



Full wwPDB X-ray Structure Validation Report ⓘ

May 21, 2020 – 03:47 am BST

PDB ID : 3M8W
Title : Phosphopentomutase from *Bacillus cereus*
Authors : Panosian, T.D.; Nannemann, D.P.; Watkins, G.; Wadzinski, B.; Bachmann, B.O.; Iverson, T.M.
Deposited on : 2010-03-19
Resolution : 1.85 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

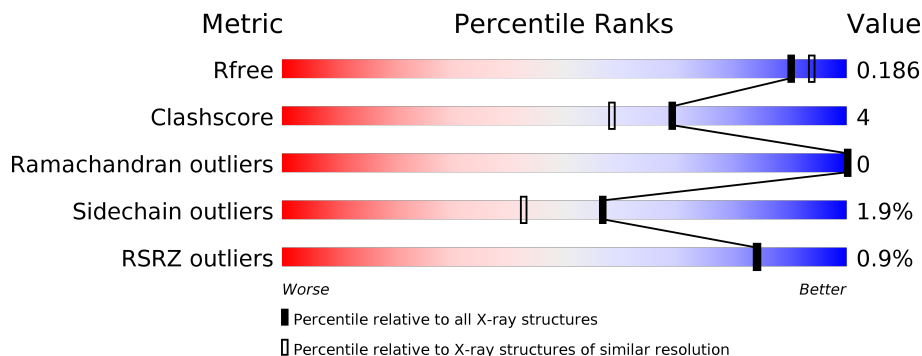
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.85 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	2469 (1.86-1.86)
Clashscore	141614	2625 (1.86-1.86)
Ramachandran outliers	138981	2592 (1.86-1.86)
Sidechain outliers	138945	2592 (1.86-1.86)
RSRZ outliers	127900	2436 (1.86-1.86)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	399	
1	B	399	
1	C	399	

2 Entry composition i

There are 5 unique types of molecules in this entry. The entry contains 10228 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 Phosphopentomutase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	P	S			
1	A	391	Total 3084	C 1948	N 507	O 610	P 1	S 18	11	2	0
1	B	391	Total 3098	C 1956	N 514	O 609	P 1	S 18	7	3	0
1	C	390	Total 3060	C 1935	N 503	O 604	P 1	S 17	47	0	0

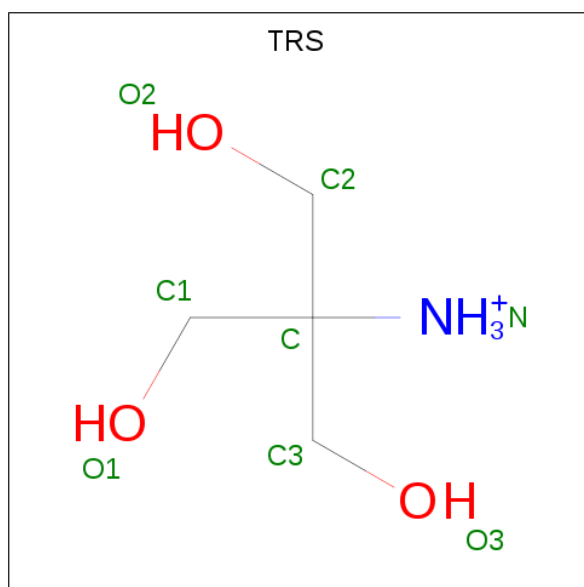
There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	GLY	-	EXPRESSION TAG	UNP Q818Z9
A	-3	SER	-	EXPRESSION TAG	UNP Q818Z9
A	-2	HIS	-	EXPRESSION TAG	UNP Q818Z9
A	-1	MET	-	EXPRESSION TAG	UNP Q818Z9
A	0	ALA	-	EXPRESSION TAG	UNP Q818Z9
A	1	SER	-	EXPRESSION TAG	UNP Q818Z9
B	-4	GLY	-	EXPRESSION TAG	UNP Q818Z9
B	-3	SER	-	EXPRESSION TAG	UNP Q818Z9
B	-2	HIS	-	EXPRESSION TAG	UNP Q818Z9
B	-1	MET	-	EXPRESSION TAG	UNP Q818Z9
B	0	ALA	-	EXPRESSION TAG	UNP Q818Z9
B	1	SER	-	EXPRESSION TAG	UNP Q818Z9
C	-4	GLY	-	EXPRESSION TAG	UNP Q818Z9
C	-3	SER	-	EXPRESSION TAG	UNP Q818Z9
C	-2	HIS	-	EXPRESSION TAG	UNP Q818Z9
C	-1	MET	-	EXPRESSION TAG	UNP Q818Z9
C	0	ALA	-	EXPRESSION TAG	UNP Q818Z9
C	1	SER	-	EXPRESSION TAG	UNP Q818Z9

- Molecule 2 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

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

- Molecule 3 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: TRS) (formula: $C_4H_{12}NO_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N O 8 4 1 3	0	0
3	B	1	Total C N O 8 4 1 3	0	0

- Molecule 4 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



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

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	348	Total O 348 348	0	0
5	B	382	Total O 382 382	0	0
5	C	218	Total O 218 218	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	91.24Å 76.55Å 106.56Å 90.00° 108.89° 90.00°	Depositor
Resolution (Å)	20.00 – 1.85 45.76 – 1.85	Depositor EDS
% Data completeness (in resolution range)	100.0 (20.00-1.85) 98.6 (45.76-1.85)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.91 (at 1.86Å)	Xtrriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.157 , 0.186 0.159 , 0.186	Depositor DCC
R_{free} test set	5851 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	24.3	Xtrriage
Anisotropy	0.497	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 48.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	10228	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.24% 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: TPO, TRS, MN, ACT

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	0.43	1/3133 (0.0%)	0.56	0/4229
1	B	0.42	0/3147	0.56	0/4246
1	C	0.39	0/3109	0.53	0/4197
All	All	0.41	1/9389 (0.0%)	0.55	0/12672

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	256	THR	C-N	-5.83	1.20	1.34

There are no bond angle outliers.

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	3084	0	3017	20	0
1	B	3098	0	3039	23	0
1	C	3060	0	3001	29	0
2	A	3	0	0	0	0
2	B	4	0	0	0	0
2	C	3	0	0	0	0
3	A	8	0	12	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	8	0	12	1	0
4	A	12	0	9	1	0
5	A	348	0	0	1	0
5	B	382	0	0	0	0
5	C	218	0	0	1	0
All	All	10228	0	9090	67	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 (67) 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:4:TYR:H	1:A:376:ASN:HD21	1.12	0.94
1:B:4:TYR:H	1:B:376:ASN:HD21	1.16	0.88
1:A:164:HIS:HD2	1:A:166:GLU:H	1.21	0.87
1:C:4:TYR:H	1:C:376:ASN:HD21	1.18	0.85
1:C:164:HIS:HD2	1:C:166:GLU:H	1.30	0.80
1:B:56:ASN:HD21	1:B:66:VAL:H	1.30	0.77
1:A:56:ASN:HD21	1:A:66:VAL:H	1.33	0.77
1:A:45:GLN:H	1:A:303:GLN:HE21	1.37	0.73
1:B:164:HIS:HD2	1:B:166:GLU:H	1.37	0.73
1:A:36:HIS:HE1	5:A:939:HOH:O	1.72	0.71
1:B:45:GLN:H	1:B:303:GLN:HE21	1.39	0.68
1:A:36:HIS:HD2	1:A:331:ASP:OD2	1.78	0.66
1:B:227:GLU:HG3	1:B:379:VAL:HB	1.76	0.66
1:C:45:GLN:H	1:C:303:GLN:HE21	1.47	0.62
1:B:164:HIS:HE1	1:B:201:GLY:O	1.83	0.62
1:B:213:HIS:HD2	1:C:234:ASP:OD1	1.83	0.61
1:B:234:ASP:OD1	1:C:213:HIS:HD2	1.84	0.59
1:B:56:ASN:ND2	1:B:66:VAL:H	1.99	0.59
1:C:186:ASP:OD1	1:C:188:LYS:HB2	2.03	0.58
1:A:164:HIS:HE1	1:A:201:GLY:O	1.87	0.58
1:C:14:SER:HB2	1:C:330:ASN:HB2	1.86	0.57
1:C:164:HIS:HE1	1:C:201:GLY:O	1.86	0.57
1:A:193:ARG:HD3	1:A:214:ASP:OD2	2.06	0.56
1:C:101:PHE:HE2	1:C:217:LEU:HD23	1.72	0.54
1:A:354:LYS:NZ	4:A:399:ACT:O	2.36	0.53
1:C:56:ASN:HD21	1:C:66:VAL:HG22	1.73	0.53
1:A:212:ARG:HD3	1:A:214:ASP:OD1	2.09	0.53
1:B:232:ASP:OD1	1:C:213:HIS:HE1	1.92	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:14:SER:HB2	1:A:330:ASN:HB2	1.90	0.52
1:A:56:ASN:ND2	1:A:66:VAL:H	2.03	0.52
1:B:273:ASP:OD2	1:C:165:GLU:OE2	2.29	0.51
1:B:143:GLN:HG2	1:B:148:SER:O	2.11	0.50
1:B:45:GLN:H	1:B:303:GLN:NE2	2.09	0.50
1:C:186:ASP:OD1	1:C:188:LYS:N	2.33	0.50
1:B:222[B]:ARG:NH2	1:B:230:ASP:OD1	2.44	0.50
1:B:14:SER:HB2	1:B:330:ASN:HB2	1.92	0.49
1:A:333:ILE:HG22	1:A:333:ILE:O	2.11	0.49
1:A:36:HIS:CD2	1:A:331:ASP:OD2	2.63	0.48
1:C:56:ASN:HD21	1:C:66:VAL:H	1.61	0.48
1:B:164:HIS:CD2	1:B:166:GLU:H	2.25	0.47
1:B:111:GLU:HB2	1:B:189:TYR:OH	2.14	0.46
1:C:101:PHE:CE2	1:C:217:LEU:HD23	2.50	0.46
1:A:256:THR:HG21	1:A:262:GLY:HA2	1.97	0.45
1:C:14:SER:HB2	1:C:330:ASN:CB	2.46	0.45
1:C:50:VAL:HG22	1:C:63:ILE:HG23	1.98	0.45
1:C:257:LYS:HG2	1:C:261:ASP:OD2	2.16	0.45
1:B:213:HIS:HE1	1:C:232:ASP:OD1	2.00	0.45
1:B:96:TYR:CZ	3:B:399:TRS:N	2.85	0.45
1:C:72:TYR:HB3	1:C:360:LEU:HD13	1.99	0.45
1:C:143:GLN:HG2	1:C:148:SER:O	2.18	0.44
1:B:133:THR:OG1	1:B:208:ARG:NH1	2.51	0.44
1:C:317:LYS:HE2	5:C:789:HOH:O	2.18	0.43
1:C:331:ASP:HB3	1:C:334:HIS:HB2	2.00	0.43
1:C:193:ARG:NH1	1:C:216:ALA:HB2	2.32	0.43
1:C:256:THR:HG21	1:C:262:GLY:HA2	2.00	0.43
1:B:227:GLU:CG	1:B:379:VAL:HB	2.46	0.43
1:B:256:THR:HG21	1:B:262:GLY:HA2	2.00	0.43
1:A:14:SER:HB2	1:A:330:ASN:CB	2.49	0.43
1:C:267:VAL:HA	1:C:270:LEU:HD12	2.02	0.42
1:C:4:TYR:N	1:C:376:ASN:HD21	2.00	0.42
1:B:14:SER:HB2	1:B:330:ASN:CB	2.50	0.42
1:A:45:GLN:H	1:A:303:GLN:NE2	2.09	0.41
1:C:132:GLY:O	1:C:136:LEU:HG	2.20	0.41
1:C:67:GLU:O	1:C:69:PRO:HD3	2.20	0.41
1:A:4:TYR:N	1:A:376:ASN:HD21	1.96	0.41
1:A:56:ASN:HB3	1:A:73:TYR:CE2	2.56	0.41
1:A:101:PHE:HE2	1:A:217:LEU:HD12	1.86	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	390/399 (98%)	377 (97%)	13 (3%)	0	100	100
1	B	391/399 (98%)	381 (97%)	10 (3%)	0	100	100
1	C	387/399 (97%)	376 (97%)	11 (3%)	0	100	100
All	All	1168/1197 (98%)	1134 (97%)	34 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	334/338 (99%)	329 (98%)	5 (2%)	65	53
1	B	335/338 (99%)	330 (98%)	5 (2%)	65	53
1	C	331/338 (98%)	322 (97%)	9 (3%)	44	29
All	All	1000/1014 (99%)	981 (98%)	19 (2%)	57	43

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	136	LEU
1	A	212	ARG
1	A	279	PHE
1	A	298	TYR
1	A	360	LEU

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Mol	Chain	Res	Type
1	B	58	ARG
1	B	110	LYS
1	B	279	PHE
1	B	298	TYR
1	B	391	GLU
1	C	61	LYS
1	C	65	LYS
1	C	110	LYS
1	C	185	LEU
1	C	188	LYS
1	C	189	TYR
1	C	217	LEU
1	C	298	TYR
1	C	316	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (39) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	36	HIS
1	A	48	ASN
1	A	56	ASN
1	A	77	GLN
1	A	89	HIS
1	A	164	HIS
1	A	205	ASN
1	A	211	ASN
1	A	259	ASN
1	A	281	ASN
1	A	303	GLN
1	A	358	GLN
1	A	376	ASN
1	A	390	ASN
1	B	25	GLN
1	B	45	GLN
1	B	56	ASN
1	B	77	GLN
1	B	89	HIS
1	B	102	GLN
1	B	164	HIS
1	B	205	ASN
1	B	211	ASN
1	B	213	HIS

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Mol	Chain	Res	Type
1	B	259	ASN
1	B	281	ASN
1	B	303	GLN
1	B	376	ASN
1	C	45	GLN
1	C	56	ASN
1	C	77	GLN
1	C	89	HIS
1	C	164	HIS
1	C	205	ASN
1	C	213	HIS
1	C	259	ASN
1	C	281	ASN
1	C	303	GLN
1	C	376	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](#)

3 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	TPO	A	85	1,2	8,10,11	0.89	0	10,14,16	1.01	0
1	TPO	B	85	1,2	8,10,11	0.94	0	10,14,16	0.93	0
1	TPO	C	85	1,2	8,10,11	0.85	0	10,14,16	0.94	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
1	TPO	A	85	1,2	-	2/9/11/13	-
1	TPO	B	85	1,2	-	2/9/11/13	-
1	TPO	C	85	1,2	-	3/9/11/13	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	85	TPO	O-C-CA-CB
1	B	85	TPO	O-C-CA-CB
1	A	85	TPO	C-CA-CB-CG2
1	B	85	TPO	C-CA-CB-CG2
1	C	85	TPO	C-CA-CB-CG2
1	C	85	TPO	CB-OG1-P-O1P
1	C	85	TPO	O-C-CA-CB

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 15 ligands modelled in this entry, 10 are monoatomic - leaving 5 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	$\# Z > 2$
4	ACT	A	401	-	1,3,3	1.50	0	0,3,3	0.00	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	ACT	A	399	-	1,3,3	1.39	0	0,3,3	0.00	-
3	TRS	B	399	-	7,7,7	0.41	0	9,9,9	0.32	0
3	TRS	A	398	-	7,7,7	0.32	0	9,9,9	0.26	0
4	ACT	A	400	-	1,3,3	1.34	0	0,3,3	0.00	-

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	TRS	B	399	-	-	1/9/9/9	-
3	TRS	A	398	-	-	0/9/9/9	-

There are no bond length outliers.

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	399	TRS	C3-C-C2-O2

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	399	ACT	1	0
3	B	399	TRS	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	390/399 (97%)	-0.44	1 (0%) 94 93	17, 25, 39, 51	16 (4%)
1	B	390/399 (97%)	-0.52	2 (0%) 91 91	17, 24, 38, 48	11 (2%)
1	C	389/399 (97%)	-0.15	7 (1%) 68 68	19, 36, 59, 71	23 (5%)
All	All	1169/1197 (97%)	-0.37	10 (0%) 84 84	17, 28, 50, 71	50 (4%)

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	189	TYR	3.9
1	B	2	ASN	3.5
1	C	133	THR	3.0
1	A	2	ASN	2.7
1	C	110	LYS	2.7
1	C	355	GLU	2.5
1	B	390	ASN	2.4
1	C	105	PRO	2.1
1	C	103	VAL	2.1
1	C	390	ASN	2.1

6.2 Non-standard residues in protein, DNA, RNA chains [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(Å ²)	Q<0.9
1	TPO	A	85	11/12	0.94	0.15	20,21,25,26	4
1	TPO	B	85	11/12	0.95	0.10	21,23,25,26	4
1	TPO	C	85	11/12	0.96	0.11	28,30,32,32	4

6.3 Carbohydrates [i](#)

There are no carbohydrates 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(Å ²)	Q<0.9
4	ACT	A	400	4/4	0.75	0.18	70,70,70,70	0
3	TRS	B	399	8/8	0.76	0.23	45,46,47,48	0
4	ACT	A	401	4/4	0.77	0.19	39,40,40,41	0
3	TRS	A	398	8/8	0.80	0.18	45,46,46,47	0
4	ACT	A	399	4/4	0.81	0.16	45,46,46,46	0
2	MN	B	397	1/1	0.97	0.04	53,53,53,53	1
2	MN	B	398	1/1	0.98	0.04	35,35,35,35	1
2	MN	C	397	1/1	0.98	0.03	46,46,46,46	0
2	MN	C	396	1/1	0.99	0.11	28,28,28,28	0
2	MN	C	395	1/1	0.99	0.08	32,32,32,32	0
2	MN	A	397	1/1	0.99	0.03	35,35,35,35	1
2	MN	A	396	1/1	1.00	0.12	20,20,20,20	0
2	MN	B	396	1/1	1.00	0.10	21,21,21,21	0
2	MN	B	395	1/1	1.00	0.09	22,22,22,22	0
2	MN	A	395	1/1	1.00	0.09	20,20,20,20	0

6.5 Other polymers [i](#)

There are no such residues in this entry.