



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 23, 2024 – 03:33 AM EDT

PDB ID : 5MX6
Title : Crystal structure of *H. pylori* purine nucleoside phosphorylase from clinical isolate HpPNP-2
Authors : Stefanic, Z.
Deposited on : 2017-01-21
Resolution : 2.41 Å (reported)

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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 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
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

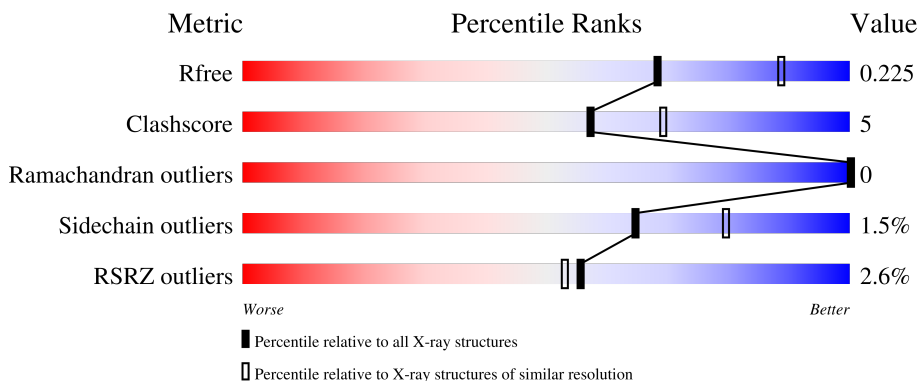
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.41 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.



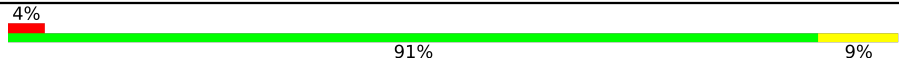
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	4647 (2.44-2.40)
Clashscore	141614	5161 (2.44-2.40)
Ramachandran outliers	138981	5073 (2.44-2.40)
Sidechain outliers	138945	5074 (2.44-2.40)
RSRZ outliers	127900	4543 (2.44-2.40)

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	233	 5% 91% 9%
1	B	233	 5% 85% 15%
1	C	233	 % 91% 9%
1	D	233	 91% 9%
1	E	233	 4% 82% 18%

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Mol	Chain	Length	Quality of chain
1	F	233	

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	303	-	-	-	X

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 11499 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 Purine nucleoside phosphorylase DeoD-type.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	233	1802	1150	300	335	17	0	0	0
1	B	233	1813	1157	301	338	17	0	2	0
1	C	233	1805	1152	300	335	18	0	1	0
1	D	233	1802	1150	300	335	17	0	0	0
1	E	233	1802	1150	300	335	17	0	0	0
1	F	233	1808	1154	300	336	18	0	2	0

There are 6 discrepancies between the modelled and reference sequences:

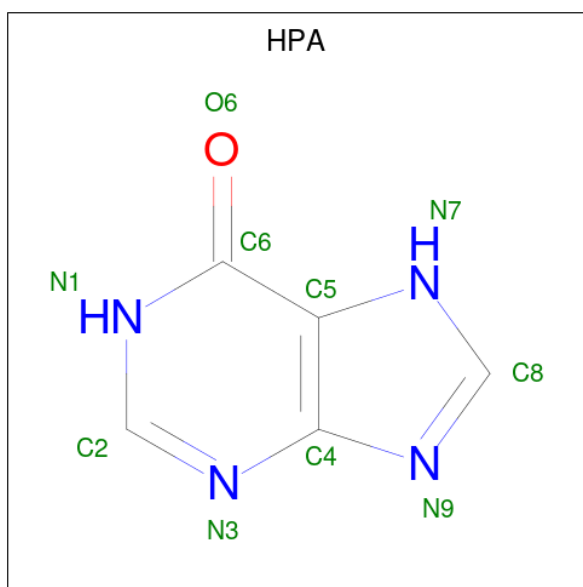
Chain	Residue	Modelled	Actual	Comment	Reference
A	107	THR	ILE	conflict	UNP K2JXG0
B	107	THR	ILE	conflict	UNP K2JXG0
C	107	THR	ILE	conflict	UNP K2JXG0
D	107	THR	ILE	conflict	UNP K2JXG0
E	107	THR	ILE	conflict	UNP K2JXG0
F	107	THR	ILE	conflict	UNP K2JXG0

- Molecule 2 is SULFATE ION (three-letter code: 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	B	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	E	1	Total	O	S	0	0
			5	4	1		
2	F	1	Total	O	S	0	0
			5	4	1		
2	F	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is HYPOXANTHINE (three-letter code: HPA) (formula: C₅H₄N₄O).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	A	1	Total 10	C 5	N 4	O 1	0	0
3	B	1	Total 10	C 5	N 4	O 1	0	0
3	C	1	Total 10	C 5	N 4	O 1	0	0
3	D	1	Total 10	C 5	N 4	O 1	0	0
3	E	1	Total 10	C 5	N 4	O 1	0	0
3	F	1	Total 10	C 5	N 4	O 1	0	0

- Molecule 4 is ACETATE ION (three-letter code: ACT) (formula: C₂H₃O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			4	2	2		
4	F	1	Total	C	O	0	0
			4	2	2		

- Molecule 5 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).



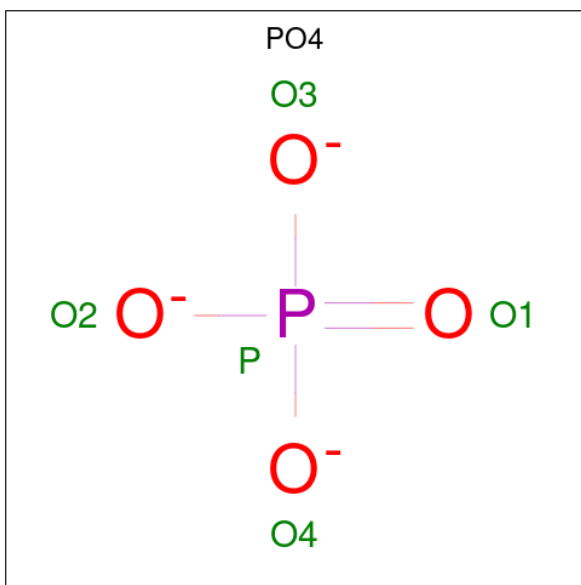
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			7	4	3		
5	B	1	Total	C	O	0	0
			7	4	3		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	C	1	Total	C	O	0	0
			7	4	3		
5	D	1	Total	C	O	0	0
			7	4	3		
5	E	1	Total	C	O	0	0
			7	4	3		

- Molecule 6 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



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

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	100	Total	O	0	0
			100	100		
7	B	70	Total	O	0	0
			70	70		
7	C	94	Total	O	0	0
			94	94		
7	D	93	Total	O	0	0
			93	93		
7	E	71	Total	O	0	0
			71	71		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	F	86	Total	O	0	0
			86	86		

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.

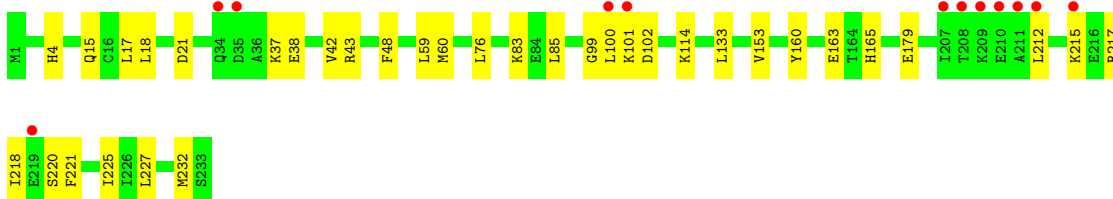
- Molecule 1: Purine nucleoside phosphorylase DeoD-type

Chain A:  91% 9%

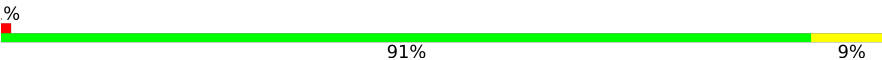


- Molecule 1: Purine nucleoside phosphorylase DeoD-type

Chain B:  5% 85% 15%



- Molecule 1: Purine nucleoside phosphorylase DeoD-type

Chain C:  91% 9%




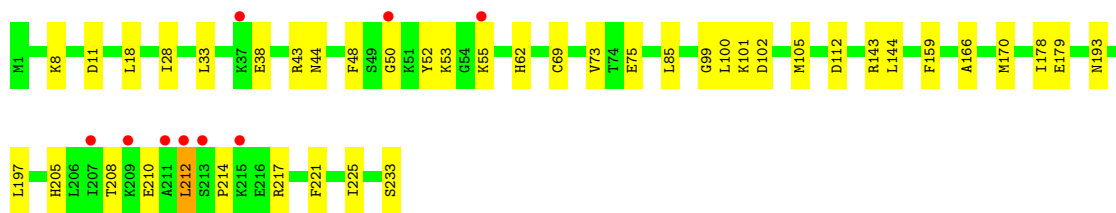
- Molecule 1: Purine nucleoside phosphorylase DeoD-type

Chain D:  91% 9%

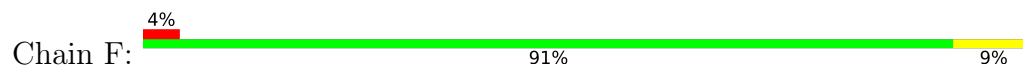


- Molecule 1: Purine nucleoside phosphorylase DeoD-type

Chain E:  4% 82% 18%



● Molecule 1: Purine nucleoside phosphorylase DeoD-type



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	104.26Å 119.86Å 139.22Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.80 – 2.41 34.80 – 2.41	Depositor EDS
% Data completeness (in resolution range)	99.5 (34.80-2.41) 99.6 (34.80-2.41)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.20 (at 2.42Å)	Xtrriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.175 , 0.225 0.174 , 0.225	Depositor DCC
R_{free} test set	3369 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	30.6	Xtrriage
Anisotropy	0.028	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 54.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	11499	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.02% 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: PEG, ACT, PO4, HPA, 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	1/1833 (0.1%)	0.58	0/2467
1	B	0.41	0/1850	0.58	0/2490
1	C	0.45	0/1839	0.59	0/2475
1	D	0.42	0/1833	0.57	0/2467
1	E	0.42	0/1833	0.61	1/2467 (0.0%)
1	F	0.43	0/1845	0.61	0/2483
All	All	0.43	1/11033 (0.0%)	0.59	1/14849 (0.0%)

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	E	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	19	CYS	CB-SG	-5.63	1.72	1.81

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	212	LEU	CA-CB-CG	5.45	127.83	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	E	212	LEU	Peptide

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	1802	0	1836	13	1
1	B	1813	0	1849	21	0
1	C	1805	0	1842	13	0
1	D	1802	0	1837	13	0
1	E	1802	0	1837	35	0
1	F	1808	0	1847	19	0
2	A	10	0	0	0	0
2	B	5	0	0	0	0
2	C	5	0	0	0	0
2	D	10	0	0	0	0
2	E	5	0	0	0	0
2	F	10	0	0	1	0
3	A	10	0	4	0	0
3	B	10	0	4	0	0
3	C	10	0	4	0	0
3	D	10	0	4	0	0
3	E	10	0	4	0	0
3	F	10	0	4	0	0
4	A	4	0	3	0	0
4	F	4	0	3	0	0
5	A	7	0	10	2	0
5	B	7	0	10	0	0
5	C	7	0	10	0	0
5	D	7	0	10	0	0
5	E	7	0	10	1	0
6	C	5	0	0	0	0
7	A	100	0	0	0	0
7	B	70	0	0	1	0
7	C	94	0	0	1	0
7	D	93	0	0	1	0
7	E	71	0	0	1	0
7	F	86	0	0	6	1
All	All	11499	0	11128	109	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 5.

The worst 5 of 109 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:F:24:ARG:NH1	1:F:221:PHE:CE1	2.08	1.21
1:F:24:ARG:NH1	1:F:221:PHE:CD1	2.32	0.94
1:F:26:SER:O	7:F:401:HOH:O	1.98	0.82
1:F:212:LEU:O	1:F:217:ARG:NH2	2.15	0.80
1:D:101:LYS:HD3	1:D:220:SER:HB2	1.68	0.74

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)
1:A:210:GLU:OE1	7:F:401:HOH:O[4_445]	1.98	0.22

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	231/233 (99%)	223 (96%)	8 (4%)	0	100	100
1	B	233/233 (100%)	222 (95%)	11 (5%)	0	100	100
1	C	232/233 (100%)	228 (98%)	4 (2%)	0	100	100
1	D	231/233 (99%)	223 (96%)	8 (4%)	0	100	100
1	E	231/233 (99%)	219 (95%)	12 (5%)	0	100	100
1	F	233/233 (100%)	225 (97%)	8 (3%)	0	100	100
All	All	1391/1398 (100%)	1340 (96%)	51 (4%)	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	196/196 (100%)	192 (98%)	4 (2%)	55	72
1	B	198/196 (101%)	195 (98%)	3 (2%)	65	79
1	C	197/196 (100%)	194 (98%)	3 (2%)	65	79
1	D	196/196 (100%)	192 (98%)	4 (2%)	55	72
1	E	196/196 (100%)	194 (99%)	2 (1%)	76	87
1	F	198/196 (101%)	196 (99%)	2 (1%)	76	87
All	All	1181/1176 (100%)	1163 (98%)	18 (2%)	65	79

5 of 18 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	44	ASN
1	F	179	GLU
1	F	142	LYS
1	C	122	ASN
1	D	179	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 monosaccharides in this entry.

5.6 Ligand geometry

23 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	HPA	F	302	-	8,11,11	2.26	3 (37%)	5,15,15	3.23	3 (60%)
2	SO4	B	301	-	4,4,4	0.21	0	6,6,6	0.19	0
2	SO4	F	301	-	4,4,4	0.14	0	6,6,6	0.53	0
2	SO4	A	301	-	4,4,4	0.35	0	6,6,6	0.33	0
3	HPA	E	302	-	8,11,11	2.16	3 (37%)	5,15,15	3.02	2 (40%)
5	PEG	C	304	-	6,6,6	0.48	0	5,5,5	0.62	0
3	HPA	C	302	-	8,11,11	2.34	3 (37%)	5,15,15	3.09	3 (60%)
5	PEG	A	305	-	6,6,6	0.46	0	5,5,5	0.89	0
3	HPA	D	302	-	8,11,11	2.11	3 (37%)	5,15,15	3.18	4 (80%)
2	SO4	A	303	1	4,4,4	0.37	0	6,6,6	0.13	0
2	SO4	F	303	-	4,4,4	0.17	0	6,6,6	0.27	0
5	PEG	D	304	-	6,6,6	0.46	0	5,5,5	0.56	0
4	ACT	F	304	-	3,3,3	0.60	0	3,3,3	1.24	0
3	HPA	A	302	-	8,11,11	2.09	3 (37%)	5,15,15	2.94	3 (60%)
4	ACT	A	304	-	3,3,3	0.64	0	3,3,3	1.67	1 (33%)
6	PO4	C	301	-	4,4,4	1.30	0	6,6,6	0.84	0
5	PEG	E	303	-	6,6,6	0.45	0	5,5,5	0.50	0
2	SO4	D	301	-	4,4,4	0.18	0	6,6,6	0.28	0
5	PEG	B	303	-	6,6,6	0.46	0	5,5,5	0.43	0
2	SO4	D	303	-	4,4,4	0.17	0	6,6,6	0.25	0
2	SO4	E	301	-	4,4,4	0.14	0	6,6,6	0.59	0
2	SO4	C	303	-	4,4,4	0.11	0	6,6,6	0.24	0
3	HPA	B	302	-	8,11,11	1.96	3 (37%)	5,15,15	3.22	4 (80%)

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	HPA	F	302	-	-	-	0/2/2/2
5	PEG	E	303	-	-	2/4/4/4	-
3	HPA	D	302	-	-	-	0/2/2/2
5	PEG	D	304	-	-	1/4/4/4	-
5	PEG	B	303	-	-	3/4/4/4	-
3	HPA	E	302	-	-	-	0/2/2/2
5	PEG	C	304	-	-	4/4/4/4	-
3	HPA	C	302	-	-	-	0/2/2/2
5	PEG	A	305	-	-	0/4/4/4	-
3	HPA	A	302	-	-	-	0/2/2/2
3	HPA	B	302	-	-	-	0/2/2/2

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	302	HPA	C2-N3	4.62	1.39	1.32
3	F	302	HPA	C2-N3	4.26	1.39	1.32
3	E	302	HPA	C2-N3	4.21	1.38	1.32
3	A	302	HPA	C2-N3	4.12	1.38	1.32
3	D	302	HPA	C2-N3	4.11	1.38	1.32

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	302	HPA	N3-C2-N1	-5.68	119.80	128.68
3	C	302	HPA	N3-C2-N1	-5.54	120.02	128.68
3	D	302	HPA	N3-C2-N1	-5.48	120.11	128.68
3	B	302	HPA	N3-C2-N1	-5.47	120.12	128.68
3	E	302	HPA	N3-C2-N1	-5.15	120.63	128.68

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	303	PEG	O1-C1-C2-O2
5	D	304	PEG	O1-C1-C2-O2
5	E	303	PEG	O1-C1-C2-O2
5	E	303	PEG	O2-C3-C4-O4
5	B	303	PEG	O2-C3-C4-O4

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	301	SO4	1	0
5	A	305	PEG	2	0
5	E	303	PEG	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	233/233 (100%)	-0.50	1 (0%) 92 91	18, 27, 43, 61	0
1	B	233/233 (100%)	-0.03	12 (5%) 27 25	22, 39, 66, 92	0
1	C	233/233 (100%)	-0.34	3 (1%) 77 75	18, 28, 49, 60	0
1	D	233/233 (100%)	-0.35	1 (0%) 92 91	18, 29, 49, 62	0
1	E	233/233 (100%)	0.02	9 (3%) 39 37	20, 41, 66, 94	0
1	F	233/233 (100%)	-0.21	10 (4%) 35 32	16, 29, 57, 89	0
All	All	1398/1398 (100%)	-0.23	36 (2%) 56 53	16, 32, 57, 94	0

The worst 5 of 36 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	212	LEU	5.7
1	B	212	LEU	5.1
1	F	213	SER	4.5
1	F	214	PRO	4.3
1	B	211	ALA	3.9

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 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
2	SO4	A	303	5/5	0.61	0.42	66,73,80,95	0
3	HPA	E	302	10/10	0.73	0.27	46,49,57,58	10
3	HPA	B	302	10/10	0.83	0.25	32,37,43,47	10
3	HPA	D	302	10/10	0.84	0.18	33,41,48,48	10
5	PEG	A	305	7/7	0.84	0.18	36,42,45,51	0
3	HPA	F	302	10/10	0.86	0.21	32,41,49,50	10
2	SO4	D	303	5/5	0.86	0.16	57,57,69,80	0
5	PEG	B	303	7/7	0.86	0.29	55,56,63,66	0
3	HPA	A	302	10/10	0.87	0.24	27,30,34,37	10
4	ACT	A	304	4/4	0.89	0.15	39,43,46,47	0
5	PEG	E	303	7/7	0.89	0.19	40,48,53,58	0
4	ACT	F	304	4/4	0.90	0.21	32,34,35,37	0
5	PEG	C	304	7/7	0.93	0.19	28,38,39,49	0
5	PEG	D	304	7/7	0.94	0.20	34,39,45,47	0
2	SO4	C	303	5/5	0.95	0.29	58,64,68,81	0
2	SO4	E	301	5/5	0.96	0.14	36,40,59,65	0
3	HPA	C	302	10/10	0.96	0.09	25,30,34,37	0
2	SO4	F	303	5/5	0.98	0.32	50,53,61,65	0
2	SO4	A	301	5/5	0.98	0.15	27,34,38,42	0
2	SO4	F	301	5/5	0.99	0.10	29,32,39,47	0
2	SO4	B	301	5/5	0.99	0.13	39,44,51,55	0
2	SO4	D	301	5/5	0.99	0.11	29,32,38,42	0
6	PO4	C	301	5/5	1.00	0.22	34,34,34,34	0

6.5 Other polymers [i](#)

There are no such residues in this entry.