



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 1, 2026 – 02:59 PM UTC

PDB ID : 3SRF / pdb_00003srf
Title : Human M1 pyruvate kinase
Authors : Morgan, H.P.; O'Reilly, F.; Palmer, R.; McNae, I.W.; Nowicki, M.W.; Wear, M.A.; Fothergill-Gilmore, L.A.; Walkinshaw, M.D.
Deposited on : 2011-07-07
Resolution : 2.85 Å (reported)

This is a wwPDB X-ray Structure Validation Summary 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 : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

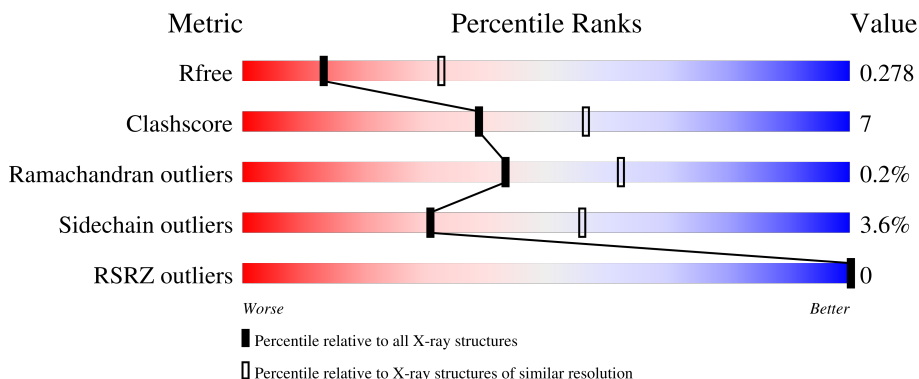
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.85 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}	180053	1520 (2.86-2.82)
Clashscore	190562	1559 (2.86-2.82)
Ramachandran outliers	187476	1517 (2.86-2.82)
Sidechain outliers	187428	1518 (2.86-2.82)
RSRZ outliers	180081	1521 (2.86-2.82)

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	551	 79% 13% • 6%
1	B	551	 79% 14% • 6%
1	C	551	 75% 16% • 6%
1	D	551	 78% 14% • 7%
1	E	551	 79% 12% • 7%

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Mol	Chain	Length	Quality of chain
1	F	551	 78% 14% • 6%
1	G	551	 80% 12% • 7%
1	H	551	 75% 18% • 6%

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 32320 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 isozymes M1/M2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	C	517	3968	2493	704	743	28	0	0	0
1	A	517	3968	2493	704	743	28	0	0	0
1	B	517	3966	2490	704	744	28	0	0	0
1	D	515	3957	2487	702	740	28	0	0	0
1	E	514	3949	2481	701	739	28	0	0	0
1	F	516	3960	2487	703	742	28	0	0	0
1	G	513	3944	2478	700	738	28	0	0	0
1	H	519	3978	2498	706	746	28	0	0	0

There are 160 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-20	MET	-	expression tag	UNP P14618
C	-19	GLY	-	expression tag	UNP P14618
C	-18	SER	-	expression tag	UNP P14618
C	-17	SER	-	expression tag	UNP P14618
C	-16	HIS	-	expression tag	UNP P14618
C	-15	HIS	-	expression tag	UNP P14618
C	-14	HIS	-	expression tag	UNP P14618
C	-13	HIS	-	expression tag	UNP P14618
C	-12	HIS	-	expression tag	UNP P14618
C	-11	HIS	-	expression tag	UNP P14618
C	-10	SER	-	expression tag	UNP P14618
C	-9	SER	-	expression tag	UNP P14618
C	-8	GLY	-	expression tag	UNP P14618

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-7	LEU	-	expression tag	UNP P14618
C	-6	VAL	-	expression tag	UNP P14618
C	-5	PRO	-	expression tag	UNP P14618
C	-4	ARG	-	expression tag	UNP P14618
C	-3	GLY	-	expression tag	UNP P14618
C	-2	SER	-	expression tag	UNP P14618
C	-1	HIS	-	expression tag	UNP P14618
A	-20	MET	-	expression tag	UNP P14618
A	-19	GLY	-	expression tag	UNP P14618
A	-18	SER	-	expression tag	UNP P14618
A	-17	SER	-	expression tag	UNP P14618
A	-16	HIS	-	expression tag	UNP P14618
A	-15	HIS	-	expression tag	UNP P14618
A	-14	HIS	-	expression tag	UNP P14618
A	-13	HIS	-	expression tag	UNP P14618
A	-12	HIS	-	expression tag	UNP P14618
A	-11	HIS	-	expression tag	UNP P14618
A	-10	SER	-	expression tag	UNP P14618
A	-9	SER	-	expression tag	UNP P14618
A	-8	GLY	-	expression tag	UNP P14618
A	-7	LEU	-	expression tag	UNP P14618
A	-6	VAL	-	expression tag	UNP P14618
A	-5	PRO	-	expression tag	UNP P14618
A	-4	ARG	-	expression tag	UNP P14618
A	-3	GLY	-	expression tag	UNP P14618
A	-2	SER	-	expression tag	UNP P14618
A	-1	HIS	-	expression tag	UNP P14618
B	-20	MET	-	expression tag	UNP P14618
B	-19	GLY	-	expression tag	UNP P14618
B	-18	SER	-	expression tag	UNP P14618
B	-17	SER	-	expression tag	UNP P14618
B	-16	HIS	-	expression tag	UNP P14618
B	-15	HIS	-	expression tag	UNP P14618
B	-14	HIS	-	expression tag	UNP P14618
B	-13	HIS	-	expression tag	UNP P14618
B	-12	HIS	-	expression tag	UNP P14618
B	-11	HIS	-	expression tag	UNP P14618
B	-10	SER	-	expression tag	UNP P14618
B	-9	SER	-	expression tag	UNP P14618
B	-8	GLY	-	expression tag	UNP P14618
B	-7	LEU	-	expression tag	UNP P14618
B	-6	VAL	-	expression tag	UNP P14618

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-5	PRO	-	expression tag	UNP P14618
B	-4	ARG	-	expression tag	UNP P14618
B	-3	GLY	-	expression tag	UNP P14618
B	-2	SER	-	expression tag	UNP P14618
B	-1	HIS	-	expression tag	UNP P14618
D	-20	MET	-	expression tag	UNP P14618
D	-19	GLY	-	expression tag	UNP P14618
D	-18	SER	-	expression tag	UNP P14618
D	-17	SER	-	expression tag	UNP P14618
D	-16	HIS	-	expression tag	UNP P14618
D	-15	HIS	-	expression tag	UNP P14618
D	-14	HIS	-	expression tag	UNP P14618
D	-13	HIS	-	expression tag	UNP P14618
D	-12	HIS	-	expression tag	UNP P14618
D	-11	HIS	-	expression tag	UNP P14618
D	-10	SER	-	expression tag	UNP P14618
D	-9	SER	-	expression tag	UNP P14618
D	-8	GLY	-	expression tag	UNP P14618
D	-7	LEU	-	expression tag	UNP P14618
D	-6	VAL	-	expression tag	UNP P14618
D	-5	PRO	-	expression tag	UNP P14618
D	-4	ARG	-	expression tag	UNP P14618
D	-3	GLY	-	expression tag	UNP P14618
D	-2	SER	-	expression tag	UNP P14618
D	-1	HIS	-	expression tag	UNP P14618
E	-20	MET	-	expression tag	UNP P14618
E	-19	GLY	-	expression tag	UNP P14618
E	-18	SER	-	expression tag	UNP P14618
E	-17	SER	-	expression tag	UNP P14618
E	-16	HIS	-	expression tag	UNP P14618
E	-15	HIS	-	expression tag	UNP P14618
E	-14	HIS	-	expression tag	UNP P14618
E	-13	HIS	-	expression tag	UNP P14618
E	-12	HIS	-	expression tag	UNP P14618
E	-11	HIS	-	expression tag	UNP P14618
E	-10	SER	-	expression tag	UNP P14618
E	-9	SER	-	expression tag	UNP P14618
E	-8	GLY	-	expression tag	UNP P14618
E	-7	LEU	-	expression tag	UNP P14618
E	-6	VAL	-	expression tag	UNP P14618
E	-5	PRO	-	expression tag	UNP P14618
E	-4	ARG	-	expression tag	UNP P14618

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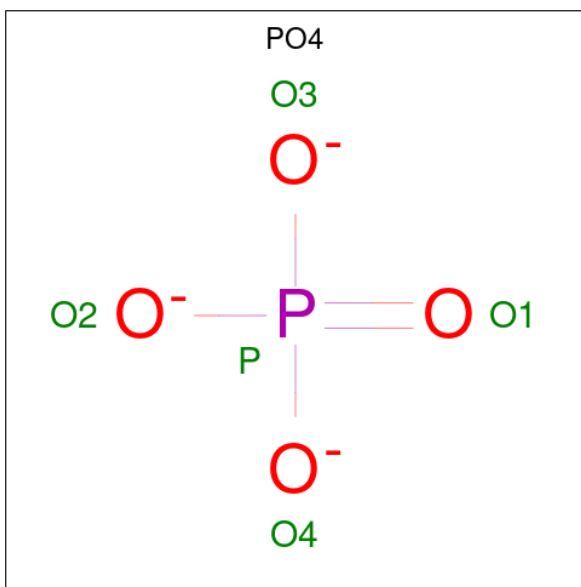
Chain	Residue	Modelled	Actual	Comment	Reference
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E	-2	SER	-	expression tag	UNP P14618
E	-1	HIS	-	expression tag	UNP P14618
F	-20	MET	-	expression tag	UNP P14618
F	-19	GLY	-	expression tag	UNP P14618
F	-18	SER	-	expression tag	UNP P14618
F	-17	SER	-	expression tag	UNP P14618
F	-16	HIS	-	expression tag	UNP P14618
F	-15	HIS	-	expression tag	UNP P14618
F	-14	HIS	-	expression tag	UNP P14618
F	-13	HIS	-	expression tag	UNP P14618
F	-12	HIS	-	expression tag	UNP P14618
F	-11	HIS	-	expression tag	UNP P14618
F	-10	SER	-	expression tag	UNP P14618
F	-9	SER	-	expression tag	UNP P14618
F	-8	GLY	-	expression tag	UNP P14618
F	-7	LEU	-	expression tag	UNP P14618
F	-6	VAL	-	expression tag	UNP P14618
F	-5	PRO	-	expression tag	UNP P14618
F	-4	ARG	-	expression tag	UNP P14618
F	-3	GLY	-	expression tag	UNP P14618
F	-2	SER	-	expression tag	UNP P14618
F	-1	HIS	-	expression tag	UNP P14618
G	-20	MET	-	expression tag	UNP P14618
G	-19	GLY	-	expression tag	UNP P14618
G	-18	SER	-	expression tag	UNP P14618
G	-17	SER	-	expression tag	UNP P14618
G	-16	HIS	-	expression tag	UNP P14618
G	-15	HIS	-	expression tag	UNP P14618
G	-14	HIS	-	expression tag	UNP P14618
G	-13	HIS	-	expression tag	UNP P14618
G	-12	HIS	-	expression tag	UNP P14618
G	-11	HIS	-	expression tag	UNP P14618
G	-10	SER	-	expression tag	UNP P14618
G	-9	SER	-	expression tag	UNP P14618
G	-8	GLY	-	expression tag	UNP P14618
G	-7	LEU	-	expression tag	UNP P14618
G	-6	VAL	-	expression tag	UNP P14618
G	-5	PRO	-	expression tag	UNP P14618
G	-4	ARG	-	expression tag	UNP P14618
G	-3	GLY	-	expression tag	UNP P14618
G	-2	SER	-	expression tag	UNP P14618

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Chain	Residue	Modelled	Actual	Comment	Reference
G	-1	HIS	-	expression tag	UNP P14618
H	-20	MET	-	expression tag	UNP P14618
H	-19	GLY	-	expression tag	UNP P14618
H	-18	SER	-	expression tag	UNP P14618
H	-17	SER	-	expression tag	UNP P14618
H	-16	HIS	-	expression tag	UNP P14618
H	-15	HIS	-	expression tag	UNP P14618
H	-14	HIS	-	expression tag	UNP P14618
H	-13	HIS	-	expression tag	UNP P14618
H	-12	HIS	-	expression tag	UNP P14618
H	-11	HIS	-	expression tag	UNP P14618
H	-10	SER	-	expression tag	UNP P14618
H	-9	SER	-	expression tag	UNP P14618
H	-8	GLY	-	expression tag	UNP P14618
H	-7	LEU	-	expression tag	UNP P14618
H	-6	VAL	-	expression tag	UNP P14618
H	-5	PRO	-	expression tag	UNP P14618
H	-4	ARG	-	expression tag	UNP P14618
H	-3	GLY	-	expression tag	UNP P14618
H	-2	SER	-	expression tag	UNP P14618
H	-1	HIS	-	expression tag	UNP P14618

- Molecule 2 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	P		
2	C	1	5	4	1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total O P 5 4 1	0	0
2	B	1	Total O P 5 4 1	0	0
2	D	1	Total O P 5 4 1	0	0
2	E	1	Total O P 5 4 1	0	0
2	F	1	Total O P 5 4 1	0	0
2	G	1	Total O P 5 4 1	0	0
2	H	1	Total O P 5 4 1	0	0

- Molecule 3 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	C	1	Total K 1 1	0	0
3	A	1	Total K 1 1	0	0
3	B	1	Total K 1 1	0	0
3	D	1	Total K 1 1	0	0
3	E	1	Total K 1 1	0	0
3	F	1	Total K 1 1	0	0
3	G	1	Total K 1 1	0	0
3	H	1	Total K 1 1	0	0

- Molecule 4 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

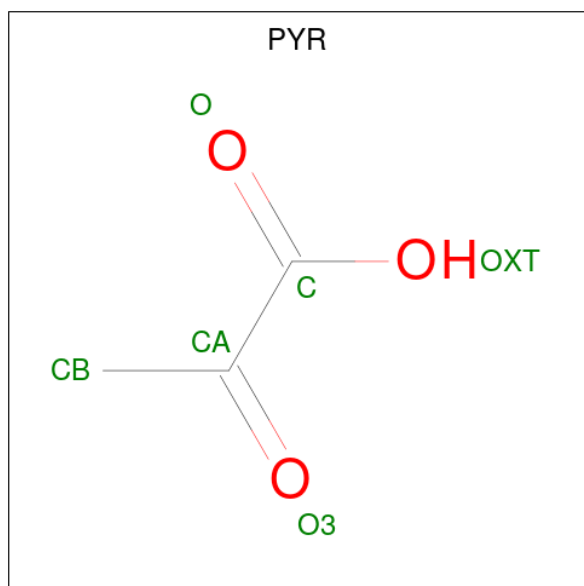
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	C	1	Total Mg 1 1	0	0
4	A	1	Total Mg 1 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total Mg 1 1	0	0
4	D	1	Total Mg 1 1	0	0
4	E	1	Total Mg 1 1	0	0
4	F	1	Total Mg 1 1	0	0
4	G	1	Total Mg 1 1	0	0
4	H	1	Total Mg 1 1	0	0

- Molecule 5 is PYRUVIC ACID (CCD ID: PYR) (formula: C₃H₄O₃).



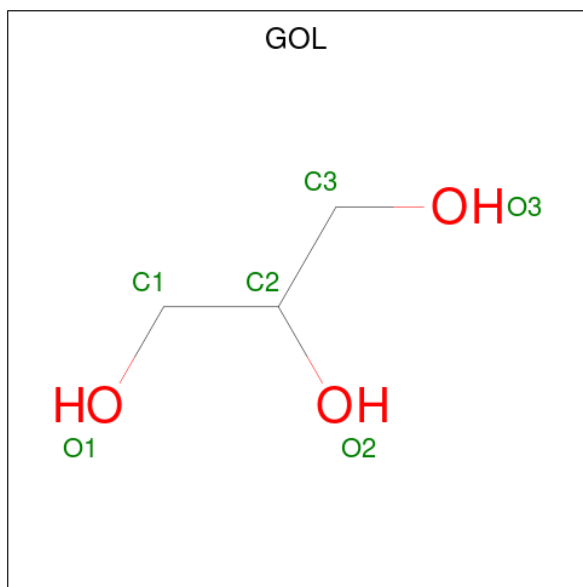
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	C	1	Total C O 6 3 3	0	0
5	A	1	Total C O 6 3 3	0	0
5	B	1	Total C O 6 3 3	0	0
5	D	1	Total C O 6 3 3	0	0
5	E	1	Total C O 6 3 3	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	F	1	Total	C	O	0	0
			6	3	3		
5	G	1	Total	C	O	0	0
			6	3	3		
5	H	1	Total	C	O	0	0
			6	3	3		

- Molecule 6 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 7 is water.

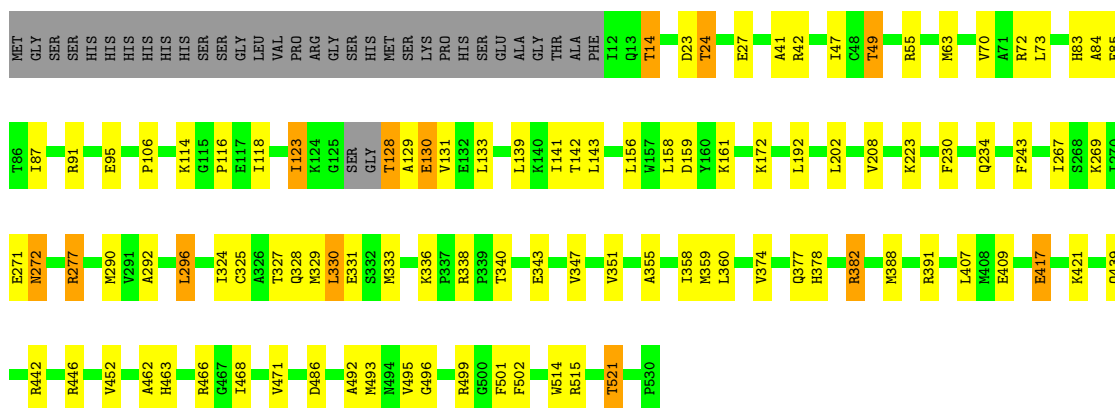
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	C	59	Total O 59 59	0	0
7	A	67	Total O 67 67	0	0
7	B	71	Total O 71 71	0	0
7	D	76	Total O 76 76	0	0
7	E	42	Total O 42 42	0	0
7	F	62	Total O 62 62	0	0
7	G	50	Total O 50 50	0	0
7	H	51	Total O 51 51	0	0

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.

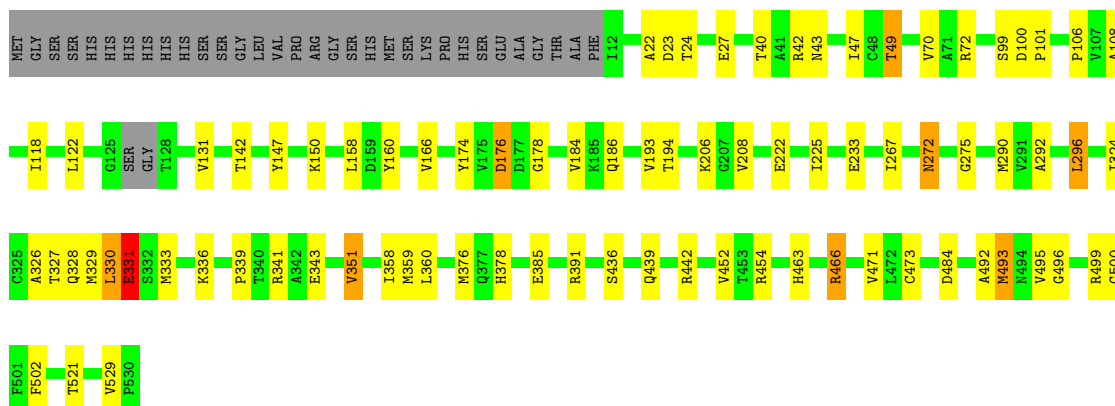
- Molecule 1: Pyruvate kinase isozymes M1/M2

Chain C:  75% 16% • 6%




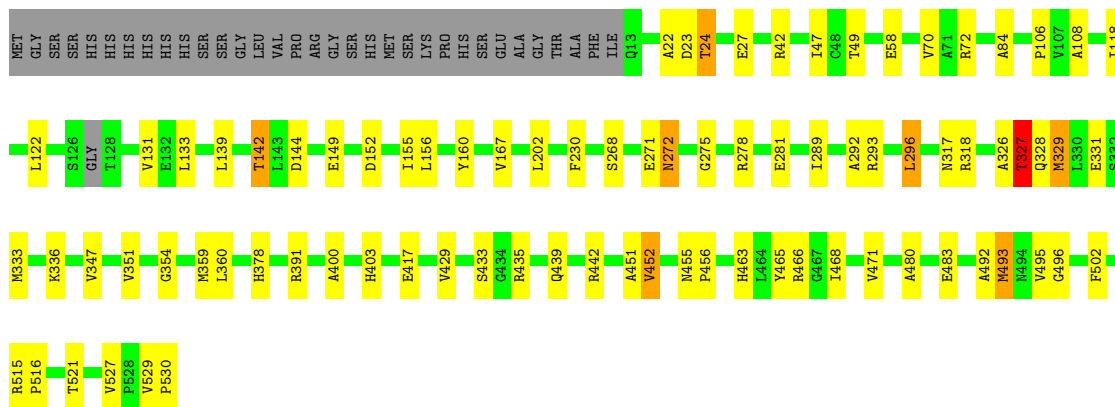
- Molecule 1: Pyruvate kinase isozymes M1/M2

Chain A:  79% 13% • 6%



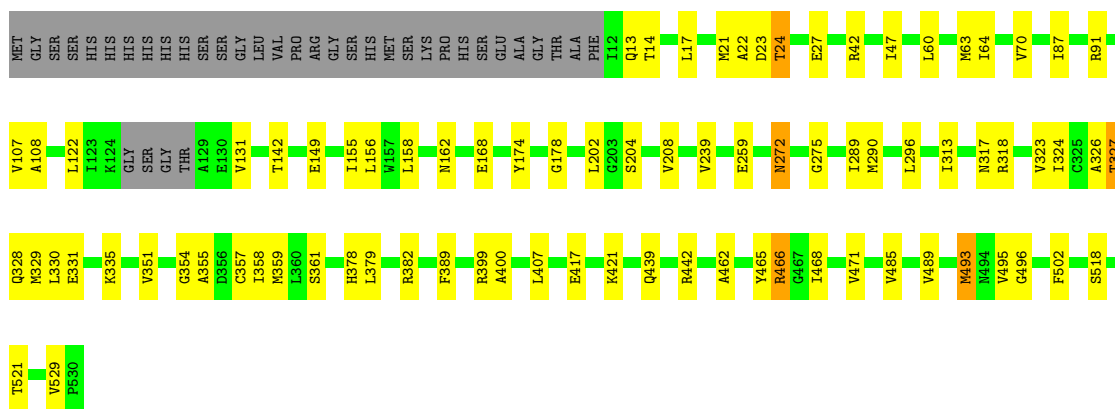
- Molecule 1: Pyruvate kinase isozymes M1/M2

Chain B:  79% 14% • 6%



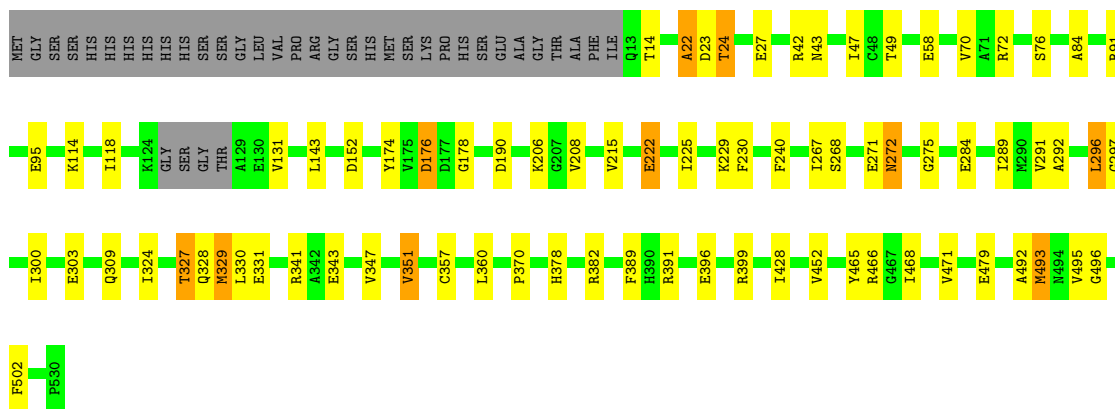
- Molecule 1: Pyruvate kinase isozymes M1/M2

Chain D: 78% 14% 7%



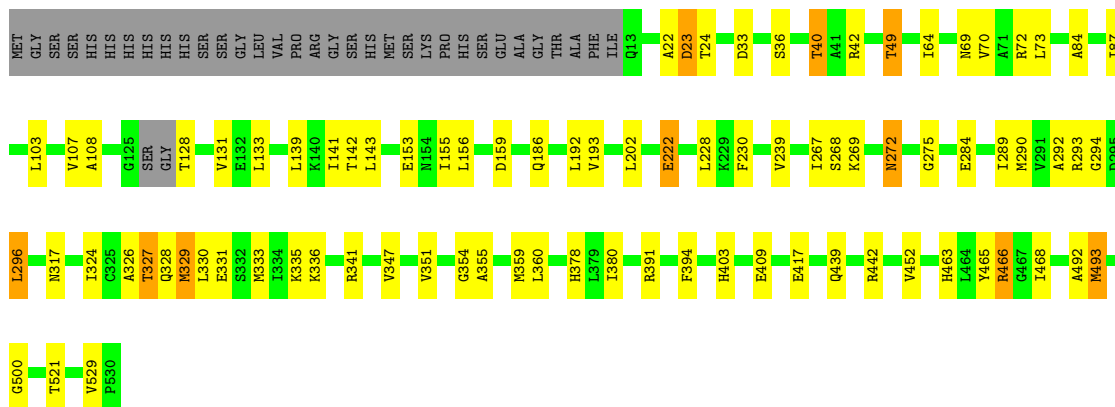
- Molecule 1: Pyruvate kinase isozymes M1/M2

Chain E: 79% 12% 7%

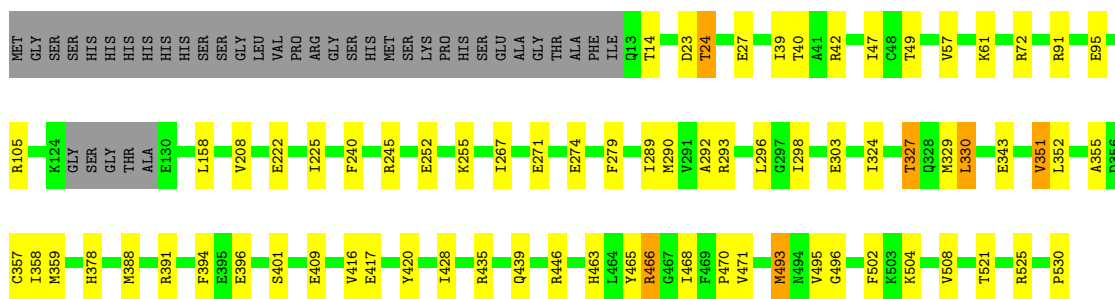
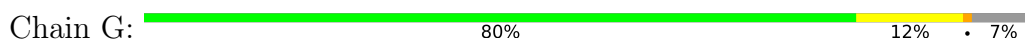


- Molecule 1: Pyruvate kinase isozymes M1/M2

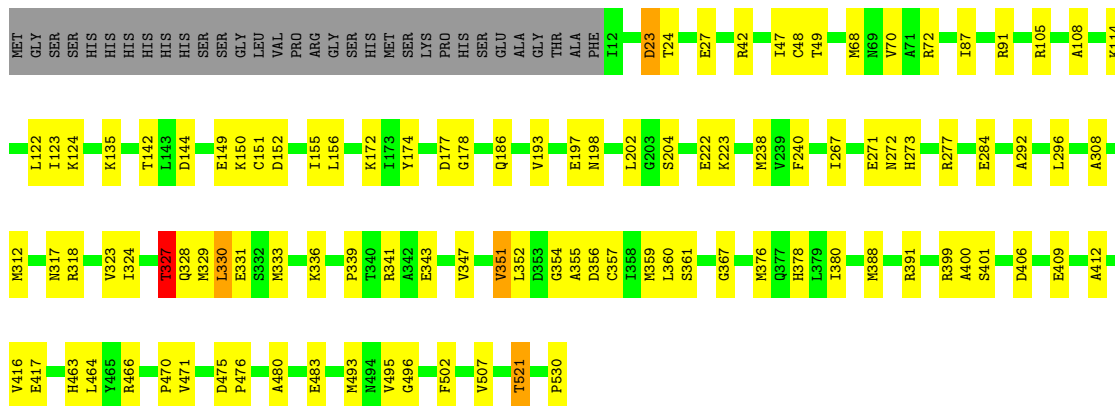
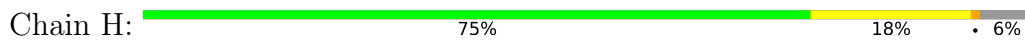
Chain F: 78% 14% 6%



• Molecule 1: Pyruvate kinase isozymes M1/M2



• Molecule 1: Pyruvate kinase isozymes M1/M2



4 Data and refinement statistics i

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	238.00Å 192.22Å 109.06Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 2.85 40.00 – 2.85	Depositor EDS
% Data completeness (in resolution range)	100.0 (40.00-2.85) 93.5 (40.00-2.85)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.23 (at 2.85Å)	Xtrriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.221 , 0.280 0.221 , 0.278	Depositor DCC
R_{free} test set	5346 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	41.8	Xtrriage
Anisotropy	0.153	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 13.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.41$, $\langle L^2 \rangle = 0.23$	Xtrriage
Estimated twinning fraction	0.129 for -h,-k,l	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	32320	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 22.28 % 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 5.8839e-03.*

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: PO4, K, GOL, PYR, MG

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	0.44	0/4030	0.81	2/5435 (0.0%)
1	B	0.44	0/4028	0.81	0/5432
1	C	0.44	0/4030	0.81	0/5435
1	D	0.45	0/4019	0.81	0/5420
1	E	0.45	0/4011	0.82	2/5409 (0.0%)
1	F	0.44	0/4022	0.81	1/5424 (0.0%)
1	G	0.44	0/4006	0.79	0/5402
1	H	0.44	0/4041	0.81	1/5451 (0.0%)
All	All	0.44	0/32187	0.81	6/43408 (0.0%)

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	176	ASP	N-CA-C	12.36	125.37	110.91
1	E	22	ALA	N-CA-C	6.44	118.09	111.14
1	A	176	ASP	N-CA-C	6.16	123.93	110.80
1	A	331	GLU	N-CA-C	5.18	117.60	111.33
1	H	367	GLY	N-CA-C	5.11	117.95	112.33

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	3968	0	4049	57	0
1	B	3966	0	4043	58	0
1	C	3968	0	4048	71	0
1	D	3957	0	4038	50	0
1	E	3949	0	4028	50	0
1	F	3960	0	4037	55	0
1	G	3944	0	4023	48	0
1	H	3978	0	4057	67	0
2	A	5	0	0	1	0
2	B	5	0	0	0	0
2	C	5	0	0	0	0
2	D	5	0	0	0	0
2	E	5	0	0	0	0
2	F	5	0	0	0	0
2	G	5	0	0	0	0
2	H	5	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
3	E	1	0	0	0	0
3	F	1	0	0	0	0
3	G	1	0	0	0	0
3	H	1	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
4	E	1	0	0	0	0
4	F	1	0	0	0	0
4	G	1	0	0	0	0
4	H	1	0	0	0	0
5	A	6	0	0	0	0
5	B	6	0	0	0	0
5	C	6	0	0	0	0
5	D	6	0	0	0	0
5	E	6	0	0	0	0
5	F	6	0	0	0	0
5	G	6	0	0	0	0
5	H	6	0	0	0	0
6	A	6	0	8	0	0
6	B	6	0	8	0	0
6	C	6	0	8	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	D	6	0	8	0	0
6	E	6	0	8	0	0
6	F	12	0	16	1	0
6	G	6	0	8	1	0
7	A	67	0	0	1	0
7	B	71	0	0	0	0
7	C	59	0	0	3	0
7	D	76	0	0	1	0
7	E	42	0	0	1	0
7	F	62	0	0	1	0
7	G	50	0	0	2	0
7	H	51	0	0	0	0
All	All	32320	0	32387	436	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 7.

The worst 5 of 436 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:G:23:ASP:HA	1:G:391:ARG:HH12	1.40	0.84
1:C:128:THR:N	1:C:129:ALA:HA	1.92	0.84
1:G:42:ARG:HE	1:G:378:HIS:HD2	1.29	0.80
1:F:49:THR:HG23	1:F:360:LEU:O	1.81	0.80
1:C:49:THR:HG21	1:C:72:ARG:HH11	1.45	0.80

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	513/551 (93%)	493 (96%)	19 (4%)	1 (0%)	43	62
1	B	513/551 (93%)	492 (96%)	20 (4%)	1 (0%)	43	62
1	C	513/551 (93%)	497 (97%)	15 (3%)	1 (0%)	43	62
1	D	511/551 (93%)	494 (97%)	16 (3%)	1 (0%)	43	62
1	E	510/551 (93%)	495 (97%)	14 (3%)	1 (0%)	43	62
1	F	512/551 (93%)	488 (95%)	23 (4%)	1 (0%)	43	62
1	G	509/551 (92%)	490 (96%)	18 (4%)	1 (0%)	43	62
1	H	517/551 (94%)	492 (95%)	24 (5%)	1 (0%)	43	62
All	All	4098/4408 (93%)	3941 (96%)	149 (4%)	8 (0%)	43	62

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	327	THR
1	G	327	THR
1	C	327	THR
1	B	327	THR
1	D	327	THR

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	426/453 (94%)	415 (97%)	11 (3%)	40	65
1	B	426/453 (94%)	412 (97%)	14 (3%)	33	58
1	C	426/453 (94%)	402 (94%)	24 (6%)	19	40
1	D	425/453 (94%)	410 (96%)	15 (4%)	32	57
1	E	424/453 (94%)	409 (96%)	15 (4%)	32	57
1	F	425/453 (94%)	405 (95%)	20 (5%)	23	47
1	G	424/453 (94%)	412 (97%)	12 (3%)	38	62
1	H	427/453 (94%)	415 (97%)	12 (3%)	38	62

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	3403/3624 (94%)	3280 (96%)	123 (4%)	31 56

5 of 123 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	296	LEU
1	G	493	MET
1	E	296	LEU
1	G	466	ARG
1	H	330	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 89 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	378	HIS
1	G	378	HIS
1	F	439	GLN
1	G	198	ASN
1	H	43	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 40 ligands modelled in this entry, 16 are monoatomic - leaving 24 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
5	PYR	A	534	4	5,5,5	1.33	0	3,6,6	0.50	0
2	PO4	A	531	-	4,4,4	1.02	0	6,6,6	0.49	0
5	PYR	C	534	4	5,5,5	1.34	0	3,6,6	0.83	0
5	PYR	H	534	4	5,5,5	1.33	0	3,6,6	0.87	0
2	PO4	H	531	-	4,4,4	1.03	0	6,6,6	0.46	0
5	PYR	D	534	4	5,5,5	1.33	1 (20%)	3,6,6	0.86	0
6	GOL	A	535	-	5,5,5	0.34	0	5,5,5	0.48	0
6	GOL	E	535	-	5,5,5	0.39	0	5,5,5	0.27	0
6	GOL	D	535	-	5,5,5	0.37	0	5,5,5	0.34	0
5	PYR	F	534	4	5,5,5	1.30	0	3,6,6	0.81	0
2	PO4	F	531	-	4,4,4	1.00	0	6,6,6	0.52	0
5	PYR	E	534	4	5,5,5	1.34	1 (20%)	3,6,6	0.71	0
2	PO4	G	531	-	4,4,4	1.01	0	6,6,6	0.39	0
2	PO4	C	531	-	4,4,4	0.98	0	6,6,6	0.44	0
6	GOL	F	536	-	5,5,5	0.41	0	5,5,5	0.29	0
6	GOL	G	535	-	5,5,5	0.34	0	5,5,5	0.33	0
6	GOL	F	535	-	5,5,5	0.33	0	5,5,5	0.47	0
2	PO4	E	531	-	4,4,4	0.98	0	6,6,6	0.55	0
2	PO4	D	531	-	4,4,4	0.99	0	6,6,6	0.47	0
5	PYR	B	534	4	5,5,5	1.22	0	3,6,6	0.97	0
2	PO4	B	531	-	4,4,4	0.94	0	6,6,6	0.54	0
6	GOL	C	535	-	5,5,5	0.42	0	5,5,5	0.33	0
6	GOL	B	535	-	5,5,5	0.35	0	5,5,5	0.37	0
5	PYR	G	534	4	5,5,5	1.27	0	3,6,6	0.84	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
5	PYR	A	534	4	-	0/4/4/4	-
6	GOL	E	535	-	-	2/4/4/4	-
5	PYR	C	534	4	-	0/4/4/4	-
6	GOL	D	535	-	-	2/4/4/4	-
5	PYR	F	534	4	-	0/4/4/4	-
6	GOL	C	535	-	-	2/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	PYR	H	534	4	-	0/4/4/4	-
6	GOL	F	536	-	-	2/4/4/4	-
6	GOL	G	535	-	-	2/4/4/4	-
5	PYR	D	534	4	-	0/4/4/4	-
6	GOL	A	535	-	-	2/4/4/4	-
6	GOL	B	535	-	-	4/4/4/4	-
5	PYR	G	534	4	-	0/4/4/4	-
6	GOL	F	535	-	-	1/4/4/4	-
5	PYR	E	534	4	-	0/4/4/4	-
5	PYR	B	534	4	-	0/4/4/4	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	E	534	PYR	CB-CA	2.02	1.54	1.50
5	D	534	PYR	OXT-C	-2.01	1.25	1.30

There are no bond angle outliers.

There are no chirality outliers.

5 of 17 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	C	535	GOL	C1-C2-C3-O3
6	A	535	GOL	O1-C1-C2-C3
6	B	535	GOL	O1-C1-C2-C3
6	E	535	GOL	O1-C1-C2-C3
6	F	536	GOL	C1-C2-C3-O3

There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	531	PO4	1	0
6	F	536	GOL	1	0
6	G	535	GOL	1	0
6	C	535	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	517/551 (93%)	-1.80	0 100 100	23, 33, 67, 78	0
1	B	517/551 (93%)	-1.81	0 100 100	24, 33, 58, 70	0
1	C	517/551 (93%)	-1.81	0 100 100	25, 35, 48, 59	0
1	D	515/551 (93%)	-1.80	0 100 100	27, 36, 50, 55	0
1	E	514/551 (93%)	-1.67	0 100 100	34, 51, 95, 101	0
1	F	516/551 (93%)	-1.80	0 100 100	27, 40, 50, 59	0
1	G	513/551 (93%)	-1.73	0 100 100	26, 42, 81, 84	0
1	H	519/551 (94%)	-1.78	0 100 100	28, 38, 60, 66	0
All	All	4128/4408 (93%)	-1.77	0 100 100	23, 38, 67, 101	0

There are no RSRZ outliers to report.

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 oligosaccharides 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(\AA^2)	Q<0.9
5	PYR	G	534	6/6	0.97	0.07	66,67,67,67	0
5	PYR	E	534	6/6	0.98	0.06	62,63,63,63	0
3	K	H	532	1/1	0.99	0.02	48,48,48,48	0
4	MG	C	533	1/1	0.99	0.05	45,45,45,45	0
5	PYR	C	534	6/6	0.99	0.05	46,46,46,46	0
5	PYR	A	534	6/6	0.99	0.04	38,38,39,39	0
5	PYR	B	534	6/6	0.99	0.04	42,43,43,43	0
5	PYR	D	534	6/6	0.99	0.05	51,51,52,52	0
3	K	B	532	1/1	0.99	0.05	94,94,94,94	0
5	PYR	F	534	6/6	0.99	0.03	38,38,38,39	0
3	K	E	532	1/1	0.99	0.05	85,85,85,85	0
5	PYR	H	534	6/6	0.99	0.08	69,70,70,70	0
6	GOL	A	535	6/6	0.99	0.05	58,58,59,60	0
6	GOL	F	535	6/6	0.99	0.03	50,50,50,50	0
3	K	G	532	1/1	1.00	0.02	60,60,60,60	0
2	PO4	B	531	5/5	1.00	0.03	37,38,38,38	0
2	PO4	D	531	5/5	1.00	0.04	47,47,47,47	0
4	MG	A	533	1/1	1.00	0.02	26,26,26,26	0
4	MG	B	533	1/1	1.00	0.02	26,26,26,26	0
4	MG	D	533	1/1	1.00	0.03	51,51,51,51	0
4	MG	E	533	1/1	1.00	0.03	58,58,58,58	0
4	MG	F	533	1/1	1.00	0.02	21,21,21,21	0
4	MG	G	533	1/1	1.00	0.02	33,33,33,33	0
4	MG	H	533	1/1	1.00	0.02	14,14,14,14	0
2	PO4	E	531	5/5	1.00	0.02	45,45,45,45	0
2	PO4	F	531	5/5	1.00	0.02	45,46,46,46	0
2	PO4	G	531	5/5	1.00	0.03	45,45,46,46	0
2	PO4	H	531	5/5	1.00	0.04	36,36,36,36	0
3	K	C	532	1/1	1.00	0.02	58,58,58,58	0
3	K	A	532	1/1	1.00	0.01	37,37,37,37	0
2	PO4	C	531	5/5	1.00	0.02	40,40,40,41	0
3	K	D	532	1/1	1.00	0.02	48,48,48,48	0
6	GOL	C	535	6/6	1.00	0.03	32,32,33,33	0
2	PO4	A	531	5/5	1.00	0.02	41,41,41,41	0
6	GOL	B	535	6/6	1.00	0.03	46,46,47,47	0
6	GOL	D	535	6/6	1.00	0.02	31,31,31,31	0
6	GOL	E	535	6/6	1.00	0.03	41,42,42,43	0
3	K	F	532	1/1	1.00	0.01	46,46,46,46	0
6	GOL	F	536	6/6	1.00	0.03	43,44,44,44	0
6	GOL	G	535	6/6	1.00	0.02	34,34,34,34	0

6.5 Other polymers [i](#)

There are no such residues in this entry.