



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 31, 2026 – 01:44 AM UTC

PDB ID : 6PC0 / pdb_00006pc0
Title : Crystal structure of Helicobacter pylori PPX/GppA
Authors : Song, H.; Wang, C.; Shaw, G.X.; Ji, X.
Deposited on : 2019-06-15
Resolution : 1.70 Å(reported)

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

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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>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

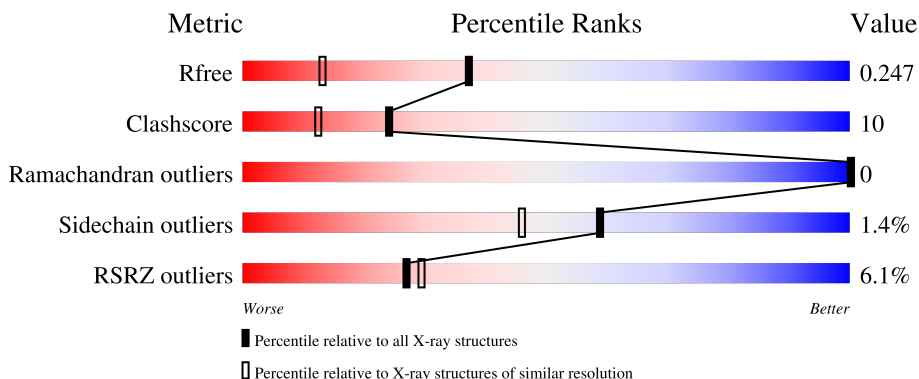
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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}	180053	5551 (1.70-1.70)
Clashscore	190562	5924 (1.70-1.70)
Ramachandran outliers	187476	5846 (1.70-1.70)
Sidechain outliers	187428	5846 (1.70-1.70)
RSRZ outliers	180081	5554 (1.70-1.70)

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 $\leq 5\%$. 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	495	 7% 74% 21% ..
1	B	495	 5% 83% 14% ..

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	SO4	A	509	-	-	X	-
4	MLT	A	514	-	-	X	-
4	MLT	A	515	-	-	X	-
5	LMR	B	520	-	X	-	-

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 8756 atoms, of which 76 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 Guanosine pentaphosphate phosphohydrolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	478	3860	2506	661	672	21	0	14	0
1	B	484	3962	2562	676	700	24	0	21	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-10	MET	-	initiating methionine	UNP B5ZA44
A	-9	ARG	-	expression tag	UNP B5ZA44
A	-8	GLY	-	expression tag	UNP B5ZA44
A	-7	SER	-	expression tag	UNP B5ZA44
A	-6	HIS	-	expression tag	UNP B5ZA44
A	-5	HIS	-	expression tag	UNP B5ZA44
A	-4	HIS	-	expression tag	UNP B5ZA44
A	-3	HIS	-	expression tag	UNP B5ZA44
A	-2	HIS	-	expression tag	UNP B5ZA44
A	-1	HIS	-	expression tag	UNP B5ZA44
A	0	GLY	-	expression tag	UNP B5ZA44
A	1	SER	-	expression tag	UNP B5ZA44
B	-10	MET	-	initiating methionine	UNP B5ZA44
B	-9	ARG	-	expression tag	UNP B5ZA44
B	-8	GLY	-	expression tag	UNP B5ZA44
B	-7	SER	-	expression tag	UNP B5ZA44
B	-6	HIS	-	expression tag	UNP B5ZA44
B	-5	HIS	-	expression tag	UNP B5ZA44
B	-4	HIS	-	expression tag	UNP B5ZA44
B	-3	HIS	-	expression tag	UNP B5ZA44
B	-2	HIS	-	expression tag	UNP B5ZA44
B	-1	HIS	-	expression tag	UNP B5ZA44
B	0	GLY	-	expression tag	UNP B5ZA44
B	1	SER	-	expression tag	UNP B5ZA44

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



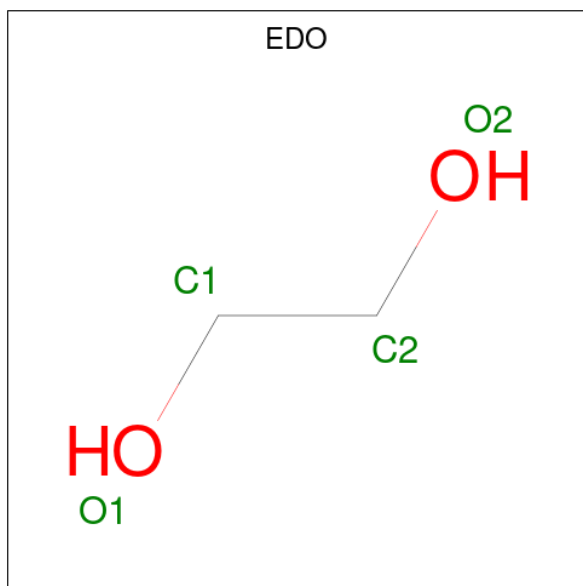
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total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

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

- Molecule 3 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



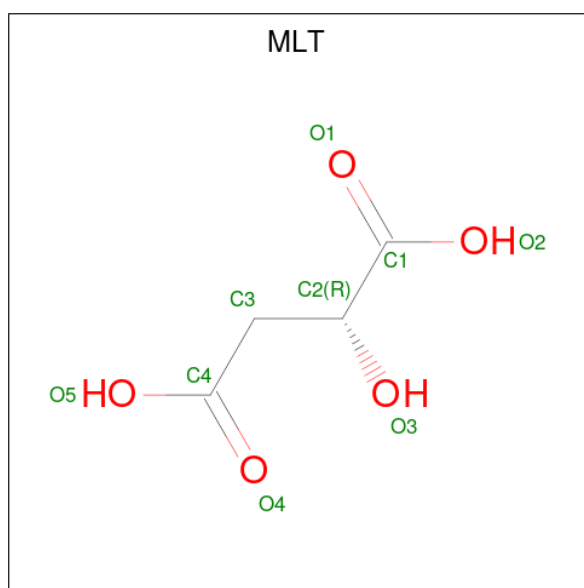
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	H	O	0	0
			10	2	6	2		
3	A	1	Total	C	H	O	0	0
			10	2	6	2		

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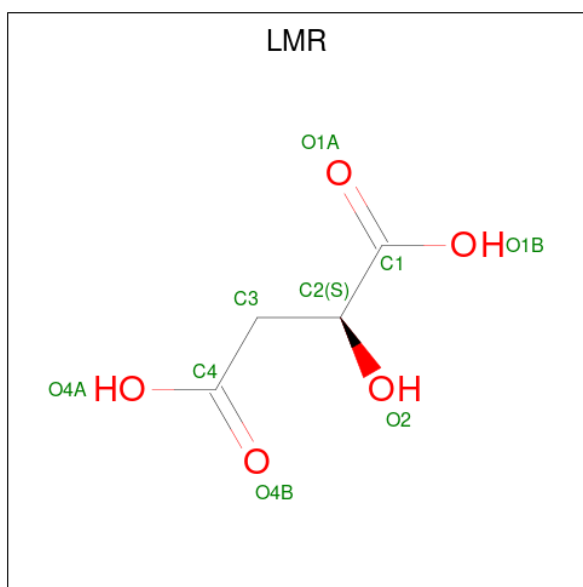
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	H	O	0	0
			10	2	6	2		
3	B	1	Total	C	H	O	0	0
			10	2	6	2		
3	B	1	Total	C	H	O	0	0
			10	2	6	2		
3	B	1	Total	C	H	O	0	1
			20	4	12	4		
3	B	1	Total	C	H	O	0	0
			10	2	6	2		
3	B	1	Total	C	H	O	0	0
			10	2	6	2		

- Molecule 4 is D-MALATE (CCD ID: MLT) (formula: C₄H₆O₅).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	H	O	0	0
			13	4	4	5		
4	A	1	Total	C	H	O	0	0
			13	4	4	5		

- Molecule 5 is (2S)-2-hydroxybutanedioic acid (CCD ID: LMR) (formula: C₄H₆O₅).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	
5	B	1	Total	C	H	O	0	0
			13	4	4	5		
5	B	1	Total	C	H	O	0	0
			13	4	4	5		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	290	Total	O	0	1
			290	290		
6	B	382	Total	O	0	1
			382	382		

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	51.36Å 129.46Å 166.75Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.11 – 1.70 39.11 – 1.70	Depositor EDS
% Data completeness (in resolution range)	98.6 (39.11-1.70) 99.1 (39.11-1.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.51 (at 1.70Å)	Xtrriage
Refinement program	PHENIX (dev_3352: ???)	Depositor
R, R_{free}	0.189 , 0.212 0.191 , 0.247	Depositor DCC
R_{free} test set	1000 reflections (0.80%)	wwPDB-VP
Wilson B-factor (Å ²)	29.3	Xtrriage
Anisotropy	0.315	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 41.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	8756	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.25% of the height of the origin peak. No significant pseudotranslation is detected.*

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: EDO, LMR, SO4, MLT

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	0.48	0/3955	0.84	14/5312 (0.3%)
1	B	0.51	0/4048	0.86	12/5436 (0.2%)
All	All	0.50	0/8003	0.85	26/10748 (0.2%)

There are no bond length outliers.

The worst 5 of 26 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	36	SER	CA-C-N	-8.01	111.71	122.85
1	B	36	SER	C-N-CA	-8.01	111.71	122.85
1	A	125	ASN	N-CA-C	6.94	122.10	112.45
1	A	190	LEU	CA-C-N	6.88	126.51	119.56
1	A	190	LEU	C-N-CA	6.88	126.51	119.56

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	3860	0	4094	101	0
1	B	3962	0	4177	64	0
2	A	55	0	0	2	0
2	B	55	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	8	12	12	4	0
3	B	32	48	48	7	0
4	A	18	8	8	9	0
5	B	18	8	8	2	0
6	A	290	0	0	12	0
6	B	382	0	0	12	0
All	All	8680	76	8347	163	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 10.

The worst 5 of 163 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:256:ARG:HH22	4:A:515:MLT:H2	1.14	1.11
1:B:342:LEU:HD13	1:B:450:LEU:HD21	1.40	1.02
1:B:390:GLN:HA	1:B:415[B]:MET:HE1	1.41	1.02
1:A:256:ARG:HH22	4:A:515:MLT:C2	1.79	0.95
1:A:212:MET:HE1	1:A:222:LEU:HD13	1.48	0.94

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	488/495 (99%)	476 (98%)	12 (2%)	0	100	100
1	B	504/495 (102%)	494 (98%)	10 (2%)	0	100	100
All	All	992/990 (100%)	970 (98%)	22 (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	429/430 (100%)	422 (98%)	7 (2%)	55	41
1	B	442/430 (103%)	436 (99%)	6 (1%)	59	46
All	All	871/860 (101%)	858 (98%)	13 (2%)	59	43

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	103[A]	CYS
1	B	103[B]	CYS
1	B	322	GLU
1	B	174	LEU
1	B	298	ASN

Sometimes 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	230	HIS
1	B	232	ASN
1	B	453	ASN
1	B	113	GLN
1	A	321	HIS

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

36 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
2	SO4	A	510	-	4,4,4	0.29	0	6,6,6	0.39	0
2	SO4	B	505	-	4,4,4	0.22	0	6,6,6	0.18	0
2	SO4	B	501	-	4,4,4	0.24	0	6,6,6	0.06	0
3	EDO	B	512	-	3,3,3	0.46	0	2,2,2	0.37	0
2	SO4	A	507	-	4,4,4	0.24	0	6,6,6	0.11	0
4	MLT	A	515	-	8,8,8	0.70	0	10,10,10	1.91	2 (20%)
2	SO4	B	509	-	4,4,4	0.25	0	6,6,6	0.05	0
2	SO4	B	503	-	4,4,4	0.24	0	6,6,6	0.11	0
3	EDO	A	513	-	3,3,3	0.40	0	2,2,2	0.37	0
2	SO4	B	502	-	4,4,4	0.24	0	6,6,6	0.22	0
2	SO4	B	506	-	4,4,4	0.26	0	6,6,6	0.07	0
2	SO4	A	501	-	4,4,4	0.25	0	6,6,6	0.16	0
2	SO4	B	510	-	4,4,4	0.31	0	6,6,6	0.30	0
3	EDO	B	516[A]	-	3,3,3	0.45	0	2,2,2	0.31	0
3	EDO	B	517	-	3,3,3	0.48	0	2,2,2	0.21	0
5	LMR	B	520	-	8,8,8	2.53	4 (50%)	10,10,10	1.57	2 (20%)
3	EDO	A	512	-	3,3,3	0.46	0	2,2,2	0.18	0
3	EDO	B	518	-	3,3,3	0.40	0	2,2,2	0.40	0
2	SO4	B	504	-	4,4,4	0.27	0	6,6,6	0.15	0
2	SO4	B	508	-	4,4,4	0.25	0	6,6,6	0.04	0
2	SO4	B	511	-	4,4,4	0.36	0	6,6,6	0.44	0
2	SO4	B	507	-	4,4,4	0.23	0	6,6,6	0.07	0
2	SO4	A	509	-	4,4,4	0.21	0	6,6,6	0.17	0
3	EDO	B	515	-	3,3,3	0.41	0	2,2,2	0.41	0
2	SO4	A	504	-	4,4,4	0.24	0	6,6,6	0.08	0
2	SO4	A	506	-	4,4,4	0.25	0	6,6,6	0.08	0
2	SO4	A	511	-	4,4,4	0.23	0	6,6,6	0.24	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	LMR	B	519	-	8,8,8	1.79	2 (25%)	10,10,10	1.62	1 (10%)
2	SO4	A	508	-	4,4,4	0.29	0	6,6,6	0.12	0
3	EDO	B	516[B]	-	3,3,3	0.43	0	2,2,2	0.22	0
3	EDO	B	514	-	3,3,3	0.39	0	2,2,2	0.38	0
3	EDO	B	513	-	3,3,3	0.46	0	2,2,2	0.42	0
4	MLT	A	514	-	8,8,8	1.86	2 (25%)	10,10,10	1.48	1 (10%)
2	SO4	A	505	-	4,4,4	0.24	0	6,6,6	0.11	0
2	SO4	A	503	-	4,4,4	0.25	0	6,6,6	0.14	0
2	SO4	A	502	-	4,4,4	0.26	0	6,6,6	0.12	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
3	EDO	A	512	-	-	0/1/1/1	-
3	EDO	B	514	-	-	0/1/1/1	-
3	EDO	B	513	-	-	0/1/1/1	-
3	EDO	B	512	-	-	1/1/1/1	-
3	EDO	B	518	-	-	1/1/1/1	-
3	EDO	B	517	-	-	1/1/1/1	-
4	MLT	A	515	-	-	6/8/8/8	-
4	MLT	A	514	-	-	6/8/8/8	-
5	LMR	B	519	-	-	0/8/8/8	-
3	EDO	A	513	-	-	1/1/1/1	-
5	LMR	B	520	-	-	6/8/8/8	-
3	EDO	B	516[A]	-	-	1/1/1/1	-
3	EDO	B	515	-	-	0/1/1/1	-
3	EDO	B	516[B]	-	-	1/1/1/1	-

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	520	LMR	O1A-C1	4.46	1.35	1.22
4	A	514	MLT	O4-C4	4.03	1.35	1.22
5	B	520	LMR	O4B-C4	3.90	1.34	1.22
5	B	519	LMR	O4B-C4	3.79	1.34	1.22
5	B	519	LMR	O4A-C4	-2.96	1.21	1.30

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	515	MLT	O2-C1-C2	4.30	121.83	112.74
5	B	519	LMR	O1B-C1-C2	3.34	119.80	112.74
4	A	514	MLT	O2-C1-C2	3.15	119.41	112.74
5	B	520	LMR	O1B-C1-C2	3.12	119.33	112.74
5	B	520	LMR	O4A-C4-C3	2.28	121.08	114.00

There are no chirality outliers.

5 of 24 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	514	MLT	O1-C1-C2-O3
4	A	514	MLT	O2-C1-C2-O3
4	A	514	MLT	C1-C2-C3-C4
4	A	514	MLT	O3-C2-C3-C4
4	A	515	MLT	O1-C1-C2-O3

There are no ring outliers.

12 monomers are involved in 26 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	515	MLT	5	0
2	B	509	SO4	1	0
3	A	513	EDO	3	0
3	B	517	EDO	3	0
5	B	520	LMR	2	0
3	A	512	EDO	1	0
3	B	518	EDO	2	0
2	B	508	SO4	1	0
2	A	509	SO4	2	0
3	B	515	EDO	1	0
3	B	513	EDO	1	0
4	A	514	MLT	4	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	478/495 (96%)	0.62	35 (7%) 21 23	15, 36, 67, 82	14 (2%)
1	B	484/495 (97%)	0.20	24 (4%) 34 38	9, 30, 51, 74	21 (4%)
All	All	962/990 (97%)	0.41	59 (6%) 27 29	9, 32, 61, 82	35 (3%)

The worst 5 of 59 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	45[A]	TYR	5.0
1	B	484	ALA	4.7
1	A	484	ALA	4.4
1	A	178	LEU	4.3
1	A	249	LEU	4.2

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 oligosaccharides 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	SO4	B	507	5/5	0.67	0.10	75,80,108,112	0
2	SO4	A	508	5/5	0.68	0.12	58,72,84,105	0
5	LMR	B	520	9/9	0.69	0.14	59,65,72,76	0
2	SO4	A	507	5/5	0.70	0.10	88,91,112,113	0
2	SO4	B	506	5/5	0.73	0.12	67,68,90,102	0
2	SO4	B	505	5/5	0.74	0.18	42,45,60,61	5
3	EDO	B	515	4/4	0.74	0.15	50,67,71,83	0
2	SO4	A	506	5/5	0.74	0.08	85,86,96,107	0
3	EDO	B	516[A]	4/4	0.78	0.13	34,43,52,52	10
3	EDO	B	516[B]	4/4	0.78	0.13	32,43,51,52	10
3	EDO	B	518	4/4	0.78	0.12	49,60,69,73	0
3	EDO	B	513	4/4	0.78	0.14	36,57,68,68	0
3	EDO	A	513	4/4	0.79	0.11	39,57,69,74	0
4	MLT	A	515	9/9	0.80	0.13	49,59,71,74	0
2	SO4	B	508	5/5	0.80	0.08	77,83,88,95	0
5	LMR	B	519	9/9	0.81	0.12	51,56,64,67	0
4	MLT	A	514	9/9	0.81	0.12	50,58,63,65	0
2	SO4	A	504	5/5	0.82	0.10	76,77,92,94	0
2	SO4	A	505	5/5	0.84	0.07	69,72,89,90	5
3	EDO	B	517	4/4	0.85	0.11	43,54,58,65	0
3	EDO	B	514	4/4	0.85	0.09	52,63,68,68	0
3	EDO	B	512	4/4	0.86	0.10	35,52,61,74	0
2	SO4	B	501	5/5	0.86	0.10	48,56,66,67	0
2	SO4	B	502	5/5	0.87	0.09	34,49,58,60	5
2	SO4	B	511	5/5	0.87	0.11	39,40,47,51	0
3	EDO	A	512	4/4	0.87	0.11	36,46,56,58	0
2	SO4	A	503	5/5	0.87	0.10	47,48,56,60	5
2	SO4	A	501	5/5	0.88	0.08	60,66,83,85	0
2	SO4	B	503	5/5	0.89	0.11	38,53,57,59	5
2	SO4	A	511	5/5	0.90	0.09	46,52,56,57	0
2	SO4	B	504	5/5	0.91	0.07	61,71,75,81	0
2	SO4	A	502	5/5	0.91	0.07	58,62,65,66	0
2	SO4	A	510	5/5	0.94	0.08	36,41,47,49	0
2	SO4	B	509	5/5	0.98	0.08	31,32,35,40	0
2	SO4	A	509	5/5	0.98	0.05	34,40,43,49	0
2	SO4	B	510	5/5	0.99	0.06	28,28,31,32	0

6.5 Other polymers [i](#)

There are no such residues in this entry.