wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 12, 2024 – 12:24 AM EDT

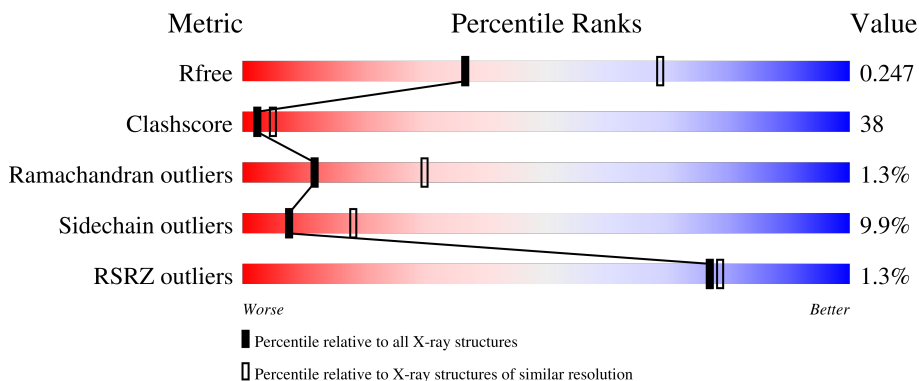|		
PDB ID	:	2NLX
Title	:	Crystal structure of the apo E. coli xylulose kinase
Authors	:	di Luccio, E.; Voegtli, J.; Wilson, D.K.
Deposited on	:	2006-10-20
Resolution	:	2.70 Å(reported)

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	Percentile Ranks	Value
Rfree		0.247
Clashscore		38
Ramachandran outliers		1.3%
Sidechain outliers		9.9%
RSRZ outliers		1.3%

Worse ← → *Better*

▮ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R$_{free}$	130704	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (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 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 <=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	484	59% 33% 6%
1	B	484	50% 38% 6%

2 Entry composition ⓘ

There are 2 unique types of molecules in this entry. The entry contains 7394 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 Xylulose kinase.

| Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	476	Total 3631	C 2297	N 637	O 673	S 24	0	0	0
1	B	472	Total 3605	C 2281	N 633	O 668	S 23	0	0	0

- Molecule 2 is water.

| Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	82	Total 82	O 82	0	0
2	B	76	Total 76	O 76	0	0

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: Xylulose kinase
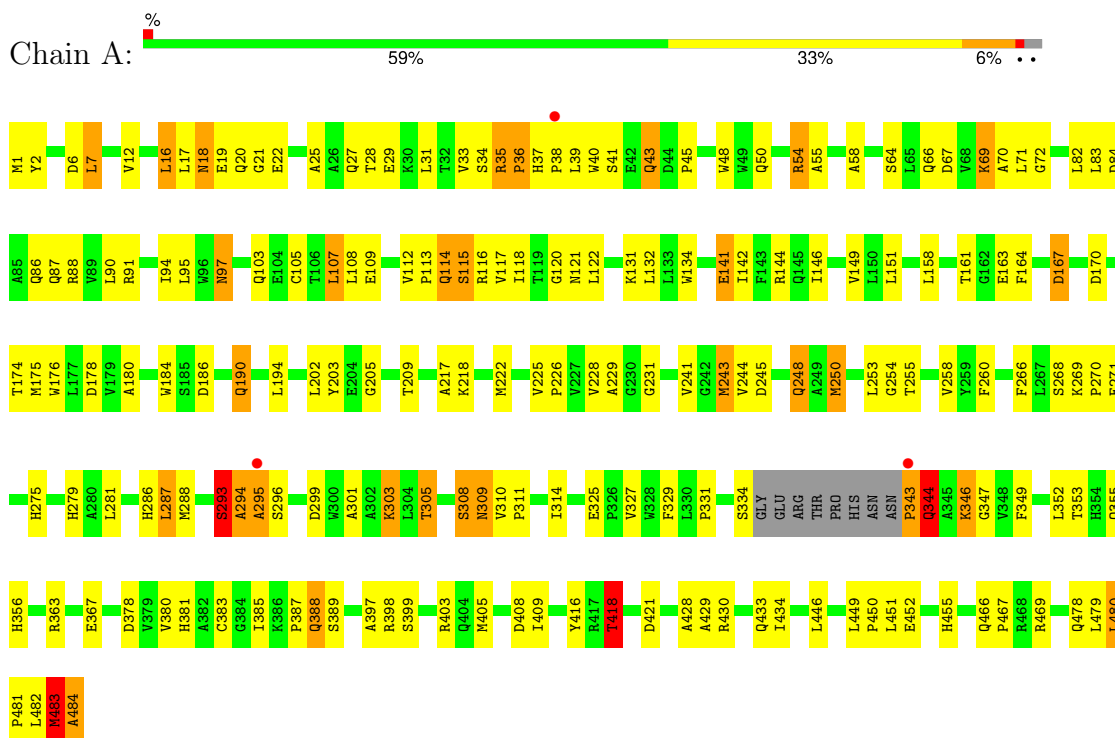
- Molecule 1: Xylulose kinase
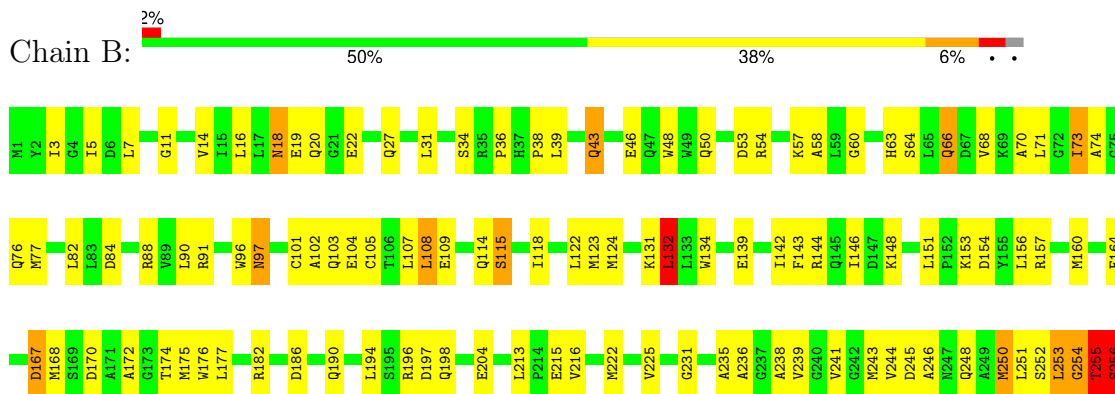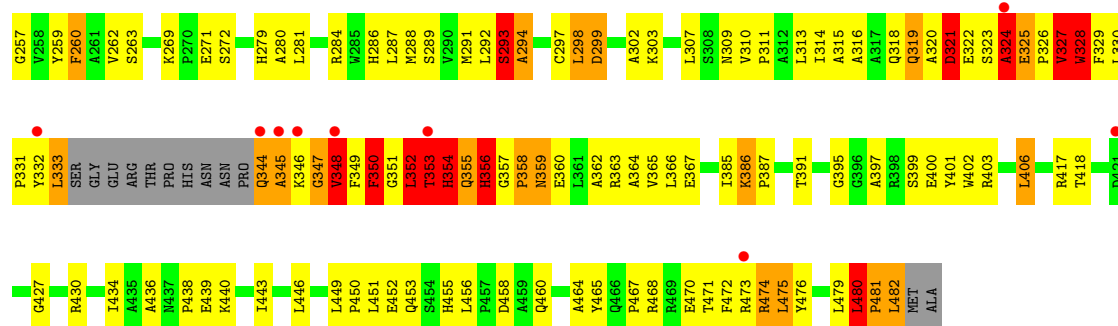
4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	67.78Å 112.02Å 138.80Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	24.88 – 2.70 24.87 – 2.70	Depositor EDS
% Data completeness (in resolution range)	96.8 (24.88-2.70) 96.7 (24.87-2.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$<I/\sigma(I)>$ [1]	5.37 (at 2.72Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.205 , 0.254 0.201 , 0.247	Depositor DCC
R_{free} test set	1182 reflections (4.12%)	wwPDB-VP
Wilson B-factor (Å^2)	37.6	Xtriage
Anisotropy	0.181	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 50.6	EDS
L-test for twinning[2]	$<|L|> = 0.49, <L^2> = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	7394	wwPDB-VP
Average B, all atoms (Å^2)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.11% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.
[2]Theoretical values of $<|L|>$, $<L^2>$ 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	0.74	5/3712 (0.1%)	0.80	9/5046 (0.2%)
1	B	0.69	5/3685 (0.1%)	0.83	15/5010 (0.3%)
All	All	0.71	10/7397 (0.1%)	0.82	24/10056 (0.2%)

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	5
1	B	1	14
All	All	1	19

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	325	GLU	CD-OE1	-8.95	1.15	1.25
1	A	484	ALA	C-O	6.58	1.35	1.23
1	B	109	GLU	CD-OE2	-6.35	1.18	1.25
1	A	109	GLU	CD-OE2	-6.13	1.19	1.25
1	A	105	CYS	CB-SG	-5.34	1.73	1.81

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	295	ALA	CB-CA-C	-17.37	84.04	110.10
1	A	308	SER	CB-CA-C	-12.13	87.04	110.10
1	B	256	SER	CB-CA-C	11.61	132.15	110.10
1	A	294	ALA	CB-CA-C	-11.29	93.17	110.10
1	A	309	ASN	N-CA-CB	9.60	127.89	110.60

All (1) chirality outliers are listed below:

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Mol	Chain	Res	Type	Atom
1	B	353	THR	CA

5 of 19 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	293	SER	Peptide
1	A	343	PRO	Peptide
1	A	344	GLN	Peptide
1	A	35	ARG	Peptide
1	A	418	THR	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	3631	0	3607	198	1
1	B	3605	0	3580	361	0
2	A	82	0	0	11	0
2	B	76	0	0	11	1
All	All	7394	0	7187	542	1

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 38.

The worst 5 of 542 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:344:GLN:HG3	1:B:345:ALA:CA	1.25	1.61
1:B:344:GLN:CG	1:B:345:ALA:HA	1.51	1.40
1:B:344:GLN:CG	1:B:345:ALA:CA	2.01	1.39
1:B:351:GLY:C	1:B:352:LEU:HD22	1.40	1.38
1:B:327:VAL:HG11	1:B:364:ALA:CB	1.55	1.36

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:484:ALA:O	2:B:543:HOH:O[4_445]	1.20	1.00

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	472/484 (98%)	440 (93%)	31 (7%)	1 (0%)	47	73
1	B	468/484 (97%)	413 (88%)	44 (9%)	11 (2%)	6	15
All	All	940/968 (97%)	853 (91%)	75 (8%)	12 (1%)	12	30

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	328	TRP
1	B	350	PHE
1	B	352	LEU
1	B	353	THR
1	B	481	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	375/382 (98%)	341 (91%)	34 (9%)	9	21
1	B	372/382 (97%)	332 (89%)	40 (11%)	6	15
All	All	747/764 (98%)	673 (90%)	74 (10%)	8	18

5 of 74 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	299	ASP
1	B	475	LEU
1	B	321	ASP
1	B	355	GLN
1	A	314	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 30 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	404	GLN
1	B	412	GLN
1	B	43	GLN
1	B	453	GLN
1	B	286	HIS

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 monosaccharides 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 ⓘ

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(Å²)	Q<0.9
1	A	476/484 (98%)	-0.44	3 (0%)	89	91	9, 28, 54, 85	0
1	B	472/484 (97%)	-0.27	9 (1%)	66	69	8, 32, 67, 92	0
All	All	948/968 (97%)	-0.35	12 (1%)	77	78	8, 30, 61, 92	0

The worst 5 of 12 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	345	ALA	5.6
1	B	348	VAL	5.5
1	B	344	GLN	4.8
1	B	353	THR	4.4
1	B	324	ALA	3.1

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

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

6.3 Carbohydrates ⓘ

There are no monosaccharides in this entry.

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.

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