



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 16, 2024 – 08:49 PM EDT

PDB ID : 5O5X
Title : Crystal structure of Thermococcus litoralis ADP-dependent glucokinase (GK)
Authors : Herrera-Morande, A.; Castro-Fernandez, V.; Merino, F.; Ramirez-Sarmiento, C.A.; Fernandez, F.J.; Guixe, V.; Vega, M.C.
Deposited on : 2017-06-02
Resolution : 2.15 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

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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

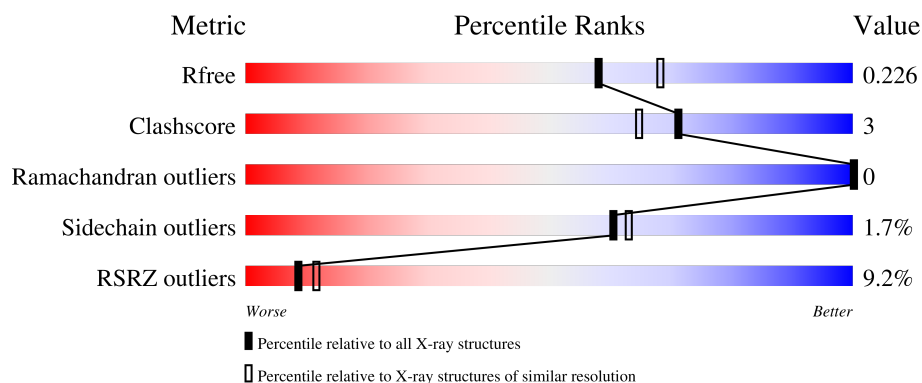
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.15 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	2523 (2.16-2.12)
Clashscore	141614	2653 (2.16-2.12)
Ramachandran outliers	138981	2618 (2.16-2.12)
Sidechain outliers	138945	2617 (2.16-2.12)
RSRZ outliers	127900	2485 (2.16-2.12)

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	464	<div> <div>2%</div> <div>89%</div> <div>9%</div> <div>.</div> </div>
1	B	464	<div> <div>16%</div> <div>86%</div> <div>11%</div> <div>.</div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7550 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 ADP-dependent glucokinase,ADP-dependent glucokinase,ADP-dependent glucokinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	454	Total	C	N	O	S	0	1	0
			3643	2332	621	682	8			
1	B	449	Total	C	N	O	S	0	2	0
			3605	2306	614	677	8			

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	49	ALA	LYS	conflict	UNP Q7M537
A	59	LYS	ILE	conflict	UNP Q7M537
A	256	LYS	ARG	conflict	UNP Q7M537
A	363	GLY	-	linker	UNP Q7M537
A	364	GLY	-	linker	UNP Q7M537
A	365	GLY	-	linker	UNP Q7M537
A	399	GLY	-	linker	UNP Q7M537
A	400	GLY	-	linker	UNP Q7M537
A	401	GLY	-	linker	UNP Q7M537
A	402	GLY	-	linker	UNP Q7M537
A	403	GLY	-	linker	UNP Q7M537
B	49	ALA	LYS	conflict	UNP Q7M537
B	59	LYS	ILE	conflict	UNP Q7M537
B	256	LYS	ARG	conflict	UNP Q7M537
B	363	GLY	-	linker	UNP Q7M537
B	364	GLY	-	linker	UNP Q7M537
B	365	GLY	-	linker	UNP Q7M537
B	399	GLY	-	linker	UNP Q7M537
B	400	GLY	-	linker	UNP Q7M537
B	401	GLY	-	linker	UNP Q7M537
B	402	GLY	-	linker	UNP Q7M537
B	403	GLY	-	linker	UNP Q7M537

- 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	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	135	Total	O	0	0
			135	135		

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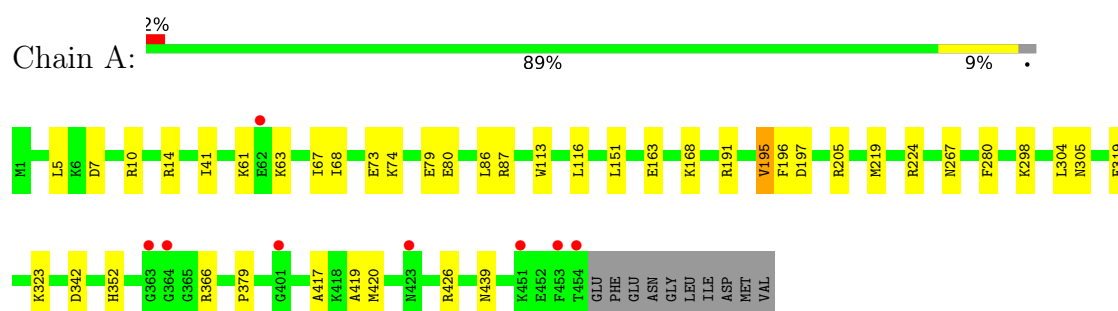
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	71	Total	O	0	0
			71	71		

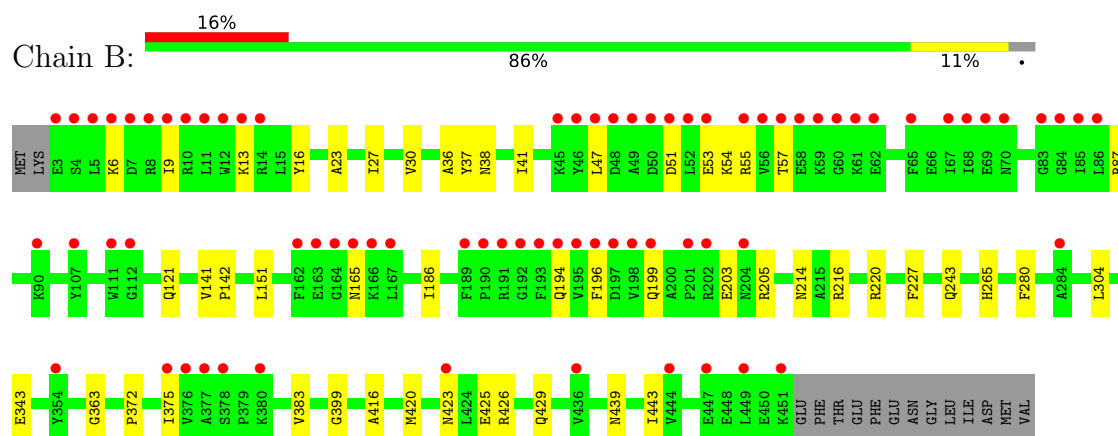
3 Residue-property plots [i](#)

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: ADP-dependent glucokinase,ADP-dependent glucokinase,ADP-dependent glucokinase



- Molecule 1: ADP-dependent glucokinase,ADP-dependent glucokinase,ADP-dependent glucokinase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	95.19Å 99.27Å 113.45Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.73 – 2.15 48.73 – 2.15	Depositor EDS
% Data completeness (in resolution range)	98.9 (48.73-2.15) 98.9 (48.73-2.15)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.00 (at 2.14Å)	Xtriage
Refinement program	PHENIX 1.10.1_2155	Depositor
R, R_{free}	0.194 , 0.226 0.194 , 0.226	Depositor DCC
R_{free} test set	2930 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	46.8	Xtriage
Anisotropy	0.522	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 46.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.017 for k,h,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	7550	wwPDB-VP
Average B, all atoms (Å ²)	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.35% 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 ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, 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	0.28	0/3716	0.43	0/5021
1	B	0.28	0/3674	0.43	0/4966
All	All	0.28	0/7390	0.43	0/9987

There are no bond length outliers.

There are no bond angle outliers.

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	3643	0	3658	20	0
1	B	3605	0	3610	33	0
2	A	15	0	0	0	0
2	B	15	0	0	1	0
3	A	30	0	40	1	0
3	B	36	0	48	0	0
4	A	135	0	0	0	0
4	B	71	0	0	1	0
All	All	7550	0	7356	51	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 (51) 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:38:ASN:HD21	1:B:121:GLN:HE21	1.32	0.78
1:A:68:ILE:O	1:A:87:ARG:NH1	2.20	0.73
1:B:30:VAL:HG12	1:B:399:GLY:HA3	1.71	0.72
1:A:219:MET:O	1:A:224:ARG:NH2	2.24	0.70
1:A:417:ALA:HA	1:A:420:MET:HE2	1.74	0.69
1:A:7:ASP:OD1	1:A:10:ARG:NH2	2.34	0.61
1:B:87:ARG:NH1	4:B:601:HOH:O	2.35	0.59
1:A:342:ASP:OD2	1:A:366:ARG:NH2	2.37	0.56
1:B:375:ILE:HD12	1:B:439:ASN:HD22	1.71	0.55
1:B:216:ARG:NH2	2:B:503:SO4:O2	2.39	0.55
1:B:425:GLU:H	1:B:429:GLN:HE22	1.54	0.54
1:B:121:GLN:HE22	1:B:243:GLN:HE22	1.55	0.54
1:B:53:GLU:HG3	1:B:196:PHE:CZ	2.43	0.54
1:A:163:GLU:HG3	1:A:168:LYS:HG3	1.90	0.52
1:B:426:ARG:HG3	1:B:429:GLN:HG3	1.92	0.52
1:B:121:GLN:NE2	1:B:243:GLN:HE22	2.08	0.51
1:A:73:GLU:HG2	1:A:74:LYS:HG3	1.91	0.51
1:A:267:ASN:HD21	1:A:298:LYS:NZ	2.08	0.51
1:A:61:LYS:HE3	1:A:196:PHE:CE1	2.46	0.51
1:B:38:ASN:HA	1:B:214:ASN:ND2	2.25	0.51
1:B:416:ALA:O	1:B:420:MET:HG3	2.11	0.50
1:B:51:ASP:OD2	1:B:55:ARG:NH1	2.46	0.48
1:B:186:ILE:HD13	1:B:383:VAL:HG21	1.95	0.48
1:B:38:ASN:ND2	1:B:121:GLN:HE21	2.05	0.47
1:A:379:PRO:HB3	1:A:419:ALA:HB1	1.95	0.47
1:B:425:GLU:H	1:B:429:GLN:NE2	2.13	0.46
1:A:305:ASN:HB3	1:A:352:HIS:CE1	2.51	0.46
1:A:191:ARG:NH2	1:B:343:GLU:OE1	2.50	0.45
1:B:141:VAL:O	1:B:220:ARG:HD2	2.16	0.44
1:B:36:ALA:HB1	1:B:37:TYR:CD1	2.52	0.44
1:A:113:TRP:CE2	1:A:116:LEU:HD13	2.53	0.44
1:A:14:ARG:HE	3:A:506:GOL:H31	1.82	0.43
1:B:54:LYS:O	1:B:57:THR:HG22	2.18	0.43
1:B:420:MET:HB2	1:B:420:MET:HE2	1.89	0.43
1:A:41:ILE:HG23	1:A:151:LEU:HD11	2.00	0.43
1:B:439:ASN:O	1:B:443:ILE:HG12	2.19	0.43
1:A:86:LEU:HD22	1:A:195:VAL:HG11	2.00	0.43
1:B:6:LYS:HA	1:B:9:ILE:HG22	2.01	0.42
1:B:13:LYS:HA	1:B:13:LYS:HD3	1.93	0.42
1:A:67:ILE:HD13	1:A:80:GLU:HA	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:319:GLU:OE2	1:A:323:LYS:NZ	2.53	0.42
1:B:16:TYR:OH	1:B:372:PRO:O	2.27	0.41
1:B:142:PRO:HG2	1:B:214:ASN:HD21	1.84	0.41
1:B:227:PHE:CZ	1:B:265:HIS:HB3	2.56	0.41
1:B:203:GLU:O	1:B:203:GLU:HG2	2.20	0.41
1:B:23:ALA:O	1:B:27:ILE:HG12	2.20	0.41
1:B:194:GLN:HB3	1:B:199:GLN:HA	2.03	0.41
1:B:38:ASN:HD21	1:B:121:GLN:NE2	2.10	0.40
1:A:63:LYS:HD2	1:A:79:GLU:HG2	2.03	0.40
1:B:41:ILE:HG23	1:B:151:LEU:HD11	2.02	0.40
1:A:439:ASN:HD21	1:B:363:GLY:CA	2.34	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	453/464 (98%)	448 (99%)	5 (1%)	0	100	100
1	B	449/464 (97%)	441 (98%)	8 (2%)	0	100	100
All	All	902/928 (97%)	889 (99%)	13 (1%)	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	386/394 (98%)	379 (98%)	7 (2%)	59	60
1	B	382/394 (97%)	376 (98%)	6 (2%)	62	65
All	All	768/788 (98%)	755 (98%)	13 (2%)	60	63

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	LEU
1	A	195	VAL
1	A	197	ASP
1	A	205	ARG
1	A	280	PHE
1	A	304	LEU
1	A	426	ARG
1	B	47	LEU
1	B	165	ASN
1	B	205	ARG
1	B	280	PHE
1	B	304	LEU
1	B	423	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	199	GLN
1	A	267	ASN
1	B	121	GLN
1	B	165	ASN
1	B	214	ASN
1	B	350	HIS
1	B	429	GLN

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 [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

17 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	SO4	A	501	-	4,4,4	0.15	0	6,6,6	0.08	0
3	GOL	B	509	-	5,5,5	0.35	0	5,5,5	0.26	0
2	SO4	A	503	-	4,4,4	0.14	0	6,6,6	0.09	0
3	GOL	A	504	-	5,5,5	0.34	0	5,5,5	0.44	0
3	GOL	A	507	-	5,5,5	0.39	0	5,5,5	0.29	0
3	GOL	B	504	-	5,5,5	0.45	0	5,5,5	0.14	0
3	GOL	B	507	-	5,5,5	0.37	0	5,5,5	0.23	0
2	SO4	A	502	-	4,4,4	0.14	0	6,6,6	0.08	0
3	GOL	B	506	-	5,5,5	0.35	0	5,5,5	0.27	0
2	SO4	B	503	-	4,4,4	0.13	0	6,6,6	0.08	0
3	GOL	A	505	-	5,5,5	0.36	0	5,5,5	0.25	0
3	GOL	B	505	-	5,5,5	0.37	0	5,5,5	0.27	0
3	GOL	A	508	-	5,5,5	0.37	0	5,5,5	0.48	0
3	GOL	B	508	-	5,5,5	0.36	0	5,5,5	0.30	0
2	SO4	B	501	-	4,4,4	0.13	0	6,6,6	0.07	0
2	SO4	B	502	-	4,4,4	0.13	0	6,6,6	0.05	0
3	GOL	A	506	-	5,5,5	0.37	0	5,5,5	0.31	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
3	GOL	B	509	-	-	2/4/4/4	-
3	GOL	A	504	-	-	2/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	A	507	-	-	2/4/4/4	-
3	GOL	B	504	-	-	2/4/4/4	-
3	GOL	B	507	-	-	2/4/4/4	-
3	GOL	B	506	-	-	0/4/4/4	-
3	GOL	A	505	-	-	2/4/4/4	-
3	GOL	B	505	-	-	2/4/4/4	-
3	GOL	A	508	-	-	1/4/4/4	-
3	GOL	B	508	-	-	4/4/4/4	-
3	GOL	A	506	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (21) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	507	GOL	O1-C1-C2-O2
3	B	504	GOL	O1-C1-C2-C3
3	B	505	GOL	O1-C1-C2-C3
3	B	507	GOL	O1-C1-C2-C3
3	B	508	GOL	O1-C1-C2-C3
3	B	509	GOL	O1-C1-C2-C3
3	A	504	GOL	O1-C1-C2-O2
3	A	505	GOL	O1-C1-C2-O2
3	A	504	GOL	O1-C1-C2-C3
3	A	505	GOL	O1-C1-C2-C3
3	A	506	GOL	O1-C1-C2-C3
3	A	507	GOL	O1-C1-C2-C3
3	A	508	GOL	O1-C1-C2-C3
3	B	504	GOL	O1-C1-C2-O2
3	B	505	GOL	O1-C1-C2-O2
3	B	507	GOL	O1-C1-C2-O2
3	A	506	GOL	O1-C1-C2-O2
3	B	508	GOL	O1-C1-C2-O2
3	B	509	GOL	O1-C1-C2-O2
3	B	508	GOL	O2-C2-C3-O3
3	B	508	GOL	C1-C2-C3-O3

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	503	SO4	1	0
3	A	506	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 [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	454/464 (97%)	0.07	8 (1%) 68 74	37, 55, 85, 117	0
1	B	449/464 (96%)	0.92	75 (16%) 1 2	36, 70, 118, 145	0
All	All	903/928 (97%)	0.49	83 (9%) 9 12	36, 60, 111, 145	0

All (83) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	364	GLY	10.5
1	B	197	ASP	8.6
1	B	196	PHE	8.2
1	B	199	GLN	7.8
1	B	198	VAL	6.7
1	B	5	LEU	6.5
1	B	8	ARG	6.4
1	B	57	THR	6.3
1	B	52	LEU	6.1
1	B	56	VAL	6.1
1	B	65	PHE	5.9
1	B	3	GLU	5.7
1	B	90	LYS	5.1
1	B	6	LYS	5.0
1	B	47	LEU	4.9
1	B	68	ILE	4.5
1	B	193	PHE	4.5
1	B	111	TRP	4.5
1	B	191	ARG	4.4
1	B	7	ASP	4.3
1	B	375	ILE	4.3
1	B	4	SER	4.2
1	B	46	TYR	4.1
1	B	61	LYS	4.0

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Mol	Chain	Res	Type	RSRZ
1	B	449	LEU	3.9
1	B	195	VAL	3.8
1	B	9	ILE	3.7
1	B	51	ASP	3.7
1	B	48	ASP	3.6
1	B	194	GLN	3.5
1	B	107	TYR	3.5
1	A	363	GLY	3.4
1	B	190	PRO	3.3
1	A	401	GLY	3.3
1	B	10	ARG	3.2
1	B	49	ALA	3.1
1	B	167	LEU	3.1
1	B	69	GLU	3.1
1	B	62	GLU	3.1
1	B	85	ILE	3.1
1	B	162	PHE	3.1
1	B	451	LYS	3.0
1	B	50	ASP	3.0
1	B	201	PRO	3.0
1	B	423	ASN	3.0
1	B	11	LEU	3.0
1	A	453	PHE	3.0
1	B	380	LYS	2.9
1	B	189	PHE	2.8
1	B	378	SER	2.7
1	A	62	GLU	2.7
1	B	53	GLU	2.7
1	A	454	THR	2.7
1	B	55	ARG	2.7
1	B	84	GLY	2.6
1	B	112	GLY	2.6
1	B	14	ARG	2.5
1	B	59	LYS	2.5
1	B	377	ALA	2.5
1	B	13	LYS	2.5
1	B	58	GLU	2.4
1	B	436	VAL	2.4
1	B	164	GLY	2.4
1	A	423	ASN	2.3
1	B	67	ILE	2.2
1	B	202	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	444	VAL	2.2
1	B	163	GLU	2.2
1	B	60	GLY	2.2
1	B	354	TYR	2.2
1	A	451	LYS	2.2
1	B	70	ASN	2.2
1	B	166	LYS	2.1
1	B	45	LYS	2.1
1	B	447	GLU	2.1
1	B	376	VAL	2.1
1	B	204	ASN	2.1
1	B	12	TRP	2.1
1	B	83	GLY	2.1
1	B	86	LEU	2.0
1	B	192	GLY	2.0
1	B	284	ALA	2.0
1	B	165	ASN	2.0

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
3	GOL	B	505	6/6	0.70	0.39	101,104,105,109	0
3	GOL	B	509	6/6	0.73	0.14	83,85,87,87	0
3	GOL	A	507	6/6	0.81	0.25	80,94,95,96	0
3	GOL	B	504	6/6	0.87	0.14	58,61,65,70	0
3	GOL	A	506	6/6	0.87	0.23	83,86,87,87	0
3	GOL	A	508	6/6	0.87	0.16	49,51,52,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	SO4	A	502	5/5	0.89	0.18	82,83,83,84	5
3	GOL	B	506	6/6	0.90	0.12	69,73,75,77	0
2	SO4	B	503	5/5	0.90	0.22	65,67,70,71	5
2	SO4	A	503	5/5	0.91	0.39	87,88,89,93	5
3	GOL	B	508	6/6	0.92	0.13	50,53,57,59	0
3	GOL	B	507	6/6	0.92	0.12	63,65,69,69	0
2	SO4	B	502	5/5	0.93	0.12	95,100,101,102	5
3	GOL	A	504	6/6	0.93	0.14	55,59,63,70	0
3	GOL	A	505	6/6	0.93	0.16	61,66,68,70	0
2	SO4	B	501	5/5	0.94	0.28	56,59,61,62	5
2	SO4	A	501	5/5	0.95	0.21	55,55,57,58	5

6.5 Other polymers [i](#)

There are no such residues in this entry.