



# Full wwPDB X-ray Structure Validation Report ⓘ

Nov 21, 2017 – 02:19 AM EST

PDB ID : 1XLC  
Title : MECHANISM FOR ALDOSE-KETOSE INTERCONVERSION BY D-XYLOSE ISOMERASE INVOLVING RING OPENING FOLLOWED BY A 1,2-HYDRIDE SHIFT  
Authors : Collyer, C.A.; Henrick, K.; Blow, D.M.  
Deposited on : unknown  
Resolution : 2.50 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](mailto: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.

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

MolProbity	:	4.02b-467
Mogul	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20030345

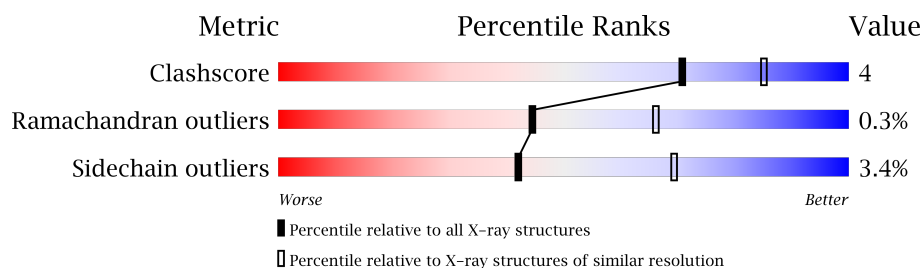
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.50 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))
Clashscore	112137	4554 (2.50-2.50)
Ramachandran outliers	110173	4463 (2.50-2.50)
Sidechain outliers	110143	4465 (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  $\geq 3$ , 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	394	
1	B	394	

## 2 Entry composition [i](#)

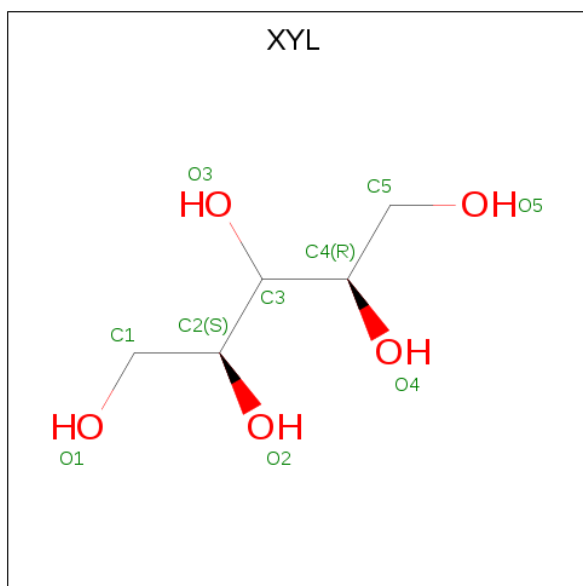
There are 4 unique types of molecules in this entry. The entry contains 6628 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called D-XYLOSE ISOMERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	393	Total	C	N	O	S	0	1	0
			3035	1923	521	582	9			
1	B	393	Total	C	N	O	S	0	1	0
			3035	1923	521	582	9			

- Molecule 2 is D-XYLITOL (three-letter code: XYL) (formula: C<sub>5</sub>H<sub>12</sub>O<sub>5</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			10	5	5		
2	B	1	Total	C	O	0	0
			10	5	5		

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total 1	Mg 1	0	0
3	A	1	Total 1	Mg 1	0	0

- Molecule 4 is water.

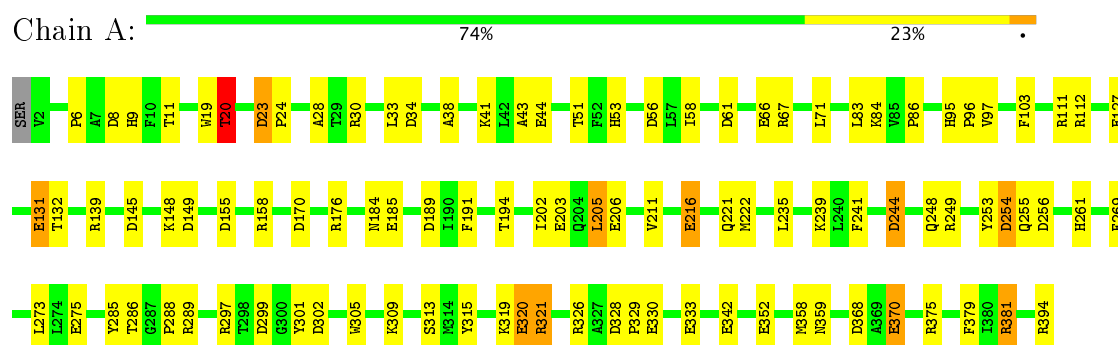
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	262	Total 262	O 262	0	0
4	B	274	Total 274	O 274	0	0

### 3 Residue-property plots [i](#)

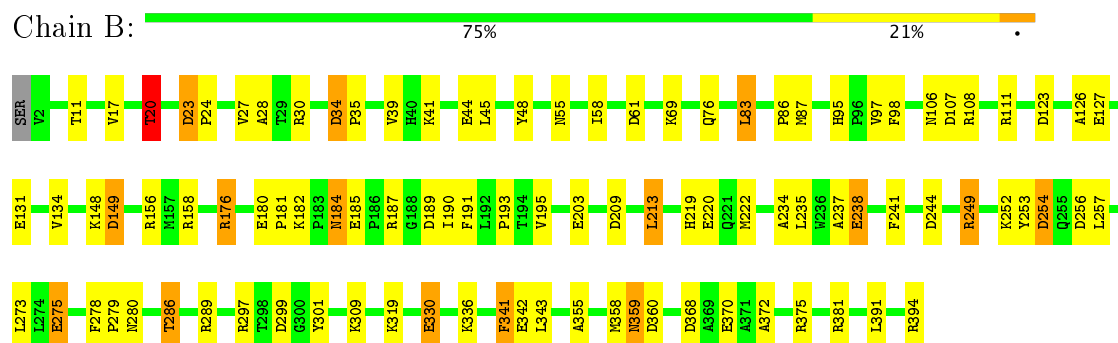
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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.

Note EDS was not executed.

#### • Molecule 1: D-XYLOSE ISOMERASE



#### • Molecule 1: D-XYLOSE ISOMERASE



## 4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	105.60 Å   105.60 Å   152.70 Å 90.00°   90.00°   120.00°	Depositor
Resolution (Å)	10.00 – 2.50	Depositor
% Data completeness (in resolution range)	(Not available) (10.00-2.50)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	PROLSQ	Depositor
R, $R_{free}$	0.155 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6628	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	23.0	wwPDB-VP

## 5 Model quality

### 5.1 Standard geometry

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

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	1.05	0/3109	1.99	94/4215 (2.2%)
1	B	1.08	0/3109	2.04	95/4215 (2.3%)
All	All	1.07	0/6218	2.01	189/8430 (2.2%)

There are no bond length outliers.

All (189) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	158	ARG	NE-CZ-NH2	-21.02	109.79	120.30
1	B	381	ARG	NE-CZ-NH2	-19.92	110.34	120.30
1	B	187	ARG	NE-CZ-NH2	-19.38	110.61	120.30
1	B	249	ARG	NE-CZ-NH1	16.10	128.35	120.30
1	B	108	ARG	NE-CZ-NH1	15.19	127.90	120.30
1	B	30	ARG	NE-CZ-NH1	14.25	127.42	120.30
1	B	108	ARG	NE-CZ-NH2	-14.21	113.20	120.30
1	B	375	ARG	NE-CZ-NH2	-14.20	113.20	120.30
1	A	394	ARG	CD-NE-CZ	14.18	143.46	123.60
1	A	111	ARG	NE-CZ-NH1	12.56	126.58	120.30
1	B	297	ARG	NE-CZ-NH2	12.03	126.31	120.30
1	A	30	ARG	NE-CZ-NH1	11.56	126.08	120.30
1	A	375	ARG	NE-CZ-NH2	-11.20	114.70	120.30
1	B	381	ARG	NE-CZ-NH1	11.08	125.84	120.30
1	A	139	ARG	NE-CZ-NH2	10.90	125.75	120.30
1	A	149	ASP	CB-CG-OD1	10.80	128.02	118.30
1	A	289	ARG	NE-CZ-NH2	-10.53	115.03	120.30
1	A	176	ARG	NE-CZ-NH1	10.42	125.51	120.30
1	B	394	ARG	NE-CZ-NH2	-10.19	115.21	120.30
1	A	375	ARG	NE-CZ-NH1	10.06	125.33	120.30
1	B	44	GLU	CA-CB-CG	10.01	135.42	113.40
1	B	299	ASP	CB-CG-OD1	9.97	127.27	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	156	ARG	NE-CZ-NH2	-9.84	115.38	120.30
1	A	241	PHE	CB-CG-CD1	9.82	127.67	120.80
1	A	301	TYR	CB-CG-CD1	-9.74	115.16	121.00
1	B	187	ARG	NE-CZ-NH1	9.73	125.17	120.30
1	B	158	ARG	NE-CZ-NH1	9.57	125.09	120.30
1	A	326	ARG	NE-CZ-NH1	9.37	124.99	120.30
1	B	48	TYR	CB-CG-CD1	-9.31	115.42	121.00
1	A	23	ASP	CB-CG-OD1	9.20	126.58	118.30
1	A	30	ARG	NE-CZ-NH2	-9.03	115.79	120.30
1	B	213	LEU	CA-CB-CG	8.78	135.50	115.30
1	B	30	ARG	NE-CZ-NH2	-8.75	115.93	120.30
1	A	394	ARG	NE-CZ-NH1	8.70	124.65	120.30
1	A	326	ARG	NE-CZ-NH2	-8.63	115.99	120.30
1	B	244	ASP	CB-CG-OD1	8.62	126.06	118.30
1	A	254[A]	ASP	CB-CG-OD1	8.55	126.00	118.30
1	A	254[B]	ASP	CB-CG-OD1	8.55	126.00	118.30
1	A	254[A]	ASP	CB-CG-OD2	-8.53	110.62	118.30
1	A	254[B]	ASP	CB-CG-OD2	-8.53	110.62	118.30
1	A	285	TYR	CB-CG-CD2	-8.33	116.00	121.00
1	B	256	ASP	CB-CG-OD2	-8.30	110.83	118.30
1	A	320	GLU	OE1-CD-OE2	-8.11	113.56	123.30
1	A	381	ARG	NE-CZ-NH2	-7.99	116.30	120.30
1	A	6	PRO	C-N-CA	7.92	141.49	121.70
1	B	176	ARG	NE-CZ-NH2	-7.91	116.34	120.30
1	A	131	GLU	CB-CG-CD	7.90	135.53	114.20
1	A	299	ASP	CB-CG-OD1	7.86	125.38	118.30
1	B	330	GLU	CA-CB-CG	7.77	130.49	113.40
1	A	112	ARG	NE-CZ-NH2	-7.76	116.42	120.30
1	B	34	ASP	CB-CG-OD2	7.60	125.14	118.30
1	B	48	TYR	CB-CG-CD2	7.58	125.55	121.00
1	A	170	ASP	CB-CG-OD1	7.53	125.08	118.30
1	A	321	ARG	NE-CZ-NH2	-7.48	116.56	120.30
1	A	381	ARG	NE-CZ-NH1	7.41	124.01	120.30
1	B	289	ARG	NE-CZ-NH2	-7.37	116.62	120.30
1	A	249	ARG	NE-CZ-NH1	7.35	123.98	120.30
1	A	194	THR	CA-CB-CG2	7.22	122.51	112.40
1	B	189	ASP	CB-CG-OD2	7.22	124.80	118.30
1	A	203	GLU	OE1-CD-OE2	-7.19	114.67	123.30
1	B	23	ASP	CB-CA-C	7.15	124.70	110.40
1	A	66	GLU	CG-CD-OE2	7.14	132.57	118.30
1	A	269	PHE	CB-CG-CD1	-7.10	115.83	120.80
1	B	372	ALA	CB-CA-C	7.08	120.72	110.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	34	ASP	CB-CG-OD2	7.06	124.65	118.30
1	B	375	ARG	NE-CZ-NH1	7.01	123.80	120.30
1	A	111	ARG	NE-CZ-NH2	-7.01	116.80	120.30
1	A	145	ASP	CB-CG-OD1	6.99	124.59	118.30
1	B	391	LEU	C-N-CA	6.98	136.95	122.30
1	A	96	PRO	O-C-N	-6.93	111.61	122.70
1	B	341	PHE	CB-CG-CD2	-6.91	115.96	120.80
1	B	83	LEU	CA-CB-CG	6.89	131.15	115.30
1	B	17	VAL	C-N-CA	6.87	136.72	122.30
1	B	20	THR	N-CA-CB	-6.85	97.28	110.30
1	A	61	ASP	CB-CG-OD1	6.78	124.40	118.30
1	A	352	GLU	OE1-CD-OE2	-6.77	115.17	123.30
1	B	286	THR	N-CA-CB	-6.77	97.44	110.30
1	B	209	ASP	CB-CG-OD2	6.74	124.37	118.30
1	B	87	MET	CG-SD-CE	6.68	110.88	100.20
1	A	320	GLU	CG-CD-OE2	6.67	131.64	118.30
1	A	241	PHE	CB-CG-CD2	-6.62	116.17	120.80
1	A	368	ASP	CB-CG-OD2	6.62	124.26	118.30
1	A	342	GLU	OE1-CD-OE2	6.56	131.17	123.30
1	B	254[A]	ASP	CB-CG-OD1	6.55	124.20	118.30
1	B	254[B]	ASP	CB-CG-OD1	6.55	124.20	118.30
1	B	394	ARG	NH1-CZ-NH2	6.54	126.59	119.40
1	B	330	GLU	CG-CD-OE1	-6.51	105.27	118.30
1	B	342	GLU	CG-CD-OE2	-6.50	105.31	118.30
1	B	253	TYR	CB-CG-CD1	6.46	124.88	121.00
1	B	176	ARG	NE-CZ-NH1	6.42	123.51	120.30
1	A	297	ARG	CG-CD-NE	6.42	125.28	111.80
1	A	261	HIS	C-N-CA	6.40	135.73	122.30
1	A	19	TRP	C-N-CA	6.36	137.59	121.70
1	A	394	ARG	NE-CZ-NH2	-6.35	117.13	120.30
1	B	343	LEU	C-N-CA	6.33	135.60	122.30
1	A	205	LEU	CA-CB-CG	6.29	129.76	115.30
1	B	238	GLU	CG-CD-OE1	-6.28	105.74	118.30
1	A	103	PHE	CB-CG-CD1	6.22	125.15	120.80
1	A	216	GLU	OE1-CD-OE2	6.21	130.75	123.30
1	B	176	ARG	CB-CG-CD	6.18	127.68	111.60
1	B	360	ASP	CB-CG-OD1	6.17	123.86	118.30
1	B	249	ARG	NH1-CZ-NH2	-6.16	112.62	119.40
1	B	107	ASP	CB-CG-OD1	6.12	123.81	118.30
1	B	254[A]	ASP	CA-CB-CG	6.11	126.85	113.40
1	B	254[B]	ASP	CA-CB-CG	6.11	126.85	113.40
1	B	275	GLU	OE1-CD-OE2	-6.11	115.96	123.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	20	THR	CA-CB-CG2	6.11	120.96	112.40
1	A	203	GLU	CG-CD-OE2	6.11	130.51	118.30
1	B	61	ASP	CB-CG-OD1	6.09	123.78	118.30
1	B	149	ASP	N-CA-C	-6.08	94.58	111.00
1	B	297	ARG	NH1-CZ-NH2	-6.05	112.74	119.40
1	B	299	ASP	OD1-CG-OD2	-6.05	111.81	123.30
1	A	254[A]	ASP	CB-CA-C	6.04	122.48	110.40
1	A	254[B]	ASP	CB-CA-C	6.04	122.48	110.40
1	B	254[A]	ASP	CB-CA-C	5.97	122.34	110.40
1	B	254[B]	ASP	CB-CA-C	5.97	122.34	110.40
1	A	253	TYR	CB-CG-CD1	5.92	124.55	121.00
1	A	330	GLU	CG-CD-OE1	-5.89	106.53	118.30
1	A	379	PHE	CB-CG-CD2	-5.88	116.68	120.80
1	B	111	ARG	NE-CZ-NH1	5.85	123.23	120.30
1	A	127	GLU	CG-CD-OE2	-5.84	106.62	118.30
1	A	44	GLU	CA-CB-CG	5.81	126.19	113.40
1	A	370	GLU	CG-CD-OE2	5.79	129.87	118.30
1	A	269	PHE	CA-C-N	5.77	129.89	117.20
1	B	238	GLU	OE1-CD-OE2	5.68	130.11	123.30
1	B	219	HIS	CB-CG-ND1	-5.66	109.04	123.20
1	A	149	ASP	N-CA-CB	5.64	120.75	110.60
1	B	368	ASP	CB-CG-OD1	5.64	123.38	118.30
1	B	134	VAL	CA-CB-CG1	5.63	119.34	110.90
1	A	206	GLU	N-CA-CB	5.62	120.72	110.60
1	A	149	ASP	N-CA-C	-5.61	95.85	111.00
1	B	342	GLU	CG-CD-OE1	5.61	129.51	118.30
1	A	352	GLU	CG-CD-OE2	5.57	129.44	118.30
1	A	315	TYR	CB-CG-CD1	5.56	124.34	121.00
1	B	289	ARG	CD-NE-CZ	5.56	131.38	123.60
1	A	176	ARG	NE-CZ-NH2	-5.56	117.52	120.30
1	A	370	GLU	CG-CD-OE1	-5.54	107.21	118.30
1	B	189	ASP	CB-CG-OD1	-5.52	113.33	118.30
1	B	330	GLU	OE1-CD-OE2	5.52	129.92	123.30
1	A	6	PRO	O-C-N	-5.51	113.89	122.70
1	B	301	TYR	CG-CD2-CE2	-5.50	116.90	121.30
1	A	297	ARG	O-C-N	-5.49	113.92	122.70
1	B	123	ASP	CB-CG-OD2	5.48	123.23	118.30
1	A	53	HIS	CB-CA-C	-5.47	99.46	110.40
1	A	20	THR	CA-CB-CG2	5.44	120.02	112.40
1	A	189	ASP	CB-CG-OD1	-5.43	113.41	118.30
1	A	342	GLU	CG-CD-OE2	-5.40	107.51	118.30
1	A	66	GLU	CG-CD-OE1	-5.39	107.52	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	98	PHE	CB-CG-CD2	-5.38	117.04	120.80
1	B	126	ALA	CB-CA-C	5.36	118.14	110.10
1	B	241	PHE	CB-CG-CD1	5.36	124.55	120.80
1	B	394	ARG	CG-CD-NE	-5.36	100.55	111.80
1	A	51	THR	CA-CB-CG2	5.35	119.90	112.40
1	B	254[A]	ASP	CB-CG-OD2	-5.35	113.49	118.30
1	B	254[B]	ASP	CB-CG-OD2	-5.35	113.49	118.30
1	A	56	ASP	N-CA-CB	5.35	120.22	110.60
1	A	155	ASP	CB-CG-OD1	5.33	123.10	118.30
1	B	156	ARG	NE-CZ-NH1	5.32	122.96	120.30
1	A	244	ASP	CB-CG-OD2	-5.32	113.51	118.30
1	B	253	TYR	CB-CG-CD2	-5.27	117.84	121.00
1	A	315	TYR	CB-CG-CD2	-5.27	117.84	121.00
1	B	127	GLU	CG-CD-OE1	-5.25	107.81	118.30
1	A	139	ARG	NH1-CZ-NH2	-5.24	113.63	119.40
1	A	84	LYS	C-N-CA	5.24	134.81	121.70
1	B	106	ASN	C-N-CA	5.23	134.78	121.70
1	B	358	MET	CG-SD-CE	5.23	108.57	100.20
1	A	83	LEU	CA-CB-CG	5.22	127.31	115.30
1	A	305	TRP	O-C-N	-5.22	114.34	122.70
1	B	158	ARG	NH1-CZ-NH2	5.20	125.12	119.40
1	A	211	VAL	CA-CB-CG2	5.18	118.67	110.90
1	B	370	GLU	OE1-CD-OE2	5.17	129.50	123.30
1	A	358	MET	CA-CB-CG	5.16	122.08	113.30
1	A	286	THR	CA-CB-OG1	-5.16	98.17	109.00
1	B	193	PRO	O-C-N	-5.15	114.45	122.70
1	A	43	ALA	CB-CA-C	5.14	117.82	110.10
1	B	203	GLU	CG-CD-OE2	5.14	128.58	118.30
1	B	370	GLU	CG-CD-OE1	-5.13	108.03	118.30
1	A	20	THR	N-CA-CB	-5.12	100.58	110.30
1	B	257	LEU	O-C-N	5.12	130.89	122.70
1	A	320	GLU	CA-CB-CG	5.10	124.62	113.40
1	B	27	VAL	CA-CB-CG2	5.09	118.54	110.90
1	B	244	ASP	CB-CG-OD2	-5.08	113.73	118.30
1	B	234	ALA	CB-CA-C	5.06	117.69	110.10
1	B	131	GLU	CG-CD-OE2	5.06	128.42	118.30
1	A	155	ASP	CB-CG-OD2	-5.06	113.75	118.30
1	A	289	ARG	CG-CD-NE	-5.04	101.22	111.80
1	A	249	ARG	NH1-CZ-NH2	-5.03	113.87	119.40
1	B	48	TYR	N-CA-CB	-5.03	101.54	110.60
1	B	257	LEU	CA-CB-CG	5.00	126.81	115.30

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	3035	0	2883	25	0
1	B	3035	0	2885	24	0
2	A	10	0	12	0	0
2	B	10	0	10	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	262	0	0	1	0
4	B	274	0	0	3	0
All	All	6628	0	5790	49	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 4.

All (49) 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:95:HIS:HD2	1:A:97:VAL:H	1.37	0.72
1:B:39:VAL:HG13	1:B:83:LEU:HD12	1.71	0.71
1:A:58:ILE:HD11	1:A:71:LEU:HD21	1.78	0.65
1:B:95:HIS:HD2	1:B:97:VAL:H	1.44	0.64
1:B:235:LEU:HD12	1:B:273:LEU:HD21	1.78	0.64
1:B:275:GLU:HG3	1:B:319:LYS:HG3	1.81	0.62
1:A:221:GLN:HE21	1:A:248:GLN:HB3	1.64	0.61
1:A:202:ILE:HG21	1:A:239:LYS:HE3	1.82	0.60
1:A:235:LEU:HD12	1:A:273:LEU:HD21	1.88	0.54
1:B:55:ASN:HA	1:B:58:ILE:O	2.08	0.54
1:B:148:LYS:HG3	1:B:191:PHE:HZ	1.73	0.53
1:B:35:PRO:O	1:B:39:VAL:HG23	2.10	0.52
1:A:158:ARG:HG3	1:A:205:LEU:HD23	1.92	0.51
1:A:222:MET:SD	1:A:254[A]:ASP:HB3	2.50	0.51
1:B:20:THR:HG23	1:B:28:ALA:HB1	1.93	0.51
1:A:8:ASP:O	1:A:9:HIS:HB2	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:11:THR:HG21	1:B:86:PRO:HG2	1.92	0.51
1:B:249:ARG:O	1:B:252:LYS:HE3	2.11	0.50
1:B:20:THR:HG23	1:B:28:ALA:CB	2.44	0.48
1:B:180:GLU:HA	1:B:181:PRO:HD3	1.70	0.47
1:B:359:ASN:HD22	1:B:359:ASN:C	2.17	0.47
1:B:278:PHE:HA	1:B:279:PRO:HD3	1.87	0.46
1:A:11:THR:HG21	1:A:86:PRO:HG2	1.98	0.46
1:B:182:LYS:HE2	1:B:184:ASN:O	2.16	0.46
1:A:148:LYS:HG3	1:A:191:PHE:HZ	1.81	0.46
1:A:131:GLU:HG3	1:A:132:THR:N	2.31	0.46
1:B:222:MET:SD	1:B:254[A]:ASP:HB3	2.57	0.45
1:B:45:LEU:HD22	1:B:309:LYS:HG3	1.98	0.45
1:A:23:ASP:HB2	1:A:24:PRO:CD	2.47	0.44
1:A:20:THR:HG23	1:A:28:ALA:CB	2.47	0.44
1:A:328:ASP:HA	1:A:329:PRO:HD3	1.76	0.44
1:A:381:ARG:HG3	4:B:871:HOH:O	2.18	0.44
1:A:216:GLU:HB2	1:A:244:ASP:HB2	2.00	0.43
1:A:23:ASP:HB2	1:A:24:PRO:HD2	2.01	0.43
1:A:255:GLN:O	1:A:256:ASP:HB2	2.18	0.43
1:B:237:ALA:O	1:B:238:GLU:HB2	2.19	0.43
1:A:95:HIS:CD2	1:A:97:VAL:H	2.27	0.42
1:B:23:ASP:HB2	1:B:24:PRO:HD2	2.01	0.42
1:B:184:ASN:HA	1:B:190:ILE:HG13	2.02	0.41
1:B:195:VAL:HG23	1:B:220:GLU:CD	2.41	0.41
1:B:280:ASN:OD1	1:B:341:PHE:HA	2.19	0.41
1:A:158:ARG:HG3	1:A:205:LEU:CD2	2.50	0.41
1:A:67:ARG:HG2	1:A:67:ARG:HH11	1.86	0.41
1:A:333:GLU:HG3	4:A:615:HOH:O	2.21	0.41
1:A:320:GLU:OE2	1:A:321:ARG:NH1	2.54	0.41
1:B:355:ALA:HB2	4:B:930:HOH:O	2.20	0.41
1:A:275:GLU:HG3	1:A:319:LYS:HG3	2.03	0.40
1:B:76:GLN:HB3	4:B:833:HOH:O	2.21	0.40
1:A:33:LEU:HD21	1:A:38:ALA:HB2	2.04	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	392/394 (100%)	375 (96%)	16 (4%)	1 (0%)	44	66
1	B	392/394 (100%)	373 (95%)	18 (5%)	1 (0%)	44	66
All	All	784/788 (100%)	748 (95%)	34 (4%)	2 (0%)	44	66

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	185	GLU
1	B	185	GLU

### 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	306/310 (99%)	297 (97%)	9 (3%)	48	75
1	B	306/310 (99%)	294 (96%)	12 (4%)	37	63
All	All	612/620 (99%)	591 (97%)	21 (3%)	42	69

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	20	THR
1	A	41	LYS
1	A	184	ASN
1	A	288	PRO

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Mol	Chain	Res	Type
1	A	302	ASP
1	A	309	LYS
1	A	313	SER
1	A	359	ASN
1	A	370	GLU
1	B	20	THR
1	B	34	ASP
1	B	41	LYS
1	B	69	LYS
1	B	149	ASP
1	B	176	ARG
1	B	184	ASN
1	B	213	LEU
1	B	286	THR
1	B	330	GLU
1	B	336	LYS
1	B	359	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	75	ASN
1	A	95	HIS
1	A	120	HIS
1	A	184	ASN
1	A	221	GLN
1	A	384	GLN
1	B	9	HIS
1	B	95	HIS
1	B	184	ASN
1	B	359	ASN
1	B	384	GLN

### 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

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	XYL	A	400	3	9,9,9	0.82	0	11,11,11	1.33	3 (27%)
2	XYL	B	400	3	9,9,9	0.73	0	11,11,11	0.96	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	XYL	A	400	3	-	0/12/12/12	0/0/0/0
2	XYL	B	400	3	-	0/12/12/12	0/0/0/0

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	400	XYL	C5-C4-C3	2.02	116.91	112.41
2	A	400	XYL	O3-C3-C2	2.38	114.71	108.82
2	A	400	XYL	O4-C4-C5	2.40	114.75	109.21

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.



## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

### 6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

### 6.4 Ligands

EDS was not executed - this section is therefore empty.

### 6.5 Other polymers

EDS was not executed - this section is therefore empty.