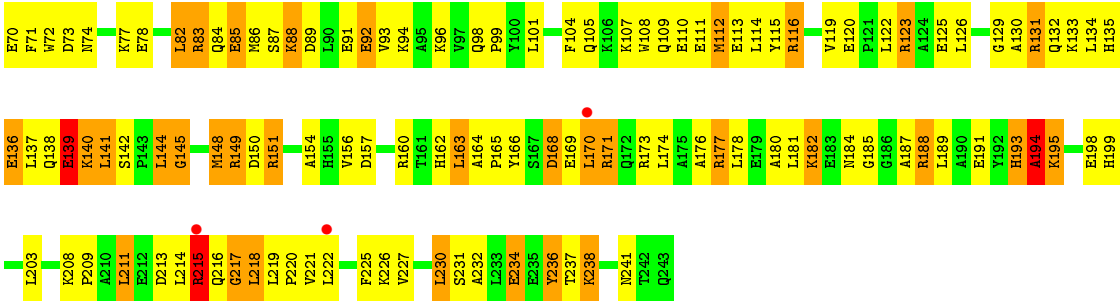
Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	B	1	Total	C	Cr	O	0	0
			22	15	1	6		
2	B	1	Total	C	Cr	O	0	0
			22	15	1	6		
2	C	1	Total	C	Cr	O	0	0
			22	15	1	6		
2	C	1	Total	C	Cr	O	0	0
			22	15	1	6		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	117	Total	O	0	0
			117	117		
3	B	190	Total	O	0	0
			190	190		
3	C	230	Total	O	0	0
			230	230		



4 Data and refinement statistics

Property	Value	Source
Space group	P 43	Depositor
Cell constants a, b, c, α , β , γ	127.78Å 127.78Å 130.13Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	91.20 – 2.40 29.57 – 2.35	Depositor EDS
% Data completeness (in resolution range)	100.0 (91.20-2.40) 100.0 (29.57-2.35)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.77 (at 2.36Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.228 , 0.249 0.285 , 0.299	Depositor DCC
R_{free} test set	4079 reflections (5.27%)	DCC
Wilson B-factor (Å ²)	36.1	Xtriage
Anisotropy	0.052	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 139.7	EDS
Estimated twinning fraction	0.008 for -h,-l,-k 0.001 for -h,l,k 0.001 for l,-k,h 0.009 for -l,-k,-h 0.027 for h,-k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 86817 reflections	Xtriage
F_o, F_c correlation	0.84	EDS
Total number of atoms	6628	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.65% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² Theoretical 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: AC9

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	0.70	0/2014	1.17	22/2714 (0.8%)
1	B	0.37	0/2014	1.05	19/2714 (0.7%)
1	C	0.37	0/2014	1.14	32/2714 (1.2%)
All	All	0.50	0/6042	1.12	73/8142 (0.9%)

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

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

There are no bond length outliers.

All (73) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	194	ALA	N-CA-C	7.30	130.70	111.00
1	C	123	ARG	NE-CZ-NH2	7.10	123.85	120.30
1	C	188	ARG	NE-CZ-NH1	7.04	123.82	120.30
1	B	10	ARG	NE-CZ-NH2	7.03	123.81	120.30
1	C	193	HIS	C-N-CA	6.89	138.94	121.70
1	B	177	ARG	NE-CZ-NH2	6.87	123.73	120.30
1	C	215	ARG	NE-CZ-NH2	6.86	123.73	120.30
1	C	131	ARG	NE-CZ-NH1	6.80	123.70	120.30
1	C	83	ARG	NE-CZ-NH1	6.78	123.69	120.30
1	B	83	ARG	NE-CZ-NH1	6.74	123.67	120.30
1	C	61	ARG	NE-CZ-NH1	6.58	123.59	120.30
1	C	177	ARG	CD-NE-CZ	6.49	132.69	123.60
1	B	160	ARG	NE-CZ-NH1	6.47	123.54	120.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	149	ARG	NE-CZ-NH1	6.47	123.53	120.30
1	C	171	ARG	NE-CZ-NH1	6.43	123.52	120.30
1	C	151	ARG	NE-CZ-NH2	6.34	123.47	120.30
1	B	188	ARG	NE-CZ-NH1	6.28	123.44	120.30
1	A	29	TYR	CB-CG-CD2	6.23	124.74	121.00
1	C	116	ARG	NE-CZ-NH2	6.20	123.40	120.30
1	C	10	ARG	NE-CZ-NH2	6.19	123.40	120.30
1	B	145	GLY	N-CA-C	-6.15	97.73	113.10
1	B	5	GLN	N-CA-C	6.13	127.54	111.00
1	B	149	ARG	NE-CZ-NH2	6.12	123.36	120.30
1	B	215	ARG	NE-CZ-NH2	6.11	123.35	120.30
1	A	27	ARG	NE-CZ-NH1	5.97	123.28	120.30
1	C	10	ARG	CD-NE-CZ	5.96	131.94	123.60
1	C	7	PRO	C-N-CA	5.95	136.57	121.70
1	A	10	ARG	NE-CZ-NH1	5.89	123.24	120.30
1	A	215	ARG	NE-CZ-NH1	5.89	123.24	120.30
1	C	7	PRO	O-C-N	-5.88	113.29	122.70
1	A	61	ARG	NE-CZ-NH1	5.87	123.23	120.30
1	A	173	ARG	NE-CZ-NH1	5.86	123.23	120.30
1	A	131	ARG	NE-CZ-NH1	5.82	123.21	120.30
1	B	215	ARG	N-CA-CB	-5.81	100.14	110.60
1	A	160	ARG	NE-CZ-NH1	5.81	123.20	120.30
1	A	116	ARG	NE-CZ-NH1	5.80	123.20	120.30
1	A	151	ARG	NE-CZ-NH1	5.79	123.20	120.30
1	A	218	LEU	N-CA-C	5.77	126.59	111.00
1	A	149	ARG	NE-CZ-NH1	5.76	123.18	120.30
1	A	123	ARG	NE-CZ-NH1	5.75	123.17	120.30
1	A	177	ARG	NE-CZ-NH1	5.75	123.17	120.30
1	B	141	LEU	C-N-CA	5.72	136.01	121.70
1	A	153	ARG	NE-CZ-NH1	5.71	123.15	120.30
1	A	83	ARG	NE-CZ-NH1	5.68	123.14	120.30
1	B	149	ARG	CD-NE-CZ	5.66	131.52	123.60
1	A	171	ARG	NE-CZ-NH1	5.65	123.12	120.30
1	C	194	ALA	O-C-N	-5.55	113.82	122.70
1	C	116	ARG	CD-NE-CZ	5.53	131.34	123.60
1	A	86	MET	CA-CB-CG	5.52	122.69	113.30
1	B	215	ARG	CD-NE-CZ	5.51	131.32	123.60
1	B	145	GLY	CA-C-O	5.46	130.42	120.60
1	B	188	ARG	CD-NE-CZ	5.45	131.23	123.60
1	A	188	ARG	NE-CZ-NH1	5.44	123.02	120.30
1	C	171	ARG	CD-NE-CZ	5.40	131.16	123.60
1	C	149	ARG	CD-NE-CZ	5.35	131.08	123.60

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	217	GLY	N-CA-C	5.29	126.33	113.10
1	C	151	ARG	CD-NE-CZ	5.26	130.97	123.60
1	B	215	ARG	N-CA-C	5.25	125.18	111.00
1	B	160	ARG	CD-NE-CZ	5.25	130.95	123.60
1	C	194	ALA	N-CA-CB	-5.22	102.79	110.10
1	C	123	ARG	CD-NE-CZ	5.19	130.86	123.60
1	A	188	ARG	CD-NE-CZ	5.16	130.83	123.60
1	C	61	ARG	CD-NE-CZ	5.16	130.83	123.60
1	B	177	ARG	CD-NE-CZ	5.13	130.78	123.60
1	C	8	TRP	N-CA-C	5.09	124.74	111.00
1	A	177	ARG	CD-NE-CZ	5.08	130.71	123.60
1	C	131	ARG	CD-NE-CZ	5.07	130.70	123.60
1	C	145	GLY	C-N-CA	5.06	134.36	121.70
1	B	83	ARG	CD-NE-CZ	5.06	130.69	123.60
1	C	215	ARG	CD-NE-CZ	5.06	130.68	123.60
1	C	140	LYS	N-CA-C	5.03	124.58	111.00
1	C	83	ARG	CD-NE-CZ	5.03	130.64	123.60
1	A	217	GLY	C-N-CA	5.02	134.25	121.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	35	GLY	Mainchain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1979	0	1968	109	16
1	B	1979	0	1967	435	5
1	C	1979	0	1968	390	2
2	A	44	0	42	13	0
2	B	66	0	63	60	0
2	C	44	0	42	24	0
3	A	117	0	0	39	2
3	B	190	0	0	69	11

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	230	0	0	80	0
All	All	6628	0	6050	921	18

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 76.

All (921) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:4:PRO:HA	1:C:86:MET:SD	1.29	1.69
1:B:8:TRP:CE3	1:B:11:VAL:HG21	1.31	1.62
1:B:92:GLU:CG	1:B:189:LEU:HD23	1.25	1.61
1:C:237:THR:HB	1:C:238:LYS:NZ	1.18	1.46
1:B:211:LEU:HD12	1:B:221:VAL:CG1	1.50	1.41
1:B:8:TRP:CE3	1:B:11:VAL:CG2	2.05	1.40
1:B:122:LEU:HD12	1:B:162:HIS:CB	1.53	1.38
1:C:214:LEU:CD2	1:C:216:GLN:HE21	1.35	1.37
1:C:8:TRP:CB	1:C:12:LYS:HE3	1.55	1.36
1:B:219:LEU:CG	1:C:226:LYS:HE3	1.55	1.35
1:A:171:ARG:NH1	1:A:172:GLN:HB2	1.38	1.35
1:B:8:TRP:CZ3	1:B:11:VAL:HG21	1.60	1.34
1:B:92:GLU:CG	1:B:189:LEU:CD2	2.08	1.32
1:C:36:SER:O	1:C:40:LYS:HB2	1.30	1.32
1:C:4:PRO:CA	1:C:86:MET:SD	2.18	1.31
1:B:92:GLU:HG2	1:B:189:LEU:CD2	1.58	1.31
1:C:56:THR:O	1:C:60:LEU:HD23	1.23	1.30
1:C:163:LEU:O	1:C:163:LEU:HD13	1.25	1.29
1:B:3:PRO:HB2	1:B:4:PRO:CD	1.58	1.26
1:C:13:ASP:O	1:C:17:VAL:HG23	1.31	1.26
1:B:173:ARG:NH2	1:B:173:ARG:HB3	1.48	1.26
1:B:226:LYS:O	1:B:230:LEU:HD13	1.32	1.26
1:C:170:LEU:O	1:C:174:LEU:HD13	1.12	1.24
1:B:36:SER:O	1:B:40:LYS:HD3	1.26	1.24
1:C:26:GLY:O	1:C:30:VAL:HG23	1.35	1.24
1:B:46:LEU:HD12	1:B:50:TRP:CG	1.73	1.23
1:B:211:LEU:CD1	1:B:221:VAL:HG13	1.68	1.22
1:C:53:VAL:CG1	1:C:123:ARG:CD	2.17	1.22
1:B:174:LEU:HD12	1:B:175:ALA:N	1.57	1.19
1:B:83:ARG:CZ	1:B:84:GLN:HE22	1.53	1.19
1:B:44:LEU:CD2	1:B:47:LEU:HD12	1.72	1.18
1:C:237:THR:CB	1:C:238:LYS:HZ2	1.57	1.18

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:110:GLU:O	1:C:114:LEU:HD13	1.39	1.18
1:C:150:ASP:O	1:C:154:ALA:HB2	1.42	1.18
1:B:44:LEU:HD23	1:B:47:LEU:CD1	1.73	1.17
1:B:83:ARG:NH1	1:B:84:GLN:HE22	1.41	1.17
1:C:8:TRP:HB2	1:C:12:LYS:CE	1.75	1.15
1:A:226:LYS:HD2	1:C:219:LEU:HD13	1.23	1.14
1:B:114:LEU:HD11	1:B:118:LYS:HE3	1.20	1.14
1:C:82:LEU:HG	1:C:86:MET:HE1	1.26	1.14
1:B:3:PRO:CB	1:B:4:PRO:HD3	1.77	1.14
1:B:139:GLU:OE2	1:B:141:LEU:HD22	1.46	1.14
1:A:226:LYS:HD2	1:C:219:LEU:CD1	1.77	1.14
1:C:53:VAL:HG11	1:C:123:ARG:NE	1.61	1.14
1:C:15:ALA:O	1:C:19:VAL:HG22	1.48	1.14
1:B:46:LEU:HD12	1:B:50:TRP:CD1	1.83	1.13
1:B:46:LEU:HD12	1:B:50:TRP:CB	1.78	1.13
1:B:46:LEU:CD1	1:B:50:TRP:CD1	2.32	1.13
1:B:219:LEU:HG	1:C:226:LYS:HE3	1.17	1.13
1:B:195:LYS:HD3	2:B:604:AC9:H2	1.14	1.12
1:C:53:VAL:CG1	1:C:123:ARG:HD2	1.77	1.12
1:B:97:VAL:HG12	1:B:101:LEU:CD1	1.79	1.12
1:B:122:LEU:CD1	1:B:162:HIS:HB3	1.78	1.12
1:A:171:ARG:HH11	1:A:172:GLN:CB	1.62	1.12
1:C:82:LEU:HD23	1:C:86:MET:HB3	1.32	1.11
1:C:237:THR:CB	1:C:238:LYS:NZ	2.10	1.11
1:B:3:PRO:CB	1:B:4:PRO:CD	2.27	1.11
1:C:144:LEU:HD23	1:C:144:LEU:H	1.14	1.10
1:B:46:LEU:CD1	1:B:50:TRP:CG	2.34	1.10
1:C:53:VAL:HG11	1:C:123:ARG:CD	1.80	1.10
1:A:171:ARG:HD3	1:A:172:GLN:N	1.66	1.10
1:C:227:VAL:O	3:C:782:HOH:O	1.68	1.10
1:B:97:VAL:HG12	1:B:101:LEU:HD12	1.31	1.09
1:C:214:LEU:CD2	1:C:216:GLN:NE2	2.14	1.09
1:C:208:LYS:HG3	1:C:209:PRO:HD3	1.12	1.09
1:C:214:LEU:HD23	1:C:216:GLN:HE21	0.94	1.09
1:B:3:PRO:HG2	1:B:4:PRO:HD2	1.35	1.09
1:C:216:GLN:OE1	1:C:220:PRO:HG3	1.51	1.08
1:C:36:SER:HB2	1:C:40:LYS:CE	1.83	1.07
1:C:107:LYS:HG2	1:C:177:ARG:HD2	1.34	1.07
1:C:74:ASN:O	1:C:78:GLU:HG3	1.53	1.07
1:B:60:LEU:HD21	1:B:115:TYR:CE2	1.89	1.07
1:C:211:LEU:CD1	1:C:221:VAL:HG13	1.85	1.06

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:170:LEU:O	1:C:174:LEU:CD1	2.03	1.06
1:B:188:ARG:HG3	1:B:195:LYS:HE3	1.33	1.05
1:B:114:LEU:CD1	1:B:118:LYS:HE3	1.86	1.05
1:B:88:LYS:HE3	1:B:88:LYS:H	1.08	1.05
1:B:8:TRP:CZ3	1:B:11:VAL:CG2	2.32	1.04
1:B:92:GLU:CD	1:B:189:LEU:HB3	1.75	1.04
1:A:236:TYR:HA	1:A:239:LYS:HE2	1.35	1.04
1:B:195:LYS:HD3	2:B:604:AC9:C2	1.88	1.03
1:B:218:LEU:HD22	2:B:603:AC9:C7	1.86	1.03
1:C:53:VAL:CG1	1:C:123:ARG:NE	2.19	1.03
1:C:163:LEU:CD1	1:C:163:LEU:O	2.07	1.03
1:B:219:LEU:CD2	2:B:603:AC9:H92	1.89	1.03
1:C:110:GLU:O	1:C:114:LEU:CD1	2.05	1.03
1:B:92:GLU:HG2	1:B:189:LEU:HD23	1.21	1.03
1:B:102:ASP:O	1:B:106:LYS:HB2	1.58	1.02
1:C:17:VAL:O	1:C:21:VAL:HG23	1.60	1.02
1:B:40:LYS:HE2	1:B:44:LEU:HD13	1.35	1.02
1:B:122:LEU:HD12	1:B:162:HIS:HB3	1.03	1.02
1:B:219:LEU:HD22	2:B:603:AC9:C9	1.90	1.02
1:B:92:GLU:O	1:B:96:LYS:HB2	1.59	1.02
1:C:199:HIS:CE1	1:C:203:LEU:HD11	1.96	1.01
1:B:90:LEU:O	1:B:90:LEU:HD23	1.61	1.01
1:B:92:GLU:HG2	1:B:189:LEU:CB	1.90	1.00
1:C:211:LEU:HD13	1:C:221:VAL:HG13	1.38	1.00
1:B:8:TRP:HE3	1:B:11:VAL:CG2	1.68	1.00
1:B:173:ARG:HH21	1:B:173:ARG:CB	1.74	1.00
1:B:176:ALA:HB2	2:B:605:AC9:C15	1.92	0.99
1:B:14:LEU:HD11	1:B:71:PHE:CE1	1.98	0.99
1:B:46:LEU:HD12	1:B:50:TRP:HB2	1.38	0.99
1:B:226:LYS:HA	1:B:226:LYS:HE2	1.42	0.98
1:B:219:LEU:CD2	1:C:226:LYS:HE3	1.93	0.98
1:C:82:LEU:HG	1:C:86:MET:CE	1.92	0.98
1:C:53:VAL:HG11	1:C:123:ARG:HE	1.22	0.98
1:B:40:LYS:HE2	1:B:44:LEU:CD1	1.93	0.98
1:C:214:LEU:HD21	1:C:216:GLN:NE2	1.75	0.98
1:C:70:GLU:HG2	3:C:737:HOH:O	1.64	0.97
1:C:60:LEU:HD12	1:C:115:TYR:OH	1.65	0.97
1:B:226:LYS:O	1:B:230:LEU:CD1	2.13	0.97
1:B:115:TYR:HE1	1:B:170:LEU:HD22	1.28	0.97
1:C:8:TRP:O	1:C:12:LYS:CG	2.12	0.97
1:B:219:LEU:HD22	2:B:603:AC9:H92	0.97	0.97

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:215:ARG:HG2	3:C:685:HOH:O	1.65	0.97
1:C:14:LEU:HD12	1:C:178:LEU:HD11	1.45	0.96
1:B:122:LEU:CD1	1:B:162:HIS:CB	2.40	0.96
1:B:42:LEU:HD22	3:B:662:HOH:O	1.64	0.96
1:C:53:VAL:HG13	1:C:123:ARG:CD	1.89	0.96
2:B:603:AC9:C5	1:C:222:LEU:HD11	1.94	0.96
1:C:208:LYS:CG	1:C:209:PRO:HD3	1.96	0.95
1:A:239:LYS:HG3	3:A:613:HOH:O	1.66	0.95
1:C:36:SER:HB2	1:C:40:LYS:HE3	1.41	0.95
1:C:11:VAL:HG21	3:C:732:HOH:O	1.63	0.95
1:B:236:TYR:CZ	2:B:604:AC9:H92	2.01	0.95
1:A:70:GLU:HG3	3:A:666:HOH:O	1.64	0.95
1:C:208:LYS:HG3	1:C:209:PRO:CD	1.96	0.95
1:C:214:LEU:HD23	1:C:216:GLN:NE2	1.78	0.95
1:B:92:GLU:HG3	1:B:189:LEU:HD23	0.97	0.95
1:C:56:THR:O	1:C:60:LEU:CD2	2.15	0.94
1:C:86:MET:HE2	3:C:825:HOH:O	1.65	0.94
1:B:92:GLU:CG	1:B:189:LEU:HB3	1.96	0.94
1:C:148:MET:HE2	3:C:835:HOH:O	1.65	0.94
1:B:173:ARG:HH21	1:B:173:ARG:HB3	1.20	0.94
1:B:174:LEU:HD12	1:B:175:ALA:H	1.17	0.94
1:B:86:MET:O	1:B:88:LYS:CE	2.15	0.94
1:C:214:LEU:HD21	1:C:216:GLN:HE21	1.29	0.94
1:B:42:LEU:H	1:B:42:LEU:HD23	1.33	0.94
1:B:86:MET:O	1:B:88:LYS:HE2	1.68	0.94
1:C:184:ASN:OD1	2:C:606:AC9:H53	1.67	0.94
1:B:90:LEU:O	1:B:93:VAL:HG23	1.68	0.93
1:C:132:GLN:O	1:C:136:GLU:HG2	1.69	0.93
1:B:26:GLY:HA2	1:B:29:TYR:HB2	1.50	0.93
1:B:176:ALA:HB2	2:B:605:AC9:H151	1.48	0.93
1:C:82:LEU:CG	1:C:86:MET:HE1	1.99	0.93
1:A:238:LYS:HD3	3:A:610:HOH:O	1.69	0.93
1:B:219:LEU:HG	1:C:226:LYS:CE	1.97	0.93
1:C:230:LEU:HD13	1:C:230:LEU:O	1.69	0.93
1:B:211:LEU:CD1	1:B:221:VAL:CG1	2.35	0.93
1:C:150:ASP:HA	3:C:812:HOH:O	1.67	0.93
1:B:115:TYR:CE1	1:B:170:LEU:HD22	2.03	0.93
1:C:8:TRP:HB2	1:C:12:LYS:HE3	0.93	0.92
1:B:83:ARG:NH1	1:B:84:GLN:NE2	2.17	0.92
1:B:97:VAL:CG1	1:B:101:LEU:HD11	1.98	0.92
1:B:72:TRP:HH2	1:B:105:GLN:HG3	1.34	0.92

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:10:ARG:HB2	1:B:71:PHE:CE1	2.03	0.92
1:B:92:GLU:HG3	1:B:189:LEU:CD2	1.85	0.92
1:C:13:ASP:O	1:C:17:VAL:CG2	2.16	0.92
1:B:122:LEU:HD12	1:B:162:HIS:HB2	1.52	0.92
1:C:227:VAL:N	3:C:701:HOH:O	2.03	0.92
1:B:236:TYR:OH	2:B:604:AC9:H92	1.69	0.92
1:B:133:LYS:HZ3	1:B:133:LYS:HB2	1.35	0.92
1:B:189:LEU:N	1:B:189:LEU:HD12	1.84	0.92
1:C:234:GLU:O	1:C:238:LYS:HD2	1.68	0.92
1:C:45:LYS:HB3	3:C:654:HOH:O	1.67	0.92
1:C:26:GLY:O	1:C:30:VAL:CG2	2.17	0.91
1:A:218:LEU:HD22	2:B:603:AC9:H151	1.52	0.91
1:B:83:ARG:HD2	1:B:84:GLN:OE1	1.71	0.91
1:C:144:LEU:H	1:C:144:LEU:CD2	1.83	0.91
1:B:2:GLU:HB2	3:B:638:HOH:O	1.69	0.91
1:B:26:GLY:O	1:B:30:VAL:HG13	1.70	0.91
1:C:82:LEU:HD23	1:C:86:MET:CB	2.00	0.90
1:C:237:THR:HB	1:C:238:LYS:HZ1	1.32	0.90
2:B:603:AC9:H52	1:C:222:LEU:HD11	1.53	0.90
1:C:62:GLU:HB2	3:C:657:HOH:O	1.69	0.90
1:B:218:LEU:CD2	2:B:603:AC9:H7	2.02	0.90
1:B:199:HIS:CD2	2:B:604:AC9:H52	2.06	0.90
1:A:223:GLU:HA	3:A:626:HOH:O	1.70	0.90
1:C:53:VAL:HG11	1:C:123:ARG:HD2	1.43	0.90
1:B:3:PRO:HB2	1:B:4:PRO:HD3	0.90	0.90
1:B:88:LYS:H	1:B:88:LYS:CE	1.84	0.90
1:B:184:ASN:O	1:B:188:ARG:HB2	1.73	0.89
1:B:200:LEU:CD2	1:B:233:LEU:HD21	2.03	0.89
1:B:26:GLY:N	1:B:29:TYR:HD1	1.69	0.89
1:B:195:LYS:CD	2:B:604:AC9:H2	2.02	0.89
1:C:139:GLU:CD	1:C:140:LYS:H	1.75	0.89
1:B:92:GLU:HG2	1:B:189:LEU:CG	2.03	0.89
1:C:211:LEU:HD12	1:C:225:PHE:CE1	2.07	0.89
1:C:82:LEU:CG	1:C:86:MET:CE	2.51	0.89
1:C:8:TRP:O	1:C:12:LYS:HG3	1.73	0.89
1:B:83:ARG:CZ	1:B:84:GLN:NE2	2.35	0.89
1:B:60:LEU:HD21	1:B:115:TYR:HE2	1.38	0.88
1:C:188:ARG:CZ	2:C:606:AC9:H42	2.03	0.88
2:B:603:AC9:C4	1:C:219:LEU:HD23	2.03	0.88
1:C:53:VAL:HG13	1:C:123:ARG:HD2	1.47	0.88
1:B:40:LYS:CE	1:B:44:LEU:HD13	2.03	0.88

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:36:SER:HB2	1:C:40:LYS:HE2	1.54	0.88
1:C:82:LEU:HD21	1:C:86:MET:HG2	1.55	0.88
1:C:12:LYS:HE2	3:C:807:HOH:O	1.74	0.87
1:C:150:ASP:O	1:C:154:ALA:CB	2.23	0.87
1:B:138:GLN:HB3	3:B:687:HOH:O	1.74	0.87
1:C:182:LYS:HB3	1:C:182:LYS:NZ	1.90	0.87
1:B:26:GLY:H	1:B:29:TYR:HD1	0.91	0.87
1:B:46:LEU:HD13	1:B:50:TRP:CD1	2.10	0.87
1:B:3:PRO:CG	1:B:4:PRO:HD2	2.04	0.87
1:B:173:ARG:NH2	1:B:173:ARG:CB	2.31	0.87
1:B:36:SER:O	1:B:40:LYS:CD	2.18	0.87
1:B:236:TYR:CE1	2:B:604:AC9:H92	2.09	0.86
1:B:45:LYS:HD2	3:B:670:HOH:O	1.74	0.86
1:C:73:ASP:HB3	1:C:77:LYS:NZ	1.89	0.86
1:B:200:LEU:HD21	1:B:233:LEU:CD2	2.05	0.86
1:B:97:VAL:CG1	1:B:101:LEU:CD1	2.52	0.86
1:B:200:LEU:CD2	1:B:233:LEU:CD2	2.52	0.86
1:A:171:ARG:HD3	1:A:171:ARG:C	1.96	0.85
1:A:171:ARG:HH11	1:A:172:GLN:HB2	0.74	0.85
1:A:38:LEU:HB2	3:A:693:HOH:O	1.76	0.85
1:C:8:TRP:HB3	1:C:12:LYS:HE3	1.58	0.85
1:B:46:LEU:CD1	1:B:50:TRP:CB	2.53	0.85
1:C:15:ALA:O	1:C:19:VAL:CG2	2.24	0.85
1:C:237:THR:HB	1:C:238:LYS:CE	2.06	0.85
1:B:118:LYS:HD2	1:B:166:TYR:HB3	1.59	0.85
1:A:26:GLY:HA3	3:A:709:HOH:O	1.77	0.85
1:C:132:GLN:O	1:C:136:GLU:CG	2.25	0.85
2:C:607:AC9:H7	3:C:736:HOH:O	1.76	0.85
1:A:188:ARG:HH12	2:A:601:AC9:H152	1.42	0.85
1:B:116:ARG:O	1:B:119:VAL:HG12	1.77	0.85
1:B:92:GLU:OE1	1:B:189:LEU:HB3	1.77	0.84
1:B:6:SER:O	1:B:8:TRP:N	2.10	0.84
1:B:8:TRP:CE3	1:B:11:VAL:HG23	2.12	0.84
1:C:36:SER:O	1:C:40:LYS:CB	2.21	0.84
1:C:8:TRP:O	1:C:12:LYS:CD	2.26	0.83
1:B:218:LEU:CD2	2:B:603:AC9:C7	2.55	0.83
1:B:90:LEU:HD23	1:B:90:LEU:C	1.97	0.83
1:B:219:LEU:CD1	1:C:226:LYS:HE3	2.07	0.83
1:B:13:ASP:O	1:B:17:VAL:HG12	1.77	0.83
2:B:604:AC9:H143	3:B:718:HOH:O	1.78	0.83
1:B:226:LYS:HA	1:B:226:LYS:CE	2.08	0.83

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:240:LEU:HD21	3:B:758:HOH:O	1.78	0.83
1:B:10:ARG:HB2	1:B:71:PHE:HE1	1.42	0.83
1:C:148:MET:HB2	3:C:726:HOH:O	1.76	0.83
1:C:238:LYS:N	1:C:238:LYS:HE3	1.94	0.82
1:A:171:ARG:CD	1:A:172:GLN:N	2.40	0.82
1:C:19:VAL:HG11	3:C:746:HOH:O	1.79	0.82
1:B:92:GLU:CB	1:B:189:LEU:HD23	2.09	0.82
1:B:88:LYS:N	1:B:88:LYS:HE3	1.92	0.82
1:C:176:ALA:HB2	2:C:607:AC9:C15	2.10	0.82
1:A:240:LEU:HG	3:A:613:HOH:O	1.78	0.82
1:B:176:ALA:CB	2:B:605:AC9:H151	2.09	0.82
1:B:133:LYS:O	1:B:137:LEU:HB3	1.79	0.82
1:B:57:PHE:HZ	1:B:123:ARG:NH1	1.78	0.82
1:C:8:TRP:O	1:C:12:LYS:HD2	1.79	0.81
1:C:145:GLY:HA3	3:C:763:HOH:O	1.79	0.81
1:A:173:ARG:N	1:A:173:ARG:HD2	1.95	0.81
1:C:236:TYR:CE2	2:C:606:AC9:H92	2.15	0.81
1:A:202:THR:HG21	3:A:615:HOH:O	1.80	0.81
1:A:137:LEU:HB3	3:A:631:HOH:O	1.79	0.81
1:B:92:GLU:HG2	1:B:189:LEU:HB3	1.57	0.81
1:B:219:LEU:HB3	3:B:751:HOH:O	1.81	0.81
1:B:116:ARG:C	1:B:119:VAL:HG12	2.00	0.81
1:B:188:ARG:HG3	1:B:195:LYS:CE	2.10	0.81
1:B:82:LEU:HD23	1:B:86:MET:CB	2.11	0.81
1:A:171:ARG:NH1	1:A:172:GLN:CB	2.33	0.80
1:B:133:LYS:HB2	1:B:133:LYS:NZ	1.95	0.80
1:B:224:SER:HB3	3:B:649:HOH:O	1.80	0.80
1:C:73:ASP:O	1:C:77:LYS:HE2	1.82	0.80
1:B:151:ARG:O	1:B:155:HIS:HD2	1.65	0.80
1:B:54:THR:O	1:B:58:SER:HB3	1.79	0.80
1:B:72:TRP:CH2	1:B:105:GLN:HG3	2.15	0.80
1:B:139:GLU:OE2	1:B:141:LEU:CD2	2.27	0.80
1:C:176:ALA:HA	3:C:826:HOH:O	1.81	0.80
1:B:6:SER:N	1:B:7:PRO:HD2	1.97	0.80
1:B:133:LYS:O	1:B:137:LEU:CB	2.30	0.80
1:C:163:LEU:C	1:C:163:LEU:HD13	2.02	0.80
1:C:144:LEU:O	1:C:148:MET:HE3	1.82	0.80
1:C:132:GLN:O	1:C:136:GLU:CD	2.20	0.80
1:C:211:LEU:HD13	1:C:221:VAL:CG1	2.12	0.79
1:A:156:VAL:HA	3:A:675:HOH:O	1.82	0.79
1:B:98:GLN:HB3	1:B:99:PRO:HD3	1.65	0.79

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:89:ASP:HB3	1:C:92:GLU:HB2	1.64	0.79
1:B:44:LEU:HD23	1:B:47:LEU:HD12	0.85	0.79
1:B:219:LEU:CG	1:C:226:LYS:CE	2.50	0.79
1:C:83:ARG:HA	1:C:88:LYS:HG2	1.65	0.79
1:B:41:GLN:HB3	3:B:682:HOH:O	1.82	0.79
1:B:222:LEU:HD12	2:B:603:AC9:H7	1.63	0.79
1:B:218:LEU:HD21	2:B:603:AC9:H101	1.65	0.78
1:B:229:PHE:HB2	3:B:793:HOH:O	1.82	0.78
1:B:3:PRO:CG	1:B:4:PRO:CD	2.59	0.78
1:C:164:ALA:HB3	1:C:165:PRO:HD3	1.65	0.78
1:C:82:LEU:CD2	1:C:86:MET:HB3	2.12	0.78
1:C:82:LEU:HD11	1:C:86:MET:HE2	1.65	0.78
1:B:14:LEU:HD11	1:B:71:PHE:CZ	2.18	0.78
1:A:215:ARG:HD3	3:A:714:HOH:O	1.83	0.78
1:C:8:TRP:CB	1:C:12:LYS:CE	2.47	0.78
1:B:3:PRO:HG2	1:B:4:PRO:CD	2.13	0.77
1:C:211:LEU:HD12	1:C:225:PHE:CD1	2.18	0.77
1:C:211:LEU:HD13	1:C:221:VAL:HA	1.66	0.77
1:B:144:LEU:H	1:B:144:LEU:HD23	1.48	0.77
1:C:84:GLN:HB2	3:C:676:HOH:O	1.85	0.77
1:B:82:LEU:HD23	1:B:86:MET:HB2	1.67	0.77
1:C:44:LEU:HD11	3:C:706:HOH:O	1.84	0.77
1:B:143:PRO:HB3	3:B:720:HOH:O	1.83	0.77
1:C:144:LEU:O	1:C:148:MET:CE	2.33	0.77
1:B:6:SER:N	1:B:7:PRO:CD	2.47	0.77
1:B:114:LEU:O	1:B:114:LEU:HD13	1.84	0.77
1:C:199:HIS:HE1	1:C:203:LEU:HD11	1.46	0.77
1:C:4:PRO:O	1:C:86:MET:HE3	1.85	0.77
1:C:163:LEU:C	1:C:163:LEU:CD1	2.54	0.77
1:B:174:LEU:CD1	1:B:175:ALA:N	2.45	0.77
1:B:39:GLY:HA2	3:B:742:HOH:O	1.84	0.77
1:B:238:LYS:HG3	1:B:239:LYS:N	1.98	0.77
1:C:2:GLU:HG2	3:C:731:HOH:O	1.84	0.76
1:C:82:LEU:CD1	1:C:86:MET:CE	2.64	0.76
1:B:86:MET:O	1:B:88:LYS:N	2.18	0.76
1:C:234:GLU:O	1:C:238:LYS:CD	2.33	0.76
1:B:92:GLU:CG	1:B:189:LEU:CB	2.58	0.76
1:C:216:GLN:OE1	1:C:220:PRO:CG	2.33	0.76
1:B:103:ASP:HB3	1:B:181:LEU:HD11	1.68	0.75
1:C:82:LEU:CD2	1:C:86:MET:HG2	2.16	0.75
1:C:170:LEU:C	1:C:174:LEU:HD13	2.05	0.75

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:62:GLU:HG2	3:C:802:HOH:O	1.85	0.75
1:C:209:PRO:HA	3:C:656:HOH:O	1.86	0.75
1:A:226:LYS:CD	1:C:219:LEU:HD13	2.11	0.75
1:B:125:GLU:HB3	3:B:628:HOH:O	1.86	0.75
1:C:213:ASP:HA	3:C:709:HOH:O	1.87	0.75
1:C:78:GLU:HB3	3:C:625:HOH:O	1.85	0.75
1:A:94:LYS:HE2	3:A:629:HOH:O	1.87	0.75
1:B:8:TRP:HE3	1:B:11:VAL:HG23	1.46	0.74
1:B:179:GLU:HB3	3:B:740:HOH:O	1.86	0.74
1:C:211:LEU:HB3	1:C:221:VAL:HG13	1.67	0.74
1:B:211:LEU:HD12	1:B:221:VAL:HG13	0.79	0.74
1:B:92:GLU:O	1:B:96:LYS:CB	2.34	0.74
1:B:148:MET:CE	1:B:149:ARG:HD2	2.17	0.74
1:C:82:LEU:HD11	1:C:86:MET:CE	2.16	0.74
1:B:57:PHE:O	1:B:61:ARG:HB2	1.86	0.74
1:C:139:GLU:CD	1:C:140:LYS:N	2.41	0.73
1:C:144:LEU:HD23	1:C:144:LEU:N	1.96	0.73
1:B:92:GLU:CG	1:B:189:LEU:CG	2.64	0.73
1:B:46:LEU:CD1	1:B:50:TRP:HB2	2.18	0.73
1:B:60:LEU:CD2	1:B:115:TYR:CE2	2.70	0.73
1:C:36:SER:CB	1:C:40:LYS:HE3	2.16	0.73
1:B:185:GLY:O	1:B:189:LEU:HD13	1.88	0.73
1:B:98:GLN:HB3	1:B:99:PRO:CD	2.19	0.73
1:A:226:LYS:CD	1:C:219:LEU:CD1	2.64	0.73
1:C:222:LEU:O	1:C:226:LYS:HG3	1.88	0.73
1:B:10:ARG:CB	1:B:71:PHE:HE1	2.01	0.73
1:C:236:TYR:CE2	2:C:606:AC9:C9	2.72	0.73
1:A:230:LEU:HD23	1:A:231:SER:N	2.03	0.73
1:B:113:GLU:HB2	3:B:750:HOH:O	1.89	0.72
1:B:222:LEU:HD12	2:B:603:AC9:C7	2.18	0.72
1:B:189:LEU:N	1:B:189:LEU:CD1	2.53	0.72
1:B:173:ARG:HB3	1:B:173:ARG:CZ	2.17	0.72
1:C:176:ALA:CA	2:C:607:AC9:H151	2.19	0.72
1:C:214:LEU:O	1:C:216:GLN:N	2.23	0.72
1:B:221:VAL:HG21	3:B:778:HOH:O	1.90	0.72
1:B:78:GLU:O	1:B:82:LEU:HD12	1.88	0.72
1:C:73:ASP:HB3	1:C:77:LYS:HZ3	1.54	0.72
1:C:231:SER:HB3	3:C:782:HOH:O	1.90	0.72
1:A:239:LYS:HE3	3:A:690:HOH:O	1.89	0.72
1:B:147:GLU:O	1:B:151:ARG:CD	2.38	0.72
1:B:38:LEU:CD2	1:B:156:VAL:HG21	2.19	0.72

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:227:VAL:CA	3:C:701:HOH:O	2.38	0.71
1:B:200:LEU:HD23	1:B:233:LEU:HD21	1.70	0.71
1:C:29:TYR:HB3	1:C:33:PHE:CE1	2.25	0.71
1:C:198:GLU:HA	3:C:817:HOH:O	1.89	0.71
1:B:219:LEU:HD21	1:C:226:LYS:HE3	1.70	0.71
1:B:107:LYS:HZ3	1:B:174:LEU:N	1.88	0.71
1:A:218:LEU:HB3	2:B:603:AC9:H12	1.71	0.71
1:B:15:ALA:O	1:B:19:VAL:HG23	1.91	0.71
1:B:86:MET:O	1:B:88:LYS:CD	2.39	0.71
1:B:214:LEU:HD11	3:B:757:HOH:O	1.91	0.71
1:B:60:LEU:CD2	1:B:115:TYR:HE2	2.01	0.71
1:C:230:LEU:CD1	1:C:230:LEU:O	2.38	0.70
1:B:218:LEU:HD22	2:B:603:AC9:H7	1.63	0.70
1:A:188:ARG:HD2	2:A:601:AC9:H41	1.72	0.70
1:A:220:PRO:HB2	3:A:673:HOH:O	1.92	0.70
1:C:134:LEU:HD21	3:C:663:HOH:O	1.91	0.70
1:B:176:ALA:HB2	2:B:605:AC9:H153	1.73	0.70
1:B:121:PRO:HG3	3:B:783:HOH:O	1.91	0.70
1:B:240:LEU:HD11	3:B:758:HOH:O	1.92	0.70
1:B:189:LEU:HG	3:B:632:HOH:O	1.91	0.69
1:B:218:LEU:HA	3:B:684:HOH:O	1.91	0.69
1:B:118:LYS:HB3	3:B:672:HOH:O	1.92	0.69
1:A:82:LEU:HA	1:A:86:MET:HG2	1.75	0.69
1:A:171:ARG:HD3	1:A:172:GLN:CA	2.23	0.68
1:B:200:LEU:HD21	1:B:233:LEU:HD22	1.74	0.68
1:C:73:ASP:HB3	1:C:77:LYS:HZ1	1.59	0.68
1:B:142:SER:OG	1:B:143:PRO:HD2	1.93	0.68
2:B:603:AC9:H43	1:C:219:LEU:HD23	1.74	0.68
1:B:219:LEU:HD11	1:C:226:LYS:CE	2.22	0.68
1:B:57:PHE:CZ	1:B:123:ARG:NH1	2.60	0.68
1:A:46:LEU:HD21	3:A:694:HOH:O	1.92	0.68
1:C:13:ASP:HB3	3:C:717:HOH:O	1.94	0.68
1:C:211:LEU:CD1	1:C:221:VAL:HA	2.22	0.68
1:C:211:LEU:CD1	1:C:225:PHE:CE1	2.76	0.68
1:B:195:LYS:HE2	2:B:604:AC9:H41	1.76	0.68
1:C:45:LYS:HE3	3:C:654:HOH:O	1.94	0.68
1:C:39:GLY:HA3	3:C:770:HOH:O	1.91	0.68
1:B:50:TRP:O	1:B:54:THR:HG22	1.93	0.67
1:B:132:GLN:O	1:B:136:GLU:HG2	1.94	0.67
1:B:219:LEU:CD1	1:C:226:LYS:CE	2.72	0.67
1:C:211:LEU:CD1	1:C:221:VAL:CG1	2.69	0.67

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:601:AC9:H43	3:A:639:HOH:O	1.93	0.67
1:C:182:LYS:HB3	1:C:182:LYS:HZ3	1.59	0.67
1:C:82:LEU:CD1	1:C:86:MET:HE1	2.24	0.67
1:B:11:VAL:HA	1:B:178:LEU:HD21	1.77	0.67
1:A:22:LEU:HD11	1:A:170:LEU:HD23	1.77	0.67
1:B:14:LEU:HD11	1:B:71:PHE:CD1	2.30	0.67
1:B:211:LEU:HD12	1:B:221:VAL:HG11	1.66	0.67
1:C:131:ARG:HA	3:C:631:HOH:O	1.94	0.67
1:B:42:LEU:H	1:B:42:LEU:CD2	2.06	0.67
1:C:232:ALA:O	1:C:236:TYR:CZ	2.48	0.67
1:B:10:ARG:CB	1:B:71:PHE:CE1	2.76	0.66
1:C:237:THR:C	1:C:238:LYS:HE3	2.15	0.66
1:B:219:LEU:HD23	1:B:219:LEU:N	2.10	0.66
1:B:93:VAL:HG13	3:B:618:HOH:O	1.93	0.66
2:C:607:AC9:H91	3:C:736:HOH:O	1.95	0.66
1:C:51:ASP:HB3	3:C:805:HOH:O	1.94	0.66
1:C:166:TYR:O	1:C:170:LEU:HD22	1.94	0.66
1:C:21:VAL:CG1	1:C:63:GLN:HE21	2.08	0.66
1:C:176:ALA:HA	2:C:607:AC9:H151	1.77	0.66
1:C:93:VAL:HB	3:C:679:HOH:O	1.96	0.66
1:B:147:GLU:O	1:B:151:ARG:HD2	1.96	0.66
1:B:86:MET:O	1:B:88:LYS:HD3	1.96	0.66
1:B:116:ARG:O	1:B:119:VAL:CG1	2.43	0.66
2:B:603:AC9:C5	1:C:222:LEU:CD1	2.73	0.65
1:C:9:ASP:O	1:C:13:ASP:OD2	2.13	0.65
1:C:17:VAL:HG11	3:C:813:HOH:O	1.95	0.65
2:C:607:AC9:H153	3:C:801:HOH:O	1.96	0.65
1:B:90:LEU:CD2	1:B:90:LEU:C	2.65	0.65
1:A:111:GLU:HG2	3:A:647:HOH:O	1.96	0.65
1:C:133:LYS:HA	1:C:137:LEU:HD12	1.78	0.65
1:B:47:LEU:HD21	3:B:773:HOH:O	1.96	0.65
1:B:139:GLU:HG2	1:B:140:LYS:H	1.61	0.65
1:B:97:VAL:HG13	1:B:101:LEU:HD11	1.78	0.65
1:B:42:LEU:HD11	3:B:680:HOH:O	1.97	0.64
1:C:108:TRP:HA	1:C:111:GLU:OE1	1.97	0.64
1:B:159:LEU:HD13	1:B:159:LEU:O	1.97	0.64
1:B:144:LEU:HD12	1:B:148:MET:HB3	1.79	0.64
1:B:222:LEU:CD1	2:B:603:AC9:H7	2.27	0.64
1:B:51:ASP:HA	1:B:54:THR:HG22	1.80	0.64
1:C:82:LEU:CG	1:C:86:MET:HE2	2.27	0.64
1:B:236:TYR:OH	2:B:604:AC9:C9	2.45	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:171:ARG:CD	1:A:171:ARG:C	2.56	0.64
1:B:21:VAL:CG2	1:B:63:GLN:CD	2.65	0.64
1:B:148:MET:HE1	1:B:149:ARG:HD2	1.79	0.64
1:B:92:GLU:HG2	1:B:189:LEU:HD22	1.73	0.64
1:B:10:ARG:HB2	1:B:71:PHE:CZ	2.32	0.64
1:B:195:LYS:CE	2:B:604:AC9:H41	2.27	0.64
1:C:21:VAL:HG13	1:C:63:GLN:HE21	1.62	0.64
2:B:603:AC9:H51	1:C:222:LEU:HD11	1.79	0.64
1:B:71:PHE:CE2	1:B:75:LEU:HD21	2.33	0.64
1:C:214:LEU:C	1:C:216:GLN:H	1.98	0.64
1:B:219:LEU:H	1:B:219:LEU:HD23	1.63	0.64
1:B:82:LEU:O	1:B:88:LYS:HD3	1.98	0.64
1:B:44:LEU:HA	3:B:715:HOH:O	1.97	0.64
1:B:86:MET:SD	1:B:86:MET:N	2.71	0.64
1:B:96:LYS:HE3	3:B:616:HOH:O	1.98	0.64
1:B:159:LEU:HD21	3:B:760:HOH:O	1.98	0.64
1:C:27:ARG:HD3	3:C:834:HOH:O	1.97	0.64
1:B:111:GLU:OE2	1:B:170:LEU:HD11	1.98	0.63
1:B:14:LEU:CD1	1:B:71:PHE:CE1	2.80	0.63
1:C:82:LEU:HA	1:C:86:MET:HB3	1.80	0.63
1:A:31:SER:HB3	3:A:695:HOH:O	1.98	0.63
1:B:44:LEU:HB3	1:B:47:LEU:HB2	1.78	0.63
1:C:53:VAL:CG1	1:C:123:ARG:HE	1.98	0.63
1:A:176:ALA:HA	2:A:602:AC9:H151	1.79	0.63
1:B:3:PRO:HG3	3:B:623:HOH:O	1.98	0.63
1:A:176:ALA:HB2	2:A:602:AC9:C15	2.28	0.63
1:C:109:GLN:O	1:C:113:GLU:HG3	1.98	0.63
1:B:188:ARG:HB3	1:B:189:LEU:HD12	1.81	0.63
1:B:219:LEU:HD21	1:C:226:LYS:CE	2.28	0.63
1:B:82:LEU:HD23	1:B:86:MET:HB3	1.81	0.63
1:C:145:GLY:HA2	1:C:148:MET:CE	2.28	0.62
1:B:38:LEU:HD23	1:B:156:VAL:HG21	1.80	0.62
1:B:139:GLU:CD	1:B:141:LEU:HD22	2.18	0.62
1:C:87:SER:HB3	3:C:754:HOH:O	1.97	0.62
1:C:130:ALA:HB2	3:C:738:HOH:O	1.99	0.62
1:B:42:LEU:O	1:B:44:LEU:HD12	1.99	0.62
1:C:112:MET:HE2	1:C:116:ARG:HH11	1.64	0.62
1:B:218:LEU:HD21	2:B:603:AC9:C10	2.29	0.62
1:A:188:ARG:NH1	2:A:601:AC9:H152	2.13	0.62
1:C:122:LEU:O	1:C:126:LEU:HG	1.98	0.62
1:C:82:LEU:CD2	1:C:86:MET:CG	2.78	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:24:ASP:O	1:B:27:ARG:N	2.25	0.62
1:C:168:ASP:O	1:C:171:ARG:HB3	2.00	0.62
1:B:222:LEU:HD11	2:B:603:AC9:H101	1.82	0.61
1:C:53:VAL:HG13	1:C:123:ARG:HD3	1.76	0.61
1:B:139:GLU:CG	1:B:140:LYS:H	2.11	0.61
1:A:236:TYR:CA	1:A:239:LYS:HE2	2.22	0.61
1:C:211:LEU:HD12	1:C:221:VAL:HG13	1.79	0.61
1:C:222:LEU:HG	3:C:729:HOH:O	2.00	0.61
1:B:111:GLU:OE2	1:B:170:LEU:CD1	2.49	0.61
1:B:147:GLU:O	1:B:151:ARG:HD3	1.98	0.61
1:B:151:ARG:O	1:B:155:HIS:CD2	2.52	0.61
1:B:229:PHE:CE2	3:B:719:HOH:O	2.53	0.61
1:C:216:GLN:CD	1:C:220:PRO:HG3	2.21	0.61
1:A:200:LEU:HD21	1:A:233:LEU:HD21	1.81	0.61
1:C:4:PRO:CB	1:C:86:MET:SD	2.89	0.61
1:B:199:HIS:NE2	2:B:604:AC9:H52	2.15	0.61
1:B:114:LEU:HD11	1:B:118:LYS:CE	2.13	0.61
1:C:82:LEU:CD1	1:C:86:MET:HE2	2.27	0.61
1:C:238:LYS:N	1:C:238:LYS:CE	2.64	0.61
1:C:188:ARG:CZ	2:C:606:AC9:C4	2.76	0.61
1:A:236:TYR:C	1:A:236:TYR:CD2	2.74	0.61
1:C:176:ALA:HB2	2:C:607:AC9:H151	1.82	0.61
2:B:603:AC9:H42	1:C:219:LEU:HD23	1.83	0.60
1:B:116:ARG:HA	1:B:119:VAL:CG1	2.31	0.60
1:C:122:LEU:HD13	1:C:162:HIS:CG	2.35	0.60
1:B:71:PHE:CE2	1:B:75:LEU:CD2	2.84	0.60
1:C:216:GLN:CD	1:C:220:PRO:CG	2.69	0.60
1:C:177:ARG:O	1:C:181:LEU:HB2	2.00	0.60
1:C:45:LYS:HG3	1:C:45:LYS:O	2.01	0.60
1:B:42:LEU:N	1:B:42:LEU:HD23	2.10	0.60
1:A:218:LEU:O	1:A:222:LEU:HG	2.02	0.60
1:C:82:LEU:HD21	1:C:86:MET:HE2	1.82	0.60
1:B:130:ALA:HA	1:B:133:LYS:HZ1	1.66	0.60
1:A:192:TYR:HA	3:A:652:HOH:O	2.02	0.60
1:B:226:LYS:CA	1:B:226:LYS:HE2	2.21	0.60
1:B:133:LYS:O	1:B:137:LEU:HB2	2.00	0.60
1:B:148:MET:SD	1:B:149:ARG:HD2	2.41	0.60
1:B:238:LYS:HG3	1:B:239:LYS:H	1.63	0.60
1:B:30:VAL:O	1:B:34:GLU:HB2	2.02	0.59
1:B:44:LEU:HG	3:B:715:HOH:O	2.01	0.59
1:C:148:MET:SD	1:C:149:ARG:N	2.73	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:235:GLU:HA	1:B:238:LYS:HG2	1.84	0.59
1:B:66:PRO:O	1:B:70:GLU:HG2	2.02	0.59
1:A:225:PHE:HE1	3:A:703:HOH:O	1.84	0.59
1:B:116:ARG:CA	1:B:119:VAL:HG12	2.33	0.59
1:A:240:LEU:CD1	3:A:690:HOH:O	2.51	0.58
1:C:237:THR:CB	1:C:238:LYS:HZ1	1.96	0.58
1:C:237:THR:HB	1:C:238:LYS:HZ2	0.74	0.58
1:C:236:TYR:HE2	2:C:606:AC9:C9	2.15	0.58
1:C:176:ALA:HB2	2:C:607:AC9:H153	1.85	0.58
1:C:110:GLU:O	1:C:114:LEU:HD12	2.00	0.58
1:B:21:VAL:HG21	1:B:63:GLN:CD	2.24	0.58
1:B:212:GLU:HG3	3:B:688:HOH:O	2.03	0.58
1:A:173:ARG:N	1:A:173:ARG:CD	2.65	0.58
1:C:65:GLY:HA3	3:C:761:HOH:O	2.03	0.58
1:C:193:HIS:O	1:C:195:LYS:HG3	2.04	0.58
1:B:102:ASP:O	1:B:106:LYS:CB	2.43	0.58
1:C:145:GLY:HA2	1:C:148:MET:HE3	1.86	0.58
1:C:112:MET:C	1:C:112:MET:SD	2.82	0.58
1:A:218:LEU:HD22	2:B:603:AC9:C15	2.31	0.57
1:B:51:ASP:HA	1:B:54:THR:CG2	2.33	0.57
1:B:135:HIS:HB2	1:B:136:GLU:OE1	2.04	0.57
1:A:169:GLU:O	1:A:173:ARG:HG2	2.04	0.57
1:B:60:LEU:HD21	1:B:115:TYR:CZ	2.39	0.57
1:C:176:ALA:CB	2:C:607:AC9:H151	2.33	0.57
1:C:112:MET:CE	1:C:116:ARG:HH11	2.17	0.57
1:C:49:ASN:N	1:C:49:ASN:HD22	2.02	0.57
1:C:216:GLN:HG3	1:C:216:GLN:O	2.04	0.57
1:B:107:LYS:NZ	1:B:174:LEU:HA	2.19	0.57
1:B:115:TYR:HE1	1:B:170:LEU:CD2	2.11	0.57
1:B:57:PHE:HZ	1:B:123:ARG:CZ	2.16	0.57
1:C:7:PRO:HG3	3:C:824:HOH:O	2.04	0.57
1:B:21:VAL:HG21	1:B:63:GLN:CG	2.35	0.57
1:C:93:VAL:CB	3:C:679:HOH:O	2.51	0.57
1:A:187:ALA:CB	1:A:198:GLU:OE1	2.53	0.57
1:B:6:SER:H	1:B:7:PRO:CD	2.16	0.57
1:C:164:ALA:HB3	1:C:165:PRO:CD	2.34	0.57
1:C:211:LEU:CG	1:C:225:PHE:HE1	2.18	0.57
1:B:212:GLU:HA	1:B:212:GLU:OE1	2.05	0.57
1:B:188:ARG:CB	1:B:189:LEU:HD12	2.35	0.57
1:C:8:TRP:O	1:C:12:LYS:CB	2.53	0.57
1:C:237:THR:CG2	1:C:238:LYS:HZ1	2.17	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:122:LEU:CD1	1:B:162:HIS:HB2	2.21	0.56
1:A:218:LEU:O	1:A:222:LEU:CG	2.53	0.56
1:A:218:LEU:O	1:A:222:LEU:HD11	2.05	0.56
1:B:40:LYS:HE2	1:B:44:LEU:HD12	1.85	0.56
1:B:83:ARG:CD	1:B:84:GLN:OE1	2.50	0.56
1:B:107:LYS:HZ1	1:B:174:LEU:HA	1.70	0.56
1:B:169:GLU:HG2	1:B:173:ARG:HE	1.70	0.56
1:C:134:LEU:CD1	1:C:151:ARG:HH21	2.19	0.56
1:B:229:PHE:CZ	3:B:719:HOH:O	2.52	0.56
1:C:82:LEU:HD11	3:C:825:HOH:O	2.05	0.56
1:B:65:GLY:N	1:B:66:PRO:HD2	2.21	0.56
1:C:108:TRP:O	1:C:111:GLU:HG2	2.06	0.56
1:C:182:LYS:HB3	1:C:182:LYS:HZ2	1.70	0.56
1:C:156:VAL:O	1:C:160:ARG:HG2	2.05	0.56
1:C:82:LEU:CD2	1:C:86:MET:CB	2.77	0.56
1:B:46:LEU:HB2	3:B:674:HOH:O	2.06	0.56
1:C:211:LEU:HD12	1:C:225:PHE:HE1	1.65	0.56
1:C:65:GLY:CA	3:C:761:HOH:O	2.54	0.56
1:C:176:ALA:O	1:C:180:ALA:HB3	2.06	0.56
1:B:188:ARG:C	1:B:189:LEU:HD12	2.26	0.55
1:B:184:ASN:O	1:B:188:ARG:CB	2.51	0.55
1:A:222:LEU:CD2	2:B:603:AC9:H151	2.36	0.55
1:A:176:ALA:CA	2:A:602:AC9:H151	2.36	0.55
1:B:86:MET:C	1:B:88:LYS:HE2	2.26	0.55
1:B:26:GLY:CA	1:B:29:TYR:HB2	2.29	0.55
1:C:8:TRP:HB3	1:C:12:LYS:HG3	1.87	0.55
1:B:196:ALA:HB2	1:B:240:LEU:HD22	1.88	0.55
1:B:145:GLY:CA	3:B:745:HOH:O	2.54	0.55
1:C:94:LYS:HD3	3:C:644:HOH:O	2.05	0.55
1:C:132:GLN:O	1:C:136:GLU:OE1	2.24	0.55
1:B:26:GLY:N	1:B:29:TYR:CD1	2.57	0.55
1:A:219:LEU:HD13	2:B:603:AC9:H143	1.88	0.55
1:B:110:GLU:O	1:B:114:LEU:HB2	2.07	0.55
1:C:120:GLU:CG	3:C:760:HOH:O	2.54	0.55
1:B:219:LEU:HA	2:B:603:AC9:H91	1.89	0.55
1:B:38:LEU:HD21	1:B:156:VAL:HG21	1.86	0.55
1:B:93:VAL:O	1:B:97:VAL:HG23	2.07	0.54
1:B:82:LEU:HA	1:B:86:MET:HB2	1.89	0.54
1:B:116:ARG:HA	1:B:119:VAL:HG12	1.90	0.54
1:C:53:VAL:HG12	1:C:123:ARG:NE	2.19	0.54
1:C:227:VAL:HA	3:C:701:HOH:O	2.04	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:230:LEU:C	1:C:230:LEU:CD1	2.75	0.54
1:C:232:ALA:O	1:C:236:TYR:CE1	2.61	0.54
1:C:211:LEU:HD13	1:C:221:VAL:CA	2.37	0.54
2:B:603:AC9:H2	1:C:218:LEU:HB3	1.89	0.54
1:B:219:LEU:HD11	1:C:226:LYS:HE3	1.85	0.54
1:B:173:ARG:HH21	1:B:173:ARG:HB2	1.68	0.54
1:B:90:LEU:HD12	3:B:627:HOH:O	2.08	0.54
1:C:164:ALA:CB	3:C:690:HOH:O	2.56	0.54
1:C:134:LEU:HD12	1:C:151:ARG:HH21	1.72	0.53
1:C:68:THR:HG22	1:C:108:TRP:CZ3	2.43	0.53
1:B:92:GLU:OE1	1:B:189:LEU:O	2.26	0.53
1:A:172:GLN:HG2	1:A:173:ARG:CZ	2.38	0.53
1:C:139:GLU:OE1	1:C:140:LYS:N	2.24	0.53
1:C:125:GLU:O	1:C:129:GLY:HA3	2.08	0.53
1:C:193:HIS:O	1:C:195:LYS:HE2	2.07	0.53
1:C:164:ALA:CB	3:C:752:HOH:O	2.56	0.53
1:A:207:ALA:HB2	3:A:649:HOH:O	2.08	0.53
1:B:199:HIS:HD2	2:B:604:AC9:H52	1.69	0.53
1:B:188:ARG:HB3	1:B:189:LEU:CD1	2.38	0.53
1:C:193:HIS:HB3	1:C:195:LYS:HE3	1.90	0.53
1:C:230:LEU:HD13	1:C:230:LEU:C	2.29	0.53
1:B:185:GLY:O	1:B:189:LEU:CD1	2.55	0.52
1:B:176:ALA:O	1:B:180:ALA:CB	2.58	0.52
1:C:29:TYR:HB3	1:C:33:PHE:CD1	2.44	0.52
1:C:17:VAL:CG1	3:C:813:HOH:O	2.54	0.52
1:B:46:LEU:HD11	1:B:50:TRP:CG	2.39	0.52
1:C:74:ASN:O	1:C:78:GLU:CG	2.42	0.52
1:C:185:GLY:O	1:C:189:LEU:HD23	2.09	0.52
1:C:112:MET:SD	1:C:113:GLU:N	2.82	0.52
1:B:114:LEU:CD1	1:B:114:LEU:C	2.78	0.52
1:B:109:GLN:HG3	3:B:710:HOH:O	2.08	0.52
1:A:226:LYS:HE3	1:C:219:LEU:HD12	1.91	0.52
1:B:88:LYS:HG2	1:B:88:LYS:O	2.08	0.52
1:B:103:ASP:CB	1:B:181:LEU:HD11	2.39	0.52
1:A:226:LYS:HD2	1:C:219:LEU:HD12	1.84	0.52
1:C:50:TRP:HZ3	3:C:810:HOH:O	1.90	0.52
1:A:195:LYS:HD2	2:A:601:AC9:C2	2.40	0.52
1:C:8:TRP:O	1:C:12:LYS:HB2	2.10	0.52
1:A:222:LEU:HD21	2:B:603:AC9:H151	1.92	0.52
2:B:603:AC9:H42	1:C:219:LEU:CD2	2.40	0.52
1:C:195:LYS:NZ	2:C:606:AC9:H43	2.24	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:179:GLU:O	1:B:183:GLU:HG3	2.09	0.52
1:B:2:GLU:O	1:B:86:MET:HE3	2.09	0.52
1:A:195:LYS:HE2	1:A:239:LYS:NZ	2.25	0.52
1:B:230:LEU:HD12	1:B:230:LEU:N	2.25	0.52
1:B:44:LEU:HD22	3:B:607:HOH:O	2.09	0.52
1:B:54:THR:O	1:B:58:SER:CB	2.57	0.52
1:C:120:GLU:HG2	3:C:760:HOH:O	2.10	0.52
1:C:237:THR:O	1:C:241:ASN:OD1	2.28	0.51
1:B:145:GLY:HA2	3:B:745:HOH:O	2.09	0.51
1:C:226:LYS:C	3:C:701:HOH:O	2.44	0.51
1:C:98:GLN:HB2	1:C:99:PRO:HD3	1.92	0.51
1:A:218:LEU:O	1:A:222:LEU:CD1	2.58	0.51
1:A:65:GLY:HA2	3:A:679:HOH:O	2.10	0.51
1:B:58:SER:O	1:B:62:GLU:HG3	2.10	0.51
1:A:34:GLU:HG2	1:A:156:VAL:CG1	2.40	0.51
1:C:6:SER:HB2	3:C:661:HOH:O	2.10	0.51
1:C:7:PRO:HB3	3:C:824:HOH:O	2.11	0.51
1:C:156:VAL:HG13	1:C:157:ASP:N	2.25	0.51
1:C:82:LEU:CD2	1:C:86:MET:HE2	2.40	0.51
1:A:176:ALA:HB2	2:A:602:AC9:H153	1.92	0.51
1:B:75:LEU:O	1:B:79:THR:HG22	2.11	0.51
1:B:120:GLU:HB3	1:B:121:PRO:HD3	1.92	0.51
1:C:211:LEU:CD1	1:C:225:PHE:HE1	2.23	0.51
1:B:133:LYS:HG3	1:B:137:LEU:CD1	2.40	0.51
1:C:21:VAL:CG1	1:C:63:GLN:NE2	2.73	0.51
1:B:126:LEU:CD2	3:B:766:HOH:O	2.57	0.51
1:A:31:SER:CB	3:A:695:HOH:O	2.59	0.51
1:B:46:LEU:O	1:B:50:TRP:HB2	2.11	0.50
1:B:114:LEU:HD13	1:B:114:LEU:C	2.32	0.50
1:C:21:VAL:HG13	1:C:63:GLN:NE2	2.25	0.50
1:C:104:PHE:CZ	3:C:793:HOH:O	2.55	0.50
1:B:10:ARG:HH11	1:B:182:LYS:HE2	1.77	0.50
1:A:222:LEU:HD11	2:B:603:AC9:C12	2.41	0.50
1:C:211:LEU:CG	1:C:225:PHE:CE1	2.94	0.50
1:B:57:PHE:CE1	1:B:123:ARG:HD2	2.46	0.50
1:B:208:LYS:HB2	1:B:209:PRO:HD3	1.93	0.50
1:A:219:LEU:HD13	2:B:603:AC9:C14	2.41	0.50
1:B:219:LEU:CD2	1:C:226:LYS:CE	2.77	0.50
1:B:46:LEU:HD22	3:B:674:HOH:O	2.11	0.50
1:B:137:LEU:HD22	1:B:138:GLN:OE1	2.11	0.50
1:C:20:ASP:O	1:C:24:ASP:OD2	2.29	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:187:ALA:O	1:C:194:ALA:HB3	2.11	0.50
1:B:107:LYS:NZ	1:B:174:LEU:CA	2.75	0.50
1:B:144:LEU:CD2	1:B:144:LEU:H	2.21	0.50
1:C:208:LYS:CG	1:C:209:PRO:CD	2.74	0.50
1:C:91:GLU:O	1:C:93:VAL:N	2.44	0.50
1:B:126:LEU:HD22	3:B:766:HOH:O	2.11	0.50
1:B:243:GLN:HG3	3:B:689:HOH:O	2.12	0.50
1:B:107:LYS:HZ3	1:B:173:ARG:C	2.15	0.50
1:B:53:VAL:HG11	1:B:123:ARG:HE	1.77	0.50
1:A:133:LYS:HA	1:A:137:LEU:HD12	1.94	0.50
2:B:603:AC9:H41	1:C:219:LEU:HA	1.93	0.50
1:C:133:LYS:CA	1:C:137:LEU:HD12	2.41	0.50
1:C:14:LEU:HG	3:C:622:HOH:O	2.11	0.50
1:C:85:GLU:HB3	3:C:673:HOH:O	2.11	0.50
2:B:603:AC9:C4	1:C:219:LEU:CD2	2.85	0.49
1:B:44:LEU:CD2	3:B:607:HOH:O	2.60	0.49
1:C:188:ARG:NH2	2:C:606:AC9:H42	2.26	0.49
1:B:42:LEU:CD1	3:B:680:HOH:O	2.56	0.49
1:C:134:LEU:HD11	1:C:151:ARG:NH2	2.27	0.49
1:C:144:LEU:N	1:C:144:LEU:CD2	2.60	0.49
1:C:214:LEU:C	1:C:216:GLN:N	2.65	0.49
1:B:90:LEU:O	1:B:93:VAL:CG2	2.52	0.49
1:B:126:LEU:CD1	3:B:766:HOH:O	2.61	0.49
1:A:222:LEU:HD22	2:B:603:AC9:C15	2.43	0.49
1:C:144:LEU:C	1:C:148:MET:HE3	2.33	0.49
1:C:108:TRP:HA	1:C:111:GLU:HG2	1.95	0.49
1:B:211:LEU:CD1	1:B:221:VAL:HG11	2.35	0.49
1:A:188:ARG:HD2	2:A:601:AC9:C4	2.39	0.49
1:B:228:SER:HB2	3:B:725:HOH:O	2.11	0.49
1:C:238:LYS:N	1:C:238:LYS:CD	2.76	0.49
1:C:211:LEU:HG	1:C:225:PHE:CE1	2.47	0.49
1:A:31:SER:CA	3:A:695:HOH:O	2.61	0.49
1:A:197:THR:HG21	3:A:668:HOH:O	2.12	0.49
1:B:188:ARG:CD	3:B:632:HOH:O	2.61	0.49
1:B:236:TYR:OH	2:B:604:AC9:C6	2.61	0.49
1:C:178:LEU:HD23	3:C:793:HOH:O	2.12	0.49
1:A:215:ARG:CD	3:A:714:HOH:O	2.50	0.49
1:C:216:GLN:CD	1:C:220:PRO:HG2	2.32	0.49
1:C:199:HIS:ND1	1:C:203:LEU:HD11	2.27	0.49
2:C:607:AC9:C13	3:C:801:HOH:O	2.60	0.48
1:A:202:THR:CG2	3:A:615:HOH:O	2.51	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:143:PRO:HD3	3:B:619:HOH:O	2.12	0.48
1:A:31:SER:HA	3:A:695:HOH:O	2.13	0.48
1:C:136:GLU:N	1:C:136:GLU:OE1	2.44	0.48
1:C:7:PRO:CG	3:C:824:HOH:O	2.59	0.48
1:A:173:ARG:HA	1:A:173:ARG:HE	1.77	0.48
1:A:34:GLU:HG2	1:A:156:VAL:HG13	1.96	0.48
1:C:164:ALA:HB2	3:C:690:HOH:O	2.13	0.48
1:B:111:GLU:O	1:B:115:TYR:HB2	2.14	0.48
1:A:206:LYS:CE	2:A:602:AC9:H93	2.43	0.48
1:A:187:ALA:HB1	1:A:198:GLU:OE1	2.14	0.48
1:B:222:LEU:HD11	2:B:603:AC9:C10	2.43	0.48
1:C:227:VAL:HG13	3:C:701:HOH:O	2.13	0.48
1:C:122:LEU:HD13	1:C:162:HIS:CD2	2.48	0.48
2:B:603:AC9:H52	1:C:222:LEU:CD1	2.37	0.48
1:C:151:ARG:O	1:C:154:ALA:HB3	2.14	0.48
1:C:144:LEU:O	1:C:148:MET:HE2	2.14	0.48
1:C:209:PRO:CA	3:C:656:HOH:O	2.56	0.48
1:B:41:GLN:HG2	3:B:665:HOH:O	2.13	0.48
1:C:133:LYS:CB	1:C:137:LEU:HD12	2.44	0.48
1:A:179:GLU:C	1:A:179:GLU:CD	2.72	0.48
1:C:211:LEU:CB	1:C:221:VAL:HG13	2.42	0.47
1:B:21:VAL:CG2	1:B:63:GLN:CG	2.92	0.47
1:B:156:VAL:CG1	3:B:788:HOH:O	2.61	0.47
1:A:219:LEU:HD22	2:B:603:AC9:C14	2.44	0.47
1:B:238:LYS:HG3	1:B:239:LYS:HG3	1.95	0.47
1:C:195:LYS:NZ	2:C:606:AC9:C4	2.78	0.47
1:B:45:LYS:HB2	1:B:46:LEU:H	1.63	0.47
1:C:6:SER:N	1:C:7:PRO:HD2	2.29	0.47
1:B:3:PRO:CG	3:B:623:HOH:O	2.60	0.47
1:B:1:ASP:C	1:B:2:GLU:HG2	2.34	0.47
1:B:24:ASP:O	1:B:27:ARG:CB	2.63	0.47
1:B:8:TRP:HZ3	1:B:11:VAL:CG2	2.18	0.47
1:B:40:LYS:O	1:B:40:LYS:HG3	2.15	0.47
1:C:134:LEU:HD23	1:C:134:LEU:O	2.15	0.47
1:B:134:LEU:HD13	1:B:151:ARG:HE	1.80	0.47
1:C:82:LEU:O	1:C:86:MET:O	2.33	0.47
1:B:176:ALA:O	1:B:180:ALA:HB2	2.15	0.47
1:C:33:PHE:O	1:C:37:ALA:HB3	2.14	0.47
1:C:91:GLU:C	1:C:93:VAL:H	2.17	0.47
1:B:122:LEU:HD12	1:B:162:HIS:CG	2.39	0.47
1:A:195:LYS:HZ3	2:A:601:AC9:C1	2.27	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:130:ALA:HA	1:B:133:LYS:NZ	2.30	0.47
1:B:116:ARG:HA	1:B:119:VAL:HG11	1.96	0.47
1:B:224:SER:CB	3:B:649:HOH:O	2.51	0.47
1:C:8:TRP:C	1:C:12:LYS:HD2	2.36	0.47
1:B:156:VAL:HB	3:B:788:HOH:O	2.14	0.47
1:B:140:LYS:HD2	3:B:635:HOH:O	2.15	0.47
1:C:176:ALA:HB2	3:C:801:HOH:O	2.15	0.47
1:B:65:GLY:O	1:B:69:GLN:HB2	2.15	0.47
1:C:145:GLY:HA2	1:C:148:MET:HE1	1.94	0.46
1:C:211:LEU:HD13	1:C:221:VAL:CB	2.44	0.46
1:C:236:TYR:CD2	1:C:236:TYR:N	2.82	0.46
1:B:188:ARG:HD3	3:B:632:HOH:O	2.15	0.46
1:B:114:LEU:CD1	1:B:114:LEU:O	2.58	0.46
1:C:46:LEU:O	1:C:50:TRP:HB2	2.15	0.46
1:C:211:LEU:HB3	1:C:221:VAL:CG1	2.39	0.46
1:B:6:SER:H	1:B:7:PRO:HD2	1.77	0.46
1:B:189:LEU:H	1:B:189:LEU:CD1	2.29	0.46
1:B:86:MET:CE	3:B:638:HOH:O	2.64	0.46
1:A:62:GLU:CD	3:A:618:HOH:O	2.54	0.46
1:B:95:ALA:HA	3:B:705:HOH:O	2.16	0.46
1:B:71:PHE:CE2	1:B:75:LEU:HD22	2.50	0.46
1:C:238:LYS:HE3	1:C:238:LYS:CA	2.46	0.46
1:C:195:LYS:HZ3	2:C:606:AC9:H43	1.80	0.46
1:B:208:LYS:O	1:B:212:GLU:HG2	2.16	0.46
1:B:140:LYS:CD	3:B:635:HOH:O	2.64	0.46
1:B:129:GLY:O	1:B:133:LYS:NZ	2.49	0.46
1:B:204:SER:HA	1:B:229:PHE:HZ	1.81	0.46
1:C:141:LEU:HD22	3:C:759:HOH:O	2.16	0.46
1:A:172:GLN:HG2	1:A:173:ARG:NH1	2.31	0.45
1:C:36:SER:CB	1:C:40:LYS:CE	2.74	0.45
1:B:53:VAL:CG1	1:B:123:ARG:HE	2.28	0.45
1:C:108:TRP:O	1:C:111:GLU:CG	2.64	0.45
1:A:124:ALA:HB1	3:A:651:HOH:O	2.16	0.45
1:B:126:LEU:HD13	3:B:766:HOH:O	2.17	0.45
1:B:219:LEU:HG	1:C:226:LYS:CD	2.47	0.45
1:C:191:GLU:OE1	1:C:194:ALA:HB2	2.16	0.45
1:A:47:LEU:HA	1:A:51:ASP:HB2	1.99	0.45
1:B:145:GLY:HA3	3:B:698:HOH:O	2.16	0.45
1:C:176:ALA:CB	3:C:787:HOH:O	2.64	0.45
1:B:238:LYS:HB2	3:B:753:HOH:O	2.16	0.45
1:B:70:GLU:O	1:B:74:ASN:HB2	2.17	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:110:GLU:HG2	3:B:792:HOH:O	2.16	0.45
1:A:195:LYS:HG3	3:A:690:HOH:O	2.16	0.45
1:A:177:ARG:HD3	1:A:181:LEU:HD23	1.99	0.45
1:C:216:GLN:HG3	1:C:220:PRO:HG2	1.98	0.45
1:C:44:LEU:HD21	1:C:46:LEU:HD12	1.99	0.45
1:B:222:LEU:CD1	2:B:603:AC9:C7	2.89	0.45
1:C:188:ARG:NE	2:C:606:AC9:C4	2.80	0.45
1:B:236:TYR:O	1:B:240:LEU:HD13	2.17	0.44
1:A:105:GLN:HG2	1:A:109:GLN:HE21	1.81	0.44
1:A:226:LYS:CD	1:C:219:LEU:HD12	2.44	0.44
1:B:139:GLU:HG2	1:B:140:LYS:N	2.30	0.44
1:C:238:LYS:H	1:C:238:LYS:HD2	1.82	0.44
1:C:232:ALA:HB1	1:C:236:TYR:OH	2.18	0.44
1:C:227:VAL:CG1	3:C:701:HOH:O	2.66	0.44
1:A:240:LEU:HD11	3:A:690:HOH:O	2.17	0.44
1:C:169:GLU:HG3	1:C:173:ARG:HH11	1.81	0.44
1:C:65:GLY:C	3:C:761:HOH:O	2.55	0.44
1:C:135:HIS:HB2	1:C:136:GLU:OE1	2.18	0.44
1:B:8:TRP:HZ3	1:B:182:LYS:HD3	1.83	0.44
1:B:166:TYR:O	1:B:170:LEU:HB2	2.18	0.44
1:B:141:LEU:HD13	1:B:141:LEU:H	1.83	0.44
1:C:54:THR:HG21	3:C:713:HOH:O	2.18	0.44
1:B:141:LEU:N	1:B:141:LEU:CD1	2.80	0.43
1:A:14:LEU:HD12	1:A:178:LEU:HD21	2.00	0.43
1:B:232:ALA:O	1:B:236:TYR:HD1	2.00	0.43
1:C:101:LEU:HD13	1:C:101:LEU:HA	1.91	0.43
1:C:195:LYS:H	1:C:195:LYS:HG3	1.31	0.43
1:C:71:PHE:HD1	3:C:622:HOH:O	1.98	0.43
1:B:179:GLU:O	1:B:183:GLU:CG	2.66	0.43
1:B:65:GLY:N	1:B:66:PRO:CD	2.82	0.43
1:B:95:ALA:CA	3:B:705:HOH:O	2.64	0.43
1:C:60:LEU:CD1	1:C:115:TYR:OH	2.52	0.43
1:B:60:LEU:O	1:B:64:LEU:HG	2.19	0.43
1:C:107:LYS:HE3	1:C:177:ARG:HE	1.84	0.43
1:C:195:LYS:HZ3	2:C:606:AC9:C4	2.31	0.43
1:C:188:ARG:NE	2:C:606:AC9:H41	2.33	0.43
1:B:19:VAL:O	1:B:23:LYS:HB2	2.18	0.43
1:B:230:LEU:H	1:B:230:LEU:HD12	1.83	0.43
1:C:108:TRP:C	1:C:111:GLU:HG2	2.39	0.43
1:A:206:LYS:C	1:A:206:LYS:HD3	2.39	0.43
1:B:193:HIS:CE1	1:B:195:LYS:HE2	2.53	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:7:PRO:HB2	3:A:657:HOH:O	2.18	0.43
1:C:29:TYR:HB3	1:C:33:PHE:HE1	1.80	0.43
1:C:133:LYS:HG2	1:C:137:LEU:CD1	2.49	0.43
1:B:44:LEU:HD21	3:B:646:HOH:O	2.18	0.43
1:C:88:LYS:HB2	1:C:88:LYS:HZ3	1.83	0.43
1:A:219:LEU:HD22	2:B:603:AC9:H141	2.01	0.42
1:C:73:ASP:C	1:C:77:LYS:HE2	2.40	0.42
1:B:158:ALA:O	1:B:162:HIS:HD2	2.03	0.42
1:A:218:LEU:HB3	1:A:222:LEU:HD21	2.01	0.42
2:B:603:AC9:H51	1:C:218:LEU:HD22	2.02	0.42
1:C:211:LEU:HA	1:C:211:LEU:HD23	1.76	0.42
1:B:133:LYS:HA	1:B:137:LEU:HB2	2.01	0.42
1:A:107:LYS:HE2	1:A:177:ARG:HB2	2.01	0.42
1:C:119:VAL:HG22	3:C:700:HOH:O	2.19	0.42
1:B:188:ARG:HD3	1:B:189:LEU:HD11	2.00	0.42
1:B:230:LEU:H	1:B:230:LEU:CD1	2.33	0.42
1:C:134:LEU:CD1	1:C:151:ARG:NH2	2.82	0.42
1:A:70:GLU:N	3:A:666:HOH:O	2.52	0.42
1:A:7:PRO:CB	3:A:657:HOH:O	2.66	0.42
2:B:603:AC9:H43	3:C:629:HOH:O	2.20	0.42
1:C:88:LYS:NZ	1:C:89:ASP:O	2.48	0.42
1:C:160:ARG:HG3	3:C:609:HOH:O	2.18	0.42
1:C:96:LYS:HG2	1:C:189:LEU:HD22	2.02	0.42
1:B:46:LEU:HB3	3:B:794:HOH:O	2.18	0.42
1:B:110:GLU:O	1:B:114:LEU:CB	2.68	0.42
1:C:11:VAL:HA	1:C:178:LEU:HD13	2.00	0.42
1:B:137:LEU:CD2	1:B:138:GLN:OE1	2.67	0.42
1:C:182:LYS:NZ	1:C:182:LYS:CB	2.73	0.42
1:B:177:ARG:HG3	1:B:181:LEU:HD12	2.01	0.42
1:B:40:LYS:HZ3	1:B:44:LEU:H	1.66	0.42
1:B:49:ASN:O	1:B:53:VAL:HG23	2.20	0.42
1:B:159:LEU:HD23	3:B:766:HOH:O	2.20	0.42
1:A:116:ARG:HD3	3:A:664:HOH:O	2.19	0.42
1:B:169:GLU:HG3	1:B:173:ARG:HH11	1.85	0.42
1:C:5:GLN:HA	1:C:5:GLN:HE21	1.85	0.42
1:C:53:VAL:CG1	1:C:123:ARG:HD3	2.31	0.41
1:C:151:ARG:HA	1:C:154:ALA:HB3	2.02	0.41
1:C:82:LEU:HD21	1:C:86:MET:CG	2.37	0.41
1:C:39:GLY:O	1:C:40:LYS:O	2.38	0.41
1:B:112:MET:O	1:B:116:ARG:HG3	2.19	0.41
1:C:122:LEU:HD13	1:C:162:HIS:CB	2.50	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:17:VAL:O	1:B:21:VAL:HB	2.21	0.41
1:C:82:LEU:HD23	1:C:86:MET:C	2.40	0.41
1:C:8:TRP:HB2	1:C:12:LYS:NZ	2.27	0.41
1:B:219:LEU:CD2	2:B:603:AC9:C9	2.73	0.41
1:B:57:PHE:O	1:B:61:ARG:CB	2.63	0.41
1:C:85:GLU:CB	3:C:673:HOH:O	2.69	0.41
1:C:241:ASN:HB3	3:C:814:HOH:O	2.20	0.41
1:B:44:LEU:CD2	1:B:47:LEU:CD1	2.59	0.41
1:B:84:GLN:HG2	3:B:656:HOH:O	2.20	0.41
1:C:56:THR:C	1:C:60:LEU:HD23	2.21	0.41
1:A:240:LEU:N	3:A:613:HOH:O	2.53	0.41
1:B:146:GLU:HB3	1:B:147:GLU:H	1.61	0.41
1:C:164:ALA:HB2	3:C:752:HOH:O	2.20	0.41
1:B:156:VAL:HG12	3:B:788:HOH:O	2.19	0.41
1:B:190:ALA:HB3	1:B:191:GLU:OE1	2.21	0.41
1:C:72:TRP:HZ2	1:C:105:GLN:HA	1.85	0.41
1:B:115:TYR:CE1	1:B:170:LEU:CD2	2.91	0.41
1:B:51:ASP:CA	1:B:54:THR:HG22	2.48	0.40
1:B:141:LEU:CD1	1:B:141:LEU:H	2.34	0.40
1:B:183:GLU:O	1:B:187:ALA:HB3	2.21	0.40
1:A:195:LYS:HZ2	2:A:601:AC9:C3	2.35	0.40
1:A:191:GLU:HG2	3:A:689:HOH:O	2.21	0.40
1:B:107:LYS:HZ3	1:B:173:ARG:HG3	1.87	0.40
1:C:107:LYS:NZ	3:C:764:HOH:O	2.53	0.40
1:C:199:HIS:HD2	2:C:606:AC9:H52	1.86	0.40
1:A:222:LEU:H	1:A:222:LEU:HG	1.43	0.40
1:C:166:TYR:HD1	3:C:672:HOH:O	2.04	0.40
1:C:45:LYS:CG	1:C:45:LYS:O	2.67	0.40

All (18) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2:GLU:CA	3:B:690:HOH:O[1_556]	0.74	1.46
1:A:1:ASP:CB	3:B:670:HOH:O[1_556]	1.15	1.05
1:A:2:GLU:CB	3:B:690:HOH:O[1_556]	1.27	0.93
1:A:1:ASP:CG	3:B:737:HOH:O[1_556]	1.41	0.79
1:A:1:ASP:O	1:B:45:LYS:NZ[1_556]	1.49	0.71
1:A:140:LYS:CB	1:C:227:VAL:CG1[4_655]	1.55	0.65
1:B:220:PRO:CA	3:A:625:HOH:O[3_544]	1.78	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1:ASP:OD2	3:B:737:HOH:O[1_556]	1.80	0.40
1:A:1:ASP:OD1	3:B:737:HOH:O[1_556]	1.81	0.39
1:A:2:GLU:N	3:B:690:HOH:O[1_556]	1.84	0.36
1:A:2:GLU:CG	3:B:690:HOH:O[1_556]	1.94	0.26
1:B:220:PRO:N	3:A:625:HOH:O[3_544]	2.06	0.14
1:A:140:LYS:O	1:C:227:VAL:CG2[4_655]	2.09	0.11
1:A:2:GLU:C	3:B:690:HOH:O[1_556]	2.11	0.09
1:A:1:ASP:CG	3:B:670:HOH:O[1_556]	2.16	0.04
1:A:1:ASP:C	1:B:45:LYS:NZ[1_556]	2.16	0.04
1:A:84:GLN:OE1	3:B:658:HOH:O[3_545]	2.18	0.02
1:A:1:ASP:O	1:B:45:LYS:CE[1_556]	2.19	0.01

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	241/243 (99%)	220 (91%)	14 (6%)	7 (3%)	6	5
1	B	241/243 (99%)	207 (86%)	20 (8%)	14 (6%)	2	1
1	C	241/243 (99%)	213 (88%)	15 (6%)	13 (5%)	2	1
All	All	723/729 (99%)	640 (88%)	49 (7%)	34 (5%)	3	2

All (34) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	144	LEU
1	B	7	PRO
1	B	36	SER
1	B	46	LEU
1	B	87	SER
1	B	142	SER
1	B	143	PRO
1	C	2	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	8	TRP
1	C	40	LYS
1	C	92	GLU
1	C	139	GLU
1	C	142	SER
1	C	194	ALA
1	C	215	ARG
1	C	217	GLY
1	C	218	LEU
1	A	8	TRP
1	A	40	LYS
1	A	194	ALA
1	B	3	PRO
1	B	41	GLN
1	B	194	ALA
1	C	141	LEU
1	A	142	SER
1	B	5	GLN
1	B	45	LYS
1	B	141	LEU
1	A	146	GLU
1	B	139	GLU
1	C	3	PRO
1	A	145	GLY
1	C	7	PRO
1	B	4	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	214/214 (100%)	191 (89%)	23 (11%)	8	11
1	B	214/214 (100%)	192 (90%)	22 (10%)	9	13
1	C	214/214 (100%)	191 (89%)	23 (11%)	8	11
All	All	642/642 (100%)	574 (89%)	68 (11%)	8	12

All (68) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	SER
1	A	57	PHE
1	A	73	ASP
1	A	82	LEU
1	A	86	MET
1	A	88	LYS
1	A	91	GLU
1	A	115	TYR
1	A	138	GLN
1	A	139	GLU
1	A	171	ARG
1	A	173	ARG
1	A	179	GLU
1	A	188	ARG
1	A	192	TYR
1	A	193	HIS
1	A	195	LYS
1	A	197	THR
1	A	199	HIS
1	A	206	LYS
1	A	222	LEU
1	A	230	LEU
1	A	236	TYR
1	B	20	ASP
1	B	21	VAL
1	B	23	LYS
1	B	42	LEU
1	B	45	LYS
1	B	85	GLU
1	B	86	MET
1	B	88	LYS
1	B	112	MET
1	B	114	LEU
1	B	131	ARG
1	B	133	LYS
1	B	148	MET
1	B	151	ARG
1	B	173	ARG
1	B	174	LEU
1	B	189	LEU
1	B	192	TYR
1	B	199	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	219	LEU
1	B	223	GLU
1	B	238	LYS
1	C	6	SER
1	C	28	ASP
1	C	49	ASN
1	C	82	LEU
1	C	85	GLU
1	C	88	LYS
1	C	112	MET
1	C	136	GLU
1	C	138	GLN
1	C	139	GLU
1	C	144	LEU
1	C	148	MET
1	C	163	LEU
1	C	168	ASP
1	C	170	LEU
1	C	182	LYS
1	C	195	LYS
1	C	211	LEU
1	C	215	ARG
1	C	230	LEU
1	C	234	GLU
1	C	236	TYR
1	C	238	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	109	GLN
1	A	127	GLN
1	A	138	GLN
1	B	84	GLN
1	B	98	GLN
1	B	155	HIS
1	B	162	HIS
1	B	243	GLN
1	C	5	GLN
1	C	49	ASN
1	C	63	GLN
1	C	69	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	132	GLN
1	C	172	GLN
1	C	199	HIS
1	C	216	GLN
1	C	243	GLN

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](#)

7 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	$\# Z > 2$
2	AC9	A	601	-	24,24,24	1.28	3 (12%)	21,42,42	1.93	2 (9%)
2	AC9	A	602	-	24,24,24	1.39	3 (12%)	21,42,42	2.00	2 (9%)
2	AC9	B	603	-	24,24,24	1.29	3 (12%)	21,42,42	1.87	3 (14%)
2	AC9	B	604	-	24,24,24	1.27	3 (12%)	21,42,42	1.97	2 (9%)
2	AC9	B	605	-	24,24,24	1.37	3 (12%)	21,42,42	1.97	2 (9%)
2	AC9	C	606	-	24,24,24	1.25	3 (12%)	21,42,42	1.84	2 (9%)
2	AC9	C	607	-	24,24,24	1.29	2 (8%)	21,42,42	2.01	2 (9%)

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	AC9	A	601	-	-	0/0/54/54	0/3/3/3
2	AC9	A	602	-	-	0/0/54/54	0/3/3/3
2	AC9	B	603	-	-	0/0/54/54	0/3/3/3
2	AC9	B	604	-	-	0/0/54/54	0/3/3/3
2	AC9	B	605	-	-	0/0/54/54	0/3/3/3
2	AC9	C	606	-	-	0/0/54/54	0/3/3/3
2	AC9	C	607	-	-	0/0/54/54	0/3/3/3

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	602	AC9	C9-C6	-4.65	1.41	1.51
2	A	601	AC9	C9-C6	-4.33	1.41	1.51
2	C	607	AC9	C9-C6	-3.87	1.42	1.51
2	B	605	AC9	CR-O4	-3.72	1.90	1.95
2	B	604	AC9	C9-C6	-3.69	1.43	1.51
2	C	606	AC9	C9-C6	-3.67	1.43	1.51
2	B	603	AC9	CR-O4	-3.59	1.91	1.95
2	B	605	AC9	C9-C6	-3.43	1.43	1.51
2	B	603	AC9	C9-C6	-3.24	1.44	1.51
2	C	606	AC9	CR-O4	-2.65	1.92	1.95
2	A	601	AC9	CR-O4	-2.62	1.92	1.95
2	A	602	AC9	CR-O4	-2.53	1.92	1.95
2	B	604	AC9	CR-O4	-2.24	1.92	1.95
2	B	605	AC9	C6-C7	2.17	1.45	1.39
2	B	604	AC9	C6-C7	2.43	1.45	1.39
2	A	602	AC9	C6-C7	2.71	1.46	1.39
2	A	601	AC9	C6-C7	2.82	1.46	1.39
2	C	607	AC9	C6-C7	2.82	1.46	1.39
2	B	603	AC9	C6-C7	2.90	1.46	1.39
2	C	606	AC9	C6-C7	3.07	1.47	1.39

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	607	AC9	O3-C6-C7	-7.54	116.55	124.78
2	A	602	AC9	O3-C6-C7	-7.52	116.57	124.78
2	B	604	AC9	O3-C6-C7	-7.36	116.74	124.78

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	605	AC9	O3-C6-C7	-7.31	116.79	124.78
2	A	601	AC9	O3-C6-C7	-7.30	116.81	124.78
2	B	603	AC9	O3-C6-C7	-6.80	117.36	124.78
2	C	606	AC9	O3-C6-C7	-6.63	117.54	124.78
2	B	603	AC9	O5-C11-C12	2.05	127.02	124.78
2	B	605	AC9	O3-C6-C9	3.54	119.75	115.12
2	B	604	AC9	O3-C6-C9	3.85	120.15	115.12
2	A	601	AC9	O3-C6-C9	3.96	120.31	115.12
2	B	603	AC9	O3-C6-C9	4.04	120.41	115.12
2	A	602	AC9	O3-C6-C9	4.17	120.58	115.12
2	C	606	AC9	O3-C6-C9	4.27	120.71	115.12
2	C	607	AC9	O3-C6-C9	4.27	120.71	115.12

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

7 monomers are involved in 97 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	AC9	8	0
2	A	602	AC9	5	0
2	B	603	AC9	42	0
2	B	604	AC9	14	0
2	B	605	AC9	4	0
2	C	606	AC9	14	0
2	C	607	AC9	10	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	243/243 (100%)	0.18	8 (3%)	50	50	22, 27, 31, 33	0
1	B	243/243 (100%)	0.31	8 (3%)	50	50	20, 27, 31, 33	0
1	C	243/243 (100%)	0.19	6 (2%)	61	60	23, 27, 31, 32	0
All	All	729/729 (100%)	0.23	22 (3%)	54	53	20, 27, 31, 33	0

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	42	LEU	7.7
1	B	83	ARG	4.2
1	B	229	PHE	4.0
1	B	190	ALA	3.8
1	B	144	LEU	3.6
1	C	38	LEU	3.6
1	A	152	ALA	3.3
1	C	3	PRO	3.2
1	C	222	LEU	2.8
1	A	41	GLN	2.6
1	A	30	VAL	2.6
1	C	215	ARG	2.5
1	B	197	THR	2.4
1	B	1	ASP	2.4
1	A	5	GLN	2.2
1	C	65	GLY	2.2
1	C	170	LEU	2.2
1	B	37	ALA	2.1
1	A	242	THR	2.1
1	A	14	LEU	2.0
1	A	187	ALA	2.0
1	A	16	THR	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(Å ²)	Q<0.9
2	AC9	A	601	22/22	0.95	0.15	-0.20	16,18,20,20	0
2	AC9	B	605	22/22	0.96	0.15	-0.27	16,17,18,19	0
2	AC9	C	607	22/22	0.93	0.14	-0.40	16,18,20,21	0
2	AC9	A	602	22/22	0.94	0.14	-0.55	16,19,20,21	0
2	AC9	B	603	22/22	0.96	0.15	-1.12	17,19,20,20	0
2	AC9	C	606	22/22	0.96	0.13	-1.28	16,18,19,20	0
2	AC9	B	604	22/22	0.97	0.10	-6.76	16,18,19,20	0

6.5 Other polymers [i](#)

There are no such residues in this entry.