



# Full wwPDB X-ray Structure Validation Report ⓘ

Sep 4, 2022 – 08:07 PM JST

PDB ID : 7WZD  
Title : Crystal Structure of cis-4,5-dihydrodiol phthalate dehydrogenase from Comamonas testosteroni KF1  
Authors : Sharma, M.; Mahto, J.K.; Kumar, P.  
Deposited on : 2022-02-17  
Resolution : 2.80 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](mailto: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>.

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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	:	2.30
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)	:	2.30

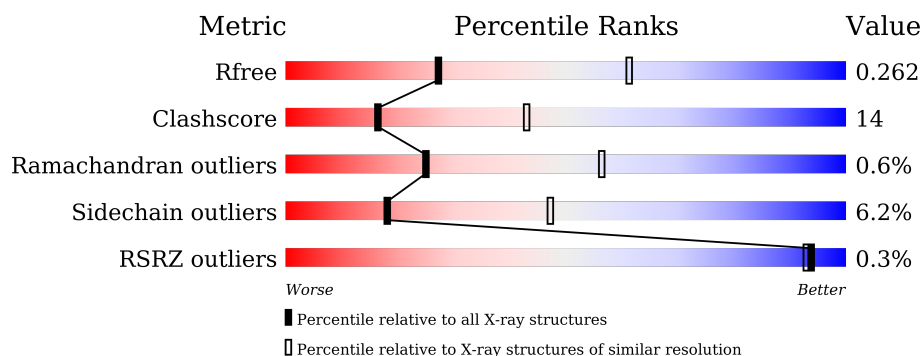
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 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	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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  $\geq 3$ , 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	392	<div> <div style="width: 100%; height: 10px; position: relative;"> <div style="position: absolute; top: -10px; left: 0;">%</div> <div style="position: absolute; top: 0; left: 0; width: 100%; height: 100%; background: linear-gradient(to right, red 0%, red 1%, orange 1%, orange 19%, yellow 19%, yellow 20%, green 20%, green 66%, green 67%, grey 67%, grey 100%);"></div> <div style="position: absolute; bottom: -10px; left: 0;">66%19%•13%</div> </div> </div>
1	B	392	<div> <div style="width: 100%; height: 10px; position: relative;"> <div style="position: absolute; top: 0; left: 0; width: 100%; height: 100%; background: linear-gradient(to right, green 0%, green 65%, green 66%, yellow 66%, yellow 20%, orange 20%, red 20%, grey 20%, grey 100%);"></div> <div style="position: absolute; bottom: -10px; left: 0;">65%20%•13%</div> </div> </div>

## 2 Entry composition [i](#)

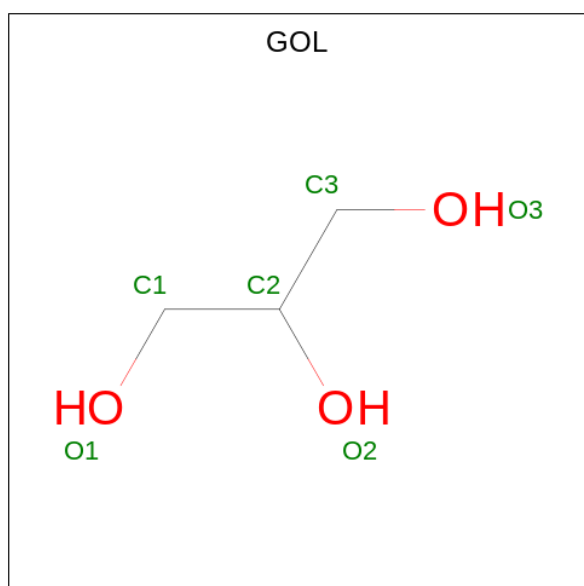
There are 3 unique types of molecules in this entry. The entry contains 5852 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 4,5-dihydroxyphthalate dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	342	Total	C	N	O	S	0	0	0
			2677	1693	489	481	14			
1	B	342	Total	C	N	O	S	0	0	0
			2674	1690	489	481	14			

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



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

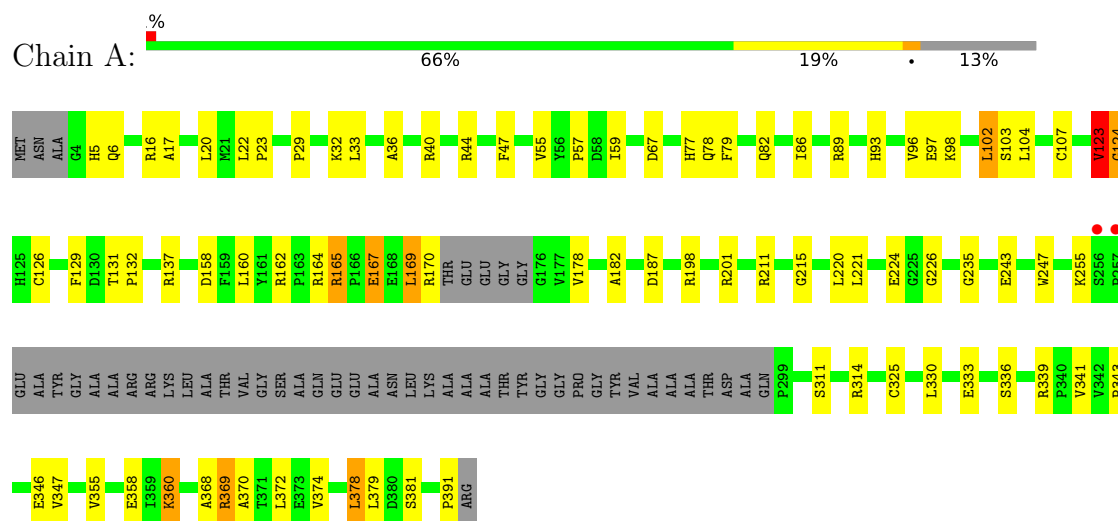
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	237	Total 237	O 237	0	0
3	B	246	Total 246	O 246	0	0

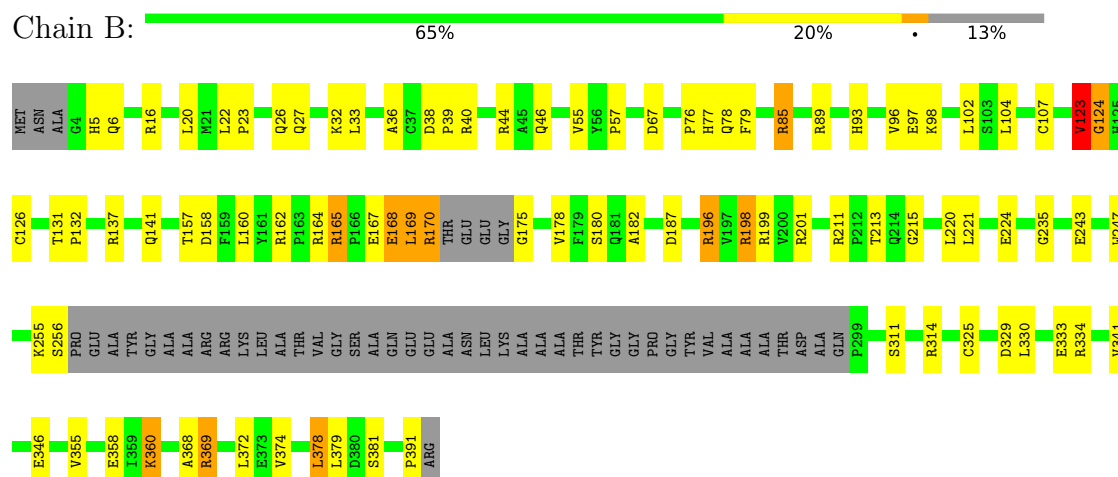
### 3 Residue-property plots

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: 4,5-dihydroxyphthalate dehydrogenase



- Molecule 1: 4,5-dihydroxyphthalate dehydrogenase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	54.18Å 90.70Å 164.11Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	60.92 – 2.80 60.85 – 2.80	Depositor EDS
% Data completeness (in resolution range)	95.2 (60.92-2.80) 95.2 (60.85-2.80)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.66 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, $R_{free}$	0.191 , 0.262 0.191 , 0.262	Depositor DCC
$R_{free}$ test set	965 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	19.5	Xtriage
Anisotropy	0.320	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 54.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	5852	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 53.35 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 4.2715e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL

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	0.45	0/2747	0.85	3/3732 (0.1%)
1	B	0.44	0/2743	0.84	1/3725 (0.0%)
All	All	0.44	0/5490	0.84	4/7457 (0.1%)

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	A	0	1
1	B	0	1
All	All	0	2

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	137	ARG	CB-CG-CD	6.41	128.26	111.60
1	A	123	VAL	C-N-CA	5.53	133.91	122.30
1	A	391	PRO	N-CA-CB	-5.22	96.86	102.60
1	B	123	VAL	C-N-CA	5.15	133.12	122.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	123	VAL	Peptide
1	B	123	VAL	Peptide

## 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	2677	0	2616	64	0
1	B	2674	0	2612	86	0
2	A	12	0	16	1	0
2	B	6	0	8	2	0
3	A	237	0	0	12	0
3	B	246	0	0	18	0
All	All	5852	0	5252	152	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 14.

All (152) 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:175:GLY:HA2	1:B:180:SER:HB2	1.24	1.17
1:B:369:ARG:HG2	1:B:369:ARG:HH11	1.21	1.03
1:A:16:ARG:HD3	1:A:165:ARG:HG3	1.42	1.02
1:A:369:ARG:HH11	1:A:369:ARG:HG2	1.23	0.98
1:B:341:VAL:HG22	3:B:586:HOH:O	1.65	0.96
1:B:16:ARG:HD3	1:B:165:ARG:HG3	1.43	0.96
1:B:98:LYS:NZ	1:B:126:CYS:SG	2.41	0.94
1:A:98:LYS:NZ	1:A:126:CYS:SG	2.44	0.90
1:B:360:LYS:HE2	3:B:517:HOH:O	1.71	0.88
1:B:175:GLY:CA	1:B:180:SER:HB2	2.04	0.88
1:B:175:GLY:HA2	1:B:180:SER:CB	2.03	0.88
1:A:369:ARG:HH11	1:A:369:ARG:CG	1.86	0.87
1:B:369:ARG:HH11	1:B:369:ARG:CG	1.86	0.87
1:B:78:GLN:HA	1:B:102:LEU:HD11	1.54	0.87
1:B:256:SER:HB2	3:B:643:HOH:O	1.75	0.87
1:B:169:LEU:O	1:B:170:ARG:HB2	1.77	0.84
1:B:131:THR:HG23	1:B:346:GLU:OE2	1.78	0.83
1:A:131:THR:HG23	1:A:346:GLU:OE2	1.78	0.82
1:B:85:ARG:HH11	1:B:89:ARG:HH22	1.29	0.78
1:A:131:THR:HG22	3:A:724:HOH:O	1.86	0.75
1:B:96:VAL:O	1:B:124:GLY:N	2.21	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:96:VAL:O	1:A:124:GLY:N	2.21	0.73
1:A:16:ARG:NH1	1:A:165:ARG:HE	1.88	0.70
1:A:78:GLN:OE1	1:A:78:GLN:N	2.23	0.70
1:A:160:LEU:HB2	1:A:235:GLY:O	1.91	0.70
1:B:160:LEU:HB2	1:B:235:GLY:O	1.93	0.68
1:B:104:LEU:HD23	1:B:372:LEU:HD23	1.75	0.68
1:A:369:ARG:HG2	1:A:369:ARG:NH1	2.05	0.67
1:B:391:PRO:HA	3:B:646:HOH:O	1.94	0.67
1:B:78:GLN:OE1	1:B:78:GLN:N	2.23	0.66
1:B:168:GLU:HG3	1:B:169:LEU:N	2.10	0.66
2:A:402:GOL:H32	3:A:655:HOH:O	1.97	0.64
1:B:16:ARG:NH1	1:B:165:ARG:HH21	1.96	0.63
1:B:334:ARG:NH2	3:B:502:HOH:O	2.31	0.63
1:B:16:ARG:HH21	1:B:20:LEU:HD21	1.63	0.62
1:A:16:ARG:HH21	1:A:20:LEU:CD2	2.13	0.62
1:A:104:LEU:HD23	1:A:372:LEU:HD23	1.80	0.62
1:B:369:ARG:HG2	1:B:369:ARG:NH1	2.03	0.61
1:A:160:LEU:HD11	1:A:215:GLY:HA3	1.81	0.61
1:B:160:LEU:HD11	1:B:215:GLY:HA3	1.82	0.61
1:A:97:GLU:HA	1:A:124:GLY:HA3	1.82	0.61
1:A:341:VAL:HG22	3:A:575:HOH:O	2.00	0.61
1:B:16:ARG:HH21	1:B:20:LEU:CD2	2.14	0.61
1:A:339:ARG:HB2	3:A:520:HOH:O	2.01	0.61
1:A:5:HIS:CD2	3:A:554:HOH:O	2.53	0.60
1:B:26:GLN:HG2	3:B:563:HOH:O	2.00	0.60
1:B:97:GLU:HA	1:B:124:GLY:HA3	1.82	0.60
1:A:131:THR:CG2	1:A:346:GLU:HG2	2.33	0.58
1:B:131:THR:CG2	1:B:346:GLU:HG2	2.34	0.57
1:B:157:THR:HA	3:B:625:HOH:O	2.04	0.57
1:A:370:ALA:HA	3:A:535:HOH:O	2.04	0.56
1:B:6:GLN:HE21	1:B:32:LYS:HB2	1.69	0.56
1:A:6:GLN:NE2	1:A:29:PRO:O	2.28	0.55
1:B:196:ARG:HH11	1:B:196:ARG:CG	2.20	0.55
1:A:343:PRO:HD3	3:A:600:HOH:O	2.05	0.55
1:A:17:ALA:HB1	1:A:97:GLU:HG3	1.88	0.55
1:B:6:GLN:HG2	1:B:32:LYS:HB2	1.88	0.55
1:B:360:LYS:CE	3:B:517:HOH:O	2.40	0.55
1:B:16:ARG:HH12	1:B:165:ARG:HH21	1.53	0.55
1:B:199:ARG:NE	3:B:507:HOH:O	2.36	0.54
1:A:158:ASP:OD1	1:A:162:ARG:NE	2.41	0.53
1:A:131:THR:HG22	1:A:346:GLU:HG2	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:256:SER:HB3	3:B:656:HOH:O	2.09	0.53
1:A:369:ARG:CG	1:A:369:ARG:NH1	2.58	0.52
1:A:226:GLY:HA3	3:A:555:HOH:O	2.08	0.52
2:B:401:GOL:H32	3:B:541:HOH:O	2.08	0.52
1:B:123:VAL:HG21	1:B:368:ALA:CB	2.41	0.51
1:B:46:GLN:HG3	2:B:401:GOL:H12	1.93	0.51
1:B:77:HIS:HD1	1:B:102:LEU:HG	1.75	0.51
1:B:158:ASP:OD1	1:B:162:ARG:NE	2.44	0.51
1:A:178:VAL:O	1:A:182:ALA:HB3	2.11	0.51
1:A:16:ARG:HH21	1:A:20:LEU:HD21	1.73	0.51
1:A:36:ALA:HB2	1:A:47:PHE:CE2	2.46	0.50
1:B:5:HIS:CD2	1:B:5:HIS:C	2.85	0.50
1:A:77:HIS:CE1	1:A:102:LEU:HD23	2.47	0.50
1:B:178:VAL:O	1:B:182:ALA:HB3	2.11	0.49
1:B:158:ASP:OD1	1:B:158:ASP:C	2.51	0.49
1:B:27:GLN:O	3:B:501:HOH:O	2.20	0.49
1:B:168:GLU:OE2	1:B:170:ARG:O	2.30	0.49
1:B:198:ARG:HD2	1:B:224:GLU:OE2	2.13	0.49
1:B:358:GLU:O	1:B:358:GLU:HG3	2.13	0.48
1:A:129:PHE:CE2	1:A:347:VAL:HA	2.49	0.48
1:B:44:ARG:NH1	1:B:57:PRO:HA	2.29	0.48
1:B:20:LEU:HD12	3:B:710:HOH:O	2.14	0.48
1:B:169:LEU:HD12	3:B:734:HOH:O	2.13	0.47
1:B:168:GLU:HG3	1:B:169:LEU:H	1.77	0.47
1:A:6:GLN:HG2	1:A:32:LYS:HB2	1.96	0.47
1:B:131:THR:HG22	1:B:346:GLU:HG2	1.97	0.47
1:A:158:ASP:OD1	1:A:158:ASP:C	2.53	0.47
1:B:137:ARG:O	1:B:141:GLN:HG2	2.14	0.47
1:B:243:GLU:HG3	1:B:247:TRP:CZ2	2.49	0.47
1:A:169:LEU:HD21	3:A:714:HOH:O	2.15	0.46
1:A:169:LEU:CD2	3:A:714:HOH:O	2.64	0.46
1:A:220:LEU:O	1:A:221:LEU:HD12	2.16	0.46
1:B:201:ARG:HD2	1:B:381:SER:OG	2.16	0.46
1:B:355:VAL:HA	3:B:548:HOH:O	2.16	0.46
1:A:358:GLU:O	1:A:358:GLU:HG3	2.15	0.45
1:B:131:THR:HG23	1:B:346:GLU:HG2	1.98	0.45
1:B:167:GLU:H	1:B:167:GLU:CD	2.18	0.45
1:A:44:ARG:NH1	1:A:57:PRO:HA	2.32	0.45
1:A:77:HIS:HD2	3:A:643:HOH:O	2.00	0.45
1:B:220:LEU:O	1:B:221:LEU:HD12	2.17	0.45
1:B:77:HIS:NE2	1:B:170:ARG:NH1	2.65	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:22:LEU:N	1:A:23:PRO:CD	2.80	0.44
1:A:167:GLU:H	1:A:167:GLU:CD	2.20	0.44
1:B:22:LEU:N	1:B:23:PRO:CD	2.81	0.44
1:A:16:ARG:HH21	1:A:20:LEU:HD23	1.81	0.44
1:B:36:ALA:HB3	1:B:55:VAL:HG12	1.99	0.44
1:B:78:GLN:H	1:B:78:GLN:CD	2.17	0.44
1:B:40:ARG:NH1	1:B:169:LEU:HD13	2.32	0.44
1:B:196:ARG:CG	1:B:196:ARG:NH1	2.81	0.44
1:B:369:ARG:CG	1:B:369:ARG:NH1	2.57	0.44
1:A:40:ARG:NH2	1:A:167:GLU:O	2.51	0.43
1:A:123:VAL:HG21	1:A:368:ALA:CB	2.47	0.43
1:B:44:ARG:HH11	1:B:57:PRO:HA	1.83	0.43
1:B:169:LEU:CD1	3:B:734:HOH:O	2.65	0.43
1:A:243:GLU:HG3	1:A:247:TRP:CZ2	2.53	0.43
1:B:131:THR:HG23	1:B:346:GLU:CG	2.48	0.43
1:B:325:CYS:HA	1:B:333:GLU:O	2.19	0.43
1:B:374:VAL:O	1:B:378:LEU:HB2	2.19	0.43
1:A:107:CYS:SG	1:A:372:LEU:HD22	2.59	0.43
1:A:201:ARG:HD2	1:A:381:SER:OG	2.19	0.43
1:A:374:VAL:O	1:A:378:LEU:HB2	2.19	0.43
1:B:16:ARG:HA	1:B:16:ARG:HD2	1.88	0.43
1:A:44:ARG:HH11	1:A:57:PRO:HA	1.84	0.42
1:A:59:ILE:HG23	1:A:86:ILE:HG21	2.00	0.42
1:A:360:LYS:HD3	1:A:360:LYS:HA	1.93	0.42
1:A:93:HIS:CD2	1:A:355:VAL:HG22	2.54	0.42
1:B:93:HIS:CD2	1:B:355:VAL:HG22	2.54	0.42
1:B:168:GLU:CG	1:B:169:LEU:N	2.78	0.42
1:B:341:VAL:CG2	3:B:586:HOH:O	2.45	0.42
1:A:96:VAL:O	1:A:124:GLY:CA	2.68	0.42
1:B:96:VAL:O	1:B:124:GLY:CA	2.67	0.42
1:B:314:ARG:NH1	1:B:329:ASP:OD2	2.53	0.42
1:A:36:ALA:HB2	1:A:47:PHE:CZ	2.55	0.41
1:A:89:ARG:HD2	3:A:646:HOH:O	2.19	0.41
1:A:36:ALA:HB3	1:A:55:VAL:HG12	2.01	0.41
1:B:76:PRO:HD2	1:B:79:PHE:HD2	1.84	0.41
1:B:131:THR:N	1:B:132:PRO:CD	2.83	0.41
1:B:255:LYS:O	1:B:256:SER:C	2.58	0.41
1:A:198:ARG:HD3	1:A:224:GLU:OE2	2.21	0.41
1:B:102:LEU:HD21	3:B:719:HOH:O	2.21	0.41
1:A:82:GLN:O	1:A:86:ILE:HG12	2.21	0.41
1:A:131:THR:HG23	1:A:346:GLU:CG	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:211:ARG:HG3	1:B:211:ARG:O	2.21	0.41
1:A:131:THR:N	1:A:132:PRO:CD	2.84	0.41
1:A:211:ARG:O	1:A:211:ARG:HG3	2.21	0.41
1:B:38:ASP:OD1	1:B:39:PRO:HD2	2.21	0.41
1:A:77:HIS:C	1:A:79:PHE:H	2.25	0.40
1:B:360:LYS:HD3	1:B:360:LYS:HA	1.93	0.40
1:B:107:CYS:CB	1:B:369:ARG:HD2	2.52	0.40
1:A:325:CYS:HA	1:A:333:GLU:O	2.21	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	336/392 (86%)	316 (94%)	19 (6%)	1 (0%)	41	72
1	B	336/392 (86%)	314 (94%)	19 (6%)	3 (1%)	17	46
All	All	672/784 (86%)	630 (94%)	38 (6%)	4 (1%)	25	56

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	124	GLY
1	B	124	GLY
1	B	168	GLU
1	B	169	LEU

### 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	281/310 (91%)	262 (93%)	19 (7%)	16	42
1	B	280/310 (90%)	264 (94%)	16 (6%)	20	50
All	All	561/620 (90%)	526 (94%)	35 (6%)	18	47

All (35) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	33	LEU
1	A	67	ASP
1	A	102	LEU
1	A	103	SER
1	A	164	ARG
1	A	165	ARG
1	A	167	GLU
1	A	169	LEU
1	A	170	ARG
1	A	187	ASP
1	A	255	LYS
1	A	311	SER
1	A	314	ARG
1	A	330	LEU
1	A	336	SER
1	A	360	LYS
1	A	369	ARG
1	A	378	LEU
1	A	379	LEU
1	B	33	LEU
1	B	67	ASP
1	B	85	ARG
1	B	164	ARG
1	B	165	ARG
1	B	170	ARG
1	B	187	ASP
1	B	196	ARG
1	B	198	ARG
1	B	213	THR
1	B	311	SER
1	B	330	LEU
1	B	360	LYS
1	B	369	ARG

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Mol	Chain	Res	Type
1	B	378	LEU
1	B	379	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	77	HIS
1	A	90	HIS
1	B	6	GLN
1	B	181	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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

3 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	GOL	A	402	-	5,5,5	0.22	0	5,5,5	0.52	0
2	GOL	A	401	-	5,5,5	0.11	0	5,5,5	0.47	0
2	GOL	B	401	-	5,5,5	0.11	0	5,5,5	0.44	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
2	GOL	A	402	-	-	1/4/4/4	-
2	GOL	A	401	-	-	2/4/4/4	-
2	GOL	B	401	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	GOL	C1-C2-C3-O3
2	B	401	GOL	O2-C2-C3-O3
2	B	401	GOL	C1-C2-C3-O3
2	A	401	GOL	O2-C2-C3-O3
2	A	402	GOL	O1-C1-C2-O2

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	402	GOL	1	0
2	B	401	GOL	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	342/392 (87%)	-0.57	2 (0%) 89 86	6, 16, 39, 76	1 (0%)
1	B	342/392 (87%)	-0.55	0 100 100	7, 17, 43, 102	1 (0%)
All	All	684/784 (87%)	-0.56	2 (0%) 94 93	6, 17, 41, 102	2 (0%)

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	257	PRO	2.2
1	A	256	SER	2.2

### 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 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
2	GOL	A	402	6/6	0.86	0.20	20,20,20,20	0
2	GOL	A	401	6/6	0.93	0.20	41,44,47,50	0
2	GOL	B	401	6/6	0.95	0.20	20,20,20,20	0



## 6.5 Other polymers ⓘ

There are no such residues in this entry.