



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 10, 2020 – 05:14 AM BST

PDB ID : 4LEF
Title : Crystal structure of PHOSPHOTRIESTERASE HOMOLOGY PROTEIN FROM ESCHERICHIA COLI complexed with phosphate in active site
Authors : Fedorov, A.A.; Fedorov, E.V.; Xiang, D.F.; Raushel, F.M.; Almo, S.C.
Deposited on : 2013-06-25
Resolution : 1.84 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	:	2.13.1
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)	:	2.13.1

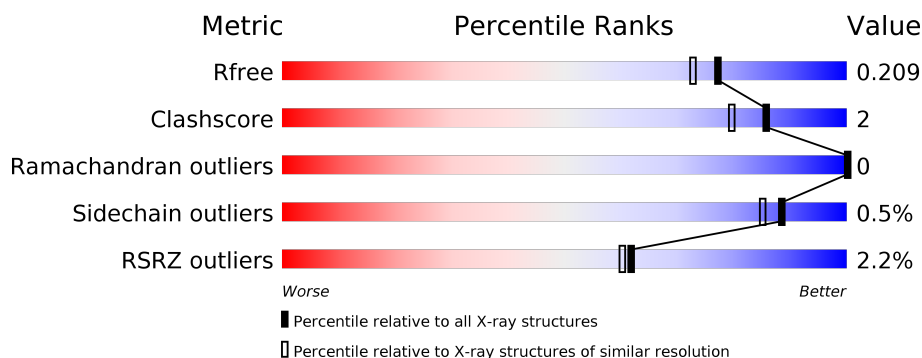
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.84 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	4003 (1.86-1.82)
Clashscore	141614	4233 (1.86-1.82)
Ramachandran outliers	138981	4185 (1.86-1.82)
Sidechain outliers	138945	4186 (1.86-1.82)
RSRZ outliers	127900	3957 (1.86-1.82)

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	292	<div> <div>95%</div> <div>5%</div> </div>
1	B	292	<div> <div>96%</div> <div>• •</div> </div>
1	C	292	<div> <div>91%</div> <div>8%</div> <div>•</div> </div>
1	D	292	<div> <div>%</div> <div>91%</div> <div>9%</div> <div>•</div> </div>
1	E	292	<div> <div>92%</div> <div>7%</div> <div>•</div> </div>
1	F	292	<div> <div>%</div> <div>95%</div> <div>5%</div> </div>

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Mol	Chain	Length	Quality of chain
1	G	292	<div><div></div><div>3%</div><div>96%</div><div></div><div></div></div>
1	H	292	<div><div></div><div>12%</div><div>93%</div><div></div><div>6%</div><div></div></div>

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 20380 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 Phosphotriesterase homology protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	290	Total	C	N	O	S	0	1	0
			2308	1445	402	442	19			
1	D	290	Total	C	N	O	S	0	0	0
			2292	1435	400	440	17			
1	A	291	Total	C	N	O	S	0	3	0
			2325	1453	408	446	18			
1	B	290	Total	C	N	O	S	0	3	0
			2319	1452	406	443	18			
1	E	290	Total	C	N	O	S	0	1	0
			2303	1441	404	441	17			
1	F	291	Total	C	N	O	S	0	2	0
			2315	1448	404	445	18			
1	G	291	Total	C	N	O	S	0	1	0
			2306	1443	402	443	18			
1	H	290	Total	C	N	O	S	0	1	0
			2300	1440	401	441	18			

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	G	2	Total	Zn	0	0
			2	2		
2	D	2	Total	Zn	0	0
			2	2		
2	E	2	Total	Zn	0	0
			2	2		
2	H	2	Total	Zn	0	0
			2	2		
2	B	2	Total	Zn	0	0
			2	2		
2	C	2	Total	Zn	0	0
			2	2		

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

- Molecule 3 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	C	1	Total	O	P	0	0
			5	4	1		
3	C	1	Total	O	P	0	0
			5	4	1		
3	C	1	Total	O	P	0	0
			5	4	1		
3	D	1	Total	O	P	0	0
			5	4	1		
3	D	1	Total	O	P	0	0
			5	4	1		
3	D	1	Total	O	P	0	0
			5	4	1		
3	A	1	Total	O	P	0	0
			5	4	1		
3	A	1	Total	O	P	0	0
			5	4	1		

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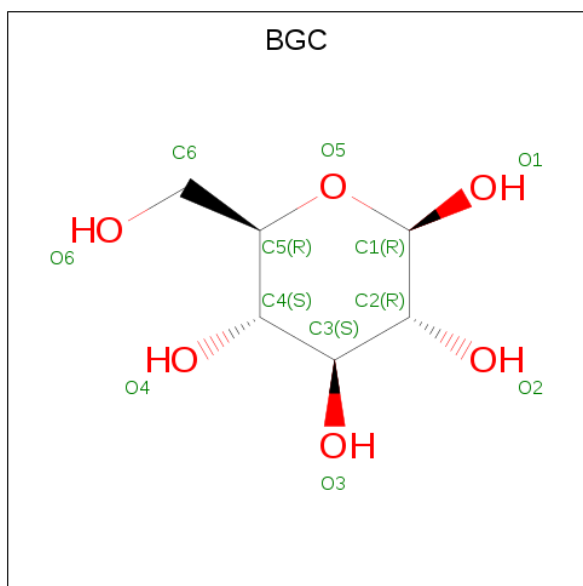
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	P	0	0
			5	4	1		
3	A	1	Total	O	P	0	0
			5	4	1		
3	B	1	Total	O	P	0	0
			5	4	1		
3	B	1	Total	O	P	0	0
			5	4	1		
3	B	1	Total	O	P	0	0
			5	4	1		
3	B	1	Total	O	P	0	0
			5	4	1		
3	B	1	Total	O	P	0	0
			5	4	1		
3	E	1	Total	O	P	0	0
			5	4	1		
3	E	1	Total	O	P	0	0
			5	4	1		
3	E	1	Total	O	P	0	0
			5	4	1		
3	E	1	Total	O	P	0	0
			5	4	1		
3	F	1	Total	O	P	0	0
			5	4	1		
3	F	1	Total	O	P	0	0
			5	4	1		
3	F	1	Total	O	P	0	0
			5	4	1		
3	F	1	Total	O	P	0	0
			5	4	1		
3	G	1	Total	O	P	0	0
			5	4	1		
3	G	1	Total	O	P	0	0
			5	4	1		
3	G	1	Total	O	P	0	0
			5	4	1		
3	G	1	Total	O	P	0	0
			5	4	1		
3	H	1	Total	O	P	0	0
			5	4	1		
3	H	1	Total	O	P	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	H	1	Total	O	P	0	0
			5	4	1		

- Molecule 4 is beta-D-glucopyranose (three-letter code: BGC) (formula: C₆H₁₂O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			12	6	6		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	C	248	Total	O	0	1
			249	249		
5	D	198	Total	O	0	1
			199	199		
5	A	283	Total	O	0	3
			286	286		
5	B	261	Total	O	0	1
			262	262		
5	E	186	Total	O	0	1
			187	187		
5	F	258	Total	O	0	2
			260	260		
5	G	151	Total	O	0	1
			152	152		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	H	134	Total 134	O 134	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: Phosphotriesterase homology protein

Chain C:  91% 8%



- Molecule 1: Phosphotriesterase homology protein

Chain D:  91% 9%



- Molecule 1: Phosphotriesterase homology protein

Chain A:  95% 5%



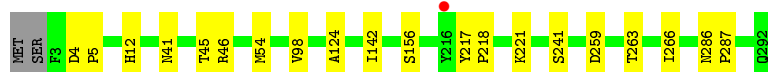
- Molecule 1: Phosphotriesterase homology protein

Chain B:  96%

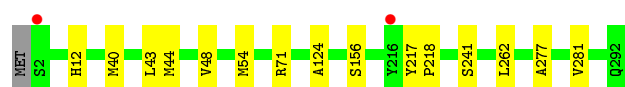


- Molecule 1: Phosphotriesterase homology protein

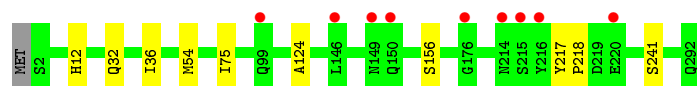
Chain E:  92% 7%



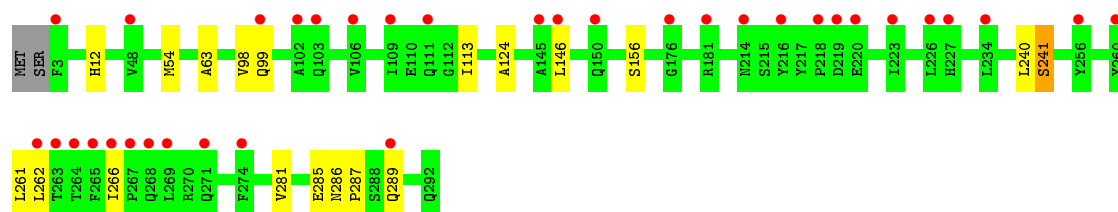
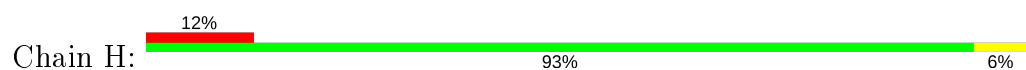
- Molecule 1: Phosphotriesterase homology protein



- Molecule 1: Phosphotriesterase homology protein



- Molecule 1: Phosphotriesterase homology protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	83.05Å 100.31Å 168.04Å 90.00° 104.48° 90.00°	Depositor
Resolution (Å)	42.57 – 1.84 42.57 – 1.84	Depositor EDS
% Data completeness (in resolution range)	99.3 (42.57-1.84) 99.2 (42.57-1.84)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.68 (at 1.84Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8_1069)	Depositor
R, R_{free}	0.175 , 0.208 0.176 , 0.209	Depositor DCC
R_{free} test set	6884 reflections (3.01%)	wwPDB-VP
Wilson B-factor (Å ²)	20.2	Xtriage
Anisotropy	0.277	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 48.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.000 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	20380	wwPDB-VP
Average B, all atoms (Å ²)	26.0	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 34.65 % 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 6.5965e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² 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: ZN, BGC, PO4

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	0.40	0/2365	0.56	0/3191
1	B	0.38	0/2359	0.56	0/3183
1	C	0.36	0/2348	0.55	0/3168
1	D	0.34	0/2332	0.51	0/3148
1	E	0.34	0/2343	0.50	0/3162
1	F	0.40	0/2355	0.56	0/3178
1	G	0.32	0/2346	0.49	0/3166
1	H	0.32	0/2340	0.50	0/3158
All	All	0.36	0/18788	0.53	0/25354

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	124	ALA	Peptide

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	2325	0	2271	8	0
1	B	2319	0	2271	8	0
1	C	2308	0	2258	13	0
1	D	2292	0	2241	14	0
1	E	2303	0	2253	11	0
1	F	2315	0	2261	10	0
1	G	2306	0	2254	4	0
1	H	2300	0	2249	13	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
2	G	2	0	0	0	0
2	H	2	0	0	0	0
3	A	20	0	0	0	0
3	B	25	0	0	1	0
3	C	15	0	0	1	0
3	D	20	0	0	2	0
3	E	20	0	0	0	0
3	F	20	0	0	0	0
3	G	20	0	0	0	0
3	H	15	0	0	0	0
4	B	12	0	11	0	0
5	A	286	0	0	0	0
5	B	262	0	0	4	0
5	C	249	0	0	0	0
5	D	199	0	0	1	0
5	E	187	0	0	0	0
5	F	260	0	0	2	0
5	G	152	0	0	0	0
5	H	134	0	0	2	0
All	All	20380	0	18069	82	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.

The worst 5 of 82 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:E:217:TYR:CZ	1:E:221:LYS:HB3	2.32	0.65
1:H:99:GLN:NE2	5:H:509:HOH:O	2.30	0.65
1:E:46[B]:ARG:NH1	1:E:259:ASP:OD2	2.29	0.65
1:C:48:VAL:HG23	1:C:262:LEU:HD11	1.83	0.61
1:H:240:LEU:HD23	1:H:241:SER:N	2.16	0.60

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	292/292 (100%)	287 (98%)	5 (2%)	0	100	100
1	B	291/292 (100%)	284 (98%)	7 (2%)	0	100	100
1	C	290/292 (99%)	284 (98%)	6 (2%)	0	100	100
1	D	288/292 (99%)	280 (97%)	8 (3%)	0	100	100
1	E	289/292 (99%)	283 (98%)	6 (2%)	0	100	100
1	F	291/292 (100%)	285 (98%)	6 (2%)	0	100	100
1	G	290/292 (99%)	282 (97%)	8 (3%)	0	100	100
1	H	289/292 (99%)	281 (97%)	8 (3%)	0	100	100
All	All	2320/2336 (99%)	2266 (98%)	54 (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	252/250 (101%)	251 (100%)	1 (0%)	91	88
1	B	251/250 (100%)	250 (100%)	1 (0%)	91	88
1	C	250/250 (100%)	249 (100%)	1 (0%)	91	88
1	D	248/250 (99%)	246 (99%)	2 (1%)	81	75
1	E	249/250 (100%)	248 (100%)	1 (0%)	91	88
1	F	251/250 (100%)	250 (100%)	1 (0%)	91	88
1	G	250/250 (100%)	248 (99%)	2 (1%)	81	75
1	H	249/250 (100%)	248 (100%)	1 (0%)	91	88
All	All	2000/2000 (100%)	1990 (100%)	10 (0%)	88	85

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	241	SER
1	E	241	SER
1	G	75	ILE
1	A	241	SER
1	F	241	SER

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 monosaccharides in this entry.

5.6 Ligand geometry

Of 48 ligands modelled in this entry, 16 are monoatomic - leaving 32 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	PO4	F	306	-	4,4,4	0.88	0	6,6,6	0.42	0
3	PO4	H	303	2	4,4,4	0.99	0	6,6,6	0.55	0
3	PO4	C	304	-	4,4,4	0.95	0	6,6,6	0.47	0
3	PO4	A	304	-	4,4,4	1.09	0	6,6,6	0.45	0
3	PO4	B	303	2	4,4,4	1.02	0	6,6,6	0.34	0
3	PO4	D	304	-	4,4,4	0.87	0	6,6,6	0.47	0
3	PO4	C	305	-	4,4,4	0.88	0	6,6,6	0.44	0
3	PO4	G	306	-	4,4,4	0.87	0	6,6,6	0.44	0
3	PO4	H	305	-	4,4,4	0.85	0	6,6,6	0.49	0
3	PO4	B	305	-	4,4,4	0.91	0	6,6,6	0.47	0
3	PO4	G	305	-	4,4,4	0.89	0	6,6,6	0.41	0
3	PO4	B	306	-	4,4,4	0.88	0	6,6,6	0.45	0
3	PO4	G	304	-	4,4,4	0.87	0	6,6,6	0.40	0
3	PO4	D	306	-	4,4,4	0.82	0	6,6,6	0.42	0
3	PO4	H	304	-	4,4,4	0.87	0	6,6,6	0.62	0
3	PO4	C	303	2	4,4,4	0.98	0	6,6,6	0.85	0
3	PO4	B	307	-	4,4,4	0.89	0	6,6,6	0.45	0
3	PO4	F	305	-	4,4,4	0.89	0	6,6,6	0.41	0
3	PO4	D	305	-	4,4,4	0.85	0	6,6,6	0.51	0
3	PO4	E	303	2	4,4,4	1.23	0	6,6,6	0.48	0
3	PO4	B	304	-	4,4,4	0.86	0	6,6,6	0.44	0
3	PO4	D	303	2	4,4,4	1.10	0	6,6,6	0.72	0
3	PO4	A	303	2	4,4,4	0.95	0	6,6,6	0.60	0
3	PO4	F	303	2	4,4,4	0.94	0	6,6,6	0.66	0
3	PO4	E	306	-	4,4,4	0.91	0	6,6,6	0.34	0
3	PO4	A	306	-	4,4,4	0.86	0	6,6,6	0.41	0
3	PO4	F	304	-	4,4,4	0.81	0	6,6,6	0.51	0
3	PO4	E	305	-	4,4,4	0.85	0	6,6,6	0.45	0
3	PO4	A	305	-	4,4,4	0.83	0	6,6,6	0.54	0
4	BGC	B	308	-	12,12,12	2.12	5 (41%)	17,17,17	1.35	4 (23%)
3	PO4	E	304	-	4,4,4	0.84	0	6,6,6	0.52	0
3	PO4	G	303	2	4,4,4	0.92	0	6,6,6	0.51	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
4	BGC	B	308	-	-	0/2/22/22	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	308	BGC	C6-C5	-3.50	1.40	1.51
4	B	308	BGC	O5-C5	3.34	1.52	1.44
4	B	308	BGC	C3-C2	-3.30	1.43	1.52
4	B	308	BGC	C4-C3	-2.60	1.45	1.52
4	B	308	BGC	C1-C2	-2.11	1.47	1.52

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	308	BGC	C3-C4-C5	2.30	114.34	110.24
4	B	308	BGC	C1-O5-C5	-2.20	109.51	113.66
4	B	308	BGC	O5-C5-C4	-2.16	105.77	109.69
4	B	308	BGC	O6-C6-C5	2.10	118.50	111.29

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	304	PO4	1	0
3	D	304	PO4	1	0
3	B	305	PO4	1	0
3	D	306	PO4	1	0

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 ⓘ

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	291/292 (99%)	-0.66	0 100 100	7, 15, 26, 45	0
1	B	290/292 (99%)	-0.61	0 100 100	8, 16, 31, 40	0
1	C	290/292 (99%)	-0.50	1 (0%) 94 93	10, 18, 32, 76	0
1	D	290/292 (99%)	-0.13	3 (1%) 82 82	12, 28, 47, 84	0
1	E	290/292 (99%)	-0.43	1 (0%) 94 93	14, 25, 39, 81	0
1	F	291/292 (99%)	-0.62	2 (0%) 87 87	8, 16, 30, 80	0
1	G	291/292 (99%)	-0.26	9 (3%) 49 46	15, 29, 50, 97	0
1	H	290/292 (99%)	0.55	35 (12%) 4 3	18, 42, 76, 89	0
All	All	2323/2336 (99%)	-0.33	51 (2%) 62 60	7, 22, 51, 97	0

The worst 5 of 51 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	216	TYR	8.0
1	G	216	TYR	7.3
1	H	266	ILE	6.8
1	C	216	TYR	6.6
1	D	216	TYR	6.3

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
3	PO4	E	306	5/5	0.68	0.21	83,84,87,87	0
3	PO4	G	306	5/5	0.71	0.22	79,82,84,87	0
3	PO4	D	306	5/5	0.78	0.33	64,64,68,71	0
3	PO4	F	306	5/5	0.82	0.24	90,91,92,93	0
3	PO4	A	305	5/5	0.83	0.23	70,72,75,77	0
3	PO4	D	305	5/5	0.85	0.21	83,86,86,89	0
3	PO4	G	304	5/5	0.85	0.15	80,82,83,86	0
3	PO4	D	304	5/5	0.86	0.15	77,79,81,82	0
3	PO4	B	307	5/5	0.86	0.18	84,86,87,87	0
3	PO4	H	305	5/5	0.87	0.16	69,70,75,75	0
3	PO4	F	305	5/5	0.89	0.14	72,73,74,75	0
3	PO4	C	304	5/5	0.89	0.19	68,73,76,79	0
3	PO4	G	305	5/5	0.89	0.25	84,84,84,85	0
3	PO4	E	304	5/5	0.89	0.12	63,71,72,74	0
3	PO4	E	305	5/5	0.90	0.12	74,75,78,78	0
3	PO4	C	305	5/5	0.91	0.26	70,72,75,76	0
3	PO4	F	304	5/5	0.92	0.12	53,54,64,65	0
3	PO4	B	306	5/5	0.92	0.23	66,70,72,72	0
3	PO4	B	305	5/5	0.93	0.18	66,71,72,75	0
3	PO4	A	306	5/5	0.93	0.26	59,62,66,66	0
4	BGC	B	308	12/12	0.95	0.09	10,15,17,26	0
3	PO4	H	304	5/5	0.95	0.10	60,62,64,70	0
2	ZN	H	301	1/1	0.97	0.06	21,21,21,21	0
3	PO4	B	304	5/5	0.98	0.07	29,35,38,46	0
3	PO4	D	303	5/5	0.98	0.08	14,15,17,21	0
3	PO4	A	304	5/5	0.98	0.08	21,23,30,36	0
3	PO4	H	303	5/5	0.98	0.08	20,20,27,31	0
2	ZN	H	302	1/1	0.98	0.05	21,21,21,21	0
3	PO4	G	303	5/5	0.98	0.06	19,19,21,21	0
3	PO4	B	303	5/5	0.99	0.07	11,14,18,19	0
2	ZN	E	302	1/1	0.99	0.06	16,16,16,16	0
3	PO4	E	303	5/5	0.99	0.07	12,20,22,25	0
2	ZN	E	301	1/1	0.99	0.07	17,17,17,17	0
2	ZN	D	302	1/1	0.99	0.06	14,14,14,14	0
3	PO4	C	303	5/5	0.99	0.08	8,13,16,18	0
2	ZN	G	302	1/1	0.99	0.06	18,18,18,18	0
3	PO4	A	303	5/5	0.99	0.08	11,13,18,19	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	PO4	F	303	5/5	0.99	0.06	10,10,18,19	0
2	ZN	D	301	1/1	0.99	0.07	15,15,15,15	0
2	ZN	B	302	1/1	1.00	0.08	12,12,12,12	0
2	ZN	C	301	1/1	1.00	0.05	11,11,11,11	0
2	ZN	C	302	1/1	1.00	0.07	12,12,12,12	0
2	ZN	A	302	1/1	1.00	0.07	10,10,10,10	0
2	ZN	A	301	1/1	1.00	0.07	10,10,10,10	0
2	ZN	G	301	1/1	1.00	0.05	16,16,16,16	0
2	ZN	F	302	1/1	1.00	0.06	11,11,11,11	0
2	ZN	F	301	1/1	1.00	0.07	10,10,10,10	0
2	ZN	B	301	1/1	1.00	0.07	10,10,10,10	0

6.5 Other polymers [i](#)

There are no such residues in this entry.