



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 7, 2020 – 01:32 am BST

PDB ID : 6FU0
Title : Phosphotriesterase PTE_A53_4
Authors : Dym, O.; Aggarwal, N.; Albeck, S.; Unger, T.; Hamer Rogotner, S.; Silman, I.; Leader, H.; Ashani, Y.; Goldsmith, M.; Greisen, P.; Tawfik, D.; Sussman, L.J.
Deposited on : 2018-02-26
Resolution : 3.20 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/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 : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
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) : 2.11

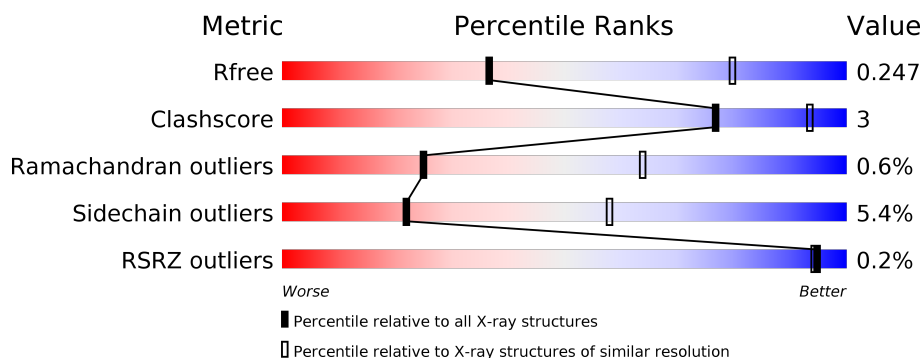
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)

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 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	332	<div> <div>86%</div> <div>11% ..</div> </div>
1	B	332	<div> <div>88%</div> <div>9% ...</div> </div>
1	C	332	<div> <div>89%</div> <div>9% ..</div> </div>
1	D	332	<div> <div>88%</div> <div>10% .</div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 9917 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 Parathion hydrolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	328	Total	C	N	O	S	0	4	0
			2463	1559	432	465	7			
1	B	327	Total	C	N	O	S	0	3	0
			2470	1564	432	467	7			
1	C	327	Total	C	N	O	S	0	4	0
			2473	1563	439	464	7			
1	D	326	Total	C	N	O	S	0	5	0
			2487	1569	441	470	7			

There are 32 discrepancies between the modelled and reference sequences:

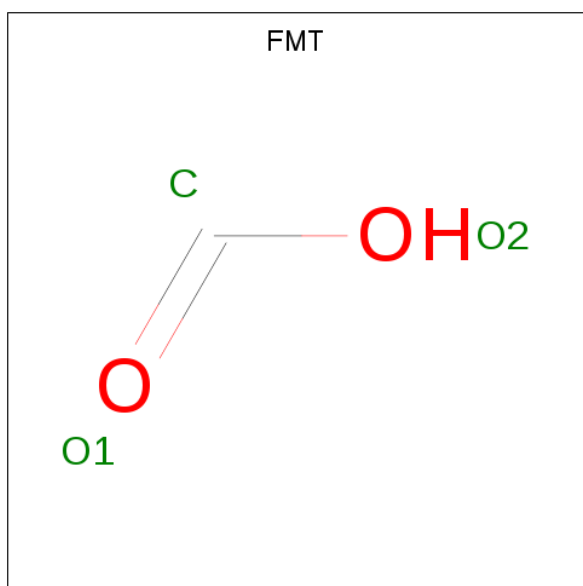
Chain	Residue	Modelled	Actual	Comment	Reference
A	77	ALA	LYS	conflict	UNP P0A434
A	80	VAL	ALA	conflict	UNP P0A434
A	132	GLU	PHE	conflict	UNP P0A434
A	173	ASN	THR	conflict	UNP P0A434
A	185	ARG	LYS	conflict	UNP P0A434
A	254	GLY	HIS	conflict	UNP P0A434
A	274	ASN	ILE	conflict	UNP P0A434
A	319	SER	ARG	conflict	UNP P0A434
B	77	ALA	LYS	conflict	UNP P0A434
B	80	VAL	ALA	conflict	UNP P0A434
B	132	GLU	PHE	conflict	UNP P0A434
B	173	ASN	THR	conflict	UNP P0A434
B	185	ARG	LYS	conflict	UNP P0A434
B	254	GLY	HIS	conflict	UNP P0A434
B	274	ASN	ILE	conflict	UNP P0A434
B	319	SER	ARG	conflict	UNP P0A434
C	77	ALA	LYS	conflict	UNP P0A434
C	80	VAL	ALA	conflict	UNP P0A434
C	132	GLU	PHE	conflict	UNP P0A434
C	173	ASN	THR	conflict	UNP P0A434
C	185	ARG	LYS	conflict	UNP P0A434

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Chain	Residue	Modelled	Actual	Comment	Reference
C	254	GLY	HIS	conflict	UNP P0A434
C	274	ASN	ILE	conflict	UNP P0A434
C	319	SER	ARG	conflict	UNP P0A434
D	77	ALA	LYS	conflict	UNP P0A434
D	80	VAL	ALA	conflict	UNP P0A434
D	132	GLU	PHE	conflict	UNP P0A434
D	173	ASN	THR	conflict	UNP P0A434
D	185	ARG	LYS	conflict	UNP P0A434
D	254	GLY	HIS	conflict	UNP P0A434
D	274	ASN	ILE	conflict	UNP P0A434
D	319	SER	ARG	conflict	UNP P0A434

- Molecule 2 is FORMIC ACID (three-letter code: FMT) (formula: CH₂O₂).



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

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	2	Total 2	Zn 2	0	0
3	A	2	Total 2	Zn 2	0	0
3	D	2	Total 2	Zn 2	0	0
3	C	2	Total 2	Zn 2	0	0

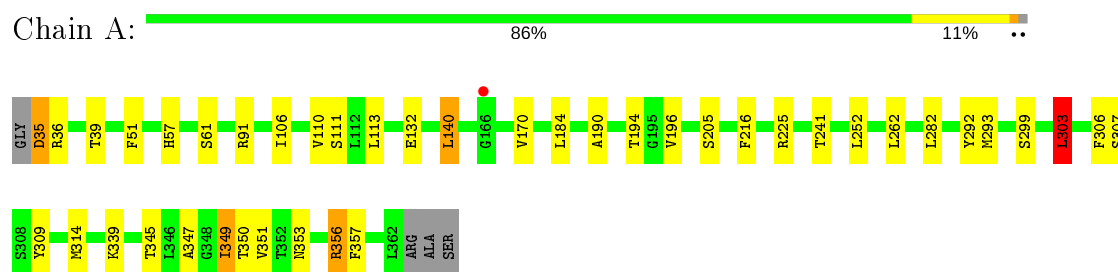
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total 1	O 1	0	0
4	B	1	Total 1	O 1	0	0
4	C	1	Total 1	O 1	0	0
4	D	1	Total 1	O 1	0	0

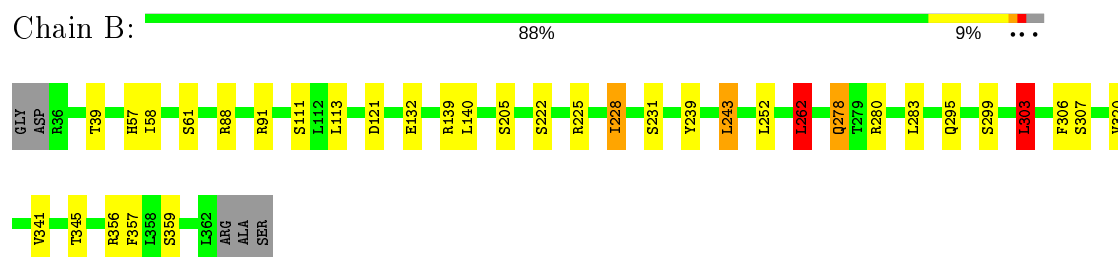
3 Residue-property plots [i](#)

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

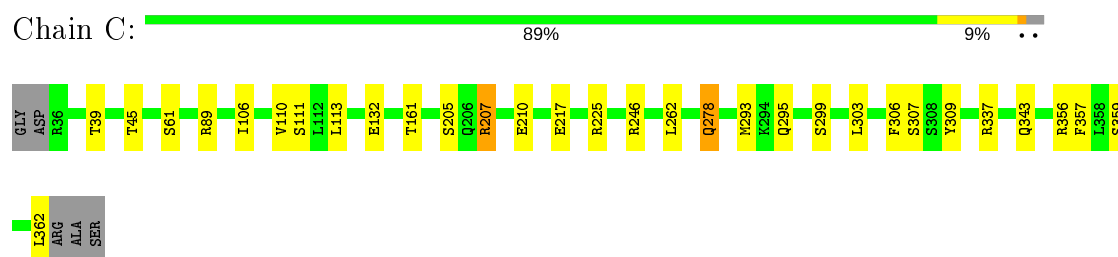
• Molecule 1: Parathion hydrolase



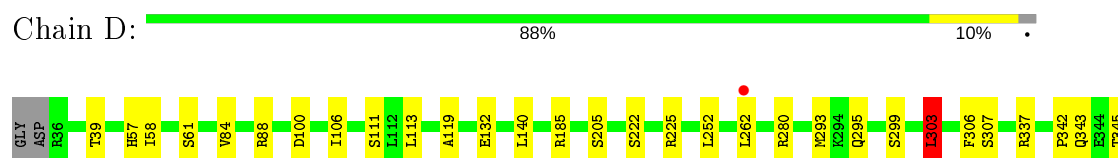
• Molecule 1: Parathion hydrolase



• Molecule 1: Parathion hydrolase



• Molecule 1: Parathion hydrolase



P354
A355
R356
F357
L358
S359
F360
T361
LEU
ARG
ALA
SER

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	88.89Å 119.90Å 161.49Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	77.87 – 3.20 77.87 – 3.20	Depositor EDS
% Data completeness (in resolution range)	99.8 (77.87-3.20) 99.9 (77.87-3.20)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.70 (at 3.19Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.215 , 0.249 0.219 , 0.247	Depositor DCC
R_{free} test set	1417 reflections (4.86%)	wwPDB-VP
Wilson B-factor (Å ²)	42.9	Xtriage
Anisotropy	1.360	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 21.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	9917	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 23.57 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 4.5439e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: ZN, FMT

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	0/2529	0.80	3/3442 (0.1%)
1	B	0.55	0/2531	0.82	7/3445 (0.2%)
1	C	0.56	0/2539	0.81	2/3453 (0.1%)
1	D	0.54	0/2556	0.83	4/3476 (0.1%)
All	All	0.55	0/10155	0.81	16/13816 (0.1%)

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	140	LEU	CB-CG-CD2	7.91	124.44	111.00
1	B	139	ARG	CG-CD-NE	6.38	125.20	111.80
1	D	100	ASP	CB-CG-OD2	6.37	124.03	118.30
1	D	185	ARG	NE-CZ-NH2	-6.20	117.20	120.30
1	C	207	ARG	NE-CZ-NH1	5.94	123.27	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	2463	0	2460	25	0
1	B	2470	0	2468	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	2473	0	2485	8	0
1	D	2487	0	2500	15	0
2	A	3	0	0	0	0
2	B	3	0	0	0	0
2	C	3	0	0	0	0
2	D	3	0	0	1	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
3	C	2	0	0	0	0
3	D	2	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
All	All	9917	0	9913	60	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.

The worst 5 of 60 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:293:MET:HG3	1:A:345:THR:HG23	1.47	0.95
1:B:91:ARG:NH1	1:B:121:ASP:O	2.11	0.83
1:D:342:PRO:HG2	1:D:345:THR:HG23	1.62	0.82
1:A:190:ALA:O	1:A:194:THR:HG22	1.82	0.78
1:A:347:ALA:O	1:A:351:VAL:HG22	1.84	0.77

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	330/332 (99%)	314 (95%)	14 (4%)	2 (1%)	25	64
1	B	328/332 (99%)	312 (95%)	14 (4%)	2 (1%)	25	64
1	C	329/332 (99%)	313 (95%)	14 (4%)	2 (1%)	25	64
1	D	329/332 (99%)	314 (95%)	13 (4%)	2 (1%)	25	64
All	All	1316/1328 (99%)	1253 (95%)	55 (4%)	8 (1%)	25	64

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	132	GLU
1	A	132	GLU
1	A	205	SER
1	B	132	GLU
1	B	205	SER

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	258/265 (97%)	243 (94%)	15 (6%)	20	55
1	B	259/265 (98%)	245 (95%)	14 (5%)	22	58
1	C	261/265 (98%)	242 (93%)	19 (7%)	14	46
1	D	266/265 (100%)	252 (95%)	14 (5%)	22	58
All	All	1044/1060 (98%)	982 (94%)	62 (6%)	22	54

5 of 62 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	359[B]	SER
1	C	111[B]	SER
1	D	303	LEU
1	C	89	ARG
1	C	278	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	295	GLN
1	D	295	GLN
1	C	278	GLN
1	B	278	GLN
1	C	295	GLN

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 ⓘ

Of 12 ligands modelled in this entry, 8 are monoatomic - leaving 4 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	$\# Z > 2$
2	FMT	B	401	1,3	0,2,2	0.00	-	0,1,1	0.00	-
2	FMT	C	401	1,3	0,2,2	0.00	-	0,1,1	0.00	-
2	FMT	A	401	1,3	0,2,2	0.00	-	0,1,1	0.00	-
2	FMT	D	401	1,3	0,2,2	0.00	-	0,1,1	0.00	-

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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	401	FMT	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 [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, 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	328/332 (98%)	0.13	1 (0%) 94 92	32, 58, 86, 114	0
1	B	327/332 (98%)	-0.05	0 100 100	28, 46, 72, 96	0
1	C	327/332 (98%)	-0.08	0 100 100	26, 45, 67, 88	0
1	D	326/332 (98%)	-0.04	1 (0%) 94 92	29, 44, 68, 99	0
All	All	1308/1328 (98%)	-0.01	2 (0%) 95 94	26, 48, 77, 114	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	166	GLY	2.1
1	D	262	LEU	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 carbohydrates 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(\AA^2)	Q<0.9
2	FMT	A	401	3/3	0.97	0.14	46,46,49,49	0
3	ZN	C	403	1/1	0.98	0.12	40,40,40,40	0
2	FMT	D	401	3/3	0.98	0.10	43,43,44,46	0
3	ZN	A	403	1/1	0.98	0.09	51,51,51,51	0
3	ZN	D	403	1/1	0.98	0.11	41,41,41,41	0
3	ZN	D	402	1/1	0.98	0.10	37,37,37,37	0
3	ZN	A	402	1/1	0.99	0.10	49,49,49,49	0
3	ZN	B	403	1/1	0.99	0.10	40,40,40,40	0
2	FMT	B	401	3/3	0.99	0.12	34,34,36,36	0
2	FMT	C	401	3/3	0.99	0.13	40,40,40,41	0
3	ZN	C	402	1/1	0.99	0.11	32,32,32,32	0
3	ZN	B	402	1/1	0.99	0.11	34,34,34,34	0

6.5 Other polymers [i](#)

There are no such residues in this entry.