



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 15, 2017 – 06:11 am GMT

PDB ID : 1AQF
Title : PYRUVATE KINASE FROM RABBIT MUSCLE WITH MG, K, AND L-PHOSPHOLACTATE
Authors : Larsen, T.M.; Benning, M.M.; Wesenberg, G.E.; Rayment, I.; Reed, G.H.
Deposited on : 1997-07-29
Resolution : 2.70 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

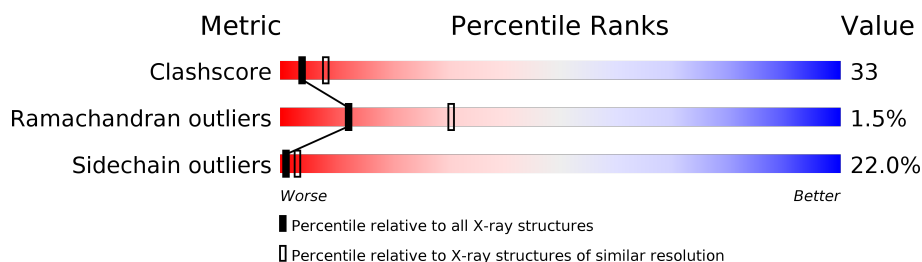
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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))
Clashscore	112137	2590 (2.70-2.70)
Ramachandran outliers	110173	2550 (2.70-2.70)
Sidechain outliers	110143	2550 (2.70-2.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	530	
1	B	530	
1	C	530	
1	D	530	
1	E	530	
1	F	530	
1	G	530	

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Mol	Chain	Length	Quality of chain
1	H	530	 A horizontal bar chart showing the quality of chain 1. The bar is divided into three segments: green (31%), yellow (45%), and orange (20%). The total length of the bar represents 100%.

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
4	PEQ	B	532	-	-	X	-
4	PEQ	F	532	-	-	X	-
4	PEQ	H	532	-	-	X	-

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 31410 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
1	A	519	Total	C	N	O	S	0	0	0
			3979	2498	708	745	28			
1	B	519	Total	C	N	O	S	0	0	0
			3979	2498	708	745	28			
1	C	519	Total	C	N	O	S	0	0	0
			3978	2498	708	744	28			
1	D	519	Total	C	N	O	S	0	0	0
			3979	2498	708	745	28			
1	E	426	Total	C	N	O	S	0	0	0
			3268	2045	592	606	25			
1	F	519	Total	C	N	O	S	0	0	0
			3979	2498	708	745	28			
1	G	519	Total	C	N	O	S	0	0	0
			3979	2498	708	745	28			
1	H	519	Total	C	N	O	S	0	0	0
			3979	2498	708	745	28			

- Molecule 2 is POTASSIUM ION (three-letter code: K) (formula: K).

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

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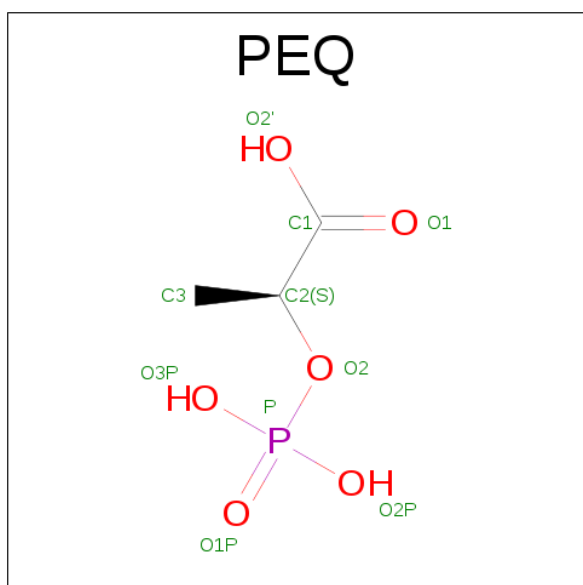
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total K 1 1	0	0
2	F	1	Total K 1 1	0	0

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 4 is L-PHOSPHOLACTATE (three-letter code: PEQ) (formula: C₃H₇O₆P).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	O	P	0	0
			10	3	6	1		
4	B	1	Total	C	O	P	0	0
			10	3	6	1		
4	C	1	Total	C	O	P	0	0
			10	3	6	1		
4	D	1	Total	C	O	P	0	0
			10	3	6	1		
4	E	1	Total	C	O	P	0	0
			10	3	6	1		
4	F	1	Total	C	O	P	0	0
			10	3	6	1		
4	G	1	Total	C	O	P	0	0
			10	3	6	1		
4	H	1	Total	C	O	P	0	0
			10	3	6	1		

- Molecule 5 is water.

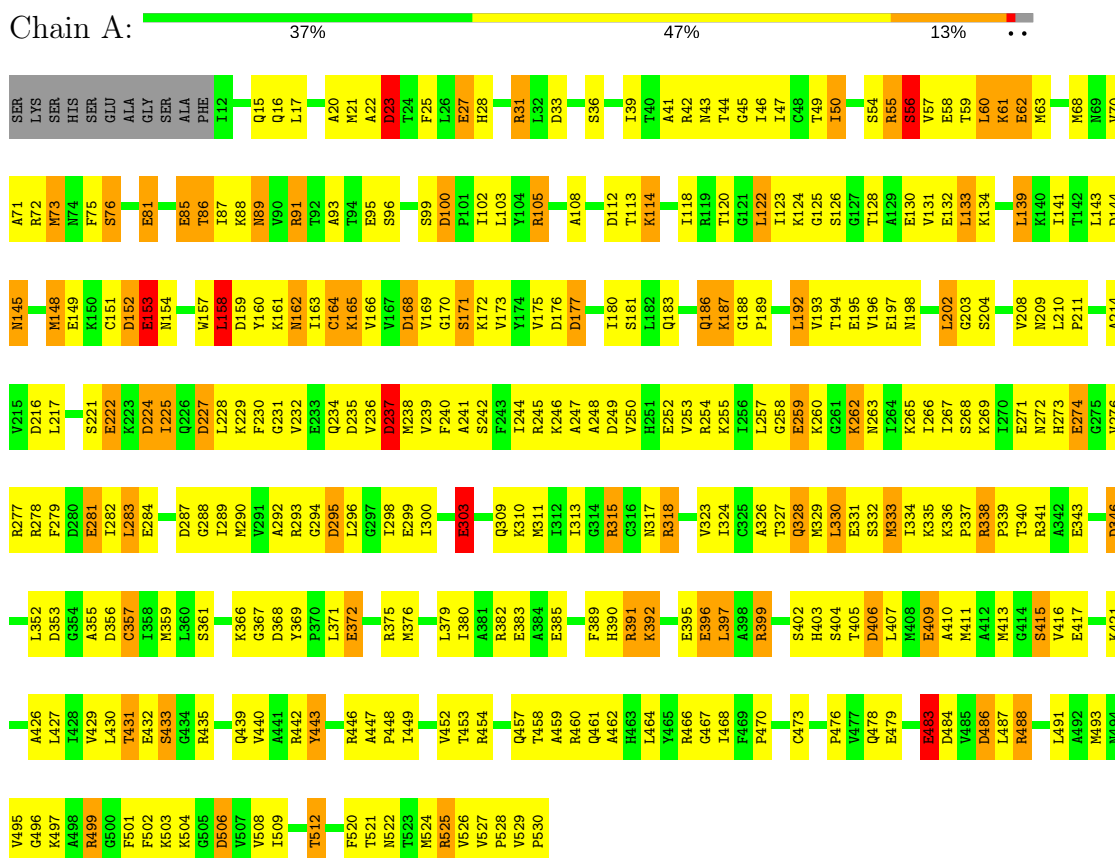
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	36	Total	O	0	0
			36	36		
5	B	25	Total	O	0	0
			25	25		
5	C	35	Total	O	0	0
			35	35		
5	D	35	Total	O	0	0
			35	35		
5	E	16	Total	O	0	0
			16	16		
5	F	18	Total	O	0	0
			18	18		
5	G	14	Total	O	0	0
			14	14		
5	H	15	Total	O	0	0
			15	15		

3 Residue-property plots

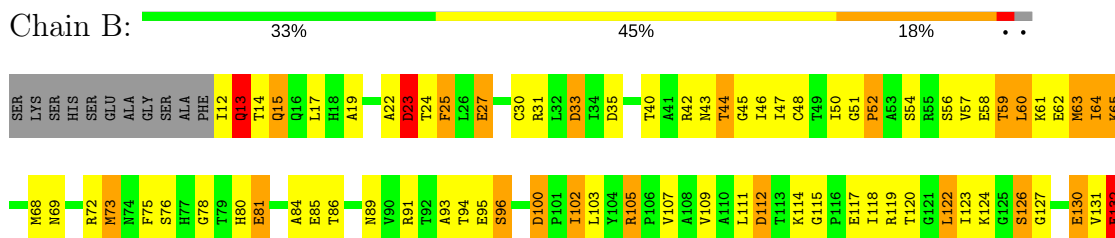
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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.

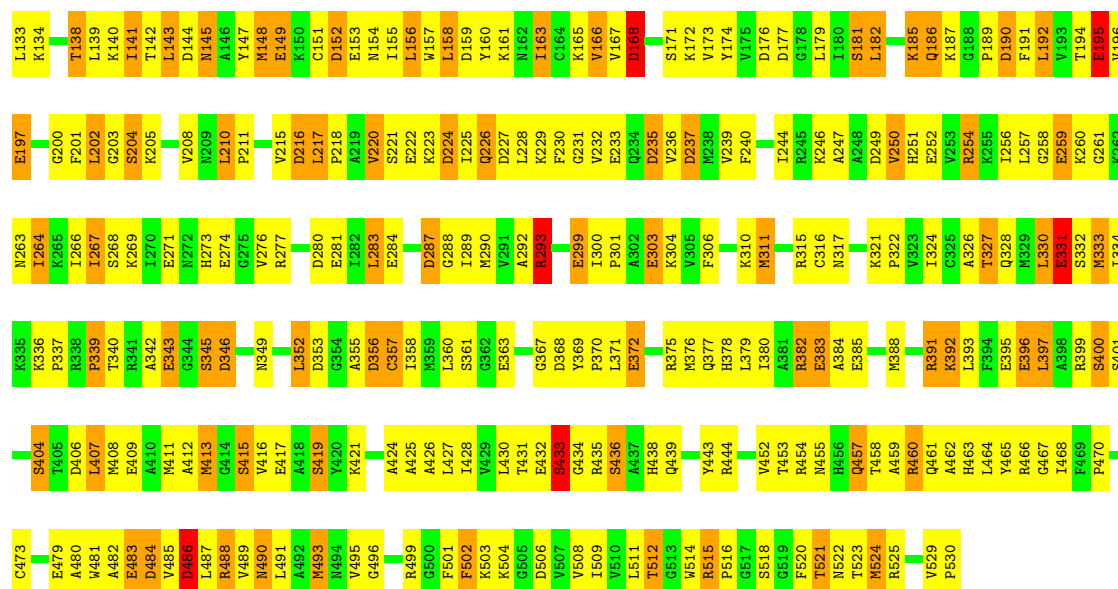
Note EDS was not executed.

• Molecule 1: PYRUVATE KINASE

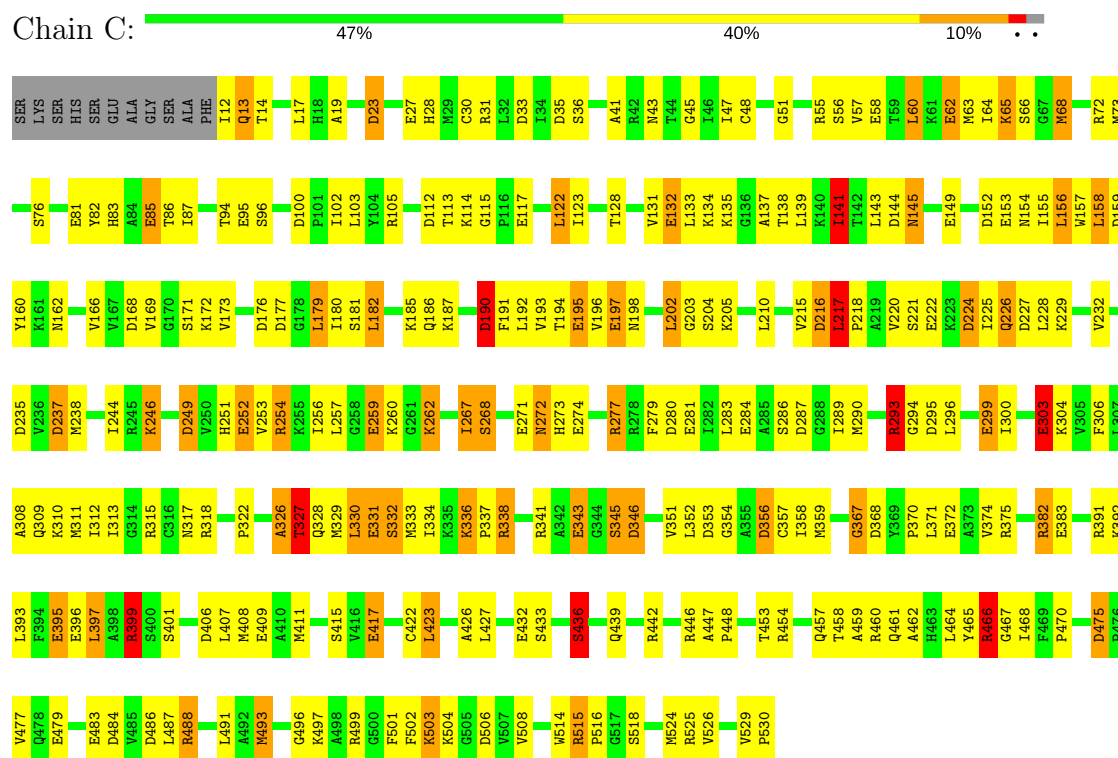


• Molecule 1: PYRUVATE KINASE

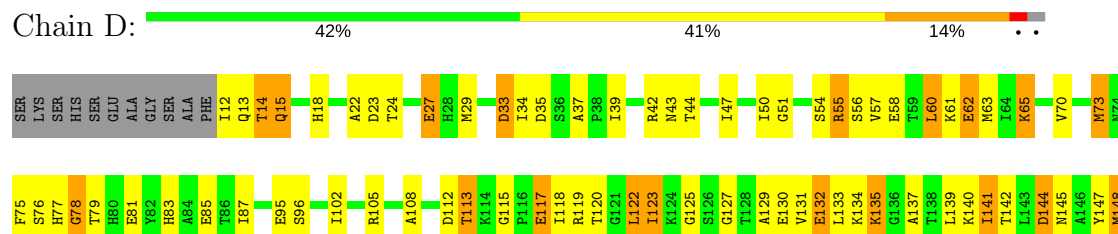


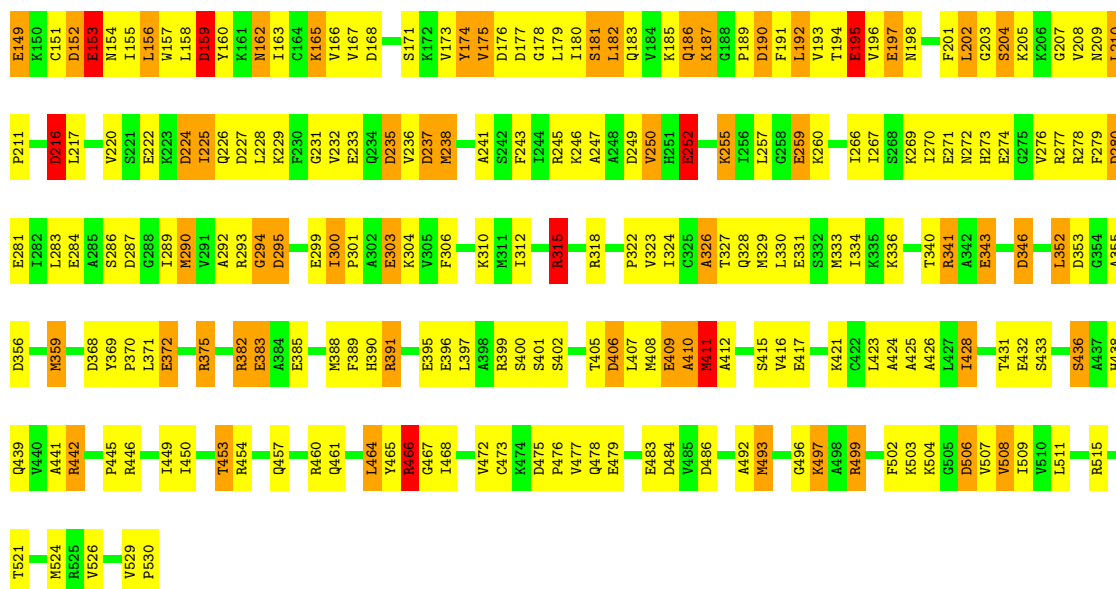


• Molecule 1: PYRUVATE KINASE



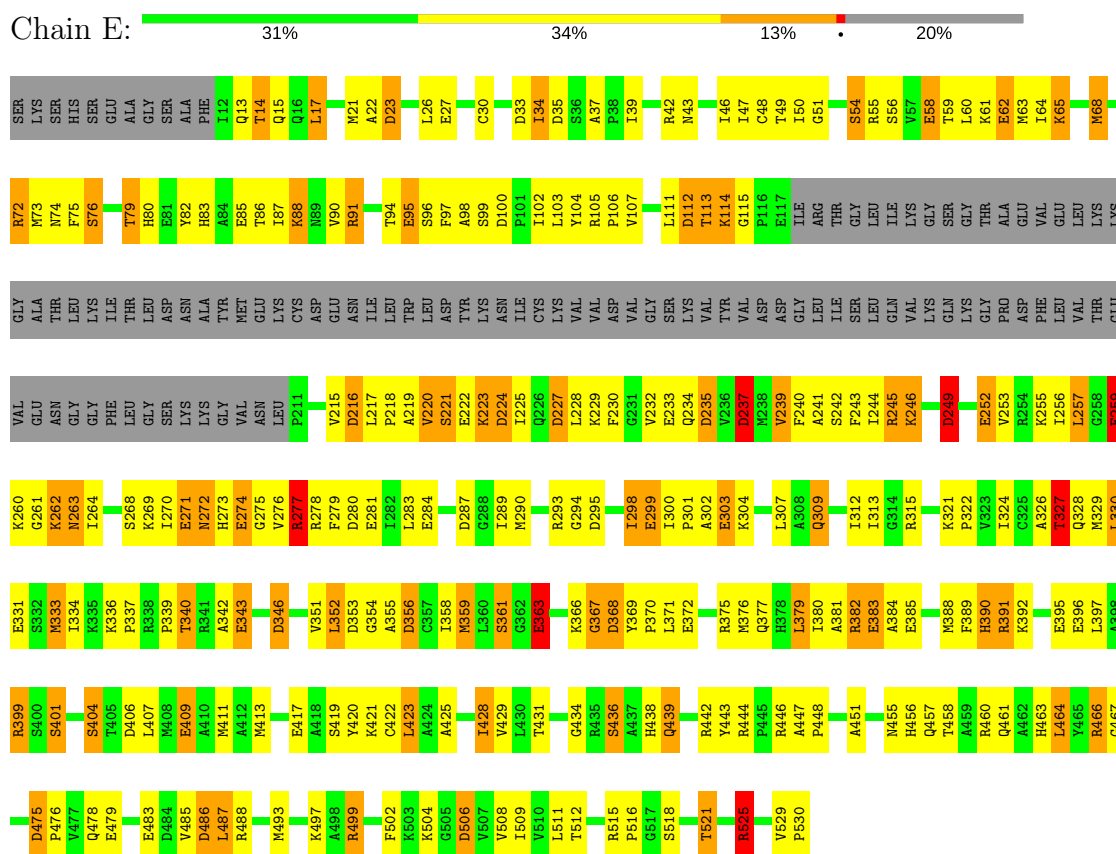
• Molecule 1: PYRUVATE KINASE





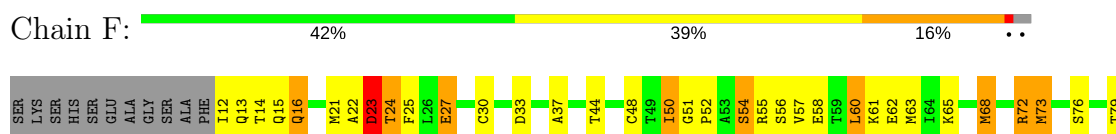
• Molecule 1: PYRUVATE KINASE

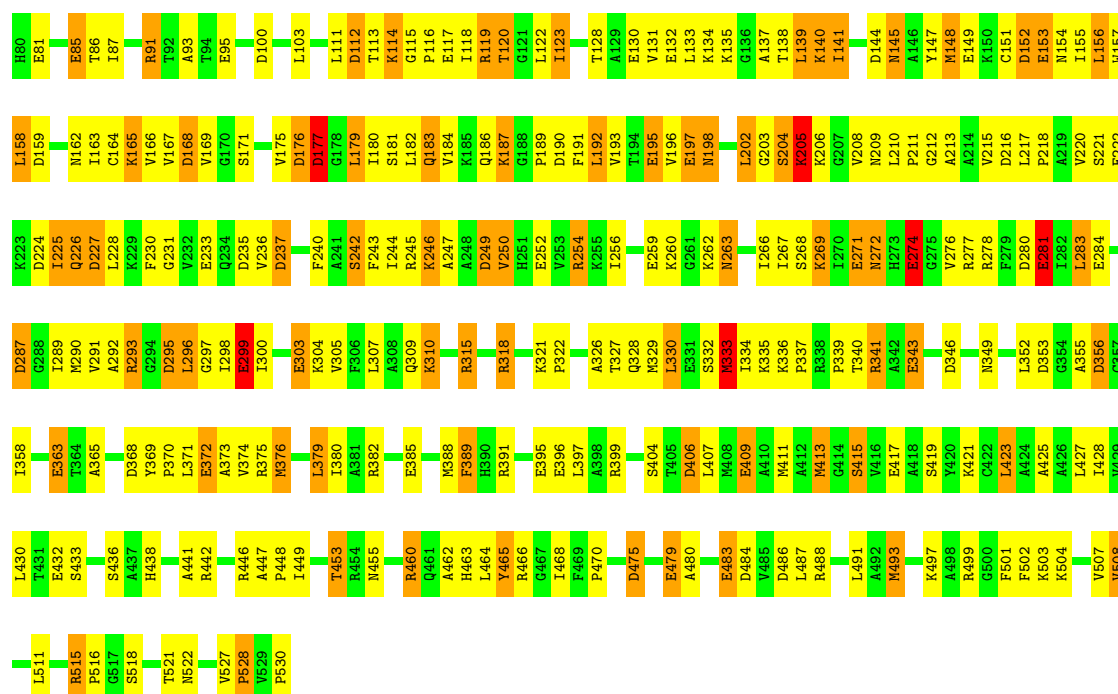
Chain E:



• Molecule 1: PYRUVATE KINASE

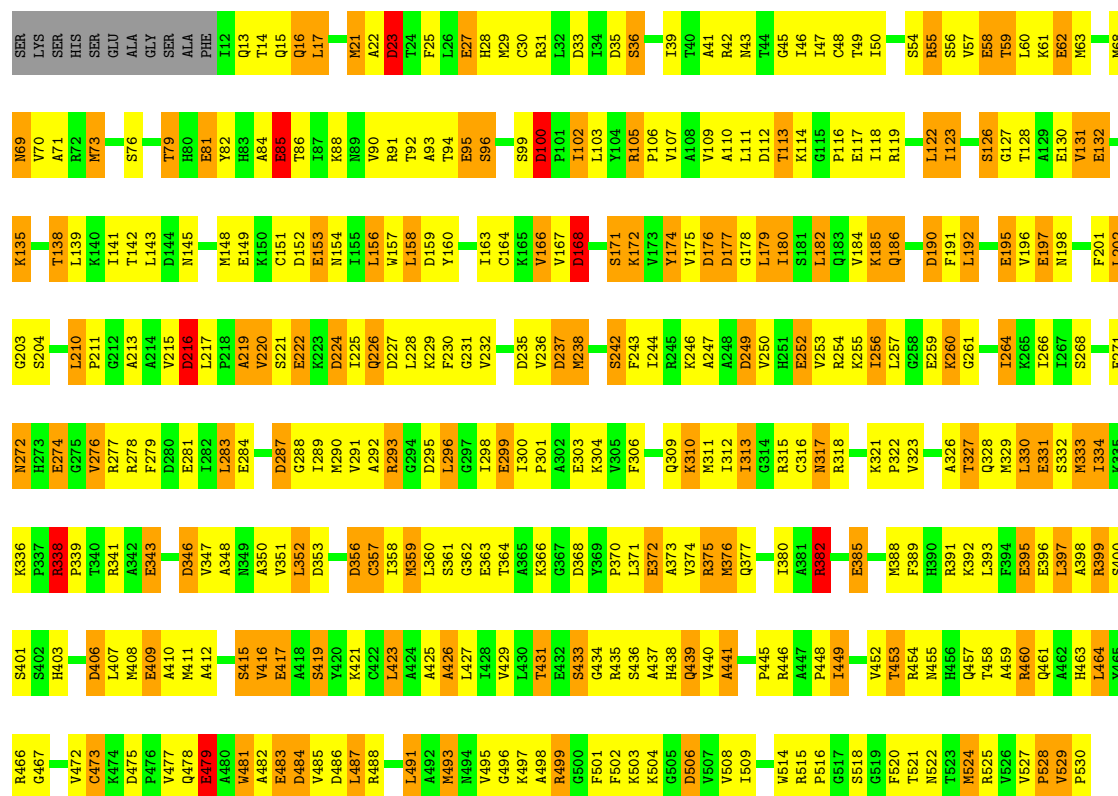
Chain F:





• Molecule 1: PYRUVATE KINASE

Chain G: 32% 43% 22% • •



• Molecule 1: PYRUVATE KINASE

Chain H: 31% 45% 20% • •



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	144.40Å 112.60Å 171.20Å 90.00° 93.70° 90.00°	Depositor
Resolution (Å)	30.00 – 2.70	Depositor
% Data completeness (in resolution range)	93.0 (30.00-2.70)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	TNT V. 5-E	Depositor
R, R_{free}	0.196 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	31410	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MG, K, PEQ

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	1.03	27/4042 (0.7%)	1.40	54/5452 (1.0%)
1	B	1.06	34/4042 (0.8%)	1.43	55/5452 (1.0%)
1	C	1.05	26/4041 (0.6%)	1.45	62/5452 (1.1%)
1	D	1.03	30/4042 (0.7%)	1.39	56/5452 (1.0%)
1	E	1.02	25/3322 (0.8%)	1.39	42/4482 (0.9%)
1	F	1.02	31/4042 (0.8%)	1.40	59/5452 (1.1%)
1	G	1.01	29/4042 (0.7%)	1.44	56/5452 (1.0%)
1	H	1.03	31/4042 (0.8%)	1.44	56/5452 (1.0%)
All	All	1.03	233/31615 (0.7%)	1.42	440/42646 (1.0%)

The worst 5 of 233 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	395	GLU	CD-OE1	9.26	1.35	1.25
1	F	372	GLU	CD-OE1	8.74	1.35	1.25
1	C	395	GLU	CD-OE1	8.68	1.35	1.25
1	B	396	GLU	CD-OE1	8.28	1.34	1.25
1	A	395	GLU	CD-OE1	8.23	1.34	1.25

The worst 5 of 440 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	293	ARG	NE-CZ-NH1	10.40	125.50	120.30
1	H	42	ARG	NE-CZ-NH1	9.77	125.19	120.30
1	E	112	ASP	CB-CG-OD2	9.57	126.92	118.30
1	D	295	ASP	CB-CG-OD2	9.49	126.84	118.30
1	A	188	GLY	C-N-CD	-9.36	100.01	120.60

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	3979	0	4055	259	0
1	B	3979	0	4055	321	0
1	C	3978	0	4055	208	0
1	D	3979	0	4056	230	0
1	E	3268	0	3315	222	0
1	F	3979	0	4055	266	0
1	G	3979	0	4056	347	0
1	H	3979	0	4056	352	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
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	10	0	4	1	0
4	B	10	0	4	4	0
4	C	10	0	4	2	0
4	D	10	0	4	3	0
4	E	10	0	4	1	0
4	F	10	0	4	4	0
4	G	10	0	4	1	0
4	H	10	0	4	6	0
5	A	36	0	0	3	0
5	B	25	0	0	2	0
5	C	35	0	0	7	0
5	D	35	0	0	3	0
5	E	16	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	F	18	0	0	2	0
5	G	14	0	0	1	0
5	H	15	0	0	0	0
All	All	31410	0	31735	2105	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 33.

The worst 5 of 2105 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:C:141:ILE:HG22	1:C:156:LEU:HB3	1.27	1.13
1:F:186:GLN:HB3	1:F:193:VAL:HB	1.30	1.12
1:E:47:ILE:HB	1:E:359:MET:HG2	1.27	1.12
1:H:15:GLN:HB3	1:H:17:LEU:HD23	1.29	1.09
1:E:391:ARG:NH1	1:F:399:ARG:HH21	1.51	1.09

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	517/530 (98%)	470 (91%)	41 (8%)	6 (1%)	15 37
1	B	517/530 (98%)	468 (90%)	43 (8%)	6 (1%)	15 37
1	C	517/530 (98%)	477 (92%)	37 (7%)	3 (1%)	28 56
1	D	517/530 (98%)	459 (89%)	49 (10%)	9 (2%)	11 27
1	E	422/530 (80%)	370 (88%)	43 (10%)	9 (2%)	8 21
1	F	517/530 (98%)	469 (91%)	39 (8%)	9 (2%)	11 27
1	G	517/530 (98%)	453 (88%)	56 (11%)	8 (2%)	12 30

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	H	517/530 (98%)	452 (87%)	56 (11%)	9 (2%)	11	27
All	All	4041/4240 (95%)	3618 (90%)	364 (9%)	59 (2%)	12	30

5 of 59 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	367	GLY
1	B	13	GLN
1	D	15	GLN
1	D	137	ALA
1	F	137	ALA

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	426/434 (98%)	353 (83%)	73 (17%)	2	6
1	B	426/434 (98%)	331 (78%)	95 (22%)	1	3
1	C	426/434 (98%)	345 (81%)	81 (19%)	2	4
1	D	426/434 (98%)	336 (79%)	90 (21%)	1	3
1	E	347/434 (80%)	267 (77%)	80 (23%)	1	2
1	F	426/434 (98%)	333 (78%)	93 (22%)	1	3
1	G	426/434 (98%)	315 (74%)	111 (26%)	0	2
1	H	426/434 (98%)	318 (75%)	108 (25%)	0	2
All	All	3329/3472 (96%)	2598 (78%)	731 (22%)	1	3

5 of 731 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	464	LEU
1	E	464	LEU
1	H	243	PHE
1	E	14	THR

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Mol	Chain	Res	Type
1	E	260	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 101 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	15	GLN
1	E	77	HIS
1	H	186	GLN
1	D	89	ASN
1	D	457	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 24 ligands modelled in this entry, 16 are monoatomic - leaving 8 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	PEQ	A	532	3,2	6,9,9	1.35	1 (16%)	7,13,13	2.03	1 (14%)
4	PEQ	B	532	2	6,9,9	1.35	2 (33%)	7,13,13	2.04	1 (14%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	PEQ	C	532	2	6,9,9	1.35	1 (16%)	7,13,13	2.04	1 (14%)
4	PEQ	D	532	2	6,9,9	1.35	2 (33%)	7,13,13	2.05	1 (14%)
4	PEQ	E	532	3,2	6,9,9	1.37	1 (16%)	7,13,13	2.04	1 (14%)
4	PEQ	F	532	2	6,9,9	1.38	2 (33%)	7,13,13	2.06	1 (14%)
4	PEQ	G	532	2	6,9,9	1.32	1 (16%)	7,13,13	2.04	1 (14%)
4	PEQ	H	532	2	6,9,9	1.34	1 (16%)	7,13,13	2.04	1 (14%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	PEQ	A	532	3,2	-	0/5/9/9	0/0/0/0
4	PEQ	B	532	2	-	0/5/9/9	0/0/0/0
4	PEQ	C	532	2	-	0/5/9/9	0/0/0/0
4	PEQ	D	532	2	-	0/5/9/9	0/0/0/0
4	PEQ	E	532	3,2	-	0/5/9/9	0/0/0/0
4	PEQ	F	532	2	-	0/5/9/9	0/0/0/0
4	PEQ	G	532	2	-	0/5/9/9	0/0/0/0
4	PEQ	H	532	2	-	0/5/9/9	0/0/0/0

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	E	532	PEQ	O2-C2	-2.36	1.43	1.45
4	F	532	PEQ	O2-C2	-2.30	1.43	1.45
4	C	532	PEQ	O2-C2	-2.30	1.43	1.45
4	A	532	PEQ	O2-C2	-2.28	1.43	1.45
4	B	532	PEQ	O2-C2	-2.28	1.43	1.45

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	F	532	PEQ	C3-C2-C1	-5.05	106.91	113.35
4	D	532	PEQ	C3-C2-C1	-5.04	106.92	113.35
4	B	532	PEQ	C3-C2-C1	-5.01	106.95	113.35
4	E	532	PEQ	C3-C2-C1	-5.01	106.96	113.35
4	H	532	PEQ	C3-C2-C1	-4.99	106.98	113.35

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

8 monomers are involved in 22 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	532	PEQ	1	0
4	B	532	PEQ	4	0
4	C	532	PEQ	2	0
4	D	532	PEQ	3	0
4	E	532	PEQ	1	0
4	F	532	PEQ	4	0
4	G	532	PEQ	1	0
4	H	532	PEQ	6	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](#)

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section is therefore empty.

6.4 Ligands [i](#)

EDS was not executed - this section is therefore empty.

6.5 Other polymers [i](#)

EDS was not executed - this section is therefore empty.