



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 11:43 AM GMT

PDB ID : 3PM5
Title : Crystal Structure of BoxB in mixed valent state with bound benzoyl-CoA
Authors : Weinert, T.; Rather, L.; Fuchs, G.; Ermler, U.
Deposited on : 2010-11-16
Resolution : 2.30 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
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

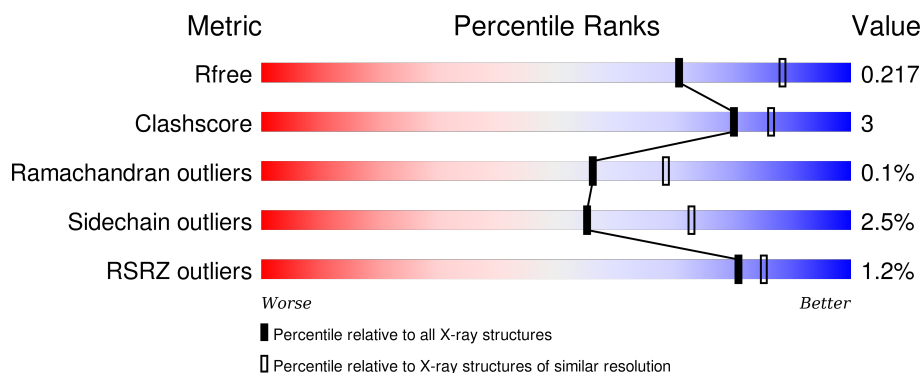
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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}	91344	3852 (2.30-2.30)
Clashscore	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)
RSRZ outliers	91569	3857 (2.30-2.30)

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. 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	481	<div> <div>2%</div> <div>89% 9% ..</div> </div>
1	B	481	<div> <div>%</div> <div>86% 10% ..</div> </div>
1	C	481	<div> <div></div> <div>91% 7% ..</div> </div>
1	D	481	<div> <div>%</div> <div>87% 10% .</div> </div>

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	483	-	-	-	X
2	SO4	A	484	-	-	-	X
2	SO4	C	483	-	-	-	X
5	PGO	D	484	-	-	-	X
6	BYC	D	1003	-	-	-	X
8	PGE	D	486	-	-	-	X

2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 16504 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 Benzoyl-CoA oxygenase component B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	472	Total	C	N	O	S	0	4	0
			3892	2466	690	724	12			
1	B	470	Total	C	N	O	S	0	5	0
			3887	2462	695	718	12			
1	C	475	Total	C	N	O	S	0	5	0
			3917	2484	695	725	13			
1	D	469	Total	C	N	O	S	0	5	0
			3866	2447	688	719	12			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	474	TRP	-	SEE REMARK 999	UNP Q9AIX7
A	475	SER	-	SEE REMARK 999	UNP Q9AIX7
A	476	HIS	-	SEE REMARK 999	UNP Q9AIX7
A	477	PRO	-	SEE REMARK 999	UNP Q9AIX7
A	478	GLN	-	SEE REMARK 999	UNP Q9AIX7
A	479	PHE	-	SEE REMARK 999	UNP Q9AIX7
A	480	GLU	-	SEE REMARK 999	UNP Q9AIX7
A	481	LYS	-	SEE REMARK 999	UNP Q9AIX7
B	474	TRP	-	SEE REMARK 999	UNP Q9AIX7
B	475	SER	-	SEE REMARK 999	UNP Q9AIX7
B	476	HIS	-	SEE REMARK 999	UNP Q9AIX7
B	477	PRO	-	SEE REMARK 999	UNP Q9AIX7
B	478	GLN	-	SEE REMARK 999	UNP Q9AIX7
B	479	PHE	-	SEE REMARK 999	UNP Q9AIX7
B	480	GLU	-	SEE REMARK 999	UNP Q9AIX7
B	481	LYS	-	SEE REMARK 999	UNP Q9AIX7
C	474	TRP	-	SEE REMARK 999	UNP Q9AIX7
C	475	SER	-	SEE REMARK 999	UNP Q9AIX7
C	476	HIS	-	SEE REMARK 999	UNP Q9AIX7
C	477	PRO	-	SEE REMARK 999	UNP Q9AIX7
C	478	GLN	-	SEE REMARK 999	UNP Q9AIX7

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Chain	Residue	Modelled	Actual	Comment	Reference
C	479	PHE	-	SEE REMARK 999	UNP Q9AIX7
C	480	GLU	-	SEE REMARK 999	UNP Q9AIX7
C	481	LYS	-	SEE REMARK 999	UNP Q9AIX7
D	474	TRP	-	SEE REMARK 999	UNP Q9AIX7
D	475	SER	-	SEE REMARK 999	UNP Q9AIX7
D	476	HIS	-	SEE REMARK 999	UNP Q9AIX7
D	477	PRO	-	SEE REMARK 999	UNP Q9AIX7
D	478	GLN	-	SEE REMARK 999	UNP Q9AIX7
D	479	PHE	-	SEE REMARK 999	UNP Q9AIX7
D	480	GLU	-	SEE REMARK 999	UNP Q9AIX7
D	481	LYS	-	SEE REMARK 999	UNP Q9AIX7

- Molecule 2 is SULFATE ION (three-letter code: SO₄) (formula: O₄S).



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

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

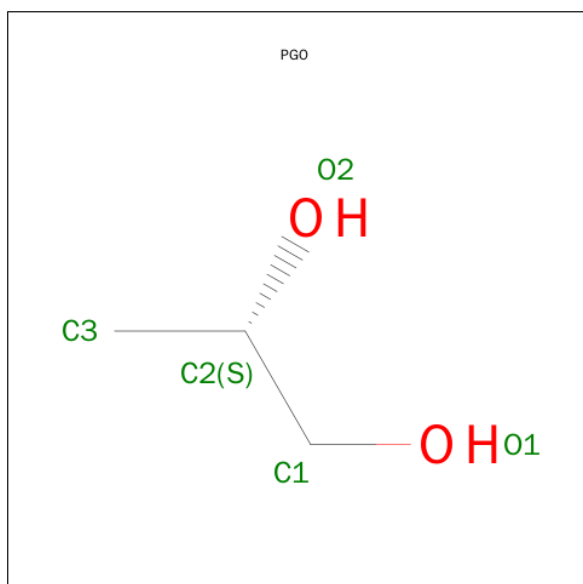
- Molecule 3 is FE (III) ION (three-letter code: FE) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	2	Total	Fe	0	0
			2	2		
3	A	2	Total	Fe	0	0
			2	2		
3	D	2	Total	Fe	0	0
			2	2		
3	C	2	Total	Fe	0	0
			2	2		

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

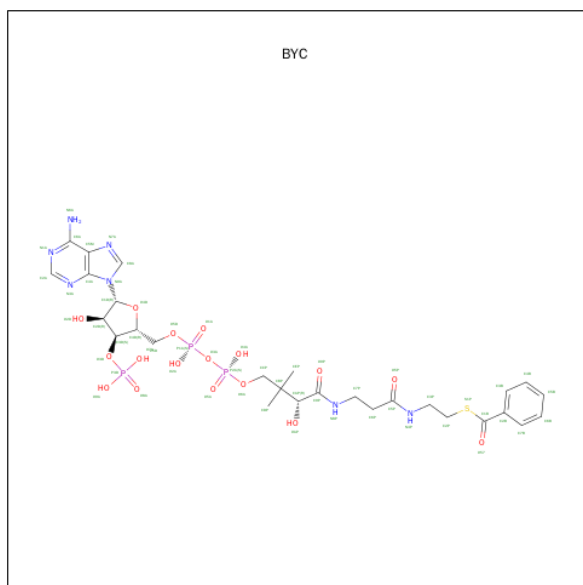
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total	Cl	0	0
			2	2		
4	D	1	Total	Cl	0	0
			1	1		
4	C	1	Total	Cl	0	0
			1	1		

- Molecule 5 is S-1,2-PROPANEDIOL (three-letter code: PGO) (formula: C₃H₈O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			5	3	2		
5	B	1	Total	C	O	0	0
			5	3	2		
5	B	1	Total	C	O	0	0
			5	3	2		
5	D	1	Total	C	O	0	0
			5	3	2		

- Molecule 6 is BENZOYL COENZYME A (three-letter code: BYC) (formula: $C_{28}H_{40}N_7O_{17}P_3S$).



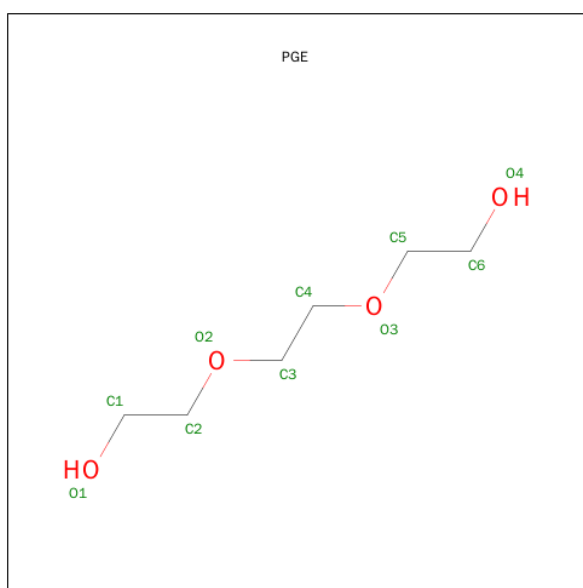
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
6	A	1	Total	C	N	O	P	S	0	0
			56	28	7	17	3	1		
6	B	1	Total	C	N	O	P	S	0	0
			56	28	7	17	3	1		
6	C	1	Total	C	N	O	P	S	0	0
			56	28	7	17	3	1		
6	D	1	Total	C	N	O	P	S	0	0
			56	28	7	17	3	1		

- Molecule 7 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	C	1	Total	C	O	0	0
			6	3	3		
7	D	1	Total	C	O	0	0
			6	3	3		

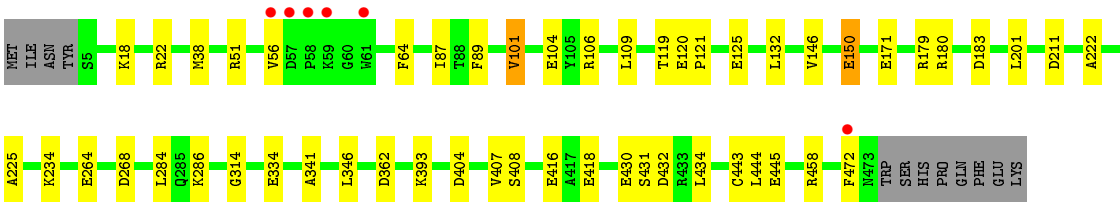
- Molecule 8 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: $C_6H_{14}O_4$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	D	1	Total	C	O	0	0
			10	6	4		

- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	178	Total 178	O 178	0	0
9	B	176	Total 176	O 176	0	0
9	C	158	Total 158	O 158	0	0
9	D	117	Total 117	O 117	0	0



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	208.18Å 76.65Å 148.20Å 90.00° 108.34° 90.00°	Depositor
Resolution (Å)	49.40 – 2.30 49.40 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.2 (49.40-2.30) 99.2 (49.40-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.76 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.174 , 0.224 0.171 , 0.217	Depositor DCC
R_{free} test set	4887 reflections (5.25%)	DCC
Wilson B-factor (Å ²)	45.0	Xtriage
Anisotropy	0.137	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 35.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	1 of 98025 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	16504	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.42% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: GOL, PGE, CL, PGO, FE, BYC, 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	0.97	4/3999 (0.1%)	0.85	1/5422 (0.0%)
1	B	0.98	2/3994 (0.1%)	0.86	3/5413 (0.1%)
1	C	1.00	2/4034 (0.0%)	0.88	6/5468 (0.1%)
1	D	0.96	6/3973 (0.2%)	0.83	0/5384
All	All	0.98	14/16000 (0.1%)	0.86	10/21687 (0.0%)

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	150[A]	GLU	CG-CD	7.02	1.62	1.51
1	C	150[B]	GLU	CG-CD	7.02	1.62	1.51
1	A	334	GLU	CB-CG	-6.45	1.39	1.52
1	D	445	GLU	CG-CD	6.26	1.61	1.51
1	A	150[A]	GLU	CG-CD	6.06	1.61	1.51

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	212	ARG	NE-CZ-NH2	-7.26	116.67	120.30
1	C	205	MET	CG-SD-CE	-6.67	89.52	100.20
1	B	348	ARG	NE-CZ-NH1	6.41	123.50	120.30
1	C	268	ASP	CB-CG-OD1	-5.69	113.18	118.30
1	C	139	ASP	CB-CG-OD1	-5.47	113.38	118.30

There are no chirality outliers.

There are no planarity outliers.

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	3892	0	3705	24	0
1	B	3887	0	3711	31	0
1	C	3917	0	3747	21	0
1	D	3866	0	3693	32	0
2	A	15	0	0	0	0
2	C	15	0	0	0	0
2	D	5	0	0	0	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
3	C	2	0	0	0	0
3	D	2	0	0	0	0
4	A	2	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
5	A	5	0	8	0	0
5	B	10	0	16	4	0
5	D	5	0	8	0	0
6	A	56	0	36	2	0
6	B	56	0	36	1	0
6	C	56	0	36	2	0
6	D	56	0	36	2	0
7	C	6	0	8	0	0
7	D	6	0	8	0	0
8	D	10	0	14	0	0
9	A	178	0	0	3	0
9	B	176	0	0	3	0
9	C	158	0	0	3	0
9	D	117	0	0	3	0
All	All	16504	0	15062	106	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 3.

The worst 5 of 106 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:B:41:GLU:OE1	1:B:129[A]:HIS:ND1	2.10	0.84
1:D:444:LEU:HD13	1:D:472:PHE:CZ	2.14	0.82
1:D:341:ALA:CB	1:D:346:LEU:HD12	2.13	0.78
1:A:341:ALA:CB	1:A:346:LEU:HD12	2.25	0.67
1:A:48:VAL:HG13	1:A:470:VAL:HG22	1.75	0.67

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	474/481 (98%)	459 (97%)	15 (3%)	0	100	100
1	B	473/481 (98%)	461 (98%)	12 (2%)	0	100	100
1	C	478/481 (99%)	468 (98%)	10 (2%)	0	100	100
1	D	472/481 (98%)	456 (97%)	15 (3%)	1 (0%)	52	64
All	All	1897/1924 (99%)	1844 (97%)	52 (3%)	1 (0%)	56	68

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	443	CYS

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	410/415 (99%)	399 (97%)	11 (3%)	52	70
1	B	409/415 (99%)	397 (97%)	12 (3%)	50	66
1	C	414/415 (100%)	404 (98%)	10 (2%)	57	74
1	D	408/415 (98%)	400 (98%)	8 (2%)	63	79
All	All	1641/1660 (99%)	1600 (98%)	41 (2%)	55	73

5 of 41 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	211	ASP
1	B	424	LYS
1	D	171	GLU
1	B	268	ASP
1	B	337	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 23 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	21	GLN
1	B	99	GLN
1	D	33	ASN
1	B	33	ASN
1	B	437	HIS

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 carbohydrates in this entry.

5.6 Ligand geometry

Of 30 ligands modelled in this entry, 12 are monoatomic - leaving 18 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	BYC	A	1003	-	49,59,59	2.60	15 (30%)	63,87,87	2.30	12 (19%)
2	SO4	A	482	-	4,4,4	0.14	0	6,6,6	0.54	0
2	SO4	A	483	-	4,4,4	0.26	0	6,6,6	0.64	0
2	SO4	A	484	-	4,4,4	0.17	0	6,6,6	0.19	0
5	PGO	A	487	-	4,4,4	0.75	0	2,4,4	0.68	0
6	BYC	B	1003	-	49,59,59	2.74	17 (34%)	63,87,87	2.34	18 (28%)
5	PGO	B	482	-	4,4,4	0.91	0	2,4,4	0.50	0
5	PGO	B	483	-	4,4,4	0.89	0	2,4,4	0.69	0
6	BYC	C	1003	-	49,59,59	2.61	12 (24%)	63,87,87	2.02	14 (22%)
2	SO4	C	482	-	4,4,4	0.54	0	6,6,6	0.58	0
2	SO4	C	483	-	4,4,4	0.14	0	6,6,6	0.15	0
2	SO4	C	484	-	4,4,4	0.11	0	6,6,6	0.09	0
7	GOL	C	486	-	5,5,5	0.46	0	5,5,5	0.85	0
6	BYC	D	1003	-	49,59,59	2.53	14 (28%)	63,87,87	2.24	14 (22%)
2	SO4	D	482	-	4,4,4	0.25	0	6,6,6	0.17	0
5	PGO	D	484	-	4,4,4	0.47	0	2,4,4	0.29	0
7	GOL	D	485	-	5,5,5	0.35	0	5,5,5	0.60	0
8	PGE	D	486	-	9,9,9	0.96	0	8,8,8	0.91	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	BYC	A	1003	-	-	0/50/71/71	0/4/4/4
2	SO4	A	482	-	-	0/0/0/0	0/0/0/0
2	SO4	A	483	-	-	0/0/0/0	0/0/0/0
2	SO4	A	484	-	-	0/0/0/0	0/0/0/0
5	PGO	A	487	-	-	0/2/2/2	0/0/0/0
6	BYC	B	1003	-	-	0/50/71/71	0/4/4/4

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	PGO	B	482	-	-	0/2/2/2	0/0/0/0
5	PGO	B	483	-	-	0/2/2/2	0/0/0/0
6	BYC	C	1003	-	-	0/50/71/71	0/4/4/4
2	SO4	C	482	-	-	0/0/0/0	0/0/0/0
2	SO4	C	483	-	-	0/0/0/0	0/0/0/0
2	SO4	C	484	-	-	0/0/0/0	0/0/0/0
7	GOL	C	486	-	-	0/4/4/4	0/0/0/0
6	BYC	D	1003	-	-	0/50/71/71	0/4/4/4
2	SO4	D	482	-	-	0/0/0/0	0/0/0/0
5	PGO	D	484	-	-	0/2/2/2	0/0/0/0
7	GOL	D	485	-	-	0/4/4/4	0/0/0/0
8	PGE	D	486	-	-	0/7/7/7	0/0/0/0

The worst 5 of 58 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	B	1003	BYC	C2D-C3D	-3.23	1.45	1.53
6	C	1003	BYC	C2D-C3D	-3.05	1.46	1.53
6	A	1003	BYC	C2D-C3D	-2.68	1.47	1.53
6	B	1003	BYC	CDP-CBP	-2.66	1.48	1.53
6	D	1003	BYC	C2D-C3D	-2.51	1.47	1.53

The worst 5 of 58 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	D	1003	BYC	N3A-C2A-N1A	-11.97	119.73	128.89
6	B	1003	BYC	N3A-C2A-N1A	-11.88	119.80	128.89
6	A	1003	BYC	N3A-C2A-N1A	-10.95	120.51	128.89
6	C	1003	BYC	N3A-C2A-N1A	-10.58	120.80	128.89
6	A	1003	BYC	P2A-O3A-P1A	-4.62	119.76	132.73

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	1003	BYC	2	0
6	B	1003	BYC	1	0
5	B	482	PGO	2	0
5	B	483	PGO	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	C	1003	BYC	2	0
6	D	1003	BYC	2	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	472/481 (98%)	0.04	10 (2%) 67 74	28, 42, 61, 83	0
1	B	470/481 (97%)	-0.20	5 (1%) 82 86	28, 41, 59, 82	0
1	C	475/481 (98%)	-0.17	1 (0%) 95 97	29, 42, 62, 79	0
1	D	469/481 (97%)	-0.16	6 (1%) 79 84	27, 47, 69, 87	0
All	All	1886/1924 (98%)	-0.12	22 (1%) 81 85	27, 43, 63, 87	0

The worst 5 of 22 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	59	LYS	4.4
1	A	474	TRP	4.3
1	A	3	ASN	3.9
1	D	58	PRO	3.8
1	A	190	LEU	3.2

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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
2	SO4	A	484	5/5	0.86	0.45	15.23	125,126,126,126	0
8	PGE	D	486	10/10	0.74	0.23	10.88	67,70,72,72	0
2	SO4	C	483	5/5	0.84	0.42	9.87	118,119,119,120	0
2	SO4	A	483	5/5	0.90	0.31	8.86	96,96,96,98	0
5	PGO	D	484	5/5	0.83	0.22	4.08	64,66,67,68	0
6	BYC	D	1003	56/56	0.85	0.20	2.65	49,71,103,106	0
4	CL	D	483	1/1	0.98	0.16	1.34	42,42,42,42	0
6	BYC	C	1003	56/56	0.91	0.18	1.05	43,65,101,103	0
3	FE	C	1001	1/1	0.94	0.16	0.95	86,86,86,86	0
6	BYC	A	1003	56/56	0.87	0.23	0.89	49,71,98,101	0
5	PGO	A	487	5/5	0.90	0.17	0.59	59,62,66,67	0
6	BYC	B	1003	56/56	0.90	0.17	0.52	47,69,98,99	0
2	SO4	A	482	5/5	0.89	0.15	-0.17	87,89,89,90	0
3	FE	A	1001	1/1	0.95	0.17	-0.47	74,74,74,74	0
4	CL	C	485	1/1	0.96	0.12	-0.78	44,44,44,44	0
2	SO4	C	482	5/5	0.98	0.10	-0.94	58,58,63,64	0
3	FE	A	1002	1/1	0.99	0.14	-1.23	59,59,59,59	0
4	CL	A	485	1/1	0.98	0.09	-1.49	40,40,40,40	0
3	FE	B	1001	1/1	0.97	0.09	-1.78	72,72,72,72	0
3	FE	C	1002	1/1	0.99	0.12	-3.14	63,63,63,63	0
4	CL	A	486	1/1	0.99	0.06	-3.28	39,39,39,39	0
3	FE	D	1001	1/1	0.98	0.06	-3.59	74,74,74,74	0
3	FE	D	1002	1/1	0.97	0.05	-3.67	73,73,73,73	0
3	FE	B	1002	1/1	0.95	0.07	-12.51	63,63,63,63	0
2	SO4	C	484	5/5	0.91	0.36	-	120,121,121,121	0
7	GOL	D	485	6/6	0.90	0.14	-	86,88,89,89	0
5	PGO	B	482	5/5	0.92	0.17	-	60,68,70,71	0
7	GOL	C	486	6/6	0.79	0.15	-	74,76,77,77	0
5	PGO	B	483	5/5	0.73	0.18	-	67,68,69,70	0
2	SO4	D	482	5/5	0.86	0.40	-	102,103,103,103	0

6.5 Other polymers [i](#)

There are no such residues in this entry.