



# wwPDB X-ray Structure Validation Summary Report

Apr 28, 2024 – 06:31 am BST

PDB ID : 2BWB  
Title : Crystal structure of the UBA domain of Dsk2 from *S. cerevisiae*  
Authors : Lowe, E.D.; Hasan, N.; Trempe, J.-F.; Fonso, L.; Noble, M.E.M.; Endicott, J.A.; Johnson, L.N.; Brown, N.R.  
Deposited on : 2005-07-13  
Resolution : 2.30 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

<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 : 4.02b-467  
Xtriage (Phenix) : 1.13  
EDS : 2.36.2  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36.2

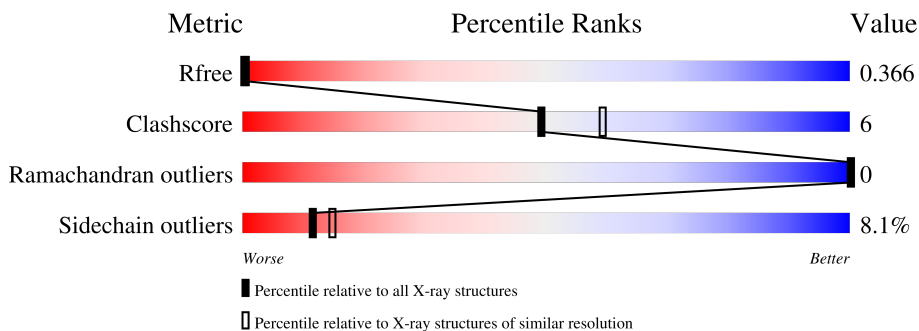
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 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))
$R_{free}$	130704	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)

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  $\geq 3$ , 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  $\leq 5\%$ .

Mol	Chain	Length	Quality of chain
1	A	46	76% (green), 20% (yellow), 4% (orange), 0% (red), 0% (grey)
1	B	46	78% (green), 13% (yellow), 7% (orange), 2% (red), 2% (grey)
1	C	46	98% (green), 2% (yellow), 0% (orange), 0% (red), 0% (grey)
1	D	46	91% (green), 7% (yellow), 2% (orange), 0% (red), 0% (grey)
1	E	46	76% (green), 20% (yellow), 4% (orange), 0% (red), 0% (grey)
1	F	46	83% (green), 9% (yellow), 8% (orange), 0% (red), 0% (grey)
1	G	46	85% (green), 13% (yellow), 2% (orange), 0% (red), 0% (grey)

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Length	Quality of chain
1	H	46	 85% 9% . .
1	I	46	 59% 20% 9% 13%

## 2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 3337 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 UBIQUITIN-LIKE PROTEIN DSK2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	46	Total 366	C 224	N 69	O 72	S 1	0	0	0
1	B	44	Total 354	C 216	N 67	O 70	S 1	0	0	0
1	C	46	Total 366	C 224	N 69	O 72	S 1	0	0	0
1	D	45	Total 358	C 218	N 68	O 71	S 1	0	0	0
1	E	44	Total 354	C 216	N 67	O 70	S 1	0	0	0
1	F	44	Total 354	C 216	N 67	O 70	S 1	0	0	0
1	G	45	Total 358	C 218	N 68	O 71	S 1	0	0	0
1	H	44	Total 354	C 216	N 67	O 70	S 1	0	0	0
1	I	40	Total 323	C 196	N 63	O 64		0	0	0

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	24	Total 24	O 24	0	0
2	B	28	Total 28	O 28	0	0
2	C	18	Total 18	O 18	0	0
2	D	19	Total 19	O 19	0	0
2	E	10	Total 10	O 10	0	0

*Continued on next page...*

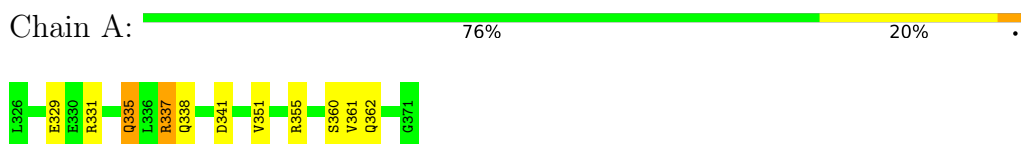
*Continued from previous page...*

<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
2	F	13	Total 13	O 13	0	0
2	G	15	Total 15	O 15	0	0
2	H	15	Total 15	O 15	0	0
2	I	8	Total 8	O 8	0	0

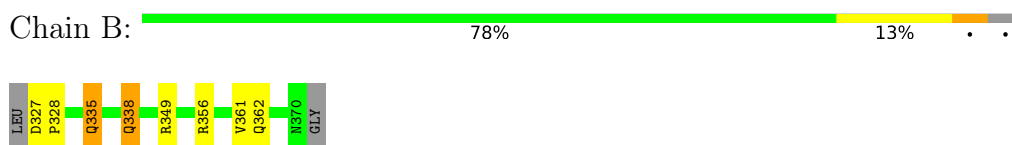
### 3 Residue-property plots [i](#)

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. 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. 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.

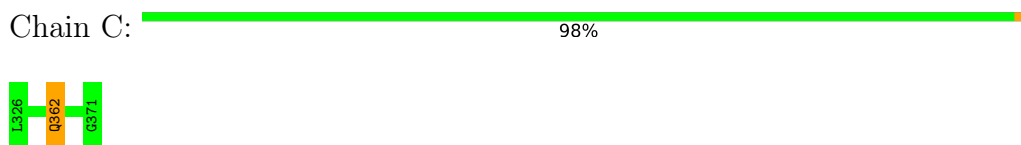
- Molecule 1: UBIQUITIN-LIKE PROTEIN DSK2



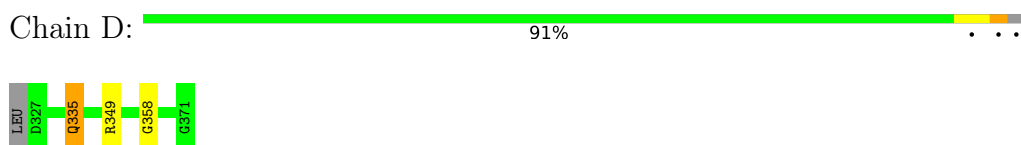
- Molecule 1: UBIQUITIN-LIKE PROTEIN DSK2



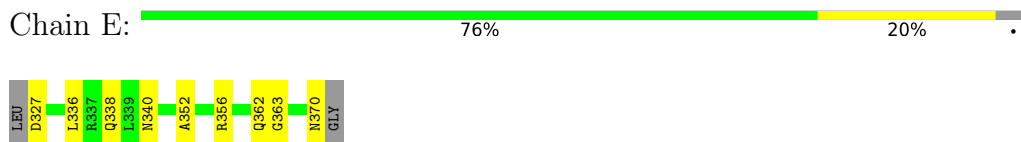
- Molecule 1: UBIQUITIN-LIKE PROTEIN DSK2



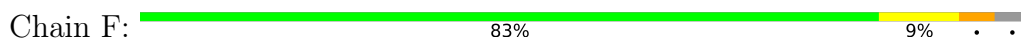
- Molecule 1: UBIQUITIN-LIKE PROTEIN DSK2



- Molecule 1: UBIQUITIN-LIKE PROTEIN DSK2



- Molecule 1: UBIQUITIN-LIKE PROTEIN DSK2





- Molecule 1: UBIQUITIN-LIKE PROTEIN DSK2

Chain G: 85% 13%



- Molecule 1: UBIQUITIN-LIKE PROTEIN DSK2

Chain H: 85% 9%



- Molecule 1: UBIQUITIN-LIKE PROTEIN DSK2

Chain I: 59% 20% 9% 13%



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	116.31Å 44.07Å 111.53Å 90.00° 114.87° 90.00°	Depositor
Resolution (Å)	101.02 – 2.30 29.06 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.8 (101.02-2.30) 99.8 (29.06-2.30)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.28 (at 2.31Å)	Xtrriage
Refinement program	REFMAC 5.2.0005	Depositor
R, $R_{free}$	0.243 , 0.307 0.299 , 0.366	Depositor DCC
$R_{free}$ test set	1127 reflections (4.87%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	48.5	Xtrriage
Anisotropy	0.318	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 49.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	3337	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	77.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.16% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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

### 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	0.48	0/371	0.72	1/497 (0.2%)
1	B	0.51	0/359	0.62	0/481
1	C	0.50	0/371	0.58	0/497
1	D	0.43	0/363	0.65	0/486
1	E	0.99	2/359 (0.6%)	0.68	0/481
1	F	0.45	0/359	0.70	2/481 (0.4%)
1	G	0.43	0/363	0.55	0/486
1	H	0.44	0/359	0.60	0/481
1	I	0.46	0/326	0.67	0/436
All	All	0.55	2/3230 (0.1%)	0.64	3/4326 (0.1%)

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	F	0	1
All	All	0	2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	370	ASN	CG-OD1	13.11	1.52	1.24
1	E	370	ASN	CG-ND2	8.38	1.53	1.32

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	327	ASP	C-N-CD	-7.24	104.68	120.60
1	F	327	ASP	C-N-CA	5.41	144.71	122.00
1	A	337	ARG	NE-CZ-NH1	5.06	122.83	120.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	329	GLU	Peptide
1	F	327	ASP	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	366	0	343	4	0
1	B	354	0	329	4	0
1	C	366	0	343	1	0
1	D	358	0	332	7	0
1	E	354	0	329	3	0
1	F	354	0	329	3	0
1	G	358	0	332	2	0
1	H	354	0	329	3	0
1	I	323	0	303	15	0
2	A	24	0	0	2	0
2	B	28	0	0	1	0
2	C	18	0	0	2	0
2	D	19	0	0	0	0
2	E	10	0	0	0	0
2	F	13	0	0	0	0
2	G	15	0	0	0	0
2	H	15	0	0	0	0
2	I	8	0	0	1	0
All	All	3337	0	2969	36	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 36 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:D:335:GLN:HE21	1:D:335:GLN:H	1.16	0.90

*Continued on next page...*

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:335:GLN:HE21	1:I:335:GLN:H	1.35	0.75
1:A:338:GLN:NE2	2:A:2007:HOH:O	2.16	0.72
1:B:335:GLN:HE21	1:B:335:GLN:H	1.43	0.66
1:F:335:GLN:HE21	1:F:335:GLN:H	1.45	0.62

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	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
1	B	42/46 (91%)	42 (100%)	0	0	100	100
1	C	44/46 (96%)	44 (100%)	0	0	100	100
1	D	43/46 (94%)	42 (98%)	1 (2%)	0	100	100
1	E	42/46 (91%)	42 (100%)	0	0	100	100
1	F	42/46 (91%)	42 (100%)	0	0	100	100
1	G	43/46 (94%)	43 (100%)	0	0	100	100
1	H	42/46 (91%)	42 (100%)	0	0	100	100
1	I	36/46 (78%)	35 (97%)	1 (3%)	0	100	100
All	All	378/414 (91%)	375 (99%)	3 (1%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains [i](#)

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	38/38 (100%)	33 (87%)	5 (13%)	4	4
1	B	37/38 (97%)	33 (89%)	4 (11%)	6	7
1	C	38/38 (100%)	37 (97%)	1 (3%)	46	63
1	D	37/38 (97%)	35 (95%)	2 (5%)	22	30
1	E	37/38 (97%)	34 (92%)	3 (8%)	11	15
1	F	37/38 (97%)	35 (95%)	2 (5%)	22	30
1	G	37/38 (97%)	34 (92%)	3 (8%)	11	15
1	H	37/38 (97%)	35 (95%)	2 (5%)	22	30
1	I	34/38 (90%)	29 (85%)	5 (15%)	3	3
All	All	332/342 (97%)	305 (92%)	27 (8%)	11	15

5 of 27 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	362	GLN
1	G	337	ARG
1	I	361	VAL
1	F	337	ARG
1	G	356	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	350	ASN
1	H	340	ASN
1	I	370	ASN
1	I	338	GLN
1	I	350	ASN

### 5.3.3 RNA

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 monosaccharides 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

### 6.1 Protein, DNA and RNA chains

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.4 Ligands

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.5 Other polymers

Unable to reproduce the depositors R factor - this section is therefore empty.