



# wwPDB X-ray Structure Validation Summary Report

Aug 22, 2023 – 06:51 PM EDT

PDB ID : 3D03  
Title : 1.9A structure of Glycerophosphodiesterase (GpdQ) from *Enterobacter aerogenes*  
Authors : Hadler, K.S.; Tanifum, E.; Yip, S.H.-C.; Miti, N.; Guddat, L.W.; Jackson, C.J.; Gahan, L.R.; Carr, P.D.; Nguyen, K.; Ollis, D.L.; Hengge, A.C.; Larrabee, J.A.; Schenk, G.  
Deposited on : 2008-04-30  
Resolution : 1.90 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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

MolProbity : 4.02b-467  
Xtriage (Phenix) : 1.13  
EDS : 2.35  
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) : 2.35

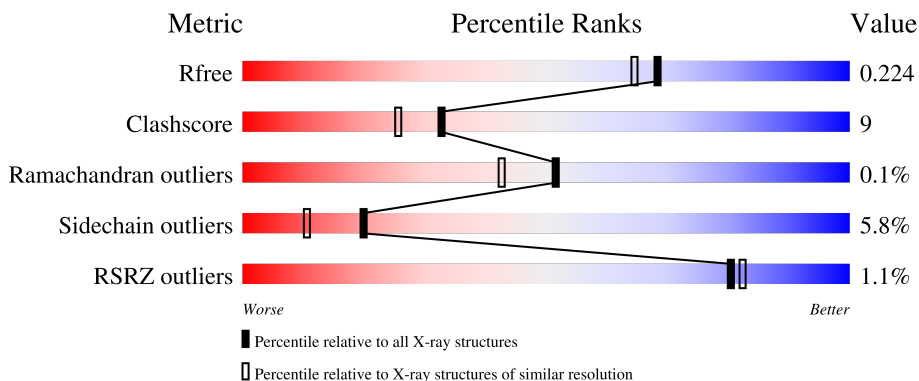
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.90 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.



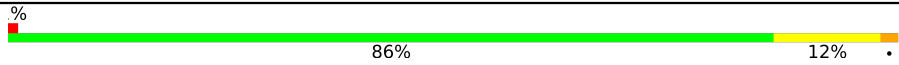
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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  $\geq 3$ , 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	274	
1	B	274	
1	C	274	
1	D	274	
1	E	274	

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Mol	Chain	Length	Quality of chain
1	F	274	 <p>A horizontal bar chart representing the quality of the chain. The bar is primarily green, indicating a high quality score of 86%. A small portion at the end is yellow, indicating a lower quality score of 12%. A small red square is visible at the very beginning of the bar. The percentage values '86%' and '12%' are printed below the bar. A '%' symbol is located above the start of the bar, and a small black dot is at the end of the bar.</p>

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 13904 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 Phosphohydrolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	274	2163	1364	378	407	14	0	0	0
1	B	271	2133	1348	372	399	14	0	0	0
1	C	271	2133	1348	372	399	14	0	0	0
1	D	271	2133	1348	372	399	14	0	0	0
1	E	271	2133	1348	372	399	14	0	0	0
1	F	274	2163	1364	378	407	14	0	0	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	224	ALA	GLU	SEE REMARK 999	UNP Q6XBH1
A	227	ASP	ARG	SEE REMARK 999	UNP Q6XBH1
B	224	ALA	GLU	SEE REMARK 999	UNP Q6XBH1
B	227	ASP	ARG	SEE REMARK 999	UNP Q6XBH1
C	224	ALA	GLU	SEE REMARK 999	UNP Q6XBH1
C	227	ASP	ARG	SEE REMARK 999	UNP Q6XBH1
D	224	ALA	GLU	SEE REMARK 999	UNP Q6XBH1
D	227	ASP	ARG	SEE REMARK 999	UNP Q6XBH1
E	224	ALA	GLU	SEE REMARK 999	UNP Q6XBH1
E	227	ASP	ARG	SEE REMARK 999	UNP Q6XBH1
F	224	ALA	GLU	SEE REMARK 999	UNP Q6XBH1
F	227	ASP	ARG	SEE REMARK 999	UNP Q6XBH1

- Molecule 2 is COBALT (II) ION (three-letter code: CO) (formula: Co).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total 2	Co 2	0	0
2	B	2	Total 2	Co 2	0	0
2	C	2	Total 2	Co 2	0	0
2	D	2	Total 2	Co 2	0	0
2	E	2	Total 2	Co 2	0	0
2	F	2	Total 2	Co 2	0	0

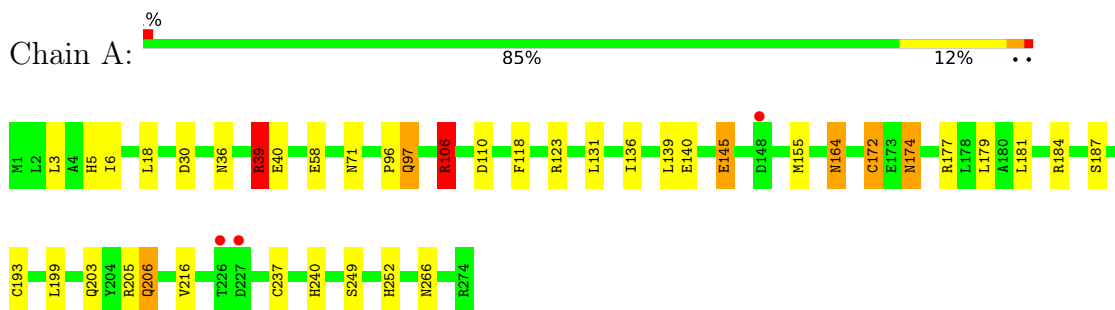
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	179	Total 179	O 179	0	0
3	B	178	Total 178	O 178	0	0
3	C	178	Total 178	O 178	0	0
3	D	181	Total 181	O 181	0	0
3	E	139	Total 139	O 139	0	0
3	F	179	Total 179	O 179	0	0

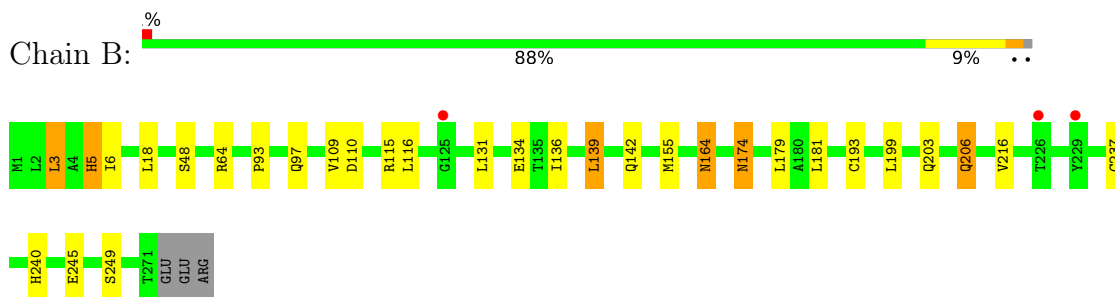
### 3 Residue-property plots [i](#)

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.

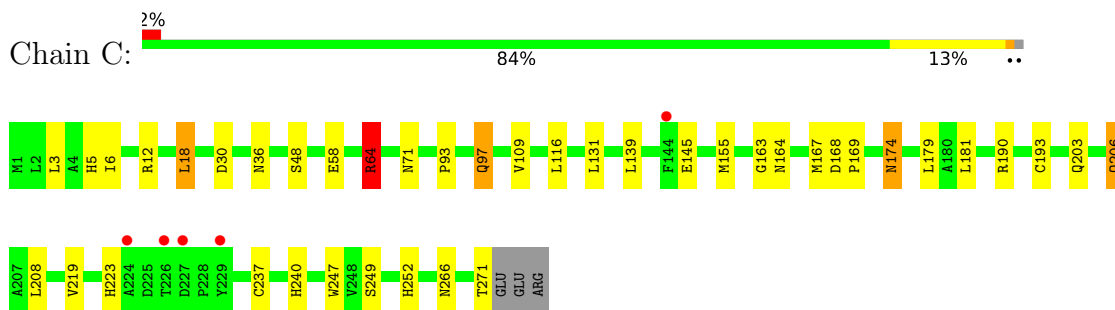
- Molecule 1: Phosphohydrolase



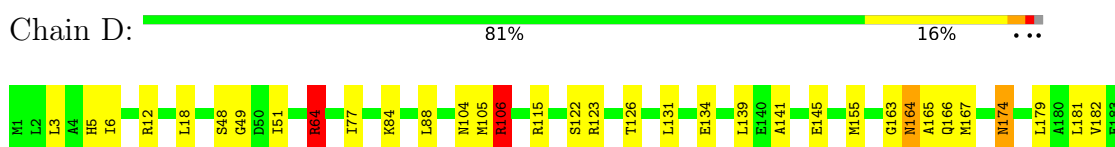
- Molecule 1: Phosphohydrolase



- Molecule 1: Phosphohydrolase

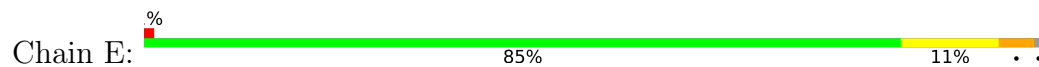


- Molecule 1: Phosphohydrolase

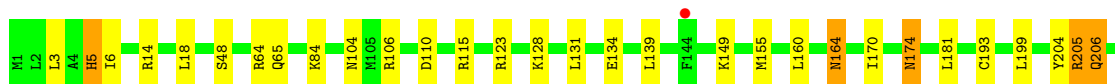
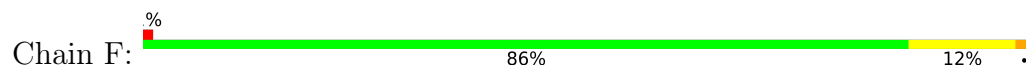




- Molecule 1: Phosphohydrolase



- Molecule 1: Phosphohydrolase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	94.97Å 133.84Å 168.94Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.27 – 1.90 43.26 – 1.90	Depositor EDS
% Data completeness (in resolution range)	96.7 (43.27-1.90) 96.7 (43.26-1.90)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.10	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.72 (at 1.89Å)	Xtrriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.184 , 0.223 0.187 , 0.224	Depositor DCC
$R_{free}$ test set	8219 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	16.5	Xtrriage
Anisotropy	0.188	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 37.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	13904	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	8.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.34% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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:  
CO

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	0.81	1/2222 (0.0%)	0.82	3/3029 (0.1%)
1	B	0.79	1/2192 (0.0%)	0.75	2/2991 (0.1%)
1	C	0.79	0/2192	0.79	4/2991 (0.1%)
1	D	0.80	1/2192 (0.0%)	0.81	4/2991 (0.1%)
1	E	0.68	0/2192	0.73	2/2991 (0.1%)
1	F	0.78	0/2222	0.78	1/3029 (0.0%)
All	All	0.77	3/13212 (0.0%)	0.78	16/18022 (0.1%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	134	GLU	CG-CD	5.30	1.59	1.51
1	D	237	CYS	CB-SG	-5.15	1.73	1.81
1	A	172	CYS	CB-SG	-5.01	1.73	1.81

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	106	ARG	NE-CZ-NH2	-5.95	117.33	120.30
1	A	39	ARG	NE-CZ-NH1	5.93	123.27	120.30
1	E	139	LEU	CA-CB-CG	5.88	128.83	115.30
1	A	30	ASP	CB-CG-OD1	5.87	123.59	118.30
1	C	12	ARG	NE-CZ-NH2	-5.81	117.39	120.30

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	2163	0	2071	48	0
1	B	2133	0	2046	31	0
1	C	2133	0	2046	36	0
1	D	2133	0	2046	44	0
1	E	2133	0	2046	44	0
1	F	2163	0	2071	38	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
2	E	2	0	0	0	0
2	F	2	0	0	0	0
3	A	179	0	0	4	0
3	B	178	0	0	1	0
3	C	178	0	0	6	0
3	D	181	0	0	5	0
3	E	139	0	0	2	0
3	F	179	0	0	6	0
All	All	13904	0	12326	218	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 9.

The worst 5 of 218 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:199:LEU:CD2	1:B:199:LEU:CD2	2.26	1.14
1:A:39:ARG:HD3	1:A:39:ARG:N	1.56	1.12
1:A:199:LEU:HD21	1:B:199:LEU:CD2	1.87	1.01
1:B:97:GLN:HG3	3:B:2124:HOH:O	1.60	1.01
1:E:106:ARG:HH11	1:E:106:ARG:HG3	0.87	1.01

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	272/274 (99%)	262 (96%)	9 (3%)	1 (0%)	34	24
1	B	269/274 (98%)	263 (98%)	5 (2%)	1 (0%)	34	24
1	C	269/274 (98%)	261 (97%)	8 (3%)	0	100	100
1	D	269/274 (98%)	258 (96%)	11 (4%)	0	100	100
1	E	269/274 (98%)	260 (97%)	9 (3%)	0	100	100
1	F	272/274 (99%)	264 (97%)	8 (3%)	0	100	100
All	All	1620/1644 (98%)	1568 (97%)	50 (3%)	2 (0%)	51	42

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	216	VAL
1	A	216	VAL

### 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	235/235 (100%)	218 (93%)	17 (7%)	14	6
1	B	232/235 (99%)	220 (95%)	12 (5%)	23	14
1	C	232/235 (99%)	221 (95%)	11 (5%)	26	16
1	D	232/235 (99%)	218 (94%)	14 (6%)	19	9
1	E	232/235 (99%)	217 (94%)	15 (6%)	17	8

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	F	235/235 (100%)	223 (95%)	12 (5%)	24	14
All	All	1398/1410 (99%)	1317 (94%)	81 (6%)	20	10

5 of 81 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	106	ARG
1	F	18	LEU
1	E	115	ARG
1	E	177	ARG
1	F	164	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 82 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	28	ASN
1	F	5	HIS
1	E	61	GLN
1	E	206	GLN
1	F	164	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](#)

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

### 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 12 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	274/274 (100%)	-0.21	3 (1%) 80 82	2, 4, 14, 19	0
1	B	271/274 (98%)	-0.27	3 (1%) 80 82	2, 5, 15, 19	0
1	C	271/274 (98%)	-0.24	5 (1%) 68 71	2, 5, 18, 24	0
1	D	271/274 (98%)	-0.32	1 (0%) 92 93	2, 5, 17, 26	0
1	E	271/274 (98%)	-0.14	3 (1%) 80 82	2, 9, 22, 27	0
1	F	274/274 (100%)	-0.28	3 (1%) 80 82	2, 6, 18, 26	0
All	All	1632/1644 (99%)	-0.24	18 (1%) 80 82	2, 6, 19, 27	0

The worst 5 of 18 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	125	GLY	2.8
1	A	226	THR	2.7
1	C	227	ASP	2.7
1	C	144	PHE	2.6
1	C	229	TYR	2.6

### 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 monosaccharides 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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
2	CO	E	1002	1/1	0.98	0.04	8,8,8,8	1
2	CO	B	1002	1/1	0.99	0.06	5,5,5,5	1
2	CO	C	1002	1/1	0.99	0.05	7,7,7,7	1
2	CO	D	1002	1/1	0.99	0.04	6,6,6,6	1
2	CO	A	1002	1/1	0.99	0.04	3,3,3,3	1
2	CO	F	1002	1/1	0.99	0.05	7,7,7,7	1
2	CO	D	1001	1/1	1.00	0.04	4,4,4,4	1
2	CO	A	1001	1/1	1.00	0.05	3,3,3,3	1
2	CO	E	1001	1/1	1.00	0.05	7,7,7,7	1
2	CO	C	1001	1/1	1.00	0.05	4,4,4,4	1
2	CO	F	1001	1/1	1.00	0.04	4,4,4,4	1
2	CO	B	1001	1/1	1.00	0.06	4,4,4,4	1

## 6.5 Other polymers [i](#)

There are no such residues in this entry.