



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 26, 2026 – 06:20 AM EDT

PDB ID : 9M3K / pdb_00009m3k
Title : Crystal structure of GinKR1
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Deposited on : 2025-03-02
Resolution : 2.25 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
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

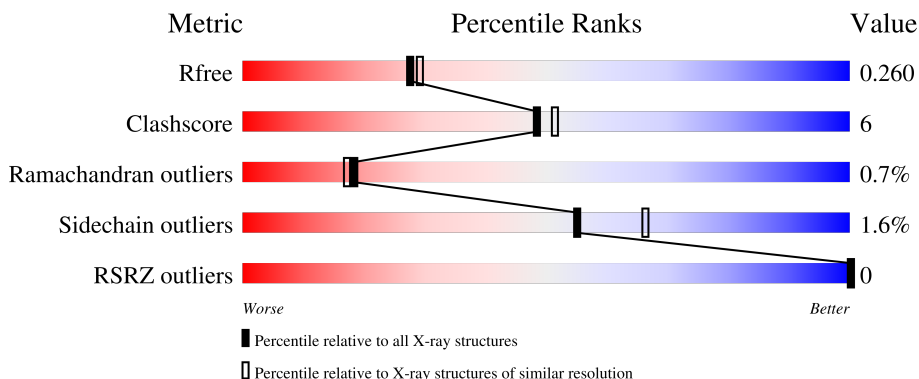
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.25 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	1898 (2.26-2.26)
Clashscore	190562	2005 (2.26-2.26)
Ramachandran outliers	187476	1965 (2.26-2.26)
Sidechain outliers	187428	1966 (2.26-2.26)
RSRZ outliers	180081	1898 (2.26-2.26)

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	339	
1	B	339	
1	C	339	
1	D	339	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 10444 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 ketoreductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	325	Total	C	N	O	S	0	0	0
			2528	1628	418	465	17			
1	B	326	Total	C	N	O	S	0	0	0
			2521	1621	420	462	18			
1	C	322	Total	C	N	O	S	0	0	0
			2497	1605	417	457	18			
1	D	316	Total	C	N	O	S	0	0	0
			2465	1586	405	456	18			

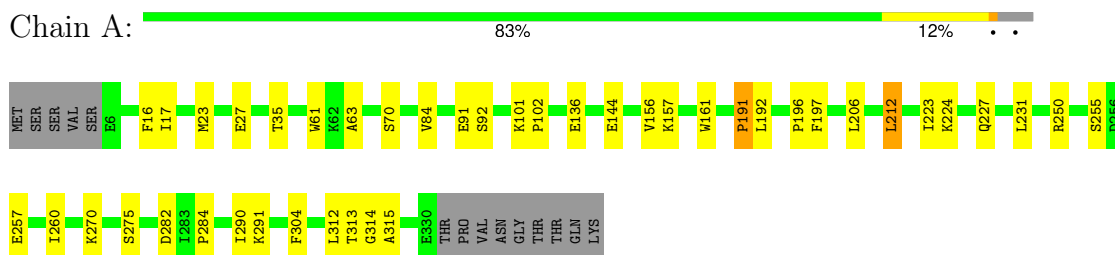
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	108	Total	O	0	0
			108	108		
2	B	116	Total	O	0	0
			116	116		
2	C	114	Total	O	0	0
			114	114		
2	D	95	Total	O	0	0
			95	95		

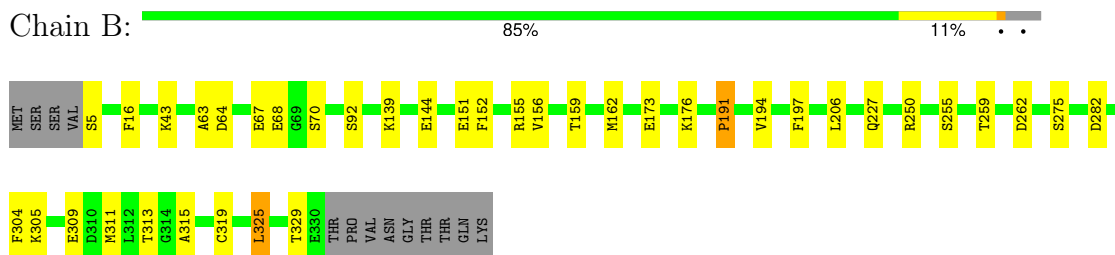
3 Residue-property plots

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.

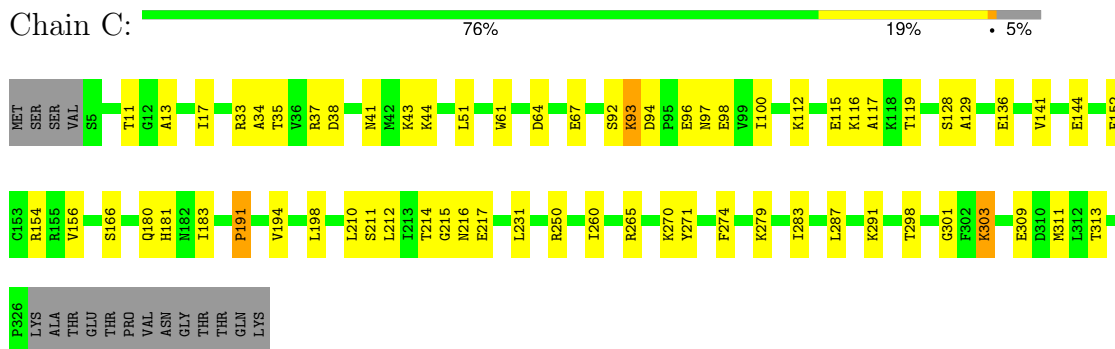
- Molecule 1: ketoreductase



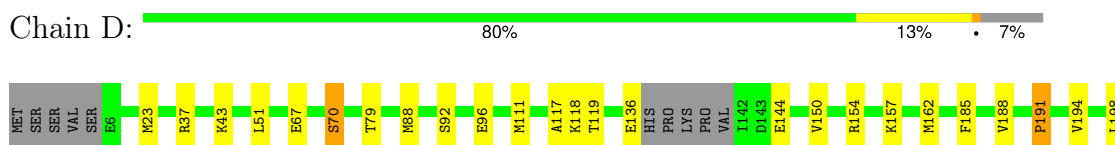
- Molecule 1: ketoreductase



- Molecule 1: ketoreductase



- Molecule 1: ketoreductase



P203	L206	L212	E217	Y220	Q227	H230	I252	S255	T259	I260	H261	D262	V263	S275	F280	I283	Q286	L287	K291	F292	F304	F326	LYS	ALA	THR	GLU	THR	PRO	VAL	ASN	GLY	THR	THR	GLN	LYS
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4 Data and refinement statistics

Property	Value	Source
Space group	P 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	105.46Å 66.61Å 109.47Å 90.00° 90.24° 90.00°	Depositor
Resolution (Å)	54.74 – 2.25 54.74 – 2.25	Depositor EDS
% Data completeness (in resolution range)	99.9 (54.74-2.25) 98.8 (54.74-2.25)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.21 (at 2.25Å)	Xtriage
Refinement program	PHENIX 5.8.0123, PHENIX 1.20.1-4487	Depositor
R, R_{free}	0.203 , 0.260 0.204 , 0.260	Depositor DCC
R_{free} test set	3744 reflections (5.16%)	wwPDB-VP
Wilson B-factor (Å ²)	37.9	Xtriage
Anisotropy	0.313	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 24.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.007 for l,k,-h 0.156 for h,-k,-l 0.016 for l,-k,h	Xtriage
F_o , F_c correlation	0.96	EDS
Total number of atoms	10444	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.58% 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](#)

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	0.33	0/2588	0.53	0/3513
1	B	0.34	0/2581	0.52	0/3502
1	C	0.37	0/2554	0.56	0/3462
1	D	0.36	0/2521	0.54	0/3418
All	All	0.35	0/10244	0.54	0/13895

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
1	D	0	1
All	All	0	3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	92	SER	Peptide
1	B	92	SER	Peptide
1	D	92	SER	Peptide

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	2528	0	2521	22	0
1	B	2521	0	2508	22	0
1	C	2497	0	2518	41	0
1	D	2465	0	2458	31	0
2	A	108	0	0	1	0
2	B	116	0	0	5	0
2	C	114	0	0	1	0
2	D	95	0	0	0	0
All	All	10444	0	10005	110	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 6.

The worst 5 of 110 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:151:GLU:OE2	1:B:155:ARG:NH1	2.16	0.78
1:B:64:ASP:HB3	1:B:67:GLU:HG3	1.70	0.71
1:B:151:GLU:OE1	2:B:401:HOH:O	2.10	0.69
1:B:139:LYS:O	2:B:402:HOH:O	2.12	0.66
1:A:27:GLU:OE2	2:A:401:HOH:O	2.15	0.65

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	323/339 (95%)	313 (97%)	7 (2%)	3 (1%)	14	12
1	B	324/339 (96%)	307 (95%)	14 (4%)	3 (1%)	14	12

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	320/339 (94%)	308 (96%)	10 (3%)	2 (1%)	21	21
1	D	312/339 (92%)	301 (96%)	10 (3%)	1 (0%)	36	40
All	All	1279/1356 (94%)	1229 (96%)	41 (3%)	9 (1%)	18	17

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	191	PRO
1	B	191	PRO
1	B	282	ASP
1	C	191	PRO
1	D	191	PRO

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	275/298 (92%)	269 (98%)	6 (2%)	45	56
1	B	273/298 (92%)	270 (99%)	3 (1%)	65	75
1	C	274/298 (92%)	270 (98%)	4 (2%)	57	68
1	D	270/298 (91%)	265 (98%)	5 (2%)	50	61
All	All	1092/1192 (92%)	1074 (98%)	18 (2%)	55	66

5 of 18 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	70	SER
1	D	188	VAL
1	D	150	VAL
1	B	325	LEU
1	D	43	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	137	HIS
1	B	180	GLN
1	B	181	HIS
1	C	97	ASN
1	D	105	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](#)

There are no ligands in this entry.

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	325/339 (95%)	-1.21	0 100 100	25, 41, 65, 86	0
1	B	326/339 (96%)	-1.18	0 100 100	25, 42, 67, 87	0
1	C	322/339 (94%)	-1.16	0 100 100	23, 41, 68, 80	0
1	D	316/339 (93%)	-1.13	0 100 100	23, 43, 62, 81	0
All	All	1289/1356 (95%)	-1.17	0 100 100	23, 41, 66, 87	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.