Full wwPDB X-ray Structure Validation Report (i)

Jan 31, 2016 – 11:38 PM GMT

PDB ID	:	1XYC
Title	:	X-RAY CRYSTALLOGRAPHIC STRUCTURES OF D-XYLOSE ISOMERASE-SUBSTRATE COMPLEXES POSITION THE SUBSTRATE AND PROVIDE EVIDENCE FOR METAL MOVEMENT DURING CATALYSIS
Authors	:	Lavie, A.; Allen, K.N.; Petsko, G.A.; Ringe, D.
Deposited on	:	1994-01-03
Resolution	:	2.19 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 (i) symbol.

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

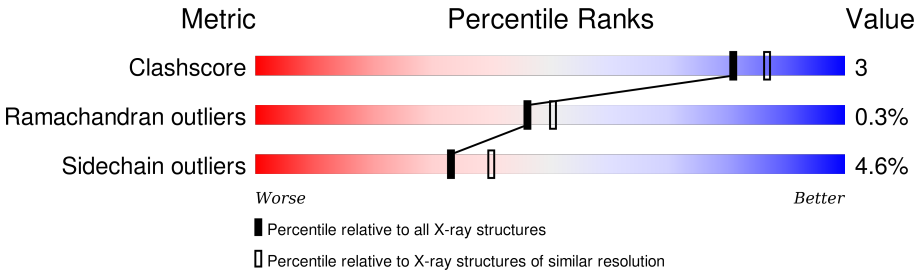
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.19 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	102246	4477 (2.20-2.20)
Ramachandran outliers	100387	4404 (2.20-2.20)
Sidechain outliers	100360	4405 (2.20-2.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	386	82% 16%
1	B	386	82% 16%

2 Entry composition

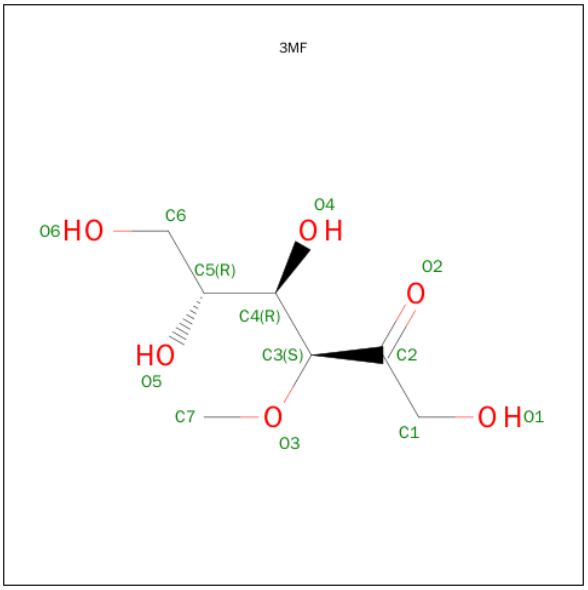
There are 4 unique types of molecules in this entry. The entry contains 6530 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 XYLOSE ISOMERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	386	Total	C	N	O	S	0	0	0
			3024	1904	540	572	8			
1	B	386	Total	C	N	O	S	0	0	0
			3024	1904	540	572	8			

- Molecule 2 is SUGAR (3-O-METHYLFRUCTOSE IN LINEAR FORM) (three-letter code: 3MF) (formula: $C_7H_{14}O_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	O		0	0
			13	7	6			
2	B	1	Total	C	O		0	0
			13	7	6			

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	2	Total Mg 3 3	0	1
3	A	2	Total Mg 3 3	0	1

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	218	Total O 218 218	0	0
4	B	232	Total O 232 232	0	0

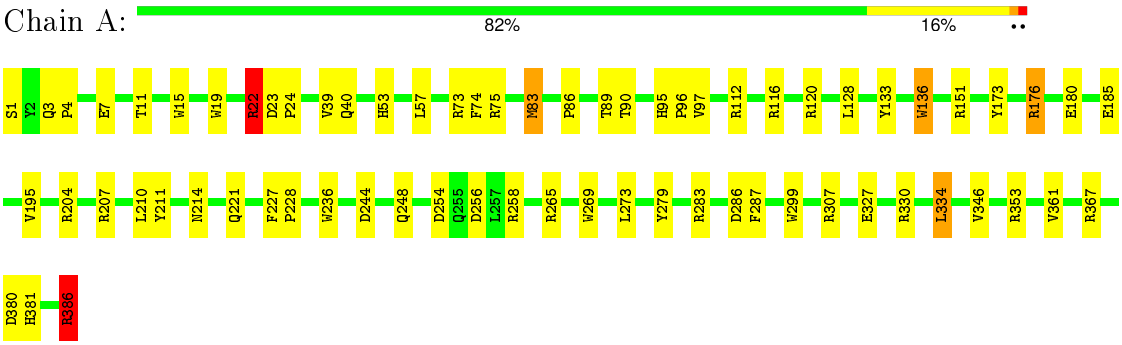
3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.

Note EDS was not executed.

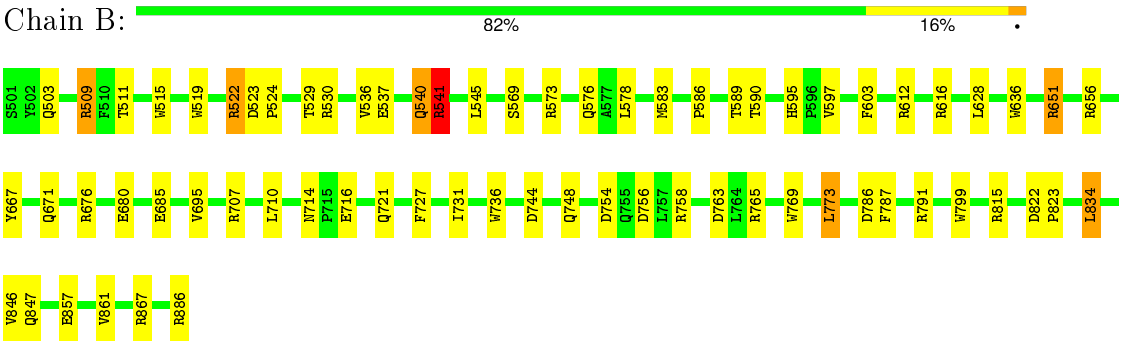
• Molecule 1: XYLOSE ISOMERASE

Chain A:



• Molecule 1: XYLOSE ISOMERASE

Chain B:



4 Data and refinement statistics (i)

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

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	87.70Å 99.30Å 94.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 2.19	Depositor
% Data completeness (in resolution range)	(Not available) (10.00-2.19)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.159 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6530	wwPDB-VP
Average B, all atoms (Å^2)	16.0	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: 3MF, MG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|>5$	RMSZ	#$\|Z\|>5$
1	A	0.78	0/3096	1.45	54/4197 (1.3%)
1	B	0.78	1/3096 (0.0%)	1.41	51/4197 (1.2%)
All	All	0.78	1/6192 (0.0%)	1.43	105/8394 (1.3%)

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	B	716	GLU	CD-OE1	-5.16	1.20	1.25

All (105) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	176	ARG	NE-CZ-NH1	12.99	126.79	120.30
1	B	765	ARG	NE-CZ-NH1	10.45	125.53	120.30
1	A	265	ARG	NE-CZ-NH2	-10.26	115.17	120.30
1	B	765	ARG	NE-CZ-NH2	-9.65	115.47	120.30
1	B	583	MET	CG-SD-CE	-9.52	84.96	100.20
1	A	367	ARG	NE-CZ-NH2	-9.07	115.76	120.30
1	B	541	ARG	NE-CZ-NH1	8.99	124.79	120.30
1	B	612	ARG	NE-CZ-NH1	8.94	124.77	120.30
1	A	299	TRP	CD1-CG-CD2	8.60	113.18	106.30
1	A	286	ASP	CB-CG-OD1	8.39	125.85	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	367	ARG	NE-CZ-NH1	8.39	124.49	120.30
1	A	116	ARG	NE-CZ-NH1	8.27	124.44	120.30
1	B	867	ARG	NE-CZ-NH1	8.25	124.43	120.30
1	A	299	TRP	CE2-CD2-CG	-7.88	101.00	107.30
1	A	353	ARG	NE-CZ-NH1	7.81	124.20	120.30
1	A	15	TRP	CE2-CD2-CG	-7.65	101.18	107.30
1	A	299	TRP	CG-CD2-CE3	7.62	140.76	133.90
1	A	15	TRP	CD1-CG-CD2	7.55	112.34	106.30
1	B	515	TRP	CE2-CD2-CG	-7.44	101.35	107.30
1	A	136	TRP	CD1-CG-CD2	7.42	112.23	106.30
1	B	515	TRP	CD1-CG-CD2	7.36	112.19	106.30
1	A	73	ARG	NE-CZ-NH2	-7.35	116.63	120.30
1	A	265	ARG	NE-CZ-NH1	7.32	123.96	120.30
1	B	736	TRP	CD1-CG-CD2	7.29	112.13	106.30
1	A	136	TRP	CE2-CD2-CG	-7.27	101.48	107.30
1	B	541	ARG	NE-CZ-NH2	-7.20	116.70	120.30
1	B	530	ARG	NE-CZ-NH1	7.19	123.90	120.30
1	A	83	MET	CG-SD-CE	-7.16	88.74	100.20
1	B	799	TRP	CE2-CD2-CG	-7.09	101.62	107.30
1	B	754	ASP	N-CA-CB	-7.09	97.84	110.60
1	A	116	ARG	NE-CZ-NH2	-7.04	116.78	120.30
1	B	786	ASP	CB-CG-OD1	6.93	124.54	118.30
1	A	236	TRP	CE2-CD2-CG	-6.93	101.76	107.30
1	A	19	TRP	CD1-CG-CD2	6.93	111.84	106.30
1	B	736	TRP	CE2-CD2-CG	-6.92	101.77	107.30
1	A	195	VAL	CG1-CB-CG2	-6.89	99.88	110.90
1	B	769	TRP	CD1-CG-CD2	6.89	111.81	106.30
1	B	799	TRP	CD1-CG-CD2	6.88	111.81	106.30
1	A	19	TRP	CE2-CD2-CG	-6.87	101.81	107.30
1	A	269	TRP	CD1-CG-CD2	6.87	111.79	106.30
1	B	846	VAL	CG1-CB-CG2	-6.84	99.95	110.90
1	A	176	ARG	NE-CZ-NH2	-6.80	116.90	120.30
1	A	236	TRP	CG-CD2-CE3	6.78	140.00	133.90
1	B	707	ARG	NE-CZ-NH1	6.74	123.67	120.30
1	B	636	TRP	CD1-CG-CD2	6.72	111.67	106.30
1	A	244	ASP	CB-CG-OD1	6.70	124.33	118.30
1	B	791	ARG	NE-CZ-NH2	-6.67	116.97	120.30
1	A	236	TRP	CD1-CG-CD2	6.65	111.62	106.30
1	B	656	ARG	NE-CZ-NH1	6.63	123.62	120.30
1	A	269	TRP	CE2-CD2-CG	-6.62	102.00	107.30
1	A	22	ARG	NE-CZ-NH2	-6.44	117.08	120.30
1	A	299	TRP	CB-CG-CD1	-6.36	118.74	127.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	769	TRP	CE2-CD2-CG	-6.33	102.23	107.30
1	B	616	ARG	NE-CZ-NH1	6.31	123.46	120.30
1	A	112	ARG	NE-CZ-NH2	-6.30	117.15	120.30
1	B	519	TRP	CD1-CG-CD2	6.30	111.34	106.30
1	B	867	ARG	NE-CZ-NH2	-6.30	117.15	120.30
1	B	515	TRP	CG-CD2-CE3	6.28	139.55	133.90
1	B	636	TRP	CE2-CD2-CG	-6.22	102.32	107.30
1	B	744	ASP	CB-CG-OD1	6.08	123.77	118.30
1	B	758	ARG	NE-CZ-NH2	-6.07	117.27	120.30
1	A	386	ARG	NE-CZ-NH1	5.89	123.24	120.30
1	B	603	PHE	CB-CG-CD2	-5.88	116.69	120.80
1	B	522	ARG	NE-CZ-NH1	5.88	123.24	120.30
1	A	211	TYR	CB-CG-CD1	-5.85	117.49	121.00
1	A	22	ARG	CA-CB-CG	5.83	126.23	113.40
1	B	695	VAL	CG1-CB-CG2	-5.83	101.57	110.90
1	B	763	ASP	CB-CG-OD1	5.82	123.54	118.30
1	A	151	ARG	NE-CZ-NH1	5.81	123.21	120.30
1	A	299	TRP	CG-CD1-NE1	-5.81	104.29	110.10
1	B	519	TRP	CE2-CD2-CG	-5.77	102.68	107.30
1	A	176	ARG	CD-NE-CZ	5.77	131.68	123.60
1	A	207	ARG	NE-CZ-NH1	5.75	123.17	120.30
1	A	176	ARG	CG-CD-NE	5.73	123.83	111.80
1	A	283	ARG	NE-CZ-NH2	-5.72	117.44	120.30
1	A	136	TRP	CG-CD2-CE3	5.72	139.05	133.90
1	A	15	TRP	CG-CD2-CE3	5.66	138.99	133.90
1	B	754	ASP	CB-CG-OD2	-5.63	113.23	118.30
1	A	334	LEU	CA-CB-CG	-5.54	102.55	115.30
1	B	834	LEU	CA-CB-CG	-5.54	102.55	115.30
1	A	254	ASP	N-CA-CB	-5.54	100.63	110.60
1	A	173	TYR	CB-CG-CD2	-5.52	117.69	121.00
1	B	651	ARG	NE-CZ-NH1	5.49	123.05	120.30
1	B	515	TRP	CB-CG-CD1	-5.45	119.92	127.00
1	B	636	TRP	CG-CD2-CE3	5.42	138.78	133.90
1	A	75	ARG	NE-CZ-NH2	-5.39	117.61	120.30
1	B	736	TRP	CG-CD1-NE1	-5.38	104.72	110.10
1	A	279	TYR	CB-CG-CD2	-5.37	117.78	121.00
1	B	736	TRP	CG-CD2-CE3	5.36	138.72	133.90
1	B	509	ARG	NE-CZ-NH1	5.35	122.97	120.30
1	A	353	ARG	NE-CZ-NH2	-5.32	117.64	120.30
1	A	258	ARG	NE-CZ-NH1	5.29	122.94	120.30
1	B	815	ARG	NE-CZ-NH2	-5.27	117.66	120.30
1	A	330	ARG	NE-CZ-NH1	5.21	122.91	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	573	ARG	NE-CZ-NH2	-5.15	117.72	120.30
1	B	569	SER	N-CA-CB	-5.14	102.80	110.50
1	A	73	ARG	NE-CZ-NH1	5.11	122.86	120.30
1	A	381	HIS	CA-CB-CG	-5.10	104.93	113.60
1	A	120	ARG	NE-CZ-NH1	5.08	122.84	120.30
1	B	799	TRP	CB-CG-CD1	-5.08	120.40	127.00
1	B	886	ARG	NE-CZ-NH1	5.07	122.83	120.30
1	B	773	LEU	CA-CB-CG	5.05	126.91	115.30
1	B	612	ARG	NE-CZ-NH2	-5.02	117.79	120.30
1	A	40	GLN	CA-CB-CG	-5.01	102.38	113.40
1	B	515	TRP	CG-CD1-NE1	-5.00	105.10	110.10

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	133	TYR	Sidechain

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3024	0	2909	21	0
1	B	3024	0	2906	19	0
2	A	13	0	14	4	0
2	B	13	0	14	2	0
3	A	3	0	0	0	0
3	B	3	0	0	0	0
4	A	218	0	0	2	0
4	B	232	0	0	2	0
All	All	6530	0	5843	39	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 3.

All (39) 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:537:GLU:HB2	1:B:541:ARG:NH2	2.03	0.73
1:B:595:HIS:HD2	1:B:597:VAL:H	1.36	0.71
1:B:537:GLU:HB2	1:B:541:ARG:HH22	1.64	0.62
1:A:136:TRP:CE2	2:A:950:3MF:H11	2.34	0.62
1:B:523:ASP:HB2	1:B:524:PRO:HD2	1.82	0.62
1:A:95:HIS:HD2	1:A:97:VAL:H	1.49	0.61
1:A:1:SER:HB2	1:A:307:ARG:HH12	1.64	0.60
1:B:680:GLU:HG3	1:B:714:ASN:O	2.02	0.59
1:A:136:TRP:CZ2	2:A:950:3MF:H11	2.40	0.57
1:A:89:THR:HG21	2:A:950:3MF:H62	1.87	0.56
1:B:589:THR:HG21	2:B:960:3MF:H61	1.88	0.55
1:B:595:HIS:CD2	1:B:597:VAL:H	2.22	0.54
1:A:96:PRO:HB3	1:B:529:THR:HG22	1.89	0.54
1:A:89:THR:HG21	2:A:950:3MF:C6	2.38	0.53
1:A:221:GLN:HE21	1:A:248:GLN:HB3	1.73	0.53
1:A:95:HIS:CD2	1:A:97:VAL:H	2.28	0.52
1:A:180:GLU:HG3	1:A:214:ASN:O	2.10	0.52
1:A:380:ASP:HB3	1:A:386:ARG:HB2	1.94	0.50
1:B:589:THR:HG21	2:B:960:3MF:C6	2.42	0.49
1:A:256:ASP:HB3	1:A:287:PHE:HA	1.97	0.47
1:A:11:THR:HG21	1:A:86:PRO:HG2	1.96	0.46
1:B:721:GLN:HE21	1:B:748:GLN:HB3	1.81	0.46
1:B:727:PHE:CZ	1:B:731:ILE:HD11	2.52	0.45
1:A:57:LEU:HD11	1:A:74:PHE:HB2	1.98	0.45
1:B:756:ASP:HB3	1:B:787:PHE:HA	1.99	0.45
1:A:53:HIS:CD2	1:A:89:THR:HG23	2.53	0.44
1:B:511:THR:HG21	1:B:586:PRO:HG2	2.00	0.43
1:B:822:ASP:HA	1:B:823:PRO:HD3	1.90	0.41
1:A:327:GLU:HG3	4:A:1286:HOH:O	2.20	0.41
1:A:22:ARG:HB3	4:A:1220:HOH:O	2.21	0.41
1:B:522:ARG:HD2	4:B:1350:HOH:O	2.20	0.41
1:A:227:PHE:HB3	1:A:228:PRO:HD3	2.01	0.41
1:B:651:ARG:HD3	4:B:1329:HOH:O	2.20	0.41
1:A:3:GLN:HA	1:A:4:PRO:HD2	1.99	0.40
1:A:23:ASP:HB2	1:A:24:PRO:HD2	2.02	0.40
1:B:667:TYR:O	1:B:671:GLN:HG2	2.21	0.40
1:B:540:GLN:HG2	1:B:540:GLN:H	1.73	0.40
1:B:536:VAL:O	1:B:540:GLN:HG2	2.21	0.40
1:A:39:VAL:HG13	1:A:83:MET:HG3	2.03	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	384/386 (100%)	371 (97%)	12 (3%)	1 (0%)	46 50
1	B	384/386 (100%)	372 (97%)	11 (3%)	1 (0%)	46 50
All	All	768/772 (100%)	743 (97%)	23 (3%)	2 (0%)	46 50

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	185	GLU
1	B	685	GLU

5.3.2 Protein sidechains (i)

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	302/302 (100%)	290 (96%)	12 (4%)	38 47
1	B	302/302 (100%)	286 (95%)	16 (5%)	28 32
All	All	604/604 (100%)	576 (95%)	28 (5%)	33 40

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	GLU
1	A	22	ARG
1	A	90	THR
1	A	128	LEU

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Mol	Chain	Res	Type
1	A	176	ARG
1	A	204	ARG
1	A	210	LEU
1	A	273	LEU
1	A	334	LEU
1	A	346	VAL
1	A	361	VAL
1	A	386	ARG
1	B	503	GLN
1	B	509	ARG
1	B	540	GLN
1	B	541	ARG
1	B	545	LEU
1	B	576	GLN
1	B	578	LEU
1	B	590	THR
1	B	628	LEU
1	B	676	ARG
1	B	710	LEU
1	B	773	LEU
1	B	834	LEU
1	B	847	GLN
1	B	857	GLU
1	B	861	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	95	HIS
1	A	221	GLN
1	A	308	ASN
1	A	326	GLN
1	A	339	GLN
1	B	595	HIS
1	B	684	ASN
1	B	721	GLN
1	B	808	ASN

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)

Of 8 ligands modelled in this entry, 6 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	3MF	A	950	3	12,12,12	0.75	0	10,15,15	1.12	0
2	3MF	B	960	3	12,12,12	1.15	1 (8%)	10,15,15	1.72	2 (20%)

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	3MF	A	950	3	-	0/18/18/18	0/0/0/0
2	3MF	B	960	3	-	0/18/18/18	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	960	3MF	C3-C2	2.95	1.57	1.52

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	960	3MF	O2-C2-C1	-2.11	116.48	120.13

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	960	3MF	C7-O3-C3	4.18	119.96	113.90

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	950	3MF	4	0
2	B	960	3MF	2	0

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 will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates

EDS was not executed - this section will therefore be empty.

6.4 Ligands

EDS was not executed - this section will therefore be empty.

6.5 Other polymers

EDS was not executed - this section will therefore be empty.