



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:03 PM GMT

PDB ID : 4NME
Title : Crystal structure of proline utilization A (PutA) from *Geobacter sulfurreducens* PCA inactivated by N-propargylglycine
Authors : Singh, H.; Tanner, J.J.
Deposited on : 2013-11-14
Resolution : 2.09 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
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

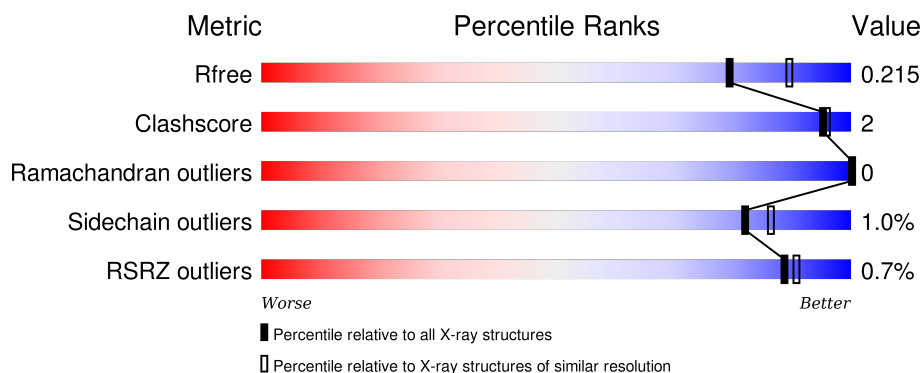
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.09 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}	91344	4546 (2.10-2.06)
Clashscore	102246	5101 (2.10-2.06)
Ramachandran outliers	100387	5048 (2.10-2.06)
Sidechain outliers	100360	5049 (2.10-2.06)
RSRZ outliers	91569	4556 (2.10-2.06)

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. 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	1005	<div> <div>%</div> <div> <div></div> <div>93%</div> <div>5%</div> <div>.</div> <div>.</div> </div> </div>
1	B	1005	<div> <div></div> <div>92%</div> <div>5%</div> <div>.</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	EDO	A	1102	-	-	-	X
3	EDO	A	1103	-	-	-	X
3	EDO	A	1104	-	-	-	X
3	EDO	A	1106	-	-	-	X
3	EDO	A	1108	-	-	-	X
3	EDO	A	1109	-	-	-	X

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 16256 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.

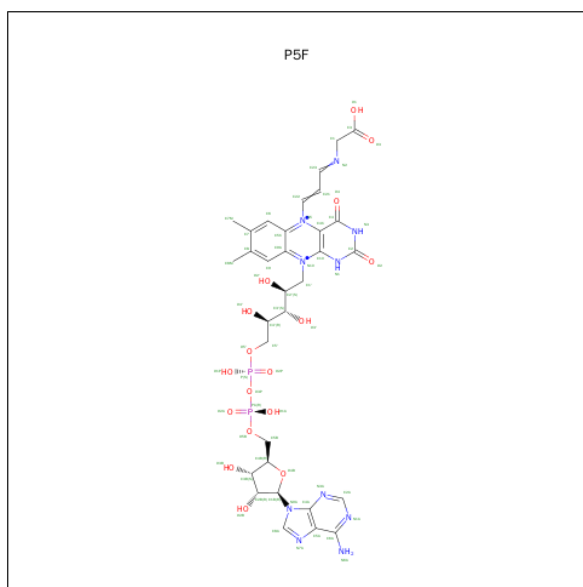
- Molecule 1 is a protein called Proline dehydrogenase and Delta-1-pyrroline-5-carboxylate dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	972	Total	C	N	O	S	0	1	0
			7522	4801	1297	1388	36			
1	B	978	Total	C	N	O	S	0	2	0
			7607	4855	1314	1400	38			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	SER	-	EXPRESSION TAG	UNP Q746X3
B	0	SER	-	EXPRESSION TAG	UNP Q746X3

- Molecule 2 is N-PROPARGYLGLYCINE-MODIFIED FLAVIN ADENINE DINUCLEOTIDE (three-letter code: P5F) (formula: $C_{32}H_{40}N_{10}O_{17}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			56	30	9	15	2		
2	B	1	Total	C	N	O	P	0	0
			56	30	9	15	2		

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: 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	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	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		

Continued on next page...

Continued from previous page...

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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	462	Total 462	O 462	0	0
4	B	489	Total 489	O 489	0	0

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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 ($\text{RSRZ} > 2$). 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.

- Chain A:
-
- Sequence logo for Chain A. The y-axis represents information content in bits (0.00 to 0.25). The x-axis shows positions 1 to 300. A green bar at the top indicates 93% identity. A legend at the bottom identifies amino acids by color: G971 (green), V1003 (yellow), ASP (grey).

- Chain B:
-
- 92% 5%
- SER MET LEU N3 R13 L28 M39 R66 SER THR GLY ALA LYS VAL ALA GLY MET LEU GLY SER PHE GLY A102 T109 E113 F119 I120 V121 G122 A128 L132 K137 V143 D187 F188 G189 G193 K197 P204 I243 Y278
- I329 E332 F353 R371 Y380 Q383 M388 R404 L405 Y406 A407 M412 E448 R456 R461 ALA ALA LYS PAD LYS LYS GLU ARG K470 G471 L472 N479 V484 D566 P567 R568 L585 Y604 K645 L726 A765 C793 R798
- A488 K852 F881 L917 F936 R991 W1002 V1003 ASP

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	95.23Å 151.18Å 175.18Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	87.59 – 2.09 114.45 – 2.09	Depositor EDS
% Data completeness (in resolution range)	99.6 (87.59-2.09) 99.6 (114.45-2.09)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.17 (at 2.08Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8_1069)	Depositor
R, R_{free}	0.169 , 0.208 0.176 , 0.215	Depositor DCC
R_{free} test set	7527 reflections (5.30%)	DCC
Wilson B-factor (Å ²)	23.4	Xtriage
Anisotropy	0.516	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 53.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 149671 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	16256	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.50% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: P5F, 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	0.36	0/7693	0.50	0/10429
1	B	0.37	0/7784	0.50	0/10546
All	All	0.36	0/15477	0.50	0/20975

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	7522	0	7315	21	0
1	B	7607	0	7453	27	0
2	A	56	0	35	3	0
2	B	56	0	35	1	0
3	A	32	0	48	3	0
3	B	32	0	48	0	0
4	A	462	0	0	0	0
4	B	489	0	0	0	0
All	All	16256	0	14934	47	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 2.

All (47) 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:26:PRO:HG2	1:A:29:PHE:HD2	1.61	0.66
1:A:406:TYR:HB2	2:A:1101:P5F:H18	1.78	0.66
1:B:119:PHE:HE1	1:B:388:MET:HB3	1.67	0.59
1:B:406:TYR:HB2	2:B:1101:P5F:H18	1.85	0.58
1:A:34:TRP:NE1	1:A:85:PHE:O	2.40	0.54
1:A:119:PHE:HE1	1:A:388:MET:HG3	1.75	0.52
1:A:397:LEU:HB2	1:A:403:ILE:HG21	1.92	0.52
2:A:1101:P5F:N1	2:A:1101:P5F:O2'	2.42	0.52
1:B:13:ARG:HH11	1:B:371:ARG:HH12	1.59	0.51
1:B:484:VAL:HB	1:B:604:TYR:CG	2.46	0.50
1:A:699:LEU:HB3	3:A:1107:EDO:H11	1.93	0.50
1:B:204:PRO:HG3	1:B:243:ILE:HG23	1.93	0.50
1:B:189:GLY:O	1:B:197:LYS:HE3	2.12	0.49
1:A:513:PHE:HE2	3:A:1107:EDO:H22	1.79	0.48
1:B:765:ALA:HA	1:B:798:ARG:O	2.14	0.48
1:B:143:VAL:HG13	1:B:406:TYR:HA	1.95	0.47
1:B:448:GLU:OE1	1:B:456:ARG:NH2	2.38	0.47
1:B:120:ILE:HG22	1:B:122:GLY:H	1.80	0.47
1:A:636:GLU:HB2	3:A:1106:EDO:H22	1.97	0.47
1:A:484:VAL:HB	1:A:604:TYR:CG	2.50	0.47
1:B:793:CYS:O	1:B:917:LEU:HD23	2.15	0.47
1:B:28:LEU:HD22	1:B:39:MET:HG3	1.96	0.46
1:B:13:ARG:HH11	1:B:371:ARG:NH1	2.14	0.46
1:A:1:MET:O	1:A:5:GLU:HG3	2.17	0.45
1:A:765:ALA:HA	1:A:798:ARG:O	2.17	0.45
1:A:26:PRO:HG2	1:A:29:PHE:CD2	2.47	0.44
1:A:421:ARG:NH2	1:B:991:ARG:O	2.50	0.44
1:A:328:THR:HG21	1:B:1003:VAL:HG11	2.01	0.42
1:B:187:ASP:O	1:B:193:GLY:HA2	2.19	0.42
1:B:484:VAL:HB	1:B:604:TYR:CD1	2.54	0.42
1:B:848:ALA:O	1:B:852:LYS:HG3	2.20	0.42
1:B:121:VAL:HG11	1:B:407:ALA:HB1	2.02	0.41
1:A:28:LEU:HG	1:A:39:MET:HG3	2.01	0.41
1:B:128:ALA:O	1:B:132:LEU:HG	2.21	0.41
1:A:359:ASN:HD22	2:A:1101:P5F:H1	1.66	0.41
1:B:329:ILE:HB	1:B:332:GLU:HG3	2.03	0.41
1:A:421:ARG:NH2	1:A:424:LEU:HD13	2.36	0.41
1:B:353:PHE:O	1:B:380:TYR:HA	2.21	0.41
1:A:416:MET:O	1:A:420:VAL:HG23	2.20	0.41
1:A:956:PRO:HB3	1:A:971:GLY:HA3	2.03	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1002:TRP:CG	1:B:1003:VAL:N	2.89	0.41
1:A:187:ASP:O	1:A:193:GLY:HA2	2.21	0.41
1:B:645:LYS:HD2	1:B:726:LEU:HD12	2.02	0.40
1:A:585:LEU:HD22	1:A:604:TYR:CZ	2.55	0.40
1:B:566:ASP:OD2	1:B:568:ARG:HB3	2.21	0.40
1:B:383:GLN:HG2	1:B:404:ARG:HB3	2.03	0.40
1:B:109:THR:O	1:B:113:GLU:HG3	2.21	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	963/1005 (96%)	940 (98%)	23 (2%)	0	100	100
1	B	974/1005 (97%)	952 (98%)	22 (2%)	0	100	100
All	All	1937/2010 (96%)	1892 (98%)	45 (2%)	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	759/821 (92%)	751 (99%)	8 (1%)	80	84

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	774/821 (94%)	767 (99%)	7 (1%)	84	88
All	All	1533/1642 (93%)	1518 (99%)	15 (1%)	82	86

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	108	LEU
1	A	266	ARG
1	A	278	TYR
1	A	392	VAL
1	A	585	LEU
1	A	838	ASP
1	A	891	PHE
1	A	936	PHE
1	B	137	LYS
1	B	278	TYR
1	B	412	MET
1	B	479	ASN
1	B	585	LEU
1	B	891	PHE
1	B	936	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

18 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	P5F	A	1101	1	46,61,66	2.43	16 (34%)	52,93,99	2.44	12 (23%)
3	EDO	A	1102	-	3,3,3	0.54	0	2,2,2	0.47	0
3	EDO	A	1103	-	3,3,3	0.57	0	2,2,2	0.65	0
3	EDO	A	1104	-	3,3,3	0.49	0	2,2,2	0.20	0
3	EDO	A	1105	-	3,3,3	0.50	0	2,2,2	0.33	0
3	EDO	A	1106	-	3,3,3	0.53	0	2,2,2	0.54	0
3	EDO	A	1107	-	3,3,3	0.46	0	2,2,2	0.11	0
3	EDO	A	1108	-	3,3,3	0.58	0	2,2,2	0.50	0
3	EDO	A	1109	-	3,3,3	0.55	0	2,2,2	0.51	0
2	P5F	B	1101	1	46,61,66	2.38	14 (30%)	52,93,99	2.39	12 (23%)
3	EDO	B	1102	-	3,3,3	0.50	0	2,2,2	0.27	0
3	EDO	B	1103	-	3,3,3	0.53	0	2,2,2	0.54	0
3	EDO	B	1104	-	3,3,3	0.50	0	2,2,2	0.33	0
3	EDO	B	1105	-	3,3,3	0.52	0	2,2,2	0.55	0
3	EDO	B	1106	-	3,3,3	0.50	0	2,2,2	0.49	0
3	EDO	B	1107	-	3,3,3	0.48	0	2,2,2	0.39	0
3	EDO	B	1108	-	3,3,3	0.45	0	2,2,2	0.21	0
3	EDO	B	1109	-	3,3,3	0.49	0	2,2,2	0.41	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	P5F	A	1101	1	-	0/31/53/58	0/6/6/6
3	EDO	A	1102	-	-	0/1/1/1	0/0/0/0
3	EDO	A	1103	-	-	0/1/1/1	0/0/0/0
3	EDO	A	1104	-	-	0/1/1/1	0/0/0/0
3	EDO	A	1105	-	-	0/1/1/1	0/0/0/0
3	EDO	A	1106	-	-	0/1/1/1	0/0/0/0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	EDO	A	1107	-	-	0/1/1/1	0/0/0/0
3	EDO	A	1108	-	-	0/1/1/1	0/0/0/0
3	EDO	A	1109	-	-	0/1/1/1	0/0/0/0
2	P5F	B	1101	1	-	0/31/53/58	0/6/6/6
3	EDO	B	1102	-	-	0/1/1/1	0/0/0/0
3	EDO	B	1103	-	-	0/1/1/1	0/0/0/0
3	EDO	B	1104	-	-	0/1/1/1	0/0/0/0
3	EDO	B	1105	-	-	0/1/1/1	0/0/0/0
3	EDO	B	1106	-	-	0/1/1/1	0/0/0/0
3	EDO	B	1107	-	-	0/1/1/1	0/0/0/0
3	EDO	B	1108	-	-	0/1/1/1	0/0/0/0
3	EDO	B	1109	-	-	0/1/1/1	0/0/0/0

All (30) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1101	P5F	C9A-C5X	-3.16	1.35	1.42
2	A	1101	P5F	C9A-C5X	-2.69	1.36	1.42
2	A	1101	P5F	O3B-C3B	-2.41	1.37	1.43
2	A	1101	P5F	O2'-C2'	-2.23	1.38	1.43
2	B	1101	P5F	O3B-C3B	-2.19	1.37	1.43
2	A	1101	P5F	PA-O5B	-2.05	1.49	1.59
2	B	1101	P5F	PA-O5B	-2.00	1.49	1.59
2	B	1101	P5F	P-O2P	2.09	1.58	1.51
2	A	1101	P5F	C5'-C4'	2.13	1.54	1.51
2	A	1101	P5F	P-O2P	2.23	1.59	1.51
2	A	1101	P5F	C2A-N3A	2.34	1.36	1.32
2	B	1101	P5F	C2A-N3A	2.68	1.36	1.32
2	B	1101	P5F	C6A-N6A	3.04	1.44	1.34
2	A	1101	P5F	C6A-N6A	3.16	1.44	1.34
2	B	1101	P5F	C6-C5X	3.73	1.48	1.40
2	A	1101	P5F	C9-C9A	3.77	1.49	1.40
2	B	1101	P5F	C9-C9A	3.82	1.49	1.40
2	A	1101	P5F	C6-C5X	3.83	1.49	1.40
2	B	1101	P5F	C4-N3	4.16	1.40	1.33
2	A	1101	P5F	C4-C4X	4.24	1.49	1.41
2	A	1101	P5F	C4-N3	4.29	1.41	1.33
2	B	1101	P5F	C10-N10	4.35	1.44	1.39
2	A	1101	P5F	C10-N10	4.52	1.44	1.39
2	B	1101	P5F	C4-C4X	4.74	1.50	1.41
2	B	1101	P5F	C9A-N10	5.00	1.45	1.38
2	A	1101	P5F	O4-C4	5.62	1.38	1.24

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1101	P5F	C9A-N10	5.71	1.46	1.38
2	B	1101	P5F	O4-C4	5.89	1.38	1.24
2	B	1101	P5F	C10-N1	6.07	1.45	1.35
2	A	1101	P5F	C10-N1	6.36	1.46	1.35

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1101	P5F	N3A-C2A-N1A	-11.18	120.33	128.89
2	B	1101	P5F	N3A-C2A-N1A	-11.15	120.36	128.89
2	A	1101	P5F	C4X-N5-C5X	-5.80	114.12	121.64
2	B	1101	P5F	C4X-N5-C5X	-5.00	115.15	121.64
2	B	1101	P5F	C4X-C4-N3	-3.58	118.69	123.59
2	A	1101	P5F	PA-O3P-P	-3.45	123.05	132.73
2	A	1101	P5F	O5'-P-O2P	-3.34	96.67	109.62
2	B	1101	P5F	O5B-PA-O2A	-3.21	97.16	109.62
2	A	1101	P5F	C1B-N9A-C4A	-2.90	122.56	126.94
2	A	1101	P5F	O5B-PA-O2A	-2.89	98.39	109.62
2	A	1101	P5F	C4X-C4-N3	-2.85	119.69	123.59
2	B	1101	P5F	C4X-C10-N10	-2.80	118.87	120.52
2	B	1101	P5F	O5'-P-O2P	-2.61	99.48	109.62
2	B	1101	P5F	C1B-N9A-C4A	-2.25	123.55	126.94
2	B	1101	P5F	C4A-C5A-N7A	-2.15	107.50	109.48
2	A	1101	P5F	C6-C5X-C9A	2.01	121.09	119.06
2	B	1101	P5F	O1A-PA-O3P	2.26	115.35	105.09
2	A	1101	P5F	O1P-P-O3P	3.01	118.77	105.09
2	B	1101	P5F	O1P-P-O3P	3.22	119.68	105.09
2	B	1101	P5F	C1'-N10-C9A	3.37	122.64	118.86
2	A	1101	P5F	O1A-PA-O3P	3.68	121.77	105.09
2	A	1101	P5F	C1'-N10-C9A	3.69	123.00	118.86
2	A	1101	P5F	C4-N3-C2	5.66	120.14	115.25
2	B	1101	P5F	C4-N3-C2	6.65	121.00	115.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1101	P5F	3	0
3	A	1106	EDO	1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1107	EDO	2	0
2	B	1101	P5F	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 ⓘ

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	972/1005 (96%)	-0.49	13 (1%) 79 83	12, 22, 57, 84	0
1	B	978/1005 (97%)	-0.62	1 (0%) 95 96	10, 20, 40, 66	0
All	All	1950/2010 (97%)	-0.55	14 (0%) 89 91	10, 21, 50, 84	0

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	438	ALA	4.0
1	A	27	SER	3.5
1	A	85	PHE	3.1
1	A	437	PHE	3.0
1	A	26	PRO	2.9
1	A	28	LEU	2.7
1	A	2	LEU	2.6
1	A	394	LYS	2.6
1	A	83	PRO	2.6
1	A	104	LEU	2.5
1	A	439	GLU	2.2
1	A	34	TRP	2.2
1	A	17	PHE	2.1
1	B	472	LEU	2.1

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 carbohydrates in this entry.

6.4 Ligands ⓘ

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
3	EDO	A	1109	4/4	0.95	0.19	11.13	36,39,41,45	0
3	EDO	A	1104	4/4	0.86	0.16	8.43	39,41,43,43	0
3	EDO	A	1103	4/4	0.98	0.17	6.10	19,20,25,25	0
3	EDO	A	1108	4/4	0.93	0.12	4.06	19,33,35,38	0
3	EDO	A	1106	4/4	0.95	0.16	3.34	30,32,33,34	0
3	EDO	A	1102	4/4	0.97	0.09	2.03	17,20,20,27	0
3	EDO	B	1108	4/4	0.94	0.10	1.77	28,28,31,34	0
3	EDO	A	1107	4/4	0.94	0.14	1.65	27,31,33,36	0
3	EDO	B	1109	4/4	0.98	0.12	0.95	22,23,27,27	0
3	EDO	B	1102	4/4	0.98	0.10	0.65	15,22,22,23	0
3	EDO	B	1104	4/4	0.96	0.09	0.48	15,20,21,25	0
2	P5F	B	1101	56/61	0.98	0.09	0.18	11,16,23,31	0
2	P5F	A	1101	56/61	0.97	0.10	-0.01	13,20,30,35	0
3	EDO	B	1107	4/4	0.95	0.09	-0.09	31,32,33,37	0
3	EDO	A	1105	4/4	0.96	0.09	-0.24	30,30,34,37	0
3	EDO	B	1106	4/4	0.94	0.09	-0.53	23,25,26,29	0
3	EDO	B	1103	4/4	0.96	0.08	-1.40	21,26,28,29	0
3	EDO	B	1105	4/4	0.96	0.06	-2.53	20,21,21,22	0

6.5 Other polymers ⓘ

There are no such residues in this entry.