

# Full wwPDB X-ray Structure Validation Report (i)

#### Mar 10, 2024 – 09:45 AM EDT

PDB ID	:	4IC4
Title	:	Crystal structure of Osh3 ORD from Saccharomyces cerevisiae
Authors	:	Tong, J.; Im, Y.J.
Deposited on	:	2012-12-09
Resolution	:	1.50  Å(reported)

This is a Full wwPDB X-ray Structure Validation 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 (i) 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 (1)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
$\mathrm{EDS}$	:	2.36
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

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:  $X\text{-}RAY \, DIFFRACTION$ 

The reported resolution of this entry is 1.50 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R <sub>free</sub>	130704	2936 (1.50-1.50)
Clashscore	141614	3144 (1.50-1.50)
Ramachandran outliers	138981	3066 (1.50-1.50)
Sidechain outliers	138945	3064 (1.50-1.50)
RSRZ outliers	127900	2884 (1.50-1.50)

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				
			13%				
1	А	397	74%	18%	• 6%		



# 2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 3332 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 Oxysterol-binding protein homolog 3.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	А	372	Total 3041	C 1947	N 521	0 568	S 5	0	0	0

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	600	GLY	-	expression tag	UNP P38713
А	601	ALA	-	expression tag	UNP P38713
А	602	MET	-	expression tag	UNP P38713
А	603	ASP	-	expression tag	UNP P38713
А	604	PRO	-	expression tag	UNP P38713

• Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	291	Total         O           291         291	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 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: Oxysterol-binding protein homolog 3



## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	40.87Å 89.20Å 96.10Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $90.00^{\circ}$	Depositor
Bosolution(A)	32.69 - 1.50	Depositor
Resolution (A)	32.69 - 1.50	EDS
% Data completeness	99.5 (32.69-1.50)	Depositor
(in resolution range)	99.6 (32.69-1.50)	EDS
$R_{merge}$	0.08	Depositor
R <sub>sym</sub>	(Not available)	Depositor
$< I/\sigma(I) > 1$	$4.66 (at 1.50 \text{\AA})$	Xtriage
Refinement program	CNS 1.1	Depositor
P. P.	0.217 , $0.234$	Depositor
$n, n_{free}$	0.218 , $0.216$	DCC
$R_{free}$ test set	2887  reflections  (5.07%)	wwPDB-VP
Wilson B-factor $(Å^2)$	13.4	Xtriage
Anisotropy	0.510	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.39 , $49.4$	EDS
L-test for twinning <sup>2</sup>	$ < L >=0.49, < L^2>=0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	3332	wwPDB-VP
Average B, all atoms $(Å^2)$	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.98% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;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.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

# 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	А	0.30	0/3120	0.60	0/4218

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

#### 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	А	3041	0	3034	58	0
2	А	291	0	0	4	0
All	All	3332	0	3034	58	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 10.

All (58) 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:A:655:LEU:HB3	1:A:769:GLN:OE1	1.83	0.78
1:A:640:PRO:HG3	1:A:716:ARG:CZ	2.17	0.75
1:A:686:LYS:HB2	1:A:686:LYS:HZ2	1.54	0.73
1:A:650:ASN:ND2	1:A:658:ILE:HD12	2.04	0.71

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	iouo puge	Interatomic	Clash
Atom-1	Atom-2	distance $(Å)$	overlap (Å)
1:A:650:ASN:HD22	1:A:658:ILE:HD12	1.56	0.68
1:A:860:LYS:HA	1:A:860:LYS:HZ3	1.61	0.65
1:A:833:LEU:HD23	1:A:833:LEU:H	1.62	0.64
1:A:914:ASN:HD22	1:A:987:HIS:HE1	1.46	0.62
1:A:742:LYS:NZ	1:A:745:HIS:HD2	1.98	0.61
1:A:877:THR:O	1:A:878:HIS:HB2	1.99	0.61
1:A:672:GLN:HE22	1:A:905:ASN:HD22	1.46	0.61
1:A:640:PRO:HG3	1:A:716:ARG:NH2	2.17	0.59
1:A:952:ARG:HG3	1:A:957:ASP:OD2	2.02	0.59
1:A:686:LYS:HB2	1:A:686:LYS:NZ	2.18	0.58
1:A:833:LEU:HD23	1:A:848:LYS:O	2.05	0.57
1:A:837:ALA:HA	2:A:1163:HOH:O	2.04	0.57
1:A:860:LYS:HA	1:A:860:LYS:NZ	2.21	0.56
1:A:777:GLU:HA	1:A:803:ILE:HD13	1.88	0.56
1:A:946:GLN:HE22	1:A:950:GLU:CG	2.20	0.55
1:A:655:LEU:HD23	1:A:656:SER:N	2.22	0.54
1:A:858:ASN:HD22	1:A:859:ARG:N	2.05	0.54
1:A:969:ASN:HA	2:A:1145:HOH:O	2.07	0.54
1:A:849:VAL:HB	1:A:864:LEU:HB2	1.90	0.53
1:A:702:ILE:HD11	1:A:832:ILE:HG12	1.91	0.53
1:A:833:LEU:HD23	1:A:833:LEU:N	2.24	0.53
1:A:914:ASN:ND2	1:A:987:HIS:HE1	2.09	0.51
1:A:627:VAL:HG11	1:A:910:ILE:HG13	1.92	0.51
1:A:723:LEU:O	1:A:724:ALA:HB3	2.11	0.51
1:A:673:LEU:HD22	1:A:718:PRO:HG2	1.92	0.50
1:A:946:GLN:NE2	1:A:950:GLU:HG2	2.27	0.50
1:A:778:LEU:HD12	1:A:778:LEU:N	2.26	0.49
1:A:776:ILE:HG13	1:A:807:LEU:HD11	1.94	0.49
1:A:946:GLN:HE22	1:A:950:GLU:HG2	1.78	0.49
1:A:832:ILE:HD12	1:A:832:ILE:N	2.27	0.48
1:A:672:GLN:HE22	1:A:905:ASN:ND2	2.12	0.47
1:A:914:ASN:HD22	1:A:987:HIS:CE1	2.31	0.47
1:A:666:GLU:OE2	1:A:718:PRO:HG3	2.15	0.47
1:A:887:LEU:HA	1:A:898:THR:HA	1.96	0.47
1:A:905:ASN:HD21	1:A:921:ARG:HA	1.80	0.46
1:A:858:ASN:HD22	1:A:858:ASN:N	2.12	0.46
1:A:742:LYS:HZ3	1:A:745:HIS:HD2	1.62	0.46
1:A:665:ASN:HA	1:A:717:LYS:O	2.15	0.46
1:A:845:GLU:O	1:A:867:LYS:HA	2.15	0.45
1:A:855:PRO:O	1:A:856:SER:HB2	2.15	0.45
1:A:985:LYS:HE3	1:A:985:LYS:HB2	1.81	0.45

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Atom 1	Atom 2	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:738:LEU:C	1:A:738:LEU:HD23	2.37	0.45
1:A:954:LYS:HG3	2:A:1263:HOH:O	2.16	0.44
1:A:905:ASN:ND2	1:A:921:ARG:HA	2.32	0.44
1:A:840:PHE:C	1:A:842:GLY:H	2.21	0.43
1:A:674:ILE:HB	1:A:752:PHE:CZ	2.53	0.43
1:A:681:ALA:N	1:A:682:PRO:CD	2.82	0.43
1:A:826:LYS:HE2	2:A:1096:HOH:O	2.19	0.43
1:A:742:LYS:HE2	1:A:745:HIS:HA	2.01	0.42
1:A:927:ARG:O	1:A:931:GLU:HG3	2.20	0.41
1:A:653:LYS:NZ	1:A:653:LYS:CB	2.83	0.41
1:A:647:LEU:HD11	1:A:776:ILE:HD11	2.03	0.41
1:A:655:LEU:HD21	1:A:717:LYS:HD2	2.02	0.41
1:A:853:PRO:HD2	1:A:861:LYS:HG2	2.03	0.41

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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	А	370/397~(93%)	354 (96%)	12 (3%)	4 (1%)	14 2

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	655	LEU
1	А	839	MET
1	А	841	SER
1	А	651	VAL



#### 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 side chain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	А	337/358~(94%)	327~(97%)	10 (3%)	41 12

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	654	ASP
1	А	780	ASN
1	А	858	ASN
1	А	860	LYS
1	А	870	GLN
1	А	878	HIS
1	А	935	ASP
1	А	945	GLU
1	А	949	ARG
1	А	957	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	650	ASN
1	А	745	HIS
1	А	780	ASN
1	А	799	GLN
1	А	806	ASN
1	А	818	ASN
1	А	858	ASN
1	А	905	ASN
1	А	914	ASN
1	А	933	ASN
1	А	946	GLN
1	А	994	GLN



#### 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 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 (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,  $95^{th}$  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	А	372/397~(93%)	1.00	52 (13%) 2 2	6, 15, 43, 60	0

All (52) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	840	PHE	19.8
1	А	655	LEU	18.0
1	А	771	PHE	16.8
1	А	838	GLY	16.0
1	А	772	TRP	10.8
1	А	837	ALA	8.4
1	А	841	SER	7.5
1	А	658	ILE	7.2
1	А	839	MET	7.1
1	А	856	SER	7.1
1	А	654	ASP	6.8
1	А	625	LYS	6.5
1	А	855	PRO	6.5
1	А	774	LYS	6.4
1	А	651	VAL	5.8
1	А	653	LYS	5.6
1	А	858	ASN	5.1
1	А	626	SER	4.9
1	А	808	ILE	4.9
1	А	656	SER	4.6
1	А	773	GLY	4.6
1	А	833	LEU	4.5
1	A	637	ALA	4.4
1	А	860	LYS	4.3
1	А	650	ASN	3.6
1	А	770	LYS	3.5
1	А	966	VAL	3.5

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Mol	Chain	Res	Type	RSRZ
1	А	935	ASP	3.4
1	А	775	SER	3.4
1	А	732	GLU	3.2
1	А	809	ALA	3.2
1	А	659	ALA	2.9
1	А	769	GLN	2.9
1	А	969	ASN	2.9
1	А	810	GLY	2.8
1	А	660	MET	2.8
1	А	647	LEU	2.7
1	А	870	GLN	2.7
1	А	652	GLY	2.6
1	А	657	SER	2.6
1	А	857	SER	2.6
1	А	648	ARG	2.4
1	А	811	GLU	2.2
1	А	936	LYS	2.1
1	А	933	ASN	2.1
1	А	968	LYS	2.1
1	А	702	ILE	2.1
1	А	949	ARG	2.1
1	А	778	LEU	2.1
1	А	812	ARG	2.0
1	А	854	PRO	2.0
1	А	690	ARG	2.0

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#### 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 monosaccharides 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.

