



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 11:27 AM GMT

PDB ID : 3P14
Title : Crystal structure of L-rhamnose isomerase with a novel high thermo-stability from *Bacillus halodurans*
Authors : Doan, T.T.N.; Prabhu, P.; Kang, L.W.; Lee, J.K.
Deposited on : 2010-09-30
Resolution : 2.51 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

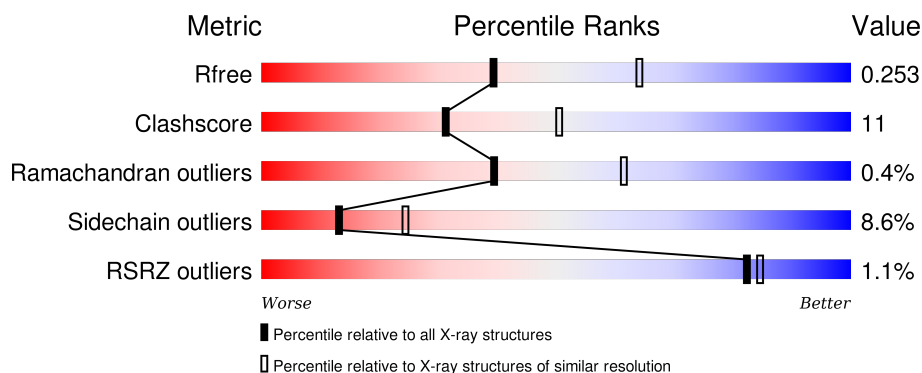
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.51 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	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (2.50-2.50)

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	424	<div> <div>2%</div> <div>73%</div> <div>18%</div> <div>• 5%</div> </div>
1	B	424	<div> <div>%</div> <div>71%</div> <div>20%</div> <div>• 5%</div> </div>
1	C	424	<div> <div>%</div> <div>66%</div> <div>25%</div> <div>• 5%</div> </div>
1	D	424	<div> <div>69%</div> <div>22%</div> <div>• 5%</div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 13611 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 L-rhamnose isomerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	402	Total	C	N	O	S	0	0	0
			3290	2109	566	606	9			
1	B	403	Total	C	N	O	S	0	0	0
			3298	2114	567	607	10			
1	C	402	Total	C	N	O	S	0	0	0
			3294	2112	566	606	10			
1	D	401	Total	C	N	O	S	0	0	0
			3278	2103	561	604	10			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	HIS	-	EXPRESSION TAG	UNP Q9KCL9
A	-4	HIS	-	EXPRESSION TAG	UNP Q9KCL9
A	-3	HIS	-	EXPRESSION TAG	UNP Q9KCL9
A	-2	HIS	-	EXPRESSION TAG	UNP Q9KCL9
A	-1	HIS	-	EXPRESSION TAG	UNP Q9KCL9
A	0	HIS	-	EXPRESSION TAG	UNP Q9KCL9
B	-5	HIS	-	EXPRESSION TAG	UNP Q9KCL9
B	-4	HIS	-	EXPRESSION TAG	UNP Q9KCL9
B	-3	HIS	-	EXPRESSION TAG	UNP Q9KCL9
B	-2	HIS	-	EXPRESSION TAG	UNP Q9KCL9
B	-1	HIS	-	EXPRESSION TAG	UNP Q9KCL9
B	0	HIS	-	EXPRESSION TAG	UNP Q9KCL9
C	-5	HIS	-	EXPRESSION TAG	UNP Q9KCL9
C	-4	HIS	-	EXPRESSION TAG	UNP Q9KCL9
C	-3	HIS	-	EXPRESSION TAG	UNP Q9KCL9
C	-2	HIS	-	EXPRESSION TAG	UNP Q9KCL9
C	-1	HIS	-	EXPRESSION TAG	UNP Q9KCL9
C	0	HIS	-	EXPRESSION TAG	UNP Q9KCL9
D	-5	HIS	-	EXPRESSION TAG	UNP Q9KCL9
D	-4	HIS	-	EXPRESSION TAG	UNP Q9KCL9
D	-3	HIS	-	EXPRESSION TAG	UNP Q9KCL9

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-2	HIS	-	EXPRESSION TAG	UNP Q9KCL9
D	-1	HIS	-	EXPRESSION TAG	UNP Q9KCL9
D	0	HIS	-	EXPRESSION TAG	UNP Q9KCL9

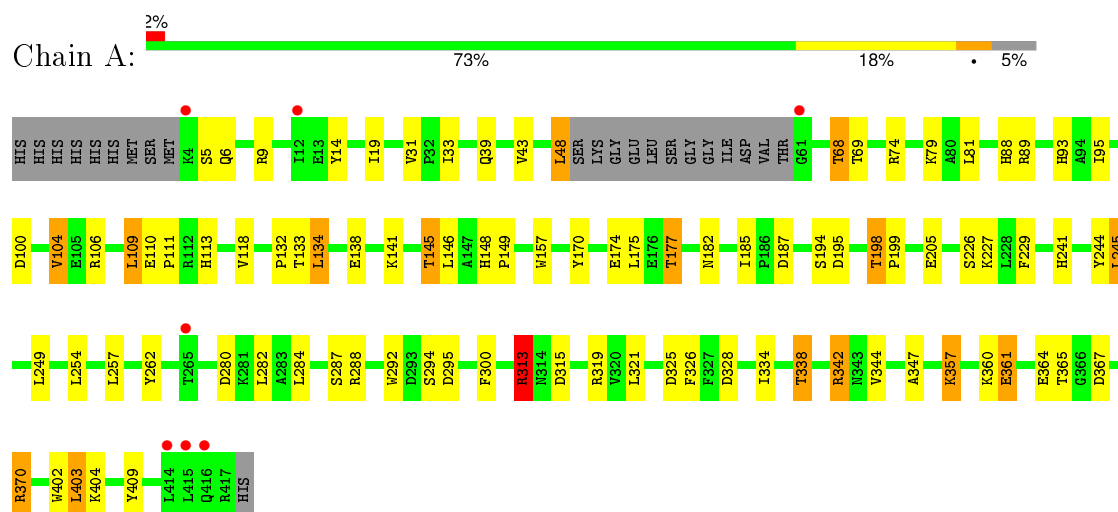
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	114	Total 114	O 114	0	0
2	B	114	Total 114	O 114	0	0
2	C	119	Total 119	O 119	0	0
2	D	104	Total 104	O 104	0	0

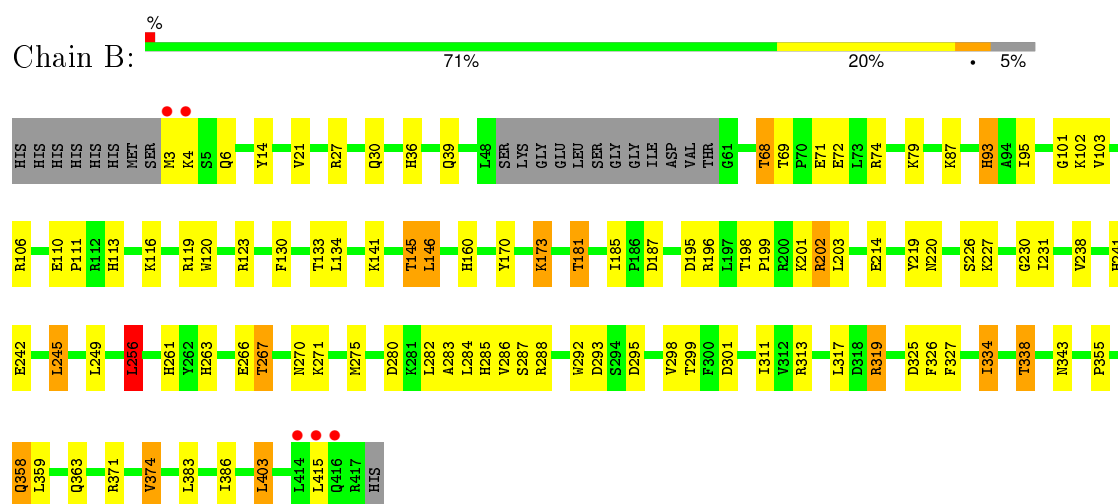
3 Residue-property plots

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.

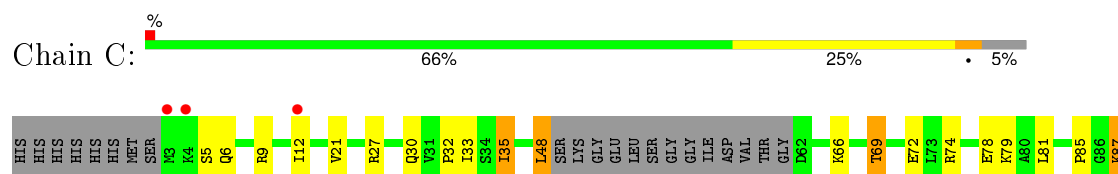
• Molecule 1: L-rhamnose isomerase



• Molecule 1: L-rhamnose isomerase



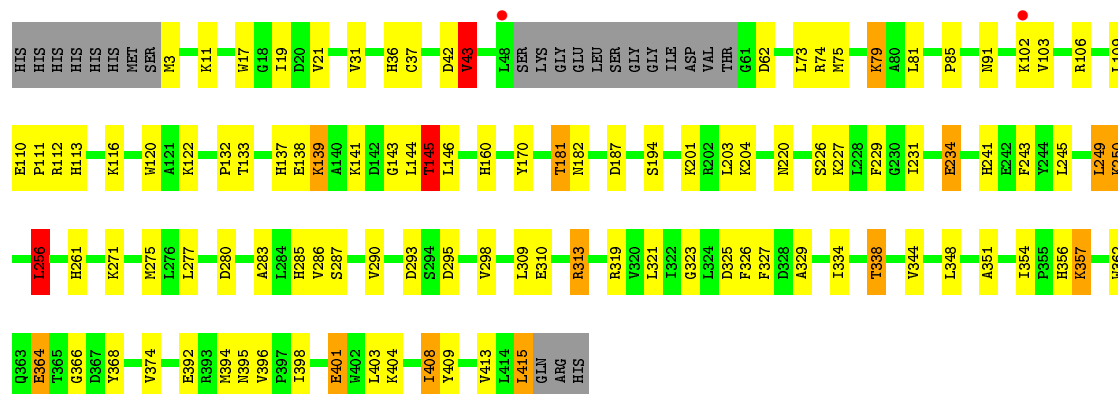
• Molecule 1: L-rhamnose isomerase





• Molecule 1: L-rhamnose isomerase

Chain D: 69% 22% 5%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	83.24Å 164.88Å 92.01Å 90.00° 115.97° 90.00°	Depositor
Resolution (Å)	45.78 – 2.51 45.78 – 2.51	Depositor EDS
% Data completeness (in resolution range)	97.7 (45.78-2.51) 97.7 (45.78-2.51)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.20 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.185 , 0.256 0.187 , 0.253	Depositor DCC
R_{free} test set	3745 reflections (5.29%)	DCC
Wilson B-factor (Å ²)	34.4	Xtriage
Anisotropy	0.022	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 39.4	EDS
Estimated twinning fraction	0.018 for h,-k,-h-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 74739 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	13611	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.18% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

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	0.91	1/3371 (0.0%)	0.90	5/4564 (0.1%)
1	B	0.90	1/3379 (0.0%)	0.91	13/4574 (0.3%)
1	C	0.93	3/3375 (0.1%)	0.89	1/4569 (0.0%)
1	D	0.90	0/3359	0.90	7/4548 (0.2%)
All	All	0.91	5/13484 (0.0%)	0.90	26/18255 (0.1%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	392	GLU	CG-CD	9.23	1.65	1.51
1	C	255	CYS	CB-SG	-5.53	1.72	1.81
1	C	392	GLU	CB-CG	5.37	1.62	1.52
1	B	71	GLU	CG-CD	5.24	1.59	1.51
1	A	205	GLU	CG-CD	5.07	1.59	1.51

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	256	LEU	CA-CB-CG	7.60	132.79	115.30
1	B	202	ARG	NE-CZ-NH2	-7.37	116.62	120.30
1	C	282	LEU	CB-CG-CD2	-6.88	99.30	111.00
1	B	415	LEU	CA-CB-CG	6.71	130.72	115.30
1	B	403	LEU	CA-CB-CG	6.59	130.47	115.30
1	B	256	LEU	CA-CB-CG	6.47	130.19	115.30
1	D	415	LEU	CA-CB-CG	6.42	130.07	115.30
1	B	313	ARG	NE-CZ-NH2	-6.41	117.10	120.30
1	B	319	ARG	NE-CZ-NH2	-6.38	117.11	120.30
1	D	362	TRP	CA-CB-CG	5.97	125.04	113.70
1	A	313	ARG	NE-CZ-NH1	5.88	123.24	120.30
1	D	106	ARG	NE-CZ-NH1	5.79	123.20	120.30
1	A	342	ARG	NE-CZ-NH2	-5.64	117.48	120.30
1	B	288	ARG	NE-CZ-NH1	-5.51	117.54	120.30
1	A	284	LEU	CA-CB-CG	5.38	127.68	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	202	ARG	NE-CZ-NH1	5.37	122.98	120.30
1	B	319	ARG	NE-CZ-NH1	5.32	122.96	120.30
1	D	256	LEU	CB-CG-CD1	5.28	119.97	111.00
1	B	313	ARG	CB-CA-C	-5.26	99.88	110.40
1	B	301	ASP	CB-CG-OD1	5.22	123.00	118.30
1	A	134	LEU	CA-CB-CG	5.21	127.29	115.30
1	D	144	LEU	CA-CB-CG	5.21	127.28	115.30
1	B	334	ILE	CG1-CB-CG2	-5.16	100.04	111.40
1	B	313	ARG	CB-CG-CD	-5.02	98.55	111.60
1	D	348	LEU	CB-CG-CD1	-5.01	102.48	111.00
1	A	74	ARG	NE-CZ-NH2	-5.00	117.80	120.30

There are no chirality outliers.

There are no planarity outliers.

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	3290	0	3244	66	0
1	B	3298	0	3253	71	0
1	C	3294	0	3250	80	0
1	D	3278	0	3232	72	0
2	A	114	0	0	2	0
2	B	114	0	0	1	0
2	C	119	0	0	2	0
2	D	104	0	0	2	0
All	All	13611	0	12979	281	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 11.

All (281) 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:14:TYR:HB3	1:A:19:ILE:CD1	1.62	1.27

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:14:TYR:CB	1:A:19:ILE:HD11	1.64	1.26
1:B:145:THR:HG22	1:B:146:LEU:H	1.11	1.14
1:A:145:THR:HG22	1:A:146:LEU:H	1.13	1.08
1:C:99:THR:HG21	1:C:102:LYS:O	1.51	1.08
1:C:99:THR:CG2	1:C:102:LYS:O	2.03	1.07
1:C:286:VAL:HG23	1:C:298:VAL:HG21	1.29	1.07
1:A:357:LYS:N	1:A:357:LYS:HD3	1.68	1.05
1:D:357:LYS:CD	1:D:357:LYS:H	1.69	1.05
1:D:357:LYS:HD3	1:D:357:LYS:H	0.91	1.05
1:A:357:LYS:H	1:A:357:LYS:HD3	0.87	1.03
1:B:227:LYS:HG3	1:B:261:HIS:CE1	1.92	1.02
1:D:357:LYS:HD3	1:D:357:LYS:N	1.77	0.99
1:A:89:ARG:HH12	1:A:177:THR:HG21	1.25	0.98
1:B:110:GLU:H	1:B:113:HIS:HD2	1.07	0.98
1:A:357:LYS:CD	1:A:357:LYS:H	1.76	0.98
1:B:145:THR:CG2	1:B:146:LEU:H	1.79	0.95
1:B:133:THR:H	1:B:160:HIS:HE1	1.13	0.95
1:C:69:THR:HG22	1:C:72:GLU:H	1.31	0.94
1:D:286:VAL:HG23	1:D:298:VAL:HG21	1.50	0.94
1:D:110:GLU:H	1:D:113:HIS:HD2	1.18	0.90
1:B:286:VAL:HG23	1:B:298:VAL:HG21	1.54	0.89
1:B:287:SER:HB3	1:B:325:ASP:O	1.73	0.89
1:D:133:THR:H	1:D:160:HIS:HE1	1.20	0.87
1:A:287:SER:HB3	1:A:325:ASP:O	1.75	0.86
1:A:14:TYR:HB3	1:A:19:ILE:HD11	0.87	0.85
1:A:145:THR:HG22	1:A:146:LEU:N	1.87	0.85
1:B:145:THR:HG22	1:B:146:LEU:N	1.93	0.83
1:A:14:TYR:HB3	1:A:19:ILE:CG1	2.09	0.82
1:D:356:HIS:HD2	2:D:492:HOH:O	1.61	0.82
1:A:110:GLU:H	1:A:113:HIS:HD2	1.24	0.82
1:D:145:THR:CG2	1:D:146:LEU:H	1.93	0.81
1:B:271:LYS:O	1:B:275:MET:HG2	1.81	0.81
1:B:145:THR:CG2	1:B:146:LEU:N	2.44	0.80
1:A:364:GLU:OE2	1:C:202:ARG:NH2	2.14	0.79
1:A:195:ASP:OD2	1:A:198:THR:HG23	1.82	0.79
1:C:286:VAL:HG23	1:C:298:VAL:CG2	2.09	0.78
1:A:145:THR:CG2	1:A:146:LEU:H	1.94	0.78
1:A:145:THR:HB	1:A:187:ASP:OD1	1.84	0.77
1:B:363:GLN:HE21	1:B:371:ARG:HH11	1.32	0.77
1:A:280:ASP:O	1:A:319:ARG:HD2	1.85	0.77
1:C:288:ARG:HD2	2:C:455:HOH:O	1.83	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:228:LEU:HD13	1:C:263:HIS:CE1	2.21	0.76
1:B:363:GLN:NE2	1:D:194:SER:H	1.83	0.76
1:B:110:GLU:H	1:B:113:HIS:CD2	1.99	0.75
1:A:110:GLU:H	1:A:113:HIS:CD2	2.04	0.75
1:B:68:THR:HG22	1:B:69:THR:HG23	1.69	0.75
1:B:363:GLN:HE22	1:D:194:SER:H	1.31	0.75
1:D:413:VAL:O	1:D:413:VAL:HG12	1.87	0.75
1:A:145:THR:CG2	1:A:146:LEU:N	2.47	0.74
1:B:280:ASP:O	1:B:319:ARG:HD2	1.88	0.74
1:C:267:THR:HG22	1:C:270:ASN:H	1.53	0.73
1:C:309:LEU:O	1:C:313:ARG:HB2	1.89	0.73
1:C:257:LEU:HD22	1:C:262:TYR:OH	1.90	0.72
1:C:286:VAL:CG2	1:C:298:VAL:HG21	2.16	0.71
1:D:145:THR:HG23	1:D:146:LEU:H	1.55	0.71
1:A:68:THR:HG22	1:A:69:THR:HG23	1.72	0.71
1:D:271:LYS:O	1:D:275:MET:HG2	1.91	0.70
1:B:145:THR:HB	1:B:187:ASP:OD1	1.90	0.70
1:D:334:ILE:O	1:D:338:THR:HG23	1.92	0.69
1:B:119:ARG:HH12	1:B:123:ARG:HH21	1.40	0.69
1:C:295:ASP:HB3	1:C:326:PHE:HA	1.74	0.69
1:B:68:THR:HB	1:B:72:GLU:OE1	1.92	0.69
1:D:287:SER:HB3	1:D:325:ASP:O	1.93	0.68
1:B:110:GLU:N	1:B:113:HIS:HD2	1.87	0.68
1:C:35:ILE:HD13	1:C:337:TRP:CD1	2.28	0.68
1:C:115:GLU:HG2	1:C:119:ARG:NH2	2.09	0.67
1:B:119:ARG:NH1	1:B:123:ARG:HH21	1.92	0.67
1:B:133:THR:N	1:B:160:HIS:HE1	1.89	0.66
1:B:256:LEU:HD22	1:B:283:ALA:CB	2.25	0.66
1:B:181:THR:CG2	1:B:220:ASN:OD1	2.42	0.66
1:A:5:SER:O	1:A:9:ARG:HG2	1.95	0.66
1:A:89:ARG:HH12	1:A:177:THR:CG2	2.07	0.65
1:D:181:THR:CG2	1:D:220:ASN:OD1	2.45	0.65
1:D:256:LEU:HD21	1:D:285:HIS:CE1	2.32	0.65
1:A:19:ILE:O	1:A:19:ILE:HD12	1.97	0.65
1:D:181:THR:HG22	1:D:220:ASN:OD1	1.97	0.65
1:C:287:SER:HB3	1:C:325:ASP:O	1.97	0.65
1:C:106:ARG:HA	1:C:109:LEU:HD22	1.80	0.64
1:D:145:THR:CG2	1:D:146:LEU:N	2.60	0.64
1:B:93:HIS:HD2	1:B:133:THR:OG1	1.81	0.63
1:A:104:VAL:CG2	1:A:109:LEU:HD13	2.27	0.63
1:C:99:THR:HG23	1:C:102:LYS:O	1.96	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:282:LEU:HD22	1:C:283:ALA:N	2.15	0.61
1:B:287:SER:CB	1:B:325:ASP:O	2.46	0.61
1:A:295:ASP:HB3	1:A:326:PHE:HA	1.81	0.61
1:C:35:ILE:CD1	1:C:337:TRP:CD1	2.83	0.61
1:B:295:ASP:HB3	1:B:326:PHE:HA	1.83	0.61
1:B:146:LEU:HD22	1:B:185:ILE:HG21	1.82	0.60
1:A:134:LEU:HG	1:A:185:ILE:HG22	1.82	0.60
1:A:48:LEU:HD22	1:A:48:LEU:C	2.21	0.60
1:B:231:ILE:HD13	1:B:292:TRP:CE3	2.37	0.60
1:A:106:ARG:HA	1:A:109:LEU:HD22	1.84	0.59
1:B:119:ARG:HH12	1:B:123:ARG:NH2	2.01	0.59
1:D:398:ILE:O	1:D:401:GLU:HB2	2.03	0.59
1:A:357:LYS:CD	1:A:357:LYS:N	2.50	0.59
1:D:133:THR:N	1:D:160:HIS:HE1	1.98	0.59
1:B:241:HIS:O	1:B:245:LEU:HB2	2.02	0.59
1:B:256:LEU:HD22	1:B:283:ALA:HB1	1.85	0.59
1:B:202:ARG:NH2	1:D:364:GLU:OE1	2.35	0.59
1:D:145:THR:HG23	1:D:146:LEU:N	2.18	0.58
1:D:110:GLU:H	1:D:113:HIS:CD2	2.09	0.58
1:D:413:VAL:CG1	1:D:413:VAL:O	2.50	0.58
1:C:148:HIS:O	1:C:154:ARG:HD3	2.03	0.58
1:C:398:ILE:HG13	1:C:399:LYS:HG3	1.85	0.58
1:C:133:THR:H	1:C:160:HIS:HE1	1.50	0.58
1:C:267:THR:CG2	1:C:270:ASN:H	2.17	0.58
1:B:133:THR:H	1:B:160:HIS:CE1	2.06	0.57
1:B:181:THR:HG23	1:B:220:ASN:OD1	2.03	0.57
1:C:48:LEU:HD22	1:C:103:VAL:HG12	1.87	0.57
1:B:227:LYS:CG	1:B:261:HIS:CE1	2.81	0.57
1:C:206:SER:O	1:C:210:ILE:HG13	2.05	0.57
1:D:137:HIS:HE1	1:D:139:LYS:HD3	1.70	0.57
1:B:263:HIS:HB2	1:B:266:GLU:OE1	2.04	0.56
1:D:357:LYS:CD	1:D:357:LYS:N	2.49	0.56
1:C:180:LEU:HD22	1:C:321:LEU:HD23	1.87	0.56
1:D:133:THR:H	1:D:160:HIS:CE1	2.12	0.56
1:A:334:ILE:O	1:A:338:THR:HG23	2.06	0.56
1:D:256:LEU:HB2	1:D:283:ALA:HB3	1.86	0.56
1:C:227:LYS:HD2	1:C:261:HIS:CE1	2.41	0.56
1:D:227:LYS:HE3	1:D:229:PHE:O	2.05	0.55
1:C:35:ILE:CD1	1:C:337:TRP:NE1	2.69	0.55
1:D:111:PRO:HB3	1:D:170:TYR:CD2	2.41	0.55
1:B:334:ILE:O	1:B:338:THR:HG23	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:226:SER:O	1:C:261:HIS:ND1	2.29	0.55
1:D:17:TRP:HB2	1:D:19:ILE:HD12	1.89	0.54
1:A:194:SER:H	1:C:363:GLN:NE2	2.05	0.54
1:B:256:LEU:HD22	1:B:283:ALA:HB3	1.89	0.54
1:C:231:ILE:CD1	1:C:292:TRP:CE3	2.90	0.54
1:D:404:LYS:O	1:D:408:ILE:HG23	2.08	0.54
1:A:288:ARG:HD2	2:A:462:HOH:O	2.08	0.54
1:C:398:ILE:O	1:C:401:GLU:HG2	2.08	0.54
1:C:115:GLU:HG2	1:C:119:ARG:HH22	1.73	0.53
1:C:282:LEU:HD22	1:C:283:ALA:H	1.74	0.53
1:A:241:HIS:CE1	1:A:245:LEU:HD12	2.43	0.53
1:C:228:LEU:CD1	1:C:263:HIS:CE1	2.90	0.53
1:C:280:ASP:O	1:C:319:ARG:HD2	2.09	0.53
1:A:19:ILE:HD12	1:A:19:ILE:C	2.29	0.52
1:B:363:GLN:HE22	1:D:194:SER:N	2.05	0.52
1:D:290:VAL:O	1:D:290:VAL:HG23	2.09	0.52
1:D:143:GLY:O	1:D:187:ASP:HA	2.09	0.52
1:C:363:GLN:HE21	1:C:371:ARG:HH11	1.56	0.52
1:C:112:ARG:NH2	1:C:113:HIS:HE1	2.08	0.52
1:C:402:TRP:CZ3	1:C:403:LEU:HD13	2.45	0.52
1:C:309:LEU:HD21	1:C:354:ILE:HG13	1.92	0.52
1:C:231:ILE:HD13	1:C:292:TRP:CZ3	2.45	0.51
1:D:295:ASP:HB3	1:D:326:PHE:HA	1.93	0.51
1:B:106:ARG:HB3	1:B:160:HIS:CD2	2.45	0.51
1:D:203:LEU:HD23	1:D:243:PHE:CE2	2.46	0.51
1:B:111:PRO:HB3	1:B:170:TYR:CD2	2.46	0.50
1:A:227:LYS:HE2	1:A:229:PHE:O	2.11	0.50
1:D:145:THR:HG22	1:D:146:LEU:H	1.70	0.50
1:B:130:PHE:O	1:B:181:THR:HA	2.11	0.50
1:D:250:LYS:HD2	1:D:250:LYS:O	2.12	0.50
1:A:39:GLN:HE22	1:A:328:ASP:H	1.59	0.50
1:A:334:ILE:O	1:A:338:THR:CG2	2.59	0.50
1:D:231:ILE:HA	1:D:234:GLU:OE2	2.12	0.50
1:B:359:LEU:HD21	1:B:374:VAL:HG22	1.93	0.49
1:A:257:LEU:CD2	1:A:262:TYR:OH	2.60	0.49
1:A:95:ILE:HG23	1:A:133:THR:HG21	1.93	0.49
1:A:313:ARG:HD3	2:C:481:HOH:O	2.12	0.49
1:D:11:LYS:HG3	1:D:21:VAL:HG22	1.94	0.49
1:C:257:LEU:CD2	1:C:262:TYR:OH	2.59	0.49
1:D:79:LYS:HE3	1:D:79:LYS:HA	1.95	0.49
1:C:85:PRO:HD3	1:C:396:VAL:HG21	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:367:ASP:OD2	1:A:370:ARG:HG3	2.12	0.49
1:C:231:ILE:HD13	1:C:292:TRP:CE3	2.47	0.49
1:C:226:SER:HB3	1:C:244:TYR:HD2	1.77	0.49
1:A:404:LYS:HA	1:A:404:LYS:HE3	1.95	0.49
1:D:137:HIS:CE1	1:D:139:LYS:HD3	2.48	0.49
1:D:309:LEU:O	1:D:313:ARG:HB3	2.12	0.48
1:B:267:THR:CG2	1:B:270:ASN:H	2.26	0.48
1:D:37:CYS:HB2	1:D:73:LEU:HD21	1.94	0.48
1:D:226:SER:O	1:D:261:HIS:ND1	2.37	0.48
1:C:410:GLU:HA	1:C:414:LEU:HB2	1.95	0.48
1:C:334:ILE:O	1:C:338:THR:HG23	2.14	0.48
1:C:359:LEU:HD21	1:C:374:VAL:HG22	1.95	0.48
1:A:338:THR:O	1:A:342:ARG:HB2	2.14	0.47
1:C:112:ARG:HH21	1:C:113:HIS:HE1	1.62	0.47
1:A:14:TYR:O	1:A:19:ILE:HG13	2.14	0.47
1:A:134:LEU:HD13	1:A:157:TRP:CE3	2.49	0.47
1:C:231:ILE:HD11	1:C:292:TRP:CE3	2.49	0.47
1:B:242:GLU:OE2	1:D:241:HIS:HE1	1.97	0.47
1:B:355:PRO:HB2	1:B:358:GLN:HG3	1.96	0.47
1:D:145:THR:HG22	1:D:187:ASP:OD1	2.14	0.47
1:C:172:GLY:HA2	1:C:177:THR:O	2.15	0.47
1:C:256:LEU:HD21	1:C:285:HIS:CG	2.49	0.47
1:D:249:LEU:HD23	1:D:249:LEU:HA	1.71	0.47
1:B:95:ILE:HG23	1:B:133:THR:HG21	1.95	0.47
1:A:79:LYS:HG3	1:A:409:TYR:CD1	2.49	0.47
1:D:394:MET:O	1:D:395:ASN:HB2	2.15	0.47
1:B:196:ARG:HD2	1:D:310:GLU:OE2	2.14	0.47
1:A:257:LEU:HD23	1:A:262:TYR:OH	2.14	0.47
1:B:74:ARG:HD2	1:B:120:TRP:CG	2.50	0.47
1:A:361:GLU:O	1:A:365:THR:OG1	2.27	0.47
1:A:6:GLN:HA	1:A:6:GLN:OE1	2.15	0.46
1:D:227:LYS:HD2	1:D:261:HIS:CE1	2.50	0.46
1:D:62:ASP:HB2	1:D:329:ALA:O	2.15	0.46
1:C:111:PRO:HB3	1:C:170:TYR:CG	2.50	0.46
1:C:112:ARG:NH2	1:C:113:HIS:CE1	2.83	0.46
1:D:351:ALA:O	1:D:356:HIS:HE1	1.99	0.46
1:B:241:HIS:CE1	1:B:245:LEU:HD12	2.51	0.46
1:D:79:LYS:HD2	1:D:409:TYR:CD1	2.51	0.46
1:A:402:TRP:CZ3	1:A:403:LEU:HD13	2.51	0.46
1:A:33:ILE:O	1:A:88:HIS:HB3	2.15	0.46
1:A:367:ASP:OD1	1:A:370:ARG:HG2	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:74:ARG:HD2	1:D:120:TRP:CD1	2.51	0.46
1:C:357:LYS:HD3	1:C:357:LYS:HA	1.79	0.45
1:A:148:HIS:CG	1:A:149:PRO:HD2	2.52	0.45
1:B:36:HIS:NE2	1:B:39:GLN:HB2	2.31	0.45
1:C:79:LYS:HA	1:C:79:LYS:HD2	1.75	0.45
1:D:42:ASP:C	1:D:43:VAL:HG23	2.37	0.45
1:B:226:SER:O	1:B:261:HIS:ND1	2.37	0.45
1:B:198:THR:HB	1:B:199:PRO:HD3	1.98	0.45
1:B:173:LYS:HG2	1:B:219:TYR:CE1	2.51	0.45
1:C:87:LYS:HE3	1:C:124:HIS:O	2.16	0.45
1:A:104:VAL:HG23	1:A:109:LEU:HD13	1.97	0.44
1:A:404:LYS:CE	1:A:404:LYS:HA	2.47	0.44
1:C:267:THR:HG23	1:C:269:SER:OG	2.17	0.44
1:D:287:SER:CB	1:D:325:ASP:O	2.64	0.44
1:C:35:ILE:HD12	1:C:337:TRP:NE1	2.32	0.44
1:A:132:PRO:HD2	1:A:182:ASN:O	2.17	0.44
1:B:256:LEU:HD11	1:B:285:HIS:CG	2.53	0.44
1:B:130:PHE:HB3	1:B:181:THR:HB	2.00	0.44
1:B:231:ILE:CD1	1:B:292:TRP:CE3	3.01	0.44
1:C:143:GLY:O	1:C:187:ASP:HA	2.18	0.44
1:C:375:LEU:HA	1:C:375:LEU:HD23	1.90	0.44
1:B:3:MET:O	1:B:6:GLN:HB2	2.17	0.44
1:A:292:TRP:NE1	1:A:294:SER:HB3	2.33	0.44
1:A:118:VAL:HG11	1:A:174:GLU:HG2	2.00	0.43
1:B:203:LEU:HD22	1:B:238:VAL:HG12	2.00	0.43
1:D:280:ASP:O	1:D:319:ARG:HD2	2.18	0.43
1:D:366:GLY:HA2	1:D:368:TYR:CE1	2.54	0.43
1:B:227:LYS:HE3	1:B:293:ASP:OD2	2.18	0.43
1:A:226:SER:HB3	1:A:244:TYR:HD2	1.82	0.43
1:D:201:LYS:HE2	2:D:487:HOH:O	2.17	0.43
1:C:241:HIS:O	1:C:245:LEU:HB2	2.18	0.43
1:C:33:ILE:O	1:C:88:HIS:HB3	2.18	0.43
1:A:300:PHE:HE1	1:A:347:ALA:HA	1.84	0.43
1:C:302:ASP:OD1	1:C:305:ARG:NH1	2.52	0.42
1:C:415:LEU:HA	1:C:415:LEU:HD23	1.71	0.42
1:C:192:THR:HA	1:C:193:PRO:HD2	1.87	0.42
1:D:145:THR:CG2	1:D:187:ASP:OD1	2.67	0.42
1:D:138:GLU:OE2	1:D:141:LYS:HE3	2.19	0.42
1:C:9:ARG:O	1:C:12:ILE:HG12	2.19	0.42
1:D:285:HIS:HA	1:D:323:GLY:O	2.20	0.42
1:C:30:GLN:O	1:C:32:PRO:HD3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:309:LEU:HD21	1:D:354:ILE:HG13	2.02	0.42
1:C:133:THR:H	1:C:160:HIS:CE1	2.35	0.42
1:D:286:VAL:HG23	1:D:298:VAL:CG2	2.36	0.42
1:C:282:LEU:HD23	1:C:282:LEU:HA	1.67	0.42
1:A:367:ASP:OD2	1:A:370:ARG:CG	2.68	0.42
1:A:79:LYS:HE2	1:A:409:TYR:HB2	2.01	0.42
1:A:111:PRO:HB3	1:A:170:TYR:CG	2.55	0.42
1:A:367:ASP:CG	1:A:370:ARG:HG2	2.40	0.41
1:B:267:THR:HG22	1:B:270:ASN:H	1.85	0.41
1:C:302:ASP:HA	1:C:305:ARG:NH1	2.35	0.41
1:C:260:GLY:HA2	1:C:289:PRO:HG3	2.02	0.41
1:B:79:LYS:HD2	1:B:79:LYS:HA	1.96	0.41
1:C:161:CYS:CB	1:C:210:ILE:HD13	2.50	0.41
1:C:370:ARG:O	1:C:374:VAL:HG13	2.20	0.41
1:B:27:ARG:HH11	1:B:30:GLN:HB2	1.85	0.41
1:B:231:ILE:HD13	1:B:292:TRP:CZ3	2.55	0.41
1:D:234:GLU:HG2	1:D:234:GLU:H	1.58	0.41
1:D:85:PRO:HD3	1:D:396:VAL:HG21	2.03	0.41
1:B:214:GLU:H	1:B:214:GLU:HG2	1.62	0.41
1:D:132:PRO:HD2	1:D:182:ASN:O	2.20	0.41
1:C:109:LEU:HD12	1:C:113:HIS:CD2	2.56	0.41
1:C:74:ARG:O	1:C:78:GLU:HG3	2.20	0.41
1:B:230:GLY:HA3	2:B:528:HOH:O	2.20	0.41
1:C:99:THR:HG22	1:C:102:LYS:H	1.86	0.41
1:B:195:ASP:OD2	1:B:198:THR:OG1	2.34	0.41
1:B:299:THR:HA	1:B:343:ASN:ND2	2.35	0.41
1:C:166:LYS:HD3	1:C:166:LYS:HA	1.93	0.41
1:D:36:HIS:HA	1:D:91:ASN:HB3	2.02	0.41
1:B:311:ILE:HG22	1:B:317:LEU:HD23	2.03	0.41
1:B:14:TYR:CE2	1:B:386:ILE:HD13	2.56	0.40
1:C:141:LYS:HA	1:C:141:LYS:HD2	1.84	0.40
1:A:138:GLU:O	1:A:141:LYS:HG2	2.22	0.40
1:D:408:ILE:HG12	1:D:409:TYR:N	2.37	0.40
1:A:9:ARG:NH1	2:A:522:HOH:O	2.53	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	398/424 (94%)	382 (96%)	15 (4%)	1 (0%)	46	68
1	B	399/424 (94%)	379 (95%)	19 (5%)	1 (0%)	46	68
1	C	398/424 (94%)	380 (96%)	17 (4%)	1 (0%)	46	68
1	D	397/424 (94%)	373 (94%)	20 (5%)	4 (1%)	19	34
All	All	1592/1696 (94%)	1514 (95%)	71 (4%)	7 (0%)	39	61

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	293	ASP
1	D	112	ARG
1	D	43	VAL
1	D	145	THR
1	C	138	GLU
1	B	101	GLY
1	A	43	VAL

5.3.2 Protein sidechains

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	351/370 (95%)	324 (92%)	27 (8%)	16	30
1	B	352/370 (95%)	325 (92%)	27 (8%)	16	30
1	C	352/370 (95%)	319 (91%)	33 (9%)	11	20

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	350/370 (95%)	316 (90%)	34 (10%)	10	19
All	All	1405/1480 (95%)	1284 (91%)	121 (9%)	13	24

All (121) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	31	VAL
1	A	48	LEU
1	A	68	THR
1	A	81	LEU
1	A	93	HIS
1	A	100	ASP
1	A	104	VAL
1	A	109	LEU
1	A	145	THR
1	A	175	LEU
1	A	177	THR
1	A	198	THR
1	A	199	PRO
1	A	245	LEU
1	A	249	LEU
1	A	254	LEU
1	A	282	LEU
1	A	313	ARG
1	A	315	ASP
1	A	321	LEU
1	A	338	THR
1	A	344	VAL
1	A	357	LYS
1	A	360	LYS
1	A	361	GLU
1	A	370	ARG
1	A	403	LEU
1	B	4	LYS
1	B	21	VAL
1	B	68	THR
1	B	87	LYS
1	B	93	HIS
1	B	102	LYS
1	B	103	VAL
1	B	116	LYS
1	B	134	LEU

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Mol	Chain	Res	Type
1	B	141	LYS
1	B	145	THR
1	B	146	LEU
1	B	173	LYS
1	B	181	THR
1	B	201	LYS
1	B	245	LEU
1	B	249	LEU
1	B	256	LEU
1	B	267	THR
1	B	282	LEU
1	B	284	LEU
1	B	327	PHE
1	B	338	THR
1	B	358	GLN
1	B	374	VAL
1	B	383	LEU
1	B	403	LEU
1	C	5	SER
1	C	6	GLN
1	C	21	VAL
1	C	27	ARG
1	C	35	ILE
1	C	48	LEU
1	C	66	LYS
1	C	69	THR
1	C	81	LEU
1	C	87	LYS
1	C	93	HIS
1	C	99	THR
1	C	100	ASP
1	C	103	VAL
1	C	109	LEU
1	C	234	GLU
1	C	237	VAL
1	C	245	LEU
1	C	250	LYS
1	C	253	LYS
1	C	265	THR
1	C	267	THR
1	C	282	LEU
1	C	284	LEU

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Mol	Chain	Res	Type
1	C	294	SER
1	C	327	PHE
1	C	338	THR
1	C	353	LEU
1	C	395	ASN
1	C	398	ILE
1	C	403	LEU
1	C	408	ILE
1	C	414	LEU
1	D	3	MET
1	D	31	VAL
1	D	43	VAL
1	D	75	MET
1	D	79	LYS
1	D	81	LEU
1	D	102	LYS
1	D	103	VAL
1	D	109	LEU
1	D	116	LYS
1	D	122	LYS
1	D	139	LYS
1	D	145	THR
1	D	181	THR
1	D	204	LYS
1	D	234	GLU
1	D	245	LEU
1	D	249	LEU
1	D	250	LYS
1	D	256	LEU
1	D	277	LEU
1	D	313	ARG
1	D	321	LEU
1	D	327	PHE
1	D	338	THR
1	D	344	VAL
1	D	357	LYS
1	D	364	GLU
1	D	374	VAL
1	D	392	GLU
1	D	401	GLU
1	D	403	LEU
1	D	408	ILE

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Mol	Chain	Res	Type
1	D	415	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (31) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	39	GLN
1	A	113	HIS
1	A	182	ASN
1	A	209	GLN
1	A	388	ASN
1	B	30	GLN
1	B	39	GLN
1	B	93	HIS
1	B	113	HIS
1	B	160	HIS
1	B	182	ASN
1	B	251	ASN
1	B	279	HIS
1	B	363	GLN
1	B	388	ASN
1	C	39	GLN
1	C	113	HIS
1	C	131	ASN
1	C	160	HIS
1	C	314	ASN
1	C	363	GLN
1	D	16	GLN
1	D	39	GLN
1	D	113	HIS
1	D	131	ASN
1	D	160	HIS
1	D	182	ASN
1	D	209	GLN
1	D	241	HIS
1	D	314	ASN
1	D	356	HIS

5.3.3 RNA ⓘ

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 ⓘ

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	402/424 (94%)	-0.28	7 (1%)	73 76	17, 30, 45, 66	0
1	B	403/424 (95%)	-0.36	5 (1%)	81 83	17, 30, 50, 85	0
1	C	402/424 (94%)	-0.33	3 (0%)	89 90	19, 30, 45, 81	0
1	D	401/424 (94%)	-0.28	2 (0%)	91 92	18, 31, 50, 71	0
All	All	1608/1696 (94%)	-0.31	17 (1%)	82 84	17, 30, 48, 85	0

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	415	LEU	4.2
1	B	3	MET	4.1
1	A	4	LYS	4.1
1	C	4	LYS	3.7
1	A	61	GLY	3.7
1	A	415	LEU	3.7
1	B	4	LYS	3.4
1	A	12	ILE	3.2
1	A	414	LEU	3.0
1	D	48	LEU	2.8
1	C	3	MET	2.5
1	B	414	LEU	2.5
1	A	265	THR	2.3
1	D	102	LYS	2.2
1	A	416	GLN	2.2
1	B	416	GLN	2.1
1	C	12	ILE	2.1

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

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.