



wwPDB X-ray Structure Validation Summary Report

Feb 28, 2014 – 02:30 PM GMT

PDB ID : 1FWL
Title : CRYSTAL STRUCTURE OF HOMOSERINE KINASE
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Deposited on : 2000-09-22
Resolution : 2.25 Å(reported)

This is a wwPDB 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/ValidationPDFNotes.html>

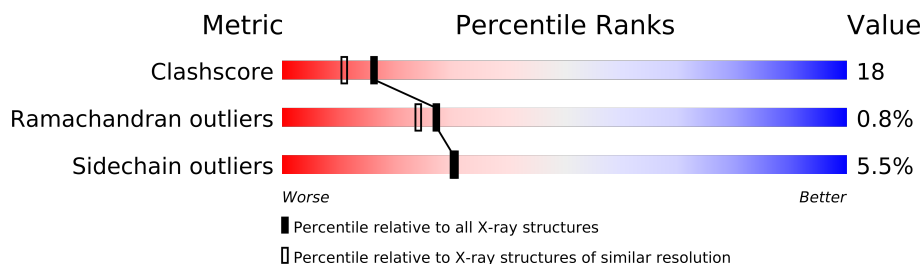
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	21963
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

1 Overall quality at a glance

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))
Clashscore	79885	1326 (2.28-2.24)
Ramachandran outliers	78287	1291 (2.28-2.24)
Sidechain outliers	78261	1291 (2.28-2.24)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	296	
1	B	296	
1	C	296	
1	D	296	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 9582 atoms, of which 0 are hydrogen and 0 are deuterium.

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 HOMOSERINE KINASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	296	Total	C	N	O	S	0	0	0
			2269	1460	366	434	9			
1	B	296	Total	C	N	O	S	0	0	0
			2269	1460	366	434	9			
1	C	296	Total	C	N	O	S	0	0	0
			2269	1460	366	434	9			
1	D	296	Total	C	N	O	S	0	0	0
			2269	1460	366	434	9			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	164	Total	O	0	0
			164	164		
2	B	77	Total	O	0	0
			77	77		
2	C	142	Total	O	0	0
			142	142		
2	D	123	Total	O	0	0
			123	123		

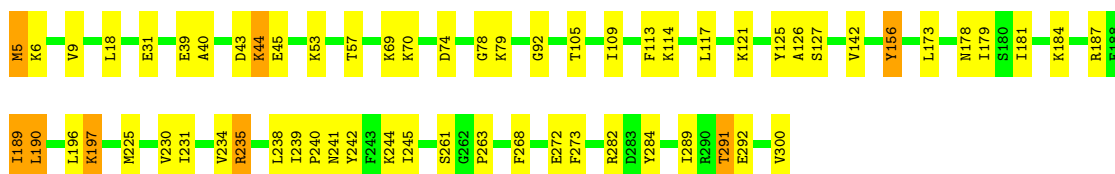
3 Residue-property plots

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.

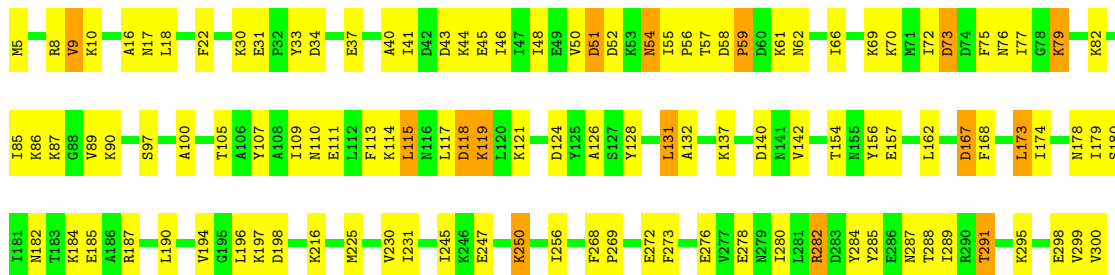
• Molecule 1: HOMOSERINE KINASE

Chain A: 



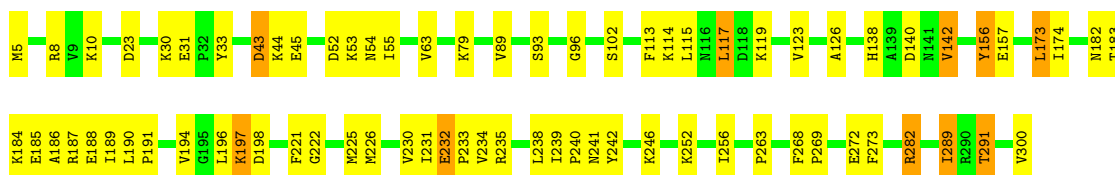
• Molecule 1: HOMOSERINE KINASE

Chain B: 



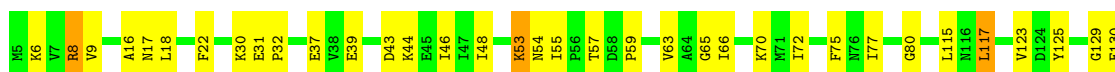
• Molecule 1: HOMOSERINE KINASE

Chain C: 



• Molecule 1: HOMOSERINE KINASE

Chain D: 



L131	R282	D283	Y284	Y285	E286	I289	R290	T291	E292	V300	L132	S133	S134	G135	A136	K137	H138	A139	V142	E157	L173	I179	M182	T183	K184	E185	A186	R187	E188	T189	L190	L196	M225	K229	V230	I231	E232	P233	V234	R235	L238	N241	K244	I245	K252	S261	G262	P263	F268	E271	E272	F273	E276
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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, α , β , γ	61.99Å 128.72Å 109.42Å 90.00° 105.57° 90.00°	Depositor
Resolution (Å)	20.00 – 2.25	Depositor
% Data completeness (in resolution range)	97.9 (20.00-2.25)	Depositor
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.204 , 0.248	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	9582	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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	0.65	0/2306	0.78	0/3112
1	B	0.55	0/2306	0.73	1/3112 (0.0%)
1	C	0.68	0/2306	0.80	1/3112 (0.0%)
1	D	0.64	0/2306	0.79	2/3112 (0.1%)
All	All	0.63	0/9224	0.78	4/12448 (0.0%)

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

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	C	156	TYR	N-CA-C	-5.77	95.43	111.00
1	D	80	GLY	N-CA-C	-5.55	99.21	113.10
1	D	285	TYR	N-CA-C	-5.44	96.32	111.00
1	B	54	ASN	N-CA-C	-5.43	96.34	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	156	TYR	Sidechain

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2269	0	2339	49	0
1	B	2269	0	2339	130	0
1	C	2269	0	2339	69	0
1	D	2269	0	2339	89	0
2	A	164	0	0	6	0
2	B	77	0	0	3	0
2	C	142	0	0	5	0
2	D	123	0	0	7	0
All	All	9582	0	9356	336	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 18.

The worst 5 of 336 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:58:ASP:HB3	1:B:61:LYS:HE2	1.26	1.09
1:D:130:GLU:HB3	1:D:138:HIS:HB2	1.35	1.03
1:B:119:LYS:H	1:B:119:LYS:HD2	1.22	1.00
1:D:31:GLU:H	1:D:291:THR:HG21	1.26	0.99
1:B:167:ASP:HB3	2:B:329:HOH:O	1.67	0.94

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	294/296 (99%)	286 (97%)	7 (2%)	1 (0%)	50	54
1	B	294/296 (99%)	272 (92%)	18 (6%)	4 (1%)	16	10
1	C	294/296 (99%)	274 (93%)	18 (6%)	2 (1%)	30	29
1	D	294/296 (99%)	277 (94%)	15 (5%)	2 (1%)	30	29
All	All	1176/1184 (99%)	1109 (94%)	58 (5%)	9 (1%)	27	24

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	134	SER
1	A	44	LYS
1	B	51	ASP
1	C	44	LYS
1	B	44	LYS

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	248/248 (100%)	234 (94%)	14 (6%)	30	30
1	B	248/248 (100%)	233 (94%)	15 (6%)	27	26
1	C	248/248 (100%)	235 (95%)	13 (5%)	32	34
1	D	248/248 (100%)	235 (95%)	13 (5%)	32	34
All	All	992/992 (100%)	937 (94%)	55 (6%)	30	30

5 of 55 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	197	LYS
1	C	43	ASP
1	D	196	LEU
1	B	282	ARG
1	B	289	ILE

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

Mol	Chain	Res	Type
1	A	138	HIS
1	A	141	ASN
1	A	178	ASN
1	A	215	ASN
1	C	138	HIS

5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

There are no ligands in this entry.

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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

6.3 Carbohydrates ⓘ

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

6.4 Ligands ⓘ

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

6.5 Other polymers ⓘ

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