WORLDWIDE PDB

PROTEIN DATA BANK

Full wwPDB X-ray Structure Validation Report (i)

Jul 25, 2022 – 01:07 pm BST

PDB ID	:	7P85
Title	:	Engineered phosphotriesterase BdPTE 10-2-C3(C59V/C227V) in complex with ethyl-4-methylbenzylphosphonate
Authors	:	Eichinger, A.; Skerra, A.
Deposited on	:	2021-07-21
Resolution	:	1.47 Å(reported)

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

|		
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.29
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0267
CCP4	:	7.1.010 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.29

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 1.47 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.
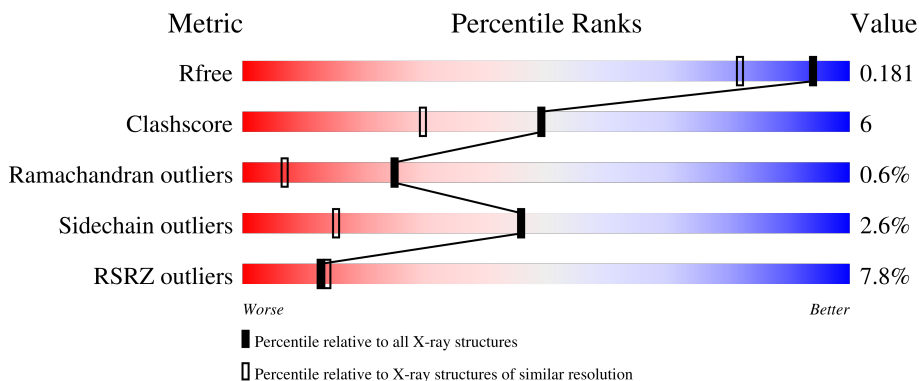
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	4690 (1.50-1.46)
Clashscore	141614	4955 (1.50-1.46)
Ramachandran outliers	138981	4846 (1.50-1.46)
Sidechain outliers	138945	4844 (1.50-1.46)
RSRZ outliers	127900	4614 (1.50-1.46)

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	348	7% / 86% / 10% · ·

2 Entry composition ⓘ

There are 7 unique types of molecules in this entry. The entry contains 2920 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
			Total	C	N	O	S			
1	A	335	2617	1658	462	492	5	0	9	0

There are 35 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	17	ALA	-	expression tag	UNP P0A434
A	18	SER	-	expression tag	UNP P0A434
A	19	ARG	-	expression tag	UNP P0A434
A	20	GLY	-	expression tag	UNP P0A434
A	21	SER	-	expression tag	UNP P0A434
A	22	HIS	-	expression tag	UNP P0A434
A	23	HIS	-	expression tag	UNP P0A434
A	24	HIS	-	expression tag	UNP P0A434
A	25	HIS	-	expression tag	UNP P0A434
A	26	HIS	-	expression tag	UNP P0A434
A	27	HIS	-	expression tag	UNP P0A434
A	28	GLY	-	expression tag	UNP P0A434
A	29	ALA	-	expression tag	UNP P0A434
A	59	VAL	CYS	engineered mutation	UNP P0A434
A	77	ALA	LYS	engineered mutation	UNP P0A434
A	80	MET	ALA	engineered mutation	UNP P0A434
A	118	GLU	ARG	engineered mutation	UNP P0A434
A	132	GLU	PHE	engineered mutation	UNP P0A434
A	173	ASN	THR	engineered mutation	UNP P0A434
A	185	ARG	LYS	engineered mutation	UNP P0A434
A	203	ASP	ALA	engineered mutation	UNP P0A434
A	222	ASP	SER	engineered mutation	UNP P0A434
A	227	VAL	CYS	engineered mutation	UNP P0A434
A	233	GLY	ASP	engineered mutation	UNP P0A434
A	238	ASP	SER	engineered mutation	UNP P0A434
A	254	GLY	HIS	engineered mutation	UNP P0A434
A	270	SER	ALA	engineered mutation	UNP P0A434

Continued on next page...

W O R L D W I D E
PDB
PROTEIN DATA BANK

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	271	TRP	LEU	engineered mutation	UNP P0A434
A	274	ASN	ILE	engineered mutation	UNP P0A434
A	293	VAL	MET	engineered mutation	UNP P0A434
A	309	TRP	TYR	engineered mutation	UNP P0A434
A	319	SER	ARG	engineered mutation	UNP P0A434
A	342	SER	PRO	engineered mutation	UNP P0A434
A	348	THR	GLY	engineered mutation	UNP P0A434
A	352	GLU	THR	engineered mutation	UNP P0A434

- Molecule 2 is ethyl-4-methylbenzylphosphonate (three-letter code: 5ZG) (formula: $C_{10}H_{15}O_3P$) (labeled as "Ligand of Interest" by depositor).
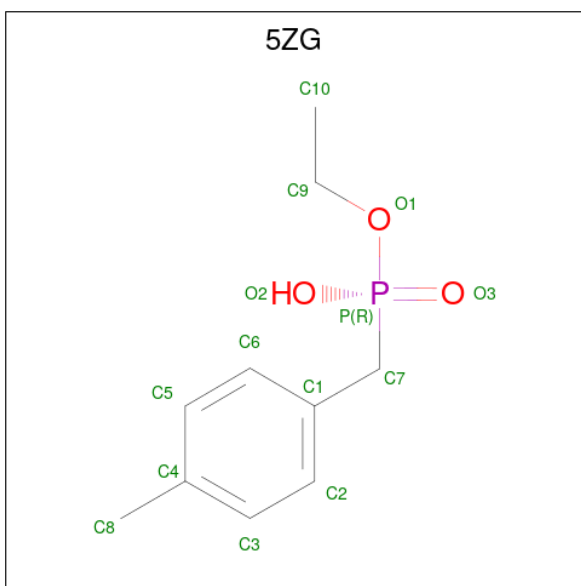
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	O	P	0	0
			14	10	3	1		

- Molecule 3 is FORMIC ACID (three-letter code: FMT) (formula: CH_2O_2) (labeled as "Ligand of Interest" by depositor).
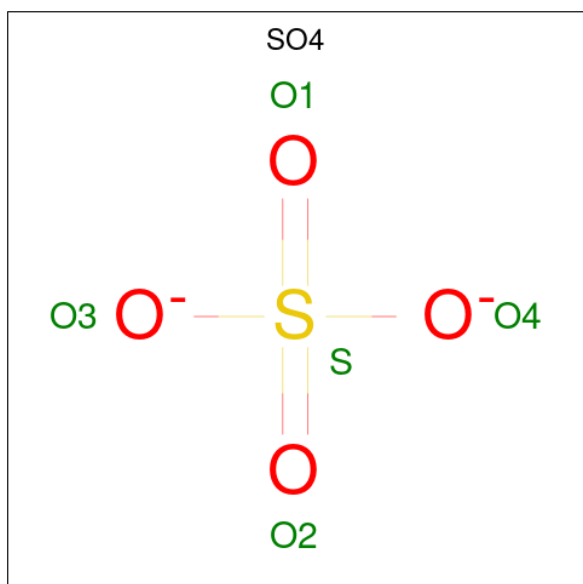
FMT

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

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total 2	Zn 2	0	0

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O_4S).

SO4

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total 5	O 4	S 1	0	0
5	A	1	Total 5	O 4	S 1	0	0
5	A	1	Total 5	O 4	S 1	0	0

- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).

GOL
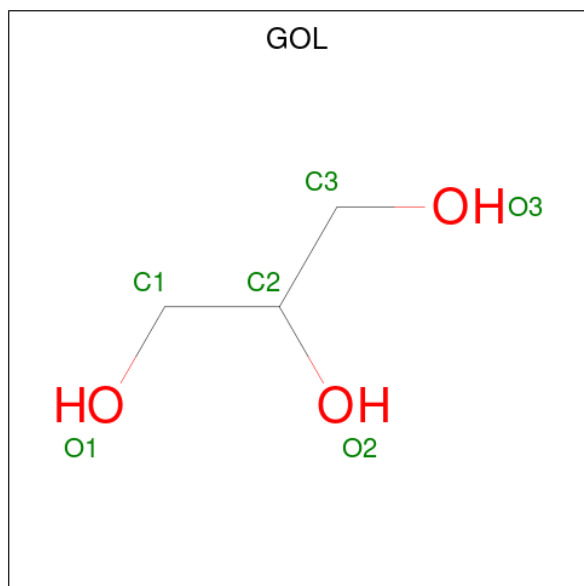
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total 6	C 3	O 3	0	0
6	A	1	Total 6	C 3	O 3	0	0
6	A	1	Total 6	C 3	O 3	0	0

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	251	Total 251	O 251	0	0

3 Residue-property plots ⓘ

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: Parathion hydrolase
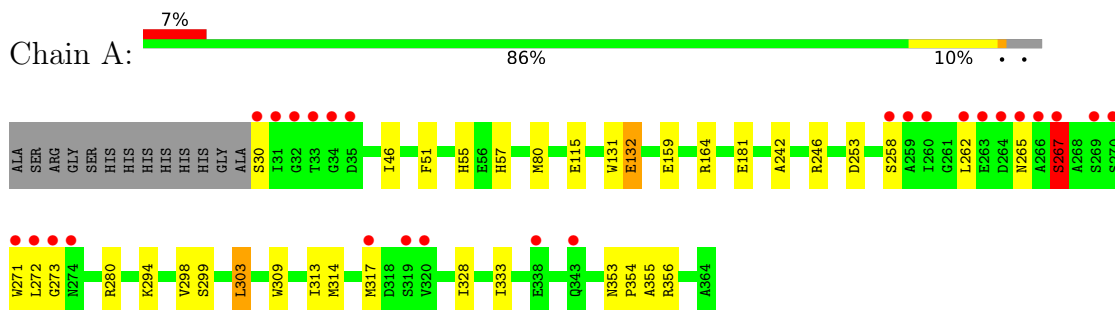
4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α, β, γ	69.30Å 69.30Å 186.93Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.05 – 1.47 49.00 – 1.47	Depositor EDS
% Data completeness (in resolution range)	100.0 (49.05-1.47) 100.0 (49.00-1.47)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.20	Depositor
$< I/\sigma(I) >$ [1]	2.58 (at 1.46Å)	Xtriage
Refinement program	REFMAC 5.8.0266	Depositor
R, R_{free}	0.157 , 0.174 0.166 , 0.181	Depositor DCC
R_{free} test set	3864 reflections (4.90%)	wwPDB-VP
Wilson B-factor (Å^2)	12.8	Xtriage
Anisotropy	0.157	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	(Not available) , (Not available)	EDS
L-test for twinning[2]	$< |L| > = 0.46$, $< L^2 > = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	2920	wwPDB-VP
Average B, all atoms (Å^2)	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.86% 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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: SO4, GOL, FMT, ZN, 5ZG

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	0.84	5/2694 (0.2%)	0.93	2/3660 (0.1%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	159[A]	GLU	CD-OE1	-7.82	1.17	1.25
1	A	159[B]	GLU	CD-OE1	-7.82	1.17	1.25
1	A	159[A]	GLU	CD-OE2	-6.93	1.18	1.25
1	A	159[B]	GLU	CD-OE2	-6.93	1.18	1.25
1	A	132	GLU	CD-OE1	-6.12	1.19	1.25

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	280[A]	ARG	NE-CZ-NH2	-5.05	117.77	120.30
1	A	280[B]	ARG	NE-CZ-NH2	-5.05	117.77	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	2617	0	2640	31	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	14	0	0	0	0
3	A	3	0	0	0	0
4	A	2	0	0	0	0
5	A	15	0	0	0	0
6	A	18	0	24	0	0
7	A	251	0	0	3	1
All	All	2920	0	2664	31	1

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 6.

All (31) 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:314:MET:HA	1:A:317:MET:HE3	1.33	1.08
1:A:271:TRP:CZ2	1:A:317:MET:HG2	2.18	0.78
1:A:314:MET:CA	1:A:317:MET:HE3	2.16	0.75
1:A:271:TRP:CE2	1:A:317:MET:HG2	2.23	0.74
1:A:353:ASN:HA	1:A:356[B]:ARG:HD3	1.68	0.73
1:A:313:ILE:HG13	1:A:317:MET:HE2	1.73	0.70
1:A:294:LYS:HE2	7:A:682:HOH:O	1.92	0.69
1:A:46:ILE:HG23	1:A:355:ALA:HB1	1.81	0.62
1:A:353:ASN:HA	1:A:356[B]:ARG:CD	2.29	0.61
1:A:356[B]:ARG:CG	1:A:356[B]:ARG:HH11	2.21	0.53
1:A:57:HIS:O	1:A:303[A]:LEU:HA	2.09	0.52
1:A:298[B]:VAL:HG12	1:A:328:ILE:HD12	1.94	0.50
1:A:298[B]:VAL:CG1	1:A:328:ILE:HD12	2.43	0.49
1:A:356[B]:ARG:CG	1:A:356[B]:ARG:NH1	2.76	0.48
1:A:356[B]:ARG:HH11	1:A:356[B]:ARG:HG2	1.77	0.48
1:A:313:ILE:HG23	1:A:317:MET:CE	2.44	0.48
1:A:181:GLU:OE1	7:A:501:HOH:O	2.21	0.47
1:A:353:ASN:HB2	1:A:354:PRO:HD3	1.97	0.46
1:A:271:TRP:CH2	1:A:317:MET:SD	3.09	0.46
1:A:80:MET:HE2	1:A:115:GLU:HG2	1.98	0.45
1:A:267:SER:HB3	1:A:309[A]:TRP:HZ2	1.82	0.45
1:A:258:SER:HB2	1:A:273:GLY:CA	2.47	0.45
1:A:30:SER:O	1:A:164:ARG:NH2	2.44	0.44
1:A:313:ILE:HG23	1:A:317:MET:HE2	2.00	0.43
1:A:309[B]:TRP:CD1	1:A:313:ILE:HG12	2.54	0.42
1:A:314:MET:HE1	7:A:561:HOH:O	2.20	0.42
1:A:46:ILE:HD12	1:A:46:ILE:N	2.35	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:57:HIS:HB2	1:A:303[A]:LEU:HB3	2.01	0.41
1:A:242:ALA:O	1:A:246:ARG:HG3	2.20	0.41
1:A:55:HIS:HB3	1:A:253:ASP:HB2	2.02	0.41
1:A:131:TRP:CG	1:A:132:GLU:N	2.88	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:635:HOH:O	7:A:635:HOH:O[7_645]	1.78	0.42

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	342/348 (98%)	323 (94%)	17 (5%)	2 (1%)	25	7

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	267	SER
1	A	265	ASN

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	278/278 (100%)	270 (97%)	8 (3%)	42	12

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	51	PHE
1	A	262	LEU
1	A	267	SER
1	A	272	LEU
1	A	299	SER
1	A	303[A]	LEU
1	A	303[B]	LEU
1	A	333	ILE

Sometimes 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 monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 10 ligands modelled in this entry, 2 are monoatomic - leaving 8 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
6	GOL	A	409	-	5,5,5	0.24	0	5,5,5	0.67	0
6	GOL	A	410	-	5,5,5	0.19	0	5,5,5	0.54	0
6	GOL	A	408	-	5,5,5	0.21	0	5,5,5	0.44	0
5	SO4	A	405	-	4,4,4	0.38	0	6,6,6	0.13	0
5	SO4	A	407	-	4,4,4	0.39	0	6,6,6	0.10	0
3	FMT	A	402	1,4	2,2,2	0.37	0	1,1,1	0.49	0
2	5ZG	A	401	4	14,14,14	0.46	0	16,19,19	1.01	1 (6%)
5	SO4	A	406	-	4,4,4	0.93	0	6,6,6	0.23	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
6	GOL	A	410	-	-	2/4/4/4	-
2	5ZG	A	401	4	-	2/9/9/9	0/1/1/1
6	GOL	A	409	-	-	0/4/4/4	-
6	GOL	A	408	-	-	0/4/4/4	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	401	5ZG	O3-P-C7	3.05	115.55	109.02

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	5ZG	C9-O1-P-O3
6	A	410	GOL	O1-C1-C2-O2
6	A	410	GOL	O1-C1-C2-C3
2	A	401	5ZG	C9-O1-P-O2

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will

also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.
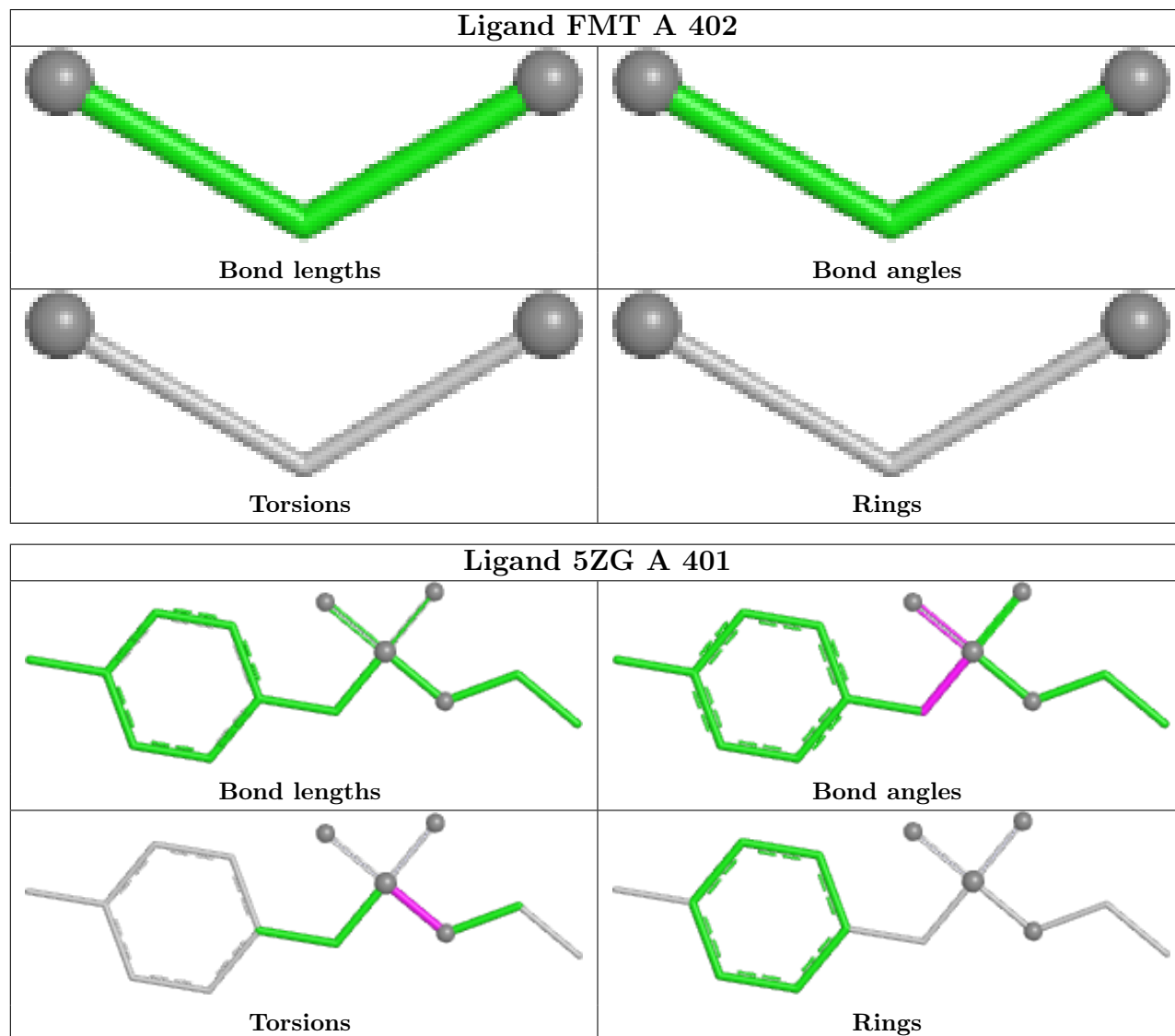
5.7 Other polymers ⓘ

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	335/348 (96%)	0.37	26 (7%)	13	14	8, 14, 38, 118	4 (1%)

All (26) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	263	GLU	40.8
1	A	265	ASN	28.7
1	A	266	ALA	20.2
1	A	264	ASP	18.9
1	A	272	LEU	12.1
1	A	271	TRP	9.3
1	A	269	SER	8.2
1	A	267	SER	7.7
1	A	262	LEU	6.5
1	A	260	ILE	5.8
1	A	33	THR	5.1
1	A	259	ALA	5.0
1	A	274	ASN	4.8
1	A	273	GLY	4.6
1	A	31	ILE	4.1
1	A	320	VAL	3.8
1	A	35	ASP	3.7
1	A	30	SER	3.7
1	A	32	GLY	3.7
1	A	258	SER	3.4
1	A	270	SER	3.1
1	A	319	SER	2.6
1	A	317	MET	2.5
1	A	343	GLN	2.5
1	A	34	GLY	2.4
1	A	338[A]	GLU	2.3

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 monosaccharides 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. 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
6	GOL	A	409	6/6	0.78	0.16	18,25,27,34	0
5	SO4	A	407	5/5	0.88	0.28	55,56,61,65	0
6	GOL	A	410	6/6	0.91	0.14	21,28,33,36	0
5	SO4	A	406	5/5	0.94	0.11	18,20,21,25	0
2	5ZG	A	401	14/14	0.96	0.12	8,12,15,15	14
6	GOL	A	408	6/6	0.96	0.07	12,16,18,23	0
5	SO4	A	405	5/5	0.98	0.21	35,37,39,42	0
3	FMT	A	402	3/3	0.99	0.05	9,9,9,10	0
4	ZN	A	403	1/1	1.00	0.05	10,10,10,10	0
4	ZN	A	404	1/1	1.00	0.04	10,10,10,10	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.
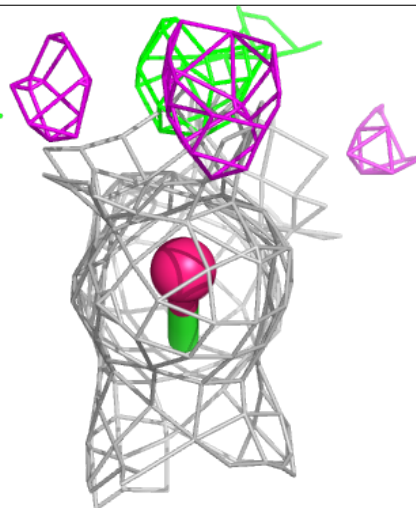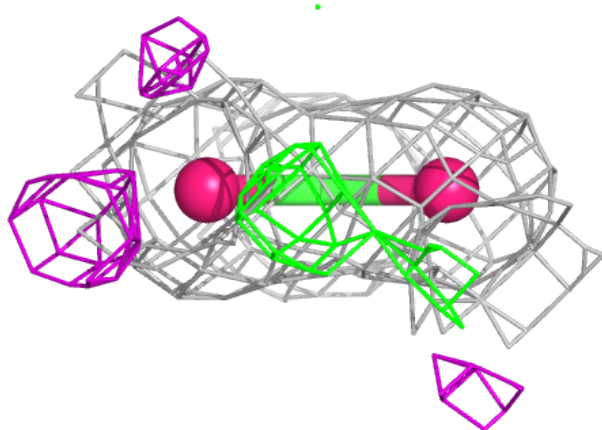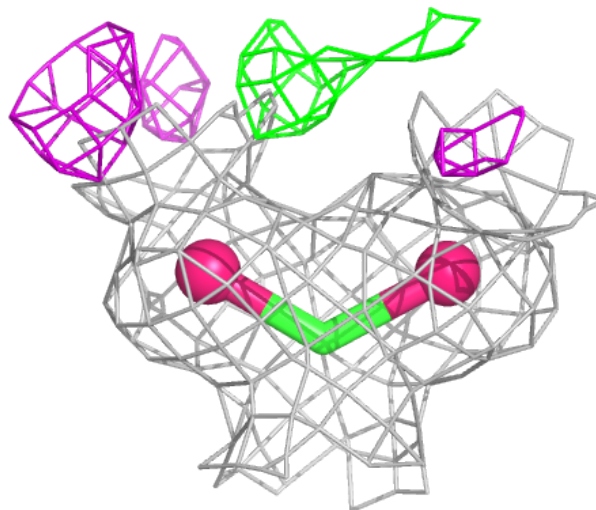
WORLDWIDE
wwPDB
PROTEIN DATA BANK

Electron density around 5ZG A 401:

2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
and green (positive)
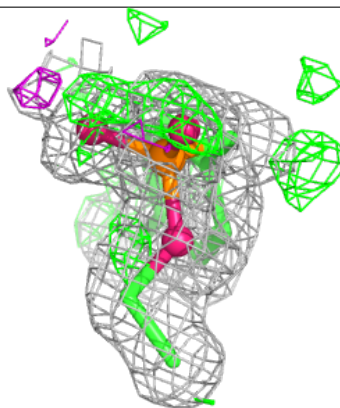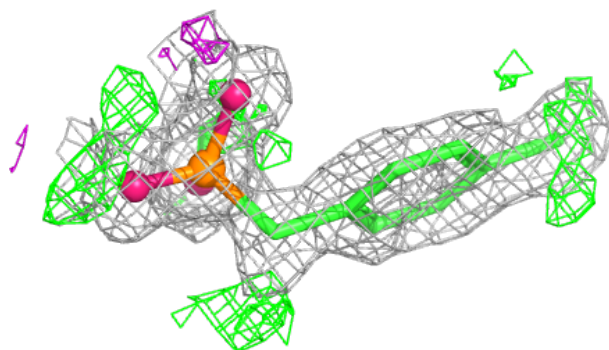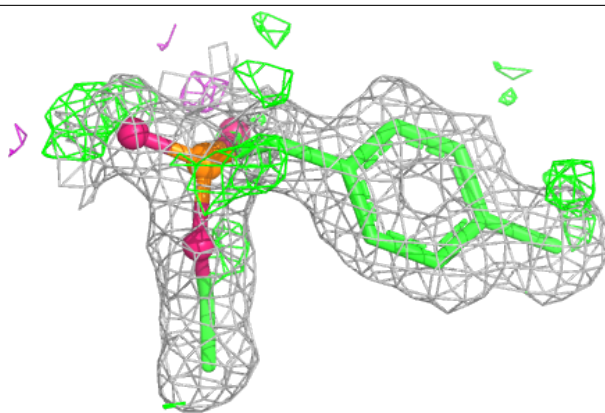
Electron density around FMT A 402:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

Full wwPDB X-ray Structure Validation Report

Electron density around ZN A 403:

$2mF_o\text{-}DF_c$ (at 0.7 rmsd) in gray
$mF_o\text{-}DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)

Electron density around ZN A 404:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)
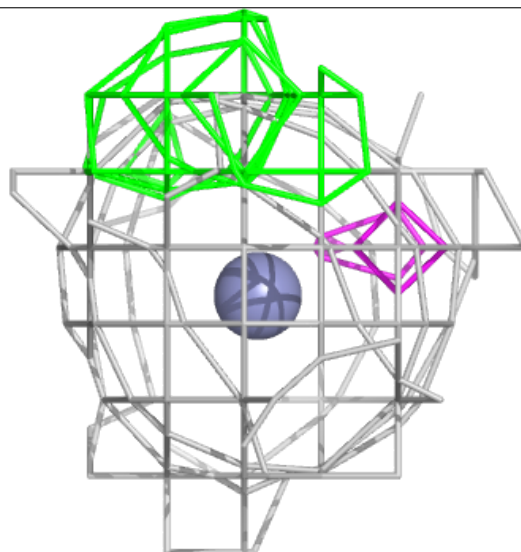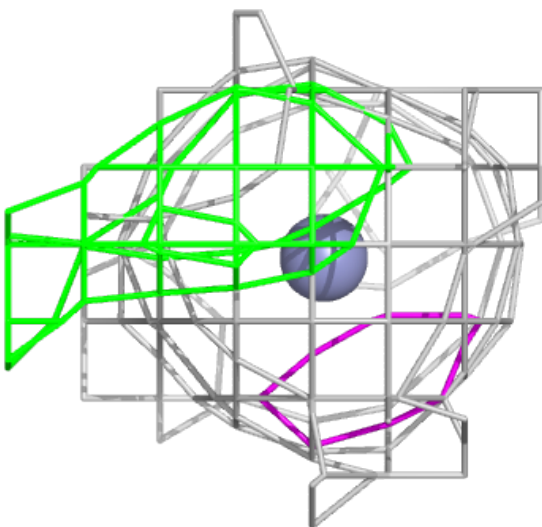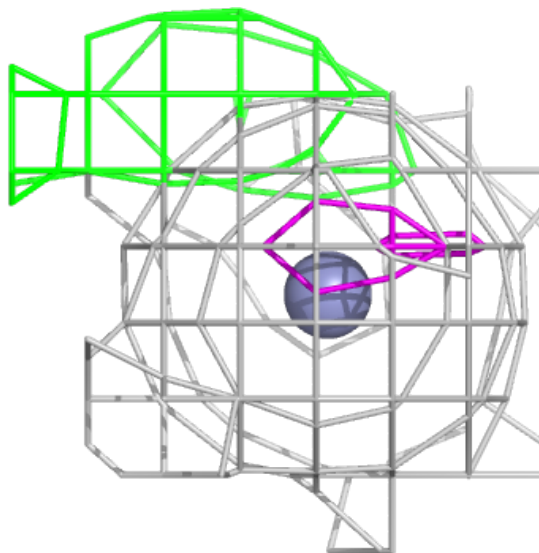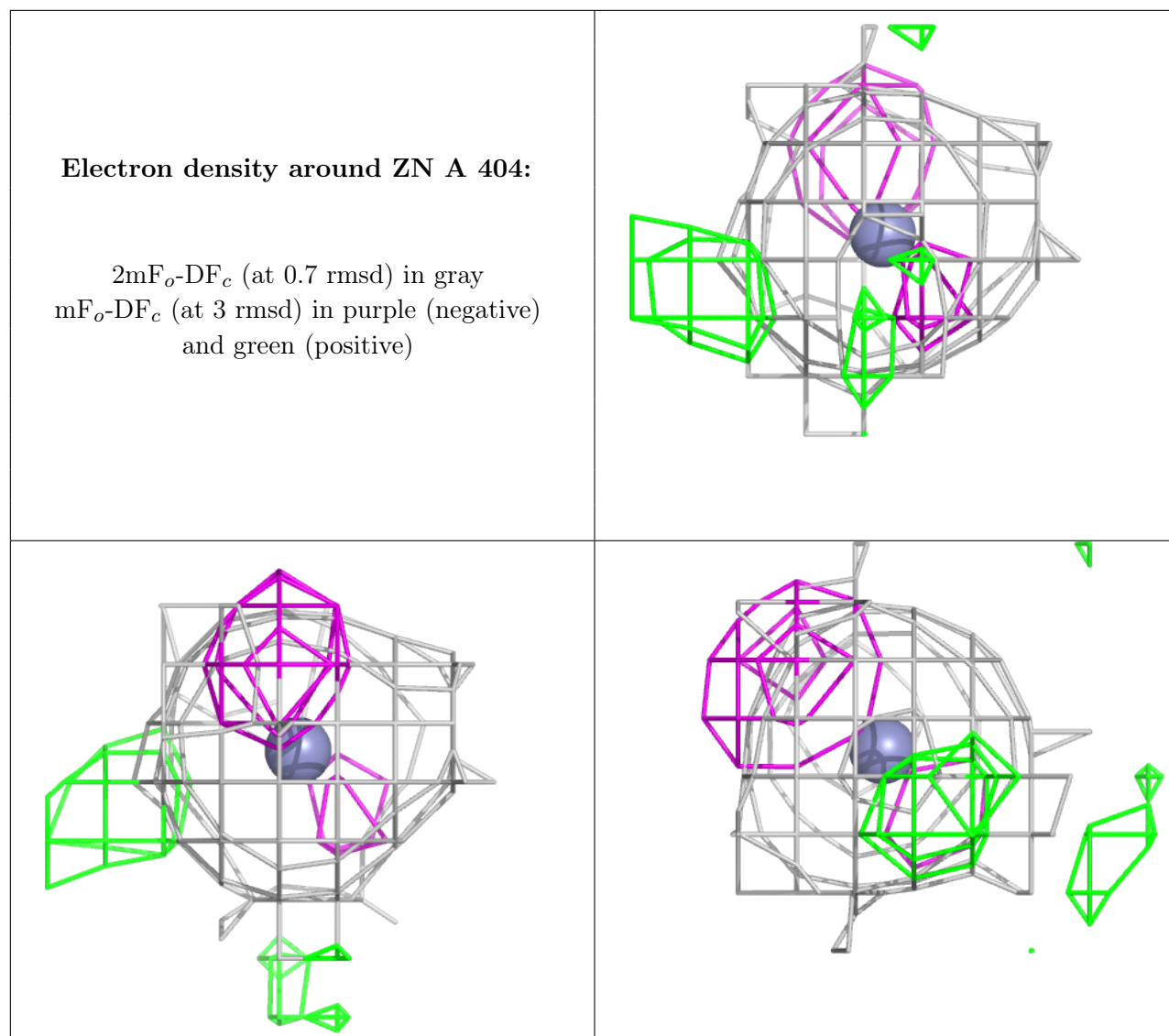
6.5 Other polymers (i)

There are no such residues in this entry.