



Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 11:43 am BST

PDB ID : 2IG9
Title : Structure of a full-length Homoprotocatechuate 2,3-Dioxygenase from *B. fus-*
cum in a new spacegroup.
Authors : Kovaleva, E.G.; Lipscomb, J.D.
Deposited on : 2006-09-22
Resolution : 1.90 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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 ⓘ symbol.

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 : 2.11
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) : 2.11

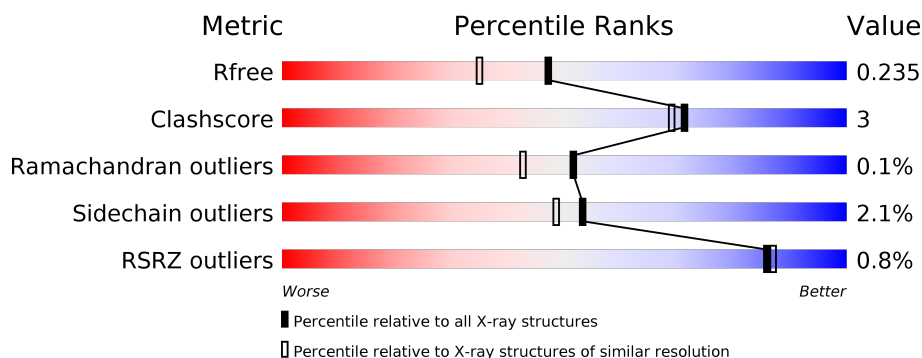
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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 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	365	<div> <div>%</div> <div> <div></div> <div>88%</div> <div>10%</div> <div>..</div> </div> </div>
1	B	365	<div> <div></div> <div>90%</div> <div>8%</div> <div>.</div> </div>
1	C	365	<div> <div>%</div> <div> <div></div> <div>86%</div> <div>12%</div> <div>.</div> </div> </div>
1	D	365	<div> <div>%</div> <div> <div></div> <div>90%</div> <div>7%</div> <div>..</div> </div> </div>

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 13106 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 Homoprotocatechuate 2,3-dioxygenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	359	Total	C	N	O	S	0	5	0
			2936	1850	517	562	7			
1	B	359	Total	C	N	O	S	0	7	0
			2950	1858	520	564	8			
1	C	359	Total	C	N	O	S	0	5	0
			2937	1849	518	563	7			
1	D	359	Total	C	N	O	S	0	8	0
			2960	1864	521	568	7			

- Molecule 2 is FE (II) ION (three-letter code: FE2) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Fe	0	0
			1	1		
2	A	1	Total	Fe	0	0
			1	1		
2	D	1	Total	Fe	0	0
			1	1		
2	C	1	Total	Fe	0	0
			1	1		

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Cl	0	0
			1	1		
3	A	1	Total	Cl	0	0
			1	1		
3	D	1	Total	Cl	0	0
			1	1		
3	C	1	Total	Cl	0	0
			1	1		

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			6	3	3		
4	A	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		
4	C	1	Total	C	O	0	0
			6	3	3		
4	C	1	Total	C	O	0	0
			6	3	3		
4	D	1	Total	C	O	0	0
			6	3	3		
4	D	1	Total	C	O	0	0
			6	3	3		
4	D	1	Total	C	O	0	0
			6	3	3		

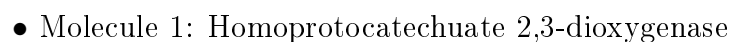
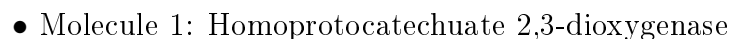
- Molecule 5 is CALCIUM ION (three-letter code: CA) (formula: Ca).

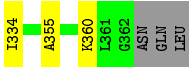
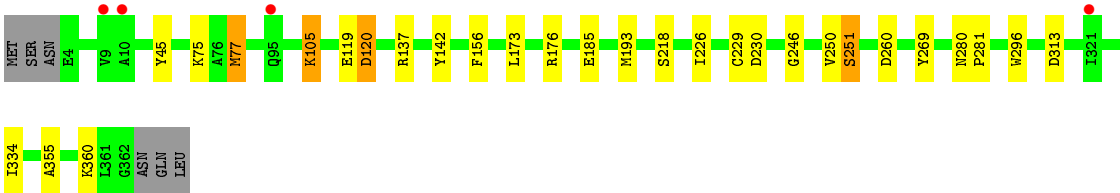
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total 1	Ca 1	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	318	Total 318	O 318	0	0
6	B	350	Total 350	O 350	0	0
6	C	268	Total 268	O 268	0	0
6	D	312	Total 312	O 312	0	0

- Molecule 1: Homoprotocatechuate 2,3-dioxygenase





4 Data and refinement statistics

Property	Value	Source
Space group	P 2 ₁ 2 ₁ 2	Depositor
Cell constants a, b, c, α , β , γ	110.44Å 152.80Å 99.71Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.08 – 1.90 46.06 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.7 (46.08-1.90) 99.7 (46.06-1.90)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.23 (at 1.90Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.187 , 0.234 0.189 , 0.235	Depositor DCC
R_{free} test set	6680 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	22.4	Xtriage
Anisotropy	0.100	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 45.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	13106	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.07% 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: GOL, CA, FE2, CL

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	0.72	0/3015	0.75	2/4094 (0.0%)
1	B	0.74	0/3032	0.76	1/4114 (0.0%)
1	C	0.70	0/3016	0.72	1/4094 (0.0%)
1	D	0.69	0/3039	0.71	1/4127 (0.0%)
All	All	0.71	0/12102	0.74	5/16429 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	120	ASP	CB-CG-OD1	6.19	123.87	118.30
1	A	292	ARG	NE-CZ-NH2	-5.93	117.33	120.30
1	C	243	ARG	NE-CZ-NH2	-5.74	117.43	120.30
1	B	54	ARG	NE-CZ-NH1	5.09	122.85	120.30
1	A	176	ARG	NE-CZ-NH1	5.01	122.81	120.30

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	2936	0	2786	23	0
1	B	2950	0	2801	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	2937	0	2782	29	0
1	D	2960	0	2804	19	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	12	0	16	0	0
4	B	18	0	24	2	0
4	C	12	0	16	0	0
4	D	24	0	32	3	0
5	B	1	0	0	0	0
6	A	318	0	0	2	0
6	B	350	0	0	4	0
6	C	268	0	0	4	0
6	D	312	0	0	6	0
All	All	13106	0	11261	80	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.

All (80) 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:33:ASN:HB2	6:A:976:HOH:O	1.47	1.11
1:B:362:GLY:HA2	1:D:360:LYS:HG3	1.53	0.89
1:A:83:THR:OG1	1:A:85:GLU:HG2	1.78	0.84
1:C:152[B]:ARG:NH2	6:C:995:HOH:O	2.14	0.79
1:A:360:LYS:HG3	1:C:362:GLY:HA2	1.64	0.77
1:A:119:GLU:HG3	1:A:314:LEU:HG	1.72	0.70
1:D:75:LYS:NZ	6:D:1086:HOH:O	2.25	0.69
1:A:8:PRO:HG3	1:A:97:LEU:HD13	1.77	0.67
1:B:74:LEU:HD21	1:B:77[A]:MET:HG3	1.78	0.65
1:B:176:ARG:NH1	1:B:278:PRO:O	2.30	0.64
4:D:804:GOL:H12	6:D:837:HOH:O	1.98	0.64
1:A:74:LEU:HD21	1:A:77:MET:HG3	1.82	0.61
1:C:176:ARG:HD2	6:C:938:HOH:O	2.00	0.61
1:B:68:LYS:HE2	6:B:893:HOH:O	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:151:VAL:HG11	1:A:220:HIS:CE1	2.37	0.59
1:C:281:PRO:HD2	1:D:137[B]:ARG:HH21	1.67	0.59
1:C:101:THR:HG22	1:C:118:VAL:HG12	1.85	0.58
1:C:250:VAL:HG22	1:C:285:TRP:CD1	2.39	0.57
4:B:809:GOL:H11	6:B:974:HOH:O	2.03	0.56
1:D:137[B]:ARG:NE	6:D:882:HOH:O	2.38	0.56
1:C:218[A]:SER:HA	1:C:269:TYR:O	2.06	0.56
1:B:119:GLU:HG3	1:B:314:LEU:HG	1.86	0.56
1:A:218:SER:HA	1:A:269:TYR:O	2.05	0.55
1:C:101:THR:HB	1:C:116:LEU:HD11	1.87	0.55
1:C:151:VAL:HG11	1:C:220:HIS:CE1	2.41	0.55
1:A:101:THR:HG22	1:A:118:VAL:HG12	1.89	0.55
1:D:77:MET:HE3	1:D:156:PHE:CD2	2.41	0.55
1:A:330:LEU:C	1:A:330:LEU:HD23	2.27	0.54
1:A:246:GLY:HA2	1:A:296:TRP:CZ3	2.42	0.53
1:A:142:TYR:CG	1:D:230:ASP:HB3	2.43	0.53
1:A:301[A]:VAL:HG13	1:C:357:LYS:O	2.08	0.53
1:A:230:ASP:HB3	1:D:142:TYR:CG	2.43	0.53
1:C:77:MET:HE3	1:C:156:PHE:CD2	2.44	0.53
1:B:218[A]:SER:HA	1:B:269:TYR:O	2.09	0.52
1:C:48:GLU:CD	1:C:48:GLU:H	2.13	0.52
1:A:101:THR:HB	1:A:116:LEU:HD11	1.91	0.51
1:B:142:TYR:CG	1:C:230:ASP:HB3	2.45	0.51
1:B:218[B]:SER:HA	1:B:269:TYR:O	2.11	0.51
1:B:226:ILE:HD11	1:D:226[A]:ILE:HD11	1.91	0.51
1:D:185:GLU:HB2	6:D:937:HOH:O	2.11	0.50
1:D:334:ILE:HG22	1:D:355:ALA:HA	1.94	0.49
1:C:223:HIS:HE1	6:C:1030:HOH:O	1.95	0.49
1:A:362:GLY:HA2	1:C:360:LYS:HG3	1.96	0.48
4:D:810:GOL:H11	6:D:1113:HOH:O	2.14	0.48
1:D:119:GLU:OE2	1:D:313:ASP:HB2	2.13	0.47
1:D:218:SER:HA	1:D:269:TYR:O	2.14	0.47
1:C:218[B]:SER:HA	1:C:269:TYR:O	2.13	0.47
1:C:32:ARG:HG3	1:C:51:ILE:HD13	1.96	0.47
1:B:248:HIS:HB3	1:B:250:VAL:O	2.15	0.46
1:C:10:ALA:HB1	6:C:877:HOH:O	2.15	0.46
1:B:296:TRP:CD1	1:D:229:CYS:HB3	2.51	0.46
1:B:176:ARG:HD3	6:B:1061:HOH:O	2.16	0.45
1:B:241:ILE:HG23	1:B:256:LEU:HD11	1.97	0.45
1:A:48[B]:GLU:CD	1:A:48[B]:GLU:H	2.20	0.45
1:C:246:GLY:HA2	1:C:296:TRP:CZ3	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:285:TRP:HA	4:B:803:GOL:H12	2.00	0.44
1:C:330:LEU:C	1:C:330:LEU:HD23	2.37	0.44
1:B:30[A]:LYS:HD3	6:B:1140:HOH:O	2.16	0.44
1:A:301[A]:VAL:HG11	6:A:902:HOH:O	2.17	0.44
1:B:230:ASP:HB3	1:C:142:TYR:CG	2.52	0.44
1:C:183:ASP:HB3	1:C:287:VAL:HG12	2.00	0.43
1:A:18:CYS:HB2	1:A:156:PHE:CE2	2.54	0.42
1:C:280:ASN:OD1	1:D:137[B]:ARG:NH2	2.51	0.42
1:D:250:VAL:O	1:D:251:SER:CB	2.67	0.42
1:D:280:ASN:HA	1:D:281:PRO:HD3	1.92	0.42
1:C:119:GLU:OE2	1:C:313:ASP:HB2	2.18	0.42
1:C:117:ARG:HG2	1:C:127:GLU:HB2	2.00	0.42
1:C:152[B]:ARG:NH1	1:C:218[B]:SER:CB	2.82	0.42
1:C:74:LEU:HD13	1:C:212:LEU:HD22	2.02	0.41
1:A:34:PHE:O	1:A:38:VAL:HB	2.21	0.41
1:B:152:ARG:HB2	1:B:218[A]:SER:OG	2.20	0.41
1:A:296:TRP:CD1	1:C:229:CYS:HB3	2.55	0.41
1:D:45:TYR:CD1	4:D:811:GOL:H11	2.56	0.41
1:B:101:THR:HB	1:B:116:LEU:HD11	2.03	0.41
1:C:248:HIS:HB3	1:C:250:VAL:O	2.21	0.41
1:A:124:PHE:CZ	1:A:158:GLN:HB3	2.56	0.40
1:B:246:GLY:HA2	1:B:296:TRP:CZ3	2.56	0.40
1:D:105:LYS:HD3	6:D:1081:HOH:O	2.21	0.40
1:D:246:GLY:HA2	1:D:296:TRP:CZ3	2.56	0.40

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	362/365 (99%)	349 (96%)	13 (4%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	364/365 (100%)	356 (98%)	8 (2%)	0	100	100
1	C	362/365 (99%)	351 (97%)	11 (3%)	0	100	100
1	D	365/365 (100%)	354 (97%)	10 (3%)	1 (0%)	41	31
All	All	1453/1460 (100%)	1410 (97%)	42 (3%)	1 (0%)	51	43

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	251	SER

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	312/313 (100%)	305 (98%)	7 (2%)	52	47
1	B	314/313 (100%)	308 (98%)	6 (2%)	57	53
1	C	312/313 (100%)	306 (98%)	6 (2%)	57	53
1	D	315/313 (101%)	308 (98%)	7 (2%)	52	47
All	All	1253/1252 (100%)	1227 (98%)	26 (2%)	53	48

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	68	LYS
1	A	97	LEU
1	A	105	LYS
1	A	120	ASP
1	A	193	MET
1	A	321	ILE
1	A	328	SER
1	B	105	LYS
1	B	120	ASP
1	B	169	TYR

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Mol	Chain	Res	Type
1	B	173	LEU
1	B	193	MET
1	B	361	LEU
1	C	105	LYS
1	C	120	ASP
1	C	169	TYR
1	C	176	ARG
1	C	193	MET
1	C	314	LEU
1	D	77	MET
1	D	105	LYS
1	D	120	ASP
1	D	173	LEU
1	D	176	ARG
1	D	193	MET
1	D	260	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	95	GLN
1	C	95	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](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 20 ligands modelled in this entry, 9 are monoatomic - leaving 11 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	$\# Z > 2$
4	GOL	C	805	-	5,5,5	0.48	0	5,5,5	0.60	0
4	GOL	D	810	-	5,5,5	0.37	0	5,5,5	0.35	0
4	GOL	B	803	-	5,5,5	0.58	0	5,5,5	0.67	0
4	GOL	D	804	-	5,5,5	0.46	0	5,5,5	0.58	0
4	GOL	C	808	-	5,5,5	0.44	0	5,5,5	0.78	0
4	GOL	B	809	-	5,5,5	0.48	0	5,5,5	0.84	0
4	GOL	A	807	-	5,5,5	0.31	0	5,5,5	0.75	0
4	GOL	B	801	-	5,5,5	0.38	0	5,5,5	0.98	0
4	GOL	D	811	-	5,5,5	0.32	0	5,5,5	0.95	0
4	GOL	D	806	-	5,5,5	0.51	0	5,5,5	0.84	0
4	GOL	A	802	-	5,5,5	0.46	0	5,5,5	1.04	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
4	GOL	C	805	-	-	0/4/4/4	-
4	GOL	D	810	-	-	2/4/4/4	-
4	GOL	B	803	-	-	1/4/4/4	-
4	GOL	D	804	-	-	2/4/4/4	-
4	GOL	C	808	-	-	0/4/4/4	-
4	GOL	B	809	-	-	3/4/4/4	-
4	GOL	A	807	-	-	2/4/4/4	-
4	GOL	B	801	-	-	1/4/4/4	-
4	GOL	D	811	-	-	1/4/4/4	-
4	GOL	D	806	-	-	4/4/4/4	-
4	GOL	A	802	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (16) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	D	810	GOL	C1-C2-C3-O3
4	A	807	GOL	O1-C1-C2-C3
4	D	806	GOL	O1-C1-C2-C3
4	D	804	GOL	O1-C1-C2-O2
4	B	809	GOL	O1-C1-C2-O2
4	B	803	GOL	O1-C1-C2-C3
4	D	811	GOL	C1-C2-C3-O3
4	D	804	GOL	O1-C1-C2-C3
4	B	809	GOL	O1-C1-C2-C3
4	B	809	GOL	C1-C2-C3-O3
4	B	801	GOL	C1-C2-C3-O3
4	D	806	GOL	C1-C2-C3-O3
4	D	810	GOL	O2-C2-C3-O3
4	A	807	GOL	O1-C1-C2-O2
4	D	806	GOL	O1-C1-C2-O2
4	D	806	GOL	O2-C2-C3-O3

There are no ring outliers.

5 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	810	GOL	1	0
4	B	803	GOL	1	0
4	D	804	GOL	1	0
4	B	809	GOL	1	0
4	D	811	GOL	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 ⓘ

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	359/365 (98%)	-0.10	2 (0%) 89 90	14, 21, 32, 43	0
1	B	359/365 (98%)	-0.13	1 (0%) 94 94	13, 19, 30, 38	0
1	C	359/365 (98%)	0.18	5 (1%) 75 77	14, 24, 36, 49	0
1	D	359/365 (98%)	0.00	4 (1%) 80 82	13, 22, 34, 47	0
All	All	1436/1460 (98%)	-0.01	12 (0%) 86 87	13, 22, 34, 49	0

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	362	GLY	3.1
1	C	345	GLY	2.9
1	B	362	GLY	2.8
1	D	10	ALA	2.7
1	C	362	GLY	2.6
1	D	321	ILE	2.4
1	C	323	GLU	2.4
1	A	85	GLU	2.4
1	C	185	GLU	2.2
1	D	9	VAL	2.2
1	D	95	GLN	2.0
1	C	152[A]	ARG	2.0

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. 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
4	GOL	B	809	6/6	0.81	0.20	42,45,46,47	0
4	GOL	C	805	6/6	0.84	0.14	45,49,49,51	0
4	GOL	C	808	6/6	0.85	0.17	36,39,40,40	0
4	GOL	D	811	6/6	0.85	0.25	44,48,48,49	0
4	GOL	D	804	6/6	0.88	0.15	44,45,47,48	0
4	GOL	B	803	6/6	0.89	0.20	38,42,46,46	0
4	GOL	A	807	6/6	0.90	0.16	41,45,46,47	0
4	GOL	D	806	6/6	0.90	0.15	23,28,29,31	0
4	GOL	A	802	6/6	0.90	0.15	23,32,32,32	0
4	GOL	D	810	6/6	0.92	0.22	51,54,54,55	0
4	GOL	B	801	6/6	0.95	0.11	19,22,24,25	0
3	CL	B	702	1/1	0.99	0.07	21,21,21,21	0
5	CA	B	601	1/1	0.99	0.04	23,23,23,23	0
3	CL	A	701	1/1	0.99	0.09	28,28,28,28	0
3	CL	D	704	1/1	0.99	0.07	26,26,26,26	0
2	FE2	C	500	1/1	0.99	0.06	21,21,21,21	0
3	CL	C	703	1/1	0.99	0.06	29,29,29,29	0
2	FE2	D	500	1/1	1.00	0.07	19,19,19,19	0
2	FE2	B	500	1/1	1.00	0.07	18,18,18,18	0
2	FE2	A	500	1/1	1.00	0.09	20,20,20,20	0

6.5 Other polymers

There are no such residues in this entry.