wwPDB X-ray Structure Validation Summary Report (i)

Jun 18, 2024 – 01:35 PM EDT

PDB ID	:	4D9K
Title	:	Crystal structure of Escherichia coli Diaminopropionate ammonia lyase in apo form
Authors	:	Bisht, S.; Rajaram, V.; Bharath, S.R.; Murthy, M.R.N.
Deposited on	:	2012-01-11
Resolution	:	2.19 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 (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

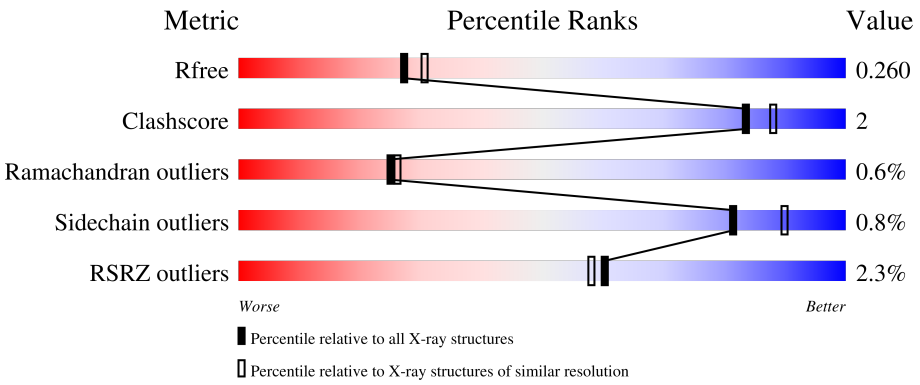
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.19 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	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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 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	398	4% 86% 6% 8%
1	B	398	% 82% 8% 10%
1	C	398	2% 86% 5% 9%
1	D	398	2% 85% 6% • 8%

2 Entry composition (i)

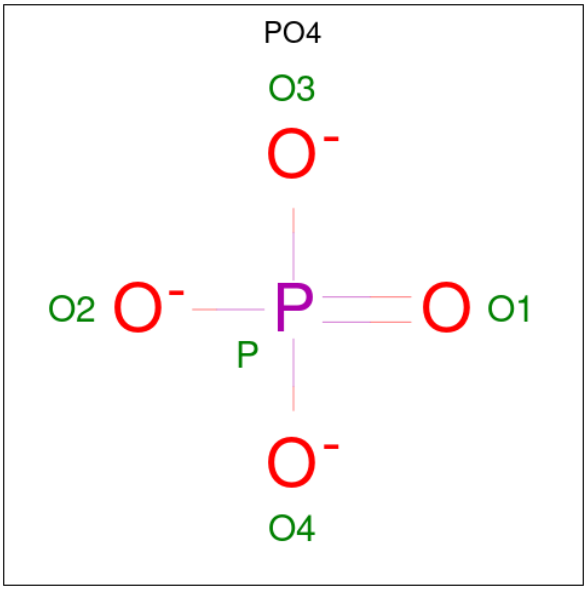
There are 4 unique types of molecules in this entry. The entry contains 11560 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Diaminopropionate ammonia-lyase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	366	2786	1767	477	525	17	0	0	0
1	D	367	2793	1773	478	525	17	0	0	0
1	B	357	2713	1719	464	513	17	0	0	0
1	C	363	2730	1727	469	517	17	0	1	0

- Molecule 2 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).



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

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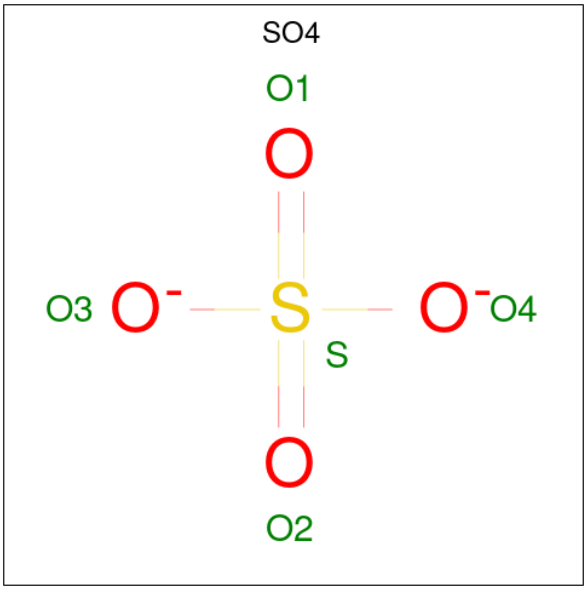
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total O P 5 4 1	0	0
2	C	1	Total O P 5 4 1	0	0

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



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

- Molecule 4 is water.

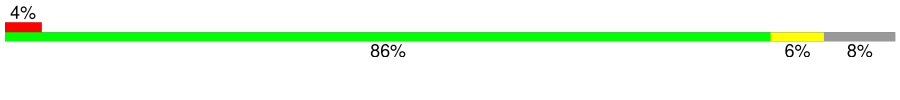
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	166	Total O 166 166	0	0
4	D	97	Total O 97 97	0	0
4	B	153	Total O 153 153	0	0
4	C	87	Total O 87 87	0	0

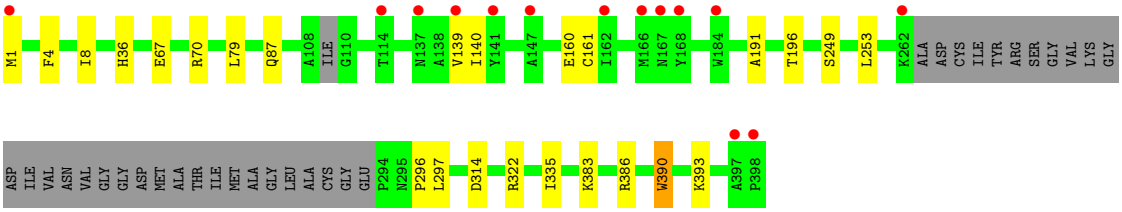
3 Residue-property plots (i)

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: Diaminopropionate ammonia-lyase

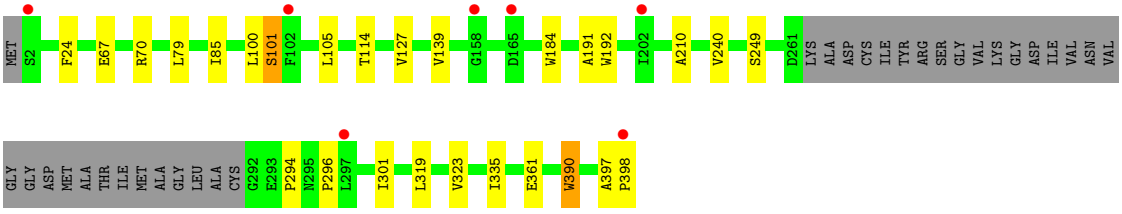
Chain A:





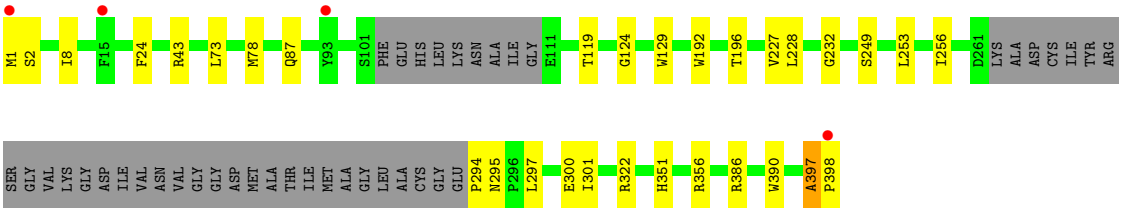
• Molecule 1: Diaminopropionate ammonia-lyase

Chain D:



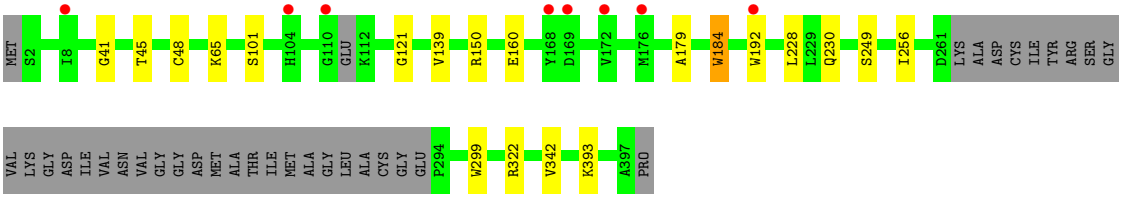
• Molecule 1: Diaminopropionate ammonia-lyase

Chain B:



• Molecule 1: Diaminopropionate ammonia-lyase

Chain C:


MET
S2
I8
G41
T45
C48
K65
S101
H104
G110
GLU
K112
G121
V139
R150
E160
Y168
D169
V172
M176
A179
W184
W192
L228
L229
Q230
S249
I256
D261
LYS
ALA
ASP
CYS
ILE
TYR
ARG
SER
GLY
VAL
LYS
GLY
ASP
ILE
VAL
ASN
VAL
GLY
GLY
ASP
MET
ALA
THR
ILE
MET
ALA
GLY
LEU
ALA
CYS
GLY
GLU
P294
W299
R322
V342
K393
A397
PRO

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	85.78Å 94.14Å 94.69Å 90.00° 110.01° 90.00°	Depositor
Resolution (Å)	40.65 – 2.19 40.65 – 2.19	Depositor EDS
% Data completeness (in resolution range)	98.0 (40.65-2.19) 98.1 (40.65-2.19)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.48 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.213 , 0.261 0.212 , 0.260	Depositor DCC
R_{free} test set	3590 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å^2)	34.4	Xtriage
Anisotropy	0.415	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 37.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	11560	wwPDB-VP
Average B, all atoms (Å^2)	43.0	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 20.59 % 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 8.4131e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[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: PO4, CME, SO4

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	0.47	1/2833 (0.0%)	0.51	0/3847
1	B	0.47	1/2758 (0.0%)	0.51	0/3748
1	C	0.46	3/2768 (0.1%)	0.48	0/3765
1	D	0.46	2/2841 (0.1%)	0.50	0/3859
All	All	0.47	7/11200 (0.1%)	0.50	0/15219

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	390	TRP	CD2-CE2	5.24	1.47	1.41
1	D	192	TRP	CD2-CE2	5.13	1.47	1.41
1	B	192	TRP	CD2-CE2	5.07	1.47	1.41
1	D	390	TRP	CD2-CE2	5.06	1.47	1.41
1	C	192	TRP	CD2-CE2	5.04	1.47	1.41

There are no bond angle outliers.

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	2786	0	2714	13	0
1	B	2713	0	2635	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	2730	0	2604	10	0
1	D	2793	0	2723	14	0
2	A	5	0	0	0	0
2	B	5	0	0	1	0
2	C	5	0	0	0	0
2	D	5	0	0	0	0
3	A	10	0	0	0	0
3	C	5	0	0	0	0
4	A	166	0	0	1	0
4	B	153	0	0	0	0
4	C	87	0	0	0	0
4	D	97	0	0	1	0
All	All	11560	0	10676	52	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 52 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:383:LYS:HG3	1:B:1:MET:HA	1.64	0.78
1:B:398:PRO:HB3	1:C:41:GLY:HA2	1.67	0.76
1:B:397:ALA:HB1	1:B:398:PRO:CD	2.19	0.73
1:D:67:GLU:OE1	1:D:70:ARG:HD2	1.94	0.67
1:A:8:ILE:HG22	1:A:8:ILE:O	1.95	0.65

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	359/398 (90%)	346 (96%)	12 (3%)	1 (0%)	41	46
1	B	350/398 (88%)	337 (96%)	11 (3%)	2 (1%)	25	26
1	C	356/398 (89%)	342 (96%)	12 (3%)	2 (1%)	25	26
1	D	362/398 (91%)	345 (95%)	14 (4%)	3 (1%)	19	19
All	All	1427/1592 (90%)	1370 (96%)	49 (3%)	8 (1%)	25	26

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	101	SER
1	B	397	ALA
1	C	101	SER
1	D	294	PRO
1	A	249	SER

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	286/318 (90%)	283 (99%)	3 (1%)	76	86
1	B	278/318 (87%)	274 (99%)	4 (1%)	67	80
1	C	270/318 (85%)	270 (100%)	0	100	100
1	D	286/318 (90%)	284 (99%)	2 (1%)	84	91
All	All	1120/1272 (88%)	1111 (99%)	9 (1%)	81	90

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	87	GLN
1	B	300	GLU
1	D	105	LEU
1	D	361	GLU
1	B	2	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	394	HIS
1	B	87	GLN
1	C	330	ASN
1	B	330	ASN
1	A	355	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

5 non-standard protein/DNA/RNA residues 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	$\#\|Z\| > 2$
1	CME	D	48	1	8,9,10	0.82	0	6,9,11	0.71	0
1	CME	C	48[B]	-	8,9,10	0.78	0	6,9,11	0.68	0
1	CME	A	48	1	8,9,10	0.89	0	6,9,11	1.06	0
1	CME	C	48[A]	-	8,9,10	0.81	0	6,9,11	0.79	0
1	CME	B	48	1	8,9,10	0.81	0	6,9,11	0.67	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
1	CME	D	48	1	-	2/5/8/10	-
1	CME	C	48[B]	-	-	1/5/8/10	-
1	CME	A	48	1	-	1/5/8/10	-
1	CME	C	48[A]	-	-	3/5/8/10	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	CME	B	48	1	-	2/5/8/10	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	D	48	CME	SD-CE-CZ-OH
1	C	48[A]	CME	N-CA-CB-SG
1	C	48[B]	CME	SD-CE-CZ-OH
1	C	48[A]	CME	SD-CE-CZ-OH
1	A	48	CME	SD-CE-CZ-OH

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	C	48[A]	CME	1	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

7 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	$\#\|Z\| > 2$
3	SO4	A	502	-	4,4,4	0.44	0	6,6,6	0.09	0
2	PO4	D	401	-	4,4,4	1.03	0	6,6,6	0.43	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	PO4	A	501	-	4,4,4	1.13	0	6,6,6	0.62	0
2	PO4	C	401	-	4,4,4	1.02	0	6,6,6	0.45	0
3	SO4	C	402	-	4,4,4	0.44	0	6,6,6	0.07	0
2	PO4	B	401	-	4,4,4	1.05	0	6,6,6	0.74	0
3	SO4	A	503	-	4,4,4	0.45	0	6,6,6	0.13	0

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	B	401	PO4	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	365/398 (91%)	0.28	14 (3%)	40	38	23, 36, 72, 88	0
1	B	356/398 (89%)	0.11	4 (1%)	80	79	22, 37, 56, 83	0
1	C	362/398 (90%)	0.26	8 (2%)	62	59	29, 50, 87, 109	0
1	D	366/398 (91%)	0.20	7 (1%)	66	65	31, 45, 67, 83	0
All	All	1449/1592 (91%)	0.21	33 (2%)	60	58	22, 41, 71, 109	0

The worst 5 of 33 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1	MET	6.3
1	A	1	MET	5.6
1	C	176	MET	4.8
1	A	184	TRP	4.4
1	A	168	TYR	4.1

6.2 Non-standard residues in protein, DNA, RNA chains (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(Å^2)	Q<0.9
1	CME	C	48[A]	10/11	0.80	0.19	34,36,37,38	7
1	CME	C	48[B]	10/11	0.80	0.19	34,36,40,40	7
1	CME	D	48	10/11	0.86	0.12	37,41,50,50	0
1	CME	A	48	10/11	0.89	0.15	29,33,45,45	0
1	CME	B	48	10/11	0.89	0.14	32,35,46,48	0

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, 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	SO4	C	402	5/5	0.90	0.22	82,83,84,85	0
2	PO4	B	401	5/5	0.95	0.14	38,42,43,44	0
2	PO4	C	401	5/5	0.95	0.15	63,64,66,66	0
3	SO4	A	503	5/5	0.95	0.16	47,48,48,49	0
2	PO4	D	401	5/5	0.95	0.12	59,62,62,63	0
2	PO4	A	501	5/5	0.97	0.14	46,47,49,50	0
3	SO4	A	502	5/5	0.98	0.17	53,53,54,56	0

6.5 Other polymers (i)

There are no such residues in this entry.