



Full wwPDB X-ray Structure Validation Report ⓘ

May 22, 2020 – 11:01 am BST

PDB ID : 4E85
Title : crystal STRUCTURE OF HAT DOMAIN OF RNA14
Authors : Paulson, A.R.; Tong, L.
Deposited on : 2012-03-19
Resolution : 3.00 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/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)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

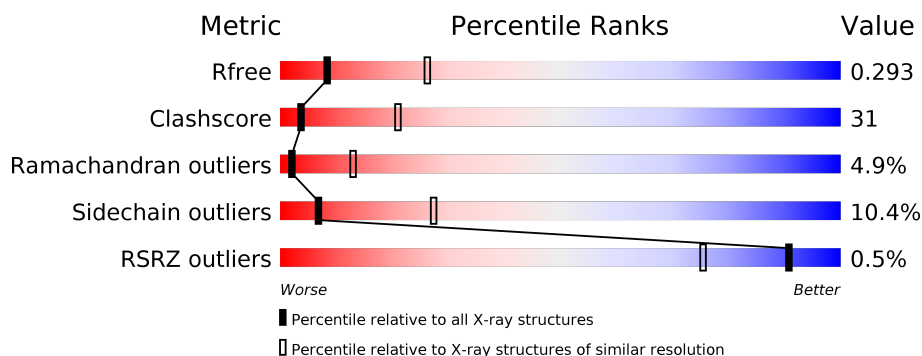
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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	678	<div> <div style="width: 37%; background-color: red;"></div> <div style="width: 37%; background-color: yellow;"></div> <div style="width: 8%; background-color: orange;"></div> <div style="width: 18%; background-color: grey;"></div> </div> <div>37% 37% 8% 18%</div>
1	B	678	<div> <div style="width: 37%; background-color: red;"></div> <div style="width: 36%; background-color: yellow;"></div> <div style="width: 8%; background-color: orange;"></div> <div style="width: 19%; background-color: grey;"></div> </div> <div>37% 36% 8% 19%</div>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 9221 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 mRNA 3'-end-processing protein RNA14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	555	Total	C	N	O	S	0	0	0
			4623	2976	765	856	26			
1	B	552	Total	C	N	O	S	0	0	0
			4598	2962	760	851	25			

There are 68 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-16	MET	-	EXPRESSION TAG	UNP Q6CII8
A	-15	GLY	-	EXPRESSION TAG	UNP Q6CII8
A	-14	SER	-	EXPRESSION TAG	UNP Q6CII8
A	-13	SER	-	EXPRESSION TAG	UNP Q6CII8
A	-12	HIS	-	EXPRESSION TAG	UNP Q6CII8
A	-11	HIS	-	EXPRESSION TAG	UNP Q6CII8
A	-10	HIS	-	EXPRESSION TAG	UNP Q6CII8
A	-9	HIS	-	EXPRESSION TAG	UNP Q6CII8
A	-8	HIS	-	EXPRESSION TAG	UNP Q6CII8
A	-7	HIS	-	EXPRESSION TAG	UNP Q6CII8
A	-6	SER	-	EXPRESSION TAG	UNP Q6CII8
A	-5	SER	-	EXPRESSION TAG	UNP Q6CII8
A	-4	GLY	-	EXPRESSION TAG	UNP Q6CII8
A	-3	LEU	-	EXPRESSION TAG	UNP Q6CII8
A	-2	VAL	-	EXPRESSION TAG	UNP Q6CII8
A	-1	PRO	-	EXPRESSION TAG	UNP Q6CII8
A	0	ARG	-	EXPRESSION TAG	UNP Q6CII8
A	1	GLY	-	EXPRESSION TAG	UNP Q6CII8
A	2	SER	-	EXPRESSION TAG	UNP Q6CII8
A	3	HIS	-	EXPRESSION TAG	UNP Q6CII8
A	4	MET	-	EXPRESSION TAG	UNP Q6CII8
A	5	ALA	-	EXPRESSION TAG	UNP Q6CII8
A	6	SER	-	EXPRESSION TAG	UNP Q6CII8
A	7	MET	-	EXPRESSION TAG	UNP Q6CII8
A	8	THR	-	EXPRESSION TAG	UNP Q6CII8

Continued on next page...

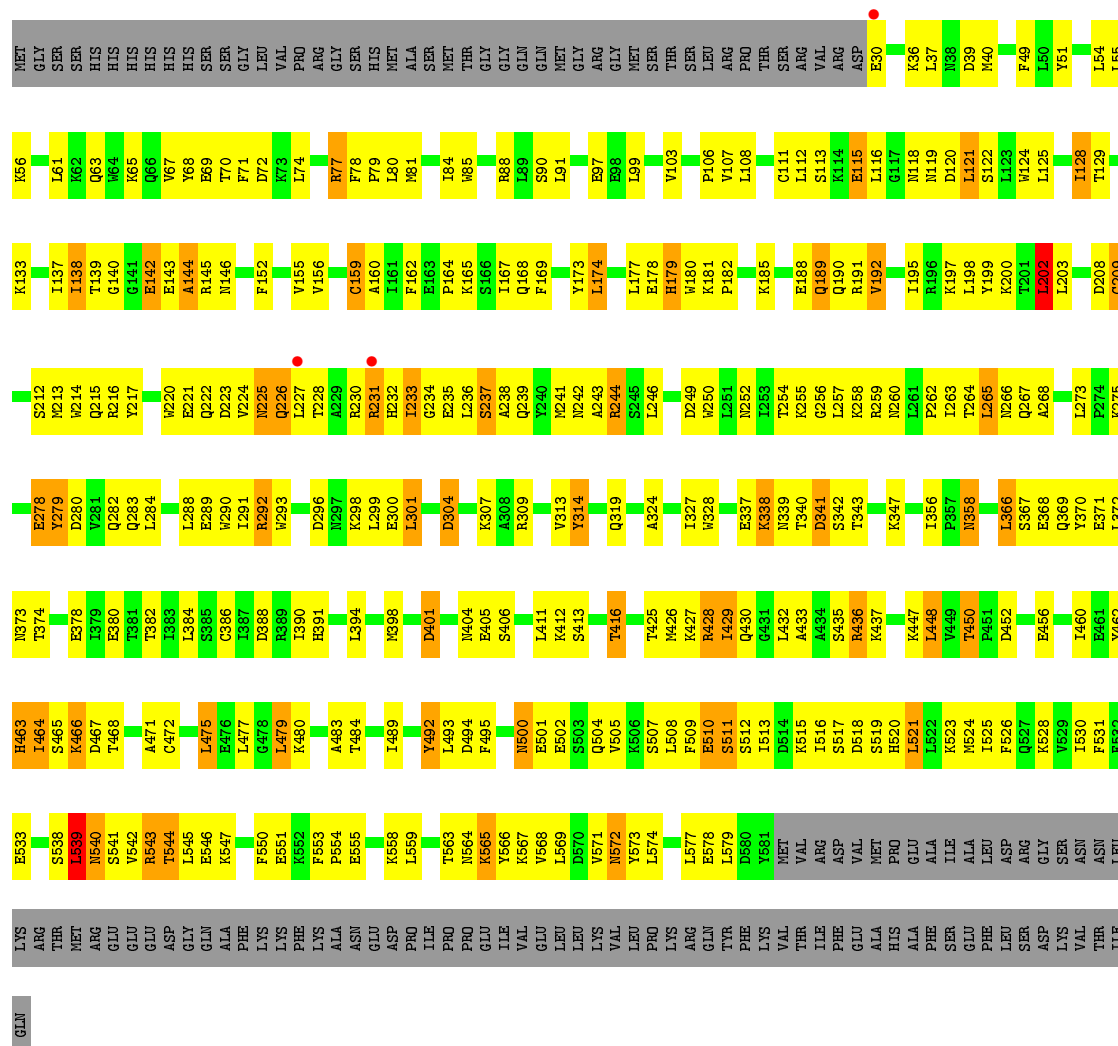
Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	9	GLY	-	EXPRESSION TAG	UNP Q6CII8
A	10	GLY	-	EXPRESSION TAG	UNP Q6CII8
A	11	GLN	-	EXPRESSION TAG	UNP Q6CII8
A	12	GLN	-	EXPRESSION TAG	UNP Q6CII8
A	13	MET	-	EXPRESSION TAG	UNP Q6CII8
A	14	GLY	-	EXPRESSION TAG	UNP Q6CII8
A	15	ARG	-	EXPRESSION TAG	UNP Q6CII8
A	16	GLY	-	EXPRESSION TAG	UNP Q6CII8
A	17	MET	-	EXPRESSION TAG	UNP Q6CII8
B	-16	MET	-	EXPRESSION TAG	UNP Q6CII8
B	-15	GLY	-	EXPRESSION TAG	UNP Q6CII8
B	-14	SER	-	EXPRESSION TAG	UNP Q6CII8
B	-13	SER	-	EXPRESSION TAG	UNP Q6CII8
B	-12	HIS	-	EXPRESSION TAG	UNP Q6CII8
B	-11	HIS	-	EXPRESSION TAG	UNP Q6CII8
B	-10	HIS	-	EXPRESSION TAG	UNP Q6CII8
B	-9	HIS	-	EXPRESSION TAG	UNP Q6CII8
B	-8	HIS	-	EXPRESSION TAG	UNP Q6CII8
B	-7	HIS	-	EXPRESSION TAG	UNP Q6CII8
B	-6	SER	-	EXPRESSION TAG	UNP Q6CII8
B	-5	SER	-	EXPRESSION TAG	UNP Q6CII8
B	-4	GLY	-	EXPRESSION TAG	UNP Q6CII8
B	-3	LEU	-	EXPRESSION TAG	UNP Q6CII8
B	-2	VAL	-	EXPRESSION TAG	UNP Q6CII8
B	-1	PRO	-	EXPRESSION TAG	UNP Q6CII8
B	0	ARG	-	EXPRESSION TAG	UNP Q6CII8
B	1	GLY	-	EXPRESSION TAG	UNP Q6CII8
B	2	SER	-	EXPRESSION TAG	UNP Q6CII8
B	3	HIS	-	EXPRESSION TAG	UNP Q6CII8
B	4	MET	-	EXPRESSION TAG	UNP Q6CII8
B	5	ALA	-	EXPRESSION TAG	UNP Q6CII8
B	6	SER	-	EXPRESSION TAG	UNP Q6CII8
B	7	MET	-	EXPRESSION TAG	UNP Q6CII8
B	8	THR	-	EXPRESSION TAG	UNP Q6CII8
B	9	GLY	-	EXPRESSION TAG	UNP Q6CII8
B	10	GLY	-	EXPRESSION TAG	UNP Q6CII8
B	11	GLN	-	EXPRESSION TAG	UNP Q6CII8
B	12	GLN	-	EXPRESSION TAG	UNP Q6CII8
B	13	MET	-	EXPRESSION TAG	UNP Q6CII8
B	14	GLY	-	EXPRESSION TAG	UNP Q6CII8
B	15	ARG	-	EXPRESSION TAG	UNP Q6CII8
B	16	GLY	-	EXPRESSION TAG	UNP Q6CII8

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	17	MET	-	EXPRESSION TAG	UNP Q6CII8



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	114.87Å 241.73Å 49.02Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.77 – 3.00 46.77 – 2.99	Depositor EDS
% Data completeness (in resolution range)	87.8 (46.77-3.00) 87.2 (46.77-2.99)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.08 (at 3.01Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.233 , 0.293 0.233 , 0.293	Depositor DCC
R_{free} test set	1280 reflections (4.83%)	wwPDB-VP
Wilson B-factor (Å ²)	61.0	Xtriage
Anisotropy	0.474	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 52.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	9221	wwPDB-VP
Average B, all atoms (Å ²)	72.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.35% 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	0.67	1/4724 (0.0%)	0.81	2/6385 (0.0%)
1	B	0.64	0/4699	0.80	1/6353 (0.0%)
All	All	0.66	1/9423 (0.0%)	0.80	3/12738 (0.0%)

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

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

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	355	CYS	CB-SG	-5.01	1.73	1.81

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	202	LEU	CA-CB-CG	6.11	129.35	115.30
1	A	202	LEU	CA-CB-CG	5.68	128.37	115.30
1	A	27	VAL	N-CA-C	-5.15	97.10	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	348	TYR	Sidechain

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	4623	0	4620	296	0
1	B	4598	0	4598	296	0
All	All	9221	0	9218	576	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 31.

All (576) 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:200:LYS:HD3	1:B:236:LEU:HD21	1.27	1.14
1:B:61:LEU:HD12	1:B:63:GLN:NE2	1.70	1.06
1:B:264:THR:HB	1:B:267:GLN:HG3	1.43	1.00
1:B:533:GLU:HG3	1:B:545:LEU:HD11	1.40	0.98
1:B:244:ARG:HB3	1:B:244:ARG:HH11	1.27	0.98
1:A:475:LEU:H	1:A:475:LEU:HD12	1.25	0.97
1:A:428:ARG:HH11	1:A:428:ARG:HG2	1.26	0.97
1:A:264:THR:HB	1:A:267:GLN:HG3	1.43	0.96
1:B:475:LEU:H	1:B:475:LEU:HD12	1.31	0.94
1:A:307:LYS:HD3	1:A:338:LYS:HD2	1.50	0.94
1:A:546:GLU:O	1:A:550:PHE:HD1	1.51	0.92
1:A:341:ASP:OD2	1:A:343:THR:HG22	1.72	0.89
1:A:61:LEU:HD12	1:A:63:GLN:NE2	1.88	0.89
1:B:61:LEU:HD12	1:B:63:GLN:HE21	1.34	0.88
1:B:307:LYS:HD3	1:B:338:LYS:HD2	1.54	0.88
1:A:480:LYS:HE2	1:A:480:LYS:HA	1.59	0.84
1:B:115:GLU:H	1:B:115:GLU:CD	1.82	0.83
1:B:299:LEU:HB3	1:B:301:LEU:HD21	1.61	0.83
1:A:115:GLU:HG2	1:A:116:LEU:H	1.45	0.82
1:A:428:ARG:HH11	1:A:428:ARG:CG	1.92	0.82
1:A:560:GLU:HA	1:A:582:MET:HE1	1.62	0.82
1:A:191:ARG:O	1:A:195:ILE:HG13	1.80	0.81
1:B:137:ILE:HD12	1:B:138:ILE:HG13	1.63	0.81
1:B:386:CYS:O	1:B:390:ILE:HG13	1.80	0.81
1:B:231:ARG:O	1:B:231:ARG:HD2	1.81	0.80

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:341:ASP:OD2	1:B:343:THR:HG22	1.80	0.80
1:A:386:CYS:O	1:A:390:ILE:HG13	1.81	0.80
1:A:202:LEU:HD21	1:A:213:MET:HG2	1.62	0.79
1:B:546:GLU:O	1:B:550:PHE:HD1	1.63	0.79
1:B:480:LYS:HE2	1:B:480:LYS:HA	1.62	0.79
1:A:560:GLU:HA	1:A:582:MET:CE	2.13	0.79
1:A:61:LEU:HD12	1:A:63:GLN:HE21	1.46	0.79
1:A:378:GLU:O	1:A:382:THR:HG22	1.83	0.78
1:B:307:LYS:NZ	1:B:338:LYS:HG3	1.98	0.78
1:B:258:LYS:H	1:B:283:GLN:HE22	1.30	0.77
1:A:26:ARG:HH11	1:A:26:ARG:HG2	1.51	0.76
1:A:99:LEU:CD1	1:A:133:LYS:HD3	2.15	0.76
1:A:427:LYS:HB2	1:A:435:SER:OG	1.87	0.75
1:B:230:ARG:NH1	1:B:230:ARG:HB3	2.01	0.75
1:B:254:THR:O	1:B:256:GLY:N	2.19	0.75
1:A:550:PHE:CE2	1:A:558:LYS:HD3	2.22	0.75
1:A:237:SER:O	1:A:241:MET:HG2	1.86	0.75
1:B:80:LEU:HA	1:B:118:ASN:HD21	1.52	0.75
1:A:200:LYS:HD3	1:A:236:LEU:HD21	1.68	0.75
1:A:258:LYS:H	1:A:283:GLN:HE22	1.36	0.74
1:A:536:VAL:O	1:A:536:VAL:HG12	1.87	0.74
1:A:423:MET:HA	1:A:438:ILE:HD12	1.69	0.73
1:A:538:SER:C	1:A:540:ASN:H	1.92	0.73
1:B:231:ARG:HG3	1:B:232:HIS:HD2	1.54	0.73
1:B:128:ILE:HD11	1:B:152:PHE:HA	1.70	0.72
1:B:224:VAL:O	1:B:225:ASN:HB2	1.87	0.72
1:B:230:ARG:HB3	1:B:230:ARG:HH11	1.53	0.72
1:B:238:ALA:HB3	1:B:239:GLN:NE2	2.04	0.72
1:B:227:LEU:HD23	1:B:228:THR:HG23	1.71	0.72
1:B:533:GLU:HG3	1:B:545:LEU:CD1	2.19	0.72
1:B:278:GLU:O	1:B:279:TYR:HB3	1.88	0.71
1:A:140:GLY:HA3	1:A:144:ALA:HB2	1.72	0.71
1:B:115:GLU:HG2	1:B:116:LEU:H	1.55	0.70
1:B:299:LEU:HB3	1:B:301:LEU:CD2	2.22	0.70
1:A:546:GLU:O	1:A:550:PHE:CD1	2.40	0.70
1:B:511:SER:O	1:B:515:LYS:HE2	1.92	0.69
1:A:99:LEU:HD11	1:A:133:LYS:HD3	1.74	0.69
1:B:167:ILE:HG23	1:B:168:GLN:N	2.08	0.69
1:A:167:ILE:HG23	1:A:168:GLN:N	2.08	0.69
1:A:292:ARG:HB3	1:A:292:ARG:HH11	1.56	0.69
1:A:501:GLU:O	1:A:504:GLN:HB2	1.92	0.69

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:394:LEU:HD11	1:A:398:MET:HE3	1.75	0.69
1:A:380:GLU:O	1:A:384:LEU:HB2	1.93	0.69
1:A:342:SER:HB2	1:A:373:ASN:OD1	1.92	0.69
1:A:569:LEU:HD12	1:B:452:ASP:OD2	1.93	0.68
1:A:214:TRP:CH2	1:A:233:ILE:HG23	2.29	0.68
1:B:202:LEU:HD21	1:B:213:MET:HG2	1.74	0.68
1:A:462:TYR:O	1:A:464:ILE:N	2.26	0.68
1:B:428:ARG:HG2	1:B:428:ARG:HH11	1.58	0.68
1:B:378:GLU:O	1:B:382:THR:HG22	1.94	0.68
1:A:358:ASN:C	1:A:358:ASN:HD22	1.96	0.68
1:A:468:THR:HG22	1:A:468:THR:O	1.94	0.68
1:B:521:LEU:O	1:B:525:ILE:HG13	1.93	0.68
1:B:538:SER:C	1:B:540:ASN:H	1.98	0.68
1:A:350:LYS:NZ	1:A:354:GLN:HE21	1.92	0.67
1:B:244:ARG:NH1	1:B:244:ARG:HB3	2.06	0.67
1:B:358:ASN:HD22	1:B:358:ASN:C	1.98	0.67
1:B:533:GLU:CG	1:B:545:LEU:HD11	2.22	0.66
1:A:78:PHE:HB3	1:A:81:MET:HG2	1.77	0.66
1:B:156:VAL:HA	1:B:160:ALA:HB3	1.77	0.66
1:B:99:LEU:HD11	1:B:133:LYS:HD3	1.77	0.66
1:B:290:TRP:HD1	1:B:290:TRP:O	1.79	0.66
1:A:371:GLU:OE1	1:B:539:LEU:HD22	1.94	0.66
1:A:36:LYS:O	1:A:40:MET:HG3	1.96	0.66
1:B:237:SER:O	1:B:241:MET:HG2	1.96	0.66
1:A:278:GLU:O	1:A:279:TYR:HB3	1.96	0.66
1:A:282:GLN:HA	1:A:282:GLN:HE21	1.60	0.65
1:A:428:ARG:NH1	1:A:428:ARG:CG	2.57	0.65
1:A:398:MET:O	1:A:402:PRO:HB3	1.97	0.65
1:A:22:ARG:HA	1:A:22:ARG:NE	2.12	0.64
1:A:394:LEU:CD1	1:A:398:MET:HE3	2.27	0.64
1:B:78:PHE:HB3	1:B:81:MET:HG2	1.79	0.64
1:B:138:ILE:HG22	1:B:139:THR:N	2.13	0.63
1:B:307:LYS:HZ1	1:B:338:LYS:HG3	1.62	0.63
1:B:554:PRO:O	1:B:555:GLU:HB3	1.97	0.63
1:A:299:LEU:HB3	1:A:301:LEU:HD21	1.81	0.63
1:B:543:ARG:HA	1:B:543:ARG:HH11	1.63	0.63
1:B:546:GLU:O	1:B:550:PHE:CD1	2.50	0.63
1:A:477:LEU:O	1:A:480:LYS:HB2	1.99	0.62
1:B:61:LEU:HD12	1:B:63:GLN:HE22	1.62	0.62
1:B:99:LEU:CD1	1:B:133:LYS:HD3	2.29	0.62
1:A:456:GLU:CG	1:B:568:VAL:HG13	2.29	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:480:LYS:HA	1:A:480:LYS:CE	2.29	0.62
1:B:145:ARG:O	1:B:145:ARG:HG2	1.98	0.62
1:A:80:LEU:HA	1:A:118:ASN:HD21	1.64	0.62
1:A:178:GLU:O	1:A:180:TRP:N	2.32	0.62
1:A:137:ILE:HD12	1:A:138:ILE:HG13	1.82	0.62
1:A:115:GLU:H	1:A:115:GLU:CD	2.03	0.62
1:A:275:LYS:O	1:A:278:GLU:HB2	2.00	0.62
1:B:36:LYS:O	1:B:40:MET:HG3	1.99	0.62
1:B:142:GLU:HG3	1:B:143:GLU:N	2.15	0.61
1:B:366:LEU:HD22	1:B:370:TYR:CE1	2.35	0.61
1:B:37:LEU:HD23	1:B:54:LEU:HA	1.82	0.61
1:A:232:HIS:HA	1:A:235:GLU:OE1	1.99	0.61
1:A:472:CYS:O	1:A:476:GLU:HG3	2.00	0.61
1:A:489:ILE:HD12	1:A:508:LEU:HD11	1.81	0.61
1:B:162:PHE:CD2	1:B:309:ARG:HG3	2.36	0.61
1:A:394:LEU:CG	1:A:398:MET:HE3	2.31	0.61
1:A:465:SER:O	1:A:467:ASP:N	2.34	0.60
1:A:543:ARG:HA	1:A:543:ARG:HH11	1.66	0.60
1:B:264:THR:HG22	1:B:266:ASN:H	1.66	0.60
1:A:282:GLN:HA	1:A:282:GLN:NE2	2.16	0.60
1:B:290:TRP:O	1:B:290:TRP:CD1	2.54	0.60
1:B:61:LEU:CD1	1:B:63:GLN:HE21	2.10	0.60
1:A:167:ILE:HB	1:A:208:ASP:OD1	2.02	0.60
1:B:559:LEU:HD21	1:B:579:LEU:HD11	1.84	0.60
1:B:275:LYS:O	1:B:278:GLU:HB2	2.01	0.59
1:A:254:THR:HG23	1:A:257:LEU:HB2	1.84	0.59
1:A:368:GLU:O	1:A:372:LEU:HD13	2.01	0.59
1:B:538:SER:O	1:B:540:ASN:N	2.35	0.59
1:A:23:PRO:O	1:A:25:SER:N	2.34	0.59
1:A:178:GLU:C	1:A:180:TRP:H	2.05	0.59
1:A:173:TYR:CE2	1:A:198:LEU:HD13	2.38	0.59
1:A:427:LYS:O	1:A:427:LYS:HE2	2.02	0.59
1:B:254:THR:HG23	1:B:257:LEU:HB2	1.84	0.59
1:B:140:GLY:HA3	1:B:144:ALA:HB2	1.85	0.59
1:B:528:LYS:NZ	1:B:528:LYS:HB2	2.17	0.59
1:B:37:LEU:HD23	1:B:54:LEU:CA	2.33	0.59
1:B:167:ILE:HB	1:B:208:ASP:OD1	2.02	0.59
1:A:479:LEU:CD1	1:A:483:ALA:HA	2.33	0.58
1:B:401:ASP:OD2	1:B:404:ASN:HB2	2.02	0.58
1:A:138:ILE:HG22	1:A:139:THR:N	2.19	0.58
1:A:189:GLN:HE21	1:A:190:GLN:N	2.01	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:280:ASP:OD1	1:A:282:GLN:HB3	2.04	0.58
1:B:65:LYS:O	1:B:69:GLU:HG3	2.03	0.58
1:A:224:VAL:O	1:A:225:ASN:HB2	2.02	0.58
1:A:533:GLU:HG3	1:A:545:LEU:HD11	1.86	0.58
1:B:538:SER:HB2	1:B:541:SER:OG	2.04	0.58
1:A:429:ILE:HG22	1:A:430:GLN:HG3	1.84	0.57
1:B:232:HIS:O	1:B:234:GLY:N	2.37	0.57
1:A:236:LEU:O	1:A:238:ALA:N	2.37	0.57
1:B:264:THR:HB	1:B:267:GLN:CG	2.24	0.57
1:B:191:ARG:O	1:B:195:ILE:HG13	2.04	0.57
1:B:199:TYR:CD1	1:B:217:TYR:HB2	2.40	0.57
1:A:429:ILE:CG2	1:A:430:GLN:HG3	2.34	0.57
1:A:538:SER:O	1:A:540:ASN:N	2.37	0.57
1:A:417:TYR:CD1	1:B:573:TYR:HB2	2.38	0.57
1:B:55:LEU:HD21	1:B:70:THR:HB	1.87	0.57
1:A:26:ARG:NH1	1:A:26:ARG:HG2	2.16	0.57
1:B:292:ARG:HH11	1:B:292:ARG:HB3	1.70	0.57
1:A:433:ALA:O	1:A:437:LYS:HG3	2.04	0.57
1:A:475:LEU:N	1:A:475:LEU:HD12	2.07	0.57
1:A:361:VAL:HG21	1:B:579:LEU:HD21	1.86	0.57
1:A:520:HIS:HE1	1:A:524:MET:CE	2.18	0.57
1:A:142:GLU:HG3	1:A:143:GLU:N	2.20	0.57
1:A:394:LEU:HG	1:A:398:MET:HE3	1.85	0.57
1:A:143:GLU:HA	1:A:146:ASN:HB3	1.86	0.56
1:B:299:LEU:CB	1:B:301:LEU:HD21	2.34	0.56
1:A:521:LEU:O	1:A:525:ILE:HG13	2.05	0.56
1:B:559:LEU:HD21	1:B:579:LEU:CD1	2.35	0.56
1:A:482:PHE:HB2	1:A:488:TYR:CD2	2.40	0.56
1:B:30:GLU:N	1:B:36:LYS:HZ1	2.02	0.56
1:B:489:ILE:HD12	1:B:508:LEU:HD11	1.85	0.56
1:A:479:LEU:HD12	1:A:483:ALA:HA	1.88	0.56
1:A:432:LEU:HD23	1:A:436:ARG:HD3	1.88	0.56
1:B:220:TRP:O	1:B:224:VAL:HG23	2.06	0.56
1:A:167:ILE:HG23	1:A:168:GLN:H	1.70	0.55
1:B:450:THR:HG23	1:B:452:ASP:H	1.72	0.55
1:A:202:LEU:HD12	1:A:202:LEU:C	2.27	0.55
1:A:224:VAL:HG12	1:A:224:VAL:O	2.07	0.55
1:B:520:HIS:HE1	1:B:524:MET:CE	2.19	0.55
1:B:61:LEU:CD1	1:B:63:GLN:NE2	2.56	0.55
1:A:307:LYS:NZ	1:A:338:LYS:HG3	2.21	0.55
1:A:539:LEU:HD22	1:B:371:GLU:OE1	2.06	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:538:SER:C	1:A:540:ASN:N	2.60	0.55
1:B:178:GLU:C	1:B:180:TRP:H	2.10	0.55
1:B:178:GLU:O	1:B:180:TRP:N	2.39	0.55
1:A:299:LEU:CB	1:A:301:LEU:HD21	2.37	0.54
1:A:489:ILE:HG21	1:A:516:ILE:HD11	1.88	0.54
1:A:78:PHE:HB3	1:A:81:MET:CG	2.37	0.54
1:A:232:HIS:O	1:A:234:GLY:N	2.40	0.54
1:A:66:GLN:HA	1:A:69:GLU:HG3	1.90	0.54
1:A:26:ARG:O	1:A:28:ARG:N	2.40	0.54
1:B:230:ARG:CB	1:B:230:ARG:HH11	2.20	0.54
1:A:456:GLU:HG3	1:B:568:VAL:HG13	1.89	0.54
1:A:181:LYS:NZ	1:A:181:LYS:H	2.06	0.54
1:B:173:TYR:CE2	1:B:198:LEU:HD13	2.43	0.54
1:A:350:LYS:HZ1	1:A:354:GLN:HE21	1.54	0.54
1:A:345:ILE:HB	1:A:369:GLN:OE1	2.08	0.54
1:B:291:ILE:HD13	1:B:314:TYR:CE1	2.42	0.54
1:B:463:HIS:HD2	1:B:466:LYS:HE2	1.72	0.54
1:B:468:THR:O	1:B:472:CYS:HB2	2.08	0.54
1:A:489:ILE:HG13	1:A:516:ILE:HD11	1.90	0.53
1:B:428:ARG:HG2	1:B:428:ARG:NH1	2.23	0.53
1:A:99:LEU:HD13	1:A:133:LYS:HD3	1.89	0.53
1:A:538:SER:HB2	1:A:541:SER:OG	2.08	0.53
1:A:568:VAL:O	1:A:569:LEU:HB2	2.08	0.53
1:B:426:MET:HA	1:B:426:MET:HE2	1.89	0.53
1:B:342:SER:HB2	1:B:373:ASN:OD1	2.08	0.53
1:A:531:PHE:O	1:A:531:PHE:CD1	2.61	0.53
1:A:518:ASP:CG	1:A:519:SER:H	2.12	0.53
1:A:199:TYR:CD1	1:A:217:TYR:HB2	2.43	0.53
1:B:202:LEU:HD12	1:B:202:LEU:C	2.29	0.53
1:B:551:GLU:O	1:B:554:PRO:HD3	2.09	0.53
1:A:245:SER:O	1:A:248:GLN:HB2	2.09	0.53
1:A:432:LEU:CD2	1:A:436:ARG:HD3	2.39	0.53
1:A:531:PHE:C	1:A:531:PHE:CD1	2.82	0.53
1:A:511:SER:O	1:A:515:LYS:HE2	2.09	0.53
1:B:202:LEU:HD12	1:B:203:LEU:N	2.24	0.53
1:A:220:TRP:O	1:A:224:VAL:HG23	2.09	0.52
1:B:304:ASP:N	1:B:304:ASP:OD2	2.42	0.52
1:A:140:GLY:CA	1:A:144:ALA:HB2	2.40	0.52
1:A:254:THR:HG23	1:A:257:LEU:CB	2.39	0.52
1:A:232:HIS:N	1:A:232:HIS:CD2	2.77	0.52
1:A:299:LEU:O	1:A:300:GLU:HB2	2.09	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:340:THR:O	1:A:341:ASP:HB3	2.09	0.52
1:A:307:LYS:HE3	1:A:335:GLN:HE22	1.74	0.52
1:B:238:ALA:HB3	1:B:239:GLN:HE21	1.73	0.52
1:B:509:PHE:O	1:B:513:ILE:HG13	2.09	0.52
1:A:401:ASP:CG	1:A:401:ASP:O	2.47	0.52
1:B:137:ILE:CD1	1:B:138:ILE:HG13	2.37	0.52
1:B:468:THR:HG22	1:B:468:THR:O	2.10	0.52
1:B:531:PHE:CD1	1:B:531:PHE:C	2.83	0.52
1:A:156:VAL:HA	1:A:160:ALA:HB3	1.92	0.52
1:A:264:THR:HG22	1:A:265:LEU:N	2.24	0.52
1:B:432:LEU:C	1:B:432:LEU:HD23	2.30	0.52
1:B:433:ALA:O	1:B:437:LYS:HG3	2.10	0.52
1:B:231:ARG:HG3	1:B:232:HIS:CD2	2.39	0.51
1:B:37:LEU:HD23	1:B:54:LEU:HB2	1.92	0.51
1:A:307:LYS:HE3	1:A:335:GLN:NE2	2.26	0.51
1:B:543:ARG:HA	1:B:543:ARG:NH1	2.25	0.51
1:B:167:ILE:CG2	1:B:168:GLN:N	2.72	0.51
1:A:192:VAL:HG12	1:A:220:TRP:HZ2	1.75	0.51
1:A:547:LYS:O	1:A:551:GLU:HG3	2.10	0.51
1:A:579:LEU:C	1:A:581:TYR:H	2.12	0.51
1:B:162:PHE:HD2	1:B:309:ARG:HG3	1.75	0.51
1:B:520:HIS:HE1	1:B:524:MET:HE1	1.75	0.51
1:A:304:ASP:N	1:A:304:ASP:OD2	2.44	0.51
1:B:307:LYS:HZ2	1:B:338:LYS:HG3	1.76	0.50
1:B:68:TYR:CD2	1:B:68:TYR:N	2.78	0.50
1:A:189:GLN:C	1:A:189:GLN:NE2	2.65	0.50
1:B:202:LEU:HD21	1:B:213:MET:CG	2.42	0.50
1:A:259:ARG:C	1:A:260:ASN:HD22	2.13	0.50
1:A:292:ARG:O	1:A:295:SER:OG	2.23	0.50
1:A:452:ASP:O	1:A:456:GLU:HB2	2.11	0.50
1:B:173:TYR:CD2	1:B:198:LEU:HD13	2.46	0.50
1:B:81:MET:CE	1:B:319:GLN:HA	2.41	0.50
1:B:192:VAL:HG12	1:B:220:TRP:HZ2	1.76	0.50
1:B:56:LYS:HG3	1:B:265:LEU:HD23	1.94	0.50
1:A:326:GLU:O	1:A:326:GLU:HG3	2.09	0.50
1:A:538:SER:OG	1:A:541:SER:HB2	2.12	0.50
1:A:89:LEU:HD21	1:A:107:VAL:CG1	2.41	0.50
1:B:189:GLN:HE21	1:B:190:GLN:N	2.08	0.50
1:B:290:TRP:C	1:B:290:TRP:CD1	2.84	0.50
1:A:315:MET:HG3	1:A:331:MET:HE3	1.94	0.50
1:B:509:PHE:CE2	1:B:513:ILE:HD11	2.47	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:544:THR:O	1:B:547:LYS:N	2.45	0.50
1:B:432:LEU:HD23	1:B:436:ARG:HD3	1.94	0.50
1:A:262:PRO:HG3	1:A:272:ASN:ND2	2.27	0.50
1:A:493:LEU:HD23	1:A:496:LEU:HD12	1.93	0.50
1:A:315:MET:HG3	1:A:331:MET:CE	2.42	0.49
1:B:282:GLN:HE21	1:B:282:GLN:HA	1.77	0.49
1:A:554:PRO:O	1:A:555:GLU:HB3	2.11	0.49
1:B:72:ASP:OD1	1:B:88:ARG:NH1	2.43	0.49
1:A:81:MET:CE	1:A:319:GLN:HA	2.42	0.49
1:A:426:MET:HG3	1:A:438:ILE:HD11	1.93	0.49
1:B:280:ASP:OD1	1:B:282:GLN:HB3	2.13	0.49
1:A:167:ILE:CG2	1:A:168:GLN:N	2.75	0.49
1:B:192:VAL:HG12	1:B:220:TRP:CZ2	2.47	0.49
1:B:429:ILE:HG22	1:B:430:GLN:HG3	1.92	0.49
1:B:236:LEU:O	1:B:238:ALA:N	2.46	0.49
1:B:493:LEU:O	1:B:494:ASP:C	2.50	0.49
1:A:22:ARG:CZ	1:A:22:ARG:HA	2.43	0.49
1:A:550:PHE:HE2	1:A:558:LYS:HA	1.78	0.49
1:B:258:LYS:H	1:B:283:GLN:NE2	2.04	0.49
1:A:22:ARG:CB	1:A:23:PRO:HD3	2.43	0.49
1:B:489:ILE:HG21	1:B:516:ILE:HD11	1.94	0.49
1:A:294:GLU:HG3	1:A:313:VAL:HG21	1.95	0.49
1:B:282:GLN:NE2	1:B:282:GLN:HA	2.27	0.49
1:B:299:LEU:O	1:B:300:GLU:HB2	2.13	0.49
1:A:371:GLU:CD	1:B:539:LEU:HD22	2.33	0.49
1:A:366:LEU:O	1:A:369:GLN:N	2.46	0.48
1:B:394:LEU:HG	1:B:398:MET:HE3	1.95	0.48
1:A:338:LYS:HE2	1:A:338:LYS:HA	1.95	0.48
1:B:309:ARG:O	1:B:313:VAL:HG23	2.13	0.48
1:B:563:THR:HB	1:B:572:ASN:HD21	1.78	0.48
1:A:414:LYS:HB2	1:B:577:LEU:HD13	1.95	0.48
1:A:472:CYS:SG	1:A:504:GLN:NE2	2.87	0.48
1:A:61:LEU:HB2	1:A:63:GLN:HG3	1.95	0.48
1:B:214:TRP:CH2	1:B:233:ILE:HG23	2.48	0.48
1:B:542:VAL:HG12	1:B:546:GLU:HG3	1.95	0.48
1:B:264:THR:HG22	1:B:265:LEU:N	2.28	0.48
1:B:501:GLU:O	1:B:504:GLN:HB2	2.12	0.48
1:A:145:ARG:O	1:A:145:ARG:HG2	2.12	0.48
1:A:428:ARG:NH2	1:B:539:LEU:HD13	2.29	0.48
1:B:550:PHE:CE2	1:B:558:LYS:HD3	2.48	0.48
1:A:89:LEU:HD21	1:A:107:VAL:HG12	1.95	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:180:TRP:CE3	1:A:191:ARG:HG3	2.48	0.48
1:A:474:VAL:O	1:A:477:LEU:HB2	2.13	0.48
1:B:292:ARG:O	1:B:293:TRP:C	2.50	0.48
1:B:55:LEU:HD22	1:B:67:VAL:HG13	1.94	0.48
1:A:181:LYS:H	1:A:181:LYS:HZ3	1.61	0.48
1:A:52:VAL:HG11	1:A:268:ALA:HB3	1.95	0.48
1:A:553:PHE:HB3	1:A:556:VAL:CG2	2.44	0.48
1:A:359:SER:HA	1:B:578:GLU:OE2	2.13	0.48
1:A:277:ASN:ND2	1:A:358:ASN:OD1	2.45	0.48
1:A:401:ASP:OD2	1:A:404:ASN:HB2	2.14	0.48
1:A:350:LYS:HZ1	1:A:354:GLN:NE2	2.12	0.48
1:B:189:GLN:NE2	1:B:190:GLN:N	2.62	0.48
1:B:224:VAL:O	1:B:224:VAL:HG12	2.14	0.47
1:B:539:LEU:HA	1:B:542:VAL:CG2	2.43	0.47
1:A:192:VAL:HG12	1:A:220:TRP:CZ2	2.49	0.47
1:B:358:ASN:ND2	1:B:358:ASN:C	2.66	0.47
1:A:512:SER:HB2	1:A:516:ILE:HG13	1.96	0.47
1:B:225:ASN:C	1:B:227:LEU:H	2.18	0.47
1:B:565:LYS:NZ	1:B:565:LYS:CB	2.77	0.47
1:B:432:LEU:CD2	1:B:436:ARG:HD3	2.44	0.47
1:B:55:LEU:CD2	1:B:70:THR:HB	2.44	0.47
1:A:462:TYR:C	1:A:464:ILE:H	2.17	0.47
1:B:518:ASP:CG	1:B:519:SER:H	2.17	0.47
1:B:246:LEU:HD22	1:B:293:TRP:CZ2	2.50	0.47
1:A:372:LEU:C	1:A:374:THR:H	2.17	0.47
1:B:121:LEU:HD21	1:B:169:PHE:HB2	1.96	0.47
1:B:538:SER:C	1:B:540:ASN:N	2.66	0.47
1:A:212:SER:O	1:A:216:ARG:HG3	2.14	0.47
1:A:553:PHE:C	1:A:554:PRO:O	2.50	0.47
1:B:222:GLN:C	1:B:224:VAL:H	2.18	0.47
1:B:293:TRP:NE1	1:B:298:LYS:HD2	2.29	0.47
1:B:479:LEU:HD12	1:B:483:ALA:HA	1.97	0.47
1:B:221:GLU:HA	1:B:221:GLU:OE1	2.15	0.47
1:B:479:LEU:HD22	1:B:492:TYR:HE2	1.80	0.47
1:A:445:LEU:O	1:A:446:LYS:HB2	2.14	0.47
1:A:297:ASN:HB2	1:A:306:HIS:CD2	2.50	0.46
1:B:155:VAL:HG11	1:B:169:PHE:CE1	2.50	0.46
1:B:489:ILE:HG13	1:B:516:ILE:HD11	1.96	0.46
1:A:479:LEU:HD12	1:A:483:ALA:CA	2.44	0.46
1:A:509:PHE:HZ	1:A:526:PHE:CE2	2.34	0.46
1:B:112:LEU:HD22	1:B:124:TRP:CH2	2.51	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:329:PHE:CG	1:B:559:LEU:HD13	2.51	0.46
1:B:307:LYS:CD	1:B:338:LYS:HD2	2.38	0.46
1:A:520:HIS:HE1	1:A:524:MET:HE1	1.80	0.46
1:A:543:ARG:HA	1:A:543:ARG:NH1	2.30	0.46
1:A:350:LYS:HZ2	1:A:354:GLN:HE21	1.63	0.46
1:A:407:ALA:O	1:A:411:LEU:HD13	2.15	0.46
1:B:568:VAL:O	1:B:569:LEU:HB2	2.15	0.46
1:A:439:PHE:CD2	1:A:457:ASN:OD1	2.69	0.46
1:B:284:LEU:O	1:B:288:LEU:HG	2.15	0.46
1:A:189:GLN:NE2	1:A:190:GLN:N	2.63	0.46
1:A:307:LYS:CE	1:A:335:GLN:HE22	2.28	0.46
1:B:77:ARG:C	1:B:79:PRO:HD3	2.36	0.46
1:A:454:TYR:CE1	1:A:482:PHE:HE1	2.34	0.46
1:A:509:PHE:CE2	1:A:513:ILE:HD11	2.51	0.46
1:B:448:LEU:HA	1:B:448:LEU:HD12	1.75	0.46
1:A:519:SER:OG	1:A:520:HIS:N	2.49	0.45
1:B:107:VAL:HG12	1:B:108:LEU:N	2.31	0.45
1:B:244:ARG:CB	1:B:244:ARG:HH11	2.14	0.45
1:B:401:ASP:O	1:B:401:ASP:CG	2.55	0.45
1:B:569:LEU:O	1:B:571:VAL:HG23	2.16	0.45
1:A:142:GLU:O	1:A:146:ASN:HB2	2.16	0.45
1:B:209:CYS:O	1:B:213:MET:HB2	2.16	0.45
1:B:452:ASP:O	1:B:456:GLU:HB2	2.17	0.45
1:B:484:THR:O	1:B:484:THR:HG22	2.16	0.45
1:A:550:PHE:CD2	1:A:558:LYS:HD3	2.52	0.45
1:A:569:LEU:O	1:A:571:VAL:HG23	2.16	0.45
1:B:125:LEU:HA	1:B:125:LEU:HD23	1.53	0.45
1:B:425:THR:HG22	1:B:426:MET:HE3	1.97	0.45
1:B:416:THR:HG21	1:B:450:THR:HG22	1.99	0.45
1:B:564:ASN:O	1:B:567:LYS:HG3	2.16	0.45
1:A:264:THR:HG22	1:A:266:ASN:H	1.81	0.45
1:A:484:THR:HG22	1:A:484:THR:O	2.16	0.45
1:A:37:LEU:HD23	1:A:54:LEU:HA	1.98	0.45
1:A:560:GLU:HA	1:A:582:MET:HE3	1.97	0.45
1:B:144:ALA:C	1:B:146:ASN:H	2.19	0.45
1:B:380:GLU:O	1:B:384:LEU:HB2	2.17	0.45
1:A:115:GLU:HG2	1:A:116:LEU:N	2.23	0.45
1:A:128:ILE:HD11	1:A:152:PHE:HA	1.99	0.45
1:A:236:LEU:O	1:A:237:SER:C	2.55	0.45
1:A:475:LEU:H	1:A:475:LEU:CD1	2.04	0.45
1:B:115:GLU:N	1:B:115:GLU:CD	2.60	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:49:PHE:HD1	1:B:273:LEU:HD12	1.82	0.45
1:B:523:LYS:HB2	1:B:553:PHE:CE2	2.52	0.45
1:B:547:LYS:O	1:B:551:GLU:HG3	2.17	0.45
1:B:78:PHE:HB3	1:B:81:MET:CG	2.45	0.45
1:A:573:TYR:O	1:A:574:LEU:C	2.56	0.44
1:B:125:LEU:CD1	1:B:168:GLN:NE2	2.80	0.44
1:B:182:PRO:HG2	1:B:188:GLU:HA	1.98	0.44
1:B:519:SER:O	1:B:521:LEU:N	2.50	0.44
1:B:565:LYS:NZ	1:B:565:LYS:HB3	2.32	0.44
1:A:485:ASP:CG	1:A:487:GLU:HB3	2.38	0.44
1:B:115:GLU:HG2	1:B:116:LEU:N	2.27	0.44
1:B:200:LYS:HD3	1:B:236:LEU:CD2	2.20	0.44
1:B:436:ARG:O	1:B:437:LYS:C	2.55	0.44
1:B:520:HIS:O	1:B:520:HIS:ND1	2.49	0.44
1:A:244:ARG:HB3	1:A:244:ARG:HH11	1.81	0.44
1:A:428:ARG:HD2	1:A:428:ARG:O	2.17	0.44
1:B:337:GLU:O	1:B:338:LYS:O	2.35	0.44
1:B:177:LEU:HA	1:B:177:LEU:HD23	1.77	0.44
1:B:254:THR:HG23	1:B:257:LEU:CB	2.48	0.44
1:B:565:LYS:HD2	1:B:566:TYR:CE1	2.53	0.44
1:A:508:LEU:HD12	1:A:508:LEU:O	2.17	0.44
1:A:81:MET:HE2	1:A:319:GLN:HA	1.98	0.44
1:B:212:SER:O	1:B:216:ARG:HG3	2.17	0.44
1:A:520:HIS:HE1	1:A:524:MET:HE3	1.81	0.44
1:A:560:GLU:HG3	1:A:582:MET:HE3	2.00	0.44
1:A:572:ASN:HD21	1:A:574:LEU:HB2	1.83	0.44
1:A:61:LEU:CD1	1:A:63:GLN:NE2	2.72	0.44
1:B:140:GLY:CA	1:B:144:ALA:HB2	2.46	0.44
1:B:174:LEU:HA	1:B:174:LEU:HD23	1.77	0.44
1:B:493:LEU:HD22	1:B:505:VAL:HG13	1.99	0.44
1:B:79:PRO:HB3	1:B:116:LEU:HD13	1.99	0.44
1:A:454:TYR:HE1	1:A:482:PHE:HE1	1.64	0.44
1:A:438:ILE:O	1:A:441:LYS:HG2	2.18	0.44
1:A:468:THR:CG2	1:A:468:THR:O	2.65	0.44
1:A:579:LEU:HD23	1:A:579:LEU:N	2.32	0.44
1:A:207:MET:HB3	1:A:207:MET:HE3	1.64	0.43
1:A:25:SER:O	1:A:27:VAL:N	2.46	0.43
1:B:508:LEU:O	1:B:508:LEU:HD12	2.17	0.43
1:A:173:TYR:CD2	1:A:198:LEU:HD13	2.54	0.43
1:A:425:THR:O	1:A:429:ILE:HB	2.17	0.43
1:B:181:LYS:H	1:B:181:LYS:NZ	2.16	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:214:TRP:O	1:B:215:GLN:C	2.57	0.43
1:A:197:LYS:O	1:A:197:LYS:HG2	2.19	0.43
1:A:477:LEU:HD13	1:A:477:LEU:HA	1.87	0.43
1:A:528:LYS:HB2	1:A:528:LYS:NZ	2.33	0.43
1:A:52:VAL:HG11	1:A:268:ALA:CB	2.48	0.43
1:B:225:ASN:O	1:B:227:LEU:N	2.51	0.43
1:B:426:MET:CE	1:B:426:MET:HA	2.48	0.43
1:A:187:GLU:C	1:A:189:GLN:N	2.70	0.43
1:A:22:ARG:HB3	1:A:23:PRO:HD3	2.00	0.43
1:A:456:GLU:HG3	1:B:568:VAL:CG1	2.48	0.43
1:A:84:ILE:HA	1:A:87:MET:CE	2.49	0.43
1:B:137:ILE:HD12	1:B:138:ILE:N	2.33	0.43
1:A:121:LEU:O	1:A:121:LEU:HD23	2.19	0.43
1:A:441:LYS:O	1:A:444:ARG:HB3	2.19	0.43
1:B:115:GLU:HB2	1:B:347:LYS:NZ	2.33	0.43
1:B:539:LEU:HA	1:B:542:VAL:HG23	2.00	0.43
1:B:372:LEU:C	1:B:374:THR:H	2.22	0.43
1:B:462:TYR:O	1:B:464:ILE:N	2.52	0.43
1:B:492:TYR:O	1:B:495:PHE:HB3	2.19	0.43
1:A:385:SER:O	1:A:386:CYS:C	2.56	0.43
1:B:37:LEU:CD2	1:B:54:LEU:HA	2.48	0.43
1:B:143:GLU:HA	1:B:146:ASN:HB3	2.01	0.43
1:B:232:HIS:C	1:B:234:GLY:N	2.72	0.43
1:B:56:LYS:CG	1:B:265:LEU:HD23	2.48	0.43
1:A:520:HIS:CE1	1:A:524:MET:HE3	2.54	0.43
1:B:259:ARG:C	1:B:260:ASN:HD22	2.21	0.43
1:B:289:GLU:OE2	1:B:289:GLU:HA	2.19	0.43
1:A:299:LEU:HB3	1:A:301:LEU:CD2	2.49	0.42
1:A:451:PRO:HG3	1:A:482:PHE:CG	2.54	0.42
1:B:366:LEU:O	1:B:369:GLN:N	2.52	0.42
1:B:366:LEU:O	1:B:367:SER:C	2.57	0.42
1:B:37:LEU:HD23	1:B:54:LEU:CB	2.49	0.42
1:B:191:ARG:O	1:B:191:ARG:HG2	2.18	0.42
1:A:297:ASN:CG	1:A:297:ASN:O	2.56	0.42
1:A:430:GLN:O	1:A:434:ALA:HB2	2.19	0.42
1:A:492:TYR:O	1:A:495:PHE:HB3	2.19	0.42
1:B:128:ILE:CD1	1:B:152:PHE:CD1	3.03	0.42
1:B:327:ILE:HG23	1:B:328:TRP:N	2.35	0.42
1:B:90:SER:O	1:B:91:LEU:C	2.58	0.42
1:A:180:TRP:C	1:A:180:TRP:CD1	2.91	0.42
1:B:140:GLY:C	1:B:144:ALA:HB2	2.38	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:165:LYS:HE3	1:B:208:ASP:HB3	2.02	0.42
1:B:368:GLU:O	1:B:372:LEU:HD13	2.20	0.42
1:B:471:ALA:O	1:B:475:LEU:HD11	2.19	0.42
1:A:436:ARG:HG2	1:A:436:ARG:HH11	1.85	0.42
1:A:575:GLN:O	1:A:580:ASP:HA	2.19	0.42
1:B:137:ILE:HG22	1:B:145:ARG:HB2	2.01	0.42
1:B:460:ILE:C	1:B:462:TYR:N	2.73	0.42
1:A:479:LEU:HD12	1:A:479:LEU:HA	1.78	0.42
1:A:232:HIS:O	1:A:235:GLU:OE1	2.37	0.42
1:B:103:VAL:O	1:B:106:PRO:HG2	2.20	0.42
1:B:120:ASP:OD2	1:B:122:SER:HB2	2.19	0.42
1:B:531:PHE:O	1:B:531:PHE:CD1	2.72	0.42
1:B:262:PRO:HG2	1:B:268:ALA:HA	2.02	0.42
1:B:279:TYR:CE2	1:B:324:ALA:HA	2.54	0.42
1:A:493:LEU:HD23	1:A:493:LEU:HA	1.89	0.42
1:B:263:ILE:HG13	1:B:263:ILE:H	1.80	0.42
1:B:512:SER:HB2	1:B:516:ILE:HG13	2.01	0.42
1:B:77:ARG:O	1:B:79:PRO:HD3	2.20	0.42
1:A:112:LEU:HD22	1:A:124:TRP:CH2	2.54	0.41
1:B:231:ARG:HD2	1:B:231:ARG:C	2.40	0.41
1:B:324:ALA:O	1:B:327:ILE:HG22	2.19	0.41
1:B:394:LEU:HD13	1:B:411:LEU:HB3	2.02	0.41
1:B:412:LYS:NZ	1:B:447:LYS:O	2.39	0.41
1:B:51:TYR:CD2	1:B:74:LEU:HD21	2.55	0.41
1:A:236:LEU:C	1:A:238:ALA:N	2.71	0.41
1:A:37:LEU:HD23	1:A:54:LEU:CA	2.50	0.41
1:A:550:PHE:CE2	1:A:558:LYS:HA	2.55	0.41
1:A:77:ARG:HG2	1:A:78:PHE:CD1	2.54	0.41
1:A:80:LEU:HA	1:A:118:ASN:ND2	2.32	0.41
1:B:119:ASN:OD1	1:B:159:CYS:HB2	2.19	0.41
1:B:142:GLU:C	1:B:144:ALA:N	2.74	0.41
1:B:202:LEU:HD11	1:B:213:MET:HG2	2.02	0.41
1:B:81:MET:HE2	1:B:319:GLN:HA	2.01	0.41
1:A:177:LEU:HD23	1:A:177:LEU:HA	1.84	0.41
1:A:446:LYS:HB3	1:A:447:LYS:H	1.45	0.41
1:B:164:PRO:HG2	1:B:250:TRP:CZ2	2.55	0.41
1:A:539:LEU:HD23	1:B:372:LEU:HD11	2.01	0.41
1:A:195:ILE:HG22	1:A:195:ILE:O	2.21	0.41
1:B:144:ALA:C	1:B:146:ASN:N	2.74	0.41
1:B:249:ASP:O	1:B:250:TRP:C	2.59	0.41
1:B:519:SER:C	1:B:521:LEU:N	2.74	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:138:ILE:HG22	1:A:139:THR:HG23	2.02	0.41
1:A:164:PRO:HG3	1:A:250:TRP:CE2	2.55	0.41
1:A:261:LEU:HA	1:A:262:PRO:HD3	1.87	0.41
1:A:574:LEU:HA	1:A:574:LEU:HD23	1.64	0.41
1:B:125:LEU:HD21	1:B:169:PHE:HD1	1.85	0.41
1:A:187:GLU:O	1:A:189:GLN:N	2.54	0.41
1:A:253:ILE:HG23	1:A:289:GLU:HG3	2.02	0.41
1:A:479:LEU:HD11	1:A:483:ALA:HA	2.01	0.41
1:B:394:LEU:CG	1:B:398:MET:HE3	2.51	0.41
1:B:526:PHE:O	1:B:530:ILE:HG13	2.21	0.41
1:A:464:ILE:HB	1:A:465:SER:H	1.65	0.41
1:A:493:LEU:HD22	1:A:505:VAL:HG13	2.02	0.41
1:B:195:ILE:HG22	1:B:195:ILE:O	2.20	0.41
1:B:232:HIS:HA	1:B:235:GLU:OE1	2.20	0.41
1:B:243:ALA:O	1:B:246:LEU:N	2.54	0.41
1:B:464:ILE:HB	1:B:465:SER:H	1.71	0.41
1:A:416:THR:HG23	1:A:449:VAL:HB	2.03	0.41
1:A:24:THR:CB	1:A:43:GLU:OE2	2.69	0.41
1:A:466:LYS:HZ1	1:B:500:ASN:HB3	1.86	0.41
1:A:579:LEU:O	1:A:581:TYR:N	2.54	0.41
1:B:246:LEU:HA	1:B:246:LEU:HD23	1.86	0.41
1:A:466:LYS:HA	1:A:466:LYS:HD3	1.94	0.41
1:A:485:ASP:OD2	1:A:487:GLU:HB3	2.21	0.41
1:B:137:ILE:H	1:B:137:ILE:HG13	1.69	0.41
1:B:465:SER:O	1:B:467:ASP:N	2.54	0.41
1:B:574:LEU:HA	1:B:574:LEU:HD23	1.81	0.41
1:B:74:LEU:HA	1:B:74:LEU:HD23	1.86	0.41
1:A:127:TYR:O	1:A:131:VAL:HG23	2.21	0.41
1:A:77:ARG:C	1:A:79:PRO:HD3	2.42	0.41
1:B:85:TRP:CD2	1:B:111:CYS:HB3	2.56	0.41
1:B:463:HIS:CD2	1:B:466:LYS:HE2	2.55	0.41
1:A:178:GLU:C	1:A:180:TRP:N	2.72	0.40
1:A:299:LEU:O	1:A:300:GLU:CB	2.68	0.40
1:A:358:ASN:C	1:A:358:ASN:ND2	2.66	0.40
1:A:394:LEU:HD21	1:A:398:MET:HE1	2.03	0.40
1:A:411:LEU:N	1:A:411:LEU:CD1	2.84	0.40
1:A:469:LYS:O	1:A:473:LYS:HG3	2.21	0.40
1:A:254:THR:HG22	1:A:255:LYS:N	2.36	0.40
1:A:301:LEU:HB3	1:A:305:LEU:HB3	2.03	0.40
1:A:34:ILE:CG1	1:A:57:HIS:CD2	3.04	0.40
1:B:340:THR:O	1:B:341:ASP:HB3	2.21	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:510:GLU:OE1	1:B:510:GLU:HA	2.19	0.40
1:A:202:LEU:HD12	1:A:203:LEU:N	2.36	0.40
1:A:292:ARG:CB	1:A:292:ARG:HH11	2.27	0.40
1:A:358:ASN:O	1:A:414:LYS:NZ	2.54	0.40
1:A:366:LEU:HD22	1:A:370:TYR:CE1	2.56	0.40
1:A:417:TYR:OH	1:B:574:LEU:HG	2.20	0.40
1:A:453:ILE:HA	1:A:453:ILE:HD12	1.93	0.40
1:A:520:HIS:ND1	1:A:520:HIS:O	2.54	0.40
1:A:533:GLU:HG3	1:A:545:LEU:CD1	2.50	0.40
1:A:538:SER:CB	1:A:541:SER:OG	2.69	0.40
1:B:464:ILE:HG13	1:B:464:ILE:H	1.74	0.40
1:B:74:LEU:HD13	1:B:84:ILE:HD13	2.04	0.40
1:A:389:ARG:HD2	1:A:389:ARG:HA	1.86	0.40
1:A:128:ILE:HD13	1:A:152:PHE:CE1	2.57	0.40
1:B:173:TYR:CD2	1:B:198:LEU:CD1	3.04	0.40
1:B:394:LEU:HA	1:B:411:LEU:HD23	2.02	0.40
1:B:394:LEU:HG	1:B:398:MET:CE	2.51	0.40
1:B:85:TRP:CD2	1:B:111:CYS:CB	3.05	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	551/678 (81%)	430 (78%)	91 (16%)	30 (5%)	2	11
1	B	550/678 (81%)	439 (80%)	87 (16%)	24 (4%)	2	15
All	All	1101/1356 (81%)	869 (79%)	178 (16%)	54 (5%)	2	13

All (54) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	113	SER
1	A	142	GLU
1	A	179	HIS
1	A	233	ILE
1	A	338	LYS
1	A	340	THR
1	A	463	HIS
1	A	466	LYS
1	B	113	SER
1	B	142	GLU
1	B	179	HIS
1	B	225	ASN
1	B	255	LYS
1	B	338	LYS
1	A	144	ALA
1	A	237	SER
1	A	464	ILE
1	A	500	ASN
1	A	502	GLU
1	A	517	SER
1	B	144	ALA
1	B	226	GLN
1	B	233	ILE
1	B	237	SER
1	B	279	TYR
1	B	341	ASP
1	B	463	HIS
1	B	466	LYS
1	B	500	ASN
1	B	502	GLU
1	B	539	LEU
1	A	31	SER
1	A	255	LYS
1	A	580	ASP
1	B	405	GLU
1	B	464	ILE
1	B	511	SER
1	A	223	ASP
1	A	235	GLU
1	A	279	TYR
1	A	538	SER
1	A	539	LEU
1	A	557	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	138	ILE
1	B	197	LYS
1	B	517	SER
1	A	34	ILE
1	A	138	ILE
1	A	254	THR
1	A	341	ASP
1	A	374	THR
1	A	511	SER
1	A	524	MET
1	B	223	ASP

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	517/623 (83%)	468 (90%)	49 (10%)	8	32
1	B	513/623 (82%)	455 (89%)	58 (11%)	6	24
All	All	1030/1246 (83%)	923 (90%)	107 (10%)	7	27

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

Mol	Chain	Res	Type
1	A	26	ARG
1	A	39	ASP
1	A	71	PHE
1	A	97	GLU
1	A	121	LEU
1	A	126	SER
1	A	129	THR
1	A	159	CYS
1	A	174	LEU
1	A	179	HIS
1	A	185	LYS
1	A	189	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	191	ARG
1	A	192	VAL
1	A	202	LEU
1	A	242	ASN
1	A	244	ARG
1	A	263	ILE
1	A	265	LEU
1	A	278	GLU
1	A	292	ARG
1	A	296	ASP
1	A	301	LEU
1	A	304	ASP
1	A	314	TYR
1	A	326	GLU
1	A	358	ASN
1	A	382	THR
1	A	384	LEU
1	A	391	HIS
1	A	406	SER
1	A	416	THR
1	A	427	LYS
1	A	428	ARG
1	A	429	ILE
1	A	436	ARG
1	A	448	LEU
1	A	450	THR
1	A	475	LEU
1	A	477	LEU
1	A	479	LEU
1	A	480	LYS
1	A	492	TYR
1	A	507	SER
1	A	521	LEU
1	A	540	ASN
1	A	543	ARG
1	A	544	THR
1	A	572	ASN
1	B	39	ASP
1	B	71	PHE
1	B	77	ARG
1	B	97	GLU
1	B	115	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	121	LEU
1	B	128	ILE
1	B	129	THR
1	B	159	CYS
1	B	174	LEU
1	B	179	HIS
1	B	185	LYS
1	B	189	GLN
1	B	192	VAL
1	B	202	LEU
1	B	209	CYS
1	B	226	GLN
1	B	231	ARG
1	B	242	ASN
1	B	244	ARG
1	B	252	ASN
1	B	265	LEU
1	B	278	GLU
1	B	292	ARG
1	B	296	ASP
1	B	301	LEU
1	B	304	ASP
1	B	314	TYR
1	B	339	ASN
1	B	356	ILE
1	B	358	ASN
1	B	366	LEU
1	B	388	ASP
1	B	391	HIS
1	B	401	ASP
1	B	406	SER
1	B	413	SER
1	B	416	THR
1	B	427	LYS
1	B	428	ARG
1	B	429	ILE
1	B	435	SER
1	B	436	ARG
1	B	448	LEU
1	B	450	THR
1	B	475	LEU
1	B	477	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	479	LEU
1	B	492	TYR
1	B	507	SER
1	B	510	GLU
1	B	521	LEU
1	B	539	LEU
1	B	540	ASN
1	B	543	ARG
1	B	544	THR
1	B	565	LYS
1	B	572	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (33) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	63	GLN
1	A	118	ASN
1	A	189	GLN
1	A	232	HIS
1	A	239	GLN
1	A	260	ASN
1	A	282	GLN
1	A	283	GLN
1	A	330	ASN
1	A	335	GLN
1	A	354	GLN
1	A	504	GLN
1	A	520	HIS
1	A	527	GLN
1	A	572	ASN
1	B	63	GLN
1	B	66	GLN
1	B	118	ASN
1	B	168	GLN
1	B	189	GLN
1	B	232	HIS
1	B	239	GLN
1	B	260	ASN
1	B	282	GLN
1	B	283	GLN
1	B	330	ASN
1	B	335	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	391	HIS
1	B	410	GLN
1	B	500	ASN
1	B	504	GLN
1	B	520	HIS
1	B	527	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](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

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

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	555/678 (81%)	-0.15	2 (0%) 92 79	30, 69, 113, 128	0
1	B	552/678 (81%)	-0.16	3 (0%) 91 75	30, 70, 115, 138	0
All	All	1107/1356 (81%)	-0.15	5 (0%) 91 75	30, 70, 114, 138	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	227	LEU	3.4
1	A	137	ILE	3.0
1	B	30	GLU	2.5
1	B	231	ARG	2.2
1	A	471	ALA	2.2

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.