



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 7B08 / pdb_00007b08
Title : TgoT apo
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Deposited on : 2020-11-18
Resolution : 2.39 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

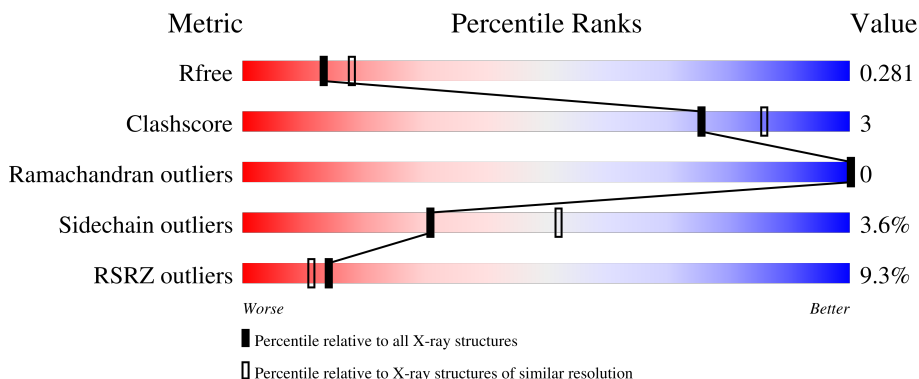
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.39 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	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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	773	9% 86% 9% ...

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 6174 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.

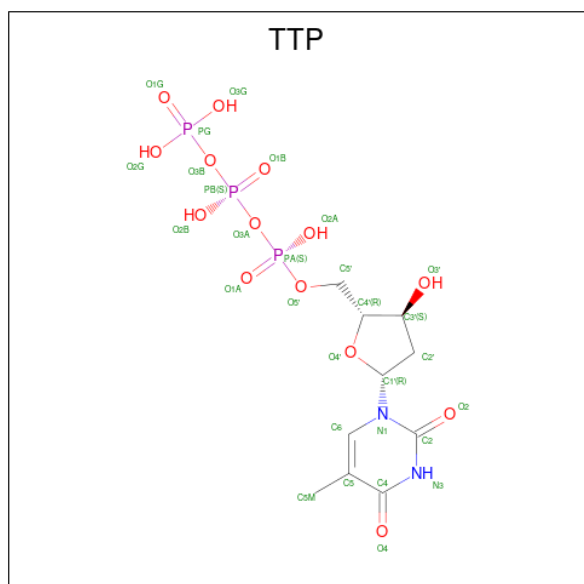
- Molecule 1 is a protein called DNA polymerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	742	6094	3935	1024	1122	13	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

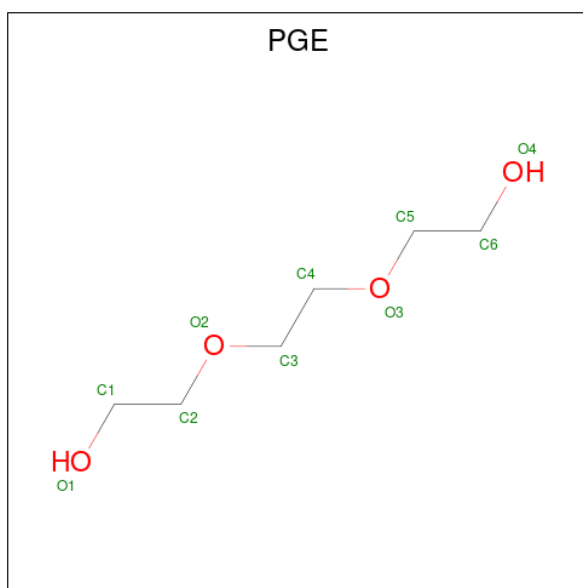
Chain	Residue	Modelled	Actual	Comment	Reference
A	93	GLN	VAL	conflict	UNP P56689
A	141	ALA	ASP	conflict	UNP P56689
A	143	ALA	GLU	conflict	UNP P56689
A	485	LEU	ALA	conflict	UNP P56689

- Molecule 2 is THYMIDINE-5'-TRIPHOSPHATE (CCD ID: TTP) (formula: $C_{10}H_{17}N_2O_{14}P_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	P	0	0
			13	10	3		

- Molecule 3 is TRIETHYLENE GLYCOL (CCD ID: PGE) (formula: $C_6H_{14}O_4$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			10	6	4		

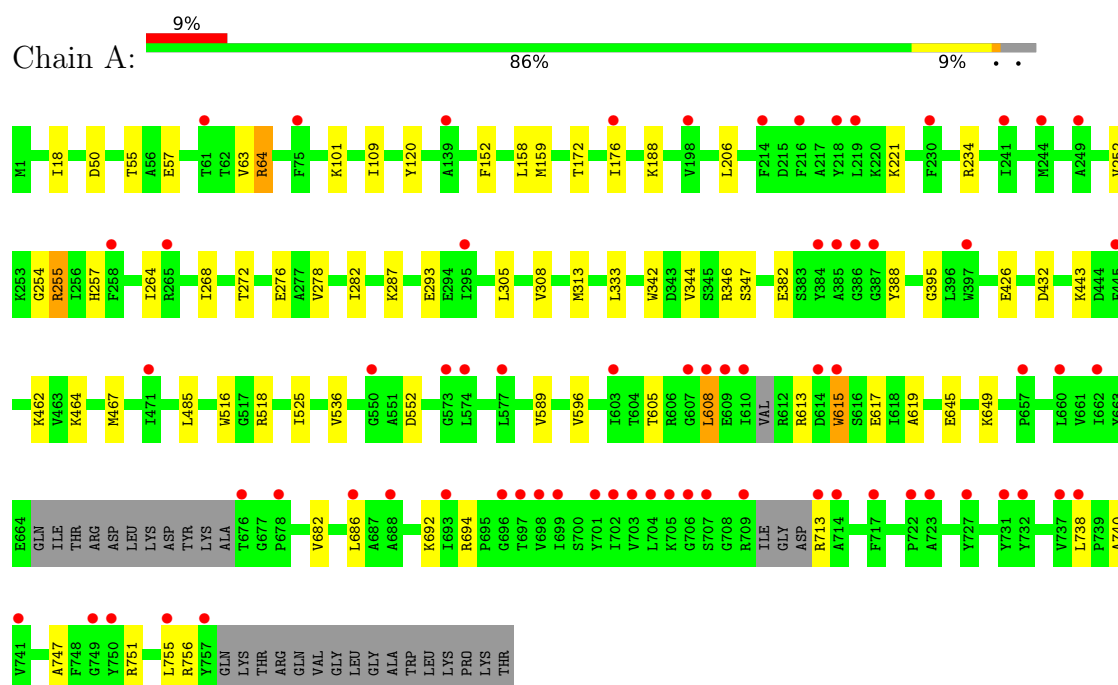
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	57	Total	O	0	0
			57	57		

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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.

• Molecule 1: DNA polymerase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	65.06Å 105.22Å 152.86Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.86 – 2.39 45.86 – 2.39	Depositor EDS
% Data completeness (in resolution range)	99.5 (45.86-2.39) 99.5 (45.86-2.39)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.25 (at 2.39Å)	Xtriage
Refinement program	BUSTER 2.10.3 (20-MAY-2020)	Depositor
R, R_{free}	0.241 , 0.261 0.262 , 0.281	Depositor DCC
R_{free} test set	2098 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	71.4	Xtriage
Anisotropy	0.384	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 49.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6174	wwPDB-VP
Average B, all atoms (Å ²)	100.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.71% 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: TTP, PGE

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	0.54	0/6229	0.90	3/8395 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	395	GLY	N-CA-C	6.13	119.54	111.70
1	A	596	VAL	N-CA-CB	-5.30	104.46	112.35
1	A	552	ASP	CA-CB-CG	5.22	117.82	112.60

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	6094	0	6127	37	0
2	A	13	0	0	0	0
3	A	10	0	14	2	0
4	A	57	0	0	0	0
All	All	6174	0	6141	37	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 (37) 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:605:THR:HB	1:A:608:LEU:HD21	1.63	0.78
1:A:188:LYS:NZ	3:A:802:PGE:H32	2.01	0.75
1:A:608:LEU:H	1:A:608:LEU:HD22	1.51	0.75
1:A:589:VAL:HG13	1:A:747:ALA:HB2	1.72	0.71
1:A:615:TRP:HD1	1:A:619:ALA:HB3	1.62	0.65
1:A:333:LEU:HD13	1:A:485:LEU:HD22	1.81	0.63
1:A:608:LEU:HD22	1:A:608:LEU:N	2.18	0.58
1:A:342:TRP:CD1	1:A:346:ARG:HH21	2.21	0.58
1:A:172:THR:HG21	1:A:176:ILE:HD12	1.87	0.57
1:A:738:LEU:HD11	1:A:756:ARG:HB3	1.87	0.55
1:A:305:LEU:HA	1:A:308:VAL:HG22	1.88	0.55
1:A:264:ILE:HD13	1:A:278:VAL:HG11	1.88	0.55
1:A:18:ILE:HD11	1:A:120:TYR:CE2	2.41	0.55
1:A:342:TRP:NE1	1:A:346:ARG:HH21	2.06	0.53
1:A:188:LYS:HZ2	3:A:802:PGE:H32	1.73	0.52
1:A:252:VAL:HG12	1:A:257:HIS:HB2	1.92	0.52
1:A:615:TRP:CD1	1:A:619:ALA:HB3	2.43	0.51
1:A:257:HIS:O	1:A:346:ARG:NH2	2.44	0.50
1:A:293:GLU:HG2	1:A:692:LYS:HE3	1.93	0.50
1:A:268:ILE:HD13	1:A:282:ILE:HD11	1.95	0.48
1:A:276:GLU:HG3	1:A:287:LYS:HG2	1.94	0.48
1:A:525:ILE:HG23	1:A:536:VAL:HG21	1.95	0.48
1:A:252:VAL:HG22	1:A:255:ARG:HG3	1.96	0.47
1:A:159:MET:HE1	1:A:308:VAL:HG23	1.97	0.46
1:A:615:TRP:CD1	1:A:619:ALA:CB	2.99	0.45
1:A:55:THR:HG22	1:A:64:ARG:HB3	1.99	0.44
1:A:432:ASP:CG	1:A:443:LYS:HD2	2.40	0.44
1:A:234:ARG:HB2	1:A:254:GLY:HA3	2.00	0.44
1:A:152:PHE:HD2	1:A:221:LYS:HD2	1.82	0.44
1:A:101:LYS:HE3	1:A:109:ILE:HG12	1.99	0.44
1:A:615:TRP:HE1	1:A:740:ALA:HB2	1.83	0.43
1:A:645:GLU:O	1:A:649:LYS:HG2	2.19	0.42
1:A:206:LEU:HD12	1:A:252:VAL:HG11	2.03	0.41
1:A:464:LYS:HA	1:A:467:MET:HE3	2.02	0.41
1:A:462:LYS:HE2	1:A:462:LYS:HB3	1.86	0.41
1:A:388:TYR:HB2	1:A:518:ARG:HG2	2.03	0.41
1:A:159:MET:HG2	1:A:172:THR:HB	2.03	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	733/773 (95%)	715 (98%)	18 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	642/669 (96%)	619 (96%)	23 (4%)	31	52

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	50	ASP
1	A	57	GLU
1	A	63	VAL
1	A	64	ARG
1	A	158	LEU
1	A	255	ARG
1	A	272	THR
1	A	313	MET
1	A	344	VAL
1	A	347	SER
1	A	382	GLU
1	A	426	GLU
1	A	516	TRP

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Mol	Chain	Res	Type
1	A	608	LEU
1	A	613	ARG
1	A	615	TRP
1	A	617	GLU
1	A	682	VAL
1	A	686	LEU
1	A	694	ARG
1	A	713	ARG
1	A	751	ARG
1	A	755	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	23	ASN
1	A	351	ASN
1	A	491	ASN
1	A	519	GLN

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](#)

2 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	TTP	A	801	-	10,12,30	0.69	0	17,20,47	0.84	0
3	PGE	A	802	-	9,9,9	0.10	0	8,8,8	0.05	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	TTP	A	801	-	-	0/12/12/34	-
3	PGE	A	802	-	-	1/7/7/7	-

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	A	802	PGE	C1-C2-O2-C3

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	802	PGE	2	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	756:ARG	C	757:TYR	N	3.82

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	742/773 (95%)	0.82	69 (9%) 14 11	63, 96, 144, 188	0

All (69) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	757	TYR	8.1
1	A	697	THR	6.0
1	A	615	TRP	5.4
1	A	610	ILE	5.0
1	A	703	VAL	5.0
1	A	608	LEU	4.4
1	A	698	VAL	4.2
1	A	603	ILE	4.0
1	A	387	GLY	4.0
1	A	386	GLY	3.9
1	A	738	LEU	3.8
1	A	702	ILE	3.7
1	A	614	ASP	3.6
1	A	713	ARG	3.6
1	A	699	ILE	3.5
1	A	676	THR	3.5
1	A	295	ILE	3.4
1	A	732	TYR	3.3
1	A	609	GLU	3.3
1	A	717	PHE	3.1
1	A	696	GLY	3.1
1	A	741	VAL	3.0
1	A	258	PHE	3.0
1	A	573	GLY	3.0
1	A	722	PRO	2.9
1	A	714	ALA	2.8
1	A	693	ILE	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	750	TYR	2.8
1	A	704	LEU	2.8
1	A	230	PHE	2.7
1	A	385	ALA	2.7
1	A	737	VAL	2.7
1	A	214	PHE	2.6
1	A	176	ILE	2.6
1	A	139	ALA	2.6
1	A	384	TYR	2.6
1	A	678	PRO	2.5
1	A	241	ILE	2.5
1	A	731	TYR	2.5
1	A	471	ILE	2.5
1	A	249	ALA	2.5
1	A	749	GLY	2.5
1	A	219	LEU	2.4
1	A	686	LEU	2.4
1	A	218	TYR	2.4
1	A	550	GLY	2.4
1	A	701	TYR	2.3
1	A	705	LYS	2.3
1	A	198	VAL	2.3
1	A	75	PHE	2.3
1	A	755	LEU	2.3
1	A	607	GLY	2.3
1	A	660	LEU	2.3
1	A	244	MET	2.3
1	A	688	ALA	2.2
1	A	709	ARG	2.2
1	A	445	PHE	2.2
1	A	574	LEU	2.1
1	A	662	ILE	2.1
1	A	216	PHE	2.1
1	A	397	TRP	2.1
1	A	707	SER	2.1
1	A	61	THR	2.1
1	A	723	ALA	2.0
1	A	577	LEU	2.0
1	A	727	TYR	2.0
1	A	265	ARG	2.0
1	A	706	GLY	2.0
1	A	657	PRO	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
3	PGE	A	802	10/10	0.61	0.26	134,134,135,135	0
2	TTP	A	801	13/29	0.75	0.11	172,172,173,173	0

6.5 Other polymers [i](#)

There are no such residues in this entry.