



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 6, 2023 – 08:27 AM EDT

PDB ID : 4DRS
Title : Crystal structure of *Cryptosporidium parvum* pyruvate kinase
Authors : Cook, W.J.; Chattopadhyay, D.
Deposited on : 2012-02-17
Resolution : 2.50 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 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 : 2.35
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) : 2.35

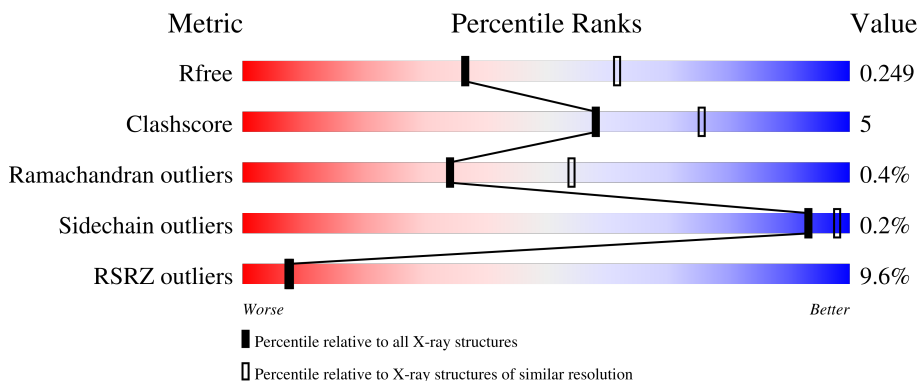
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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	526	 7% 82% 10% 8%
1	B	526	 11% 82% 11% 8%

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
3	GOL	B	604	-	-	X	-

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 7505 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 Pyruvate kinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	485	Total 3644	C 2279	N 629	O 704	S 32	0	0	0
1	B	485	Total 3644	C 2279	N 629	O 704	S 32	0	0	0

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



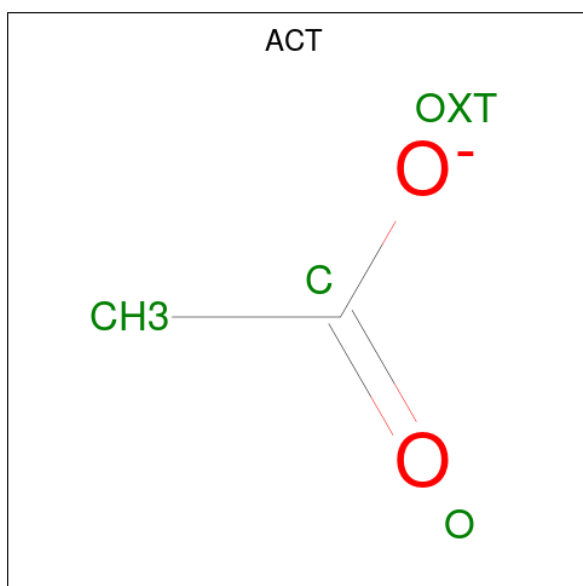
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
2	A	1	Total 5	O 4	S 1	0	0
2	A	1	Total 5	O 4	S 1	0	0
2	B	1	Total 5	O 4	S 1	0	0
2	B	1	Total 5	O 4	S 1	0	0

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 4 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



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

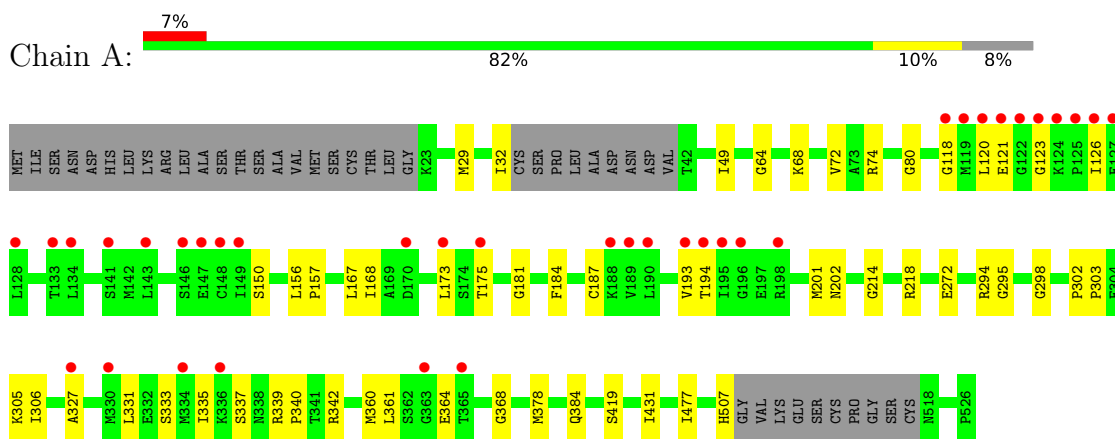
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	74	Total O 74 74	0	0
5	B	75	Total O 75 75	0	0

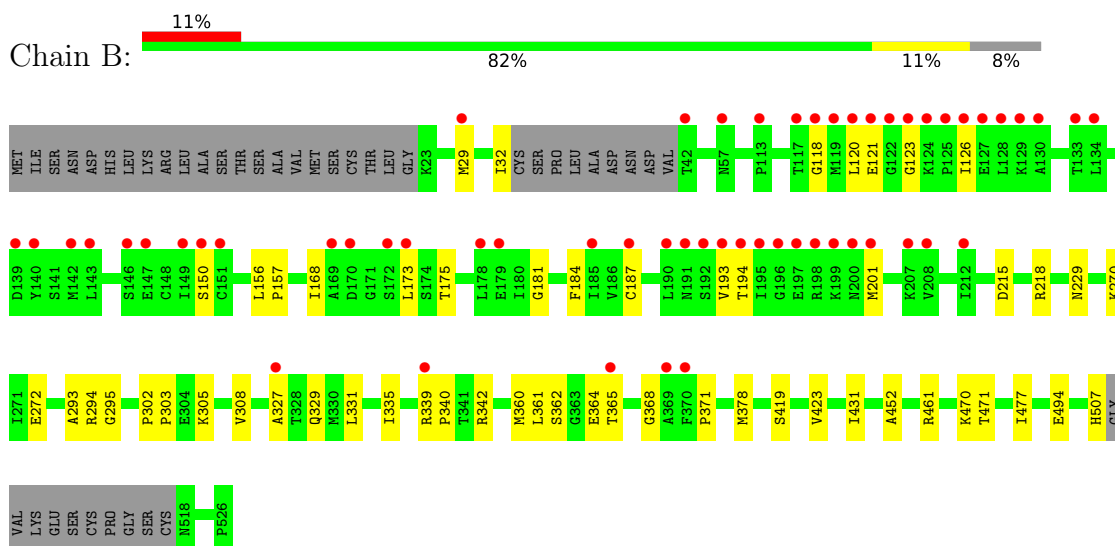
3 Residue-property plots

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: Pyruvate kinase



- Molecule 1: Pyruvate kinase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	129.90Å 136.94Å 77.23Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.71 – 2.50 49.71 – 2.50	Depositor EDS
% Data completeness (in resolution range)	97.8 (49.71-2.50) 97.8 (49.71-2.50)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.39 (at 2.51Å)	Xtrriage
Refinement program	REFMAC 5.5.0109, CNS	Depositor
R, R_{free}	0.213 , 0.249 0.213 , 0.249	Depositor DCC
R_{free} test set	2344 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	47.3	Xtrriage
Anisotropy	0.133	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 39.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7505	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.46% 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, ACT, 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	0.35	0/3692	0.48	0/4991
1	B	0.35	0/3692	0.48	0/4991
All	All	0.35	0/7384	0.48	0/9982

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 [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	3644	0	3733	36	0
1	B	3644	0	3733	41	0
2	A	10	0	0	0	0
2	B	10	0	0	0	0
3	A	12	0	16	1	0
3	B	12	0	16	5	0
4	A	12	0	9	1	0
4	B	12	0	9	0	0
5	A	74	0	0	0	0
5	B	75	0	0	0	0
All	All	7505	0	7516	72	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 5.

All (72) 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:229:ASN:HD21	3:B:604:GOL:H31	1.52	0.73
1:B:339:ARG:HG2	1:B:340:PRO:HD2	1.71	0.72
1:B:229:ASN:ND2	3:B:604:GOL:H31	2.06	0.69
1:B:229:ASN:HD21	3:B:604:GOL:C3	2.05	0.69
1:A:175:THR:HB	1:A:187:CYS:HB3	1.79	0.65
1:A:168:ILE:HD12	1:A:173:LEU:HD23	1.78	0.65
1:B:331:LEU:HD12	1:B:361:LEU:HD21	1.78	0.64
1:B:168:ILE:HG12	1:B:201:MET:HG3	1.80	0.64
1:B:335:ILE:HG23	1:B:368:GLY:HA2	1.81	0.62
1:A:339:ARG:HG2	1:A:340:PRO:HD2	1.81	0.62
1:A:32:ILE:HG12	1:B:305:LYS:HD3	1.81	0.62
1:B:175:THR:HB	1:B:187:CYS:HB3	1.81	0.61
1:A:331:LEU:HB2	1:A:364:GLU:HG2	1.82	0.60
1:A:431:ILE:HB	1:A:507:HIS:HB3	1.84	0.60
1:A:193:VAL:HG12	1:A:194:THR:N	2.16	0.59
1:A:335:ILE:HG23	1:A:368:GLY:HA2	1.84	0.59
1:B:168:ILE:HB	1:B:173:LEU:HB3	1.87	0.57
1:B:327:ALA:HB2	1:B:360:MET:HB3	1.86	0.57
1:A:298:GLY:HA2	1:A:306:ILE:HD11	1.87	0.57
1:A:384:GLN:HG3	1:B:308:VAL:HG21	1.88	0.56
1:A:120:LEU:HD22	1:A:126:ILE:HD12	1.87	0.56
1:A:331:LEU:HD12	1:A:361:LEU:HD21	1.88	0.55
1:A:168:ILE:HG12	1:A:201:MET:HG3	1.89	0.55
1:A:168:ILE:HB	1:A:173:LEU:HB3	1.91	0.53
1:A:305:LYS:HD3	1:B:32:ILE:HG12	1.91	0.52
1:B:361:LEU:HG	1:B:378:MET:CE	2.40	0.52
1:B:168:ILE:HD12	1:B:173:LEU:HD23	1.91	0.52
1:B:193:VAL:HG12	1:B:194:THR:N	2.25	0.52
1:A:361:LEU:HG	1:A:378:MET:CE	2.40	0.52
1:A:64:GLY:O	1:A:68:LYS:HG2	2.09	0.52
1:A:80:GLY:H	4:A:606:ACT:H3	1.75	0.52
1:A:193:VAL:HG12	1:A:194:THR:H	1.74	0.51
1:B:461:ARG:NH2	3:B:604:GOL:H11	2.26	0.51
1:A:342:ARG:CZ	1:B:294:ARG:HG3	2.40	0.50
1:B:120:LEU:HD22	1:B:126:ILE:HD12	1.93	0.50
1:A:167:LEU:HB2	1:A:202:ASN:HB2	1.94	0.49
1:B:331:LEU:HB2	1:B:364:GLU:HG2	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:327:ALA:CB	1:B:360:MET:HB3	2.43	0.48
1:B:452:ALA:HB3	1:B:471:THR:HG22	1.95	0.48
1:A:294:ARG:HG3	1:B:342:ARG:CZ	2.44	0.48
1:A:156:LEU:N	1:A:157:PRO:HD2	2.29	0.47
1:A:49:ILE:HG12	1:A:72:VAL:HB	1.95	0.47
1:A:118:GLY:HA3	1:A:150:SER:HB3	1.96	0.47
1:A:29:MET:HA	1:A:32:ILE:HD12	1.97	0.46
1:B:329:GLN:HG3	1:B:362:SER:HB2	1.97	0.46
1:A:214:GLY:O	1:A:218:ARG:HG3	2.16	0.46
1:A:74:ARG:HH22	3:A:603:GOL:H2	1.81	0.46
1:A:327:ALA:HB2	1:A:360:MET:HB3	1.97	0.45
1:A:181:GLY:HA3	1:A:184:PHE:CE1	2.51	0.45
1:B:431:ILE:HB	1:B:507:HIS:HB3	1.98	0.45
1:A:431:ILE:HG23	1:A:477:ILE:HG13	2.00	0.44
1:A:193:VAL:CG1	1:A:194:THR:N	2.80	0.44
1:B:156:LEU:N	1:B:157:PRO:HD2	2.33	0.43
1:B:361:LEU:HG	1:B:378:MET:HE2	2.00	0.43
1:B:365:THR:HA	1:B:371:PRO:HB3	2.01	0.43
1:B:431:ILE:HG23	1:B:477:ILE:HG13	2.00	0.43
1:B:302:PRO:HA	1:B:303:PRO:HD3	1.87	0.43
1:B:470:LYS:HE2	1:B:494:GLU:OE1	2.19	0.43
1:A:193:VAL:CG1	1:A:194:THR:H	2.32	0.42
1:B:29:MET:HA	1:B:32:ILE:HD12	2.02	0.42
1:B:118:GLY:HA3	1:B:150:SER:HB3	2.02	0.41
1:A:272:GLU:HB3	1:A:295:GLY:HA3	2.03	0.41
1:B:419:SER:O	1:B:423:VAL:HG22	2.20	0.41
1:B:181:GLY:HA3	1:B:184:PHE:CE1	2.55	0.41
1:B:218:ARG:HH11	1:B:218:ARG:HB3	1.84	0.41
1:B:270:LYS:HZ1	3:B:603:GOL:H11	1.84	0.41
1:B:339:ARG:HG2	1:B:340:PRO:CD	2.46	0.41
1:A:333:SER:O	1:A:337:SER:HB3	2.21	0.41
1:B:218:ARG:HB3	1:B:218:ARG:NH1	2.35	0.41
1:B:272:GLU:HB3	1:B:295:GLY:HA3	2.01	0.41
1:A:302:PRO:HA	1:A:303:PRO:HD3	1.83	0.41
1:B:272:GLU:HG2	1:B:293:ALA:HB3	2.02	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	479/526 (91%)	463 (97%)	14 (3%)	2 (0%)	34	54
1	B	479/526 (91%)	460 (96%)	17 (4%)	2 (0%)	34	54
All	All	958/1052 (91%)	923 (96%)	31 (3%)	4 (0%)	34	54

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	121	GLU
1	A	123	GLY
1	B	121	GLU
1	B	123	GLY

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	414/449 (92%)	413 (100%)	1 (0%)	93	98
1	B	414/449 (92%)	413 (100%)	1 (0%)	93	98
All	All	828/898 (92%)	826 (100%)	2 (0%)	93	98

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	419	SER
1	B	215	ASP

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

Mol	Chain	Res	Type
1	A	518	ASN
1	B	229	ASN

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](#)

14 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	$\# Z > 2$
4	ACT	A	607	-	3,3,3	0.77	0	3,3,3	0.70	0
4	ACT	B	606	-	3,3,3	0.79	0	3,3,3	0.71	0
2	SO4	A	601	-	4,4,4	0.26	0	6,6,6	0.18	0
2	SO4	A	602	-	4,4,4	0.33	0	6,6,6	0.19	0
4	ACT	B	607	-	3,3,3	0.78	0	3,3,3	0.74	0
3	GOL	A	603	-	5,5,5	0.33	0	5,5,5	0.29	0
3	GOL	B	603	-	5,5,5	0.34	0	5,5,5	0.33	0
2	SO4	B	602	-	4,4,4	0.34	0	6,6,6	0.14	0
4	ACT	A	606	-	3,3,3	0.76	0	3,3,3	0.75	0
4	ACT	B	605	-	3,3,3	0.80	0	3,3,3	0.62	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	GOL	B	604	-	5,5,5	0.24	0	5,5,5	0.38	0
3	GOL	A	604	-	5,5,5	0.26	0	5,5,5	0.40	0
2	SO4	B	601	-	4,4,4	0.32	0	6,6,6	0.10	0
4	ACT	A	605	-	3,3,3	0.84	0	3,3,3	0.57	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	A	603	-	-	2/4/4/4	-
3	GOL	B	603	-	-	3/4/4/4	-
3	GOL	B	604	-	-	0/4/4/4	-
3	GOL	A	604	-	-	0/4/4/4	-

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
3	A	603	GOL	C1-C2-C3-O3
3	B	603	GOL	O1-C1-C2-C3
3	B	603	GOL	C1-C2-C3-O3
3	A	603	GOL	O2-C2-C3-O3
3	B	603	GOL	O2-C2-C3-O3

There are no ring outliers.

4 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	603	GOL	1	0
3	B	603	GOL	1	0
4	A	606	ACT	1	0
3	B	604	GOL	4	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	485/526 (92%)	0.38	36 (7%) 14 15	32, 51, 111, 142	0
1	B	485/526 (92%)	0.56	57 (11%) 4 4	33, 50, 139, 176	0
All	All	970/1052 (92%)	0.47	93 (9%) 8 7	32, 51, 125, 176	0

All (93) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	119	MET	10.5
1	B	128	LEU	8.2
1	A	126	ILE	8.0
1	B	195	ILE	6.9
1	B	194	THR	6.7
1	B	134	LEU	6.6
1	B	125	PRO	6.6
1	A	173	LEU	6.3
1	B	196	GLY	5.8
1	A	195	ILE	5.8
1	A	119	MET	5.3
1	B	130	ALA	5.0
1	B	127	GLU	5.0
1	A	128	LEU	5.0
1	A	127	GLU	4.7
1	A	121	GLU	4.7
1	B	120	LEU	4.6
1	B	121	GLU	4.6
1	B	126	ILE	4.6
1	A	147	GLU	4.5
1	A	149	ILE	4.4
1	A	143	LEU	4.4
1	A	365	THR	4.3
1	A	196	GLY	4.3

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Mol	Chain	Res	Type	RSRZ
1	B	133	THR	4.2
1	B	208	VAL	4.2
1	B	140	TYR	4.2
1	A	134	LEU	4.1
1	B	143	LEU	4.0
1	A	189	VAL	4.0
1	B	191	ASN	4.0
1	B	147	GLU	3.9
1	B	146	SER	3.9
1	B	172	SER	3.8
1	B	118	GLY	3.7
1	A	118	GLY	3.7
1	B	151	CYS	3.6
1	B	150	SER	3.6
1	B	173	LEU	3.6
1	B	198	ARG	3.6
1	A	198	ARG	3.6
1	B	122	GLY	3.6
1	A	170	ASP	3.6
1	B	129	LYS	3.5
1	B	149	ILE	3.5
1	A	175	THR	3.5
1	A	193	VAL	3.4
1	B	169	ALA	3.4
1	B	117	THR	3.4
1	B	139	ASP	3.3
1	A	330	MET	3.3
1	B	42	THR	3.3
1	A	146	SER	3.2
1	B	339	ARG	3.0
1	B	193	VAL	3.0
1	A	194	THR	2.9
1	B	124	LYS	2.9
1	A	327	ALA	2.9
1	B	190	LEU	2.9
1	B	369	ALA	2.9
1	A	334	MET	2.9
1	B	185	ILE	2.9
1	B	327	ALA	2.9
1	A	336	LYS	2.9
1	B	179	GLU	2.8
1	B	192	SER	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	201	MET	2.7
1	A	120	LEU	2.7
1	B	142	MET	2.7
1	A	125	PRO	2.7
1	A	148	CYS	2.6
1	B	170	ASP	2.5
1	B	123	GLY	2.4
1	B	197	GLU	2.4
1	B	200	ASN	2.3
1	B	113	PRO	2.3
1	B	212	ILE	2.3
1	A	141	SER	2.3
1	A	123	GLY	2.3
1	A	124	LYS	2.3
1	B	365	THR	2.3
1	B	178	LEU	2.3
1	A	122	GLY	2.3
1	B	187	CYS	2.3
1	B	57	ASN	2.2
1	B	370	PHE	2.2
1	A	190	LEU	2.2
1	B	29	MET	2.2
1	A	363	GLY	2.1
1	A	133	THR	2.1
1	B	207	LYS	2.1
1	A	188	LYS	2.0
1	B	199	LYS	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	603	6/6	0.84	0.16	72,73,75,77	0
4	ACT	B	607	4/4	0.84	0.26	69,69,70,71	0
4	ACT	A	607	4/4	0.87	0.14	65,65,67,67	0
3	GOL	A	603	6/6	0.87	0.17	62,63,65,66	0
4	ACT	A	605	4/4	0.88	0.17	64,66,67,68	0
3	GOL	B	604	6/6	0.90	0.22	55,55,58,58	0
3	GOL	A	604	6/6	0.90	0.21	47,49,51,53	0
4	ACT	B	605	4/4	0.91	0.24	65,67,67,68	0
2	SO4	B	602	5/5	0.91	0.13	78,82,84,85	0
4	ACT	B	606	4/4	0.94	0.10	71,73,73,74	0
2	SO4	A	602	5/5	0.96	0.12	59,63,66,66	0
4	ACT	A	606	4/4	0.96	0.13	68,68,70,70	0
2	SO4	B	601	5/5	0.98	0.12	59,59,61,61	0
2	SO4	A	601	5/5	0.98	0.12	54,54,56,57	0

6.5 Other polymers [i](#)

There are no such residues in this entry.