



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 04:18 PM GMT

PDB ID : 4EED
Title : CorA coiled-coil mutant under Mg²⁺ presence
Authors : Pfoh, R.; Pai, E.F.
Deposited on : 2012-03-28
Resolution : 3.92 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

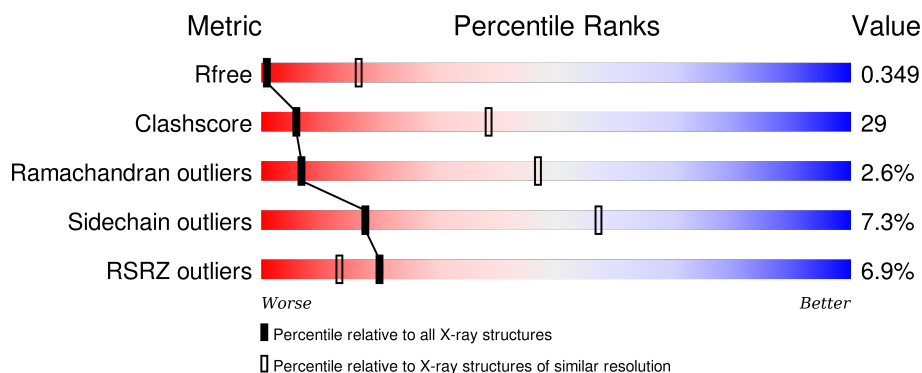
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.92 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	1047 (4.32-3.52)
Clashscore	102246	1008 (4.26-3.58)
Ramachandran outliers	100387	1044 (4.30-3.54)
Sidechain outliers	100360	1035 (4.30-3.54)
RSRZ outliers	91569	1002 (4.30-3.54)

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	330	<div> <div>3%</div> <div>44%</div> <div>47%</div> <div>5%</div> </div>
1	B	330	<div> <div>12%</div> <div>51%</div> <div>40%</div> <div>5%</div> </div>
1	C	330	<div> <div>3%</div> <div>48%</div> <div>43%</div> <div>5%</div> </div>
1	D	330	<div> <div>7%</div> <div>46%</div> <div>42%</div> <div>6%</div> <div>5%</div> </div>
1	E	330	<div> <div>8%</div> <div>48%</div> <div>42%</div> <div>5%</div> <div>5%</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	MG	A	403	-	-	-	X
2	MG	E	501	-	-	-	X

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 12979 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 Magnesium transport protein CorA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	314	Total	C	N	O	S	0	0	0
			2593	1688	418	478	9			
1	B	314	Total	C	N	O	S	0	0	0
			2593	1688	418	478	9			
1	C	314	Total	C	N	O	S	0	0	0
			2593	1688	418	478	9			
1	D	314	Total	C	N	O	S	0	0	0
			2593	1688	418	478	9			
1	E	314	Total	C	N	O	S	0	0	0
			2593	1688	418	478	9			

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	22	GLY	-	EXPRESSION TAG	UNP Q9WZ31
A	23	SER	-	EXPRESSION TAG	UNP Q9WZ31
A	24	HIS	-	EXPRESSION TAG	UNP Q9WZ31
A	25	MET	-	EXPRESSION TAG	UNP Q9WZ31
A	222	ALA	ARG	ENGINEERED MUTATION	UNP Q9WZ31
A	223	ALA	LYS	ENGINEERED MUTATION	UNP Q9WZ31
B	22	GLY	-	EXPRESSION TAG	UNP Q9WZ31
B	23	SER	-	EXPRESSION TAG	UNP Q9WZ31
B	24	HIS	-	EXPRESSION TAG	UNP Q9WZ31
B	25	MET	-	EXPRESSION TAG	UNP Q9WZ31
B	222	ALA	ARG	ENGINEERED MUTATION	UNP Q9WZ31
B	223	ALA	LYS	ENGINEERED MUTATION	UNP Q9WZ31
C	22	GLY	-	EXPRESSION TAG	UNP Q9WZ31
C	23	SER	-	EXPRESSION TAG	UNP Q9WZ31
C	24	HIS	-	EXPRESSION TAG	UNP Q9WZ31
C	25	MET	-	EXPRESSION TAG	UNP Q9WZ31
C	222	ALA	ARG	ENGINEERED MUTATION	UNP Q9WZ31
C	223	ALA	LYS	ENGINEERED MUTATION	UNP Q9WZ31
D	22	GLY	-	EXPRESSION TAG	UNP Q9WZ31

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
D	23	SER	-	EXPRESSION TAG	UNP Q9WZ31
D	24	HIS	-	EXPRESSION TAG	UNP Q9WZ31
D	25	MET	-	EXPRESSION TAG	UNP Q9WZ31
D	222	ALA	ARG	ENGINEERED MUTATION	UNP Q9WZ31
D	223	ALA	LYS	ENGINEERED MUTATION	UNP Q9WZ31
E	22	GLY	-	EXPRESSION TAG	UNP Q9WZ31
E	23	SER	-	EXPRESSION TAG	UNP Q9WZ31
E	24	HIS	-	EXPRESSION TAG	UNP Q9WZ31
E	25	MET	-	EXPRESSION TAG	UNP Q9WZ31
E	222	ALA	ARG	ENGINEERED MUTATION	UNP Q9WZ31
E	223	ALA	LYS	ENGINEERED MUTATION	UNP Q9WZ31

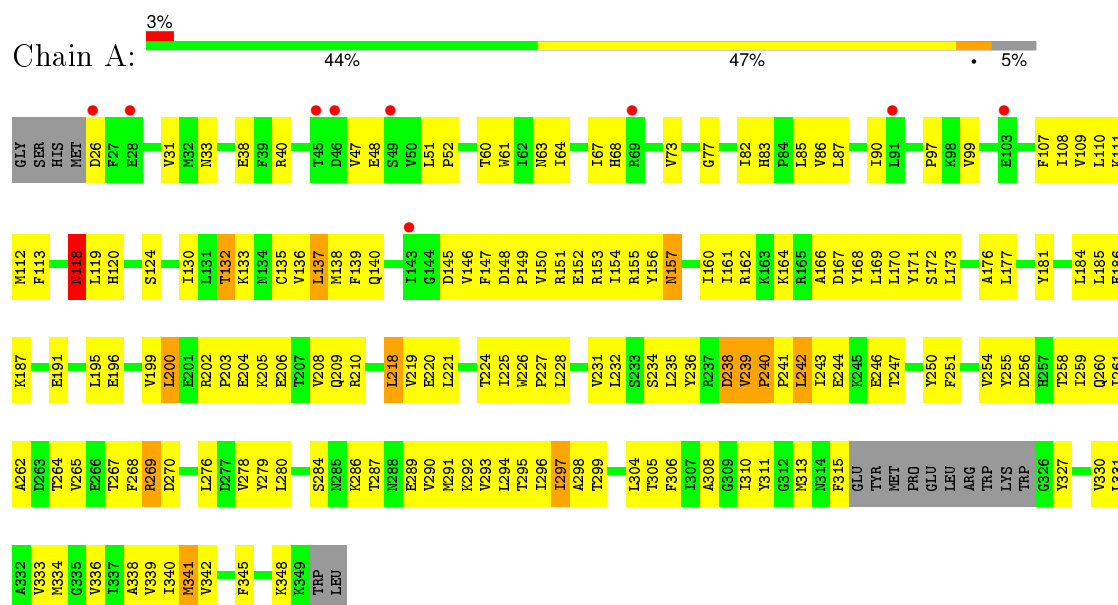
- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	3	Total Mg 3 3	0	0
2	A	4	Total Mg 4 4	0	0
2	D	3	Total Mg 3 3	0	0
2	C	2	Total Mg 2 2	0	0
2	E	2	Total Mg 2 2	0	0

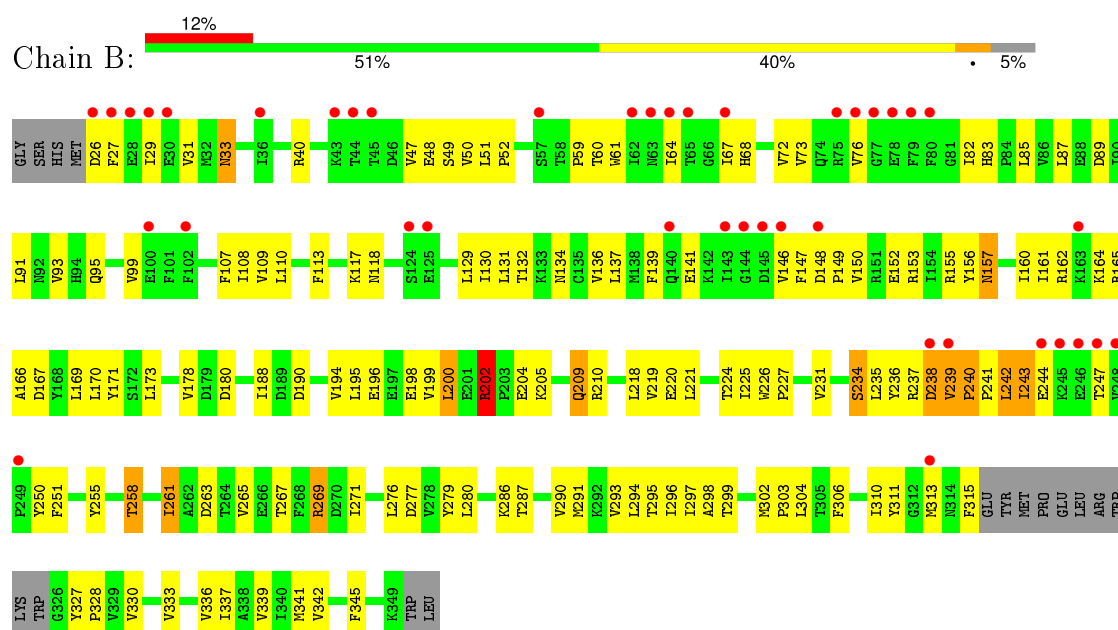
3 Residue-property plots

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

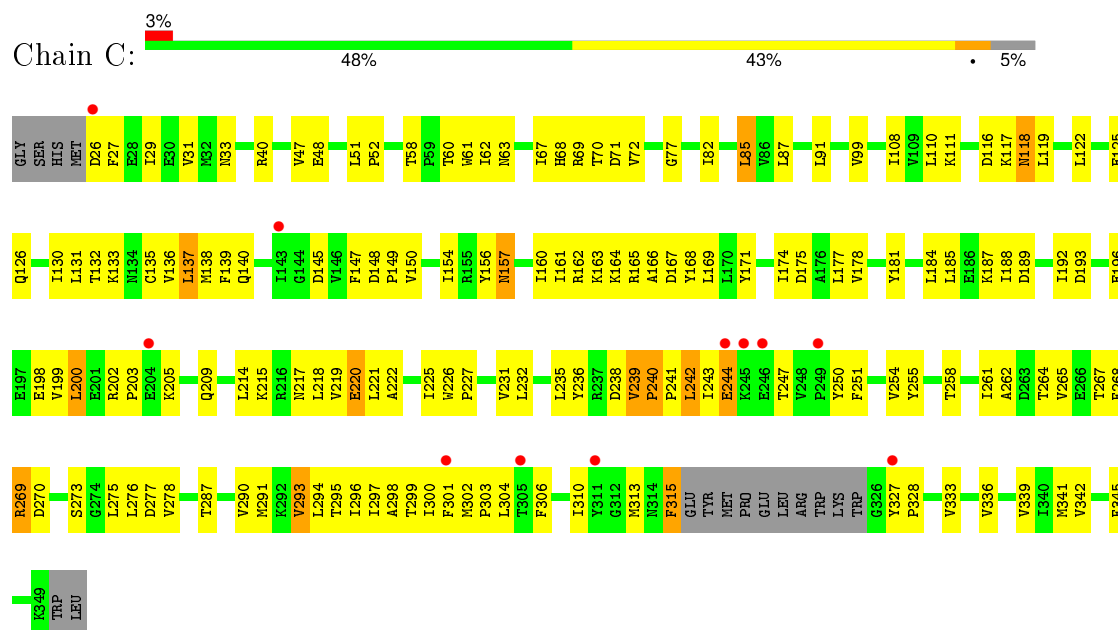
• Molecule 1: Magnesium transport protein CorA



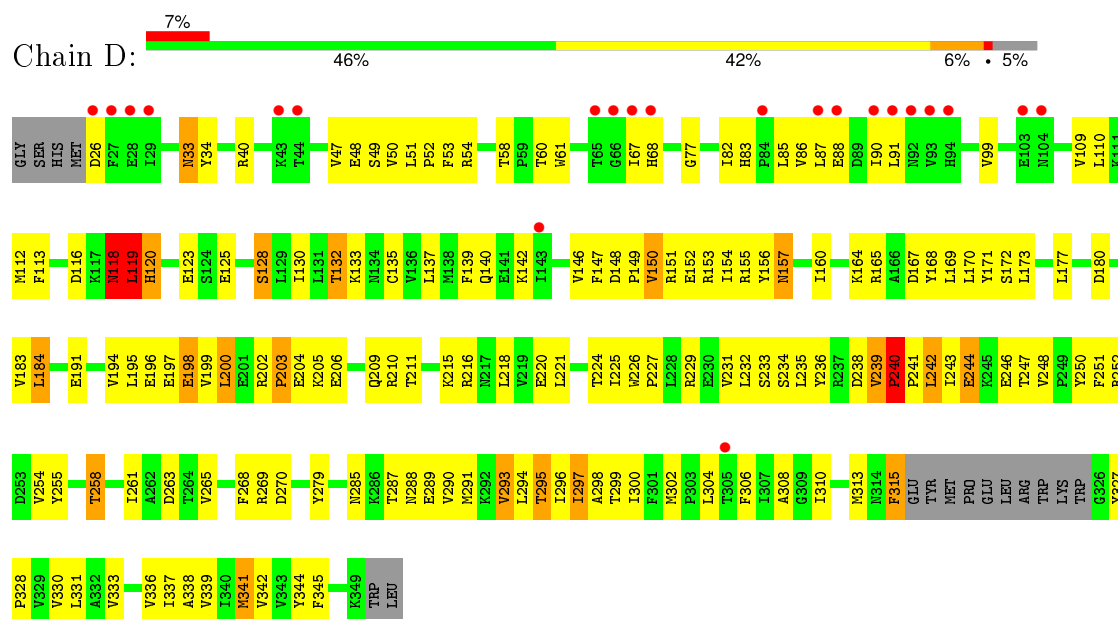
• Molecule 1: Magnesium transport protein CorA



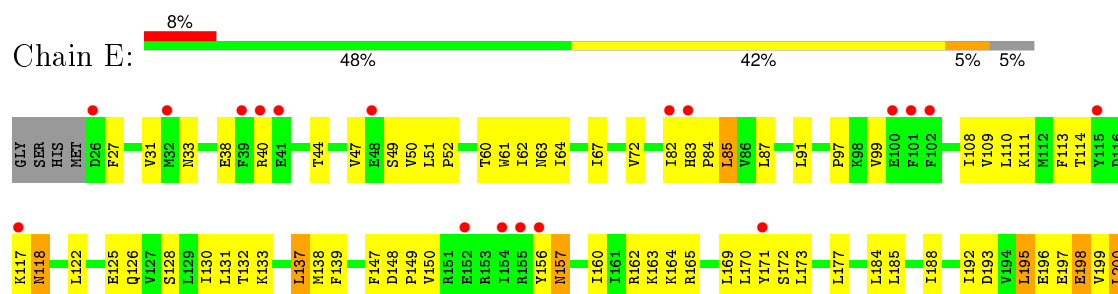
- Molecule 1: Magnesium transport protein CorA

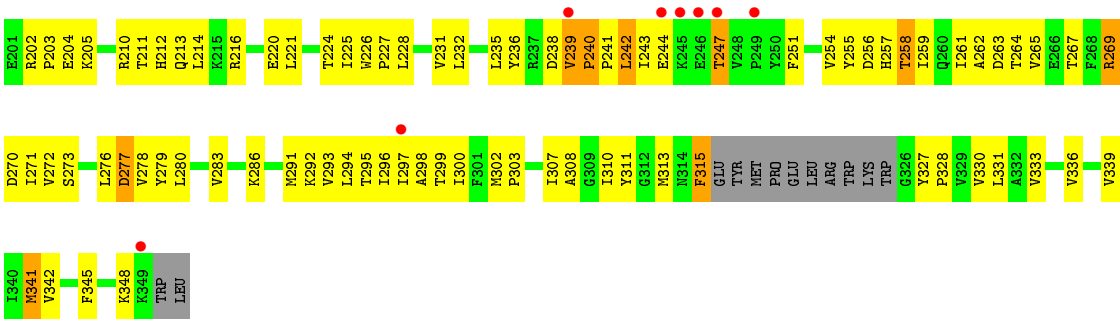


- Molecule 1: Magnesium transport protein CorA



- Molecule 1: Magnesium transport protein CorA





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	121.70 Å 132.50 Å 179.10 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.79 – 3.92 48.79 – 3.90	Depositor EDS
% Data completeness (in resolution range)	82.1 (48.79-3.92) 81.0 (48.79-3.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.27 (at 3.88 Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.297 , 0.351 0.297 , 0.349	Depositor DCC
R_{free} test set	1096 reflections (5.29%)	DCC
Wilson B-factor (Å ²)	142.1	Xtriage
Anisotropy	0.017	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.25 , 100.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.38$, $\langle L^2 \rangle = 0.21$	Xtriage
Outliers	3 of 21855 reflections (0.014%)	Xtriage
F_o, F_c correlation	0.85	EDS
Total number of atoms	12979	wwPDB-VP
Average B, all atoms (Å ²)	145.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.46% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.56	0/2646	0.67	0/3588
1	B	0.53	0/2646	0.61	0/3588
1	C	0.56	0/2646	0.64	0/3588
1	D	0.59	0/2646	0.69	0/3588
1	E	0.58	0/2646	0.66	0/3588
All	All	0.56	0/13230	0.66	0/17940

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2593	0	2630	181	0
1	B	2593	0	2630	150	0
1	C	2593	0	2630	169	0
1	D	2593	0	2630	160	0
1	E	2593	0	2630	155	0
2	A	4	0	0	0	0
2	B	3	0	0	0	0
2	C	2	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	3	0	0	0	0
2	E	2	0	0	0	0
All	All	12979	0	13150	746	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 29.

All (746) 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:221:LEU:HG	1:B:225:ILE:HD11	1.27	1.17
1:C:294:LEU:HD22	1:D:294:LEU:HD11	1.11	1.05
1:E:221:LEU:HG	1:E:225:ILE:HD11	1.36	1.04
1:C:99:VAL:HG21	1:C:235:LEU:HD13	1.42	0.99
1:D:33:ASN:CG	1:D:60:THR:HG22	1.86	0.95
1:A:276:LEU:HD23	1:E:277:ASP:HB3	1.51	0.93
1:B:255:TYR:O	1:B:258:THR:HG22	1.69	0.93
1:C:255:TYR:O	1:C:258:THR:HG22	1.68	0.93
1:C:70:THR:HG22	1:C:91:LEU:HD22	1.51	0.92
1:C:310:ILE:O	1:C:313:MET:HG2	1.71	0.91
1:A:310:ILE:O	1:A:313:MET:HG2	1.70	0.90
1:D:339:VAL:HA	1:D:342:VAL:HG12	1.54	0.90
1:D:255:TYR:O	1:D:258:THR:HG22	1.75	0.87
1:A:221:LEU:CD1	1:A:225:ILE:HD11	2.05	0.86
1:A:255:TYR:O	1:A:258:THR:HG22	1.76	0.86
1:B:294:LEU:HD22	1:C:294:LEU:CD1	2.07	0.85
1:E:211:THR:HG21	1:E:276:LEU:HD13	1.58	0.84
1:D:221:LEU:HG	1:D:225:ILE:HD11	1.60	0.83
1:E:67:ILE:HG22	1:E:91:LEU:HD23	1.60	0.83
1:B:310:ILE:O	1:B:313:MET:HG2	1.79	0.82
1:B:294:LEU:CD2	1:C:294:LEU:HD11	2.09	0.82
1:E:296:ILE:HG22	1:E:345:PHE:CE2	2.16	0.81
1:A:111:LYS:O	1:A:181:TYR:OH	1.97	0.81
1:B:291:MET:CE	1:C:290:VAL:HG12	2.11	0.81
1:E:221:LEU:CG	1:E:225:ILE:HD11	2.10	0.80
1:B:294:LEU:HD22	1:C:294:LEU:HD12	1.63	0.80
1:E:197:GLU:HA	1:E:200:LEU:HD22	1.64	0.80
1:B:236:TYR:HA	1:B:251:PHE:HZ	1.46	0.80
1:C:221:LEU:HG	1:C:225:ILE:HD11	1.62	0.80
1:E:255:TYR:O	1:E:258:THR:HG22	1.82	0.79
1:D:152:GLU:OE2	1:D:155:ARG:HD2	1.82	0.79

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:310:ILE:O	1:D:313:MET:HG2	1.83	0.78
1:C:339:VAL:HA	1:C:342:VAL:HG12	1.64	0.78
1:E:236:TYR:HA	1:E:251:PHE:HZ	1.47	0.78
1:B:47:VAL:HG23	1:B:72:VAL:HG13	1.66	0.78
1:A:99:VAL:HB	1:A:231:VAL:HG13	1.67	0.77
1:E:147:PHE:O	1:E:150:VAL:HG12	1.83	0.77
1:A:108:ILE:HD11	1:A:235:LEU:HD21	1.67	0.77
1:B:61:TRP:HB2	1:B:169:LEU:HD21	1.67	0.77
1:B:294:LEU:HD23	1:B:294:LEU:C	2.05	0.77
1:C:296:ILE:HG22	1:C:345:PHE:CE2	2.19	0.77
1:E:221:LEU:O	1:E:225:ILE:HD12	1.85	0.76
1:B:258:THR:HA	1:B:261:ILE:HD12	1.68	0.76
1:A:73:VAL:HG12	1:A:87:LEU:HD22	1.68	0.76
1:B:294:LEU:HD21	1:C:294:LEU:HD11	1.67	0.76
1:A:225:ILE:HG22	1:A:262:ALA:HB2	1.66	0.75
1:D:302:MET:CE	1:E:298:ALA:HA	2.16	0.75
1:D:330:VAL:HG13	1:D:331:LEU:HD12	1.68	0.75
1:E:327:TYR:O	1:E:330:VAL:HG12	1.86	0.75
1:D:236:TYR:HA	1:D:251:PHE:HZ	1.50	0.75
1:D:147:PHE:O	1:D:150:VAL:HG12	1.87	0.75
1:C:236:TYR:HA	1:C:251:PHE:HZ	1.53	0.74
1:A:90:ILE:HD11	1:A:130:ILE:HD11	1.68	0.74
1:C:131:LEU:HD13	1:C:136:VAL:HG22	1.68	0.73
1:C:315:PHE:CZ	1:D:327:TYR:HA	2.23	0.73
1:E:330:VAL:HG13	1:E:331:LEU:HD12	1.68	0.73
1:C:26:ASP:O	1:C:68:HIS:NE2	2.20	0.73
1:E:299:THR:HG21	1:E:345:PHE:CE2	2.24	0.73
1:C:147:PHE:O	1:C:150:VAL:HG12	1.88	0.72
1:A:299:THR:HG21	1:A:345:PHE:CZ	2.24	0.72
1:B:73:VAL:HG12	1:B:87:LEU:HD22	1.70	0.72
1:A:110:LEU:HD13	1:A:177:LEU:HD22	1.70	0.72
1:E:109:VAL:O	1:E:110:LEU:HD23	1.88	0.72
1:D:295:THR:HG23	1:E:294:LEU:HB2	1.71	0.72
1:A:239:VAL:HB	1:A:242:LEU:HD23	1.72	0.72
1:B:339:VAL:HA	1:B:342:VAL:HG12	1.72	0.72
1:E:67:ILE:O	1:E:67:ILE:HG22	1.90	0.72
1:C:313:MET:HE3	1:D:308:ALA:HB1	1.72	0.71
1:A:199:VAL:HG11	1:A:278:VAL:HB	1.72	0.71
1:A:150:VAL:HG11	1:A:173:LEU:HD23	1.72	0.71
1:A:112:MET:CE	1:A:146:VAL:HG13	2.21	0.71
1:B:302:MET:HE3	1:C:301:PHE:HB2	1.70	0.71

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:154:ILE:HG12	1:C:161:ILE:HG21	1.71	0.71
1:E:299:THR:HG21	1:E:345:PHE:CZ	2.26	0.71
1:E:296:ILE:HA	1:E:299:THR:HG22	1.74	0.70
1:C:165:ARG:HD3	1:C:243:ILE:HD11	1.73	0.69
1:B:294:LEU:CD2	1:C:294:LEU:CD1	2.69	0.69
1:C:48:GLU:HA	1:C:51:LEU:HD13	1.75	0.69
1:A:333:VAL:O	1:A:336:VAL:HG12	1.93	0.69
1:C:294:LEU:HD22	1:D:294:LEU:CD1	2.05	0.68
1:D:239:VAL:HB	1:D:242:LEU:HD23	1.76	0.68
1:A:208:VAL:HG12	1:E:278:VAL:HG13	1.74	0.68
1:C:296:ILE:CD1	1:C:297:ILE:HD12	2.23	0.68
1:A:118:ASN:O	1:A:120:HIS:N	2.26	0.68
1:A:225:ILE:HG21	1:A:261:ILE:HG22	1.76	0.68
1:E:310:ILE:O	1:E:313:MET:HG2	1.92	0.68
1:D:118:ASN:O	1:D:120:HIS:N	2.27	0.68
1:A:278:VAL:HA	1:B:276:LEU:HD21	1.76	0.68
1:D:67:ILE:HG22	1:D:67:ILE:O	1.92	0.68
1:D:232:LEU:CD2	1:D:254:VAL:HG12	2.23	0.67
1:B:296:ILE:CD1	1:B:297:ILE:HD12	2.23	0.67
1:A:82:ILE:HD13	1:A:130:ILE:HD13	1.76	0.67
1:E:160:ILE:O	1:E:160:ILE:HG22	1.95	0.67
1:D:293:VAL:HG12	1:D:294:LEU:N	2.10	0.67
1:D:296:ILE:HD11	1:D:297:ILE:HD12	1.75	0.67
1:C:67:ILE:HG22	1:C:91:LEU:HD23	1.76	0.67
1:E:150:VAL:HG11	1:E:173:LEU:HD23	1.76	0.67
1:E:267:THR:O	1:E:271:ILE:HD12	1.95	0.67
1:A:147:PHE:O	1:A:150:VAL:HG12	1.96	0.66
1:B:31:VAL:HG21	1:B:50:VAL:HG12	1.77	0.66
1:A:290:VAL:HG12	1:E:291:MET:CE	2.25	0.66
1:E:307:ILE:HA	1:E:310:ILE:HD12	1.77	0.66
1:E:267:THR:HG22	1:E:271:ILE:HD11	1.78	0.66
1:A:206:GLU:HB2	1:A:209:GLN:HG2	1.76	0.66
1:B:107:PHE:CZ	1:B:109:VAL:HG22	2.30	0.65
1:B:67:ILE:O	1:B:67:ILE:HG22	1.94	0.65
1:A:99:VAL:HG21	1:A:235:LEU:HD13	1.77	0.65
1:C:85:LEU:H	1:C:85:LEU:HD23	1.62	0.65
1:A:304:LEU:HD11	1:A:338:ALA:HB2	1.79	0.65
1:E:330:VAL:O	1:E:333:VAL:HG12	1.96	0.65
1:B:221:LEU:HG	1:B:225:ILE:CD1	2.15	0.65
1:A:221:LEU:HD12	1:A:225:ILE:HD11	1.79	0.65
1:C:196:GLU:O	1:C:200:LEU:HD22	1.97	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:236:TYR:HA	1:A:251:PHE:HZ	1.62	0.65
1:E:64:ILE:HD12	1:E:139:PHE:CE1	2.32	0.64
1:C:221:LEU:HG	1:C:225:ILE:CD1	2.27	0.64
1:B:295:THR:HG21	1:C:293:VAL:HG12	1.80	0.64
1:B:330:VAL:HA	1:B:333:VAL:HG12	1.79	0.64
1:D:191:GLU:HG3	1:D:195:LEU:HD22	1.80	0.64
1:A:196:GLU:O	1:A:200:LEU:HD22	1.96	0.64
1:B:178:VAL:HG13	1:B:261:ILE:HD11	1.78	0.64
1:C:77:GLY:HA2	1:C:82:ILE:HD12	1.79	0.64
1:B:302:MET:CE	1:C:298:ALA:HA	2.27	0.64
1:D:296:ILE:CD1	1:D:297:ILE:HD12	2.28	0.64
1:A:82:ILE:CD1	1:A:130:ILE:HD13	2.27	0.64
1:A:67:ILE:HG22	1:A:67:ILE:O	1.96	0.64
1:D:225:ILE:HG21	1:D:261:ILE:HG22	1.79	0.64
1:C:238:ASP:C	1:C:239:VAL:HG23	2.17	0.64
1:B:296:ILE:HD12	1:B:297:ILE:HD12	1.80	0.63
1:C:77:GLY:HA3	1:C:87:LEU:HD21	1.80	0.63
1:D:112:MET:CE	1:D:146:VAL:HG13	2.28	0.63
1:C:225:ILE:HG22	1:C:262:ALA:HB2	1.81	0.63
1:D:199:VAL:HG13	1:D:279:TYR:HA	1.81	0.63
1:A:160:ILE:HG22	1:A:160:ILE:O	1.98	0.63
1:A:208:VAL:CG1	1:E:278:VAL:HG13	2.29	0.62
1:A:264:THR:O	1:A:265:VAL:C	2.34	0.62
1:B:196:GLU:O	1:B:200:LEU:HD22	1.98	0.62
1:E:67:ILE:CG2	1:E:91:LEU:HD23	2.30	0.62
1:E:177:LEU:C	1:E:177:LEU:HD23	2.20	0.62
1:A:306:PHE:CE1	1:B:304:LEU:HB3	2.34	0.62
1:B:296:ILE:HA	1:B:299:THR:HG22	1.80	0.62
1:A:77:GLY:HA3	1:A:87:LEU:HD21	1.82	0.62
1:D:48:GLU:HA	1:D:51:LEU:HD13	1.81	0.62
1:D:177:LEU:HD23	1:D:177:LEU:C	2.20	0.62
1:A:225:ILE:CG2	1:A:262:ALA:HB2	2.30	0.62
1:B:302:MET:HE1	1:C:298:ALA:HA	1.80	0.62
1:D:99:VAL:HB	1:D:231:VAL:HG13	1.81	0.61
1:C:296:ILE:HG22	1:C:345:PHE:CD2	2.34	0.61
1:A:199:VAL:HG13	1:A:279:TYR:HA	1.82	0.61
1:A:293:VAL:O	1:A:296:ILE:HG13	2.01	0.61
1:D:112:MET:HE1	1:D:146:VAL:HG13	1.81	0.61
1:A:290:VAL:HG12	1:E:291:MET:HE3	1.82	0.61
1:B:310:ILE:HG22	1:B:311:TYR:HD1	1.65	0.61
1:A:270:ASP:OD2	1:B:269:ARG:NH1	2.34	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:299:THR:HG21	1:A:345:PHE:CE2	2.35	0.60
1:B:296:ILE:O	1:B:299:THR:HG22	2.01	0.60
1:D:294:LEU:HD22	1:E:294:LEU:HD11	1.83	0.60
1:E:99:VAL:HB	1:E:231:VAL:HG13	1.83	0.60
1:D:171:TYR:O	1:D:250:TYR:CE2	2.54	0.60
1:E:171:TYR:CD1	1:E:251:PHE:HB3	2.36	0.60
1:D:116:ASP:OD1	1:D:119:LEU:HB3	2.01	0.60
1:A:298:ALA:HA	1:E:302:MET:HE1	1.82	0.60
1:A:240:PRO:HB2	1:A:241:PRO:HD3	1.83	0.60
1:C:47:VAL:HG13	1:C:48:GLU:HG2	1.84	0.60
1:D:167:ASP:OD1	1:D:168:TYR:N	2.35	0.60
1:E:232:LEU:CD2	1:E:254:VAL:HG12	2.32	0.59
1:B:188:ILE:HD13	1:B:218:LEU:HD11	1.84	0.59
1:C:48:GLU:OE1	1:C:51:LEU:HD22	2.02	0.59
1:D:33:ASN:CB	1:D:60:THR:HG22	2.32	0.59
1:A:130:ILE:HD12	1:A:139:PHE:HE2	1.67	0.59
1:D:61:TRP:HB2	1:D:169:LEU:HD21	1.85	0.59
1:E:82:ILE:HD13	1:E:130:ILE:HD13	1.83	0.59
1:D:296:ILE:HD12	1:D:297:ILE:N	2.18	0.59
1:B:302:MET:HE3	1:C:301:PHE:CB	2.31	0.59
1:D:77:GLY:HA3	1:D:87:LEU:HD21	1.85	0.59
1:A:137:LEU:HD22	1:A:139:PHE:CE2	2.38	0.59
1:D:171:TYR:CD1	1:D:251:PHE:HB3	2.37	0.59
1:E:160:ILE:HG23	1:E:163:LYS:HE3	1.84	0.59
1:C:160:ILE:O	1:C:160:ILE:HG22	2.03	0.59
1:C:33:ASN:ND2	1:C:58:THR:O	2.36	0.59
1:C:300:ILE:HD11	1:C:301:PHE:CE1	2.37	0.59
1:A:137:LEU:HD23	1:A:138:MET:N	2.18	0.59
1:C:177:LEU:HD23	1:C:177:LEU:C	2.24	0.59
1:E:185:LEU:HD11	1:E:261:ILE:HG23	1.83	0.59
1:C:67:ILE:CG2	1:C:91:LEU:HD23	2.33	0.58
1:B:302:MET:CE	1:C:301:PHE:HB2	2.33	0.58
1:B:47:VAL:CG2	1:B:72:VAL:HG13	2.33	0.58
1:C:67:ILE:O	1:C:67:ILE:HG22	2.04	0.58
1:A:291:MET:HE1	1:B:291:MET:HA	1.86	0.58
1:A:64:ILE:HD12	1:A:139:PHE:CE1	2.38	0.58
1:D:33:ASN:ND2	1:D:58:THR:O	2.36	0.58
1:D:112:MET:HE1	1:D:146:VAL:N	2.18	0.58
1:E:221:LEU:CD1	1:E:225:ILE:HD11	2.32	0.58
1:D:67:ILE:HD11	1:D:139:PHE:O	2.03	0.58
1:A:108:ILE:CD1	1:A:235:LEU:HD21	2.33	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:99:VAL:HG23	1:B:108:ILE:HG12	1.84	0.58
1:D:333:VAL:HA	1:D:336:VAL:HG12	1.86	0.57
1:C:122:LEU:HD22	1:C:217:ASN:ND2	2.19	0.57
1:B:225:ILE:HG21	1:B:261:ILE:HG22	1.85	0.57
1:B:291:MET:HE2	1:C:290:VAL:HG12	1.85	0.57
1:E:199:VAL:HG13	1:E:279:TYR:HA	1.86	0.57
1:C:296:ILE:HA	1:C:299:THR:HG22	1.85	0.57
1:A:177:LEU:HD23	1:A:181:TYR:HE2	1.69	0.57
1:D:313:MET:HE1	1:E:308:ALA:O	2.04	0.57
1:C:333:VAL:HA	1:C:336:VAL:HG12	1.85	0.57
1:E:202:ARG:N	1:E:203:PRO:HD3	2.19	0.57
1:C:185:LEU:HD13	1:C:264:THR:HG21	1.86	0.57
1:E:113:PHE:HB2	1:E:184:LEU:HD21	1.85	0.57
1:E:211:THR:CG2	1:E:276:LEU:HD13	2.34	0.57
1:D:285:ASN:O	1:D:288:ASN:HB3	2.05	0.57
1:A:225:ILE:HD12	1:A:225:ILE:N	2.20	0.57
1:D:240:PRO:HB2	1:D:241:PRO:HD3	1.87	0.57
1:A:327:TYR:HA	1:E:315:PHE:CZ	2.40	0.57
1:D:225:ILE:O	1:D:229:ARG:N	2.37	0.56
1:D:299:THR:HG21	1:D:345:PHE:CZ	2.40	0.56
1:A:296:ILE:HD12	1:A:297:ILE:N	2.20	0.56
1:B:48:GLU:HA	1:B:51:LEU:HD13	1.88	0.56
1:C:296:ILE:HD11	1:C:297:ILE:HD12	1.87	0.56
1:C:296:ILE:HD12	1:C:297:ILE:HD12	1.86	0.56
1:B:296:ILE:HD11	1:B:297:ILE:CD1	2.35	0.56
1:C:171:TYR:CD1	1:C:251:PHE:HB3	2.39	0.56
1:A:31:VAL:HA	1:A:61:TRP:O	2.05	0.56
1:B:147:PHE:O	1:B:150:VAL:HG12	2.05	0.56
1:D:26:ASP:O	1:D:68:HIS:NE2	2.32	0.56
1:E:44:THR:HG21	1:E:49:SER:OG	2.06	0.56
1:A:290:VAL:HG13	1:E:295:THR:OG1	2.05	0.56
1:E:63:ASN:HB2	1:E:138:MET:HE2	1.87	0.56
1:B:310:ILE:HG22	1:B:311:TYR:CD1	2.40	0.56
1:C:300:ILE:HG13	1:C:301:PHE:N	2.21	0.56
1:C:122:LEU:CD2	1:C:217:ASN:ND2	2.69	0.56
1:A:219:VAL:HG22	1:A:269:ARG:HE	1.69	0.56
1:B:73:VAL:CG1	1:B:87:LEU:HD22	2.36	0.56
1:C:71:ASP:OD1	1:C:72:VAL:N	2.39	0.56
1:C:239:VAL:HB	1:C:242:LEU:HD23	1.87	0.56
1:E:27:PHE:CZ	1:E:72:VAL:HG21	2.41	0.56
1:E:225:ILE:HG22	1:E:262:ALA:HB2	1.88	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:171:TYR:OH	1:B:235:LEU:HG	2.05	0.56
1:C:99:VAL:HB	1:C:231:VAL:HG13	1.88	0.55
1:A:238:ASP:C	1:A:239:VAL:HG23	2.26	0.55
1:D:235:LEU:O	1:D:239:VAL:HG22	2.06	0.55
1:B:190:ASP:O	1:B:194:VAL:HG23	2.06	0.55
1:D:196:GLU:O	1:D:200:LEU:HD22	2.05	0.55
1:C:70:THR:HG22	1:C:91:LEU:CD2	2.32	0.55
1:A:311:TYR:HB2	1:E:313:MET:SD	2.47	0.55
1:E:270:ASP:O	1:E:273:SER:OG	2.24	0.55
1:C:232:LEU:HD23	1:C:255:TYR:N	2.22	0.55
1:A:331:LEU:HD12	1:A:334:MET:CE	2.36	0.55
1:E:213:GLN:O	1:E:216:ARG:HB3	2.07	0.55
1:B:240:PRO:HB2	1:B:241:PRO:HD3	1.88	0.55
1:A:170:LEU:O	1:A:172:SER:N	2.34	0.55
1:A:151:ARG:O	1:A:154:ILE:HB	2.06	0.55
1:E:221:LEU:HG	1:E:225:ILE:CD1	2.25	0.55
1:E:150:VAL:HG11	1:E:173:LEU:CD2	2.36	0.55
1:E:226:TRP:N	1:E:227:PRO:HD2	2.21	0.55
1:C:218:LEU:HD21	1:C:268:PHE:HB3	1.88	0.55
1:C:295:THR:O	1:C:299:THR:HG22	2.06	0.54
1:D:33:ASN:CG	1:D:60:THR:CG2	2.69	0.54
1:C:171:TYR:O	1:C:250:TYR:CE2	2.59	0.54
1:C:51:LEU:N	1:C:52:PRO:HD2	2.23	0.54
1:A:251:PHE:HA	1:A:254:VAL:HG23	1.88	0.54
1:B:149:PRO:O	1:B:153:ARG:HG3	2.06	0.54
1:B:171:TYR:CD1	1:B:251:PHE:HB3	2.42	0.54
1:C:167:ASP:OD1	1:C:168:TYR:N	2.40	0.54
1:B:294:LEU:HD23	1:B:294:LEU:O	2.07	0.54
1:C:174:ILE:HD13	1:C:232:LEU:HD11	1.90	0.54
1:C:291:MET:CE	1:D:290:VAL:HG12	2.38	0.54
1:A:295:THR:OG1	1:B:290:VAL:HG13	2.07	0.54
1:A:232:LEU:HD23	1:A:255:TYR:N	2.22	0.54
1:A:171:TYR:CD1	1:A:247:THR:HG22	2.43	0.54
1:D:202:ARG:N	1:D:203:PRO:HD3	2.22	0.54
1:E:240:PRO:HB2	1:E:241:PRO:HD3	1.90	0.54
1:A:221:LEU:O	1:A:225:ILE:HD12	2.07	0.54
1:D:51:LEU:N	1:D:52:PRO:HD2	2.23	0.54
1:D:232:LEU:HD23	1:D:255:TYR:N	2.23	0.54
1:D:132:THR:HG23	1:D:135:CYS:HB2	1.90	0.54
1:D:291:MET:O	1:D:295:THR:OG1	2.26	0.54
1:D:90:ILE:HG23	1:D:128:SER:OG	2.08	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:238:ASP:C	1:E:239:VAL:HG23	2.26	0.54
1:D:85:LEU:H	1:D:85:LEU:HD23	1.73	0.54
1:E:330:VAL:CG1	1:E:331:LEU:HD12	2.36	0.54
1:A:292:LYS:O	1:A:296:ILE:HG23	2.08	0.54
1:D:99:VAL:HG11	1:D:234:SER:HB3	1.89	0.54
1:B:85:LEU:HD23	1:B:85:LEU:H	1.73	0.54
1:D:291:MET:HE1	1:E:291:MET:HA	1.90	0.53
1:B:291:MET:CE	1:C:290:VAL:CG1	2.84	0.53
1:A:67:ILE:HG13	1:A:140:GLN:O	2.09	0.53
1:A:152:GLU:OE1	1:A:156:TYR:CD2	2.61	0.53
1:E:51:LEU:N	1:E:52:PRO:HD2	2.24	0.53
1:C:202:ARG:N	1:C:203:PRO:HD3	2.23	0.53
1:E:293:VAL:HG12	1:E:294:LEU:N	2.24	0.53
1:D:232:LEU:HD21	1:D:254:VAL:HG12	1.90	0.53
1:A:130:ILE:HD12	1:A:139:PHE:CE2	2.43	0.53
1:A:296:ILE:O	1:A:299:THR:HG22	2.07	0.53
1:B:51:LEU:N	1:B:52:PRO:HD2	2.24	0.53
1:A:152:GLU:OE1	1:A:156:TYR:CE2	2.62	0.53
1:D:300:ILE:HG22	1:D:341:MET:HG2	1.90	0.53
1:D:150:VAL:HG11	1:D:173:LEU:HD23	1.89	0.53
1:A:330:VAL:O	1:A:333:VAL:HG12	2.08	0.53
1:E:165:ARG:HD3	1:E:243:ILE:HD11	1.90	0.53
1:C:275:LEU:O	1:C:276:LEU:C	2.45	0.53
1:C:117:LYS:O	1:C:118:ASN:HB2	2.09	0.53
1:E:199:VAL:HG12	1:E:278:VAL:HG12	1.90	0.53
1:E:171:TYR:OH	1:E:235:LEU:HG	2.08	0.53
1:D:315:PHE:CE2	1:E:327:TYR:HA	2.44	0.53
1:D:235:LEU:O	1:D:239:VAL:CG2	2.57	0.53
1:D:304:LEU:HD11	1:D:338:ALA:HB2	1.90	0.53
1:B:327:TYR:HB3	1:B:328:PRO:HD3	1.91	0.53
1:E:236:TYR:HA	1:E:251:PHE:CZ	2.37	0.53
1:B:150:VAL:HG11	1:B:173:LEU:HD23	1.90	0.53
1:A:85:LEU:H	1:A:85:LEU:HD23	1.74	0.53
1:E:33:ASN:HA	1:E:60:THR:HA	1.91	0.52
1:A:61:TRP:HB2	1:A:169:LEU:HD21	1.92	0.52
1:B:277:ASP:HB3	1:C:276:LEU:HD23	1.91	0.52
1:C:31:VAL:HG22	1:C:62:ILE:HG23	1.91	0.52
1:D:171:TYR:CD1	1:D:247:THR:HG22	2.45	0.52
1:D:137:LEU:HD22	1:D:139:PHE:CZ	2.45	0.52
1:B:27:PHE:CZ	1:B:29:ILE:HD11	2.45	0.52
1:D:295:THR:HA	1:E:294:LEU:HD12	1.91	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:112:MET:HE1	1:A:146:VAL:N	2.25	0.52
1:D:268:PHE:C	1:D:270:ASP:H	2.13	0.52
1:B:31:VAL:HG21	1:B:50:VAL:CG1	2.39	0.52
1:B:109:VAL:O	1:B:110:LEU:HD23	2.10	0.52
1:C:33:ASN:ND2	1:C:60:THR:HG22	2.23	0.52
1:C:181:TYR:CB	1:C:261:ILE:HD13	2.40	0.52
1:B:136:VAL:CG2	1:B:169:LEU:HD23	2.40	0.52
1:A:268:PHE:C	1:A:270:ASP:H	2.13	0.52
1:A:145:ASP:OD1	1:A:147:PHE:N	2.39	0.51
1:C:303:PRO:HA	1:C:306:PHE:HB3	1.91	0.51
1:B:296:ILE:HD11	1:B:297:ILE:HD12	1.91	0.51
1:D:224:THR:CG2	1:D:224:THR:O	2.57	0.51
1:E:330:VAL:HG13	1:E:331:LEU:N	2.25	0.51
1:E:33:ASN:ND2	1:E:60:THR:HG22	2.24	0.51
1:B:295:THR:O	1:B:299:THR:HB	2.09	0.51
1:A:136:VAL:HG11	1:A:173:LEU:HD12	1.93	0.51
1:A:112:MET:HE1	1:A:146:VAL:HG13	1.92	0.51
1:B:132:THR:HG23	1:B:132:THR:O	2.11	0.51
1:C:154:ILE:CG1	1:C:161:ILE:HG21	2.40	0.51
1:D:82:ILE:HD13	1:D:130:ILE:HD13	1.92	0.51
1:B:225:ILE:HG21	1:B:261:ILE:CG2	2.41	0.51
1:B:330:VAL:O	1:B:333:VAL:HG12	2.11	0.51
1:B:33:ASN:CG	1:B:60:THR:HG22	2.30	0.51
1:A:112:MET:CE	1:A:146:VAL:HG22	2.41	0.51
1:B:165:ARG:HD3	1:B:243:ILE:HD11	1.93	0.51
1:A:67:ILE:O	1:A:67:ILE:CG2	2.59	0.51
1:C:166:ALA:O	1:C:169:LEU:HB3	2.11	0.51
1:B:267:THR:O	1:B:271:ILE:HD12	2.09	0.51
1:D:296:ILE:HG22	1:D:345:PHE:CE2	2.46	0.50
1:E:67:ILE:HD11	1:E:139:PHE:O	2.11	0.50
1:B:99:VAL:HB	1:B:231:VAL:HG13	1.93	0.50
1:D:47:VAL:O	1:D:50:VAL:HG22	2.11	0.50
1:C:240:PRO:HB2	1:C:241:PRO:HD3	1.92	0.50
1:A:48:GLU:HA	1:A:51:LEU:HD13	1.92	0.50
1:D:296:ILE:HA	1:D:299:THR:HG22	1.93	0.50
1:E:267:THR:HG22	1:E:271:ILE:CD1	2.41	0.50
1:E:33:ASN:CG	1:E:60:THR:HG22	2.32	0.50
1:D:236:TYR:OH	1:D:252:ARG:HD2	2.11	0.50
1:D:238:ASP:C	1:D:239:VAL:HG23	2.31	0.50
1:B:219:VAL:HG22	1:B:269:ARG:HE	1.76	0.50
1:A:132:THR:HG23	1:A:135:CYS:HB2	1.93	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:73:VAL:CG1	1:A:87:LEU:HD22	2.40	0.50
1:C:199:VAL:HG11	1:C:278:VAL:HB	1.93	0.50
1:D:53:PHE:O	1:D:54:ARG:C	2.50	0.50
1:B:221:LEU:O	1:B:225:ILE:HD12	2.11	0.50
1:E:200:LEU:H	1:E:200:LEU:HD13	1.76	0.50
1:A:327:TYR:O	1:A:330:VAL:HG12	2.12	0.50
1:C:222:ALA:HB2	1:C:265:VAL:CG1	2.42	0.50
1:E:61:TRP:HB2	1:E:169:LEU:HD21	1.92	0.50
1:D:243:ILE:HG22	1:D:246:GLU:HB2	1.94	0.50
1:E:254:VAL:O	1:E:255:TYR:C	2.50	0.50
1:D:67:ILE:HG13	1:D:140:GLN:O	2.12	0.50
1:A:243:ILE:HG22	1:A:246:GLU:HB2	1.93	0.50
1:B:238:ASP:C	1:B:239:VAL:HG23	2.32	0.49
1:D:225:ILE:HD13	1:D:265:VAL:HG21	1.94	0.49
1:E:47:VAL:O	1:E:50:VAL:HG22	2.12	0.49
1:C:132:THR:HG23	1:C:135:CYS:HB2	1.94	0.49
1:D:293:VAL:O	1:D:294:LEU:C	2.51	0.49
1:E:199:VAL:CG1	1:E:278:VAL:HG12	2.42	0.49
1:D:298:ALA:O	1:D:302:MET:CG	2.61	0.49
1:E:195:LEU:HD11	1:E:210:ARG:HD3	1.93	0.49
1:E:256:ASP:O	1:E:259:ILE:N	2.43	0.49
1:A:67:ILE:HD11	1:A:139:PHE:O	2.13	0.49
1:D:48:GLU:OE1	1:D:51:LEU:HD22	2.13	0.49
1:B:291:MET:O	1:B:291:MET:HE3	2.13	0.49
1:B:26:ASP:O	1:B:68:HIS:NE2	2.40	0.49
1:C:82:ILE:HD13	1:C:130:ILE:HD13	1.95	0.49
1:A:33:ASN:HB2	1:A:60:THR:HG22	1.95	0.49
1:E:333:VAL:O	1:E:336:VAL:HG12	2.12	0.49
1:A:259:ILE:HG22	1:A:260:GLN:N	2.28	0.49
1:B:67:ILE:CG2	1:B:91:LEU:HD23	2.42	0.49
1:B:221:LEU:CG	1:B:225:ILE:HD11	2.18	0.49
1:C:294:LEU:HD23	1:C:294:LEU:C	2.32	0.49
1:B:136:VAL:HG21	1:B:169:LEU:HB3	1.95	0.49
1:A:26:ASP:O	1:A:68:HIS:NE2	2.45	0.49
1:B:294:LEU:C	1:B:294:LEU:CD2	2.77	0.49
1:A:221:LEU:HD11	1:A:225:ILE:HD11	1.90	0.49
1:B:298:ALA:O	1:B:302:MET:HG2	2.13	0.49
1:C:171:TYR:CE1	1:C:251:PHE:CD2	3.00	0.49
1:A:33:ASN:CB	1:A:60:THR:HG22	2.43	0.49
1:D:88:GLU:HA	1:D:91:LEU:HD12	1.93	0.49
1:E:131:LEU:HD12	1:E:132:THR:N	2.27	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:294:LEU:HD11	1:E:294:LEU:CD2	2.43	0.48
1:E:232:LEU:HD23	1:E:255:TYR:N	2.28	0.48
1:E:31:VAL:HA	1:E:61:TRP:O	2.13	0.48
1:A:264:THR:O	1:A:267:THR:N	2.45	0.48
1:D:197:GLU:HA	1:D:200:LEU:HD23	1.95	0.48
1:E:131:LEU:HD12	1:E:132:THR:H	1.77	0.48
1:B:93:VAL:HG11	1:B:141:GLU:OE1	2.13	0.48
1:C:174:ILE:HG22	1:C:254:VAL:HG11	1.95	0.48
1:E:232:LEU:HD21	1:E:254:VAL:HG12	1.95	0.48
1:B:129:LEU:HD13	1:B:170:LEU:CD1	2.44	0.48
1:E:256:ASP:O	1:E:257:HIS:C	2.52	0.48
1:A:235:LEU:O	1:A:239:VAL:HG22	2.14	0.48
1:A:185:LEU:O	1:A:186:GLU:C	2.51	0.48
1:B:296:ILE:CD1	1:B:297:ILE:CD1	2.91	0.48
1:A:171:TYR:CD1	1:A:251:PHE:HB3	2.48	0.48
1:E:239:VAL:HB	1:E:242:LEU:HD23	1.96	0.48
1:C:226:TRP:N	1:C:227:PRO:HD2	2.28	0.48
1:C:295:THR:CG2	1:D:293:VAL:HG12	2.43	0.48
1:D:295:THR:HG23	1:E:294:LEU:CB	2.40	0.48
1:D:33:ASN:HA	1:D:60:THR:HA	1.94	0.48
1:E:67:ILE:O	1:E:67:ILE:CG2	2.61	0.48
1:C:188:ILE:HG22	1:C:268:PHE:CE2	2.49	0.48
1:C:219:VAL:HG22	1:C:269:ARG:HE	1.79	0.48
1:E:296:ILE:CG2	1:E:345:PHE:CE2	2.93	0.48
1:C:82:ILE:HD13	1:C:130:ILE:CD1	2.44	0.48
1:C:291:MET:HE2	1:D:290:VAL:HG12	1.96	0.48
1:D:202:ARG:O	1:D:204:GLU:N	2.47	0.48
1:D:315:PHE:CZ	1:E:327:TYR:HA	2.49	0.48
1:A:296:ILE:HA	1:A:345:PHE:HE2	1.77	0.48
1:B:67:ILE:HD11	1:B:139:PHE:O	2.14	0.48
1:A:202:ARG:N	1:A:203:PRO:HD3	2.28	0.48
1:D:48:GLU:O	1:D:50:VAL:N	2.47	0.47
1:C:192:ILE:O	1:C:193:ASP:C	2.51	0.47
1:C:181:TYR:HB3	1:C:261:ILE:HD13	1.96	0.47
1:E:292:LYS:HD3	1:E:348:LYS:HG2	1.96	0.47
1:A:137:LEU:HD23	1:A:138:MET:H	1.80	0.47
1:A:196:GLU:HG2	1:A:200:LEU:HD21	1.95	0.47
1:C:302:MET:HB2	1:C:303:PRO:CD	2.44	0.47
1:A:51:LEU:N	1:A:52:PRO:HD2	2.30	0.47
1:E:264:THR:O	1:E:265:VAL:C	2.52	0.47
1:E:232:LEU:HD21	1:E:254:VAL:CG1	2.45	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:306:PHE:CE1	1:C:304:LEU:HB3	2.50	0.47
1:A:137:LEU:HD22	1:A:139:PHE:CZ	2.50	0.47
1:D:33:ASN:HD22	1:D:34:TYR:N	2.13	0.47
1:C:148:ASP:N	1:C:149:PRO:HD2	2.30	0.47
1:D:211:THR:O	1:D:211:THR:HG22	2.15	0.47
1:E:224:THR:HG22	1:E:224:THR:O	2.15	0.47
1:E:333:VAL:HA	1:E:336:VAL:HG12	1.95	0.47
1:C:171:TYR:CD1	1:C:247:THR:HG22	2.50	0.47
1:A:33:ASN:ND2	1:A:60:THR:HG22	2.30	0.47
1:A:153:ARG:NE	1:A:161:ILE:HD11	2.29	0.47
1:A:195:LEU:HG	1:A:210:ARG:HD3	1.97	0.47
1:E:204:GLU:O	1:E:279:TYR:OH	2.27	0.47
1:B:296:ILE:CA	1:B:299:THR:HG22	2.45	0.47
1:C:221:LEU:O	1:C:225:ILE:HD12	2.14	0.47
1:A:186:GLU:O	1:A:187:LYS:C	2.53	0.47
1:B:131:LEU:HD21	1:B:167:ASP:CB	2.45	0.47
1:B:178:VAL:HG13	1:B:261:ILE:CD1	2.45	0.47
1:A:109:VAL:O	1:A:110:LEU:HD23	2.15	0.47
1:C:131:LEU:HD21	1:C:167:ASP:HA	1.95	0.47
1:A:136:VAL:HG11	1:A:173:LEU:CD1	2.44	0.47
1:A:311:TYR:CD1	1:A:311:TYR:N	2.83	0.47
1:E:85:LEU:H	1:E:85:LEU:HD23	1.79	0.47
1:A:290:VAL:CG1	1:E:291:MET:HE3	2.45	0.47
1:A:291:MET:HA	1:E:291:MET:HE1	1.97	0.47
1:D:293:VAL:CG1	1:D:294:LEU:N	2.78	0.47
1:B:298:ALA:O	1:B:302:MET:CG	2.63	0.47
1:D:171:TYR:HB3	1:D:250:TYR:CE2	2.50	0.47
1:B:64:ILE:HD12	1:B:139:PHE:CE1	2.50	0.47
1:C:33:ASN:HA	1:C:60:THR:HA	1.96	0.47
1:A:156:TYR:O	1:A:157:ASN:C	2.53	0.47
1:E:156:TYR:O	1:E:157:ASN:C	2.54	0.47
1:B:160:ILE:HG22	1:B:160:ILE:O	2.15	0.47
1:A:339:VAL:HA	1:A:342:VAL:HG12	1.97	0.47
1:B:296:ILE:HA	1:B:299:THR:CG2	2.45	0.46
1:B:302:MET:HE2	1:C:298:ALA:HA	1.97	0.46
1:E:197:GLU:CA	1:E:200:LEU:HD22	2.40	0.46
1:D:336:VAL:HG13	1:D:337:ILE:N	2.30	0.46
1:D:270:ASP:OD2	1:E:269:ARG:NH1	2.48	0.46
1:A:286:LYS:O	1:A:287:THR:C	2.53	0.46
1:B:171:TYR:O	1:B:250:TYR:CE2	2.68	0.46
1:D:67:ILE:O	1:D:67:ILE:CG2	2.60	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:218:LEU:HD12	1:A:218:LEU:HA	1.73	0.46
1:B:153:ARG:NE	1:B:161:ILE:HD11	2.30	0.46
1:C:306:PHE:CE1	1:D:304:LEU:HB3	2.49	0.46
1:A:226:TRP:N	1:A:227:PRO:HD2	2.31	0.46
1:A:327:TYR:HA	1:E:315:PHE:CE2	2.51	0.46
1:C:122:LEU:H	1:C:122:LEU:HD23	1.79	0.46
1:C:333:VAL:O	1:C:336:VAL:HG12	2.16	0.46
1:C:296:ILE:O	1:C:299:THR:HG22	2.16	0.46
1:A:110:LEU:HD22	1:A:228:LEU:CD1	2.45	0.46
1:B:67:ILE:O	1:B:67:ILE:CG2	2.62	0.46
1:C:222:ALA:HB2	1:C:265:VAL:HG11	1.96	0.46
1:A:286:LYS:O	1:A:289:GLU:N	2.49	0.46
1:C:29:ILE:HG23	1:C:63:ASN:O	2.15	0.46
1:A:224:THR:O	1:A:224:THR:CG2	2.63	0.46
1:C:137:LEU:HD22	1:C:139:PHE:CZ	2.50	0.46
1:E:171:TYR:CE1	1:E:251:PHE:CG	3.04	0.46
1:D:330:VAL:CG1	1:D:331:LEU:HD12	2.44	0.46
1:C:122:LEU:CD2	1:C:217:ASN:HD22	2.28	0.46
1:E:283:VAL:O	1:E:286:LYS:N	2.48	0.46
1:A:294:LEU:HD11	1:E:294:LEU:HD22	1.95	0.46
1:B:293:VAL:O	1:B:296:ILE:HG13	2.15	0.46
1:E:171:TYR:CE1	1:E:251:PHE:CD2	3.03	0.46
1:E:192:ILE:HG22	1:E:193:ASP:N	2.30	0.46
1:A:348:LYS:HZ2	1:B:290:VAL:HG22	1.81	0.46
1:A:240:PRO:CB	1:A:241:PRO:HD3	2.46	0.46
1:B:82:ILE:HG22	1:B:83:HIS:O	2.16	0.46
1:D:232:LEU:HD21	1:D:254:VAL:CG1	2.44	0.46
1:A:63:ASN:HB2	1:A:138:MET:HE2	1.96	0.46
1:D:171:TYR:O	1:D:250:TYR:CZ	2.69	0.46
1:D:170:LEU:C	1:D:172:SER:H	2.19	0.46
1:A:33:ASN:HA	1:A:60:THR:HA	1.96	0.46
1:B:117:LYS:O	1:B:118:ASN:HB2	2.16	0.46
1:A:221:LEU:CG	1:A:225:ILE:HD11	2.45	0.46
1:D:195:LEU:HD11	1:D:210:ARG:HD3	1.98	0.46
1:A:202:ARG:O	1:A:204:GLU:N	2.49	0.46
1:A:86:VAL:HG13	1:A:107:PHE:CD2	2.51	0.46
1:B:146:VAL:HG11	1:B:180:ASP:HB2	1.97	0.46
1:B:296:ILE:HD12	1:B:297:ILE:N	2.31	0.45
1:D:151:ARG:O	1:D:154:ILE:HB	2.15	0.45
1:C:184:LEU:O	1:C:185:LEU:C	2.54	0.45
1:C:313:MET:HE3	1:D:308:ALA:CB	2.43	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:225:ILE:CG2	1:C:262:ALA:HB2	2.45	0.45
1:A:136:VAL:CG2	1:A:169:LEU:HD23	2.47	0.45
1:E:212:HIS:O	1:E:213:GLN:C	2.54	0.45
1:C:188:ILE:O	1:C:189:ASP:C	2.52	0.45
1:D:289:GLU:O	1:D:290:VAL:C	2.55	0.45
1:B:202:ARG:O	1:B:204:GLU:N	2.50	0.45
1:E:199:VAL:HG13	1:E:279:TYR:CA	2.47	0.45
1:B:306:PHE:CE2	1:B:310:ILE:HD11	2.52	0.45
1:B:199:VAL:HG13	1:B:279:TYR:HA	1.98	0.45
1:E:300:ILE:HG22	1:E:341:MET:CG	2.45	0.45
1:E:200:LEU:HD13	1:E:200:LEU:N	2.32	0.45
1:D:156:TYR:O	1:D:157:ASN:C	2.54	0.45
1:B:33:ASN:CB	1:B:60:THR:HG22	2.46	0.45
1:D:180:ASP:O	1:D:183:VAL:HB	2.16	0.45
1:B:250:TYR:C	1:B:250:TYR:CD2	2.90	0.45
1:D:224:THR:HG22	1:D:224:THR:O	2.16	0.45
1:B:148:ASP:N	1:B:149:PRO:HD2	2.31	0.45
1:B:297:ILE:HG22	1:B:298:ALA:N	2.32	0.45
1:B:303:PRO:O	1:B:306:PHE:HB3	2.17	0.45
1:A:173:LEU:O	1:A:176:ALA:HB3	2.16	0.45
1:C:67:ILE:HD11	1:C:139:PHE:O	2.17	0.45
1:B:303:PRO:HA	1:B:306:PHE:HB3	1.99	0.45
1:B:99:VAL:HG21	1:B:235:LEU:HD13	1.99	0.45
1:C:145:ASP:OD1	1:C:147:PHE:N	2.46	0.45
1:E:327:TYR:HB3	1:E:328:PRO:HD3	1.99	0.45
1:A:152:GLU:OE2	1:A:155:ARG:HD2	2.17	0.45
1:E:97:PRO:HD3	1:E:111:LYS:HE2	2.00	0.44
1:E:111:LYS:HG2	1:E:126:GLN:HG3	2.00	0.44
1:A:280:LEU:HD23	1:B:280:LEU:HD21	1.99	0.44
1:A:221:LEU:HG	1:A:225:ILE:CD1	2.47	0.44
1:A:97:PRO:HD3	1:A:111:LYS:HE2	1.99	0.44
1:C:236:TYR:HA	1:C:251:PHE:CZ	2.43	0.44
1:B:330:VAL:CA	1:B:333:VAL:HG12	2.47	0.44
1:C:215:LYS:O	1:C:219:VAL:HG23	2.17	0.44
1:C:136:VAL:HG21	1:C:169:LEU:HG	2.00	0.44
1:A:333:VAL:HA	1:A:336:VAL:HG12	1.98	0.44
1:C:71:ASP:OD1	1:C:72:VAL:HG23	2.17	0.44
1:A:276:LEU:O	1:A:279:TYR:HB3	2.17	0.44
1:A:242:LEU:HD12	1:A:242:LEU:H	1.82	0.44
1:D:302:MET:HE3	1:E:298:ALA:HA	1.95	0.44
1:A:218:LEU:HB3	1:A:269:ARG:HG3	1.99	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:302:MET:HB2	1:C:303:PRO:HD3	1.98	0.44
1:C:108:ILE:HG22	1:C:110:LEU:HG	1.99	0.44
1:D:206:GLU:HB2	1:D:209:GLN:HG2	1.99	0.44
1:A:171:TYR:CE1	1:A:251:PHE:CD2	3.06	0.44
1:E:47:VAL:HG23	1:E:72:VAL:HG13	2.00	0.44
1:A:87:LEU:O	1:A:90:ILE:HB	2.17	0.44
1:E:330:VAL:CG1	1:E:331:LEU:N	2.81	0.44
1:C:296:ILE:CA	1:C:299:THR:HG22	2.48	0.44
1:B:171:TYR:CD1	1:B:247:THR:HG22	2.53	0.44
1:D:306:PHE:CE2	1:D:310:ILE:HD11	2.53	0.44
1:D:171:TYR:CE1	1:D:251:PHE:CD2	3.06	0.44
1:A:265:VAL:O	1:A:268:PHE:N	2.51	0.44
1:C:69:ARG:HB3	1:C:72:VAL:HG23	2.00	0.44
1:B:209:GLN:HG3	1:B:210:ARG:N	2.32	0.44
1:E:196:GLU:O	1:E:200:LEU:HD13	2.18	0.44
1:D:150:VAL:CG1	1:D:151:ARG:N	2.81	0.44
1:A:308:ALA:O	1:E:313:MET:HE3	2.17	0.44
1:D:119:LEU:HD12	1:D:119:LEU:C	2.39	0.44
1:A:167:ASP:OD1	1:A:168:TYR:N	2.51	0.44
1:D:313:MET:HA	1:E:311:TYR:O	2.18	0.43
1:A:296:ILE:HG22	1:A:345:PHE:CE2	2.52	0.43
1:E:113:PHE:CB	1:E:184:LEU:HD21	2.47	0.43
1:D:125:GLU:OE1	1:D:142:LYS:HG2	2.18	0.43
1:D:295:THR:CA	1:E:294:LEU:HD12	2.47	0.43
1:B:152:GLU:OE2	1:B:155:ARG:NH1	2.51	0.43
1:E:117:LYS:O	1:E:118:ASN:HB2	2.17	0.43
1:D:247:THR:O	1:D:250:TYR:HB3	2.17	0.43
1:B:156:TYR:O	1:B:157:ASN:C	2.56	0.43
1:C:296:ILE:HA	1:C:345:PHE:HE2	1.83	0.43
1:E:272:VAL:O	1:E:273:SER:C	2.57	0.43
1:D:90:ILE:HG23	1:D:128:SER:CB	2.49	0.43
1:D:165:ARG:HD3	1:D:243:ILE:HD11	2.01	0.43
1:C:214:LEU:O	1:C:215:LYS:C	2.55	0.43
1:E:214:LEU:HD12	1:E:214:LEU:HA	1.73	0.43
1:C:61:TRP:HE1	1:C:138:MET:HE2	1.83	0.43
1:A:295:THR:OG1	1:B:290:VAL:CG1	2.67	0.43
1:D:152:GLU:OE1	1:D:156:TYR:CE2	2.70	0.43
1:A:130:ILE:HB	1:A:137:LEU:HB3	2.01	0.43
1:A:82:ILE:HG22	1:A:83:HIS:O	2.17	0.43
1:E:108:ILE:HG22	1:E:110:LEU:HG	2.00	0.43
1:A:153:ARG:NH2	1:A:161:ILE:HD11	2.33	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:305:THR:O	1:A:305:THR:HG22	2.18	0.43
1:D:327:TYR:HB3	1:D:328:PRO:HD3	2.00	0.43
1:B:339:VAL:O	1:B:342:VAL:HG12	2.18	0.43
1:C:82:ILE:CD1	1:C:130:ILE:HD13	2.49	0.43
1:D:99:VAL:HG13	1:D:99:VAL:O	2.18	0.43
1:D:82:ILE:CD1	1:D:130:ILE:HD13	2.49	0.43
1:E:225:ILE:CG2	1:E:262:ALA:HB2	2.48	0.43
1:A:208:VAL:CG2	1:A:279:TYR:CZ	3.01	0.43
1:A:108:ILE:HD11	1:A:235:LEU:CD2	2.43	0.43
1:D:236:TYR:HA	1:D:251:PHE:CZ	2.39	0.43
1:C:275:LEU:O	1:C:278:VAL:N	2.49	0.43
1:C:327:TYR:HB3	1:C:328:PRO:HD3	2.00	0.43
1:E:228:LEU:HD23	1:E:228:LEU:O	2.19	0.43
1:C:238:ASP:C	1:C:239:VAL:CG2	2.87	0.42
1:B:82:ILE:HD13	1:B:130:ILE:HD13	2.01	0.42
1:A:291:MET:HE3	1:B:290:VAL:HG12	2.00	0.42
1:B:296:ILE:HG22	1:B:345:PHE:CE2	2.54	0.42
1:C:61:TRP:HB2	1:C:169:LEU:HD21	2.01	0.42
1:D:341:MET:O	1:D:344:TYR:N	2.52	0.42
1:D:83:HIS:HB2	1:D:86:VAL:CG2	2.49	0.42
1:B:291:MET:HE3	1:C:290:VAL:CG1	2.49	0.42
1:E:198:GLU:HA	1:E:202:ARG:HB3	2.01	0.42
1:B:153:ARG:HE	1:B:161:ILE:HD11	1.83	0.42
1:A:47:VAL:HG13	1:A:48:GLU:N	2.35	0.42
1:A:256:ASP:HA	1:A:259:ILE:HD12	2.02	0.42
1:D:233:SER:HA	1:D:255:TYR:CE1	2.54	0.42
1:D:330:VAL:CG1	1:D:331:LEU:N	2.82	0.42
1:C:250:TYR:C	1:C:250:TYR:CD2	2.93	0.42
1:C:156:TYR:O	1:C:157:ASN:C	2.58	0.42
1:E:148:ASP:N	1:E:149:PRO:HD2	2.34	0.42
1:A:221:LEU:HG	1:A:225:ILE:HD11	2.01	0.42
1:C:111:LYS:O	1:C:181:TYR:OH	2.22	0.42
1:C:243:ILE:O	1:C:244:GLU:C	2.58	0.42
1:B:113:PHE:CZ	1:B:224:THR:HG21	2.55	0.42
1:A:348:LYS:NZ	1:B:290:VAL:HG22	2.34	0.42
1:D:226:TRP:N	1:D:227:PRO:HD2	2.35	0.42
1:C:333:VAL:HA	1:C:336:VAL:CG1	2.49	0.42
1:C:270:ASP:O	1:C:273:SER:HB3	2.19	0.42
1:A:113:PHE:CE1	1:A:124:SER:HB2	2.54	0.42
1:B:221:LEU:O	1:B:224:THR:N	2.44	0.42
1:C:165:ARG:HD3	1:C:243:ILE:CD1	2.44	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:199:VAL:HG13	1:D:279:TYR:CA	2.49	0.42
1:B:286:LYS:O	1:B:287:THR:C	2.58	0.42
1:B:226:TRP:N	1:B:227:PRO:HD2	2.34	0.42
1:B:224:THR:HG22	1:B:224:THR:O	2.20	0.42
1:A:108:ILE:CD1	1:A:235:LEU:CD2	2.97	0.42
1:C:225:ILE:N	1:C:225:ILE:HD12	2.35	0.42
1:D:195:LEU:CD1	1:D:210:ARG:HD3	2.50	0.42
1:D:169:LEU:O	1:D:170:LEU:C	2.58	0.42
1:C:333:VAL:CA	1:C:336:VAL:HG12	2.49	0.42
1:A:149:PRO:O	1:A:153:ARG:HG3	2.20	0.42
1:D:148:ASP:N	1:D:149:PRO:HD2	2.33	0.42
1:D:149:PRO:O	1:D:153:ARG:HG3	2.19	0.42
1:C:294:LEU:HD23	1:C:294:LEU:O	2.20	0.42
1:C:299:THR:HA	1:D:297:ILE:HG21	2.02	0.42
1:B:306:PHE:CZ	1:B:310:ILE:HD11	2.55	0.42
1:C:171:TYR:CE1	1:C:251:PHE:CG	3.08	0.42
1:C:192:ILE:HG22	1:C:193:ASP:N	2.34	0.42
1:B:336:VAL:HG13	1:B:337:ILE:N	2.34	0.42
1:B:234:SER:HA	1:B:237:ARG:HG2	2.02	0.42
1:C:232:LEU:HD21	1:C:254:VAL:HG12	2.01	0.41
1:E:339:VAL:HA	1:E:342:VAL:HG12	2.01	0.41
1:D:215:LYS:O	1:D:216:ARG:C	2.57	0.41
1:E:84:PRO:O	1:E:87:LEU:HB2	2.20	0.41
1:B:302:MET:HB2	1:B:303:PRO:CD	2.50	0.41
1:E:255:TYR:O	1:E:256:ASP:C	2.57	0.41
1:A:112:MET:HE1	1:A:146:VAL:H	1.85	0.41
1:E:300:ILE:HG22	1:E:341:MET:HG2	2.03	0.41
1:D:244:GLU:O	1:D:248:VAL:HB	2.20	0.41
1:B:296:ILE:C	1:B:299:THR:HG22	2.41	0.41
1:B:67:ILE:HG22	1:B:91:LEU:HD23	2.01	0.41
1:B:196:GLU:HG2	1:B:200:LEU:HD21	2.02	0.41
1:D:333:VAL:CA	1:D:336:VAL:HG12	2.50	0.41
1:A:152:GLU:HA	1:A:155:ARG:HB2	2.01	0.41
1:C:67:ILE:O	1:C:67:ILE:CG2	2.67	0.41
1:A:108:ILE:HG22	1:A:109:VAL:N	2.35	0.41
1:D:330:VAL:HG13	1:D:331:LEU:N	2.35	0.41
1:A:184:LEU:O	1:A:185:LEU:C	2.59	0.41
1:A:268:PHE:C	1:A:270:ASP:N	2.73	0.41
1:C:160:ILE:HG23	1:C:163:LYS:HD2	2.02	0.41
1:C:333:VAL:C	1:C:336:VAL:HG12	2.41	0.41
1:B:221:LEU:HD12	1:B:221:LEU:HA	1.87	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:174:ILE:O	1:C:175:ASP:C	2.57	0.41
1:B:72:VAL:O	1:B:76:VAL:HG23	2.20	0.41
1:D:198:GLU:OE2	1:D:210:ARG:NH1	2.54	0.41
1:A:339:VAL:O	1:A:341:MET:N	2.54	0.41
1:B:195:LEU:HD11	1:B:210:ARG:HD3	2.02	0.41
1:E:83:HIS:HB3	1:E:84:PRO:HD2	2.02	0.41
1:E:62:ILE:O	1:E:137:LEU:HD23	2.20	0.41
1:C:299:THR:HG21	1:C:345:PHE:CE2	2.56	0.41
1:A:199:VAL:HG13	1:A:279:TYR:CA	2.49	0.41
1:C:232:LEU:CD2	1:C:254:VAL:HG12	2.50	0.41
1:A:191:GLU:HG3	1:A:195:LEU:HD22	2.01	0.41
1:C:99:VAL:HG21	1:C:235:LEU:CD1	2.29	0.41
1:E:279:TYR:O	1:E:280:LEU:C	2.59	0.41
1:C:67:ILE:HD11	1:C:139:PHE:HB3	2.02	0.41
1:A:221:LEU:O	1:A:225:ILE:CD1	2.67	0.41
1:E:296:ILE:O	1:E:299:THR:HG22	2.21	0.41
1:C:225:ILE:HG21	1:C:261:ILE:HG22	2.03	0.41
1:A:296:ILE:HD12	1:A:296:ILE:C	2.40	0.41
1:A:247:THR:O	1:A:250:TYR:HB3	2.21	0.41
1:D:183:VAL:O	1:D:184:LEU:C	2.58	0.41
1:B:134:ASN:HA	1:B:166:ALA:HB3	2.02	0.41
1:C:116:ASP:O	1:C:119:LEU:O	2.38	0.41
1:D:113:PHE:CE2	1:D:221:LEU:HD12	2.56	0.41
1:B:295:THR:CG2	1:C:293:VAL:HG12	2.50	0.41
1:E:109:VAL:HG13	1:E:128:SER:OG	2.21	0.41
1:D:137:LEU:HD22	1:D:139:PHE:CE2	2.56	0.41
1:C:264:THR:O	1:C:267:THR:HB	2.21	0.41
1:A:153:ARG:HE	1:A:161:ILE:HD11	1.85	0.41
1:C:67:ILE:HG13	1:C:140:GLN:O	2.21	0.40
1:A:313:MET:HE2	1:A:313:MET:HA	2.03	0.40
1:D:268:PHE:O	1:D:270:ASP:N	2.54	0.40
1:C:219:VAL:O	1:C:220:GLU:C	2.59	0.40
1:B:302:MET:HE3	1:C:301:PHE:C	2.42	0.40
1:C:300:ILE:CG1	1:C:301:PHE:N	2.84	0.40
1:A:239:VAL:CG1	1:A:242:LEU:HB3	2.51	0.40
1:D:231:VAL:O	1:D:235:LEU:HB2	2.21	0.40
1:A:298:ALA:HA	1:E:302:MET:CE	2.49	0.40
1:B:239:VAL:HB	1:B:242:LEU:HD23	2.03	0.40
1:B:89:ASP:HB3	1:B:95:GLN:HE22	1.85	0.40
1:C:221:LEU:CG	1:C:225:ILE:HD11	2.44	0.40
1:A:330:VAL:HG13	1:A:331:LEU:N	2.37	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:48:GLU:C	1:D:50:VAL:H	2.24	0.40
1:D:333:VAL:O	1:D:336:VAL:HG12	2.21	0.40
1:D:194:VAL:C	1:D:196:GLU:H	2.24	0.40
1:E:226:TRP:N	1:E:227:PRO:CD	2.84	0.40
1:E:170:LEU:C	1:E:172:SER:H	2.24	0.40
1:D:109:VAL:O	1:D:110:LEU:HD23	2.21	0.40
1:A:166:ALA:O	1:A:169:LEU:HB3	2.22	0.40
1:D:99:VAL:HG22	1:D:99:VAL:O	2.21	0.40
1:D:191:GLU:CG	1:D:195:LEU:HD22	2.50	0.40
1:D:112:MET:HE1	1:D:146:VAL:H	1.85	0.40
1:D:112:MET:HE3	1:D:146:VAL:HG13	2.01	0.40
1:C:184:LEU:O	1:C:187:LYS:N	2.55	0.40
1:C:27:PHE:CZ	1:C:72:VAL:HG21	2.57	0.40
1:A:148:ASP:N	1:A:149:PRO:HD2	2.37	0.40
1:E:188:ILE:HG21	1:E:188:ILE:HD13	1.88	0.40
1:E:122:LEU:H	1:E:122:LEU:HD23	1.86	0.40
1:E:171:TYR:CD1	1:E:247:THR:HG22	2.56	0.40
1:E:302:MET:HB2	1:E:303:PRO:CD	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	310/330 (94%)	258 (83%)	44 (14%)	8 (3%)	7	47
1	B	310/330 (94%)	257 (83%)	44 (14%)	9 (3%)	6	45
1	C	310/330 (94%)	255 (82%)	49 (16%)	6 (2%)	10	53
1	D	310/330 (94%)	250 (81%)	48 (16%)	12 (4%)	4	37
1	E	310/330 (94%)	258 (83%)	47 (15%)	5 (2%)	12	56
All	All	1550/1650 (94%)	1278 (82%)	232 (15%)	40 (3%)	7	47

All (40) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	119	LEU
1	A	244	GLU
1	B	244	GLU
1	C	157	ASN
1	A	157	ASN
1	A	240	PRO
1	B	157	ASN
1	C	244	GLU
1	D	119	LEU
1	D	157	ASN
1	E	157	ASN
1	E	244	GLU
1	B	240	PRO
1	D	49	SER
1	D	240	PRO
1	D	244	GLU
1	E	240	PRO
1	A	118	ASN
1	A	133	LYS
1	A	239	VAL
1	B	239	VAL
1	C	118	ASN
1	C	133	LYS
1	C	239	VAL
1	C	240	PRO
1	D	118	ASN
1	D	239	VAL
1	D	269	ARG
1	E	239	VAL
1	D	120	HIS
1	E	133	LYS
1	B	49	SER
1	B	59	PRO
1	D	133	LYS
1	A	340	ILE
1	B	202	ARG
1	B	243	ILE
1	B	261	ILE
1	D	160	ILE
1	D	203	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	295/310 (95%)	276 (94%)	19 (6%)	22	61
1	B	295/310 (95%)	275 (93%)	20 (7%)	20	59
1	C	295/310 (95%)	275 (93%)	20 (7%)	20	59
1	D	295/310 (95%)	270 (92%)	25 (8%)	13	51
1	E	295/310 (95%)	272 (92%)	23 (8%)	16	54
All	All	1475/1550 (95%)	1368 (93%)	107 (7%)	17	57

All (107) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	38	GLU
1	A	40	ARG
1	A	118	ASN
1	A	132	THR
1	A	137	LEU
1	A	162	ARG
1	A	164	LYS
1	A	200	LEU
1	A	205	LYS
1	A	218	LEU
1	A	220	GLU
1	A	234	SER
1	A	238	ASP
1	A	242	LEU
1	A	269	ARG
1	A	284	SER
1	A	297	ILE
1	A	315	PHE
1	A	341	MET
1	B	33	ASN
1	B	40	ARG
1	B	137	LEU
1	B	162	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	164	LYS
1	B	198	GLU
1	B	200	LEU
1	B	202	ARG
1	B	205	LYS
1	B	209	GLN
1	B	220	GLU
1	B	234	SER
1	B	238	ASP
1	B	242	LEU
1	B	258	THR
1	B	263	ASP
1	B	265	VAL
1	B	269	ARG
1	B	315	PHE
1	B	341	MET
1	C	40	ARG
1	C	85	LEU
1	C	125	GLU
1	C	126	GLN
1	C	137	LEU
1	C	162	ARG
1	C	164	LYS
1	C	178	VAL
1	C	198	GLU
1	C	200	LEU
1	C	205	LYS
1	C	209	GLN
1	C	220	GLU
1	C	242	LEU
1	C	269	ARG
1	C	277	ASP
1	C	287	THR
1	C	293	VAL
1	C	315	PHE
1	C	341	MET
1	D	33	ASN
1	D	40	ARG
1	D	118	ASN
1	D	119	LEU
1	D	123	GLU
1	D	128	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	132	THR
1	D	150	VAL
1	D	164	LYS
1	D	184	LEU
1	D	198	GLU
1	D	200	LEU
1	D	205	LYS
1	D	218	LEU
1	D	220	GLU
1	D	240	PRO
1	D	242	LEU
1	D	258	THR
1	D	263	ASP
1	D	287	THR
1	D	293	VAL
1	D	295	THR
1	D	297	ILE
1	D	315	PHE
1	D	341	MET
1	E	38	GLU
1	E	40	ARG
1	E	85	LEU
1	E	114	THR
1	E	118	ASN
1	E	125	GLU
1	E	137	LEU
1	E	162	ARG
1	E	164	LYS
1	E	195	LEU
1	E	198	GLU
1	E	200	LEU
1	E	205	LYS
1	E	220	GLU
1	E	242	LEU
1	E	247	THR
1	E	258	THR
1	E	263	ASP
1	E	269	ARG
1	E	277	ASP
1	E	297	ILE
1	E	315	PHE
1	E	341	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	33	ASN
1	A	95	GLN
1	A	120	HIS
1	A	217	ASN
1	A	288	ASN
1	A	314	ASN
1	B	33	ASN
1	B	95	GLN
1	B	118	ASN
1	B	140	GLN
1	B	217	ASN
1	B	314	ASN
1	C	33	ASN
1	C	95	GLN
1	C	140	GLN
1	C	217	ASN
1	C	314	ASN
1	D	33	ASN
1	D	120	HIS
1	D	217	ASN
1	D	285	ASN
1	E	33	ASN
1	E	95	GLN
1	E	217	ASN
1	E	314	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

Of 14 ligands modelled in this entry, 14 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	314/330 (95%)	-0.11	9 (2%) 55 42	82, 149, 185, 198	0
1	B	314/330 (95%)	0.39	41 (13%) 5 4	83, 153, 195, 210	0
1	C	314/330 (95%)	0.01	11 (3%) 48 36	81, 151, 193, 207	0
1	D	314/330 (95%)	0.15	22 (7%) 19 13	80, 145, 179, 192	0
1	E	314/330 (95%)	0.16	26 (8%) 14 10	81, 145, 181, 193	0
All	All	1570/1650 (95%)	0.12	109 (6%) 20 13	80, 149, 188, 210	0

All (109) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	245	LYS	7.0
1	B	244	GLU	6.7
1	B	28	GLU	6.2
1	E	244	GLU	6.2
1	D	28	GLU	5.9
1	B	36	ILE	5.8
1	C	245	LYS	5.8
1	D	103	GLU	5.7
1	E	245	LYS	5.7
1	B	143	ILE	5.4
1	B	65	THR	5.0
1	D	43	LYS	4.5
1	E	246	GLU	4.5
1	C	244	GLU	4.5
1	D	26	ASP	4.2
1	B	29	ILE	3.9
1	B	57	SER	3.9
1	C	26	ASP	3.7
1	B	27	PHE	3.7
1	B	26	ASP	3.7

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	D	104	ASN	3.7
1	A	143	ILE	3.7
1	E	101	PHE	3.7
1	E	349	LYS	3.6
1	D	91	LEU	3.6
1	B	146	VAL	3.6
1	B	145	ASP	3.6
1	D	143	ILE	3.6
1	D	65	THR	3.6
1	B	140	GLN	3.6
1	E	40	ARG	3.5
1	B	64	ILE	3.5
1	D	90	ILE	3.4
1	E	249	PRO	3.4
1	E	26	ASP	3.4
1	A	46	ASP	3.3
1	B	124	SER	3.3
1	E	155	ARG	3.1
1	D	27	PHE	3.1
1	E	100	GLU	3.0
1	C	204	GLU	3.0
1	B	144	GLY	2.9
1	B	239	VAL	2.9
1	B	246	GLU	2.9
1	B	313	MET	2.9
1	D	92	ASN	2.8
1	D	87	LEU	2.8
1	C	305	THR	2.8
1	C	143	ILE	2.7
1	D	44	THR	2.7
1	B	30	GLU	2.7
1	E	39	PHE	2.7
1	D	66	GLY	2.7
1	D	94	HIS	2.7
1	A	28	GLU	2.7
1	C	311	TYR	2.7
1	B	125	GLU	2.7
1	B	45	THR	2.7
1	E	247	THR	2.6
1	B	247	THR	2.6
1	B	67	ILE	2.6
1	A	26	ASP	2.6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	77	GLY	2.6
1	B	238	ASP	2.5
1	B	76	VAL	2.5
1	B	249	PRO	2.5
1	D	88	GLU	2.5
1	A	45	THR	2.4
1	B	43	LYS	2.4
1	B	75	ARG	2.4
1	E	32	MET	2.4
1	B	63	ASN	2.4
1	C	249	PRO	2.4
1	E	102	PHE	2.4
1	A	103	GLU	2.4
1	E	82	ILE	2.3
1	B	163	LYS	2.3
1	E	154	ILE	2.3
1	C	327	TYR	2.3
1	E	117	LYS	2.3
1	B	100	GLU	2.3
1	A	49	SER	2.3
1	B	44	THR	2.3
1	B	79	PHE	2.2
1	E	171	TYR	2.2
1	B	148	ASP	2.2
1	A	91	LEU	2.2
1	E	156	TYR	2.2
1	B	102	PHE	2.2
1	E	115	TYR	2.2
1	E	297	ILE	2.2
1	E	239	VAL	2.2
1	B	80	PHE	2.2
1	E	41	GLU	2.2
1	A	69	ARG	2.1
1	E	48	GLU	2.1
1	B	248	VAL	2.1
1	D	67	ILE	2.1
1	C	246	GLU	2.1
1	D	93	VAL	2.1
1	B	62	ILE	2.1
1	E	152	GLU	2.1
1	D	305	THR	2.1
1	D	29	ILE	2.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	E	83	HIS	2.0
1	D	68	HIS	2.0
1	B	78	GLU	2.0
1	C	301	PHE	2.0
1	D	84	PRO	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	MG	A	403	1/1	0.89	0.42	9.77	23,23,23,23	0
2	MG	E	501	1/1	0.92	0.34	2.25	48,48,48,48	0
2	MG	D	503	1/1	0.64	0.27	0.80	80,80,80,80	0
2	MG	A	404	1/1	0.95	0.18	-1.03	88,88,88,88	0
2	MG	B	501	1/1	0.93	0.10	-1.40	90,90,90,90	0
2	MG	C	501	1/1	0.97	0.11	-1.50	79,79,79,79	0
2	MG	D	501	1/1	0.86	0.17	-3.21	113,113,113,113	0
2	MG	D	502	1/1	0.97	0.71	-	17,17,17,17	0
2	MG	A	402	1/1	0.83	0.39	-	45,45,45,45	0
2	MG	C	502	1/1	0.89	0.26	-	47,47,47,47	0
2	MG	E	502	1/1	0.95	0.16	-	56,56,56,56	0
2	MG	B	502	1/1	0.96	0.50	-	58,58,58,58	0
2	MG	A	401	1/1	0.67	0.43	-	75,75,75,75	0
2	MG	B	503	1/1	0.88	0.72	-	22,22,22,22	0

6.5 Other polymers

There are no such residues in this entry.