



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 06:05 am GMT

PDB ID : 5CH6
Title : Crystal Structure of FRIGIDA Flowering-time Regulator
Authors : Hyun, K.; Song, J.J.
Deposited on : 2015-07-10
Resolution : 3.26 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
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

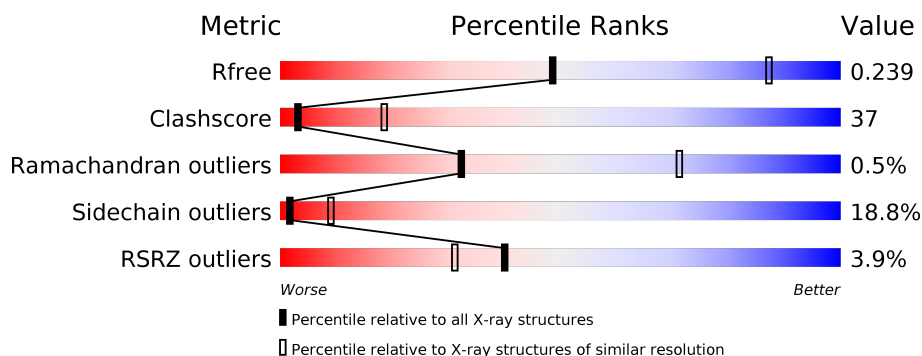
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.26 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	100719	1852 (3.32-3.20)
Clashscore	112137	2036 (3.32-3.20)
Ramachandran outliers	110173	2000 (3.32-3.20)
Sidechain outliers	110143	1998 (3.32-3.20)
RSRZ outliers	101464	1861 (3.32-3.20)

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	289	<div> <div>3%</div> <div> <div></div> <div>44%</div> <div>45%</div> <div>10%</div> <div>.</div> </div> </div>
1	B	289	<div> <div>3%</div> <div> <div></div> <div>45%</div> <div>42%</div> <div>12%</div> <div>.</div> </div> </div>
1	C	289	<div> <div>5%</div> <div> <div></div> <div>40%</div> <div>46%</div> <div>12%</div> <div>.</div> </div> </div>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 6819 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.

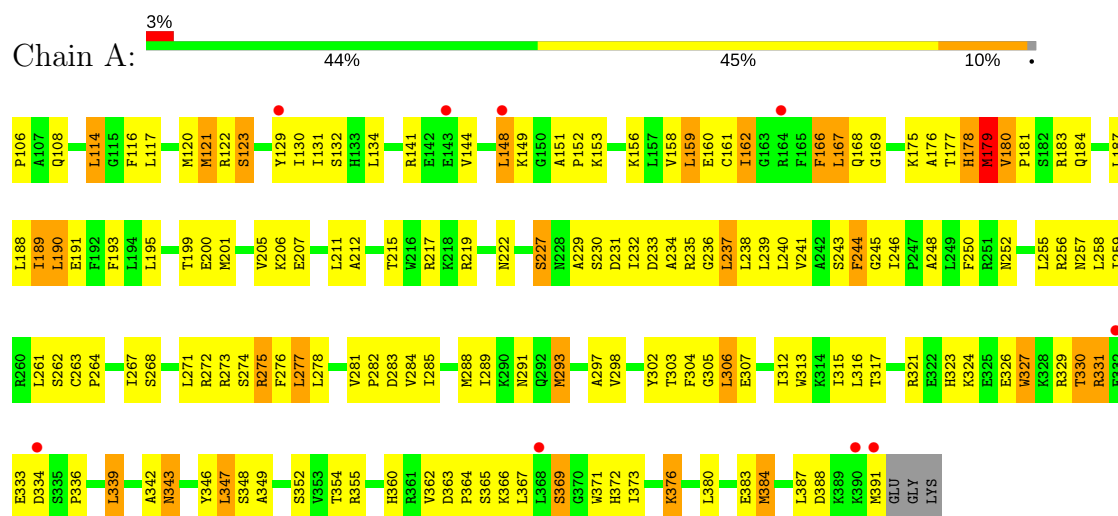
- Molecule 1 is a protein called FRIGIDA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	286	Total	C	N	O	S	0	0	0
			2279	1449	403	413	14			
1	B	285	Total	C	N	O	S	0	0	0
			2273	1445	402	412	14			
1	C	284	Total	C	N	O	S	0	0	0
			2267	1442	401	410	14			

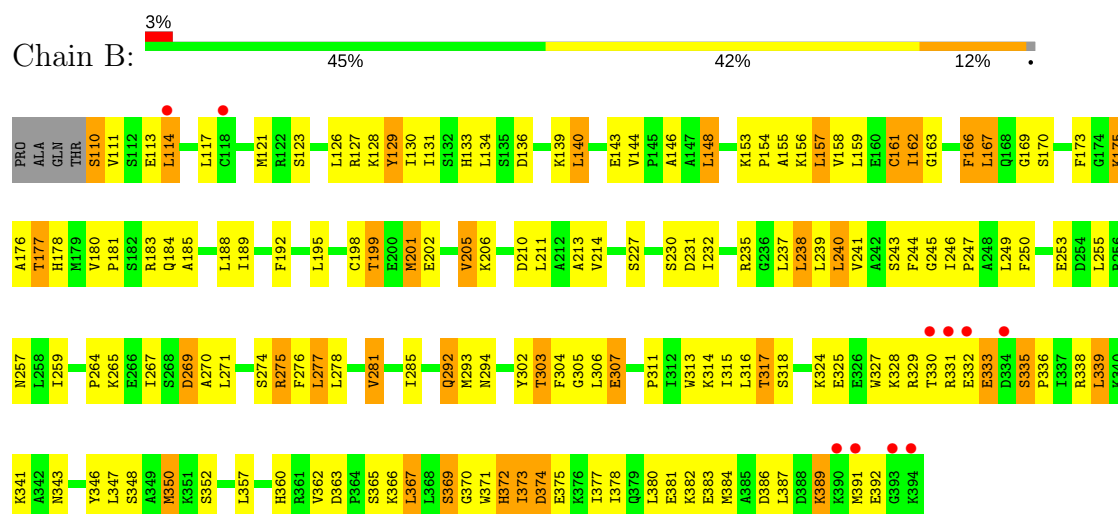
3 Residue-property plots

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

• Molecule 1: FRIGIDA

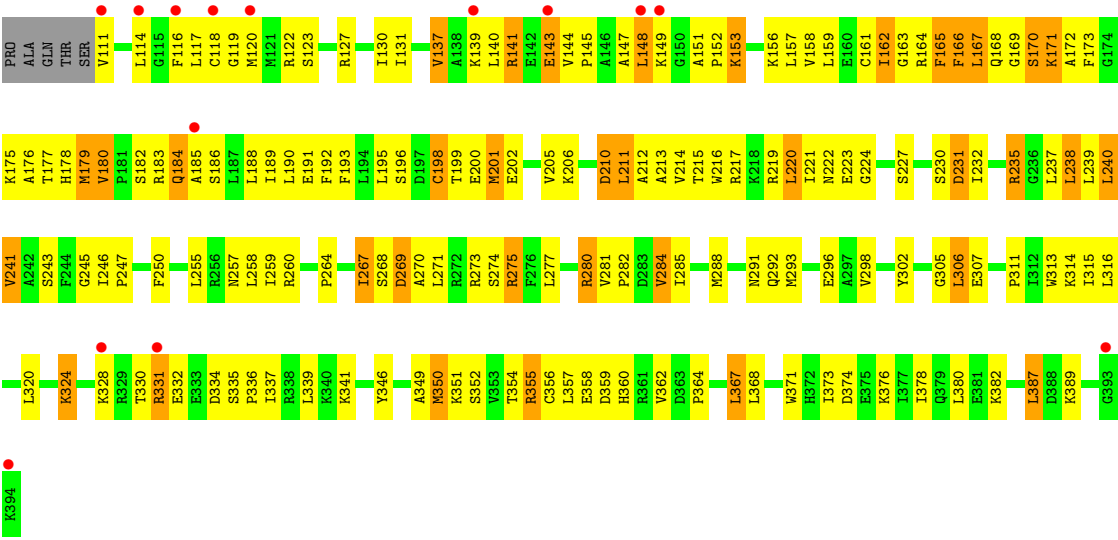


• Molecule 1: FRIGIDA



• Molecule 1: FRIGIDA





4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	148.88Å 148.88Å 262.33Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.96 – 3.26 46.96 – 3.26	Depositor EDS
% Data completeness (in resolution range)	86.7 (46.96-3.26) 86.8 (46.96-3.26)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.19 (at 3.25Å)	Xtriage
Refinement program	CNS 1.3	Depositor
R, R_{free}	0.225 , 0.239 0.225 , 0.239	Depositor DCC
R_{free} test set	3509 reflections (8.64%)	DCC
Wilson B-factor (Å ²)	99.1	Xtriage
Anisotropy	0.253	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 84.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6819	wwPDB-VP
Average B, all atoms (Å ²)	121.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.61% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

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	0.48	0/2319	0.70	2/3116 (0.1%)
1	B	0.61	2/2312 (0.1%)	0.78	1/3104 (0.0%)
1	C	0.51	0/2306	0.72	0/3096
All	All	0.54	2/6937 (0.0%)	0.73	3/9316 (0.0%)

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

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

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	292	GLN	CD-OE1	9.94	1.45	1.24
1	B	292	GLN	CD-NE2	8.97	1.55	1.32

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	370	GLY	N-CA-C	-8.47	91.91	113.10
1	A	180	VAL	N-CA-C	-6.58	93.24	111.00
1	A	334	ASP	N-CA-C	5.02	124.56	111.00

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	179	MET	Peptide
1	A	333	GLU	Peptide
1	B	369	SER	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2279	0	2352	170	0
1	B	2273	0	2346	174	0
1	C	2267	0	2341	176	0
All	All	6819	0	7039	508	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 37.

All (508) 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:A:331:ARG:HH11	1:A:331:ARG:HG3	1.08	1.12
1:C:274:SER:O	1:C:275:ARG:HB3	1.60	1.02
1:C:355:ARG:HH11	1:C:355:ARG:HG2	1.22	1.01
1:B:281:VAL:HG21	1:B:304:PHE:CE2	1.95	0.99
1:A:211:LEU:HD22	1:B:347:LEU:HD13	1.43	0.98
1:B:188:LEU:HD12	1:B:192:PHE:CZ	1.98	0.98
1:A:179:MET:HG3	1:A:181:PRO:HA	1.43	0.98
1:C:172:ALA:HB3	1:C:175:LYS:HB2	1.46	0.98
1:B:267:ILE:HG22	1:B:271:LEU:HG	1.46	0.96
1:A:162:ILE:HD11	1:A:190:LEU:HD23	1.48	0.93
1:B:114:LEU:HG	1:B:129:TYR:CE1	2.05	0.91
1:C:280:ARG:CG	1:C:280:ARG:HH11	1.84	0.90
1:A:365:SER:O	1:A:369:SER:N	2.04	0.89
1:B:247:PRO:HG2	1:B:250:PHE:CD1	2.08	0.88
1:C:280:ARG:HH11	1:C:280:ARG:HG3	1.37	0.88
1:A:331:ARG:NH1	1:A:331:ARG:HG3	1.88	0.88
1:A:162:ILE:HD11	1:A:190:LEU:CD2	2.04	0.87
1:B:372:HIS:HB3	1:B:375:GLU:HG3	1.56	0.87

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:331:ARG:HH11	1:A:331:ARG:CG	1.87	0.86
1:B:303:THR:HG22	1:B:304:PHE:HD1	1.38	0.86
1:B:114:LEU:HG	1:B:129:TYR:HE1	1.36	0.86
1:B:121:MET:CE	1:B:153:LYS:H	1.87	0.86
1:A:179:MET:HG2	1:A:179:MET:O	1.73	0.86
1:A:347:LEU:HD13	1:C:211:LEU:HG	1.56	0.86
1:B:303:THR:HG22	1:B:304:PHE:CD1	2.11	0.86
1:A:258:LEU:O	1:A:262:SER:HB2	1.75	0.86
1:A:141:ARG:NH1	1:A:191:GLU:OE2	2.10	0.85
1:C:166:PHE:O	1:C:219:ARG:NH2	2.10	0.85
1:C:172:ALA:HB2	1:C:183:ARG:HH22	1.39	0.85
1:B:267:ILE:CG2	1:B:271:LEU:HG	2.07	0.84
1:C:118:CYS:HB3	1:C:151:ALA:HB2	1.56	0.84
1:B:302:TYR:HB3	1:B:360:HIS:ND1	1.94	0.83
1:B:188:LEU:HD12	1:B:192:PHE:HZ	1.43	0.82
1:A:330:THR:HG21	1:A:342:ALA:HB2	1.62	0.82
1:A:230:SER:HB2	1:A:233:ASP:H	1.41	0.82
1:C:302:TYR:CE2	1:C:307:GLU:HG2	2.14	0.81
1:A:177:THR:C	1:A:179:MET:H	1.84	0.81
1:C:171:LYS:HG3	1:C:175:LYS:HE2	1.63	0.80
1:B:357:LEU:HD22	1:B:362:VAL:HG11	1.64	0.80
1:B:158:VAL:HG13	1:B:189:ILE:HG22	1.64	0.79
1:A:363:ASP:HB3	1:A:366:LYS:HG3	1.65	0.79
1:C:339:LEU:HB3	1:C:387:LEU:HD11	1.63	0.79
1:A:134:LEU:HD13	1:A:179:MET:CE	2.12	0.79
1:B:281:VAL:HG21	1:B:304:PHE:HE2	1.45	0.78
1:A:339:LEU:HD12	1:A:387:LEU:HD21	1.64	0.78
1:B:155:ALA:HB2	1:B:201:MET:HB3	1.63	0.78
1:C:127:ARG:O	1:C:131:ILE:HG13	1.82	0.78
1:B:129:TYR:HE2	1:B:133:HIS:CD2	2.03	0.77
1:B:372:HIS:CB	1:B:375:GLU:HG3	2.15	0.77
1:A:238:LEU:CD1	1:A:271:LEU:HD21	2.14	0.77
1:B:158:VAL:HG13	1:B:189:ILE:CG2	2.14	0.77
1:A:331:ARG:HD2	1:A:331:ARG:N	1.99	0.76
1:C:324:LYS:HE3	1:C:346:TYR:OH	1.86	0.76
1:B:367:LEU:HD22	1:B:367:LEU:O	1.87	0.75
1:B:155:ALA:CB	1:B:201:MET:HB3	2.16	0.74
1:C:157:LEU:O	1:C:161:CYS:HB2	1.86	0.74
1:B:167:LEU:H	1:B:167:LEU:HD23	1.51	0.73
1:B:185:ALA:O	1:B:189:ILE:HD12	1.87	0.73
1:B:201:MET:CE	1:B:206:LYS:HD2	2.19	0.73

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:241:VAL:HG22	1:C:246:ILE:HA	1.70	0.73
1:B:199:THR:HG22	1:B:275:ARG:NH2	2.04	0.72
1:C:232:ILE:HD12	1:C:232:ILE:H	1.54	0.72
1:C:311:PRO:O	1:C:315:ILE:HG13	1.88	0.72
1:A:134:LEU:HD13	1:A:179:MET:HE1	1.71	0.72
1:C:355:ARG:HG2	1:C:355:ARG:NH1	1.97	0.72
1:B:255:LEU:O	1:B:259:ILE:HG13	1.90	0.72
1:B:363:ASP:HB3	1:B:366:LYS:HG2	1.72	0.71
1:A:355:ARG:HH12	1:C:164:ARG:HH11	1.38	0.71
1:B:302:TYR:CD2	1:B:307:GLU:HG2	2.25	0.71
1:B:127:ARG:O	1:B:131:ILE:HG13	1.90	0.71
1:B:201:MET:HE3	1:B:206:LYS:HD2	1.72	0.70
1:C:302:TYR:CD2	1:C:307:GLU:HG2	2.26	0.70
1:B:144:VAL:HG12	1:B:148:LEU:HD12	1.72	0.70
1:A:302:TYR:HB3	1:A:360:HIS:CD2	2.27	0.69
1:C:281:VAL:HA	1:C:284:VAL:HG13	1.74	0.69
1:C:193:PHE:CE2	1:C:243:SER:HB3	2.27	0.69
1:B:302:TYR:CE2	1:B:307:GLU:HG2	2.27	0.69
1:A:302:TYR:CB	1:A:360:HIS:CD2	2.76	0.69
1:A:312:ILE:HG21	1:A:367:LEU:HD11	1.73	0.69
1:A:323:HIS:ND1	1:A:349:ALA:CB	2.56	0.68
1:B:110:SER:HB3	1:B:143:GLU:OE2	1.92	0.68
1:B:339:LEU:HB3	1:B:387:LEU:HD21	1.75	0.68
1:C:255:LEU:O	1:C:259:ILE:HG13	1.94	0.68
1:C:267:ILE:HG22	1:C:271:LEU:HD12	1.76	0.68
1:A:365:SER:O	1:A:369:SER:HB2	1.94	0.68
1:C:311:PRO:HB2	1:C:314:LYS:HB2	1.76	0.67
1:A:343:ASN:HB3	1:A:384:MET:SD	2.34	0.67
1:C:362:VAL:O	1:C:364:PRO:HD3	1.95	0.67
1:A:274:SER:O	1:A:275:ARG:HB3	1.95	0.66
1:B:253:GLU:O	1:B:257:ASN:ND2	2.28	0.66
1:B:331:ARG:HG3	1:B:332:GLU:HG2	1.76	0.66
1:C:149:LYS:HE2	1:C:196:SER:O	1.95	0.66
1:C:210:ASP:O	1:C:214:VAL:HG23	1.96	0.66
1:C:171:LYS:HE3	1:C:175:LYS:HE2	1.77	0.66
1:C:162:ILE:CG2	1:C:163:GLY:H	2.08	0.66
1:C:172:ALA:HB3	1:C:175:LYS:CB	2.25	0.66
1:C:156:LYS:HB3	1:C:205:VAL:CG2	2.26	0.65
1:A:330:THR:C	1:A:331:ARG:HD2	2.16	0.65
1:B:365:SER:O	1:B:369:SER:HB2	1.96	0.65
1:A:121:MET:HE3	1:A:153:LYS:H	1.60	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:154:PRO:O	1:B:158:VAL:HG23	1.97	0.65
1:C:354:THR:O	1:C:358:GLU:HG2	1.95	0.65
1:B:339:LEU:HD12	1:B:387:LEU:HD21	1.78	0.64
1:B:331:ARG:NH2	1:B:339:LEU:HD21	2.13	0.64
1:C:193:PHE:HE2	1:C:243:SER:HB3	1.63	0.64
1:C:162:ILE:CG2	1:C:163:GLY:N	2.60	0.64
1:C:259:ILE:O	1:C:264:PRO:HG3	1.97	0.64
1:B:336:PRO:HB2	1:B:391:MET:HG3	1.78	0.64
1:A:177:THR:C	1:A:179:MET:N	2.51	0.64
1:C:137:VAL:HA	1:C:140:LEU:HD12	1.79	0.63
1:C:267:ILE:CG2	1:C:271:LEU:HG	2.28	0.63
1:A:321:ARG:HG3	1:A:371:TRP:HZ2	1.64	0.63
1:B:114:LEU:CG	1:B:129:TYR:CE1	2.81	0.63
1:B:235:ARG:HD3	1:B:267:ILE:HD11	1.79	0.63
1:A:241:VAL:HG11	1:A:246:ILE:HG12	1.81	0.63
1:A:131:ILE:HA	1:A:134:LEU:HD12	1.81	0.62
1:B:114:LEU:CG	1:B:129:TYR:HE1	2.12	0.62
1:B:277:LEU:O	1:B:281:VAL:HB	2.00	0.62
1:C:139:LYS:O	1:C:143:GLU:HG2	1.99	0.62
1:C:198:CYS:HB3	1:C:200:GLU:HG2	1.81	0.62
1:C:357:LEU:HD22	1:C:362:VAL:HG11	1.80	0.62
1:A:177:THR:O	1:A:179:MET:N	2.33	0.62
1:A:326:GLU:HA	1:A:329:ARG:HD2	1.81	0.62
1:C:156:LYS:HB3	1:C:205:VAL:HG22	1.81	0.62
1:C:162:ILE:HG23	1:C:163:GLY:N	2.15	0.62
1:B:235:ARG:CD	1:B:267:ILE:HD11	2.30	0.62
1:A:257:ASN:O	1:A:261:LEU:HB2	1.99	0.61
1:A:304:PHE:O	1:A:306:LEU:HD23	2.01	0.61
1:A:179:MET:CG	1:A:179:MET:O	2.47	0.61
1:A:259:ILE:O	1:A:264:PRO:CG	2.49	0.61
1:A:263:CYS:N	1:A:264:PRO:HD3	2.15	0.61
1:B:311:PRO:O	1:B:315:ILE:HG13	2.00	0.61
1:C:167:LEU:HD13	1:C:212:ALA:HA	1.83	0.60
1:C:354:THR:HG22	1:C:355:ARG:HD3	1.83	0.60
1:A:327:TRP:O	1:A:331:ARG:HD3	2.01	0.60
1:B:324:LYS:O	1:B:327:TRP:HB3	2.01	0.60
1:C:172:ALA:HB2	1:C:183:ARG:NH2	2.14	0.60
1:A:241:VAL:CG1	1:A:246:ILE:HG12	2.31	0.60
1:A:306:LEU:HD23	1:A:306:LEU:N	2.15	0.60
1:A:323:HIS:ND1	1:A:349:ALA:HB2	2.16	0.60
1:B:336:PRO:CB	1:B:391:MET:HG3	2.32	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:374:ASP:O	1:B:378:ILE:HG12	2.02	0.60
1:C:306:LEU:N	1:C:306:LEU:HD23	2.17	0.60
1:C:267:ILE:HG22	1:C:271:LEU:CD1	2.32	0.59
1:A:176:ALA:C	1:A:178:HIS:H	2.03	0.59
1:A:252:ASN:HB3	1:A:284:VAL:HG22	1.84	0.59
1:B:339:LEU:CD1	1:B:387:LEU:HD21	2.32	0.59
1:C:130:ILE:HG23	1:C:140:LEU:HD22	1.85	0.59
1:B:130:ILE:HD12	1:B:189:ILE:HD11	1.85	0.59
1:B:339:LEU:HB3	1:B:387:LEU:CD2	2.32	0.59
1:C:281:VAL:O	1:C:285:ILE:HG13	2.02	0.59
1:A:274:SER:CB	1:A:277:LEU:HB2	2.33	0.58
1:C:119:GLY:HA2	1:C:152:PRO:HD3	1.84	0.58
1:B:121:MET:HE2	1:B:153:LYS:H	1.68	0.58
1:A:365:SER:C	1:A:369:SER:HB2	2.24	0.58
1:A:336:PRO:HB2	1:A:391:MET:SD	2.43	0.58
1:C:275:ARG:O	1:C:275:ARG:HG2	2.03	0.58
1:B:175:LYS:O	1:B:176:ALA:HB3	2.03	0.57
1:C:280:ARG:CG	1:C:280:ARG:NH1	2.54	0.57
1:A:238:LEU:HD11	1:A:271:LEU:HD21	1.85	0.57
1:C:216:TRP:CD1	1:C:220:LEU:HD12	2.39	0.57
1:C:171:LYS:HD2	1:C:175:LYS:HG3	1.85	0.57
1:B:129:TYR:CE2	1:B:133:HIS:CE1	2.93	0.57
1:B:274:SER:OG	1:B:275:ARG:N	2.36	0.56
1:C:171:LYS:HE3	1:C:175:LYS:CE	2.34	0.56
1:A:201:MET:SD	1:A:206:LYS:HG3	2.45	0.56
1:C:232:ILE:HD12	1:C:232:ILE:N	2.19	0.56
1:C:349:ALA:O	1:C:352:SER:HB3	2.05	0.56
1:B:176:ALA:C	1:B:178:HIS:H	2.08	0.56
1:A:346:TYR:OH	1:A:376:LYS:HE3	2.06	0.56
1:C:120:MET:HA	1:C:120:MET:CE	2.35	0.56
1:C:284:VAL:O	1:C:288:MET:HG3	2.05	0.56
1:B:247:PRO:HG2	1:B:250:PHE:CE1	2.41	0.56
1:A:298:VAL:HG23	1:A:315:ILE:HG21	1.87	0.56
1:B:169:GLY:O	1:B:170:SER:OG	2.23	0.56
1:A:215:THR:HG22	1:B:348:SER:OG	2.06	0.56
1:B:143:GLU:O	1:B:146:ALA:HB3	2.06	0.56
1:B:311:PRO:HB2	1:B:314:LYS:HB2	1.87	0.56
1:C:213:ALA:HB2	1:C:240:LEU:HD13	1.87	0.56
1:A:121:MET:CE	1:A:153:LYS:H	2.20	0.56
1:A:323:HIS:O	1:A:346:TYR:CD1	2.59	0.55
1:A:237:LEU:HD13	1:A:258:LEU:HD11	1.88	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:384:MET:O	1:A:388:ASP:HB2	2.06	0.55
1:B:130:ILE:HD12	1:B:189:ILE:CD1	2.37	0.55
1:C:216:TRP:HD1	1:C:220:LEU:HD12	1.71	0.55
1:B:129:TYR:HE2	1:B:133:HIS:CG	2.24	0.55
1:B:167:LEU:N	1:B:167:LEU:HD23	2.20	0.55
1:B:274:SER:O	1:B:275:ARG:CB	2.55	0.55
1:C:165:PHE:HD2	1:C:165:PHE:N	2.04	0.55
1:C:165:PHE:CD2	1:C:165:PHE:N	2.75	0.55
1:B:129:TYR:C	1:B:129:TYR:CD2	2.80	0.54
1:B:214:VAL:HG13	1:B:249:LEU:HD12	1.89	0.54
1:A:190:LEU:HD11	1:A:240:LEU:HA	1.88	0.54
1:A:324:LYS:HA	1:A:346:TYR:CE1	2.41	0.54
1:B:275:ARG:HA	1:B:278:LEU:HB2	1.89	0.54
1:B:346:TYR:HD2	1:B:380:LEU:HD11	1.72	0.54
1:C:216:TRP:CD1	1:C:220:LEU:CD1	2.90	0.54
1:A:331:ARG:NH2	1:A:383:GLU:OE2	2.36	0.54
1:B:134:LEU:CD1	1:B:181:PRO:HB3	2.37	0.54
1:B:331:ARG:CG	1:B:332:GLU:HG2	2.37	0.54
1:A:121:MET:HE1	1:A:153:LYS:O	2.08	0.54
1:B:199:THR:HG22	1:B:275:ARG:HH21	1.73	0.54
1:A:244:PHE:CD1	1:A:244:PHE:N	2.75	0.54
1:A:298:VAL:HG21	1:A:316:LEU:HD21	1.87	0.54
1:A:158:VAL:HG23	1:A:244:PHE:HZ	1.72	0.54
1:A:291:ASN:HB3	1:A:293:MET:HG3	1.90	0.54
1:A:298:VAL:HG21	1:A:316:LEU:CD2	2.37	0.54
1:C:201:MET:CE	1:C:206:LYS:HD2	2.38	0.54
1:C:328:LYS:O	1:C:331:ARG:HB2	2.08	0.54
1:A:162:ILE:HD11	1:A:190:LEU:HD21	1.88	0.54
1:C:131:ILE:HG12	1:C:185:ALA:HB2	1.90	0.54
1:C:201:MET:HE1	1:C:206:LYS:HD2	1.89	0.53
1:A:271:LEU:HD22	1:A:277:LEU:HD23	1.90	0.53
1:B:166:PHE:CE1	1:B:183:ARG:HG2	2.43	0.53
1:C:144:VAL:HG12	1:C:148:LEU:HD12	1.90	0.53
1:C:235:ARG:HG3	1:C:235:ARG:O	2.05	0.53
1:C:281:VAL:N	1:C:282:PRO:CD	2.71	0.53
1:C:298:VAL:HG21	1:C:316:LEU:HD21	1.90	0.53
1:C:144:VAL:N	1:C:145:PRO:HD2	2.24	0.53
1:C:281:VAL:HA	1:C:284:VAL:CG1	2.37	0.53
1:B:170:SER:HB3	1:B:183:ARG:NH1	2.23	0.53
1:A:285:ILE:O	1:A:289:ILE:HG12	2.09	0.53
1:C:184:GLN:HG3	1:C:188:LEU:HD12	1.91	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:267:ILE:HG22	1:B:271:LEU:CG	2.30	0.52
1:B:274:SER:O	1:B:275:ARG:HB3	2.09	0.52
1:C:162:ILE:HG22	1:C:163:GLY:H	1.74	0.52
1:B:175:LYS:HB3	1:C:177:THR:HB	1.91	0.52
1:C:371:TRP:O	1:C:376:LYS:NZ	2.41	0.52
1:B:114:LEU:CD1	1:B:129:TYR:CE1	2.92	0.52
1:B:126:LEU:O	1:B:130:ILE:HG13	2.10	0.52
1:B:383:GLU:O	1:B:386:ASP:HB2	2.09	0.52
1:A:323:HIS:CE1	1:A:349:ALA:HB2	2.44	0.52
1:A:248:ALA:HB1	1:B:341:LYS:HG3	1.91	0.52
1:B:176:ALA:O	1:B:178:HIS:N	2.42	0.52
1:C:246:ILE:HD13	1:C:255:LEU:HD21	1.92	0.52
1:C:298:VAL:HG21	1:C:316:LEU:CD2	2.39	0.52
1:A:307:GLU:HB2	1:A:312:ILE:HD11	1.92	0.52
1:A:339:LEU:O	1:A:343:ASN:HB2	2.09	0.52
1:A:178:HIS:O	1:A:179:MET:HB3	2.09	0.52
1:A:227:SER:O	1:A:261:LEU:HD11	2.10	0.52
1:A:245:GLY:HA2	1:A:276:PHE:CG	2.44	0.52
1:A:312:ILE:CG2	1:A:367:LEU:HD11	2.40	0.52
1:A:256:ARG:HA	1:A:259:ILE:HD12	1.91	0.51
1:C:151:ALA:HB1	1:C:152:PRO:HD2	1.92	0.51
1:B:170:SER:HB3	1:B:183:ARG:CZ	2.40	0.51
1:A:121:MET:HG3	1:A:152:PRO:HG2	1.92	0.51
1:B:269:ASP:OD2	1:B:269:ASP:N	2.43	0.51
1:C:281:VAL:O	1:C:284:VAL:HG13	2.10	0.51
1:C:346:TYR:CD2	1:C:380:LEU:HD11	2.45	0.51
1:A:275:ARG:HA	1:A:278:LEU:HB2	1.93	0.51
1:B:335:SER:HB3	1:B:338:ARG:HB2	1.92	0.51
1:C:280:ARG:NH1	1:C:280:ARG:HG3	2.17	0.51
1:B:372:HIS:N	1:B:372:HIS:ND1	2.57	0.51
1:A:274:SER:HB3	1:A:277:LEU:HB2	1.93	0.51
1:A:114:LEU:HG	1:A:129:TYR:CE2	2.46	0.50
1:A:272:ARG:HE	1:A:305:GLY:N	2.10	0.50
1:B:155:ALA:HB1	1:B:205:VAL:HG21	1.92	0.50
1:A:275:ARG:O	1:A:275:ARG:HG2	2.10	0.50
1:B:389:LYS:HB2	1:B:389:LYS:NZ	2.26	0.50
1:A:355:ARG:NH1	1:C:164:ARG:HH11	2.08	0.50
1:C:171:LYS:HE3	1:C:175:LYS:NZ	2.25	0.50
1:C:180:VAL:HG13	1:C:183:ARG:HG2	1.92	0.50
1:C:175:LYS:HG2	1:C:176:ALA:N	2.27	0.50
1:A:321:ARG:HG3	1:A:371:TRP:CZ2	2.47	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:162:ILE:HG12	1:B:163:GLY:N	2.26	0.50
1:C:180:VAL:HG22	1:C:182:SER:H	1.75	0.50
1:A:187:LEU:HD21	1:A:236:GLY:HA2	1.93	0.50
1:C:178:HIS:O	1:C:179:MET:HB2	2.12	0.50
1:C:241:VAL:CG2	1:C:247:PRO:HD2	2.41	0.50
1:C:367:LEU:HD22	1:C:367:LEU:O	2.12	0.50
1:C:350:MET:HG2	1:C:373:ILE:HG23	1.94	0.50
1:B:129:TYR:HE2	1:B:133:HIS:NE2	2.09	0.50
1:B:246:ILE:HD13	1:B:255:LEU:HD21	1.94	0.50
1:C:153:LYS:N	1:C:153:LYS:HE2	2.26	0.49
1:C:157:LEU:O	1:C:157:LEU:HD23	2.12	0.49
1:C:156:LYS:HB3	1:C:205:VAL:HG21	1.94	0.49
1:A:114:LEU:HD11	1:A:144:VAL:HG22	1.93	0.49
1:B:346:TYR:CD2	1:B:380:LEU:HD11	2.48	0.49
1:A:229:ALA:HB3	1:A:261:LEU:HD13	1.94	0.49
1:A:193:PHE:CE2	1:A:243:SER:HB3	2.48	0.49
1:A:123:SER:HB3	1:A:160:GLU:HB3	1.94	0.48
1:A:347:LEU:HD13	1:C:211:LEU:CG	2.36	0.48
1:A:302:TYR:HB2	1:A:360:HIS:CD2	2.48	0.48
1:B:184:GLN:HG2	1:B:188:LEU:HD23	1.94	0.48
1:A:190:LEU:CD1	1:A:240:LEU:HA	2.43	0.48
1:B:136:ASP:OD1	1:B:139:LYS:HB2	2.13	0.48
1:C:117:LEU:CD1	1:C:122:ARG:HB2	2.43	0.48
1:C:173:PHE:C	1:C:175:LYS:H	2.17	0.48
1:A:106:PRO:HB2	1:A:108:GLN:HG2	1.96	0.48
1:A:255:LEU:O	1:A:259:ILE:HG13	2.14	0.48
1:C:141:ARG:NH2	1:C:191:GLU:OE1	2.45	0.48
1:C:165:PHE:HA	1:C:168:GLN:HB3	1.94	0.48
1:B:111:VAL:HG22	1:B:111:VAL:O	2.13	0.48
1:C:222:ASN:C	1:C:224:GLY:H	2.16	0.48
1:A:121:MET:HG3	1:A:152:PRO:CG	2.43	0.48
1:B:238:LEU:HD13	1:B:271:LEU:HD21	1.95	0.48
1:B:372:HIS:HB2	1:B:375:GLU:HG3	1.95	0.48
1:C:167:LEU:H	1:C:167:LEU:HD23	1.79	0.48
1:C:305:GLY:C	1:C:306:LEU:HD23	2.34	0.48
1:A:193:PHE:HE2	1:A:243:SER:HB3	1.78	0.48
1:B:175:LYS:HA	1:B:175:LYS:HD2	1.73	0.48
1:B:371:TRP:O	1:B:373:ILE:HG12	2.13	0.48
1:C:232:ILE:H	1:C:232:ILE:CD1	2.24	0.48
1:A:158:VAL:HG11	1:A:193:PHE:HB2	1.95	0.47
1:B:211:LEU:HD23	1:B:211:LEU:C	2.35	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:241:VAL:HB	1:B:246:ILE:HG12	1.95	0.47
1:C:355:ARG:HH11	1:C:355:ARG:CG	2.09	0.47
1:C:211:LEU:HD13	1:C:215:THR:HG23	1.96	0.47
1:C:355:ARG:HD3	1:C:355:ARG:N	2.29	0.47
1:C:374:ASP:O	1:C:378:ILE:HG12	2.14	0.47
1:A:343:ASN:ND2	1:A:380:LEU:HD22	2.29	0.47
1:B:157:LEU:HD23	1:B:157:LEU:O	2.14	0.47
1:B:166:PHE:HB3	1:B:167:LEU:HD23	1.95	0.47
1:B:357:LEU:HD22	1:B:362:VAL:CG1	2.39	0.47
1:B:305:GLY:C	1:B:306:LEU:HD23	2.35	0.47
1:C:116:PHE:O	1:C:120:MET:HB2	2.14	0.47
1:A:323:HIS:O	1:A:346:TYR:HD1	1.97	0.47
1:C:241:VAL:O	1:C:245:GLY:N	2.48	0.47
1:C:195:LEU:HD23	1:C:270:ALA:HB2	1.96	0.47
1:B:350:MET:HG2	1:B:373:ILE:HG23	1.97	0.47
1:C:162:ILE:HD11	1:C:190:LEU:HG	1.96	0.47
1:A:302:TYR:CE1	1:A:312:ILE:HD13	2.50	0.46
1:B:180:VAL:HG13	1:B:181:PRO:CD	2.45	0.46
1:C:389:LYS:HB2	1:C:389:LYS:HE3	1.60	0.46
1:A:201:MET:CE	1:A:205:VAL:HG12	2.45	0.46
1:A:330:THR:CG2	1:A:342:ALA:HB2	2.39	0.46
1:C:271:LEU:HD22	1:C:277:LEU:CD2	2.45	0.46
1:C:274:SER:OG	1:C:277:LEU:HB2	2.15	0.46
1:B:317:THR:HG22	1:B:318:SER:N	2.29	0.46
1:C:171:LYS:CG	1:C:175:LYS:HE2	2.41	0.46
1:A:149:LYS:HB3	1:A:149:LYS:HE3	1.69	0.46
1:B:117:LEU:HD12	1:B:129:TYR:HD1	1.79	0.46
1:B:157:LEU:O	1:B:161:CYS:HB2	2.14	0.46
1:C:281:VAL:CA	1:C:284:VAL:HG13	2.43	0.46
1:A:363:ASP:HB3	1:A:366:LYS:CG	2.41	0.46
1:A:234:ALA:HA	1:A:258:LEU:CD2	2.45	0.46
1:C:288:MET:O	1:C:293:MET:HB2	2.15	0.46
1:B:129:TYR:O	1:B:129:TYR:HD2	1.98	0.46
1:B:306:LEU:N	1:B:306:LEU:HD23	2.31	0.46
1:B:302:TYR:CZ	1:B:362:VAL:HG21	2.51	0.46
1:C:158:VAL:HG21	1:C:193:PHE:HB2	1.98	0.46
1:A:176:ALA:C	1:A:178:HIS:N	2.68	0.46
1:A:187:LEU:HD21	1:A:236:GLY:CA	2.46	0.46
1:A:268:SER:HA	1:A:271:LEU:HB2	1.97	0.46
1:A:232:ILE:HD13	1:C:173:PHE:CE2	2.50	0.46
1:C:267:ILE:HG23	1:C:271:LEU:HG	1.97	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:167:LEU:HD13	1:A:212:ALA:CB	2.46	0.46
1:A:175:LYS:HD3	1:A:180:VAL:HG22	1.97	0.45
1:A:343:ASN:HD22	1:A:384:MET:HG2	1.81	0.45
1:B:371:TRP:O	1:B:372:HIS:C	2.54	0.45
1:C:198:CYS:CB	1:C:200:GLU:HG2	2.46	0.45
1:C:274:SER:O	1:C:275:ARG:CB	2.43	0.45
1:A:130:ILE:HD13	1:A:189:ILE:HG12	1.98	0.45
1:B:129:TYR:CE2	1:B:133:HIS:NE2	2.85	0.45
1:C:337:ILE:HG22	1:C:341:LYS:HE2	1.98	0.45
1:A:347:LEU:HD23	1:A:347:LEU:HA	1.74	0.45
1:C:211:LEU:HA	1:C:211:LEU:HD22	1.65	0.45
1:C:332:GLU:HA	1:C:332:GLU:OE1	2.17	0.45
1:A:281:VAL:HG12	1:A:282:PRO:HD3	1.99	0.45
1:C:238:LEU:HD13	1:C:271:LEU:HD21	1.99	0.45
1:A:167:LEU:HD13	1:A:212:ALA:HB1	1.98	0.45
1:A:241:VAL:HG21	1:A:250:PHE:CE1	2.52	0.45
1:A:288:MET:HE1	1:A:297:ALA:HA	1.99	0.45
1:B:201:MET:HE1	1:B:206:LYS:HD2	1.95	0.45
1:C:152:PRO:O	1:C:153:LYS:HB2	2.17	0.45
1:C:313:TRP:HD1	1:C:367:LEU:HD22	1.81	0.45
1:A:271:LEU:HD22	1:A:277:LEU:CD2	2.47	0.45
1:C:257:ASN:OD1	1:C:260:ARG:NH2	2.47	0.45
1:A:272:ARG:O	1:A:278:LEU:HD11	2.16	0.45
1:B:129:TYR:C	1:B:129:TYR:HD2	2.20	0.45
1:A:166:PHE:CE1	1:A:183:ARG:NH1	2.85	0.45
1:C:139:LYS:HB3	1:C:139:LYS:HE2	1.62	0.45
1:B:175:LYS:HB2	1:C:231:ASP:OD1	2.17	0.45
1:C:241:VAL:HG21	1:C:250:PHE:CE2	2.51	0.45
1:B:294:ASN:HB3	1:B:315:ILE:HG22	1.98	0.44
1:A:116:PHE:CZ	1:A:120:MET:HG3	2.52	0.44
1:B:357:LEU:HA	1:B:357:LEU:HD23	1.66	0.44
1:A:195:LEU:HA	1:A:273:ARG:NH1	2.31	0.44
1:B:386:ASP:O	1:B:389:LYS:HG2	2.17	0.44
1:B:259:ILE:O	1:B:264:PRO:HG3	2.18	0.44
1:C:144:VAL:HG11	1:C:192:PHE:CD1	2.52	0.44
1:C:258:LEU:HA	1:C:258:LEU:HD23	1.56	0.44
1:A:114:LEU:HD11	1:A:144:VAL:CG2	2.48	0.44
1:A:302:TYR:CE1	1:A:312:ILE:CD1	3.00	0.44
1:B:130:ILE:HD12	1:B:189:ILE:HG13	2.00	0.44
1:B:134:LEU:HD11	1:B:181:PRO:HB3	1.99	0.44
1:B:267:ILE:HG22	1:B:267:ILE:O	2.18	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:339:LEU:HA	1:B:339:LEU:HD23	1.64	0.44
1:B:347:LEU:HD11	1:B:381:GLU:HG2	1.99	0.44
1:B:347:LEU:HA	1:B:347:LEU:HD23	1.78	0.44
1:C:331:ARG:HD2	1:C:331:ARG:HA	1.70	0.44
1:B:213:ALA:HB2	1:B:240:LEU:HD13	1.99	0.44
1:B:304:PHE:HD1	1:B:304:PHE:N	2.16	0.44
1:B:140:LEU:O	1:B:144:VAL:HG23	2.18	0.44
1:C:296:GLU:OE1	1:C:296:GLU:N	2.44	0.43
1:C:336:PRO:HG2	1:C:337:ILE:CD1	2.48	0.43
1:B:304:PHE:CD1	1:B:304:PHE:N	2.86	0.43
1:C:195:LEU:HD12	1:C:195:LEU:O	2.17	0.43
1:A:313:TRP:O	1:A:317:THR:HB	2.18	0.43
1:A:362:VAL:HG11	1:A:367:LEU:HD12	2.01	0.43
1:B:245:GLY:HA2	1:B:276:PHE:CD2	2.53	0.43
1:C:118:CYS:SG	1:C:147:ALA:HB1	2.58	0.43
1:C:334:ASP:O	1:C:335:SER:C	2.57	0.43
1:A:176:ALA:O	1:A:178:HIS:N	2.52	0.43
1:C:217:ARG:O	1:C:221:ILE:HG13	2.17	0.43
1:C:140:LEU:O	1:C:144:VAL:HG23	2.18	0.43
1:A:190:LEU:HD12	1:A:239:LEU:C	2.38	0.43
1:A:258:LEU:HD23	1:A:258:LEU:HA	1.75	0.43
1:B:243:SER:HB2	1:B:244:PHE:CD1	2.54	0.43
1:B:294:ASN:ND2	1:B:294:ASN:H	2.16	0.43
1:C:157:LEU:C	1:C:157:LEU:HD23	2.39	0.43
1:C:169:GLY:O	1:C:170:SER:HB2	2.19	0.43
1:C:179:MET:HG2	1:C:232:ILE:HG12	2.01	0.43
1:C:291:ASN:O	1:C:292:GLN:HB2	2.18	0.43
1:B:302:TYR:OH	1:B:362:VAL:HG21	2.17	0.43
1:C:337:ILE:HD12	1:C:337:ILE:N	2.33	0.43
1:A:274:SER:O	1:A:275:ARG:CB	2.63	0.43
1:B:129:TYR:HE2	1:B:133:HIS:CE1	2.35	0.43
1:B:159:LEU:HD23	1:B:159:LEU:HA	1.48	0.43
1:B:303:THR:HG22	1:B:304:PHE:CE1	2.54	0.43
1:C:165:PHE:HZ	1:C:182:SER:HB2	1.84	0.43
1:B:140:LEU:HD23	1:B:144:VAL:CG2	2.49	0.43
1:A:117:LEU:HD23	1:A:117:LEU:HA	1.69	0.42
1:A:189:ILE:HD13	1:A:189:ILE:HA	1.87	0.42
1:B:117:LEU:HD13	1:B:126:LEU:HA	2.01	0.42
1:B:134:LEU:HD12	1:B:181:PRO:HB3	2.01	0.42
1:B:166:PHE:CD1	1:B:183:ARG:HG2	2.54	0.42
1:C:161:CYS:SG	1:C:189:ILE:HD13	2.59	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:179:MET:HE2	1:A:181:PRO:HB3	1.99	0.42
1:A:232:ILE:HG23	1:A:232:ILE:HD12	1.80	0.42
1:B:117:LEU:HA	1:B:117:LEU:HD23	1.69	0.42
1:B:121:MET:HE1	1:B:153:LYS:H	1.77	0.42
1:B:325:GLU:O	1:B:328:LYS:N	2.51	0.42
1:A:278:LEU:HD23	1:A:278:LEU:HA	1.79	0.42
1:B:128:LYS:HD3	1:B:128:LYS:HA	1.88	0.42
1:B:350:MET:HE3	1:B:377:ILE:HG13	2.00	0.42
1:C:277:LEU:HA	1:C:277:LEU:HD12	1.80	0.42
1:C:357:LEU:HD22	1:C:362:VAL:CG1	2.47	0.42
1:A:354:THR:HG22	1:A:355:ARG:N	2.33	0.42
1:B:210:ASP:O	1:B:214:VAL:HG23	2.20	0.42
1:C:162:ILE:HA	1:C:162:ILE:HD12	1.65	0.42
1:C:320:LEU:HD11	1:C:368:LEU:HD13	2.01	0.42
1:C:355:ARG:O	1:C:356:CYS:C	2.58	0.42
1:B:347:LEU:HD11	1:B:381:GLU:CG	2.50	0.42
1:A:134:LEU:CD2	1:A:184:GLN:HG2	2.50	0.42
1:B:267:ILE:CG2	1:B:267:ILE:O	2.67	0.42
1:B:367:LEU:HD22	1:B:367:LEU:C	2.35	0.42
1:A:148:LEU:HD12	1:A:193:PHE:HA	2.01	0.42
1:C:117:LEU:HD13	1:C:122:ARG:HB2	2.01	0.42
1:C:190:LEU:HD23	1:C:190:LEU:HA	1.67	0.42
1:C:213:ALA:HB2	1:C:240:LEU:CD1	2.49	0.42
1:C:118:CYS:CB	1:C:151:ALA:HB2	2.40	0.42
1:C:324:LYS:HE3	1:C:346:TYR:CZ	2.55	0.42
1:A:178:HIS:O	1:A:179:MET:CB	2.68	0.41
1:A:259:ILE:O	1:A:264:PRO:HG2	2.18	0.41
1:A:315:ILE:HG22	1:A:316:LEU:N	2.35	0.41
1:A:188:LEU:HD23	1:A:188:LEU:HA	1.82	0.41
1:A:272:ARG:HE	1:A:304:PHE:C	2.24	0.41
1:B:180:VAL:HG13	1:B:181:PRO:HD2	2.02	0.41
1:C:269:ASP:OD1	1:C:269:ASP:N	2.52	0.41
1:A:363:ASP:HA	1:A:364:PRO:HD2	1.77	0.41
1:A:331:ARG:CG	1:A:331:ARG:NH1	2.58	0.41
1:A:347:LEU:O	1:A:347:LEU:HD22	2.20	0.41
1:A:121:MET:SD	1:A:152:PRO:HG2	2.60	0.41
1:B:176:ALA:C	1:B:178:HIS:N	2.73	0.41
1:B:378:ILE:O	1:B:382:LYS:HG2	2.20	0.41
1:A:121:MET:CG	1:A:152:PRO:HG2	2.50	0.41
1:A:217:ARG:HD3	1:A:250:PHE:CE2	2.55	0.41
1:B:313:TRP:O	1:B:317:THR:HB	2.21	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:328:LYS:O	1:B:329:ARG:C	2.59	0.41
1:A:207:GLU:OE1	1:B:384:MET:HE3	2.20	0.41
1:C:291:ASN:O	1:C:292:GLN:CB	2.68	0.41
1:A:121:MET:CE	1:A:151:ALA:HB1	2.50	0.41
1:A:169:GLY:HA3	1:A:219:ARG:HE	1.86	0.41
1:A:371:TRP:O	1:A:372:HIS:HB2	2.20	0.41
1:A:371:TRP:HB3	1:A:373:ILE:HG23	2.02	0.41
1:B:239:LEU:HA	1:B:239:LEU:HD23	1.80	0.41
1:C:336:PRO:HG2	1:C:337:ILE:HD12	2.03	0.41
1:A:148:LEU:HD11	1:A:193:PHE:HB2	2.02	0.41
1:A:156:LYS:HE2	1:A:160:GLU:OE2	2.20	0.41
1:A:159:LEU:HA	1:A:159:LEU:HD23	1.80	0.41
1:A:134:LEU:HD21	1:A:184:GLN:HG2	2.03	0.41
1:B:140:LEU:HD23	1:B:144:VAL:HG23	2.03	0.41
1:C:302:TYR:HB3	1:C:360:HIS:ND1	2.35	0.41
1:C:358:GLU:HG2	1:C:358:GLU:H	1.78	0.41
1:B:183:ARG:O	1:B:184:GLN:C	2.59	0.41
1:C:268:SER:O	1:C:269:ASP:C	2.58	0.41
1:C:346:TYR:HD2	1:C:380:LEU:HD11	1.86	0.41
1:A:114:LEU:HD23	1:A:114:LEU:HA	1.83	0.40
1:A:232:ILE:HA	1:A:232:ILE:HD13	1.74	0.40
1:A:277:LEU:HD12	1:A:277:LEU:HA	1.62	0.40
1:B:195:LEU:CD2	1:B:270:ALA:HA	2.51	0.40
1:B:360:HIS:N	1:B:360:HIS:CD2	2.87	0.40
1:B:333:GLU:O	1:B:335:SER:HB2	2.21	0.40
1:C:355:ARG:NH1	1:C:355:ARG:CG	2.74	0.40
1:A:263:CYS:N	1:A:264:PRO:CD	2.82	0.40
1:B:302:TYR:HB3	1:B:360:HIS:CE1	2.56	0.40
1:B:333:GLU:O	1:B:335:SER:N	2.54	0.40
1:A:217:ARG:HD3	1:A:250:PHE:CD2	2.56	0.40
1:B:114:LEU:CD1	1:B:129:TYR:HE1	2.34	0.40
1:B:173:PHE:CE1	1:C:231:ASP:CB	3.05	0.40
1:B:316:LEU:CD1	1:B:357:LEU:HD11	2.51	0.40
1:C:211:LEU:O	1:C:215:THR:HG23	2.21	0.40
1:A:259:ILE:O	1:A:264:PRO:HG3	2.22	0.40
1:B:113:GLU:O	1:B:117:LEU:HG	2.22	0.40
1:C:144:VAL:HG12	1:C:148:LEU:CD1	2.52	0.40
1:C:219:ARG:O	1:C:223:GLU:HG3	2.21	0.40
1:C:330:THR:O	1:C:330:THR:OG1	2.32	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	284/289 (98%)	255 (90%)	28 (10%)	1 (0%)	38	74
1	B	283/289 (98%)	255 (90%)	25 (9%)	3 (1%)	17	56
1	C	282/289 (98%)	243 (86%)	39 (14%)	0	100	100
All	All	849/867 (98%)	753 (89%)	92 (11%)	4 (0%)	32	71

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	178	HIS
1	B	177	THR
1	B	392	GLU
1	B	175	LYS

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	249/251 (99%)	208 (84%)	41 (16%)	2	13
1	B	248/251 (99%)	200 (81%)	48 (19%)	1	8
1	C	247/251 (98%)	196 (79%)	51 (21%)	1	6
All	All	744/753 (99%)	604 (81%)	140 (19%)	2	9

All (140) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	114	LEU
1	A	121	MET
1	A	122	ARG
1	A	123	SER
1	A	132	SER
1	A	148	LEU
1	A	159	LEU
1	A	161	CYS
1	A	162	ILE
1	A	166	PHE
1	A	167	LEU
1	A	168	GLN
1	A	179	MET
1	A	189	ILE
1	A	190	LEU
1	A	199	THR
1	A	200	GLU
1	A	222	ASN
1	A	227	SER
1	A	231	ASP
1	A	235	ARG
1	A	237	LEU
1	A	244	PHE
1	A	267	ILE
1	A	275	ARG
1	A	277	LEU
1	A	283	ASP
1	A	293	MET
1	A	303	THR
1	A	306	LEU
1	A	327	TRP
1	A	330	THR
1	A	331	ARG
1	A	339	LEU
1	A	343	ASN
1	A	347	LEU
1	A	348	SER
1	A	352	SER
1	A	369	SER
1	A	376	LYS
1	A	384	MET
1	B	110	SER
1	B	114	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	123	SER
1	B	129	TYR
1	B	140	LEU
1	B	148	LEU
1	B	156	LYS
1	B	157	LEU
1	B	161	CYS
1	B	162	ILE
1	B	166	PHE
1	B	167	LEU
1	B	177	THR
1	B	198	CYS
1	B	199	THR
1	B	201	MET
1	B	202	GLU
1	B	205	VAL
1	B	227	SER
1	B	230	SER
1	B	231	ASP
1	B	232	ILE
1	B	237	LEU
1	B	238	LEU
1	B	240	LEU
1	B	265	LYS
1	B	269	ASP
1	B	275	ARG
1	B	277	LEU
1	B	281	VAL
1	B	285	ILE
1	B	292	GLN
1	B	293	MET
1	B	303	THR
1	B	307	GLU
1	B	317	THR
1	B	330	THR
1	B	333	GLU
1	B	335	SER
1	B	339	LEU
1	B	343	ASN
1	B	350	MET
1	B	352	SER
1	B	367	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	372	HIS
1	B	373	ILE
1	B	374	ASP
1	B	389	LYS
1	C	111	VAL
1	C	114	LEU
1	C	123	SER
1	C	137	VAL
1	C	141	ARG
1	C	143	GLU
1	C	148	LEU
1	C	153	LYS
1	C	159	LEU
1	C	162	ILE
1	C	165	PHE
1	C	166	PHE
1	C	167	LEU
1	C	170	SER
1	C	171	LYS
1	C	179	MET
1	C	180	VAL
1	C	184	GLN
1	C	186	SER
1	C	198	CYS
1	C	199	THR
1	C	201	MET
1	C	202	GLU
1	C	210	ASP
1	C	211	LEU
1	C	220	LEU
1	C	227	SER
1	C	230	SER
1	C	231	ASP
1	C	235	ARG
1	C	237	LEU
1	C	238	LEU
1	C	239	LEU
1	C	240	LEU
1	C	241	VAL
1	C	267	ILE
1	C	269	ASP
1	C	273	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	275	ARG
1	C	280	ARG
1	C	284	VAL
1	C	306	LEU
1	C	324	LYS
1	C	331	ARG
1	C	350	MET
1	C	351	LYS
1	C	355	ARG
1	C	359	ASP
1	C	367	LEU
1	C	382	LYS
1	C	387	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	294	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

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	286/289 (98%)	0.32	9 (3%)	49	40	79, 119, 181, 257	0
1	B	285/289 (98%)	0.28	10 (3%)	44	34	69, 106, 173, 234	0
1	C	284/289 (98%)	0.46	14 (4%)	30	23	73, 120, 185, 297	0
All	All	855/867 (98%)	0.35	33 (3%)	40	31	69, 114, 184, 297	0

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	394	LYS	6.4
1	C	111	VAL	5.4
1	A	334	ASP	3.9
1	C	116	PHE	3.6
1	C	118	CYS	3.6
1	C	149	LYS	3.4
1	B	390	LYS	3.1
1	B	332	GLU	3.0
1	B	330	THR	3.0
1	B	394	LYS	2.9
1	C	185	ALA	2.8
1	B	331	ARG	2.8
1	C	148	LEU	2.8
1	C	393	GLY	2.7
1	C	114	LEU	2.7
1	A	368	LEU	2.6
1	C	120	MET	2.4
1	A	391	MET	2.4
1	C	331	ARG	2.4
1	B	391	MET	2.4
1	B	334	ASP	2.4
1	B	114	LEU	2.3
1	B	393	GLY	2.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	118	CYS	2.2
1	A	148	LEU	2.2
1	C	328	LYS	2.2
1	A	390	LYS	2.2
1	A	143	GLU	2.1
1	A	164	ARG	2.1
1	A	332	GLU	2.1
1	C	143	GLU	2.0
1	A	129	TYR	2.0
1	C	139	LYS	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.