



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:15 AM UTC

PDB ID : 3ED3 / pdb_00003ed3
Title : Crystal Structure of the Yeast Dithiol/Disulfide Oxidoreductase Mpd1p
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Deposited on : 2008-09-02
Resolution : 2.00 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

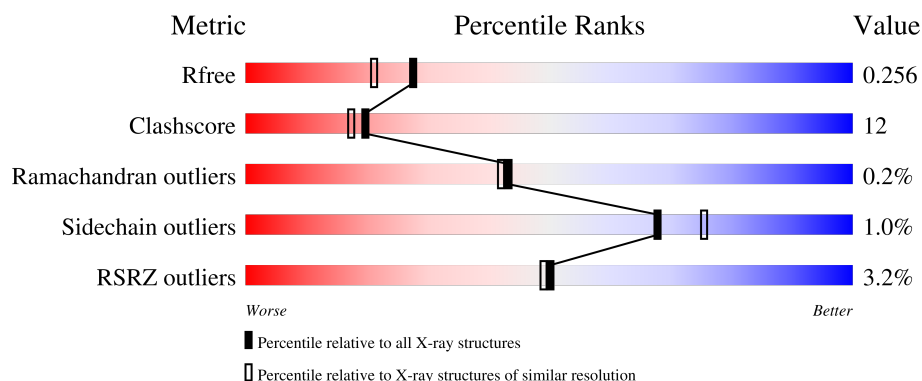
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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}	180053	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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 of 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	298	4% 64% 25% 10%
1	B	298	2% 70% 18% 11%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4656 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 Protein disulfide-isomerase MPD1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	267	Total	C	N	O	S	0	0	0
			2161	1394	366	395	6			
1	B	266	Total	C	N	O	S	0	0	0
			2152	1388	364	394	6			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	13	MET	-	expression tag	UNP Q12404
A	14	GLY	-	expression tag	UNP Q12404
A	15	SER	-	expression tag	UNP Q12404
A	16	SER	-	expression tag	UNP Q12404
A	17	HIS	-	expression tag	UNP Q12404
A	18	HIS	-	expression tag	UNP Q12404
A	19	HIS	-	expression tag	UNP Q12404
A	20	HIS	-	expression tag	UNP Q12404
A	21	HIS	-	expression tag	UNP Q12404
A	22	HIS	-	expression tag	UNP Q12404
B	13	MET	-	expression tag	UNP Q12404
B	14	GLY	-	expression tag	UNP Q12404
B	15	SER	-	expression tag	UNP Q12404
B	16	SER	-	expression tag	UNP Q12404
B	17	HIS	-	expression tag	UNP Q12404
B	18	HIS	-	expression tag	UNP Q12404
B	19	HIS	-	expression tag	UNP Q12404
B	20	HIS	-	expression tag	UNP Q12404
B	21	HIS	-	expression tag	UNP Q12404
B	22	HIS	-	expression tag	UNP Q12404

- Molecule 2 is ACETATE ION (CCD ID: ACT) (formula: C₂H₃O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			4	2	2		
2	A	1	Total	C	O	0	0
			4	2	2		
2	A	1	Total	C	O	0	0
			4	2	2		
2	A	1	Total	C	O	0	0
			4	2	2		
2	A	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 3 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



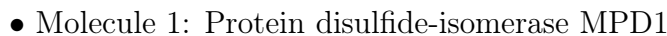
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	156	Total	O	0	0
			156	156		
4	B	135	Total	O	0	0
			135	135		

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- Molecule 1: Protein disulfide-isomerase MPD1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	48.16Å 92.27Å 79.34Å 90.00° 92.23° 90.00°	Depositor
Resolution (Å)	50.00 – 2.00 50.00 – 2.00	Depositor EDS
% Data completeness (in resolution range)	97.8 (50.00-2.00) 97.8 (50.00-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.56 (at 2.00Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.219 , 0.255 0.219 , 0.256	Depositor DCC
R_{free} test set	3243 reflections (7.07%)	wwPDB-VP
Wilson B-factor (Å ²)	32.7	Xtriage
Anisotropy	0.544	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 39.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.037 for h,-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4656	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.98% 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 [i](#)

5.1 Standard geometry [i](#)

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

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	0.37	0/2213	0.92	8/2985 (0.3%)
1	B	0.38	0/2204	0.90	4/2974 (0.1%)
All	All	0.38	0/4417	0.91	12/5959 (0.2%)

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	25	TYR	N-CA-C	8.08	123.26	111.87
1	B	25	TYR	N-CA-C	7.39	122.30	111.87
1	A	43	ILE	N-CA-C	7.37	117.97	110.82
1	B	43	ILE	N-CA-C	6.81	117.42	110.82
1	A	39	PHE	N-CA-C	5.71	117.98	111.02
1	B	132	ALA	N-CA-C	-5.63	102.15	110.48
1	A	182	SER	N-CA-C	5.62	119.08	110.20
1	A	236	ILE	CB-CA-C	-5.57	108.41	113.70
1	A	181	PHE	N-CA-C	-5.49	98.33	107.99
1	A	142	LEU	N-CA-C	5.11	117.25	111.02
1	B	182	SER	N-CA-C	5.09	118.25	110.20
1	A	49	THR	N-CA-C	-5.03	102.32	110.32

There are no chirality outliers.

There are no planarity outliers.

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	2161	0	2179	58	0
1	B	2152	0	2166	45	0
2	A	24	0	18	1	0
2	B	12	0	9	0	0
3	A	8	0	12	0	0
3	B	8	0	12	0	0
4	A	156	0	0	4	0
4	B	135	0	0	5	0
All	All	4656	0	4396	101	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 12.

All (101) 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:220:PRO:HA	1:A:223:GLU:HG3	1.61	0.82
1:B:141:THR:O	1:B:145:ILE:HD13	1.81	0.79
1:B:160:PHE:O	1:B:207:ILE:HG22	1.84	0.77
1:B:143:ALA:HB3	1:B:144:PRO:HD3	1.69	0.74
1:B:140:ARG:HA	1:B:145:ILE:HD11	1.70	0.74
1:A:163:ILE:HG23	1:A:215:LEU:HD21	1.70	0.72
1:B:171:ARG:HH22	1:B:221:THR:HG23	1.54	0.72
1:A:275:ARG:HB3	1:A:275:ARG:HH11	1.57	0.70
1:A:163:ILE:HD12	1:A:212:LEU:HD22	1.74	0.69
1:B:201:LYS:HE2	1:B:283:ASN:ND2	2.09	0.67
1:A:290:ARG:NE	1:A:294:ILE:HD11	2.11	0.66
1:A:272:LYS:HG3	1:A:275:ARG:HH12	1.58	0.66
1:B:207:ILE:HD12	1:B:207:ILE:O	1.97	0.64
1:A:290:ARG:HE	1:A:294:ILE:HD11	1.62	0.64
1:B:168:SER:HA	1:B:171:ARG:NH1	2.14	0.62
1:A:143:ALA:HB3	1:A:144:PRO:HD3	1.81	0.61
1:A:163:ILE:HD13	1:A:236:ILE:HD11	1.80	0.61
1:A:237:PRO:HG2	4:A:2905:HOH:O	1.99	0.60
1:A:220:PRO:HA	1:A:223:GLU:CG	2.30	0.60
1:A:163:ILE:HD13	1:A:236:ILE:CD1	2.31	0.60
1:A:209:ASN:HB3	1:A:239:GLN:O	2.01	0.59
1:A:90:ASN:HA	1:A:93:LYS:HE2	1.85	0.59
1:A:58:TRP:CD1	1:B:93:LYS:HD3	2.38	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:260:TYR:CZ	1:B:262:GLY:HA3	2.39	0.57
1:A:260:TYR:CZ	1:A:262:GLY:HA3	2.40	0.57
1:B:181:PHE:HA	1:B:207:ILE:HD12	1.86	0.57
1:A:236:ILE:N	1:A:237:PRO:HD2	2.19	0.57
1:A:234:LYS:O	1:A:234:LYS:HD3	2.05	0.56
1:B:171:ARG:NH2	1:B:221:THR:HG23	2.19	0.56
1:A:260:TYR:CE1	1:A:270:ILE:HD13	2.41	0.56
1:A:167:GLY:HA3	1:A:221:THR:HG22	1.89	0.53
1:B:181:PHE:CD2	1:B:207:ILE:HD11	2.44	0.53
1:B:163:ILE:HG12	1:B:236:ILE:HD11	1.90	0.53
1:B:140:ARG:HH11	1:B:140:ARG:HG2	1.73	0.53
1:B:160:PHE:CD2	1:B:207:ILE:HG23	2.44	0.53
1:A:168:SER:O	1:A:171:ARG:HG2	2.10	0.52
1:B:111:ARG:NH1	4:B:2836:HOH:O	2.43	0.52
1:A:247:LEU:C	1:A:247:LEU:HD23	2.35	0.51
1:A:140:ARG:HG2	1:A:140:ARG:HH11	1.75	0.51
1:B:201:LYS:HE3	1:B:281:THR:O	2.09	0.51
1:B:214:GLN:HA	1:B:236:ILE:HG21	1.93	0.51
1:A:201:LYS:HE2	1:A:283:ASN:ND2	2.26	0.50
1:A:57:PRO:HD2	1:A:88:ASP:OD2	2.10	0.50
1:A:162:ARG:HB3	1:A:164:ASP:OD1	2.11	0.50
1:A:73:ALA:HA	1:A:82:VAL:HG21	1.94	0.50
1:B:107:LEU:HD12	1:B:140:ARG:NH1	2.26	0.50
1:B:190:VAL:HG23	4:B:2799:HOH:O	2.11	0.50
1:A:169:LEU:HD23	1:A:172:LYS:NZ	2.28	0.49
1:B:217:ASP:O	1:B:218:MET:C	2.56	0.49
1:B:90:ASN:OD1	1:B:93:LYS:HE2	2.13	0.49
1:B:73:ALA:HA	1:B:82:VAL:HG21	1.96	0.48
1:A:209:ASN:O	1:A:240:ARG:HA	2.14	0.47
1:B:165:THR:HA	4:B:2897:HOH:O	2.14	0.47
1:A:290:ARG:HG3	1:A:294:ILE:HD12	1.96	0.47
1:A:245:SER:HB2	1:A:265:ILE:HD11	1.96	0.47
1:B:236:ILE:N	1:B:237:PRO:HD2	2.30	0.46
1:A:37:LYS:HE3	1:A:37:LYS:HB2	1.73	0.46
1:A:183:LYS:HE3	4:A:2879:HOH:O	2.15	0.46
1:B:29:PRO:O	1:B:298:LYS:HD3	2.16	0.46
1:A:247:LEU:HD23	1:A:248:VAL:N	2.31	0.45
1:A:228:ILE:HD11	1:A:256:LYS:O	2.16	0.45
1:A:36:PRO:HB3	2:A:1109:ACT:H3	1.98	0.45
1:A:103:GLY:HA2	1:B:103:GLY:HA2	1.98	0.45
1:A:245:SER:HB2	1:A:265:ILE:CD1	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:29:PRO:O	1:A:298:LYS:HD3	2.16	0.45
1:B:275:ARG:HH11	1:B:275:ARG:HB3	1.80	0.45
1:B:221:THR:HG21	4:B:2897:HOH:O	2.16	0.45
1:A:296:TYR:O	1:A:300:GLY:N	2.48	0.44
1:A:41:LYS:HD3	1:A:293:TYR:CZ	2.52	0.44
1:A:220:PRO:HA	1:A:223:GLU:CD	2.42	0.44
1:B:265:ILE:HD12	1:B:265:ILE:N	2.33	0.44
1:A:246:LYS:HE2	4:A:2886:HOH:O	2.17	0.44
1:A:35:THR:HA	1:A:92:ASN:OD1	2.17	0.44
1:B:140:ARG:HG2	1:B:140:ARG:NH1	2.32	0.43
1:A:290:ARG:HG3	1:A:294:ILE:CD1	2.48	0.43
1:B:209:ASN:HB3	1:B:239:GLN:O	2.18	0.43
1:B:36:PRO:HD3	1:B:92:ASN:OD1	2.19	0.43
1:B:272:LYS:HA	1:B:275:ARG:NH1	2.34	0.43
1:A:30:HIS:CD2	1:A:74:LYS:HG2	2.54	0.43
1:A:217:ASP:C	1:A:219:ASN:H	2.27	0.42
1:B:166:LEU:O	1:B:170:LEU:HG	2.18	0.42
1:B:140:ARG:NE	4:B:2881:HOH:O	2.44	0.42
1:B:90:ASN:HA	1:B:93:LYS:HE2	2.02	0.42
1:A:168:SER:O	1:A:172:LYS:HG3	2.19	0.41
1:A:213:LYS:O	1:A:214:GLN:C	2.63	0.41
1:A:180:LEU:HD11	1:A:265:ILE:CD1	2.50	0.41
1:B:209:ASN:O	1:B:240:ARG:HA	2.20	0.41
1:B:247:LEU:HD23	1:B:247:LEU:C	2.45	0.41
1:A:74:LYS:HD3	4:A:2853:HOH:O	2.20	0.41
1:A:217:ASP:C	1:A:219:ASN:N	2.77	0.41
1:B:108:MET:HE3	1:B:108:MET:HB2	1.91	0.41
1:B:167:GLY:O	1:B:171:ARG:HG3	2.20	0.41
1:A:183:LYS:HG2	1:A:245:SER:OG	2.21	0.41
1:B:35:THR:HA	1:B:92:ASN:OD1	2.20	0.41
1:B:232:LEU:O	1:B:236:ILE:HG12	2.20	0.41
1:B:238:GLU:OE2	1:B:246:LYS:NZ	2.53	0.41
1:A:228:ILE:HD12	1:A:250:PHE:HD2	1.86	0.41
1:A:162:ARG:HB2	1:A:165:THR:HG23	2.04	0.40
1:A:201:LYS:HE3	1:A:281:THR:O	2.22	0.40
1:A:226:PRO:O	1:A:230:LYS:HG3	2.22	0.40
1:A:228:ILE:HD11	1:A:256:LYS:C	2.47	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	263/298 (88%)	255 (97%)	7 (3%)	1 (0%)	30	27
1	B	262/298 (88%)	259 (99%)	3 (1%)	0	100	100
All	All	525/596 (88%)	514 (98%)	10 (2%)	1 (0%)	43	42

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	214	GLN

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	242/272 (89%)	240 (99%)	2 (1%)	73	80
1	B	241/272 (89%)	238 (99%)	3 (1%)	63	70
All	All	483/544 (89%)	478 (99%)	5 (1%)	68	75

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	59	CYS
1	A	275	ARG
1	B	59	CYS
1	B	207	ILE
1	B	268	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	30	HIS
1	A	268	ASN
1	A	283	ASN
1	B	81	GLN
1	B	133	ASN
1	B	283	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

13 ligands are modelled in this entry.

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	ACT	B	1102	-	3,3,3	2.07	2 (66%)	3,3,3	0.85	0
3	EDO	B	2765	-	3,3,3	0.47	0	2,2,2	0.37	0
2	ACT	A	1101	-	3,3,3	1.99	1 (33%)	3,3,3	0.85	0
3	EDO	A	2762	-	3,3,3	0.41	0	2,2,2	0.41	0
3	EDO	A	2763	-	3,3,3	0.51	0	2,2,2	0.41	0
3	EDO	B	2764	-	3,3,3	0.47	0	2,2,2	0.36	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	ACT	A	1109	-	3,3,3	2.07	2 (66%)	3,3,3	0.85	0
2	ACT	A	1108	-	3,3,3	2.06	1 (33%)	3,3,3	0.85	0
2	ACT	B	1103	-	3,3,3	2.11	2 (66%)	3,3,3	0.83	0
2	ACT	A	1105	-	3,3,3	2.09	2 (66%)	3,3,3	0.81	0
2	ACT	A	1107	-	3,3,3	2.07	1 (33%)	3,3,3	0.82	0
2	ACT	A	1106	-	3,3,3	2.09	2 (66%)	3,3,3	0.82	0
2	ACT	B	1104	-	3,3,3	2.04	2 (66%)	3,3,3	0.85	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
3	EDO	A	2762	-	-	0/1/1/1	-
3	EDO	A	2763	-	-	0/1/1/1	-
3	EDO	B	2765	-	-	1/1/1/1	-
3	EDO	B	2764	-	-	0/1/1/1	-

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1107	ACT	O-C	2.94	1.35	1.22
2	A	1105	ACT	O-C	2.91	1.35	1.22
2	B	1102	ACT	O-C	2.90	1.34	1.22
2	B	1103	ACT	O-C	2.90	1.34	1.22
2	A	1108	ACT	O-C	2.90	1.34	1.22
2	A	1109	ACT	O-C	2.90	1.34	1.22
2	A	1106	ACT	O-C	2.90	1.34	1.22
2	B	1104	ACT	O-C	2.82	1.34	1.22
2	A	1101	ACT	O-C	2.79	1.34	1.22
2	B	1103	ACT	OXT-C	-2.15	1.20	1.30
2	A	1106	ACT	OXT-C	-2.08	1.21	1.30
2	B	1104	ACT	OXT-C	-2.08	1.21	1.30
2	A	1105	ACT	OXT-C	-2.06	1.21	1.30
2	B	1102	ACT	OXT-C	-2.03	1.21	1.30
2	A	1109	ACT	OXT-C	-2.03	1.21	1.30

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	2765	EDO	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1109	ACT	1	0

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	267/298 (89%)	0.30	11 (4%) 41 40	22, 37, 59, 67	0
1	B	266/298 (89%)	0.23	6 (2%) 61 60	22, 37, 52, 66	0
All	All	533/596 (89%)	0.27	17 (3%) 50 49	22, 37, 56, 67	0

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	300	GLY	4.2
1	A	221	THR	3.8
1	A	22	HIS	2.9
1	B	22	HIS	2.9
1	A	237	PRO	2.7
1	A	223	GLU	2.5
1	A	241	GLN	2.4
1	B	207	ILE	2.3
1	B	243	ASP	2.3
1	A	171	ARG	2.2
1	B	236	ILE	2.1
1	A	289	ARG	2.1
1	A	243	ASP	2.1
1	B	115	ILE	2.1
1	A	283	ASN	2.0
1	A	301	LYS	2.0
1	A	163	ILE	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	ACT	B	1103	4/4	0.62	0.24	67,68,68,69	0
2	ACT	A	1108	4/4	0.64	0.23	80,80,80,81	0
2	ACT	A	1101	4/4	0.78	0.25	61,62,63,64	0
2	ACT	A	1105	4/4	0.78	0.17	65,65,66,66	0
2	ACT	A	1106	4/4	0.79	0.19	50,50,51,52	0
2	ACT	A	1107	4/4	0.79	0.20	64,65,65,66	0
2	ACT	A	1109	4/4	0.84	0.17	48,50,50,50	0
3	EDO	B	2765	4/4	0.86	0.16	57,58,58,59	0
2	ACT	B	1102	4/4	0.88	0.20	65,65,66,66	0
2	ACT	B	1104	4/4	0.89	0.16	69,70,71,71	0
3	EDO	A	2762	4/4	0.93	0.11	50,50,50,51	0
3	EDO	B	2764	4/4	0.97	0.06	27,29,29,29	0
3	EDO	A	2763	4/4	0.97	0.06	24,29,30,30	0

6.5 Other polymers [i](#)

There are no such residues in this entry.