



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 06:26 PM 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](mailto: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.

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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 : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

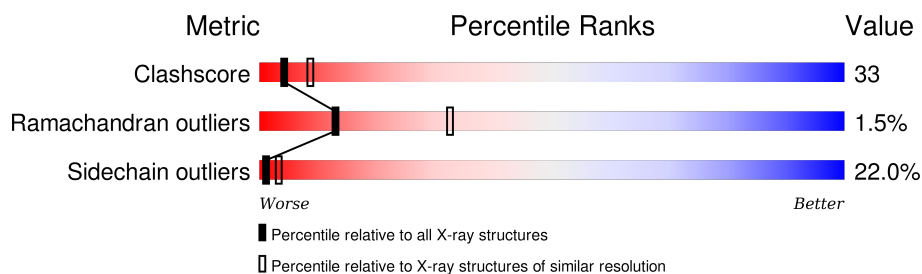
# 1 Overall quality at a glance

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	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (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  $\geq 3$ , 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	

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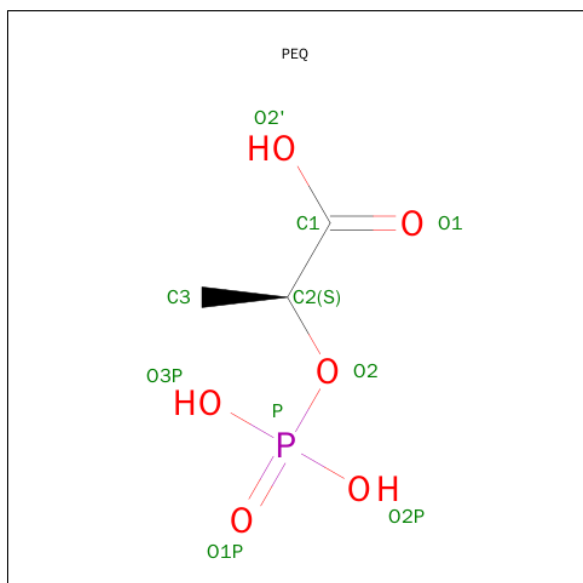
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	K	0	0
			1	1		
2	F	1	Total	K	0	0
			1	1		

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

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

- Molecule 4 is L-PHOSPHOLACTATE (three-letter code: PEQ) (formula: C<sub>3</sub>H<sub>7</sub>O<sub>6</sub>P).



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

- Molecule 5 is water.

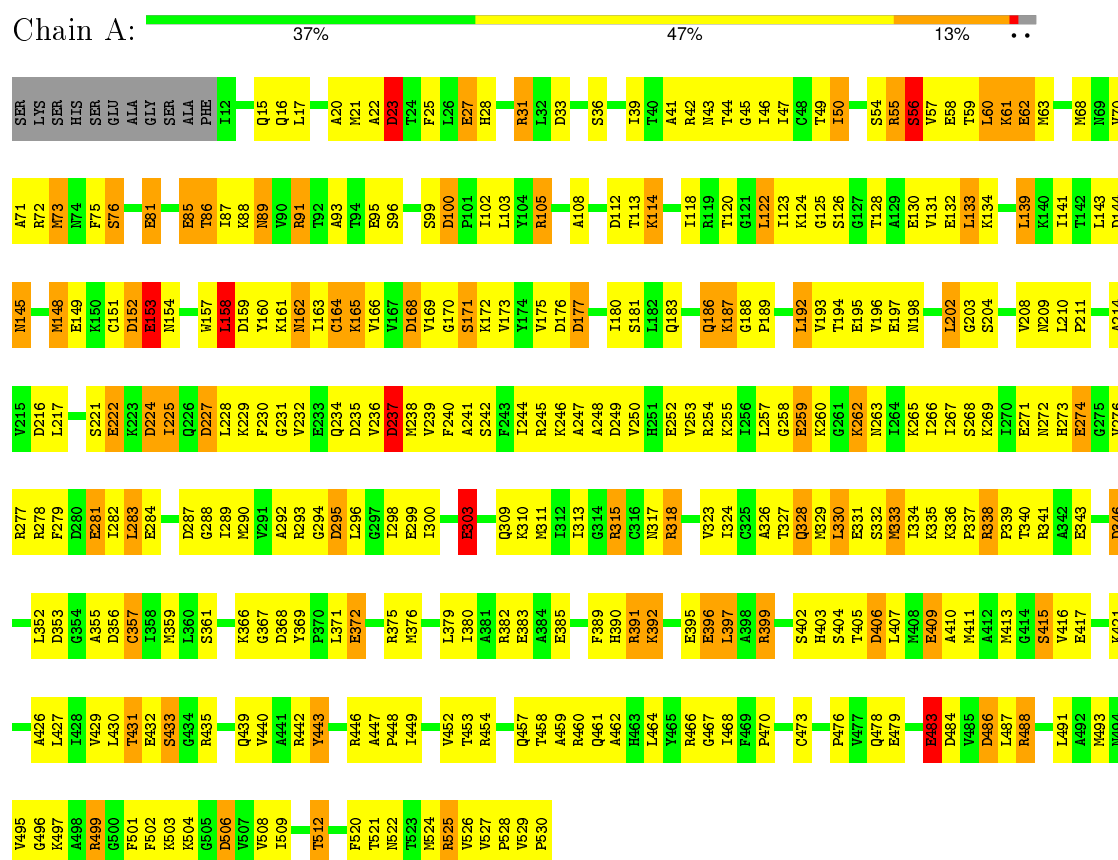
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	36	Total 36	O 36	0	0
5	B	25	Total 25	O 25	0	0
5	C	35	Total 35	O 35	0	0
5	D	35	Total 35	O 35	0	0
5	E	16	Total 16	O 16	0	0
5	F	18	Total 18	O 18	0	0
5	G	14	Total 14	O 14	0	0
5	H	15	Total 15	O 15	0	0

### 3 Residue-property plots

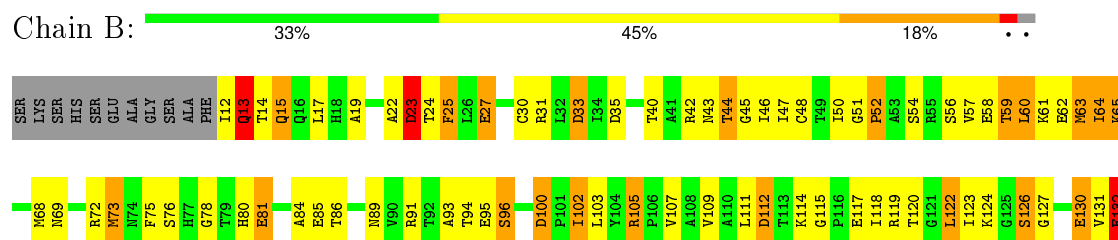
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according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

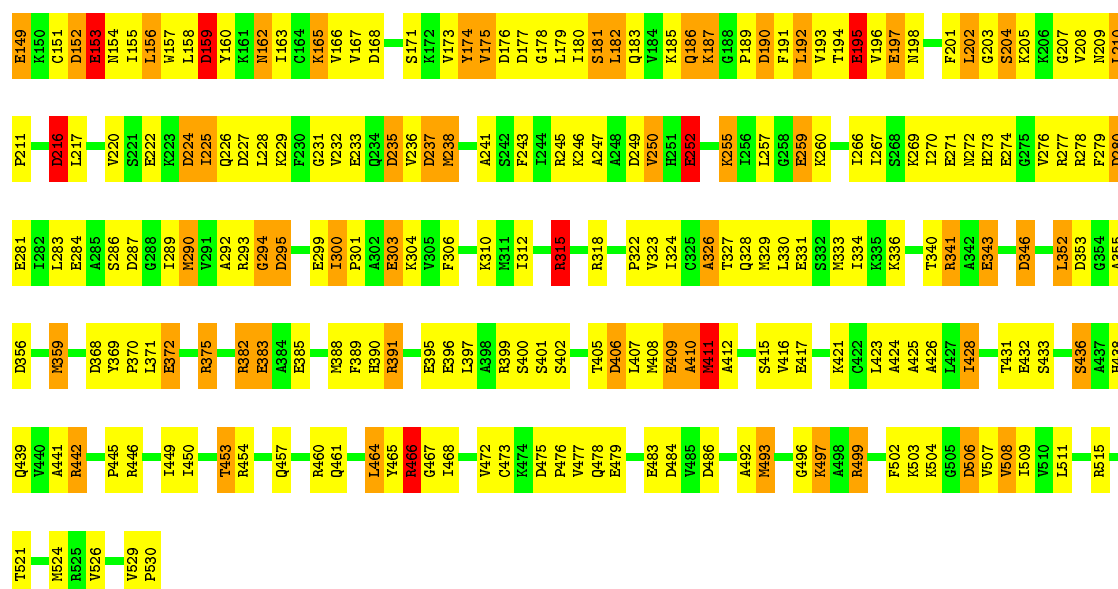


#### • Molecule 1: PYRUVATE KINASE



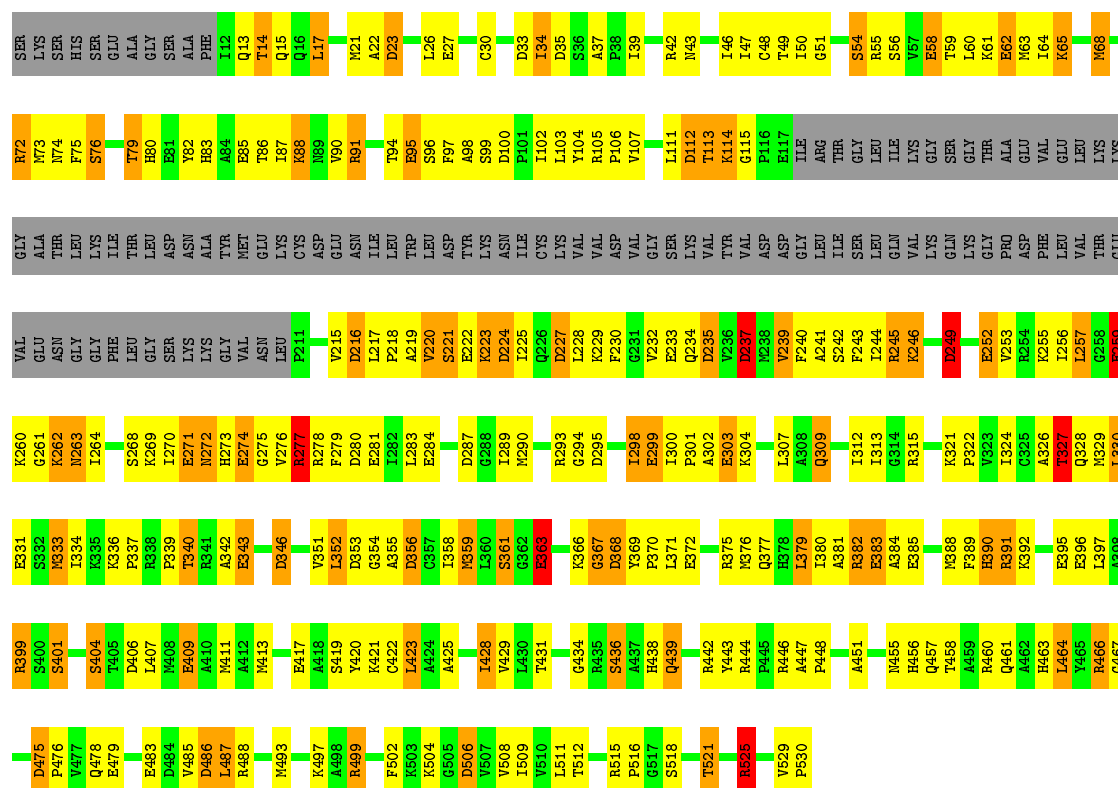






### • Molecule 1: PYRUVATE KINASE

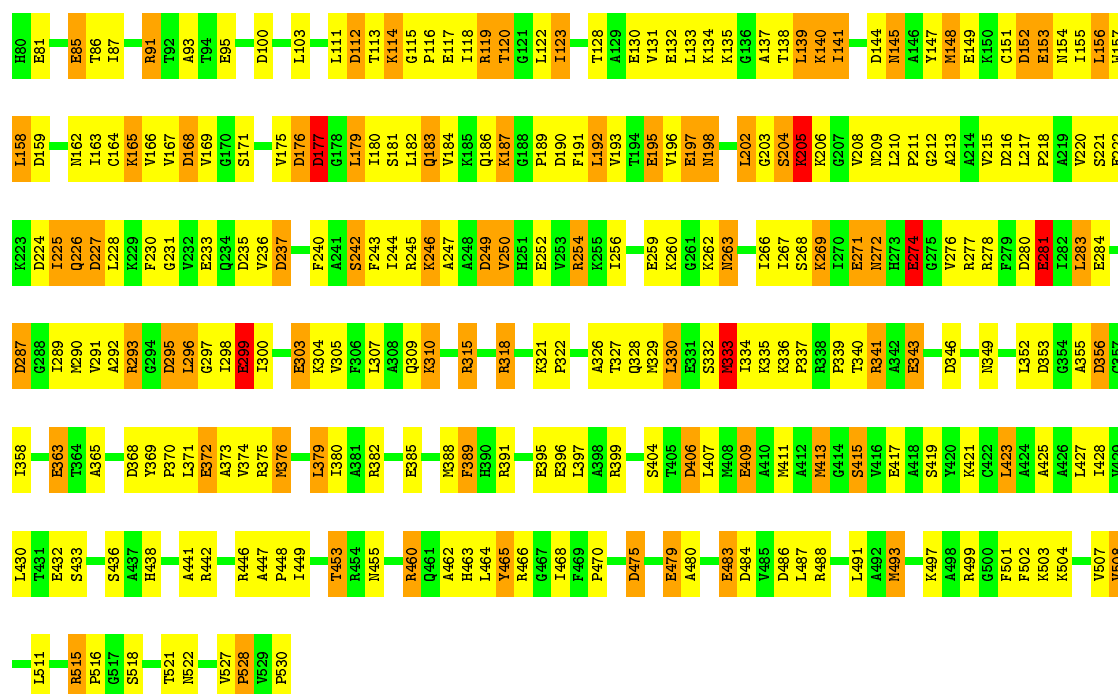
Chain E: 31% 34% 13% 20%



### • Molecule 1: PYRUVATE KINASE

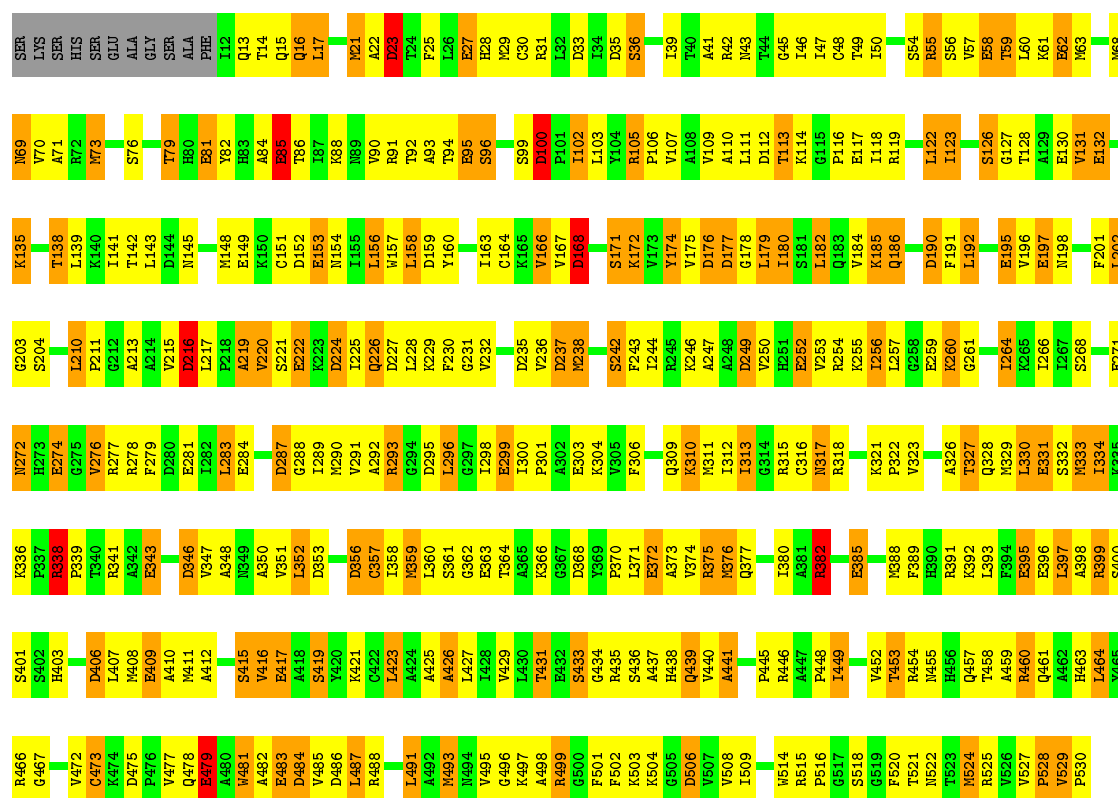
Chain F: 42% 39% 16%





## • Molecule 1: PYRUVATE KINASE

Chain G: 32% 43% 22% ..



## • Molecule 1: PYRUVATE KINASE

Chain H: 31% 45% 20% ..

P476	D406	P337	S268	V131	M63	SER
V477	L407	R338	K269	E132	I64	LYS
Q478	M408	P339	I270	L133	K65	SER
E479	E409	T340	E271	K134	S66	HIS
A480	A410	R341	N272	K135	G67	SER
E483	M411	A342	H273	G136	M68	GLU
D484	A412	E343	E274	A137	M69	ALA
V485	M413	G344		T138		GLY
D486	S415	S345	R277	L139	R72	SER
L487	V416	N349	R278	K140	M73	ALA
R488	E417		F279	I141	M74	PHE
V489		I352	D280	T142	S75	I12
M490	K421	D353	E281	L143	F76	Q13
L491	C422	G354	I282	D144	H77	T14
A492	L423	A355	L283		G78	Q15
M493	A424	D356	E284	M148	T79	Q16
N494	A425	C357	A285	E149	H80	L17
V495	A426	I358	S286	K150	E81	H18
G496	L427	M359	D287	C151	Y62	A19
R497	L428	L360	G288	D152	H83	A20
A498	V429	S361	M290	E153	A84	M21
R499	L430	G362	M291		E85	A22
G500	T431	E363	A292	L156	T86	D23
F501	E432		D227	V157	I87	T24
F502	S433	D368	L228	L158	K88	F25
R503	G434	P369	K229	D159	N89	L26
K504	R435	P370	F230	Y160	V90	E27
G505	S436	L371	G231	K161	R91	E28
D506	A437	E372	V232		T92	M29
V507	H438	A373	E233	K165	A93	C30
V508	Q439	V374	E234	V166	T94	R31
V509	V440	R375	D235	V167	E95	L32
V510	A441	M376	V236	D168	S96	D33
L511		Q377	D237	V169	F97	T34
T512	R444	H378	M238	G170	A98	D35
G513	P445	L379	V239	S171	S99	S36
K514	R446	I380	F240	K172	D100	A37
R515		A381	A241		P101	P38
P516	I449	R382	S242	D176	L102	I39
	A451	E383	F243	D177	L103	T40
T521	I450	A384	I244	G178	Y104	A41
N522	V452	A385	R245	L179	R105	R42
T523	T453	E385	K246	I180	P106	M43
M524	R454			S181	V107	T44
R525		M388	D249	L182	A108	G45
V526	Q457	F389	E252	Q183	V109	
	T458	R391	V253	V184		C48
V529	A459	K392		K185	D112	T49
P530	R460		I256	Q186	T113	I50
		E395	A326	K187	K114	G51
	H463	E396	T327	G188		
L464	L464	L397	E259	P189	E117	S54
R465	Y465	A398	K260	D190	I118	R55
R466	R466	R399	G261	F191	R119	S56
G467	G467	S400	K262	L192	T120	V57
		S401	M263	T194	G121	E58
C473	K473	H403	I264	E195	L122	T59
	K474	D475	K265	V196	I123	L60
			I266	E197	E130	B52

## 4 Data and refinement statistics

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	144.40 Å   112.60 Å   171.20 Å 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 <sup>2</sup> )	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 [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	517/530 (98%)	470 (91%)	41 (8%)	6 (1%)	16	39
1	B	517/530 (98%)	468 (90%)	43 (8%)	6 (1%)	16	39
1	C	517/530 (98%)	477 (92%)	37 (7%)	3 (1%)	30	59
1	D	517/530 (98%)	459 (89%)	49 (10%)	9 (2%)	11	29
1	E	422/530 (80%)	370 (88%)	43 (10%)	9 (2%)	9	23
1	F	517/530 (98%)	469 (91%)	39 (8%)	9 (2%)	11	29
1	G	517/530 (98%)	453 (88%)	56 (11%)	8 (2%)	13	32

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	H	517/530 (98%)	452 (87%)	56 (11%)	9 (2%)	11	29
All	All	4041/4240 (95%)	3618 (90%)	364 (9%)	59 (2%)	13	32

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	5
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%)	1	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 ⓘ

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 ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

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	5,9,9	0.76	0	5,13,13	2.31	1 (20%)
4	PEQ	B	532	2	5,9,9	0.77	0	5,13,13	2.33	1 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	PEQ	C	532	2	5,9,9	0.77	0	5,13,13	2.32	1 (20%)
4	PEQ	D	532	2	5,9,9	0.77	0	5,13,13	2.34	1 (20%)
4	PEQ	E	532	3,2	5,9,9	0.78	0	5,13,13	2.33	1 (20%)
4	PEQ	F	532	2	5,9,9	0.78	0	5,13,13	2.35	1 (20%)
4	PEQ	G	532	2	5,9,9	0.76	0	5,13,13	2.32	1 (20%)
4	PEQ	H	532	2	5,9,9	0.77	0	5,13,13	2.32	1 (20%)

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

There are no bond length outliers.

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	-4.90	106.91	113.18
4	D	532	PEQ	C3-C2-C1	-4.89	106.92	113.18
4	B	532	PEQ	C3-C2-C1	-4.86	106.95	113.18
4	E	532	PEQ	C3-C2-C1	-4.86	106.96	113.18
4	H	532	PEQ	C3-C2-C1	-4.84	106.98	113.18

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

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Clashes	Symm-Clashes
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 ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

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 will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

### 6.3 Carbohydrates [i](#)

EDS was not executed - this section will therefore be empty.

### 6.4 Ligands [i](#)

EDS was not executed - this section will therefore be empty.

### 6.5 Other polymers [i](#)

EDS was not executed - this section will therefore be empty.