



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 10:34 PM UTC

PDB ID : 6N0R / pdb_00006n0r
Title : Crystal structure of Tdp1 catalytic domain in complex with compound XZ572
Authors : Lountos, G.T.; Zhao, X.Z.; Kiselev, E.; Tropea, J.E.; Needle, D.; Burke Jr., T.R.; Pommier, Y.; Waugh, D.S.
Deposited on : 2018-11-07
Resolution : 1.54 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

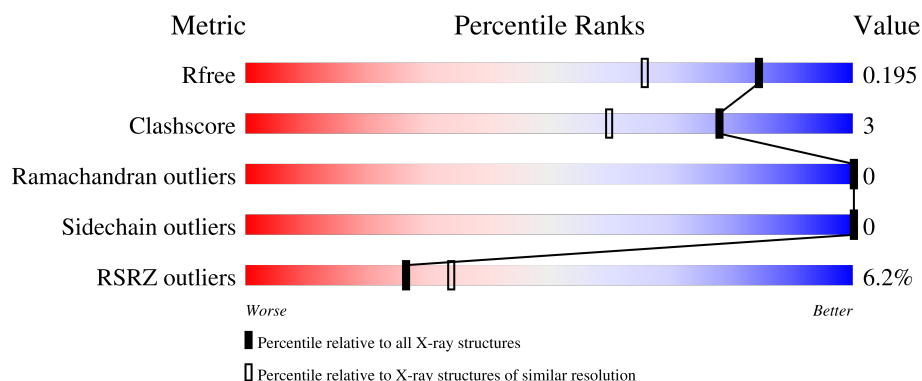
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.54 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	1003 (1.54-1.54)
Clashscore	190562	1025 (1.54-1.54)
Ramachandran outliers	187476	1007 (1.54-1.54)
Sidechain outliers	187428	1007 (1.54-1.54)
RSRZ outliers	180081	1002 (1.54-1.54)

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	461	5% 88% 7% 5%
1	B	461	7% 89% 6% 5%

2 Entry composition [i](#)

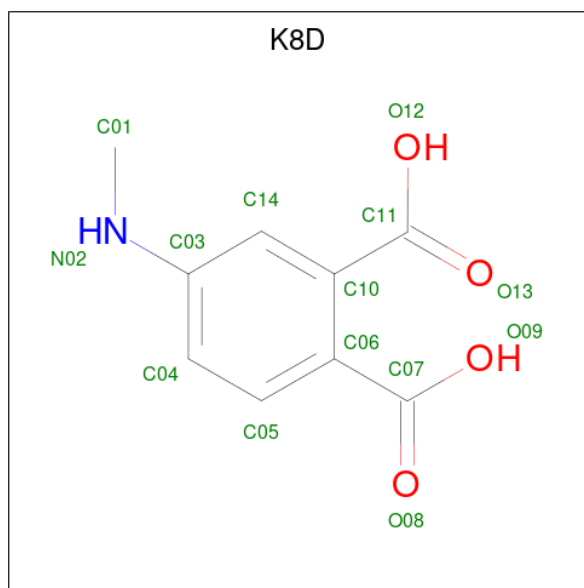
There are 5 unique types of molecules in this entry. The entry contains 8020 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Tyrosyl-DNA phosphodiesterase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	438	Total	C	N	O	S	0	17	0
			3624	2344	611	655	14			
1	B	438	Total	C	N	O	S	0	16	0
			3618	2342	610	651	15			

- Molecule 2 is 4-(methylamino)benzene-1,2-dicarboxylic acid (CCD ID: K8D) (formula: $C_9H_9NO_4$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	9	1	4		
2	B	1	Total	C	N	O	0	0
			14	9	1	4		

- Molecule 3 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



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	A	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 4 is DIMETHYL SULFOXIDE (CCD ID: DMS) (formula: C_2H_6OS).



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

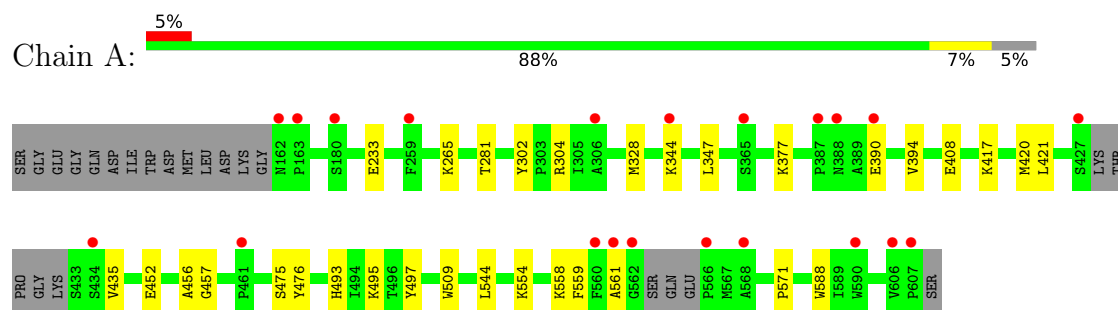
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	389	Total	O	0	0
			389	389		
5	B	341	Total	O	0	0
			341	341		

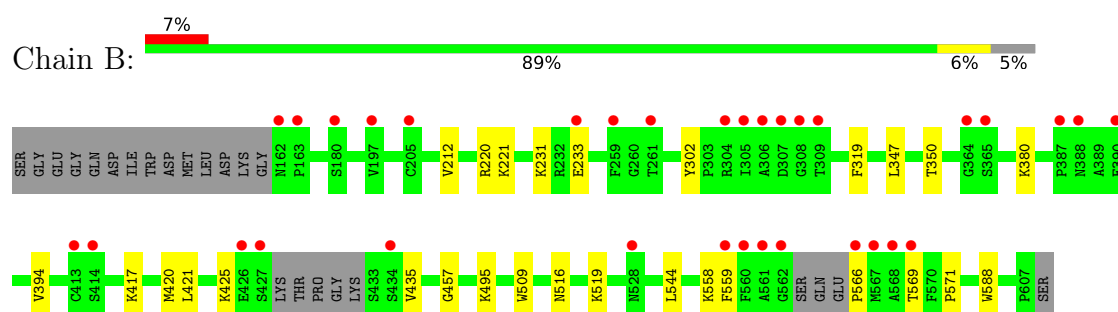
3 Residue-property plots [i](#)

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: Tyrosyl-DNA phosphodiesterase 1



• Molecule 1: Tyrosyl-DNA phosphodiesterase 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	50.04Å 105.40Å 193.59Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	37.02 – 1.54 37.02 – 1.54	Depositor EDS
% Data completeness (in resolution range)	99.3 (37.02-1.54) 99.3 (37.02-1.54)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.20 (at 1.55Å)	Xtriage
Refinement program	PHENIX (1.14_3260: ???)	Depositor
R, R_{free}	0.170 , 0.195 0.170 , 0.195	Depositor DCC
R_{free} test set	2000 reflections (1.32%)	wwPDB-VP
Wilson B-factor (Å ²)	19.8	Xtriage
Anisotropy	0.368	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 47.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	8020	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.72% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: K8D, DMS, 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	0.27	0/3741	0.50	0/5083
1	B	0.25	0/3735	0.47	0/5074
All	All	0.26	0/7476	0.49	0/10157

There are no bond length outliers.

There are no bond angle outliers.

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	3624	0	3534	21	0
1	B	3618	0	3535	19	0
2	A	14	0	0	0	0
2	B	14	0	0	0	0
3	A	12	0	18	0	0
3	B	4	0	6	0	0
4	A	4	0	6	0	0
5	A	389	0	0	5	0
5	B	341	0	0	3	0
All	All	8020	0	7099	40	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 (40) 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:394:VAL:CG1	1:B:420:MET:HE3	2.01	0.91
1:A:328[B]:MET:SD	5:A:1101:HOH:O	2.34	0.85
1:B:394:VAL:HG11	1:B:420:MET:HE3	1.64	0.78
1:A:420:MET:HE1	1:A:497:TYR:HB3	1.72	0.70
1:A:394:VAL:HG13	1:A:420:MET:HE3	1.75	0.68
1:B:417:LYS:O	1:B:421[A]:LEU:HG	2.01	0.60
1:A:421[A]:LEU:HD22	1:A:435:VAL:HG11	1.87	0.56
1:A:377:LYS:NZ	5:A:804:HOH:O	2.32	0.54
1:B:421[A]:LEU:HD22	1:B:435:VAL:HG11	1.88	0.54
1:B:519:LYS:NZ	5:B:807:HOH:O	2.40	0.54
1:A:417:LYS:O	1:A:421[A]:LEU:HG	2.08	0.54
1:A:452:GLU:HB2	1:A:456:ALA:HB2	1.91	0.51
1:B:231:LYS:NZ	5:B:808:HOH:O	2.43	0.51
1:B:558:LYS:NZ	5:B:801:HOH:O	2.26	0.50
1:A:408:GLU:OE2	1:A:476:TYR:OH	2.26	0.48
1:B:566:PRO:O	1:B:569:THR:HG23	2.13	0.48
1:A:475[B]:SER:OG	5:A:801:HOH:O	2.20	0.48
1:B:495:LYS:HE3	1:B:516:ASN:OD1	2.14	0.47
1:B:509:TRP:HB3	1:B:544:LEU:HD23	1.97	0.47
1:A:233:GLU:H	1:A:233:GLU:CD	2.23	0.46
1:A:304:ARG:NE	1:A:344:LYS:HD2	2.30	0.46
1:A:390:GLU:OE1	5:A:802:HOH:O	2.20	0.46
1:A:265:LYS:HD3	1:A:281:THR:C	2.41	0.45
1:A:493:HIS:O	1:A:495:LYS:NZ	2.41	0.45
1:A:457:GLY:HA3	1:A:588:TRP:CZ2	2.51	0.44
1:A:554:LYS:NZ	5:A:814:HOH:O	2.50	0.44
1:B:319:PHE:CG	1:B:350:THR:HG21	2.53	0.44
1:B:233:GLU:H	1:B:233:GLU:CD	2.26	0.43
1:B:302:TYR:CD1	1:B:347:LEU:HA	2.53	0.43
1:A:559:PHE:CE1	1:A:571:PRO:HB2	2.53	0.43
1:A:509:TRP:HB3	1:A:544:LEU:HD23	2.00	0.43
1:B:394:VAL:HG13	1:B:420:MET:HE3	1.91	0.42
1:B:380:LYS:HG2	1:B:425:LYS:HG2	2.01	0.42
1:A:302:TYR:CD1	1:A:347:LEU:HA	2.55	0.42
1:B:457:GLY:HA3	1:B:588:TRP:CZ2	2.55	0.41
1:B:559:PHE:CE1	1:B:571:PRO:HB2	2.55	0.41
1:B:212:VAL:HG13	1:B:220:ARG:HG2	2.02	0.41
1:A:558:LYS:HB2	1:A:561:ALA:HB2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:417:LYS:HG2	1:A:421[A]:LEU:HD21	2.02	0.41
1:B:221:LYS:HD2	1:B:221:LYS:HA	1.78	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	449/461 (97%)	443 (99%)	6 (1%)	0	100	100
1	B	448/461 (97%)	441 (98%)	7 (2%)	0	100	100
All	All	897/922 (97%)	884 (99%)	13 (1%)	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	396/400 (99%)	396 (100%)	0	100	100
1	B	395/400 (99%)	395 (100%)	0	100	100
All	All	791/800 (99%)	791 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

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	214	GLN
1	A	471	ASN
1	B	363	GLN
1	B	471	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

7 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	$\# Z > 2$
3	EDO	B	702	-	3,3,3	0.45	0	2,2,2	0.31	0
2	K8D	B	701	-	14,14,14	1.56	1 (7%)	18,19,19	0.86	0
3	EDO	A	703	-	3,3,3	0.50	0	2,2,2	0.34	0
3	EDO	A	704	-	3,3,3	0.41	0	2,2,2	0.48	0
3	EDO	A	702	-	3,3,3	0.38	0	2,2,2	0.46	0
4	DMS	A	705	-	3,3,3	0.64	0	3,3,3	0.72	0
2	K8D	A	701	-	14,14,14	1.53	1 (7%)	18,19,19	1.15	2 (11%)

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	B	702	-	-	0/1/1/1	-
2	K8D	B	701	-	-	4/10/10/10	0/1/1/1
3	EDO	A	703	-	-	0/1/1/1	-
3	EDO	A	704	-	-	0/1/1/1	-
3	EDO	A	702	-	-	1/1/1/1	-
2	K8D	A	701	-	-	4/10/10/10	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	701	K8D	C03-N02	4.27	1.46	1.37
2	B	701	K8D	C03-N02	4.16	1.45	1.37

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	701	K8D	O09-C07-C06	2.28	121.75	115.28
2	A	701	K8D	O12-C11-C10	2.16	121.43	115.28

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	701	K8D	C04-C03-N02-C01
2	A	701	K8D	C14-C03-N02-C01
3	A	702	EDO	O1-C1-C2-O2
2	A	701	K8D	C05-C06-C07-O09
2	B	701	K8D	C14-C10-C11-O12
2	A	701	K8D	C05-C06-C07-O08
2	B	701	K8D	C14-C10-C11-O13
2	B	701	K8D	C05-C06-C07-O09
2	B	701	K8D	C05-C06-C07-O08

There are no ring outliers.

No monomer is involved in short contacts.

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

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	438/461 (95%)	0.17	21 (4%) 35 44	8, 22, 44, 76	17 (3%)
1	B	438/461 (95%)	0.36	33 (7%) 20 25	9, 25, 53, 82	16 (3%)
All	All	876/922 (95%)	0.27	54 (6%) 26 34	8, 23, 50, 82	33 (3%)

All (54) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	306	ALA	7.7
1	B	568	ALA	6.6
1	B	566	PRO	6.5
1	A	344	LYS	6.2
1	A	566	PRO	5.1
1	B	163	PRO	4.7
1	A	163	PRO	4.6
1	A	162	ASN	4.5
1	A	568	ALA	4.1
1	B	567	MET	4.0
1	B	162	ASN	3.9
1	B	309	THR	3.8
1	B	560	PHE	3.8
1	A	606	VAL	3.5
1	A	365	SER	3.4
1	B	562	GLY	3.3
1	B	205[A]	CYS	3.3
1	B	414	SER	3.3
1	B	365	SER	3.2
1	A	561	ALA	3.2
1	A	427	SER	3.1
1	B	364	GLY	3.1
1	B	304	ARG	3.1
1	B	308	GLY	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	197	VAL	3.0
1	A	590	TRP	3.0
1	B	413	CYS	3.0
1	A	434	SER	2.9
1	A	306	ALA	2.9
1	B	427	SER	2.9
1	B	307	ASP	2.8
1	A	387	PRO	2.8
1	A	562	GLY	2.8
1	B	559	PHE	2.8
1	B	390	GLU	2.7
1	A	388	ASN	2.6
1	B	434	SER	2.6
1	A	461	PRO	2.6
1	A	180	SER	2.6
1	B	561	ALA	2.5
1	A	607	PRO	2.4
1	B	528	ASN	2.4
1	A	560	PHE	2.4
1	B	233	GLU	2.4
1	B	261[A]	THR	2.3
1	A	390	GLU	2.3
1	B	305	ILE	2.3
1	B	387	PRO	2.3
1	B	426	GLU	2.2
1	B	388	ASN	2.2
1	B	569	THR	2.1
1	A	259	PHE	2.1
1	B	180	SER	2.1
1	B	259	PHE	2.0

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

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

6.3 Carbohydrates ⓘ

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(Å ²)	Q<0.9
4	DMS	A	705	4/4	0.82	0.23	53,55,68,69	0
3	EDO	A	702	4/4	0.84	0.14	21,32,36,43	0
3	EDO	A	704	4/4	0.89	0.14	27,35,42,46	0
2	K8D	A	701	14/14	0.90	0.12	24,32,55,61	0
2	K8D	B	701	14/14	0.93	0.10	23,30,48,56	0
3	EDO	A	703	4/4	0.96	0.08	18,19,20,23	0
3	EDO	B	702	4/4	0.97	0.06	22,22,22,27	0

6.5 Other polymers [i](#)

There are no such residues in this entry.