



wwPDB X-ray Structure Validation Summary Report i

Feb 26, 2014 – 03:50 PM 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 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/ValidationPDFNotes.html>

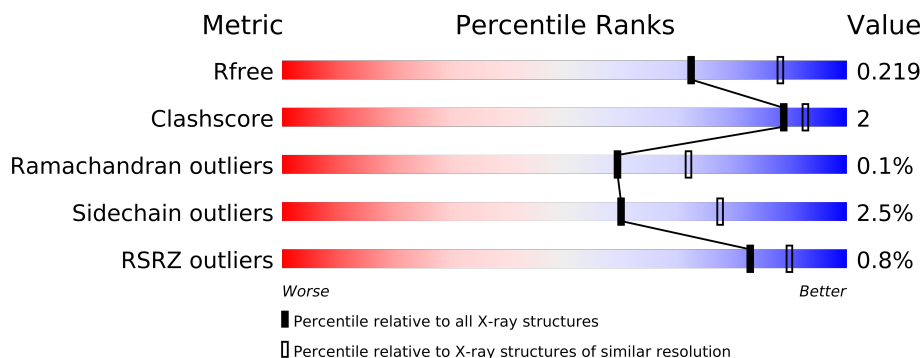
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

1 Overall quality at a glance

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}	66092	2929 (2.30-2.30)
Clashscore	79885	3679 (2.30-2.30)
Ramachandran outliers	78287	3642 (2.30-2.30)
Sidechain outliers	78261	3641 (2.30-2.30)
RSRZ outliers	66119	2930 (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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	481	
1	B	481	
1	C	481	
1	D	481	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
2	SO4	A	483	-	X
2	SO4	A	484	-	X
2	SO4	C	483	-	X
2	SO4	C	484	-	X

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Geometry	Electron density
2	SO4	D	482	-	X
5	PGO	B	482	-	X
5	PGO	B	483	-	X
5	PGO	D	484	-	X
6	BYC	D	1003	-	X
8	PGE	D	486	-	X

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 16504 atoms, of which 0 are hydrogen and 0 are deuterium.

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:

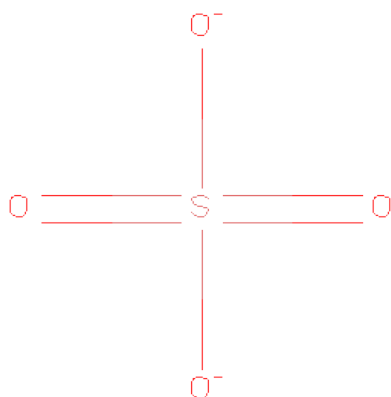
Chain	Residue	Modelled	Actual	Comment	Reference
A	474	TRP	-	SEE REMARK 999	UNP Q9AIX7
A	475	SER	-	SEE REMARK 999	UNP Q9AIX7
A	476	HIS	-	SEE REMARK 999	UNP Q9AIX7
A	477	PRO	-	SEE REMARK 999	UNP Q9AIX7
A	478	GLN	-	SEE REMARK 999	UNP Q9AIX7
A	479	PHE	-	SEE REMARK 999	UNP Q9AIX7
A	480	GLU	-	SEE REMARK 999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

Continued on next page...

Continued from previous page...

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	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	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		

Continued on next page...

Continued from previous page...

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

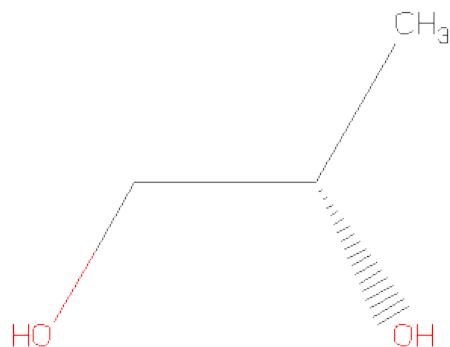
- Molecule 3 is FE (III) ION (three-letter code: FE) (formula: Fe).

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).

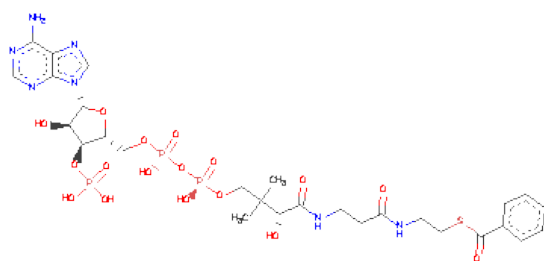
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total	Cl	0	0
			2	2		
4	D	1	Total	Cl	0	0
			1	1		
4	C	1	Total	Cl	0	0
			1	1		

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



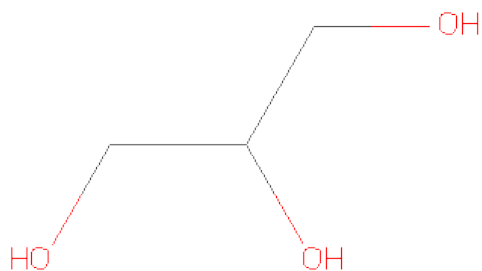
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			5	3	2		
5	B	1	Total	C	O	0	0
			5	3	2		
5	B	1	Total	C	O	0	0
			5	3	2		
5	D	1	Total	C	O	0	0
			5	3	2		

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



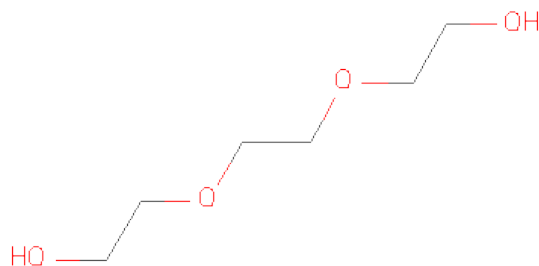
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
6	A	1	Total	C	N	O	P	S	0	0
			56	28	7	17	3	1		
6	B	1	Total	C	N	O	P	S	0	0
			56	28	7	17	3	1		
6	C	1	Total	C	N	O	P	S	0	0
			56	28	7	17	3	1		
6	D	1	Total	C	N	O	P	S	0	0
			56	28	7	17	3	1		

- 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		

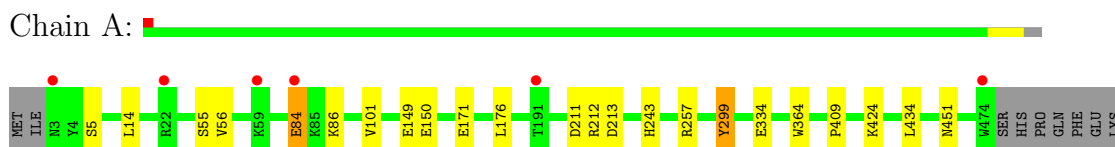
- Molecule 9 is water.

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

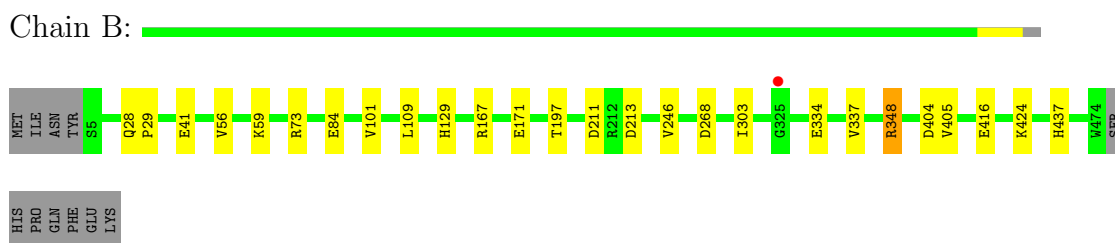
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

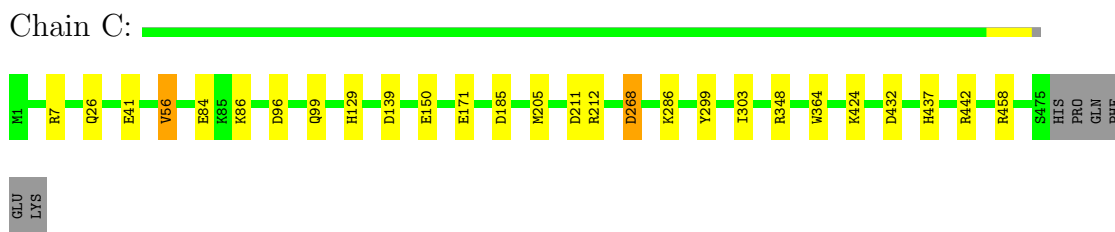
- Molecule 1: Benzoyl-CoA oxygenase component B



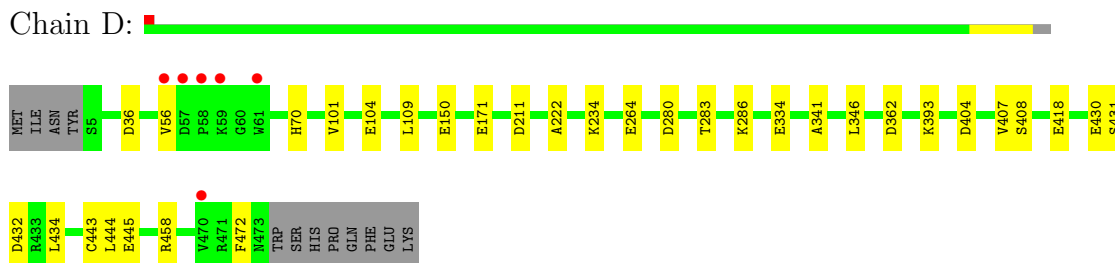
- Molecule 1: Benzoyl-CoA oxygenase component B



- Molecule 1: Benzoyl-CoA oxygenase component B



- Molecule 1: Benzoyl-CoA oxygenase component B



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) 99.3 (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 0.173 , 0.219	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)	0.33 , 29.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	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.

5 Model quality

5.1 Standard geometry

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 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3892	0	0	7	0
1	B	3887	0	0	8	0
1	C	3917	0	0	10	0
1	D	3866	0	653	13	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	2	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	1	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	1	0
9	B	176	0	0	2	0
9	C	158	0	0	1	0
9	D	117	0	0	1	0
All	All	16504	0	859	38	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 2.

The worst 5 of 38 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(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:A:56:VAL:CG1	1:A:56:VAL:O	2.43	0.66
1:D:286:LYS:NZ	1:D:432:ASP:OD2	2.30	0.64
1:B:197:THR:N	9:B:577:HOH:O	2.33	0.60

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

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%)	56	68
All	All	1897/1924 (99%)	1844 (97%)	52 (3%)	1 (0%)	59	72

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	443	CYS

5.3.2 Protein sidechains ⓘ

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%)	57	74
1	B	409/415 (99%)	397 (97%)	12 (3%)	55	71

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	414/415 (100%)	404 (98%)	10 (2%)	61	79
1	D	408/415 (98%)	400 (98%)	8 (2%)	68	84
All	All	1641/1660 (99%)	1600 (98%)	41 (2%)	60	77

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. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA chains 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	-	59,59,59	2.32	15 (25%)	87,87,87	2.38	19 (21%)
2	SO4	A	482	-	4,4,4	0.14	0	6,6,6	0.53	0
2	SO4	A	483	-	4,4,4	0.29	0	6,6,6	0.61	0
2	SO4	A	484	-	4,4,4	0.14	0	6,6,6	0.18	0
5	PGO	A	487	-	4,4,4	0.75	0	4,4,4	0.58	0
6	BYC	B	1003	-	59,59,59	2.44	16 (27%)	87,87,87	2.69	22 (25%)
5	PGO	B	482	-	4,4,4	0.91	0	4,4,4	0.51	0
5	PGO	B	483	-	4,4,4	0.88	0	4,4,4	0.79	0
6	BYC	C	1003	-	59,59,59	2.33	13 (22%)	87,87,87	2.26	16 (18%)
2	SO4	C	482	-	4,4,4	0.59	0	6,6,6	0.56	0
2	SO4	C	483	-	4,4,4	0.13	0	6,6,6	0.14	0
2	SO4	C	484	-	4,4,4	0.10	0	6,6,6	0.09	0
7	GOL	C	486	-	5,5,5	0.42	0	5,5,5	0.82	0
6	BYC	D	1003	-	59,59,59	2.25	15 (25%)	87,87,87	2.13	18 (20%)
2	SO4	D	482	-	4,4,4	0.25	0	6,6,6	0.17	0
5	PGO	D	484	-	4,4,4	0.46	0	4,4,4	0.90	0
7	GOL	D	485	-	5,5,5	0.33	0	5,5,5	0.60	0
8	PGE	D	486	-	9,9,9	0.96	0	8,8,8	0.87	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	-	-	0/54/71/71	0/2/4/4
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	-	-	0/54/71/71	0/2/4/4
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	-	-	0/54/71/71	0/2/4/4
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	-	-	0/54/71/71	0/2/4/4
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

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	PGE	D	486	-	-	0/7/7/7	0/0/0/0

The worst 5 of 59 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	D	1003	BYC	C4A-N3A	7.41	1.46	1.35
6	C	1003	BYC	C2A-N3A	7.20	1.46	1.32
6	C	1003	BYC	C4A-N3A	7.15	1.46	1.35
6	A	1003	BYC	C4A-N3A	7.06	1.46	1.35
6	B	1003	BYC	C4A-N3A	6.97	1.46	1.35

The worst 5 of 75 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	C	1003	BYC	O4D-C1D-N9A	12.92	120.46	108.44
6	B	1003	BYC	O4D-C1D-N9A	12.06	119.66	108.44
6	B	1003	BYC	CBP-CAP-C9P	11.79	124.17	112.73
6	D	1003	BYC	N3A-C2A-N1A	-10.74	119.73	128.71
6	B	1003	BYC	N3A-C2A-N1A	-10.66	119.80	128.71

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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	472/481 (98%)	-0.04	6 (1%) 74 82	28, 42, 61, 83	0
1	B	470/481 (97%)	-0.28	1 (0%) 93 97	28, 41, 59, 82	0
1	C	475/481 (98%)	-0.24	0 100 100	29, 42, 62, 79	0
1	D	469/481 (97%)	-0.20	6 (1%) 74 82	27, 47, 69, 87	0
All	All	1886/1924 (98%)	-0.19	13 (0%) 83 91	27, 43, 63, 87	0

The worst 5 of 13 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	59	LYS	5.1
1	A	474	TRP	4.4
1	A	3	ASN	4.4
1	D	58	PRO	3.9
1	D	61	TRP	2.6

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 carbohydrates 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. 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	SO4	D	482	5/5	0.33	23.62	102,103,103,103	0
2	SO4	C	484	5/5	0.39	15.93	120,121,121,121	0
2	SO4	A	484	5/5	0.46	14.55	125,126,126,126	0
8	PGE	D	486	10/10	0.21	11.26	67,70,72,72	0
2	SO4	C	483	5/5	0.39	9.22	118,119,119,120	0
2	SO4	A	483	5/5	0.24	8.74	96,96,96,98	0
6	BYC	D	1003	56/56	0.19	2.61	49,71,103,106	0
5	PGO	D	484	5/5	0.21	2.53	64,66,67,68	0
5	PGO	B	482	5/5	0.15	2.39	60,68,70,71	0
5	PGO	B	483	5/5	0.18	2.09	67,68,69,70	0
6	BYC	A	1003	56/56	0.21	1.08	49,71,98,101	0
5	PGO	A	487	5/5	0.17	0.72	59,62,66,67	0
6	BYC	C	1003	56/56	0.16	0.66	43,65,101,103	0
6	BYC	B	1003	56/56	0.16	0.64	47,69,98,99	0
3	FE	C	1001	1/1	0.14	0.27	86,86,86,86	0
7	GOL	D	485	6/6	0.14	-0.19	86,88,89,89	0
7	GOL	C	486	6/6	0.16	-0.30	74,76,77,77	0
4	CL	D	483	1/1	0.12	-0.31	42,42,42,42	0
2	SO4	A	482	5/5	0.13	-0.52	87,89,89,90	0
3	FE	A	1001	1/1	0.15	-0.82	74,74,74,74	0
2	SO4	C	482	5/5	0.10	-0.85	58,58,63,64	0
3	FE	B	1001	1/1	0.08	-1.54	72,72,72,72	0
3	FE	A	1002	1/1	0.13	-1.59	59,59,59,59	0
4	CL	A	485	1/1	0.06	-2.23	40,40,40,40	0
4	CL	C	485	1/1	0.09	-2.29	44,44,44,44	0
4	CL	A	486	1/1	0.06	-3.46	39,39,39,39	0
3	FE	C	1002	1/1	0.10	-3.59	63,63,63,63	0
3	FE	D	1002	1/1	0.04	-3.74	73,73,73,73	0
3	FE	D	1001	1/1	0.07	-3.84	74,74,74,74	0
3	FE	B	1002	1/1	0.06	-21.59	63,63,63,63	0

6.5 Other polymers ⓘ

There are no such residues in this entry.