Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 01:47 PM UTC

PDB ID	:	2R3S / pdb_00002r3s
Title	:	CRYSTAL STRUCTURE OF A PUTATIVE O-METHYLTRANSFERASE (NPUN_R0239) FROM NOSTOC PUNCTIFORME PCC 73102 AT 2.15 A RESOLUTION
Authors	:	Joint Center for Structural Genomics (JCSG)
Deposited on	:	2007-08-29
Resolution	:	2.15 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:

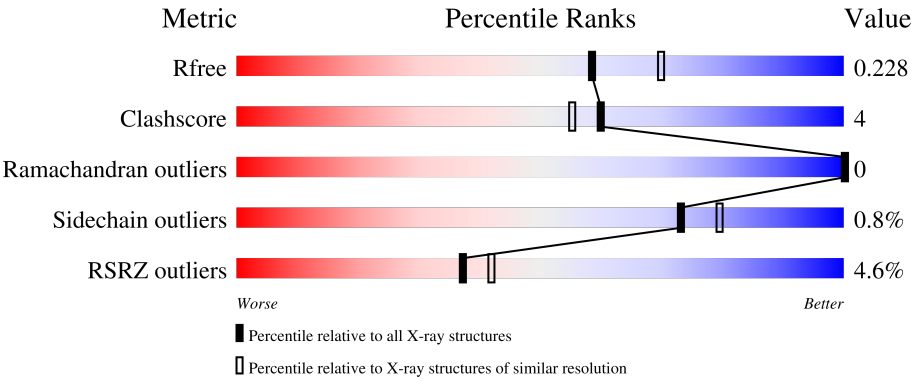
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry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

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.15 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	2057 (2.16-2.16)
Clashscore	190562	2159 (2.16-2.16)
Ramachandran outliers	187476	2134 (2.16-2.16)
Sidechain outliers	187428	2133 (2.16-2.16)
RSRZ outliers	180081	2059 (2.16-2.16)

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 <=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	335	3% 88% 10%
1	B	335	6% 84% 13%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5411 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.

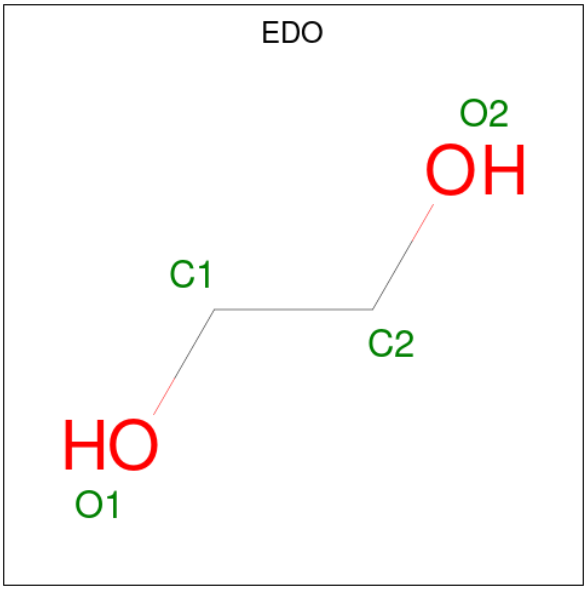
- Molecule 1 is a protein called uncharacterized protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	330	Total	C	N	O	S	Se	0	9	0
			2561	1642	419	485	3	12			
1	B	325	Total	C	N	O	S	Se	0	6	0
			2500	1606	413	466	3	12			

- Molecule 2 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

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

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

- Molecule 4 is water.

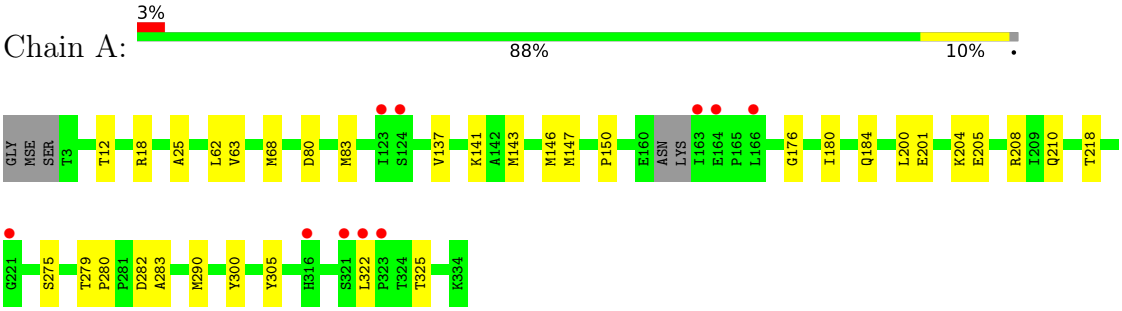
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	163	Total O 163 163	0	0
4	B	145	Total O 145 145	0	0

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.

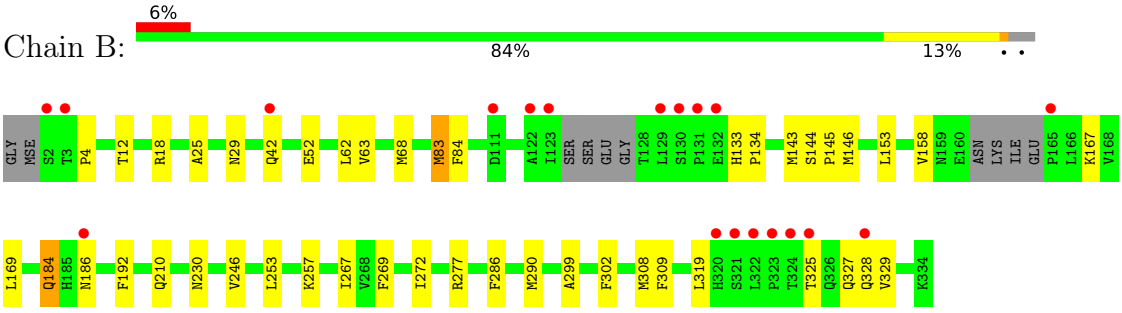
• Molecule 1: uncharacterized protein

Chain A:



• Molecule 1: uncharacterized protein

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α, β, γ	93.90Å 93.90Å 180.52Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.70 – 2.15 29.70 – 2.15	Depositor EDS
% Data completeness (in resolution range)	99.8 (29.70-2.15) 99.8 (29.70-2.15)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.68 (at 2.16Å)	Xtriage
Refinement program	REFMAC 5.2.0019, PHENIX	Depositor
R, R_{free}	0.188 , 0.228 0.191 , 0.228	Depositor DCC
R_{free} test set	2245 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å^2)	34.2	Xtriage
Anisotropy	0.356	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 43.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	5411	wwPDB-VP
Average B, all atoms (Å^2)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.53% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: EDO, CL

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	0.82	0/2633	0.87	0/3559
1	B	0.83	0/2561	0.86	1/3460 (0.0%)
All	All	0.83	0/5194	0.86	1/7019 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	329	VAL	N-CA-C	5.39	115.89	108.12

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	2561	0	2525	22	0
1	B	2500	0	2464	27	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	24	0	36	0	0
3	B	16	0	24	0	0
4	A	163	0	0	2	0
4	B	145	0	0	1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	5411	0	5049	44	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 (44) 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:246:VAL:HG12	1:B:308:MSE:HE2	1.69	0.74
1:B:272:ILE:HD12	1:B:328:GLN:HB2	1.79	0.64
1:A:184[B]:GLN:NE2	1:A:210:GLN:OE1	2.32	0.60
1:A:200:LEU:HD13	1:A:218:THR:HB	1.84	0.59
1:B:143:MSE:SE	1:B:146[A]:MSE:HE1	2.54	0.58
1:A:83[A]:MSE:SE	1:B:4:PRO:HG2	2.53	0.58
1:B:286:PHE:CZ	1:B:290:MSE:HE3	2.39	0.58
1:A:205:GLU:OE2	1:A:208:ARG:NH2	2.38	0.57
1:B:158:VAL:HG12	1:B:267:ILE:HD11	1.88	0.56
1:B:153:LEU:HD12	1:B:325:THR:CG2	2.36	0.55
1:A:83[A]:MSE:SE	1:B:4:PRO:CG	3.05	0.55
1:A:325:THR:O	4:A:486:HOH:O	2.18	0.54
1:A:322:LEU:HB3	1:A:325:THR:HG22	1.90	0.53
1:A:143:MSE:SE	1:A:146:MSE:HE1	2.60	0.51
1:B:257:LYS:NZ	4:B:440:HOH:O	2.28	0.49
1:A:80:ASP:OD1	1:B:4:PRO:HA	2.13	0.49
1:B:302:PHE:CD1	1:B:319:LEU:HD13	2.48	0.48
1:B:83:MSE:HG2	1:B:84:PHE:CE2	2.48	0.48
1:B:253:LEU:HD22	1:B:309:PHE:CE1	2.48	0.48
1:A:18:ARG:HB3	1:B:12:THR:HG23	1.96	0.48
1:B:167:LYS:NZ	1:B:230:ASN:O	2.39	0.47
1:B:63:VAL:HG22	1:B:68:MSE:HG3	1.97	0.47
1:B:169:LEU:HD12	1:B:192:PHE:O	2.15	0.46
1:A:275:SER:HB3	4:A:487:HOH:O	2.16	0.46
1:B:158:VAL:CG1	1:B:267:ILE:HD11	2.46	0.46
1:B:184:GLN:NE2	1:B:210:GLN:OE1	2.49	0.45
1:A:12:THR:HG23	1:B:18:ARG:HB3	1.98	0.45
1:B:158:VAL:CG1	1:B:267:ILE:CD1	2.95	0.45
1:A:290:MSE:HA	1:A:290:MSE:HE2	1.99	0.44
1:A:176:GLY:C	1:A:180:ILE:HD12	2.43	0.44
1:B:25:ALA:HB2	1:B:62:LEU:HD11	2.00	0.43
1:A:63:VAL:HG22	1:A:68:MSE:HG3	2.01	0.43
1:A:279:THR:HA	1:A:280:PRO:C	2.43	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:144:SER:N	1:B:145:PRO:CD	2.82	0.43
1:A:137:VAL:HG12	1:A:141:LYS:HE2	2.01	0.43
1:A:147:MSE:C	1:A:150:PRO:HD2	2.43	0.42
1:A:25:ALA:HB2	1:A:62:LEU:HD11	2.01	0.42
1:B:133:HIS:ND1	1:B:134:PRO:HD2	2.35	0.42
1:A:300:TYR:HB2	1:A:305:TYR:CZ	2.55	0.41
1:A:201[A]:GLU:OE2	1:A:204:LYS:NZ	2.54	0.41
1:B:42[A]:GLN:NE2	1:B:52:GLU:HG3	2.34	0.41
1:B:269:PHE:CZ	1:B:327:GLN:HB2	2.56	0.41
1:A:282[A]:ASP:OD1	1:A:283:ALA:N	2.51	0.41
1:B:277[B]:ARG:NH2	1:B:299:ALA:O	2.53	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	335/335 (100%)	325 (97%)	10 (3%)	0	100	100
1	B	325/335 (97%)	317 (98%)	8 (2%)	0	100	100
All	All	660/670 (98%)	642 (97%)	18 (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	273/265 (103%)	273 (100%)	0	100	100
1	B	264/265 (100%)	260 (98%)	4 (2%)	57	64
All	All	537/530 (101%)	533 (99%)	4 (1%)	73	82

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	29	ASN
1	B	83	MSE
1	B	184	GLN
1	B	186	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	210	GLN
1	B	327	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)

Of 12 ligands modelled in this entry, 2 are monoatomic - leaving 10 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	$\#\|Z\| > 2$
3	EDO	A	341	-	3,3,3	0.48	0	2,2,2	0.18	0
3	EDO	B	339	-	3,3,3	0.25	0	2,2,2	0.72	0
3	EDO	B	336	-	3,3,3	0.70	0	2,2,2	0.26	0
3	EDO	A	340	-	3,3,3	0.66	0	2,2,2	0.20	0
3	EDO	A	337	-	3,3,3	0.84	0	2,2,2	0.59	0
3	EDO	A	338	-	3,3,3	0.51	0	2,2,2	0.13	0
3	EDO	B	337	-	3,3,3	0.62	0	2,2,2	0.06	0
3	EDO	A	336	-	3,3,3	0.48	0	2,2,2	0.23	0
3	EDO	B	338	-	3,3,3	0.37	0	2,2,2	0.44	0
3	EDO	A	339	-	3,3,3	0.44	0	2,2,2	0.47	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	341	-	-	1/1/1/1	-
3	EDO	B	339	-	-	0/1/1/1	-
3	EDO	B	336	-	-	1/1/1/1	-
3	EDO	A	340	-	-	1/1/1/1	-
3	EDO	A	337	-	-	1/1/1/1	-
3	EDO	A	338	-	-	1/1/1/1	-
3	EDO	B	337	-	-	1/1/1/1	-
3	EDO	A	336	-	-	0/1/1/1	-
3	EDO	B	338	-	-	1/1/1/1	-
3	EDO	A	339	-	-	0/1/1/1	-

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
3	A	338	EDO	O1-C1-C2-O2
3	A	341	EDO	O1-C1-C2-O2
3	A	340	EDO	O1-C1-C2-O2
3	B	336	EDO	O1-C1-C2-O2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
3	B	337	EDO	O1-C1-C2-O2
3	B	338	EDO	O1-C1-C2-O2
3	A	337	EDO	O1-C1-C2-O2

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, 95^{th} 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	320/335 (95%)	0.28	10 (3%)	51	55	18, 34, 59, 86	7 (2%)
1	B	315/335 (94%)	0.35	19 (6%)	27	31	16, 36, 57, 83	4 (1%)
All	All	635/670 (94%)	0.32	29 (4%)	37	42	16, 35, 57, 86	11 (1%)

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	324	THR	4.7
1	B	131	PRO	4.4
1	B	321	SER	4.3
1	B	2	SER	4.0
1	A	163	ILE	3.7
1	B	322	LEU	3.4
1	B	122	ALA	3.1
1	B	320	HIS	2.9
1	A	166	LEU	2.9
1	B	130	SER	2.8
1	B	165	PRO	2.8
1	B	111	ASP	2.7
1	A	321	SER	2.7
1	B	186	ASN	2.6
1	B	123	ILE	2.6
1	B	323	PRO	2.6
1	A	316	HIS	2.5
1	A	123	ILE	2.5
1	B	129	LEU	2.4
1	A	164	GLU	2.3
1	A	323	PRO	2.3
1	B	325	THR	2.3
1	B	42[A]	GLN	2.2
1	A	124	SER	2.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	221	GLY	2.1
1	A	322	LEU	2.1
1	B	328	GLN	2.1
1	B	3	THR	2.1
1	B	132	GLU	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, 95^{th} 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
3	EDO	B	337	4/4	0.75	0.16	59,62,66,69	0
3	EDO	B	338	4/4	0.76	0.23	55,59,62,63	0
3	EDO	B	336	4/4	0.79	0.19	49,49,49,55	0
3	EDO	A	339	4/4	0.80	0.25	43,57,57,60	0
3	EDO	A	338	4/4	0.81	0.17	48,50,53,53	0
3	EDO	A	341	4/4	0.84	0.14	47,48,54,55	0
3	EDO	A	337	4/4	0.86	0.15	26,41,44,44	0
3	EDO	A	340	4/4	0.87	0.15	39,55,58,59	0
3	EDO	A	336	4/4	0.90	0.10	34,34,36,40	0
3	EDO	B	339	4/4	0.95	0.09	43,49,50,54	0
2	CL	A	335	1/1	0.99	0.04	35,35,35,35	0
2	CL	B	335	1/1	0.99	0.08	45,45,45,45	0

6.5 Other polymers (i)

There are no such residues in this entry.